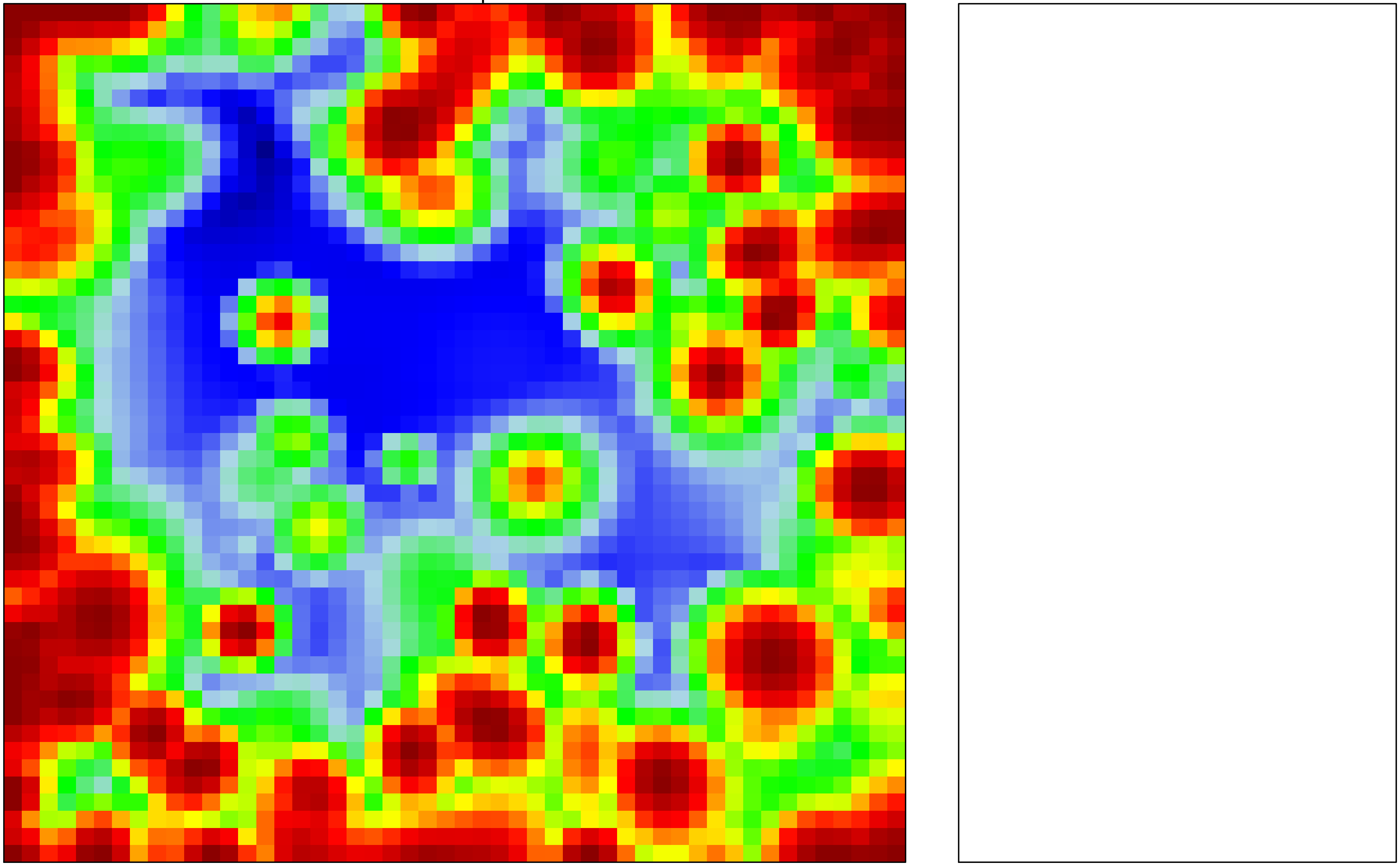
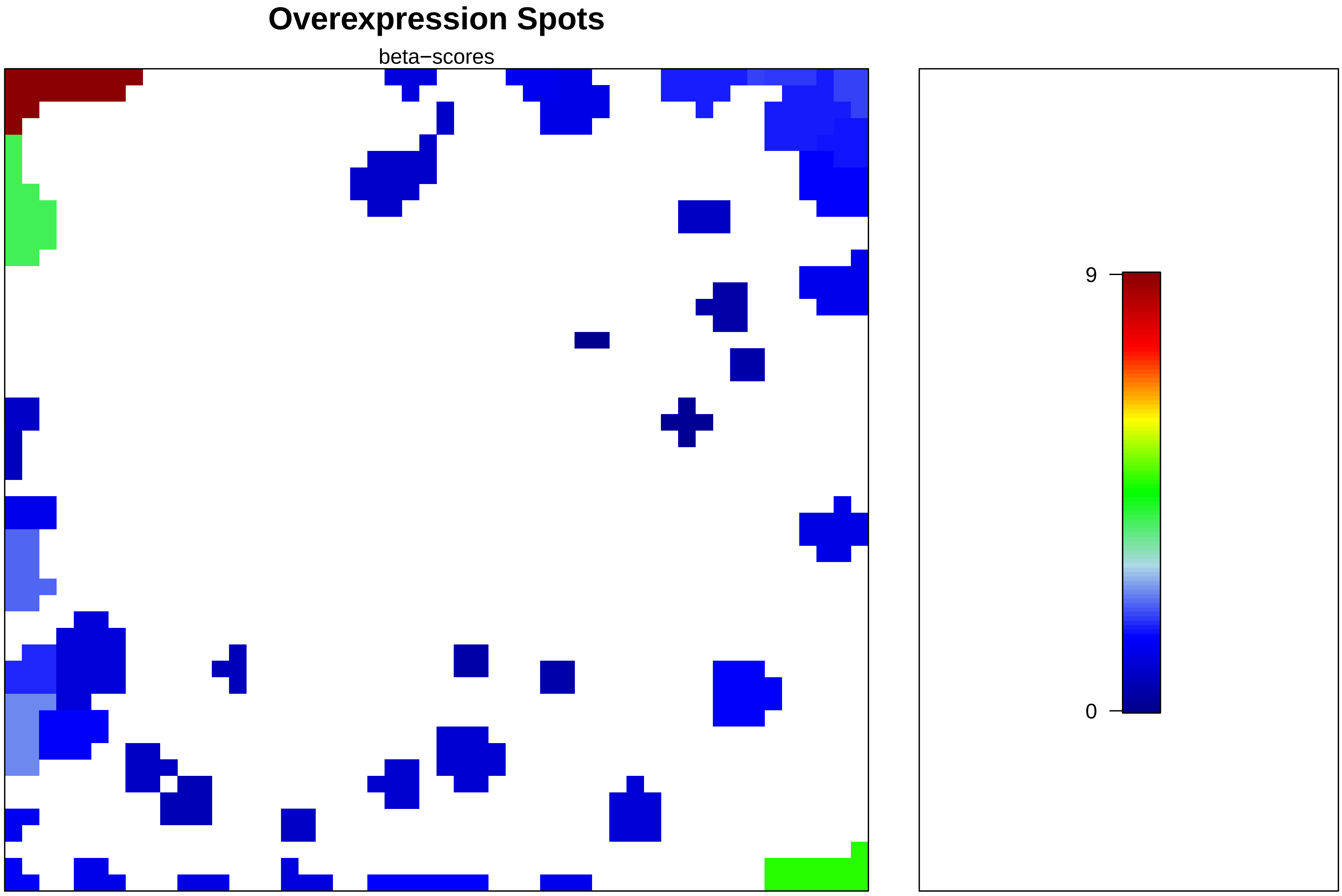
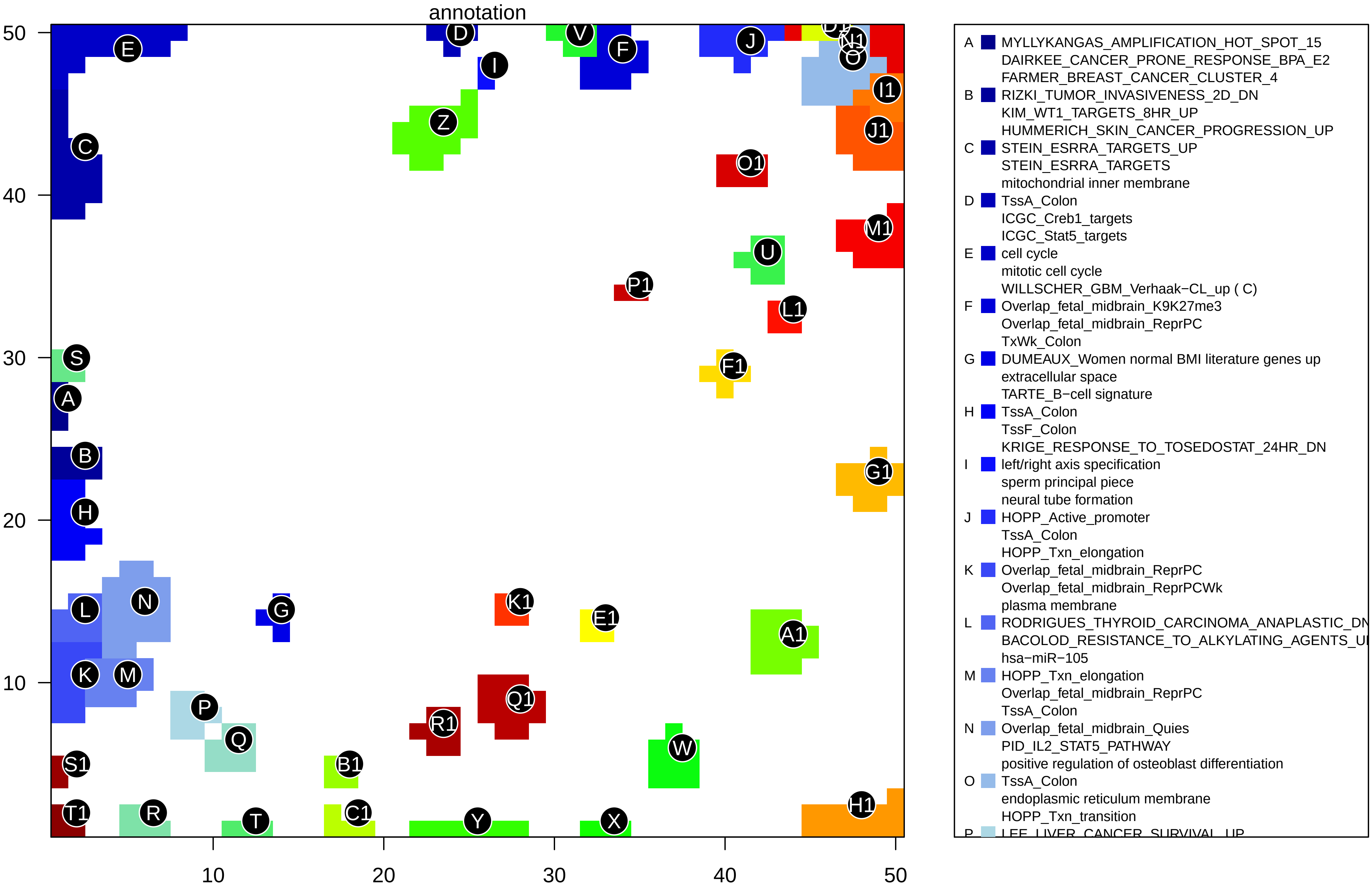
Overexpression Spots

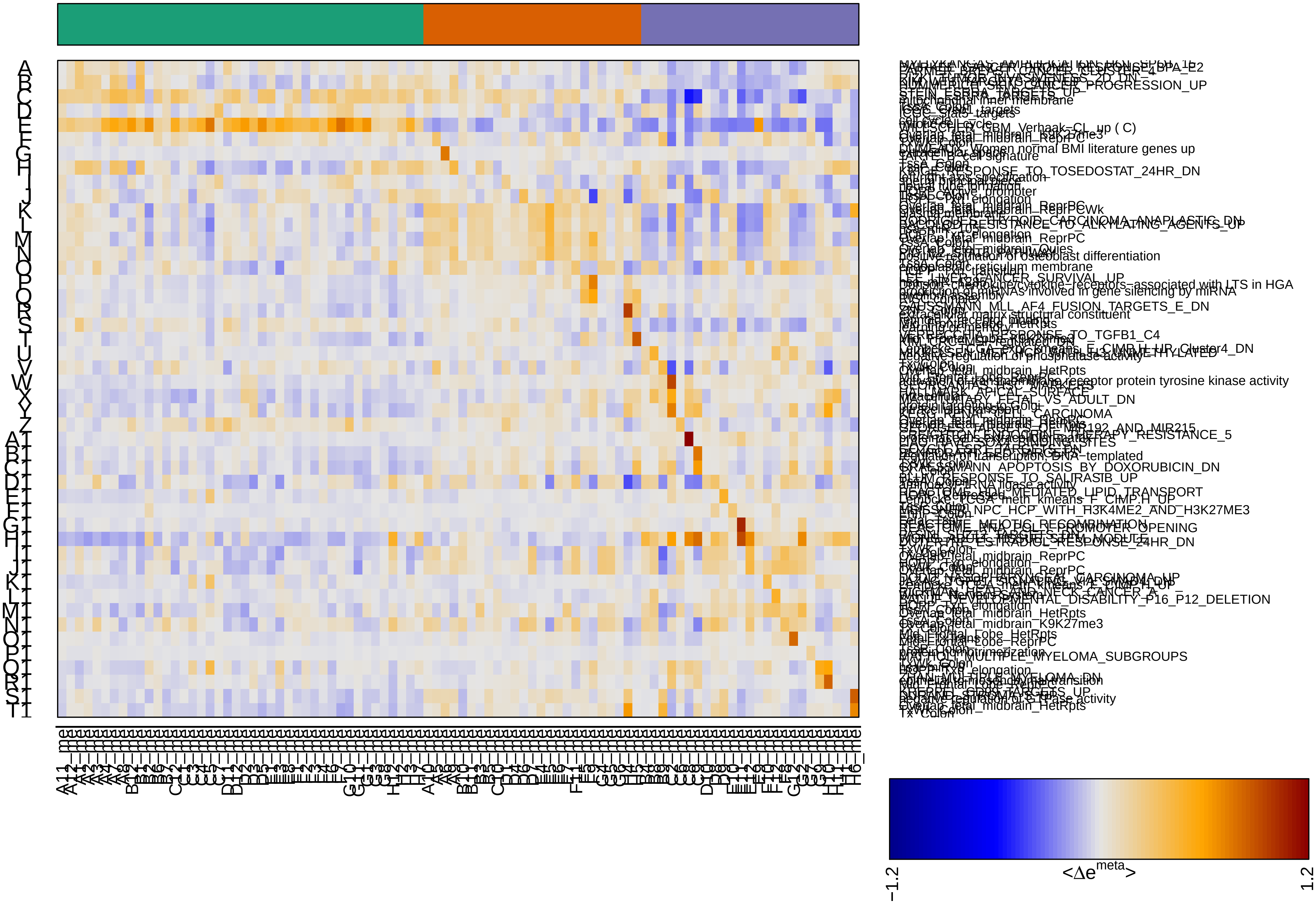
landscape

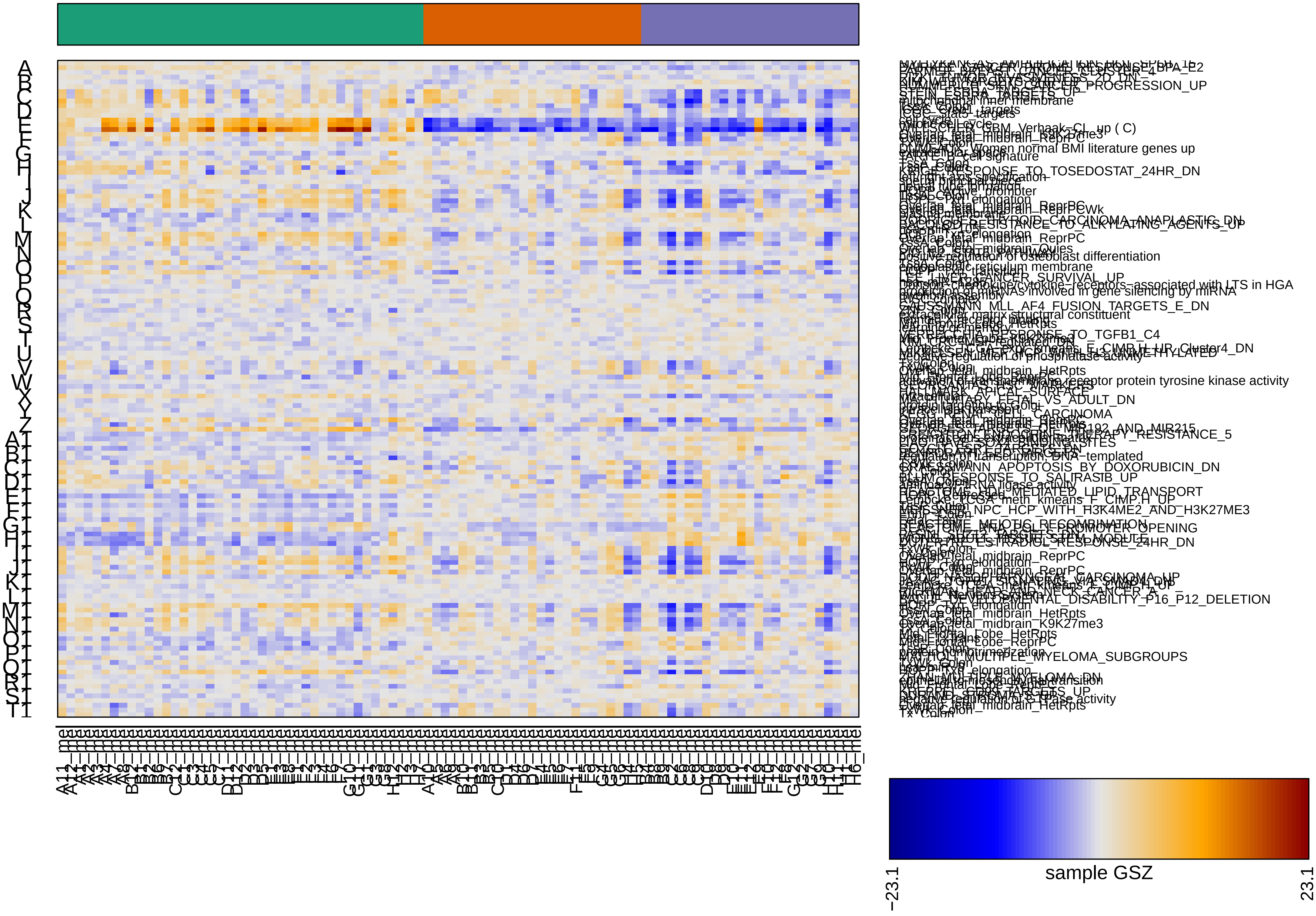



Overexpression Spots
beta−scores
9
0

Overexpression Spots




STEIN_ESRRA_TARGETS_UP
mitochondrial inner membrane
REACTOME_MEIOTIC_RECOMBINATION
VERRECCHIA_RESPONSE_TO_TGFB1_C4
negative regulation of phosphatase activity
HALLMARK_APICAL_SURFACE
regulation of transcription, DNA−templated
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT
MATTHOLI_MULTIPLE_MYELOMA_SUBGROUPS
positive regulation of osteoblast differentiation
endoplasmic reticulum membrane
extracellular matrix structural constituent
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Mid−Frontal_Lobe_ReprPC
Mid−Frontal_Lobe_HetRpts
Tx_Colon
TxWk_Colon
TSSA_Colon
negative regulation of GTPase activity
<Δe^meta>
−1.2
1.2


sample GSZ
−23.1
23.1

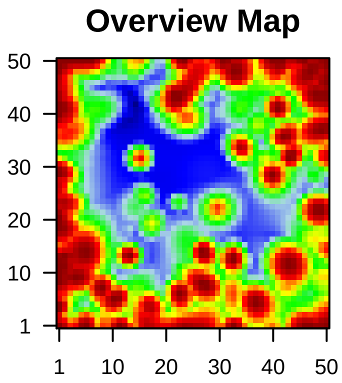
Overexpression Spots

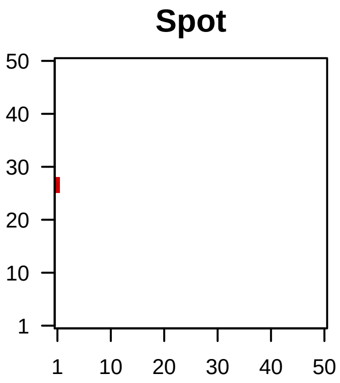
Spot Summary: A

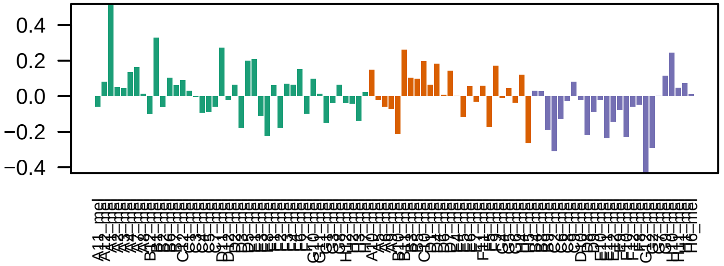
metagenes = 3
genes = 50

<r> metagenes = 0.96
<r> genes = 0.1
beta: r2= 0.68 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 5 (11.9 %)
MSC2 : 3 (12 %)
MSC3 : 1 (4 %)





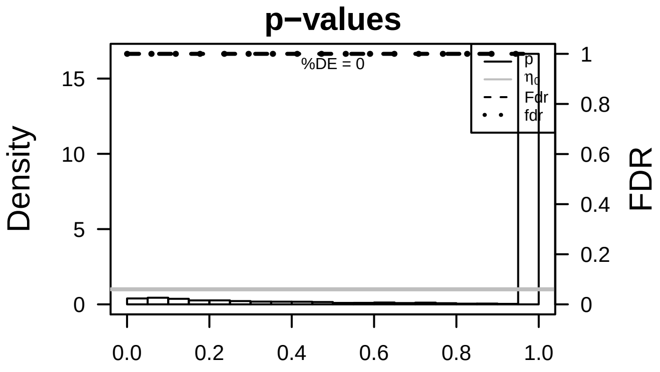


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	SIPA1L3	2.07	−0.3	0.26	SIPA1L3	signal−induced proliferation−associated 1 like 3 [Source:HGN
2	PPP1R13L	1.82	−0.03	0.32	PPP1R13L	protein phosphatase 1, regulatory subunit 13 like [Source:HG
3	CHN1	1.77	−0.26	0.26	CHN1	chimerin 1 [Source:HGNC Symbol;Acc:HGNC:1943]
4	ITGB1BP2	1.65	−0.06	0.3	ITGB1BP2	integrin beta 1 binding protein (melusin) 2 [Source:HGNC Sy
5	TFEB	1.64	−0.14	0.42	TFEB	transcription factor EB [Source:HGNC Symbol;Acc:HGNC:11
6	AP4S1	1.49	−0.27	0.31	AP4S1	adaptor−related protein complex 4, sigma 1 subunit [Source:
7	PCTP	1.48	−0.14	0.27	PCTP	phosphatidylcholine transfer protein [Source:HGNC Symbol;
8	TMEM218	1.47	−0.53	0.27	TMEM218	transmembrane protein 218 [Source:HGNC Symbol;Acc:HGN
9	LRBA	1.46	−0.36	0.31	LRBA	LPS−responsive vesicle trafficking, beach and anchor contai
10	KLHL5	1.46	−0.53	0.35	KLHL5	kelch−like family member 5 [Source:HGNC Symbol;Acc:HGN
11	GPR116	1.46	−0.08	0.31		
12	RIC1	1.45	−0.35	0.21	RIC1	RAB6A GEF complex partner 1 [Source:HGNC Symbol;Acc:
13	PPP1R21	1.43	−0.24	0.23	PPP1R21	protein phosphatase 1, regulatory subunit 21 [Source:HGNC
14	CASKIN2	1.4	−0.36	0.3	CASKIN2	CASK interacting protein 2 [Source:HGNC Symbol;Acc:HGN
15	POLM	1.37	−0.15	0.31	POLM	polymerase (DNA directed), mu [Source:HGNC Symbol;Acc:
16	SLC18A2	1.34	−0.25	0.2	SLC18A2	solute carrier family 18 (vesicular monoamine transporter), m
17	MPP6	1.34	−0.83	0.31	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily m
18	RASGEF1A	1.3	−0.25	0.38	RASGEF1A	RasGEF domain family, member 1A [Source:HGNC Symbol;
19	TBC1D1	1.29	−0.87	0.32	TBC1D1	TBC1 (tre−2/USP6, BUB2, cdc16) domain family, member 1 [
20	ECM2	1.25	−0.11	0.31	ECM2	extracellular matrix protein 2, female organ and adipocyte spe

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−06	3 / 10	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15
2	4e−04	4 / 102	GSEA	DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
3	9e−04	2 / 14	GSEA	FARMER_BREAST_CANCER_CLUSTER_4
4	1e−03	41 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	2e−03	6 / 382	BP	positive regulation of GTPase activity
6	2e−03	11 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	2e−03	2 / 21	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
8	2e−03	3 / 78	GSEA	ROVERSI_GLIOMA_COPY_NUMBER_UP
9	2e−03	5 / 287	GSEA	GRESHOCK_CANCER_COPY_NUMBER_UP
10	3e−03	3 / 83	MF	translation factor activity, RNA binding
11	3e−03	2 / 23	BP	sulfur amino acid metabolic process
12	3e−03	33 / 6929	Lymph	HOPP_Txn_elongation
13	3e−03	38 / 8580	Colon	TxWk_Colon
14	4e−03	4 / 193	GSEA	KYNG_DNA_DAMAGE_UP
15	4e−03	39 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
16	4e−03	3 / 100	GSEA	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
17	4e−03	2 / 30	BP	phospholipid transport
18	5e−03	2 / 31	GSEA	YAGI_AML_RELAPSE_PROGNOSIS
19	5e−03	4 / 209	GSEA	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
20	5e−03	2 / 32	BP	RNA phosphodiester bond hydrolysis, endonucleolytic
21	5e−03	29 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
22	5e−03	40 / 9482	Colon	TssA_Colon
23	5e−03	8 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
24	6e−03	4 / 217	MF	GTPase activator activity
25	7e−03	3 / 116	GSEA	YAGI_AML_WITH_T_9_11_TRANSLOCATION
26	7e−03	7 / 682	GSEA	KRIEG_HYPOXIA_NOT_VIA_KDM3A
27	7e−03	6 / 517	GSEA	FEVR_CTNNB1_TARGETS_DN
28	8e−03	2 / 42	GSEA	REACTOME_MRNA_SPLICING_MINOR_PATHWAY
29	9e−03	2 / 43	GSEA	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY
30	9e−03	2 / 43	GSEA	ZHAN_MULTIPLE_MYELOMA_CD2_DN
31	9e−03	5 / 393	BP	mRNA processing
32	1e−02	2 / 45	GSEA	MORI_IMMATURE_B_LYMPHOCYTE_UP
33	1e−02	5 / 398	GSEA	MOOTHA_PGC
34	1e−02	38 / 9027	Colon	Tx_Colon
35	1e−02	8 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
36	1e−02	2 / 47	Cance	PanCan_DNARepair_geneset_nanostring
37	1e−02	2 / 48	GSEA	YANG_BREAST_CANCER_ESR1_LASER_DN
38	1e−02	5 / 412	GSEA	GARY_CD5_TARGETS_DN
39	1e−02	4 / 270	GSEA	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
40	1e−02	3 / 146	GSEA	BROWNE_HCMV_INFECTION_14HR_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.04	2 / 100	HORVATH_aging_genes meth DOWN
2	1.00	0 / 111	HORVATH_aging_genes meth UP
3	1.00	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	6 / 382	positive regulation of GTPase activity
2	0.003	2 / 23	sulfur amino acid metabolic process
3	0.004	2 / 30	phospholipid transport
4	0.005	2 / 32	RNA phosphodiester bond hydrolysis, endonucleolytic
5	0.009	5 / 393	mRNA processing
6	0.013	2 / 52	nuclear−transcribed mRNA catabolic process, deadenylation−dependent deca
7	0.013	4 / 276	nucleobase−containing compound catabolic process
8	0.013	4 / 277	translation
9	0.017	4 / 298	DNA repair
10	0.018	2 / 63	locomotory behavior
11	0.021	3 / 177	mRNA splicing, via spliceosome
12	0.024	2 / 73	post−embryonic development
13	0.031	2 / 83	mitochondrial translational elongation
14	0.033	1 / 10	DNA unwinding involved in DNA replication
15	0.033	1 / 10	folic acid metabolic process
16	0.036	1 / 11	embryonic camera−type eye development
17	0.039	1 / 12	mitochondrial genome maintenance
18	0.039	1 / 12	somatic hypermutation of immunoglobulin genes
19	0.040	6 / 768	DNA metabolic process
20	0.040	3 / 229	RNA splicing

Brain

Rank	p−value	#in/all	Geneset
1	0.001	41 / 9330	Overlap_fetal_midbrain_ReprPC
2	0.004	39 / 9013	Overlap_fetal_midbrain_K9K27me3
3	0.005	29 / 5940	Overlap_fetal_midbrain_HetRpts
4	0.017	17 / 3081	Mid_Frontal_Lobe_ZNF
5	0.032	38 / 9528	Overlap_fetal_midbrain_Quies
6	0.108	5 / 769	Overlap_fetal_midbrain_ZNF
7	0.146	7 / 1333	Fetal_ReprPCWk
8	0.258	3 / 534	Mid_Frontal_Lobe_EnhG
9	0.260	4 / 786	Fetal_EnhG
10	0.311	8 / 1949	Fetal_TssF
11	0.321	2 / 349	Fetal_ZNF
12	0.409	1 / 158	Overlap_fetal_midbrain_Het
13	0.414	4 / 989	Mid_Frontal_Lobe_Quies
14	0.420	31 / 9020	Overlap_fetal_midbrain_ReprPCWk
15	0.435	8 / 2185	Fetal_TssA
16	0.460	4 / 1050	Fetal_EnhP
17	0.466	3 / 765	Mid_Frontal_Lobe_Het
18	0.471	4 / 1065	Overlap_fetal_midbrain_Enh
19	0.522	3 / 831	Fetal_HetRpts
20	0.548	3 / 862	Overlap_fetal_midbrain_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	2 / 47	PanCan_DNARepair_geneset_nanostring
2	0.05	1 / 16	GENTLES_modul2
3	0.05	1 / 16	GENTLES_modul14
4	0.05	1 / 16	GENTLES_modul16
5	0.06	1 / 20	PanCan_ChromMod_geneset_nanostring
6	0.08	3 / 298	SPANG_BCL6−index2
7	0.09	0 / 14	LIU_LIVER_CANCER
8	0.14	0 / 14	LIU_PROSTATE_CANCER_DN
9	0.15	1 / 48	KUIPER_MM poor survival
10	0.24	0 / 12	LIU_PROSTATE_CANCER_UP
11	0.38	2 / 401	Lembcke_Colonic Inflammation
12	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
13	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	1.00	0 / 12	LIU_BREAST_CANCER
17	1.00	0 / 14	LIU_COMMON_CANCER_GENES
18	1.00	0 / 15	WANG_ER_UP
19	1.00	0 / 5	WANG_ER_DN
20	1.00	0 / 16	WOLFER_overlap genes

CC

Rank	p−value	#in/all	Geneset
1	0.03	1 / 10	sperm flagellum
2	0.04	1 / 11	interstitial matrix
3	0.04	1 / 13	DNA−directed RNA polymerase I complex
4	0.04	1 / 13	Fanconi anaemia nuclear complex
5	0.05	1 / 15	centriolar satellite
6	0.05	1 / 16	DNA−directed RNA polymerase II, core complex
7	0.05	1 / 16	vacuolar membrane
8	0.06	1 / 18	DNA−directed RNA polymerase III complex
9	0.06	33 / 8205	cytoplasm
10	0.07	2 / 128	ribosome
11	0.07	1 / 22	mitochondrial large ribosomal subunit
12	0.07	40 / 10605	intracellular
13	0.08	1 / 24	mitochondrial ribosome
14	0.08	1 / 24	U12−type spliceosomal complex
15	0.08	47 / 13191	cellular_component
16	0.10	5 / 747	nucleolus
17	0.11	2 / 169	transcription factor complex
18	0.13	1 / 41	mitochondrial nucleoid
19	0.13	1 / 42	intercellular bridge
20	0.14	1 / 45	transcriptional repressor complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	7 / 840	Chr 17
2	0.04	5 / 558	Chr 4
3	0.14	5 / 838	Chr 3
4	0.30	3 / 576	Chr 9
5	0.40	3 / 687	Chr 6
6	0.40	3 / 689	Chr 7
7	0.50	3 / 801	Chr 11
8	0.52	1 / 221	Chr 18
9	0.55	2 / 551	Chr X
10	0.55	2 / 552	Chr 10
11	0.58	1 / 262	Chr 13
12	0.67	1 / 335	Chr 22
13	0.67	3 / 1037	Chr 19
14	0.79	1 / 462	Chr 14
15	0.79	1 / 465	Chr 15
16	0.79	1 / 469	Chr 8
17	0.85	2 / 993	Chr 2
18	0.88	3 / 1500	Chr 1
19	0.91	1 / 696	Chr 5
20	1.00	0 / 775	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.003	38 / 8580	TxWk_Colon
2	0.005	40 / 9482	TssA_Colon
3	0.010	38 / 9027	Tx_Colon
4	0.013	32 / 7203	TssF_Colon
5	0.023	2 / 71	Marisa_CRC−cluster−g
6	0.024	35 / 8415	Quies3_Colon
7	0.079	37 / 9653	Enh_Colon
8	0.090	22 / 5155	EnhWk1_Colon
9	0.116	24 / 5880	TssD2_Colon
10	0.135	38 / 10290	TssWk_Colon
11	0.166	3 / 427	Quies2_Colon
12	0.167	12 / 2698	EnhA_Colon
13	0.200	12 / 2798	TxEnhG1_Colon
14	0.215	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
15	0.256	5 / 1038	HetRpts_Colon
16	0.306	6 / 1386	Het_Colon
17	0.322	1 / 117	Marisa_CRC−cluster−b
18	0.353	1 / 131	Marisa_CRC−cluster−a
19	0.422	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	0.424	2 / 436	K9acLow_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.6	1 / 294	GUDJ_psoriasis down
2	1.0	0 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.04	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
2	0.09	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
3	0.12	1 / 39	OPC
4	0.19	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
5	0.20	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	0.21	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP
7	0.21	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	0.22	1 / 75	Weller_LGG_A_vs_O_DOWN
9	0.27	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
10	0.30	4 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
11	0.41	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	0.71	1 / 365	Down_b
13	1.00	0 / 15	VERHAAK_CL subtype
14	1.00	0 / 15	VERHAAK_MES subtype
15	1.00	0 / 16	VERHAAK_NL subtype
16	1.00	0 / 14	VERHAAK_PN subtype
17	1.00	0 / 23	WIRTH_PN subtype
18	1.00	0 / 74	WIRTH_Normal Brain
19	1.00	0 / 9	VERHAAK_Brain
20	1.00	0 / 8	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−06	3 / 10	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15
2	4e−04	4 / 102	DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
3	9e−04	2 / 14	FARMER_BREAST_CANCER_CLUSTER_4
4	2e−03	11 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	2e−03	2 / 21	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
6	2e−03	3 / 78	ROVERSI_GLIOMA_COPY_NUMBER_UP
7	2e−03	5 / 287	GRESHOCK_CANCER_COPY_NUMBER_UP
8	4e−03	4 / 193	KYNG_DNA_DAMAGE_UP
9	4e−03	3 / 100	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
10	5e−03	2 / 31	YAGI_AML_RELAPSE_PROGNOSIS
11	5e−03	4 / 209	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
12	5e−03	8 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
13	7e−03	3 / 116	YAGI_AML_WITH_T_9_11_TRANSLOCATION
14	7e−03	7 / 682	KRIEG_HYPOXIA_NOT_VIA_KDM3A
15	7e−03	6 / 517	FEVR_CTNNB1_TARGETS_DN
16	8e−03	2 / 42	REACTOME_MRNA_SPLICING_MINOR_PATHWAY
17	9e−03	2 / 43	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY
18	9e−03	2 / 43	ZHAN_MULTIPLE_MYELOMA_CD2_DN
19	1e−02	2 / 45	MORI_IMMATURE_B_LYMPHOCYTE_UP
20	1e−02	5 / 398	MOOTHA_PGC

HM

Rank	p−value	#in/all	Geneset
1	0.02	3 / 188	HALLMARK_MYC_TARGETS_V1
2	0.14	2 / 197	HALLMARK_E2F_TARGETS
3	0.14	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	0.30	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	0.34	1 / 127	HALLMARK_KRAS_SIGNALING_DN
6	0.37	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
7	0.38	1 / 146	HALLMARK_DNA_REPAIR
8	0.38	1 / 146	HALLMARK_UV_RESPONSE_UP
9	0.39	1 / 148	HALLMARK_KRAS_SIGNALING_UP
10	0.43	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
11	0.47	1 / 188	HALLMARK_ADIPOGENESIS
12	0.48	1 / 196	HALLMARK_G2M_CHECKPOINT
13	0.48	1 / 196	HALLMARK_MTORC1_SIGNALING
14	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	1.00	0 / 176	HALLMARK_HYPOXIA
16	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	1.00	0 / 195	HALLMARK_MITOTIC_SPINDLE
18	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
19	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
20	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	33 / 6929	HOPP_Txn_elongation
2	0.047	28 / 6564	HOPP_Strong_enhancer
3	0.048	25 / 5693	HOPP_Weak_enhancer
4	0.052	1 / 16	ROSOLOWSKI_red UP
5	0.055	23 / 5184	HOPP_Txn_transition
6	0.061	1 / 19	DAVE_c−myc BL UP
7	0.089	29 / 7209	HOPP_Weak_promoter
8	0.101	30 / 7592	HOPP_Active_promoter
9	0.107	23 / 5538	HOPP_Weak_txn
10	0.130	1 / 42	CARO_OxPhos_in_DLBCL_UP
11	0.233	1 / 80	Aukema_BCL2 DN_BCL6 UP
12	0.248	1 / 86	ROSOLOWSKI_red total
13	0.315	5 / 1128	SPANG_BCR DN
14	0.348	1 / 129	DAVE_BL−vs−DLBCL
15	0.375	5 / 1218	SPANG_BCR UP
16	0.477	9 / 2563	HOPP_Heterochrom
17	0.506	1 / 212	LENZ_Stromal signature 1
18	0.591	1 / 268	SPANG_IL21 UP
19	0.601	1 / 275	TARTE_Mature plasma cell signature
20	0.607	1 / 280	SPANG_CD40 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 83	translation factor activity, RNA binding
2	0.006	4 / 217	GTPase activator activity
3	0.012	10 / 1365	RNA binding
4	0.013	2 / 52	double−stranded RNA binding
5	0.017	3 / 164	nuclease activity
6	0.021	48 / 13179	molecular_function
7	0.033	1 / 10	DNA−(apurinic or apyrimidinic site) lyase activity
8	0.033	1 / 10	FAD binding
9	0.033	2 / 86	integrin binding
10	0.036	1 / 11	RNA helicase activity
11	0.039	1 / 12	NADPH binding
12	0.039	1 / 12	Ras guanyl−nucleotide exchange factor activity
13	0.039	1 / 12	RNA polymerase I activity
14	0.042	1 / 13	FMN binding
15	0.042	1 / 13	Ral GTPase binding
16	0.045	2 / 102	mRNA binding
17	0.046	7 / 1007	poly(A) RNA binding
18	0.048	1 / 15	retinoid X receptor binding
19	0.058	1 / 18	RNA polymerase III activity
20	0.062	2 / 123	nucleotidyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	2 / 90	hsa−miR−216b
2	0.05	2 / 104	hsa−miR−605
3	0.05	1 / 16	hsa−miR−220a
4	0.06	1 / 18	hsa−miR−564
5	0.07	2 / 132	hsa−miR−508−3p
6	0.07	2 / 133	hsa−miR−485−5p
7	0.09	2 / 154	hsa−miR−139−5p
8	0.10	1 / 31	hsa−miR−558
9	0.10	2 / 163	hsa−miR−495
10	0.12	1 / 37	hsa−miR−197
11	0.13	2 / 187	hsa−miR−944
12	0.13	1 / 42	hsa−miR−642
13	0.13	1 / 43	hsa−miR−331−5p
14	0.13	1 / 43	hsa−miR−766
15	0.15	1 / 50	hsa−miR−549
16	0.16	1 / 52	hsa−miR−431
17	0.16	2 / 217	hsa−miR−203
18	0.17	1 / 55	hsa−miR−191
19	0.17	1 / 56	hsa−miR−384
20	0.18	2 / 233	hsa−miR−26a

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	1 / 11	MYC_Protein synthesis degradation UP
2	0.04	8 / 1171	KIM_MYC targets
3	0.05	10 / 1701	HEBENSTREIT_high expression TF
4	0.16	10 / 2137	ICGC_SrfV0416101_targets
5	0.18	7 / 1400	ICGC_Myc_targets
6	0.18	19 / 4689	ICGC_Taf1_targets
7	0.18	1 / 59	MYC_Targets UP
8	0.24	16 / 4032	ICGC_Creb1_targets
9	0.24	19 / 4909	ICGC_Stat5_targets
10	0.24	16 / 4054	ICGC_Egr1_targets
11	0.26	10 / 2391	ICGC_Pbx3_targets
12	0.26	17 / 4385	ICGC_Atf2_targets
13	0.27	9 / 2136	ICGC_GabpPcr2_targets
14	0.27	17 / 4414	ICGC_Bclaf101388_targets
15	0.29	18 / 4774	ICGC_Foxm1_targets
16	0.30	15 / 3924	ICGC_Zeb1_targets
17	0.31	3 / 595	ICGC_NrsfPcr2_targets
18	0.33	6 / 1418	ICGC_Ets1_targets
19	0.33	18 / 4879	ICGC_Pmlsc71910_targets
20	0.34	17 / 4617	ICGC_Tcf12_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 17	VAQUERIZAS_Heart
2	0.18	1 / 59	VAQUERIZAS_Whole blood
3	0.38	1 / 143	VAQUERIZAS_General
4	1.00	0 / 36	VAQUERIZAS_Fetal brain
5	1.00	0 / 41	VAQUERIZAS_Placenta
6	1.00	0 / 26	VAQUERIZAS_Liver
7	1.00	0 / 33	VAQUERIZAS_Prostate
8	1.00	0 / 29	VAQUERIZAS_Smooth muscle
9	1.00	0 / 45	VAQUERIZAS_Uterus
10	1.00	0 / 9	VAQUERIZAS_Kidney
11	1.00	0 / 23	VAQUERIZAS_Spinal cord
12	1.00	0 / 38	VAQUERIZAS_Whole brain
13	1.00	0 / 37	VAQUERIZAS_Thymus
14	1.00	0 / 40	VAQUERIZAS_Thyroid
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 194	PALMER_B−Cell signature up
2	0.3	1 / 95	WIRTH_Muscle
3	0.3	2 / 350	WIRTH_Nervous System
4	0.5	1 / 225	PALMER_Granulocytes signature up
5	0.7	1 / 350	WIRTH_Immune system
6	1.0	0 / 32	WIRTH_Pancreas
7	1.0	0 / 11	WIRTH_Sec. lymphoid organs
8	1.0	0 / 11	WIRTH_Prim. lymphoid organs
9	1.0	0 / 13	WIRTH_B−cells
10	1.0	0 / 8	WIRTH_Tonsil
11	1.0	0 / 12	WIRTH_Thymus
12	1.0	0 / 12	WIRTH_Lymphocytes
13	1.0	0 / 5	WIRTH_Bone marrow
14	1.0	0 / 11	WIRTH_Globus pallidus
15	1.0	0 / 14	WIRTH_Telencephalon
16	1.0	0 / 11	WIRTH_Cortex cerebri
17	1.0	0 / 10	WIRTH_Hippocampus
18	1.0	0 / 10	WIRTH_Thalamus
19	1.0	0 / 12	WIRTH_Cerebellum
20	1.0	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	11 / 3682	LU_BPDE 0.005 DN
2	0.9	2 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

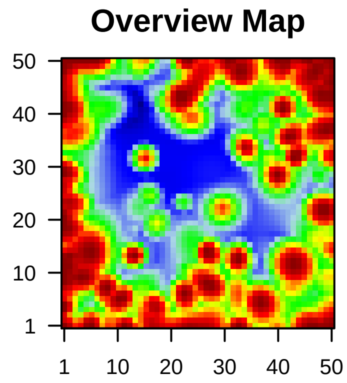
Overexpression Spots

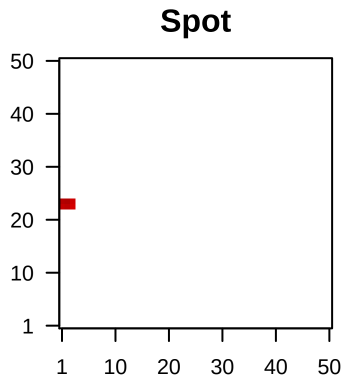
Spot Summary: B

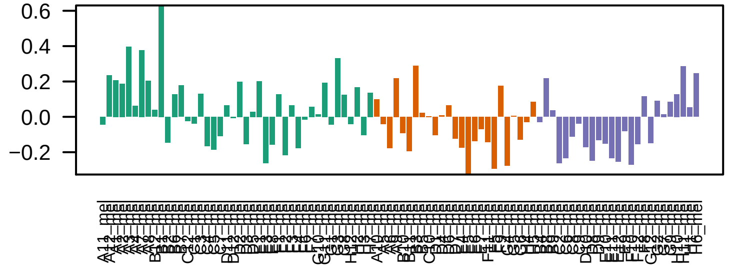
metagenes = 6
genes = 33

<r> metagenes = 0.99
<r> genes = 0.12
beta: r2= 1.23 / log p= −Inf

samples with spot = 16 (17.4 %)
MSC1 : 11 (26.2 %)
MSC2 : 2 (8 %)
MSC3 : 3 (12 %)


Overview Map


Spot

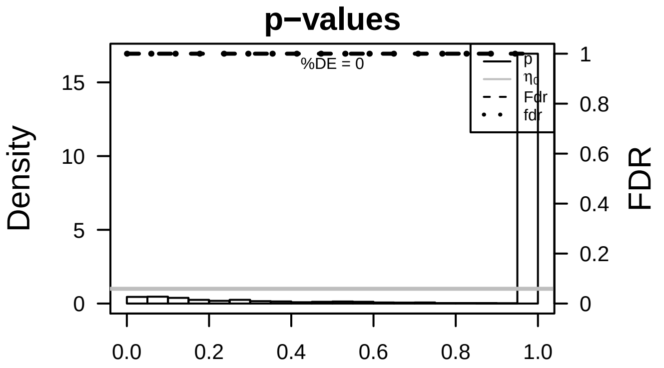


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	NSMCE4A	1.83	−0.38	0.29	NSMCE4A	non−SMC element 4 homolog A (S. cerevisiae) [Source:HGN
2	TAZ	1.78	−0.27	0.28	TAZ	tafazzin [Source:HGNC Symbol;Acc:HGNC:11577]
3	ORAI3	1.62	−0.39	0.21	ORAI3	ORAI calcium release−activated calcium modulator 3 [Source
4	KIF13B	1.58	−0.33	0.28	KIF13B	kinesin family member 13B [Source:HGNC Symbol;Acc:HGN
5	RAD51D	1.55	−0.37	0.23	RAD51D	RAD51 paralog D [Source:HGNC Symbol;Acc:HGNC:9823]
6	SPATA6	1.53	−0.48	0.2	SPATA6	spermatogenesis associated 6 [Source:HGNC Symbol;Acc:H
7	EGLN2	1.51	−0.65	0.27	EGLN2	egl−9 family hypoxia−inducible factor 2 [Source:HGNC Symb
8	TMC8	1.45	−0.25	0.31	TMC8	transmembrane channel−like 8 [Source:HGNC Symbol;Acc:H
9	EXOSC5	1.4	−0.94	0.25	EXOSC5	exosome component 5 [Source:HGNC Symbol;Acc:HGNC:24
10	RFK	1.34	−0.59	0.36	RFK	riboflavin kinase [Source:HGNC Symbol;Acc:HGNC:30324]
11	TNFRSF1A	1.32	−0.66	0.25	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A [Sour
12	JUNB	1.32	−0.18	0.34	JUNB	jun B proto−oncogene [Source:HGNC Symbol;Acc:HGNC:62
13	CUL4A	1.28	−0.7	0.3	CUL4A	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
14	MTMR1	1.28	−0.21	0.32	MTMR1	myotubularin related protein 1 [Source:HGNC Symbol;Acc:H
15	C9orf89	1.27	−0.66	0.35	C9orf89	chromosome 9 open reading frame 89 [Source:HGNC Symb
16	DGCR6L	1.17	−0.7	0.24	DGCR6L	DiGeorge syndrome critical region gene 6−like [Source:HGN
17	RNASEH2C	1.15	−0.84	0.31	RNASEH2C	ribonuclease H2, subunit C [Source:HGNC Symbol;Acc:HGN
18	PPP5C	1.14	−1.11	0.38	PPP5C	protein phosphatase 5, catalytic subunit [Source:HGNC Sym
19	NIPA2	1.13	−1.02	0.41	NIPA2	non imprinted in Prader−Willi/Angelman syndrome 2 [Source:
20	SRSF4	1.08	−1.23	0.34	SRSF4	serine/arginine−rich splicing factor 4 [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−04	3 / 56	GSEA	RIZKI_TUMOR_INVASIVENESS_2D_DN
2	4e−04	4 / 154	GSEA	KIM_WT1_TARGETS_8HR_UP
3	4e−04	3 / 67	GSEA	HUMMERICH_SKIN_CANCER_PROGRESSION_UP
4	4e−04	30 / 9482	Colon	TssA_Colon
5	5e−04	6 / 460	GSEA	ACEVEDO_LIVER_CANCER_DN
6	5e−04	2 / 15	BP	RNA catabolic process
7	5e−04	2 / 15	GSEA	KEGG_RIBOFLAVIN_METABOLISM
8	6e−04	2 / 16	GSEA	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
9	2e−03	3 / 109	Lymph	ROSOLOWSKI_green total
10	3e−03	2 / 35	GSEA	KEGG_PYRUVATE_METABOLISM
11	3e−03	2 / 37	CC	chromosome, telomeric region
12	4e−03	2 / 42	GSEA	PARK_APL_PATHOGENESIS_DN
13	4e−03	2 / 43	GSEA	SASAI_RESISTANCE_TO_NEOPLASTIC_TRANSFROMATION
14	4e−03	3 / 146	HM	HALLMARK_UV_RESPONSE_UP
15	4e−03	4 / 298	BP	DNA repair
16	4e−03	2 / 45	GSEA	BECKER_TAMOXIFEN_RESISTANCE_UP
17	5e−03	3 / 154	miRN	hsa−miR−139−5p
18	5e−03	2 / 47	HM	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
19	5e−03	4 / 314	GSEA	OSMAN_BLADDER_CANCER_DN
20	5e−03	3 / 157	GSEA	BAKKER_FOXO3_TARGETS_DN
21	5e−03	2 / 48	BP	positive regulation of protein catabolic process
22	5e−03	2 / 48	GSEA	BORLAK_LIVER_CANCER_EGF_UP
23	5e−03	5 / 517	GSEA	FEVR_CTNNB1_TARGETS_DN
24	6e−03	2 / 54	GSEA	PHONG_TNF_TARGETS_UP
25	7e−03	2 / 56	BP	regulation of cell growth
26	7e−03	3 / 181	GSEA	PENG_LEUCINE_DEPRIVATION_DN
27	8e−03	2 / 61	BP	mRNA export from nucleus
28	9e−03	2 / 63	GSEA	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP
29	1e−02	3 / 198	GSEA	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP
30	1e−02	6 / 842	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
31	1e−02	3 / 200	GSEA	LINSLEY_MIR16_TARGETS
32	1e−02	6 / 843	GSEA	LOPEZ_MBD_TARGETS
33	1e−02	2 / 69	miRN	hsa−miR−1266
34	1e−02	3 / 204	BP	in utero embryonic development
35	1e−02	2 / 70	GSEA	COATES_MACROPHAGE_M1_VS_M2_UP
36	1e−02	2 / 72	BP	hemopoiesis
37	1e−02	2 / 73	miRN	hsa−miR−657
38	1e−02	7 / 1171	TF	KIM_MYC targets
39	1e−02	1 / 6	GSEA	HE_PTEN_TARGETS_DN
40	1e−02	2 / 80	CC	mitochondrial membrane


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	2 / 15	RNA catabolic process
2	4e−03	4 / 298	DNA repair
3	5e−03	2 / 48	positive regulation of protein catabolic process
4	7e−03	2 / 56	regulation of cell growth
5	8e−03	2 / 61	mRNA export from nucleus
6	1e−02	3 / 204	in utero embryonic development
7	1e−02	2 / 72	hemopoiesis
8	2e−02	1 / 10	prostaglandin metabolic process
9	2e−02	1 / 10	regulation of cell death
10	2e−02	1 / 11	motile cilium assembly
11	3e−02	5 / 768	DNA metabolic process
12	3e−02	1 / 12	purine ribonucleoside monophosphate biosynthetic process
13	3e−02	1 / 13	magnesium ion transport
14	3e−02	1 / 13	response to lead ion
15	3e−02	1 / 14	maternal process involved in female pregnancy
16	3e−02	1 / 14	response to morphine
17	3e−02	1 / 14	trophectodermal cell differentiation
18	3e−02	1 / 15	cellular process
19	3e−02	1 / 15	nucleoside metabolic process
20	3e−02	1 / 15	positive regulation of G1/S transition of mitotic cell cycle

Brain

Rank	p−value	#in/all	Geneset
1	0.04	3 / 349	Fetal_ZNF
2	0.06	18 / 5940	Overlap_fetal_midbrain_HetRpts
3	0.08	25 / 9330	Overlap_fetal_midbrain_ReprPC
4	0.11	24 / 9013	Overlap_fetal_midbrain_K9K27me3
5	0.22	6 / 1845	Fetal_Quies
6	0.24	3 / 765	Mid_Frontal_Lobe_Het
7	0.24	3 / 769	Overlap_fetal_midbrain_ZNF
8	0.31	22 / 9020	Overlap_fetal_midbrain_ReprPCWk
9	0.42	3 / 1050	Fetal_EnhP
10	0.45	2 / 686	Overlap_fetal_midbrain_TssA
11	0.46	4 / 1548	Mid_Frontal_Lobe_K9K27me3
12	0.46	22 / 9528	Overlap_fetal_midbrain_Quies
13	0.50	1 / 304	Fetal_Het
14	0.54	7 / 3081	Mid_Frontal_Lobe_ZNF
15	0.56	2 / 831	Fetal_HetRpts
16	0.58	1 / 383	Fetal_Tx
17	0.58	3 / 1333	Fetal_ReprPCWk
18	0.59	2 / 884	Overlap_fetal_midbrain_EnhG
19	0.66	2 / 989	Mid_Frontal_Lobe_Quies
20	0.67	2 / 1013	Fetal_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 15	GENTLES_modul4
2	0.03	1 / 16	GENTLES_modul16
3	0.10	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.30	2 / 489	Lembcke_Normal vs Adenoma
5	0.49	1 / 298	SPANG_BCL6−index2
6	0.58	0 / 14	LIU_PROSTATE_CANCER_DN
7	0.60	1 / 401	Lembcke_Colonic Inflammation
8	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
9	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
10	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_COMMON_CANCER_GENES
13	1.00	0 / 14	LIU_LIVER_CANCER
14	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
15	1.00	0 / 15	WANG_ER_UP
16	1.00	0 / 5	WANG_ER_DN
17	1.00	0 / 16	WOLFER_overlap genes
18	1.00	0 / 12	BEN−PORATH_DN
19	1.00	0 / 13	BEN−PORATH_UP
20	1.00	0 / 15	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	0.003	2 / 37	chromosome, telomeric region
2	0.014	2 / 80	mitochondrial membrane
3	0.024	1 / 11	intrinsic component of membrane
4	0.026	1 / 12	cullin−RING ubiquitin ligase complex
5	0.031	1 / 14	Cul4−RING E3 ubiquitin ligase complex
6	0.031	1 / 14	exosome (RNase complex)
7	0.037	1 / 17	replication fork
8	0.037	1 / 17	transcriptionally active chromatin
9	0.058	4 / 663	chromosome
10	0.075	1 / 35	cell periphery
11	0.092	9 / 2507	cytosol
12	0.101	1 / 48	kinesin complex
13	0.109	1 / 52	perikaryon
14	0.125	1 / 60	nuclear pore
15	0.127	27 / 10605	intracellular
16	0.155	16 / 5696	nucleus
17	0.159	10 / 3214	protein complex
18	0.168	2 / 332	nuclear envelope
19	0.174	3 / 649	endoplasmic reticulum membrane
20	0.195	1 / 97	chromatin

Chr

Rank	p−value	#in/all	Geneset
1	0.1	2 / 262	Chr 13
2	0.2	4 / 1037	Chr 19
3	0.2	2 / 398	Chr 20
4	0.3	3 / 801	Chr 11
5	0.3	2 / 465	Chr 15
6	0.3	3 / 840	Chr 17
7	0.3	1 / 151	Chr 21
8	0.3	2 / 551	Chr X
9	0.4	2 / 576	Chr 9
10	0.4	1 / 221	Chr 18
11	0.4	2 / 649	Chr 16
12	0.5	1 / 335	Chr 22
13	0.7	1 / 469	Chr 8
14	0.7	1 / 552	Chr 10
15	0.7	1 / 558	Chr 4
16	0.8	1 / 687	Chr 6
17	0.8	1 / 689	Chr 7
18	0.8	1 / 775	Chr 12
19	0.9	2 / 1500	Chr 1
20	1.0	0 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	30 / 9482	TssA_Colon
2	4e−02	4 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
3	6e−02	21 / 7203	TssF_Colon
4	9e−02	23 / 8415	Quies3_Colon
5	1e−01	24 / 9027	Tx_Colon
6	1e−01	17 / 5880	TssD2_Colon
7	2e−01	24 / 9653	Enh_Colon
8	3e−01	8 / 2798	TxEnhG1_Colon
9	3e−01	21 / 8580	TxWk_Colon
10	3e−01	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	4e−01	2 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	5e−01	2 / 739	TxEnhG2_Colon
13	5e−01	2 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
14	6e−01	23 / 10290	TssWk_Colon
15	6e−01	1 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
16	6e−01	6 / 2698	EnhA_Colon
17	6e−01	2 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	6e−01	1 / 436	K9acLow_Colon
19	7e−01	1 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
20	8e−01	10 / 5155	EnhWk1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 435	GUDJ_psoriasis up
2	1	0 / 294	GUDJ_psoriasis down
3	1	0 / 11	BCHETNIA_EBM up
4	1	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.1	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
2	0.1	1 / 71	Weller_LGG_A_vs_O_UP
3	0.2	1 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	0.2	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	0.2	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	0.2	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	0.3	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.5	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	0.5	1 / 332	Up
10	0.6	1 / 365	Down_b
11	1.0	0 / 15	VERHAAK_CL subtype
12	1.0	0 / 15	VERHAAK_MES subtype
13	1.0	0 / 16	VERHAAK_NL subtype
14	1.0	0 / 14	VERHAAK_PN subtype
15	1.0	0 / 23	WIRTH_PN subtype
16	1.0	0 / 74	WIRTH_Normal Brain
17	1.0	0 / 9	VERHAAK_Brain
18	1.0	0 / 8	VERHAAK_PN_Brain
19	1.0	0 / 11	Martinez_Glio_hypermeth
20	1.0	0 / 3	Martinez_Glio_hypometh

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 56	RIZKI_TUMOR_INVASIVENESS_2D_DN
2	4e−04	4 / 154	KIM_WT1_TARGETS_8HR_UP
3	4e−04	3 / 67	HUMMERICH_SKIN_CANCER_PROGRESSION_UP
4	5e−04	6 / 460	ACEVEDO_LIVER_CANCER_DN
5	5e−04	2 / 15	KEGG_RIBOFLAVIN_METABOLISM
6	6e−04	2 / 16	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
7	3e−03	2 / 35	KEGG_PYRUVATE_METABOLISM
8	4e−03	2 / 42	PARK_APL_PATHOGENESIS_DN
9	4e−03	2 / 43	SASAI_RESISTANCE_TO_NEOPLASTIC_TRANSFROMATION
10	4e−03	2 / 45	BECKER_TAMOXIFEN_RESISTANCE_UP
11	5e−03	4 / 314	OSMAN_BLADDER_CANCER_DN
12	5e−03	3 / 157	BAKKER_FOXO3_TARGETS_DN
13	5e−03	2 / 48	BORLAK_LIVER_CANCER_EGF_UP
14	5e−03	5 / 517	FEVR_CTNNB1_TARGETS_DN
15	6e−03	2 / 54	PHONG_TNF_TARGETS_UP
16	7e−03	3 / 181	PENG_LEUCINE_DEPRIVATION_DN
17	9e−03	2 / 63	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP
18	1e−02	3 / 198	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP
19	1e−02	6 / 842	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
20	1e−02	3 / 200	LINSLEY_MIR16_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	0.004	3 / 146	HALLMARK_UV_RESPONSE_UP
2	0.005	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	0.059	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	0.111	1 / 53	HALLMARK_TGF_BETA_SIGNALING
5	0.119	1 / 57	HALLMARK_MYC_TARGETS_V2
6	0.125	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	0.152	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	0.191	1 / 95	HALLMARK_SPERMATOGENESIS
9	0.193	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	0.216	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	0.245	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
12	0.269	1 / 140	HALLMARK_APOPTOSIS
13	0.270	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
14	0.315	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
15	0.316	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
16	0.333	1 / 181	HALLMARK_P53_PATHWAY
17	0.336	1 / 183	HALLMARK_GLYCOLYSIS
18	0.355	1 / 196	HALLMARK_G2M_CHECKPOINT
19	1.000	0 / 176	HALLMARK_HYPOXIA
20	1.000	0 / 195	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	3 / 109	ROSOLOWSKI_green total
2	0.014	2 / 82	ROSOLOWSKI_green UP
3	0.020	1 / 9	Subero_B−ALL_hypo_meth
4	0.029	1 / 13	BENTINK_mBL UP
5	0.054	1 / 25	Subero_T−PLL_hypo_meth
6	0.102	5 / 1128	SPANG_BCR DN
7	0.110	2 / 256	SPANG_IL21 DN
8	0.139	15 / 5184	HOPP_Txn_transition
9	0.232	18 / 6929	HOPP_Txn_elongation
10	0.251	17 / 6564	HOPP_Strong_enhancer
11	0.285	4 / 1218	SPANG_BCR UP
12	0.378	1 / 212	LENZ_Stromal signature 1
13	0.553	17 / 7592	HOPP_Active_promoter
14	0.604	1 / 410	SPANG_CD40 6hrs DN
15	0.745	4 / 2211	HOPP_Repetitive
16	0.810	14 / 7209	HOPP_Weak_promoter
17	0.962	8 / 5538	HOPP_Weak_txn
18	0.965	2 / 2188	HOPP_Poised_promoter
19	0.985	2 / 2563	HOPP_Heterochrom
20	0.989	7 / 5693	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	0.01	2 / 83	translation factor activity, RNA binding
2	0.03	1 / 12	magnesium ion transmembrane transporter activity
3	0.03	1 / 12	Notch binding
4	0.03	1 / 14	ferrous iron binding
5	0.03	1 / 14	G−protein alpha−subunit binding
6	0.03	1 / 14	polypeptide N−acetylgalactosaminyltransferase activity
7	0.03	1 / 15	L−ascorbic acid binding
8	0.04	1 / 18	14−3−3 protein binding
9	0.04	1 / 18	gamma−tubulin binding
10	0.04	1 / 19	3'−5'−exoribonuclease activity
11	0.04	1 / 20	translation elongation factor activity
12	0.05	2 / 156	microtubule binding
13	0.05	1 / 23	DNA helicase activity
14	0.05	1 / 25	transferase activity, transferring acyl groups other than amino−acyl groups
15	0.06	1 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductic
16	0.06	1 / 27	ribosome binding
17	0.07	2 / 193	transferase activity, transferring acyl groups
18	0.07	1 / 34	DNA−dependent ATPase activity
19	0.08	1 / 35	4 iron, 4 sulfur cluster binding
20	0.08	2 / 210	transferase activity, transferring glycosyl groups

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.005	3 / 154	hsa−miR−139−5p
2	0.010	2 / 69	hsa−miR−1266
3	0.011	2 / 73	hsa−miR−657
4	0.017	2 / 89	hsa−miR−608
5	0.022	1 / 10	hsa−miR−487b
6	0.024	1 / 11	hsa−miR−604
7	0.026	1 / 12	hsa−miR−639
8	0.040	3 / 343	hsa−miR−548b−5p
9	0.042	2 / 147	hsa−miR−143
10	0.045	3 / 358	hsa−let−7d
11	0.050	1 / 23	hsa−miR−1250
12	0.052	1 / 24	hsa−miR−1225−5p
13	0.052	1 / 24	hsa−miR−220b
14	0.060	1 / 28	hsa−miR−591
15	0.063	1 / 29	hsa−miR−193a−5p
16	0.065	1 / 30	hsa−miR−371−3p
17	0.065	1 / 30	hsa−miR−654−5p
18	0.065	1 / 30	hsa−miR−1293
19	0.066	2 / 189	hsa−miR−513a−3p
20	0.067	1 / 31	hsa−miR−342−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.01	7 / 1171	KIM_MYC targets
2	0.03	7 / 1400	ICGC_Myc_targets
3	0.04	1 / 19	MYC_Metabolism UP
4	0.07	15 / 4689	ICGC_Taf1_targets
5	0.07	6 / 1314	ICGC_Usf1_targets
6	0.08	7 / 1701	HEBENSTREIT_high expression TF
7	0.11	16 / 5408	ICGC_Pou2_targets
8	0.12	1 / 59	MYC_Targets UP
9	0.16	12 / 4054	ICGC_Egr1_targets
10	0.19	16 / 5890	ICGC_Elf1_targets
11	0.20	15 / 5495	ICGC_Yy1_targets
12	0.23	12 / 4314	ICGC_Ebfsc137065_targets
13	0.24	13 / 4774	ICGC_Foxm1_targets
14	0.25	16 / 6114	ICGC_Runx3_targets
15	0.25	11 / 3966	ICGC_Pu1_targets
16	0.26	12 / 4414	ICGC_Bclaf101388_targets
17	0.27	11 / 4032	ICGC_Creb1_targets
18	0.34	6 / 2136	ICGC_GabpPcr2_targets
19	0.38	11 / 4385	ICGC_Atf2_targets
20	0.38	12 / 4829	ICGC_Nficsc81335_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 143	VAQUERIZAS_General
2	1.00	0 / 36	VAQUERIZAS_Fetal brain
3	1.00	0 / 41	VAQUERIZAS_Placenta
4	1.00	0 / 26	VAQUERIZAS_Liver
5	1.00	0 / 33	VAQUERIZAS_Prostate
6	1.00	0 / 29	VAQUERIZAS_Smooth muscle
7	1.00	0 / 45	VAQUERIZAS_Uterus
8	1.00	0 / 9	VAQUERIZAS_Kidney
9	1.00	0 / 23	VAQUERIZAS_Spinal cord
10	1.00	0 / 38	VAQUERIZAS_Whole brain
11	1.00	0 / 37	VAQUERIZAS_Thymus
12	1.00	0 / 40	VAQUERIZAS_Thyroid
13	1.00	0 / 59	VAQUERIZAS_Whole blood
14	1.00	0 / 7	VAQUERIZAS_Appendix
15	1.00	0 / 29	VAQUERIZAS_Fetal lung
16	1.00	0 / 58	VAQUERIZAS_Lung
17	1.00	0 / 16	VAQUERIZAS_Pancreas
18	1.00	0 / 23	VAQUERIZAS_Trachea
19	1.00	0 / 11	VAQUERIZAS_Fetal liver
20	1.00	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	1 / 14	WIRTH_Telencephalon
2	0.21	1 / 107	WIRTH_Testis
3	0.55	1 / 350	WIRTH_Immune system
4	1.00	0 / 32	WIRTH_Pancreas
5	1.00	0 / 11	WIRTH_Sec. lymphoid organs
6	1.00	0 / 11	WIRTH_Prim. lymphoid organs
7	1.00	0 / 13	WIRTH_B−cells
8	1.00	0 / 8	WIRTH_Tonsil
9	1.00	0 / 12	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 5	WIRTH_Bone marrow
12	1.00	0 / 350	WIRTH_Nervous System
13	1.00	0 / 11	WIRTH_Globus pallidus
14	1.00	0 / 11	WIRTH_Cortex cerebri
15	1.00	0 / 10	WIRTH_Hippocampus
16	1.00	0 / 10	WIRTH_Thalamus
17	1.00	0 / 12	WIRTH_Cerebellum
18	1.00	0 / 41	WIRTH_Homeostasis
19	1.00	0 / 46	WIRTH_Liver
20	1.00	0 / 95	WIRTH_Muscle

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	3 / 1115	LU_BPDE 1h DN
2	0.7	7 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

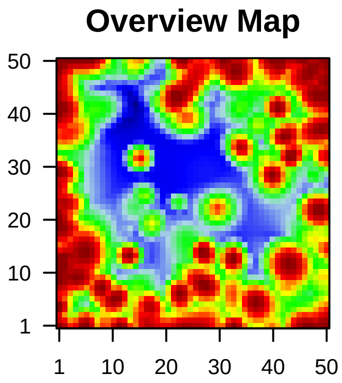
Overexpression Spots

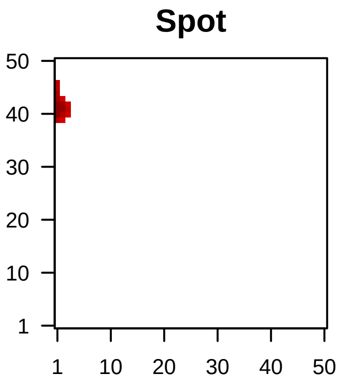
Spot Summary: C

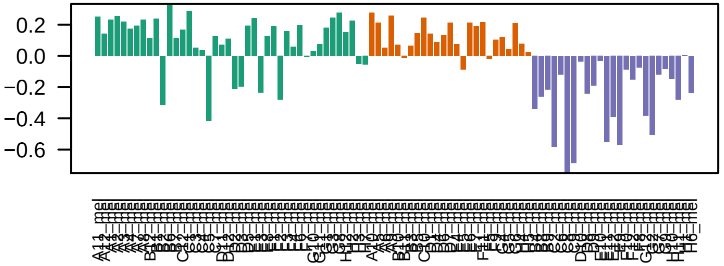
metagenes = 16
genes = 283

<r> metagenes = 0.95
<r> genes = 0.17
beta: r2= 3.92 / log p= −Inf

samples with spot = 26 (28.3 %)
MSC1 : 17 (40.5 %)
MSC2 : 9 (36 %)





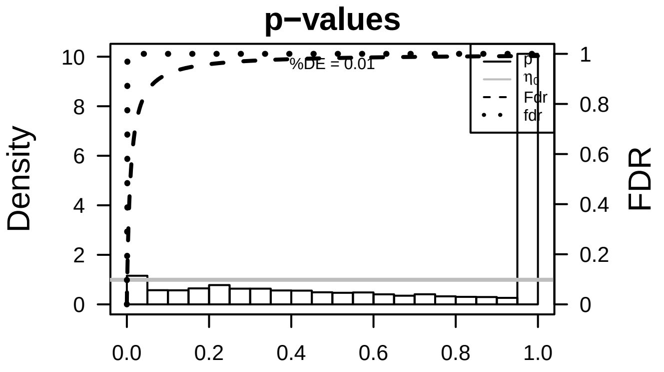


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ZNF577	1.94	−0.21	0.27	ZNF577	zinc finger protein 577 [Source:HGNC Symbol;Acc:HGNC:28
2	GAPDHS	1.71	−1.17	0.59	GAPDHS	glyceraldehyde−3−phosphate dehydrogenase, spermatogeni
3	ST6GALNAC	1.69	−0.39	0.32	ST6GALNAC3	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
4	TRMT1	1.65	−0.71	0.36	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:H
5	NMRK2	1.63	−1.2	0.71	NMRK2	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
6	NT5DC1	1.63	−0.93	0.28	NT5DC1	5'−nucleotidase domain containing 1 [Source:HGNC Symbol;
7	WIPF3	1.62	−0.29	0.33	WIPF3	WAS/WASL interacting protein family, member 3 [Source:HG
8	NT5DC2	1.62	−0.98	0.28	NT5DC2	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
9	ANO2	1.61	−0.48	0.34	ANO2	anoctamin 2, calcium activated chloride channel [Source:HG
10	MUC7	1.61	−0.26	0.44	MUC7	mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]
11	CAPG	1.58	−0.72	0.39	CAPG	capping protein (actin filament), gelsolin−like [Source:HGNC
12	MAPK10	1.57	−0.69	0.44	MAPK10	mitogen−activated protein kinase 10 [Source:HGNC Symbol;
13	SNAP29	1.56	−0.44	0.3	SNAP29	synaptosomal−associated protein, 29kDa [Source:HGNC Sy
14	MIPEP	1.55	−0.46	0.29	MIPEP	mitochondrial intermediate peptidase [Source:HGNC Symbol
15	TMEM243	1.54	−0.76	0.45	TMEM243	transmembrane protein 243, mitochondrial [Source:HGNC Sy
16	ISY1	1.53	−0.64	0.24	ISY1	ISY1 splicing factor homolog (S. cerevisiae) [Source:HGNC S
17	SNX8	1.52	−0.75	0.39	SNX8	sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
18	IFI35	1.51	−0.5	0.32	IFI35	interferon−induced protein 35 [Source:HGNC Symbol;Acc:HG
19	NENF	1.49	−0.83	0.33	NENF	neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HG
20	TCN2	1.49	−0.39	0.34	TCN2	transcobalamin II [Source:HGNC Symbol;Acc:HGNC:11653]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−13	33 / 368	GSEA	STEIN_ESRRA_TARGETS_UP
2	5e−12	36 / 500	GSEA	STEIN_ESRRA_TARGETS
3	6e−12	32 / 401	CC	mitochondrial inner membrane
4	1e−11	66 / 1468	CC	mitochondrion
5	3e−10	42 / 756	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
6	1e−09	20 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	1e−08	44 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
8	1e−08	24 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
9	1e−08	27 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
10	3e−08	27 / 421	GSEA	MOOTHA_MITOCHONDRIA
11	4e−08	181 / 7203	Colon	TssF_Colon
12	4e−07	38 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
13	4e−07	13 / 120	CC	mitochondrial outer membrane
14	6e−07	16 / 188	HM	HALLMARK_ADIPOGENESIS
15	9e−07	21 / 322	BP	mitochondrion organization
16	9e−07	15 / 171	GSEA	BURTON_ADIPOGENESIS_6
17	9e−07	61 / 1730	BP	small molecule metabolic process
18	2e−06	22 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
19	2e−06	21 / 338	GSEA	DAIRKEE_TERT_TARGETS_UP
20	2e−06	71 / 2193	CC	extracellular exosome
21	3e−06	5 / 13	BP	melanin biosynthetic process
22	5e−06	7 / 37	GSEA	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP
23	6e−06	18 / 278	GSEA	MANALO_HYPOXIA_DN
24	7e−06	22 / 398	GSEA	MOOTHA_PGC
25	1e−05	24 / 475	GSEA	ONKEN_UVEAL_MELANOMA_DN
26	1e−05	12 / 140	GSEA	ELVIDGE_HYPOXIA_DN
27	2e−05	5 / 18	BP	melanocyte differentiation
28	2e−05	212 / 9482	Colon	TssA_Colon
29	3e−05	7 / 47	BP	protein targeting to mitochondrion
30	3e−05	203 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
31	3e−05	7 / 48	GSEA	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
32	3e−05	14 / 202	GSEA	CHANG_CORE_SERUM_RESPONSE_UP
33	4e−05	188 / 8205	CC	cytoplasm
34	6e−05	11 / 136	GSEA	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
35	7e−05	3 / 5	GSEA	IGARASHI_ATF4_TARGETS_UP
36	8e−05	12 / 167	GSEA	KIM_MYC_AMPLIFICATION_TARGETS_UP
37	9e−05	10 / 120	GSEA	BURTON_ADIPOGENESIS_5
38	1e−04	24 / 541	BP	oxidation−reduction process
39	1e−04	15 / 255	BP	cellular amino acid metabolic process
40	1e−04	14 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 100	HORVATH_aging_genes meth DOWN
2	0.6	2 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−07	21 / 322	mitochondrion organization
2	9e−07	61 / 1730	small molecule metabolic process
3	3e−06	5 / 13	melanin biosynthetic process
4	2e−05	5 / 18	melanocyte differentiation
5	3e−05	7 / 47	protein targeting to mitochondrion
6	1e−04	24 / 541	oxidation−reduction process
7	1e−04	15 / 255	cellular amino acid metabolic process
8	2e−04	7 / 63	response to ethanol
9	3e−04	76 / 2755	transport
10	6e−04	19 / 435	cellular protein metabolic process
11	8e−04	4 / 23	secondary metabolic process
12	8e−04	4 / 23	sulfur amino acid metabolic process
13	1e−03	13 / 259	protein targeting
14	1e−03	18 / 431	negative regulation of apoptotic process
15	2e−03	4 / 27	positive regulation of autophagy
16	2e−03	22 / 598	membrane organization
17	3e−03	6 / 75	water−soluble vitamin metabolic process
18	4e−03	3 / 17	mitochondrial respiratory chain complex I assembly
19	4e−03	3 / 17	sialylation
20	4e−03	6 / 81	vitamin metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	3e−05	203 / 9013	Overlap_fetal_midbrain_K9K27me3
2	2e−03	204 / 9528	Overlap_fetal_midbrain_Quies
3	2e−03	79 / 3081	Mid_Frontal_Lobe_ZNF
4	3e−03	199 / 9330	Overlap_fetal_midbrain_ReprPC
5	3e−02	22 / 765	Mid_Frontal_Lobe_Het
6	5e−02	34 / 1333	Fetal_ReprPCWk
7	6e−02	57 / 2462	Mid_Frontal_Lobe_HetRpts
8	2e−01	20 / 831	Fetal_HetRpts
9	2e−01	120 / 5940	Overlap_fetal_midbrain_HetRpts
10	4e−01	2 / 69	Overlap_fetal_midbrain_Tx
11	4e−01	173 / 9020	Overlap_fetal_midbrain_ReprPCWk
12	5e−01	22 / 1122	Fetal_K9K27me3
13	5e−01	57 / 2972	Mid_Frontal_Lobe_ReprPC
14	5e−01	35 / 1845	Fetal_Quies
15	6e−01	3 / 156	Mid_Frontal_Lobe_TssA
16	6e−01	3 / 163	Fetal_ReprPC
17	6e−01	14 / 786	Fetal_EnhG
18	7e−01	6 / 349	Fetal_ZNF
19	7e−01	5 / 304	Fetal_Het
20	7e−01	13 / 769	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	3 / 16	GENTLES_modul2
2	0.007	4 / 40	ZHANG_MM up
3	0.024	16 / 489	Lembcke_Normal vs Adenoma
4	0.027	6 / 120	PanCan_CC+Apop_geneset_nanostring
5	0.113	1 / 15	RHODES_CANCER_META_SIGNATURE
6	0.147	3 / 70	SHAUGHNESSY_MM high risk
7	0.174	1 / 10	GENTLES_modul5
8	0.203	3 / 82	PanCan_TXmisReg_geneset_nanostring
9	0.205	8 / 298	SPANG_BCL6−index2
10	0.205	1 / 12	LIU_BREAST_CANCER
11	0.220	1 / 13	BEN−PORATH_UP
12	0.220	1 / 13	GENTLES_modul12
13	0.235	1 / 14	LIU_PROSTATE_CANCER_DN
14	0.249	1 / 15	GENTLES_modul1
15	0.249	1 / 15	GENTLES_modul10
16	0.255	5 / 180	SPANG_LPS−index2
17	0.264	1 / 16	WOLFER_overlap genes
18	0.264	1 / 16	GENTLES_modul7
19	0.291	1 / 18	PanCan_Notch_geneset_nanostring
20	0.318	1 / 20	PanCan_ChromMod_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−12	32 / 401	mitochondrial inner membrane
2	1e−11	66 / 1468	mitochondrion
3	4e−07	13 / 120	mitochondrial outer membrane
4	2e−06	71 / 2193	extracellular exosome
5	4e−05	188 / 8205	cytoplasm
6	4e−04	8 / 94	melanosome
7	1e−03	68 / 2507	cytosol
8	1e−03	9 / 135	myelin sheath
9	2e−03	80 / 3132	extracellular region
10	2e−03	211 / 9988	organelle
11	5e−03	16 / 412	lysosome
12	7e−03	11 / 246	mitochondrial matrix
13	1e−02	3 / 24	mitochondrial ribosome
14	1e−02	218 / 10605	intracellular
15	1e−02	20 / 616	endosome
16	2e−02	2 / 13	sperm principal piece
17	3e−02	4 / 60	lysosomal lumen
18	3e−02	15 / 456	vacuole
19	3e−02	3 / 35	cell periphery
20	3e−02	6 / 128	ribosome

Chr

Rank	p−value	#in/all	Geneset
1	0.01	10 / 221	Chr 18
2	0.01	19 / 576	Chr 9
3	0.09	25 / 993	Chr 2
4	0.10	10 / 335	Chr 22
5	0.17	16 / 649	Chr 16
6	0.25	13 / 552	Chr 10
7	0.32	22 / 1037	Chr 19
8	0.32	4 / 151	Chr 21
9	0.43	14 / 687	Chr 6
10	0.45	14 / 696	Chr 5
11	0.53	16 / 840	Chr 17
12	0.56	15 / 801	Chr 11
13	0.56	5 / 262	Chr 13
14	0.61	14 / 775	Chr 12
15	0.66	8 / 465	Chr 15
16	0.67	8 / 469	Chr 8
17	0.72	9 / 551	Chr X
18	0.83	8 / 558	Chr 4
19	0.87	6 / 462	Chr 14
20	0.88	5 / 398	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−08	181 / 7203	TssF_Colon
2	2e−05	212 / 9482	TssA_Colon
3	2e−04	200 / 9027	Tx_Colon
4	2e−03	186 / 8580	TxWk_Colon
5	3e−03	205 / 9653	Enh_Colon
6	3e−03	134 / 5880	TssD2_Colon
7	6e−03	22 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	9e−03	117 / 5155	EnhWk1_Colon
9	3e−02	22 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
10	3e−02	66 / 2798	TxEnhG1_Colon
11	3e−02	209 / 10290	TssWk_Colon
12	5e−02	173 / 8415	Quies3_Colon
13	9e−02	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
14	1e−01	2 / 33	Marisa_CRC−cluster−e
15	1e−01	11 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
16	1e−01	1 / 8	Boland_CRC−MSI−TGC
17	2e−01	18 / 739	TxEnhG2_Colon
18	2e−01	5 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
19	2e−01	1 / 15	Budinska_B_Lower crypt−like_UP
20	3e−01	54 / 2698	EnhA_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.07	13 / 435	GUDJ_psoriasis up
2	0.32	1 / 20	BCHETNIA_EBM−DM up
3	0.48	6 / 294	GUDJ_psoriasis down
4	1.00	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−04	7 / 63	Stuehler_Proteins_up_in_STS
2	3e−02	3 / 38	OL vs. OPC
3	4e−02	2 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
4	7e−02	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
5	8e−02	22 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	9e−02	2 / 26	Christensen_hypomethylated_in_ependymoma
7	1e−01	2 / 32	Donson−innate immunity−associated with LTS in HGA
8	1e−01	1 / 8	Colman_survival_robust
9	2e−01	3 / 71	Weller_LGG_A_vs_O_UP
10	2e−01	1 / 9	VERHAAK_Brain
11	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
12	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
13	2e−01	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
14	2e−01	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
15	2e−01	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
16	2e−01	3 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
17	2e−01	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
18	3e−01	9 / 365	Down_b
19	3e−01	2 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
20	3e−01	3 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−13	33 / 368	STEIN_ESRRA_TARGETS_UP
2	5e−12	36 / 500	STEIN_ESRRA_TARGETS
3	3e−10	42 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
4	1e−08	44 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
5	1e−08	24 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
6	1e−08	27 / 405	MOOTHA_HUMAN_MITODB_6_2002
7	3e−08	27 / 421	MOOTHA_MITOCHONDRIA
8	4e−07	38 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
9	9e−07	15 / 171	BURTON_ADIPOGENESIS_6
10	2e−06	22 / 363	RUTELLA_RESPONSE_TO_HGF_UP
11	2e−06	21 / 338	DAIRKEE_TERT_TARGETS_UP
12	5e−06	7 / 37	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP
13	6e−06	18 / 278	MANALO_HYPOXIA_DN
14	7e−06	22 / 398	MOOTHA_PGC
15	1e−05	24 / 475	ONKEN_UVEAL_MELANOMA_DN
16	1e−05	12 / 140	ELVIDGE_HYPOXIA_DN
17	3e−05	7 / 48	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
18	3e−05	14 / 202	CHANG_CORE_SERUM_RESPONSE_UP
19	6e−05	11 / 136	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
20	7e−05	3 / 5	IGARASHI_ATF4_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−09	20 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	6e−07	16 / 188	HALLMARK_ADIPOGENESIS
3	4e−04	11 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	4e−03	5 / 57	HALLMARK_MYC_TARGETS_V2
5	5e−03	8 / 141	HALLMARK_FATTY_ACID_METABOLISM
6	8e−03	9 / 183	HALLMARK_GLYCOLYSIS
7	3e−02	5 / 91	HALLMARK_PROTEIN_SECRETION
8	6e−02	6 / 146	HALLMARK_UV_RESPONSE_UP
9	8e−02	7 / 196	HALLMARK_MTORC1_SIGNALING
10	9e−02	6 / 162	HALLMARK_COMPLEMENT
11	1e−01	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	1e−01	6 / 188	HALLMARK_MYC_TARGETS_V1
13	2e−01	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	2e−01	5 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	2e−01	3 / 91	HALLMARK_BILE_ACID_METABOLISM
16	3e−01	3 / 94	HALLMARK_ANDROGEN_RESPONSE
17	3e−01	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	3e−01	4 / 140	HALLMARK_APOPTOSIS
19	3e−01	5 / 195	HALLMARK_MITOTIC_SPINDLE
20	4e−01	1 / 24	HALLMARK_PANCREAS_BETA_CELLS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
2	0.25	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.29	1 / 18	DUMEAUX_High bmi enriched genes
4	0.33	2 / 62	DUMEAUX_Smoking enriched genes
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.005	153 / 6929	HOPP_Txn_elongation
2	0.006	12 / 275	TARTE_Mature plasma cell signature
3	0.007	145 / 6564	HOPP_Strong_enhancer
4	0.016	162 / 7592	HOPP_Active_promoter
5	0.054	10 / 294	TARTE_Plasmablast signature
6	0.058	150 / 7209	HOPP_Weak_promoter
7	0.065	4 / 80	Aukema_BCL2 DN_BCL6 UP
8	0.070	4 / 82	ROSOLOWSKI_green UP
9	0.090	12 / 410	SPANG_CD40 6hrs DN
10	0.145	107 / 5184	HOPP_Txn_transition
11	0.152	4 / 109	ROSOLOWSKI_green total
12	0.172	26 / 1128	SPANG_BCR DN
13	0.175	2 / 40	Subero_mBL_hyper_meth
14	0.189	2 / 42	CARO_OxPhos_in_DLBCL_UP
15	0.198	3 / 81	Subero_INT_hyper_meth
16	0.205	1 / 12	BENTINK_mBL DOWN
17	0.223	3 / 86	ROSOLOWSKI_red total
18	0.223	2 / 47	Subero_FL_hyper_meth
19	0.235	1 / 14	Subero_MCL_hyper_meth
20	0.249	1 / 15	DAVE_Immune response 2

MF

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 45	NAD binding
2	2e−03	3 / 13	5'−nucleotidase activity
3	2e−03	22 / 592	oxidoreductase activity
4	4e−03	3 / 17	sialyltransferase activity
5	6e−03	4 / 39	SNARE binding
6	1e−02	3 / 26	NF−kappaB binding
7	1e−02	2 / 10	FAD binding
8	2e−02	2 / 11	protein deacetylase activity
9	2e−02	14 / 394	catalytic activity
10	2e−02	5 / 81	protein N−terminus binding
11	2e−02	2 / 12	dynein binding
12	2e−02	2 / 12	NAD−dependent histone deacetylase activity (H3−K14 specific)
13	2e−02	2 / 12	NAD−dependent histone deacetylase activity (H3−K18 specific)
14	2e−02	2 / 12	NAD−dependent histone deacetylase activity (H4−K16 specific)
15	2e−02	2 / 12	oxidoreductase activity, acting on NAD(P)H
16	2e−02	21 / 695	transmembrane transporter activity
17	2e−02	4 / 58	cysteine−type peptidase activity
18	2e−02	2 / 13	NAD+ binding
19	2e−02	2 / 13	NAD−dependent histone deacetylase activity (H3−K9 specific)
20	3e−02	3 / 35	aminoacyl−tRNA ligase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	4 / 40	hsa−miR−647
2	0.013	3 / 26	hsa−miR−337−5p
3	0.018	2 / 11	hsa−miR−604
4	0.038	13 / 395	hsa−miR−301b
5	0.040	3 / 40	hsa−miR−518d−3p
6	0.040	4 / 68	hsa−miR−361−3p
7	0.042	3 / 41	hsa−miR−518b
8	0.050	3 / 44	hsa−miR−640
9	0.056	12 / 378	hsa−miR−454
10	0.067	5 / 115	hsa−miR−154
11	0.075	2 / 24	hsa−miR−1225−5p
12	0.082	3 / 54	hsa−miR−379
13	0.088	4 / 89	hsa−miR−608
14	0.096	8 / 246	hsa−miR−27b
15	0.097	3 / 58	hsa−miR−409−5p
16	0.109	4 / 96	hsa−miR−513b
17	0.113	3 / 62	hsa−miR−556−5p
18	0.117	10 / 343	hsa−miR−548b−5p
19	0.129	2 / 33	hsa−miR−934
20	0.132	6 / 182	hsa−miR−23a

PathwAct

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_e2f3.1
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 12	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−04	127 / 5219	ICGC_Tcf3_targets
2	6e−04	102 / 4054	ICGC_Egr1_targets
3	6e−04	51 / 1701	HEBENSTREIT_high expression TF
4	6e−04	99 / 3924	ICGC_Zeb1_targets
5	6e−04	119 / 4909	ICGC_Stat5_targets
6	1e−03	137 / 5890	ICGC_Elf1_targets
7	2e−03	112 / 4689	ICGC_Taf1_targets
8	3e−03	124 / 5355	ICGC_Pol2_targets
9	3e−03	111 / 4706	ICGC_Sp1_targets
10	3e−03	41 / 1400	ICGC_Myc_targets
11	3e−03	109 / 4617	ICGC_Tcf12_targets
12	4e−03	41 / 1418	ICGC_Ets1_targets
13	4e−03	90 / 3700	ICGC_Nfatc1_targets
14	5e−03	102 / 4314	ICGC_Ebfsc137065_targets
15	5e−03	113 / 4879	ICGC_Pmlsc71910_targets
16	6e−03	125 / 5495	ICGC_Yy1_targets
17	6e−03	123 / 5408	ICGC_Pou2_targets
18	8e−03	108 / 4682	ICGC_Pol24_targets
19	1e−02	121 / 5374	ICGC_Pax5_targets
20	1e−02	55 / 2137	ICGC_SrfV0416101_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 16	VAQUERIZAS_Adrenal gland
2	0.07	2 / 23	VAQUERIZAS_Trachea
3	0.07	2 / 23	VAQUERIZAS_Adrenal cortex
4	0.13	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
5	0.16	1 / 9	VAQUERIZAS_Kidney
6	0.26	1 / 16	VAQUERIZAS_Pancreas
7	0.26	1 / 16	VAQUERIZAS_Salivary gland
8	0.28	1 / 17	VAQUERIZAS_Pituitary
9	0.36	1 / 23	VAQUERIZAS_Spinal cord
10	0.51	1 / 37	VAQUERIZAS_Thymus
11	0.52	1 / 38	VAQUERIZAS_Whole brain
12	0.58	1 / 45	VAQUERIZAS_Uterus
13	0.94	1 / 143	VAQUERIZAS_General
14	1.00	0 / 36	VAQUERIZAS_Fetal brain
15	1.00	0 / 41	VAQUERIZAS_Placenta
16	1.00	0 / 26	VAQUERIZAS_Liver
17	1.00	0 / 33	VAQUERIZAS_Prostate
18	1.00	0 / 29	VAQUERIZAS_Smooth muscle
19	1.00	0 / 40	VAQUERIZAS_Thyroid
20	1.00	0 / 59	VAQUERIZAS_Whole blood

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	11 / 350	WIRTH_Nervous System
2	0.11	4 / 95	WIRTH_Muscle
3	0.14	7 / 225	PALMER_Granulocytes signature up
4	0.19	1 / 11	WIRTH_Cortex cerebri
5	0.22	1 / 13	WIRTH_Thyroid gland
6	0.26	1 / 16	PALMER_Lymphocytes signature up
7	0.46	1 / 32	WIRTH_Pancreas
8	0.64	2 / 114	PALMER_T−Cell signature up
9	0.71	3 / 194	PALMER_B−Cell signature up
10	0.87	1 / 107	WIRTH_Testis
11	0.90	4 / 350	WIRTH_Immune system
12	1.00	0 / 11	WIRTH_Sec. lymphoid organs
13	1.00	0 / 11	WIRTH_Prim. lymphoid organs
14	1.00	0 / 13	WIRTH_B−cells
15	1.00	0 / 8	WIRTH_Tonsil
16	1.00	0 / 12	WIRTH_Thymus
17	1.00	0 / 12	WIRTH_Lymphocytes
18	1.00	0 / 5	WIRTH_Bone marrow
19	1.00	0 / 11	WIRTH_Globus pallidus
20	1.00	0 / 14	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.08	28 / 1115	LU_BPDE 1h DN
2	0.84	63 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

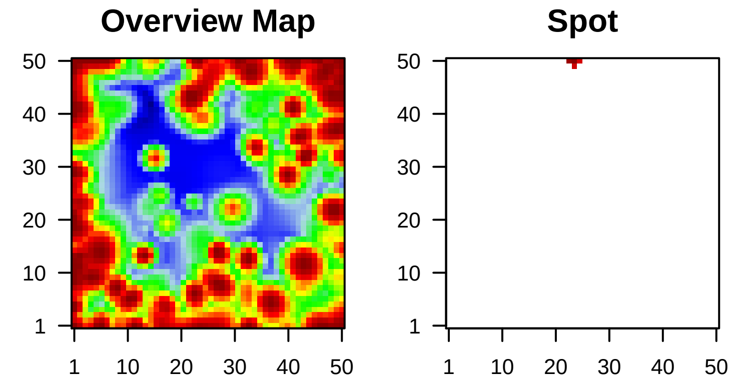
Overexpression Spots

Spot Summary: D

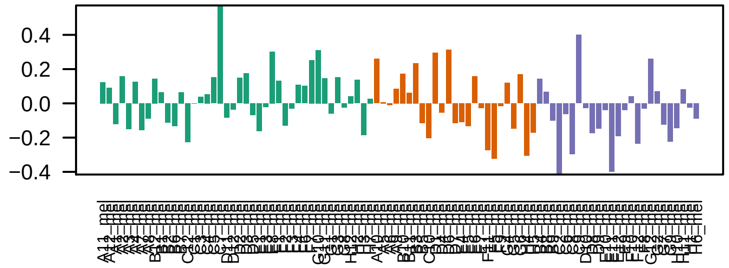
metagenes = 4
genes = 57

<r> metagenes = 0.99
<r> genes = 0.11
beta: r2= 1.06 / log p= −Inf

samples with spot = 10 (10.9 %)
MSC1 : 4 (9.5 %)
MSC2 : 4 (16 %)
MSC3 : 2 (8 %)


Overview Map

Spot

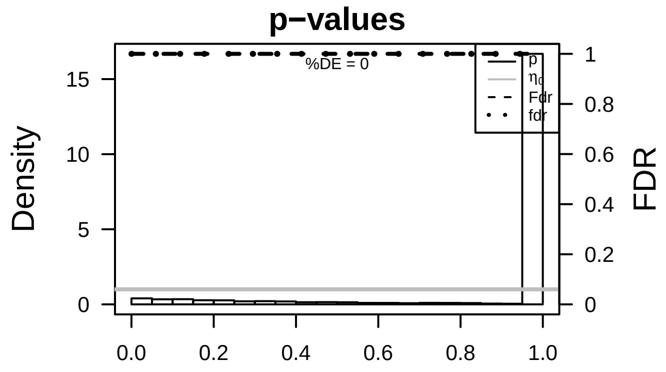


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ZNF57	1.75	−0.34	0.27	ZNF57	zinc finger protein 57 [Source:HGNC Symbol;Acc:HGNC:131
2	ZBED8	1.6	−0.16	0.32	ZBED8	zinc finger, BED−type containing 8 [Source:HGNC Symbol;Ac
3	ZNF581	1.52	−0.4	0.26	ZNF581	zinc finger protein 581 [Source:HGNC Symbol;Acc:HGNC:25
4	DENND6A	1.52	−0.47	0.35	DENND6A	DENN/MADD domain containing 6A [Source:HGNC Symbol;
5	TDRKH	1.51	−0.28	0.3	TDRKH	tudor and KH domain containing [Source:HGNC Symbol;Acc:
6	CPEB2	1.51	−0.47	0.27	CPEB2	cytoplasmic polyadenylation element binding protein 2 [Sourc
7	C16orf93	1.5	−0.17	0.22	C16orf93	chromosome 16 open reading frame 93 [Source:HGNC Symb
8	PLEKHF2	1.48	−0.28	0.36	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE
9	PNPLA4	1.44	−0.52	0.35	PNPLA4	patatin−like phospholipase domain containing 4 [Source:HGN
10	ANKMY2	1.43	−0.4	0.33	ANKMY2	ankyrin repeat and MYND domain containing 2 [Source:HGN
11	INVS	1.41	−0.64	0.28	INVS	inversin [Source:HGNC Symbol;Acc:HGNC:17870]
12	INTS10	1.39	−1.31	0.29	INTS10	integrator complex subunit 10 [Source:HGNC Symbol;Acc:HG
13	CXXC4	1.39	−0.1	0.37	CXXC4	CXXC finger protein 4 [Source:HGNC Symbol;Acc:HGNC:24
14	SLC39A4	1.38	−0.25	0.28	SLC39A4	solute carrier family 39 (zinc transporter), member 4 [Source:
15	CLK4	1.37	−0.51	0.24	CLK4	CDC−like kinase 4 [Source:HGNC Symbol;Acc:HGNC:13659
16	DDX20	1.37	−0.43	0.26	DDX20	DEAD (Asp−Glu−Ala−Asp) box polypeptide 20 [Source:HGN
17	CAPNS1	1.33	−1.11	0.38	CAPNS1	calpain, small subunit 1 [Source:HGNC Symbol;Acc:HGNC:1
18	SLC35B3	1.33	−0.61	0.3	SLC35B3	solute carrier family 35 (adenosine 3'−phospho 5'−phosphos
19	NME6	1.33	−0.84	0.33	NME6	NME/NM23 nucleoside diphosphate kinase 6 [Source:HGNC
20	ATG4B	1.33	−0.92	0.34	ATG4B	autophagy related 4B, cysteine peptidase [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−06	52 / 9482	Colon	TssA_Colon
2	4e−05	30 / 4032	TF	ICGC_Creb1_targets
3	1e−04	33 / 4909	TF	ICGC_Stat5_targets
4	1e−04	32 / 4689	TF	ICGC_Taf1_targets
5	1e−04	48 / 9027	Colon	Tx_Colon
6	2e−04	31 / 4617	TF	ICGC_Tcf12_targets
7	2e−04	32 / 4879	TF	ICGC_Pmlsc71910_targets
8	3e−04	3 / 34	miRN	hsa−miR−517b
9	3e−04	31 / 4706	TF	ICGC_Sp1_targets
10	3e−04	33 / 5200	TF	ICGC_Mta3_targets
11	3e−04	47 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
12	4e−04	48 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
13	5e−04	31 / 4829	TF	ICGC_Nficsc81335_targets
14	6e−04	33 / 5355	TF	ICGC_Pol2_targets
15	7e−04	39 / 6929	Lympl	HOPP_Txn_elongation
16	7e−04	18 / 2136	TF	ICGC_GabpPcr2_targets
17	7e−04	30 / 4682	TF	ICGC_Pol24_targets
18	7e−04	14 / 1418	TF	ICGC_Ets1_targets
19	9e−04	35 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
20	1e−03	3 / 51	miRN	hsa−miR−504
21	1e−03	50 / 10290	Colon	TssWk_Colon
22	1e−03	33 / 5495	TF	ICGC_Yy1_targets
23	1e−03	2 / 13	miRN	hsa−miR−638
24	1e−03	25 / 3700	TF	ICGC_Nfatc1_targets
25	1e−03	28 / 4385	TF	ICGC_Atf2_targets
26	1e−03	16 / 1878	TF	ICGC_Cebpbsc150_targets
27	2e−03	6 / 328	miRN	hsa−miR−18a
28	2e−03	28 / 4414	TF	ICGC_Bclaf101388_targets
29	2e−03	32 / 5374	TF	ICGC_Pax5_targets
30	2e−03	44 / 8580	Colon	TxWk_Colon
31	2e−03	34 / 5890	TF	ICGC_Elf1_targets
32	3e−03	25 / 3924	TF	ICGC_Zeb1_targets
33	3e−03	4 / 161	miRN	hsa−miR−802
34	4e−03	5 / 269	miRN	hsa−miR−30d
35	4e−03	34 / 6114	TF	ICGC_Runx3_targets
36	4e−03	21 / 3081	Brain	Mid_Frontal_Lobe_ZNF
37	4e−03	31 / 5408	TF	ICGC_Pou2_targets
38	4e−03	38 / 7209	Lympl	HOPP_Weak_promoter
39	4e−03	2 / 26	BP	negative regulation of GTPase activity
40	5e−03	3 / 88	miRN	hsa−miR−10a


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.004	2 / 26	negative regulation of GTPase activity
2	0.018	2 / 53	protein homotetramerization
3	0.019	3 / 147	tRNA metabolic process
4	0.019	2 / 55	tRNA processing
5	0.038	1 / 10	cellular response to peptide
6	0.038	1 / 10	heart contraction
7	0.038	1 / 10	maternal placenta development
8	0.038	1 / 10	necroptotic process
9	0.038	1 / 10	pantothenate metabolic process
10	0.038	1 / 10	positive regulation of mitochondrial fission
11	0.038	1 / 10	protein K11−linked deubiquitination
12	0.041	2 / 84	endoplasmic reticulum unfolded protein response
13	0.041	1 / 11	cellular response to arsenic−containing substance
14	0.041	1 / 11	coenzyme A biosynthetic process
15	0.041	1 / 11	DNA methylation involved in gamete generation
16	0.041	1 / 11	hindbrain development
17	0.041	1 / 11	positive regulation of dendritic spine morphogenesis
18	0.041	1 / 11	spliceosomal tri−snRNP complex assembly
19	0.045	1 / 12	mitochondrial fission
20	0.049	1 / 13	COPI coating of Golgi vesicle

Brain

Rank	p−value	#in/all	Geneset
1	3e−04	47 / 9013	Overlap_fetal_midbrain_K9K27me3
2	4e−04	48 / 9330	Overlap_fetal_midbrain_ReprPC
3	9e−04	35 / 5940	Overlap_fetal_midbrain_HetRpts
4	4e−03	21 / 3081	Mid_Frontal_Lobe_ZNF
5	2e−02	44 / 9528	Overlap_fetal_midbrain_Quies
6	3e−02	7 / 765	Mid_Frontal_Lobe_Het
7	2e−01	7 / 1236	Mid_Frontal_Lobe_ReprPCWk
8	3e−01	9 / 1845	Fetal_Quies
9	3e−01	37 / 9020	Overlap_fetal_midbrain_ReprPCWk
10	3e−01	4 / 769	Overlap_fetal_midbrain_ZNF
11	4e−01	6 / 1333	Fetal_ReprPCWk
12	5e−01	1 / 158	Overlap_fetal_midbrain_Het
13	5e−01	4 / 953	Fetal_Enh
14	6e−01	4 / 1013	Fetal_TssP
15	6e−01	6 / 1548	Mid_Frontal_Lobe_K9K27me3
16	6e−01	3 / 786	Fetal_EnhG
17	7e−01	2 / 656	Overlap_fetal_midbrain_EnhP
18	7e−01	3 / 989	Mid_Frontal_Lobe_Quies
19	7e−01	1 / 349	Fetal_ZNF
20	8e−01	3 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	1 / 61	PanCan_Wnt_geneset_nanostring
2	0.2	1 / 70	SHAUGHNESSY_MM high risk
3	0.3	2 / 298	SPANG_BCL6−index2
4	0.6	2 / 489	Lembcke_Normal vs Adenoma
5	0.8	0 / 14	LIU_PROSTATE_CANCER_DN
6	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
7	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
8	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1.0	0 / 12	LIU_BREAST_CANCER
11	1.0	0 / 14	LIU_COMMON_CANCER_GENES
12	1.0	0 / 14	LIU_LIVER_CANCER
13	1.0	0 / 12	LIU_PROSTATE_CANCER_UP
14	1.0	0 / 15	WANG_ER_UP
15	1.0	0 / 5	WANG_ER_DN
16	1.0	0 / 16	WOLFER_overlap genes
17	1.0	0 / 12	BEN−PORATH_DN
18	1.0	0 / 13	BEN−PORATH_UP
19	1.0	0 / 15	GENTLES_modul1
20	1.0	0 / 16	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	0.04	2 / 77	ciliary basal body
2	0.04	1 / 10	mRNA cap binding complex
3	0.04	1 / 10	vacuolar proton−transporting V−type ATPase complex
4	0.04	1 / 11	Gemini of coiled bodies
5	0.04	1 / 11	nonmotile primary cilium
6	0.05	1 / 12	HOPS complex
7	0.05	1 / 12	SMN complex
8	0.05	1 / 13	integrator complex
9	0.05	1 / 13	TCTN−B9D complex
10	0.06	1 / 17	SMN−Sm protein complex
11	0.07	6 / 745	cytoplasmic membrane−bounded vesicle
12	0.07	1 / 19	ciliary base
13	0.07	1 / 19	stereocilium
14	0.07	1 / 20	exon−exon junction complex
15	0.08	46 / 10605	intracellular
16	0.08	2 / 120	mitochondrial outer membrane
17	0.08	1 / 22	cortical cytoskeleton
18	0.09	5 / 616	endosome
19	0.09	1 / 24	polysome
20	0.10	1 / 28	cytoplasmic stress granule

Chr

Rank	p−value	#in/all	Geneset
1	0.07	5 / 576	Chr 9
2	0.17	4 / 558	Chr 4
3	0.22	5 / 840	Chr 17
4	0.24	4 / 649	Chr 16
5	0.27	3 / 469	Chr 8
6	0.35	4 / 775	Chr 12
7	0.40	4 / 838	Chr 3
8	0.50	3 / 687	Chr 6
9	0.50	3 / 689	Chr 7
10	0.50	3 / 696	Chr 5
11	0.57	4 / 1037	Chr 19
12	0.58	1 / 221	Chr 18
13	0.63	2 / 551	Chr X
14	0.63	2 / 552	Chr 10
15	0.70	5 / 1500	Chr 1
16	0.73	1 / 335	Chr 22
17	0.82	2 / 801	Chr 11
18	0.90	2 / 993	Chr 2
19	1.00	0 / 262	Chr 13
20	1.00	0 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	52 / 9482	TssA_Colon
2	1e−04	48 / 9027	Tx_Colon
3	1e−03	50 / 10290	TssWk_Colon
4	2e−03	44 / 8580	TxWk_Colon
5	9e−03	37 / 7203	TssF_Colon
6	3e−02	40 / 8415	Quies3_Colon
7	6e−02	26 / 5155	EnhWk1_Colon
8	6e−02	16 / 2798	TxEnhG1_Colon
9	1e−01	14 / 2698	EnhA_Colon
10	2e−01	5 / 739	TxEnhG2_Colon
11	2e−01	5 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
12	2e−01	41 / 9653	Enh_Colon
13	2e−01	18 / 3812	TssD1_Colon
14	2e−01	3 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
15	2e−01	26 / 5880	TssD2_Colon
16	3e−01	5 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
17	3e−01	1 / 102	Marisa_CRC−cluster−d
18	4e−01	2 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
19	6e−01	1 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
20	7e−01	2 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.8	1 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.13	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
3	0.22	1 / 63	Stuehler_Proteins_up_in_STS
4	0.22	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.22	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
6	0.23	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
7	0.25	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
8	0.30	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	0.73	1 / 332	Up
10	0.75	1 / 356	Down_a
11	0.76	1 / 365	Down_b
12	1.00	0 / 15	VERHAAK_CL subtype
13	1.00	0 / 15	VERHAAK_MES subtype
14	1.00	0 / 16	VERHAAK_NL subtype
15	1.00	0 / 14	VERHAAK_PN subtype
16	1.00	0 / 23	WIRTH_PN subtype
17	1.00	0 / 74	WIRTH_Normal Brain
18	1.00	0 / 9	VERHAAK_Brain
19	1.00	0 / 8	VERHAAK_PN_Brain
20	1.00	0 / 11	Martinez_Glio_hypermeth

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.009	2 / 38	BARRIER_COLON_CANCER_RECURRENCE_UP
2	0.010	5 / 343	THUM_SYSTOLIC_HEART_FAILURE_UP
3	0.011	2 / 41	ZHAN_V2_LATE_DIFFERENTIATION_GENES
4	0.011	2 / 41	KOHOUTEK_CCNT1_TARGETS
5	0.013	4 / 239	HOLLMANN_APOPTOSIS_VIA_CD40_DN
6	0.015	1 / 4	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_DN
7	0.017	2 / 52	BOYLAN_MULTIPLE_MYELOMA_PCA3_DN
8	0.019	1 / 5	CHEN_HOXA5_TARGETS_6HR_DN
9	0.020	5 / 410	SENESE_HDAC1_TARGETS_UP
10	0.021	5 / 416	SHEN_SMARCA2_TARGETS_UP
11	0.026	4 / 292	LIU_SOX4_TARGETS_DN
12	0.027	1 / 7	MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_UP
13	0.030	1 / 8	MARSON_FOXP3_TARGETS_STIMULATED_DN
14	0.031	3 / 178	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
15	0.033	2 / 74	SWEET_KRAS_ONCOGENIC_SIGNATURE
16	0.034	3 / 184	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
17	0.037	2 / 79	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP
18	0.037	4 / 328	MCCABE_BOUND_BY_HOXC6
19	0.038	1 / 10	KEGG_LIMONENE_AND_PINENE_DEGRADATION
20	0.038	1 / 10	BIOCARTA_P35ALZHEIMERS_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.05	2 / 91	HALLMARK_PROTEIN_SECRETION
2	0.14	2 / 174	HALLMARK_HEME_METABOLISM
3	0.25	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
4	0.34	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	0.42	1 / 140	HALLMARK_APOPTOSIS
6	0.42	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
7	0.43	1 / 146	HALLMARK_DNA_REPAIR
8	0.48	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	0.48	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
10	0.52	1 / 188	HALLMARK_ADIPOGENESIS
11	0.52	1 / 188	HALLMARK_MYC_TARGETS_V1
12	0.53	1 / 195	HALLMARK_MITOTIC_SPINDLE
13	0.53	1 / 196	HALLMARK_MTORC1_SIGNALING
14	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	1.00	0 / 176	HALLMARK_HYPOXIA
16	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
18	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	1.00	0 / 196	HALLMARK_G2M_CHECKPOINT
20	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−04	39 / 6929	HOPP_Txn_elongation
2	4e−03	38 / 7209	HOPP_Weak_promoter
3	1e−02	38 / 7592	HOPP_Active_promoter
4	2e−02	28 / 5184	HOPP_Txn_transition
5	8e−02	27 / 5538	HOPP_Weak_txn
6	9e−02	8 / 1218	SPANG_BCR UP
7	1e−01	3 / 294	TARTE_Plasmablast signature
8	1e−01	27 / 5693	HOPP_Weak_enhancer
9	2e−01	1 / 43	LENZ_Stromal signature 2
10	3e−01	28 / 6564	HOPP_Strong_enhancer
11	3e−01	2 / 268	SPANG_IL21 UP
12	3e−01	1 / 89	ROSOLOWSKI_blue total
13	3e−01	1 / 107	SPANG_LPS 6hrs UP
14	6e−01	1 / 256	SPANG_IL21 DN
15	7e−01	1 / 280	SPANG_CD40 6hrs UP
16	8e−01	1 / 410	SPANG_CD40 6hrs DN
17	8e−01	3 / 1128	SPANG_BCR DN
18	9e−01	7 / 2563	HOPP_Heterochrom
19	1e+00	4 / 2211	HOPP_Repetitive
20	1e+00	3 / 2188	HOPP_Poised_promoter

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 27	ribosome binding
2	0.016	9 / 1033	nucleic acid binding
3	0.038	1 / 10	guanylate kinase activity
4	0.038	1 / 10	lamin binding
5	0.038	1 / 10	ribosomal small subunit binding
6	0.041	1 / 11	metal ion transmembrane transporter activity
7	0.045	1 / 12	GTPase inhibitor activity
8	0.045	1 / 12	NAD−dependent histone deacetylase activity (H3−K18 specific)
9	0.049	1 / 13	ATPase activator activity
10	0.049	1 / 13	NAD+ binding
11	0.049	1 / 13	pseudouridine synthase activity
12	0.049	1 / 13	zinc ion transmembrane transporter activity
13	0.060	1 / 16	calcium−dependent cysteine−type endopeptidase activity
14	0.060	1 / 16	nucleoside diphosphate kinase activity
15	0.075	9 / 1365	RNA binding
16	0.092	1 / 25	protein serine/threonine/tyrosine kinase activity
17	0.095	1 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductic
18	0.102	1 / 28	hydrogen ion transmembrane transporter activity
19	0.106	1 / 29	Rab guanyl−nucleotide exchange factor activity
20	0.106	1 / 29	ubiquitin−like protein transferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 34	hsa−miR−517b
2	1e−03	3 / 51	hsa−miR−504
3	1e−03	2 / 13	hsa−miR−638
4	2e−03	6 / 328	hsa−miR−18a
5	3e−03	4 / 161	hsa−miR−802
6	4e−03	5 / 269	hsa−miR−30d
7	5e−03	3 / 88	hsa−miR−10a
8	6e−03	3 / 94	hsa−miR−219−2−3p
9	6e−03	3 / 96	hsa−miR−125b
10	6e−03	3 / 96	hsa−miR−125a−5p
11	6e−03	3 / 98	hsa−miR−21
12	6e−03	3 / 98	hsa−miR−590−5p
13	7e−03	5 / 312	hsa−miR−30e
14	8e−03	2 / 35	hsa−miR−621
15	8e−03	3 / 107	hsa−miR−501−5p
16	8e−03	5 / 328	hsa−miR−520d−3p
17	9e−03	2 / 37	hsa−miR−635
18	1e−02	4 / 237	hsa−miR−214
19	1e−02	2 / 46	hsa−miR−1256
20	2e−02	3 / 135	hsa−miR−28−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−05	30 / 4032	ICGC_Creb1_targets
2	1e−04	33 / 4909	ICGC_Stat5_targets
3	1e−04	32 / 4689	ICGC_Taf1_targets
4	2e−04	31 / 4617	ICGC_Tcf12_targets
5	2e−04	32 / 4879	ICGC_Pmlsc71910_targets
6	3e−04	31 / 4706	ICGC_Sp1_targets
7	3e−04	33 / 5200	ICGC_Mta3_targets
8	5e−04	31 / 4829	ICGC_Nficsc81335_targets
9	6e−04	33 / 5355	ICGC_Pol2_targets
10	7e−04	18 / 2136	ICGC_GabpPcr2_targets
11	7e−04	30 / 4682	ICGC_Pol24_targets
12	7e−04	14 / 1418	ICGC_Ets1_targets
13	1e−03	33 / 5495	ICGC_Yy1_targets
14	1e−03	25 / 3700	ICGC_Nfatc1_targets
15	1e−03	28 / 4385	ICGC_Atf2_targets
16	1e−03	16 / 1878	ICGC_Cebpbsc150_targets
17	2e−03	28 / 4414	ICGC_Bclaf101388_targets
18	2e−03	32 / 5374	ICGC_Pax5_targets
19	2e−03	34 / 5890	ICGC_Elf1_targets
20	3e−03	25 / 3924	ICGC_Zeb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	1 / 11	VAQUERIZAS_Fetal liver
2	0.10	1 / 26	VAQUERIZAS_Liver
3	1.00	0 / 36	VAQUERIZAS_Fetal brain
4	1.00	0 / 41	VAQUERIZAS_Placenta
5	1.00	0 / 33	VAQUERIZAS_Prostate
6	1.00	0 / 29	VAQUERIZAS_Smooth muscle
7	1.00	0 / 45	VAQUERIZAS_Uterus
8	1.00	0 / 143	VAQUERIZAS_General
9	1.00	0 / 9	VAQUERIZAS_Kidney
10	1.00	0 / 23	VAQUERIZAS_Spinal cord
11	1.00	0 / 38	VAQUERIZAS_Whole brain
12	1.00	0 / 37	VAQUERIZAS_Thymus
13	1.00	0 / 40	VAQUERIZAS_Thyroid
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.05	4 / 350	WIRTH_Immune system
2	0.21	2 / 225	PALMER_Granulocytes signature up
3	0.53	1 / 194	PALMER_B−Cell signature up
4	1.00	0 / 32	WIRTH_Pancreas
5	1.00	0 / 11	WIRTH_Sec. lymphoid organs
6	1.00	0 / 11	WIRTH_Prim. lymphoid organs
7	1.00	0 / 13	WIRTH_B−cells
8	1.00	0 / 8	WIRTH_Tonsil
9	1.00	0 / 12	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 5	WIRTH_Bone marrow
12	1.00	0 / 350	WIRTH_Nervous System
13	1.00	0 / 11	WIRTH_Globus pallidus
14	1.00	0 / 14	WIRTH_Telencephalon
15	1.00	0 / 11	WIRTH_Cortex cerebri
16	1.00	0 / 10	WIRTH_Hippocampus
17	1.00	0 / 10	WIRTH_Thalamus
18	1.00	0 / 12	WIRTH_Cerebellum
19	1.00	0 / 107	WIRTH_Testis
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	6 / 1115	LU_BPDE 1h DN
2	0.8	12 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

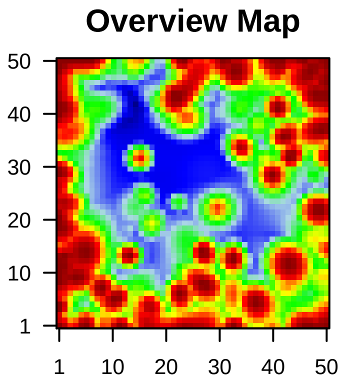
Overexpression Spots

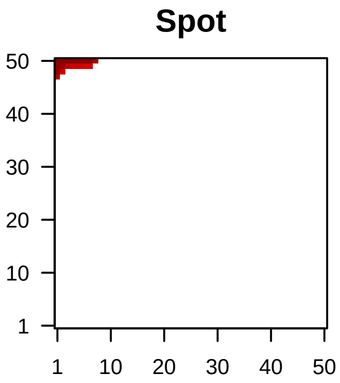
Spot Summary: E

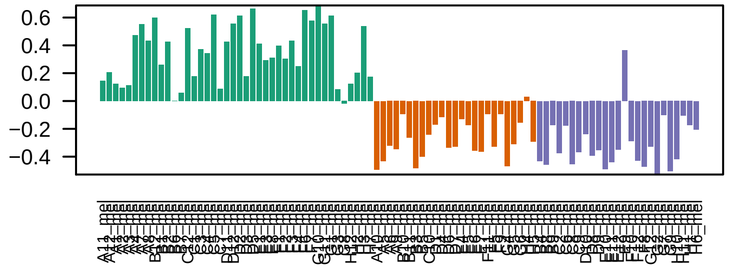
metagenes = 18
genes = 348

<r> metagenes = 0.91
<r> genes = 0.28
beta: r2= 8.96 / log p= −Inf

samples with spot = 30 (32.6 %)
MSC1 : 29 (69 %)
MSC3 : 1 (4 %)





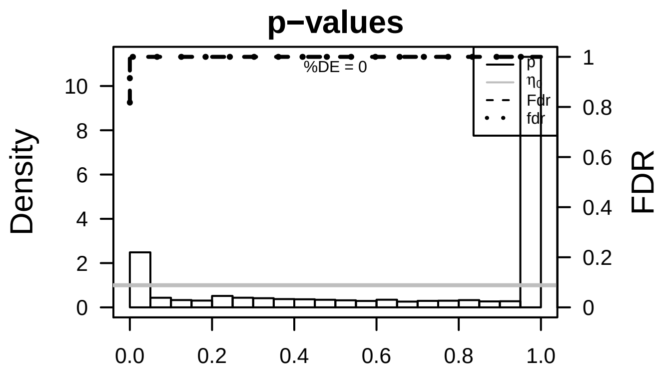


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	UBE2C	2.22	−1.05	0.87	UBE2C	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
2	NUF2	2.2	−0.57	0.84	NUF2	NUF2, NDC80 kinetochore complex component [Source:HGN
3	CDK1	2.16	−1.11	0.84	CDK1	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
4	CCNB1	2.14	−1.08	0.66	CCNB1	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
5	NEK2	2.14	−0.38	0.68	NEK2	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
6	SMCO4	2.1	−0.21	0.34	SMCO4	single−pass membrane protein with coiled−coil domains 4 [S
7	PLK1	2.09	−0.46	0.65	PLK1	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
8	AURKB	2.03	−0.61	0.79	AURKB	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
9	CKAP2L	2.01	−0.57	0.84	CKAP2L	cytoskeleton associated protein 2−like [Source:HGNC Symb
10	CDC20	2	−0.67	0.71	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
11	KIF20A	1.98	−0.39	0.74	KIF20A	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
12	NDC80	1.96	−0.62	0.87	NDC80	NDC80 kinetochore complex component [Source:HGNC Sym
13	DLGAP5	1.93	−0.47	0.78	DLGAP5	discs, large (Drosophila) homolog−associated protein 5 [Sour
14	PRR11	1.93	−0.5	0.75	PRR11	proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
15	RRM2	1.92	−0.76	0.86	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
16	SGOL1	1.91	−0.72	0.75	SGOL1	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
17	HIST1H4E	1.9	−0.46	0.45	HIST1H4E	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
18	CDCA3	1.88	−0.49	0.83	CDCA3	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
19	PBK	1.85	−0.67	0.8	PBK	PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828
20	FAM64A	1.85	−0.57	0.76	FAM64A	family with sequence similarity 64, member A [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	196 / 1110	BP	cell cycle
2	1e−99	119 / 412	BP	mitotic cell cycle
3	1e−99	117 / 142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	1e−99	103 / 197	HM	HALLMARK_E2F_TARGETS
5	1e−99	12 / 16	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	1e−99	234 / 1192	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	1e−99	202 / 1251	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	1e−99	129 / 505	GSE	BERENJENO_TRANSFORMED_BY_RHOA_UP
9	1e−99	98 / 139	GSE	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	1e−99	121 / 390	GSE	PUJANA_BRCA2_PCC_NETWORK
11	1e−99	167 / 944	GSE	NUYTTEN_EZH2_TARGETS_DN
12	1e−99	154 / 616	GSE	BENPORATH_CYCLING_GENES
13	1e−99	177 / 700	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
14	1e−99	114 / 327	GSE	BLUM_RESPONSE_TO_SALIRASIB_DN
15	1e−99	91 / 145	GSE	CHANG_CYCLING_GENES
16	1e−99	135 / 436	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	1e−99	117 / 267	GSE	ZHANG_TLX_TARGETS_60HR_DN
18	1e−99	136 / 242	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
19	1e−99	163 / 305	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
20	1e−99	218 / 550	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
21	3e−97	85 / 162	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
22	5e−95	70 / 96	GSE	CROONQUIST_IL6_DEPRIVATION_DN
23	2e−92	81 / 155	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
24	4e−92	75 / 124	GSE	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
25	2e−89	118 / 489	Canc	Lembcke_Normal vs Adenoma
26	3e−88	95 / 270	GSE	BASAKI_YBX1_TARGETS_UP
27	4e−88	66 / 93	GSE	KONG_E2F3_TARGETS
28	8e−88	106 / 373	GSE	VECCHI_GASTRIC_CANCER_EARLY_UP
29	1e−87	97 / 291	GSE	HORIUCHI_WTAP_TARGETS_DN
30	3e−87	67 / 99	GSE	BURTON_ADIPOGENESIS_3
31	3e−86	62 / 81	GSE	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
32	3e−86	69 / 110	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
33	8e−86	106 / 388	GSE	REACTOME_CELL_CYCLE
34	3e−84	83 / 198	GSE	FUJII_YBX1_TARGETS_DN
35	3e−84	132 / 724	GSE	PUJANA_CHEK2_PCC_NETWORK
36	8e−84	116 / 517	GSE	FEVR_CTNNB1_TARGETS_DN
37	1e−82	78 / 171	GSE	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
38	1e−81	94 / 301	GSE	REACTOME_CELL_CYCLE_MITOTIC
39	3e−81	64 / 99	GSE	LEE_EARLY_T_LYMPHOCYTE_UP
40	6e−79	82 / 216	GSE	MARKEY_RB1_ACUTE_LOF_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.1	5 / 111	HORVATH_aging_genes meth UP
2	0.7	2 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−99	196 / 1110	cell cycle
2	1e−99	119 / 412	mitotic cell cycle
3	2e−76	128 / 768	DNA metabolic process
4	3e−65	83 / 312	mitotic nuclear division
5	7e−62	89 / 409	cell division
6	2e−45	52 / 160	chromosome segregation
7	6e−45	49 / 139	DNA replication
8	7e−45	94 / 721	chromosome organization
9	1e−28	21 / 29	DNA strand elongation involved in DNA replication
10	1e−26	48 / 298	DNA repair
11	2e−25	34 / 139	G1/S transition of mitotic cell cycle
12	1e−22	178 / 3980	cellular nitrogen compound metabolic process
13	4e−19	14 / 20	telomere maintenance via semi−conservative replication
14	8e−18	14 / 23	DNA replication initiation
15	2e−17	14 / 24	telomere maintenance via recombination
16	5e−17	26 / 133	G2/M transition of mitotic cell cycle
17	3e−16	16 / 41	CENP−A containing nucleosome assembly
18	2e−15	12 / 20	mitotic sister chromatid segregation
19	4e−15	49 / 581	cytoskeleton organization
20	5e−15	18 / 65	telomere maintenance

Brain

Rank	p−value	#in/all	Geneset
1	6e−16	286 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−13	93 / 1845	Fetal_Quies
3	2e−06	42 / 831	Fetal_HetRpts
4	3e−06	251 / 9013	Overlap_fetal_midbrain_K9K27me3
5	9e−04	43 / 1122	Fetal_K9K27me3
6	8e−03	45 / 1333	Fetal_ReprPCWk
7	2e−01	6 / 163	Fetal_ReprPC
8	3e−01	26 / 989	Mid_Frontal_Lobe_Quies
9	4e−01	31 / 1236	Mid_Frontal_Lobe_ReprPCWk
10	4e−01	6 / 229	Mid_Frontal_Lobe_TxTrans
11	5e−01	11 / 468	Mid_Frontal_Lobe_TssF
12	7e−01	207 / 9020	Overlap_fetal_midbrain_ReprPCWk
13	7e−01	3 / 158	Overlap_fetal_midbrain_Het
14	7e−01	6 / 304	Fetal_Het
15	7e−01	20 / 953	Fetal_Enh
16	7e−01	22 / 1050	Fetal_EnhP
17	7e−01	3 / 166	Mid_Frontal_Lobe_Tx
18	9e−01	9 / 534	Mid_Frontal_Lobe_EnhG
19	9e−01	2 / 156	Mid_Frontal_Lobe_TssA
20	9e−01	5 / 349	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	12 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	2e−89	118 / 489	Lembcke_Normal vs Adenoma
3	2e−31	8 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	2e−12	14 / 47	PanCan_DNARepair_geneset_nanostring
5	5e−12	20 / 120	PanCan_CC+Apop_geneset_nanostring
6	9e−10	8 / 16	WOLFER_overlap genes
7	1e−08	9 / 29	KUIPER_MM good survival
8	3e−08	6 / 10	GENTLES_modul3
9	1e−07	10 / 48	KUIPER_MM poor survival
10	2e−07	2 / 15	RHODES_CANCER_META_SIGNATURE
11	6e−07	11 / 70	SHAUGHNESSY_MM high risk
12	7e−06	5 / 13	BEN−PORATH_UP
13	6e−03	3 / 16	GENTLES_modul2
14	4e−02	2 / 14	LIU_COMMON_CANCER_GENES
15	5e−02	2 / 15	GENTLES_modul1
16	5e−02	2 / 16	GENTLES_modul6
17	8e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
18	1e−01	5 / 113	PanCan_Driver_Gene_geneset_nanostring
19	2e−01	2 / 40	PanCan_HK_geneset_nanostring
20	2e−01	1 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	3e−74	119 / 663	chromosome
2	2e−47	264 / 5696	nucleus
3	4e−42	169 / 2577	nucleoplasm
4	3e−27	26 / 59	chromosome, centromeric region
5	2e−25	27 / 75	condensed chromosome kinetochore
6	7e−23	46 / 331	nuclear chromosome
7	3e−22	155 / 3214	protein complex
8	3e−21	26 / 93	spindle pole
9	5e−21	318 / 10605	intracellular
10	6e−21	95 / 1465	cytoskeleton
11	2e−20	307 / 9988	organelle
12	7e−19	21 / 65	kinetochore
13	5e−18	50 / 512	microtubule organizing center
14	3e−17	42 / 377	centrosome
15	1e−16	24 / 113	spindle
16	2e−14	22 / 115	midbody
17	2e−12	13 / 38	spindle microtubule
18	2e−11	320 / 11774	cell
19	4e−10	105 / 2507	cytosol
20	8e−10	16 / 97	chromatin

Chr

Rank	p−value	#in/all	Geneset
1	0.003	24 / 558	Chr 4
2	0.007	20 / 465	Chr 15
3	0.009	13 / 262	Chr 13
4	0.035	10 / 221	Chr 18
5	0.095	12 / 335	Chr 22
6	0.143	23 / 775	Chr 12
7	0.328	11 / 398	Chr 20
8	0.363	18 / 696	Chr 5
9	0.413	20 / 801	Chr 11
10	0.472	4 / 151	Chr 21
11	0.499	20 / 840	Chr 17
12	0.529	13 / 552	Chr 10
13	0.531	35 / 1500	Chr 1
14	0.643	10 / 462	Chr 14
15	0.645	15 / 687	Chr 6
16	0.660	14 / 649	Chr 16
17	0.762	17 / 838	Chr 3
18	0.794	11 / 576	Chr 9
19	0.823	13 / 689	Chr 7
20	0.926	7 / 469	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−18	57 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	5e−11	49 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
3	6e−08	284 / 10290	TssWk_Colon
4	2e−06	262 / 9482	TssA_Colon
5	2e−04	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
6	1e−03	197 / 7203	TssF_Colon
7	6e−03	220 / 8415	Quies3_Colon
8	8e−03	3 / 18	Boland_CRC−MSI−A6−A10
9	1e−02	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
10	1e−02	2 / 8	Boland_CRC−MMR−system
11	2e−02	2 / 9	KIM_MSI−in−EC
12	5e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
13	5e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
14	1e−01	1 / 5	Budinska_C_CIMP−H−like_UP
15	1e−01	99 / 3812	TssD1_Colon
16	2e−01	1 / 8	Marisa_CRC−C1
17	2e−01	1 / 8	Marisa_CRC−C3
18	2e−01	1 / 8	Marisa_CRC−C6
19	2e−01	4 / 102	Marisa_CRC−cluster−d
20	2e−01	3 / 71	Marisa_CRC−cluster−g

Disease

Rank	p−value	#in/all	Geneset
1	5e−38	69 / 435	GUDJ_psoriasis up
2	1e+00	2 / 294	GUDJ_psoriasis down
3	1e+00	0 / 11	BCHETNIA_EBM up
4	1e+00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1e−99	117 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−31	27 / 49	developing astrocytes
3	1e−27	28 / 71	Weller_LGG_gradeII−vs−III_DOWN
4	2e−07	11 / 62	cultured astroglia vs. in vivo astrocytes
5	1e−06	4 / 5	Phillips Prolif up vs PN & MES
6	4e−05	39 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
7	1e−02	4 / 39	OPC
8	3e−02	5 / 75	Weller_LGG_A_vs_O_DOWN
9	5e−02	13 / 332	Up
10	9e−02	5 / 103	GIEZELT_GBM_WT_up_VS_mut
11	2e−01	1 / 9	Mukasa_UP_in_GBM
12	2e−01	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
13	3e−01	1 / 16	KIM deleted & downregulated in LTS
14	3e−01	2 / 49	OL vs. MOG− OL
15	3e−01	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
16	4e−01	1 / 22	KIM prognostic signature LTS vs. STS
17	5e−01	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
18	5e−01	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
19	5e−01	4 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
20	6e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	12 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	1e−99	234 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	1e−99	202 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	1e−99	129 / 505	BERENJENO_TRANSFORMED_BY_RHOA_UP
5	1e−99	98 / 139	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	1e−99	121 / 390	PUJANA_BRCA2_PCC_NETWORK
7	1e−99	167 / 944	NUYTTEN_EZH2_TARGETS_DN
8	1e−99	154 / 616	BENPORATH_CYCLING_GENES
9	1e−99	177 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	1e−99	114 / 327	BLUM_RESPONSE_TO_SALIRASIB_DN
11	1e−99	91 / 145	CHANG_CYCLING_GENES
12	1e−99	135 / 436	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
13	1e−99	117 / 267	ZHANG_TLX_TARGETS_60HR_DN
14	1e−99	136 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
15	1e−99	163 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
16	1e−99	218 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
17	3e−97	85 / 162	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	5e−95	70 / 96	CROONQUIST_IL6_DEPRIVATION_DN
19	2e−92	81 / 155	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
20	4e−92	75 / 124	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR

HM

Rank	p−value	#in/all	Geneset
1	1e−99	103 / 197	HALLMARK_E2F_TARGETS
2	2e−78	79 / 196	HALLMARK_G2M_CHECKPOINT
3	3e−22	36 / 195	HALLMARK_MITOTIC_SPINDLE
4	2e−08	20 / 188	HALLMARK_MYC_TARGETS_V1
5	2e−06	15 / 146	HALLMARK_DNA_REPAIR
6	2e−06	12 / 95	HALLMARK_SPERMATOGENESIS
7	2e−03	6 / 57	HALLMARK_MYC_TARGETS_V2
8	6e−03	11 / 196	HALLMARK_MTORC1_SIGNALING
9	7e−03	10 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	5e−02	7 / 140	HALLMARK_APOPTOSIS
11	1e−01	7 / 183	HALLMARK_GLYCOLYSIS
12	2e−01	4 / 93	HALLMARK_PEROXISOME
13	2e−01	5 / 141	HALLMARK_FATTY_ACID_METABOLISM
14	2e−01	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	3e−01	5 / 146	HALLMARK_UV_RESPONSE_UP
16	4e−01	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
17	4e−01	5 / 174	HALLMARK_HEME_METABOLISM
18	4e−01	5 / 181	HALLMARK_P53_PATHWAY
19	5e−01	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
20	5e−01	4 / 162	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−37	277 / 6929	HOPP_Txn_elongation
2	4e−35	56 / 294	TARTE_Plasmablast signature
3	4e−20	204 / 5184	HOPP_Txn_transition
4	8e−19	257 / 7592	HOPP_Active_promoter
5	2e−12	21 / 129	DAVE_BL−vs−DLBCL
6	1e−09	63 / 1218	SPANG_BCR UP
7	2e−08	14 / 89	ROSOLOWSKI_blue total
8	2e−05	192 / 6564	HOPP_Strong_enhancer
9	7e−05	204 / 7209	HOPP_Weak_promoter
10	8e−03	2 / 6	MASCQUE_mBL UP
11	4e−02	11 / 256	SPANG_IL21 DN
12	7e−02	2 / 19	DAVE_c−myc BL UP
13	1e−01	143 / 5693	HOPP_Weak_enhancer
14	2e−01	2 / 30	TARTE_B−cell signature
15	2e−01	8 / 247	ZHANG_DLBCL mutated
16	3e−01	1 / 13	WRIGHT_GCB UP
17	3e−01	1 / 13	YAMANE_AICDA_targets_recruited
18	3e−01	1 / 14	Subero_mBL_hypo_meth
19	3e−01	1 / 16	DAVE_BL Inter
20	3e−01	2 / 50	SPANG_BAFF 9hrs DN

MF

Rank	p−value	#in/all	Geneset
1	6e−15	277 / 8984	protein binding
2	1e−12	73 / 1309	ATP binding
3	3e−11	33 / 364	ATPase activity
4	6e−11	93 / 2037	DNA binding
5	6e−10	20 / 156	microtubule binding
6	8e−10	14 / 71	single−stranded DNA binding
7	6e−08	12 / 69	microtubule motor activity
8	7e−08	28 / 376	chromatin binding
9	2e−07	8 / 29	DNA−directed DNA polymerase activity
10	2e−06	16 / 167	helicase activity
11	4e−06	9 / 54	damaged DNA binding
12	1e−05	6 / 23	DNA helicase activity
13	1e−05	14 / 152	histone binding
14	2e−05	21 / 316	protein kinase binding
15	2e−05	5 / 16	ATP−dependent microtubule motor activity, plus−end−directed
16	3e−05	14 / 164	nuclease activity
17	5e−05	6 / 29	ATP−dependent DNA helicase activity
18	1e−04	6 / 34	DNA−dependent ATPase activity
19	2e−04	4 / 13	nucleocytoplasmic transporter activity
20	2e−04	46 / 1149	enzyme binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	18 / 328	hsa−miR−520d−3p
2	8e−04	18 / 329	hsa−miR−302d
3	2e−03	17 / 327	hsa−miR−590−3p
4	2e−03	17 / 328	hsa−miR−18a
5	2e−03	9 / 119	hsa−miR−217
6	3e−03	8 / 101	hsa−miR−325
7	3e−03	8 / 103	hsa−miR−1284
8	3e−03	8 / 104	hsa−miR−210
9	3e−03	7 / 83	hsa−miR−576−5p
10	3e−03	11 / 179	hsa−miR−582−5p
11	4e−03	9 / 135	hsa−miR−28−5p
12	5e−03	14 / 272	hsa−miR−520b
13	6e−03	8 / 115	hsa−miR−154
14	6e−03	9 / 140	hsa−miR−522
15	6e−03	15 / 307	hsa−miR−302b
16	6e−03	13 / 250	hsa−miR−520a−3p
17	6e−03	5 / 50	hsa−miR−610
18	6e−03	5 / 50	hsa−miR−549
19	6e−03	10 / 168	hsa−miR−520h
20	6e−03	13 / 251	hsa−miR−548l

Pathw Act

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 15	BENTINK_ras.6
2	2e−03	3 / 12	GUSTAFSON_PI3K_UP
3	3e−02	2 / 12	BENTINK_e2f3.2
4	3e−02	2 / 12	BENTINK_ras.1
5	3e−01	1 / 13	BENTINK_myc.1
6	3e−01	1 / 14	BENTINK_src.2
7	1e+00	0 / 13	GUSTAFSON_PI3K_DN
8	1e+00	0 / 14	BENTINK_e2f3.1
9	1e+00	0 / 9	BENTINK_ras.4
10	1e+00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−08	58 / 1171	KIM_MYC targets
2	2e−07	158 / 4829	ICGC_Nficsc81335_targets
3	3e−06	150 / 4689	ICGC_Taf1_targets
4	9e−06	131 / 4032	ICGC_Creb1_targets
5	2e−05	58 / 1418	ICGC_Ets1_targets
6	6e−05	8 / 59	MYC_Targets UP
7	1e−04	147 / 4879	ICGC_Pmlsc71910_targets
8	2e−04	142 / 4706	ICGC_Sp1_targets
9	5e−04	141 / 4774	ICGC_Foxm1_targets
10	9e−04	155 / 5408	ICGC_Pou2_targets
11	9e−04	137 / 4682	ICGC_Pol24_targets
12	1e−03	3 / 9	MYC_DNA repair UP
13	1e−03	129 / 4385	ICGC_Atf2_targets
14	1e−03	59 / 1701	HEBENSTREIT_high expression TF
15	2e−03	165 / 5890	ICGC_Elf1_targets
16	2e−03	63 / 1878	ICGC_Cebpbsc150_targets
17	3e−03	139 / 4909	ICGC_Stat5_targets
18	4e−03	131 / 4617	ICGC_Tcf12_targets
19	5e−03	167 / 6114	ICGC_Runx3_targets
20	5e−03	2 / 5	MYC_Cell growth and proliferation UP

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 11	VAQUERIZAS_Fetal liver
2	0.05	3 / 37	VAQUERIZAS_Thymus
3	0.06	3 / 38	VAQUERIZAS_Testis
4	0.12	2 / 26	VAQUERIZAS_Liver
5	0.30	1 / 15	VAQUERIZAS_Bone marrow
6	0.75	1 / 59	VAQUERIZAS_Whole blood
7	0.85	2 / 143	VAQUERIZAS_General
8	1.00	0 / 36	VAQUERIZAS_Fetal brain
9	1.00	0 / 41	VAQUERIZAS_Placenta
10	1.00	0 / 33	VAQUERIZAS_Prostate
11	1.00	0 / 29	VAQUERIZAS_Smooth muscle
12	1.00	0 / 45	VAQUERIZAS_Uterus
13	1.00	0 / 9	VAQUERIZAS_Kidney
14	1.00	0 / 23	VAQUERIZAS_Spinal cord
15	1.00	0 / 38	VAQUERIZAS_Whole brain
16	1.00	0 / 40	VAQUERIZAS_Thyroid
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 29	VAQUERIZAS_Fetal lung
19	1.00	0 / 58	VAQUERIZAS_Lung
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.002	3 / 12	WIRTH_Thymus
2	0.229	1 / 11	WIRTH_Prim. lymphoid organs
3	0.247	1 / 12	WIRTH_Cerebellum
4	0.301	6 / 194	PALMER_B−Cell signature up
5	0.576	8 / 350	WIRTH_Immune system
6	0.750	2 / 114	PALMER_T−Cell signature up
7	0.966	4 / 350	WIRTH_Nervous System
8	0.970	2 / 225	PALMER_Granulocytes signature up
9	1.000	0 / 32	WIRTH_Pancreas
10	1.000	0 / 11	WIRTH_Sec. lymphoid organs
11	1.000	0 / 13	WIRTH_B−cells
12	1.000	0 / 8	WIRTH_Tonsil
13	1.000	0 / 12	WIRTH_Lymphocytes
14	1.000	0 / 5	WIRTH_Bone marrow
15	1.000	0 / 11	WIRTH_Globus pallidus
16	1.000	0 / 14	WIRTH_Telencephalon
17	1.000	0 / 11	WIRTH_Cortex cerebri
18	1.000	0 / 10	WIRTH_Hippocampus
19	1.000	0 / 10	WIRTH_Thalamus
20	1.000	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	27 / 1115	LU_BPDE 1n DN
2	1.0	61 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: F

metagenes = 12
genes = 81

<r> metagenes = 0.96
<r> genes = 0.1
beta: r2= 1.19 / log p= −Inf

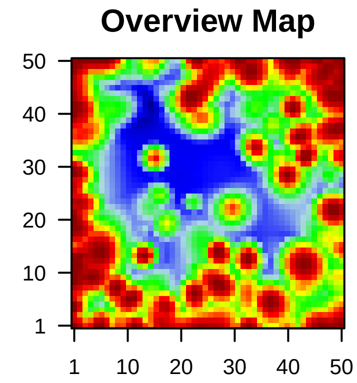
samples with spot = 11 (12 %)
MSC1 : 2 (4.8 %)
MSC2 : 5 (20 %)
MSC3 : 4 (16 %)

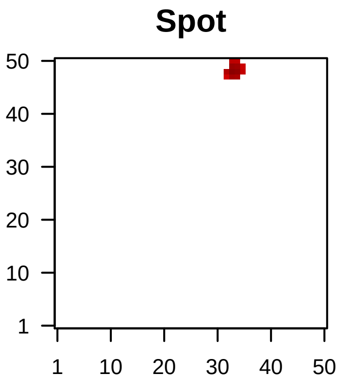
Spot Genelist

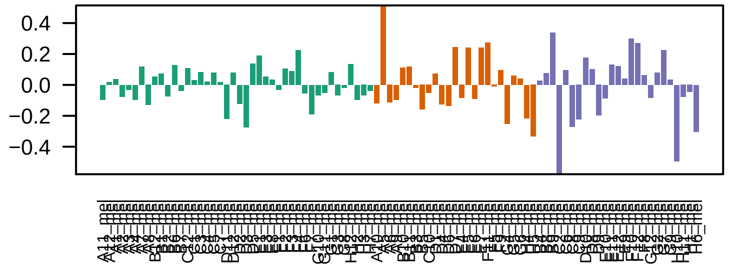
Rank	ID	max e	min e	r	Symbol	Description
1	SLC25A35	1.83	−0.09	0.35	SLC25A35	solute carrier family 25, member 35 [Source:HGNC Symbol;A
2	FBXW4	1.8	−0.4	0.22	FBXW4	F−box and WD repeat domain containing 4 [Source:HGNC Sy
3	RAD51B	1.8	−0.76	0.28	RAD51B	RAD51 paralog B [Source:HGNC Symbol;Acc:HGNC:9822]
4	PLD6	1.73	−0.29	0.35	PLD6	phospholipase D family, member 6 [Source:HGNC Symbol;Ac
5	ENPP5	1.7	−0.2	0.33	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putati
6	DHRS12	1.62	−0.43	0.27	DHRS12	dehydrogenase/reductase (SDR family) member 12 [Source:H
7	KIAA1211	1.58	−0.17	0.24	KIAA1211	KIAA1211 [Source:HGNC Symbol;Acc:HGNC:29219]
8	BCHE	1.54	−0.55	0.27	BCHE	butyrylcholinesterase [Source:HGNC Symbol;Acc:HGNC:983
9	UBXN8	1.53	−0.63	0.19	UBXN8	UBX domain protein 8 [Source:HGNC Symbol;Acc:HGNC:30
10	UBE3D	1.5	−0.35	0.36	UBE3D	ubiquitin protein ligase E3D [Source:HGNC Symbol;Acc:HGN
11	IGF2BP3	1.5	−0.64	0.24	IGF2BP3	insulin−like growth factor 2 mRNA binding protein 3 [Source:H
12	USP30	1.47	−0.19	0.25	USP30	ubiquitin specific peptidase 30 [Source:HGNC Symbol;Acc:H
13	RBM41	1.46	−0.67	0.27	RBM41	RNA binding motif protein 41 [Source:HGNC Symbol;Acc:HG
14	TOR3A	1.45	−0.15	0.29	TOR3A	torsin family 3, member A [Source:HGNC Symbol;Acc:HGNC
15	SLC1A3	1.44	−0.21	0.3	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter
16	LRAT	1.42	−0.11	0.23	LRAT	lecithin retinol acyltransferase (phosphatidylcholine−−retinol
17	TTC4	1.42	−0.66	0.21	TTC4	tetratricopeptide repeat domain 4 [Source:HGNC Symbol;Acc
18	TGS1	1.4	−0.49	0.27	TGS1	trimethylguanosine synthase 1 [Source:HGNC Symbol;Acc:H
19	ZNF708	1.37	−0.25	0.32	ZNF708	zinc finger protein 708 [Source:HGNC Symbol;Acc:HGNC:12
20	PCGF1	1.37	−0.72	0.41	PCGF1	polycomb group ring finger 1 [Source:HGNC Symbol;Acc:HG

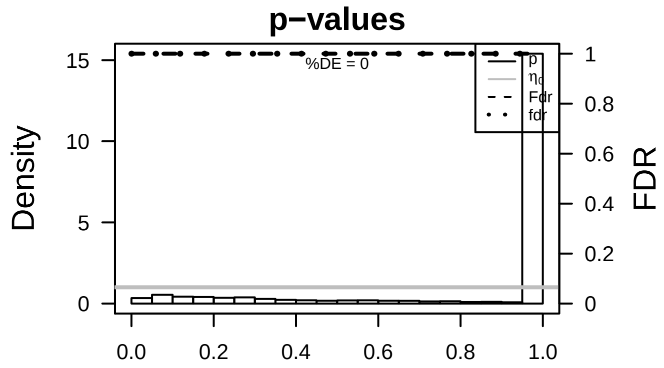
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−06	67 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
2	3e−05	67 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	2e−04	62 / 8580	Colon	TxWk_Colon
4	2e−04	3 / 23	BP	ncRNA metabolic process
5	3e−04	66 / 9528	Brain	Overlap_fetal_midbrain_Quies
6	3e−04	9 / 393	BP	mRNA processing
7	3e−04	53 / 6929	Lymp	HOPP_Txn_elongation
8	5e−04	63 / 9027	Colon	Tx_Colon
9	5e−04	3 / 29	BP	spliceosomal snRNP assembly
10	5e−04	65 / 9482	Colon	TssA_Colon
11	8e−04	17 / 1365	MF	RNA binding
12	9e−04	14 / 1007	MF	poly(A) RNA binding
13	1e−03	55 / 7592	Lymp	HOPP_Active_promoter
14	1e−03	46 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
15	1e−03	2 / 10	MF	protein phosphatase type 1 regulator activity
16	1e−03	8 / 394	MF	catalytic activity
17	2e−03	16 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
18	2e−03	2 / 12	BP	histone H2A monoubiquitination
19	2e−03	2 / 12	BP	mitochondrial fusion
20	2e−03	3 / 47	miRN	hsa−miR−518e*
21	2e−03	3 / 47	GSEA	REACTOME_METABOLISM_OF_NON_CODING_RNA
22	2e−03	5 / 167	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
23	2e−03	12 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
24	2e−03	4 / 104	miRN	hsa−miR−525−5p
25	2e−03	7 / 341	GSEA	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
26	2e−03	61 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
27	3e−03	2 / 14	BP	natural killer cell mediated cytotoxicity
28	3e−03	4 / 108	CC	late endosome
29	3e−03	2 / 15	BP	regulation of DNA−templated transcription, elongation
30	3e−03	16 / 1400	TF	ICGC_Myc_targets
31	3e−03	2 / 16	BP	cell separation after cytokinesis
32	3e−03	2 / 16	BP	regulation of centrosome duplication
33	4e−03	10 / 681	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
34	4e−03	14 / 1171	TF	KIM_MYC targets
35	4e−03	3 / 60	BP	mRNA transport
36	5e−03	14 / 1201	CC	endoplasmic reticulum
37	5e−03	3 / 65	GSEA	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
38	5e−03	4 / 131	BP	ribonucleoprotein complex assembly
39	6e−03	2 / 21	BP	positive regulation of viral genome replication
40	6e−03	2 / 22	GSEA	CHEOK_RESPONSE_TO_HD_MTX_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 23	ncRNA metabolic process
2	3e−04	9 / 393	mRNA processing
3	5e−04	3 / 29	spliceosomal snRNP assembly
4	2e−03	2 / 12	histone H2A monoubiquitination
5	2e−03	2 / 12	mitochondrial fusion
6	3e−03	2 / 14	natural killer cell mediated cytotoxicity
7	3e−03	2 / 15	regulation of DNA−templated transcription, elongation
8	3e−03	2 / 16	cell separation after cytokinesis
9	3e−03	2 / 16	regulation of centrosome duplication
10	4e−03	3 / 60	mRNA transport
11	5e−03	4 / 131	ribonucleoprotein complex assembly
12	6e−03	2 / 21	positive regulation of viral genome replication
13	1e−02	14 / 1325	catabolic process
14	1e−02	5 / 251	nucleocytoplasmic transport
15	1e−02	2 / 31	7−methylguanosine mRNA capping
16	1e−02	2 / 32	RNA phosphodiester bond hydrolysis, endonucleolytic
17	2e−02	18 / 1975	cellular protein modification process
18	2e−02	2 / 37	regulation of translational initiation
19	2e−02	2 / 40	ER−associated ubiquitin−dependent protein catabolic process
20	2e−02	2 / 42	positive regulation of viral transcription

Brain

Rank	p−value	#in/all	Geneset
1	7e−06	67 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−05	67 / 9330	Overlap_fetal_midbrain_ReprPC
3	3e−04	66 / 9528	Overlap_fetal_midbrain_Quies
4	1e−03	46 / 5940	Overlap_fetal_midbrain_HetRpts
5	2e−03	61 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	2e−02	7 / 534	Mid_Frontal_Lobe_EnhG
7	6e−02	23 / 3081	Mid_Frontal_Lobe_ZNF
8	6e−02	3 / 163	Fetal_ReprPC
9	8e−02	4 / 304	Fetal_Het
10	1e−01	7 / 769	Overlap_fetal_midbrain_ZNF
11	2e−01	8 / 1050	Fetal_EnhP
12	2e−01	2 / 166	Mid_Frontal_Lobe_Tx
13	4e−01	4 / 564	Mid_Frontal_Lobe_EnhP
14	6e−01	1 / 156	Mid_Frontal_Lobe_TssA
15	6e−01	5 / 953	Fetal_Enh
16	6e−01	2 / 383	Fetal_Tx
17	6e−01	4 / 786	Fetal_EnhG
18	6e−01	5 / 989	Mid_Frontal_Lobe_Quies
19	7e−01	4 / 831	Fetal_HetRpts
20	7e−01	5 / 1065	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	4 / 298	SPANG_BCL6−index2
2	0.08	1 / 16	GENTLES_modul14
3	0.29	0 / 15	RHODES_CANCER_META_SIGNATURE
4	0.30	0 / 14	LIU_COMMON_CANCER_GENES
5	0.36	1 / 82	PanCan_TXmisReg_geneset_nanostring
6	0.48	1 / 121	PanCan_MAPK_geneset_nanostring
7	0.56	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.62	1 / 180	SPANG_LPS−index2
9	0.88	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.89	1 / 401	Lembcke_Colonic Inflammation
11	0.93	1 / 489	Lembcke_Normal vs Adenoma
12	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1.00	0 / 12	LIU_BREAST_CANCER
15	1.00	0 / 14	LIU_LIVER_CANCER
16	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
17	1.00	0 / 15	WANG_ER_UP
18	1.00	0 / 5	WANG_ER_DN
19	1.00	0 / 16	WOLFER_overlap genes
20	1.00	0 / 12	BEN−PORATH_DN

CC

Rank	p−value	#in/all	Geneset
1	0.003	4 / 108	late endosome
2	0.005	14 / 1201	endoplasmic reticulum
3	0.015	4 / 175	early endosome
4	0.027	2 / 47	Cajal body
5	0.027	3 / 120	mitochondrial outer membrane
6	0.043	3 / 145	endoplasmic reticulum lumen
7	0.048	7 / 616	endosome
8	0.053	1 / 10	methylosome
9	0.053	1 / 10	mRNA cap binding complex
10	0.053	1 / 10	mRNA cleavage and polyadenylation specificity factor complex
11	0.053	1 / 10	nuclear pore outer ring
12	0.058	1 / 11	nuclear periphery
13	0.063	1 / 12	STAGA complex
14	0.064	3 / 170	nuclear speck
15	0.068	1 / 13	transcription factor TFTC complex
16	0.071	2 / 81	late endosome membrane
17	0.073	1 / 14	Cul4−RING E3 ubiquitin ligase complex
18	0.077	51 / 8205	cytoplasm
19	0.078	1 / 15	alpha−amino−3−hydroxy−5−methyl−4−isoxazolepropionic acid selective gluta
20	0.083	1 / 16	Ada2/Gcn5/Ada3 transcription activator complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	9 / 775	Chr 12
2	0.20	2 / 151	Chr 21
3	0.26	6 / 801	Chr 11
4	0.29	10 / 1500	Chr 1
5	0.30	6 / 838	Chr 3
6	0.31	5 / 687	Chr 6
7	0.35	4 / 552	Chr 10
8	0.46	3 / 462	Chr 14
9	0.47	3 / 469	Chr 8
10	0.54	2 / 335	Chr 22
11	0.58	3 / 558	Chr 4
12	0.63	5 / 993	Chr 2
13	0.67	5 / 1037	Chr 19
14	0.67	4 / 840	Chr 17
15	0.72	2 / 465	Chr 15
16	0.72	3 / 689	Chr 7
17	0.76	1 / 262	Chr 13
18	0.87	2 / 649	Chr 16
19	0.89	1 / 398	Chr 20
20	0.89	2 / 696	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	62 / 8580	TxWk_Colon
2	5e−04	63 / 9027	Tx_Colon
3	5e−04	65 / 9482	TssA_Colon
4	2e−02	61 / 9653	Enh_Colon
5	7e−02	46 / 7203	TssF_Colon
6	1e−01	61 / 10290	TssWk_Colon
7	2e−01	50 / 8415	Quies3_Colon
8	2e−01	18 / 2698	EnhA_Colon
9	2e−01	1 / 43	Marisa_CRC−cluster−f
10	2e−01	18 / 2798	TxEnhG1_Colon
11	2e−01	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
12	4e−01	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
13	4e−01	3 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	4e−01	4 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
15	4e−01	5 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	4e−01	6 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
17	4e−01	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
18	4e−01	3 / 436	K9acLow_Colon
19	4e−01	29 / 5155	EnhWk1_Colon
20	4e−01	2 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.7	2 / 435	GUDJ_psoriasis up
2	0.8	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
2	0.06	1 / 11	astrocytes_glio
3	0.08	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	0.08	8 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.22	1 / 47	Vishal_subnetwork signature of survival in GBM
6	0.27	3 / 332	Up
7	0.29	1 / 63	Stuehler_Proteins_up_in_STS
8	0.29	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	0.31	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	0.43	1 / 103	GIEZELT_GBM_WT_up_VS_mut
11	0.51	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
12	0.63	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
13	1.00	0 / 15	VERHAAK_CL subtype
14	1.00	0 / 15	VERHAAK_MES subtype
15	1.00	0 / 16	VERHAAK_NL subtype
16	1.00	0 / 14	VERHAAK_PN subtype
17	1.00	0 / 23	WIRTH_PN subtype
18	1.00	0 / 74	WIRTH_Normal Brain
19	1.00	0 / 9	VERHAAK_Brain
20	1.00	0 / 8	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	16 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	0.002	3 / 47	REACTOME_METABOLISM_OF_NON_CODING_RNA
3	0.002	5 / 167	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
4	0.002	12 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
5	0.002	7 / 341	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
6	0.004	10 / 681	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
7	0.005	3 / 65	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
8	0.006	2 / 22	CHEOK_RESPONSE_TO_HD_MTX_DN
9	0.006	10 / 741	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
10	0.007	2 / 23	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_
11	0.008	3 / 75	KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION
12	0.008	6 / 324	GRUETZMANN_PANCREATIC_CANCER_UP
13	0.008	6 / 324	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
14	0.010	2 / 28	REACTOME_MRNA_CAPPING
15	0.010	2 / 28	KIM_TIAL1_TARGETS
16	0.010	2 / 28	YU_BAP1_TARGETS
17	0.010	4 / 158	BENPORATH_NOS_TARGETS
18	0.013	5 / 258	BENPORATH_OCT4_TARGETS
19	0.013	2 / 32	REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPL
20	0.013	9 / 706	BENPORATH_MYC_MAX_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	0.04	3 / 146	HALLMARK_DNA_REPAIR
2	0.08	3 / 188	HALLMARK_ADIPOGENESIS
3	0.09	3 / 196	HALLMARK_G2M_CHECKPOINT
4	0.19	2 / 148	HALLMARK_KRAS_SIGNALING_UP
5	0.27	2 / 188	HALLMARK_MYC_TARGETS_V1
6	0.41	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	0.44	1 / 107	HALLMARK_COAGULATION
8	0.50	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
9	0.52	1 / 137	HALLMARK_UV_RESPONSE_DN
10	0.59	1 / 162	HALLMARK_COMPLEMENT
11	0.62	1 / 176	HALLMARK_HYPOXIA
12	0.62	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	0.65	1 / 195	HALLMARK_MITOTIC_SPINDLE
14	0.66	1 / 197	HALLMARK_E2F_TARGETS
15	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
16	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
18	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	1.00	0 / 140	HALLMARK_APOPTOSIS
20	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−04	53 / 6929	HOPP_Txn_elongation
2	1e−03	55 / 7592	HOPP_Active_promoter
3	8e−03	50 / 7209	HOPP_Weak_promoter
4	1e−02	38 / 5184	HOPP_Txn_transition
5	1e−01	1 / 19	DAVE_c−myc BL UP
6	2e−01	3 / 256	SPANG_IL21 DN
7	2e−01	1 / 50	SPANG_BAFF 9hrs DN
8	3e−01	1 / 61	SPANG_LPS 6hrs DN
9	3e−01	38 / 6564	HOPP_Strong_enhancer
10	4e−01	1 / 89	ROSOLOWSKI_blue total
11	4e−01	15 / 2563	HOPP_Heterochrom
12	4e−01	32 / 5693	HOPP_Weak_enhancer
13	4e−01	2 / 268	SPANG_IL21 UP
14	5e−01	1 / 129	DAVE_BL−vs−DLBCL
15	7e−01	5 / 1128	SPANG_BCR DN
16	7e−01	1 / 247	ZHANG_DLBCL mutated
17	8e−01	1 / 275	TARTE_Mature plasma cell signature
18	8e−01	27 / 5538	HOPP_Weak_txn
19	8e−01	1 / 280	SPANG_CD40 6hrs UP
20	9e−01	1 / 410	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	8e−04	17 / 1365	RNA binding
2	9e−04	14 / 1007	poly(A) RNA binding
3	1e−03	2 / 10	protein phosphatase type 1 regulator activity
4	1e−03	8 / 394	catalytic activity
5	9e−03	2 / 26	peptide antigen binding
6	2e−02	2 / 37	coenzyme binding
7	2e−02	2 / 37	endonuclease activity
8	2e−02	2 / 45	calcium−dependent protein binding
9	3e−02	2 / 51	ubiquitinyl hydrolase activity
10	5e−02	10 / 1033	nucleic acid binding
11	5e−02	1 / 10	cytoskeletal adaptor activity
12	6e−02	2 / 71	cysteine−type endopeptidase activity
13	6e−02	2 / 71	ubiquitin−specific protease activity
14	6e−02	5 / 386	nucleotide binding
15	6e−02	3 / 164	nuclease activity
16	6e−02	3 / 167	helicase activity
17	6e−02	1 / 12	MAP kinase tyrosine/serine/threonine phosphatase activity
18	6e−02	1 / 12	phospholipase activity
19	7e−02	1 / 13	mannosyltransferase activity
20	7e−02	1 / 13	nucleocytoplasmic transporter activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 47	hsa−miR−518e*
2	0.002	4 / 104	hsa−miR−525−5p
3	0.018	2 / 38	hsa−miR−517*
4	0.018	4 / 187	hsa−miR−382
5	0.019	2 / 39	hsa−miR−518f*
6	0.021	2 / 42	hsa−miR−769−3p
7	0.023	3 / 112	hsa−miR−297
8	0.023	5 / 300	hsa−miR−548c−3p
9	0.030	2 / 50	hsa−miR−487a
10	0.036	3 / 134	hsa−miR−488
11	0.036	3 / 135	hsa−miR−28−5p
12	0.038	2 / 57	hsa−miR−193a−3p
13	0.041	3 / 141	hsa−miR−138
14	0.043	3 / 145	hsa−miR−922
15	0.043	3 / 145	hsa−miR−491−5p
16	0.047	2 / 64	hsa−miR−485−3p
17	0.052	2 / 68	hsa−miR−193b
18	0.053	1 / 10	hsa−miR−887
19	0.059	3 / 164	hsa−miR−323b−5p
20	0.062	2 / 75	hsa−miR−877

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.003	16 / 1400	ICGC_Myc_targets
2	0.004	14 / 1171	KIM_MYC targets
3	0.007	24 / 2714	ICGC_Irf4_targets
4	0.012	9 / 690	ICGC_Atf3_targets
5	0.017	19 / 2136	ICGC_GabpPcr2_targets
6	0.017	19 / 2137	ICGC_SrfV0416101_targets
7	0.029	7 / 553	ICGC_RxraPcr1_targets
8	0.033	13 / 1383	ICGC_Six5_targets
9	0.039	13 / 1418	ICGC_Ets1_targets
10	0.041	16 / 1878	ICGC_Cebpbsc150_targets
11	0.068	32 / 4689	ICGC_Taf1_targets
12	0.075	28 / 4032	ICGC_Creb1_targets
13	0.109	31 / 4706	ICGC_Sp1_targets
14	0.127	14 / 1872	ICGC_Mef2_targets
15	0.136	17 / 2391	ICGC_Pbx3_targets
16	0.138	37 / 5890	ICGC_Elf1_targets
17	0.167	31 / 4909	ICGC_Stat5_targets
18	0.170	28 / 4385	ICGC_Atf2_targets
19	0.183	34 / 5495	ICGC_Yy1_targets
20	0.195	25 / 3924	ICGC_Zeb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.08	1 / 16	VAQUERIZAS_Pancreas
2	0.18	1 / 37	VAQUERIZAS_Thymus
3	1.00	0 / 36	VAQUERIZAS_Fetal brain
4	1.00	0 / 41	VAQUERIZAS_Placenta
5	1.00	0 / 26	VAQUERIZAS_Liver
6	1.00	0 / 33	VAQUERIZAS_Prostate
7	1.00	0 / 29	VAQUERIZAS_Smooth muscle
8	1.00	0 / 45	VAQUERIZAS_Uterus
9	1.00	0 / 143	VAQUERIZAS_General
10	1.00	0 / 9	VAQUERIZAS_Kidney
11	1.00	0 / 23	VAQUERIZAS_Spinal cord
12	1.00	0 / 38	VAQUERIZAS_Whole brain
13	1.00	0 / 40	VAQUERIZAS_Thyroid
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 23	VAQUERIZAS_Trachea
19	1.00	0 / 11	VAQUERIZAS_Fetal liver
20	1.00	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 14	WIRTH_Telencephalon
2	0.16	1 / 32	WIRTH_Placenta
3	0.57	2 / 350	WIRTH_Immune system
4	0.65	1 / 194	PALMER_B−Cell signature up
5	0.71	1 / 225	PALMER_Granulocytes signature up
6	0.85	1 / 350	WIRTH_Nervous System
7	1.00	0 / 32	WIRTH_Pancreas
8	1.00	0 / 11	WIRTH_Sec. lymphoid organs
9	1.00	0 / 11	WIRTH_Prim. lymphoid organs
10	1.00	0 / 13	WIRTH_B−cells
11	1.00	0 / 8	WIRTH_Tonsil
12	1.00	0 / 12	WIRTH_Thymus
13	1.00	0 / 12	WIRTH_Lymphocytes
14	1.00	0 / 5	WIRTH_Bone marrow
15	1.00	0 / 11	WIRTH_Globus pallidus
16	1.00	0 / 11	WIRTH_Cortex cerebri
17	1.00	0 / 10	WIRTH_Hippocampus
18	1.00	0 / 10	WIRTH_Thalamus
19	1.00	0 / 12	WIRTH_Cerebellum
20	1.00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	9 / 1115	LU_BPDE 1h DN
2	0.7	18 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

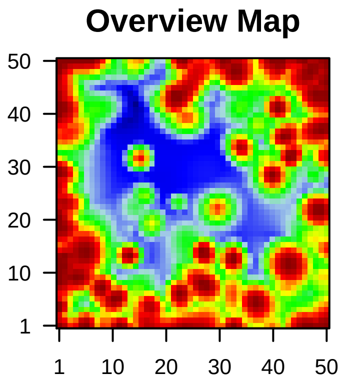
Overexpression Spots

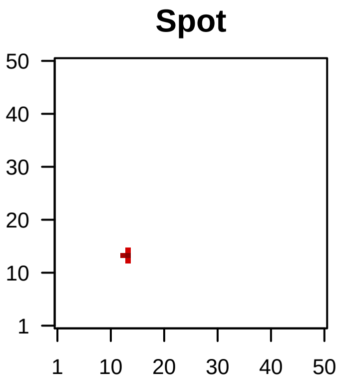
Spot Summary: G

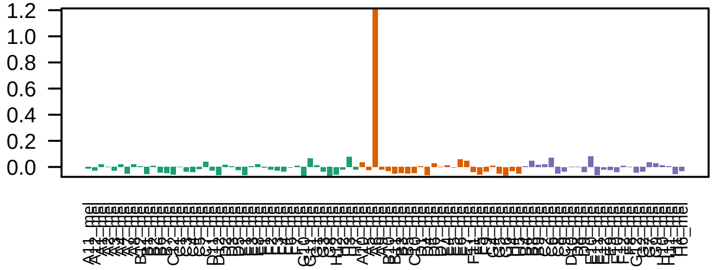
metagenes = 4
genes = 143

<r> metagenes = 1
<r> genes = 0.27
beta: r2= 0.62 / log p= −Inf

samples with spot = 1 (1.1 %)
MSC2 : 1 (4 %)





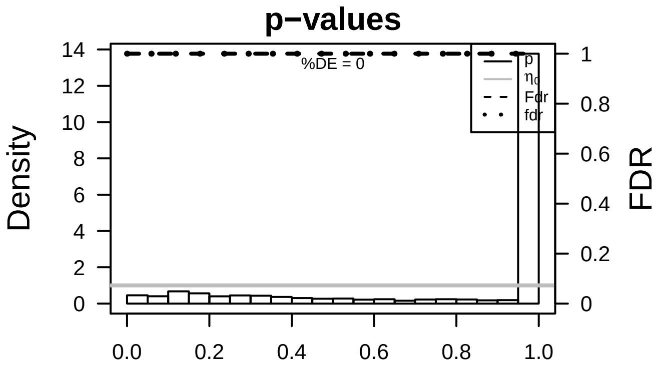


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	C3orf14	2.29	−0.16	0.39	C3orf14	chromosome 3 open reading frame 14 [Source:HGNC Symb
2	MDK	2.02	−0.1	0.54	MDK	midkine (neurite growth−promoting factor 2) [Source:HGNC
3	C10orf107	1.93	−0.08	0.67	C10orf107	chromosome 10 open reading frame 107 [Source:HGNC Sy
4	ANKS1B	1.88	−0.13	0.64	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B [
5	MEGF10	1.88	−0.23	0.44	MEGF10	multiple EGF−like−domains 10 [Source:HGNC Symbol;Acc:
6	ZNF442	1.86	−0.19	0.45	ZNF442	zinc finger protein 442 [Source:HGNC Symbol;Acc:HGNC:20
7	NEK3	1.8	−0.27	0.32	NEK3	NIMA−related kinase 3 [Source:HGNC Symbol;Acc:HGNC:7
8	C9orf92	1.79	−0.1	0.62	C9orf92	chromosome 9 open reading frame 92 [Source:HGNC Symb
9	MDGA2	1.77	−0.23	0.41	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor
10	THAP9	1.76	−0.33	0.34	THAP9	THAP domain containing 9 [Source:HGNC Symbol;Acc:HGN
11	MCU	1.74	−0.18	0.47	MCU	mitochondrial calcium uniporter [Source:HGNC Symbol;Acc:
12	NFKBIE	1.74	−0.22	0.3	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B−
13	SNAP25	1.72	−0.13	0.43	SNAP25	synaptosomal−associated protein, 25kDa [Source:HGNC Sy
14	ZSCAN26	1.72	−0.31	0.26	ZSCAN26	zinc finger and SCAN domain containing 26 [Source:HGNC
15	GIT2	1.69	−0.46	0.25	GIT2	G protein−coupled receptor kinase interacting ArfGAP 2 [Sou
16	CTIF	1.67	−0.36	0.29	CTIF	CBP80/20−dependent translation initiation factor [Source:HG
17	ALDH1A1	1.65	−0.08	0.91	ALDH1A1	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
18	TTYH2	1.65	−0.14	0.49	TTYH2	tweety family member 2 [Source:HGNC Symbol;Acc:HGNC:1
19	ZNF669	1.65	−0.44	0.2	ZNF669	zinc finger protein 669 [Source:HGNC Symbol;Acc:HGNC:25
20	PRKD2	1.64	−0.08	0.55	PRKD2	protein kinase D2 [Source:HGNC Symbol;Acc:HGNC:17293]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−05	3 / 7	Lifesty	DUMEAUX_Women normal BMI literature genes up
2	2e−04	19 / 775	CC	extracellular space
3	2e−04	4 / 30	Lymp	TARTE_B−cell signature
4	2e−04	4 / 31	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
5	2e−04	13 / 427	GSEA	NABA_MATRISOME_ASSOCIATED
6	3e−04	16 / 616	GSEA	NABA_MATRISOME
7	3e−04	8 / 179	GSEA	NABA_SECRETED_FACTORS
8	4e−04	3 / 16	BP	calcium ion−dependent exocytosis
9	6e−04	5 / 72	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
10	9e−04	7 / 160	GSEA	WIERENGA_STAT5A_TARGETS_DN
11	9e−04	32 / 1889	Colon	ReprPCWk_Colon
12	1e−03	11 / 379	GSEA	REACTOME_SIGNALING_BY_GPCR
13	1e−03	5 / 85	BP	response to virus
14	2e−03	34 / 2142	Colon	ReprPC_Colon
15	2e−03	3 / 26	GSEA	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
16	2e−03	18 / 884	Brain	Overlap_fetal_midbrain_EnhG
17	2e−03	3 / 27	MF	chemokine activity
18	2e−03	3 / 27	GSEA	HAHTOLA_SEZARY_SYNDROM_DN
19	2e−03	21 / 1115	Toxic	LU_BPDE 1h DN
20	3e−03	4 / 61	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1
21	3e−03	3 / 30	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_DN
22	3e−03	21 / 1139	TF	HEBENSTREIT_low expression TF
23	3e−03	9 / 311	GSEA	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1
24	3e−03	9 / 314	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
25	4e−03	23 / 1317	Colon	EnhP_Colon
26	4e−03	2 / 10	BP	DNA integration
27	4e−03	2 / 10	MF	ephrin receptor activity
28	4e−03	2 / 10	MF	guanylate kinase activity
29	4e−03	2 / 10	MF	proteoglycan binding
30	4e−03	2 / 10	BP	regulation of sodium ion transmembrane transporter activity
31	4e−03	2 / 10	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_D
32	4e−03	2 / 10	GSEA	IGLESIAS_E2F_TARGETS_DN
33	4e−03	10 / 385	GSEA	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
34	4e−03	33 / 2159	Colon	TssP_Colon
35	5e−03	3 / 35	BP	negative regulation of Wnt signaling pathway
36	5e−03	2 / 11	BP	positive regulation of interleukin−2 production
37	5e−03	2 / 11	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
38	5e−03	3 / 37	TF Ti	VAQUERIZAS_Thymus
39	5e−03	4 / 73	CC	basement membrane
40	6e−03	3 / 38	BP	regulation of G−protein coupled receptor protein signaling pathway



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.02	3 / 61	PanCan_Wnt_geneset_nanostring
3	0.03	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.14	1 / 15	GENTLES_modul10
5	0.18	0 / 12	LIU_BREAST_CANCER
6	0.19	1 / 22	PanCan_HH_geneset_nanostring
7	0.30	2 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.33	2 / 121	PanCan_MAPK_geneset_nanostring
9	0.33	6 / 489	Lembcke_Normal vs Adenoma
10	0.35	1 / 44	PanCan_TGF−B_geneset_nanostring
11	0.37	1 / 47	PanCan_DNARepair_geneset_nanostring
12	0.41	1 / 55	PanCan_JAK−ST_geneset_nanostring
13	0.55	1 / 82	PanCan_TXmisReg_geneset_nanostring
14	0.69	1 / 120	PanCan_CC+Apop_geneset_nanostring
15	0.75	3 / 401	Lembcke_Colonic Inflammation
16	0.83	1 / 180	SPANG_LPS−index2
17	0.95	1 / 298	SPANG_BCL6−index2
18	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
19	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
20	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	32 / 1889	ReprPCWk_Colon
2	2e−03	34 / 2142	ReprPC_Colon
3	3e−03	9 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
4	4e−03	23 / 1317	EnhP_Colon
5	4e−03	33 / 2159	TssP_Colon
6	1e−02	8 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
7	2e−02	21 / 1386	Het_Colon
8	3e−02	8 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
9	3e−02	6 / 250	K9K27me3_Colon
10	4e−02	42 / 3383	EnhWk2_Colon
11	4e−02	2 / 33	Marisa_CRC−cluster−e
12	7e−02	8 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
13	7e−02	1 / 8	Marisa_CRC−C6
14	9e−02	7 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	9e−02	7 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
16	9e−02	45 / 3897	Quies1_Colon
17	1e−01	5 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
18	1e−01	13 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
19	1e−01	14 / 1038	HetRpts_Colon
20	1e−01	2 / 66	Marisa_CRC−cluster−h

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 31	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
2	2e−04	13 / 427	NABA_MATRISOME_ASSOCIATED
3	3e−04	16 / 616	NABA_MATRISOME
4	3e−04	8 / 179	NABA_SECRETED_FACTORS
5	6e−04	5 / 72	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
6	9e−04	7 / 160	WIERENGA_STAT5A_TARGETS_DN
7	1e−03	11 / 379	REACTOME_SIGNALING_BY_GPCR
8	2e−03	3 / 26	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
9	2e−03	3 / 27	HAHTOLA_SEZARY_SYNDROM_DN
10	3e−03	4 / 61	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1
11	3e−03	3 / 30	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_DN
12	3e−03	9 / 311	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1
13	4e−03	2 / 10	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_DN
14	4e−03	2 / 10	IGLESIAS_E2F_TARGETS_DN
15	4e−03	10 / 385	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
16	6e−03	3 / 38	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
17	7e−03	3 / 40	WANG_BARRETTS_ESOPHAGUS_UP
18	7e−03	4 / 78	ROVERSI_GLIOMA_COPY_NUMBER_UP
19	7e−03	7 / 230	ROZANOV_MMP14_TARGETS_UP
20	8e−03	2 / 14	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 30	TARTE_B−cell signature
2	5e−02	5 / 212	LENZ_Stromal signature 1
3	7e−02	1 / 8	Subero_MM_hypo_meth
4	1e−01	7 / 410	SPANG_CD40 6hrs DN
5	1e−01	27 / 2188	HOPP_Poised_promoter
6	1e−01	2 / 61	SPANG_LPS 6hrs DN
7	1e−01	39 / 3396	HOPP_Repressed
8	1e−01	1 / 15	DAVE_Immune response 2
9	2e−01	1 / 20	SPANG_BAFF 9hrs UP
10	2e−01	1 / 25	Subero_T−PLL_hypo_meth
11	2e−01	4 / 256	SPANG_IL21 DN
12	2e−01	2 / 96	Subero_DLBCL_hyper_meth
13	2e−01	1 / 29	Subero_DLBCL_hypo_meth
14	3e−01	1 / 30	Subero_INT_hypo_meth
15	3e−01	4 / 275	TARTE_Mature plasma cell signature
16	3e−01	2 / 107	SPANG_LPS 6hrs UP
17	4e−01	1 / 50	SPANG_BAFF 9hrs DN
18	4e−01	3 / 247	ZHANG_DLBCL mutated
19	5e−01	22 / 2211	HOPP_Repetitive
20	5e−01	3 / 268	SPANG_IL21 UP

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p−value	#in/all	Geneset
1	0.008	2 / 14	WIRTH_Telencephalon
2	0.020	8 / 350	WIRTH_Nervous System
3	0.059	2 / 41	WIRTH_Homeostasis
4	0.075	1 / 8	WIRTH_Tonsil
5	0.118	4 / 194	PALMER_B−Cell signature up
6	0.233	2 / 95	WIRTH_Muscle
7	0.512	1 / 74	WIRTH_Mucosa
8	0.641	2 / 225	PALMER_Granulocytes signature up
9	0.659	3 / 350	WIRTH_Immune system
10	1.000	0 / 32	WIRTH_Pancreas
11	1.000	0 / 11	WIRTH_Sec. lymphoid organs
12	1.000	0 / 11	WIRTH_Prim. lymphoid organs
13	1.000	0 / 13	WIRTH_B−cells
14	1.000	0 / 12	WIRTH_Thymus
15	1.000	0 / 12	WIRTH_Lymphocytes
16	1.000	0 / 5	WIRTH_Bone marrow
17	1.000	0 / 11	WIRTH_Globus pallidus
18	1.000	0 / 11	WIRTH_Cortex cerebri
19	1.000	0 / 10	WIRTH_Hippocampus
20	1.000	0 / 10	WIRTH_Thalamus

BP

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 16	calcium ion−dependent exocytosis
2	1e−03	5 / 85	response to virus
3	4e−03	2 / 10	DNA integration
4	4e−03	2 / 10	regulation of sodium ion transmembrane transporter activity
5	5e−03	3 / 35	negative regulation of Wnt signaling pathway
6	5e−03	2 / 11	positive regulation of interleukin−2 production
7	6e−03	3 / 38	regulation of G−protein coupled receptor protein signaling pathway
8	7e−03	2 / 13	behavioral response to pain
9	7e−03	2 / 13	negative regulation of viral release from host cell
10	8e−03	2 / 14	negative regulation of interferon−gamma production
11	8e−03	2 / 14	T cell proliferation
12	9e−03	2 / 15	nucleotide phosphorylation
13	9e−03	2 / 15	positive regulation of interleukin−10 production
14	1e−02	2 / 16	positive regulation of interleukin−12 production
15	1e−02	2 / 17	adrenal gland development
16	1e−02	2 / 17	retinol metabolic process
17	1e−02	2 / 18	cellular response to interleukin−4
18	1e−02	2 / 18	entrainment of circadian clock by photoperiod
19	1e−02	2 / 19	negative regulation of endothelial cell apoptotic process
20	1e−02	2 / 19	negative regulation of mitotic cell cycle

CC

Rank	p−value	#in/all	Geneset
1	2e−04	19 / 775	extracellular space
2	5e−03	4 / 73	basement membrane
3	7e−03	3 / 41	cleavage furrow
4	9e−03	5 / 132	basolateral plasma membrane
5	4e−02	2 / 32	chloride channel complex
6	4e−02	4 / 138	cell−cell junction
7	4e−02	2 / 35	cell periphery
8	5e−02	2 / 36	T−tubule
9	5e−02	3 / 84	growth cone
10	5e−02	2 / 37	lateral plasma membrane
11	6e−02	3 / 91	nuclear matrix
12	6e−02	2 / 41	presynaptic membrane
13	6e−02	2 / 42	synaptic vesicle membrane
14	7e−02	3 / 99	receptor complex
15	8e−02	2 / 48	kinesin complex
16	8e−02	2 / 48	peroxisomal membrane
17	8e−02	5 / 239	proteinaceous extracellular matrix
18	9e−02	4 / 177	synapse
19	9e−02	1 / 10	beta−catenin destruction complex
20	9e−02	1 / 10	IkappaB kinase complex

Disease

Rank	p−value	#in/all	Geneset
1	0.2	5 / 294	GUDJ_psoriasis down
2	1.0	1 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	0.007	6 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	0.058	3 / 91	HALLMARK_BILE_ACID_METABOLISM
3	0.081	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
4	0.082	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.155	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
6	0.171	3 / 148	HALLMARK_KRAS_SIGNALING_UP
7	0.218	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
8	0.223	3 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.226	2 / 93	HALLMARK_PEROXISOME
10	0.259	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
11	0.295	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	0.343	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
13	0.402	1 / 53	HALLMARK_TGF_BETA_SIGNALING
14	0.441	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	0.464	2 / 162	HALLMARK_COMPLEMENT
16	0.474	2 / 165	HALLMARK_MYOGENESIS
17	0.483	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
18	0.502	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	0.543	2 / 188	HALLMARK_ADIPOGENESIS
20	0.570	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 27	chemokine activity
2	0.004	2 / 10	ephrin receptor activity
3	0.004	2 / 10	guanylate kinase activity
4	0.004	2 / 10	proteoglycan binding
5	0.017	3 / 56	phosphoprotein phosphatase activity
6	0.017	2 / 21	sodium channel regulator activity
7	0.020	2 / 23	ephrin receptor binding
8	0.026	2 / 26	chloride channel activity
9	0.026	2 / 26	endopeptidase inhibitor activity
10	0.026	2 / 26	olfactory receptor activity
11	0.029	3 / 69	microtubule motor activity
12	0.031	9 / 451	protein kinase activity
13	0.035	12 / 691	kinase activity
14	0.038	3 / 77	cytokine activity
15	0.039	8 / 398	protein tyrosine kinase activity
16	0.050	3 / 86	ubiquitin−like protein binding
17	0.059	2 / 41	G−protein coupled receptor binding
18	0.059	2 / 41	phosphatase binding
19	0.064	4 / 156	protein C−terminus binding
20	0.064	2 / 43	SMAD binding

TF

Rank	p−value	#in/all	Geneset
1	0.003	21 / 1139	HEBENSTREIT_low expression TF
2	0.132	34 / 2927	ICGC_Rad21_targets
3	0.156	24 / 2013	ICGC_Bcl11_targets
4	0.284	7 / 553	ICGC_RxraPcr1_targets
5	0.476	28 / 2836	ICGC_BatfPcr1_targets
6	0.672	50 / 5408	ICGC_Pou2_targets
7	0.684	11 / 1266	ICGC_NrsfPcr1_targets
8	0.712	24 / 2714	ICGC_Irf4_targets
9	0.714	49 / 5374	ICGC_Pax5_targets
10	0.730	11 / 1314	ICGC_Usf1_targets
11	0.733	36 / 4032	ICGC_Creb1_targets
12	0.733	16 / 1872	ICGC_Mef2_targets
13	0.793	10 / 1273	ICGC_P300_targets
14	0.821	54 / 6114	ICGC_Runx3_targets
15	0.830	4 / 595	ICGC_NrsfPcr2_targets
16	0.858	51 / 5890	ICGC_Elf1_targets
17	0.891	16 / 2137	ICGC_SrfV0416101_targets
18	0.900	32 / 3966	ICGC_Pu1_targets
19	0.903	46 / 5495	ICGC_Yy1_targets
20	0.904	4 / 690	ICGC_Atf3_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.002	21 / 1115	LU_BPDE 1h DN
2	0.061	44 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	0.002	18 / 884	Overlap_fetal_midbrain_EnhG
2	0.018	5 / 156	Mid_Frontal_Lobe_TssA
3	0.051	16 / 1065	Overlap_fetal_midbrain_Enh
4	0.051	10 / 574	Overlap_fetal_midbrain_TssP
5	0.071	5 / 229	Mid_Frontal_Lobe_TxTrans
6	0.101	27 / 2185	Fetal_TssA
7	0.107	20 / 1548	Mid_Frontal_Lobe_K9K27me3
8	0.110	35 / 2972	Mid_Frontal_Lobe_ReprPC
9	0.119	16 / 1207	Overlap_fetal_midbrain_TssF
10	0.142	17 / 1333	Fetal_ReprPCWk
11	0.182	9 / 656	Overlap_fetal_midbrain_EnhP
12	0.203	10 / 765	Mid_Frontal_Lobe_Het
13	0.215	3 / 166	Mid_Frontal_Lobe_Tx
14	0.247	5 / 349	Fetal_ZNF
15	0.297	6 / 468	Mid_Frontal_Lobe_TssF
16	0.336	26 / 2462	Mid_Frontal_Lobe_HetRpts
17	0.341	8 / 686	Overlap_fetal_midbrain_TssA
18	0.382	9 / 812	Mid_Frontal_Lobe_TssP
19	0.413	13 / 1236	Mid_Frontal_Lobe_ReprPCWk
20	0.451	9 / 862	Overlap_fetal_midbrain_TxTrans

Chr

Rank	p−value	#in/all	Geneset
1	0.09	9 / 551	Chr X
2	0.09	12 / 801	Chr 11
3	0.13	14 / 1037	Chr 19
4	0.16	8 / 552	Chr 10
5	0.19	8 / 576	Chr 9
6	0.22	9 / 687	Chr 6
7	0.22	5 / 335	Chr 22
8	0.43	2 / 151	Chr 21
9	0.44	7 / 649	Chr 16
10	0.47	8 / 775	Chr 12
11	0.59	14 / 1500	Chr 1
12	0.67	6 / 696	Chr 5
13	0.71	7 / 840	Chr 17
14	0.74	3 / 398	Chr 20
15	0.82	6 / 838	Chr 3
16	0.83	3 / 462	Chr 14
17	0.88	1 / 221	Chr 18
18	0.90	4 / 689	Chr 7
19	0.91	3 / 558	Chr 4
20	0.92	1 / 262	Chr 13

Glio

Rank	p−value	#in/all	Geneset
1	0.005	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
2	0.025	3 / 65	GIEZELT_GBM_STS_up_VS_LTS
3	0.035	3 / 74	WIRTH_Normal Brain
4	0.047	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
5	0.052	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
6	0.072	3 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
7	0.075	1 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
8	0.081	2 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
9	0.083	1 / 9	Mukasa_UP_in_GBM
10	0.118	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
11	0.130	6 / 356	Down_a
12	0.141	6 / 365	Down_b
13	0.144	1 / 16	KIM deleted & downregulated in LTS
14	0.160	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
15	0.192	1 / 22	KIM prognostic signature LTS vs. STS
16	0.200	1 / 23	WIRTH_PN subtype
17	0.200	1 / 23	Donson−Misc immune function−associated with LTS in HGA
18	0.204	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
19	0.229	2 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
20	0.301	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−05	3 / 7	DUMEAUX_Women normal BMI literature genes up
2	3e−01	1 / 32	DUMEAUX_Fasting enriched genes
3	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
5	1e+00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1e+00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1e+00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1e+00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1e+00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1e+00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.1	2 / 69	hsa−miR−1266
2	0.2	2 / 75	hsa−miR−513c
3	0.2	3 / 146	hsa−miR−142−3p
4	0.2	1 / 22	hsa−miR−516a−5p
5	0.2	2 / 90	hsa−miR−216b
6	0.3	1 / 32	hsa−miR−1178
7	0.3	3 / 191	hsa−miR−641
8	0.3	1 / 37	hsa−miR−635
9	0.3	1 / 40	hsa−miR−758
10	0.3	1 / 40	hsa−miR−450a
11	0.3	1 / 41	hsa−miR−601
12	0.3	1 / 44	hsa−miR−658
13	0.4	2 / 129	hsa−miR−1272
14	0.4	1 / 47	hsa−miR−1291
15	0.4	2 / 133	hsa−miR−198
16	0.4	2 / 136	hsa−miR−155
17	0.4	1 / 51	hsa−miR−571
18	0.4	1 / 52	hsa−miR−370
19	0.4	1 / 53	hsa−miR−1279
20	0.4	1 / 54	hsa−miR−513a−5p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.005	3 / 37	VAQUERIZAS_Thymus
2	0.014	2 / 19	VAQUERIZAS_Tonsil
3	0.028	2 / 27	VAQUERIZAS_Lymph node
4	0.108	2 / 58	VAQUERIZAS_Lung
5	0.135	1 / 15	VAQUERIZAS_Bone marrow
6	0.144	1 / 16	VAQUERIZAS_Salivary gland
7	0.223	1 / 26	VAQUERIZAS_Liver
8	0.245	1 / 29	VAQUERIZAS_Smooth muscle
9	0.402	2 / 143	VAQUERIZAS_General
10	0.436	1 / 59	VAQUERIZAS_Whole blood
11	1.000	0 / 36	VAQUERIZAS_Fetal brain
12	1.000	0 / 41	VAQUERIZAS_Placenta
13	1.000	0 / 33	VAQUERIZAS_Prostate
14	1.000	0 / 45	VAQUERIZAS_Uterus
15	1.000	0 / 9	VAQUERIZAS_Kidney
16	1.000	0 / 23	VAQUERIZAS_Spinal cord
17	1.000	0 / 38	VAQUERIZAS_Whole brain
18	1.000	0 / 40	VAQUERIZAS_Thyroid
19	1.000	0 / 7	VAQUERIZAS_Appendix
20	1.000	0 / 29	VAQUERIZAS_Fetal lung

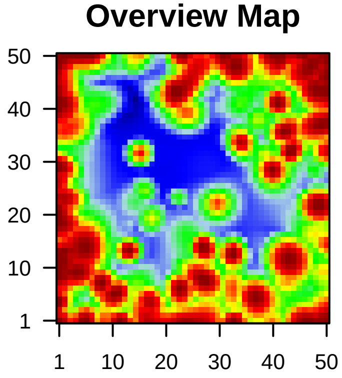
Overexpression Spots

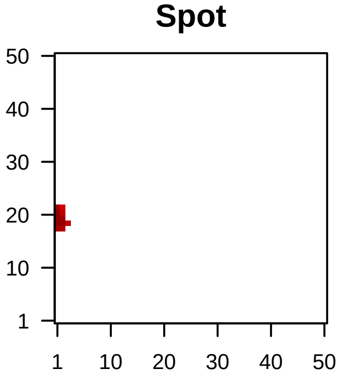
Spot Summary: H

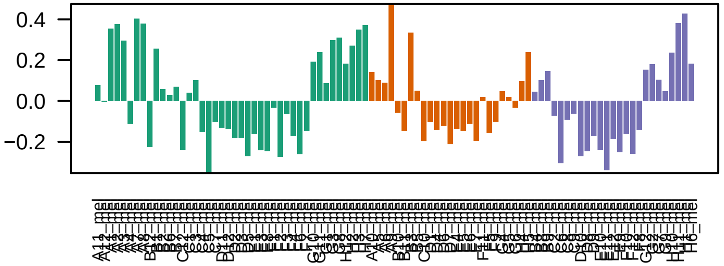
metagenes = 11
genes = 216

<r> metagenes = 0.97
<r> genes = 0.16
beta: r2= 2.2 / log p= −Inf

samples with spot = 21 (22.8 %)
MSC1 : 14 (33.3 %)
MSC2 : 3 (12 %)
MSC3 : 4 (16 %)


Overview Map


Spot

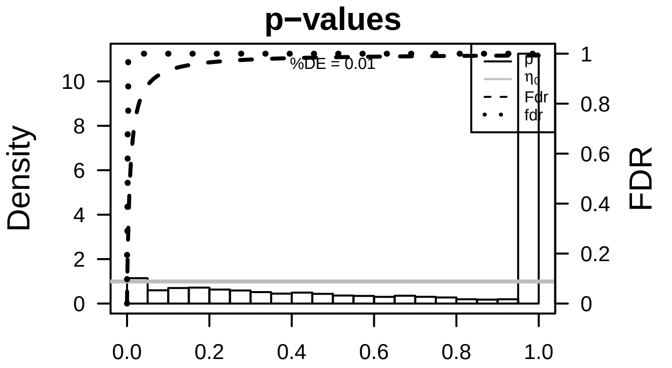


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	RAB40B	1.91	−0.31	0.29	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
2	ARRDC1	1.83	−0.36	0.26	ARRDC1	arrestin domain containing 1 [Source:HGNC Symbol;Acc:HGI
3	FAM131A	1.78	−0.18	0.29	FAM131A	family with sequence similarity 131, member A [Source:HGN
4	DBNDD2	1.77	−0.24	0.33	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing
5	IFNAR2	1.71	−0.41	0.45	IFNAR2	interferon (alpha, beta and omega) receptor 2 [Source:HGNC
6	LMLN	1.68	−0.37	0.26	LMLN	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
7	MIOS	1.64	−0.23	0.29	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila) [Sou
8	SDCCAG3	1.61	−0.51	0.35	SDCCAG3	serologically defined colon cancer antigen 3 [Source:HGNC S
9	GET4	1.6	−0.28	0.32	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:H
10	DNAJC4	1.59	−0.96	0.27	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HGN
11	SLC35A3	1.58	−0.48	0.31	SLC35A3	solute carrier family 35 (UDP−N−acetylglucosamine (UDP−G
12	E2F4	1.58	−0.5	0.36	E2F4	E2F transcription factor 4, p107/p130−binding [Source:HGNC
13	DPAGT1	1.54	−0.93	0.29	DPAGT1	dolichyl−phosphate (UDP−N−acetylglucosamine) N−acetylglu
14	TMEM18	1.53	−0.87	0.36	TMEM18	transmembrane protein 18 [Source:HGNC Symbol;Acc:HGN
15	FAM120AOS	1.53	−0.59	0.35	FAM120AOS	family with sequence similarity 120A opposite strand [Source:
16	RRAGA	1.53	−0.46	0.48	RRAGA	Ras−related GTP binding A [Source:HGNC Symbol;Acc:HGN
17	PIK3R4	1.52	−0.78	0.21	PIK3R4	phosphoinositide−3−kinase, regulatory subunit 4 [Source:HG
18	ENG	1.5	−0.47	0.28	ENG	endoglin [Source:HGNC Symbol;Acc:HGNC:3349]
19	OGFOD3	1.49	−0.6	0.44	OGFOD3	2−oxoglutarate and iron−dependent oxygenase domain conta
20	PEX10	1.49	−0.23	0.32	PEX10	peroxisomal biogenesis factor 10 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−17	192 / 9482	Colon	TssA_Colon
2	1e−13	158 / 7203	Colon	TssF_Colon
3	5e−13	45 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	1e−12	179 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
5	3e−12	168 / 8205	CC	cytoplasm
6	7e−11	39 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	6e−08	48 / 1468	CC	mitochondrion
8	7e−08	42 / 1201	CC	endoplasmic reticulum
9	1e−07	28 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
10	1e−07	23 / 440	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
11	1e−07	24 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
12	2e−07	44 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	2e−07	173 / 9528	Brain	Overlap_fetal_midbrain_Quies
14	2e−07	186 / 10605	CC	intracellular
15	2e−07	29 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
16	4e−07	166 / 9027	Colon	Tx_Colon
17	4e−07	16 / 238	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
18	6e−07	22 / 447	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_UP
19	6e−07	14 / 188	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_UP
20	8e−07	173 / 9653	Colon	Enh_Colon
21	2e−06	74 / 3081	Brain	Mid_Frontal_Lobe_ZNF
22	9e−06	174 / 9988	CC	organelle
23	2e−05	116 / 5880	Colon	TssD2_Colon
24	2e−05	4 / 12	BP	oxidative phosphorylation
25	2e−05	23 / 598	BP	membrane organization
26	5e−05	54 / 2193	CC	extracellular exosome
27	8e−05	16 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
28	9e−05	5 / 32	BP	mitochondrion degradation
29	1e−04	7 / 74	GSEA	SMITH_TERT_TARGETS_DN
30	2e−04	7 / 80	GSEA	SASSON_RESPONSE_TO_GONADOTROPHINS_UP
31	2e−04	16 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
32	2e−04	13 / 274	GSEA	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
33	2e−04	26 / 840	Chr	Chr 17
34	2e−04	29 / 990	GSEA	DANG_BOUND_BY_MYC
35	3e−04	62 / 2798	Colon	TxEnhG1_Colon
36	3e−04	14 / 327	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
37	4e−04	67 / 3132	CC	extracellular region
38	4e−04	7 / 94	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
39	5e−04	3 / 11	MF	proton−transporting ATP synthase activity, rotational mechanism
40	5e−04	18 / 510	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.8	1 / 100	HORVATH_aging_genes meth DOWN
3	0.8	1 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 12	oxidative phosphorylation
2	2e−05	23 / 598	membrane organization
3	9e−05	5 / 32	mitochondrion degradation
4	6e−04	4 / 27	phospholipid biosynthetic process
5	8e−04	3 / 13	ATP biosynthetic process
6	1e−03	3 / 15	negative regulation of release of cytochrome c from mitochondria
7	1e−03	5 / 56	cellular iron ion homeostasis
8	2e−03	3 / 19	negative regulation of proteolysis
9	4e−03	39 / 1730	small molecule metabolic process
10	4e−03	4 / 44	post−Golgi vesicle−mediated transport
11	4e−03	3 / 23	phosphatidic acid biosynthetic process
12	5e−03	4 / 47	proton transport
13	5e−03	4 / 48	hydrogen ion transmembrane transport
14	6e−03	3 / 25	lipoprotein metabolic process
15	7e−03	3 / 27	platelet aggregation
16	7e−03	5 / 83	mitochondrial translational elongation
17	7e−03	5 / 83	mitochondrial translational initiation
18	7e−03	5 / 83	mitochondrial translational termination
19	8e−03	21 / 815	cell death
20	8e−03	6 / 120	transforming growth factor beta receptor signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	1e−12	179 / 9013	Overlap_fetal_midbrain_K9K27me3
2	2e−07	173 / 9528	Overlap_fetal_midbrain_Quies
3	2e−06	74 / 3081	Mid_Frontal_Lobe_ZNF
4	4e−03	21 / 765	Mid_Frontal_Lobe_Het
5	5e−03	154 / 9330	Overlap_fetal_midbrain_ReprPC
6	6e−03	31 / 1333	Fetal_ReprPCWk
7	3e−02	55 / 2972	Mid_Frontal_Lobe_ReprPC
8	4e−01	29 / 1845	Fetal_Quies
9	4e−01	3 / 163	Fetal_ReprPC
10	4e−01	13 / 831	Fetal_HetRpts
11	5e−01	36 / 2462	Mid_Frontal_Lobe_HetRpts
12	6e−01	5 / 349	Fetal_ZNF
13	7e−01	2 / 166	Mid_Frontal_Lobe_Tx
14	7e−01	8 / 656	Overlap_fetal_midbrain_EnhP
15	8e−01	82 / 5940	Overlap_fetal_midbrain_HetRpts
16	8e−01	9 / 769	Overlap_fetal_midbrain_ZNF
17	8e−01	19 / 1548	Mid_Frontal_Lobe_K9K27me3
18	9e−01	8 / 786	Fetal_EnhG
19	9e−01	1 / 158	Overlap_fetal_midbrain_Het
20	9e−01	5 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	3 / 40	PanCan_HK_geneset_nanostring
2	0.02	2 / 16	GENTLES_modul16
3	0.05	6 / 180	SPANG_LPS−index2
4	0.11	2 / 40	ZHANG_MM up
5	0.17	1 / 13	BEN−PORATH_UP
6	0.21	1 / 16	GENTLES_modul2
7	0.27	2 / 70	SHAUGHNESSY_MM high risk
8	0.28	9 / 489	Lembcke_Normal vs Adenoma
9	0.35	1 / 29	KUIPER_MM good survival
10	0.44	5 / 298	SPANG_BCL6−index2
11	0.48	1 / 44	PanCan_TGF−B_geneset_nanostring
12	0.51	1 / 48	KUIPER_MM poor survival
13	0.52	2 / 120	PanCan_CC+Apop_geneset_nanostring
14	0.53	2 / 121	PanCan_MAPK_geneset_nanostring
15	0.55	1 / 55	PanCan_JAK−ST_geneset_nanostring
16	0.60	0 / 15	RHODES_CANCER_META_SIGNATURE
17	0.64	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	0.67	0 / 14	LIU_PROSTATE_CANCER_DN
19	0.70	0 / 12	LIU_PROSTATE_CANCER_UP
20	0.81	1 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−12	168 / 8205	cytoplasm
2	6e−08	48 / 1468	mitochondrion
3	7e−08	42 / 1201	endoplasmic reticulum
4	2e−07	186 / 10605	intracellular
5	9e−06	174 / 9988	organelle
6	5e−05	54 / 2193	extracellular exosome
7	4e−04	67 / 3132	extracellular region
8	5e−04	21 / 649	endoplasmic reticulum membrane
9	6e−04	190 / 11774	cell
10	6e−04	13 / 308	focal adhesion
11	7e−04	20 / 616	endosome
12	2e−03	6 / 94	melanosome
13	3e−03	8 / 164	endosome membrane
14	3e−03	15 / 456	vacuole
15	3e−03	21 / 745	cytoplasmic membrane−bounded vesicle
16	3e−03	14 / 412	lysosome
17	4e−03	3 / 22	pre−autophagosomal structure
18	5e−03	4 / 47	lipid particle
19	5e−03	9 / 223	lysosomal membrane
20	6e−03	4 / 51	endoplasmic reticulum−Golgi intermediate compartment

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	26 / 840	Chr 17
2	5e−03	17 / 576	Chr 9
3	7e−02	10 / 398	Chr 20
4	2e−01	13 / 649	Chr 16
5	2e−01	7 / 335	Chr 22
6	2e−01	5 / 221	Chr 18
7	3e−01	5 / 262	Chr 13
8	4e−01	3 / 151	Chr 21
9	4e−01	13 / 801	Chr 11
10	4e−01	16 / 1037	Chr 19
11	5e−01	10 / 689	Chr 7
12	6e−01	12 / 838	Chr 3
13	6e−01	8 / 558	Chr 4
14	7e−01	6 / 465	Chr 15
15	7e−01	7 / 552	Chr 10
16	8e−01	6 / 551	Chr X
17	9e−01	7 / 696	Chr 5
18	9e−01	4 / 462	Chr 14
19	9e−01	4 / 469	Chr 8
20	9e−01	10 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−17	192 / 9482	TssA_Colon
2	1e−13	158 / 7203	TssF_Colon
3	4e−07	166 / 9027	Tx_Colon
4	8e−07	173 / 9653	Enh_Colon
5	2e−05	116 / 5880	TssD2_Colon
6	3e−04	62 / 2798	TxEnhG1_Colon
7	2e−03	57 / 2698	EnhA_Colon
8	6e−03	20 / 739	TxEnhG2_Colon
9	6e−03	20 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
10	7e−03	143 / 8580	TxWk_Colon
11	9e−03	92 / 5155	EnhWk1_Colon
12	1e−02	17 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	3e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
14	7e−02	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
15	8e−02	3 / 71	Marisa_CRC−cluster−g
16	1e−01	5 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
17	1e−01	1 / 8	Marisa_CRC−C1
18	1e−01	1 / 8	Marisa_CRC−C2
19	2e−01	12 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
20	2e−01	1 / 15	TCGA_Mutated−in−CRC_hypermutated

Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 20	BCHETNIA_EBM−DM up
2	0.4	5 / 294	GUDJ_psoriasis down
3	0.4	7 / 435	GUDJ_psoriasis up
4	1.0	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.003	12 / 332	Up
2	0.038	4 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.041	10 / 365	Down_b
4	0.064	3 / 63	Stuehler_Proteins_up_in_STS
5	0.105	2 / 38	OL vs. OPC
6	0.149	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
7	0.149	1 / 11	Christensen_hypermethylated_in_ependymoma
8	0.157	3 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	0.174	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
10	0.189	3 / 103	GIEZELT_GBM_WT_up_VS_mut
11	0.197	1 / 15	VERHAAK_CL subtype
12	0.201	2 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
13	0.202	4 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
14	0.209	1 / 16	VERHAAK_NL subtype
15	0.228	2 / 62	cultured astroglia vs. in vivo astrocytes
16	0.260	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
17	0.276	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
18	0.344	14 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
19	0.414	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
20	0.419	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−13	45 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	7e−11	39 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	1e−07	28 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
4	1e−07	23 / 440	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
5	1e−07	24 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
6	2e−07	44 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	2e−07	29 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
8	4e−07	16 / 238	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
9	6e−07	22 / 447	ENK_UV_RESPONSE_KERATINOCYTE_UP
10	6e−07	14 / 188	DAZARD_RESPONSE_TO_UV_NHEK_UP
11	8e−05	16 / 363	RUTELLA_RESPONSE_TO_HGF_UP
12	1e−04	7 / 74	SMITH_TERT_TARGETS_DN
13	2e−04	7 / 80	SASSON_RESPONSE_TO_GONADOTROPHINS_UP
14	2e−04	16 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
15	2e−04	13 / 274	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
16	2e−04	29 / 990	DANG_BOUND_BY_MYC
17	3e−04	14 / 327	BLUM_RESPONSE_TO_SALIRASIB_DN
18	4e−04	7 / 94	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
19	5e−04	18 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
20	5e−04	7 / 96	BOUDOUKHA_BOUND_BY_IGF2BP2

HM

Rank	p−value	#in/all	Geneset
1	0.002	9 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.020	6 / 146	HALLMARK_UV_RESPONSE_UP
3	0.042	3 / 53	HALLMARK_TGF_BETA_SIGNALING
4	0.042	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.042	6 / 174	HALLMARK_HEME_METABOLISM
6	0.047	4 / 93	HALLMARK_PEROXISOME
7	0.048	4 / 94	HALLMARK_ANDROGEN_RESPONSE
8	0.057	6 / 188	HALLMARK_ADIPOGENESIS
9	0.057	6 / 188	HALLMARK_MYC_TARGETS_V1
10	0.062	5 / 146	HALLMARK_DNA_REPAIR
11	0.067	6 / 196	HALLMARK_MTORC1_SIGNALING
12	0.097	5 / 167	HALLMARK_APICAL_JUNCTION
13	0.112	4 / 126	HALLMARK_ALLOGRAFT_REJECTION
14	0.147	3 / 91	HALLMARK_PROTEIN_SECRETION
15	0.164	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
16	0.211	4 / 162	HALLMARK_COMPLEMENT
17	0.235	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
18	0.293	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
19	0.321	3 / 137	HALLMARK_UV_RESPONSE_DN
20	0.333	3 / 140	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.20	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	131 / 7592	HOPP_Active_promoter
2	0.008	93 / 5184	HOPP_Txn_transition
3	0.008	5 / 86	ROSOLOWSKI_red total
4	0.016	4 / 66	TARTE_Plasma cell signature
5	0.022	2 / 16	DAVE_BL Inter
6	0.028	9 / 294	TARTE_Plasmablast signature
7	0.029	4 / 80	Aukema_BCL2 DN_BCL6 UP
8	0.039	24 / 1128	SPANG_BCR DN
9	0.041	114 / 6929	HOPP_Txn_elongation
10	0.077	10 / 410	SPANG_CD40 6hrs DN
11	0.087	2 / 34	Subero_B−ALL_hyper_meth
12	0.110	2 / 39	ROSOLOWSKI_blue DOWN
13	0.136	1 / 10	DAVE_BL UP
14	0.161	1 / 12	BENTINK_mBL DOWN
15	0.174	1 / 13	WRIGHT_GCB UP
16	0.174	1 / 13	YAMANE_AICDA_targets_recruited
17	0.186	1 / 14	Subero_MCL_hyper_meth
18	0.204	102 / 6564	HOPP_Strong_enhancer
19	0.209	1 / 16	ROSOLOWSKI_red UP
20	0.221	111 / 7209	HOPP_Weak_promoter

MF

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 11	proton−transporting ATP synthase activity, rotational mechanism
2	8e−04	5 / 51	ubiquitin binding
3	1e−03	18 / 550	protein homodimerization activity
4	2e−03	3 / 18	2 iron, 2 sulfur cluster binding
5	3e−03	4 / 42	protein kinase C binding
6	4e−03	3 / 23	proton−transporting ATPase activity, rotational mechanism
7	8e−03	7 / 156	protein C−terminus binding
8	8e−03	5 / 86	ubiquitin−like protein binding
9	8e−03	3 / 29	beta−amyloid binding
10	9e−03	2 / 10	proteasome binding
11	1e−02	3 / 33	peptide binding
12	1e−02	2 / 12	misfolded protein binding
13	1e−02	2 / 13	5'−nucleotidase activity
14	2e−02	10 / 316	protein kinase binding
15	2e−02	2 / 16	K63−linked polyubiquitin binding
16	2e−02	2 / 16	RNA polymerase II carboxy−terminal domain kinase activity
17	2e−02	12 / 430	lipid binding
18	2e−02	2 / 17	glycosaminoglycan binding
19	2e−02	2 / 17	protein disulfide isomerase activity
20	3e−02	3 / 49	drug binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	6 / 96	hsa−miR−133a
2	0.003	6 / 97	hsa−miR−133b
3	0.003	5 / 68	hsa−miR−342−3p
4	0.004	6 / 105	hsa−miR−1271
5	0.005	7 / 141	hsa−miR−138
6	0.006	10 / 269	hsa−miR−449a
7	0.008	10 / 282	hsa−miR−570
8	0.009	5 / 87	hsa−miR−188−3p
9	0.013	5 / 96	hsa−miR−125b
10	0.013	5 / 96	hsa−miR−125a−5p
11	0.014	5 / 97	hsa−miR−624
12	0.014	5 / 97	hsa−miR−1303
13	0.016	7 / 179	hsa−miR−381
14	0.016	3 / 37	hsa−miR−635
15	0.019	5 / 105	hsa−miR−526b
16	0.026	5 / 115	hsa−miR−154
17	0.028	9 / 294	hsa−miR−561
18	0.029	4 / 80	hsa−miR−942
19	0.030	8 / 250	hsa−miR−524−5p
20	0.031	6 / 162	hsa−miR−96

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−04	81 / 4054	ICGC_Egr1_targets
2	1e−03	53 / 2416	ICGC_Bcl3_targets
3	2e−03	97 / 5219	ICGC_Tcf3_targets
4	2e−03	92 / 4909	ICGC_Stat5_targets
5	3e−03	109 / 6114	ICGC_Runx3_targets
6	4e−03	87 / 4689	ICGC_Taf1_targets
7	4e−03	105 / 5890	ICGC_Elf1_targets
8	6e−03	89 / 4879	ICGC_Pmlsc71910_targets
9	6e−03	28 / 1171	KIM_MYC targets
10	8e−03	75 / 4032	ICGC_Creb1_targets
11	9e−03	96 / 5408	ICGC_Pou2_targets
12	9e−03	73 / 3924	ICGC_Zeb1_targets
13	1e−02	83 / 4617	ICGC_Tcf12_targets
14	1e−02	36 / 1701	HEBENSTREIT_high expression TF
15	1e−02	96 / 5495	ICGC_Yy1_targets
16	2e−02	91 / 5200	ICGC_Mta3_targets
17	2e−02	77 / 4314	ICGC_Ebfsc137065_targets
18	2e−02	67 / 3700	ICGC_Nfatc1_targets
19	2e−02	78 / 4414	ICGC_Bclaf101388_targets
20	4e−02	91 / 5355	ICGC_Pol2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 40	VAQUERIZAS_Thyroid
2	0.2	1 / 16	VAQUERIZAS_Pancreas
3	0.2	1 / 16	VAQUERIZAS_Salivary gland
4	0.2	1 / 17	VAQUERIZAS_Heart
5	0.3	1 / 27	VAQUERIZAS_Lymph node
6	0.3	1 / 29	VAQUERIZAS_Fetal lung
7	0.4	1 / 33	VAQUERIZAS_Prostate
8	0.5	1 / 45	VAQUERIZAS_Uterus
9	0.6	1 / 58	VAQUERIZAS_Lung
10	0.6	1 / 59	VAQUERIZAS_Whole blood
11	1.0	0 / 36	VAQUERIZAS_Fetal brain
12	1.0	0 / 41	VAQUERIZAS_Placenta
13	1.0	0 / 26	VAQUERIZAS_Liver
14	1.0	0 / 29	VAQUERIZAS_Smooth muscle
15	1.0	0 / 143	VAQUERIZAS_General
16	1.0	0 / 9	VAQUERIZAS_Kidney
17	1.0	0 / 23	VAQUERIZAS_Spinal cord
18	1.0	0 / 38	VAQUERIZAS_Whole brain
19	1.0	0 / 37	VAQUERIZAS_Thymus
20	1.0	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	6 / 225	PALMER_Granulocytes signature up
2	0.2	1 / 12	WIRTH_Cerebellum
3	0.2	1 / 13	WIRTH_B−cells
4	0.5	2 / 114	PALMER_T−Cell signature up
5	0.5	3 / 194	PALMER_B−Cell signature up
6	0.8	4 / 350	WIRTH_Immune system
7	1.0	0 / 32	WIRTH_Pancreas
8	1.0	0 / 11	WIRTH_Sec. lymphoid organs
9	1.0	0 / 11	WIRTH_Prim. lymphoid organs
10	1.0	0 / 8	WIRTH_Tonsil
11	1.0	0 / 12	WIRTH_Thymus
12	1.0	0 / 12	WIRTH_Lymphocytes
13	1.0	0 / 5	WIRTH_Bone marrow
14	1.0	0 / 350	WIRTH_Nervous System
15	1.0	0 / 11	WIRTH_Globus pallidus
16	1.0	0 / 14	WIRTH_Telencephalon
17	1.0	0 / 11	WIRTH_Cortex cerebri
18	1.0	0 / 10	WIRTH_Hippocampus
19	1.0	0 / 10	WIRTH_Thalamus
20	1.0	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.09	22 / 1115	LU_BPDE 1h DN
2	0.87	47 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

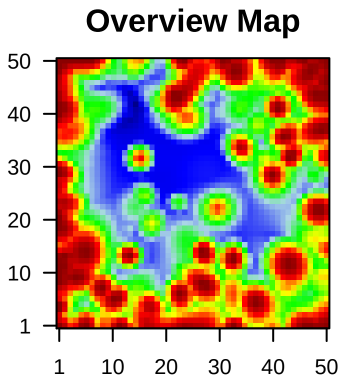
Overexpression Spots

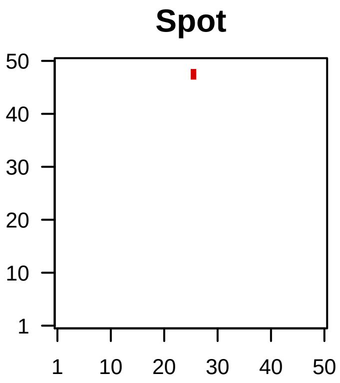
Spot Summary: I

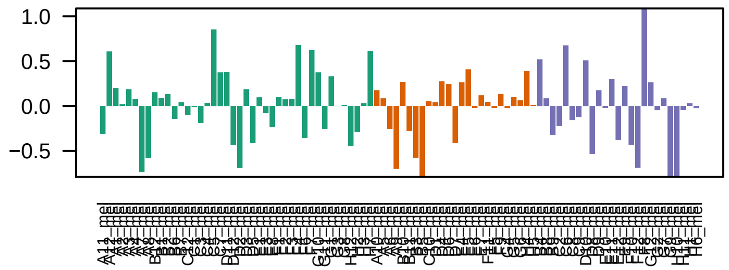
metagenes = 2
genes = 2

<r> metagenes = 1
<r> genes = 0.52
beta: r2= 0.83 / log p= −Inf

samples with spot = 25 (27.2 %)
MSC1 : 12 (28.6 %)
MSC2 : 6 (24 %)
MSC3 : 7 (28 %)


Overview Map


Spot

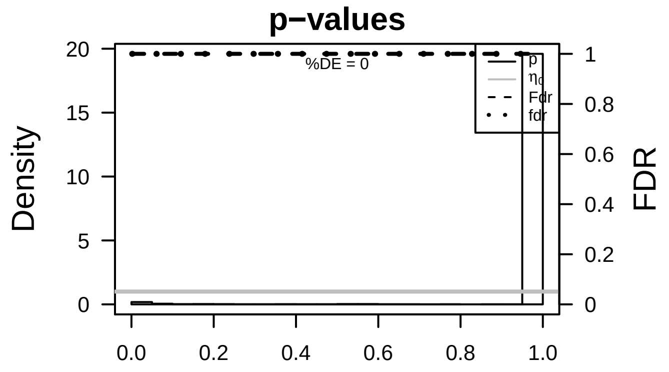


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	IFT172	1.7	−0.2	0.23	IFT172	intraflagellar transport 172 [Source:HGNC Symbol;Acc:HGNC
2	GPATCH8	0.75	−1.38	0.23	GPATCH8	G patch domain containing 8 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	0.002	1 / 13	BP	left/right axis specification
2	0.002	1 / 13	CC	sperm principal piece
3	0.002	1 / 14	BP	neural tube formation
4	0.002	1 / 16	BP	spinal cord motor neuron differentiation
5	0.002	1 / 18	CC	intraciliary transport particle B
6	0.002	1 / 18	BP	positive regulation of smoothened signaling pathway
7	0.002	1 / 18	BP	regulation of smoothened signaling pathway
8	0.003	1 / 22	BP	cytoplasmic microtubule organization
9	0.003	1 / 23	BP	limb development
10	0.004	1 / 33	BP	dorsal/ventral pattern formation
11	0.004	1 / 33	GSEA	LASTOWSKA_COAMPLIFIED_WITH_MYCN
12	0.005	1 / 35	miRN	hsa−miR−1287
13	0.005	1 / 37	BP	neural tube development
14	0.005	1 / 39	BP	bone development
15	0.006	1 / 41	CC	ciliary tip
16	0.006	1 / 41	BP	heart looping
17	0.006	1 / 43	BP	determination of left/right symmetry
18	0.006	1 / 44	BP	protein processing
19	0.006	1 / 45	GSEA	PID_HEDGEHOG_GLI_PATHWAY
20	0.006	1 / 48	BP	negative regulation of epithelial cell proliferation
21	0.007	1 / 51	CC	axoneme
22	0.007	1 / 54	miRN	hsa−miR−330−5p
23	0.008	1 / 59	BP	cilium morphogenesis
24	0.008	1 / 59	BP	epidermis development
25	0.008	1 / 59	BP	smoothened signaling pathway
26	0.008	1 / 60	miRN	hsa−miR−650
27	0.008	1 / 61	BP	palate development
28	0.008	1 / 62	miRN	hsa−miR−556−5p
29	0.009	1 / 65	miRN	hsa−miR−326
30	0.009	1 / 65	miRN	hsa−miR−9*
31	0.009	1 / 70	CC	primary cilium
32	0.010	1 / 76	BP	neural tube closure
33	0.010	1 / 77	CC	ciliary basal body
34	0.011	1 / 80	miRN	hsa−miR−942
35	0.011	1 / 83	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN
36	0.011	1 / 84	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN
37	0.011	1 / 85	miRN	hsa−miR−433
38	0.012	1 / 88	miRN	hsa−miR−587
39	0.013	1 / 97	miRN	hsa−miR−1259
40	0.013	1 / 98	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	1 / 13	left/right axis specification
2	0.002	1 / 14	neural tube formation
3	0.002	1 / 16	spinal cord motor neuron differentiation
4	0.002	1 / 18	positive regulation of smoothened signaling pathway
5	0.002	1 / 18	regulation of smoothened signaling pathway
6	0.003	1 / 22	cytoplasmic microtubule organization
7	0.003	1 / 23	limb development
8	0.004	1 / 33	dorsal/ventral pattern formation
9	0.005	1 / 37	neural tube development
10	0.005	1 / 39	bone development
11	0.006	1 / 41	heart looping
12	0.006	1 / 43	determination of left/right symmetry
13	0.006	1 / 44	protein processing
14	0.006	1 / 48	negative regulation of epithelial cell proliferation
15	0.008	1 / 59	cilium morphogenesis
16	0.008	1 / 59	epidermis development
17	0.008	1 / 59	smoothened signaling pathway
18	0.008	1 / 61	palate development
19	0.010	1 / 76	neural tube closure
20	0.014	1 / 103	cilium assembly

Brain

Rank	p−value	#in/all	Geneset
1	0.2	2 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.4	2 / 9013	Overlap_fetal_midbrain_K9K27me3
3	0.4	2 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	0.4	2 / 9330	Overlap_fetal_midbrain_ReprPC
5	0.4	2 / 9528	Overlap_fetal_midbrain_Quies
6	1.0	0 / 812	Mid_Frontal_Lobe_TssP
7	1.0	0 / 2972	Mid_Frontal_Lobe_ReprPC
8	1.0	0 / 1548	Mid_Frontal_Lobe_K9K27me3
9	1.0	0 / 765	Mid_Frontal_Lobe_Het
10	1.0	0 / 2462	Mid_Frontal_Lobe_HetRpts
11	1.0	0 / 3081	Mid_Frontal_Lobe_ZNF
12	1.0	0 / 989	Mid_Frontal_Lobe_Quies
13	1.0	0 / 156	Mid_Frontal_Lobe_TssA
14	1.0	0 / 468	Mid_Frontal_Lobe_TssF
15	1.0	0 / 229	Mid_Frontal_Lobe_TxTrans
16	1.0	0 / 166	Mid_Frontal_Lobe_Tx
17	1.0	0 / 534	Mid_Frontal_Lobe_EnhG
18	1.0	0 / 668	Mid_Frontal_Lobe_Enh
19	1.0	0 / 564	Mid_Frontal_Lobe_EnhP
20	1.0	0 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	1	0 / 15	RHODES_CANCER_META_SIGNATURE
2	1	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
3	1	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	1	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	1	0 / 12	LIU_BREAST_CANCER
6	1	0 / 14	LIU_COMMON_CANCER_GENES
7	1	0 / 14	LIU_LIVER_CANCER
8	1	0 / 14	LIU_PROSTATE_CANCER_DN
9	1	0 / 12	LIU_PROSTATE_CANCER_UP
10	1	0 / 15	WANG_ER_UP
11	1	0 / 5	WANG_ER_DN
12	1	0 / 16	WOLFER_overlap genes
13	1	0 / 12	BEN−PORATH_DN
14	1	0 / 13	BEN−PORATH_UP
15	1	0 / 15	GENTLES_modul1
16	1	0 / 16	GENTLES_modul2
17	1	0 / 10	GENTLES_modul3
18	1	0 / 15	GENTLES_modul4
19	1	0 / 10	GENTLES_modul5
20	1	0 / 16	GENTLES_modul6

CC

Rank	p−value	#in/all	Geneset
1	0.002	1 / 13	sperm principal piece
2	0.002	1 / 18	intraciliary transport particle B
3	0.006	1 / 41	ciliary tip
4	0.007	1 / 51	axoneme
5	0.009	1 / 70	primary cilium
6	0.010	1 / 77	ciliary basal body
7	0.018	1 / 131	vesicle
8	0.037	1 / 276	cilium
9	0.068	1 / 512	microtubule organizing center
10	0.188	1 / 1465	cytoskeleton
11	0.386	1 / 3214	protein complex
12	0.790	2 / 13191	cellular_component
13	0.800	1 / 8205	cytoplasm
14	0.893	1 / 9988	organelle
15	0.918	1 / 10605	intracellular
16	0.957	1 / 11774	cell
17	1.000	0 / 11	acetylcholine−gated channel complex
18	1.000	0 / 15	acrosomal membrane
19	1.000	0 / 53	acrosomal vesicle
20	1.000	0 / 202	actin cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.1	1 / 840	Chr 17
2	0.1	1 / 993	Chr 2
3	1.0	0 / 1500	Chr 1
4	1.0	0 / 552	Chr 10
5	1.0	0 / 801	Chr 11
6	1.0	0 / 775	Chr 12
7	1.0	0 / 262	Chr 13
8	1.0	0 / 462	Chr 14
9	1.0	0 / 465	Chr 15
10	1.0	0 / 649	Chr 16
11	1.0	0 / 221	Chr 18
12	1.0	0 / 1037	Chr 19
13	1.0	0 / 398	Chr 20
14	1.0	0 / 151	Chr 21
15	1.0	0 / 335	Chr 22
16	1.0	0 / 838	Chr 3
17	1.0	0 / 558	Chr 4
18	1.0	0 / 696	Chr 5
19	1.0	0 / 687	Chr 6
20	1.0	0 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 1079	ZNF_Colon
2	0.2	2 / 5880	TssD2_Colon
3	0.2	2 / 7203	TssF_Colon
4	0.3	2 / 8415	Quies3_Colon
5	0.3	2 / 8580	TxWk_Colon
6	0.4	2 / 9027	Tx_Colon
7	0.4	1 / 3383	EnhWk2_Colon
8	0.4	2 / 9482	TssA_Colon
9	0.6	1 / 5155	EnhWk1_Colon
10	0.9	1 / 9653	Enh_Colon
11	0.9	1 / 10290	TssWk_Colon
12	1.0	0 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
13	1.0	0 / 15	TCGA_Mutated−in−CRC_hypermutated
14	1.0	0 / 16	TCGA_Mutated−in−CRC_non−hypermutated
15	1.0	0 / 9	TCGA−CRC_agressive−disease−markers
16	1.0	0 / 13	TCGA−CRC_less−agressive−disease−markers
17	1.0	0 / 4	Kaneda_CIMP−group1
18	1.0	0 / 7	Kaneda_CIMP−group2
19	1.0	0 / 50	Ang_CRC_Hypermethylated
20	1.0	0 / 25	Ang_CRC_Hypomethylated

Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 435	GUDJ_psoriasis up
2	1	0 / 294	GUDJ_psoriasis down
3	1	0 / 11	BCHETNIA_EBM up
4	1	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1	0 / 15	VERHAAK_CL subtype
2	1	0 / 15	VERHAAK_MES subtype
3	1	0 / 16	VERHAAK_NL subtype
4	1	0 / 14	VERHAAK_PN subtype
5	1	0 / 23	WIRTH_PN subtype
6	1	0 / 74	WIRTH_Normal Brain
7	1	0 / 9	VERHAAK_Brain
8	1	0 / 8	VERHAAK_PN_Brain
9	1	0 / 11	Martinez_Glio_hypermeth
10	1	0 / 3	Martinez_Glio_hypometh
11	1	0 / 2	laffaire_hypometh_LGG_vs_control
12	1	0 / 72	laffaire_hypermeth_LGG_vs_control
13	1	0 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
14	1	0 / 4	Donson−adaptive−immunity−associated with LTS in HGA
15	1	0 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
16	1	0 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
17	1	0 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
18	1	0 / 32	Donson−innate immunity−associated with LTS in HGA
19	1	0 / 3	Donson−migration tethering and rolling−associated with LTS in HGA
20	1	0 / 23	Donson−Misc immune function−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.004	1 / 33	LASTOWSKA_COAMPLIFIED_WITH_MYCN
2	0.006	1 / 45	PID_HEDGEHOG_GLI_PATHWAY
3	0.011	1 / 83	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN
4	0.011	1 / 84	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN
5	0.013	1 / 98	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
6	0.018	1 / 137	JISON_SICKLE_CELL_DISEASE_DN
7	0.026	1 / 197	FOSTER_KDM1A_TARGETS_DN
8	0.027	1 / 200	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
9	0.032	1 / 238	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	0.036	1 / 273	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
11	0.038	1 / 287	JIANG_HYPOXIA_NORMAL
12	0.051	1 / 381	MARTENS_BOUND_BY_PML_RARA_FUSION
13	0.063	1 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	0.083	1 / 629	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
15	0.103	1 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
16	0.109	1 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
17	0.168	1 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
18	0.179	1 / 1394	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
19	0.215	1 / 1693	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
20	0.235	1 / 1858	PILON_KLF1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	1	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	1	0 / 176	HALLMARK_HYPOXIA
3	1	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
4	1	0 / 195	HALLMARK_MITOTIC_SPINDLE
5	1	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	1	0 / 53	HALLMARK_TGF_BETA_SIGNALING
7	1	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
8	1	0 / 146	HALLMARK_DNA_REPAIR
9	1	0 / 196	HALLMARK_G2M_CHECKPOINT
10	1	0 / 140	HALLMARK_APOPTOSIS
11	1	0 / 29	HALLMARK_NOTCH_SIGNALING
12	1	0 / 188	HALLMARK_ADIPOGENESIS
13	1	0 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	1	0 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
15	1	0 / 94	HALLMARK_ANDROGEN_RESPONSE
16	1	0 / 165	HALLMARK_MYOGENESIS
17	1	0 / 91	HALLMARK_PROTEIN_SECRETION
18	1	0 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
19	1	0 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	1	0 / 167	HALLMARK_APICAL_JUNCTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 6929	HOPP_Txn_elongation
2	0.6	1 / 5184	HOPP_Txn_transition
3	0.6	1 / 5538	HOPP_Weak_txn
4	0.6	1 / 5693	HOPP_Weak_enhancer
5	0.7	1 / 6564	HOPP_Strong_enhancer
6	0.7	1 / 7209	HOPP_Weak_promoter
7	1.0	0 / 13	BENTINK_mBL UP
8	1.0	0 / 12	BENTINK_mBL DOWN
9	1.0	0 / 129	DAVE_BL−vs−DLBCL
10	1.0	0 / 10	DAVE_BL_DN
11	1.0	0 / 16	DAVE_BL Inter
12	1.0	0 / 10	DAVE_BL UP
13	1.0	0 / 19	DAVE_c−myc BL UP
14	1.0	0 / 6	DAVE_MHCCII BL DN
15	1.0	0 / 17	DAVE_NFkB BL DN
16	1.0	0 / 23	DAVE_Immune response 1
17	1.0	0 / 15	DAVE_Immune response 2
18	1.0	0 / 212	LENZ_Stromal signature 1
19	1.0	0 / 43	LENZ_Stromal signature 2
20	1.0	0 / 50	SPANG_BAFF 9hrs DN

MF

Rank	p−value	#in/all	Geneset
1	0.05	1 / 361	binding
2	0.13	1 / 1007	poly(A) RNA binding
3	0.13	1 / 1033	nucleic acid binding
4	0.18	1 / 1365	RNA binding
5	0.23	1 / 1859	metal ion binding
6	0.37	2 / 8984	protein binding
7	0.56	1 / 4992	ion binding
8	0.79	2 / 13179	molecular_function
9	1.00	0 / 18	14−3−3 protein binding
10	1.00	0 / 19	1−phosphatidylinositol binding
11	1.00	0 / 18	2 iron, 2 sulfur cluster binding
12	1.00	0 / 22	3',5'−cyclic−nucleotide phosphodiesterase activity
13	1.00	0 / 18	3'−5' exonuclease activity
14	1.00	0 / 19	3'−5'−exoribonuclease activity
15	1.00	0 / 11	3−beta−hydroxy−delta5−steroid dehydrogenase activity
16	1.00	0 / 35	4 iron, 4 sulfur cluster binding
17	1.00	0 / 13	5'−nucleotidase activity
18	1.00	0 / 10	acetylcholine−activated cation−selective channel activity
19	1.00	0 / 10	acetylgalactosaminyltransferase activity
20	1.00	0 / 16	acetylglucosaminyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	1 / 35	hsa−miR−1287
2	0.007	1 / 54	hsa−miR−330−5p
3	0.008	1 / 60	hsa−miR−650
4	0.008	1 / 62	hsa−miR−556−5p
5	0.009	1 / 65	hsa−miR−326
6	0.009	1 / 65	hsa−miR−9*
7	0.011	1 / 80	hsa−miR−942
8	0.011	1 / 85	hsa−miR−433
9	0.012	1 / 88	hsa−miR−587
10	0.013	1 / 97	hsa−miR−1259
11	0.014	1 / 101	hsa−miR−603
12	0.018	1 / 137	hsa−miR−656
13	0.019	1 / 145	hsa−miR−922
14	0.019	1 / 145	hsa−miR−491−5p
15	0.021	1 / 153	hsa−miR−200c
16	0.021	1 / 155	hsa−miR−429
17	0.021	1 / 158	hsa−miR−200b
18	0.021	1 / 159	hsa−miR−298
19	0.022	1 / 163	hsa−miR−137
20	0.025	1 / 183	hsa−miR−1283

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.2	1 / 1266	ICGC_NrsfPcr1_targets
2	0.2	1 / 1383	ICGC_Six5_targets
3	0.2	1 / 1701	HEBENSTREIT_high expression TF
4	0.2	1 / 1878	ICGC_Cebpbsc150_targets
5	0.3	1 / 2136	ICGC_GabpPcr2_targets
6	0.3	1 / 2137	ICGC_SrfV0416101_targets
7	0.3	1 / 2714	ICGC_Irf4_targets
8	0.4	1 / 3700	ICGC_Nfatc1_targets
9	0.5	1 / 3966	ICGC_Pu1_targets
10	0.5	1 / 4032	ICGC_Creb1_targets
11	0.5	1 / 4054	ICGC_Egr1_targets
12	0.5	1 / 4314	ICGC_Ebfsc137065_targets
13	0.5	1 / 4385	ICGC_Atf2_targets
14	0.5	1 / 4414	ICGC_Bclaf101388_targets
15	0.5	1 / 4617	ICGC_Tcf12_targets
16	0.5	1 / 4682	ICGC_Pol24_targets
17	0.5	1 / 4689	ICGC_Taf1_targets
18	0.5	1 / 4706	ICGC_Sp1_targets
19	0.5	1 / 4774	ICGC_Foxm1_targets
20	0.5	1 / 4829	ICGC_Nficsc81335_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 32	WIRTH_Pancreas
2	1	0 / 350	WIRTH_Immune system
3	1	0 / 11	WIRTH_Sec. lymphoid organs
4	1	0 / 11	WIRTH_Prim. lymphoid organs
5	1	0 / 13	WIRTH_B−cells
6	1	0 / 8	WIRTH_Tonsil
7	1	0 / 12	WIRTH_Thymus
8	1	0 / 12	WIRTH_Lymphocytes
9	1	0 / 5	WIRTH_Bone marrow
10	1	0 / 350	WIRTH_Nervous System
11	1	0 / 11	WIRTH_Globus pallidus
12	1	0 / 14	WIRTH_Telencephalon
13	1	0 / 11	WIRTH_Cortex cerebri
14	1	0 / 10	WIRTH_Hippocampus
15	1	0 / 10	WIRTH_Thalamus
16	1	0 / 12	WIRTH_Cerebellum
17	1	0 / 107	WIRTH_Testis
18	1	0 / 41	WIRTH_Homeostasis
19	1	0 / 46	WIRTH_Liver
20	1	0 / 95	WIRTH_Muscle

Toxic

Rank	p−value	#in/all	Geneset
1	1	0 / 3682	LU_BPDE 0.005 DN
2	1	0 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: J

metagenes = 10
genes = 138

<r> metagenes = 0.95
<r> genes = 0.1
beta: r2= 1.7 / log p= −Inf

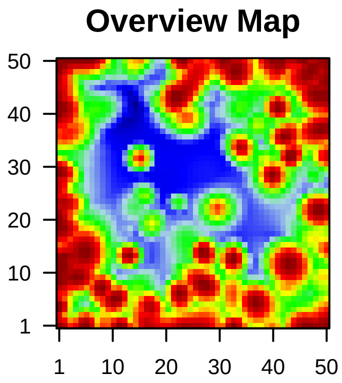
samples with spot = 14 (15.2 %)
MSC1 : 5 (11.9 %)
MSC2 : 5 (20 %)
MSC3 : 4 (16 %)

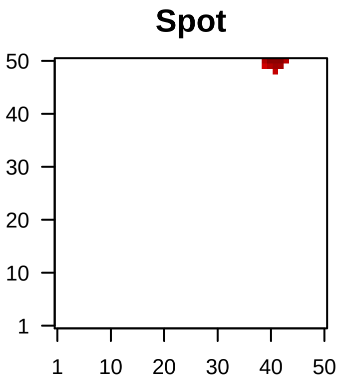
Spot Genelist

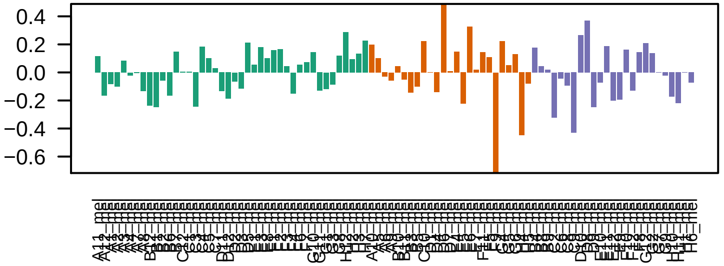
Rank	ID	max e	min e	r	Symbol	Description
1	MYO1E	1.87	−0.47	0.35	MYO1E	myosin IE [Source:HGNC Symbol;Acc:HGNC:7599]
2	EMC1	1.82	−0.59	0.33	EMC1	ER membrane protein complex subunit 1 [Source:HGNC Sym
3	SELL	1.69	−0.16	0.33	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
4	GULP1	1.65	−0.53	0.26	GULP1	GULP, engulfment adaptor PTB domain containing 1 [Source:
5	PGBD2	1.63	−0.39	0.31	PGBD2	piggyBac transposable element derived 2 [Source:HGNC Syr
6	STK11IP	1.61	−0.17	0.35	STK11IP	serine/threonine kinase 11 interacting protein [Source:HGNC
7	LIPT1	1.57	−0.38	0.29	LIPT1	lipoyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:29569]
8	FUCA1	1.57	−0.24	0.34	FUCA1	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:H
9	GPX8	1.56	−0.72	0.32	GPX8	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Ac
10	FAM114A2	1.56	−0.67	0.26	FAM114A2	family with sequence similarity 114, member A2 [Source:HGN
11	SIL1	1.56	−0.68	0.35	SIL1	SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:
12	PDLIM2	1.55	−0.27	0.24	PDLIM2	PDZ and LIM domain 2 (mystique) [Source:HGNC Symbol;Ac
13	ATG13	1.55	−0.73	0.39	ATG13	autophagy related 13 [Source:HGNC Symbol;Acc:HGNC:290
14	PLA2G4A	1.54	−0.31	0.29	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium−dependent)
15	PEX13	1.54	−0.59	0.25	PEX13	peroxisomal biogenesis factor 13 [Source:HGNC Symbol;Acc
16	PJA1	1.53	−0.56	0.36	PJA1	praja ring finger 1, E3 ubiquitin protein ligase [Source:HGNC
17	DNAJB9	1.51	−0.61	0.28	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9 [Source:HGN
18	PARP11	1.51	−0.34	0.23	PARP11	poly (ADP−ribose) polymerase family, member 11 [Source:HC
19	CFH	1.5	−0.41	0.31	CFH	complement factor H [Source:HGNC Symbol;Acc:HGNC:488
20	DDX19B	1.48	−0.89	0.3	DDX19B	DEAD (Asp−Glu−Ala−Asp) box polypeptide 19B [Source:HGN

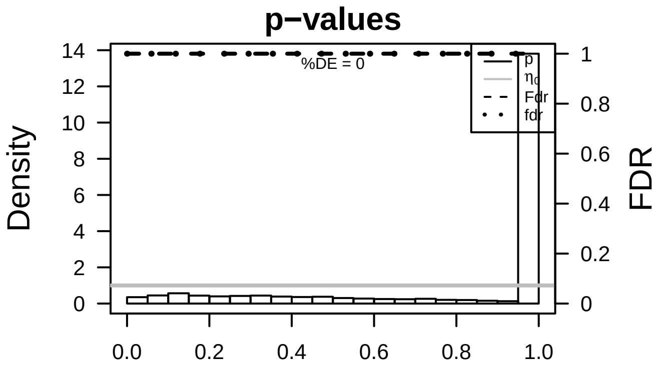
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−11	108 / 7592	Lymp	HOPP_Active_promoter
2	5e−11	122 / 9482	Colon	TssA_Colon
3	2e−10	101 / 6929	Lymp	HOPP_Txn_elongation
4	2e−10	120 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	6e−07	111 / 9027	Colon	Tx_Colon
6	1e−06	110 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
7	2e−06	106 / 8580	Colon	TxWk_Colon
8	7e−06	81 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
9	1e−05	92 / 7209	Lymp	HOPP_Weak_promoter
10	3e−05	14 / 408	GSE	ZHANG_BREAST_CANCER_PROGENITORS_UP
11	5e−05	99 / 8205	CC	cytoplasm
12	2e−04	31 / 1701	TF	HEBENSTREIT_high expression TF
13	2e−04	99 / 8415	Colon	Quies3_Colon
14	3e−04	68 / 5184	Lymp	HOPP_Txn_transition
15	6e−04	16 / 681	GSE	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
16	7e−04	10 / 315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	8e−04	11 / 379	GSE	LIM_MAMMARY_STEM_CELL_DN
18	8e−04	2 / 5	GSE	CASTELLANO_HRAS_AND_NRAS_TARGETS_UP
19	8e−04	70 / 5538	Lymp	HOPP_Weak_txn
20	1e−03	112 / 10290	Colon	TssWk_Colon
21	1e−03	7 / 175	miRN	hsa−miR−548k
22	1e−03	12 / 462	Chr	Chr 14
23	2e−03	18 / 890	GSE	ACEVEDO_LIVER_CANCER_UP
24	2e−03	7 / 182	GSE	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
25	2e−03	3 / 28	GSE	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
26	3e−03	3 / 30	BP	negative regulation of viral genome replication
27	4e−03	2 / 10	MF	glutathione binding
28	4e−03	11 / 461	GSE	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B
29	4e−03	4 / 70	Canc	SHAUGHNESSY_MM high risk
30	4e−03	3 / 36	GSE	SESTO_RESPONSE_TO_UV_C6
31	5e−03	6 / 167	HM	HALLMARK_IL2_STAT5_SIGNALING
32	5e−03	11 / 476	GSE	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
33	5e−03	23 / 1400	TF	ICGC_Myc_targets
34	5e−03	2 / 12	BP	negative regulation of DNA damage response, signal transduction by p53 c
35	6e−03	68 / 5693	Lymp	HOPP_Weak_enhancer
36	6e−03	28 / 1858	GSE	PILON_KLF1_TARGETS_DN
37	6e−03	7 / 235	GSE	BLUM_RESPONSE_TO_SALIRASIB_UP
38	7e−03	3 / 42	GSE	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
39	7e−03	2 / 14	GSE	KEGG_OTHER_GLYCAN_DEGRADATION
40	7e−03	2 / 14	GSE	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS









Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.003	3 / 30	negative regulation of viral genome replication
2	0.005	2 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
3	0.010	3 / 48	positive regulation of proteasomal ubiquitin−dependent protein catabolic proce
4	0.011	21 / 1325	catabolic process
5	0.015	4 / 101	response to oxidative stress
6	0.016	2 / 21	adipose tissue development
7	0.017	9 / 422	viral process
8	0.019	2 / 23	glycosaminoglycan catabolic process
9	0.019	3 / 61	palate development
10	0.031	2 / 30	cholesterol biosynthetic process
11	0.034	5 / 193	protein folding
12	0.034	9 / 478	protein transport
13	0.038	2 / 33	outflow tract morphogenesis
14	0.040	2 / 34	arachidonic acid metabolic process
15	0.040	2 / 34	response to nutrient levels
16	0.040	3 / 81	positive regulation of sequence−specific DNA binding transcription factor activ
17	0.044	6 / 276	nucleobase−containing compound catabolic process
18	0.049	23 / 1730	small molecule metabolic process
19	0.050	3 / 89	neuron migration
20	0.055	5 / 220	cofactor metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−10	120 / 9330	Overlap_fetal_midbrain_ReprPC
2	1e−06	110 / 9013	Overlap_fetal_midbrain_K9K27me3
3	7e−06	81 / 5940	Overlap_fetal_midbrain_HetRpts
4	2e−02	96 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	3e−02	25 / 1845	Fetal_Quies
6	2e−01	11 / 831	Fetal_HetRpts
7	2e−01	12 / 953	Fetal_Enh
8	2e−01	13 / 1050	Fetal_EnhP
9	2e−01	94 / 9528	Overlap_fetal_midbrain_Quies
10	2e−01	13 / 1065	Overlap_fetal_midbrain_Enh
11	2e−01	11 / 884	Overlap_fetal_midbrain_EnhG
12	3e−01	11 / 1013	Fetal_TssP
13	4e−01	7 / 656	Overlap_fetal_midbrain_EnhP
14	4e−01	8 / 769	Overlap_fetal_midbrain_ZNF
15	4e−01	2 / 158	Overlap_fetal_midbrain_Het
16	4e−01	10 / 989	Mid_Frontal_Lobe_Quies
17	5e−01	11 / 1122	Fetal_K9K27me3
18	6e−01	28 / 3081	Mid_Frontal_Lobe_ZNF
19	6e−01	7 / 786	Fetal_EnhG
20	6e−01	17 / 1949	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	4 / 70	SHAUGHNESSY_MM high risk
2	0.060	6 / 298	SPANG_BCL6−index2
3	0.125	0 / 14	LIU_COMMON_CANCER_GENES
4	0.139	1 / 16	GENTLES_modul6
5	0.237	1 / 29	KUIPER_MM good survival
6	0.356	1 / 47	PanCan_DNARepair_geneset_nanostring
7	0.647	1 / 111	PanCan_RAS_geneset_nanostring
8	0.678	1 / 121	PanCan_MAPK_geneset_nanostring
9	0.704	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.816	1 / 180	SPANG_LPS−index2
11	0.837	3 / 489	Lembcke_Normal vs Adenoma
12	0.891	2 / 401	Lembcke_Colonic Inflammation
13	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	1.000	0 / 12	LIU_BREAST_CANCER
18	1.000	0 / 14	LIU_LIVER_CANCER
19	1.000	0 / 12	LIU_PROSTATE_CANCER_UP
20	1.000	0 / 15	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	5e−05	99 / 8205	cytoplasm
2	1e−02	111 / 10605	intracellular
3	2e−02	3 / 57	proteasome complex
4	3e−02	2 / 31	dendritic shaft
5	3e−02	8 / 401	mitochondrial inner membrane
6	5e−02	2 / 38	cytoplasmic side of plasma membrane
7	5e−02	3 / 92	spliceosomal complex
8	6e−02	102 / 9988	organelle
9	7e−02	2 / 48	stress fiber
10	9e−02	37 / 3214	protein complex
11	9e−02	1 / 10	ER membrane protein complex
12	9e−02	1 / 10	WASH complex
13	9e−02	2 / 54	intermediate filament cytoskeleton
14	1e−01	1 / 11	CD40 receptor complex
15	1e−01	1 / 12	holo TFIIH complex
16	1e−01	1 / 12	STAGA complex
17	1e−01	1 / 12	XY body
18	1e−01	4 / 196	nuclear membrane
19	1e−01	1 / 13	integrator complex
20	1e−01	1 / 13	proteasome regulatory particle

Chr

Rank	p−value	#in/all	Geneset
1	0.001	12 / 462	Chr 14
2	0.011	17 / 993	Chr 2
3	0.029	12 / 696	Chr 5
4	0.156	18 / 1500	Chr 1
5	0.212	10 / 801	Chr 11
6	0.311	8 / 689	Chr 7
7	0.338	3 / 221	Chr 18
8	0.443	5 / 469	Chr 8
9	0.457	7 / 687	Chr 6
10	0.521	8 / 838	Chr 3
11	0.585	5 / 551	Chr X
12	0.606	3 / 335	Chr 22
13	0.632	4 / 465	Chr 15
14	0.720	3 / 398	Chr 20
15	0.727	5 / 649	Chr 16
16	0.733	6 / 775	Chr 12
17	0.758	1 / 151	Chr 21
18	0.957	4 / 840	Chr 17
19	0.973	2 / 576	Chr 9
20	0.995	1 / 552	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−11	122 / 9482	TssA_Colon
2	6e−07	111 / 9027	Tx_Colon
3	2e−06	106 / 8580	TxWk_Colon
4	2e−04	99 / 8415	Quies3_Colon
5	1e−03	112 / 10290	TssWk_Colon
6	2e−02	3 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
7	7e−02	76 / 7203	TssF_Colon
8	7e−02	1 / 8	Juehling−MSI−enriched−in−7
9	8e−02	10 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	9e−02	11 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
11	9e−02	1 / 10	KIM_MSI−in−CRC
12	1e−01	1 / 11	Budinska_B_Lower crypt−like_DOWN
13	2e−01	12 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	2e−01	1 / 29	Marisa_CRC−cluster−c
15	3e−01	12 / 1079	ZNF_Colon
16	3e−01	38 / 3812	TssD1_Colon
17	4e−01	92 / 9653	Enh_Colon
18	4e−01	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
19	5e−01	1 / 66	Marisa_CRC−cluster−h
20	5e−01	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.6	4 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	7e−04	10 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	8e−03	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
3	1e−02	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
4	2e−02	1 / 2	WILLSCHER_GBM_LTSmut_proteomics−E_UP
5	1e−01	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
6	1e−01	2 / 63	Stuehler_Proteins_up_in_STS
7	1e−01	2 / 65	GIEZELT_GBM_STS_up_VS_LTS
8	2e−01	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
9	2e−01	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
10	2e−01	1 / 25	Shaw_down_in_1p19q
11	3e−01	10 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	3e−01	1 / 32	Donson−innate immunity−associated with LTS in HGA
13	3e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
14	3e−01	1 / 38	OL vs. OPC
15	3e−01	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
16	4e−01	1 / 49	OL vs. MOG− OL
17	4e−01	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
18	4e−01	1 / 62	cultured astroglia vs. in vivo astrocytes
19	5e−01	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
20	5e−01	1 / 71	Weller_LGG_A_vs_O_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	14 / 408	ZHANG_BREAST_CANCER_PROGENITORS_UP
2	6e−04	16 / 681	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
3	8e−04	11 / 379	LIM_MAMMARY_STEM_CELL_DN
4	8e−04	2 / 5	CASTELLANO_HRAS_AND_NRAS_TARGETS_UP
5	2e−03	18 / 890	ACEVEDO_LIVER_CANCER_UP
6	2e−03	7 / 182	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
7	2e−03	3 / 28	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
8	4e−03	11 / 461	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B
9	4e−03	3 / 36	SESTO_RESPONSE_TO_UV_C6
10	5e−03	11 / 476	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
11	6e−03	28 / 1858	PILON_KLF1_TARGETS_DN
12	6e−03	7 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
13	7e−03	3 / 42	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
14	7e−03	2 / 14	KEGG_OTHER_GLYCAN_DEGRADATION
15	7e−03	2 / 14	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS
16	7e−03	6 / 183	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP
17	8e−03	19 / 1123	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
18	8e−03	2 / 15	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN
19	9e−03	7 / 248	HELLER_HDAC_TARGETS_DN
20	9e−03	3 / 47	SUNG_METASTASIS_STROMA_DN

HM

Rank	p−value	#in/all	Geneset
1	0.005	6 / 167	HALLMARK_IL2_STAT5_SIGNALING
2	0.021	5 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.021	5 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	0.031	5 / 188	HALLMARK_ADIPOGENESIS
5	0.032	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.038	5 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	0.064	4 / 162	HALLMARK_COMPLEMENT
8	0.194	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
9	0.218	2 / 94	HALLMARK_ANDROGEN_RESPONSE
10	0.269	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	0.275	3 / 196	HALLMARK_MTORC1_SIGNALING
12	0.375	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
13	0.394	2 / 146	HALLMARK_DNA_REPAIR
14	0.401	2 / 148	HALLMARK_KRAS_SIGNALING_UP
15	0.413	1 / 57	HALLMARK_MYC_TARGETS_V2
16	0.546	2 / 196	HALLMARK_G2M_CHECKPOINT
17	0.574	1 / 91	HALLMARK_PROTEIN_SECRETION
18	0.574	1 / 91	HALLMARK_BILE_ACID_METABOLISM
19	0.582	1 / 93	HALLMARK_PEROXISOME
20	0.589	1 / 95	HALLMARK_SPERMATOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
2	0.26	1 / 32	DUMEAUX_Fasting enriched genes
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−11	108 / 7592	HOPP_Active_promoter
2	2e−10	101 / 6929	HOPP_Txn_elongation
3	1e−05	92 / 7209	HOPP_Weak_promoter
4	3e−04	68 / 5184	HOPP_Txn_transition
5	8e−04	70 / 5538	HOPP_Weak_txn
6	6e−03	68 / 5693	HOPP_Weak_enhancer
7	2e−02	19 / 1218	SPANG_BCR UP
8	4e−02	1 / 4	Shaknovich_ABC_hyper_meth
9	6e−02	1 / 7	CARO_OxPhos_vs_BCR_UP
10	7e−02	1 / 8	MASCQUE_GCB UP
11	3e−01	2 / 107	SPANG_LPS 6hrs UP
12	3e−01	23 / 2211	HOPP_Repetitive
13	3e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
14	3e−01	1 / 43	LENZ_Stromal signature 2
15	3e−01	64 / 6564	HOPP_Strong_enhancer
16	4e−01	12 / 1128	SPANG_BCR DN
17	4e−01	25 / 2563	HOPP_Heterochrom
18	4e−01	1 / 61	SPANG_LPS 6hrs DN
19	5e−01	1 / 82	ROSOLOWSKI_green UP
20	6e−01	1 / 89	ROSOLOWSKI_blue total

MF

Rank	p−value	#in/all	Geneset
1	0.004	2 / 10	glutathione binding
2	0.016	2 / 21	polyubiquitin binding
3	0.022	2 / 25	cytochrome−c oxidase activity
4	0.031	8 / 394	catalytic activity
5	0.031	2 / 30	hydrolase activity, hydrolyzing O−glycosyl compounds
6	0.046	2 / 37	coenzyme binding
7	0.046	2 / 37	histone acetyltransferase activity
8	0.049	10 / 592	oxidoreductase activity
9	0.059	3 / 95	hydrolase activity, acting on glycosyl bonds
10	0.059	15 / 1040	zinc ion binding
11	0.075	6 / 316	protein kinase binding
12	0.081	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
13	0.089	1 / 10	cAMP response element binding protein binding
14	0.089	1 / 10	glycine binding
15	0.098	1 / 11	ATPase activity, coupled
16	0.098	1 / 11	cAMP response element binding
17	0.098	1 / 11	glutathione peroxidase activity
18	0.098	1 / 11	quinone binding
19	0.098	1 / 11	telomeric DNA binding
20	0.106	4 / 193	transferase activity, transferring acyl groups

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	7 / 175	hsa−miR−548k
2	0.010	5 / 140	hsa−miR−409−3p
3	0.013	3 / 53	hsa−miR−552
4	0.016	6 / 217	hsa−miR−203
5	0.022	4 / 115	hsa−miR−515−5p
6	0.025	3 / 68	hsa−miR−649
7	0.033	3 / 75	hsa−miR−509−5p
8	0.033	2 / 31	hsa−miR−617
9	0.035	4 / 132	hsa−miR−320d
10	0.039	4 / 137	hsa−miR−656
11	0.044	2 / 36	hsa−miR−1226
12	0.047	9 / 507	hsa−miR−15a
13	0.047	4 / 146	hsa−miR−320c
14	0.048	4 / 147	hsa−miR−143
15	0.050	4 / 149	hsa−miR−633
16	0.051	4 / 150	hsa−miR−338−3p
17	0.052	5 / 217	hsa−miR−181d
18	0.058	2 / 42	hsa−miR−642
19	0.066	4 / 163	hsa−miR−495
20	0.068	3 / 101	hsa−miR−603

PathwAct

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	BENTINK_e2f3.1
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 12	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−04	31 / 1701	HEBENSTREIT_high expression TF
2	5e−03	23 / 1400	ICGC_Myc_targets
3	1e−02	19 / 1171	KIM_MYC targets
4	2e−02	1 / 2	MYC_ECM cell adhesion DOWN
5	3e−02	20 / 1383	ICGC_Six5_targets
6	3e−02	10 / 553	ICGC_RxraPcr1_targets
7	6e−02	27 / 2136	ICGC_GabpPcr2_targets
8	8e−02	1 / 9	MYC_Targets DOWN
9	3e−01	54 / 5408	ICGC_Pou2_targets
10	3e−01	20 / 1878	ICGC_Cebpbsc150_targets
11	3e−01	15 / 1418	ICGC_Ets1_targets
12	4e−01	46 / 4682	ICGC_Pol24_targets
13	4e−01	47 / 4879	ICGC_Pmlsc71910_targets
14	4e−01	21 / 2137	ICGC_SrfV0416101_targets
15	5e−01	42 / 4414	ICGC_Bclaf101388_targets
16	5e−01	23 / 2391	ICGC_Pbx3_targets
17	5e−01	37 / 3924	ICGC_Zeb1_targets
18	5e−01	44 / 4689	ICGC_Taf1_targets
19	6e−01	25 / 2714	ICGC_Irf4_targets
20	6e−01	34 / 3700	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
2	0.29	1 / 36	VAQUERIZAS_Fetal brain
3	0.31	1 / 40	VAQUERIZAS_Thyroid
4	0.38	2 / 143	VAQUERIZAS_General
5	1.00	0 / 41	VAQUERIZAS_Placenta
6	1.00	0 / 26	VAQUERIZAS_Liver
7	1.00	0 / 33	VAQUERIZAS_Prostate
8	1.00	0 / 29	VAQUERIZAS_Smooth muscle
9	1.00	0 / 45	VAQUERIZAS_Uterus
10	1.00	0 / 9	VAQUERIZAS_Kidney
11	1.00	0 / 23	VAQUERIZAS_Spinal cord
12	1.00	0 / 38	VAQUERIZAS_Whole brain
13	1.00	0 / 37	VAQUERIZAS_Thymus
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	WIRTH_B−cells
2	0.2	4 / 225	PALMER_Granulocytes signature up
3	0.5	2 / 194	PALMER_B−Cell signature up
4	0.6	3 / 350	WIRTH_Immune system
5	1.0	0 / 32	WIRTH_Pancreas
6	1.0	0 / 11	WIRTH_Sec. lymphoid organs
7	1.0	0 / 11	WIRTH_Prim. lymphoid organs
8	1.0	0 / 8	WIRTH_Tonsil
9	1.0	0 / 12	WIRTH_Thymus
10	1.0	0 / 12	WIRTH_Lymphocytes
11	1.0	0 / 5	WIRTH_Bone marrow
12	1.0	0 / 350	WIRTH_Nervous System
13	1.0	0 / 11	WIRTH_Globus pallidus
14	1.0	0 / 14	WIRTH_Telencephalon
15	1.0	0 / 11	WIRTH_Cortex cerebri
16	1.0	0 / 10	WIRTH_Hippocampus
17	1.0	0 / 10	WIRTH_Thalamus
18	1.0	0 / 12	WIRTH_Cerebellum
19	1.0	0 / 107	WIRTH_Testis
20	1.0	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	8 / 1115	LU_BPDE 1h DN
2	1.0	26 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

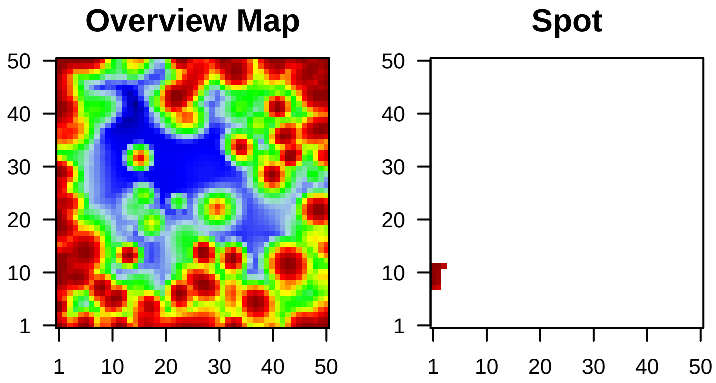
Overexpression Spots

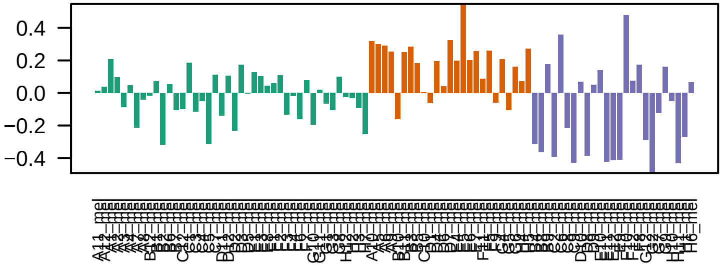
Spot Summary: K

metagenes = 11
genes = 196

<r> metagenes = 0.95
<r> genes = 0.14
beta: r2= 2.45 / log p= −Inf

samples with spot = 20 (21.7 %)
MSC1 : 2 (4.8 %)
MSC2 : 16 (64 %)
MSC3 : 2 (8 %)



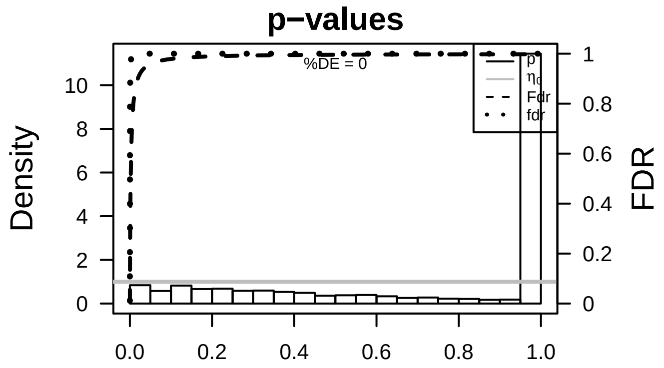


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	POPDC2	2.06	−0.33	0.46	POPDC2	popeye domain containing 2 [Source:HGNC Symbol;Acc:HG
2	EGLN3	1.89	−0.41	0.36	EGLN3	egl−9 family hypoxia−inducible factor 3 [Source:HGNC Symb
3	KCNQ5	1.87	−0.46	0.35	KCNQ5	potassium channel, voltage gated KQT−like subfamily Q, mer
4	CFAP61	1.86	−0.52	0.45	CFAP61	cilia and flagella associated protein 61 [Source:HGNC Symb
5	LYRM9	1.85	−0.31	0.28	LYRM9	LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
6	CC2D1B	1.84	−0.41	0.22	CC2D1B	coiled−coil and C2 domain containing 1B [Source:HGNC Sym
7	KRTAP19−1	1.78	−0.78	0.4	KRTAP19−1	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:
8	GAS8	1.75	−0.56	0.29	GAS8	growth arrest−specific 8 [Source:HGNC Symbol;Acc:HGNC:4
9	BBS5	1.74	−0.64	0.36	BBS5	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
10	C1orf54	1.7	−0.3	0.41	C1orf54	chromosome 1 open reading frame 54 [Source:HGNC Symb
11	SUOX	1.69	−0.67	0.27	SUOX	sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
12	PLA1A	1.68	−0.26	0.34	PLA1A	phospholipase A1 member A [Source:HGNC Symbol;Acc:HG
13	FUBP3	1.66	−0.52	0.3	FUBP3	far upstream element (FUSE) binding protein 3 [Source:HGN
14	VPS13D	1.65	−0.8	0.38	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae) [Source
15	PRKCH	1.63	−0.39	0.32	PRKCH	protein kinase C, eta [Source:HGNC Symbol;Acc:HGNC:940
16	AGPAT6	1.6	−1.04	0.45	AGPAT6	1−acylglycerol−3−phosphate O−acyltransferase 6 [Source:H
17	TGDS	1.58	−0.72	0.45	TGDS	TDP−glucose 4,6−dehydratase [Source:HGNC Symbol;Acc:
18	DGKI	1.57	−0.49	0.35	DGKI	diacylglycerol kinase, iota [Source:HGNC Symbol;Acc:HGNC
19	ZNF18	1.57	−0.32	0.29	ZNF18	zinc finger protein 18 [Source:HGNC Symbol;Acc:HGNC:129
20	CEACAM1	1.55	−1.27	0.42	CEACAM1	carcinoembryonic antigen−related cell adhesion molecule 1 (

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−07	154 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	2e−06	149 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
3	3e−06	68 / 3088	CC	plasma membrane
4	7e−06	9 / 100	miRN	hsa−miR−574−5p
5	2e−05	16 / 353	GSEA	ONDER_CDH1_TARGETS_2_DN
6	3e−05	7 / 67	BP	pigmentation
7	4e−05	4 / 15	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
8	6e−05	4 / 17	MF	Ras GTPase binding
9	7e−05	144 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
10	7e−05	15 / 356	GSEA	DELYS_THYROID_CANCER_UP
11	1e−04	19 / 552	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
12	1e−04	67 / 3383	Colon	EnhWk2_Colon
13	1e−04	22 / 705	BP	locomotion
14	2e−04	149 / 9528	Brain	Overlap_fetal_midbrain_Quies
15	2e−04	74 / 3897	Colon	Quies1_Colon
16	3e−04	3 / 10	BP	negative regulation of smooth muscle cell migration
17	3e−04	3 / 10	MF	semaphorin receptor binding
18	3e−04	27 / 995	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
19	3e−04	102 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
20	6e−04	3 / 13	GSEA	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
21	7e−04	13 / 349	GSEA	RATTENBACHER_BOUND_BY_CELF1
22	7e−04	3 / 14	GSEA	LE_SKI_TARGETS_UP
23	8e−04	5 / 55	GSEA	BILBAN_B_CLL_LPL_UP
24	8e−04	18 / 590	BP	cell morphogenesis
25	9e−04	3 / 15	BP	developmental pigmentation
26	1e−03	51 / 2576	CC	membrane
27	2e−03	15 / 475	GSEA	ONKEN_UVEAL_MELANOMA_DN
28	2e−03	3 / 18	BP	melanocyte differentiation
29	2e−03	8 / 167	GSEA	KIM_MYC_AMPLIFICATION_TARGETS_UP
30	2e−03	3 / 19	MF	1−phosphatidylinositol binding
31	2e−03	3 / 19	MF	cAMP binding
32	2e−03	3 / 19	GSEA	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN
33	2e−03	9 / 212	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
34	2e−03	8 / 174	HM	HALLMARK_ESTROGEN_RESPONSE_EARLY
35	2e−03	3 / 20	BP	semaphorin−plexin signaling pathway
36	2e−03	3 / 20	GSEA	YANG_BREAST_CANCER_ESR1_BULK_DN
37	2e−03	3 / 20	GSEA	FERRARI_RESPONSE_TO_FENRETINIDE_UP
38	2e−03	8 / 175	CC	early endosome
39	2e−03	8 / 176	GSEA	FOSTER_KDM1A_TARGETS_UP
40	2e−03	3 / 21	BP	melanosome transport



Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 100	HORVATH_aging_genes meth DOWN
2	0.4	2 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−05	7 / 67	pigmentation
2	1e−04	22 / 705	locomotion
3	3e−04	3 / 10	negative regulation of smooth muscle cell migration
4	8e−04	18 / 590	cell morphogenesis
5	9e−04	3 / 15	developmental pigmentation
6	2e−03	3 / 18	melanocyte differentiation
7	2e−03	3 / 20	semaphorin−plexin signaling pathway
8	2e−03	3 / 21	melanosome transport
9	4e−03	3 / 24	neural crest cell migration
10	4e−03	9 / 239	response to drug
11	6e−03	3 / 28	sperm motility
12	7e−03	2 / 10	temperature homeostasis
13	8e−03	3 / 31	phosphatidylinositol phosphorylation
14	8e−03	12 / 409	cell motility
15	9e−03	5 / 96	leukocyte migration
16	9e−03	2 / 11	fatty acid oxidation
17	9e−03	4 / 63	response to ethanol
18	1e−02	2 / 12	positive regulation of urine volume
19	1e−02	19 / 815	lipid metabolic process
20	1e−02	4 / 66	response to nutrient

Brain

Rank	p−value	#in/all	Geneset
1	8e−07	154 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−06	149 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	7e−05	144 / 9013	Overlap_fetal_midbrain_K9K27me3
4	2e−04	149 / 9528	Overlap_fetal_midbrain_Quies
5	3e−04	102 / 5940	Overlap_fetal_midbrain_HetRpts
6	7e−03	17 / 668	Mid_Frontal_Lobe_Enh
7	7e−03	23 / 1013	Fetal_TssP
8	9e−03	37 / 1907	Fetal_TxTrans
9	3e−02	39 / 2185	Fetal_TssA
10	3e−02	17 / 786	Fetal_EnhG
11	4e−02	21 / 1065	Overlap_fetal_midbrain_Enh
12	5e−02	23 / 1207	Overlap_fetal_midbrain_TssF
13	6e−02	3 / 69	Overlap_fetal_midbrain_Tx
14	7e−02	33 / 1949	Fetal_TssF
15	8e−02	49 / 3081	Mid_Frontal_Lobe_ZNF
16	8e−02	15 / 769	Overlap_fetal_midbrain_ZNF
17	1e−01	16 / 884	Overlap_fetal_midbrain_EnhG
18	1e−01	8 / 383	Fetal_Tx
19	2e−01	10 / 574	Overlap_fetal_midbrain_TssP
20	2e−01	11 / 656	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	4 / 111	PanCan_RAS_geneset_nanostring
2	0.08	9 / 401	Lembcke_Colonic Inflammation
3	0.09	5 / 180	SPANG_LPS−index2
4	0.09	0 / 12	LIU_PROSTATE_CANCER_UP
5	0.12	1 / 10	GENTLES_modul13
6	0.16	2 / 55	PanCan_JAK−ST_geneset_nanostring
7	0.17	1 / 14	LIU_COMMON_CANCER_GENES
8	0.23	1 / 20	PanCan_ChromMod_geneset_nanostring
9	0.25	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.35	5 / 298	SPANG_BCL6−index2
11	0.41	1 / 40	PanCan_HK_geneset_nanostring
12	0.46	1 / 47	PanCan_DNARepair_geneset_nanostring
13	0.48	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	0.59	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	0.61	2 / 156	PanCan_PI3K_geneset_nanostring
16	0.62	6 / 489	Lembcke_Normal vs Adenoma
17	0.66	1 / 82	PanCan_TXmisReg_geneset_nanostring
18	0.78	1 / 113	PanCan_Driver_Gene_geneset_nanostring
19	0.80	1 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.86	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	3e−06	68 / 3088	plasma membrane
2	1e−03	51 / 2576	membrane
3	2e−03	8 / 175	early endosome
4	5e−03	169 / 11774	cell
5	7e−03	125 / 8205	cytoplasm
6	2e−02	8 / 246	mitochondrial matrix
7	2e−02	7 / 200	axon
8	2e−02	3 / 44	motile cilium
9	2e−02	44 / 2507	cytosol
10	3e−02	3 / 49	extrinsic component of cytoplasmic side of plasma membrane
11	3e−02	2 / 20	retromer complex
12	3e−02	6 / 178	apical plasma membrane
13	3e−02	2 / 21	immunological synapse
14	3e−02	3 / 52	secretory granule
15	3e−02	2 / 22	smooth endoplasmic reticulum
16	4e−02	4 / 94	melanosome
17	5e−02	49 / 2984	integral component of membrane
18	5e−02	3 / 64	Golgi cisterna membrane
19	6e−02	2 / 29	cell−cell adherens junction
20	7e−02	2 / 32	chloride channel complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	8 / 262	Chr 13
2	0.04	11 / 465	Chr 15
3	0.10	18 / 993	Chr 2
4	0.17	9 / 469	Chr 8
5	0.21	14 / 838	Chr 3
6	0.22	14 / 840	Chr 17
7	0.23	10 / 576	Chr 9
8	0.31	11 / 696	Chr 5
9	0.32	3 / 151	Chr 21
10	0.44	11 / 775	Chr 12
11	0.45	8 / 558	Chr 4
12	0.51	20 / 1500	Chr 1
13	0.56	3 / 221	Chr 18
14	0.57	6 / 462	Chr 14
15	0.60	5 / 398	Chr 20
16	0.65	4 / 335	Chr 22
17	0.75	7 / 649	Chr 16
18	0.81	7 / 689	Chr 7
19	0.85	5 / 551	Chr X
20	0.94	4 / 552	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	67 / 3383	EnhWk2_Colon
2	2e−04	74 / 3897	Quies1_Colon
3	4e−03	129 / 8415	Quies3_Colon
4	6e−03	22 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
5	6e−03	66 / 3812	TssD1_Colon
6	1e−02	5 / 102	Marisa_CRC−cluster−d
7	2e−02	149 / 10290	TssWk_Colon
8	3e−02	11 / 436	K9acLow_Colon
9	4e−02	131 / 9027	Tx_Colon
10	4e−02	80 / 5155	EnhWk1_Colon
11	4e−02	125 / 8580	TxWk_Colon
12	5e−02	45 / 2698	EnhA_Colon
13	5e−02	138 / 9653	Enh_Colon
14	6e−02	10 / 427	Quies2_Colon
15	6e−02	7 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
16	6e−02	1 / 5	Budinska_C_CIMP−H−like_UP
17	7e−02	88 / 5880	TssD2_Colon
18	7e−02	3 / 71	Marisa_CRC−cluster−g
19	7e−02	9 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
20	8e−02	7 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.2	6 / 294	GUDJ_psoriasis down
2	0.5	6 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	9 / 356	Down_a
2	0.05	3 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
3	0.06	5 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	0.07	3 / 72	laffaire_hypermeth_LGG_vs_control
5	0.14	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
6	0.14	2 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
7	0.21	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
8	0.23	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	0.23	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
10	0.25	2 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	0.25	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
12	0.32	1 / 29	shaw_responders_down_in_oligo_glioma
13	0.36	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
14	0.38	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	0.38	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
16	0.39	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
17	0.40	1 / 38	OL vs. OPC
18	0.46	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
19	0.46	1 / 47	Vishal_subnetwork signature of survival in GBM
20	0.46	1 / 47	mature astrocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	16 / 353	ONDER_CDH1_TARGETS_2_DN
2	4e−05	4 / 15	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
3	7e−05	15 / 356	DELYS_THYROID_CANCER_UP
4	1e−04	19 / 552	HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	3e−04	27 / 995	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
6	6e−04	3 / 13	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
7	7e−04	13 / 349	RATTENBACHER_BOUND_BY_CELF1
8	7e−04	3 / 14	LE_SKI_TARGETS_UP
9	8e−04	5 / 55	BILBAN_B_CLL_LPL_UP
10	2e−03	15 / 475	ONKEN_UVEAL_MELANOMA_DN
11	2e−03	8 / 167	KIM_MYC_AMPLIFICATION_TARGETS_UP
12	2e−03	3 / 19	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN
13	2e−03	9 / 212	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
14	2e−03	3 / 20	YANG_BREAST_CANCER_ESR1_BULK_DN
15	2e−03	3 / 20	FERRARI_RESPONSE_TO_FENRETINIDE_UP
16	2e−03	8 / 176	FOSTER_KDM1A_TARGETS_UP
17	3e−03	7 / 140	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN
18	3e−03	10 / 265	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP
19	3e−03	4 / 45	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
20	3e−03	3 / 22	WILLIAMS_ESR1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.002	8 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	0.004	8 / 196	HALLMARK_MTORC1_SIGNALING
3	0.006	7 / 165	HALLMARK_MYOGENESIS
4	0.038	6 / 188	HALLMARK_ADIPOGENESIS
5	0.074	5 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.080	5 / 174	HALLMARK_HEME_METABOLISM
7	0.106	4 / 137	HALLMARK_UV_RESPONSE_DN
8	0.126	3 / 94	HALLMARK_ANDROGEN_RESPONSE
9	0.177	4 / 167	HALLMARK_APICAL_JUNCTION
10	0.177	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
11	0.254	4 / 195	HALLMARK_MITOTIC_SPINDLE
12	0.272	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
13	0.279	3 / 140	HALLMARK_APOPTOSIS
14	0.279	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
15	0.308	3 / 148	HALLMARK_KRAS_SIGNALING_UP
16	0.319	1 / 29	HALLMARK_NOTCH_SIGNALING
17	0.337	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
18	0.346	2 / 93	HALLMARK_PEROXISOME
19	0.380	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
20	0.383	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	44 / 2211	HOPP_Repetitive
2	0.006	104 / 6564	HOPP_Strong_enhancer
3	0.006	42 / 2188	HOPP_Poised_promoter
4	0.015	90 / 5693	HOPP_Weak_enhancer
5	0.015	58 / 3396	HOPP_Repressed
6	0.021	4 / 80	Aukema_BCL2 DN_BCL6 UP
7	0.049	43 / 2563	HOPP_Heterochrom
8	0.052	1 / 4	MASCQUE_mBL DOWN
9	0.061	6 / 212	LENZ_Stromal signature 1
10	0.064	1 / 5	WRIGHT_custom ABC−DLBCL UP
11	0.097	82 / 5538	HOPP_Weak_txn
12	0.103	77 / 5184	HOPP_Txn_transition
13	0.124	1 / 10	DAVE_BL_DN
14	0.147	1 / 12	BENTINK_mBL DOWN
15	0.158	19 / 1128	SPANG_BCR DN
16	0.158	1 / 13	BENTINK_mBL UP
17	0.169	1 / 14	Subero_mBL_hypo_meth
18	0.180	1 / 15	DAVE_Immune response 2
19	0.180	1 / 15	WRIGHT_ABC UP
20	0.201	1 / 17	DAVE_NFkB BL DN

MF

Rank	p−value	#in/all	Geneset
1	6e−05	4 / 17	Ras GTPase binding
2	3e−04	3 / 10	semaphorin receptor binding
3	2e−03	3 / 19	1−phosphatidylinositol binding
4	2e−03	3 / 19	cAMP binding
5	6e−03	7 / 166	receptor activity
6	7e−03	2 / 10	Rac guanyl−nucleotide exchange factor activity
7	1e−02	5 / 104	iron ion binding
8	1e−02	2 / 14	phosphatidylserine binding
9	1e−02	2 / 14	polypeptide N−acetylgalactosaminyltransferase activity
10	2e−02	3 / 41	ATPase binding
11	2e−02	2 / 16	acetylglucosaminyltransferase activity
12	2e−02	5 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activity
13	2e−02	4 / 84	RNA polymerase II core promoter proximal region sequence−specific DNA bir
14	3e−02	2 / 19	protein kinase activator activity
15	3e−02	11 / 430	lipid binding
16	3e−02	2 / 20	ligand−dependent nuclear receptor binding
17	3e−02	2 / 21	E−box binding
18	3e−02	3 / 52	RNA polymerase II distal enhancer sequence−specific DNA binding transcript
19	3e−02	2 / 22	amino acid transmembrane transporter activity
20	4e−02	2 / 23	bHLH transcription factor binding

miRNA Target

Rank	p−value	#in/all	Geneset
1	7e−06	9 / 100	hsa−miR−374−5p
2	1e−02	4 / 71	hsa−miR−331−3p
3	2e−02	11 / 395	hsa−miR−301b
4	2e−02	12 / 467	hsa−miR−301a
5	2e−02	4 / 84	hsa−miR−339−5p
6	3e−02	8 / 268	hsa−miR−363
7	3e−02	3 / 49	hsa−miR−519b−5p
8	3e−02	3 / 49	hsa−miR−519c−5p
9	3e−02	8 / 274	hsa−miR−1244
10	3e−02	2 / 22	hsa−miR−516a−5p
11	3e−02	3 / 54	hsa−miR−940
12	3e−02	3 / 54	hsa−miR−518d−5p
13	3e−02	3 / 54	hsa−miR−520c−5p
14	3e−02	4 / 93	hsa−miR−299−3p
15	4e−02	8 / 296	hsa−miR−25
16	4e−02	3 / 60	hsa−miR−532−5p
17	6e−02	3 / 66	hsa−miR−648
18	6e−02	7 / 263	hsa−miR−92b
19	6e−02	3 / 68	hsa−miR−299−5p
20	6e−02	4 / 112	hsa−miR−297

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	BENTINK_ras.4
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.009	51 / 2836	ICGC_BatfPcr1_targets
2	0.010	49 / 2714	ICGC_Irf4_targets
3	0.010	72 / 4314	ICGC_Ebfsc137065_targets
4	0.030	34 / 1872	ICGC_Mef2_targets
5	0.032	36 / 2013	ICGC_Bcl11_targets
6	0.073	32 / 1878	ICGC_Cebpbsc150_targets
7	0.083	71 / 4682	ICGC_Pol24_targets
8	0.091	67 / 4414	ICGC_Bclaf101388_targets
9	0.102	46 / 2927	ICGC_Rad21_targets
10	0.108	81 / 5495	ICGC_Yy1_targets
11	0.115	60 / 3966	ICGC_Pu1_targets
12	0.115	71 / 4774	ICGC_Foxm1_targets
13	0.126	56 / 3700	ICGC_Nfatc1_targets
14	0.128	59 / 3924	ICGC_Zeb1_targets
15	0.132	79 / 5408	ICGC_Pou2_targets
16	0.150	78 / 5374	ICGC_Pax5_targets
17	0.175	64 / 4385	ICGC_Atf2_targets
18	0.178	71 / 4909	ICGC_Stat5_targets
19	0.197	59 / 4054	ICGC_Egr1_targets
20	0.223	86 / 6114	ICGC_Runx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 27	VAQUERIZAS_Lymph node
2	0.10	2 / 40	VAQUERIZAS_Thyroid
3	0.11	1 / 9	VAQUERIZAS_Kidney
4	0.18	2 / 58	VAQUERIZAS_Lung
5	0.20	1 / 17	VAQUERIZAS_Pituitary
6	0.22	1 / 19	VAQUERIZAS_Tonsil
7	0.26	1 / 23	VAQUERIZAS_Spinal cord
8	0.26	1 / 23	VAQUERIZAS_Trachea
9	0.29	3 / 143	VAQUERIZAS_General
10	0.32	1 / 29	VAQUERIZAS_Smooth muscle
11	0.32	1 / 29	VAQUERIZAS_Fetal lung
12	0.35	1 / 33	VAQUERIZAS_Prostate
13	0.40	1 / 38	VAQUERIZAS_Whole brain
14	0.42	1 / 41	VAQUERIZAS_Placenta
15	0.45	1 / 45	VAQUERIZAS_Uterus
16	1.00	0 / 36	VAQUERIZAS_Fetal brain
17	1.00	0 / 26	VAQUERIZAS_Liver
18	1.00	0 / 37	VAQUERIZAS_Thymus
19	1.00	0 / 59	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	5 / 194	PALMER_B−Cell signature up
2	0.1	1 / 11	WIRTH_Prim. lymphoid organs
3	0.1	1 / 12	WIRTH_Thymus
4	0.1	1 / 12	WIRTH_Lymphocytes
5	0.1	1 / 12	WIRTH_Cerebellum
6	0.2	1 / 13	WIRTH_Thyroid gland
7	0.2	3 / 107	WIRTH_Testis
8	0.4	2 / 95	WIRTH_Muscle
9	0.4	1 / 41	WIRTH_Homeostasis
10	0.6	3 / 225	PALMER_Granulocytes signature up
11	0.6	1 / 74	WIRTH_Mucosa
12	0.7	4 / 350	WIRTH_Nervous System
13	0.8	1 / 114	PALMER_T−Cell signature up
14	0.8	3 / 350	WIRTH_Immune system
15	1.0	0 / 32	WIRTH_Pancreas
16	1.0	0 / 11	WIRTH_Sec. lymphoid organs
17	1.0	0 / 13	WIRTH_B−cells
18	1.0	0 / 8	WIRTH_Tonsil
19	1.0	0 / 5	WIRTH_Bone marrow
20	1.0	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	51 / 3682	LU_BPDE 0.005 DN
2	0.9	10 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

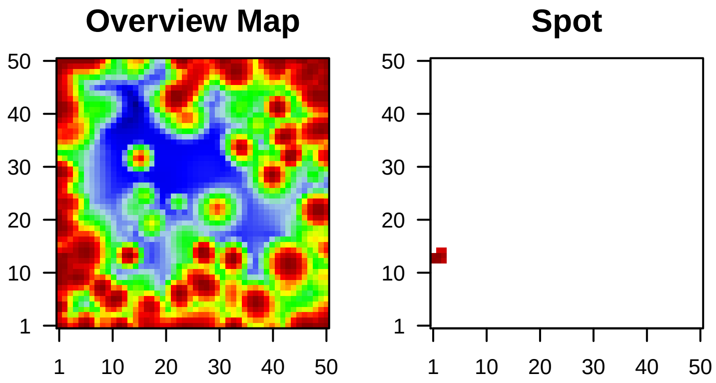
Overexpression Spots

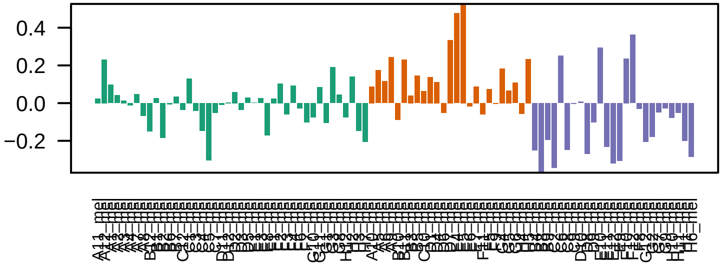
Spot Summary: L

metagenes = 8
genes = 73

<r> metagenes = 0.97
<r> genes = 0.12
beta: r2= 1.76 / log p= −Inf

samples with spot = 13 (14.1 %)
MSC1 : 2 (4.8 %)
MSC2 : 7 (28 %)
MSC3 : 4 (16 %)



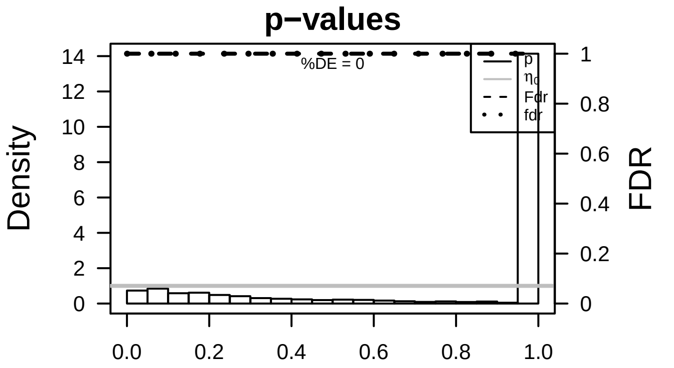


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TAPBPL	1.83	−0.08	0.34	TAPBPL	TAP binding protein−like [Source:HGNC Symbol;Acc:HGNC:3
2	SLC26A4	1.8	−0.16	0.43	SLC26A4	solute carrier family 26 (anion exchanger), member 4 [Source
3	LCMT2	1.75	−0.37	0.3	LCMT2	leucine carboxyl methyltransferase 2 [Source:HGNC Symbol;
4	STAT6	1.71	−0.38	0.29	STAT6	signal transducer and activator of transcription 6, interleukin−
5	VAV3	1.65	−0.26	0.39	VAV3	vav 3 guanine nucleotide exchange factor [Source:HGNC Syr
6	ANGPTL2	1.64	−0.53	0.39	ANGPTL2	angiopoietin−like 2 [Source:HGNC Symbol;Acc:HGNC:490]
7	TMEM133	1.57	−0.33	0.32	TMEM133	transmembrane protein 133 [Source:HGNC Symbol;Acc:HGN
8	PKIB	1.53	−0.19	0.28	PKIB	protein kinase (cAMP−dependent, catalytic) inhibitor beta [So
9	ZNF559	1.5	−0.72	0.29	ZNF559	zinc finger protein 559 [Source:HGNC Symbol;Acc:HGNC:28
10	TRAF6	1.5	−0.19	0.3	TRAF6	TNF receptor−associated factor 6, E3 ubiquitin protein ligase
11	CLUH	1.49	−0.46	0.33	CLUH	clustered mitochondria (cluA/CLU1) homolog [Source:HGNC
12	ECHDC2	1.49	−0.61	0.24	ECHDC2	enoyl CoA hydratase domain containing 2 [Source:HGNC Syr
13	ZNF589	1.49	−0.54	0.22	ZNF589	zinc finger protein 589 [Source:HGNC Symbol;Acc:HGNC:16
14	CYP7B1	1.48	−0.21	0.24	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1 [Sourc
15	HDHD3	1.47	−0.28	0.3	HDHD3	haloacid dehalogenase−like hydrolase domain containing 3 [S
16	SPACA1	1.47	−0.28	0.29	SPACA1	sperm acrosome associated 1 [Source:HGNC Symbol;Acc:H
17	PTPDC1	1.46	−0.37	0.34	PTPDC1	protein tyrosine phosphatase domain containing 1 [Source:H
18	HMG20A	1.45	−0.9	0.36	HMG20A	high mobility group 20A [Source:HGNC Symbol;Acc:HGNC:5
19	PPP2R1B	1.45	−0.39	0.24	PPP2R1B	protein phosphatase 2, regulatory subunit A, beta [Source:H
20	KIAA1551	1.45	−0.43	0.34	KIAA1551	KIAA1551 [Source:HGNC Symbol;Acc:HGNC:25559]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−04	10 / 482	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
2	1e−04	3 / 20	GSEA	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
3	3e−04	5 / 120	miRN	hsa−miR−105
4	4e−04	5 / 127	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
5	4e−04	3 / 30	GSEA	BURTON_ADIPOGENESIS_1
6	4e−04	3 / 30	GSEA	PIONTEK_PKD1_TARGETS_UP
7	5e−04	3 / 31	GSEA	HAN_JNK_SINGALING_UP
8	6e−04	3 / 34	GSEA	WENG_POR_TARGETS_LIVER_UP
9	8e−04	5 / 147	miRN	hsa−miR−506
10	9e−04	3 / 39	BP	I−kappaB kinase/NF−kappaB signaling
11	1e−03	2 / 10	BP	mammary gland epithelial cell proliferation
12	1e−03	2 / 10	GSEA	BIOCARTA_RNA_PATHWAY
13	1e−03	5 / 158	GSEA	BENPORATH_NOS_TARGETS
14	2e−03	2 / 12	GSEA	BIOCARTA_IL10_PATHWAY
15	2e−03	2 / 12	GSEA	REACTOME_METABOLISM_OF_PORPHYRINS
16	2e−03	3 / 47	GSEA	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
17	2e−03	6 / 258	GSEA	BENPORATH_OCT4_TARGETS
18	2e−03	2 / 13	BP	melanin biosynthetic process
19	2e−03	2 / 13	GSEA	BIOCARTA_RANKL_PATHWAY
20	2e−03	2 / 13	GSEA	BIOCARTA_TALL1_PATHWAY
21	2e−03	50 / 7592	Lymph	HOPP_Active_promoter
22	2e−03	2 / 14	GSEA	BIOCARTA_RELA_PATHWAY
23	2e−03	2 / 14	GSEA	BIOCARTA_CD40_PATHWAY
24	2e−03	6 / 271	BP	positive regulation of apoptotic process
25	2e−03	4 / 111	miRN	hsa−miR−361−5p
26	2e−03	3 / 53	GSEA	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NAD
27	2e−03	5 / 187	miRN	hsa−miR−382
28	2e−03	5 / 188	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_UP
29	2e−03	2 / 15	BP	membrane protein intracellular domain proteolysis
30	3e−03	5 / 193	GSEA	LEE_RECENT_THYMIC_EMIGRANT
31	3e−03	2 / 16	BP	porphyrin−containing compound metabolic process
32	3e−03	2 / 16	GSEA	WENG_POR_DOSAGE
33	3e−03	3 / 57	BP	response to hormone
34	3e−03	17 / 1693	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
35	3e−03	56 / 9027	Colon	Tx_Colon
36	3e−03	2 / 17	Lymph	DAVE_NFkB BL DN
37	3e−03	7 / 398	GSEA	MOOTHA_PGC
38	3e−03	2 / 18	BP	melanocyte differentiation
39	3e−03	2 / 18	BP	positive regulation of protein targeting to membrane
40	4e−03	3 / 63	GSEA	MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 39	I−kappaB kinase/NF−kappaB signaling
2	1e−03	2 / 10	mammary gland epithelial cell proliferation
3	2e−03	2 / 13	melanin biosynthetic process
4	2e−03	6 / 271	positive regulation of apoptotic process
5	2e−03	2 / 15	membrane protein intracellular domain proteolysis
6	3e−03	2 / 16	porphyrin−containing compound metabolic process
7	3e−03	3 / 57	response to hormone
8	3e−03	2 / 18	melanocyte differentiation
9	3e−03	2 / 18	positive regulation of protein targeting to membrane
10	5e−03	3 / 71	negative regulation of protein kinase activity
11	5e−03	2 / 22	odontogenesis
12	9e−03	2 / 29	cell development
13	1e−02	2 / 35	positive regulation of smooth muscle cell proliferation
14	1e−02	3 / 104	apoptotic signaling pathway
15	2e−02	2 / 44	protein autoubiquitination
16	2e−02	2 / 47	negative regulation of neuron differentiation
17	3e−02	2 / 53	positive regulation of protein ubiquitination
18	3e−02	4 / 236	neurotrophin TRK receptor signaling pathway
19	3e−02	2 / 54	positive regulation of neuron differentiation
20	3e−02	2 / 55	tRNA processing

Brain

Rank	p−value	#in/all	Geneset
1	0.006	55 / 9013	Overlap_fetal_midbrain_K9K27me3
2	0.007	40 / 5940	Overlap_fetal_midbrain_HetRpts
3	0.012	54 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	0.016	55 / 9330	Overlap_fetal_midbrain_ReprPC
5	0.112	8 / 989	Mid_Frontal_Lobe_Quies
6	0.155	13 / 1949	Fetal_TssF
7	0.187	51 / 9528	Overlap_fetal_midbrain_Quies
8	0.229	7 / 1013	Fetal_TssP
9	0.291	3 / 383	Fetal_Tx
10	0.312	4 / 574	Overlap_fetal_midbrain_TssP
11	0.327	5 / 769	Overlap_fetal_midbrain_ZNF
12	0.334	11 / 1907	Fetal_TxTrans
13	0.404	4 / 656	Overlap_fetal_midbrain_EnhP
14	0.407	7 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	0.418	4 / 668	Mid_Frontal_Lobe_Enh
16	0.427	6 / 1065	Overlap_fetal_midbrain_Enh
17	0.437	13 / 2462	Mid_Frontal_Lobe_HetRpts
18	0.449	16 / 3081	Mid_Frontal_Lobe_ZNF
19	0.507	5 / 953	Fetal_Enh
20	0.515	2 / 349	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	5 / 298	SPANG_BCL6−index2
2	0.04	0 / 14	LIU_PROSTATE_CANCER_DN
3	0.06	2 / 82	PanCan_TXmisReg_geneset_nanostring
4	0.06	1 / 13	GENTLES_modul12
5	0.07	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.13	4 / 401	Lembcke_Colonic Inflammation
7	0.18	1 / 40	ZHANG_MM up
8	0.20	1 / 44	PanCan_TGF−B_geneset_nanostring
9	0.21	1 / 48	KUIPER_MM poor survival
10	0.22	2 / 180	SPANG_LPS−index2
11	0.29	1 / 70	SHAUGHNESSY_MM high risk
12	0.33	0 / 12	LIU_PROSTATE_CANCER_UP
13	0.42	1 / 111	PanCan_RAS_geneset_nanostring
14	0.43	1 / 113	PanCan_Driver_Gene_geneset_nanostring
15	0.45	1 / 120	PanCan_CC+Apop_geneset_nanostring
16	0.45	1 / 121	PanCan_MAPK_geneset_nanostring
17	0.54	1 / 156	PanCan_PI3K_geneset_nanostring
18	0.70	2 / 489	Lembcke_Normal vs Adenoma
19	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
20	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.01	12 / 1201	endoplasmic reticulum
2	0.03	3 / 135	nuclear chromatin
3	0.04	7 / 649	endoplasmic reticulum membrane
4	0.05	1 / 11	CD40 receptor complex
5	0.05	1 / 11	filopodium tip
6	0.06	1 / 12	actomyosin
7	0.06	1 / 13	TCTN−B9D complex
8	0.07	1 / 14	microtubule plus−end
9	0.07	1 / 15	acrosomal membrane
10	0.07	2 / 91	nuclear matrix
11	0.08	2 / 94	melanosome
12	0.09	55 / 9988	organelle
13	0.09	1 / 20	ciliary transition zone
14	0.10	1 / 21	mitochondrial small ribosomal subunit
15	0.10	1 / 22	smooth endoplasmic reticulum
16	0.11	1 / 24	Cul3−RING ubiquitin ligase complex
17	0.12	1 / 25	clathrin−coated endocytic vesicle membrane
18	0.12	1 / 25	PcG protein complex
19	0.13	1 / 29	heterotrimeric G−protein complex
20	0.14	2 / 131	vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.007	8 / 576	Chr 9
2	0.026	6 / 462	Chr 14
3	0.056	6 / 558	Chr 4
4	0.079	5 / 465	Chr 15
5	0.181	6 / 775	Chr 12
6	0.296	2 / 221	Chr 18
7	0.359	5 / 801	Chr 11
8	0.439	4 / 687	Chr 6
9	0.514	3 / 552	Chr 10
10	0.527	1 / 151	Chr 21
11	0.665	3 / 689	Chr 7
12	0.676	2 / 469	Chr 8
13	0.728	1 / 262	Chr 13
14	0.760	6 / 1500	Chr 1
15	0.790	3 / 840	Chr 17
16	0.812	1 / 335	Chr 22
17	0.863	1 / 398	Chr 20
18	0.875	3 / 993	Chr 2
19	0.923	2 / 838	Chr 3
20	0.937	1 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.003	56 / 9027	Tx_Colon
2	0.004	3 / 66	Marisa_CRC−cluster−h
3	0.006	53 / 8580	TxWk_Colon
4	0.006	57 / 9482	TssA_Colon
5	0.014	51 / 8415	Quies3_Colon
6	0.027	3 / 131	Marisa_CRC−cluster−a
7	0.043	1 / 9	KIM_MSI−in−EC
8	0.053	1 / 11	Budinska_B_Lower crypt−like_DOWN
9	0.064	25 / 3812	TssD1_Colon
10	0.067	54 / 9653	Enh_Colon
11	0.071	1 / 15	Budinska_B_Lower crypt−like_UP
12	0.091	35 / 5880	TssD2_Colon
13	0.103	31 / 5155	EnhWk1_Colon
14	0.161	55 / 10290	TssWk_Colon
15	0.182	4 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
16	0.263	22 / 3897	Quies1_Colon
17	0.278	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
18	0.293	16 / 2798	TxEnhG1_Colon
19	0.298	5 / 739	TxEnhG2_Colon
20	0.301	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.2	3 / 294	GUDJ_psoriasis down
2	0.6	2 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	oligodendrocytes_glio
2	0.04	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
3	0.04	2 / 68	GIEZELT_GBM_WT_down_VS_mut
4	0.05	1 / 11	Christensen_hypermethylated_in_ependymoma
5	0.05	1 / 11	WILLSCHER__GBM_LTSwt_proteomics−C_UP
6	0.08	1 / 18	Barbus_GBM_STS_vs._LTS
7	0.09	2 / 103	GIEZELT_GBM_WT_up_VS_mut
8	0.10	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
9	0.11	1 / 23	Donson−Misc_immune function−associated with LTS in HGA
10	0.13	1 / 29	shaw_responders_down_in_oligo_glioma
11	0.17	1 / 38	OL vs. OPC
12	0.18	1 / 39	OPC
13	0.21	1 / 47	Vishal_subnetwork signature of survival in GBM
14	0.21	1 / 47	mature astrocytes
15	0.21	1 / 49	OL vs. MOG−_OL
16	0.23	6 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
17	0.27	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
18	0.30	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
19	0.31	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
20	0.39	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	10 / 482	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
2	1e−04	3 / 20	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
3	4e−04	5 / 127	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
4	4e−04	3 / 30	BURTON_ADIPOGENESIS_1
5	4e−04	3 / 30	PIONTEK_PKD1_TARGETS_UP
6	5e−04	3 / 31	HAN_JNK_SINGALING_UP
7	6e−04	3 / 34	WENG_POR_TARGETS_LIVER_UP
8	1e−03	2 / 10	BIOCARTA_RNA_PATHWAY
9	1e−03	5 / 158	BENPORATH_NOS_TARGETS
10	2e−03	2 / 12	BIOCARTA_IL10_PATHWAY
11	2e−03	2 / 12	REACTOME_METABOLISM_OF_PORPHYRINS
12	2e−03	3 / 47	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
13	2e−03	6 / 258	BENPORATH_OCT4_TARGETS
14	2e−03	2 / 13	BIOCARTA_RANKL_PATHWAY
15	2e−03	2 / 13	BIOCARTA_TALL1_PATHWAY
16	2e−03	2 / 14	BIOCARTA_RELA_PATHWAY
17	2e−03	2 / 14	BIOCARTA_CD40_PATHWAY
18	2e−03	3 / 53	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE
19	2e−03	5 / 188	DAZARD_RESPONSE_TO_UV_NHEK_UP
20	3e−03	5 / 193	LEE_RECENT_THYMIC_EMIGRANT

HM

Rank	p−value	#in/all	Geneset
1	0.01	4 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	0.05	3 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.05	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
4	0.05	3 / 174	HALLMARK_HEME_METABOLISM
5	0.08	2 / 94	HALLMARK_ANDROGEN_RESPONSE
6	0.08	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	0.15	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
8	0.20	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.23	1 / 53	HALLMARK_TGF_BETA_SIGNALING
10	0.36	1 / 91	HALLMARK_BILE_ACID_METABOLISM
11	0.42	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	0.47	1 / 127	HALLMARK_KRAS_SIGNALING_DN
13	0.49	1 / 137	HALLMARK_UV_RESPONSE_DN
14	0.50	1 / 140	HALLMARK_APOPTOSIS
15	0.50	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	0.52	1 / 148	HALLMARK_KRAS_SIGNALING_UP
17	0.55	1 / 162	HALLMARK_COMPLEMENT
18	0.56	1 / 165	HALLMARK_MYOGENESIS
19	0.56	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
20	0.57	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	50 / 7592	HOPP_Active_promoter
2	0.003	2 / 17	DAVE_NFkB BL DN
3	0.009	12 / 1128	SPANG_BCR DN
4	0.013	44 / 6929	HOPP_Txn_elongation
5	0.026	34 / 5184	HOPP_Txn_transition
6	0.039	1 / 8	Subero_MM_hypo_meth
7	0.051	5 / 410	SPANG_CD40 6hrs DN
8	0.071	1 / 15	DAVE_Immune response 2
9	0.078	42 / 7209	HOPP_Weak_promoter
10	0.133	1 / 29	Subero_DLBCL_hypo_meth
11	0.138	1 / 30	TARTE_B−cell signature
12	0.138	1 / 30	Subero_INT_hypo_meth
13	0.150	32 / 5538	HOPP_Weak_txn
14	0.159	37 / 6564	HOPP_Strong_enhancer
15	0.180	14 / 2188	HOPP_Poised_promoter
16	0.271	31 / 5693	HOPP_Weak_enhancer
17	0.287	13 / 2211	HOPP_Repetitive
18	0.327	1 / 80	Aukema_BCL2 DN_BCL6 UP
19	0.343	2 / 247	ZHANG_DLBCL mutated
20	0.381	2 / 268	SPANG_IL21 UP

MF

Rank	p−value	#in/all	Geneset
1	0.007	2 / 26	protein kinase inhibitor activity
2	0.008	2 / 27	potassium channel regulator activity
3	0.015	8 / 657	enzyme regulator activity
4	0.016	2 / 40	heat shock protein binding
5	0.022	2 / 47	GDP binding
6	0.042	2 / 66	Rho guanyl−nucleotide exchange factor activity
7	0.043	2 / 67	kinase binding
8	0.048	1 / 10	neutral amino acid transmembrane transporter activity
9	0.048	1 / 10	Rac guanyl−nucleotide exchange factor activity
10	0.053	1 / 11	protein kinase B binding
11	0.057	1 / 12	magnesium ion transmembrane transporter activity
12	0.057	1 / 12	misfolded protein binding
13	0.060	2 / 81	protein N−terminus binding
14	0.062	1 / 13	thioesterase binding
15	0.062	1 / 13	ubiquitin conjugating enzyme binding
16	0.066	2 / 85	histone deacetylase binding
17	0.067	1 / 14	regulatory region DNA binding
18	0.070	3 / 193	protein complex binding
19	0.071	1 / 15	microfilament motor activity
20	0.071	1 / 15	retinoid X receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 120	hsa−miR−105
2	8e−04	5 / 147	hsa−miR−506
3	2e−03	4 / 111	hsa−miR−361−5p
4	2e−03	5 / 187	hsa−miR−382
5	8e−03	3 / 82	hsa−miR−630
6	8e−03	3 / 85	hsa−miR−433
7	9e−03	2 / 29	hsa−miR−1237
8	1e−02	3 / 94	hsa−miR−219−2−3p
9	1e−02	4 / 181	hsa−miR−196b
10	1e−02	3 / 98	hsa−miR−147
11	1e−02	2 / 36	hsa−miR−127−3p
12	1e−02	4 / 191	hsa−miR−330−3p
13	1e−02	2 / 38	hsa−miR−1224−5p
14	2e−02	5 / 318	hsa−miR−340
15	3e−02	2 / 50	hsa−miR−518f
16	3e−02	4 / 228	hsa−miR−124
17	3e−02	5 / 358	hsa−let−7d
18	4e−02	2 / 60	hsa−miR−650
19	4e−02	2 / 60	hsa−miR−1243
20	4e−02	3 / 146	hsa−miR−142−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	1 / 9	BENTINK_ras.4
2	0.06	1 / 12	BENTINK_ras.1
3	0.06	1 / 13	GUSTAFSON_PI3K_DN
4	1.00	0 / 12	GUSTAFSON_PI3K_UP
5	1.00	0 / 14	BENTINK_e2f3.1
6	1.00	0 / 12	BENTINK_e2f3.2
7	1.00	0 / 13	BENTINK_myc.1
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	11 / 1273	ICGC_P300_targets
2	0.10	6 / 653	ICGC_SrfPcr2_targets
3	0.22	8 / 1171	KIM_MYC targets
4	0.36	12 / 2137	ICGC_SrfV0416101_targets
5	0.51	3 / 553	ICGC_RxraPcr1_targets
6	0.52	24 / 4829	ICGC_Nficsc81335_targets
7	0.53	20 / 4032	ICGC_Creb1_targets
8	0.54	10 / 2013	ICGC_Bcl11_targets
9	0.54	14 / 2836	ICGC_BatfPcr1_targets
10	0.55	23 / 4682	ICGC_Pol24_targets
11	0.56	3 / 595	ICGC_NrsfPcr2_targets
12	0.57	21 / 4314	ICGC_Ebfsc137065_targets
13	0.59	13 / 2714	ICGC_Irf4_targets
14	0.59	14 / 2927	ICGC_Rad21_targets
15	0.60	26 / 5408	ICGC_Pou2_targets
16	0.62	21 / 4414	ICGC_Bclaf101388_targets
17	0.65	22 / 4689	ICGC_Taf1_targets
18	0.67	5 / 1139	HEBENSTREIT_low expression TF
19	0.68	18 / 3924	ICGC_Zeb1_targets
20	0.70	20 / 4385	ICGC_Atf2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 59	VAQUERIZAS_Whole blood
2	0.09	1 / 19	VAQUERIZAS_Tonsil
3	0.13	1 / 29	VAQUERIZAS_Smooth muscle
4	0.16	2 / 143	VAQUERIZAS_General
5	0.17	1 / 37	VAQUERIZAS_Thymus
6	1.00	0 / 36	VAQUERIZAS_Fetal brain
7	1.00	0 / 41	VAQUERIZAS_Placenta
8	1.00	0 / 26	VAQUERIZAS_Liver
9	1.00	0 / 33	VAQUERIZAS_Prostate
10	1.00	0 / 45	VAQUERIZAS_Uterus
11	1.00	0 / 9	VAQUERIZAS_Kidney
12	1.00	0 / 23	VAQUERIZAS_Spinal cord
13	1.00	0 / 38	VAQUERIZAS_Whole brain
14	1.00	0 / 40	VAQUERIZAS_Thyroid
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 11	WIRTH_Cortex cerebri
2	0.18	1 / 41	WIRTH_Homeostasis
3	0.25	3 / 350	WIRTH_Immune system
4	0.30	2 / 225	PALMER_Granulocytes signature up
5	0.43	1 / 114	PALMER_T−Cell signature up
6	0.62	1 / 194	PALMER_B−Cell signature up
7	0.83	1 / 350	WIRTH_Nervous System
8	1.00	0 / 32	WIRTH_Pancreas
9	1.00	0 / 11	WIRTH_Sec. lymphoid organs
10	1.00	0 / 11	WIRTH_Prim. lymphoid organs
11	1.00	0 / 13	WIRTH_B−cells
12	1.00	0 / 8	WIRTH_Tonsil
13	1.00	0 / 12	WIRTH_Thymus
14	1.00	0 / 12	WIRTH_Lymphocytes
15	1.00	0 / 5	WIRTH_Bone marrow
16	1.00	0 / 11	WIRTH_Globus pallidus
17	1.00	0 / 14	WIRTH_Telencephalon
18	1.00	0 / 10	WIRTH_Hippocampus
19	1.00	0 / 10	WIRTH_Thalamus
20	1.00	0 / 12	WIRTH_Cerebellum

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	21 / 3682	LU_BPDE 0.005 DN
2	0.6	5 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

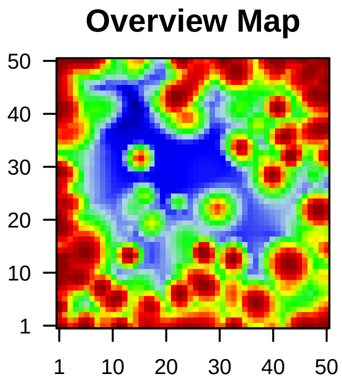
Overexpression Spots

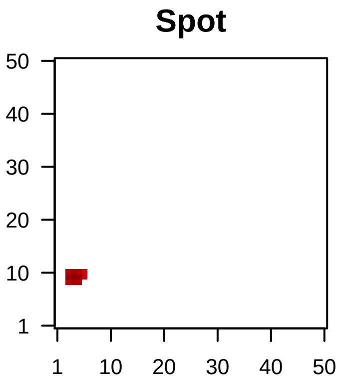
Spot Summary: M

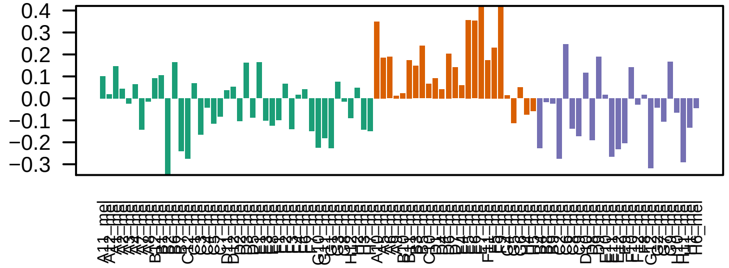
metagenes = 11
genes = 68

<r> metagenes = 0.96
<r> genes = 0.12
beta: r2= 1.46 / log p= −Inf

samples with spot = 12 (13 %)
MSC2 : 10 (40 %)
MSC3 : 2 (8 %)





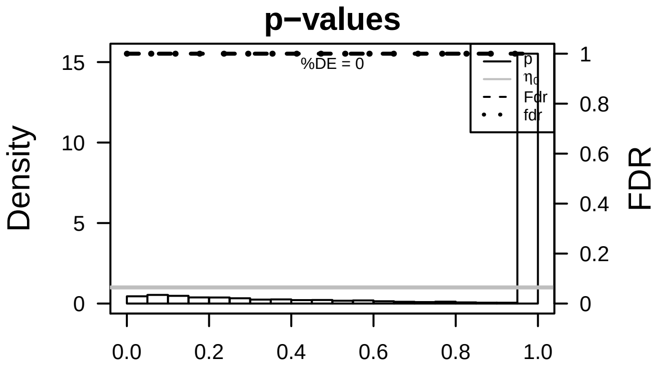


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PLA2G4B	1.82	−0.16	0.33	PLA2G4B	phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym
2	TMEM150A	1.75	−0.24	0.35	TMEM150A	transmembrane protein 150A [Source:HGNC Symbol;Acc:HG
3	RDH14	1.75	−0.43	0.31	RDH14	retinol dehydrogenase 14 (all−trans/9−cis/11−cis) [Source:HG
4	TXNDC16	1.69	−0.35	0.28	TXNDC16	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc
5	USP54	1.61	−0.41	0.31	USP54	ubiquitin specific peptidase 54 [Source:HGNC Symbol;Acc:H
6	MCF2	1.57	−0.32	0.41	MCF2	MCF.2 cell line derived transforming sequence [Source:HGN
7	HEATR6	1.55	−0.72	0.31	HEATR6	HEAT repeat containing 6 [Source:HGNC Symbol;Acc:HGNC
8	STOX2	1.53	−0.17	0.38	STOX2	storkhead box 2 [Source:HGNC Symbol;Acc:HGNC:25450]
9	MSANTD2	1.5	−0.15	0.26	MSANTD2	Myb/SANT−like DNA−binding domain containing 2 [Source:H
10	NPM3	1.47	−0.32	0.34	NPM3	nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:
11	FBXW9	1.43	−0.26	0.27	FBXW9	F−box and WD repeat domain containing 9 [Source:HGNC Sy
12	NFX1	1.41	−0.4	0.28	NFX1	nuclear transcription factor, X−box binding 1 [Source:HGNC S
13	MTFMT	1.4	−0.99	0.34	MTFMT	mitochondrial methionyl−tRNA formyltransferase [Source:HG
14	SLC9A1	1.39	−0.49	0.35	SLC9A1	solute carrier family 9, subfamily A (NHE1, cation proton antip
15	RMDN3	1.39	−0.63	0.24	RMDN3	regulator of microtubule dynamics 3 [Source:HGNC Symbol;A
16	PRKAB1	1.33	−0.49	0.28	PRKAB1	protein kinase, AMP−activated, beta 1 non−catalytic subunit [
17	FEM1B	1.32	−0.9	0.3	FEM1B	fem−1 homolog b (C. elegans) [Source:HGNC Symbol;Acc:H
18	COQ7	1.31	−0.59	0.31	COQ7	coenzyme Q7 homolog, ubiquinone (yeast) [Source:HGNC Sy
19	TARS2	1.3	−0.89	0.21	TARS2	threonyl−tRNA synthetase 2, mitochondrial (putative) [Source
20	PPP1R3B	1.3	−0.25	0.24	PPP1R3B	protein phosphatase 1, regulatory subunit 3B [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−07	52 / 6929	Lympl	HOPP_Txn_elongation
2	3e−06	60 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	2e−05	59 / 9482	Colon	TssA_Colon
4	5e−05	51 / 7592	Lympl	HOPP_Active_promoter
5	3e−04	13 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
6	3e−04	9 / 473	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
7	3e−04	55 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
8	3e−04	7 / 288	GSEA	WEST_ADRENOCORTICAL_TUMOR_UP
9	4e−04	12 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	5e−04	5 / 146	GSEA	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP
11	6e−04	2 / 8	GSEA	REACTOME_RECEPTOR_LIGAND_BINDING_INITIATES_THE_SECOND
12	7e−04	3 / 38	miRN	hsa−miR−490−5p
13	8e−04	37 / 5184	Lympl	HOPP_Txn_transition
14	9e−04	3 / 41	GSEA	AMIT_EGF_RESPONSE_480_MCF10A
15	9e−04	2 / 10	GSEA	REACTOME_SIGNALING_BY_NOTCH4
16	9e−04	2 / 10	GSEA	REACTOME_SIGNALING_BY_NOTCH2
17	9e−04	2 / 10	GSEA	REACTOME_SIGNALING_BY_NOTCH3
18	9e−04	5 / 164	miRN	hsa−miR−323b−5p
19	1e−03	51 / 8415	Colon	Quies3_Colon
20	2e−03	2 / 14	GSEA	LIU_IL13_PRIMING_MODEL
21	2e−03	5 / 198	miRN	hsa−miR−448
22	2e−03	5 / 200	GSEA	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP
23	2e−03	51 / 8580	Colon	TxWk_Colon
24	3e−03	6 / 301	GSEA	MULLIGHAN_NPM1_SIGNATURE_3_UP
25	3e−03	42 / 6564	Lympl	HOPP_Strong_enhancer
26	3e−03	39 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
27	3e−03	3 / 63	GSEA	LIN_MELANOMA_COPY_NUMBER_UP
28	3e−03	2 / 19	BP	Notch receptor processing
29	4e−03	2 / 21	GSEA	REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NU
30	4e−03	4 / 144	miRN	hsa−miR−135b
31	4e−03	10 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
32	5e−03	52 / 9027	Colon	Tx_Colon
33	5e−03	38 / 5880	Colon	TssD2_Colon
34	5e−03	54 / 9528	Brain	Overlap_fetal_midbrain_Quies
35	5e−03	3 / 75	MF	metallopeptidase activity
36	5e−03	2 / 23	miRN	hsa−miR−943
37	5e−03	5 / 247	Lympl	ZHANG_DLBCL mutated
38	6e−03	2 / 25	MF	aminopeptidase activity
39	6e−03	2 / 25	GSEA	NICK_RESPONSE_TO_PROC_TREATMENT_DN
40	6e−03	14 / 1468	CC	mitochondrion



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.003	2 / 19	Notch receptor processing
2	0.007	2 / 27	endosome organization
3	0.008	2 / 30	negative regulation of cell adhesion
4	0.010	3 / 96	antigen processing and presentation of peptide antigen via MHC class I
5	0.011	2 / 34	regulation of protein kinase activity
6	0.016	5 / 322	mitochondrion organization
7	0.024	2 / 52	cartilage development
8	0.024	3 / 136	phospholipid metabolic process
9	0.025	2 / 53	phosphatidylinositol biosynthetic process
10	0.028	2 / 57	positive regulation of cell growth
11	0.032	8 / 815	cell death
12	0.036	2 / 65	regulation of Rho protein signal transduction
13	0.038	2 / 67	pigmentation
14	0.042	7 / 705	locomotion
15	0.044	2 / 73	antigen processing and presentation of exogenous peptide antigen via MHC c
16	0.045	1 / 10	cellular response to antibiotic
17	0.045	1 / 10	cellular response to ATP
18	0.045	1 / 10	cellular response to electrical stimulus
19	0.045	1 / 10	cellular response to epinephrine stimulus
20	0.045	1 / 10	maternal placenta development

Brain

Rank	p−value	#in/all	Geneset
1	3e−06	60 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−04	55 / 9013	Overlap_fetal_midbrain_K9K27me3
3	3e−03	39 / 5940	Overlap_fetal_midbrain_HetRpts
4	5e−03	54 / 9528	Overlap_fetal_midbrain_Quies
5	3e−02	49 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	4e−02	8 / 831	Fetal_HetRpts
7	8e−02	10 / 1333	Fetal_ReprPCWk
8	2e−01	18 / 3081	Mid_Frontal_Lobe_ZNF
9	2e−01	2 / 166	Mid_Frontal_Lobe_Tx
10	3e−01	7 / 1122	Fetal_K9K27me3
11	3e−01	5 / 765	Mid_Frontal_Lobe_Het
12	3e−01	6 / 1050	Fetal_EnhP
13	4e−01	3 / 534	Mid_Frontal_Lobe_EnhG
14	5e−01	2 / 349	Fetal_ZNF
15	5e−01	4 / 786	Fetal_EnhG
16	5e−01	3 / 574	Overlap_fetal_midbrain_TssP
17	5e−01	1 / 156	Mid_Frontal_Lobe_TssA
18	5e−01	1 / 158	Overlap_fetal_midbrain_Het
19	5e−01	2 / 383	Fetal_Tx
20	6e−01	3 / 656	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	1 / 18	PanCan Notch_geneset_nanostring
2	0.17	1 / 40	ZHANG_MM up
3	0.39	3 / 489	Lembcke_Normal vs Adenoma
4	0.40	2 / 298	SPANG_BCL6−index2
5	0.53	0 / 14	LIU_PROSTATE_CANCER_DN
6	0.85	1 / 401	Lembcke_Colonic Inflammation
7	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
8	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
9	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_COMMON_CANCER_GENES
13	1.00	0 / 14	LIU_LIVER_CANCER
14	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
15	1.00	0 / 15	WANG_ER_UP
16	1.00	0 / 5	WANG_ER_DN
17	1.00	0 / 16	WOLFER_overlap genes
18	1.00	0 / 12	BEN−PORATH_DN
19	1.00	0 / 13	BEN−PORATH_UP
20	1.00	0 / 15	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	0.006	14 / 1468	mitochondrion
2	0.009	3 / 94	melanosome
3	0.018	6 / 456	vacuole
4	0.022	7 / 616	endosome
5	0.040	5 / 412	lysosome
6	0.045	1 / 10	perinuclear endoplasmic reticulum
7	0.053	4 / 308	focal adhesion
8	0.053	2 / 81	late endosome membrane
9	0.054	1 / 12	AMP−activated protein kinase complex
10	0.054	1 / 12	Golgi−associated vesicle
11	0.054	1 / 12	holo TFIIH complex
12	0.062	1 / 14	gap junction
13	0.067	2 / 92	early endosome membrane
14	0.067	1 / 15	integral component of mitochondrial inner membrane
15	0.068	11 / 1465	cytoskeleton
16	0.070	17 / 2576	membrane
17	0.075	1 / 17	desmosome
18	0.082	3 / 223	lysosomal membrane
19	0.092	1 / 21	histone methyltransferase complex
20	0.092	1 / 21	immunological synapse

Chr

Rank	p−value	#in/all	Geneset
1	0.06	5 / 465	Chr 15
2	0.08	8 / 993	Chr 2
3	0.14	6 / 775	Chr 12
4	0.20	3 / 335	Chr 22
5	0.25	9 / 1500	Chr 1
6	0.34	2 / 262	Chr 13
7	0.36	3 / 469	Chr 8
8	0.40	4 / 696	Chr 5
9	0.47	3 / 558	Chr 4
10	0.50	4 / 801	Chr 11
11	0.54	4 / 838	Chr 3
12	0.55	2 / 398	Chr 20
13	0.63	2 / 462	Chr 14
14	0.73	2 / 552	Chr 10
15	0.75	2 / 576	Chr 9
16	0.75	3 / 840	Chr 17
17	0.80	2 / 649	Chr 16
18	0.92	1 / 551	Chr X
19	0.96	2 / 1037	Chr 19
20	0.96	1 / 687	Chr 6

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	59 / 9482	TssA_Colon
2	1e−03	51 / 8415	Quies3_Colon
3	2e−03	51 / 8580	TxWk_Colon
4	5e−03	52 / 9027	Tx_Colon
5	5e−03	38 / 5880	TssD2_Colon
6	7e−03	34 / 5155	EnhWk1_Colon
7	7e−03	54 / 9653	Enh_Colon
8	3e−02	1 / 7	Kaneda_CIMP−group2
9	4e−02	1 / 8	Marisa_CRC−C2
10	6e−02	40 / 7203	TssF_Colon
11	8e−02	53 / 10290	TssWk_Colon
12	8e−02	6 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	1e−01	3 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	1e−01	6 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
15	1e−01	22 / 3812	TssD1_Colon
16	2e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
17	3e−01	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
18	3e−01	15 / 2798	TxEnhG1_Colon
19	3e−01	3 / 436	K9acLow_Colon
20	3e−01	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	4 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	1 / 11	Martinez_Glio_hypermeth
2	0.05	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
3	0.07	1 / 15	VERHAAK_CL subtype
4	0.16	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
5	0.16	1 / 39	OPC
6	0.18	3 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.19	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
8	0.23	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
9	0.27	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.29	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
11	0.34	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.36	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
13	0.37	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
14	0.42	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	0.44	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
16	0.45	2 / 332	Up
17	0.50	2 / 365	Down_b
18	0.52	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
19	0.57	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
20	1.00	0 / 15	VERHAAK_MES subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	13 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	3e−04	9 / 473	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
3	3e−04	7 / 288	WEST_ADRENOCORTICAL_TUMOR_UP
4	4e−04	12 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	5e−04	5 / 146	MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_UP
6	6e−04	2 / 8	REACTOME_RECEPTOR_LIGAND_BINDING_INITIATES_THE_SECOND_F
7	9e−04	3 / 41	AMIT_EGF_RESPONSE_480_MCF10A
8	9e−04	2 / 10	REACTOME_SIGNALING_BY_NOTCH4
9	9e−04	2 / 10	REACTOME_SIGNALING_BY_NOTCH2
10	9e−04	2 / 10	REACTOME_SIGNALING_BY_NOTCH3
11	2e−03	2 / 14	LIU_IL13_PRIMING_MODEL
12	2e−03	5 / 200	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_UP
13	3e−03	6 / 301	MULLIGHAN_NPM1_SIGNATURE_3_UP
14	3e−03	3 / 63	LIN_MELANOMA_COPY_NUMBER_UP
15	4e−03	2 / 21	REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCL
16	4e−03	10 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
17	6e−03	2 / 25	NICK_RESPONSE_TO_PROC_TREATMENT_DN
18	6e−03	3 / 81	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
19	7e−03	2 / 28	GENTILE_UV_RESPONSE_CLUSTER_D9
20	9e−03	4 / 181	PENG_LEUCINE_DEPRIVATION_DN

HM

Rank	p−value	#in/all	Geneset
1	0.03	2 / 57	HALLMARK_MYC_TARGETS_V2
2	0.05	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
3	0.11	1 / 26	HALLMARK_ANGIOGENESIS
4	0.12	1 / 29	HALLMARK_NOTCH_SIGNALING
5	0.14	2 / 146	HALLMARK_DNA_REPAIR
6	0.15	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	0.16	1 / 37	HALLMARK_APICAL_SURFACE
8	0.18	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
9	0.19	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.19	2 / 174	HALLMARK_HEME_METABOLISM
11	0.20	2 / 181	HALLMARK_P53_PATHWAY
12	0.34	1 / 91	HALLMARK_PROTEIN_SECRETION
13	0.35	1 / 94	HALLMARK_ANDROGEN_RESPONSE
14	0.48	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
15	0.53	1 / 162	HALLMARK_COMPLEMENT
16	0.56	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
17	0.58	1 / 188	HALLMARK_ADIPOGENESIS
18	0.59	1 / 195	HALLMARK_MITOTIC_SPINDLE
19	0.60	1 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
20	1.00	0 / 176	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−07	52 / 6929	HOPP_Txn_elongation
2	5e−05	51 / 7592	HOPP_Active_promoter
3	8e−04	37 / 5184	HOPP_Txn_transition
4	3e−03	42 / 6564	HOPP_Strong_enhancer
5	5e−03	57 / 247	ZHANG_DLBCL mutated
6	1e−02	11 / 1128	SPANG_BCR DN
7	2e−02	42 / 7209	HOPP_Weak_promoter
8	6e−02	33 / 5693	HOPP_Weak_enhancer
9	1e−01	31 / 5538	HOPP_Weak_txn
10	1e−01	4 / 410	SPANG_CD40 6hrs DN
11	2e−01	3 / 294	TARTE_Plasmablast signature
12	3e−01	2 / 212	LENZ_Stromal signature 1
13	3e−01	14 / 2563	HOPP_Heterochrom
14	3e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
15	3e−01	1 / 82	ROSOLOWSKI_green UP
16	3e−01	1 / 86	ROSOLOWSKI_red total
17	3e−01	1 / 89	ROSOLOWSKI_blue total
18	4e−01	1 / 109	ROSOLOWSKI_green total
19	4e−01	1 / 129	DAVE_BL−vs−DLBCL
20	7e−01	5 / 1218	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	0.005	3 / 75	metallopeptidase activity
2	0.006	2 / 25	aminopeptidase activity
3	0.009	51 / 8984	protein binding
4	0.025	5 / 361	binding
5	0.027	2 / 56	phosphoprotein phosphatase activity
6	0.037	2 / 66	Rho guanyl−nucleotide exchange factor activity
7	0.038	2 / 67	phosphotransferase activity, alcohol group as acceptor
8	0.045	1 / 10	cytoskeletal adaptor activity
9	0.045	1 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
10	0.045	1 / 10	peptidase activator activity
11	0.045	1 / 10	semaphorin receptor binding
12	0.049	1 / 11	mismatched DNA binding
13	0.054	1 / 12	GTPase activating protein binding
14	0.054	1 / 12	GTPase inhibitor activity
15	0.054	1 / 12	lysophospholipase activity
16	0.054	1 / 12	neurexin family protein binding
17	0.054	1 / 12	Notch binding
18	0.054	1 / 12	phospholipase activity
19	0.057	2 / 84	guanyl−nucleotide exchange factor activity
20	0.058	1 / 13	GTP−Rho binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 38	hsa−miR−490−5p
2	9e−04	5 / 164	hsa−miR−323b−5p
3	2e−03	5 / 198	hsa−miR−448
4	4e−03	4 / 144	hsa−miR−135b
5	5e−03	2 / 23	hsa−miR−943
6	8e−03	3 / 88	hsa−miR−149
7	1e−02	5 / 284	hsa−miR−503
8	1e−02	5 / 294	hsa−miR−561
9	1e−02	3 / 107	hsa−miR−146b−5p
10	2e−02	2 / 44	hsa−miR−658
11	2e−02	3 / 120	hsa−miR−105
12	2e−02	2 / 46	hsa−miR−346
13	2e−02	3 / 124	hsa−miR−646
14	2e−02	2 / 47	hsa−miR−329
15	2e−02	3 / 130	hsa−miR−383
16	2e−02	2 / 50	hsa−miR−1201
17	2e−02	2 / 50	hsa−miR−610
18	2e−02	3 / 132	hsa−miR−194
19	3e−02	2 / 55	hsa−miR−191
20	3e−02	3 / 145	hsa−miR−135a

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.01	13 / 1418	ICGC_Ets1_targets
2	0.01	8 / 690	ICGC_Atf3_targets
3	0.02	30 / 4689	ICGC_Taf1_targets
4	0.02	14 / 1701	HEBENSTREIT_high expression TF
5	0.03	16 / 2136	ICGC_GabpPcr2_targets
6	0.03	26 / 4032	ICGC_Creb1_targets
7	0.06	15 / 2137	ICGC_SrfV0416101_targets
8	0.06	23 / 3700	ICGC_Nfatc1_targets
9	0.07	24 / 3966	ICGC_Pu1_targets
10	0.08	10 / 1314	ICGC_Usf1_targets
11	0.09	18 / 2836	ICGC_BatfPcr1_targets
12	0.10	10 / 1383	ICGC_Six5_targets
13	0.12	25 / 4385	ICGC_Atf2_targets
14	0.13	26 / 4617	ICGC_Tcf12_targets
15	0.13	25 / 4414	ICGC_Bclaf101388_targets
16	0.13	27 / 4829	ICGC_Nficsc81335_targets
17	0.14	27 / 4879	ICGC_Pmlsc71910_targets
18	0.14	23 / 4054	ICGC_Egr1_targets
19	0.14	26 / 4682	ICGC_Pol24_targets
20	0.15	12 / 1878	ICGC_Cebpbsc150_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	3 / 350	WIRTH_Immune system
2	0.6	1 / 194	PALMER_B−Cell signature up
3	0.6	1 / 225	PALMER_Granulocytes signature up
4	1.0	0 / 32	WIRTH_Pancreas
5	1.0	0 / 11	WIRTH_Sec. lymphoid organs
6	1.0	0 / 11	WIRTH_Prim. lymphoid organs
7	1.0	0 / 13	WIRTH_B−cells
8	1.0	0 / 8	WIRTH_Tonsil
9	1.0	0 / 12	WIRTH_Thymus
10	1.0	0 / 12	WIRTH_Lymphocytes
11	1.0	0 / 5	WIRTH_Bone marrow
12	1.0	0 / 350	WIRTH_Nervous System
13	1.0	0 / 11	WIRTH_Globus pallidus
14	1.0	0 / 14	WIRTH_Telencephalon
15	1.0	0 / 11	WIRTH_Cortex cerebri
16	1.0	0 / 10	WIRTH_Hippocampus
17	1.0	0 / 10	WIRTH_Thalamus
18	1.0	0 / 12	WIRTH_Cerebellum
19	1.0	0 / 107	WIRTH_Testis
20	1.0	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	4 / 1115	LU_BPDE 1n DN
2	1.0	11 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

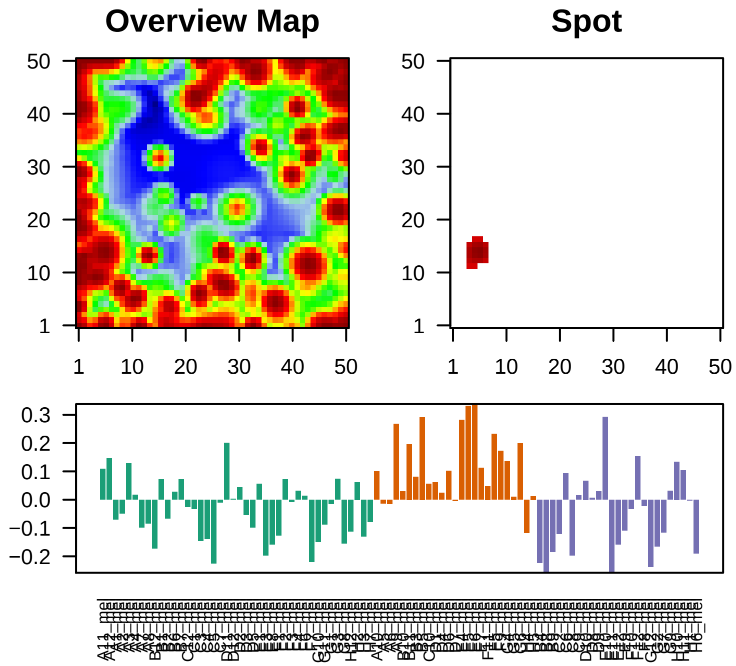
Overexpression Spots

Spot Summary: N

metagenes = 20
genes = 138

<r> metagenes = 0.92
<r> genes = 0.09
beta: r2= 1 / log p= −Inf

samples with spot = 10 (10.9 %)
MSC1 : 1 (2.4 %)
MSC2 : 8 (32 %)
MSC3 : 1 (4 %)

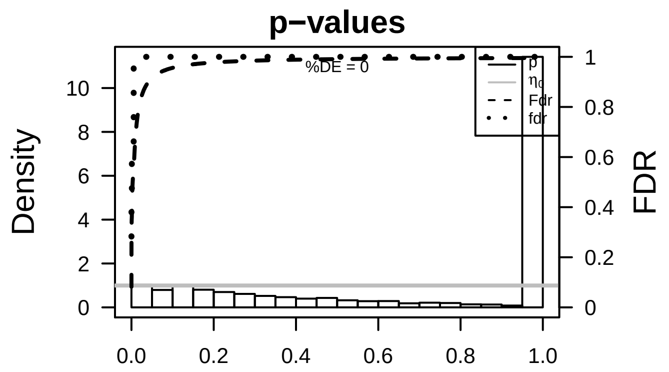


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	FZD3	2.09	−0.27	0.28	FZD3	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4
2	SLC25A14	2.08	−0.21	0.26	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member
3	TKTL1	1.87	−0.19	0.27	TKTL1	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
4	TRDMT1	1.73	−0.13	0.28	TRDMT1	tRNA aspartic acid methyltransferase 1 [Source:HGNC Symb
5	ELL	1.73	−0.16	0.25	ELL	elongation factor RNA polymerase II [Source:HGNC Symbol;
6	ATP6V1E2	1.71	−0.16	0.35	ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2 [S
7	EMCN	1.69	−0.48	0.39	EMCN	endomucin [Source:HGNC Symbol;Acc:HGNC:16041]
8	SCRN2	1.68	−0.18	0.3	SCRN2	secernin 2 [Source:HGNC Symbol;Acc:HGNC:30381]
9	SLAIN1	1.67	−0.34	0.28	SLAIN1	SLAIN motif family, member 1 [Source:HGNC Symbol;Acc:HC
10	ZNF691	1.66	−0.36	0.31	ZNF691	zinc finger protein 691 [Source:HGNC Symbol;Acc:HGNC:28
11	CPS1	1.65	−0.46	0.24	CPS1	carbamoyl−phosphate synthase 1, mitochondrial [Source:HG
12	SMAD1	1.61	−0.21	0.34	SMAD1	SMAD family member 1 [Source:HGNC Symbol;Acc:HGNC:6
13	SLC5A9	1.59	−0.04	0.38	SLC5A9	solute carrier family 5 (sodium/sugar cotransporter), member
14	PDP2	1.56	−0.21	0.24	PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2 [Sou
15	CLYBL	1.55	−0.17	0.24	CLYBL	citrate lyase beta like [Source:HGNC Symbol;Acc:HGNC:183
16	SSPN	1.55	−0.45	0.28	SSPN	sarcospan [Source:HGNC Symbol;Acc:HGNC:11322]
17	HECTD3	1.53	−0.31	0.27	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3 [Sourc
18	MTSS1	1.51	−0.68	0.37	MTSS1	metastasis suppressor 1 [Source:HGNC Symbol;Acc:HGNC:
19	ZNF527	1.49	−0.2	0.26	ZNF527	zinc finger protein 527 [Source:HGNC Symbol;Acc:HGNC:29
20	HHAT	1.45	−0.5	0.25	HHAT	hedgehog acyltransferase [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−06	112 / 9528	Brain	Overlap_fetal_midbrain_Quies
2	6e−05	4 / 23	GSEA	PID_IL2_STAT5_PATHWAY
3	7e−05	5 / 47	BP	positive regulation of osteoblast differentiation
4	1e−04	4 / 28	GSEA	PID_IL2_PI3K_PATHWAY
5	2e−04	3 / 12	BP	positive regulation of cartilage development
6	2e−04	4 / 33	miRN	hsa−miR−615−5p
7	3e−04	3 / 14	GSEA	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
8	3e−04	106 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
9	3e−04	3 / 15	GSEA	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
10	6e−04	4 / 41	GSEA	PID_IL6_7_PATHWAY
11	6e−04	3 / 18	BP	melanocyte differentiation
12	6e−04	11 / 366	miRN	hsa−miR−519b−3p
13	6e−04	5 / 74	GSEA	PID_MYC_ACTIV_PATHWAY
14	6e−04	13 / 488	miRN	hsa−miR−103
15	7e−04	3 / 19	BP	B cell homeostasis
16	7e−04	3 / 19	MF	Hsp90 protein binding
17	7e−04	3 / 19	GSEA	REACTOME_SIGNALING_BY_BMP
18	8e−04	7 / 162	miRN	hsa−miR−96
19	8e−04	3 / 20	BP	cellular response to fibroblast growth factor stimulus
20	8e−04	3 / 20	BP	semaphorin−plexin signaling pathway
21	9e−04	3 / 21	GSEA	BIOCARTA_IL6_PATHWAY
22	9e−04	4 / 47	GSEA	PID_SHP2_PATHWAY
23	9e−04	4 / 47	GSEA	PID_IL2_1PATHWAY
24	1e−03	4 / 48	GSEA	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP
25	1e−03	5 / 85	GSEA	BASSO_CD40_SIGNALING_UP
26	1e−03	2 / 6	GSEA	TAKADA_GASTRIC_CANCER_COPY_NUMBER_UP
27	1e−03	11 / 405	miRN	hsa−miR−519c−3p
28	2e−03	4 / 55	BP	BMP signaling pathway
29	2e−03	123 / 11774	CC	cell
30	2e−03	34 / 2211	Lymph	HOPP_Repetitive
31	2e−03	3 / 26	GSEA	BIOCARTA_NO1_PATHWAY
32	2e−03	2 / 7	GSEA	BAKER_HEMATOPOESIS_STAT5_TARGETS
33	2e−03	2 / 7	GSEA	BRUNEAU_SEPTATION_VENTRICULAR
34	2e−03	10 / 358	miRN	hsa−let−7d
35	2e−03	4 / 57	GSEA	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
36	2e−03	12 / 488	miRN	hsa−miR−107
37	2e−03	7 / 194	Tissu	PALMER_B−Cell signature up
38	2e−03	10 / 367	GSEA	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
39	2e−03	2 / 8	GSEA	TURJANSKI_MAPK7_TARGETS
40	2e−03	43 / 3068	BP	signal transduction



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 100	HORVATH_aging_genes meth DOWN
2	0.6	1 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−05	5 / 47	positive regulation of osteoblast differentiation
2	2e−04	3 / 12	positive regulation of cartilage development
3	6e−04	3 / 18	melanocyte differentiation
4	7e−04	3 / 19	B cell homeostasis
5	8e−04	3 / 20	cellular response to fibroblast growth factor stimulus
6	8e−04	3 / 20	semaphorin−plexin signaling pathway
7	2e−03	4 / 55	BMP signaling pathway
8	2e−03	43 / 3068	signal transduction
9	3e−03	3 / 32	chondrocyte differentiation
10	3e−03	3 / 33	ovarian follicle development
11	4e−03	2 / 10	B cell proliferation
12	4e−03	2 / 10	lymphocyte homeostasis
13	4e−03	2 / 10	response to iron ion
14	4e−03	4 / 69	negative regulation of cell migration
15	5e−03	4 / 72	hemopoiesis
16	5e−03	4 / 75	regulation of catalytic activity
17	5e−03	2 / 12	cellular response to fluid shear stress
18	6e−03	3 / 39	cellular response to drug
19	6e−03	3 / 39	membrane fusion
20	6e−03	3 / 39	ureteric bud development

Brain

Rank	p−value	#in/all	Geneset
1	9e−06	112 / 9528	Overlap_fetal_midbrain_Quies
2	3e−04	106 / 9330	Overlap_fetal_midbrain_ReprPC
3	4e−03	99 / 9013	Overlap_fetal_midbrain_K9K27me3
4	2e−02	16 / 953	Fetal_Enh
5	2e−02	96 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	7e−02	13 / 884	Overlap_fetal_midbrain_EnhG
7	9e−02	12 / 831	Fetal_HetRpts
8	1e−01	11 / 769	Overlap_fetal_midbrain_ZNF
9	1e−01	62 / 5940	Overlap_fetal_midbrain_HetRpts
10	2e−01	34 / 3081	Mid_Frontal_Lobe_ZNF
11	2e−01	5 / 304	Fetal_Het
12	3e−01	12 / 1065	Overlap_fetal_midbrain_Enh
13	4e−01	22 / 2185	Fetal_TssA
14	4e−01	8 / 765	Mid_Frontal_Lobe_Het
15	4e−01	6 / 574	Overlap_fetal_midbrain_TssP
16	5e−01	10 / 1013	Fetal_TssP
17	5e−01	10 / 1050	Fetal_EnhP
18	6e−01	6 / 656	Overlap_fetal_midbrain_EnhP
19	6e−01	7 / 786	Fetal_EnhG
20	6e−01	10 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.009	2 / 16	GENTLES_modul7
2	0.015	3 / 55	PanCan_JAK−ST_geneset_nanostring
3	0.021	4 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.026	4 / 120	PanCan_CC+Apop_geneset_nanostring
5	0.063	2 / 44	PanCan_TGF−B_geneset_nanostring
6	0.103	3 / 121	PanCan_MAPK_geneset_nanostring
7	0.110	2 / 61	PanCan_Wnt_geneset_nanostring
8	0.114	1 / 13	GENTLES_modul12
9	0.125	0 / 14	LIU_COMMON_CANCER_GENES
10	0.131	1 / 15	RHODES_CANCER_META_SIGNATURE
11	0.131	1 / 15	GENTLES_modul1
12	0.139	1 / 16	GENTLES_modul14
13	0.139	1 / 16	GENTLES_modul16
14	0.177	3 / 156	PanCan_PI3K_geneset_nanostring
15	0.276	2 / 111	PanCan_RAS_geneset_nanostring
16	0.356	1 / 47	PanCan_DNARepair_geneset_nanostring
17	0.362	1 / 48	KUIPER_MM poor survival
18	0.368	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
19	0.501	2 / 180	SPANG_LPS−index2
20	0.526	3 / 298	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	0.002	123 / 11774	cell
2	0.003	3 / 33	Golgi stack
3	0.004	3 / 34	ER to Golgi transport vesicle membrane
4	0.004	2 / 11	filopodium tip
5	0.005	4 / 76	extrinsic component of membrane
6	0.006	112 / 10605	intracellular
7	0.008	2 / 15	mitochondrial envelope
8	0.010	14 / 747	nucleolus
9	0.011	90 / 8205	cytoplasm
10	0.011	4 / 94	melanosome
11	0.015	105 / 9988	organelle
12	0.016	2 / 21	mitochondrial small ribosomal subunit
13	0.018	2 / 22	integral component of lumenal side of endoplasmic reticulum membrane
14	0.018	2 / 22	transport vesicle membrane
15	0.019	34 / 2576	membrane
16	0.021	5 / 169	transcription factor complex
17	0.026	40 / 3214	protein complex
18	0.029	6 / 249	neuronal cell body
19	0.030	21 / 1468	mitochondrion
20	0.032	4 / 128	ribosome

Chr

Rank	p−value	#in/all	Geneset
1	0.02	11 / 558	Chr 4
2	0.04	10 / 576	Chr 9
3	0.15	7 / 469	Chr 8
4	0.15	4 / 221	Chr 18
5	0.16	11 / 838	Chr 3
6	0.31	8 / 689	Chr 7
7	0.41	6 / 552	Chr 10
8	0.41	2 / 151	Chr 21
9	0.47	8 / 801	Chr 11
10	0.47	7 / 696	Chr 5
11	0.70	2 / 262	Chr 13
12	0.72	3 / 398	Chr 20
13	0.73	5 / 649	Chr 16
14	0.73	6 / 775	Chr 12
15	0.76	8 / 1037	Chr 19
16	0.77	5 / 687	Chr 6
17	0.80	6 / 840	Chr 17
18	0.82	7 / 993	Chr 2
19	0.89	3 / 551	Chr X
20	0.93	2 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.006	82 / 7203	TssF_Colon
2	0.008	102 / 9482	TssA_Colon
3	0.009	44 / 3383	EnhWk2_Colon
4	0.022	2 / 25	Ang_CRC_Hypomethylated
5	0.025	90 / 8415	Quies3_Colon
6	0.025	101 / 9653	Enh_Colon
7	0.025	47 / 3897	Quies1_Colon
8	0.030	66 / 5880	TssD2_Colon
9	0.031	95 / 9027	Tx_Colon
10	0.039	11 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	0.040	45 / 3812	TssD1_Colon
12	0.055	1 / 6	Marisa_CRC−C4
13	0.058	7 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	0.063	1 / 7	Juehling_HNPCC−mutated−in−5
15	0.081	1 / 9	Budinska_D_Mesenchymal_UP
16	0.112	7 / 436	K9acLow_Colon
17	0.119	55 / 5155	EnhWk1_Colon
18	0.121	87 / 8580	TxWk_Colon
19	0.123	3 / 131	Marisa_CRC−cluster−a
20	0.131	1 / 15	TCGA_Mutated−in−CRC_hypermutated

Disease

Rank	p−value	#in/all	Geneset
1	0.02	7 / 294	GUDJ_psoriasis down
2	0.98	1 / 435	GUDJ_psoriasis up
3	1.00	0 / 11	BCHETNIA_EBM up
4	1.00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
2	0.06	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
3	0.07	2 / 47	Vishal_subnetwork signature of survival in GBM
4	0.07	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
5	0.09	6 / 332	Up
6	0.10	1 / 11	Christensen_hypermethylated_in_ependymoma
7	0.10	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
8	0.14	1 / 16	KIM deleted & downregulated in LTS
9	0.14	2 / 71	Weller_LGG_A_vs_O_UP
10	0.15	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
11	0.16	11 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.18	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	0.19	1 / 22	KIM prognostic signature LTS vs. STS
14	0.21	1 / 25	Shaw_down_in_1p19q
15	0.24	1 / 29	shaw_responders_down_in_oligo_glioma
16	0.30	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
17	0.34	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
18	0.37	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
19	0.42	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
20	0.44	4 / 365	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−05	4 / 23	PID_IL2_STAT5_PATHWAY
2	1e−04	4 / 28	PID_IL2_PI3K_PATHWAY
3	3e−04	3 / 14	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
4	3e−04	3 / 15	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
5	6e−04	4 / 41	PID_IL6_7_PATHWAY
6	6e−04	5 / 74	PID_MYC_ACTIV_PATHWAY
7	7e−04	3 / 19	REACTOME_SIGNALING_BY_BMP
8	9e−04	3 / 21	BIOCARTA_IL6_PATHWAY
9	9e−04	4 / 47	PID_SHP2_PATHWAY
10	9e−04	4 / 47	PID_IL2_1PATHWAY
11	1e−03	4 / 48	CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP
12	1e−03	5 / 85	BASSO_CD40_SIGNALING_UP
13	1e−03	2 / 6	TAKADA_GASTRIC_CANCER_COPY_NUMBER_UP
14	2e−03	3 / 26	BIOCARTA_NO1_PATHWAY
15	2e−03	2 / 7	BAKER_HEMATOPOESIS_STAT5_TARGETS
16	2e−03	2 / 7	BRUNEAU_SEPTATION_VENTRICULAR
17	2e−03	4 / 57	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
18	2e−03	10 / 367	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
19	2e−03	2 / 8	TURJANSKI_MAPK7_TARGETS
20	2e−03	3 / 29	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP

HM

Rank	p−value	#in/all	Geneset
1	0.008	6 / 188	HALLMARK_MYC_TARGETS_V1
2	0.010	4 / 91	HALLMARK_PROTEIN_SECRETION
3	0.016	3 / 57	HALLMARK_MYC_TARGETS_V2
4	0.023	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.060	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	0.081	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.087	2 / 53	HALLMARK_TGF_BETA_SIGNALING
8	0.107	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	0.110	4 / 196	HALLMARK_MTORC1_SIGNALING
10	0.135	3 / 137	HALLMARK_UV_RESPONSE_DN
11	0.155	3 / 146	HALLMARK_UV_RESPONSE_UP
12	0.198	3 / 165	HALLMARK_MYOGENESIS
13	0.201	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
14	0.203	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
15	0.210	3 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
16	0.218	2 / 94	HALLMARK_ANDROGEN_RESPONSE
17	0.221	2 / 95	HALLMARK_SPERMATOGENESIS
18	0.227	3 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	0.286	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
20	0.331	2 / 127	HALLMARK_KRAS_SIGNALING_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 18	DUMEAUX_High bmi enriched genes
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	34 / 2211	HOPP_Repetitive
2	0.003	69 / 5693	HOPP_Weak_enhancer
3	0.004	83 / 7209	HOPP_Weak_promoter
4	0.011	65 / 5538	HOPP_Weak_txn
5	0.031	82 / 7592	HOPP_Active_promoter
6	0.069	57 / 5184	HOPP_Txn_transition
7	0.081	5 / 247	ZHANG_DLBCL mutated
8	0.102	15 / 1128	SPANG_BCR DN
9	0.105	5 / 268	SPANG_IL21 UP
10	0.112	72 / 6929	HOPP_Txn_elongation
11	0.114	1 / 13	YAMANE_AICDA_targets_recruited
12	0.125	2 / 66	TARTE_Plasma cell signature
13	0.131	1 / 15	WRIGHT_ABC UP
14	0.147	1 / 17	DAVE_NFkB BL DN
15	0.163	1 / 19	DAVE_c−myc BL UP
16	0.163	1 / 19	Subero_MM_hyper_meth
17	0.173	67 / 6564	HOPP_Strong_enhancer
18	0.183	6 / 410	SPANG_CD40 6hrs DN
19	0.201	2 / 89	ROSOLOWSKI_blue total
20	0.208	1 / 25	Subero_T−PLL_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 19	Hsp90 protein binding
2	4e−03	2 / 11	I−SMAD binding
3	5e−03	6 / 171	RNA polymerase II core promoter proximal region sequence−specific DNA bir
4	5e−03	2 / 12	Ras guanyl−nucleotide exchange factor activity
5	6e−03	18 / 1007	poly(A) RNA binding
6	7e−03	3 / 42	RNA polymerase II core promoter sequence−specific DNA binding
7	7e−03	11 / 501	identical protein binding
8	7e−03	2 / 14	endoribonuclease activity
9	7e−03	22 / 1365	RNA binding
10	8e−03	2 / 15	spectrin binding
11	1e−02	2 / 18	actin monomer binding
12	2e−02	3 / 59	syntaxin binding
13	2e−02	2 / 23	DNA helicase activity
14	2e−02	2 / 23	Hsp70 protein binding
15	2e−02	2 / 23	proton−transporting ATPase activity, rotational mechanism
16	2e−02	6 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
17	2e−02	2 / 26	growth factor binding
18	3e−02	2 / 28	ubiquitin conjugating enzyme activity
19	3e−02	2 / 30	repressing transcription factor binding
20	3e−02	27 / 2037	DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 33	hsa−miR−615−5p
2	6e−04	11 / 366	hsa−miR−519b−3p
3	6e−04	13 / 488	hsa−miR−103
4	8e−04	7 / 162	hsa−miR−96
5	1e−03	11 / 405	hsa−miR−519c−3p
6	2e−03	10 / 358	hsa−let−7d
7	2e−03	12 / 488	hsa−miR−107
8	2e−03	8 / 251	hsa−miR−548l
9	3e−03	11 / 447	hsa−miR−130b
10	4e−03	7 / 214	hsa−miR−182
11	4e−03	7 / 217	hsa−miR−181d
12	5e−03	7 / 224	hsa−miR−181b
13	5e−03	8 / 284	hsa−miR−503
14	5e−03	11 / 479	hsa−miR−16
15	5e−03	5 / 121	hsa−miR−543
16	5e−03	7 / 228	hsa−miR−124
17	6e−03	3 / 39	hsa−miR−593
18	9e−03	9 / 378	hsa−miR−454
19	1e−02	6 / 198	hsa−miR−181c
20	1e−02	10 / 459	hsa−miR−195

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	GUSTAFSON_PI3K_UP
2	0.1	1 / 12	BENTINK_ras.1
3	0.1	1 / 13	BENTINK_myc.1
4	0.1	1 / 15	BENTINK_ras.6
5	1.0	0 / 13	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 12	BENTINK_e2f3.2
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	32 / 2416	ICGC_Bcl3_targets
2	0.03	1 / 3	MYC_DNA replication UP
3	0.05	1 / 5	MYC_TF and cofactors
4	0.06	27 / 2136	ICGC_GabpPcr2_targets
5	0.06	19 / 1400	ICGC_Myc_targets
6	0.08	1 / 9	MYC_Targets DOWN
7	0.08	10 / 653	ICGC_SrfPcr2_targets
8	0.10	23 / 1872	ICGC_Mef2_targets
9	0.10	17 / 1314	ICGC_Usf1_targets
10	0.12	24 / 2013	ICGC_Bcl11_targets
11	0.14	50 / 4689	ICGC_Taf1_targets
12	0.15	46 / 4314	ICGC_Ebfsc137065_targets
13	0.18	43 / 4054	ICGC_Egr1_targets
14	0.21	21 / 1878	ICGC_Cebpbsc150_targets
15	0.23	19 / 1701	HEBENSTREIT_high expression TF
16	0.23	29 / 2714	ICGC_Irf4_targets
17	0.24	53 / 5219	ICGC_Tcf3_targets
18	0.24	50 / 4909	ICGC_Stat5_targets
19	0.24	16 / 1418	ICGC_Ets1_targets
20	0.26	7 / 553	ICGC_RxraPcr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 38	VAQUERIZAS_Whole brain
2	0.16	1 / 19	VAQUERIZAS_Tonsil
3	0.22	1 / 26	VAQUERIZAS_Liver
4	0.22	1 / 27	VAQUERIZAS_Lymph node
5	0.29	1 / 36	VAQUERIZAS_Fetal brain
6	0.31	1 / 40	VAQUERIZAS_Thyroid
7	0.38	2 / 143	VAQUERIZAS_General
8	0.42	1 / 58	VAQUERIZAS_Lung
9	0.42	1 / 59	VAQUERIZAS_Whole blood
10	1.00	0 / 41	VAQUERIZAS_Placenta
11	1.00	0 / 33	VAQUERIZAS_Prostate
12	1.00	0 / 29	VAQUERIZAS_Smooth muscle
13	1.00	0 / 45	VAQUERIZAS_Uterus
14	1.00	0 / 9	VAQUERIZAS_Kidney
15	1.00	0 / 23	VAQUERIZAS_Spinal cord
16	1.00	0 / 37	VAQUERIZAS_Thymus
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 29	VAQUERIZAS_Fetal lung
19	1.00	0 / 16	VAQUERIZAS_Pancreas
20	1.00	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.002	7 / 194	PALMER_B−Cell signature up
2	0.090	3 / 114	PALMER_T−Cell signature up
3	0.114	1 / 13	WIRTH_Thyroid gland
4	0.350	1 / 46	WIRTH_Liver
5	0.633	1 / 107	WIRTH_Testis
6	0.635	3 / 350	WIRTH_Nervous System
7	0.840	2 / 350	WIRTH_Immune system
8	1.000	0 / 32	WIRTH_Pancreas
9	1.000	0 / 11	WIRTH_Sec. lymphoid organs
10	1.000	0 / 11	WIRTH_Prim. lymphoid organs
11	1.000	0 / 13	WIRTH_B−cells
12	1.000	0 / 8	WIRTH_Tonsil
13	1.000	0 / 12	WIRTH_Thymus
14	1.000	0 / 12	WIRTH_Lymphocytes
15	1.000	0 / 5	WIRTH_Bone marrow
16	1.000	0 / 11	WIRTH_Globus pallidus
17	1.000	0 / 14	WIRTH_Telencephalon
18	1.000	0 / 11	WIRTH_Cortex cerebri
19	1.000	0 / 10	WIRTH_Hippocampus
20	1.000	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	14 / 1115	LU_BPDE 1h DN
2	0.3	38 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

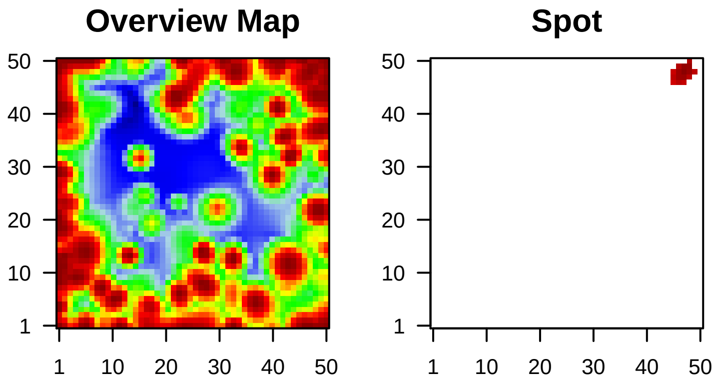
Overexpression Spots

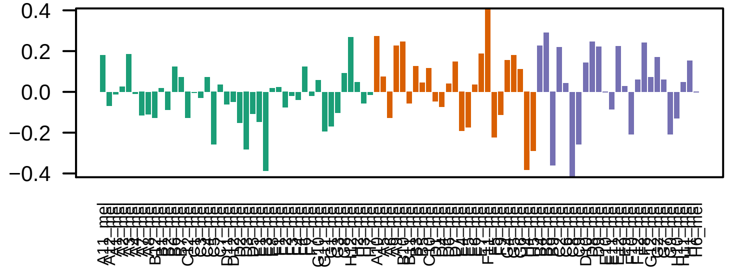
Spot Summary: O

metagenes = 16
genes = 121

<r> metagenes = 0.93
<r> genes = 0.11
beta: r2= 1.69 / log p= −Inf

samples with spot = 15 (16.3 %)
MSC1 : 3 (7.1 %)
MSC2 : 5 (20 %)
MSC3 : 7 (28 %)



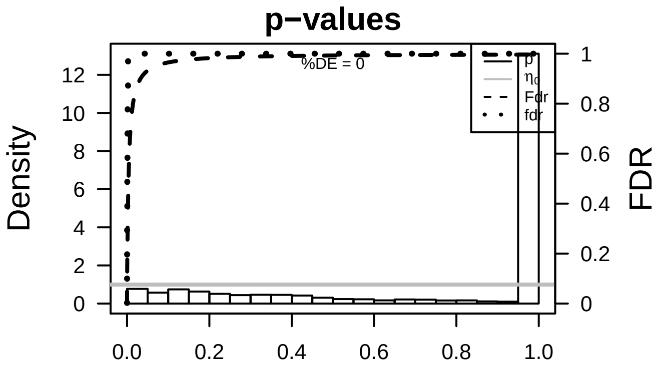


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	OAS1	1.86	−0.2	0.37	OAS1	2'−5'−oligoadenylate synthetase 1, 40/46kDa [Source:HGNC
2	CYP19A1	1.7	−0.37	0.31	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1 [Sour
3	MXI1	1.66	−0.86	0.23	MXI1	MAX interactor 1, dimerization protein [Source:HGNC Symbo
4	RNF170	1.65	−0.21	0.3	RNF170	ring finger protein 170 [Source:HGNC Symbol;Acc:HGNC:25
5	HSPBAP1	1.58	−0.39	0.36	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1 [Source:HGN
6	METTL1	1.57	−1.04	0.29	METTL1	methyltransferase like 1 [Source:HGNC Symbol;Acc:HGNC:7
7	WDR27	1.54	−0.32	0.21	WDR27	WD repeat domain 27 [Source:HGNC Symbol;Acc:HGNC:21
8	CYB561A3	1.51	−1.09	0.25	CYB561A3	cytochrome b561 family, member A3 [Source:HGNC Symbol;
9	MED29	1.51	−0.56	0.37	MED29	mediator complex subunit 29 [Source:HGNC Symbol;Acc:HG
10	GATSL3	1.49	−0.08	0.28	GATSL3	GATS protein−like 3 [Source:HGNC Symbol;Acc:HGNC:3442
11	PIGV	1.49	−0.28	0.34	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V [Sou
12	CCND1	1.49	−1.24	0.39	CCND1	cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]
13	COG5	1.49	−0.47	0.24	COG5	component of oligomeric golgi complex 5 [Source:HGNC Sym
14	RABGGTA	1.41	−0.76	0.27	RABGGTA	Rab geranylgeranyltransferase, alpha subunit [Source:HGNC
15	TNFAIP1	1.4	−0.97	0.33	TNFAIP1	tumor necrosis factor, alpha−induced protein 1 (endothelial) [
16	COG7	1.39	−0.34	0.32	COG7	component of oligomeric golgi complex 7 [Source:HGNC Sym
17	GSTZ1	1.38	−0.56	0.28	GSTZ1	glutathione S−transferase zeta 1 [Source:HGNC Symbol;Acc:
18	CAPN10	1.37	−0.2	0.29	CAPN10	calpain 10 [Source:HGNC Symbol;Acc:HGNC:1477]
19	YBEY	1.37	−0.69	0.36	YBEY	ybeY metallopeptidase (putative) [Source:HGNC Symbol;Acc
20	SPRYD3	1.37	−0.39	0.39	SPRYD3	SPRY domain containing 3 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−11	109 / 9482	Colon	TssA_Colon
2	3e−07	20 / 649	CC	endoplasmic reticulum membrane
3	5e−07	69 / 5184	Lymph	HOPP_Txn_transition
4	1e−06	98 / 9027	Colon	Tx_Colon
5	3e−06	94 / 8580	Colon	TxWk_Colon
6	3e−06	26 / 1201	CC	endoplasmic reticulum
7	4e−06	99 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
8	1e−05	8 / 135	GSEA	KAAB_FAILED_HEART_ATRIUM_DN
9	2e−05	95 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
10	4e−05	27 / 1468	CC	mitochondrion
11	5e−05	8 / 162	BP	ribosome biogenesis
12	6e−05	78 / 6929	Lymph	HOPP_Txn_elongation
13	6e−05	23 / 1171	TF	KIM_MYC targets
14	7e−05	8 / 167	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
15	8e−05	9 / 221	GSEA	DANG_REGULATED_BY_MYC_DN
16	1e−04	3 / 12	CC	Golgi transport complex
17	1e−04	87 / 8205	CC	cytoplasm
18	1e−04	13 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
19	2e−04	5 / 63	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
20	2e−04	5 / 69	GSEA	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
21	3e−04	17 / 800	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
22	3e−04	6 / 111	GSEA	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
23	3e−04	5 / 73	GSEA	CARD_MIR302A_TARGETS
24	3e−04	10 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
25	4e−04	16 / 752	GSEA	GRADE_COLON_CANCER_UP
26	5e−04	30 / 1975	BP	cellular protein modification process
27	5e−04	5 / 80	BP	rRNA processing
28	6e−04	98 / 9988	CC	organelle
29	6e−04	6 / 126	GSEA	LU_AGING_BRAIN_DN
30	6e−04	5 / 83	GSEA	LI_DCP2_BOUND_MRNA
31	7e−04	102 / 10605	CC	intracellular
32	8e−04	31 / 2136	TF	ICGC_GabpPcr2_targets
33	8e−04	4 / 51	GSEA	JIANG_AGING_CEREBRAL_CORTEX_DN
34	8e−04	4 / 52	GSEA	NADLER_OBESITY_UP
35	9e−04	11 / 435	BP	cellular protein metabolic process
36	9e−04	3 / 24	MF	snoRNA binding
37	1e−03	8 / 250	miRN	hsa−miR−520a−3p
38	1e−03	5 / 94	GSEA	TAKAO_RESPONSE_TO_UVB_RADIATION_DN
39	1e−03	15 / 747	CC	nucleolus
40	1e−03	10 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−05	8 / 162	ribosome biogenesis
2	5e−04	30 / 1975	cellular protein modification process
3	5e−04	5 / 80	rRNA processing
4	9e−04	11 / 435	cellular protein metabolic process
5	1e−03	3 / 27	intra−Golgi vesicle−mediated transport
6	1e−03	7 / 204	post−translational protein modification
7	3e−03	3 / 34	retrograde vesicle−mediated transport, Golgi to ER
8	3e−03	2 / 10	DNA catabolic process
9	3e−03	2 / 10	protein localization to Golgi apparatus
10	3e−03	4 / 76	protein glycosylation
11	3e−03	2 / 11	positive regulation of B cell differentiation
12	3e−03	2 / 11	protein transmembrane transport
13	5e−03	2 / 13	mannosylation
14	5e−03	19 / 1237	metabolic process
15	6e−03	24 / 1730	small molecule metabolic process
16	8e−03	2 / 17	cellular response to nitrogen starvation
17	8e−03	2 / 17	zinc II ion transport
18	1e−02	2 / 19	protein palmitoylation
19	1e−02	14 / 863	transmembrane transport
20	1e−02	3 / 56	cellular iron ion homeostasis

Brain

Rank	p−value	#in/all	Geneset
1	4e−06	99 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−05	95 / 9013	Overlap_fetal_midbrain_K9K27me3
3	2e−02	18 / 1333	Fetal_ReprPCWk
4	3e−02	88 / 9528	Overlap_fetal_midbrain_Quies
5	5e−02	11 / 765	Mid_Frontal_Lobe_Het
6	7e−02	57 / 5940	Overlap_fetal_midbrain_HetRpts
7	1e−01	10 / 769	Overlap_fetal_midbrain_ZNF
8	1e−01	31 / 3081	Mid_Frontal_Lobe_ZNF
9	1e−01	3 / 163	Fetal_ReprPC
10	2e−01	9 / 831	Fetal_HetRpts
11	3e−01	23 / 2462	Mid_Frontal_Lobe_HetRpts
12	3e−01	4 / 349	Fetal_ZNF
13	3e−01	17 / 1845	Fetal_Quies
14	4e−01	76 / 9020	Overlap_fetal_midbrain_ReprPCWk
15	5e−01	9 / 1050	Fetal_EnhP
16	6e−01	10 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	6e−01	8 / 989	Mid_Frontal_Lobe_Quies
18	6e−01	7 / 884	Overlap_fetal_midbrain_EnhG
19	7e−01	7 / 953	Fetal_Enh
20	7e−01	2 / 304	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	6 / 298	SPANG_BCL6−index2
2	0.08	1 / 10	GENTLES_modul3
3	0.09	0 / 15	RHODES_CANCER_META_SIGNATURE
4	0.09	1 / 12	LIU_BREAST_CANCER
5	0.10	1 / 13	GENTLES_modul12
6	0.12	1 / 16	GENTLES_modul6
7	0.13	3 / 156	PanCan_PI3K_geneset_nanostring
8	0.18	3 / 180	SPANG_LPS−index2
9	0.21	1 / 29	KUIPER_MM good survival
10	0.28	1 / 40	ZHANG_MM up
11	0.28	1 / 40	PanCan_HK_geneset_nanostring
12	0.30	1 / 44	PanCan_TGF−B_geneset_nanostring
13	0.33	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	0.36	1 / 55	PanCan_JAK−ST_geneset_nanostring
15	0.39	1 / 61	PanCan_Wnt_geneset_nanostring
16	0.42	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
17	0.49	0 / 12	LIU_PROSTATE_CANCER_UP
18	0.60	1 / 111	PanCan_RAS_geneset_nanostring
19	0.60	1 / 113	PanCan_Driver_Gene_geneset_nanostring
20	0.63	1 / 120	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−07	20 / 649	endoplasmic reticulum membrane
2	3e−06	26 / 1201	endoplasmic reticulum
3	4e−05	27 / 1468	mitochondrion
4	1e−04	3 / 12	Golgi transport complex
5	1e−04	87 / 8205	cytoplasm
6	6e−04	98 / 9988	organelle
7	7e−04	102 / 10605	intracellular
8	1e−03	15 / 747	nucleolus
9	2e−03	13 / 616	endosome
10	2e−03	7 / 223	lysosomal membrane
11	4e−03	10 / 456	vacuole
12	5e−03	18 / 1132	Golgi apparatus
13	5e−03	116 / 13191	cellular_component
14	6e−03	2 / 15	autophagic vacuole membrane
15	1e−02	4 / 105	ribonucleoprotein complex
16	1e−02	106 / 11774	cell
17	1e−02	2 / 22	pre−autophagosomal structure
18	2e−02	8 / 412	lysosome
19	3e−02	3 / 81	late endosome membrane
20	3e−02	2 / 35	mediator complex

Chr

Rank	p−value	#in/all	Geneset
1	0.03	12 / 801	Chr 11
2	0.04	14 / 1037	Chr 19
3	0.15	10 / 840	Chr 17
4	0.15	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
5	0.27	3 / 221	Chr 18
6	0.28	7 / 649	Chr 16
7	0.30	8 / 775	Chr 12
8	0.32	5 / 462	Chr 14
9	0.36	3 / 262	Chr 13
10	0.47	5 / 551	Chr X
11	0.47	5 / 552	Chr 10
12	0.50	6 / 696	Chr 5
13	0.51	5 / 576	Chr 9
14	0.53	4 / 469	Chr 8
15	0.66	5 / 687	Chr 6
16	0.71	1 / 151	Chr 21
17	0.76	2 / 335	Chr 22
18	0.82	4 / 689	Chr 7
19	0.82	5 / 838	Chr 3
20	0.84	2 / 398	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−11	109 / 9482	TssA_Colon
2	1e−06	98 / 9027	Tx_Colon
3	3e−06	94 / 8580	TxWk_Colon
4	5e−03	35 / 2798	TxEnhG1_Colon
5	6e−03	73 / 7203	TssF_Colon
6	2e−02	90 / 9653	Enh_Colon
7	4e−02	93 / 10290	TssWk_Colon
8	7e−02	29 / 2698	EnhA_Colon
9	7e−02	77 / 8415	Quies3_Colon
10	8e−02	56 / 5880	TssD2_Colon
11	1e−01	48 / 5155	EnhWk1_Colon
12	2e−01	1 / 33	Marisa_CRC−cluster−e
13	4e−01	2 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
14	4e−01	7 / 739	TxEnhG2_Colon
15	4e−01	7 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	4e−01	1 / 66	Marisa_CRC−cluster−h
17	4e−01	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
18	4e−01	6 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
19	5e−01	4 / 427	Quies2_Colon
20	6e−01	1 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.7	3 / 435	GUDJ_psoriasis up
2	0.9	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
2	0.04	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.09	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	0.12	1 / 15	WILLSCHER_GBM_STSwt_proteomics−Q_UP
5	0.18	2 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	0.20	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
7	0.23	1 / 32	Colman_survival_associated
8	0.27	1 / 39	OPC
9	0.32	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
10	0.34	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	0.35	4 / 365	Down_b
12	0.37	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	0.40	1 / 62	cultured astroglia vs. in vivo astrocytes
14	0.40	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	0.43	1 / 68	GIEZELT_GBM_WT_down_VS_mut
16	0.43	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
17	0.46	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
18	0.51	1 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
19	0.51	3 / 332	Up
20	0.54	7 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−05	8 / 135	KAAB_FAILED_HEART_ATRIUM_DN
2	7e−05	8 / 167	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
3	8e−05	9 / 221	DANG_REGULATED_BY_MYC_DN
4	1e−04	13 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
5	2e−04	5 / 63	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
6	2e−04	5 / 69	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
7	3e−04	17 / 800	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
8	3e−04	6 / 111	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
9	3e−04	5 / 73	CARD_MIR302A_TARGETS
10	3e−04	10 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
11	4e−04	16 / 752	GRADE_COLON_CANCER_UP
12	6e−04	6 / 126	LU_AGING_BRAIN_DN
13	6e−04	5 / 83	LI_DCP2_BOUND_MRNA
14	8e−04	4 / 51	JIANG_AGING_CEREBRAL_CORTEX_DN
15	8e−04	4 / 52	NADLER_OBESITY_UP
16	1e−03	5 / 94	TAKAO_RESPONSE_TO_UVB_RADIATION_DN
17	1e−03	10 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
18	1e−03	9 / 324	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
19	2e−03	5 / 104	LAIHO_COLORECTAL_CANCER_SERRATED_UP
20	2e−03	11 / 476	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR

HM

Rank	p−value	#in/all	Geneset
1	0.004	6 / 188	HALLMARK_ADIPOGENESIS
2	0.054	4 / 174	HALLMARK_HEME_METABOLISM
3	0.060	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.079	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	0.117	3 / 146	HALLMARK_DNA_REPAIR
6	0.158	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	0.178	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
8	0.198	3 / 188	HALLMARK_MYC_TARGETS_V1
9	0.211	1 / 29	HALLMARK_NOTCH_SIGNALING
10	0.217	2 / 107	HALLMARK_COAGULATION
11	0.224	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
12	0.274	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
13	0.316	2 / 140	HALLMARK_APOPTOSIS
14	0.320	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	0.352	1 / 53	HALLMARK_TGF_BETA_SIGNALING
16	0.373	1 / 57	HALLMARK_MYC_TARGETS_V2
17	0.381	2 / 162	HALLMARK_COMPLEMENT
18	0.389	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	0.402	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
20	0.422	2 / 176	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 32	DUMEAUX_Fasting enriched genes
2	0.4	1 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−07	69 / 5184	HOPP_Txn_transition
2	6e−05	78 / 6929	HOPP_Txn_elongation
3	6e−03	76 / 7592	HOPP_Active_promoter
4	9e−03	67 / 6564	HOPP_Strong_enhancer
5	2e−02	17 / 1218	SPANG_BCR UP
6	6e−02	1 / 8	YAMANE_AICDA_targets_nonrecruited
7	8e−02	14 / 1128	SPANG_BCR DN
8	9e−02	2 / 60	Subero_T−ALL_hyper_meth
9	1e−01	2 / 66	TARTE_Plasma cell signature
10	2e−01	4 / 268	SPANG_IL21 UP
11	2e−01	1 / 30	TARTE_B−cell signature
12	3e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
13	3e−01	62 / 7209	HOPP_Weak_promoter
14	3e−01	1 / 47	Subero_FL_hyper_meth
15	4e−01	1 / 61	SPANG_LPS 6hrs DN
16	4e−01	3 / 280	SPANG_CD40 6hrs UP
17	4e−01	4 / 410	SPANG_CD40 6hrs DN
18	5e−01	1 / 81	Subero_INT_hyper_meth
19	5e−01	1 / 82	ROSOLOWSKI_green UP
20	5e−01	1 / 96	Subero_DLBCL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 24	snoRNA binding
2	3e−03	2 / 10	deoxyribonuclease activity
3	3e−03	2 / 10	ribosomal small subunit binding
4	3e−03	2 / 11	metal ion transmembrane transporter activity
5	4e−03	3 / 39	SNARE binding
6	5e−03	2 / 13	myosin V binding
7	6e−03	2 / 15	hydrolase activity, acting on acid anhydrides
8	7e−03	20 / 1365	RNA binding
9	8e−03	2 / 17	FK506 binding
10	9e−03	2 / 18	palmitoyltransferase activity
11	1e−02	2 / 19	protein phosphatase type 2A regulator activity
12	1e−02	2 / 22	transferase activity, transferring hexosyl groups
13	1e−02	2 / 23	Hsp70 protein binding
14	1e−02	2 / 23	proton−transporting ATPase activity, rotational mechanism
15	2e−02	2 / 24	protein−cysteine S−palmitoyltransferase activity
16	2e−02	15 / 1007	poly(A) RNA binding
17	2e−02	2 / 25	protein serine/threonine/tyrosine kinase activity
18	2e−02	5 / 193	transferase activity, transferring acyl groups
19	2e−02	2 / 29	carboxylic ester hydrolase activity
20	3e−02	8 / 433	peptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	8 / 250	hsa−miR−520a−3p
2	0.004	8 / 314	hsa−miR−520c−3p
3	0.005	4 / 84	hsa−miR−220c
4	0.006	3 / 46	hsa−miR−874
5	0.006	5 / 144	hsa−miR−135b
6	0.007	4 / 91	hsa−miR−378
7	0.007	7 / 272	hsa−miR−520b
8	0.007	6 / 208	hsa−miR−432
9	0.012	5 / 168	hsa−miR−520h
10	0.013	3 / 60	hsa−miR−671−5p
11	0.013	4 / 112	hsa−miR−875−3p
12	0.014	3 / 62	hsa−miR−1236
13	0.015	2 / 23	hsa−miR−1227
14	0.016	5 / 179	hsa−miR−520f
15	0.016	4 / 118	hsa−miR−509−3p
16	0.018	7 / 328	hsa−miR−18a
17	0.022	4 / 130	hsa−miR−145
18	0.023	3 / 74	hsa−miR−422a
19	0.023	3 / 74	hsa−miR−708
20	0.026	2 / 31	hsa−miR−296−5p

PathwAct

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_myc.1
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−05	23 / 1171	KIM_MYC targets
2	8e−04	31 / 2136	ICGC_GabpPcr2_targets
3	1e−02	48 / 4385	ICGC_Atf2_targets
4	2e−02	19 / 1383	ICGC_Six5_targets
5	2e−02	19 / 1400	ICGC_Myc_targets
6	4e−02	42 / 4032	ICGC_Creb1_targets
7	5e−02	45 / 4414	ICGC_Bclaf101388_targets
8	5e−02	49 / 4909	ICGC_Stat5_targets
9	5e−02	47 / 4689	ICGC_Taf1_targets
10	6e−02	48 / 4829	ICGC_Nficsc81335_targets
11	6e−02	46 / 4617	ICGC_Tcf12_targets
12	7e−02	48 / 4879	ICGC_Pmlsc71910_targets
13	9e−02	39 / 3924	ICGC_Zeb1_targets
14	1e−01	45 / 4706	ICGC_Sp1_targets
15	1e−01	1 / 19	MYC_Metabolism UP
16	2e−01	28 / 2836	ICGC_BatfPcr1_targets
17	2e−01	48 / 5200	ICGC_Mta3_targets
18	2e−01	49 / 5355	ICGC_Pol2_targets
19	2e−01	35 / 3700	ICGC_Nfatc1_targets
20	2e−01	14 / 1314	ICGC_Usf1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	VAQUERIZAS_Bone marrow
2	0.2	1 / 26	VAQUERIZAS_Liver
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 33	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 45	VAQUERIZAS_Uterus
8	1.0	0 / 143	VAQUERIZAS_General
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 59	VAQUERIZAS_Whole blood
15	1.0	0 / 7	VAQUERIZAS_Appendix
16	1.0	0 / 29	VAQUERIZAS_Fetal lung
17	1.0	0 / 58	VAQUERIZAS_Lung
18	1.0	0 / 16	VAQUERIZAS_Pancreas
19	1.0	0 / 23	VAQUERIZAS_Trachea
20	1.0	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	5 / 225	PALMER_Granulocytes signature up
2	0.09	1 / 11	WIRTH_Globus pallidus
3	0.10	1 / 13	WIRTH_B−cells
4	0.11	1 / 14	WIRTH_Telencephalon
5	0.12	1 / 16	PALMER_Lymphocytes signature up
6	0.21	3 / 194	PALMER_B−Cell signature up
7	0.23	1 / 32	WIRTH_Placenta
8	0.61	1 / 114	PALMER_T−Cell signature up
9	0.78	2 / 350	WIRTH_Immune system
10	1.00	0 / 32	WIRTH_Pancreas
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 8	WIRTH_Tonsil
14	1.00	0 / 12	WIRTH_Thymus
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 350	WIRTH_Nervous System
18	1.00	0 / 11	WIRTH_Cortex cerebri
19	1.00	0 / 10	WIRTH_Hippocampus
20	1.00	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.07	14 / 1115	LU_BPDE 1h DN
2	0.30	33 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

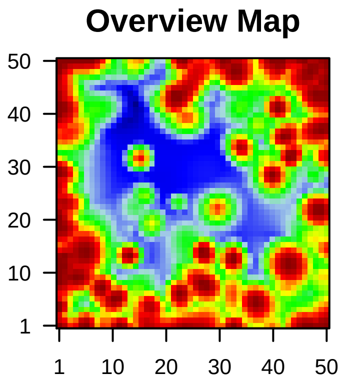
Overexpression Spots

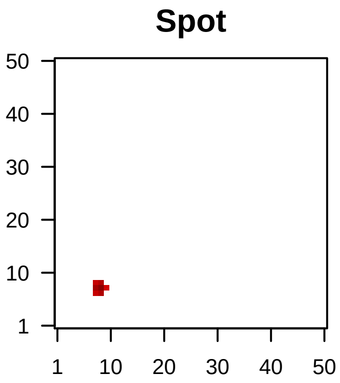
Spot Summary: P

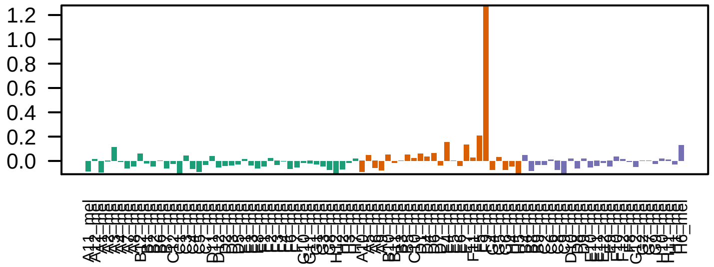
metagenes = 7
genes = 97

<r> metagenes = 0.98
<r> genes = 0.22
beta: r2= 0.74 / log p= −Inf

samples with spot = 2 (2.2 %)
MSC2 : 2 (8 %)





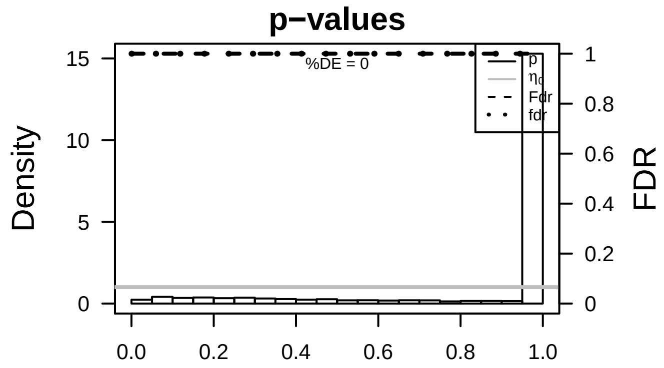


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	METAP1D	2.04	−0.33	0.31	METAP1D	methionyl aminopeptidase type 1D (mitochondrial) [Source:H
2	SLC24A1	1.94	−0.09	0.54	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchange
3	GPR183	1.92	−0.15	0.49	GPR183	G protein−coupled receptor 183 [Source:HGNC Symbol;Acc:
4	RHPN2	1.85	−0.17	0.36	RHPN2	rhophilin, Rho GTPase binding protein 2 [Source:HGNC Sym
5	KCNIP4	1.84	−0.07	0.63	KCNIP4	Kv channel interacting protein 4 [Source:HGNC Symbol;Acc:
6	ACP6	1.8	−0.24	0.32	ACP6	acid phosphatase 6, lysophosphatidic [Source:HGNC Symbo
7	GPR171	1.8	−0.08	0.72	GPR171	G protein−coupled receptor 171 [Source:HGNC Symbol;Acc:
8	JAM3	1.8	−0.24	0.47	JAM3	junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:H
9	TMEM27	1.79	−0.08	0.5	TMEM27	transmembrane protein 27 [Source:HGNC Symbol;Acc:HGN
10	CHAMP1	1.78	−0.27	0.33	CHAMP1	chromosome alignment maintaining phosphoprotein 1 [Sourc
11	ZNF530	1.78	−0.18	0.28	ZNF530	zinc finger protein 530 [Source:HGNC Symbol;Acc:HGNC:29
12	UGT3A2	1.78	−0.08	0.49	UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2 [Source:HG
13	CFAP46	1.73	−0.09	0.51	CFAP46	cilia and flagella associated protein 46 [Source:HGNC Symbo
14	ADAM22	1.7	−0.14	0.59	ADAM22	ADAM metallopeptidase domain 22 [Source:HGNC Symbol;A
15	TRPC1	1.7	−0.16	0.36	TRPC1	transient receptor potential cation channel, subfamily C, mem
16	SLC29A3	1.68	−0.08	0.39	SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter),
17	RD3L	1.67	−0.09	0.49	RD3L	retinal degeneration 3−like [Source:HGNC Symbol;Acc:HGN
18	PDCD2L	1.66	−0.43	0.32	PDCD2L	programmed cell death 2−like [Source:HGNC Symbol;Acc:H
19	ZNF546	1.65	−0.15	0.42	ZNF546	zinc finger protein 546 [Source:HGNC Symbol;Acc:HGNC:28
20	ZNF248	1.65	−0.3	0.33	ZNF248	zinc finger protein 248 [Source:HGNC Symbol;Acc:HGNC:13

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−04	6 / 138	GSE	LEE_LIVER_CANCER_SURVIVAL_UP
2	8e−04	4 / 63	miRN	hsa−miR−1285
3	3e−03	2 / 12	Glio	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	4e−03	3 / 47	GSE	LEE_EARLY_T_LYMPHOCYTE_DN
5	4e−03	2 / 14	BP	histone H4−K5 acetylation
6	4e−03	2 / 14	BP	histone H4−K8 acetylation
7	4e−03	3 / 48	miRN	hsa−miR−524−3p
8	4e−03	8 / 388	BP	proteolysis
9	4e−03	2 / 15	BP	peptide hormone processing
10	4e−03	2 / 15	GSE	GEISS_RESPONSE_TO_DSRNA_DN
11	4e−03	4 / 101	miRN	hsa−miR−325
12	5e−03	2 / 17	BP	pseudouridine synthesis
13	6e−03	15 / 1122	Brain	Fetal_K9K27me3
14	7e−03	3 / 61	miRN	hsa−miR−612
15	7e−03	2 / 20	GSE	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
16	8e−03	2 / 21	GSE	LA_MEN1_TARGETS
17	9e−03	2 / 22	MF	delayed rectifier potassium channel activity
18	9e−03	2 / 22	CC	histone acetyltransferase complex
19	9e−03	2 / 22	GSE	HEIDENBLAD_AMPLICON_12P11_12_DN
20	9e−03	9 / 545	GSE	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
21	1e−02	2 / 23	MF	hydrolase activity, acting on ester bonds
22	1e−02	2 / 24	MF	cation channel activity
23	1e−02	2 / 24	MF	N−acetyltransferase activity
24	1e−02	3 / 72	GSE	SAFFORD_T_LYMPHOCYTE_ANERGY
25	1e−02	2 / 26	BP	cellular response to organic substance
26	1e−02	2 / 26	GSE	VALK_AML_CLUSTER_4
27	1e−02	1 / 2	Glio	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
28	1e−02	2 / 28	MF	Ran GTPase binding
29	2e−02	4 / 145	miRN	hsa−miR−922
30	2e−02	2 / 29	GSE	ZHENG_IL22_SIGNALING_DN
31	2e−02	2 / 30	GSE	LEE_LIVER_CANCER
32	2e−02	2 / 30	GSE	PIONTEK_PKD1_TARGETS_UP
33	2e−02	3 / 82	GSE	WINZEN_DEGRADED_VIA_KHSRP
34	2e−02	20 / 1872	TF	ICGC_Mef2_targets
35	2e−02	2 / 31	CC	brush border membrane
36	2e−02	2 / 31	GSE	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
37	2e−02	6 / 319	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
38	2e−02	6 / 321	miRN	hsa−miR−32
39	2e−02	3 / 87	GSE	MATZUK_SPERMATOZOA
40	2e−02	1 / 3	GSE	CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.1	2 / 100	HORVATH_aging_genes meth DOWN
2	0.5	1 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.004	2 / 14	histone H4−K5 acetylation
2	0.004	2 / 14	histone H4−K8 acetylation
3	0.004	8 / 388	proteolysis
4	0.004	2 / 15	peptide hormone processing
5	0.005	2 / 17	pseudouridine synthesis
6	0.012	2 / 26	cellular response to organic substance
7	0.026	7 / 443	anatomical structure formation involved in morphogenesis
8	0.028	2 / 40	histone H3 acetylation
9	0.033	2 / 44	protein processing
10	0.035	2 / 45	cell growth
11	0.047	2 / 53	phosphatidylinositol biosynthetic process
12	0.053	4 / 216	immune response
13	0.060	3 / 136	phospholipid metabolic process
14	0.060	4 / 225	ion transport
15	0.060	2 / 61	palate development
16	0.063	1 / 10	adherens junction assembly
17	0.063	1 / 10	biotin metabolic process
18	0.063	1 / 10	cardiac muscle cell proliferation
19	0.063	1 / 10	cerebellar Purkinje cell differentiation
20	0.063	1 / 10	heart trabecula formation

Brain

Rank	p−value	#in/all	Geneset
1	0.006	15 / 1122	Fetal_K9K27me3
2	0.044	12 / 1065	Overlap_fetal_midbrain_Enh
3	0.047	19 / 1949	Fetal_TssF
4	0.058	11 / 989	Mid_Frontal_Lobe_Quies
5	0.076	7 / 564	Mid_Frontal_Lobe_EnhP
6	0.174	20 / 2462	Mid_Frontal_Lobe_HetRpts
7	0.220	15 / 1845	Fetal_Quies
8	0.220	8 / 884	Overlap_fetal_midbrain_EnhG
9	0.258	6 / 656	Overlap_fetal_midbrain_EnhP
10	0.270	5 / 534	Mid_Frontal_Lobe_EnhG
11	0.280	7 / 812	Mid_Frontal_Lobe_TssP
12	0.298	62 / 9020	Overlap_fetal_midbrain_ReprPCWk
13	0.366	4 / 468	Mid_Frontal_Lobe_TssF
14	0.409	6 / 786	Fetal_EnhG
15	0.418	9 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	0.443	2 / 229	Mid_Frontal_Lobe_TxTrans
17	0.444	5 / 668	Mid_Frontal_Lobe_Enh
18	0.459	3 / 383	Fetal_Tx
19	0.480	13 / 1907	Fetal_TxTrans
20	0.497	6 / 862	Overlap_fetal_midbrain_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	1 / 10	GENTLES_modul13
2	0.09	1 / 15	GENTLES_modul4
3	0.09	1 / 15	GENTLES_modul11
4	0.10	1 / 16	GENTLES_modul14
5	0.17	2 / 113	PanCan_Driver_Gene_geneset_nanostring
6	0.23	1 / 40	ZHANG_MM up
7	0.28	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.30	1 / 55	PanCan_JAK−ST_geneset_nanostring
9	0.33	1 / 61	PanCan_Wnt_geneset_nanostring
10	0.42	1 / 82	PanCan_TXmisReg_geneset_nanostring
11	0.49	3 / 401	Lembcke_Colonic Inflammation
12	0.55	1 / 121	PanCan_MAPK_geneset_nanostring
13	0.62	3 / 489	Lembcke_Normal vs Adenoma
14	0.64	1 / 156	PanCan_PI3K_geneset_nanostring
15	0.86	1 / 298	SPANG_BCL6−index2
16	0.92	0 / 14	LIU_PROSTATE_CANCER_DN
17	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
18	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
19	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.00	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.009	2 / 22	histone acetyltransferase complex
2	0.017	2 / 31	brush border membrane
3	0.022	3 / 91	nuclear matrix
4	0.031	2 / 42	intercellular bridge
5	0.032	2 / 43	cytoplasmic microtubule
6	0.038	2 / 47	Cajal body
7	0.044	2 / 51	axoneme
8	0.044	2 / 51	voltage−gated potassium channel complex
9	0.063	1 / 10	cell−cell contact zone
10	0.068	3 / 144	membrane raft
11	0.076	1 / 12	XY body
12	0.082	1 / 13	microvillus membrane
13	0.082	1 / 13	neuronal cell body membrane
14	0.082	1 / 13	phagocytic cup
15	0.082	1 / 13	Sin3 complex
16	0.088	1 / 14	microtubule plus−end
17	0.094	1 / 15	alpha−amino−3−hydroxy−5−methyl−4−isoxazolepropionic acid selective gluta
18	0.094	1 / 15	autophagic vacuole membrane
19	0.094	1 / 15	pre−autophagosomal structure membrane
20	0.102	2 / 83	endomembrane system

Chr

Rank	p−value	#in/all	Geneset
1	0.07	7 / 552	Chr 10
2	0.08	11 / 1037	Chr 19
3	0.08	3 / 151	Chr 21
4	0.19	5 / 465	Chr 15
5	0.24	3 / 262	Chr 13
6	0.38	3 / 335	Chr 22
7	0.43	6 / 801	Chr 11
8	0.47	6 / 838	Chr 3
9	0.47	5 / 689	Chr 7
10	0.47	7 / 993	Chr 2
11	0.49	4 / 551	Chr X
12	0.50	4 / 558	Chr 4
13	0.52	10 / 1500	Chr 1
14	0.73	3 / 576	Chr 9
15	0.77	1 / 221	Chr 18
16	0.81	4 / 840	Chr 17
17	0.82	2 / 469	Chr 8
18	0.84	3 / 696	Chr 5
19	0.89	3 / 775	Chr 12
20	0.93	2 / 649	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.02	6 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	0.04	3 / 117	Marisa_CRC−cluster−b
3	0.08	4 / 250	K9K27me3_Colon
4	0.08	1 / 13	TCGA−CRC_less−agressive−disease−markers
5	0.09	11 / 1079	ZNF_Colon
6	0.10	19 / 2142	ReprPC_Colon
7	0.11	17 / 1889	ReprPCWk_Colon
8	0.12	8 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	0.14	10 / 1038	HetRpts_Colon
10	0.16	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
11	0.19	12 / 1386	Het_Colon
12	0.21	3 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
13	0.22	4 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
14	0.25	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
15	0.25	4 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
16	0.30	20 / 2698	EnhA_Colon
17	0.33	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
18	0.34	4 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
19	0.35	27 / 3812	TssD1_Colon
20	0.35	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.07	1 / 11	BCHETNIA_EBM up
2	0.13	4 / 294	GUDJ_psoriasis down
3	0.32	4 / 435	GUDJ_psoriasis up
4	1.00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.003	2 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
2	0.013	1 / 2	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
3	0.039	1 / 6	neurons_glio
4	0.079	2 / 71	Weller_LGG_A_vs_O_UP
5	0.151	1 / 25	Shaw_down_in_1p19q
6	0.162	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
7	0.275	1 / 49	OL_vs_MOG−_OL
8	0.312	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
9	0.339	3 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	0.348	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
11	0.348	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
12	0.360	1 / 68	GIEZELT_GBM_WT_down_VS_mut
13	0.360	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	0.360	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
15	0.389	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
16	0.482	1 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
17	0.492	1 / 103	GIEZELT_GBM_WT_up_VS_mut
18	0.693	2 / 365	Down_b
19	0.906	1 / 356	Down_a
20	0.997	1 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−04	6 / 138	LEE_LIVER_CANCER_SURVIVAL_UP
2	4e−03	3 / 47	LEE_EARLY_T_LYMPHOCYTE_DN
3	4e−03	2 / 15	GEISS_RESPONSE_TO_DSRNA_DN
4	7e−03	2 / 20	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
5	8e−03	2 / 21	LA_MEN1_TARGETS
6	9e−03	2 / 22	HEIDENBLAD_AMPLICON_12P11_12_DN
7	9e−03	9 / 545	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
8	1e−02	3 / 72	SAFFORD_T_LYMPHOCYTE_ANERGY
9	1e−02	2 / 26	VALK_AML_CLUSTER_4
10	2e−02	2 / 29	ZHENG_IL22_SIGNALING_DN
11	2e−02	2 / 30	LEE_LIVER_CANCER
12	2e−02	2 / 30	PIONTEK_PKD1_TARGETS_UP
13	2e−02	3 / 82	WINZEN_DEGRADED_VIA_KHSRP
14	2e−02	2 / 31	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
15	2e−02	3 / 87	MATZUK_SPERMATOZOA
16	2e−02	1 / 3	CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN
17	2e−02	1 / 3	DIERICK_SEROTONIN_FUNCTION_GENES
18	2e−02	2 / 33	ONO_FOXP3_TARGETS_DN
19	2e−02	6 / 325	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
20	2e−02	9 / 629	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.2	2 / 127	HALLMARK_KRAS_SIGNALING_DN
3	0.2	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
4	0.2	2 / 146	HALLMARK_UV_RESPONSE_UP
5	0.3	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
6	0.5	1 / 91	HALLMARK_BILE_ACID_METABOLISM
7	0.5	1 / 95	HALLMARK_SPERMATOGENESIS
8	0.6	1 / 137	HALLMARK_UV_RESPONSE_DN
9	0.6	1 / 140	HALLMARK_APOPTOSIS
10	0.6	1 / 148	HALLMARK_KRAS_SIGNALING_UP
11	0.7	1 / 167	HALLMARK_APICAL_JUNCTION
12	0.7	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	0.7	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.7	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.7	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
16	0.7	1 / 181	HALLMARK_P53_PATHWAY
17	0.7	1 / 188	HALLMARK_ADIPOGENESIS
18	0.7	1 / 188	HALLMARK_MYC_TARGETS_V1
19	0.7	1 / 195	HALLMARK_MITOTIC_SPINDLE
20	0.7	1 / 197	HALLMARK_E2F_TARGETS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	1 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.19	1 / 32	DUMEAUX_Fasting enriched genes
3	0.33	1 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.08	1 / 13	YAMANE_AICDA_targets_recruited
2	0.23	20 / 2563	HOPP_Heterochrom
3	0.23	3 / 256	SPANG_IL21 DN
4	0.27	3 / 275	TARTE_Mature plasma cell signature
5	0.30	46 / 6564	HOPP_Strong_enhancer
6	0.32	9 / 1128	SPANG_BCR DN
7	0.35	1 / 66	TARTE_Plasma cell signature
8	0.42	1 / 82	ROSOLOWSKI_green UP
9	0.47	37 / 5538	HOPP_Weak_txn
10	0.47	38 / 5693	HOPP_Weak_enhancer
11	0.50	3 / 410	SPANG_CD40 6hrs DN
12	0.51	1 / 109	ROSOLOWSKI_green total
13	0.57	1 / 129	DAVE_BL−vs−DLBCL
14	0.58	14 / 2188	HOPP_Poised_promoter
15	0.65	21 / 3396	HOPP_Repressed
16	0.70	45 / 7209	HOPP_Weak_promoter
17	0.74	47 / 7592	HOPP_Active_promoter
18	0.75	1 / 212	LENZ_Stromal signature 1
19	0.80	1 / 247	ZHANG_DLBCL mutated
20	0.82	6 / 1218	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	0.009	2 / 22	delayed rectifier potassium channel activity
2	0.010	2 / 23	hydrolase activity, acting on ester bonds
3	0.011	2 / 24	cation channel activity
4	0.011	2 / 24	N−acetyltransferase activity
5	0.014	2 / 28	Ran GTPase binding
6	0.023	7 / 433	peptidase activity
7	0.024	3 / 95	heparin binding
8	0.027	8 / 550	protein homodimerization activity
9	0.044	2 / 51	endopeptidase activity
10	0.063	1 / 10	microtubule plus−end binding
11	0.076	1 / 12	activin binding
12	0.076	1 / 12	nitric−oxide synthase binding
13	0.079	2 / 71	PDZ domain binding
14	0.082	1 / 13	glucuronosyltransferase activity
15	0.082	1 / 13	neuropeptide hormone activity
16	0.082	1 / 13	pseudouridine synthase activity
17	0.088	5 / 361	binding
18	0.088	1 / 14	inward rectifier potassium channel activity
19	0.088	1 / 14	transforming growth factor beta−activated receptor activity
20	0.094	1 / 15	fibroblast growth factor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 63	hsa−miR−1285
2	4e−03	3 / 48	hsa−miR−524−3p
3	4e−03	4 / 101	hsa−miR−325
4	7e−03	3 / 61	hsa−miR−612
5	2e−02	4 / 145	hsa−miR−922
6	2e−02	6 / 321	hsa−miR−32
7	3e−02	3 / 98	hsa−miR−590−5p
8	3e−02	5 / 264	hsa−miR−30a
9	3e−02	3 / 103	hsa−miR−1284
10	3e−02	2 / 44	hsa−miR−640
11	3e−02	6 / 370	hsa−miR−144
12	4e−02	2 / 46	hsa−miR−1256
13	4e−02	2 / 49	hsa−miR−1224−3p
14	4e−02	2 / 49	hsa−miR−302b*
15	4e−02	2 / 51	hsa−miR−571
16	5e−02	2 / 53	hsa−miR−337−3p
17	6e−02	2 / 58	hsa−miR−219−1−3p
18	6e−02	2 / 58	hsa−miR−324−3p
19	6e−02	1 / 9	hsa−miR−720
20	6e−02	5 / 327	hsa−miR−367

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	1 / 14	BENTINK_src.2
2	1.00	0 / 12	GUSTAFSON_PI3K_UP
3	1.00	0 / 13	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	BENTINK_e2f3.1
5	1.00	0 / 12	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 9	BENTINK_ras.4
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	20 / 1872	ICGC_Mef2_targets
2	0.04	44 / 5355	ICGC_Pol2_targets
3	0.05	17 / 1701	HEBENSTREIT_high expression TF
4	0.06	20 / 2136	ICGC_GabpPcr2_targets
5	0.06	20 / 2137	ICGC_SrfV0416101_targets
6	0.08	33 / 4032	ICGC_Creb1_targets
7	0.09	41 / 5219	ICGC_Tcf3_targets
8	0.10	21 / 2416	ICGC_Bcl3_targets
9	0.11	45 / 5890	ICGC_Elf1_targets
10	0.13	41 / 5374	ICGC_Pax5_targets
11	0.13	13 / 1418	ICGC_Ets1_targets
12	0.13	7 / 653	ICGC_SrfPcr2_targets
13	0.14	41 / 5408	ICGC_Pou2_targets
14	0.14	36 / 4689	ICGC_Taf1_targets
15	0.16	37 / 4879	ICGC_Pmlsc71910_targets
16	0.17	41 / 5495	ICGC_Yy1_targets
17	0.17	45 / 6114	ICGC_Runx3_targets
18	0.19	30 / 3924	ICGC_Zeb1_targets
19	0.19	23 / 2927	ICGC_Rad21_targets
20	0.20	30 / 3966	ICGC_Pu1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 36	VAQUERIZAS_Fetal brain
2	0.2	1 / 38	VAQUERIZAS_Whole brain
3	0.2	2 / 143	VAQUERIZAS_General
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 26	VAQUERIZAS_Liver
6	1.0	0 / 33	VAQUERIZAS_Prostate
7	1.0	0 / 29	VAQUERIZAS_Smooth muscle
8	1.0	0 / 45	VAQUERIZAS_Uterus
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 37	VAQUERIZAS_Thymus
12	1.0	0 / 40	VAQUERIZAS_Thyroid
13	1.0	0 / 59	VAQUERIZAS_Whole blood
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 29	VAQUERIZAS_Fetal lung
16	1.0	0 / 58	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 23	VAQUERIZAS_Trachea
19	1.0	0 / 11	VAQUERIZAS_Fetal liver
20	1.0	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	2 / 74	WIRTH_Mucosa
2	0.24	1 / 41	WIRTH_Homeostasis
3	0.26	1 / 46	WIRTH_Liver
4	0.51	1 / 107	WIRTH_Testis
5	0.53	1 / 114	PALMER_T−Cell signature up
6	0.67	2 / 350	WIRTH_Immune system
7	0.72	1 / 194	PALMER_B−Cell signature up
8	0.90	1 / 350	WIRTH_Nervous System
9	1.00	0 / 32	WIRTH_Pancreas
10	1.00	0 / 11	WIRTH_Sec. lymphoid organs
11	1.00	0 / 11	WIRTH_Prim. lymphoid organs
12	1.00	0 / 13	WIRTH_B−cells
13	1.00	0 / 8	WIRTH_Tonsil
14	1.00	0 / 12	WIRTH_Thymus
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	11 / 1115	LU_BPDE 1h DN
2	0.4	26 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

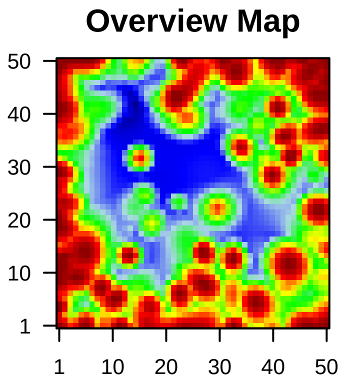
Spot Summary: Q

metagenes = 8
genes = 53

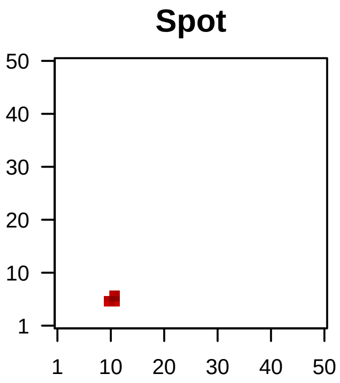
<r> metagenes = 0.96
<r> genes = 0.21
beta: r2= 0.56 / log p= −Inf

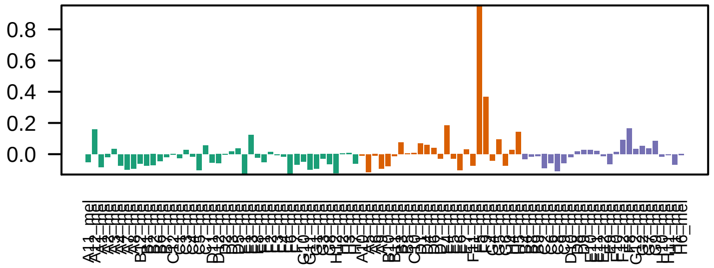
samples with spot = 3 (3.3 %)
MSC2 : 3 (12 %)

Overview Map



Spot





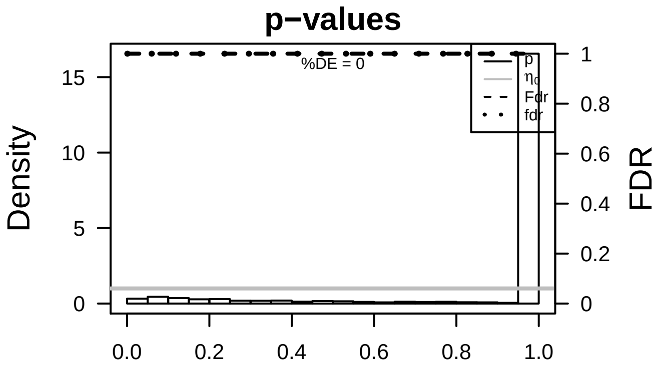
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TRAF2	1.82	−0.16	0.33	TRAF2	TNF receptor−associated factor 2 [Source:HGNC Symbol;Acc
2	TBC1D32	1.81	−0.38	0.29	TBC1D32	TBC1 domain family, member 32 [Source:HGNC Symbol;Acc
3	KDM7A	1.73	−0.05	0.48	KDM7A	lysine (K)−specific demethylase 7A [Source:HGNC Symbol;A
4	HKDC1	1.69	−0.03	0.53	HKDC1	hexokinase domain containing 1 [Source:HGNC Symbol;Acc:
5	NEK1	1.68	−0.72	0.27	NEK1	NIMA−related kinase 1 [Source:HGNC Symbol;Acc:HGNC:77
6	PSG4	1.67	−0.11	0.31	PSG4	pregnancy specific beta−1−glycoprotein 4 [Source:HGNC Sy
7	DNAJA4	1.67	−0.13	0.35	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4 [Source:HGN
8	PYGL	1.64	−0.21	0.31	PYGL	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:H
9	ZNF627	1.6	−0.29	0.46	ZNF627	zinc finger protein 627 [Source:HGNC Symbol;Acc:HGNC:30
10	JRK	1.6	−0.15	0.65	JRK	Jrk homolog (mouse) [Source:HGNC Symbol;Acc:HGNC:619
11	DQX1	1.58	−0.02	0.59	DQX1	DEAQ box RNA−dependent ATPase 1 [Source:HGNC Symbo
12	SYN3	1.52	−0.09	0.42	SYN3	synapsin III [Source:HGNC Symbol;Acc:HGNC:11496]
13	NEURL2	1.52	−0.06	0.32	NEURL2	neuralized E3 ubiquitin protein ligase 2 [Source:HGNC Symb
14	AGO3	1.48	−0.63	0.34	AGO3	argonaute RISC catalytic component 3 [Source:HGNC Symb
15	MBTD1	1.48	−0.29	0.37	MBTD1	mbt domain containing 1 [Source:HGNC Symbol;Acc:HGNC:
16	EPB41L1	1.42	−0.14	0.42	EPB41L1	erythrocyte membrane protein band 4.1−like 1 [Source:HGNC
17	AGO4	1.41	−0.33	0.26	AGO4	argonaute RISC catalytic component 4 [Source:HGNC Symb
18	EEF1E1−BLC	1.38	−0.14	0.3	EEF1E1−BLOC1S5	EEF1E1−BLOC1S5 readthrough (NMD candidate) [Source:H
19	NADK	1.38	−0.31	0.34	NADK	NAD kinase [Source:HGNC Symbol;Acc:HGNC:29831]
20	DHRS3	1.32	−0.03	0.51	DHRS3	dehydrogenase/reductase (SDR family) member 3 [Source:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−04	2 / 10	BP	production of miRNAs involved in gene silencing by miRNA
2	7e−04	2 / 11	BP	myofibril assembly
3	7e−04	2 / 11	CC	RISC complex
4	7e−04	2 / 11	Tissu	WIRTH_Prim. lymphoid organs
5	8e−04	4 / 116	GSEA	YAGI_AML_WITH_T_9_11_TRANSLOCATION
6	8e−04	2 / 12	MF	miRNA binding
7	8e−04	2 / 12	BP	pre−miRNA processing
8	2e−03	2 / 18	BP	mRNA catabolic process
9	2e−03	3 / 71	GSEA	WALLACE_PROSTATE_CANCER_RACE_DN
10	3e−03	2 / 21	GSEA	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_5
11	3e−03	8 / 683	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
12	3e−03	2 / 22	GSEA	REACTOME_MICRORNA_MIRNA_BIOGENESIS
13	4e−03	2 / 25	BP	lens development in camera−type eye
14	4e−03	2 / 25	GSEA	REACTOME_REGULATORY_RNA_PATHWAYS
15	4e−03	3 / 90	GSEA	BROWNE_HCMV_INFECTION_8HR_UP
16	4e−03	2 / 27	GSEA	REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION
17	5e−03	2 / 30	GSEA	NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
18	6e−03	2 / 33	MF	single−stranded RNA binding
19	7e−03	5 / 338	GSEA	BASAKI_YBX1_TARGETS_DN
20	7e−03	3 / 111	Aging	HORVATH_aging_genes meth UP
21	8e−03	4 / 219	GSEA	DOANE_RESPONSE_TO_ANDROGEN_DN
22	8e−03	2 / 37	miRN	hsa−miR−501−3p
23	8e−03	2 / 37	miRN	hsa−miR−1274a
24	9e−03	2 / 39	miRN	hsa−miR−502−3p
25	9e−03	26 / 4829	TF	ICGC_Nficsc81335_targets
26	9e−03	2 / 41	GSEA	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING
27	9e−03	8 / 842	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
28	1e−02	2 / 42	BP	camera−type eye development
29	1e−02	5 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
30	1e−02	3 / 129	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_U
31	1e−02	2 / 45	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
32	1e−02	2 / 46	BP	response to ionizing radiation
33	1e−02	3 / 133	GSEA	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES
34	1e−02	13 / 1872	TF	ICGC_Mef2_targets
35	1e−02	21 / 3700	TF	ICGC_Nfatc1_targets
36	1e−02	2 / 49	GSEA	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_DN
37	1e−02	10 / 1273	TF	ICGC_P300_targets
38	1e−02	2 / 50	GSEA	HENDRICKS_SMARCA4_TARGETS_UP
39	1e−02	2 / 51	GSEA	ZWANG_EGF_PERSISTENTLY_DN
40	1e−02	2 / 52	MF	double−stranded RNA binding

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.007	3 / 111	HORVATH_aging_genes meth UP
2	1.000	0 / 100	HORVATH_aging_genes meth DOWN
3	1.000	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	6e−04	2 / 10	production of miRNAs involved in gene silencing by miRNA
2	7e−04	2 / 11	myofibril assembly
3	8e−04	2 / 12	pre−miRNA processing
4	2e−03	2 / 18	mRNA catabolic process
5	4e−03	2 / 25	lens development in camera−type eye
6	1e−02	2 / 42	camera−type eye development
7	1e−02	2 / 46	response to ionizing radiation
8	2e−02	2 / 55	regulation of signal transduction
9	3e−02	5 / 491	innate immune response
10	3e−02	2 / 77	male gonad development
11	3e−02	9 / 1255	cellular component assembly
12	3e−02	2 / 81	ephrin receptor signaling pathway
13	4e−02	1 / 10	acrosome assembly
14	4e−02	1 / 10	cellular glucose homeostasis
15	4e−02	1 / 10	cellular response to nitric oxide
16	4e−02	1 / 10	hematopoietic stem cell differentiation
17	4e−02	1 / 10	morphogenesis of an epithelial sheet
18	4e−02	1 / 10	necroptotic process
19	4e−02	1 / 10	regulation of ossification
20	4e−02	1 / 11	positive regulation of interleukin−2 production

Brain

Rank	p−value	#in/all	Geneset
1	0.1	9 / 1548	Mid_Frontal_Lobe_K9K27me3
2	0.1	37 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	0.1	26 / 5940	Overlap_fetal_midbrain_HetRpts
4	0.1	5 / 786	Fetal_EnhG
5	0.2	4 / 656	Overlap_fetal_midbrain_EnhP
6	0.2	1 / 69	Overlap_fetal_midbrain_Tx
7	0.2	3 / 468	Mid_Frontal_Lobe_TssF
8	0.3	13 / 2972	Mid_Frontal_Lobe_ReprPC
9	0.3	5 / 953	Fetal_Enh
10	0.3	6 / 1207	Overlap_fetal_midbrain_TssF
11	0.3	5 / 989	Mid_Frontal_Lobe_Quies
12	0.3	5 / 1013	Fetal_TssP
13	0.3	3 / 564	Mid_Frontal_Lobe_EnhP
14	0.4	4 / 862	Overlap_fetal_midbrain_TxTrans
15	0.4	9 / 2185	Fetal_TssA
16	0.4	1 / 156	Mid_Frontal_Lobe_TssA
17	0.4	1 / 158	Overlap_fetal_midbrain_Het
18	0.4	1 / 163	Fetal_ReprPC
19	0.4	1 / 166	Mid_Frontal_Lobe_Tx
20	0.5	3 / 765	Mid_Frontal_Lobe_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	1 / 11	GENTLES_modul17
2	0.22	1 / 70	SHAUGHNESSY_MM high risk
3	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
4	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
5	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	1.00	0 / 12	LIU_BREAST_CANCER
8	1.00	0 / 14	LIU_COMMON_CANCER_GENES
9	1.00	0 / 14	LIU_LIVER_CANCER
10	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
11	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
12	1.00	0 / 15	WANG_ER_UP
13	1.00	0 / 5	WANG_ER_DN
14	1.00	0 / 16	WOLFER_overlap genes
15	1.00	0 / 12	BEN−PORATH_DN
16	1.00	0 / 13	BEN−PORATH_UP
17	1.00	0 / 15	GENTLES_modul1
18	1.00	0 / 16	GENTLES_modul2
19	1.00	0 / 10	GENTLES_modul3
20	1.00	0 / 15	GENTLES_modul4

CC

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 11	RISC complex
2	2e−02	2 / 61	cytoplasmic mRNA processing body
3	4e−02	1 / 10	low−density lipoprotein particle
4	4e−02	1 / 10	very−low−density lipoprotein particle
5	4e−02	1 / 11	Arp2/3 protein complex
6	4e−02	1 / 11	CD40 receptor complex
7	4e−02	1 / 11	photoreceptor outer segment membrane
8	5e−02	2 / 99	cell cortex
9	5e−02	1 / 14	exosome (RNase complex)
10	5e−02	1 / 15	mitochondrial envelope
11	5e−02	1 / 15	pericentriolar material
12	7e−02	1 / 21	vesicle membrane
13	8e−02	1 / 22	cortical cytoskeleton
14	1e−01	1 / 28	myofibril
15	1e−01	13 / 2507	cytosol
16	1e−01	1 / 30	COP9 signalosome
17	1e−01	1 / 30	sarcomere
18	1e−01	2 / 159	extracellular matrix
19	1e−01	1 / 35	integral component of Golgi membrane
20	1e−01	1 / 38	cytoplasmic side of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.05	4 / 398	Chr 20
2	0.15	4 / 576	Chr 9
3	0.18	5 / 840	Chr 17
4	0.23	4 / 687	Chr 6
5	0.32	3 / 552	Chr 10
6	0.32	3 / 558	Chr 4
7	0.34	2 / 335	Chr 22
8	0.42	1 / 151	Chr 21
9	0.45	3 / 689	Chr 7
10	0.45	6 / 1500	Chr 1
11	0.50	2 / 465	Chr 15
12	0.61	1 / 262	Chr 13
13	0.68	2 / 649	Chr 16
14	0.70	3 / 993	Chr 2
15	0.73	3 / 1037	Chr 19
16	0.81	1 / 462	Chr 14
17	0.82	1 / 469	Chr 8
18	0.92	1 / 696	Chr 5
19	0.95	1 / 801	Chr 11
20	0.95	1 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.05	2 / 102	Marisa_CRC−cluster−d
2	0.05	4 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
3	0.10	1 / 29	Marisa_CRC−cluster−c
4	0.15	30 / 7203	TssF_Colon
5	0.15	13 / 2698	EnhA_Colon
6	0.21	1 / 66	Marisa_CRC−cluster−h
7	0.23	2 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	0.34	1 / 117	Marisa_CRC−cluster−b
9	0.35	3 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
10	0.36	8 / 1889	ReprPCWk_Colon
11	0.38	2 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
12	0.41	2 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	0.43	4 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	0.43	13 / 3383	EnhWk2_Colon
15	0.45	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
16	0.45	31 / 8415	Quies3_Colon
17	0.46	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
18	0.50	3 / 739	TxEnhG2_Colon
19	0.50	3 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
20	0.50	8 / 2142	ReprPC_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.5	2 / 435	GUDJ_psoriasis up
2	0.7	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	1 / 9	Phillips PN up vs MES & Prolif
2	0.05	2 / 103	GIEZELT_GBM_WT_up_VS_mut
3	0.11	1 / 32	Colman_survival_associated
4	0.14	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
5	0.16	1 / 49	OL vs. MOG−OL
6	0.16	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
7	0.22	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	0.22	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.22	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP
10	0.27	1 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
11	0.68	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
12	0.72	1 / 356	Down_a
13	1.00	0 / 15	VERHAAK_CL subtype
14	1.00	0 / 15	VERHAAK_MES subtype
15	1.00	0 / 16	VERHAAK_NL subtype
16	1.00	0 / 14	VERHAAK_PN subtype
17	1.00	0 / 23	WIRTH_PN subtype
18	1.00	0 / 74	WIRTH_Normal Brain
19	1.00	0 / 9	VERHAAK_Brain
20	1.00	0 / 8	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 116	YAGI_AML_WITH_T_9_11_TRANSLOCATION
2	2e−03	3 / 71	WALLACE_PROSTATE_CANCER_RACE_DN
3	3e−03	2 / 21	MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_5
4	3e−03	8 / 683	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
5	3e−03	2 / 22	REACTOME_MICRORNA_MIRNA_BIOGENESIS
6	4e−03	2 / 25	REACTOME_REGULATORY_RNA_PATHWAYS
7	4e−03	3 / 90	BROWNE_HCMV_INFECTION_8HR_UP
8	4e−03	2 / 27	REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION
9	5e−03	2 / 30	NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
10	7e−03	5 / 338	BASAKI_YBX1_TARGETS_DN
11	8e−03	4 / 219	DOANE_RESPONSE_TO_ANDROGEN_DN
12	9e−03	2 / 41	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING
13	9e−03	8 / 842	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
14	1e−02	5 / 376	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
15	1e−02	3 / 129	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP
16	1e−02	2 / 45	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
17	1e−02	3 / 133	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES
18	1e−02	2 / 49	MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_DN
19	1e−02	2 / 50	HENDRICKS_SMARCA4_TARGETS_UP
20	1e−02	2 / 51	ZWANG_EGF_PERSISTENTLY_DN

HM

Rank	p−value	#in/all	Geneset
1	0.03	3 / 183	HALLMARK_GLYCOLYSIS
2	0.05	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.09	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
4	0.28	1 / 93	HALLMARK_PEROXISOME
5	0.32	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	0.36	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
7	0.40	1 / 140	HALLMARK_APOPTOSIS
8	0.41	1 / 146	HALLMARK_DNA_REPAIR
9	0.41	1 / 148	HALLMARK_KRAS_SIGNALING_UP
10	0.45	1 / 165	HALLMARK_MYOGENESIS
11	0.45	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.46	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	0.46	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
14	0.47	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.47	1 / 174	HALLMARK_HEME_METABOLISM
16	0.49	1 / 188	HALLMARK_MYC_TARGETS_V1
17	0.51	1 / 196	HALLMARK_MTORC1_SIGNALING
18	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	1.00	0 / 176	HALLMARK_HYPOXIA
20	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	1 / 18	DUMEAUX_High bmi enriched genes
2	0.20	1 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.05	1 / 15	DAVE_Immune response 2
2	0.22	23 / 5538	HOPP_Weak_txn
3	0.27	23 / 5693	HOPP_Weak_enhancer
4	0.42	27 / 7209	HOPP_Weak_promoter
5	0.59	1 / 247	ZHANG_DLBCL mutated
6	0.60	1 / 256	SPANG_IL21 DN
7	0.61	18 / 5184	HOPP_Txn_transition
8	0.64	4 / 1218	SPANG_BCR UP
9	0.69	7 / 2211	HOPP_Repetitive
10	0.72	8 / 2563	HOPP_Heterochrom
11	0.73	23 / 6929	HOPP_Txn_elongation
12	0.76	25 / 7592	HOPP_Active_promoter
13	0.77	1 / 410	SPANG_CD40 6hrs DN
14	0.78	3 / 1128	SPANG_BCR DN
15	0.79	21 / 6564	HOPP_Strong_enhancer
16	0.81	6 / 2188	HOPP_Poised_promoter
17	0.94	8 / 3396	HOPP_Repressed
18	1.00	0 / 13	BENTINK_mBL UP
19	1.00	0 / 12	BENTINK_mBL DOWN
20	1.00	0 / 129	DAVE_BL−vs−DLBCL

MF

Rank	p−value	#in/all	Geneset
1	8e−04	2 / 12	miRNA binding
2	6e−03	2 / 33	single−stranded RNA binding
3	1e−02	2 / 52	double−stranded RNA binding
4	4e−02	1 / 10	tropomyosin binding
5	4e−02	1 / 11	retinol dehydrogenase activity
6	4e−02	9 / 1309	ATP binding
7	5e−02	1 / 13	thioesterase binding
8	5e−02	2 / 102	actin filament binding
9	5e−02	1 / 15	histone demethylase activity (H4−K20 specific)
10	6e−02	1 / 16	metallocarboxypeptidase activity
11	6e−02	1 / 16	NAD+ kinase activity
12	6e−02	1 / 17	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
13	6e−02	1 / 18	galactosyltransferase activity
14	6e−02	1 / 18	mitogen−activated protein kinase kinase kinase binding
15	7e−02	1 / 19	GTPase regulator activity
16	7e−02	1 / 19	MAP kinase kinase activity
17	7e−02	1 / 21	polyubiquitin binding
18	7e−02	7 / 1033	nucleic acid binding
19	8e−02	1 / 23	ephrin receptor binding
20	8e−02	1 / 23	tumor necrosis factor receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	2 / 37	hsa−miR−501−3p
2	0.008	2 / 37	hsa−miR−1274a
3	0.009	2 / 39	hsa−miR−502−3p
4	0.027	3 / 182	hsa−miR−374a
5	0.032	1 / 9	hsa−miR−720
6	0.036	2 / 84	hsa−miR−339−5p
7	0.041	3 / 214	hsa−miR−182
8	0.050	2 / 101	hsa−miR−516b
9	0.053	2 / 104	hsa−miR−605
10	0.066	1 / 19	hsa−miR−542−5p
11	0.069	2 / 121	hsa−miR−212
12	0.088	2 / 139	hsa−miR−132
13	0.095	2 / 145	hsa−miR−922
14	0.096	4 / 488	hsa−miR−103
15	0.096	4 / 488	hsa−miR−107
16	0.097	3 / 307	hsa−miR−302b
17	0.105	3 / 318	hsa−miR−302a
18	0.111	1 / 33	hsa−miR−1274b
19	0.114	2 / 162	hsa−miR−96
20	0.115	2 / 163	hsa−miR−137

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.009	26 / 4829	ICGC_Nficsc81335_targets
2	0.013	13 / 1872	ICGC_Mef2_targets
3	0.013	21 / 3700	ICGC_Nfatc1_targets
4	0.013	10 / 1273	ICGC_P300_targets
5	0.022	23 / 4385	ICGC_Atf2_targets
6	0.024	16 / 2714	ICGC_Irf4_targets
7	0.028	21 / 3966	ICGC_Pu1_targets
8	0.035	13 / 2137	ICGC_SrfV0416101_targets
9	0.035	16 / 2836	ICGC_BatfPcr1_targets
10	0.045	16 / 2927	ICGC_Rad21_targets
11	0.048	12 / 2013	ICGC_Bcl11_targets
12	0.056	23 / 4774	ICGC_Foxm1_targets
13	0.065	11 / 1878	ICGC_Cebpbsc150_targets
14	0.079	24 / 5200	ICGC_Mta3_targets
15	0.079	21 / 4414	ICGC_Bclaf101388_targets
16	0.079	13 / 2416	ICGC_Bcl3_targets
17	0.082	22 / 4689	ICGC_Taf1_targets
18	0.082	24 / 5219	ICGC_Tcf3_targets
19	0.083	25 / 5495	ICGC_Yy1_targets
20	0.096	27 / 6114	ICGC_Runx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 11	WIRTH_Prim. lymphoid organs
2	4e−02	4 / 350	WIRTH_Immune system
3	1e−01	1 / 32	WIRTH_Pancreas
4	1e−01	1 / 32	WIRTH_Placenta
5	2e−01	2 / 225	PALMER_Granulocytes signature up
6	3e−01	1 / 114	PALMER_T−Cell signature up
7	7e−01	1 / 350	WIRTH_Nervous System
8	1e+00	0 / 11	WIRTH_Sec. lymphoid organs
9	1e+00	0 / 13	WIRTH_B−cells
10	1e+00	0 / 8	WIRTH_Tonsil
11	1e+00	0 / 12	WIRTH_Thymus
12	1e+00	0 / 12	WIRTH_Lymphocytes
13	1e+00	0 / 5	WIRTH_Bone marrow
14	1e+00	0 / 11	WIRTH_Globus pallidus
15	1e+00	0 / 14	WIRTH_Telencephalon
16	1e+00	0 / 11	WIRTH_Cortex cerebri
17	1e+00	0 / 10	WIRTH_Hippocampus
18	1e+00	0 / 10	WIRTH_Thalamus
19	1e+00	0 / 12	WIRTH_Cerebellum
20	1e+00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	4 / 1115	LU_BPDE 1h DN
2	0.9	10 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: R

metagenes = 5
genes = 183

<r> metagenes = 0.98
<r> genes = 0.21
beta: r2= 1.22 / log p= −Inf

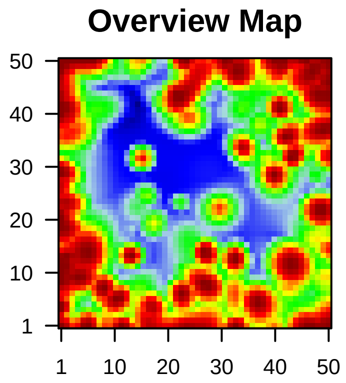
samples with spot = 1 (1.1 %)
MSC2 : 1 (4 %)

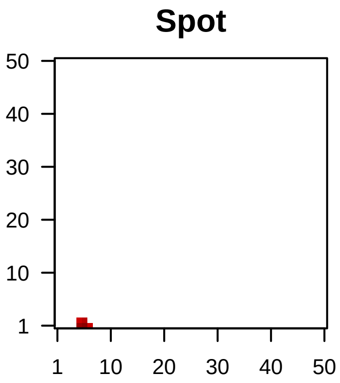
Spot Genelist

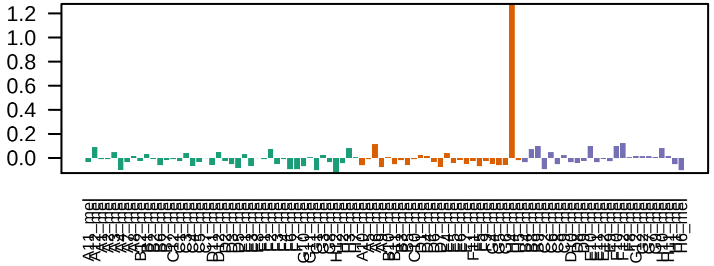
Rank	ID	max e	min e	r	Symbol	Description
1	NINL	2.26	−0.04	0.79	NINL	ninein−like [Source:HGNC Symbol;Acc:HGNC:29163]
2	PAN2	2.19	−0.24	0.32	PAN2	PAN2 poly(A) specific ribonuclease subunit [Source:HGNC Sy
3	C14orf93	2.1	−0.34	0.43	C14orf93	chromosome 14 open reading frame 93 [Source:HGNC Symb
4	NPL	2.03	−0.15	0.37	NPL	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
5	COL4A5	2.01	−0.07	0.46	COL4A5	collagen, type IV, alpha 5 [Source:HGNC Symbol;Acc:HGNC:
6	FAM154B	1.99	−0.18	0.3		
7	TMEM164	1.95	−0.23	0.42	TMEM164	transmembrane protein 164 [Source:HGNC Symbol;Acc:HGN
8	CFP	1.94	−0.03	0.87	CFP	complement factor properdin [Source:HGNC Symbol;Acc:HG
9	RANBP3L	1.9	−0.03	0.86	RANBP3L	RAN binding protein 3−like [Source:HGNC Symbol;Acc:HGN
10	WWC1	1.86	−0.12	0.48	WWC1	WW and C2 domain containing 1 [Source:HGNC Symbol;Acc
11	FCN3	1.84	−0.08	0.55	FCN3	ficolin (collagen/fibrinogen domain containing) 3 [Source:HGN
12	TMEM17	1.83	−0.3	0.22	TMEM17	transmembrane protein 17 [Source:HGNC Symbol;Acc:HGN
13	ACTN2	1.81	−0.15	0.58	ACTN2	actinin, alpha 2 [Source:HGNC Symbol;Acc:HGNC:164]
14	TSSK4	1.81	−0.08	0.4	TSSK4	testis−specific serine kinase 4 [Source:HGNC Symbol;Acc:H
15	DOPEY2	1.81	−0.21	0.36	DOPEY2	dopey family member 2 [Source:HGNC Symbol;Acc:HGNC:1
16	GRIP1	1.8	−0.22	0.34	GRIP1	glutamate receptor interacting protein 1 [Source:HGNC Symb
17	TMPRSS5	1.78	−0.09	0.35	TMPRSS5	transmembrane protease, serine 5 [Source:HGNC Symbol;Ac
18	ARNTL	1.77	−0.29	0.24	ARNTL	aryl hydrocarbon receptor nuclear translocator−like [Source:H
19	STX4	1.76	−0.3	0.32	STX4	syntaxin 4 [Source:HGNC Symbol;Acc:HGNC:11439]
20	SEMA3B	1.76	−0.11	0.47	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic doma

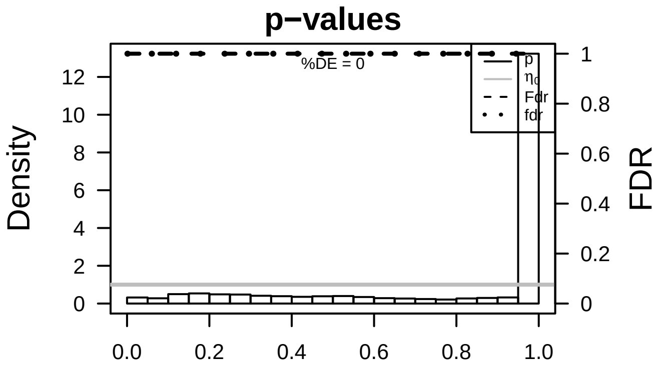
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−04	3 / 16	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
2	1e−03	25 / 1079	Colon	ZNF_Colon
3	1e−03	4 / 40	MF	extracellular matrix structural constituent
4	2e−03	12 / 370	BP	intracellular signal transduction
5	2e−03	3 / 22	BP	positive regulation of transforming growth factor beta receptor signaling pat
6	2e−03	4 / 47	Glio	Weller_LGG_gradeII−vs−III_UP
7	3e−03	3 / 23	GSEA	BIOCARTA_PGC1A_PATHWAY
8	3e−03	4 / 49	GSEA	LEE_LIVER_CANCER_MYC_E2F1_UP
9	3e−03	2 / 7	GSEA	SCHUHMACHER_MYC_TARGETS_DN
10	4e−03	5 / 87	Glio	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
11	5e−03	2 / 9	GSEA	BIOCARTA_ACE2_PATHWAY
12	6e−03	3 / 30	GSEA	REACTOME_NCAM1_INTERACTIONS
13	6e−03	2 / 10	BP	negative regulation of calcium ion transport
14	6e−03	2 / 10	GSEA	BIOCARTA_PLATELETAPP_PATHWAY
15	6e−03	2 / 10	GSEA	BIOCARTA_VITCB_PATHWAY
16	6e−03	16 / 656	Brain	Overlap_fetal_midbrain_EnhP
17	6e−03	11 / 378	MF	structural molecule activity
18	7e−03	2 / 11	BP	negative regulation of transcription regulatory region DNA binding
19	7e−03	2 / 11	MF	telomeric DNA binding
20	7e−03	2 / 11	BP	tRNA modification
21	8e−03	7 / 188	GSEA	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN
22	8e−03	4 / 66	GSEA	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS
23	9e−03	4 / 67	GSEA	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
24	9e−03	2 / 12	MF	RNA polymerase II core promoter proximal region sequence−specific DNA
25	9e−03	2 / 12	MF	RNA polymerase II transcription factor binding transcription factor activity
26	9e−03	2 / 12	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENT
27	9e−03	27 / 1386	Colon	Het_Colon
28	1e−02	7 / 195	GSEA	SHEN_SMARCA2_TARGETS_DN
29	1e−02	3 / 37	GSEA	TSENG_ADIPOGENIC_POTENTIAL_DN
30	1e−02	4 / 70	GSEA	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_DN
31	1e−02	2 / 13	BP	epithelial cell morphogenesis
32	1e−02	2 / 13	GSEA	BIOCARTA_AMI_PATHWAY
33	1e−02	2 / 13	GSEA	GHO_ATF5_TARGETS_UP
34	1e−02	3 / 38	MF	protein complex scaffold
35	1e−02	3 / 38	GSEA	LUI_THYROID_CANCER_CLUSTER_2
36	1e−02	42 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
37	1e−02	2 / 14	GSEA	BIOCARTA_INTRINSIC_PATHWAY
38	1e−02	2 / 15	BP	complement activation
39	1e−02	2 / 15	BP	nucleotide phosphorylation
40	1e−02	2 / 15	BP	osteoblast development









Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 100	HORVATH_aging_genes meth DOWN
2	0.4	1 / 38	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	12 / 370	intracellular signal transduction
2	0.002	37 / 22	positive regulation of transforming growth factor beta receptor signaling pathw
3	0.006	2 / 10	negative regulation of calcium ion transport
4	0.007	2 / 11	negative regulation of transcription regulatory region DNA binding
5	0.007	2 / 11	tRNA modification
6	0.010	2 / 13	epithelial cell morphogenesis
7	0.014	2 / 15	complement activation
8	0.014	2 / 15	nucleotide phosphorylation
9	0.014	2 / 15	osteoblast development
10	0.016	4 / 80	anterior/posterior pattern specification
11	0.018	2 / 17	neuron fate commitment
12	0.018	2 / 17	regulation of complement activation
13	0.018	3 / 46	embryonic digit morphogenesis
14	0.018	10 / 382	positive regulation of GTPase activity
15	0.020	2 / 18	cellular amino acid biosynthetic process
16	0.020	2 / 18	mRNA catabolic process
17	0.021	28 / 1556	cell differentiation
18	0.022	2 / 19	negative regulation of extrinsic apoptotic signaling pathway via death domain
19	0.024	37 / 2210	anatomical structure development
20	0.024	2 / 20	telencephalon development

Brain

Rank	p−value	#in/all	Geneset
1	0.006	16 / 656	Overlap_fetal_midbrain_EnhP
2	0.012	42 / 2462	Mid_Frontal_Lobe_HetRpts
3	0.018	48 / 2972	Mid_Frontal_Lobe_ReprPC
4	0.030	12 / 534	Mid_Frontal_Lobe_EnhG
5	0.058	19 / 1065	Overlap_fetal_midbrain_Enh
6	0.118	15 / 884	Overlap_fetal_midbrain_EnhG
7	0.141	29 / 1949	Fetal_TssF
8	0.187	13 / 812	Mid_Frontal_Lobe_TssP
9	0.196	31 / 2185	Fetal_TssA
10	0.224	12 / 769	Overlap_fetal_midbrain_ZNF
11	0.260	114 / 9013	Overlap_fetal_midbrain_K9K27me3
12	0.263	19 / 1333	Fetal_ReprPCWk
13	0.269	120 / 9528	Overlap_fetal_midbrain_Quies
14	0.290	26 / 1907	Fetal_TxTrans
15	0.292	10 / 668	Mid_Frontal_Lobe_Enh
16	0.327	3 / 166	Mid_Frontal_Lobe_Tx
17	0.340	7 / 468	Mid_Frontal_Lobe_TssF
18	0.417	5 / 349	Fetal_ZNF
19	0.427	11 / 831	Fetal_HetRpts
20	0.450	10 / 765	Mid_Frontal_Lobe_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.07	7 / 298	SPANG_BCL6−index2
3	0.16	1 / 14	LIU_LIVER_CANCER
4	0.18	1 / 16	GENTLES_modul2
5	0.18	1 / 16	GENTLES_modul7
6	0.21	7 / 401	Lembcke_Colonic Inflammation
7	0.37	3 / 180	SPANG_LPS−index2
8	0.38	7 / 489	Lembcke_Normal vs Adenoma
9	0.39	1 / 40	ZHANG_MM up
10	0.40	2 / 113	PanCan_Driver_Gene_geneset_nanostring
11	0.42	1 / 44	PanCan_TGF−B_geneset_nanostring
12	0.43	2 / 120	PanCan_CC+Apop_geneset_nanostring
13	0.53	1 / 61	PanCan_Wnt_geneset_nanostring
14	0.57	2 / 156	PanCan_PI3K_geneset_nanostring
15	0.58	1 / 70	SHAUGHNESSY_MM high risk
16	0.63	0 / 12	LIU_PROSTATE_CANCER_UP
17	0.63	1 / 82	PanCan_TXmisReg_geneset_nanostring
18	0.74	1 / 111	PanCan_RAS_geneset_nanostring
19	0.77	1 / 121	PanCan_MAPK_geneset_nanostring
20	0.84	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	0.01	2 / 15	RNA polymerase II transcription factor complex
2	0.02	2 / 17	basal lamina
3	0.02	5 / 127	cytoplasmic vesicle
4	0.02	3 / 48	clathrin−coated vesicle
5	0.02	3 / 51	collagen trimer
6	0.03	2 / 24	cortical actin cytoskeleton
7	0.05	3 / 70	primary cilium
8	0.06	3 / 73	basement membrane
9	0.07	14 / 745	cytoplasmic membrane−bounded vesicle
10	0.07	2 / 36	microvillus
11	0.07	2 / 36	nuclear body
12	0.07	2 / 37	chromosome, telomeric region
13	0.09	2 / 41	ciliary tip
14	0.09	19 / 1132	Golgi apparatus
15	0.11	1 / 10	nuclear exosome (RNase complex)
16	0.11	1 / 10	pronucleus
17	0.13	1 / 11	CD40 receptor complex
18	0.13	1 / 11	filopodium tip
19	0.13	2 / 51	axoneme
20	0.13	2 / 51	filopodium

Chr

Rank	p−value	#in/all	Geneset
1	0.01	21 / 1037	Chr 19
2	0.05	12 / 576	Chr 9
3	0.07	11 / 551	Chr X
4	0.11	14 / 801	Chr 11
5	0.17	11 / 649	Chr 16
6	0.34	11 / 775	Chr 12
7	0.49	6 / 462	Chr 14
8	0.55	2 / 151	Chr 21
9	0.57	10 / 840	Chr 17
10	0.58	4 / 335	Chr 22
11	0.60	8 / 689	Chr 7
12	0.61	8 / 696	Chr 5
13	0.62	3 / 262	Chr 13
14	0.65	17 / 1500	Chr 1
15	0.67	5 / 465	Chr 15
16	0.82	4 / 469	Chr 8
17	0.86	9 / 993	Chr 2
18	0.89	7 / 838	Chr 3
19	0.91	4 / 552	Chr 10
20	0.92	5 / 687	Chr 6

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	25 / 1079	ZNF_Colon
2	0.009	27 / 1386	Het_Colon
3	0.047	19 / 1038	HetRpts_Colon
4	0.048	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
5	0.053	43 / 2798	TxEnhG1_Colon
6	0.082	1 / 7	Kaneda_CIMP−group2
7	0.096	2 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
8	0.110	96 / 7203	TssF_Colon
9	0.115	1 / 10	KIM_MSI−in−CRC
10	0.136	70 / 5155	EnhWk1_Colon
11	0.161	8 / 436	K9acLow_Colon
12	0.167	1 / 15	Juehling_HNPCC−mutated−in−4
13	0.177	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
14	0.177	1 / 16	Vilar_non−hypermutated−in−CRC
15	0.177	1 / 16	Juehling−MSI−enriched−in−6
16	0.184	8 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
17	0.187	1 / 17	Vilar_mutated−in−CRC−CamP
18	0.187	1 / 17	Vilar_hypermutated−in−CRC
19	0.197	1 / 18	Ang_CRC−CIMPH−vs−L_hypo
20	0.197	1 / 18	Boland_CRC−MSI−A6−A10

Disease

Rank	p−value	#in/all	Geneset
1	0.9	2 / 294	GUDJ_psoriasis down
2	0.9	3 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	4 / 47	Weller_LGG_gradeII−vs−III_UP
2	0.004	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.021	3 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
4	0.077	2 / 38	OL vs. OPC
5	0.093	1 / 8	VERHAAK_PN_Brain
6	0.119	2 / 49	OL vs. MOG− OL
7	0.126	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
8	0.147	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
9	0.197	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
10	0.208	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
11	0.226	2 / 74	WIRTH_Normal Brain
12	0.231	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
13	0.231	2 / 75	Weller_LGG_A_vs_O_DOWN
14	0.236	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
15	0.371	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
16	0.387	1 / 40	in vivo astrocytes vs. cultured astroglia
17	0.470	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
18	0.502	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
19	0.570	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
20	0.580	1 / 71	Weller_LGG_gradeII−vs−III_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 16	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
2	3e−03	3 / 23	BIOCARTA_PGC1A_PATHWAY
3	3e−03	4 / 49	LEE_LIVER_CANCER_MYC_E2F1_UP
4	3e−03	2 / 7	SCHUHMACHER_MYC_TARGETS_DN
5	5e−03	2 / 9	BIOCARTA_ACE2_PATHWAY
6	6e−03	3 / 30	REACTOME_NCAM1_INTERACTIONS
7	6e−03	2 / 10	BIOCARTA_PLATELETAPP_PATHWAY
8	6e−03	2 / 10	BIOCARTA_VITCB_PATHWAY
9	8e−03	7 / 188	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN
10	8e−03	4 / 66	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS
11	9e−03	4 / 67	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
12	9e−03	2 / 12	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_
13	1e−02	7 / 195	SHEN_SMARCA2_TARGETS_DN
14	1e−02	3 / 37	TSENG_ADIPOGENIC_POTENTIAL_DN
15	1e−02	4 / 70	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_DN
16	1e−02	2 / 13	BIOCARTA_AMI_PATHWAY
17	1e−02	2 / 13	GHO_ATF5_TARGETS_UP
18	1e−02	3 / 38	LUI_THYROID_CANCER_CLUSTER_2
19	1e−02	2 / 14	BIOCARTA_INTRINSIC_PATHWAY
20	1e−02	2 / 15	PID_CIRCADIAN_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 167	HALLMARK_APICAL_JUNCTION
2	0.2	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
3	0.3	3 / 148	HALLMARK_KRAS_SIGNALING_UP
4	0.3	3 / 162	HALLMARK_COMPLEMENT
5	0.3	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
6	0.4	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	0.4	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.4	1 / 37	HALLMARK_APICAL_SURFACE
9	0.5	1 / 53	HALLMARK_TGF_BETA_SIGNALING
10	0.5	2 / 137	HALLMARK_UV_RESPONSE_DN
11	0.5	2 / 146	HALLMARK_UV_RESPONSE_UP
12	0.6	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	0.6	2 / 165	HALLMARK_MYOGENESIS
14	0.6	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	0.6	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
16	0.7	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
17	0.7	1 / 91	HALLMARK_BILE_ACID_METABOLISM
18	0.7	1 / 95	HALLMARK_SPERMATOGENESIS
19	0.7	2 / 196	HALLMARK_MTORC1_SIGNALING
20	0.7	2 / 197	HALLMARK_E2F_TARGETS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	3 / 62	DUMEAUX_Smoking enriched genes
2	1.00	0 / 10	DUMEAUX_Smoking literature genes up
3	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.06	2 / 33	LEE_Developmental_regulators
2	0.10	49 / 3396	HOPP_Repressed
3	0.11	1 / 10	DAVE_BL_DN
4	0.12	33 / 2211	HOPP_Repetitive
5	0.15	1 / 13	YAMANE_AICDA_targets_recruited
6	0.18	1 / 16	DAVE_BL_Inter
7	0.20	31 / 2188	HOPP_Poised_promoter
8	0.25	5 / 280	SPANG_CD40 6hrs UP
9	0.29	2 / 89	ROSOLOWSKI_blue total
10	0.34	1 / 34	Subero_B−ALL_hyper_meth
11	0.38	6 / 410	SPANG_CD40 6hrs DN
12	0.40	1 / 42	CARO_OxPhos_in_DLBCL_UP
13	0.46	1 / 50	SPANG_BAFF 9hrs DN
14	0.53	1 / 61	SPANG_LPS 6hrs DN
15	0.58	3 / 247	ZHANG_DLBCL mutated
16	0.62	1 / 80	Aukema_BCL2 DN_BCL6 UP
17	0.69	29 / 2563	HOPP_Heterochrom
18	0.79	1 / 129	DAVE_BL−vs−DLBCL
19	0.81	12 / 1218	SPANG_BCR UP
20	0.85	2 / 275	TARTE_Mature plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 40	extracellular matrix structural constituent
2	0.006	11 / 378	structural molecule activity
3	0.007	2 / 11	telomeric DNA binding
4	0.009	2 / 12	RNA polymerase II core promoter proximal region sequence−specific DNA bir
5	0.009	2 / 12	RNA polymerase II transcription factor binding transcription factor activity
6	0.011	3 / 38	protein complex scaffold
7	0.022	2 / 19	3'−5'−exoribonuclease activity
8	0.026	20 / 1033	nucleic acid binding
9	0.026	2 / 21	exonuclease activity
10	0.026	2 / 21	R−SMAD binding
11	0.029	2 / 22	RNA polymerase II transcription coactivator activity
12	0.031	2 / 23	virus receptor activity
13	0.034	2 / 24	protein−cysteine S−palmitoyltransferase activity
14	0.037	2 / 25	phosphatidylinositol−3−phosphate binding
15	0.042	2 / 27	frizzled binding
16	0.050	5 / 164	nuclease activity
17	0.055	4 / 118	carbohydrate binding
18	0.062	30 / 1859	metal ion binding
19	0.067	2 / 35	receptor signaling protein activity
20	0.074	2 / 37	endonuclease activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	3 / 65	hsa−miR−518c*
2	0.05	5 / 163	hsa−miR−137
3	0.06	3 / 74	hsa−miR−1254
4	0.09	2 / 41	hsa−miR−532−3p
5	0.11	3 / 96	hsa−miR−125b
6	0.16	2 / 58	hsa−miR−409−5p
7	0.17	1 / 15	hsa−miR−191*
8	0.18	1 / 16	hsa−miR−220a
9	0.19	2 / 65	hsa−miR−550
10	0.24	1 / 23	hsa−miR−1250
11	0.24	1 / 23	hsa−miR−1228
12	0.26	1 / 25	hsa−miR−1273
13	0.26	1 / 25	hsa−miR−99a
14	0.26	1 / 25	hsa−miR−100
15	0.26	1 / 25	hsa−miR−432*
16	0.27	2 / 84	hsa−miR−486−3p
17	0.28	2 / 85	hsa−miR−423−5p
18	0.28	2 / 87	hsa−miR−134
19	0.31	3 / 162	hsa−miR−96
20	0.32	1 / 31	hsa−miR−296−5p

PathwAct

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	42 / 2714	ICGC_Irf4_targets
2	0.08	33 / 2136	ICGC_GabpPcr2_targets
3	0.16	40 / 2836	ICGC_BatfPcr1_targets
4	0.23	53 / 3966	ICGC_Pu1_targets
5	0.26	76 / 5890	ICGC_Elf1_targets
6	0.27	20 / 1418	ICGC_Ets1_targets
7	0.28	29 / 2137	ICGC_SrfV0416101_targets
8	0.30	67 / 5219	ICGC_Tcf3_targets
9	0.32	19 / 1383	ICGC_Six5_targets
10	0.37	56 / 4414	ICGC_Bclaf101388_targets
11	0.38	17 / 1273	ICGC_P300_targets
12	0.40	9 / 653	ICGC_SrfPcr2_targets
13	0.40	67 / 5355	ICGC_Pol2_targets
14	0.42	76 / 6114	ICGC_Runx3_targets
15	0.48	53 / 4314	ICGC_Ebfsc137065_targets
16	0.52	49 / 4032	ICGC_Creb1_targets
17	0.53	56 / 4617	ICGC_Tcf12_targets
18	0.54	65 / 5374	ICGC_Pax5_targets
19	0.56	59 / 4909	ICGC_Stat5_targets
20	0.57	35 / 2927	ICGC_Rad21_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 27	VAQUERIZAS_Lymph node
2	0.07	2 / 36	VAQUERIZAS_Fetal brain
3	0.08	2 / 38	VAQUERIZAS_Whole brain
4	0.19	1 / 17	VAQUERIZAS_Pituitary
5	0.19	1 / 17	VAQUERIZAS_Heart
6	0.21	1 / 19	VAQUERIZAS_Tonsil
7	0.30	1 / 29	VAQUERIZAS_Fetal lung
8	0.39	1 / 41	VAQUERIZAS_Placenta
9	0.42	1 / 45	VAQUERIZAS_Uterus
10	0.51	1 / 58	VAQUERIZAS_Lung
11	0.52	2 / 143	VAQUERIZAS_General
12	1.00	0 / 26	VAQUERIZAS_Liver
13	1.00	0 / 33	VAQUERIZAS_Prostate
14	1.00	0 / 29	VAQUERIZAS_Smooth muscle
15	1.00	0 / 9	VAQUERIZAS_Kidney
16	1.00	0 / 23	VAQUERIZAS_Spinal cord
17	1.00	0 / 37	VAQUERIZAS_Thymus
18	1.00	0 / 40	VAQUERIZAS_Thyroid
19	1.00	0 / 59	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 74	WIRTH_Mucosa
2	0.3	2 / 95	WIRTH_Muscle
3	0.4	1 / 46	WIRTH_Liver
4	0.5	3 / 225	PALMER_Granulocytes signature up
5	0.7	2 / 194	PALMER_B−Cell signature up
6	0.7	1 / 107	WIRTH_Testis
7	0.8	1 / 114	PALMER_T−Cell signature up
8	0.8	3 / 350	WIRTH_Immune system
9	0.9	2 / 350	WIRTH_Nervous System
10	1.0	0 / 32	WIRTH_Pancreas
11	1.0	0 / 11	WIRTH_Sec. lymphoid organs
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 13	WIRTH_B−cells
14	1.0	0 / 8	WIRTH_Tonsil
15	1.0	0 / 12	WIRTH_Thymus
16	1.0	0 / 12	WIRTH_Lymphocytes
17	1.0	0 / 5	WIRTH_Bone marrow
18	1.0	0 / 11	WIRTH_Globus pallidus
19	1.0	0 / 14	WIRTH_Telencephalon
20	1.0	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.01	58 / 3682	LU_BPDE 0.005 DN
2	0.28	16 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

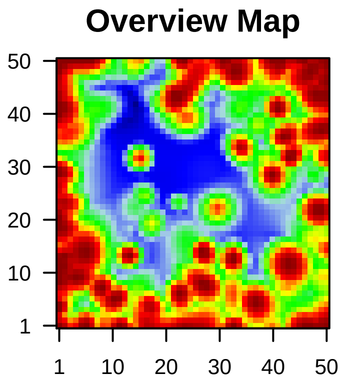
Overexpression Spots

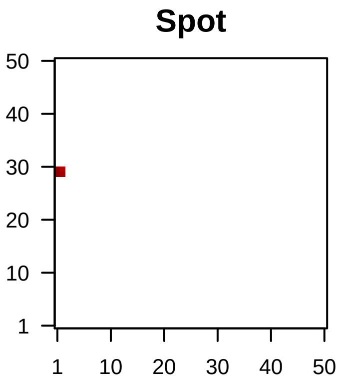
Spot Summary: S

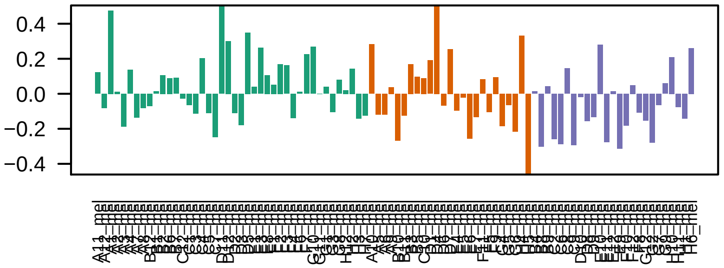
metagenes = 4
genes = 23

<r> metagenes = 0.99
<r> genes = 0.14
beta: r2= 0.78 / log p= −Inf

samples with spot = 16 (17.4 %)
MSC1 : 8 (19 %)
MSC2 : 5 (20 %)
MSC3 : 3 (12 %)


Overview Map


Spot

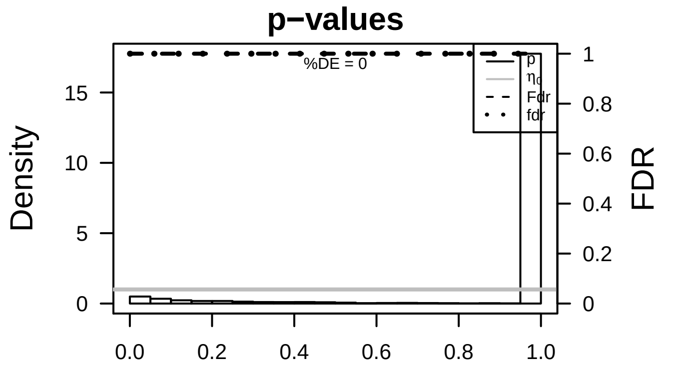


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PEX16	1.94	−0.14	0.3	PEX16	peroxisomal biogenesis factor 16 [Source:HGNC Symbol;Acc
2	MAP4K3	1.86	−0.43	0.25	MAP4K3	mitogen−activated protein kinase kinase kinase kinase 3 [Sou
3	SPATS1	1.73	−0.14	0.39	SPATS1	spermatogenesis associated, serine−rich 1 [Source:HGNC Sy
4	TBCK	1.7	−0.42	0.27	TBCK	TBC1 domain containing kinase [Source:HGNC Symbol;Acc:
5	GIMAP2	1.66	−0.11	0.22	GIMAP2	GTPase, IMAP family member 2 [Source:HGNC Symbol;Acc:
6	DOCK6	1.45	−0.36	0.31	DOCK6	dedicator of cytokinesis 6 [Source:HGNC Symbol;Acc:HGNC
7	WLS	1.41	−0.59	0.2	WLS	wntless Wnt ligand secretion mediator [Source:HGNC Symbo
8	CYB5RL	1.4	−0.14	0.28	CYB5RL	cytochrome b5 reductase−like [Source:HGNC Symbol;Acc:H
9	FHL2	1.39	−0.17	0.23	FHL2	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:H
10	GADL1	1.3	−0.33	0.32	GADL1	glutamate decarboxylase−like 1 [Source:HGNC Symbol;Acc:
11	SYS1	1.29	−0.9	0.37	SYS1	Sys1 golgi trafficking protein [Source:HGNC Symbol;Acc:HG
12	TADA1	1.26	−0.77	0.34	TADA1	transcriptional adaptor 1 [Source:HGNC Symbol;Acc:HGNC:
13	PSEN2	1.19	−1.09	0.3	PSEN2	presenilin 2 [Source:HGNC Symbol;Acc:HGNC:9509]
14	INO80C	1.12	−0.9	0.26	INO80C	INO80 complex subunit C [Source:HGNC Symbol;Acc:HGNC
15	TMEM161B	1.11	−0.81	0.27	TMEM161B	transmembrane protein 161B [Source:HGNC Symbol;Acc:HG
16	TSHZ1	1.04	−0.6	0.27	TSHZ1	teashirt zinc finger homeobox 1 [Source:HGNC Symbol;Acc:
17	PRKAR1B	1.01	−0.29	0.28	PRKAR1B	protein kinase, cAMP−dependent, regulatory, type I, beta [So
18	CKLF−CMTM	1	−0.1	0.33	CKLF−CMTM1	CKLF−CMTM1 readthrough [Source:HGNC Symbol;Acc:HGN
19	NSD1	0.95	−1.06	0.25	NSD1	nuclear receptor binding SET domain protein 1 [Source:HGN
20	NR1H2	0.89	−1.11	0.28	NR1H2	nuclear receptor subfamily 1, group H, member 2 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	2 / 15	MF	retinoid X receptor binding
2	5e−04	11 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
3	1e−03	2 / 35	BP	learning or memory
4	2e−03	2 / 38	miRN	hsa−miR−490−5p
5	2e−03	2 / 39	MF	androgen receptor binding
6	4e−03	2 / 62	GSE	RAMASWAMY_METASTASIS_UP
7	4e−03	14 / 4774	TF	ICGC_Foxm1_targets
8	5e−03	14 / 4829	TF	ICGC_Nficsc81335_targets
9	5e−03	2 / 68	GSE	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_UP
10	5e−03	2 / 72	GSE	HOEBEKE_LYMPHOID_STEM_CELL_DN
11	6e−03	2 / 75	miRN	hsa−miR−513c
12	6e−03	13 / 4385	TF	ICGC_Atf2_targets
13	6e−03	20 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
14	7e−03	2 / 80	BP	chromatin remodeling
15	8e−03	10 / 2927	TF	ICGC_Rad21_targets
16	8e−03	2 / 89	CC	Z disc
17	8e−03	19 / 8415	Colon	Quies3_Colon
18	1e−02	2 / 98	GSE	CERVERA_SDHB_TARGETS_1_UP
19	1e−02	13 / 4617	TF	ICGC_Tcf12_targets
20	1e−02	14 / 5200	TF	ICGC_Mta3_targets
21	1e−02	9 / 2563	Lymp	HOPP_Heterochrom
22	1e−02	1 / 7	GSE	PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_DN
23	1e−02	2 / 103	GSE	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPM
24	1e−02	13 / 4689	TF	ICGC_Taf1_targets
25	1e−02	8 / 2137	TF	ICGC_SrfV0416101_targets
26	1e−02	3 / 314	GSE	OSMAN_BLADDER_CANCER_DN
27	1e−02	1 / 8	GSE	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
28	1e−02	3 / 318	miRN	hsa−miR−340
29	1e−02	16 / 6564	Lymp	HOPP_Strong_enhancer
30	1e−02	21 / 10290	Colon	TssWk_Colon
31	1e−02	1 / 9	GSE	EHRLICH_ICF_SYNDROM_UP
32	1e−02	2 / 119	miRN	hsa−miR−380
33	1e−02	11 / 3700	TF	ICGC_Nfatc1_targets
34	1e−02	20 / 9528	Brain	Overlap_fetal_midbrain_Quies
35	2e−02	1 / 10	BP	beta−amyloid metabolic process
36	2e−02	1 / 10	BP	DNA integration
37	2e−02	1 / 10	BP	heart trabecula formation
38	2e−02	1 / 10	BP	negative regulation of macrophage derived foam cell differentiation
39	2e−02	1 / 10	GSE	REACTOME_SIGNALING_BY_NOTCH4
40	2e−02	1 / 10	GSE	REACTOME_SIGNALING_BY_NOTCH2


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	2 / 35	learning or memory
2	0.007	2 / 80	chromatin remodeling
3	0.015	1 / 10	beta−amyloid metabolic process
4	0.015	1 / 10	DNA integration
5	0.015	1 / 10	heart trabecula formation
6	0.015	1 / 10	negative regulation of macrophage derived foam cell differentiation
7	0.017	1 / 11	cell fate specification
8	0.017	1 / 11	positive regulation of triglyceride biosynthetic process
9	0.017	1 / 11	protein import into peroxisome matrix
10	0.018	1 / 12	brain morphogenesis
11	0.018	1 / 12	carboxylic acid metabolic process
12	0.018	1 / 12	endoplasmic reticulum calcium ion homeostasis
13	0.020	2 / 140	cellular lipid metabolic process
14	0.020	1 / 13	positive regulation of cellular protein metabolic process
15	0.020	1 / 13	positive regulation of cholesterol efflux
16	0.021	1 / 14	anterior/posterior axis specification
17	0.021	1 / 14	dorsal/ventral neural tube patterning
18	0.021	1 / 14	negative regulation of protein complex assembly
19	0.021	1 / 14	positive regulation of Ras protein signal transduction
20	0.023	1 / 15	activation of protein kinase A activity

Brain

Rank	p−value	#in/all	Geneset
1	5e−04	11 / 2462	Mid_Frontal_Lobe_HetRpts
2	6e−03	20 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	1e−02	20 / 9528	Overlap_fetal_midbrain_Quies
4	2e−02	5 / 1065	Overlap_fetal_midbrain_Enh
5	2e−02	7 / 1949	Fetal_TssF
6	4e−02	7 / 2185	Fetal_TssA
7	7e−02	6 / 1907	Fetal_TxTrans
8	7e−02	8 / 2972	Mid_Frontal_Lobe_ReprPC
9	8e−02	3 / 656	Overlap_fetal_midbrain_EnhP
10	8e−02	5 / 1548	Mid_Frontal_Lobe_K9K27me3
11	1e−01	2 / 383	Fetal_Tx
12	1e−01	17 / 9013	Overlap_fetal_midbrain_K9K27me3
13	2e−01	7 / 3081	Mid_Frontal_Lobe_ZNF
14	2e−01	3 / 1013	Fetal_TssP
15	2e−01	1 / 158	Overlap_fetal_midbrain_Het
16	3e−01	3 / 1207	Overlap_fetal_midbrain_TssF
17	3e−01	2 / 786	Fetal_EnhG
18	4e−01	2 / 884	Overlap_fetal_midbrain_EnhG
19	4e−01	10 / 5940	Overlap_fetal_midbrain_HetRpts
20	5e−01	2 / 1050	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 15	GENTLES_modul11
2	0.03	1 / 20	PanCan_ChromMod_geneset_nanostring
3	0.17	1 / 120	PanCan_CC+Apop_geneset_nanostring
4	0.54	1 / 489	Lembcke_Normal vs Adenoma
5	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
6	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
7	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	1.00	0 / 12	LIU_BREAST_CANCER
10	1.00	0 / 14	LIU_COMMON_CANCER_GENES
11	1.00	0 / 14	LIU_LIVER_CANCER
12	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
13	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
14	1.00	0 / 15	WANG_ER_UP
15	1.00	0 / 5	WANG_ER_DN
16	1.00	0 / 16	WOLFER_overlap genes
17	1.00	0 / 12	BEN−PORATH_DN
18	1.00	0 / 13	BEN−PORATH_UP
19	1.00	0 / 15	GENTLES_modul1
20	1.00	0 / 16	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	0.008	2 / 89	Z disc
2	0.018	1 / 12	dendrite membrane
3	0.018	1 / 12	STAGA complex
4	0.021	1 / 14	integral component of peroxisomal membrane
5	0.023	1 / 15	dendrite cytoplasm
6	0.023	1 / 15	Ino80 complex
7	0.025	1 / 16	M band
8	0.029	1 / 19	ciliary base
9	0.029	3 / 438	Golgi membrane
10	0.034	8 / 2577	nucleoplasm
11	0.038	1 / 25	MLL1 complex
12	0.047	1 / 31	dendritic shaft
13	0.047	1 / 31	nuclear inner membrane
14	0.053	1 / 35	integral component of Golgi membrane
15	0.063	1 / 42	neuromuscular junction
16	0.067	2 / 276	cilium
17	0.070	1 / 47	lipid particle
18	0.072	1 / 48	peroxisomal membrane
19	0.081	3 / 663	chromosome
20	0.082	2 / 308	focal adhesion

Chr

Rank	p−value	#in/all	Geneset
1	0.05	2 / 221	Chr 18
2	0.08	5 / 1500	Chr 1
3	0.29	2 / 689	Chr 7
4	0.29	2 / 696	Chr 5
5	0.46	2 / 993	Chr 2
6	0.47	1 / 398	Chr 20
7	0.48	2 / 1037	Chr 19
8	0.52	1 / 465	Chr 15
9	0.59	1 / 558	Chr 4
10	0.64	1 / 649	Chr 16
11	0.66	1 / 687	Chr 6
12	0.72	1 / 801	Chr 11
13	0.74	1 / 838	Chr 3
14	0.74	1 / 840	Chr 17
15	1.00	0 / 552	Chr 10
16	1.00	0 / 775	Chr 12
17	1.00	0 / 262	Chr 13
18	1.00	0 / 462	Chr 14
19	1.00	0 / 151	Chr 21
20	1.00	0 / 335	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.008	19 / 8415	Quies3_Colon
2	0.013	21 / 10290	TssWk_Colon
3	0.019	57 / 1038	HetRpts_Colon
4	0.034	16 / 7203	TssF_Colon
5	0.034	18 / 8580	TxWk_Colon
6	0.041	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
7	0.053	8 / 2798	TxEnhG1_Colon
8	0.055	10 / 3897	Quies1_Colon
9	0.057	5 / 1386	Het_Colon
10	0.062	3 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	0.063	18 / 9027	Tx_Colon
12	0.064	12 / 5155	EnhWk1_Colon
13	0.109	7 / 2698	EnhA_Colon
14	0.109	18 / 9482	TssA_Colon
15	0.146	2 / 436	K9acLow_Colon
16	0.154	12 / 5880	TssD2_Colon
17	0.227	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
18	0.232	3 / 1079	ZNF_Colon
19	0.236	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	0.254	17 / 9653	Enh_Colon

Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 435	GUDJ_psoriasis up
2	1	0 / 294	GUDJ_psoriasis down
3	1	0 / 11	BCHETNIA_EBM up
4	1	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
2	0.02	1 / 15	VERHAAK_CL subtype
3	0.02	1 / 15	VERHAAK_MES subtype
4	0.10	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
5	0.14	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.43	1 / 356	Down_a
7	1.00	0 / 16	VERHAAK_NL subtype
8	1.00	0 / 14	VERHAAK_PN subtype
9	1.00	0 / 23	WIRTH_PN subtype
10	1.00	0 / 74	WIRTH_Normal Brain
11	1.00	0 / 9	VERHAAK_Brain
12	1.00	0 / 8	VERHAAK_PN_Brain
13	1.00	0 / 11	Martinez_Glio_hypermeth
14	1.00	0 / 3	Martinez_Glio_hypometh
15	1.00	0 / 2	laffaire_hypometh_LGG_vs_control
16	1.00	0 / 72	laffaire_hypermeth_LGG_vs_control
17	1.00	0 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
18	1.00	0 / 4	Donson−adaptive−immunity−associated with LTS in HGA
19	1.00	0 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
20	1.00	0 / 8	Donson−chemokines/cytokines−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.004	2 / 62	RAMASWAMY_METASTASIS_UP
2	0.005	2 / 68	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_UP
3	0.005	2 / 72	HOEBEKE_LYMPHOID_STEM_CELL_DN
4	0.010	2 / 98	CERVERA_SDHB_TARGETS_1_UP
5	0.011	1 / 7	PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_DN
6	0.011	2 / 103	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPME
7	0.012	3 / 314	OSMAN_BLADDER_CANCER_DN
8	0.012	1 / 8	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
9	0.014	1 / 9	EHRLICH_ICF_SYNDROM_UP
10	0.015	1 / 10	REACTOME_SIGNALING_BY_NOTCH4
11	0.015	1 / 10	REACTOME_SIGNALING_BY_NOTCH2
12	0.015	1 / 10	REACTOME_SIGNALING_BY_NOTCH3
13	0.015	1 / 10	REACTOME_REGULATED_PROTEOLYSIS_OF_P75NTR
14	0.017	1 / 11	BIOCARTA_CFTR_PATHWAY
15	0.017	1 / 11	BIOCARTA_PLCE_PATHWAY
16	0.017	1 / 11	AMIT_EGF_RESPONSE_20_HELA
17	0.018	1 / 12	BIOCARTA_AGPCR_PATHWAY
18	0.018	1 / 12	BIOCARTA_GATA3_PATHWAY
19	0.018	1 / 12	BIOCARTA_CARM1_PATHWAY
20	0.018	1 / 12	REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS

HM

Rank	p−value	#in/all	Geneset
1	0.04	1 / 29	HALLMARK_NOTCH_SIGNALING
2	0.05	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.13	1 / 91	HALLMARK_BILE_ACID_METABOLISM
4	0.19	1 / 137	HALLMARK_UV_RESPONSE_DN
5	0.20	1 / 140	HALLMARK_APOPTOSIS
6	0.23	1 / 165	HALLMARK_MYOGENESIS
7	0.23	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
8	0.23	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.24	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.25	1 / 183	HALLMARK_GLYCOLYSIS
11	0.25	1 / 188	HALLMARK_ADIPOGENESIS
12	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	1.00	0 / 176	HALLMARK_HYPOXIA
14	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1.00	0 / 195	HALLMARK_MITOTIC_SPINDLE
16	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
17	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
18	1.00	0 / 146	HALLMARK_DNA_REPAIR
19	1.00	0 / 196	HALLMARK_G2M_CHECKPOINT
20	1.00	0 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	9 / 2563	HOPP_Heterochrom
2	0.01	16 / 6564	HOPP_Strong_enhancer
3	0.06	15 / 6929	HOPP_Txn_elongation
4	0.13	12 / 5693	HOPP_Weak_enhancer
5	0.13	2 / 410	SPANG_CD40 6hrs DN
6	0.25	3 / 1128	SPANG_BCR DN
7	0.28	1 / 212	LENZ_Stromal signature 1
8	0.29	13 / 7209	HOPP_Weak_promoter
9	0.32	1 / 247	ZHANG_DLBCL mutated
10	0.34	10 / 5538	HOPP_Weak_txn
11	0.35	1 / 280	SPANG_CD40 6hrs UP
12	0.41	9 / 5184	HOPP_Txn_transition
13	0.44	6 / 3396	HOPP_Repressed
14	0.45	4 / 2188	HOPP_Poised_promoter
15	0.54	12 / 7592	HOPP_Active_promoter
16	0.57	2 / 1218	SPANG_BCR UP
17	0.88	2 / 2211	HOPP_Repetitive
18	1.00	0 / 13	BENTINK_mBL UP
19	1.00	0 / 12	BENTINK_mBL DOWN
20	1.00	0 / 129	DAVE_BL−vs−DLBCL

MF

Rank	p−value	#in/all	Geneset
1	2e−04	2 / 15	retinoid X receptor binding
2	2e−03	2 / 39	androgen receptor binding
3	2e−02	1 / 12	protein kinase A catalytic subunit binding
4	3e−02	1 / 17	aspartic−type endopeptidase activity
5	3e−02	1 / 19	cAMP binding
6	3e−02	1 / 19	protein phosphatase type 2A regulator activity
7	3e−02	1 / 21	retinoic acid receptor binding
8	3e−02	3 / 456	protein binding transcription factor activity
9	3e−02	1 / 22	histone−lysine N−methyltransferase activity
10	3e−02	1 / 22	Wnt−protein binding
11	4e−02	1 / 25	ATP−dependent helicase activity
12	4e−02	1 / 25	protein phosphatase inhibitor activity
13	4e−02	1 / 27	potassium channel regulator activity
14	4e−02	1 / 27	protein phosphatase 2A binding
15	4e−02	1 / 27	thyroid hormone receptor binding
16	4e−02	2 / 217	transcription coactivator activity
17	4e−02	1 / 29	ATP−dependent DNA helicase activity
18	5e−02	1 / 33	estrogen receptor binding
19	5e−02	1 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
20	5e−02	1 / 35	receptor signaling protein serine/threonine kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	2 / 38	hsa−miR−490−5p
2	0.006	2 / 75	hsa−miR−513c
3	0.013	3 / 318	hsa−miR−340
4	0.014	2 / 119	hsa−miR−380
5	0.018	2 / 132	hsa−miR−320d
6	0.020	2 / 141	hsa−miR−138
7	0.021	2 / 146	hsa−miR−320c
8	0.022	2 / 150	hsa−miR−338−3p
9	0.024	3 / 408	hsa−miR−497
10	0.028	3 / 432	hsa−miR−424
11	0.028	2 / 170	hsa−miR−320b
12	0.032	2 / 181	hsa−miR−196b
13	0.032	1 / 21	hsa−miR−1282
14	0.033	3 / 459	hsa−miR−195
15	0.034	2 / 189	hsa−miR−513a−3p
16	0.035	2 / 191	hsa−miR−520d−5p
17	0.035	3 / 471	hsa−miR−15b
18	0.037	3 / 479	hsa−miR−16
19	0.041	2 / 209	hsa−miR−196a
20	0.042	3 / 507	hsa−miR−15a

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.004	14 / 4774	ICGC_Foxm1_targets
2	0.005	14 / 4829	ICGC_Nficsc81335_targets
3	0.006	13 / 4385	ICGC_Atf2_targets
4	0.008	10 / 2927	ICGC_Rad21_targets
5	0.010	13 / 4617	ICGC_Tcf12_targets
6	0.010	14 / 5200	ICGC_Mta3_targets
7	0.012	13 / 4689	ICGC_Taf1_targets
8	0.012	8 / 2137	ICGC_SrfV0416101_targets
9	0.014	11 / 3700	ICGC_Nfatc1_targets
10	0.016	13 / 4879	ICGC_Pmlsc71910_targets
11	0.020	12 / 4414	ICGC_Bclaf101388_targets
12	0.023	8 / 2391	ICGC_Pbx3_targets
13	0.024	8 / 2416	ICGC_Bcl3_targets
14	0.024	11 / 3966	ICGC_Pu1_targets
15	0.032	12 / 4682	ICGC_Pol24_targets
16	0.032	14 / 5890	ICGC_Elf1_targets
17	0.036	13 / 5355	ICGC_Pol2_targets
18	0.039	13 / 5408	ICGC_Pou2_targets
19	0.041	6 / 1701	HEBENSTREIT_high expression TF
20	0.042	5 / 1273	ICGC_P300_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	1 / 17	VAQUERIZAS_Heart
2	0.09	1 / 58	VAQUERIZAS_Lung
3	1.00	0 / 36	VAQUERIZAS_Fetal brain
4	1.00	0 / 41	VAQUERIZAS_Placenta
5	1.00	0 / 26	VAQUERIZAS_Liver
6	1.00	0 / 33	VAQUERIZAS_Prostate
7	1.00	0 / 29	VAQUERIZAS_Smooth muscle
8	1.00	0 / 45	VAQUERIZAS_Uterus
9	1.00	0 / 143	VAQUERIZAS_General
10	1.00	0 / 9	VAQUERIZAS_Kidney
11	1.00	0 / 23	VAQUERIZAS_Spinal cord
12	1.00	0 / 38	VAQUERIZAS_Whole brain
13	1.00	0 / 37	VAQUERIZAS_Thymus
14	1.00	0 / 40	VAQUERIZAS_Thyroid
15	1.00	0 / 59	VAQUERIZAS_Whole blood
16	1.00	0 / 7	VAQUERIZAS_Appendix
17	1.00	0 / 29	VAQUERIZAS_Fetal lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 114	PALMER_T−Cell signature up
2	0.3	1 / 194	PALMER_B−Cell signature up
3	0.4	1 / 350	WIRTH_Immune system
4	0.4	1 / 350	WIRTH_Nervous System
5	1.0	0 / 32	WIRTH_Pancreas
6	1.0	0 / 11	WIRTH_Sec. lymphoid organs
7	1.0	0 / 11	WIRTH_Prim. lymphoid organs
8	1.0	0 / 13	WIRTH_B−cells
9	1.0	0 / 8	WIRTH_Tonsil
10	1.0	0 / 12	WIRTH_Thymus
11	1.0	0 / 12	WIRTH_Lymphocytes
12	1.0	0 / 5	WIRTH_Bone marrow
13	1.0	0 / 11	WIRTH_Globus pallidus
14	1.0	0 / 14	WIRTH_Telencephalon
15	1.0	0 / 11	WIRTH_Cortex cerebri
16	1.0	0 / 10	WIRTH_Hippocampus
17	1.0	0 / 10	WIRTH_Thalamus
18	1.0	0 / 12	WIRTH_Cerebellum
19	1.0	0 / 107	WIRTH_Testis
20	1.0	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	3 / 3682	LU_BPDE 0.005 DN
2	1.0	0 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

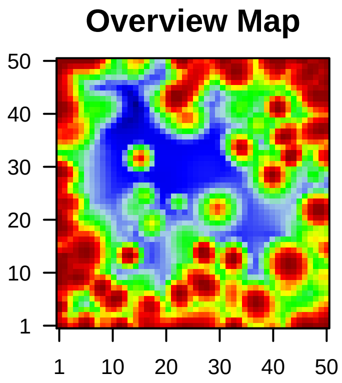
Overexpression Spots

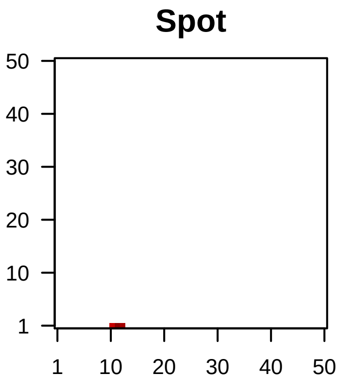
Spot Summary: T

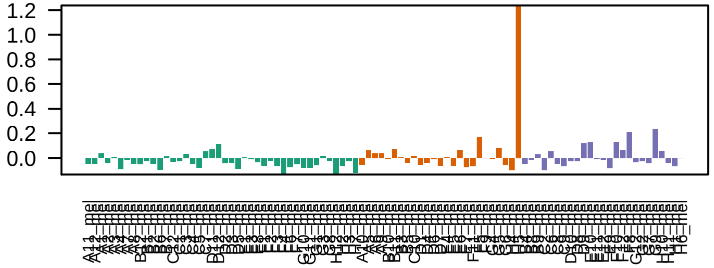
metagenes = 3
genes = 129

<r> metagenes = 0.98
<r> genes = 0.19
beta: r2= 1.14 / log p= −Inf

samples with spot = 3 (3.3 %)
MSC2 : 1 (4 %)
MSC3 : 2 (8 %)


Overview Map


Spot

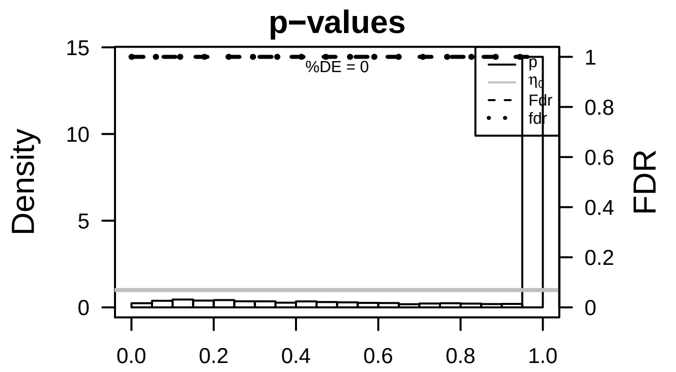


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ZNF483	2.09	−0.13	0.46	ZNF483	zinc finger protein 483 [Source:HGNC Symbol;Acc:HGNC:23
2	C1orf111	2.02	−0.07	0.66	C1orf111	chromosome 1 open reading frame 111 [Source:HGNC Symb
3	SEPP1	1.92	−0.03	0.77	SEPP1	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGNC
4	C11orf71	1.91	−0.28	0.42	C11orf71	chromosome 11 open reading frame 71 [Source:HGNC Symb
5	FCGRT	1.9	−0.05	0.36	FCGRT	Fc fragment of IgG, receptor, transporter, alpha [Source:HGN
6	PIGL	1.84	−0.33	0.26	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L [Sou
7	FGFBP2	1.83	−0.07	0.48	FGFBP2	fibroblast growth factor binding protein 2 [Source:HGNC Sym
8	ZNF77	1.83	−0.17	0.42	ZNF77	zinc finger protein 77 [Source:HGNC Symbol;Acc:HGNC:131
9	STKLD1	1.82	−0.11	0.34	STKLD1	serine/threonine kinase−like domain containing 1 [Source:HG
10	TENM3	1.79	−0.26	0.39	TENM3	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
11	CCDC80	1.79	−0.18	0.47	CCDC80	coiled−coil domain containing 80 [Source:HGNC Symbol;Acc
12	BAX	1.78	−0.22	0.41	BAX	BCL2−associated X protein [Source:HGNC Symbol;Acc:HGN
13	LGALS9	1.77	−0.09	0.41	LGALS9	lectin, galactoside−binding, soluble, 9 [Source:HGNC Symbol
14	ASPA	1.77	−0.16	0.41	ASPA	aspartoacylase [Source:HGNC Symbol;Acc:HGNC:756]
15	SERPINE3	1.75	−0.09	0.39	SERPINE3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
16	PTPRU	1.75	−0.1	0.44	PTPRU	protein tyrosine phosphatase, receptor type, U [Source:HGNC
17	ZNF606	1.71	−0.07	0.47	ZNF606	zinc finger protein 606 [Source:HGNC Symbol;Acc:HGNC:25
18	MYOT	1.71	−0.1	0.38	MYOT	myotilin [Source:HGNC Symbol;Acc:HGNC:12399]
19	INTS1	1.69	−0.29	0.37	INTS1	integrator complex subunit 1 [Source:HGNC Symbol;Acc:HG
20	ZNF609	1.68	−0.43	0.34	ZNF609	zinc finger protein 609 [Source:HGNC Symbol;Acc:HGNC:29

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−04	3 / 12	GSEA	VERRECCHIA_RESPONSE_TO_TGFB1_C4
2	3e−04	27 / 1548	Brain	Mid_Frontal_Lobe_K9K27me3
3	2e−03	2 / 8	Colon	KIM_CRC−MSI−regulated_DN
4	2e−03	8 / 271	GSEA	ZHANG_TLX_TARGETS_60HR_UP
5	3e−03	2 / 10	BP	response to dietary excess
6	4e−03	3 / 37	GSEA	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
7	5e−03	2 / 12	MF	channel activity
8	5e−03	2 / 13	MF	antigen binding
9	5e−03	2 / 13	BP	positive regulation of myoblast differentiation
10	5e−03	2 / 13	MF	ubiquitin conjugating enzyme binding
11	5e−03	2 / 13	GSEA	TSAI_DNAJB4_TARGETS_UP
12	6e−03	38 / 2984	CC	integral component of membrane
13	7e−03	32 / 2416	TF	ICGC_Bcl3_targets
14	7e−03	12 / 622	GSEA	LEE_BMP2_TARGETS_UP
15	8e−03	5 / 143	BP	protein homooligomerization
16	8e−03	8 / 331	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
17	8e−03	6 / 203	GSEA	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_DN
18	9e−03	3 / 49	Glio	OL vs. MOG− OL
19	9e−03	2 / 17	BP	cellular respiration
20	9e−03	2 / 17	GSEA	ALONSO_METASTASIS_NEURAL_UP
21	1e−02	2 / 18	BP	camera−type eye morphogenesis
22	1e−02	2 / 18	BP	double−strand break repair via nonhomologous end joining
23	1e−02	2 / 18	GSEA	AMIT_EGF_RESPONSE_240_MCF10A
24	1e−02	2 / 19	MF	acyl−CoA dehydrogenase activity
25	1e−02	3 / 55	miRN	hsa−miR−28−3p
26	1e−02	3 / 55	GSEA	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
27	1e−02	4 / 104	GSEA	DAIRKEE_TERT_TARGETS_DN
28	1e−02	2 / 20	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
29	1e−02	2 / 21	BP	positive regulation of muscle cell differentiation
30	1e−02	2 / 21	GSEA	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_UP
31	1e−02	2 / 21	GSEA	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP
32	1e−02	6 / 228	GSEA	WANG_MLL_TARGETS
33	1e−02	6 / 231	GSEA	DURAND_STROMA_S_UP
34	2e−02	2 / 22	MF	oxidoreductase activity, acting on the CH−CH group of donors
35	2e−02	31 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
36	2e−02	5 / 175	CC	early endosome
37	2e−02	3 / 64	MF	beta−catenin binding
38	2e−02	3 / 64	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16
39	2e−02	2 / 24	GSEA	IVANOVA_HEMATOPOIESIS_STEM_CELL_SHORT_TERM
40	2e−02	2 / 24	GSEA	IKEDA_MIR30_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 100	HORVATH_aging_genes meth DOWN
2	0.6	1 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	GENTLES_modul11
2	0.2	3 / 180	SPANG_LPS−index2
3	0.6	1 / 120	PanCan_CC+Apop_geneset_nanostring
4	0.9	1 / 298	SPANG_BCL6−index2
5	1.0	1 / 489	Lembcke_Normal vs Adenoma
6	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
7	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
8	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1.0	0 / 12	LIU_BREAST_CANCER
11	1.0	0 / 14	LIU_COMMON_CANCER_GENES
12	1.0	0 / 14	LIU_LIVER_CANCER
13	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
14	1.0	0 / 12	LIU_PROSTATE_CANCER_UP
15	1.0	0 / 15	WANG_ER_UP
16	1.0	0 / 5	WANG_ER_DN
17	1.0	0 / 16	WOLFER_overlap genes
18	1.0	0 / 12	BEN−PORATH_DN
19	1.0	0 / 13	BEN−PORATH_UP
20	1.0	0 / 15	GENTLES_modul1

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	2 / 8	KIM_CRC−MSI−regulated_DN
2	0.026	62 / 5880	TssD2_Colon
3	0.030	14 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
4	0.033	32 / 2698	EnhA_Colon
5	0.033	2 / 33	Marisa_CRC−cluster−e
6	0.034	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
7	0.045	15 / 1079	ZNF_Colon
8	0.058	6 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	0.058	3 / 102	Marisa_CRC−cluster−d
10	0.059	9 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	0.059	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
12	0.067	1 / 8	Boland_CRC−MSI−TGC
13	0.068	25 / 2142	ReprPC_Colon
14	0.075	1 / 9	Budinska_D_Mesenchymal_UP
15	0.083	7 / 436	K9acLow_Colon
16	0.092	36 / 3383	EnhWk2_Colon
17	0.095	52 / 5155	EnhWk1_Colon
18	0.106	80 / 8415	Quies3_Colon
19	0.112	24 / 2159	TssP_Colon
20	0.114	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 12	VERRECCHIA_RESPONSE_TO_TGFB1_C4
2	2e−03	8 / 271	ZHANG_TLX_TARGETS_60HR_UP
3	4e−03	3 / 37	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
4	5e−03	2 / 13	TSAI_DNAJB4_TARGETS_UP
5	7e−03	12 / 622	LEE_BMP2_TARGETS_UP
6	8e−03	8 / 331	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
7	8e−03	6 / 203	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_DN
8	9e−03	2 / 17	ALONSO_METASTASIS_NEURAL_UP
9	1e−02	2 / 18	AMIT_EGF_RESPONSE_240_MCF10A
10	1e−02	3 / 55	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
11	1e−02	4 / 104	DAIRKEE_TERT_TARGETS_DN
12	1e−02	2 / 20	FARMER_BREAST_CANCER_CLUSTER_1
13	1e−02	2 / 21	YORDY_RECIPROCAL_REGULATION_BY_ETS1_AND_SP100_UP
14	1e−02	2 / 21	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP
15	1e−02	6 / 228	WANG_MLL_TARGETS
16	1e−02	6 / 231	DURAND_STROMA_S_UP
17	2e−02	3 / 64	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16
18	2e−02	2 / 24	IVANOVA_HEMATOPOIESIS_STEM_CELL_SHORT_TERM
19	2e−02	2 / 24	IKEDA_MIR30_TARGETS_DN
20	2e−02	2 / 25	NGUYEN_NOTCH1_TARGETS_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.07	1 / 8	Subero_MM_hypo_meth
2	0.07	29 / 2563	HOPP_Heterochrom
3	0.11	2 / 66	TARTE_Plasma cell signature
4	0.14	35 / 3396	HOPP_Repressed
5	0.18	1 / 23	DAVE_Immune response 1
6	0.22	1 / 29	Subero_DLBCL_hypo_meth
7	0.23	1 / 30	Subero_INT_hypo_meth
8	0.28	3 / 212	LENZ_Stromal signature 1
9	0.33	21 / 2188	HOPP_Poised_promoter
10	0.35	1 / 50	SPANG_BAFF 9hrs DN
11	0.47	50 / 5693	HOPP_Weak_enhancer
12	0.52	48 / 5538	HOPP_Weak_txn
13	0.54	1 / 89	ROSOLOWSKI_blue total
14	0.64	18 / 2211	HOPP_Repetitive
15	0.69	2 / 275	TARTE_Mature plasma cell signature
16	0.69	3 / 410	SPANG_CD40 6hrs DN
17	0.72	2 / 294	TARTE_Plasmablast signature
18	0.86	51 / 6564	HOPP_Strong_enhancer
19	0.86	7 / 1128	SPANG_BCR DN
20	0.89	1 / 256	SPANG_IL21 DN

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p−value	#in/all	Geneset
1	0.05	3 / 95	WIRTH_Muscle
2	0.08	3 / 114	PALMER_T−Cell signature up
3	0.23	3 / 194	PALMER_B−Cell signature up
4	0.24	2 / 107	WIRTH_Testis
5	0.24	1 / 32	WIRTH_Placenta
6	0.31	3 / 225	PALMER_Granulocytes signature up
7	0.36	4 / 350	WIRTH_Nervous System
8	0.47	1 / 74	WIRTH_Mucosa
9	0.81	2 / 350	WIRTH_Immune system
10	1.00	0 / 32	WIRTH_Pancreas
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 13	WIRTH_B−cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 12	WIRTH_Lymphocytes
17	1.00	0 / 5	WIRTH_Bone marrow
18	1.00	0 / 11	WIRTH_Globus pallidus
19	1.00	0 / 14	WIRTH_Telencephalon
20	1.00	0 / 11	WIRTH_Cortex cerebri

BP

Rank	p−value	#in/all	Geneset
1	0.003	2 / 10	response to dietary excess
2	0.005	2 / 13	positive regulation of myoblast differentiation
3	0.008	5 / 143	protein homooligomerization
4	0.009	2 / 17	cellular respiration
5	0.010	2 / 18	camera−type eye morphogenesis
6	0.010	2 / 18	double−strand break repair via nonhomologous end joining
7	0.014	2 / 21	positive regulation of muscle cell differentiation
8	0.024	2 / 28	synapse organization
9	0.029	2 / 31	muscle cell differentiation
10	0.029	2 / 31	response to cold
11	0.033	2 / 33	neuron apoptotic process
12	0.035	2 / 34	dendrite morphogenesis
13	0.035	13 / 863	transmembrane transport
14	0.044	2 / 39	fatty acid beta−oxidation
15	0.044	2 / 39	positive regulation of neuron apoptotic process
16	0.060	2 / 46	odontogenesis of dentin−containing tooth
17	0.062	2 / 47	response to insulin
18	0.074	2 / 52	regulation of growth
19	0.076	2 / 53	chloride transmembrane transport
20	0.077	4 / 186	ion transmembrane transport

CC

Rank	p−value	#in/all	Geneset
1	0.006	38 / 2984	integral component of membrane
2	0.018	5 / 175	early endosome
3	0.029	17 / 1201	endoplasmic reticulum
4	0.032	3 / 80	mitochondrial membrane
5	0.047	2 / 40	recycling endosome membrane
6	0.060	8 / 487	intracellular membrane−bounded organelle
7	0.079	2 / 54	intermediate filament cytoskeleton
8	0.083	1 / 10	beta−catenin destruction complex
9	0.083	1 / 10	endoplasmic reticulum chaperone complex
10	0.083	1 / 10	ionotropic glutamate receptor complex
11	0.083	1 / 10	pericentric heterochromatin
12	0.091	1 / 11	interstitial matrix
13	0.095	4 / 200	axon
14	0.099	1 / 12	axonal growth cone
15	0.107	1 / 13	integrator complex
16	0.108	9 / 649	endoplasmic reticulum membrane
17	0.114	1 / 14	male germ cell nucleus
18	0.122	1 / 15	dendrite cytoplasm
19	0.152	1 / 19	site of double−strand break
20	0.152	1 / 19	stereocilium

Disease

Rank	p−value	#in/all	Geneset
1	0.5	3 / 294	GUDJ_psoriasis down
2	0.5	4 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	0.04	4 / 148	HALLMARK_KRAS_SIGNALING_UP
2	0.10	3 / 127	HALLMARK_KRAS_SIGNALING_DN
3	0.17	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
4	0.19	2 / 94	HALLMARK_ANDROGEN_RESPONSE
5	0.27	1 / 37	HALLMARK_APICAL_SURFACE
6	0.34	2 / 140	HALLMARK_APOPTOSIS
7	0.41	2 / 162	HALLMARK_COMPLEMENT
8	0.43	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	0.43	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.44	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.45	2 / 176	HALLMARK_HYPOXIA
12	0.51	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	0.56	1 / 95	HALLMARK_SPERMATOGENESIS
14	0.61	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	0.67	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
16	0.76	1 / 165	HALLMARK_MYOGENESIS
17	0.77	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
18	0.78	1 / 174	HALLMARK_HEME_METABOLISM
19	0.79	1 / 181	HALLMARK_P53_PATHWAY
20	0.80	1 / 183	HALLMARK_GLYCOLYSIS

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 12	channel activity
2	0.005	2 / 13	antigen binding
3	0.005	2 / 13	ubiquitin conjugating enzyme binding
4	0.011	2 / 19	acyl−CoA dehydrogenase activity
5	0.015	2 / 22	oxidoreductase activity, acting on the CH−CH group of donors
6	0.018	3 / 64	beta−catenin binding
7	0.023	6 / 255	receptor binding
8	0.033	2 / 33	receptor tyrosine kinase binding
9	0.038	11 / 695	transmembrane transporter activity
10	0.042	2 / 38	protein serine/threonine phosphatase activity
11	0.082	2 / 55	serine−type endopeptidase inhibitor activity
12	0.083	1 / 10	anion transmembrane transporter activity
13	0.083	1 / 10	ephrin receptor activity
14	0.083	1 / 10	estradiol 17−beta−dehydrogenase activity
15	0.083	1 / 10	Rac guanyl−nucleotide exchange factor activity
16	0.091	1 / 11	inorganic anion exchanger activity
17	0.091	1 / 11	methyl−CpG binding
18	0.099	1 / 12	alpha−actinin binding
19	0.099	1 / 12	lysophospholipase activity
20	0.099	1 / 12	misfolded protein binding

TF

Rank	p−value	#in/all	Geneset
1	0.007	32 / 2416	ICGC_Bcl3_targets
2	0.018	17 / 1139	HEBENSTREIT_low expression TF
3	0.020	52 / 4706	ICGC_Sp1_targets
4	0.037	47 / 4314	ICGC_Ebfsc137065_targets
5	0.037	25 / 2013	ICGC_Bcl11_targets
6	0.042	1 / 5	MYC_Apoptosis UP
7	0.050	43 / 3966	ICGC_Pu1_targets
8	0.056	33 / 2927	ICGC_Rad21_targets
9	0.076	46 / 4414	ICGC_Bclaf101388_targets
10	0.081	50 / 4879	ICGC_Pmlsc71910_targets
11	0.092	41 / 3924	ICGC_Zeb1_targets
12	0.096	55 / 5495	ICGC_Yy1_targets
13	0.098	42 / 4054	ICGC_Egr1_targets
14	0.101	47 / 4617	ICGC_Tcf12_targets
15	0.121	26 / 2391	ICGC_Pbx3_targets
16	0.122	47 / 4682	ICGC_Pol24_targets
17	0.122	1 / 15	NOWICK_TF
18	0.146	51 / 5200	ICGC_Mta3_targets
19	0.160	15 / 1314	ICGC_Usf1_targets
20	0.162	52 / 5355	ICGC_Pol2_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	33 / 3682	LU_BPDE 0.005 DN
2	0.6	9 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	3e−04	27 / 1548	Mid_Frontal_Lobe_K9K27me3
2	2e−02	31 / 2462	Mid_Frontal_Lobe_HetRpts
3	4e−02	24 / 1907	Fetal_TxTrans
4	6e−02	10 / 656	Overlap_fetal_midbrain_EnhP
5	7e−02	16 / 1236	Mid_Frontal_Lobe_ReprPCWk
6	7e−02	11 / 769	Overlap_fetal_midbrain_ZNF
7	7e−02	23 / 1949	Fetal_TssF
8	1e−01	31 / 2972	Mid_Frontal_Lobe_ReprPC
9	1e−01	11 / 884	Overlap_fetal_midbrain_EnhG
10	1e−01	12 / 989	Mid_Frontal_Lobe_Quies
11	2e−01	12 / 1013	Fetal_TssP
12	2e−01	12 / 1065	Overlap_fetal_midbrain_Enh
13	2e−01	7 / 574	Overlap_fetal_midbrain_TssP
14	3e−01	14 / 1333	Fetal_ReprPCWk
15	3e−01	9 / 831	Fetal_HetRpts
16	3e−01	21 / 2185	Fetal_TssA
17	3e−01	85 / 9528	Overlap_fetal_midbrain_Quies
18	3e−01	8 / 765	Mid_Frontal_Lobe_Het
19	4e−01	5 / 468	Mid_Frontal_Lobe_TssF
20	4e−01	28 / 3081	Mid_Frontal_Lobe_ZNF

Chr

Rank	p−value	#in/all	Geneset
1	0.03	15 / 1037	Chr 19
2	0.06	9 / 576	Chr 9
3	0.25	8 / 696	Chr 5
4	0.31	15 / 1500	Chr 1
5	0.44	8 / 840	Chr 17
6	0.45	4 / 398	Chr 20
7	0.49	6 / 649	Chr 16
8	0.54	7 / 801	Chr 11
9	0.55	6 / 687	Chr 6
10	0.57	4 / 465	Chr 15
11	0.59	7 / 838	Chr 3
12	0.63	8 / 993	Chr 2
13	0.66	2 / 262	Chr 13
14	0.70	4 / 551	Chr X
15	0.71	4 / 552	Chr 10
16	0.71	4 / 558	Chr 4
17	0.73	1 / 151	Chr 21
18	0.77	3 / 462	Chr 14
19	0.77	3 / 469	Chr 8
20	0.85	1 / 221	Chr 18

Glio

Rank	p−value	#in/all	Geneset
1	0.009	3 / 49	OL vs. MOG− OL
2	0.034	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
3	0.042	2 / 38	OL vs. OPC
4	0.059	1 / 7	KIM amplified & overexpressed in LTS
5	0.062	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
6	0.075	1 / 9	VERHAAK_Brain
7	0.122	1 / 15	VERHAAK_MES subtype
8	0.137	2 / 75	Weller_LGG_A_vs_O_DOWN
9	0.137	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
10	0.174	1 / 22	KIM prognostic signature LTS vs. STS
11	0.195	1 / 25	Shaw_down_in_1p19q
12	0.222	1 / 29	shaw_responders_down_in_oligo_glioma
13	0.255	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
14	0.281	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
15	0.303	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
16	0.335	1 / 47	mature astrocytes
17	0.346	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
18	0.363	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
19	0.390	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
20	0.416	1 / 62	cultured astroglia vs. in vivo astrocytes

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 10	DUMEAUX_Smoking literature genes up
2	0.42	1 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	3 / 55	hsa−miR−28−3p
2	0.03	2 / 33	hsa−miR−1296
3	0.03	3 / 83	hsa−miR−582−3p
4	0.04	4 / 143	hsa−miR−24
5	0.05	1 / 6	hsa−miR−937
6	0.06	2 / 44	hsa−miR−885−3p
7	0.06	2 / 48	hsa−miR−524−3p
8	0.07	1 / 9	hsa−miR−615−3p
9	0.08	1 / 10	hsa−miR−487b
10	0.08	2 / 56	hsa−miR−384
11	0.09	2 / 57	hsa−miR−889
12	0.09	2 / 58	hsa−miR−328
13	0.09	1 / 11	hsa−miR−1180
14	0.12	2 / 68	hsa−miR−342−3p
15	0.12	2 / 69	hsa−miR−499−3p
16	0.12	1 / 15	hsa−miR−744
17	0.15	2 / 79	hsa−miR−569
18	0.15	2 / 80	hsa−miR−876−5p
19	0.16	2 / 84	hsa−miR−486−3p
20	0.17	1 / 21	hsa−miR−596

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 41	VAQUERIZAS_Placenta
2	0.18	1 / 23	VAQUERIZAS_Spinal cord
3	0.28	1 / 38	VAQUERIZAS_Whole brain
4	0.28	1 / 38	VAQUERIZAS_Testis
5	0.29	1 / 40	VAQUERIZAS_Thyroid
6	0.71	1 / 143	VAQUERIZAS_General
7	1.00	0 / 36	VAQUERIZAS_Fetal brain
8	1.00	0 / 26	VAQUERIZAS_Liver
9	1.00	0 / 33	VAQUERIZAS_Prostate
10	1.00	0 / 29	VAQUERIZAS_Smooth muscle
11	1.00	0 / 45	VAQUERIZAS_Uterus
12	1.00	0 / 9	VAQUERIZAS_Kidney
13	1.00	0 / 37	VAQUERIZAS_Thymus
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Overexpression Spots

Spot Summary: U

metagenes = 7
genes = 69

<r> metagenes = 0.97
<r> genes = 0.32
beta: r2= 0.37 / log p= −9.85

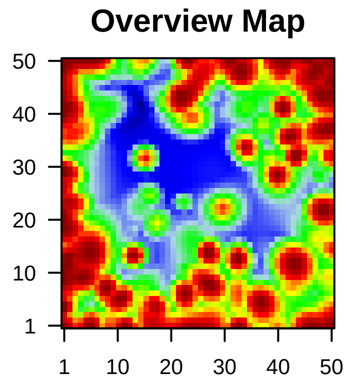
samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

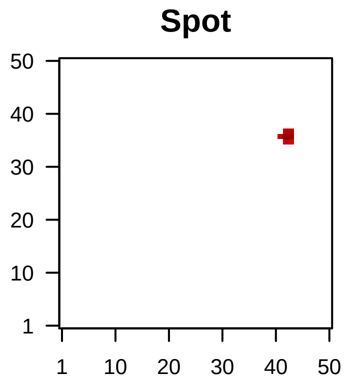
Spot Genelist

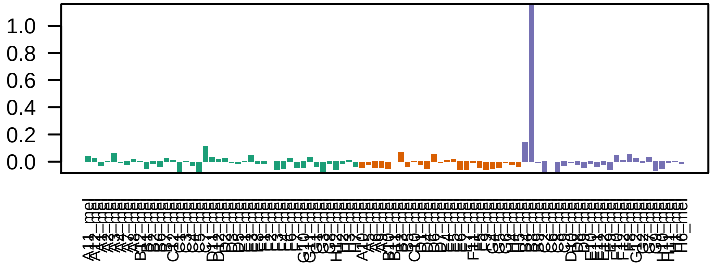
Rank	ID	max e	min e	r	Symbol	Description
1	CXCL1	2.09	−0.14	0.29	CXCL1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
2	CCDC159	1.72	−0.09	0.32	CCDC159	coiled−coil domain containing 159 [Source:HGNC Symbol;Ac
3	NR0B1	1.71	−0.04	0.67	NR0B1	nuclear receptor subfamily 0, group B, member 1 [Source:HG
4	CARD10	1.7	−0.09	0.34	CARD10	caspase recruitment domain family, member 10 [Source:HGN
5	DNAJC22	1.7	−0.09	0.44	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22 [Source:HG
6	EDC4	1.67	−0.68	0.38	EDC4	enhancer of mRNA decapping 4 [Source:HGNC Symbol;Acc:
7	SCGB1D2	1.66	−0.11	0.45	SCGB1D2	secretoglobin, family 1D, member 2 [Source:HGNC Symbol;A
8	COL4A2	1.65	−0.1	0.49	COL4A2	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:HGNC:
9	WDR66	1.6	−0.1	0.42	WDR66	WD repeat domain 66 [Source:HGNC Symbol;Acc:HGNC:28
10	GDPD1	1.57	−0.16	0.35	GDPD1	glycerophosphodiester phosphodiesterase domain containing
11	FUZ	1.55	−0.06	0.41	FUZ	fuzzy planar cell polarity protein [Source:HGNC Symbol;Acc:
12	NRG1	1.54	−0.02	0.72	NRG1	neuregulin 1 [Source:HGNC Symbol;Acc:HGNC:7997]
13	CSRNP3	1.53	−0.06	0.44	CSRNP3	cysteine−serine−rich nuclear protein 3 [Source:HGNC Symbo
14	CSRNP2	1.53	−0.15	0.42	CSRNP2	cysteine−serine−rich nuclear protein 2 [Source:HGNC Symbo
15	FAM217A	1.5	−0.13	0.4	FAM217A	family with sequence similarity 217, member A [Source:HGN
16	FBXO34	1.49	−0.46	0.33	FBXO34	F−box protein 34 [Source:HGNC Symbol;Acc:HGNC:20201]
17	TMEM184B	1.49	−0.38	0.25	TMEM184B	transmembrane protein 184B [Source:HGNC Symbol;Acc:HG
18	LSMEM1	1.47	−0.08	0.3	LSMEM1	leucine−rich single−pass membrane protein 1 [Source:HGNC
19	PIGO	1.46	−0.07	0.39	PIGO	phosphatidylinositol glycan anchor biosynthesis, class O [Sou
20	SOSTDC1	1.45	−0.02	0.63	SOSTDC1	sclerostin domain containing 1 [Source:HGNC Symbol;Acc:H

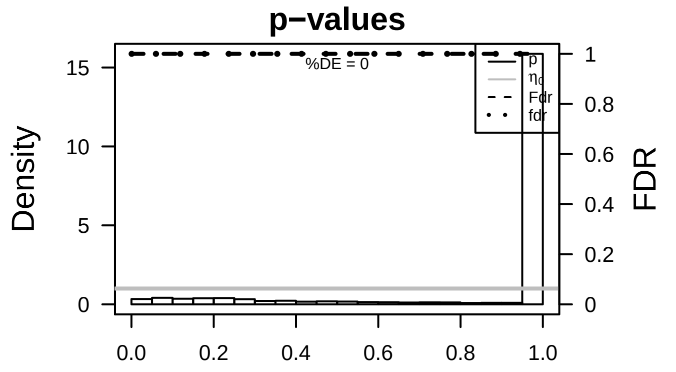
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	9 / 452	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−04	5 / 134	GSEA	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
3	9e−04	3 / 41	BP	negative regulation of phosphatase activity
4	2e−03	7 / 377	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
5	2e−03	2 / 15	BP	positive regulation of cardiac muscle cell proliferation
6	3e−03	3 / 63	MF	RNA polymerase II transcription regulatory region sequence−specific DNA
7	3e−03	6 / 310	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
8	4e−03	2 / 20	GSEA	PID_GLYPICAN_1PATHWAY
9	4e−03	8 / 558	Chr	Chr 4
10	5e−03	3 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
11	5e−03	2 / 22	CC	transport vesicle membrane
12	5e−03	3 / 74	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
13	6e−03	5 / 250	CC	microtubule
14	6e−03	2 / 26	GSEA	TERAO_AOX4_TARGETS_HG_UP
15	7e−03	4 / 162	HM	HALLMARK_COMPLEMENT
16	7e−03	2 / 28	BP	sperm motility
17	8e−03	5 / 263	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
18	9e−03	2 / 30	BP	activation of JUN kinase activity
19	1e−02	2 / 32	GSEA	OSADA_ASCL1_TARGETS_UP
20	1e−02	2 / 33	miRN	hsa−miR−615−5p
21	1e−02	6 / 401	Canc	Lembcke_Colonic Inflammation
22	1e−02	2 / 35	GSEA	LIU_TARGETS_OF_VMYB_VS_CMYB_DN
23	1e−02	3 / 104	MF	growth factor activity
24	1e−02	8 / 674	GSEA	BENPORATH_SUZ12_TARGETS
25	1e−02	2 / 37	GSEA	ZUCCHI_METASTASIS_DN
26	1e−02	2 / 39	BP	synapse assembly
27	1e−02	2 / 39	GSEA	PARENT_MTOR_SIGNALING_DN
28	1e−02	2 / 39	GSEA	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
29	1e−02	2 / 39	GSEA	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
30	1e−02	2 / 40	GSEA	CHOI_ATL_STAGE_PREDICTOR
31	1e−02	2 / 40	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_2_UP
32	1e−02	3 / 111	Canc	PanCan_RAS_geneset_nanostring
33	2e−02	2 / 41	MF	phosphatase binding
34	2e−02	2 / 41	BP	positive regulation of MAP kinase activity
35	2e−02	2 / 41	GSEA	ZHAN_V2_LATE_DIFFERENTIATION_GENES
36	2e−02	4 / 209	GSEA	KEGG_MAPK_SIGNALING_PATHWAY
37	2e−02	2 / 42	GSEA	BURTON_ADIPOGENESIS_4
38	2e−02	3 / 115	miRN	hsa−miR−515−5p
39	2e−02	4 / 214	GSEA	WANG_CISPLATIN_RESPONSE_AND_XPC_DN
40	2e−02	1 / 4	GSEA	FUJIWARA_PARK2_IN_LIVER_CANCER_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 38	TESCHENDORFF_age_hypermethylated
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	6 / 401	Lembcke_Colonic Inflammation
2	0.01	3 / 111	PanCan_RAS_geneset_nanostring
3	0.02	3 / 121	PanCan_MAPK_geneset_nanostring
4	0.16	2 / 156	PanCan_PI3K_geneset_nanostring
5	0.17	1 / 40	ZHANG_MM up
6	0.23	1 / 55	PanCan_JAK−ST_geneset_nanostring
7	0.41	1 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.43	1 / 120	PanCan_CC+Apop_geneset_nanostring
9	0.54	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.75	1 / 298	SPANG_BCL6−index2
11	0.90	1 / 489	Lembcke_Normal vs Adenoma
12	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
13	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	1.00	0 / 12	LIU_BREAST_CANCER
17	1.00	0 / 14	LIU_COMMON_CANCER_GENES
18	1.00	0 / 14	LIU_LIVER_CANCER
19	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
20	1.00	0 / 15	WANG_ER_UP

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−02	1 / 9	TCGA−CRC_agressive−disease−markers
3	7e−02	15 / 2159	TssP_Colon
4	9e−02	13 / 1889	ReprPCWk_Colon
5	1e−01	14 / 2142	ReprPC_Colon
6	1e−01	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
7	1e−01	4 / 427	Quies2_Colon
8	1e−01	5 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
9	1e−01	7 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	2e−01	16 / 2698	EnhA_Colon
11	2e−01	1 / 45	Ang_CRC−CIMPH−vs−L_hyper
12	2e−01	1 / 50	Ang_CRC_Hypermethylated
13	2e−01	7 / 1079	ZNF_Colon
14	2e−01	2 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
15	3e−01	8 / 1386	Het_Colon
16	3e−01	2 / 250	K9K27me3_Colon
17	4e−01	6 / 1038	HetRpts_Colon
18	4e−01	2 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	5e−01	4 / 739	TxEnhG2_Colon
20	5e−01	1 / 131	Marisa_CRC−cluster−a

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	5 / 134	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
2	2e−03	7 / 377	SMID_BREAST_CANCER_LUMINAL_B_DN
3	3e−03	6 / 310	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
4	4e−03	2 / 20	PID_GLYPICAN_1PATHWAY
5	5e−03	3 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
6	5e−03	3 / 74	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
7	6e−03	2 / 26	TERAO_AOX4_TARGETS_HG_UP
8	8e−03	5 / 263	IVANOVA_HEMATOPOIESIS_MATURE_CELL
9	1e−02	2 / 32	OSADA_ASCL1_TARGETS_UP
10	1e−02	2 / 35	LIU_TARGETS_OF_VMYB_VS_CMYB_DN
11	1e−02	8 / 674	BENPORATH_SUZ12_TARGETS
12	1e−02	2 / 37	ZUCCHI_METASTASIS_DN
13	1e−02	2 / 39	PARENT_MTOR_SIGNALING_DN
14	1e−02	2 / 39	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
15	1e−02	2 / 39	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
16	1e−02	2 / 40	CHOI_ATL_STAGE_PREDICTOR
17	1e−02	2 / 40	FIGUEROA_AML_METHYLATION_CLUSTER_2_UP
18	2e−02	2 / 41	ZHAN_V2_LATE_DIFFERENTIATION_GENES
19	2e−02	4 / 209	KEGG_MAPK_SIGNALING_PATHWAY
20	2e−02	2 / 42	BURTON_ADIPOGENESIS_4

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.03	23 / 3396	HOPP_Repressed
2	0.03	2 / 60	Subero_T−ALL_hyper_meth
3	0.05	1 / 10	DAVE_BL UP
4	0.06	1 / 14	Subero_MCL_hyper_meth
5	0.17	1 / 40	Subero_mBL_hyper_meth
6	0.21	13 / 2188	HOPP_Poised_promoter
7	0.27	1 / 66	TARTE_Plasma cell signature
8	0.32	1 / 81	Subero_INT_hyper_meth
9	0.33	2 / 256	SPANG_IL21 DN
10	0.34	7 / 1218	SPANG_BCR UP
11	0.36	1 / 96	Subero_DLBCL_hyper_meth
12	0.40	1 / 109	ROSOLOWSKI_green total
13	0.41	13 / 2563	HOPP_Heterochrom
14	0.45	1 / 129	DAVE_BL−vs−DLBCL
15	0.57	2 / 410	SPANG_CD40 6hrs DN
16	0.59	10 / 2211	HOPP_Repetitive
17	0.69	1 / 247	ZHANG_DLBCL mutated
18	0.73	1 / 275	TARTE_Mature plasma cell signature
19	0.73	1 / 280	SPANG_CD40 6hrs UP
20	0.90	3 / 1128	SPANG_BCR DN

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 13	GUSTAFSON_PI3K_DN
2	1.00	0 / 12	GUSTAFSON_PI3K_UP
3	1.00	0 / 14	BENTINK_e2f3.1
4	1.00	0 / 12	BENTINK_e2f3.2
5	1.00	0 / 13	BENTINK_myc.1
6	1.00	0 / 12	BENTINK_ras.1
7	1.00	0 / 9	BENTINK_ras.4
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	4 / 350	WIRTH_Nervous System
2	0.19	1 / 46	WIRTH_Liver
3	0.39	1 / 107	WIRTH_Testis
4	0.49	2 / 350	WIRTH_Immune system
5	0.60	1 / 194	PALMER_B−Cell signature up
6	1.00	0 / 32	WIRTH_Pancreas
7	1.00	0 / 11	WIRTH_Sec. lymphoid organs
8	1.00	0 / 11	WIRTH_Prim. lymphoid organs
9	1.00	0 / 13	WIRTH_B−cells
10	1.00	0 / 8	WIRTH_Tonsil
11	1.00	0 / 12	WIRTH_Thymus
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 11	WIRTH_Globus pallidus
15	1.00	0 / 14	WIRTH_Telencephalon
16	1.00	0 / 11	WIRTH_Cortex cerebri
17	1.00	0 / 10	WIRTH_Hippocampus
18	1.00	0 / 10	WIRTH_Thalamus
19	1.00	0 / 12	WIRTH_Cerebellum
20	1.00	0 / 41	WIRTH_Homeostasis

BP

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 41	negative regulation of phosphatase activity
2	2e−03	2 / 15	positive regulation of cardiac muscle cell proliferation
3	7e−03	2 / 28	sperm motility
4	9e−03	2 / 30	activation of JUN kinase activity
5	1e−02	2 / 39	synapse assembly
6	2e−02	2 / 41	positive regulation of MAP kinase activity
7	2e−02	2 / 52	positive regulation of protein kinase activity
8	3e−02	2 / 53	phosphatidylinositol biosynthetic process
9	3e−02	2 / 60	positive regulation of protein kinase B signaling
10	4e−02	4 / 272	embryo development
11	4e−02	7 / 694	protein complex assembly
12	5e−02	2 / 73	chemotaxis
13	5e−02	1 / 10	activation of transmembrane receptor protein tyrosine kinase activity
14	5e−02	1 / 10	cerebral cortex neuron differentiation
15	5e−02	1 / 10	establishment of planar polarity
16	5e−02	1 / 10	Leydig cell differentiation
17	5e−02	1 / 10	negative regulation of cardiac muscle cell apoptotic process
18	5e−02	1 / 10	neural crest cell development
19	5e−02	2 / 74	wound healing
20	5e−02	1 / 11	glycerol metabolic process

CC

Rank	p−value	#in/all	Geneset
1	0.005	2 / 22	transport vesicle membrane
2	0.006	5 / 250	microtubule
3	0.020	2 / 47	phagocytic vesicle membrane
4	0.046	1 / 10	endoplasmic reticulum chaperone complex
5	0.046	1 / 10	high−density lipoprotein particle
6	0.046	1 / 10	sperm flagellum
7	0.048	2 / 75	blood microparticle
8	0.049	3 / 177	synapse
9	0.050	1 / 11	phosphatidylinositol 3−kinase complex
10	0.059	1 / 13	pseudopodium
11	0.059	1 / 13	sperm principal piece
12	0.068	7 / 775	extracellular space
13	0.076	5 / 487	intracellular membrane−bounded organelle
14	0.089	1 / 20	dynein complex
15	0.093	1 / 21	secretory granule membrane
16	0.093	1 / 21	synaptonemal complex
17	0.093	1 / 21	transcription elongation factor complex
18	0.097	1 / 22	presynaptic active zone
19	0.118	1 / 27	photoreceptor inner segment
20	0.131	1 / 30	endoplasmic reticulum−Golgi intermediate compartment membrane

Disease

Rank	p−value	#in/all	Geneset
1	0.3	3 / 435	GUDJ_psoriasis up
2	0.7	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	0.007	4 / 162	HALLMARK_COMPLEMENT
2	0.027	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
3	0.032	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	0.043	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	0.047	3 / 174	HALLMARK_HEME_METABOLISM
6	0.072	2 / 95	HALLMARK_SPERMATOGENESIS
7	0.116	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
8	0.151	2 / 148	HALLMARK_KRAS_SIGNALING_UP
9	0.179	2 / 165	HALLMARK_MYOGENESIS
10	0.206	2 / 181	HALLMARK_P53_PATHWAY
11	0.346	1 / 91	HALLMARK_PROTEIN_SECRETION
12	0.352	1 / 93	HALLMARK_PEROXISOME
13	0.399	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.543	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
15	0.564	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
16	0.586	1 / 188	HALLMARK_MYC_TARGETS_V1
17	0.599	1 / 195	HALLMARK_MITOTIC_SPINDLE
18	1.000	0 / 176	HALLMARK_HYPOXIA
19	1.000	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	1.000	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 63	RNA polymerase II transcription regulatory region sequence−specific DNA bir
2	0.013	3 / 104	growth factor activity
3	0.016	2 / 41	phosphatase binding
4	0.032	7 / 657	enzyme regulator activity
5	0.050	2 / 77	cytokine activity
6	0.050	1 / 11	small GTPase binding
7	0.050	1 / 11	substrate−specific transmembrane transporter activity
8	0.054	1 / 12	nitric−oxide synthase binding
9	0.055	2 / 81	protein N−terminus binding
10	0.059	2 / 85	transmembrane signaling receptor activity
11	0.062	2 / 87	unfolded protein binding
12	0.068	1 / 15	dioxygenase activity
13	0.068	1 / 15	mitogen−activated protein kinase kinase binding
14	0.076	1 / 17	chemoattractant activity
15	0.076	1 / 17	receptor signaling complex scaffold activity
16	0.076	1 / 17	RNA polymerase II core binding
17	0.076	1 / 17	sulfuric ester hydrolase activity
18	0.080	1 / 18	mitogen−activated protein kinase kinase kinase binding
19	0.080	1 / 18	palmitoyltransferase activity
20	0.085	1 / 19	protein kinase activator activity

TF

Rank	p−value	#in/all	Geneset
1	0.2	13 / 2137	ICGC_SmV0416101_targets
2	0.2	16 / 2836	ICGC_BatfPcr1_targets
3	0.2	8 / 1273	ICGC_P300_targets
4	0.3	11 / 1878	ICGC_Cebpbsc150_targets
5	0.3	4 / 553	ICGC_RxraPcr1_targets
6	0.3	10 / 1701	HEBENSTREIT_high expression TF
7	0.3	16 / 2927	ICGC_Rad21_targets
8	0.3	21 / 4032	ICGC_Creb1_targets
9	0.3	8 / 1383	ICGC_Six5_targets
10	0.4	26 / 5200	ICGC_Mta3_targets
11	0.4	26 / 5219	ICGC_Tcf3_targets
12	0.4	22 / 4385	ICGC_Atf2_targets
13	0.4	4 / 690	ICGC_Atf3_targets
14	0.4	24 / 4879	ICGC_Pmlsc71910_targets
15	0.4	23 / 4706	ICGC_Sp1_targets
16	0.4	26 / 5355	ICGC_Pol2_targets
17	0.5	18 / 3700	ICGC_Nfatc1_targets
18	0.5	23 / 4774	ICGC_Foxm1_targets
19	0.5	28 / 5890	ICGC_Elf1_targets
20	0.5	21 / 4414	ICGC_Bclaf101388_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	20 / 3682	LU_BPDE 0.005 DN
2	0.9	3 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	0.02	12 / 1333	Fetal_ReprPCWk
2	0.05	8 / 862	Overlap_fetal_midbrain_TxTrans
3	0.05	6 / 574	Overlap_fetal_midbrain_TssP
4	0.08	6 / 656	Overlap_fetal_midbrain_EnhP
5	0.09	3 / 229	Mid_Frontal_Lobe_TxTrans
6	0.10	6 / 686	Overlap_fetal_midbrain_TssA
7	0.11	9 / 1207	Overlap_fetal_midbrain_TssF
8	0.13	18 / 2972	Mid_Frontal_Lobe_ReprPC
9	0.14	12 / 1845	Fetal_Quies
10	0.17	4 / 468	Mid_Frontal_Lobe_TssF
11	0.17	7 / 989	Mid_Frontal_Lobe_Quies
12	0.18	6 / 812	Mid_Frontal_Lobe_TssP
13	0.24	4 / 534	Mid_Frontal_Lobe_EnhG
14	0.28	1 / 69	Overlap_fetal_midbrain_Tx
15	0.28	6 / 953	Fetal_Enh
16	0.31	12 / 2185	Fetal_TssA
17	0.37	6 / 1065	Overlap_fetal_midbrain_Enh
18	0.39	5 / 884	Overlap_fetal_midbrain_EnhG
19	0.50	4 / 786	Fetal_EnhG
20	0.52	1 / 156	Mid_Frontal_Lobe_TssA

Chr

Rank	p−value	#in/all	Geneset
1	0.004	8 / 558	Chr 4
2	0.031	7 / 649	Chr 16
3	0.089	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
4	0.150	6 / 775	Chr 12
5	0.204	3 / 335	Chr 22
6	0.216	5 / 689	Chr 7
7	0.397	4 / 687	Chr 6
8	0.515	4 / 801	Chr 11
9	0.533	5 / 1037	Chr 19
10	0.556	2 / 398	Chr 20
11	0.638	2 / 462	Chr 14
12	0.708	1 / 262	Chr 13
13	0.732	2 / 551	Chr X
14	0.732	2 / 552	Chr 10
15	0.757	3 / 840	Chr 17
16	0.841	2 / 696	Chr 5
17	0.849	3 / 993	Chr 2
18	0.889	1 / 465	Chr 15
19	0.891	1 / 469	Chr 8
20	0.907	2 / 838	Chr 3

Glio

Rank	p−value	#in/all	Geneset
1	0.03	1 / 7	KIM amplified & overexpressed in LTS
2	0.03	1 / 7	Phillips MES up vs Prolif & PN
3	0.04	1 / 8	VERHAAK_PN_Brain
4	0.04	1 / 9	Phillips PN up vs MES & Prolif
5	0.05	1 / 11	Mukasa_UP_in_Astroglioma
6	0.05	3 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
7	0.06	1 / 14	VERHAAK_PN subtype
8	0.09	4 / 365	Down_b
9	0.10	1 / 22	KIM prognostic signature LTS vs. STS
10	0.10	1 / 23	WIRTH_PN subtype
11	0.12	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
12	0.14	1 / 32	Donson−innate immunity−associated with LTS in HGA
13	0.20	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
14	0.23	3 / 356	Down_a
15	0.25	1 / 62	cultured astroglia vs. in vivo astrocytes
16	0.28	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP
17	0.28	1 / 71	Weller_LGG_A_vs_O_UP
18	0.28	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
19	0.30	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
20	0.30	1 / 75	Weller_LGG_A_vs_O_DOWN

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	2 / 33	hsa−miR−615−5p
2	0.02	3 / 115	hsa−miR−515−5p
3	0.03	2 / 63	hsa−miR−637
4	0.04	2 / 65	hsa−miR−550
5	0.08	2 / 104	hsa−miR−210
6	0.09	2 / 105	hsa−miR−1271
7	0.09	2 / 107	hsa−miR−33b
8	0.10	4 / 386	hsa−let−7c
9	0.11	2 / 124	hsa−miR−223
10	0.13	1 / 31	hsa−miR−342−5p
11	0.13	1 / 31	hsa−miR−558
12	0.14	4 / 428	hsa−let−7b
13	0.14	1 / 32	hsa−miR−1178
14	0.14	2 / 144	hsa−miR−548f
15	0.15	2 / 150	hsa−miR−338−3p
16	0.16	1 / 37	hsa−miR−760
17	0.16	1 / 38	hsa−miR−490−5p
18	0.16	1 / 38	hsa−miR−484
19	0.17	2 / 162	hsa−miR−96
20	0.18	1 / 42	hsa−miR−769−3p

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 143	VAQUERIZAS_General
2	0.2	1 / 38	VAQUERIZAS_Testis
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 26	VAQUERIZAS_Liver
6	1.0	0 / 33	VAQUERIZAS_Prostate
7	1.0	0 / 29	VAQUERIZAS_Smooth muscle
8	1.0	0 / 45	VAQUERIZAS_Uterus
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 59	VAQUERIZAS_Whole blood
15	1.0	0 / 7	VAQUERIZAS_Appendix
16	1.0	0 / 29	VAQUERIZAS_Fetal lung
17	1.0	0 / 58	VAQUERIZAS_Lung
18	1.0	0 / 16	VAQUERIZAS_Pancreas
19	1.0	0 / 23	VAQUERIZAS_Trachea
20	1.0	0 / 11	VAQUERIZAS_Fetal liver

Overexpression Spots

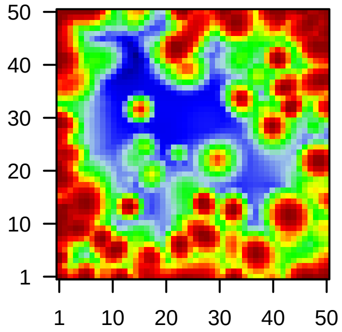
Spot Summary: V

metagenes = 5
genes = 72

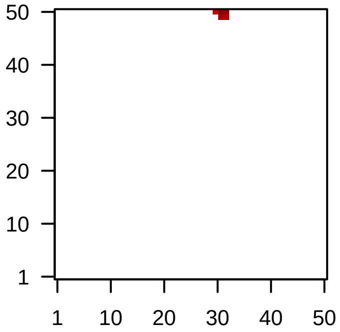
<r> metagenes = 0.98
<r> genes = 0.1
beta: r2= 1.32 / log p= −Inf

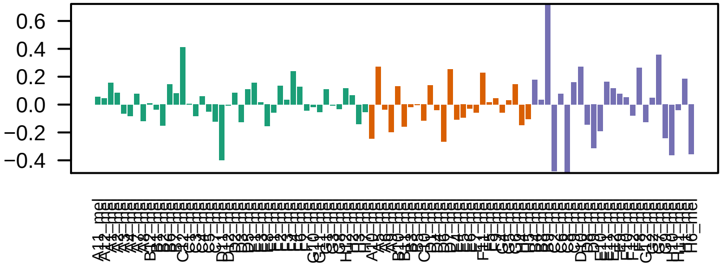
samples with spot = 10 (10.9 %)
MSC1 : 2 (4.8 %)
MSC2 : 3 (12 %)
MSC3 : 5 (20 %)

Overview Map



Spot





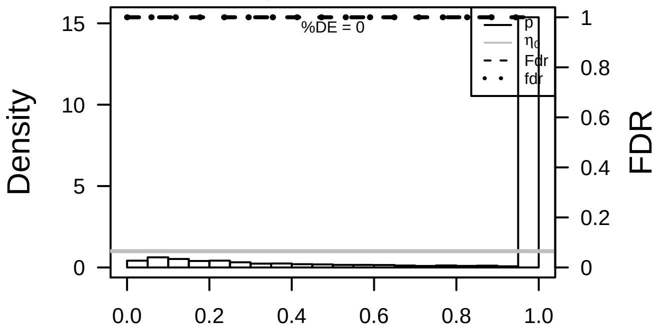
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TYK2	2.19	−0.38	0.23	TYK2	tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:12440]
2	BAAT	1.99	−0.45	0.28	BAAT	bile acid CoA:amino acid N−acyltransferase [Source:HGNC S
3	PLCG1	1.83	−0.72	0.36	PLCG1	phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
4	PCK2	1.77	−0.36	0.39	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial) [Sourc
5	TRIM68	1.72	−0.24	0.3	TRIM68	tripartite motif containing 68 [Source:HGNC Symbol;Acc:HGN
6	DMWD	1.7	−0.24	0.22	DMWD	dystrophia myotonica, WD repeat containing [Source:HGNC
7	DAK	1.69	−0.31	0.33	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae) [Source:
8	POLR3F	1.67	−0.67	0.28	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa [
9	POLI	1.67	−0.5	0.34	POLI	polymerase (DNA directed) iota [Source:HGNC Symbol;Acc:
10	MTRF1	1.66	−0.48	0.25	MTRF1	mitochondrial translational release factor 1 [Source:HGNC Sy
11	COG3	1.64	−0.54	0.39	COG3	component of oligomeric golgi complex 3 [Source:HGNC Syn
12	APPL2	1.58	−0.55	0.35	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and
13	ZNF561	1.55	−0.49	0.27	ZNF561	zinc finger protein 561 [Source:HGNC Symbol;Acc:HGNC:28
14	ZNF613	1.51	−0.13	0.31	ZNF613	zinc finger protein 613 [Source:HGNC Symbol;Acc:HGNC:25
15	DPY19L3	1.46	−0.45	0.33	DPY19L3	dpy−19−like 3 (C. elegans) [Source:HGNC Symbol;Acc:HGN
16	FKTN	1.46	−0.71	0.26	FKTN	fukutin [Source:HGNC Symbol;Acc:HGNC:3622]
17	ZNF343	1.39	−0.25	0.27	ZNF343	zinc finger protein 343 [Source:HGNC Symbol;Acc:HGNC:16
18	CREB1	1.39	−1.12	0.24	CREB1	cAMP responsive element binding protein 1 [Source:HGNC S
19	CD9	1.38	−1.01	0.32	CD9	CD9 molecule [Source:HGNC Symbol;Acc:HGNC:1709]
20	XPO5	1.37	−1.25	0.21	XPO5	exportin 5 [Source:HGNC Symbol;Acc:HGNC:17675]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−08	65 / 9027	Colon	Tx_Colon
2	2e−07	62 / 8580	Colon	TxWk_Colon
3	4e−06	48 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
4	6e−06	63 / 9482	Colon	TssA_Colon
5	3e−05	60 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
6	4e−05	42 / 5184	Lympl	HOPP_Txn_transition
7	3e−04	5 / 120	GSEA	KARLSSON_TGFB1_TARGETS_UP
8	5e−04	48 / 6929	Lympl	HOPP_Txn_elongation
9	7e−04	3 / 36	MF	tRNA binding
10	7e−04	5 / 147	BP	tRNA metabolic process
11	8e−04	2 / 9	GSEA	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
12	9e−04	58 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
13	9e−04	6 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
14	1e−03	7 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
15	1e−03	4 / 92	miRN	hsa−miR−425
16	1e−03	14 / 1149	MF	enzyme binding
17	1e−03	3 / 45	GSEA	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN
18	1e−03	9 / 552	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
19	2e−03	5 / 185	GSEA	WELCSH_BRCA1_TARGETS_UP
20	2e−03	2 / 15	GSEA	BIOCARTA_ERK5_PATHWAY
21	3e−03	3 / 58	BP	ER to Golgi vesicle−mediated transport
22	3e−03	9 / 615	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
23	3e−03	2 / 17	MF	RNA polymerase II core binding
24	3e−03	3 / 60	GSEA	SESTO_RESPONSE_TO_UV_C7
25	4e−03	3 / 67	GSEA	RADMACHER_AML_PROGNOSIS
26	4e−03	22 / 2577	CC	nucleoplasm
27	5e−03	39 / 5696	CC	nucleus
28	5e−03	52 / 8415	Colon	Quies3_Colon
29	5e−03	4 / 143	GSEA	VANTVEER_BREAST_CANCER_ESR1_UP
30	5e−03	3 / 73	GSEA	TOOKER_GEMCITABINE_RESISTANCE_UP
31	5e−03	14 / 1365	MF	RNA binding
32	5e−03	2 / 23	MF	rRNA binding
33	6e−03	2 / 24	MF	histone acetyltransferase binding
34	6e−03	5 / 239	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_DN
35	6e−03	61 / 10605	CC	intracellular
36	7e−03	3 / 79	GSEA	MORI_SMALL_PRE_BII_LYMPHOCYTE_UP
37	7e−03	2 / 26	GSEA	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS
38	7e−03	4 / 159	GSEA	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN
39	8e−03	2 / 27	GSEA	REACTOME_DAG_AND_IP3_SIGNALING
40	8e−03	2 / 28	BP	positive regulation of multicellular organism growth

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−04	5 / 147	tRNA metabolic process
2	3e−03	3 / 58	ER to Golgi vesicle−mediated transport
3	8e−03	2 / 28	positive regulation of multicellular organism growth
4	1e−02	3 / 91	protein stabilization
5	1e−02	2 / 37	transcription from RNA polymerase III promoter
6	2e−02	6 / 422	viral process
7	2e−02	8 / 687	gene expression
8	2e−02	2 / 43	cellular response to growth factor stimulus
9	2e−02	7 / 570	symbiosis, encompassing mutualism through parasitism
10	2e−02	2 / 48	activation of phospholipase C activity
11	3e−02	3 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
12	3e−02	2 / 56	stem cell maintenance
13	3e−02	6 / 491	innate immune response
14	4e−02	4 / 255	cellular amino acid metabolic process
15	4e−02	2 / 65	Fc−gamma receptor signaling pathway involved in phagocytosis
16	4e−02	3 / 162	ribosome biogenesis
17	5e−02	4 / 277	translation
18	5e−02	1 / 10	biomineral tissue development
19	5e−02	1 / 10	negative regulation of transcription by competitive promoter binding
20	5e−02	1 / 10	paraxial mesoderm development

Brain

Rank	p−value	#in/all	Geneset
1	4e−06	48 / 5940	Overlap_fetal_midbrain_HetRpts
2	3e−05	60 / 9013	Overlap_fetal_midbrain_K9K27me3
3	9e−04	58 / 9330	Overlap_fetal_midbrain_ReprPC
4	2e−02	55 / 9528	Overlap_fetal_midbrain_Quies
5	3e−02	12 / 1333	Fetal_ReprPCWk
6	6e−02	21 / 3081	Mid_Frontal_Lobe_ZNF
7	2e−01	6 / 769	Overlap_fetal_midbrain_ZNF
8	2e−01	6 / 831	Fetal_HetRpts
9	3e−01	46 / 9020	Overlap_fetal_midbrain_ReprPCWk
10	5e−01	6 / 1122	Fetal_K9K27me3
11	5e−01	4 / 765	Mid_Frontal_Lobe_Het
12	5e−01	3 / 564	Mid_Frontal_Lobe_EnhP
13	6e−01	3 / 656	Overlap_fetal_midbrain_EnhP
14	7e−01	5 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	7e−01	2 / 534	Mid_Frontal_Lobe_EnhG
16	7e−01	3 / 786	Fetal_EnhG
17	8e−01	1 / 304	Fetal_Het
18	8e−01	1 / 349	Fetal_ZNF
19	8e−01	2 / 668	Mid_Frontal_Lobe_Enh
20	8e−01	1 / 383	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	WANG_ER_DN
2	0.05	1 / 10	GENTLES_modul5
3	0.06	4 / 298	SPANG_BCL6−index2
4	0.07	1 / 14	LIU_LIVER_CANCER
5	0.07	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.07	1 / 15	GENTLES_modul1
7	0.07	1 / 15	GENTLES_modul4
8	0.07	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	0.07	1 / 16	GENTLES_modul6
10	0.13	1 / 29	KUIPER_MM good survival
11	0.29	1 / 70	SHAUGHNESSY_MM high risk
12	0.33	0 / 12	LIU_PROSTATE_CANCER_UP
13	0.42	3 / 489	Lembcke_Normal vs Adenoma
14	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
15	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
16	1.00	0 / 12	LIU_BREAST_CANCER
17	1.00	0 / 14	LIU_COMMON_CANCER_GENES
18	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
19	1.00	0 / 15	WANG_ER_UP
20	1.00	0 / 16	WOLFER_overlap genes

CC

Rank	p−value	#in/all	Geneset
1	0.004	22 / 2577	nucleoplasm
2	0.005	39 / 5696	nucleus
3	0.006	61 / 10605	intracellular
4	0.009	58 / 9988	organelle
5	0.015	2 / 38	cis−Golgi network
6	0.034	69 / 13191	cellular_component
7	0.047	1 / 10	nuclear exosome (RNase complex)
8	0.050	3 / 170	nuclear speck
9	0.053	2 / 76	cell projection
10	0.057	1 / 12	Golgi transport complex
11	0.057	1 / 12	holo TFIIH complex
12	0.066	1 / 14	ER to Golgi transport vesicle
13	0.066	1 / 14	exosome (RNase complex)
14	0.070	7 / 747	nucleolus
15	0.070	1 / 15	eukaryotic 43S preinitiation complex
16	0.070	1 / 15	eukaryotic 48S preinitiation complex
17	0.070	1 / 15	integral component of mitochondrial inner membrane
18	0.075	1 / 16	eukaryotic translation initiation factor 3 complex
19	0.075	1 / 16	lamellipodium membrane
20	0.079	1 / 17	transcriptionally active chromatin

Chr

Rank	p−value	#in/all	Geneset
1	0.03	10 / 1037	Chr 19
2	0.04	4 / 262	Chr 13
3	0.04	5 / 398	Chr 20
4	0.05	7 / 687	Chr 6
5	0.08	7 / 775	Chr 12
6	0.25	5 / 696	Chr 5
7	0.29	2 / 221	Chr 18
8	0.39	3 / 462	Chr 14
9	0.43	4 / 689	Chr 7
10	0.53	3 / 576	Chr 9
11	0.75	3 / 801	Chr 11
12	0.76	2 / 558	Chr 4
13	0.81	1 / 335	Chr 22
14	0.83	2 / 649	Chr 16
15	0.87	5 / 1500	Chr 1
16	0.87	3 / 993	Chr 2
17	0.90	1 / 465	Chr 15
18	0.90	1 / 469	Chr 8
19	0.92	2 / 840	Chr 17
20	0.94	1 / 552	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−08	65 / 9027	Tx_Colon
2	2e−07	62 / 8580	TxWk_Colon
3	6e−06	63 / 9482	TssA_Colon
4	5e−03	52 / 8415	Quies3_Colon
5	4e−02	1 / 8	KIM_CRC−MSI−regulated_DN
6	5e−02	19 / 2698	EnhA_Colon
7	6e−02	32 / 5155	EnhWk1_Colon
8	8e−02	35 / 5880	TssD2_Colon
9	1e−01	18 / 2798	TxEnhG1_Colon
10	1e−01	40 / 7203	TssF_Colon
11	2e−01	7 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
12	2e−01	5 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	3e−01	50 / 9653	Enh_Colon
14	3e−01	7 / 1079	ZNF_Colon
15	3e−01	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
16	3e−01	1 / 71	Marisa_CRC−cluster−g
17	3e−01	5 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
18	4e−01	20 / 3812	TssD1_Colon
19	4e−01	51 / 10290	TssWk_Colon
20	5e−01	4 / 739	TxEnhG2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.6	2 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	2 / 47	Vishal_subnetwork signature of survival in GBM
2	0.02	5 / 332	Up
3	0.03	1 / 7	KIM amplified & overexpressed in LTS
4	0.05	8 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.07	1 / 15	VERHAAK_CL subtype
6	0.10	1 / 22	KIM prognostic signature LTS vs. STS
7	0.12	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	0.16	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
9	0.24	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
10	0.26	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	0.27	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
12	0.29	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
13	0.29	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
14	0.30	1 / 72	laffaire_hypermeth_LGG_vs_control
15	0.38	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
16	0.39	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
17	0.39	1 / 103	GIEZELT_GBM_WT_up_VS_mut
18	0.44	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
19	0.45	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
20	0.53	2 / 365	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	5 / 120	KARLSSON_TGFB1_TARGETS_UP
2	8e−04	2 / 9	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
3	9e−04	6 / 233	PENG_RAPAMYCIN_RESPONSE_DN
4	1e−03	7 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
5	1e−03	3 / 45	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN
6	1e−03	9 / 552	HAMAI_APOPTOSIS_VIA_TRAIL_UP
7	2e−03	5 / 185	WELCSH_BRCA1_TARGETS_UP
8	2e−03	2 / 15	BIOCARTA_ERK5_PATHWAY
9	3e−03	9 / 615	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
10	3e−03	3 / 60	SESTO_RESPONSE_TO_UV_C7
11	4e−03	3 / 67	RADMACHER_AML_PROGNOSIS
12	5e−03	4 / 143	VANTVEER_BREAST_CANCER_ESR1_UP
13	5e−03	3 / 73	TOOKER_GEMCITABINE_RESISTANCE_UP
14	6e−03	5 / 239	HOLLMANN_APOPTOSIS_VIA_CD40_DN
15	7e−03	3 / 79	MORI_SMALL_PRE_BII_LYMPHOCYTE_UP
16	7e−03	2 / 26	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_I
17	7e−03	4 / 159	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN
18	8e−03	2 / 27	REACTOME_DAG_AND_IP3_SIGNALING
19	8e−03	2 / 28	LANG_MYB_FAMILY_TARGETS
20	8e−03	4 / 164	GOLDRATH_HOMEOSTATIC_PROLIFERATION

HM

Rank	p−value	#in/all	Geneset
1	0.009	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
2	0.034	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	0.050	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
4	0.070	3 / 196	HALLMARK_MTORC1_SIGNALING
5	0.149	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
6	0.194	2 / 167	HALLMARK_APICAL_JUNCTION
7	0.232	2 / 188	HALLMARK_MYC_TARGETS_V1
8	0.242	1 / 57	HALLMARK_MYC_TARGETS_V2
9	0.249	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.365	1 / 93	HALLMARK_PEROXISOME
11	0.374	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.407	1 / 107	HALLMARK_COAGULATION
13	0.459	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
14	0.488	1 / 137	HALLMARK_UV_RESPONSE_DN
15	0.562	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
16	0.565	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
17	0.591	1 / 183	HALLMARK_GLYCOLYSIS
18	0.601	1 / 188	HALLMARK_ADIPOGENESIS
19	1.000	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	1.000	0 / 176	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	1 / 10	DUMEAUX_Smoking literature genes up
2	1.00	0 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−05	42 / 5184	HOPP_Txn_transition
2	5e−04	48 / 6929	HOPP_Txn_elongation
3	3e−02	45 / 7592	HOPP_Active_promoter
4	4e−02	1 / 8	MASCQUE_ABC UP
5	4e−02	10 / 1128	SPANG_BCR DN
6	5e−02	4 / 294	TARTE_Plasmablast signature
7	7e−02	1 / 16	ROSOLOWSKI_red UP
8	1e−01	3 / 247	ZHANG_DLBCL mutated
9	1e−01	4 / 410	SPANG_CD40 6hrs DN
10	2e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
11	2e−01	36 / 6564	HOPP_Strong_enhancer
12	2e−01	1 / 50	SPANG_BAFF 9hrs DN
13	3e−01	1 / 66	TARTE_Plasma cell signature
14	3e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
15	3e−01	1 / 82	ROSOLOWSKI_green UP
16	3e−01	1 / 86	ROSOLOWSKI_red total
17	4e−01	2 / 256	SPANG_IL21 DN
18	4e−01	37 / 7209	HOPP_Weak_promoter
19	4e−01	2 / 275	TARTE_Mature plasma cell signature
20	4e−01	1 / 109	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 36	tRNA binding
2	1e−03	14 / 1149	enzyme binding
3	3e−03	2 / 17	RNA polymerase II core binding
4	5e−03	14 / 1365	RNA binding
5	5e−03	2 / 23	rRNA binding
6	6e−03	2 / 24	histone acetyltransferase binding
7	9e−03	11 / 1007	poly(A) RNA binding
8	3e−02	52 / 8984	protein binding
9	3e−02	3 / 136	lyase activity
10	5e−02	1 / 11	cAMP response element binding
11	5e−02	1 / 11	methyl−CpG binding
12	5e−02	1 / 11	phospholipase C activity
13	6e−02	2 / 79	protein transporter activity
14	6e−02	1 / 13	mannosyltransferase activity
15	6e−02	1 / 13	pseudouridine synthase activity
16	6e−02	2 / 83	translation factor activity, RNA binding
17	7e−02	2 / 86	ubiquitin−like protein binding
18	7e−02	1 / 14	RNA polymerase II transcription factor binding transcription factor activity invo
19	7e−02	1 / 15	amino acid binding
20	7e−02	1 / 16	RNA polymerase II carboxy−terminal domain kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	4 / 92	hsa−miR−425
2	0.014	3 / 103	hsa−miR−653
3	0.043	3 / 161	hsa−miR−802
4	0.045	3 / 164	hsa−miR−323b−5p
5	0.050	3 / 170	hsa−miR−183
6	0.051	2 / 75	hsa−miR−509−5p
7	0.053	2 / 76	hsa−miR−509−3−5p
8	0.057	1 / 12	hsa−miR−369−5p
9	0.061	2 / 83	hsa−miR−582−3p
10	0.114	2 / 119	hsa−miR−217
11	0.115	1 / 25	hsa−miR−1273
12	0.117	2 / 121	hsa−miR−543
13	0.123	1 / 27	hsa−miR−521
14	0.138	2 / 134	hsa−miR−488
15	0.140	1 / 31	hsa−miR−342−5p
16	0.141	2 / 136	hsa−miR−155
17	0.148	1 / 33	hsa−miR−1296
18	0.157	1 / 35	hsa−miR−1287
19	0.161	1 / 36	hsa−miR−518e
20	0.165	1 / 37	hsa−miR−1274a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 12	BENTINK_e2f3.2
2	0.06	1 / 12	BENTINK_ras.1
3	0.06	1 / 13	BENTINK_myc.1
4	1.00	0 / 12	GUSTAFSON_PI3K_UP
5	1.00	0 / 13	GUSTAFSON_PI3K_DN
6	1.00	0 / 14	BENTINK_e2f3.1
7	1.00	0 / 9	BENTINK_ras.4
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.07	17 / 2416	ICGC_Bcl3_targets
2	0.12	12 / 1701	HEBENSTREIT_high expression TF
3	0.14	26 / 4385	ICGC_Atf2_targets
4	0.17	22 / 3700	ICGC_Nfatc1_targets
5	0.17	27 / 4689	ICGC_Taf1_targets
6	0.21	8 / 1171	KIM_MYC targets
7	0.23	13 / 2136	ICGC_GabpPcr2_targets
8	0.23	13 / 2137	ICGC_SrfV0416101_targets
9	0.24	9 / 1400	ICGC_Myc_targets
10	0.24	27 / 4879	ICGC_Pmlsc71910_targets
11	0.25	27 / 4909	ICGC_Stat5_targets
12	0.26	14 / 2391	ICGC_Pbx3_targets
13	0.27	8 / 1266	ICGC_NrsfPcr1_targets
14	0.29	16 / 2836	ICGC_BatfPcr1_targets
15	0.30	26 / 4829	ICGC_Nficsc81335_targets
16	0.30	22 / 4032	ICGC_Creb1_targets
17	0.36	25 / 4774	ICGC_Foxm1_targets
18	0.37	27 / 5200	ICGC_Mta3_targets
19	0.37	28 / 5408	ICGC_Pou2_targets
20	0.39	4 / 653	ICGC_SrfPcr2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	1 / 7	VAQUERIZAS_Appendix
2	0.17	1 / 38	VAQUERIZAS_Testis
3	0.25	1 / 59	VAQUERIZAS_Whole blood
4	0.50	1 / 143	VAQUERIZAS_General
5	1.00	0 / 36	VAQUERIZAS_Fetal brain
6	1.00	0 / 41	VAQUERIZAS_Placenta
7	1.00	0 / 26	VAQUERIZAS_Liver
8	1.00	0 / 33	VAQUERIZAS_Prostate
9	1.00	0 / 29	VAQUERIZAS_Smooth muscle
10	1.00	0 / 45	VAQUERIZAS_Uterus
11	1.00	0 / 9	VAQUERIZAS_Kidney
12	1.00	0 / 23	VAQUERIZAS_Spinal cord
13	1.00	0 / 38	VAQUERIZAS_Whole brain
14	1.00	0 / 37	VAQUERIZAS_Thymus
15	1.00	0 / 40	VAQUERIZAS_Thyroid
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.09	4 / 350	WIRTH_Immune system
2	0.61	1 / 194	PALMER_B−Cell signature up
3	0.67	1 / 225	PALMER_Granulocytes signature up
4	1.00	0 / 32	WIRTH_Pancreas
5	1.00	0 / 11	WIRTH_Sec. lymphoid organs
6	1.00	0 / 11	WIRTH_Prim. lymphoid organs
7	1.00	0 / 13	WIRTH_B−cells
8	1.00	0 / 8	WIRTH_Tonsil
9	1.00	0 / 12	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 5	WIRTH_Bone marrow
12	1.00	0 / 350	WIRTH_Nervous System
13	1.00	0 / 11	WIRTH_Globus pallidus
14	1.00	0 / 14	WIRTH_Telencephalon
15	1.00	0 / 11	WIRTH_Cortex cerebri
16	1.00	0 / 10	WIRTH_Hippocampus
17	1.00	0 / 10	WIRTH_Thalamus
18	1.00	0 / 12	WIRTH_Cerebellum
19	1.00	0 / 107	WIRTH_Testis
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	16 / 3682	LU_BPDE 0.005 DN
2	1.0	2 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

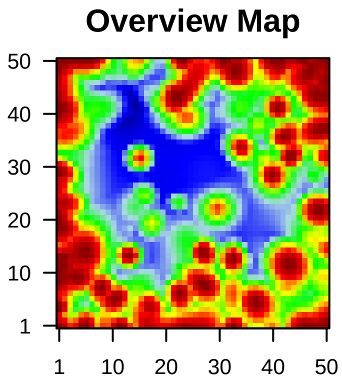
Spot Summary: W

metagenes = 10
genes = 166

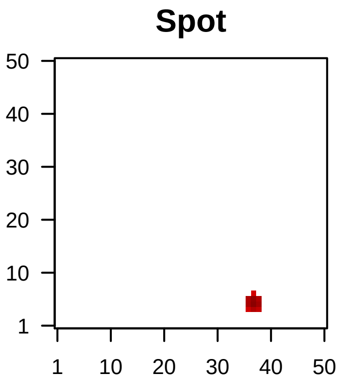
<r> metagenes = 0.98
<r> genes = 0.28
beta: r2= 0.98 / log p= −Inf

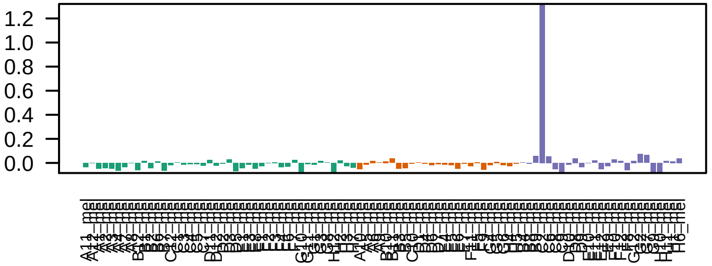
samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

Overview Map



Spot





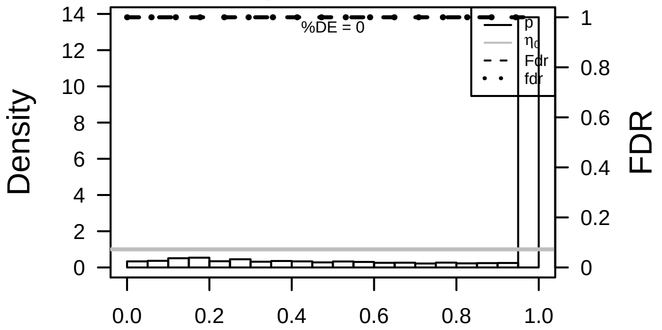
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	FAP	2.68	−0.06	0.83	FAP	fibroblast activation protein, alpha [Source:HGNC Symbol;Ac
2	CLU	2.35	−0.13	0.5	CLU	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
3	CPNE7	2.15	−0.03	0.94	CPNE7	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
4	WDR90	2.04	−0.35	0.29	WDR90	WD repeat domain 90 [Source:HGNC Symbol;Acc:HGNC:26
5	HSF4	1.98	−0.15	0.42	HSF4	heat shock transcription factor 4 [Source:HGNC Symbol;Acc:
6	CLDN15	1.9	−0.12	0.65	CLDN15	claudin 15 [Source:HGNC Symbol;Acc:HGNC:2036]
7	SLC10A7	1.89	−0.17	0.4	SLC10A7	solute carrier family 10, member 7 [Source:HGNC Symbol;Ac
8	SNX16	1.89	−0.17	0.26	SNX16	sorting nexin 16 [Source:HGNC Symbol;Acc:HGNC:14980]
9	BBS1	1.84	−0.26	0.32	BBS1	Bardet−Biedl syndrome 1 [Source:HGNC Symbol;Acc:HGNC
10	FHL3	1.83	−0.11	0.6	FHL3	four and a half LIM domains 3 [Source:HGNC Symbol;Acc:H
11	PPP1R12B	1.81	−0.43	0.28	PPP1R12B	protein phosphatase 1, regulatory subunit 12B [Source:HGN
12	C15orf65	1.79	−0.07	0.65	C15orf65	chromosome 15 open reading frame 65 [Source:HGNC Sym
13	GPRC5A	1.78	−0.07	0.48	GPRC5A	G protein−coupled receptor, class C, group 5, member A [So
14	MRAS	1.78	−0.21	0.43	MRAS	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:
15	TMEM140	1.78	−0.21	0.44	TMEM140	transmembrane protein 140 [Source:HGNC Symbol;Acc:HG
16	FAM149A	1.78	−0.07	0.59	FAM149A	family with sequence similarity 149, member A [Source:HGN
17	ZNF350	1.76	−0.62	0.27	ZNF350	zinc finger protein 350 [Source:HGNC Symbol;Acc:HGNC:16
18	TEP1	1.75	−0.14	0.46	TEP1	telomerase−associated protein 1 [Source:HGNC Symbol;Acc
19	AQPEP	1.75	−0.06	0.9		
20	SOBP	1.74	−0.18	0.43	SOBP	sine oculis binding protein homolog (Drosophila) [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−05	55 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
2	2e−04	3 / 10	BP	activation of transmembrane receptor protein tyrosine kinase activity
3	3e−04	5 / 55	GSE	GEORGANTAS_HSC_MARKERS
4	4e−04	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
5	9e−04	8 / 180	GSE	GAL_LEUKEMIC_STEM_CELL_DN
6	1e−03	6 / 103	GSE	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP
7	1e−03	17 / 668	Brain	Mid_Frontal_Lobe_Enh
8	1e−03	27 / 1317	Colon	EnhP_Colon
9	2e−03	3 / 21	GSE	GENTLES_LEUKEMIC_STEM_CELL_UP
10	2e−03	5 / 77	GSE	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP
11	2e−03	54 / 3396	Lymp	HOPP_Repressed
12	2e−03	4 / 49	GSE	DELASERNA_MYOD_TARGETS_DN
13	2e−03	4 / 50	GSE	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
14	2e−03	2 / 7	GSE	OXFORD_RALB_TARGETS_UP
15	4e−03	15 / 618	GSE	GOZGIT_ESR1_TARGETS_DN
16	4e−03	10 / 332	GSE	PEDRIOLI_MIR31_TARGETS_DN
17	5e−03	37 / 2188	Lymp	HOPP_Poised_promoter
18	5e−03	25 / 1308	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_UP
19	5e−03	2 / 10	BP	positive regulation of interleukin−4 production
20	5e−03	4 / 63	GSE	HECKER_IFNB1_TARGETS
21	5e−03	5 / 102	CC	cytoplasmic vesicle membrane
22	6e−03	3 / 33	GSE	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
23	6e−03	4 / 66	GSE	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCY
24	6e−03	4 / 66	GSE	BAELDE_DIABETIC_NEPHROPATHY_UP
25	6e−03	4 / 66	GSE	ZWANG_EGF_INTERVAL_UP
26	6e−03	2 / 11	GSE	SHI_SPARC_TARGETS_DN
27	6e−03	2 / 11	GSE	WU_HBX_TARGETS_3_DN
28	7e−03	3 / 35	BP	learning or memory
29	7e−03	3 / 35	BP	skeletal muscle cell differentiation
30	7e−03	9 / 304	GSE	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
31	8e−03	3 / 37	CC	lateral plasma membrane
32	8e−03	20 / 1013	Brain	Fetal_TssP
33	8e−03	4 / 72	GSE	SAFFORD_T_LYMPHOCYTE_ANERGY
34	8e−03	3 / 38	BP	cellular response to amino acid stimulus
35	9e−03	4 / 73	Glio	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
36	9e−03	2 / 13	BP	actin filament−based movement
37	9e−03	2 / 13	BP	calcium−independent cell−cell adhesion via plasma membrane cell−adhesi
38	9e−03	8 / 263	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
39	9e−03	5 / 115	BP	cell cycle arrest
40	9e−03	8 / 266	GSE	VECCHI_GASTRIC_CANCER_EARLY_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	3 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 10	activation of transmembrane receptor protein tyrosine kinase activity
2	5e−03	2 / 10	positive regulation of interleukin−4 production
3	7e−03	3 / 35	learning or memory
4	7e−03	3 / 35	skeletal muscle cell differentiation
5	8e−03	3 / 38	cellular response to amino acid stimulus
6	9e−03	2 / 13	actin filament−based movement
7	9e−03	2 / 13	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion
8	9e−03	5 / 115	cell cycle arrest
9	1e−02	2 / 14	negative regulation of interferon−gamma production
10	1e−02	2 / 14	regulation of peptidyl−tyrosine phosphorylation
11	1e−02	5 / 122	plasma membrane organization
12	2e−02	2 / 19	neuronal action potential
13	2e−02	2 / 19	positive regulation of cell cycle arrest
14	2e−02	2 / 19	positive regulation of TOR signaling
15	2e−02	5 / 141	actin cytoskeleton organization
16	2e−02	2 / 20	negative regulation of T cell proliferation
17	2e−02	3 / 56	intrinsic apoptotic signaling pathway
18	2e−02	3 / 56	regulation of cell growth
19	2e−02	2 / 22	release of cytochrome c from mitochondria
20	3e−02	2 / 23	negative regulation of fibroblast proliferation

Brain

Rank	p−value	#in/all	Geneset
1	3e−05	55 / 2972	Mid_Frontal_Lobe_ReprPC
2	1e−03	17 / 668	Mid_Frontal_Lobe_Enh
3	8e−03	20 / 1013	Fetal_TssP
4	1e−02	35 / 2185	Fetal_TssA
5	2e−02	22 / 1236	Mid_Frontal_Lobe_ReprPCWk
6	3e−02	18 / 989	Mid_Frontal_Lobe_Quies
7	3e−02	25 / 1548	Mid_Frontal_Lobe_K9K27me3
8	4e−02	29 / 1907	Fetal_TxTrans
9	6e−02	29 / 1949	Fetal_TssF
10	7e−02	10 / 534	Mid_Frontal_Lobe_EnhG
11	8e−02	9 / 468	Mid_Frontal_Lobe_TssF
12	1e−01	14 / 862	Overlap_fetal_midbrain_TxTrans
13	1e−01	15 / 953	Fetal_Enh
14	1e−01	41 / 3081	Mid_Frontal_Lobe_ZNF
15	1e−01	16 / 1050	Fetal_EnhP
16	2e−01	12 / 786	Fetal_EnhG
17	2e−01	32 / 2462	Mid_Frontal_Lobe_HetRpts
18	2e−01	12 / 812	Mid_Frontal_Lobe_TssP
19	2e−01	11 / 765	Mid_Frontal_Lobe_Het
20	3e−01	16 / 1207	Overlap_fetal_midbrain_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	0 / 14	LIU_PROSTATE_CANCER_DN
2	1e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	1e−01	6 / 298	SPANG_BCL6−index2
4	1e−01	1 / 11	GENTLES_modul17
5	1e−01	1 / 13	GENTLES_modul12
6	2e−01	1 / 15	RHODES_CANCER_META_SIGNATURE
7	2e−01	7 / 401	Lembcke_Colonic Inflammation
8	5e−01	1 / 55	PanCan_JAK−ST_geneset_nanostring
9	5e−01	1 / 61	PanCan_Wnt_geneset_nanostring
10	5e−01	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	7e−01	1 / 111	PanCan_RAS_geneset_nanostring
12	7e−01	1 / 120	PanCan_CC+Apop_geneset_nanostring
13	7e−01	1 / 121	PanCan_MAPK_geneset_nanostring
14	8e−01	1 / 156	PanCan_PI3K_geneset_nanostring
15	9e−01	3 / 489	Lembcke_Normal vs Adenoma
16	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	1e+00	0 / 12	LIU_BREAST_CANCER
18	1e+00	0 / 14	LIU_COMMON_CANCER_GENES
19	1e+00	0 / 14	LIU_LIVER_CANCER
20	1e+00	0 / 12	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	0.005	5 / 102	cytoplasmic vesicle membrane
2	0.008	3 / 37	lateral plasma membrane
3	0.016	3 / 48	stress fiber
4	0.038	2 / 28	SCF ubiquitin ligase complex
5	0.043	2 / 30	endoplasmic reticulum−Golgi intermediate compartment membrane
6	0.063	2 / 37	platelet alpha granule lumen
7	0.076	3 / 89	tight junction
8	0.077	4 / 145	endoplasmic reticulum lumen
9	0.080	3 / 91	nuclear matrix
10	0.082	3 / 92	early endosome membrane
11	0.085	2 / 44	terminal bouton
12	0.088	13 / 775	extracellular space
13	0.088	2 / 45	SNARE complex
14	0.105	1 / 10	apical dendrite
15	0.105	1 / 10	fascia adherens
16	0.109	2 / 51	axoneme
17	0.116	2 / 53	acrosomal vesicle
18	0.121	17 / 1132	Golgi apparatus
19	0.125	1 / 12	actomyosin
20	0.125	1 / 12	basal part of cell

Chr

Rank	p−value	#in/all	Geneset
1	0.1	11 / 689	Chr 7
2	0.2	15 / 1037	Chr 19
3	0.2	10 / 649	Chr 16
4	0.2	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
5	0.3	7 / 469	Chr 8
6	0.3	4 / 262	Chr 13
7	0.4	10 / 801	Chr 11
8	0.4	6 / 465	Chr 15
9	0.4	7 / 552	Chr 10
10	0.4	7 / 558	Chr 4
11	0.4	5 / 398	Chr 20
12	0.5	7 / 576	Chr 9
13	0.5	8 / 687	Chr 6
14	0.6	6 / 551	Chr X
15	0.6	5 / 462	Chr 14
16	0.6	16 / 1500	Chr 1
17	0.6	8 / 775	Chr 12
18	0.8	9 / 993	Chr 2
19	0.8	1 / 151	Chr 21
20	0.9	6 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	27 / 1317	EnhP_Colon
2	0.009	8 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	0.022	55 / 3897	Quies1_Colon
4	0.028	33 / 2142	ReprPC_Colon
5	0.044	3 / 71	Marisa_CRC−cluster−g
6	0.046	47 / 3383	EnhWk2_Colon
7	0.048	32 / 2159	TssP_Colon
8	0.053	9 / 436	K9acLow_Colon
9	0.054	1 / 5	Budinska_A_Surface crypt−like_UP
10	0.060	7 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
11	0.063	28 / 1889	ReprPCWk_Colon
12	0.064	6 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
13	0.071	8 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
14	0.088	17 / 1079	ZNF_Colon
15	0.103	3 / 102	Marisa_CRC−cluster−d
16	0.126	49 / 3812	TssD1_Colon
17	0.128	8 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
18	0.129	114 / 9653	Enh_Colon
19	0.165	2 / 66	Marisa_CRC−cluster−h
20	0.165	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	6 / 294	GUDJ_psoriasis down
2	0.9	3 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.009	4 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
2	0.025	3 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
3	0.026	2 / 23	WIRTH_PN subtype
4	0.054	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
5	0.072	2 / 40	in vivo astrocytes vs. cultured astroglia
6	0.115	1 / 11	Mukasa_UP_in_Astroglioma
7	0.135	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
8	0.154	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	0.173	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.181	1 / 18	Barbus_GBM_STS_vs._LTS
11	0.181	1 / 18	Shinawi_with_increased_methylation_in_STS
12	0.181	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
13	0.197	2 / 74	WIRTH_Normal Brain
14	0.257	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	0.276	1 / 29	shaw_responders_down_in_oligo_glioma
16	0.299	1 / 32	Donson−innate immunity−associated with LTS in HGA
17	0.303	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
18	0.315	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
19	0.332	3 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
20	0.358	5 / 356	Down_a

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 55	GEORGANTAS_HSC_MARKERS
2	4e−04	0 / 14	LIU_PROSTATE_CANCER_DN
3	9e−04	8 / 180	GAL_LEUKEMIC_STEM_CELL_DN
4	1e−03	6 / 103	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP
5	2e−03	3 / 21	GENTLES_LEUKEMIC_STEM_CELL_UP
6	2e−03	5 / 77	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP
7	2e−03	4 / 49	DELASERNA_MYOD_TARGETS_DN
8	2e−03	4 / 50	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
9	2e−03	2 / 7	OXFORD_RALB_TARGETS_UP
10	4e−03	15 / 618	GOZGIT_ESR1_TARGETS_DN
11	4e−03	10 / 332	PEDRIOLI_MIR31_TARGETS_DN
12	5e−03	25 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
13	5e−03	4 / 63	HECKER_IFNB1_TARGETS
14	6e−03	3 / 33	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
15	6e−03	4 / 66	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE
16	6e−03	4 / 66	BAELDE_DIABETIC_NEPHROPATHY_UP
17	6e−03	4 / 66	ZWANG_EGF_INTERVAL_UP
18	6e−03	2 / 11	SHI_SPARC_TARGETS_DN
19	6e−03	2 / 11	WU_HBX_TARGETS_3_DN
20	7e−03	9 / 304	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 162	HALLMARK_COMPLEMENT
2	0.1	4 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.2	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
4	0.2	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	0.2	3 / 148	HALLMARK_KRAS_SIGNALING_UP
6	0.2	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	0.3	3 / 165	HALLMARK_MYOGENESIS
8	0.4	2 / 127	HALLMARK_KRAS_SIGNALING_DN
9	0.5	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	0.6	2 / 167	HALLMARK_APICAL_JUNCTION
11	0.6	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	0.6	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	0.6	2 / 183	HALLMARK_GLYCOLYSIS
14	0.6	1 / 91	HALLMARK_BILE_ACID_METABOLISM
15	0.6	1 / 93	HALLMARK_PEROXISOME
16	0.7	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
17	0.7	1 / 107	HALLMARK_COAGULATION
18	0.7	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
19	0.8	1 / 137	HALLMARK_UV_RESPONSE_DN
20	0.8	1 / 140	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 32	DUMEAUX_Fasting enriched genes
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	54 / 3396	HOPP_Repressed
2	0.005	37 / 2188	HOPP_Poised_promoter
3	0.010	36 / 2211	HOPP_Repetitive
4	0.069	2 / 39	ROSOLOWSKI_blue DOWN
5	0.105	2 / 50	SPANG_BAFF 9hrs DN
6	0.198	5 / 280	SPANG_CD40 6hrs UP
7	0.208	4 / 212	LENZ_Stromal signature 1
8	0.246	2 / 86	ROSOLOWSKI_red total
9	0.307	1 / 33	LEE_Developmental_regulators
10	0.319	31 / 2563	HOPP_Heterochrom
11	0.331	2 / 107	SPANG_LPS 6hrs UP
12	0.361	4 / 275	TARTE_Mature plasma cell signature
13	0.376	75 / 6564	HOPP_Strong_enhancer
14	0.407	1 / 47	Subero_FL_hyper_meth
15	0.418	2 / 129	DAVE_BL−vs−DLBCL
16	0.520	1 / 66	TARTE_Plasma cell signature
17	0.590	1 / 80	Aukema_BCL2 DN_BCL6 UP
18	0.593	13 / 1218	SPANG_BCR UP
19	0.594	1 / 81	Subero_INT_hyper_meth
20	0.629	1 / 89	ROSOLOWSKI_blue total

MF

Rank	p−value	#in/all	Geneset
1	0.03	7 / 271	actin binding
2	0.04	2 / 27	voltage−gated calcium channel activity
3	0.05	2 / 33	receptor tyrosine kinase binding
4	0.06	2 / 36	SNAP receptor activity
5	0.06	3 / 81	serine−type endopeptidase activity
6	0.07	2 / 39	SNARE binding
7	0.07	4 / 142	calmodulin binding
8	0.08	2 / 42	glycoprotein binding
9	0.10	5 / 223	phosphatase activity
10	0.10	3 / 102	actin filament binding
11	0.11	1 / 10	actin−dependent ATPase activity
12	0.11	1 / 10	calcium−activated potassium channel activity
13	0.11	1 / 10	glucocorticoid receptor binding
14	0.11	1 / 10	polysaccharide binding
15	0.11	151 / 13179	molecular_function
16	0.11	3 / 104	growth factor activity
17	0.11	2 / 51	ubiquitinyl hydrolase activity
18	0.12	1 / 11	metal ion transmembrane transporter activity
19	0.12	1 / 11	structural constituent of eye lens
20	0.12	1 / 12	misfolded protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 54	hsa−miR−940
2	0.07	1 / 7	hsa−miR−339−3p
3	0.08	3 / 89	hsa−miR−608
4	0.09	1 / 8	hsa−miR−566
5	0.09	2 / 45	hsa−miR−518a−3p
6	0.10	3 / 102	hsa−miR−500
7	0.11	1 / 10	hsa−miR−887
8	0.13	1 / 13	hsa−miR−1234
9	0.14	1 / 14	hsa−miR−891a
10	0.15	1 / 15	hsa−miR−744
11	0.16	2 / 65	hsa−miR−550
12	0.16	1 / 16	hsa−miR−302a*
13	0.17	3 / 130	hsa−miR−145
14	0.20	2 / 74	hsa−miR−1254
15	0.20	1 / 20	hsa−miR−1288
16	0.21	1 / 21	hsa−miR−662
17	0.23	1 / 23	hsa−miR−609
18	0.24	1 / 25	hsa−miR−1273
19	0.24	1 / 25	hsa−miR−432*
20	0.24	1 / 25	hsa−miR−99b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_src.10
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 15	BENTINK_ras.6
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.03	43 / 2927	ICGC_Rad21_targets
2	0.05	19 / 1139	HEBENSTREIT_low expression TF
3	0.08	34 / 2416	ICGC_Bcl3_targets
4	0.11	11 / 653	ICGC_SrfPcr2_targets
5	0.13	26 / 1872	ICGC_Mef2_targets
6	0.14	19 / 1314	ICGC_Usf1_targets
7	0.20	46 / 3700	ICGC_Nfatc1_targets
8	0.22	59 / 4879	ICGC_Pmlsc71910_targets
9	0.24	17 / 1273	ICGC_P300_targets
10	0.25	62 / 5200	ICGC_Mta3_targets
11	0.27	65 / 5495	ICGC_Yy1_targets
12	0.30	25 / 2013	ICGC_Bcl11_targets
13	0.33	34 / 2836	ICGC_BatfPcr1_targets
14	0.35	9 / 690	ICGC_Atf3_targets
15	0.36	62 / 5374	ICGC_Pax5_targets
16	0.37	50 / 4314	ICGC_Ebfsc137065_targets
17	0.41	25 / 2137	ICGC_SrfV0416101_targets
18	0.41	45 / 3924	ICGC_Zeb1_targets
19	0.42	22 / 1878	ICGC_Cebpbsc150_targets
20	0.45	54 / 4774	ICGC_Foxm1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	2 / 38	VAQUERIZAS_Whole brain
2	0.07	2 / 40	VAQUERIZAS_Thyroid
3	0.07	4 / 143	VAQUERIZAS_General
4	0.08	2 / 41	VAQUERIZAS_Placenta
5	0.16	1 / 16	VAQUERIZAS_Adrenal gland
6	0.17	1 / 17	VAQUERIZAS_Pituitary
7	0.23	1 / 23	VAQUERIZAS_Adrenal cortex
8	0.28	1 / 29	VAQUERIZAS_Fetal lung
9	0.31	1 / 33	VAQUERIZAS_Prostate
10	0.39	1 / 45	VAQUERIZAS_Uterus
11	0.48	1 / 58	VAQUERIZAS_Lung
12	1.00	0 / 36	VAQUERIZAS_Fetal brain
13	1.00	0 / 26	VAQUERIZAS_Liver
14	1.00	0 / 29	VAQUERIZAS_Smooth muscle
15	1.00	0 / 9	VAQUERIZAS_Kidney
16	1.00	0 / 23	VAQUERIZAS_Spinal cord
17	1.00	0 / 37	VAQUERIZAS_Thymus
18	1.00	0 / 59	VAQUERIZAS_Whole blood
19	1.00	0 / 7	VAQUERIZAS_Appendix
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.3	2 / 95	WIRTH_Muscle
2	0.3	1 / 32	WIRTH_Pancreas
3	0.3	1 / 32	WIRTH_Placenta
4	0.3	2 / 107	WIRTH_Testis
5	0.5	4 / 350	WIRTH_Nervous System
6	0.6	1 / 74	WIRTH_Mucosa
7	0.7	1 / 114	PALMER_T−Cell signature up
8	0.9	1 / 194	PALMER_B−Cell signature up
9	0.9	2 / 350	WIRTH_Immune system
10	0.9	1 / 225	PALMER_Granulocytes signature up
11	1.0	0 / 11	WIRTH_Sec. lymphoid organs
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 13	WIRTH_B−cells
14	1.0	0 / 8	WIRTH_Tonsil
15	1.0	0 / 12	WIRTH_Thymus
16	1.0	0 / 12	WIRTH_Lymphocytes
17	1.0	0 / 5	WIRTH_Bone marrow
18	1.0	0 / 11	WIRTH_Globus pallidus
19	1.0	0 / 14	WIRTH_Telencephalon
20	1.0	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.08	49 / 3682	LU_BPDE 0.005 DN
2	0.46	13 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

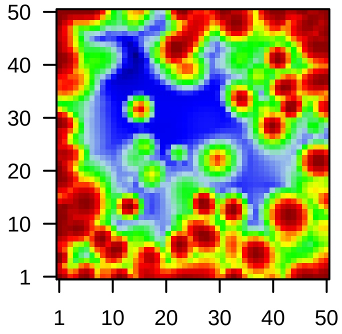
Spot Summary: X

metagenes = 3
genes = 69

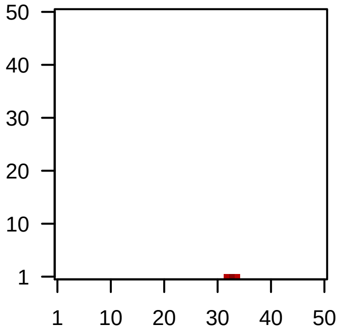
<r> metagenes = 0.98
<r> genes = 0.16
beta: r2= 1.25 / log p= −Inf

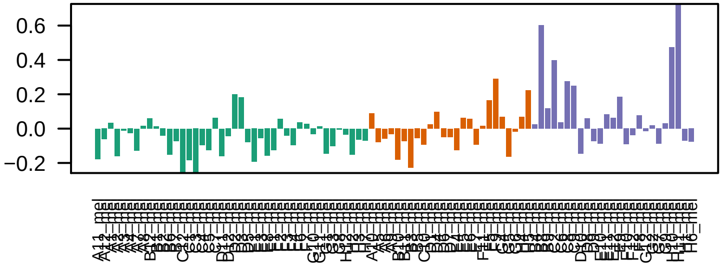
samples with spot = 11 (12 %)
MSC1 : 2 (4.8 %)
MSC2 : 2 (8 %)
MSC3 : 7 (28 %)

Overview Map



Spot





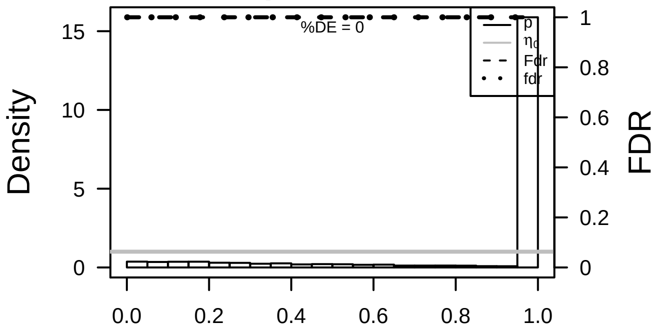
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PIGB	1.97	−0.55	0.32	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B [Sou
2	AKAP7	1.92	−0.37	0.36	AKAP7	A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Ac
3	CAPNS2	1.85	−0.05	0.5	CAPNS2	calpain, small subunit 2 [Source:HGNC Symbol;Acc:HGNC:1
4	RFX3	1.8	−0.12	0.34	RFX3	regulatory factor X, 3 (influences HLA class II expression) [Sc
5	MED18	1.74	−0.28	0.28	MED18	mediator complex subunit 18 [Source:HGNC Symbol;Acc:HG
6	ITPR1	1.7	−0.28	0.26	ITPR1	inositol 1,4,5−trisphosphate receptor, type 1 [Source:HGNC S
7	ZNF701	1.68	−0.41	0.35	ZNF701	zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25
8	ZNF28	1.61	−0.51	0.35	ZNF28	zinc finger protein 28 [Source:HGNC Symbol;Acc:HGNC:130
9	APOBEC3H	1.6	−0.16	0.4	APOBEC3H	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
10	GBX2	1.56	−0.05	0.4	GBX2	gastrulation brain homeobox 2 [Source:HGNC Symbol;Acc:H
11	ABHD14A	1.55	−0.55	0.29	ABHD14A	abhydrolase domain containing 14A [Source:HGNC Symbol;
12	APBB3	1.54	−0.21	0.3	APBB3	amyloid beta (A4) precursor protein−binding, family B, membe
13	NAP1L5	1.54	−0.4	0.37	NAP1L5	nucleosome assembly protein 1−like 5 [Source:HGNC Symbo
14	SEPT4	1.53	−0.38	0.4	SEPT4	septin 4 [Source:HGNC Symbol;Acc:HGNC:9165]
15	GYG2	1.53	−0.5	0.27	GYG2	glycogenin 2 [Source:HGNC Symbol;Acc:HGNC:4700]
16	TMCO3	1.5	−0.71	0.29	TMCO3	transmembrane and coiled−coil domains 3 [Source:HGNC Sy
17	LZTFL1	1.5	−0.72	0.31	LZTFL1	leucine zipper transcription factor−like 1 [Source:HGNC Sym
18	AFAP1L2	1.49	−0.16	0.68	AFAP1L2	actin filament associated protein 1−like 2 [Source:HGNC Sym
19	L3HYPDH	1.47	−0.77	0.29	L3HYPDH	L−3−hydroxyproline dehydratase (trans−) [Source:HGNC Syn
20	AK8	1.44	−0.09	0.66	AK8	adenylate kinase 8 [Source:HGNC Symbol;Acc:HGNC:26526

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−04	3 / 37	HM	HALLMARK_APICAL_SURFACE
2	1e−03	59 / 10605	CC	intracellular
3	2e−03	2 / 16	GSEA	MA_PITUITARY_FETAL_VS_ADULT_DN
4	3e−03	2 / 17	GSEA	BIOCARTA_UCALPAIN_PATHWAY
5	3e−03	3 / 61	GSEA	HOSHIDA_LIVER_CANCER_SURVIVAL_UP
6	3e−03	7 / 427	GSEA	PILON_KLF1_TARGETS_UP
7	3e−03	24 / 3081	Brain	Mid_Frontal_Lobe_ZNF
8	3e−03	2 / 19	GSEA	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN
9	4e−03	3 / 68	GSEA	PID_AVB3_INTEGRIN_PATHWAY
10	4e−03	6 / 329	GSEA	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECUL
11	4e−03	2 / 22	BP	patterning of blood vessels
12	4e−03	2 / 22	GSEA	BIOCARTA_MCALPAIN_PATHWAY
13	4e−03	2 / 22	GSEA	MATZUK_MALE_REPRODUCTION_SERTOLI
14	5e−03	2 / 23	GSEA	XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR
15	5e−03	9 / 730	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
16	6e−03	3 / 80	GSEA	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
17	6e−03	2 / 26	GSEA	MAYBURD_RESPONSE_TO_L663536_UP
18	7e−03	37 / 5880	Colon	TssD2_Colon
19	7e−03	2 / 28	GSEA	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_UP
20	7e−03	2 / 28	GSEA	MATZUK_SPERMATID_DIFFERENTIATION
21	7e−03	3 / 87	GSEA	MATZUK_SPERMATOZOA
22	7e−03	5 / 268	Lymph	SPANG_IL21 UP
23	8e−03	2 / 30	GSEA	RODRIGUES_NTN1_AND_DCC_TARGETS
24	8e−03	2 / 30	GSEA	GRADE_COLON_CANCER_DN
25	9e−03	1 / 2	Colon	Budinska_C_CIMP−H−like_DOWN
26	1e−02	3 / 100	Aging	HORVATH_aging_genes meth DOWN
27	1e−02	2 / 35	CC	mediator complex
28	1e−02	2 / 35	GSEA	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN
29	1e−02	2 / 37	GSEA	BIOCARTA_INTEGRIN_PATHWAY
30	1e−02	3 / 108	GSEA	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN
31	1e−02	4 / 201	GSEA	WHITFIELD_CELL_CYCLE_G2_M
32	1e−02	48 / 8580	Colon	TxWk_Colon
33	1e−02	5 / 315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
34	1e−02	2 / 40	GSEA	WANG_BARRETTS_ESOPHAGUS_UP
35	2e−02	12 / 1333	Brain	Fetal_ReprPCWk
36	2e−02	2 / 42	GSEA	JIANG_AGING_HYPOTHALAMUS_UP
37	2e−02	21 / 2927	TF	ICGC_Rad21_targets
38	2e−02	65 / 13191	CC	cellular_component
39	2e−02	6 / 456	MF	protein binding transcription factor activity
40	2e−02	46 / 8205	CC	cytoplasm

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	3 / 100	HORVATH_aging_genes meth DOWN
2	0.40	1 / 111	HORVATH_aging_genes meth UP
3	1.00	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.004	2 / 22	patterning of blood vessels
2	0.019	4 / 225	ion transport
3	0.024	2 / 53	chloride transmembrane transport
4	0.026	2 / 56	spermatid development
5	0.031	2 / 61	palate development
6	0.032	2 / 62	canonical Wnt signaling pathway
7	0.034	2 / 64	regulation of insulin secretion
8	0.035	2 / 65	regulation of Rho protein signal transduction
9	0.039	3 / 166	epidermal growth factor receptor signaling pathway
10	0.043	2 / 73	post−embryonic development
11	0.044	1 / 10	diaphragm development
12	0.044	1 / 10	histone ubiquitination
13	0.044	1 / 10	negative regulation of viral transcription
14	0.044	1 / 10	porphyrin−containing compound biosynthetic process
15	0.046	23 / 3644	biosynthetic process
16	0.049	1 / 11	alpha−linolenic acid metabolic process
17	0.049	1 / 11	branching involved in mammary gland duct morphogenesis
18	0.049	1 / 11	detection of mechanical stimulus involved in sensory perception of sound
19	0.049	1 / 11	fatty acid beta−oxidation using acyl−CoA oxidase
20	0.049	1 / 11	hindbrain development

Brain

Rank	p−value	#in/all	Geneset
1	0.003	24 / 3081	Mid_Frontal_Lobe_ZNF
2	0.015	12 / 1333	Fetal_ReprPCWk
3	0.048	34 / 5940	Overlap_fetal_midbrain_HetRpts
4	0.080	6 / 668	Mid_Frontal_Lobe_Enh
5	0.095	4 / 383	Fetal_Tx
6	0.168	2 / 163	Fetal_ReprPC
7	0.171	6 / 831	Fetal_HetRpts
8	0.196	46 / 9330	Overlap_fetal_midbrain_ReprPC
9	0.241	7 / 1122	Fetal_K9K27me3
10	0.263	5 / 765	Mid_Frontal_Lobe_Het
11	0.276	12 / 2185	Fetal_TssA
12	0.314	13 / 2462	Mid_Frontal_Lobe_HetRpts
13	0.327	43 / 9013	Overlap_fetal_midbrain_K9K27me3
14	0.336	6 / 1050	Fetal_EnhP
15	0.355	45 / 9528	Overlap_fetal_midbrain_Quies
16	0.357	10 / 1907	Fetal_TxTrans
17	0.425	42 / 9020	Overlap_fetal_midbrain_ReprPCWk
18	0.456	9 / 1845	Fetal_Quies
19	0.460	4 / 769	Overlap_fetal_midbrain_ZNF
20	0.471	3 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	4 / 298	SPANG_BCL6−index2
2	0.54	2 / 401	Lembcke_Colonic Inflammation
3	0.56	1 / 180	SPANG_LPS−index2
4	0.83	0 / 14	LIU_PROSTATE_CANCER_DN
5	0.89	1 / 489	Lembcke_Normal vs Adenoma
6	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
7	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
8	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1.00	0 / 12	LIU_BREAST_CANCER
11	1.00	0 / 14	LIU_COMMON_CANCER_GENES
12	1.00	0 / 14	LIU_LIVER_CANCER
13	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
14	1.00	0 / 15	WANG_ER_UP
15	1.00	0 / 5	WANG_ER_DN
16	1.00	0 / 16	WOLFER_overlap genes
17	1.00	0 / 12	BEN−PORATH_DN
18	1.00	0 / 13	BEN−PORATH_UP
19	1.00	0 / 15	GENTLES_modul1
20	1.00	0 / 16	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	0.001	59 / 10605	intracellular
2	0.011	2 / 35	mediator complex
3	0.016	65 / 13191	cellular_component
4	0.017	46 / 8205	cytoplasm
5	0.021	60 / 11774	cell
6	0.041	3 / 169	transcription factor complex
7	0.044	52 / 9988	organelle
8	0.044	1 / 10	sperm flagellum
9	0.044	1 / 10	vacuolar proton−transporting V−type ATPase complex
10	0.046	3 / 178	apical plasma membrane
11	0.048	2 / 78	ubiquitin ligase complex
12	0.049	1 / 11	intrinsic component of the cytoplasmic side of the plasma membrane
13	0.049	1 / 11	phosphatidylinositol 3−kinase complex
14	0.053	1 / 12	STAGA complex
15	0.057	1 / 13	transcription factor TFTC complex
16	0.061	1 / 14	NuA4 histone acetyltransferase complex
17	0.066	1 / 15	Ino80 complex
18	0.080	3 / 223	lysosomal membrane
19	0.095	1 / 22	cortical cytoskeleton
20	0.118	2 / 131	vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.08	7 / 838	Chr 3
2	0.11	4 / 398	Chr 20
3	0.18	6 / 840	Chr 17
4	0.20	5 / 689	Chr 7
5	0.33	2 / 262	Chr 13
6	0.35	3 / 462	Chr 14
7	0.35	3 / 465	Chr 15
8	0.39	4 / 696	Chr 5
9	0.46	3 / 552	Chr 10
10	0.46	3 / 558	Chr 4
11	0.48	3 / 576	Chr 9
12	0.61	3 / 687	Chr 6
13	0.70	4 / 1037	Chr 19
14	0.78	1 / 335	Chr 22
15	0.82	5 / 1500	Chr 1
16	0.83	3 / 993	Chr 2
17	0.87	2 / 775	Chr 12
18	0.88	2 / 801	Chr 11
19	0.88	1 / 469	Chr 8
20	0.92	1 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	37 / 5880	TssD2_Colon
2	0.009	1 / 2	Budinska_C_CIMP−H−like_DOWN
3	0.013	48 / 8580	TxWk_Colon
4	0.027	54 / 10290	TssWk_Colon
5	0.036	1 / 8	Marisa_CRC−C2
6	0.042	24 / 3812	TssD1_Colon
7	0.043	48 / 9027	Tx_Colon
8	0.050	18 / 2698	EnhA_Colon
9	0.091	29 / 5155	EnhWk1_Colon
10	0.115	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
11	0.193	42 / 8415	Quies3_Colon
12	0.257	4 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	0.258	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
14	0.259	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
15	0.263	3 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
16	0.272	15 / 2798	TxEnhG1_Colon
17	0.298	2 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
18	0.336	45 / 9482	TssA_Colon
19	0.371	1 / 102	Marisa_CRC−cluster−d
20	0.424	2 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.6	2 / 435	GUDJ_psoriasis up
2	0.7	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.01	5 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.03	1 / 7	Phillips MES up vs Prolif & PN
3	0.08	1 / 18	Shinawi_with_increased_methylation_in_STS
4	0.19	1 / 47	Vishal_subnetwork signature of survival in GBM
5	0.21	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
6	0.25	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	0.27	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
8	0.28	1 / 71	Weller_LGG_A_vs_O_UP
9	0.28	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
10	0.28	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	0.44	2 / 332	Up
12	0.48	2 / 356	Down_a
13	0.49	2 / 365	Down_b
14	0.51	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	0.53	4 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
16	0.57	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
17	1.00	0 / 15	VERHAAK_CL subtype
18	1.00	0 / 15	VERHAAK_MES subtype
19	1.00	0 / 16	VERHAAK_NL subtype
20	1.00	0 / 14	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	7 / 16	MA_PITUITARY_FETAL_VS_ADULT_DN
2	0.003	2 / 17	BIOCARTA_UCALPAIN_PATHWAY
3	0.003	3 / 61	HOSHIDA_LIVER_CANCER_SURVIVAL_UP
4	0.003	7 / 427	PILON_KLF1_TARGETS_UP
5	0.003	2 / 19	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN
6	0.004	3 / 68	PID_AVB3_INTEGRIN_PATHWAY
7	0.004	6 / 329	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES
8	0.004	2 / 22	BIOCARTA_MCALPAIN_PATHWAY
9	0.004	2 / 22	MATZUK_MALE_REPRODUCTION_SERTOLI
10	0.005	2 / 23	XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR
11	0.005	9 / 730	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
12	0.006	3 / 80	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
13	0.006	2 / 26	MAYBURD_RESPONSE_TO_L663536_UP
14	0.007	2 / 28	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_UP
15	0.007	2 / 28	MATZUK_SPERMATID_DIFFERENTIATION
16	0.007	3 / 87	MATZUK_SPERMATOZOA
17	0.008	2 / 30	RODRIGUES_NTN1_AND_DCC_TARGETS
18	0.008	2 / 30	GRADE_COLON_CANCER_DN
19	0.011	2 / 35	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN
20	0.012	2 / 37	BIOCARTA_INTEGRIN_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 37	HALLMARK_APICAL_SURFACE
2	7e−02	2 / 95	HALLMARK_SPERMATOGENESIS
3	2e−01	2 / 195	HALLMARK_MITOTIC_SPINDLE
4	3e−01	1 / 91	HALLMARK_BILE_ACID_METABOLISM
5	3e−01	1 / 93	HALLMARK_PEROXISOME
6	4e−01	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	5e−01	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
8	5e−01	1 / 146	HALLMARK_DNA_REPAIR
9	5e−01	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	5e−01	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
11	5e−01	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	5e−01	1 / 174	HALLMARK_HEME_METABOLISM
13	6e−01	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	6e−01	1 / 181	HALLMARK_P53_PATHWAY
15	6e−01	1 / 188	HALLMARK_ADIPOGENESIS
16	6e−01	1 / 196	HALLMARK_G2M_CHECKPOINT
17	6e−01	1 / 196	HALLMARK_MTORC1_SIGNALING
18	1e+00	0 / 176	HALLMARK_HYPOXIA
19	1e+00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	1e+00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.007	5 / 268	SPANG_IL21 UP
2	0.066	1 / 15	DAVE_Immune response 2
3	0.074	1 / 17	Aukema_BCL2 UP_BCL6 DN
4	0.100	40 / 7592	HOPP_Active_promoter
5	0.127	1 / 30	TARTE_B−cell signature
6	0.139	1 / 33	LEE_Developmental_regulators
7	0.180	13 / 2188	HOPP_Poised_promoter
8	0.239	33 / 6564	HOPP_Strong_enhancer
9	0.292	34 / 6929	HOPP_Txn_elongation
10	0.307	2 / 247	ZHANG_DLBCL mutated
11	0.310	7 / 1218	SPANG_BCR UP
12	0.348	27 / 5538	HOPP_Weak_txn
13	0.353	2 / 275	TARTE_Mature plasma cell signature
14	0.358	17 / 3396	HOPP_Repressed
15	0.390	1 / 109	ROSOLOWSKI_green total
16	0.406	34 / 7209	HOPP_Weak_promoter
17	0.414	11 / 2211	HOPP_Repetitive
18	0.416	27 / 5693	HOPP_Weak_enhancer
19	0.586	23 / 5184	HOPP_Txn_transition
20	0.623	11 / 2563	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	0.02	6 / 456	protein binding transcription factor activity
2	0.02	10 / 1040	zinc ion binding
3	0.02	2 / 50	RNA polymerase II distal enhancer sequence−specific DNA binding
4	0.03	2 / 64	beta−catenin binding
5	0.04	2 / 66	Rho guanyl−nucleotide exchange factor activity
6	0.04	2 / 67	phosphatidylinositol binding
7	0.04	2 / 67	phosphotransferase activity, alcohol group as acceptor
8	0.04	1 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
9	0.04	1 / 10	neutral amino acid transmembrane transporter activity
10	0.05	1 / 11	vinculin binding
11	0.06	1 / 13	mannosyltransferase activity
12	0.06	1 / 13	protein kinase A binding
13	0.06	1 / 13	protein kinase A regulatory subunit binding
14	0.06	1 / 13	solute:proton antiporter activity
15	0.06	1 / 14	aldehyde dehydrogenase (NAD) activity
16	0.06	1 / 14	ankyrin binding
17	0.07	1 / 15	phospholipid−translocating ATPase activity
18	0.07	1 / 16	calcium−dependent cysteine−type endopeptidase activity
19	0.07	1 / 16	nucleoside diphosphate kinase activity
20	0.07	1 / 16	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD o

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 123	hsa−miR−204
2	0.02	3 / 129	hsa−miR−218
3	0.03	3 / 141	hsa−miR−138
4	0.03	3 / 146	hsa−miR−655
5	0.03	3 / 153	hsa−miR−583
6	0.04	1 / 8	hsa−miR−886−3p
7	0.04	2 / 66	hsa−miR−140−3p
8	0.04	4 / 284	hsa−miR−503
9	0.04	2 / 71	hsa−miR−1290
10	0.05	2 / 80	hsa−miR−584
11	0.05	2 / 82	hsa−miR−365
12	0.06	2 / 84	hsa−miR−486−3p
13	0.08	1 / 19	hsa−miR−645
14	0.09	2 / 108	hsa−miR−211
15	0.10	2 / 116	hsa−miR−376c
16	0.10	1 / 23	hsa−miR−1250
17	0.10	1 / 24	hsa−miR−220b
18	0.11	1 / 25	hsa−miR−663b
19	0.11	1 / 25	hsa−miR−432*
20	0.13	1 / 32	hsa−miR−1178

PathwACT

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	21 / 2927	ICGC_Rad21_targets
2	0.13	12 / 1872	ICGC_Mef2_targets
3	0.21	8 / 1266	ICGC_NrsfPcr1_targets
4	0.24	4 / 553	ICGC_RxraPcr1_targets
5	0.32	20 / 3966	ICGC_Pu1_targets
6	0.33	27 / 5495	ICGC_Yy1_targets
7	0.37	11 / 2137	ICGC_SrfV0416101_targets
8	0.37	26 / 5374	ICGC_Pax5_targets
9	0.41	12 / 2416	ICGC_Bcl3_targets
10	0.43	7 / 1383	ICGC_Six5_targets
11	0.49	20 / 4314	ICGC_Ebfsc137065_targets
12	0.50	27 / 5890	ICGC_Elf1_targets
13	0.51	18 / 3924	ICGC_Zeb1_targets
14	0.52	22 / 4829	ICGC_Nficsc81335_targets
15	0.57	3 / 653	ICGC_SrfPcr2_targets
16	0.57	21 / 4706	ICGC_Sp1_targets
17	0.59	23 / 5200	ICGC_Mta3_targets
18	0.60	21 / 4774	ICGC_Foxm1_targets
19	0.60	27 / 6114	ICGC_Runx3_targets
20	0.61	6 / 1400	ICGC_Myc_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 27	VAQUERIZAS_Lymph node
2	1.0	0 / 36	VAQUERIZAS_Fetal brain
3	1.0	0 / 41	VAQUERIZAS_Placenta
4	1.0	0 / 26	VAQUERIZAS_Liver
5	1.0	0 / 33	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 45	VAQUERIZAS_Uterus
8	1.0	0 / 143	VAQUERIZAS_General
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 59	VAQUERIZAS_Whole blood
15	1.0	0 / 7	VAQUERIZAS_Appendix
16	1.0	0 / 29	VAQUERIZAS_Fetal lung
17	1.0	0 / 58	VAQUERIZAS_Lung
18	1.0	0 / 16	VAQUERIZAS_Pancreas
19	1.0	0 / 23	VAQUERIZAS_Trachea
20	1.0	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 194	PALMER_B−Cell signature up
2	0.3	1 / 74	WIRTH_Mucosa
3	0.4	1 / 114	PALMER_T−Cell signature up
4	0.5	2 / 350	WIRTH_Nervous System
5	0.8	1 / 350	WIRTH_Immune system
6	1.0	0 / 32	WIRTH_Pancreas
7	1.0	0 / 11	WIRTH_Sec. lymphoid organs
8	1.0	0 / 11	WIRTH_Prim. lymphoid organs
9	1.0	0 / 13	WIRTH_B−cells
10	1.0	0 / 8	WIRTH_Tonsil
11	1.0	0 / 12	WIRTH_Thymus
12	1.0	0 / 12	WIRTH_Lymphocytes
13	1.0	0 / 5	WIRTH_Bone marrow
14	1.0	0 / 11	WIRTH_Globus pallidus
15	1.0	0 / 14	WIRTH_Telencephalon
16	1.0	0 / 11	WIRTH_Cortex cerebri
17	1.0	0 / 10	WIRTH_Hippocampus
18	1.0	0 / 10	WIRTH_Thalamus
19	1.0	0 / 12	WIRTH_Cerebellum
20	1.0	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	15 / 3682	LU_BPDE 0.005 DN
2	0.9	3 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

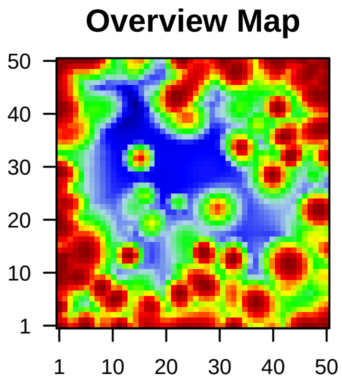
Overexpression Spots

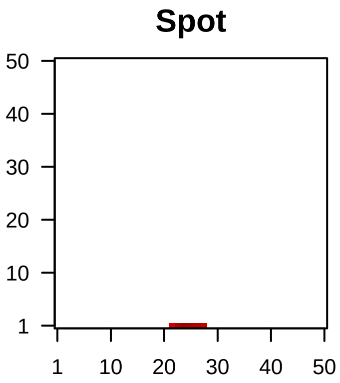
Spot Summary: Y

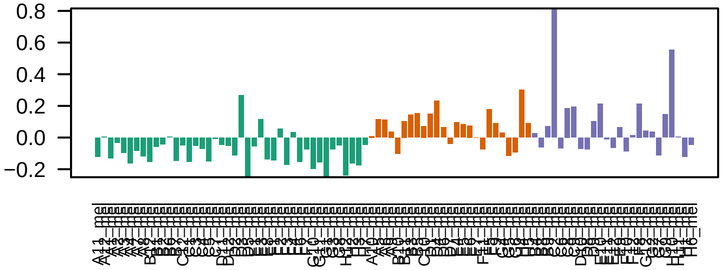
metagenes = 7
genes = 166

<r> metagenes = 0.94
<r> genes = 0.18
beta: r2= 1.48 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 1 (2.4 %)
MSC2 : 2 (8 %)
MSC3 : 6 (24 %)


Overview Map


Spot

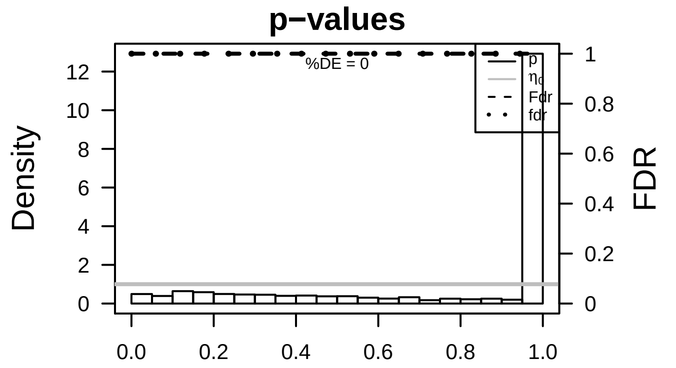


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PELP1	1.9	−0.32	0.55	PELP1	proline, glutamate and leucine rich protein 1 [Source:HGNC S
2	RCBTB2	1.87	−0.27	0.37	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (PC
3	BMP4	1.84	−0.21	0.45	BMP4	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:H
4	BBS10	1.74	−0.2	0.49	BBS10	Bardet−Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGN
5	ATG2B	1.7	−0.32	0.46	ATG2B	autophagy related 2B [Source:HGNC Symbol;Acc:HGNC:201
6	ATG4A	1.64	−0.6	0.24	ATG4A	autophagy related 4A, cysteine peptidase [Source:HGNC Sy
7	GALK2	1.64	−0.44	0.28	GALK2	galactokinase 2 [Source:HGNC Symbol;Acc:HGNC:4119]
8	ZNF525	1.63	−0.32	0.36	ZNF525	zinc finger protein 525 [Source:HGNC Symbol;Acc:HGNC:29
9	ITSN2	1.62	−0.64	0.33	ITSN2	intersectin 2 [Source:HGNC Symbol;Acc:HGNC:6184]
10	IKBKE	1.62	−0.27	0.43	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B−cells,
11	RNF25	1.6	−0.33	0.28	RNF25	ring finger protein 25 [Source:HGNC Symbol;Acc:HGNC:146
12	AKR1C3	1.59	−0.15	0.54	AKR1C3	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
13	FBXO36	1.58	−0.24	0.35	FBXO36	F−box protein 36 [Source:HGNC Symbol;Acc:HGNC:27020]
14	TLE1	1.57	−0.57	0.46	TLE1	transducin−like enhancer of split 1 (E(sp1) homolog, Drosoph
15	POLL	1.56	−0.27	0.33	POLL	polymerase (DNA directed), lambda [Source:HGNC Symbol;
16	ADCY6	1.55	−0.31	0.46	ADCY6	adenylate cyclase 6 [Source:HGNC Symbol;Acc:HGNC:237]
17	NCKAP5L	1.46	−0.2	0.4	NCKAP5L	NCK−associated protein 5−like [Source:HGNC Symbol;Acc:H
18	WDR73	1.46	−0.53	0.31	WDR73	WD repeat domain 73 [Source:HGNC Symbol;Acc:HGNC:25
19	ARNT	1.44	−0.88	0.36	ARNT	aryl hydrocarbon receptor nuclear translocator [Source:HGN
20	DIRC2	1.43	−0.34	0.39	DIRC2	disrupted in renal carcinoma 2 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−06	5 / 19	BP	protein targeting to Golgi
2	1e−05	5 / 28	BP	intracellular transport
3	1e−04	6 / 68	GSEA	KEGG_RENAL_CELL_CARCINOMA
4	1e−04	5 / 43	BP	autophagic vacuole assembly
5	5e−04	6 / 93	GSEA	REACTOME_SIGNALING_BY_FGFR
6	6e−04	10 / 259	BP	protein targeting
7	7e−04	6 / 99	GSEA	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
8	8e−04	3 / 17	BP	cellular response to nitrogen starvation
9	1e−03	6 / 107	GSEA	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
10	1e−03	2 / 5	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
11	1e−03	10 / 287	GSEA	GRESHOCK_CANCER_COPY_NUMBER_UP
12	1e−03	4 / 44	GSEA	PID_HES_HEY_PATHWAY
13	1e−03	3 / 21	BP	nucleophagy
14	2e−03	3 / 23	BP	response to tumor necrosis factor
15	2e−03	4 / 49	miRN	hsa−miR−1224−3p
16	2e−03	6 / 120	GSEA	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_ME
17	2e−03	5 / 83	GSEA	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR
18	2e−03	5 / 84	GSEA	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION
19	2e−03	2 / 7	GSEA	JIANG_CORE_DUPLICON_GENES
20	3e−03	5 / 89	GSEA	REACTOME_SIGNALING_BY_ERBB2
21	3e−03	3 / 27	BP	retina homeostasis
22	3e−03	3 / 27	GSEA	WANG_RESPONSE_TO_ANDROGEN_UP
23	3e−03	3 / 27	GSEA	NOJIMA_SFRP2_TARGETS_UP
24	3e−03	3 / 27	GSEA	CHOW_RASSF1_TARGETS_DN
25	4e−03	6 / 136	GSEA	KEGG_CHEMOKINE_SIGNALING_PATHWAY
26	4e−03	3 / 29	MF	ubiquitin−like protein transferase activity
27	4e−03	30 / 1664	BP	transcription, DNA−templated
28	4e−03	4 / 59	GSEA	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY
29	4e−03	3 / 30	BP	cellular response to calcium ion
30	4e−03	6 / 139	GSEA	FIRESTEIN_PROLIFERATION
31	4e−03	4 / 61	GSEA	REACTOME_SIGNALING_BY_NOTCH1
32	5e−03	4 / 63	GSEA	LIN_MELANOMA_COPY_NUMBER_UP
33	5e−03	3 / 32	BP	mitochondrion degradation
34	5e−03	3 / 32	BP	positive regulation of cell death
35	5e−03	8 / 244	MF	ubiquitin−protein transferase activity
36	6e−03	3 / 34	GSEA	PID_HIF2PATHWAY
37	6e−03	3 / 34	GSEA	PID_CD8_TCR_DOWNSTREAM_PATHWAY
38	6e−03	2 / 11	BP	stress fiber assembly
39	6e−03	5 / 107	GSEA	REACTOME_SIGNALING_BY_PDGF
40	7e−03	7 / 201	GSEA	RAO_BOUND_BY_SALL4


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.[illegible]	0 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−06	5 / 19	protein targeting to Golgi
2	1e−05	5 / 28	intracellular transport
3	1e−04	5 / 43	autophagic vacuole assembly
4	6e−04	10 / 259	protein targeting
5	8e−04	3 / 17	cellular response to nitrogen starvation
6	1e−03	3 / 21	nucleophagy
7	2e−03	3 / 23	response to tumor necrosis factor
8	3e−03	3 / 27	retina homeostasis
9	4e−03	30 / 1664	transcription, DNA−templated
10	4e−03	3 / 30	cellular response to calcium ion
11	5e−03	3 / 32	mitochondrion degradation
12	5e−03	3 / 32	positive regulation of cell death
13	6e−03	2 / 11	stress fiber assembly
14	9e−03	2 / 13	cellular response to prostaglandin E stimulus
15	1e−02	3 / 41	cellular response to hydrogen peroxide
16	1e−02	3 / 41	positive regulation of protein binding
17	1e−02	3 / 41	protein peptidyl−prolyl isomerization
18	1e−02	2 / 15	positive regulation of histone acetylation
19	1e−02	2 / 16	renal system development
20	1e−02	3 / 45	protein K48−linked ubiquitination

Brain

Rank	p−value	#in/all	Geneset
1	0.04	18 / 1050	Fetal_EnhP
2	0.04	76 / 5940	Overlap_fetal_midbrain_HetRpts
3	0.18	6 / 349	Fetal_ZNF
4	0.24	11 / 786	Fetal_EnhG
5	0.25	3 / 158	Overlap_fetal_midbrain_Het
6	0.28	37 / 3081	Mid_Frontal_Lobe_ZNF
7	0.45	13 / 1122	Fetal_K9K27me3
8	0.49	15 / 1333	Fetal_ReprPCWk
9	0.53	6 / 534	Mid_Frontal_Lobe_EnhG
10	0.53	2 / 163	Fetal_ReprPC
11	0.58	7 / 656	Overlap_fetal_midbrain_EnhP
12	0.59	101 / 9330	Overlap_fetal_midbrain_ReprPC
13	0.60	7 / 668	Mid_Frontal_Lobe_Enh
14	0.60	8 / 765	Mid_Frontal_Lobe_Het
15	0.61	8 / 769	Overlap_fetal_midbrain_ZNF
16	0.65	3 / 304	Fetal_Het
17	0.82	1 / 156	Mid_Frontal_Lobe_TssA
18	0.83	93 / 9013	Overlap_fetal_midbrain_K9K27me3
19	0.87	4 / 564	Mid_Frontal_Lobe_EnhP
20	0.90	6 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 18	PanCan_Notch_geneset_nanostring
2	0.04	4 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.05	5 / 180	SPANG_LPS−index2
4	0.08	2 / 44	PanCan_TGF−B_geneset_nanostring
5	0.12	2 / 55	PanCan_JAK−ST_geneset_nanostring
6	0.13	1 / 13	GENTLES_modul12
7	0.14	1 / 14	LIU_COMMON_CANCER_GENES
8	0.15	3 / 121	PanCan_MAPK_geneset_nanostring
9	0.15	1 / 15	GENTLES_modul4
10	0.16	1 / 16	GENTLES_modul6
11	0.16	1 / 16	GENTLES_modul16
12	0.21	1 / 22	PanCan_HH_geneset_nanostring
13	0.34	2 / 111	PanCan_RAS_geneset_nanostring
14	0.38	2 / 120	PanCan_CC+Apop_geneset_nanostring
15	0.49	1 / 61	PanCan_Wnt_geneset_nanostring
16	0.51	2 / 156	PanCan_PI3K_geneset_nanostring
17	0.62	0 / 14	LIU_PROSTATE_CANCER_DN
18	0.63	3 / 298	SPANG_BCL6−index2
19	0.79	4 / 489	Lembcke_Normal vs Adenoma
20	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	0.007	78 / 5696	nucleus
2	0.011	2 / 15	pre−autophagosomal structure membrane
3	0.019	3 / 52	coated pit
4	0.028	2 / 24	Cul3−RING ubiquitin ligase complex
5	0.040	2 / 29	heterotrimeric G−protein complex
6	0.044	37 / 2577	nucleoplasm
7	0.053	2 / 34	ER to Golgi transport vesicle membrane
8	0.056	2 / 35	condensed nuclear chromosome
9	0.065	13 / 747	nucleolus
10	0.079	3 / 92	early endosome membrane
11	0.090	3 / 97	chromatin
12	0.097	5 / 223	lysosomal membrane
13	0.104	1 / 10	MHC class I protein complex
14	0.104	1 / 10	WASH complex
15	0.114	1 / 11	filopodium tip
16	0.114	1 / 11	Gemini of coiled bodies
17	0.114	4 / 169	transcription factor complex
18	0.123	1 / 12	holo TFIIH complex
19	0.123	1 / 12	SMN complex
20	0.123	1 / 12	U4/U6 x U5 tri−snRNP complex

Chr

Rank	p−value	#in/all	Geneset
1	0.1	16 / 1037	Chr 19
2	0.1	15 / 993	Chr 2
3	0.1	11 / 687	Chr 6
4	0.1	11 / 689	Chr 7
5	0.1	21 / 1500	Chr 1
6	0.3	8 / 552	Chr 10
7	0.3	6 / 398	Chr 20
8	0.3	4 / 262	Chr 13
9	0.5	4 / 335	Chr 22
10	0.6	6 / 551	Chr X
11	0.6	7 / 649	Chr 16
12	0.6	5 / 465	Chr 15
13	0.7	2 / 221	Chr 18
14	0.8	7 / 838	Chr 3
15	0.9	6 / 801	Chr 11
16	0.9	3 / 462	Chr 14
17	0.9	3 / 469	Chr 8
18	0.9	6 / 840	Chr 17
19	0.9	5 / 775	Chr 12
20	0.9	3 / 558	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
2	0.08	1 / 8	KIM_CRC−MSI−regulated_DN
3	0.15	1 / 15	TCGA_Mutated−in−CRC_hypermutated
4	0.16	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
5	0.16	1 / 16	Vilar_non−hypermutated−in−CRC
6	0.17	1 / 17	Vilar_mutated−in−CRC−CamP
7	0.17	1 / 17	Vilar_hypermutated−in−CRC
8	0.18	1 / 18	Ang_CRC−CIMPH−vs−L_hypo
9	0.22	6 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
10	0.24	1 / 25	Ang_CRC_Hypomethylated
11	0.27	3 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	0.27	34 / 2798	TxEnhG1_Colon
13	0.31	2 / 102	Marisa_CRC−cluster−d
14	0.32	12 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	0.37	2 / 117	Marisa_CRC−cluster−b
16	0.38	96 / 8580	TxWk_Colon
17	0.42	2 / 131	Marisa_CRC−cluster−a
18	0.43	9 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
19	0.46	12 / 1038	HetRpts_Colon
20	0.49	30 / 2698	EnhA_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.6	3 / 294	GUDJ_psoriasis down
2	1.0	2 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.09	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
2	0.15	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
3	0.20	2 / 75	Weller_LGG_A_vs_O_DOWN
4	0.21	12 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.25	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	0.26	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
7	0.34	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
8	0.36	1 / 40	in vivo astrocytes vs. cultured astroglia
9	0.39	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
10	0.40	1 / 47	Vishal_subnetwork signature of survival in GBM
11	0.47	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
12	0.51	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
13	0.53	1 / 68	GIEZELT_GBM_WT_down_VS_mut
14	0.53	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
15	0.53	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
16	0.54	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
17	0.55	1 / 72	laffaire_hypermeth_LGG_vs_control
18	0.56	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
19	0.56	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
20	0.57	4 / 365	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	6 / 68	KEGG_RENAL_CELL_CARCINOMA
2	5e−04	6 / 93	REACTOME_SIGNALING_BY_FGFR
3	7e−04	6 / 99	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
4	1e−03	6 / 107	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
5	1e−03	2 / 5	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
6	1e−03	10 / 287	GRESHOCK_CANCER_COPY_NUMBER_UP
7	1e−03	4 / 44	PID_HES_HEY_PATHWAY
8	2e−03	6 / 120	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMB
9	2e−03	5 / 83	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR
10	2e−03	5 / 84	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION
11	2e−03	2 / 7	JIANG_CORE_DUPLICON_GENES
12	3e−03	5 / 89	REACTOME_SIGNALING_BY_ERBB2
13	3e−03	3 / 27	WANG_RESPONSE_TO_ANDROGEN_UP
14	3e−03	3 / 27	NOJIMA_SFRP2_TARGETS_UP
15	3e−03	3 / 27	CHOW_RASSF1_TARGETS_DN
16	4e−03	6 / 136	KEGG_CHEMOKINE_SIGNALING_PATHWAY
17	4e−03	4 / 59	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY
18	4e−03	6 / 139	FIRESTEIN_PROLIFERATION
19	4e−03	4 / 61	REACTOME_SIGNALING_BY_NOTCH1
20	5e−03	4 / 63	LIN_MELANOMA_COPY_NUMBER_UP

HM

Rank	p−value	#in/all	Geneset
1	0.04	2 / 29	HALLMARK_NOTCH_SIGNALING
2	0.06	4 / 137	HALLMARK_UV_RESPONSE_DN
3	0.08	3 / 94	HALLMARK_ANDROGEN_RESPONSE
4	0.13	2 / 57	HALLMARK_MYC_TARGETS_V2
5	0.16	3 / 127	HALLMARK_KRAS_SIGNALING_DN
6	0.21	3 / 146	HALLMARK_DNA_REPAIR
7	0.23	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
8	0.26	2 / 91	HALLMARK_PROTEIN_SECRETION
9	0.28	2 / 95	HALLMARK_SPERMATOGENESIS
10	0.29	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
11	0.30	3 / 176	HALLMARK_HYPOXIA
12	0.33	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	0.34	3 / 188	HALLMARK_MYC_TARGETS_V1
14	0.40	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
15	0.45	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	0.48	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
17	0.55	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
18	0.56	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
19	0.57	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	0.58	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	1.00	0 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	21 / 1128	SPANG_BCR DN
2	0.06	1 / 6	DAVE_MHCCII BL DN
3	0.12	18 / 1218	SPANG_BCR UP
4	0.13	1 / 13	BENTINK_mBL UP
5	0.30	1 / 33	LEE_Developmental_regulators
6	0.33	2 / 109	ROSOLOWSKI_green total
7	0.34	4 / 268	SPANG_IL21 UP
8	0.37	1 / 42	CARO_OxPhos_in_DLBCL_UP
9	0.40	1 / 47	Subero_FL_hyper_meth
10	0.42	1 / 50	SPANG_BAFF 9hrs DN
11	0.44	58 / 5184	HOPP_Txn_transition
12	0.46	5 / 410	SPANG_CD40 6hrs DN
13	0.51	3 / 247	ZHANG_DLBCL mutated
14	0.59	3 / 280	SPANG_CD40 6hrs UP
15	0.59	1 / 82	ROSOLOWSKI_green UP
16	0.65	1 / 96	Subero_DLBCL_hyper_meth
17	0.68	58 / 5538	HOPP_Weak_txn
18	0.69	26 / 2563	HOPP_Heterochrom
19	0.72	59 / 5693	HOPP_Weak_enhancer
20	0.75	79 / 7592	HOPP_Active_promoter

MF

Rank	p−value	#in/all	Geneset
1	0.004	3 / 29	ubiquitin−like protein transferase activity
2	0.005	8 / 244	ubiquitin−protein transferase activity
3	0.009	2 / 13	GABA receptor binding
4	0.010	3 / 41	peptidyl−prolyl cis−trans isomerase activity
5	0.011	2 / 15	mitogen−activated protein kinase kinase binding
6	0.014	2 / 17	receptor signaling complex scaffold activity
7	0.022	2 / 21	RNA polymerase II transcription corepressor activity
8	0.025	6 / 205	ubiquitin protein ligase binding
9	0.030	9 / 397	transcription factor binding
10	0.032	2 / 26	NF−kappaB binding
11	0.033	18 / 1033	nucleic acid binding
12	0.042	2 / 30	RNA polymerase II transcription factor binding
13	0.050	2 / 33	estrogen receptor binding
14	0.056	2 / 35	phosphoprotein binding
15	0.061	2 / 37	DNA−directed RNA polymerase activity
16	0.061	2 / 37	histone acetyltransferase activity
17	0.066	7 / 325	protein serine/threonine kinase activity
18	0.066	9 / 461	transferase activity, transferring phosphorus−containing groups
19	0.067	2 / 39	androgen receptor binding
20	0.070	4 / 142	isomerase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	4 / 49	hsa−miR−1224−3p
2	0.007	2 / 12	hsa−miR−614
3	0.008	4 / 71	hsa−miR−331−3p
4	0.010	2 / 14	hsa−miR−891a
5	0.010	5 / 121	hsa−miR−212
6	0.015	5 / 132	hsa−miR−320d
7	0.015	3 / 48	hsa−miR−628−5p
8	0.016	4 / 88	hsa−miR−587
9	0.016	5 / 134	hsa−miR−488
10	0.018	5 / 139	hsa−miR−132
11	0.022	4 / 97	hsa−miR−1303
12	0.022	2 / 21	hsa−miR−596
13	0.022	5 / 146	hsa−miR−320c
14	0.024	2 / 22	hsa−miR−151−5p
15	0.024	4 / 100	hsa−miR−1299
16	0.026	2 / 23	hsa−miR−517a
17	0.028	2 / 24	hsa−miR−483−3p
18	0.029	3 / 61	hsa−miR−324−5p
19	0.030	6 / 214	hsa−miR−182
20	0.030	2 / 25	hsa−miR−517c

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	NOWICK_TF
2	0.3	8 / 553	ICGC_RxraPcr1_targets
3	0.3	21 / 1701	HEBENSTREIT_high expression TF
4	0.4	25 / 2136	ICGC_GabpPcr2_targets
5	0.4	45 / 3966	ICGC_Pu1_targets
6	0.5	31 / 2836	ICGC_BatfPcr1_targets
7	0.5	14 / 1273	ICGC_P300_targets
8	0.5	59 / 5408	ICGC_Pou2_targets
9	0.6	50 / 4617	ICGC_Tcf12_targets
10	0.6	56 / 5219	ICGC_Tcf3_targets
11	0.6	50 / 4689	ICGC_Taf1_targets
12	0.7	42 / 4032	ICGC_Creb1_targets
13	0.7	27 / 2714	ICGC_Irf4_targets
14	0.7	48 / 4706	ICGC_Sp1_targets
15	0.8	55 / 5374	ICGC_Pax5_targets
16	0.8	54 / 5355	ICGC_Pol2_targets
17	0.8	5 / 653	ICGC_SrfPcr2_targets
18	0.9	46 / 4829	ICGC_Nficsc81335_targets
19	0.9	4 / 595	ICGC_NrsfPcr2_targets
20	0.9	44 / 4682	ICGC_Pol24_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.09	1 / 9	VAQUERIZAS_Kidney
2	0.12	1 / 12	VAQUERIZAS_Skin
3	0.16	1 / 16	VAQUERIZAS_Pancreas
4	0.25	1 / 26	VAQUERIZAS_Liver
5	0.26	1 / 27	VAQUERIZAS_Lymph node
6	0.30	1 / 33	VAQUERIZAS_Prostate
7	0.39	1 / 45	VAQUERIZAS_Uterus
8	0.47	1 / 58	VAQUERIZAS_Lung
9	0.48	1 / 59	VAQUERIZAS_Whole blood
10	0.79	1 / 143	VAQUERIZAS_General
11	1.00	0 / 36	VAQUERIZAS_Fetal brain
12	1.00	0 / 41	VAQUERIZAS_Placenta
13	1.00	0 / 29	VAQUERIZAS_Smooth muscle
14	1.00	0 / 23	VAQUERIZAS_Spinal cord
15	1.00	0 / 38	VAQUERIZAS_Whole brain
16	1.00	0 / 37	VAQUERIZAS_Thymus
17	1.00	0 / 40	VAQUERIZAS_Thyroid
18	1.00	0 / 7	VAQUERIZAS_Appendix
19	1.00	0 / 29	VAQUERIZAS_Fetal lung
20	1.00	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	WIRTH_Cerebellum
2	0.3	5 / 350	WIRTH_Immune system
3	0.4	3 / 194	PALMER_B−Cell signature up
4	0.7	1 / 107	WIRTH_Testis
5	0.7	1 / 114	PALMER_T−Cell signature up
6	0.9	1 / 225	PALMER_Granulocytes signature up
7	1.0	1 / 350	WIRTH_Nervous System
8	1.0	0 / 32	WIRTH_Pancreas
9	1.0	0 / 11	WIRTH_Sec. lymphoid organs
10	1.0	0 / 11	WIRTH_Prim. lymphoid organs
11	1.0	0 / 13	WIRTH_B−cells
12	1.0	0 / 8	WIRTH_Tonsil
13	1.0	0 / 12	WIRTH_Thymus
14	1.0	0 / 12	WIRTH_Lymphocytes
15	1.0	0 / 5	WIRTH_Bone marrow
16	1.0	0 / 11	WIRTH_Globus pallidus
17	1.0	0 / 14	WIRTH_Telencephalon
18	1.0	0 / 11	WIRTH_Cortex cerebri
19	1.0	0 / 10	WIRTH_Hippocampus
20	1.0	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	10 / 1115	LU_BPDE 1h DN
2	0.9	32 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: Z

metagenes = 16
genes = 104

<r> metagenes = 0.94
<r> genes = 0.1
beta: r2= 0.82 / log p= −Inf

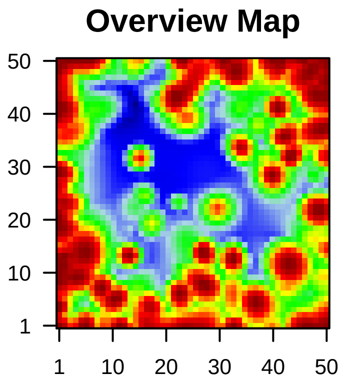
samples with spot = 8 (8.7 %)
MSC1 : 5 (11.9 %)
MSC2 : 2 (8 %)
MSC3 : 1 (4 %)

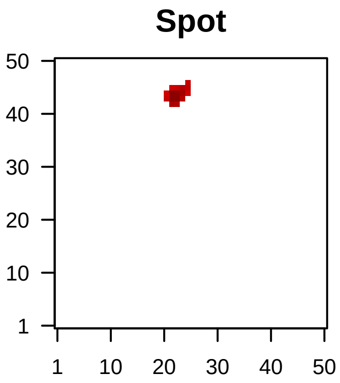
Spot Genelist

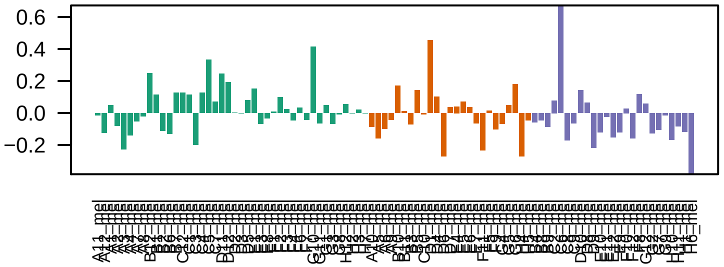
Rank	ID	max e	min e	r	Symbol	Description
1	MPP3	1.79	−0.19	0.22	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily m
2	FAXC	1.75	−0.16	0.43	FAXC	failed axon connections homolog (Drosophila) [Source:HGNC
3	GPRC5D	1.69	−0.02	0.4	GPRC5D	G protein−coupled receptor, class C, group 5, member D [Sou
4	AP3M2	1.69	−0.65	0.34	AP3M2	adaptor−related protein complex 3, mu 2 subunit [Source:HG
5	DISP1	1.64	−0.17	0.29	DISP1	dispatched homolog 1 (Drosophila) [Source:HGNC Symbol;A
6	TXNRD3	1.63	−0.07	0.27	TXNRD3	thioredoxin reductase 3 [Source:HGNC Symbol;Acc:HGNC:2
7	LRRC6	1.62	−0.12	0.25	LRRC6	leucine rich repeat containing 6 [Source:HGNC Symbol;Acc:
8	KLHDC2	1.62	−0.65	0.25	KLHDC2	kelch domain containing 2 [Source:HGNC Symbol;Acc:HGNC
9	CCDC101	1.62	−0.38	0.44	CCDC101	coiled−coil domain containing 101 [Source:HGNC Symbol;Ac
10	GPR146	1.61	−0.08	0.35	GPR146	G protein−coupled receptor 146 [Source:HGNC Symbol;Acc:
11	ZNF699	1.59	−0.05	0.36	ZNF699	zinc finger protein 699 [Source:HGNC Symbol;Acc:HGNC:24
12	ERAP1	1.57	−0.25	0.37	ERAP1	endoplasmic reticulum aminopeptidase 1 [Source:HGNC Sym
13	C11orf74	1.56	−0.37	0.35	C11orf74	chromosome 11 open reading frame 74 [Source:HGNC Symb
14	NDUFAF7	1.56	−0.7	0.33	NDUFAF7	NADH dehydrogenase (ubiquinone) complex I, assembly fact
15	HEXIM2	1.55	−0.19	0.26	HEXIM2	hexamethylene bis−acetamide inducible 2 [Source:HGNC Sy
16	TTC21A	1.53	−0.1	0.23	TTC21A	tetratricopeptide repeat domain 21A [Source:HGNC Symbol;
17	ZBTB17	1.53	−0.51	0.2	ZBTB17	zinc finger and BTB domain containing 17 [Source:HGNC Sy
18	C2orf44	1.51	−0.32	0.33	C2orf44	chromosome 2 open reading frame 44 [Source:HGNC Symbo
19	COQ3	1.5	−0.41	0.38	COQ3	coenzyme Q3 methyltransferase [Source:HGNC Symbol;Acc:
20	TFB1M	1.5	−0.61	0.26	TFB1M	transcription factor B1, mitochondrial [Source:HGNC Symbol;

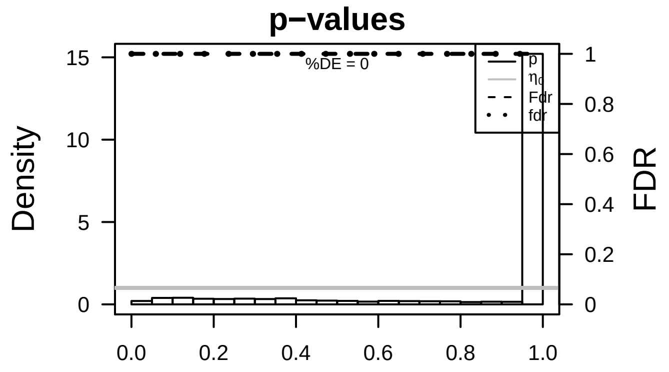
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−07	88 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	7e−06	64 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
3	2e−04	16 / 840	GSEA	GEORGES_TARGETS_OF_MIR192_AND_MIR215
4	5e−04	8 / 265	MF	hydrolase activity
5	1e−03	13 / 687	Chr	Chr 6
6	1e−03	69 / 7592	Lympl	HOPP_Active_promoter
7	1e−03	3 / 30	GSEA	YANG_BREAST_CANCER_ESR1_LASER_UP
8	1e−03	86 / 10290	Colon	TssWk_Colon
9	2e−03	5 / 120	CC	mitochondrial outer membrane
10	2e−03	78 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
11	2e−03	75 / 8580	Colon	TxWk_Colon
12	2e−03	8 / 322	BP	mitochondrion organization
13	3e−03	2 / 11	BP	motile cilium assembly
14	3e−03	80 / 9482	Colon	TssA_Colon
15	3e−03	63 / 6929	Lympl	HOPP_Txn_elongation
16	3e−03	19 / 1394	GSEA	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
17	4e−03	2 / 13	MF	protein kinase C activity
18	4e−03	2 / 13	BP	rRNA methylation
19	5e−03	2 / 15	BP	Golgi to plasma membrane transport
20	5e−03	5 / 157	GSEA	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
21	5e−03	64 / 7209	Lympl	HOPP_Weak_promoter
22	5e−03	2 / 16	GSEA	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN
23	6e−03	76 / 9027	Colon	Tx_Colon
24	6e−03	12 / 748	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
25	6e−03	2 / 17	CC	integral component of mitochondrial outer membrane
26	7e−03	4 / 107	GSEA	SANSOM_APC_TARGETS_UP
27	7e−03	13 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
28	8e−03	2 / 19	BP	mitochondrion morphogenesis
29	8e−03	3 / 59	TF Ti	VAQUERIZAS_Whole blood
30	8e−03	4 / 114	Tissu	PALMER_T−Cell signature up
31	9e−03	8 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
32	1e−02	6 / 263	GSEA	MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN
33	1e−02	2 / 24	BP	anterograde axon cargo transport
34	1e−02	9 / 532	GSEA	PARENT_MTOR_SIGNALING_UP
35	1e−02	3 / 70	BP	positive regulation of neuron projection development
36	1e−02	11 / 729	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
37	2e−02	2 / 27	GSEA	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS
38	2e−02	5 / 209	GSEA	BROWNE_HCMV_INFECTION_16HR_UP
39	2e−02	37 / 3812	Colon	TssD1_Colon
40	2e−02	2 / 28	GSEA	TCGA_GLIOBLASTOMA_COPY_NUMBER_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 38	TESCHENDORFF_age_hypermethylated
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	8 / 322	mitochondrion organization
2	0.003	2 / 11	motile cilium assembly
3	0.004	2 / 13	rRNA methylation
4	0.005	2 / 15	Golgi to plasma membrane transport
5	0.008	2 / 19	mitochondrion morphogenesis
6	0.012	2 / 24	anterograde axon cargo transport
7	0.013	3 / 70	positive regulation of neuron projection development
8	0.017	2 / 29	sphingolipid biosynthetic process
9	0.018	4 / 143	protein homooligomerization
10	0.019	3 / 81	cytoskeleton−dependent intracellular transport
11	0.051	2 / 52	cellular response to oxidative stress
12	0.051	2 / 52	fat cell differentiation
13	0.059	8 / 598	membrane organization
14	0.059	10 / 815	lipid metabolic process
15	0.062	3 / 129	autophagy
16	0.062	2 / 58	ER to Golgi vesicle−mediated transport
17	0.064	2 / 59	Golgi organization
18	0.066	3 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
19	0.068	1 / 10	calcium−mediated signaling using intracellular calcium source
20	0.068	1 / 10	diaphragm development

Brain

Rank	p−value	#in/all	Geneset
1	8e−07	88 / 9330	Overlap_fetal_midbrain_ReprPC
2	7e−06	64 / 5940	Overlap_fetal_midbrain_HetRpts
3	2e−03	78 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	5e−02	13 / 1122	Fetal_K9K27me3
5	5e−02	75 / 9528	Overlap_fetal_midbrain_Quies
6	6e−02	5 / 304	Fetal_Het
7	7e−02	71 / 9013	Overlap_fetal_midbrain_K9K27me3
8	1e−01	7 / 564	Mid_Frontal_Lobe_EnhP
9	2e−01	9 / 884	Overlap_fetal_midbrain_EnhG
10	2e−01	10 / 1050	Fetal_EnhP
11	2e−01	10 / 1065	Overlap_fetal_midbrain_Enh
12	3e−01	15 / 1845	Fetal_Quies
13	3e−01	6 / 656	Overlap_fetal_midbrain_EnhP
14	4e−01	23 / 3081	Mid_Frontal_Lobe_ZNF
15	4e−01	3 / 349	Fetal_ZNF
16	5e−01	6 / 769	Overlap_fetal_midbrain_ZNF
17	5e−01	11 / 1548	Mid_Frontal_Lobe_K9K27me3
18	5e−01	7 / 989	Mid_Frontal_Lobe_Quies
19	6e−01	17 / 2462	Mid_Frontal_Lobe_HetRpts
20	6e−01	8 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	1 / 12	LIU_PROSTATE_CANCER_UP
2	0.26	5 / 489	Lembcke_Normal vs Adenoma
3	0.29	1 / 48	KUIPER_MM poor survival
4	0.29	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.37	0 / 14	LIU_COMMON_CANCER_GENES
6	0.44	1 / 82	PanCan_TXmisReg_geneset_nanostring
7	0.94	1 / 401	Lembcke_Colonic Inflammation
8	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
9	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
10	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_LIVER_CANCER
13	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
14	1.00	0 / 15	WANG_ER_UP
15	1.00	0 / 5	WANG_ER_DN
16	1.00	0 / 16	WOLFER_overlap genes
17	1.00	0 / 12	BEN−PORATH_DN
18	1.00	0 / 13	BEN−PORATH_UP
19	1.00	0 / 15	GENTLES_modul1
20	1.00	0 / 16	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	0.002	5 / 120	mitochondrial outer membrane
2	0.006	2 / 17	integral component of mitochondrial outer membrane
3	0.050	2 / 51	filopodium
4	0.060	2 / 57	proteasome complex
5	0.074	1 / 11	nuclear periphery
6	0.081	1 / 12	npBAF complex
7	0.081	1 / 12	transcription export complex
8	0.084	5 / 332	cell junction
9	0.085	8 / 649	endoplasmic reticulum membrane
10	0.087	1 / 13	Fanconi anaemia nuclear complex
11	0.087	1 / 13	integrator complex
12	0.087	1 / 13	nBAF complex
13	0.087	1 / 13	SWI/SNF complex
14	0.094	1 / 14	exocyst
15	0.094	1 / 14	integral component of peroxisomal membrane
16	0.094	1 / 14	trans−Golgi network transport vesicle
17	0.094	4 / 246	mitochondrial matrix
18	0.100	1 / 15	alpha−amino−3−hydroxy−5−methyl−4−isoxazolepropionic acid selective gluta
19	0.100	1 / 15	BAF−type complex
20	0.104	2 / 78	ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.001	13 / 687	Chr 6
2	0.106	6 / 462	Chr 14
3	0.133	9 / 838	Chr 3
4	0.176	8 / 775	Chr 12
5	0.202	3 / 221	Chr 18
6	0.260	9 / 993	Chr 2
7	0.353	6 / 689	Chr 7
8	0.353	5 / 558	Chr 4
9	0.362	6 / 696	Chr 5
10	0.418	4 / 469	Chr 8
11	0.418	3 / 335	Chr 22
12	0.531	3 / 398	Chr 20
13	0.544	4 / 552	Chr 10
14	0.551	2 / 262	Chr 13
15	0.656	1 / 151	Chr 21
16	0.839	3 / 649	Chr 16
17	0.860	5 / 1037	Chr 19
18	0.903	2 / 551	Chr X
19	0.939	3 / 840	Chr 17
20	0.964	1 / 465	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	86 / 10290	TssWk_Colon
2	0.002	75 / 8580	TxWk_Colon
3	0.003	80 / 9482	TssA_Colon
4	0.006	76 / 9027	Tx_Colon
5	0.006	12 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
6	0.016	37 / 3812	TssD1_Colon
7	0.017	70 / 8415	Quies3_Colon
8	0.059	12 / 1038	HetRpts_Colon
9	0.070	5 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
10	0.104	14 / 1386	Het_Colon
11	0.113	1 / 17	Vilar_mutated−in−CRC−CamP
12	0.169	7 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	0.223	10 / 1079	ZNF_Colon
14	0.261	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
15	0.307	30 / 3897	Quies1_Colon
16	0.353	70 / 9653	Enh_Colon
17	0.418	25 / 3383	EnhWk2_Colon
18	0.497	51 / 7203	TssF_Colon
19	0.513	1 / 102	Marisa_CRC−cluster−d
20	0.517	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.8	2 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
2	0.07	2 / 63	Stuehler_Proteins_up_in_STS
3	0.08	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
4	0.12	1 / 18	Barbus_GBM_STS_vs._LTS
5	0.15	1 / 23	WIRTH_PN subtype
6	0.18	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.37	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
8	0.37	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
9	0.38	1 / 68	GIEZELT_GBM_WT_down_VS_mut
10	0.38	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	0.41	1 / 75	Weller_LGG_A_vs_O_DOWN
12	0.41	3 / 332	Up
13	0.67	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
14	0.71	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
15	0.72	2 / 356	Down_a
16	0.73	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
17	1.00	0 / 15	VERHAAK_CL subtype
18	1.00	0 / 15	VERHAAK_MES subtype
19	1.00	0 / 16	VERHAAK_NL subtype
20	1.00	0 / 14	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	16 / 840	GEORGES_TARGETS_OF_MIR192_AND_MIR215
2	1e−03	3 / 30	YANG_BREAST_CANCER_ESR1_LASER_UP
3	3e−03	19 / 1394	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
4	5e−03	5 / 157	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
5	5e−03	2 / 16	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN
6	7e−03	4 / 107	SANSOM_APC_TARGETS_UP
7	7e−03	13 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
8	9e−03	8 / 416	SHEN_SMARCA2_TARGETS_UP
9	1e−02	6 / 263	MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN
10	1e−02	9 / 532	PARENT_MTOR_SIGNALING_UP
11	1e−02	11 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
12	2e−02	2 / 27	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS
13	2e−02	5 / 209	BROWNE_HCMV_INFECTION_16HR_UP
14	2e−02	2 / 28	TCGA_GLIOBLASTOMA_COPY_NUMBER_DN
15	2e−02	2 / 28	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP
16	2e−02	7 / 376	OSMAN_BLADDER_CANCER_UP
17	2e−02	2 / 30	CAFFAREL_RESPONSE_TO_THC_UP
18	2e−02	2 / 31	MARZEC_IL2_SIGNALING_DN
19	2e−02	5 / 222	UDAYAKUMAR_MED1_TARGETS_DN
20	2e−02	3 / 83	LEIN_CHOROID_PLEXUS_MARKERS

HM

Rank	p−value	#in/all	Geneset
1	0.04	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	0.15	3 / 188	HALLMARK_ADIPOGENESIS
3	0.22	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
4	0.22	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.26	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
6	0.41	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	0.46	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.47	1 / 91	HALLMARK_BILE_ACID_METABOLISM
9	0.48	1 / 93	HALLMARK_PEROXISOME
10	0.49	1 / 95	HALLMARK_SPERMATOGENESIS
11	0.49	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.63	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
13	0.64	1 / 146	HALLMARK_DNA_REPAIR
14	0.65	1 / 148	HALLMARK_KRAS_SIGNALING_UP
15	0.69	1 / 167	HALLMARK_APICAL_JUNCTION
16	0.69	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
17	0.70	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	0.70	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
19	0.71	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	0.71	1 / 174	HALLMARK_HEME_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	69 / 7592	HOPP_Active_promoter
2	0.003	63 / 6929	HOPP_Txn_elongation
3	0.005	64 / 7209	HOPP_Weak_promoter
4	0.042	49 / 5693	HOPP_Weak_enhancer
5	0.047	45 / 5184	HOPP_Txn_transition
6	0.051	13 / 1128	SPANG_BCR DN
7	0.060	47 / 5538	HOPP_Weak_txn
8	0.087	1 / 13	WRIGHT_GCB UP
9	0.094	1 / 14	Subero_MCL_hyper_meth
10	0.131	1 / 20	SPANG_BAFF 9hrs UP
11	0.178	2 / 109	ROSOLOWSKI_green total
12	0.232	11 / 1218	SPANG_BCR UP
13	0.282	1 / 47	Subero_FL_hyper_meth
14	0.290	3 / 268	SPANG_IL21 UP
15	0.345	1 / 60	Subero_T−ALL_hyper_meth
16	0.433	19 / 2563	HOPP_Heterochrom
17	0.435	1 / 81	Subero_INT_hyper_meth
18	0.439	1 / 82	ROSOLOWSKI_green UP
19	0.492	1 / 96	Subero_DLBCL_hyper_meth
20	0.519	2 / 247	ZHANG_DLBCL_mutated

MF

Rank	p−value	#in/all	Geneset
1	5e−04	8 / 265	hydrolase activity
2	4e−03	2 / 13	protein kinase C activity
3	3e−02	13 / 1033	nucleic acid binding
4	4e−02	4 / 189	methyltransferase activity
5	5e−02	2 / 51	ubiquitin binding
6	7e−02	1 / 10	guanylate kinase activity
7	7e−02	1 / 10	hedgehog receptor activity
8	7e−02	1 / 10	protein phosphatase type 1 regulator activity
9	7e−02	1 / 10	sodium channel activity
10	8e−02	1 / 12	cyclin−dependent protein serine/threonine kinase inhibitor activity
11	8e−02	1 / 12	miRNA binding
12	8e−02	1 / 12	phosphorus−oxygen lyase activity
13	8e−02	1 / 12	poly(U) RNA binding
14	9e−02	1 / 13	Ral GTPase binding
15	9e−02	97 / 13179	molecular_function
16	9e−02	1 / 14	phospholipase A2 activity
17	9e−02	1 / 14	polypeptide N−acetylgalactosaminyltransferase activity
18	1e−01	18 / 1859	metal ion binding
19	1e−01	1 / 15	ARF guanyl−nucleotide exchange factor activity
20	1e−01	2 / 77	electron carrier activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	6 / 294	hsa−miR−561
2	0.03	1 / 5	hsa−miR−1268
3	0.04	4 / 183	hsa−miR−1283
4	0.04	3 / 110	hsa−miR−491−3p
5	0.05	3 / 118	hsa−miR−509−3p
6	0.07	3 / 133	hsa−miR−485−5p
7	0.07	2 / 63	hsa−miR−1278
8	0.08	3 / 144	hsa−miR−548f
9	0.09	2 / 70	hsa−miR−502−5p
10	0.10	3 / 155	hsa−miR−31
11	0.10	2 / 75	hsa−miR−651
12	0.10	3 / 157	hsa−miR−512−3p
13	0.11	5 / 358	hsa−let−7d
14	0.11	2 / 80	hsa−miR−584
15	0.11	1 / 17	hsa−miR−1298
16	0.12	4 / 269	hsa−miR−101
17	0.13	3 / 177	hsa−miR−548e
18	0.13	3 / 181	hsa−miR−548a−3p
19	0.14	3 / 183	hsa−miR−129−5p
20	0.15	2 / 96	hsa−miR−513b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	1 / 12	BENTINK_e2f3.2
2	1.00	0 / 12	GUSTAFSON_PI3K_UP
3	1.00	0 / 13	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_myc.1
6	1.00	0 / 12	BENTINK_ras.1
7	1.00	0 / 9	BENTINK_ras.4
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.2	15 / 1701	HEBENSTREIT_high expression TF
2	0.4	20 / 2714	ICGC_Irf4_targets
3	0.5	33 / 4682	ICGC_Pol24_targets
4	0.5	9 / 1266	ICGC_NrsfPcr1_targets
5	0.6	8 / 1139	HEBENSTREIT_low expression TF
6	0.6	14 / 2013	ICGC_Bcl11_targets
7	0.6	8 / 1171	KIM_MYC targets
8	0.6	4 / 595	ICGC_NrsfPcr2_targets
9	0.6	16 / 2391	ICGC_Pbx3_targets
10	0.7	4 / 653	ICGC_SrfPcr2_targets
11	0.7	32 / 4829	ICGC_Nficsc81335_targets
12	0.7	4 / 690	ICGC_Atf3_targets
13	0.7	34 / 5219	ICGC_Tcf3_targets
14	0.8	28 / 4385	ICGC_Atf2_targets
15	0.8	8 / 1383	ICGC_Six5_targets
16	0.8	11 / 1872	ICGC_Mef2_targets
17	0.8	23 / 3700	ICGC_Nfatc1_targets
18	0.8	34 / 5355	ICGC_Pol2_targets
19	0.8	29 / 4689	ICGC_Taf1_targets
20	0.8	7 / 1314	ICGC_Usf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.008	3 / 59	VAQUERIZAS_Whole blood
2	0.074	1 / 11	VAQUERIZAS_Fetal liver
3	0.149	1 / 23	VAQUERIZAS_Spinal cord
4	0.167	1 / 26	VAQUERIZAS_Liver
5	0.173	1 / 27	VAQUERIZAS_Lymph node
6	0.185	1 / 29	VAQUERIZAS_Fetal lung
7	0.207	1 / 33	VAQUERIZAS_Prostate
8	0.224	1 / 36	VAQUERIZAS_Fetal brain
9	0.229	1 / 37	VAQUERIZAS_Thymus
10	0.235	1 / 38	VAQUERIZAS_Testis
11	0.245	1 / 40	VAQUERIZAS_Thyroid
12	0.265	2 / 143	VAQUERIZAS_General
13	0.335	1 / 58	VAQUERIZAS_Lung
14	1.000	0 / 41	VAQUERIZAS_Placenta
15	1.000	0 / 29	VAQUERIZAS_Smooth muscle
16	1.000	0 / 45	VAQUERIZAS_Uterus
17	1.000	0 / 9	VAQUERIZAS_Kidney
18	1.000	0 / 38	VAQUERIZAS_Whole brain
19	1.000	0 / 7	VAQUERIZAS_Appendix
20	1.000	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.008	4 / 114	PALMER_T−Cell signature up
2	0.081	1 / 12	WIRTH_Cerebellum
3	0.747	1 / 194	PALMER_B−Cell signature up
4	0.917	1 / 350	WIRTH_Immune system
5	0.917	1 / 350	WIRTH_Nervous System
6	1.000	0 / 32	WIRTH_Pancreas
7	1.000	0 / 11	WIRTH_Sec. lymphoid organs
8	1.000	0 / 11	WIRTH_Prim. lymphoid organs
9	1.000	0 / 13	WIRTH_B−cells
10	1.000	0 / 8	WIRTH_Tonsil
11	1.000	0 / 12	WIRTH_Thymus
12	1.000	0 / 12	WIRTH_Lymphocytes
13	1.000	0 / 5	WIRTH_Bone marrow
14	1.000	0 / 11	WIRTH_Globus pallidus
15	1.000	0 / 14	WIRTH_Telencephalon
16	1.000	0 / 11	WIRTH_Cortex cerebri
17	1.000	0 / 10	WIRTH_Hippocampus
18	1.000	0 / 10	WIRTH_Thalamus
19	1.000	0 / 107	WIRTH_Testis
20	1.000	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	32 / 3682	LU_BPDE 0.005 DN
2	0.8	6 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

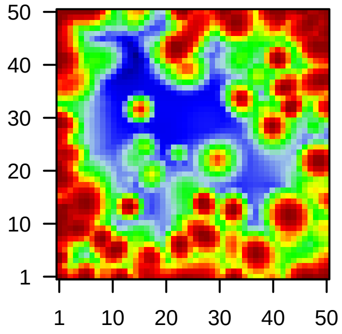
Spot Summary: A1

metagenes = 14
genes = 177

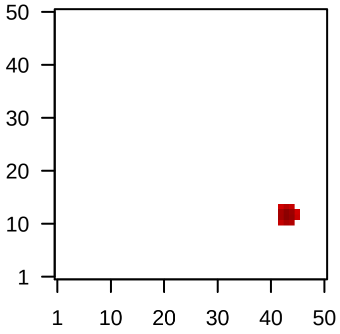
<r> metagenes = 0.98
<r> genes = 0.25
beta: r2= 1.46 / log p= −Inf

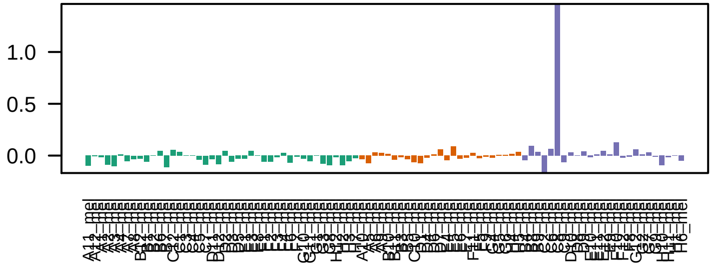
samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

Overview Map



Spot





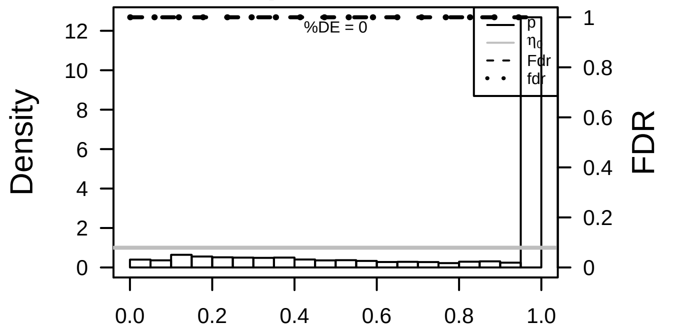
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	KRTAP21−2	2.37	−0.09	0.56	KRTAP21−2	keratin associated protein 21−2 [Source:HGNC Symbol;Acc:H
2	GPR133	2.19	−0.03	0.96		
3	FBXL2	2.11	−0.4	0.39	FBXL2	F−box and leucine−rich repeat protein 2 [Source:HGNC Symb
4	MNDA	2.08	−0.03	0.96	MNDA	myeloid cell nuclear differentiation antigen [Source:HGNC Sy
5	NREP	2.03	−0.33	0.4	NREP	neuronal regeneration related protein [Source:HGNC Symbol
6	TUBA4A	2.01	−0.13	0.45	TUBA4A	tubulin, alpha 4a [Source:HGNC Symbol;Acc:HGNC:12407]
7	PHKA2	2.01	−0.19	0.51	PHKA2	phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
8	NCAM2	2	−0.23	0.4	NCAM2	neural cell adhesion molecule 2 [Source:HGNC Symbol;Acc:H
9	DCN	1.98	−0.06	0.65	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
10	SLC14A1	1.98	−0.03	0.93	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd bl
11	KIAA1324L	1.97	−0.39	0.3	KIAA1324L	KIAA1324−like [Source:HGNC Symbol;Acc:HGNC:21945]
12	PRKAG2	1.92	−0.36	0.32	PRKAG2	protein kinase, AMP−activated, gamma 2 non−catalytic subu
13	WFDC3	1.92	−0.04	0.65	WFDC3	WAP four−disulfide core domain 3 [Source:HGNC Symbol;Ac
14	GAB1	1.9	−0.32	0.44	GAB1	GRB2−associated binding protein 1 [Source:HGNC Symbol;
15	CCDC149	1.89	−0.13	0.59	CCDC149	coiled−coil domain containing 149 [Source:HGNC Symbol;Ac
16	MMAA	1.89	−0.07	0.49	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type [Sou
17	SPAG4	1.86	−0.02	0.97	SPAG4	sperm associated antigen 4 [Source:HGNC Symbol;Acc:HG
18	PCNXL2	1.86	−0.44	0.42	PCNXL2	pecanex−like 2 (Drosophila) [Source:HGNC Symbol;Acc:HG
19	RECQL4	1.86	−0.2	0.3	RECQL4	RecQ protein−like 4 [Source:HGNC Symbol;Acc:HGNC:9949
20	ANXA10	1.85	−0.07	0.88	ANXA10	annexin A10 [Source:HGNC Symbol;Acc:HGNC:534]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−04	14 / 422	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
2	5e−04	10 / 239	CC	proteinaceous extracellular matrix
3	1e−03	4 / 39	GSEA	LIAO_HAVE_SOX4_BINDING_SITES
4	1e−03	3 / 18	CC	podosome
5	1e−03	4 / 40	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN
6	1e−03	9 / 222	GSEA	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
7	1e−03	2 / 5	Lifesty	DUMEAUX_Estrogen related in non smokers literature genes up
8	2e−03	7 / 146	GSEA	BROWNE_HCMV_INFECTION_14HR_UP
9	2e−03	10 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	3e−03	7 / 156	GSEA	RIGGI_EWING_SARCOMA_PROGENITOR_DN
11	3e−03	14 / 506	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
12	3e−03	3 / 25	CC	clathrin−coated endocytic vesicle membrane
13	3e−03	3 / 25	BP	positive regulation of reactive oxygen species metabolic process
14	3e−03	4 / 52	GSEA	NOUZOVA_METHYLATED_IN_APL
15	3e−03	3 / 26	Glio	Christensen_hypomethylated_in_ependymoma
16	3e−03	3 / 26	GSEA	AIGNER_ZEB1_TARGETS
17	5e−03	3 / 30	BP	activation of JUN kinase activity
18	6e−03	3 / 31	BP	cellular defense response
19	6e−03	15 / 616	GSEA	NABA_MATRISOME
20	7e−03	21 / 995	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
21	7e−03	2 / 11	BP	UV protection
22	7e−03	2 / 11	GSEA	WHITESIDE_CISPLATIN_RESISTANCE_UP
23	7e−03	11 / 396	GSEA	JOHNSTONE_PARVB_TARGETS_3_UP
24	8e−03	4 / 66	GSEA	CAMPS_COLON_CANCER_COPY_NUMBER_UP
25	8e−03	2 / 12	BP	male meiosis I
26	8e−03	2 / 12	GSEA	HUMMERICH_BENIGN_SKIN_TUMOR_DN
27	8e−03	2 / 12	GSEA	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
28	8e−03	2 / 12	GSEA	JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN
29	9e−03	3 / 36	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
30	9e−03	3 / 36	GSEA	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2
31	9e−03	4 / 70	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0
32	1e−02	5 / 110	BP	response to lipopolysaccharide
33	1e−02	4 / 71	MF	PDZ domain binding
34	1e−02	3 / 38	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
35	1e−02	6 / 156	GSEA	BROWNE_HCMV_INFECTION_48HR_UP
36	1e−02	7 / 205	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
37	1e−02	6 / 159	CC	extracellular matrix
38	1e−02	2 / 14	BP	negative regulation of microtubule depolymerization
39	1e−02	2 / 14	GSEA	REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1
40	1e−02	4 / 75	GSEA	BHAT_ESR1_TARGETS_VIA_AKT1_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.07	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.33	2 / 100	HORVATH_aging_genes meth DOWN
3	0.38	2 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.003	3 / 25	positive regulation of reactive oxygen species metabolic process
2	0.005	3 / 30	activation of JUN kinase activity
3	0.006	3 / 31	cellular defense response
4	0.007	2 / 11	UV protection
5	0.008	2 / 12	male meiosis I
6	0.009	3 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
7	0.010	5 / 110	response to lipopolysaccharide
8	0.011	2 / 14	negative regulation of microtubule depolymerization
9	0.013	2 / 15	cellular response to lithium ion
10	0.015	2 / 16	cellular response to nerve growth factor stimulus
11	0.015	4 / 81	vitamin metabolic process
12	0.017	2 / 17	synaptic vesicle endocytosis
13	0.019	2 / 18	cellular response to dexamethasone stimulus
14	0.019	3 / 48	regulation of protein localization
15	0.020	3 / 49	cellular response to tumor necrosis factor
16	0.020	3 / 49	response to mechanical stimulus
17	0.023	3 / 52	protein heterooligomerization
18	0.025	4 / 94	sensory perception of sound
19	0.027	2 / 22	patterning of blood vessels
20	0.032	2 / 24	blood vessel morphogenesis

Brain

Rank	p−value	#in/all	Geneset
1	0.04	45 / 2972	Mid_Frontal_Lobe_ReprPC
2	0.05	16 / 862	Overlap_fetal_midbrain_TxTrans
3	0.06	25 / 1548	Mid_Frontal_Lobe_K9K27me3
4	0.10	121 / 9528	Overlap_fetal_midbrain_Quies
5	0.14	13 / 786	Fetal_EnhG
6	0.14	10 / 574	Overlap_fetal_midbrain_TssP
7	0.21	112 / 9020	Overlap_fetal_midbrain_ReprPCWk
8	0.26	17 / 1207	Overlap_fetal_midbrain_TssF
9	0.27	29 / 2185	Fetal_TssA
10	0.28	3 / 156	Mid_Frontal_Lobe_TssA
11	0.31	7 / 468	Mid_Frontal_Lobe_TssF
12	0.33	13 / 953	Fetal_Enh
13	0.34	15 / 1122	Fetal_K9K27me3
14	0.35	12 / 884	Overlap_fetal_midbrain_EnhG
15	0.38	14 / 1065	Overlap_fetal_midbrain_Enh
16	0.40	17 / 1333	Fetal_ReprPCWk
17	0.41	38 / 3081	Mid_Frontal_Lobe_ZNF
18	0.42	10 / 769	Overlap_fetal_midbrain_ZNF
19	0.49	23 / 1907	Fetal_TxTrans
20	0.50	7 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	9 / 401	Lembcke_Colonic Inflammation
2	0.08	2 / 40	PanCan_HK_geneset_nanostring
3	0.17	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.30	0 / 14	LIU_LIVER_CANCER
5	0.38	1 / 40	ZHANG_MM_up
6	0.41	1 / 44	PanCan_TGF−B_geneset_nanostring
7	0.42	2 / 121	PanCan_MAPK_geneset_nanostring
8	0.44	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	0.52	1 / 61	PanCan_Wnt_geneset_nanostring
10	0.55	2 / 156	PanCan_PI3K_geneset_nanostring
11	0.62	0 / 12	LIU_PROSTATE_CANCER_UP
12	0.62	1 / 82	PanCan_TXmisReg_geneset_nanostring
13	0.73	1 / 111	PanCan_RAS_geneset_nanostring
14	0.88	1 / 180	SPANG_LPS−index2
15	0.97	1 / 298	SPANG_BCL6−index2
16	1.00	1 / 489	Lembcke_Normal vs Adenoma
17	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
18	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
19	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.00	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	5e−04	10 / 239	proteinaceous extracellular matrix
2	1e−03	3 / 18	podosome
3	3e−03	3 / 25	clathrin−coated endocytic vesicle membrane
4	1e−02	6 / 159	extracellular matrix
5	1e−02	2 / 15	autophagic vacuole membrane
6	2e−02	4 / 84	PML body
7	2e−02	5 / 132	basolateral plasma membrane
8	4e−02	15 / 775	extracellular space
9	5e−02	2 / 31	microtubule associated complex
10	6e−02	3 / 73	basement membrane
11	6e−02	4 / 125	lamellipodium
12	6e−02	3 / 76	cell projection
13	6e−02	2 / 35	adherens junction
14	7e−02	2 / 37	platelet alpha granule lumen
15	8e−02	6 / 250	microtubule
16	8e−02	2 / 39	autophagic vacuole
17	1e−01	2 / 47	Cajal body
18	1e−01	1 / 10	DNA replication factor A complex
19	1e−01	1 / 10	fascia adherens
20	1e−01	1 / 10	mRNA cap binding complex

Chr

Rank	p−value	#in/all	Geneset
1	0.04	15 / 775	Chr 12
2	0.10	8 / 398	Chr 20
3	0.11	12 / 689	Chr 7
4	0.12	10 / 558	Chr 4
5	0.17	22 / 1500	Chr 1
6	0.20	9 / 552	Chr 10
7	0.24	12 / 801	Chr 11
8	0.32	8 / 551	Chr X
9	0.34	14 / 1037	Chr 19
10	0.36	5 / 335	Chr 22
11	0.48	3 / 221	Chr 18
12	0.51	12 / 993	Chr 2
13	0.53	2 / 151	Chr 21
14	0.60	3 / 262	Chr 13
15	0.81	4 / 469	Chr 8
16	0.81	5 / 576	Chr 9
17	0.83	6 / 687	Chr 6
18	0.89	5 / 649	Chr 16
19	0.91	3 / 462	Chr 14
20	0.93	6 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	9 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	0.01	84 / 5880	TssD2_Colon
3	0.02	36 / 2159	TssP_Colon
4	0.02	13 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	0.03	18 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	0.04	7 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
7	0.06	1 / 5	Juehling−MSI−enriched−in−8−to−9
8	0.07	4 / 131	Marisa_CRC−cluster−a
9	0.08	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
10	0.08	1 / 7	Marisa_CRC−C5
11	0.08	1 / 7	Juehling_HNPCC−mutated−in−5
12	0.08	6 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
13	0.09	1 / 8	Boland_CRC−MSI−TGC
14	0.11	1 / 10	KIM_MSI−in−CRC
15	0.12	6 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
16	0.12	47 / 3383	EnhWk2_Colon
17	0.14	10 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
18	0.16	5 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
19	0.16	1 / 15	TCGA_Mutated−in−CRC_hypermutated
20	0.17	1 / 16	Juehling−MSI−enriched−in−6

Disease

Rank	p−value	#in/all	Geneset
1	0.9	2 / 294	GUDJ_psoriasis down
2	0.9	3 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.003	3 / 26	Christensen_hypomethylated_in_ependymoma
2	0.020	3 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
3	0.022	6 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
4	0.025	9 / 356	Down_a
5	0.035	1 / 3	Martinez_Glio_hypometh
6	0.057	2 / 33	Christensen_hypomethylated_in_primary_glioblastoma
7	0.069	1 / 6	neurons_glio
8	0.070	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
9	0.112	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
10	0.122	1 / 11	astrocytes_glio
11	0.122	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
12	0.125	2 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
13	0.133	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
14	0.170	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	0.178	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
16	0.204	2 / 71	Weller_LGG_A_vs_O_UP
17	0.257	1 / 25	Shaw_down_in_1p19q
18	0.262	6 / 365	Down_b
19	0.274	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
20	0.289	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	14 / 422	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
2	1e−03	4 / 39	LIAO_HAVE_SOX4_BINDING_SITES
3	1e−03	4 / 40	SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN
4	1e−03	9 / 222	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
5	2e−03	7 / 146	BROWNE_HCMV_INFECTION_14HR_UP
6	2e−03	10 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
7	3e−03	7 / 156	RIGGI_EWING_SARCOMA_PROGENITOR_DN
8	3e−03	14 / 506	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
9	3e−03	4 / 52	NOUZOVA_METHYLATED_IN_APL
10	3e−03	3 / 26	AIGNER_ZEB1_TARGETS
11	6e−03	15 / 616	NABA_MATRISOME
12	7e−03	21 / 995	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
13	7e−03	2 / 11	WHITESIDE_CISPLATIN_RESISTANCE_UP
14	7e−03	11 / 396	JOHNSTONE_PARVB_TARGETS_3_UP
15	8e−03	4 / 66	CAMPS_COLON_CANCER_COPY_NUMBER_UP
16	8e−03	2 / 12	HUMMERICH_BENIGN_SKIN_TUMOR_DN
17	8e−03	2 / 12	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
18	8e−03	2 / 12	JI_CARCINOGENESIS_BY_KRAS_AND_STK11_DN
19	9e−03	3 / 36	WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2
20	9e−03	4 / 70	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	0.2	4 / 176	HALLMARK_HYPOXIA
3	0.2	4 / 183	HALLMARK_GLYCOLYSIS
4	0.2	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
5	0.3	3 / 165	HALLMARK_MYOGENESIS
6	0.3	2 / 95	HALLMARK_SPERMATOGENESIS
7	0.3	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	0.3	3 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.4	3 / 188	HALLMARK_ADIPOGENESIS
10	0.4	2 / 127	HALLMARK_KRAS_SIGNALING_DN
11	0.5	1 / 53	HALLMARK_TGF_BETA_SIGNALING
12	0.5	2 / 137	HALLMARK_UV_RESPONSE_DN
13	0.5	2 / 146	HALLMARK_UV_RESPONSE_UP
14	0.6	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	0.6	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
16	0.6	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
17	0.6	2 / 181	HALLMARK_P53_PATHWAY
18	0.7	2 / 188	HALLMARK_MYC_TARGETS_V1
19	0.7	1 / 91	HALLMARK_PROTEIN_SECRETION
20	0.7	1 / 91	HALLMARK_BILE_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.001	2 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.035	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
3	0.112	1 / 10	DUMEAUX_Smoking literature genes up
4	0.163	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	1.000	0 / 62	DUMEAUX_Smoking enriched genes
6	1.000	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.000	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.000	0 / 18	DUMEAUX_High bmi enriched genes
11	1.000	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	2 / 15	DAVE_Immune response 2
2	0.05	34 / 2188	HOPP_Poised_promoter
3	0.07	49 / 3396	HOPP_Repressed
4	0.09	1 / 8	Subero_MM_hypo_meth
5	0.10	74 / 5538	HOPP_Weak_txn
6	0.11	5 / 212	LENZ_Stromal signature 1
7	0.12	32 / 2211	HOPP_Repetitive
8	0.13	3 / 107	SPANG_LPS 6hrs UP
9	0.15	1 / 14	Subero_mBL_hypo_meth
10	0.16	92 / 7209	HOPP_Weak_promoter
11	0.24	5 / 280	SPANG_CD40 6hrs UP
12	0.25	34 / 2563	HOPP_Heterochrom
13	0.26	1 / 25	Subero_T−PLL_hypo_meth
14	0.29	1 / 29	Subero_DLBCL_hypo_meth
15	0.30	1 / 30	TARTE_B−cell signature
16	0.30	1 / 30	Subero_INT_hypo_meth
17	0.39	4 / 268	SPANG_IL21 UP
18	0.40	1 / 43	LENZ_Stromal signature 2
19	0.45	1 / 50	SPANG_BAFF 9hrs DN
20	0.52	1 / 61	SPANG_LPS 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	0.01	4 / 71	PDZ domain binding
2	0.01	2 / 16	extracellular matrix binding
3	0.01	2 / 16	transforming growth factor beta binding
4	0.02	2 / 17	glycosaminoglycan binding
5	0.02	2 / 18	mitogen−activated protein kinase kinase kinase binding
6	0.02	2 / 19	protein kinase activator activity
7	0.04	2 / 27	RNA polymerase II repressing transcription factor binding
8	0.05	11 / 530	calcium ion binding
9	0.06	3 / 75	metallopeptidase activity
10	0.07	2 / 36	enzyme activator activity
11	0.08	5 / 193	protein complex binding
12	0.08	3 / 86	integrin binding
13	0.08	2 / 41	copper ion binding
14	0.09	4 / 142	calmodulin binding
15	0.10	5 / 205	ubiquitin protein ligase binding
16	0.10	3 / 95	hydrolase activity, acting on glycosyl bonds
17	0.11	1 / 10	acetylgalactosaminyltransferase activity
18	0.11	1 / 10	gamma−catenin binding
19	0.11	1 / 10	glutathione binding
20	0.11	1 / 10	hedgehog receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	5 / 133	hsa−miR−485−5p
2	0.04	3 / 61	hsa−miR−324−5p
3	0.06	2 / 35	hsa−miR−770−5p
4	0.09	2 / 42	hsa−miR−192
5	0.10	2 / 46	hsa−miR−581
6	0.13	2 / 52	hsa−miR−370
7	0.16	2 / 60	hsa−miR−634
8	0.21	2 / 73	hsa−miR−1304
9	0.22	2 / 75	hsa−miR−877
10	0.23	2 / 78	hsa−miR−1321
11	0.25	1 / 24	hsa−miR−602
12	0.25	1 / 24	hsa−miR−483−3p
13	0.26	2 / 84	hsa−miR−220c
14	0.26	6 / 366	hsa−miR−519b−3p
15	0.29	2 / 90	hsa−miR−216a
16	0.29	2 / 90	hsa−miR−216b
17	0.29	1 / 29	hsa−miR−193a−5p
18	0.29	7 / 456	hsa−miR−130a
19	0.30	2 / 93	hsa−miR−299−3p
20	0.31	1 / 31	hsa−miR−617

PathwAct

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.03	74 / 5219	ICGC_Tcf3_targets
2	0.03	67 / 4682	ICGC_Pol24_targets
3	0.04	59 / 4054	ICGC_Egr1_targets
4	0.05	20 / 1139	HEBENSTREIT_low expression TF
5	0.07	73 / 5374	ICGC_Pax5_targets
6	0.10	81 / 6114	ICGC_Runx3_targets
7	0.11	35 / 2416	ICGC_Bcl3_targets
8	0.12	12 / 690	ICGC_Atf3_targets
9	0.12	55 / 4032	ICGC_Creb1_targets
10	0.12	54 / 3966	ICGC_Pu1_targets
11	0.13	69 / 5200	ICGC_Mta3_targets
12	0.16	70 / 5355	ICGC_Pol2_targets
13	0.16	62 / 4706	ICGC_Sp1_targets
14	0.21	20 / 1400	ICGC_Myc_targets
15	0.23	69 / 5408	ICGC_Pou2_targets
16	0.23	29 / 2137	ICGC_SrfV0416101_targets
17	0.28	62 / 4909	ICGC_Stat5_targets
18	0.28	69 / 5495	ICGC_Yy1_targets
19	0.30	59 / 4689	ICGC_Taf1_targets
20	0.31	31 / 2391	ICGC_Pbx3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	VAQUERIZAS_Salivary gland
2	0.2	1 / 17	VAQUERIZAS_Pituitary
3	0.2	1 / 23	VAQUERIZAS_Spinal cord
4	0.3	1 / 33	VAQUERIZAS_Prostate
5	0.3	1 / 36	VAQUERIZAS_Fetal brain
6	0.4	1 / 37	VAQUERIZAS_Thymus
7	0.4	1 / 38	VAQUERIZAS_Whole brain
8	0.4	1 / 45	VAQUERIZAS_Uterus
9	0.5	1 / 59	VAQUERIZAS_Whole blood
10	0.5	2 / 143	VAQUERIZAS_General
11	1.0	0 / 41	VAQUERIZAS_Placenta
12	1.0	0 / 26	VAQUERIZAS_Liver
13	1.0	0 / 29	VAQUERIZAS_Smooth muscle
14	1.0	0 / 9	VAQUERIZAS_Kidney
15	1.0	0 / 40	VAQUERIZAS_Thyroid
16	1.0	0 / 7	VAQUERIZAS_Appendix
17	1.0	0 / 29	VAQUERIZAS_Fetal lung
18	1.0	0 / 58	VAQUERIZAS_Lung
19	1.0	0 / 16	VAQUERIZAS_Pancreas
20	1.0	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	2 / 41	WIRTH_Homeostasis
2	0.10	3 / 95	WIRTH_Muscle
3	0.11	1 / 10	WIRTH_Hippocampus
4	0.12	1 / 11	WIRTH_Globus pallidus
5	0.12	1 / 11	WIRTH_Cortex cerebri
6	0.13	1 / 12	WIRTH_Thymus
7	0.22	2 / 74	WIRTH_Mucosa
8	0.36	2 / 107	WIRTH_Testis
9	0.40	5 / 350	WIRTH_Immune system
10	0.50	3 / 225	PALMER_Granulocytes signature up
11	0.74	1 / 114	PALMER_T−Cell signature up
12	0.78	3 / 350	WIRTH_Nervous System
13	1.00	0 / 32	WIRTH_Pancreas
14	1.00	0 / 11	WIRTH_Sec. lymphoid organs
15	1.00	0 / 11	WIRTH_Prim. lymphoid organs
16	1.00	0 / 13	WIRTH_B−cells
17	1.00	0 / 8	WIRTH_Tonsil
18	1.00	0 / 12	WIRTH_Lymphocytes
19	1.00	0 / 5	WIRTH_Bone marrow
20	1.00	0 / 14	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.07	19 / 1115	LU_BPDE 1h DN
2	0.42	45 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

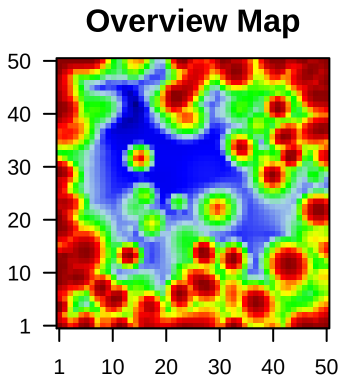
Spot Summary: B1

metagenes = 4
genes = 82

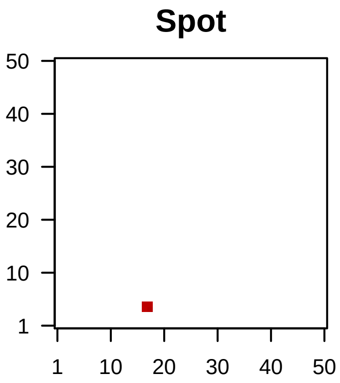
<r> metagenes = 0.99
<r> genes = 0.25
beta: r2= 0.78 / log p= −Inf

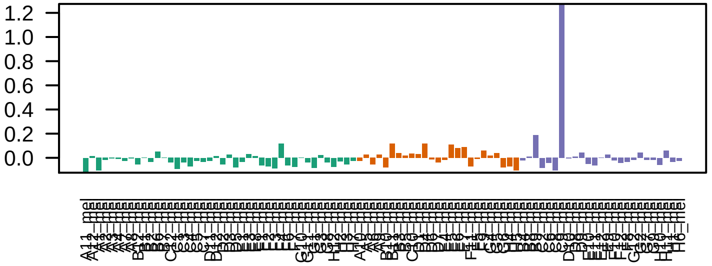
samples with spot = 2 (2.2 %)
MSC3 : 2 (8 %)

Overview Map



Spot





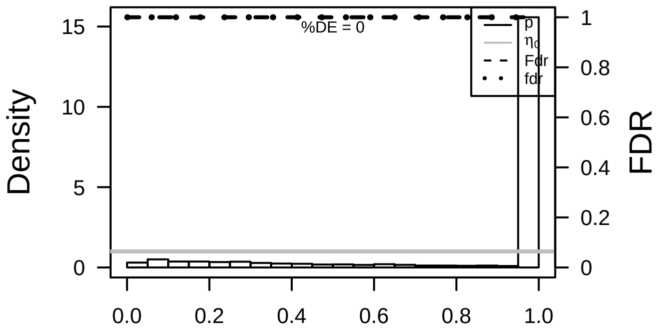
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LRRC27	2.04	−0.16	0.57	LRRC27	leucine rich repeat containing 27 [Source:HGNC Symbol;Acc:
2	IFT46	1.98	−0.27	0.26	IFT46	intraflagellar transport 46 [Source:HGNC Symbol;Acc:HGNC:
3	CLCN5	1.98	−0.19	0.6	CLCN5	chloride channel, voltage−sensitive 5 [Source:HGNC Symbol;
4	SLC25A53	1.94	−0.16	0.42	SLC25A53	solute carrier family 25, member 53 [Source:HGNC Symbol;A
5	E2F5	1.86	−0.2	0.38	E2F5	E2F transcription factor 5, p130−binding [Source:HGNC Sym
6	OSR2	1.84	−0.06	0.67	OSR2	odd−skipped related transciption factor 2 [Source:HGNC Sym
7	WDR54	1.78	−0.34	0.3	WDR54	WD repeat domain 54 [Source:HGNC Symbol;Acc:HGNC:25
8	MBD5	1.78	−0.22	0.32	MBD5	methyl−CpG binding domain protein 5 [Source:HGNC Symbo
9	HDGFRP2	1.77	−0.28	0.34		
10	SPATA25	1.76	−0.03	0.77	SPATA25	spermatogenesis associated 25 [Source:HGNC Symbol;Acc:
11	RELL1	1.69	−0.22	0.43	RELL1	RELT−like 1 [Source:HGNC Symbol;Acc:HGNC:27379]
12	DNAJB2	1.67	−0.1	0.61	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:HGN
13	BMF	1.66	−0.16	0.54	BMF	Bcl2 modifying factor [Source:HGNC Symbol;Acc:HGNC:241
14	PCDH18	1.66	−0.21	0.29	PCDH18	protocadherin 18 [Source:HGNC Symbol;Acc:HGNC:14268]
15	CTTNBP2	1.65	−0.09	0.5	CTTNBP2	cortactin binding protein 2 [Source:HGNC Symbol;Acc:HGNC
16	RHOV	1.62	−0.04	0.67	RHOV	ras homolog family member V [Source:HGNC Symbol;Acc:HG
17	DUSP5	1.62	−0.06	0.74	DUSP5	dual specificity phosphatase 5 [Source:HGNC Symbol;Acc:H
18	KCNH8	1.6	−0.04	0.42	KCNH8	potassium channel, voltage gated eag related subfamily H, m
19	GMEB2	1.55	−0.09	0.43	GMEB2	glucocorticoid modulatory element binding protein 2 [Source:
20	CA11	1.54	−0.11	0.45	CA11	carbonic anhydrase XI [Source:HGNC Symbol;Acc:HGNC:13

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−04	11 / 618	GSEA	GOZGIT_ESR1_TARGETS_DN
2	5e−04	12 / 724	GSEA	BENPORATH_EED_TARGETS
3	6e−04	19 / 1565	BP	regulation of transcription, DNA−templated
4	8e−04	2 / 8	Lifesty	DUMEAUX_Hormon therapy in non smokers literature genes up
5	8e−04	4 / 77	CC	ciliary basal body
6	1e−03	11 / 674	GSEA	BENPORATH_SUZ12_TARGETS
7	2e−03	2 / 11	BP	phosphorelay signal transduction system
8	2e−03	3 / 43	BP	rhythmic process
9	2e−03	3 / 45	TF Tis	VAQUERIZAS_Uterus
10	2e−03	3 / 45	GSEA	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
11	2e−03	4 / 97	Glio	Christensen_hypermethylated_in_grade3_astrocytoma
12	2e−03	3 / 46	BP	response to unfolded protein
13	2e−03	3 / 46	GSEA	BROWNE_HCMV_INFECTION_1HR_UP
14	2e−03	4 / 98	GSEA	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
15	2e−03	21 / 2037	MF	DNA binding
16	3e−03	2 / 15	TF Tis	VAQUERIZAS_Fetal thyroid
17	4e−03	3 / 58	Glio	Christensen_hypermethylated_in_grade2_astrocytoma
18	4e−03	2 / 18	BP	intraciliary transport
19	4e−03	2 / 18	CC	intraciliary transport particle B
20	5e−03	12 / 936	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
21	5e−03	44 / 5880	Colon	TssD2_Colon
22	6e−03	10 / 720	GSEA	BENPORATH_ES_WITH_H3K27ME3
23	6e−03	2 / 21	miRN	hsa−miR−1282
24	7e−03	2 / 23	BP	endoderm development
25	7e−03	2 / 23	TF Tis	VAQUERIZAS_Spinal cord
26	8e−03	2 / 24	GSEA	MCCABE_HOXC6_TARGETS_CANCER_UP
27	8e−03	17 / 1664	BP	transcription, DNA−templated
28	8e−03	2 / 25	miRN	hsa−miR−941
29	9e−03	3 / 77	GSEA	BILD_CTNNB1_ONCOGENIC_SIGNATURE
30	9e−03	6 / 325	GSEA	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
31	9e−03	5 / 232	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
32	9e−03	2 / 26	MF	chloride channel activity
33	9e−03	2 / 26	GSEA	REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE
34	1e−02	3 / 82	GSEA	WINZEN_DEGRADED_VIA_KHSRP
35	1e−02	18 / 1859	MF	metal ion binding
36	1e−02	2 / 29	MF	insulin receptor binding
37	1e−02	2 / 29	TF Tis	VAQUERIZAS_Smooth muscle
38	1e−02	2 / 29	TF Tis	VAQUERIZAS_Fetal lung
39	1e−02	2 / 29	GSEA	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP
40	1e−02	3 / 85	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	6e−04	19 / 1565	regulation of transcription, DNA−templated
2	2e−03	2 / 11	phosphorelay signal transduction system
3	2e−03	3 / 43	rhythmic process
4	2e−03	3 / 46	response to unfolded protein
5	4e−03	2 / 18	intraciliary transport
6	7e−03	2 / 23	endoderm development
7	8e−03	17 / 1664	transcription, DNA−templated
8	1e−02	2 / 32	chondrocyte differentiation
9	2e−02	2 / 37	transcription from RNA polymerase III promoter
10	2e−02	3 / 103	cilium assembly
11	2e−02	4 / 191	brain development
12	3e−02	2 / 45	chloride transport
13	3e−02	2 / 45	memory
14	3e−02	2 / 46	hippocampus development
15	3e−02	2 / 53	chloride transmembrane transport
16	4e−02	2 / 57	regulation of membrane potential
17	4e−02	2 / 58	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
18	4e−02	2 / 59	smoothened signaling pathway
19	4e−02	2 / 59	sodium ion transmembrane transport
20	5e−02	2 / 63	negative regulation of transforming growth factor beta receptor signaling pathw

Brain

Rank	p−value	#in/all	Geneset
1	0.01	9 / 686	Overlap_fetal_midbrain_TssA
2	0.02	17 / 1845	Fetal_Quies
3	0.02	10 / 884	Overlap_fetal_midbrain_EnhG
4	0.03	13 / 1333	Fetal_ReprPCWk
5	0.05	2 / 69	Overlap_fetal_midbrain_Tx
6	0.10	9 / 1013	Fetal_TssP
7	0.16	21 / 3081	Mid_Frontal_Lobe_ZNF
8	0.19	7 / 862	Overlap_fetal_midbrain_TxTrans
9	0.22	2 / 163	Fetal_ReprPC
10	0.26	16 / 2462	Mid_Frontal_Lobe_HetRpts
11	0.27	8 / 1122	Fetal_K9K27me3
12	0.28	6 / 812	Mid_Frontal_Lobe_TssP
13	0.30	52 / 9013	Overlap_fetal_midbrain_K9K27me3
14	0.34	8 / 1207	Overlap_fetal_midbrain_TssF
15	0.34	12 / 1907	Fetal_TxTrans
16	0.36	2 / 229	Mid_Frontal_Lobe_TxTrans
17	0.36	7 / 1065	Overlap_fetal_midbrain_Enh
18	0.41	5 / 765	Mid_Frontal_Lobe_Het
19	0.50	11 / 1949	Fetal_TssF
20	0.51	6 / 1050	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.07	0 / 12	LIU_PROSTATE_CANCER_UP
3	0.07	1 / 14	LIU_COMMON_CANCER_GENES
4	0.08	1 / 15	RHODES_CANCER_META_SIGNATURE
5	0.08	1 / 15	GENTLES_modul11
6	0.08	4 / 298	SPANG_BCL6−index2
7	0.08	1 / 16	GENTLES_modul16
8	0.21	1 / 44	PanCan_TGF−B_geneset_nanostring
9	0.26	1 / 55	PanCan_JAK−ST_geneset_nanostring
10	0.28	1 / 61	PanCan_Wnt_geneset_nanostring
11	0.48	1 / 120	PanCan_CC+Apop_geneset_nanostring
12	0.49	1 / 121	PanCan_MAPK_geneset_nanostring
13	0.50	3 / 489	Lembcke_Normal vs Adenoma
14	0.58	1 / 156	PanCan_PI3K_geneset_nanostring
15	0.63	1 / 180	SPANG_LPS−index2
16	0.65	2 / 401	Lembcke_Colonic Inflammation
17	0.88	0 / 14	LIU_PROSTATE_CANCER_DN
18	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
19	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.00	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 77	ciliary basal body
2	4e−03	2 / 18	intraciliary transport particle B
3	1e−02	2 / 31	membrane coat
4	1e−02	2 / 32	nuclear nucleosome
5	2e−02	2 / 41	ciliary tip
6	5e−02	4 / 249	neuronal cell body
7	5e−02	1 / 10	neuron projection terminus
8	6e−02	2 / 70	primary cilium
9	6e−02	1 / 12	axonal growth cone
10	6e−02	1 / 12	node of Ranvier
11	7e−02	2 / 78	dendritic spine
12	7e−02	1 / 13	chromocenter
13	7e−02	1 / 13	contractile fiber
14	7e−02	1 / 13	COPI vesicle coat
15	7e−02	38 / 5696	nucleus
16	7e−02	2 / 81	apical part of cell
17	8e−02	2 / 87	recycling endosome
18	9e−02	1 / 17	basal lamina
19	9e−02	1 / 17	membrane−bounded vesicle
20	9e−02	1 / 18	DNA−directed RNA polymerase III complex

Chr

Rank	p−value	#in/all	Geneset
1	0.08	7 / 689	Chr 7
2	0.11	5 / 465	Chr 15
3	0.11	9 / 1037	Chr 19
4	0.17	4 / 398	Chr 20
5	0.18	5 / 551	Chr X
6	0.25	4 / 469	Chr 8
7	0.31	6 / 838	Chr 3
8	0.34	2 / 221	Chr 18
9	0.36	4 / 552	Chr 10
10	0.42	5 / 775	Chr 12
11	0.49	5 / 840	Chr 17
12	0.56	1 / 151	Chr 21
13	0.59	3 / 558	Chr 4
14	0.61	3 / 576	Chr 9
15	0.64	5 / 993	Chr 2
16	0.76	1 / 262	Chr 13
17	0.87	2 / 649	Chr 16
18	0.89	2 / 687	Chr 6
19	0.90	2 / 696	Chr 5
20	0.92	1 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.005	44 / 5880	TssD2_Colon
2	0.029	22 / 2698	EnhA_Colon
3	0.068	9 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
4	0.068	10 / 1079	ZNF_Colon
5	0.090	5 / 436	K9acLow_Colon
6	0.091	6 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
7	0.095	3 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
8	0.122	16 / 2159	TssP_Colon
9	0.123	45 / 7203	TssF_Colon
10	0.165	1 / 33	Marisa_CRC−cluster−e
11	0.204	4 / 427	Quies2_Colon
12	0.210	1 / 43	Marisa_CRC−cluster−f
13	0.253	3 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
14	0.263	55 / 9482	TssA_Colon
15	0.280	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
16	0.289	59 / 10290	TssWk_Colon
17	0.304	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
18	0.323	1 / 71	Marisa_CRC−cluster−g
19	0.326	23 / 3812	TssD1_Colon
20	0.330	3 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	0.2	3 / 294	GUDJ_psoriasis down
2	0.9	1 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	4 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
2	0.004	3 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
3	0.022	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
4	0.027	3 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
5	0.031	3 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	0.058	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
7	0.059	2 / 72	laffaire_hypermeth_LGG_vs_control
8	0.062	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
9	0.074	1 / 14	VERHAAK_PN subtype
10	0.103	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.118	1 / 23	WIRTH_PN subtype
12	0.219	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
13	0.227	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
14	0.312	6 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
15	0.319	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP
16	0.323	1 / 71	Weller_LGG_A_vs_O_UP
17	0.334	1 / 74	WIRTH_Normal Brain
18	0.337	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
19	0.403	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
20	0.422	1 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	11 / 618	GOZGIT_ESR1_TARGETS_DN
2	5e−04	12 / 724	BENPORATH_EED_TARGETS
3	1e−03	11 / 674	BENPORATH_SUZ12_TARGETS
4	2e−03	3 / 45	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
5	2e−03	3 / 46	BROWNE_HCMV_INFECTION_1HR_UP
6	2e−03	4 / 98	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
7	5e−03	12 / 936	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
8	6e−03	10 / 720	BENPORATH_ES_WITH_H3K27ME3
9	8e−03	2 / 24	MCCABE_HOXC6_TARGETS_CANCER_UP
10	9e−03	3 / 77	BILD_CTNNB1_ONCOGENIC_SIGNATURE
11	9e−03	6 / 325	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
12	9e−03	5 / 232	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
13	9e−03	2 / 26	REACTOME_RNA_POL_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3
14	1e−02	3 / 82	WINZEN_DEGRADED_VIA_KHSRP
15	1e−02	2 / 29	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP
16	1e−02	3 / 85	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP
17	1e−02	2 / 33	REACTOME_RNA_POL_III_TRANSCRIPTION
18	1e−02	2 / 33	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP
19	1e−02	2 / 33	SHAFFER_IRF4_MULTIPLE_MYELOMA_PROGRAM
20	2e−02	1 / 3	WAGSCHAL_EHMT2_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.2	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
2	0.2	2 / 140	HALLMARK_APOPTOSIS
3	0.2	2 / 146	HALLMARK_UV_RESPONSE_UP
4	0.2	2 / 162	HALLMARK_COMPLEMENT
5	0.2	2 / 167	HALLMARK_APICAL_JUNCTION
6	0.2	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.4	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.4	1 / 95	HALLMARK_SPERMATOGENESIS
9	0.5	1 / 137	HALLMARK_UV_RESPONSE_DN
10	0.6	1 / 146	HALLMARK_DNA_REPAIR
11	0.6	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.6	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	0.6	1 / 176	HALLMARK_HYPOXIA
14	0.6	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	0.6	1 / 181	HALLMARK_P53_PATHWAY
16	0.6	1 / 183	HALLMARK_GLYCOLYSIS
17	1.0	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
18	1.0	0 / 195	HALLMARK_MITOTIC_SPINDLE
19	1.0	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
20	1.0	0 / 53	HALLMARK_TGF_BETA_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−04	2 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
2	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
3	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
4	1e+00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1e+00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1e+00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1e+00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1e+00	0 / 18	DUMEAUX_High bmi enriched genes
11	1e+00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	2 / 34	Subero_B−ALL_hyper_meth
2	0.03	1 / 5	WRIGHT_custom ABC−DLBCL UP
3	0.04	2 / 60	Subero_T−ALL_hyper_meth
4	0.04	1 / 8	MASCQUE_ABC UP
5	0.05	4 / 247	ZHANG_DLBCL mutated
6	0.05	1 / 9	Subero_B−ALL_hypo_meth
7	0.07	11 / 1218	SPANG_BCR UP
8	0.07	2 / 81	Subero_INT_hyper_meth
9	0.10	2 / 96	Subero_DLBCL_hyper_meth
10	0.13	1 / 25	Subero_T−PLL_hypo_meth
11	0.15	1 / 30	Subero_INT_hypo_meth
12	0.16	3 / 256	SPANG_IL21 DN
13	0.17	1 / 33	LEE_Developmental_regulators
14	0.20	1 / 40	Subero_mBL_hyper_meth
15	0.21	1 / 43	LENZ_Stromal signature 2
16	0.23	1 / 47	Subero_FL_hyper_meth
17	0.29	21 / 3396	HOPP_Repressed
18	0.36	1 / 80	Aukema_BCL2 DN_BCL6 UP
19	0.42	13 / 2188	HOPP_Poised_promoter
20	0.43	2 / 268	SPANG_IL21 UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	21 / 2037	DNA binding
2	0.009	2 / 26	chloride channel activity
3	0.010	18 / 1859	metal ion binding
4	0.011	2 / 29	insulin receptor binding
5	0.016	3 / 98	ion channel activity
6	0.022	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
7	0.022	2 / 42	protein kinase C binding
8	0.034	9 / 820	sequence−specific DNA binding transcription factor activity
9	0.036	6 / 450	sequence−specific DNA binding
10	0.037	9 / 830	nucleic acid binding transcription factor activity
11	0.046	2 / 63	RNA polymerase II transcription regulatory region sequence−specific DNA bir
12	0.053	1 / 10	cAMP response element binding protein binding
13	0.053	1 / 10	proteasome binding
14	0.053	1 / 10	sodium channel activity
15	0.057	2 / 71	PDZ domain binding
16	0.058	1 / 11	antiporter activity
17	0.058	1 / 11	cAMP response element binding
18	0.058	1 / 11	insulin−like growth factor receptor binding
19	0.058	1 / 11	protein kinase B binding
20	0.064	1 / 12	alpha−actinin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.006	2 / 21	hsa−miR−1282
2	0.008	2 / 25	hsa−miR−941
3	0.028	2 / 48	hsa−miR−628−5p
4	0.044	2 / 61	hsa−miR−612
5	0.048	1 / 9	hsa−miR−615−3p
6	0.062	2 / 74	hsa−miR−1254
7	0.066	2 / 77	hsa−miR−205
8	0.069	1 / 13	hsa−miR−1234
9	0.089	1 / 17	hsa−miR−1298
10	0.094	1 / 18	hsa−miR−380*
11	0.107	2 / 102	hsa−miR−377
12	0.118	1 / 23	hsa−miR−943
13	0.136	2 / 118	hsa−miR−625
14	0.142	1 / 28	hsa−miR−591
15	0.142	1 / 28	hsa−miR−1292
16	0.147	1 / 29	hsa−miR−1225−3p
17	0.147	1 / 29	hsa−miR−1237
18	0.156	1 / 31	hsa−miR−892b
19	0.173	3 / 263	hsa−miR−92b
20	0.174	1 / 35	hsa−miR−621

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.06	22 / 2927	ICGC_Rad21_targets
2	0.17	26 / 3966	ICGC_Pu1_targets
3	0.17	30 / 4689	ICGC_Taf1_targets
4	0.17	38 / 6114	ICGC_Runx3_targets
5	0.17	6 / 690	ICGC_Atf3_targets
6	0.18	30 / 4706	ICGC_Sp1_targets
7	0.20	26 / 4054	ICGC_Egr1_targets
8	0.21	34 / 5495	ICGC_Yy1_targets
9	0.22	5 / 595	ICGC_NrsfPcr2_targets
10	0.27	14 / 2136	ICGC_GabpPcr2_targets
11	0.27	23 / 3700	ICGC_Nfatc1_targets
12	0.27	14 / 2137	ICGC_SrfV0416101_targets
13	0.29	28 / 4617	ICGC_Tcf12_targets
14	0.30	32 / 5374	ICGC_Pax5_targets
15	0.31	31 / 5200	ICGC_Mta3_targets
16	0.32	12 / 1872	ICGC_Mef2_targets
17	0.32	11 / 1701	HEBENSTREIT_high expression TF
18	0.34	15 / 2416	ICGC_Bcl3_targets
19	0.34	29 / 4909	ICGC_Stat5_targets
20	0.35	26 / 4385	ICGC_Atf2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.002	3 / 45	VAQUERIZAS_Uterus
2	0.003	2 / 15	VAQUERIZAS_Fetal thyroid
3	0.007	2 / 23	VAQUERIZAS_Spinal cord
4	0.011	2 / 29	VAQUERIZAS_Smooth muscle
5	0.011	2 / 29	VAQUERIZAS_Fetal lung
6	0.018	2 / 38	VAQUERIZAS_Testis
7	0.020	2 / 40	VAQUERIZAS_Thyroid
8	0.040	2 / 58	VAQUERIZAS_Lung
9	0.048	1 / 9	VAQUERIZAS_Kidney
10	0.074	1 / 14	VAQUERIZAS_Ovary
11	0.084	1 / 16	VAQUERIZAS_Adrenal gland
12	0.089	1 / 17	VAQUERIZAS_Pituitary
13	0.089	1 / 17	VAQUERIZAS_Heart
14	0.165	1 / 33	VAQUERIZAS_Prostate
15	0.179	1 / 36	VAQUERIZAS_Fetal brain
16	0.183	1 / 37	VAQUERIZAS_Thymus
17	0.201	1 / 41	VAQUERIZAS_Placenta
18	0.276	1 / 59	VAQUERIZAS_Whole blood
19	1.000	0 / 26	VAQUERIZAS_Liver
20	1.000	0 / 143	VAQUERIZAS_General

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 32	WIRTH_Pancreas
2	0.2	1 / 32	WIRTH_Placenta
3	0.2	1 / 41	WIRTH_Homeostasis
4	0.3	2 / 194	PALMER_B−Cell signature up
5	0.3	1 / 74	WIRTH_Mucosa
6	0.6	2 / 350	WIRTH_Nervous System
7	1.0	0 / 350	WIRTH_Immune system
8	1.0	0 / 11	WIRTH_Sec. lymphoid organs
9	1.0	0 / 11	WIRTH_Prim. lymphoid organs
10	1.0	0 / 13	WIRTH_B−cells
11	1.0	0 / 8	WIRTH_Tonsil
12	1.0	0 / 12	WIRTH_Thymus
13	1.0	0 / 12	WIRTH_Lymphocytes
14	1.0	0 / 5	WIRTH_Bone marrow
15	1.0	0 / 11	WIRTH_Globus pallidus
16	1.0	0 / 14	WIRTH_Telencephalon
17	1.0	0 / 11	WIRTH_Cortex cerebri
18	1.0	0 / 10	WIRTH_Hippocampus
19	1.0	0 / 10	WIRTH_Thalamus
20	1.0	0 / 12	WIRTH_Cerebellum

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	9 / 1115	LU_BPDE 1h DN
2	0.3	23 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

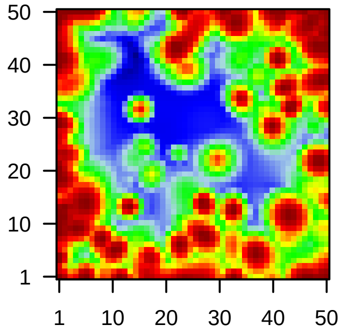
Overexpression Spots

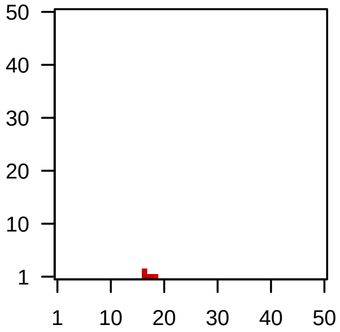
Spot Summary: C1

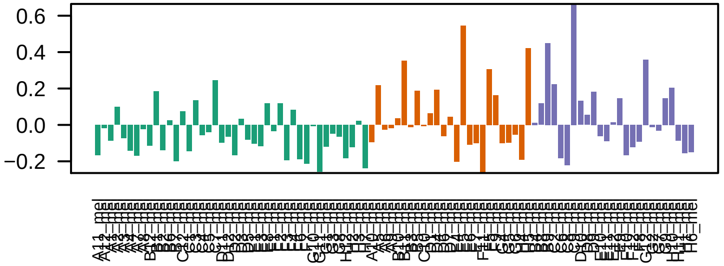
metagenes = 4
genes = 52

<r> metagenes = 0.97
<r> genes = 0.14
beta: r2= 1.09 / log p= −Inf

samples with spot = 15 (16.3 %)
MSC1 : 2 (4.8 %)
MSC2 : 7 (28 %)
MSC3 : 6 (24 %)


Overview Map


Spot

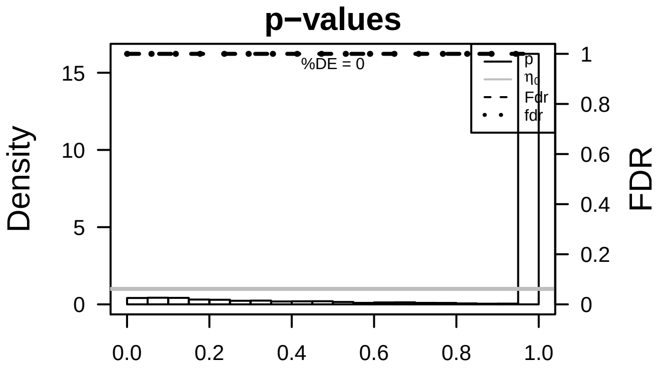


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	RORB	1.67	−0.16	0.4	RORB	RAR−related orphan receptor B [Source:HGNC Symbol;Acc:
2	SLC39A3	1.61	−0.35	0.41	SLC39A3	solute carrier family 39 (zinc transporter), member 3 [Source:
3	SARS2	1.6	−0.55	0.31	SARS2	seryl−tRNA synthetase 2, mitochondrial [Source:HGNC Sym
4	NFIX	1.57	−0.33	0.44	NFIX	nuclear factor I/X (CCAAT−binding transcription factor) [Sour
5	MPDZ	1.54	−0.52	0.36	MPDZ	multiple PDZ domain protein [Source:HGNC Symbol;Acc:HG
6	ADCK1	1.53	−0.23	0.3	ADCK1	aarF domain containing kinase 1 [Source:HGNC Symbol;Acc
7	PRMT9	1.48	−0.3	0.25	PRMT9	protein arginine methyltransferase 9 [Source:HGNC Symbol;
8	KIAA0586	1.48	−0.54	0.33	KIAA0586	KIAA0586 [Source:HGNC Symbol;Acc:HGNC:19960]
9	AREL1	1.46	−0.72	0.31	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1 [Source:HGN
10	ANKS3	1.42	−0.39	0.41	ANKS3	ankyrin repeat and sterile alpha motif domain containing 3 [S
11	AHSA2	1.41	−0.46	0.22	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolo
12	SLC30A6	1.41	−0.59	0.29	SLC30A6	solute carrier family 30 (zinc transporter), member 6 [Source:
13	AP1G1	1.4	−1.07	0.33	AP1G1	adaptor−related protein complex 1, gamma 1 subunit [Source
14	CAB39	1.4	−0.62	0.31	CAB39	calcium binding protein 39 [Source:HGNC Symbol;Acc:HGN
15	RRP8	1.39	−0.89	0.31	RRP8	ribosomal RNA processing 8, methyltransferase, homolog (ye
16	BTBD9	1.36	−0.39	0.4	BTBD9	BTB (POZ) domain containing 9 [Source:HGNC Symbol;Acc:
17	PGS1	1.36	−0.54	0.33	PGS1	phosphatidylglycerophosphate synthase 1 [Source:HGNC Sy
18	PPP2R4	1.33	−0.47	0.36	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4 [Sourc
19	DAG1	1.3	−0.89	0.26	DAG1	dystroglycan 1 (dystrophin−associated glycoprotein 1) [Sourc
20	SLC35D1	1.26	−0.25	0.45	SLC35D1	solute carrier family 35 (UDP−GlcA/UDP−GalNAc transporter

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−05	44 / 8580	Colon	TxWk_Colon
2	1e−04	16 / 1693	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
3	2e−04	44 / 9027	Colon	Tx_Colon
4	4e−04	4 / 102	miRN	hsa−miR−1301
5	8e−04	2 / 12	GSEA	IVANOV_MUTATED_IN_COLON_CANCER
6	8e−04	36 / 6929	Lymp	HOPP_Txn_elongation
7	9e−04	2 / 13	BP	zinc II ion transmembrane transport
8	9e−04	2 / 13	MF	zinc ion transmembrane transporter activity
9	1e−03	3 / 60	miRN	hsa−miR−296−3p
10	1e−03	32 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
11	2e−03	43 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
12	2e−03	2 / 17	CC	costamere
13	2e−03	2 / 17	BP	zinc II ion transport
14	2e−03	2 / 17	GSEA	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURF
15	2e−03	2 / 18	BP	regulation of cell morphogenesis
16	2e−03	4 / 155	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
17	2e−03	6 / 391	miRN	hsa−miR−519a
18	2e−03	2 / 21	CC	clathrin adaptor complex
19	3e−03	2 / 22	BP	regulation of defense response to virus by virus
20	3e−03	2 / 22	GSEA	REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISE
21	3e−03	3 / 83	GSEA	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
22	3e−03	6 / 422	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
23	4e−03	8 / 729	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
24	4e−03	2 / 27	BP	phospholipid biosynthetic process
25	4e−03	2 / 28	GSEA	BILANGES_RAPAMYCIN_SENSITIVE_GENES
26	4e−03	6 / 443	miRN	hsa−miR−19a
27	5e−03	3 / 96	miRN	hsa−miR−513b
28	5e−03	4 / 196	GSEA	AMUNDSON_RESPONSE_TO_ARSENITE
29	5e−03	2 / 31	CC	membrane coat
30	7e−03	2 / 35	MF	ligand−activated sequence−specific DNA binding RNA polymerase II trans
31	7e−03	2 / 37	BP	intracellular receptor signaling pathway
32	8e−03	6 / 506	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
33	9e−03	8 / 843	Glio	Sturm_GBM_Meth_overexpression_E_G34_UP
34	9e−03	27 / 5184	Lymp	HOPP_Txn_transition
35	9e−03	2 / 41	MF	peptidyl−prolyl cis−trans isomerase activity
36	9e−03	2 / 41	BP	protein peptidyl−prolyl isomerization
37	9e−03	2 / 42	GSEA	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY
38	1e−02	2 / 43	BP	rhythmic process
39	1e−02	9 / 1050	Brain	Fetal_EnhP
40	1e−02	1 / 3	GSEA	YANG_MUC2_TARGETS_DUODENUM_6MO_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−04	2 / 13	zinc II ion transmembrane transport
2	2e−03	2 / 17	zinc II ion transport
3	2e−03	2 / 18	regulation of cell morphogenesis
4	3e−03	2 / 22	regulation of defense response to virus by virus
5	4e−03	2 / 27	phospholipid biosynthetic process
6	7e−03	2 / 37	intracellular receptor signaling pathway
7	9e−03	2 / 41	protein peptidyl−prolyl isomerization
8	1e−02	2 / 43	rhythmic process
9	1e−02	2 / 45	regulation of circadian rhythm
10	1e−02	2 / 50	steroid hormone mediated signaling pathway
11	1e−02	6 / 570	symbiosis, encompassing mutualism through parasitism
12	2e−02	2 / 58	protein ubiquitination involved in ubiquitin−dependent protein catabolic process
13	3e−02	2 / 77	glycerophospholipid biosynthetic process
14	3e−02	6 / 687	gene expression
15	3e−02	1 / 10	endosome to melanosome transport
16	3e−02	1 / 10	histone H3−K4 trimethylation
17	3e−02	1 / 10	morphogenesis of an epithelial sheet
18	3e−02	1 / 10	positive regulation of cellular metabolic process
19	3e−02	1 / 10	positive regulation of phosphoprotein phosphatase activity
20	3e−02	1 / 10	Schwann cell development

Brain

Rank	p−value	#in/all	Geneset
1	0.001	32 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.002	43 / 9330	Overlap_fetal_midbrain_ReprPC
3	0.010	9 / 1050	Fetal_EnhP
4	0.022	39 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	0.043	38 / 9013	Overlap_fetal_midbrain_K9K27me3
6	0.051	6 / 769	Overlap_fetal_midbrain_ZNF
7	0.106	2 / 158	Overlap_fetal_midbrain_Het
8	0.115	38 / 9528	Overlap_fetal_midbrain_Quies
9	0.191	2 / 229	Mid_Frontal_Lobe_TxTrans
10	0.197	6 / 1122	Fetal_K9K27me3
11	0.272	13 / 3081	Mid_Frontal_Lobe_ZNF
12	0.279	4 / 765	Mid_Frontal_Lobe_Het
13	0.316	8 / 1845	Fetal_Quies
14	0.332	4 / 831	Fetal_HetRpts
15	0.347	2 / 349	Fetal_ZNF
16	0.373	8 / 1949	Fetal_TssF
17	0.405	3 / 656	Overlap_fetal_midbrain_EnhP
18	0.506	5 / 1333	Fetal_ReprPCWk
19	0.563	2 / 534	Mid_Frontal_Lobe_EnhG
20	0.593	2 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	1 / 14	LIU_COMMON_CANCER_GENES
2	0.05	1 / 16	GENTLES_modul16
3	0.13	2 / 180	SPANG_LPS−index2
4	0.16	1 / 48	KUIPER_MM poor survival
5	0.33	1 / 113	PanCan_Driver_Gene_geneset_nanostring
6	0.51	2 / 489	Lembcke_Normal vs Adenoma
7	0.65	1 / 298	SPANG_BCL6−index2
8	0.75	0 / 14	LIU_PROSTATE_CANCER_DN
9	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
10	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.00	0 / 12	LIU_BREAST_CANCER
14	1.00	0 / 14	LIU_LIVER_CANCER
15	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
16	1.00	0 / 15	WANG_ER_UP
17	1.00	0 / 5	WANG_ER_DN
18	1.00	0 / 16	WOLFER_overlap genes
19	1.00	0 / 12	BEN−PORATH_DN
20	1.00	0 / 13	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	0.002	2 / 17	costamere
2	0.002	2 / 21	clathrin adaptor complex
3	0.005	2 / 31	membrane coat
4	0.014	3 / 144	postsynaptic membrane
5	0.041	1 / 12	node of Ranvier
6	0.043	3 / 223	lysosomal membrane
7	0.045	1 / 13	dystrophin−associated glycoprotein complex
8	0.048	1 / 14	clathrin−coated vesicle membrane
9	0.053	2 / 106	trans−Golgi network
10	0.055	3 / 246	mitochondrial matrix
11	0.061	1 / 18	protein phosphatase type 2A complex
12	0.065	1 / 19	calcium channel complex
13	0.081	1 / 24	polysome
14	0.084	1 / 25	clathrin−coated endocytic vesicle membrane
15	0.097	1 / 29	cell−cell adherens junction
16	0.116	1 / 35	trans−Golgi network membrane
17	0.119	5 / 747	nucleolus
18	0.128	1 / 39	endocytic vesicle membrane
19	0.134	1 / 41	mitochondrial nucleoid
20	0.155	1 / 48	clathrin−coated vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.07	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
2	0.17	5 / 838	Chr 3
3	0.22	3 / 462	Chr 14
4	0.23	3 / 469	Chr 8
5	0.27	5 / 993	Chr 2
6	0.31	3 / 558	Chr 4
7	0.33	3 / 576	Chr 9
8	0.40	3 / 649	Chr 16
9	0.41	1 / 151	Chr 21
10	0.43	3 / 687	Chr 6
11	0.57	3 / 840	Chr 17
12	0.70	1 / 335	Chr 22
13	0.71	2 / 696	Chr 5
14	0.71	3 / 1037	Chr 19
15	0.76	1 / 398	Chr 20
16	0.76	2 / 775	Chr 12
17	0.78	4 / 1500	Chr 1
18	0.81	1 / 465	Chr 15
19	0.86	1 / 551	Chr X
20	0.92	1 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	44 / 8580	TxWk_Colon
2	2e−04	44 / 9027	Tx_Colon
3	1e−02	41 / 9482	TssA_Colon
4	2e−02	37 / 8415	Quies3_Colon
5	4e−02	1 / 13	TCGA−CRC_less−agressive−disease−markers
6	5e−02	1 / 15	Budinska_B_Lower crypt−like_UP
7	8e−02	26 / 5880	TssD2_Colon
8	1e−01	14 / 2798	TxEnhG1_Colon
9	1e−01	30 / 7203	TssF_Colon
10	2e−01	16 / 3812	TssD1_Colon
11	3e−01	1 / 102	Marisa_CRC−cluster−d
12	3e−01	1 / 117	Marisa_CRC−cluster−b
13	3e−01	11 / 2698	EnhA_Colon
14	4e−01	2 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
15	4e−01	2 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
16	4e−01	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
17	4e−01	2 / 427	Quies2_Colon
18	5e−01	37 / 10290	TssWk_Colon
19	5e−01	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	5e−01	3 / 739	TxEnhG2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.8	1 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.009	8 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.024	2 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
3	0.084	1 / 25	Shaw_down_in_1p19q
4	0.097	1 / 29	shaw_responders_down_in_oligo_glioma
5	0.122	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	0.136	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
7	0.152	1 / 47	mature astrocytes
8	0.199	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	0.213	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.213	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	0.232	1 / 75	Weller_LGG_A_vs_O_DOWN
12	0.303	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
13	0.304	1 / 103	GIEZELT_GBM_WT_up_VS_mut
14	0.429	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	0.692	1 / 332	Up
16	0.718	1 / 356	Down_a
17	1.000	0 / 15	VERHAAK_CL subtype
18	1.000	0 / 15	VERHAAK_MES subtype
19	1.000	0 / 16	VERHAAK_NL subtype
20	1.000	0 / 14	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	16 / 1693	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
2	8e−04	2 / 12	IVANOV_MUTATED_IN_COLON_CANCER
3	2e−03	2 / 17	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACI
4	2e−03	4 / 155	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
5	3e−03	2 / 22	REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEAS
6	3e−03	3 / 83	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
7	3e−03	6 / 422	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
8	4e−03	8 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
9	4e−03	2 / 28	BILANGES_RAPAMYCIN_SENSITIVE_GENES
10	5e−03	4 / 196	AMUNDSON_RESPONSE_TO_ARSENITE
11	8e−03	6 / 506	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
12	9e−03	2 / 42	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY
13	1e−02	1 / 3	YANG_MUC2_TARGETS_DUODENUM_6MO_UP
14	1e−02	2 / 47	RASHI_RESPONSE_TO_IONIZING_RADIATION_3
15	1e−02	2 / 48	RAMASWAMY_METASTASIS_DN
16	1e−02	1 / 4	WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_LIVER_DAMAGE
17	2e−02	3 / 148	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_UP
18	2e−02	2 / 55	KYNG_DNA_DAMAGE_BY_UV
19	2e−02	5 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
20	2e−02	1 / 5	ST_INTERLEUKIN_13_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.04	2 / 91	HALLMARK_PROTEIN_SECRETION
3	0.12	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	0.13	2 / 181	HALLMARK_P53_PATHWAY
5	0.14	2 / 188	HALLMARK_ADIPOGENESIS
6	0.15	2 / 196	HALLMARK_MTORC1_SIGNALING
7	0.19	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
8	0.28	1 / 94	HALLMARK_ANDROGEN_RESPONSE
9	0.28	1 / 95	HALLMARK_SPERMATOGENESIS
10	0.29	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.38	1 / 137	HALLMARK_UV_RESPONSE_DN
12	0.39	1 / 140	HALLMARK_APOPTOSIS
13	0.46	1 / 174	HALLMARK_HEME_METABOLISM
14	0.46	1 / 176	HALLMARK_HYPOXIA
15	0.48	1 / 183	HALLMARK_GLYCOLYSIS
16	0.50	1 / 196	HALLMARK_G2M_CHECKPOINT
17	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
18	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
19	1.00	0 / 195	HALLMARK_MITOTIC_SPINDLE
20	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−04	36 / 6929	HOPP_Txn_elongation
2	9e−03	27 / 5184	HOPP_Txn_transition
3	2e−02	27 / 5538	HOPP_Weak_txn
4	5e−02	33 / 7592	HOPP_Active_promoter
5	5e−02	1 / 16	ROSOLOWSKI_red UP
6	7e−02	31 / 7209	HOPP_Weak_promoter
7	1e−01	25 / 5693	HOPP_Weak_enhancer
8	3e−01	2 / 280	SPANG_CD40 6hrs UP
9	3e−01	1 / 86	ROSOLOWSKI_red total
10	3e−01	1 / 89	ROSOLOWSKI_blue total
11	3e−01	1 / 107	SPANG_LPS 6hrs UP
12	3e−01	25 / 6564	HOPP_Strong_enhancer
13	4e−01	9 / 2211	HOPP_Repetitive
14	4e−01	10 / 2563	HOPP_Heterochrom
15	4e−01	5 / 1218	SPANG_BCR UP
16	6e−01	1 / 247	ZHANG_DLBCL mutated
17	6e−01	1 / 294	TARTE_Plasmablast signature
18	9e−01	2 / 1128	SPANG_BCR DN
19	1e+00	4 / 2188	HOPP_Poised_promoter
20	1e+00	6 / 3396	HOPP_Repressed

MF

Rank	p−value	#in/all	Geneset
1	9e−04	2 / 13	zinc ion transmembrane transporter activity
2	7e−03	2 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
3	9e−03	2 / 41	peptidyl−prolyl cis−trans isomerase activity
4	1e−02	2 / 46	steroid hormone receptor activity
5	2e−02	2 / 67	kinase binding
6	3e−02	3 / 193	transferase activity, transferring acyl groups
7	3e−02	2 / 79	protein transporter activity
8	4e−02	1 / 11	metal ion transmembrane transporter activity
9	4e−02	1 / 11	vinculin binding
10	4e−02	1 / 12	alpha−actinin binding
11	4e−02	1 / 12	protein methyltransferase activity
12	4e−02	1 / 13	ATPase activator activity
13	5e−02	4 / 386	nucleotide binding
14	5e−02	1 / 14	ferrous iron binding
15	5e−02	2 / 102	mRNA binding
16	5e−02	1 / 15	cation transmembrane transporter activity
17	5e−02	1 / 15	protein serine/threonine kinase activator activity
18	5e−02	4 / 405	ligase activity
19	5e−02	1 / 16	RNA polymerase II carboxy−terminal domain kinase activity
20	6e−02	1 / 17	GTP−dependent protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 102	hsa−miR−1301
2	1e−03	3 / 60	hsa−miR−296−3p
3	2e−03	6 / 391	hsa−miR−519a
4	4e−03	6 / 443	hsa−miR−19a
5	5e−03	3 / 96	hsa−miR−513b
6	1e−02	3 / 132	hsa−miR−199b−5p
7	1e−02	3 / 132	hsa−miR−320d
8	1e−02	2 / 48	hsa−miR−553
9	1e−02	2 / 50	hsa−miR−518f
10	1e−02	5 / 405	hsa−miR−519c−3p
11	1e−02	3 / 146	hsa−miR−140−5p
12	1e−02	3 / 146	hsa−miR−142−3p
13	1e−02	3 / 146	hsa−miR−320c
14	1e−02	3 / 147	hsa−miR−143
15	2e−02	3 / 153	hsa−miR−583
16	2e−02	2 / 56	hsa−miR−151−3p
17	2e−02	5 / 437	hsa−miR−19b
18	2e−02	4 / 291	hsa−miR−34c−5p
19	2e−02	4 / 300	hsa−miR−548c−3p
20	2e−02	3 / 170	hsa−miR−320b

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.03	1 / 9	MYC_Targets DOWN
2	0.06	11 / 1878	ICGC_Cebpbsc150_targets
3	0.11	7 / 1171	KIM_MYC targets
4	0.15	7 / 1273	ICGC_P300_targets
5	0.21	10 / 2136	ICGC_GabpPcr2_targets
6	0.24	8 / 1701	HEBENSTREIT_high expression TF
7	0.25	20 / 4909	ICGC_Stat5_targets
8	0.25	18 / 4385	ICGC_Atf2_targets
9	0.26	19 / 4689	ICGC_Taf1_targets
10	0.27	9 / 2013	ICGC_Bcl11_targets
11	0.34	10 / 2416	ICGC_Bcl3_targets
12	0.36	6 / 1383	ICGC_Six5_targets
13	0.38	6 / 1418	ICGC_Ets1_targets
14	0.40	15 / 3924	ICGC_Zeb1_targets
15	0.40	18 / 4774	ICGC_Foxm1_targets
16	0.41	11 / 2836	ICGC_BatfPcr1_targets
17	0.42	18 / 4829	ICGC_Nficsc81335_targets
18	0.44	3 / 690	ICGC_Atf3_targets
19	0.45	11 / 2927	ICGC_Rad21_targets
20	0.45	15 / 4054	ICGC_Egr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 17	VAQUERIZAS_Pituitary
2	0.13	1 / 40	VAQUERIZAS_Thyroid
3	0.15	1 / 45	VAQUERIZAS_Uterus
4	1.00	0 / 36	VAQUERIZAS_Fetal brain
5	1.00	0 / 41	VAQUERIZAS_Placenta
6	1.00	0 / 26	VAQUERIZAS_Liver
7	1.00	0 / 33	VAQUERIZAS_Prostate
8	1.00	0 / 29	VAQUERIZAS_Smooth muscle
9	1.00	0 / 143	VAQUERIZAS_General
10	1.00	0 / 9	VAQUERIZAS_Kidney
11	1.00	0 / 23	VAQUERIZAS_Spinal cord
12	1.00	0 / 38	VAQUERIZAS_Whole brain
13	1.00	0 / 37	VAQUERIZAS_Thymus
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 23	VAQUERIZAS_Trachea
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	1 / 11	WIRTH_Globus pallidus
2	0.04	1 / 13	WIRTH_B−cells
3	0.55	1 / 225	PALMER_Granulocytes signature up
4	0.71	1 / 350	WIRTH_Immune system
5	1.00	0 / 32	WIRTH_Pancreas
6	1.00	0 / 11	WIRTH_Sec. lymphoid organs
7	1.00	0 / 11	WIRTH_Prim. lymphoid organs
8	1.00	0 / 8	WIRTH_Tonsil
9	1.00	0 / 12	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 5	WIRTH_Bone marrow
12	1.00	0 / 350	WIRTH_Nervous System
13	1.00	0 / 14	WIRTH_Telencephalon
14	1.00	0 / 11	WIRTH_Cortex cerebri
15	1.00	0 / 10	WIRTH_Hippocampus
16	1.00	0 / 10	WIRTH_Thalamus
17	1.00	0 / 12	WIRTH_Cerebellum
18	1.00	0 / 107	WIRTH_Testis
19	1.00	0 / 41	WIRTH_Homeostasis
20	1.00	0 / 46	WIRTH_Liver

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	11 / 3682	LU_BPDE 0.005 DN
2	0.9	2 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

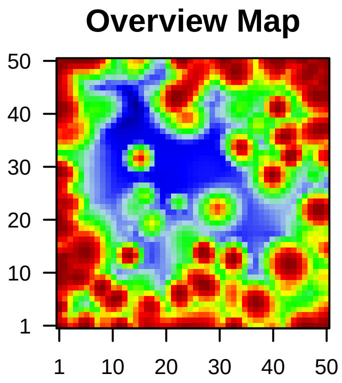
Overexpression Spots

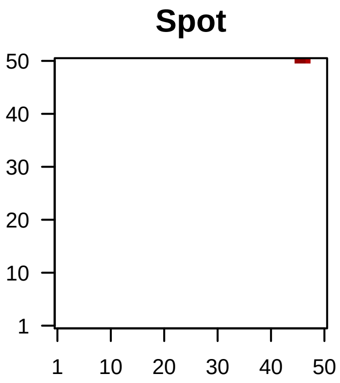
Spot Summary: D1

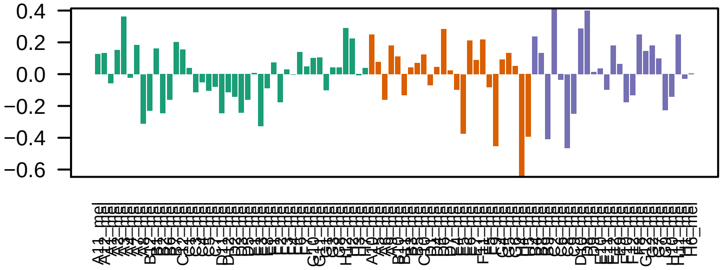
metagenes = 3
genes = 79

<r> metagenes = 0.98
<r> genes = 0.11
beta: r2= 1.88 / log p= −Inf

samples with spot = 17 (18.5 %)
MSC1 : 5 (11.9 %)
MSC2 : 5 (20 %)
MSC3 : 7 (28 %)


Overview Map


Spot

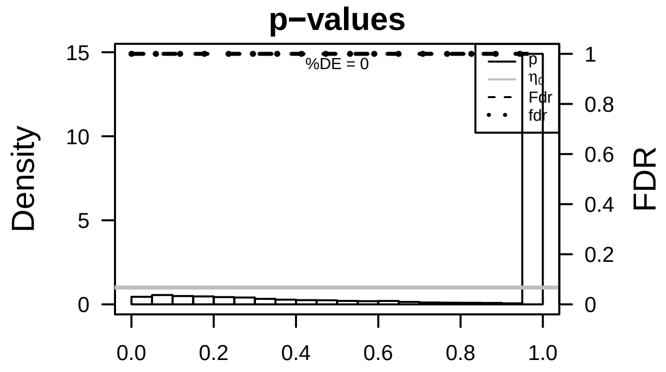


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	GDF15	1.77	−1.15	0.38	GDF15	growth differentiation factor 15 [Source:HGNC Symbol;Acc:H
2	PPCDC	1.72	−0.42	0.2	PPCDC	phosphopantothenoylcysteine decarboxylase [Source:HGNC
3	BBS4	1.71	−0.53	0.31	BBS4	Bardet−Biedl syndrome 4 [Source:HGNC Symbol;Acc:HGNC
4	PISD	1.67	−0.46	0.24	PISD	phosphatidylserine decarboxylase [Source:HGNC Symbol;Ac
5	TRIB3	1.65	−0.81	0.34	TRIB3	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:1
6	PTPRR	1.65	−0.28	0.31	PTPRR	protein tyrosine phosphatase, receptor type, R [Source:HGN
7	C2orf74	1.63	−0.75	0.24	C2orf74	chromosome 2 open reading frame 74 [Source:HGNC Symb
8	ORMDL3	1.56	−0.27	0.34	ORMDL3	ORMDL sphingolipid biosynthesis regulator 3 [Source:HGNC
9	PKN1	1.55	−0.45	0.28	PKN1	protein kinase N1 [Source:HGNC Symbol;Acc:HGNC:9405]
10	ELOVL6	1.55	−0.58	0.26	ELOVL6	ELOVL fatty acid elongase 6 [Source:HGNC Symbol;Acc:HG
11	MARCH9	1.49	−0.56	0.26	MARCH9	membrane−associated ring finger (C3HC4) 9 [Source:HGNC
12	TSEN2	1.47	−0.64	0.17	TSEN2	TSEN2 tRNA splicing endonuclease subunit [Source:HGNC
13	ARHGEF2	1.47	−0.64	0.32	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Sourc
14	POC5	1.43	−0.71	0.27	POC5	POC5 centriolar protein [Source:HGNC Symbol;Acc:HGNC:2
15	NMRK1	1.42	−0.6	0.38	NMRK1	nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:H
16	PDK4	1.41	−1.3	0.27	PDK4	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S
17	CCDC51	1.41	−0.75	0.4	CCDC51	coiled−coil domain containing 51 [Source:HGNC Symbol;Acc
18	THG1L	1.39	−0.53	0.26	THG1L	tRNA−histidine guanylyltransferase 1−like (S. cerevisiae) [Sou
19	GRIPAP1	1.34	−0.6	0.35	GRIPAP1	GRIP1 associated protein 1 [Source:HGNC Symbol;Acc:HGN
20	UBIAD1	1.34	−0.47	0.28	UBIAD1	UbiA prenyltransferase domain containing 1 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−07	10 / 235	GSEA	BLUM_RESPONSE_TO_SALIRASIB_UP
2	3e−06	68 / 9482	Colon	TssA_Colon
3	3e−05	4 / 35	MF	aminoacyl−tRNA ligase activity
4	4e−05	7 / 176	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
5	5e−05	6 / 126	GSEA	PENG_LEUCINE_DEPRIVATION_UP
6	6e−05	4 / 41	GSEA	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
7	6e−05	65 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
8	7e−05	4 / 42	GSEA	REACTOME_TRNA_AMINOACYLATION
9	7e−05	3 / 16	GSEA	TOMIDA_METASTASIS_DN
10	8e−05	4 / 44	BP	tRNA aminoacylation for protein translation
11	1e−04	3 / 18	GSEA	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN
12	1e−04	6 / 147	BP	tRNA metabolic process
13	2e−04	5 / 98	GSEA	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
14	3e−04	3 / 24	GSEA	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
15	3e−04	9 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
16	3e−04	3 / 26	GSEA	KRIGE_AMINO_ACID_DEPRIVATION
17	4e−04	9 / 421	GSEA	MOOTHA_MITOCHONDRIA
18	4e−04	2 / 6	GSEA	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS
19	4e−04	7 / 260	GSEA	ENK_UV_RESPONSE_EPIDERMIS_UP
20	5e−04	12 / 743	GSEA	ONKEN_UVEAL_MELANOMA_UP
21	5e−04	20 / 1730	BP	small molecule metabolic process
22	5e−04	18 / 1468	CC	mitochondrion
23	6e−04	7 / 277	BP	translation
24	7e−04	2 / 8	GSEA	VANLOO_SP3_TARGETS_UP
25	9e−04	0 / 12	Canc	LIU_PROSTATE_CANCER_UP
26	9e−04	54 / 7592	Lymp	HOPP_Active_promoter
27	9e−04	57 / 8205	CC	cytoplasm
28	1e−03	2 / 10	CC	nuclear exosome (RNase complex)
29	1e−03	2 / 11	BP	negative regulation of B cell proliferation
30	1e−03	2 / 11	GSEA	LUI_THYROID_CANCER_CLUSTER_4
31	2e−03	9 / 532	GSEA	PARENT_MTOR_SIGNALING_UP
32	2e−03	5 / 168	MF	magnesium ion binding
33	2e−03	3 / 47	GSEA	MARCHINI_TRABECTEDIN_RESISTANCE_DN
34	2e−03	8 / 435	GSEA	GARY_CD5_TARGETS_UP
35	2e−03	40 / 5184	Lymp	HOPP_Txn_transition
36	2e−03	2 / 14	CC	exosome (RNase complex)
37	3e−03	4 / 108	GSEA	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
38	3e−03	4 / 109	GSEA	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON
39	3e−03	3 / 55	BP	tRNA processing
40	3e−03	3 / 56	GSEA	CAFFAREL_RESPONSE_TO_THC_24HR_5_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−05	4 / 44	tRNA aminoacylation for protein translation
2	1e−04	6 / 147	tRNA metabolic process
3	5e−04	20 / 1730	small molecule metabolic process
4	6e−04	7 / 277	translation
5	1e−03	2 / 11	negative regulation of B cell proliferation
6	3e−03	3 / 55	tRNA processing
7	6e−03	2 / 22	regulation of angiogenesis
8	7e−03	4 / 142	positive regulation of I−kappaB kinase/NF−kappaB signaling
9	7e−03	2 / 24	mitotic cytokinesis
10	9e−03	3 / 83	mitochondrial translational elongation
11	9e−03	3 / 83	mitochondrial translational initiation
12	9e−03	3 / 83	mitochondrial translational termination
13	1e−02	5 / 255	cellular amino acid metabolic process
14	1e−02	3 / 96	mitochondrial translation
15	2e−02	3 / 110	defense response to virus
16	3e−02	2 / 48	JNK cascade
17	3e−02	5 / 322	mitochondrion organization
18	3e−02	8 / 687	gene expression
19	3e−02	4 / 220	cofactor metabolic process
20	3e−02	2 / 53	protein homotetramerization

Brain

Rank	p−value	#in/all	Geneset
1	6e−05	65 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−02	7 / 564	Mid_Frontal_Lobe_EnhP
3	3e−02	10 / 989	Mid_Frontal_Lobe_Quies
4	5e−02	55 / 9013	Overlap_fetal_midbrain_K9K27me3
5	5e−02	39 / 5940	Overlap_fetal_midbrain_HetRpts
6	1e−01	12 / 1548	Mid_Frontal_Lobe_K9K27me3
7	1e−01	53 / 9020	Overlap_fetal_midbrain_ReprPCWk
8	2e−01	6 / 765	Mid_Frontal_Lobe_Het
9	2e−01	3 / 304	Fetal_Het
10	3e−01	19 / 3081	Mid_Frontal_Lobe_ZNF
11	3e−01	3 / 349	Fetal_ZNF
12	3e−01	7 / 1050	Fetal_EnhP
13	4e−01	11 / 1845	Fetal_Quies
14	5e−01	7 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	6e−01	1 / 163	Fetal_ReprPC
16	7e−01	12 / 2462	Mid_Frontal_Lobe_HetRpts
17	7e−01	1 / 229	Mid_Frontal_Lobe_TxTrans
18	7e−01	5 / 1122	Fetal_K9K27me3
19	7e−01	48 / 9528	Overlap_fetal_midbrain_Quies
20	7e−01	4 / 953	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	0 / 12	LIU_PROSTATE_CANCER_UP
2	7e−02	2 / 82	PanCan_TXmisReg_geneset_nanostring
3	8e−02	1 / 15	WANG_ER_UP
4	8e−02	1 / 15	GENTLES_modul1
5	8e−02	1 / 16	GENTLES_modul14
6	2e−01	3 / 298	SPANG_BCL6−index2
7	2e−01	1 / 47	PanCan_DNARepair_geneset_nanostring
8	2e−01	1 / 48	KUIPER_MM poor survival
9	2e−01	2 / 180	SPANG_LPS−index2
10	3e−01	0 / 14	LIU_COMMON_CANCER_GENES
11	3e−01	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	3e−01	1 / 70	SHAUGHNESSY_MM high risk
13	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
14	5e−01	1 / 120	PanCan_CC+Apop_geneset_nanostring
15	5e−01	1 / 121	PanCan_MAPK_geneset_nanostring
16	7e−01	2 / 489	Lembcke_Normal vs Adenoma
17	9e−01	0 / 14	LIU_PROSTATE_CANCER_DN
18	9e−01	1 / 401	Lembcke_Colonic Inflammation
19	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
20	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	5e−04	18 / 1468	mitochondrion
2	9e−04	57 / 8205	cytoplasm
3	1e−03	2 / 10	nuclear exosome (RNase complex)
4	2e−03	2 / 14	exosome (RNase complex)
5	5e−03	2 / 21	mitochondrial small ribosomal subunit
6	9e−03	3 / 81	late endosome membrane
7	9e−03	5 / 246	mitochondrial matrix
8	2e−02	8 / 616	endosome
9	2e−02	6 / 401	mitochondrial inner membrane
10	2e−02	2 / 41	cleavage furrow
11	3e−02	3 / 128	ribosome
12	3e−02	3 / 131	vesicle
13	3e−02	2 / 54	transport vesicle
14	6e−02	1 / 11	intrinsic component of membrane
15	6e−02	1 / 11	nonmotile primary cilium
16	6e−02	3 / 175	early endosome
17	7e−02	2 / 81	centriole
18	7e−02	59 / 9988	organelle
19	8e−02	1 / 15	centriolar satellite
20	8e−02	1 / 15	mitochondrial envelope

Chr

Rank	p−value	#in/all	Geneset
1	0.04	6 / 469	Chr 8
2	0.19	2 / 151	Chr 21
3	0.25	5 / 649	Chr 16
4	0.30	5 / 689	Chr 7
5	0.33	4 / 552	Chr 10
6	0.44	3 / 462	Chr 14
7	0.44	3 / 465	Chr 15
8	0.45	5 / 840	Chr 17
9	0.49	4 / 687	Chr 6
10	0.50	4 / 696	Chr 5
11	0.61	4 / 801	Chr 11
12	0.62	2 / 398	Chr 20
13	0.69	7 / 1500	Chr 1
14	0.69	1 / 221	Chr 18
15	0.75	1 / 262	Chr 13
16	0.78	3 / 775	Chr 12
17	0.79	2 / 551	Chr X
18	0.80	2 / 558	Chr 4
19	0.80	4 / 1037	Chr 19
20	0.81	2 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−06	68 / 9482	TssA_Colon
2	4e−03	59 / 9027	Tx_Colon
3	8e−03	49 / 7203	TssF_Colon
4	1e−02	55 / 8580	TxWk_Colon
5	4e−02	1 / 8	Marisa_CRC−C2
6	8e−02	1 / 16	Vilar_non−hypermutated−in−CRC
7	9e−02	6 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
8	1e−01	7 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	1e−01	19 / 2698	EnhA_Colon
10	1e−01	50 / 8415	Quies3_Colon
11	1e−01	59 / 10290	TssWk_Colon
12	1e−01	36 / 5880	TssD2_Colon
13	3e−01	54 / 9653	Enh_Colon
14	3e−01	30 / 5155	EnhWk1_Colon
15	3e−01	1 / 71	Marisa_CRC−cluster−g
16	3e−01	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
17	4e−01	6 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	4e−01	1 / 102	Marisa_CRC−cluster−d
19	6e−01	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	6e−01	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.7	2 / 435	GUDJ_psoriasis up
2	0.8	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	5 / 332	Up
2	0.06	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
3	0.13	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
4	0.15	7 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.18	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	0.22	1 / 47	Vishal_subnetwork signature of survival in GBM
7	0.22	1 / 47	mature astrocytes
8	0.22	1 / 47	Weller_LGG_gradeII−vs−III_UP
9	0.22	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
10	0.23	1 / 49	OL vs. MOG−OL
11	0.26	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.29	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
13	0.39	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	0.42	1 / 103	GIEZELT_GBM_WT_up_VS_mut
15	0.62	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
16	0.85	1 / 356	Down_a
17	0.86	1 / 365	Down_b
18	1.00	0 / 15	VERHAAK_CL subtype
19	1.00	0 / 15	VERHAAK_MES subtype
20	1.00	0 / 16	VERHAAK_NL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−07	10 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
2	4e−05	7 / 176	TIEN_INTESTINE_PROBIOTICS_24HR_DN
3	5e−05	6 / 126	PENG_LEUCINE_DEPRIVATION_UP
4	6e−05	4 / 41	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
5	7e−05	4 / 42	REACTOME_TRNA_AMINOACYLATION
6	7e−05	3 / 16	TOMIDA_METASTASIS_DN
7	1e−04	3 / 18	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN
8	2e−04	5 / 98	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
9	3e−04	3 / 24	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
10	3e−04	9 / 405	MOOTHA_HUMAN_MITODB_6_2002
11	3e−04	3 / 26	KRIGE_AMINO_ACID_DEPRIVATION
12	4e−04	9 / 421	MOOTHA_MITOCHONDRIA
13	4e−04	2 / 6	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS
14	4e−04	7 / 260	ENK_UV_RESPONSE_EPIDERMIS_UP
15	5e−04	12 / 743	ONKEN_UVEAL_MELANOMA_UP
16	7e−04	2 / 8	VANLOO_SP3_TARGETS_UP
17	9e−04	0 / 12	LIU_PROSTATE_CANCER_UP
18	1e−03	2 / 11	LUI_THYROID_CANCER_CLUSTER_4
19	2e−03	9 / 532	PARENT_MTOR_SIGNALING_UP
20	2e−03	3 / 47	MARCHINI_TRABECTEDIN_RESISTANCE_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	4 / 196	HALLMARK_MTORC1_SIGNALING
2	0.06	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
3	0.07	3 / 183	HALLMARK_GLYCOLYSIS
4	0.08	3 / 188	HALLMARK_ADIPOGENESIS
5	0.08	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	0.09	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	0.11	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.17	2 / 140	HALLMARK_APOPTOSIS
9	0.17	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
10	0.22	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
11	0.22	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	0.22	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
13	0.24	2 / 176	HALLMARK_HYPOXIA
14	0.25	2 / 181	HALLMARK_P53_PATHWAY
15	0.27	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
16	0.28	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
17	0.38	1 / 91	HALLMARK_BILE_ACID_METABOLISM
18	0.39	1 / 93	HALLMARK_PEROXISOME
19	0.49	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
20	0.53	1 / 141	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.00	0 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−04	54 / 7592	HOPP_Active_promoter
2	2e−03	40 / 5184	HOPP_Txn_transition
3	6e−03	48 / 6929	HOPP_Txn_elongation
4	2e−02	5 / 294	TARTE_Plasmablast signature
5	5e−02	2 / 66	TARTE_Plasma cell signature
6	5e−02	11 / 1218	SPANG_BCR UP
7	5e−02	42 / 6564	HOPP_Strong_enhancer
8	1e−01	1 / 20	SPANG_BAFF 9hrs UP
9	1e−01	44 / 7209	HOPP_Weak_promoter
10	1e−01	2 / 107	SPANG_LPS 6hrs UP
11	2e−01	3 / 268	SPANG_IL21 UP
12	2e−01	3 / 280	SPANG_CD40 6hrs UP
13	3e−01	1 / 61	SPANG_LPS 6hrs DN
14	3e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
15	4e−01	1 / 82	ROSOLOWSKI_green UP
16	4e−01	32 / 5693	HOPP_Weak_enhancer
17	4e−01	3 / 410	SPANG_CD40 6hrs DN
18	4e−01	2 / 256	SPANG_IL21 DN
19	4e−01	1 / 109	ROSOLOWSKI_green total
20	5e−01	30 / 5538	HOPP_Weak_txn

MF

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 35	aminoacyl−tRNA ligase activity
2	2e−03	5 / 168	magnesium ion binding
3	9e−03	2 / 27	RNA polymerase II repressing transcription factor binding
4	1e−02	2 / 32	Rac GTPase binding
5	2e−02	2 / 36	tRNA binding
6	3e−02	3 / 136	lyase activity
7	5e−02	1 / 10	lamin binding
8	5e−02	1 / 10	proteasome binding
9	5e−02	1 / 10	Rac guanyl−nucleotide exchange factor activity
10	6e−02	1 / 12	NADPH binding
11	6e−02	1 / 12	oxidoreductase activity, acting on NAD(P)H
12	6e−02	1 / 12	RNA polymerase II core promoter proximal region sequence−specific DNA bir
13	6e−02	5 / 405	ligase activity
14	7e−02	1 / 13	GTP−Rho binding
15	7e−02	1 / 13	protein kinase C activity
16	7e−02	2 / 81	protein N−terminus binding
17	7e−02	1 / 14	transmembrane receptor protein tyrosine phosphatase activity
18	8e−02	1 / 15	mitogen−activated protein kinase kinase binding
19	8e−02	11 / 1309	ATP binding
20	9e−02	1 / 17	alpha−tubulin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	7 / 459	hsa−miR−195
2	0.01	2 / 35	hsa−miR−588
3	0.02	2 / 39	hsa−miR−593
4	0.02	3 / 111	hsa−miR−361−5p
5	0.03	2 / 51	hsa−miR−571
6	0.03	1 / 6	hsa−miR−126
7	0.03	2 / 54	hsa−miR−330−5p
8	0.04	2 / 60	hsa−miR−671−5p
9	0.05	2 / 65	hsa−miR−326
10	0.05	1 / 9	hsa−miR−1306
11	0.05	1 / 9	hsa−miR−720
12	0.05	3 / 157	hsa−miR−512−3p
13	0.05	6 / 507	hsa−miR−15a
14	0.05	2 / 69	hsa−miR−873
15	0.06	2 / 78	hsa−miR−1321
16	0.06	2 / 79	hsa−miR−542−3p
17	0.07	1 / 13	hsa−miR−1234
18	0.07	5 / 426	hsa−miR−519d
19	0.10	2 / 99	hsa−miR−376a
20	0.10	3 / 208	hsa−miR−432

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.06	1 / 11	MYC_Protein synthesis degradation UP
2	0.10	1 / 19	MYC_Metabolism UP
3	0.18	13 / 1872	ICGC_Mef2_targets
4	0.27	1 / 59	MYC_Targets UP
5	0.27	8 / 1171	KIM_MYC targets
6	0.30	9 / 1383	ICGC_Six5_targets
7	0.31	17 / 2836	ICGC_BatfPcr1_targets
8	0.32	27 / 4689	ICGC_Taf1_targets
9	0.34	28 / 4909	ICGC_Stat5_targets
10	0.35	25 / 4385	ICGC_Atf2_targets
11	0.40	11 / 1878	ICGC_Cebpbsc150_targets
12	0.40	10 / 1701	HEBENSTREIT_high expression TF
13	0.41	24 / 4314	ICGC_Ebfsc137065_targets
14	0.41	27 / 4879	ICGC_Pmlsc71910_targets
15	0.46	8 / 1400	ICGC_Myc_targets
16	0.46	22 / 4032	ICGC_Creb1_targets
17	0.46	24 / 4414	ICGC_Bclaf101388_targets
18	0.47	22 / 4054	ICGC_Egr1_targets
19	0.49	4 / 690	ICGC_Atf3_targets
20	0.49	11 / 2013	ICGC_Bcl11_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 45	VAQUERIZAS_Uterus
2	0.3	1 / 59	VAQUERIZAS_Whole blood
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 26	VAQUERIZAS_Liver
6	1.0	0 / 33	VAQUERIZAS_Prostate
7	1.0	0 / 29	VAQUERIZAS_Smooth muscle
8	1.0	0 / 143	VAQUERIZAS_General
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 29	VAQUERIZAS_Fetal lung
16	1.0	0 / 58	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 23	VAQUERIZAS_Trachea
19	1.0	0 / 11	VAQUERIZAS_Fetal liver
20	1.0	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 12	WIRTH_Lymphocytes
2	0.06	1 / 12	WIRTH_Cerebellum
3	0.33	2 / 225	PALMER_Granulocytes signature up
4	0.45	1 / 114	PALMER_T−Cell signature up
5	0.64	1 / 194	PALMER_B−Cell signature up
6	1.00	0 / 32	WIRTH_Pancreas
7	1.00	0 / 350	WIRTH_Immune system
8	1.00	0 / 11	WIRTH_Sec. lymphoid organs
9	1.00	0 / 11	WIRTH_Prim. lymphoid organs
10	1.00	0 / 13	WIRTH_B−cells
11	1.00	0 / 8	WIRTH_Tonsil
12	1.00	0 / 12	WIRTH_Thymus
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 350	WIRTH_Nervous System
15	1.00	0 / 11	WIRTH_Globus pallidus
16	1.00	0 / 14	WIRTH_Telencephalon
17	1.00	0 / 11	WIRTH_Cortex cerebri
18	1.00	0 / 10	WIRTH_Hippocampus
19	1.00	0 / 10	WIRTH_Thalamus
20	1.00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	7 / 1115	LU_BPDE 1h DN
2	0.9	15 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

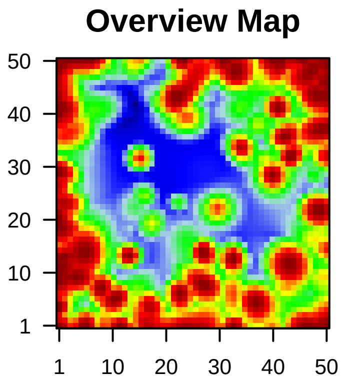
Overexpression Spots

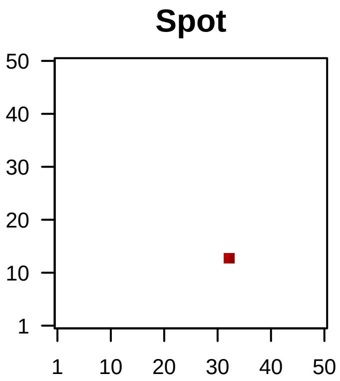
Spot Summary: E1

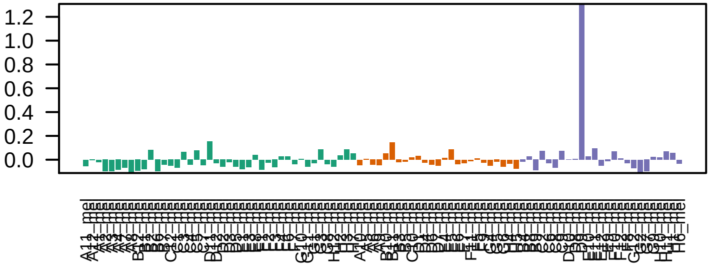
metagenes = 4
genes = 51

<r> metagenes = 0.99
<r> genes = 0.27
beta: r2= 0.41 / log p= −11.35

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)


Overview Map


Spot

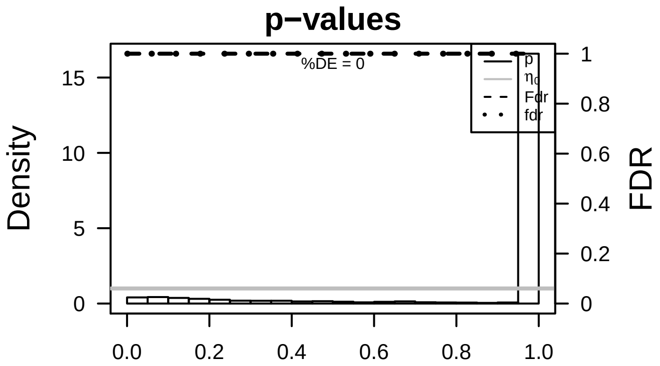


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	IGF2BP2	2.5	−0.05	0.75	IGF2BP2	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
2	ACSF2	2.1	−0.18	0.48	ACSF2	acyl−CoA synthetase family member 2 [Source:HGNC Symbo
3	CFAP44	2.06	−0.34	0.27	CFAP44	cilia and flagella associated protein 44 [Source:HGNC Symbo
4	KLF4	1.99	−0.11	0.44	KLF4	Kruppel−like factor 4 (gut) [Source:HGNC Symbol;Acc:HGNC
5	SHISA2	1.94	−0.19	0.38	SHISA2	shisa family member 2 [Source:HGNC Symbol;Acc:HGNC:20
6	PLXDC1	1.9	−0.05	0.51	PLXDC1	plexin domain containing 1 [Source:HGNC Symbol;Acc:HGN
7	SLC9B1	1.83	−0.14	0.37	SLC9B1	solute carrier family 9, subfamily B (NHA1, cation proton antip
8	ANKMY1	1.82	−0.19	0.47	ANKMY1	ankyrin repeat and MYND domain containing 1 [Source:HGN
9	EPGN	1.77	−0.02	0.79	EPGN	epithelial mitogen [Source:HGNC Symbol;Acc:HGNC:17470]
10	APLP1	1.75	−0.26	0.41	APLP1	amyloid beta (A4) precursor−like protein 1 [Source:HGNC Sy
11	PTHLH	1.75	−0.05	0.6	PTHLH	parathyroid hormone−like hormone [Source:HGNC Symbol;A
12	NRCAM	1.74	−0.1	0.52	NRCAM	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:
13	DLX6	1.69	−0.22	0.37	DLX6	distal−less homeobox 6 [Source:HGNC Symbol;Acc:HGNC:2
14	GRB14	1.68	−0.09	0.45	GRB14	growth factor receptor−bound protein 14 [Source:HGNC Sym
15	RPUSD4	1.68	−0.32	0.26	RPUSD4	RNA pseudouridylate synthase domain containing 4 [Source:
16	ZNF782	1.58	−0.11	0.36	ZNF782	zinc finger protein 782 [Source:HGNC Symbol;Acc:HGNC:33
17	NLGN1	1.57	−0.26	0.35	NLGN1	neuroligin 1 [Source:HGNC Symbol;Acc:HGNC:14291]
18	RNF169	1.52	−0.5	0.28	RNF169	ring finger protein 169 [Source:HGNC Symbol;Acc:HGNC:26
19	CCDC30	1.51	−0.12	0.43	CCDC30	coiled−coil domain containing 30 [Source:HGNC Symbol;Acc
20	TMEM241	1.47	−0.58	0.34	TMEM241	transmembrane protein 241 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−04	2 / 11	GSEA	REACTOME_HDL_MEDIATED_LIPID_TRANSPORT
2	1e−03	22 / 3396	Lympl	HOPP_Repressed
3	2e−03	6 / 371	Colon	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
4	2e−03	16 / 2159	Colon	TssP_Colon
5	2e−03	6 / 391	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2
6	2e−03	2 / 21	GSEA	REACTOME_LIPOPROTEIN_METABOLISM
7	3e−03	4 / 177	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	3e−03	6 / 427	Colon	Quies2_Colon
9	3e−03	2 / 25	BP	lipoprotein metabolic process
10	3e−03	4 / 182	GSEA	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
11	4e−03	2 / 26	BP	positive regulation of nitric oxide biosynthetic process
12	4e−03	6 / 443	BP	anatomical structure formation involved in morphogenesis
13	4e−03	11 / 1317	Colon	EnhP_Colon
14	5e−03	2 / 31	miRN	hsa−miR−617
15	5e−03	2 / 32	GSEA	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT
16	7e−03	22 / 3897	Colon	Quies1_Colon
17	8e−03	3 / 118	GSEA	REACTOME_DIABETES_PATHWAYS
18	8e−03	2 / 39	BP	synapse assembly
19	8e−03	2 / 40	GSEA	MELLMAN_TUT1_TARGETS_DN
20	9e−03	2 / 41	GSEA	BROWNE_HCMV_INFECTION_30MIN_UP
21	1e−02	13 / 1889	Colon	ReprPCWk_Colon
22	1e−02	5 / 394	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
23	1e−02	4 / 260	BP	nervous system development
24	1e−02	2 / 49	miRN	hsa−miR−654−3p
25	1e−02	3 / 142	GSEA	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
26	1e−02	6 / 574	Brain	Overlap_fetal_midbrain_TssP
27	1e−02	14 / 2188	Lympl	HOPP_Poised_promoter
28	1e−02	2 / 52	BP	fat cell differentiation
29	1e−02	2 / 53	GSEA	FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP
30	1e−02	3 / 149	GSEA	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
31	1e−02	2 / 54	BP	positive regulation of epithelial cell proliferation
32	2e−02	2 / 56	GSEA	WONG_ENDMETRIUM_CANCER_DN
33	2e−02	3 / 157	GSEA	GRUETZMANN_PANCREATIC_CANCER_DN
34	2e−02	2 / 58	GSEA	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
35	2e−02	1 / 5	Cance	WANG_ER_DN
36	2e−02	1 / 5	Glio	oligodendrocytes_glio
37	2e−02	7 / 786	Brain	Fetal_EnhG
38	2e−02	2 / 59	GSEA	MCCLUNG_COCAIN_REWARD_4WK
39	2e−02	2 / 60	GSEA	AMIT_SERUM_RESPONSE_120_MCF10A
40	2e−02	6 / 615	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.003	2 / 25	lipoprotein metabolic process
2	0.004	2 / 26	positive regulation of nitric oxide biosynthetic process
3	0.004	6 / 443	anatomical structure formation involved in morphogenesis
4	0.008	2 / 39	synapse assembly
5	0.012	4 / 260	nervous system development
6	0.014	2 / 52	fat cell differentiation
7	0.015	2 / 54	positive regulation of epithelial cell proliferation
8	0.020	2 / 64	epithelial cell differentiation
9	0.026	3 / 187	angiogenesis
10	0.034	1 / 10	cellular response to peptide
11	0.034	1 / 10	lipoprotein transport
12	0.034	1 / 10	negative regulation of chondrocyte differentiation
13	0.034	1 / 10	negative regulation of phosphatidylinositol 3−kinase signaling
14	0.034	1 / 10	negative regulation of programmed cell death
15	0.034	1 / 10	neuron cell−cell adhesion
16	0.034	1 / 10	positive regulation of myoblast fusion
17	0.034	1 / 10	positive regulation of tyrosine phosphorylation of Stat5 protein
18	0.034	1 / 10	protein localization to synapse
19	0.034	1 / 10	regulation of axon extension
20	0.034	1 / 10	regulation of respiratory gaseous exchange by neurological system process

Brain

Rank	p−value	#in/all	Geneset
1	0.01	6 / 574	Overlap_fetal_midbrain_TssP
2	0.02	7 / 786	Fetal_EnhG
3	0.03	6 / 668	Mid_Frontal_Lobe_Enh
4	0.03	7 / 862	Overlap_fetal_midbrain_TxTrans
5	0.07	5 / 656	Overlap_fetal_midbrain_EnhP
6	0.11	2 / 166	Mid_Frontal_Lobe_Tx
7	0.12	11 / 2185	Fetal_TssA
8	0.16	5 / 831	Fetal_HetRpts
9	0.16	6 / 1065	Overlap_fetal_midbrain_Enh
10	0.18	9 / 1845	Fetal_Quies
11	0.19	5 / 884	Overlap_fetal_midbrain_EnhG
12	0.19	2 / 229	Mid_Frontal_Lobe_TxTrans
13	0.21	13 / 2972	Mid_Frontal_Lobe_ReprPC
14	0.21	4 / 686	Overlap_fetal_midbrain_TssA
15	0.22	3 / 468	Mid_Frontal_Lobe_TssF
16	0.23	6 / 1207	Overlap_fetal_midbrain_TssF
17	0.25	5 / 989	Mid_Frontal_Lobe_Quies
18	0.28	3 / 534	Mid_Frontal_Lobe_EnhG
19	0.30	4 / 812	Mid_Frontal_Lobe_TssP
20	0.35	8 / 1949	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	WANG_ER_DN
2	0.05	1 / 14	LIU_LIVER_CANCER
3	0.15	1 / 48	KUIPER_MM poor survival
4	0.17	1 / 55	PanCan_JAK−ST_geneset_nanostring
5	0.19	0 / 15	RHODES_CANCER_META_SIGNATURE
6	0.20	0 / 14	LIU_COMMON_CANCER_GENES
7	0.32	1 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.74	0 / 14	LIU_PROSTATE_CANCER_DN
9	0.75	1 / 401	Lembcke_Colonic Inflammation
10	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.00	0 / 12	LIU_BREAST_CANCER
14	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
15	1.00	0 / 15	WANG_ER_UP
16	1.00	0 / 16	WOLFER_overlap genes
17	1.00	0 / 12	BEN−PORATH_DN
18	1.00	0 / 13	BEN−PORATH_UP
19	1.00	0 / 15	GENTLES_modul1
20	1.00	0 / 16	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	0.04	1 / 11	filopodium tip
2	0.05	1 / 14	exocyst
3	0.05	1 / 14	male germ cell nucleus
4	0.05	1 / 16	excitatory synapse
5	0.06	2 / 119	external side of plasma membrane
6	0.06	4 / 438	Golgi membrane
7	0.06	1 / 19	site of double−strand break
8	0.07	1 / 21	synaptonemal complex
9	0.08	1 / 23	nuclear euchromatin
10	0.09	1 / 26	sarcoplasmic reticulum membrane
11	0.09	7 / 1132	Golgi apparatus
12	0.10	1 / 31	brush border membrane
13	0.10	1 / 31	dendritic shaft
14	0.11	2 / 164	endosome membrane
15	0.11	1 / 35	condensed nuclear chromosome
16	0.11	1 / 35	integral component of Golgi membrane
17	0.11	2 / 169	transcription factor complex
18	0.12	1 / 36	T−tubule
19	0.12	1 / 37	platelet alpha granule lumen
20	0.12	2 / 177	synapse

Chr

Rank	p−value	#in/all	Geneset
1	0.1	4 / 576	Chr 9
2	0.2	2 / 262	Chr 13
3	0.3	7 / 1500	Chr 1
4	0.3	3 / 552	Chr 10
5	0.3	3 / 558	Chr 4
6	0.3	4 / 838	Chr 3
7	0.4	2 / 398	Chr 20
8	0.4	1 / 151	Chr 21
9	0.4	3 / 689	Chr 7
10	0.5	2 / 465	Chr 15
11	0.5	2 / 469	Chr 8
12	0.5	3 / 801	Chr 11
13	0.5	1 / 221	Chr 18
14	0.7	2 / 649	Chr 16
15	0.7	3 / 993	Chr 2
16	0.7	1 / 335	Chr 22
17	0.8	2 / 775	Chr 12
18	0.8	2 / 840	Chr 17
19	0.9	2 / 1037	Chr 19
20	1.0	0 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	6 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
2	0.002	16 / 2159	TssP_Colon
3	0.003	6 / 427	Quies2_Colon
4	0.004	11 / 1317	EnhP_Colon
5	0.007	22 / 3897	Quies1_Colon
6	0.010	13 / 1889	ReprPCWk_Colon
7	0.011	5 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	0.026	13 / 2142	ReprPC_Colon
9	0.060	1 / 18	Boland_CRC−MSI−A6−A10
10	0.119	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	0.138	1 / 43	Marisa_CRC−cluster−f
12	0.163	6 / 1079	ZNF_Colon
13	0.202	2 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
14	0.218	2 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
15	0.297	1 / 102	Marisa_CRC−cluster−d
16	0.300	2 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
17	0.319	15 / 3812	TssD1_Colon
18	0.332	3 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
19	0.352	22 / 5880	TssD2_Colon
20	0.374	13 / 3383	EnhWk2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.3	2 / 294	GUDJ_psoriasis down
2	1.0	0 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	oligodendrocytes_glio
2	0.02	2 / 62	cultured astroglia vs. in vivo astrocytes
3	0.02	2 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
4	0.03	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
5	0.04	1 / 11	Christensen_hypermethylated_in_ependymoma
6	0.04	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
7	0.06	1 / 18	Shinawi_with_increased_methylation_in_STS
8	0.12	1 / 38	OL vs. OPC
9	0.13	1 / 39	OPC
10	0.16	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
11	0.18	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.20	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
13	0.22	1 / 71	Weller_LGG_A_vs_O_UP
14	0.28	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
15	0.33	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
16	0.35	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
17	0.67	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
18	0.71	1 / 356	Down_a
19	0.72	1 / 365	Down_b
20	0.79	2 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	2 / 11	REACTOME_HDL_MEDIATED_LIPID_TRANSPORT
2	2e−03	6 / 391	MEISSNER_NPC_HCP_WITH_H3K4ME2
3	2e−03	2 / 21	REACTOME_LIPOPROTEIN_METABOLISM
4	3e−03	4 / 182	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
5	5e−03	2 / 32	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT
6	8e−03	3 / 118	REACTOME_DIABETES_PATHWAYS
7	8e−03	2 / 40	MELLMAN_TUT1_TARGETS_DN
8	9e−03	2 / 41	BROWNE_HCMV_INFECTION_30MIN_UP
9	1e−02	3 / 142	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
10	1e−02	2 / 53	FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP
11	1e−02	3 / 149	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
12	2e−02	2 / 56	WONG_ENDMETRIUM_CANCER_DN
13	2e−02	3 / 157	GRUETZMANN_PANCREATIC_CANCER_DN
14	2e−02	2 / 58	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
15	2e−02	2 / 59	MCCLUNG_COCAIN_REWARD_4WK
16	2e−02	2 / 60	AMIT_SERUM_RESPONSE_120_MCF10A
17	2e−02	6 / 615	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
18	2e−02	2 / 61	MAHAJAN_RESPONSE_TO_IL1A_UP
19	2e−02	3 / 165	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
20	2e−02	2 / 62	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP

HM

Rank	p−value	#in/all	Geneset
1	0.003	4 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	0.101	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
3	0.113	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	0.167	1 / 53	HALLMARK_TGF_BETA_SIGNALING
5	0.187	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.275	1 / 93	HALLMARK_PEROXISOME
7	0.280	1 / 95	HALLMARK_SPERMATOGENESIS
8	0.353	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
9	0.384	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
10	0.401	1 / 148	HALLMARK_KRAS_SIGNALING_UP
11	0.439	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.445	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.452	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.466	1 / 181	HALLMARK_P53_PATHWAY
15	1.000	0 / 176	HALLMARK_HYPOXIA
16	1.000	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	1.000	0 / 195	HALLMARK_MITOTIC_SPINDLE
18	1.000	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
19	1.000	0 / 146	HALLMARK_DNA_REPAIR
20	1.000	0 / 196	HALLMARK_G2M_CHECKPOINT

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	22 / 3396	HOPP_Repressed
2	0.013	14 / 2188	HOPP_Poised_promoter
3	0.037	1 / 11	Subero_T−ALL_hypo_meth
4	0.054	1 / 16	DAVE_BL Inter
5	0.076	1 / 23	DAVE_Immune response 1
6	0.083	1 / 25	Subero_T−PLL_hypo_meth
7	0.089	13 / 2563	HOPP_Heterochrom
8	0.496	8 / 2211	HOPP_Repetitive
9	0.549	4 / 1128	SPANG_BCR DN
10	0.576	1 / 247	ZHANG_DLBCL mutated
11	0.589	1 / 256	SPANG_IL21 DN
12	0.606	1 / 268	SPANG_IL21 UP
13	0.761	1 / 410	SPANG_CD40 6hrs DN
14	0.801	3 / 1218	SPANG_BCR UP
15	0.810	17 / 5693	HOPP_Weak_enhancer
16	0.847	16 / 5538	HOPP_Weak_txn
17	0.924	18 / 6564	HOPP_Strong_enhancer
18	0.961	19 / 7209	HOPP_Weak_promoter
19	0.997	17 / 7592	HOPP_Active_promoter
20	0.998	14 / 6929	HOPP_Txn_elongation

MF

Rank	p−value	#in/all	Geneset
1	0.02	3 / 166	receptor activity
2	0.02	7 / 820	sequence−specific DNA binding transcription factor activity
3	0.02	3 / 176	transcription regulatory region DNA binding
4	0.02	7 / 830	nucleic acid binding transcription factor activity
5	0.03	2 / 84	RNA polymerase II core promoter proximal region sequence−specific DNA bir
6	0.03	1 / 10	tropomyosin binding
7	0.04	3 / 210	transferase activity, transferring glycosyl groups
8	0.04	1 / 11	nucleosome binding
9	0.04	1 / 11	substrate−specific transmembrane transporter activity
10	0.04	1 / 12	core promoter proximal region sequence−specific DNA binding
11	0.04	1 / 12	neurexin family protein binding
12	0.04	1 / 12	nitric−oxide synthase binding
13	0.04	1 / 13	fatty acid binding
14	0.04	1 / 13	pseudouridine synthase activity
15	0.04	1 / 13	Ral GTPase binding
16	0.04	1 / 13	solute:proton antiporter activity
17	0.05	1 / 14	ankyrin binding
18	0.05	1 / 14	polypeptide N−acetylgalactosaminyltransferase activity
19	0.05	1 / 14	RNA polymerase II transcription factor binding transcription factor activity invo
20	0.05	1 / 16	acetylglucosaminyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	2 / 31	hsa−miR−617
2	0.012	2 / 49	hsa−miR−654−3p
3	0.031	2 / 80	hsa−miR−876−5p
4	0.052	4 / 411	hsa−miR−372
5	0.068	3 / 275	hsa−miR−577
6	0.077	3 / 289	hsa−miR−186
7	0.079	1 / 24	hsa−miR−632
8	0.083	1 / 25	hsa−miR−941
9	0.095	1 / 29	hsa−miR−486−5p
10	0.098	1 / 30	hsa−miR−371−3p
11	0.098	1 / 30	hsa−miR−1293
12	0.099	2 / 155	hsa−miR−429
13	0.114	1 / 35	hsa−miR−621
14	0.120	1 / 37	hsa−miR−635
15	0.120	1 / 37	hsa−miR−215
16	0.120	1 / 37	hsa−miR−760
17	0.120	1 / 37	hsa−miR−501−3p
18	0.120	2 / 174	hsa−miR−539
19	0.122	2 / 176	hsa−miR−199b−3p
20	0.126	1 / 39	hsa−miR−502−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	12 / 2013	ICGC_Bcl11_targets
2	0.04	8 / 1139	HEBENSTREIT_low expression TF
3	0.05	5 / 595	ICGC_NrsfPcr2_targets
4	0.07	8 / 1273	ICGC_P300_targets
5	0.09	5 / 690	ICGC_Atf3_targets
6	0.09	14 / 2836	ICGC_BatfPcr1_targets
7	0.11	18 / 3966	ICGC_Pu1_targets
8	0.14	7 / 1266	ICGC_NrsfPcr1_targets
9	0.16	7 / 1314	ICGC_Usf1_targets
10	0.19	20 / 4829	ICGC_Nficsc81335_targets
11	0.28	15 / 3700	ICGC_Nfatc1_targets
12	0.30	17 / 4314	ICGC_Ebfsc137065_targets
13	0.30	18 / 4617	ICGC_Tcf12_targets
14	0.31	8 / 1872	ICGC_Mef2_targets
15	0.31	10 / 2416	ICGC_Bcl3_targets
16	0.31	8 / 1878	ICGC_Cebpbsc150_targets
17	0.32	21 / 5495	ICGC_Yy1_targets
18	0.32	17 / 4385	ICGC_Atf2_targets
19	0.32	11 / 2714	ICGC_Irf4_targets
20	0.36	6 / 1418	ICGC_Ets1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	1 / 12	VAQUERIZAS_Skin
2	0.08	1 / 23	VAQUERIZAS_Trachea
3	0.13	1 / 41	VAQUERIZAS_Placenta
4	0.18	1 / 58	VAQUERIZAS_Lung
5	0.39	1 / 143	VAQUERIZAS_General
6	1.00	0 / 36	VAQUERIZAS_Fetal brain
7	1.00	0 / 26	VAQUERIZAS_Liver
8	1.00	0 / 33	VAQUERIZAS_Prostate
9	1.00	0 / 29	VAQUERIZAS_Smooth muscle
10	1.00	0 / 45	VAQUERIZAS_Uterus
11	1.00	0 / 9	VAQUERIZAS_Kidney
12	1.00	0 / 23	VAQUERIZAS_Spinal cord
13	1.00	0 / 38	VAQUERIZAS_Whole brain
14	1.00	0 / 37	VAQUERIZAS_Thymus
15	1.00	0 / 40	VAQUERIZAS_Thyroid
16	1.00	0 / 59	VAQUERIZAS_Whole blood
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 29	VAQUERIZAS_Fetal lung
19	1.00	0 / 16	VAQUERIZAS_Pancreas
20	1.00	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	1 / 10	WIRTH_Thalamus
2	0.05	2 / 107	WIRTH_Testis
3	0.13	1 / 41	WIRTH_Homeostasis
4	0.14	2 / 194	PALMER_B−Cell signature up
5	0.15	1 / 46	WIRTH_Liver
6	0.28	1 / 95	WIRTH_Muscle
7	0.33	1 / 114	PALMER_T−Cell signature up
8	0.34	2 / 350	WIRTH_Nervous System
9	1.00	0 / 32	WIRTH_Pancreas
10	1.00	0 / 350	WIRTH_Immune system
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 13	WIRTH_B−cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 12	WIRTH_Lymphocytes
17	1.00	0 / 5	WIRTH_Bone marrow
18	1.00	0 / 11	WIRTH_Globus pallidus
19	1.00	0 / 14	WIRTH_Telencephalon
20	1.00	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	5 / 1115	LU_BPDE 1h DN
2	0.5	13 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

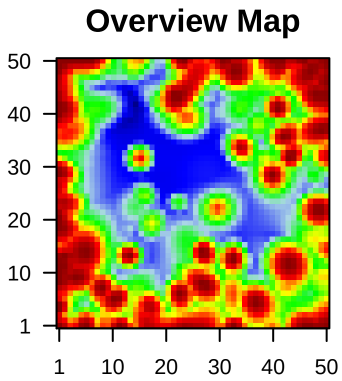
Overexpression Spots

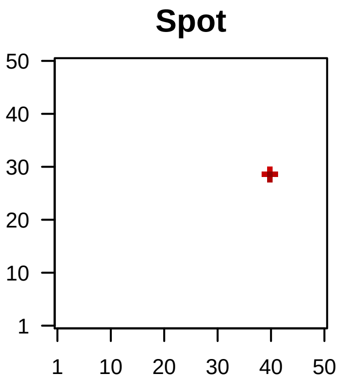
Spot Summary: F1

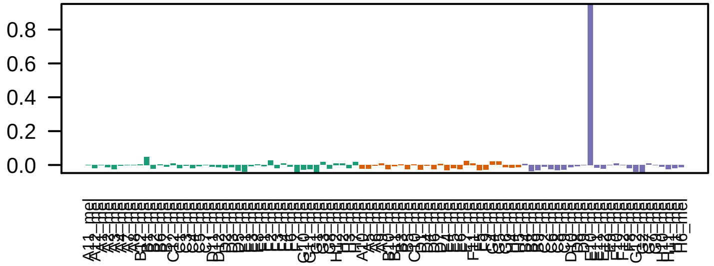
metagenes = 5
genes = 89

<r> metagenes = 0.97
<r> genes = 0.46
beta: r2= 0.14 / log p= −3.52

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)





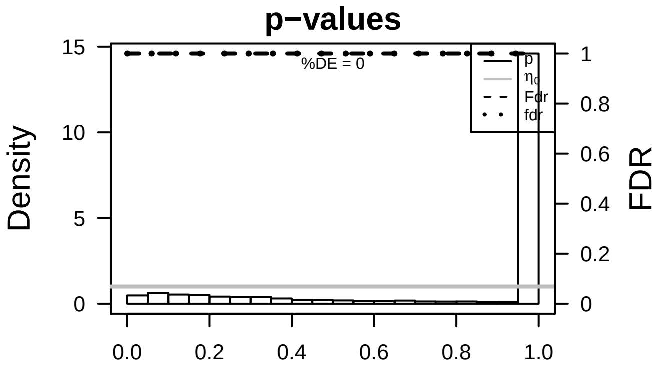


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	UBB	1.97	−0.09	0.41	UBB	ubiquitin B [Source:HGNC Symbol;Acc:HGNC:12463]
2	IKZF4	1.85	−0.22	0.34	IKZF4	IKAROS family zinc finger 4 (Eos) [Source:HGNC Symbol;Ac
3	MFSD2A	1.84	−0.03	0.65	MFSD2A	major facilitator superfamily domain containing 2A [Source:H
4	FGF9	1.81	−0.02	0.75	FGF9	fibroblast growth factor 9 [Source:HGNC Symbol;Acc:HGNC:
5	ZNF232	1.78	−0.03	0.77	ZNF232	zinc finger protein 232 [Source:HGNC Symbol;Acc:HGNC:13
6	RAP1GAP2	1.73	−0.02	0.75	RAP1GAP2	RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac
7	ZNF25	1.73	−0.1	0.5	ZNF25	zinc finger protein 25 [Source:HGNC Symbol;Acc:HGNC:130
8	MLKL	1.71	−0.1	0.3	MLKL	mixed lineage kinase domain−like [Source:HGNC Symbol;Ac
9	LMF1	1.65	−0.11	0.33	LMF1	lipase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC:
10	HOXA10	1.61	−0.05	0.57	HOXA10	homeobox A10 [Source:HGNC Symbol;Acc:HGNC:5100]
11	NR1H3	1.56	−0.05	0.34	NR1H3	nuclear receptor subfamily 1, group H, member 3 [Source:HG
12	WIF1	1.55	−0.02	0.75	WIF1	WNT inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC:1
13	BATF3	1.55	−0.09	0.42	BATF3	basic leucine zipper transcription factor, ATF−like 3 [Source:H
14	SDK1	1.53	−0.13	0.37	SDK1	sidekick cell adhesion molecule 1 [Source:HGNC Symbol;Ac
15	CCDC88B	1.49	−0.05	0.29	CCDC88B	coiled−coil domain containing 88B [Source:HGNC Symbol;Ac
16	C16orf45	1.49	−0.1	0.49	C16orf45	chromosome 16 open reading frame 45 [Source:HGNC Sym
17	KRTAP13−2	1.46	−0.04	0.48	KRTAP13−2	keratin associated protein 13−2 [Source:HGNC Symbol;Acc:
18	TTC24	1.45	−0.03	0.61	TTC24	tetratricopeptide repeat domain 24 [Source:HGNC Symbol;Ac
19	ZNF491	1.44	−0.04	0.54	ZNF491	zinc finger protein 491 [Source:HGNC Symbol;Acc:HGNC:23
20	FAM72A	1.44	−0.11	0.39	FAM72A	family with sequence similarity 72, member A [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−08	33 / 2159	Colon	TssP_Colon
2	6e−07	10 / 217	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
3	2e−05	21 / 1317	Colon	EnhP_Colon
4	2e−05	8 / 199	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
5	7e−05	27 / 2142	Colon	ReprPC_Colon
6	2e−04	24 / 1889	Colon	ReprPCWk_Colon
7	2e−04	13 / 686	Brain	Overlap_fetal_midbrain_TssA
8	3e−04	2 / 5	GSEA	ST_INTERLEUKIN_13_PATHWAY
9	3e−04	2 / 5	GSEA	ST_IL_13_PATHWAY
10	5e−04	9 / 391	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2
11	5e−04	14 / 862	Brain	Overlap_fetal_midbrain_TxTrans
12	5e−04	8 / 314	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	5e−04	6 / 172	GSEA	WIERENGA_STAT5A_TARGETS_UP
14	7e−04	25 / 2188	Lympl	HOPP_Poised_promoter
15	1e−03	2 / 8	GSEA	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
16	1e−03	2 / 8	GSEA	MIKKELSEN_PLURIPOTENT_STATE_DN
17	1e−03	13 / 812	Brain	Mid_Frontal_Lobe_TssP
18	1e−03	3 / 34	GSEA	WIERENGA_PML_INTERACTOME
19	1e−03	13 / 823	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
20	2e−03	2 / 10	GSEA	SASAKI_TARGETS_OF_TP73_AND_TP63
21	2e−03	7 / 291	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
22	2e−03	2 / 11	GSEA	FINETTI_BREAST_CANCER_KINOME_GREEN
23	2e−03	2 / 12	BP	axon regeneration
24	2e−03	2 / 12	BP	regulation of canonical Wnt signaling pathway
25	2e−03	2 / 12	Glio	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
26	2e−03	5 / 155	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
27	2e−03	3 / 45	BP	embryonic limb morphogenesis
28	3e−03	4 / 96	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_UP
29	3e−03	3 / 46	GSEA	HALMOS_CEBPA_TARGETS_UP
30	3e−03	2 / 13	BP	cellular response to estradiol stimulus
31	3e−03	2 / 13	BP	positive regulation of vascular endothelial growth factor receptor signaling
32	3e−03	7 / 316	MF	protein kinase binding
33	3e−03	2 / 14	GSEA	REACTOME_RAP1_SIGNALLING
34	3e−03	4 / 102	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
35	3e−03	13 / 936	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
36	3e−03	2 / 15	BP	protein homotrimerization
37	3e−03	2 / 15	GSEA	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_UP
38	4e−03	19 / 1664	BP	transcription, DNA−templated
39	4e−03	12 / 840	Chr	Chr 17
40	4e−03	2 / 16	GSEA	STEGER_ADIPOGENESIS_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.4	1 / 100	HORVATH_aging_genes meth DOWN
3	0.5	1 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	axon regeneration
2	0.002	2 / 12	regulation of canonical Wnt signaling pathway
3	0.002	3 / 45	embryonic limb morphogenesis
4	0.003	2 / 13	cellular response to estradiol stimulus
5	0.003	2 / 13	positive regulation of vascular endothelial growth factor receptor signaling patl
6	0.003	2 / 15	protein homotrimerization
7	0.004	19 / 1664	transcription, DNA−templated
8	0.008	5 / 206	cytokine−mediated signaling pathway
9	0.008	2 / 23	negative regulation of fibroblast proliferation
10	0.008	2 / 23	positive regulation of DNA binding
11	0.010	2 / 26	detection of chemical stimulus involved in sensory perception of smell
12	0.011	7 / 409	cell motility
13	0.011	2 / 27	retina homeostasis
14	0.012	8 / 519	cell−cell signaling
15	0.012	3 / 81	muscle organ development
16	0.017	2 / 34	embryonic skeletal system development
17	0.018	2 / 35	neurogenesis
18	0.021	2 / 38	protein import into nucleus
19	0.023	2 / 40	regulation of inflammatory response
20	0.026	2 / 42	mitotic nuclear envelope disassembly

Brain

Rank	p−value	#in/all	Geneset
1	2e−04	13 / 686	Overlap_fetal_midbrain_TssA
2	5e−04	14 / 862	Overlap_fetal_midbrain_TxTrans
3	1e−03	13 / 812	Mid_Frontal_Lobe_TssP
4	5e−03	15 / 1207	Overlap_fetal_midbrain_TssF
5	2e−02	21 / 2185	Fetal_TssA
6	2e−02	12 / 1065	Overlap_fetal_midbrain_Enh
7	3e−02	22 / 2462	Mid_Frontal_Lobe_HetRpts
8	4e−02	25 / 2972	Mid_Frontal_Lobe_ReprPC
9	6e−02	2 / 69	Overlap_fetal_midbrain_Tx
10	7e−02	3 / 156	Mid_Frontal_Lobe_TssA
11	7e−02	16 / 1845	Fetal_Quies
12	1e−01	16 / 1949	Fetal_TssF
13	1e−01	9 / 1013	Fetal_TssP
14	2e−01	7 / 786	Fetal_EnhG
15	2e−01	4 / 383	Fetal_Tx
16	3e−01	2 / 166	Mid_Frontal_Lobe_Tx
17	3e−01	7 / 884	Overlap_fetal_midbrain_EnhG
18	3e−01	11 / 1548	Mid_Frontal_Lobe_K9K27me3
19	3e−01	13 / 1907	Fetal_TxTrans
20	4e−01	7 / 989	Mid_Frontal_Lobe_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	3 / 61	PanCan_Wnt_geneset_nanostring
2	0.006	4 / 121	PanCan_MAPK_geneset_nanostring
3	0.028	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.042	2 / 55	PanCan_JAK−ST_geneset_nanostring
5	0.065	3 / 156	PanCan_PI3K_geneset_nanostring
6	0.080	1 / 14	LIU_COMMON_CANCER_GENES
7	0.085	2 / 82	PanCan_TXmisReg_geneset_nanostring
8	0.141	2 / 111	PanCan_RAS_geneset_nanostring
9	0.145	2 / 113	PanCan_Driver_Gene_geneset_nanostring
10	0.159	2 / 120	PanCan_CC+Apop_geneset_nanostring
11	0.164	0 / 14	LIU_LIVER_CANCER
12	0.244	1 / 47	PanCan_DNARepair_geneset_nanostring
13	0.341	1 / 70	SHAUGHNESSY_MM high risk
14	0.383	0 / 12	LIU_PROSTATE_CANCER_UP
15	0.530	2 / 298	SPANG_BCL6−index2
16	0.911	1 / 401	Lembcke_Colonic Inflammation
17	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
18	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
19	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	0.01	28 / 3088	plasma membrane
2	0.02	2 / 39	autophagic vacuole
3	0.03	2 / 42	synaptic vesicle membrane
4	0.03	4 / 200	axon
5	0.03	4 / 205	neuron projection
6	0.04	2 / 53	intermediate filament
7	0.06	2 / 64	anchored component of membrane
8	0.06	1 / 10	connexon complex
9	0.06	1 / 10	MHC class I protein complex
10	0.06	1 / 10	perinuclear endoplasmic reticulum
11	0.06	4 / 246	dendrite
12	0.06	24 / 2984	integral component of membrane
13	0.07	2 / 73	basement membrane
14	0.08	8 / 751	integral component of plasma membrane
15	0.08	3 / 169	transcription factor complex
16	0.08	1 / 14	gap junction
17	0.09	1 / 15	RNA polymerase II transcription factor complex
18	0.09	2 / 83	synaptic vesicle
19	0.09	8 / 775	extracellular space
20	0.09	1 / 16	excitatory synapse

Chr

Rank	p−value	#in/all	Geneset
1	0.004	12 / 840	Chr 17
2	0.038	8 / 649	Chr 16
3	0.070	4 / 262	Chr 13
4	0.224	6 / 689	Chr 7
5	0.339	6 / 801	Chr 11
6	0.447	4 / 576	Chr 9
7	0.529	3 / 469	Chr 8
8	0.537	9 / 1500	Chr 1
9	0.585	6 / 1037	Chr 19
10	0.594	1 / 151	Chr 21
11	0.641	3 / 552	Chr 10
12	0.681	4 / 775	Chr 12
13	0.688	2 / 398	Chr 20
14	0.709	5 / 993	Chr 2
15	0.734	1 / 221	Chr 18
16	0.767	2 / 465	Chr 15
17	0.867	1 / 335	Chr 22
18	0.881	3 / 838	Chr 3
19	0.923	2 / 696	Chr 5
20	0.939	1 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−08	33 / 2159	TssP_Colon
2	2e−05	21 / 1317	EnhP_Colon
3	7e−05	27 / 2142	ReprPC_Colon
4	2e−04	24 / 1889	ReprPCWk_Colon
5	5e−04	8 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
6	1e−02	1 / 2	Hewish_dMMR−secondary−mutations_Immune_surveillance
7	3e−02	6 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	4e−02	11 / 1038	HetRpts_Colon
9	6e−02	13 / 1386	Het_Colon
10	6e−02	4 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
11	7e−02	1 / 13	TCGA−CRC_less−agressive−disease−markers
12	9e−02	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
13	9e−02	1 / 16	Vilar_non−hypermutated−in−CRC
14	1e−01	29 / 3897	Quies1_Colon
15	1e−01	10 / 1079	ZNF_Colon
16	1e−01	3 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
17	1e−01	25 / 3383	EnhWk2_Colon
18	1e−01	5 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
19	2e−01	2 / 117	Marisa_CRC−cluster−b
20	2e−01	3 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	4 / 294	GUDJ_psoriasis down
2	0.5	3 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
2	0.010	3 / 74	WIRTH_Normal Brain
3	0.063	1 / 11	Mukasa_UP_in_Astroglioma
4	0.070	2 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
5	0.094	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
6	0.102	1 / 18	Shinawi_with_increased_methylation_in_STS
7	0.119	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
8	0.128	1 / 23	WIRTH_PN subtype
9	0.202	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	0.206	2 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
11	0.244	1 / 47	Vishal_subnetwork signature of survival in GBM
12	0.288	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
13	0.298	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
14	0.333	1 / 68	GIEZELT_GBM_WT_down_VS_mut
15	0.333	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
16	0.337	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
17	0.349	1 / 72	laffaire_hypermeth_LGG_vs_control
18	0.354	3 / 356	Down_a
19	0.360	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
20	0.368	3 / 365	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−07	10 / 217	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
2	2e−05	8 / 199	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
3	3e−04	2 / 5	ST_INTERLEUKIN_13_PATHWAY
4	3e−04	2 / 5	ST_IL_13_PATHWAY
5	5e−04	9 / 391	MEISSNER_NPC_HCP_WITH_H3K4ME2
6	5e−04	6 / 172	WIERENGA_STAT5A_TARGETS_UP
7	1e−03	2 / 8	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
8	1e−03	2 / 8	MIKKELSEN_PLURIPOTENT_STATE_DN
9	1e−03	3 / 34	WIERENGA_PML_INTERACTOME
10	1e−03	13 / 823	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
11	2e−03	2 / 10	SASAKI_TARGETS_OF_TP73_AND_TP63
12	2e−03	7 / 291	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
13	2e−03	2 / 11	FINETTI_BREAST_CANCER_KINOME_GREEN
14	2e−03	5 / 155	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
15	3e−03	4 / 96	LENAOUR_DENDRITIC_CELL_MATURATION_UP
16	3e−03	3 / 46	HALMOS_CEBPA_TARGETS_UP
17	3e−03	2 / 14	REACTOME_RAP1_SIGNALLING
18	3e−03	4 / 102	MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
19	3e−03	13 / 936	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
20	3e−03	2 / 15	SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_UP

HM

Rank	p−value	#in/all	Geneset
1	0.007	4 / 126	HALLMARK_ALLOGRAFT_REJECTION
2	0.017	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
3	0.049	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	0.050	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
5	0.085	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	0.143	1 / 26	HALLMARK_ANGIOGENESIS
7	0.193	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.202	2 / 140	HALLMARK_APOPTOSIS
9	0.219	2 / 148	HALLMARK_KRAS_SIGNALING_UP
10	0.265	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	0.265	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
12	0.271	1 / 53	HALLMARK_TGF_BETA_SIGNALING
13	0.357	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	0.405	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	0.419	1 / 91	HALLMARK_BILE_ACID_METABOLISM
16	0.433	1 / 95	HALLMARK_SPERMATOGENESIS
17	0.436	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	0.532	1 / 127	HALLMARK_KRAS_SIGNALING_DN
19	0.620	1 / 162	HALLMARK_COMPLEMENT
20	0.632	1 / 167	HALLMARK_APICAL_JUNCTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	2 / 62	DUMEAUX_Smoking enriched genes
2	0.09	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−04	25 / 2188	HOPP_Poised_promoter
2	6e−03	31 / 3396	HOPP_Repressed
3	2e−02	2 / 39	ROSOLOWSKI_blue DOWN
4	3e−02	1 / 5	WRIGHT_custom ABC−DLBCL UP
5	5e−02	1 / 8	MASCQUE_ABC UP
6	6e−02	4 / 247	ZHANG_DLBCL mutated
7	9e−02	1 / 15	WRIGHT_ABC UP
8	9e−02	2 / 86	ROSOLOWSKI_red total
9	1e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
10	1e−01	3 / 212	LENZ_Stromal signature 1
11	2e−01	1 / 30	TARTE_B−cell signature
12	2e−01	1 / 40	Subero_mBL_hyper_meth
13	3e−01	3 / 294	TARTE_Plasmablast signature
14	3e−01	1 / 61	SPANG_LPS 6hrs DN
15	4e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
16	5e−01	2 / 268	SPANG_IL21 UP
17	5e−01	2 / 275	TARTE_Mature plasma cell signature
18	5e−01	7 / 1128	SPANG_BCR DN
19	5e−01	1 / 129	DAVE_BL−vs−DLBCL
20	6e−01	13 / 2211	HOPP_Repetitive

MF

Rank	p−value	#in/all	Geneset
1	0.003	7 / 316	protein kinase binding
2	0.009	11 / 820	sequence−specific DNA binding transcription factor activity
3	0.010	11 / 830	nucleic acid binding transcription factor activity
4	0.010	2 / 26	olfactory receptor activity
5	0.012	2 / 28	cholesterol binding
6	0.012	5 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
7	0.014	2 / 30	repressing transcription factor binding
8	0.014	2 / 31	kinesin binding
9	0.018	13 / 1149	enzyme binding
10	0.019	4 / 171	RNA polymerase II core promoter proximal region sequence−specific DNA bir
11	0.020	4 / 174	transcription corepressor activity
12	0.040	4 / 217	G−protein coupled receptor activity
13	0.054	6 / 456	protein binding transcription factor activity
14	0.058	1 / 10	deoxyribonuclease activity
15	0.063	1 / 11	steroid hydroxylase activity
16	0.068	2 / 72	structural constituent of cytoskeleton
17	0.069	1 / 12	dynein binding
18	0.069	1 / 12	endodeoxyribonuclease activity
19	0.069	1 / 12	insulin receptor substrate binding
20	0.074	1 / 13	platelet−derived growth factor receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.006	3 / 61	hsa−miR−1275
2	0.013	3 / 83	hsa−miR−1265
3	0.017	3 / 91	hsa−miR−378
4	0.019	4 / 172	hsa−miR−29a
5	0.023	4 / 181	hsa−miR−29c
6	0.026	4 / 190	hsa−miR−548d−3p
7	0.039	4 / 215	hsa−miR−29b
8	0.042	3 / 130	hsa−miR−145
9	0.043	6 / 432	hsa−miR−424
10	0.052	1 / 9	hsa−miR−373*
11	0.058	1 / 10	hsa−miR−933
12	0.063	1 / 11	hsa−miR−1180
13	0.066	3 / 157	hsa−miR−450b−5p
14	0.071	2 / 74	hsa−miR−422a
15	0.074	3 / 164	hsa−miR−323b−5p
16	0.080	2 / 79	hsa−miR−569
17	0.080	1 / 14	hsa−miR−891a
18	0.082	2 / 80	hsa−miR−942
19	0.083	2 / 81	hsa−miR−557
20	0.085	2 / 82	hsa−miR−767−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	12 / 1139	HEBENSTREIT_low expression TF
2	0.05	1 / 8	MYC_Cell cycle UP
3	0.23	6 / 690	ICGC_Atf3_targets
4	0.30	1 / 59	MYC_Targets UP
5	0.30	14 / 2013	ICGC_Bcl11_targets
6	0.31	13 / 1872	ICGC_Mef2_targets
7	0.34	16 / 2391	ICGC_Pbx3_targets
8	0.42	18 / 2836	ICGC_BatfPcr1_targets
9	0.49	8 / 1273	ICGC_P300_targets
10	0.52	8 / 1314	ICGC_Usf1_targets
11	0.63	7 / 1266	ICGC_NrsfPcr1_targets
12	0.66	15 / 2714	ICGC_Irf4_targets
13	0.68	24 / 4314	ICGC_Ebfsc137065_targets
14	0.69	30 / 5355	ICGC_Pol2_targets
15	0.69	13 / 2416	ICGC_Bcl3_targets
16	0.74	7 / 1400	ICGC_Myc_targets
17	0.75	3 / 653	ICGC_SrfPcr2_targets
18	0.77	29 / 5374	ICGC_Pax5_targets
19	0.77	25 / 4682	ICGC_Pol24_targets
20	0.77	15 / 2927	ICGC_Rad21_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 26	VAQUERIZAS_Liver
2	0.1	1 / 27	VAQUERIZAS_Lymph node
3	0.2	1 / 36	VAQUERIZAS_Fetal brain
4	0.2	1 / 38	VAQUERIZAS_Whole brain
5	0.2	1 / 38	VAQUERIZAS_Testis
6	1.0	0 / 41	VAQUERIZAS_Placenta
7	1.0	0 / 33	VAQUERIZAS_Prostate
8	1.0	0 / 29	VAQUERIZAS_Smooth muscle
9	1.0	0 / 45	VAQUERIZAS_Uterus
10	1.0	0 / 143	VAQUERIZAS_General
11	1.0	0 / 9	VAQUERIZAS_Kidney
12	1.0	0 / 23	VAQUERIZAS_Spinal cord
13	1.0	0 / 37	VAQUERIZAS_Thymus
14	1.0	0 / 40	VAQUERIZAS_Thyroid
15	1.0	0 / 59	VAQUERIZAS_Whole blood
16	1.0	0 / 7	VAQUERIZAS_Appendix
17	1.0	0 / 29	VAQUERIZAS_Fetal lung
18	1.0	0 / 58	VAQUERIZAS_Lung
19	1.0	0 / 16	VAQUERIZAS_Pancreas
20	1.0	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 32	WIRTH_Placenta
2	0.06	5 / 350	WIRTH_Nervous System
3	0.07	1 / 13	WIRTH_Thyroid gland
4	0.09	1 / 16	PALMER_Lymphocytes signature up
5	0.15	2 / 114	PALMER_T−Cell signature up
6	0.69	1 / 194	PALMER_B−Cell signature up
7	1.00	0 / 32	WIRTH_Pancreas
8	1.00	0 / 350	WIRTH_Immune system
9	1.00	0 / 11	WIRTH_Sec. lymphoid organs
10	1.00	0 / 11	WIRTH_Prim. lymphoid organs
11	1.00	0 / 13	WIRTH_B−cells
12	1.00	0 / 8	WIRTH_Tonsil
13	1.00	0 / 12	WIRTH_Thymus
14	1.00	0 / 12	WIRTH_Lymphocytes
15	1.00	0 / 5	WIRTH_Bone marrow
16	1.00	0 / 11	WIRTH_Globus pallidus
17	1.00	0 / 14	WIRTH_Telencephalon
18	1.00	0 / 11	WIRTH_Cortex cerebri
19	1.00	0 / 10	WIRTH_Hippocampus
20	1.00	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	27 / 3682	LU_BPDE 0.005 DN
2	1.0	3 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

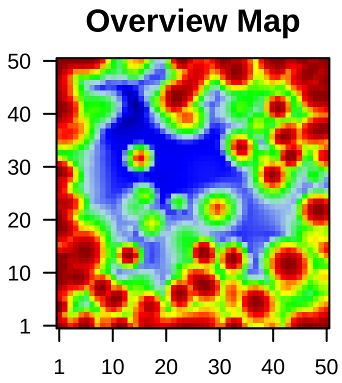
Overexpression Spots

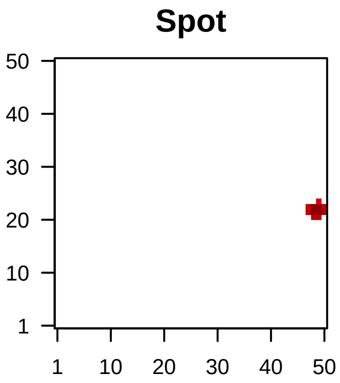
Spot Summary: G1

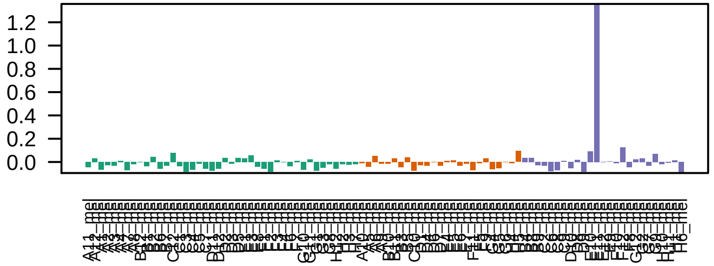
metagenes = 11
genes = 160

<r> metagenes = 0.99
<r> genes = 0.24
beta: r2= 1.17 / log p= −Inf

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)





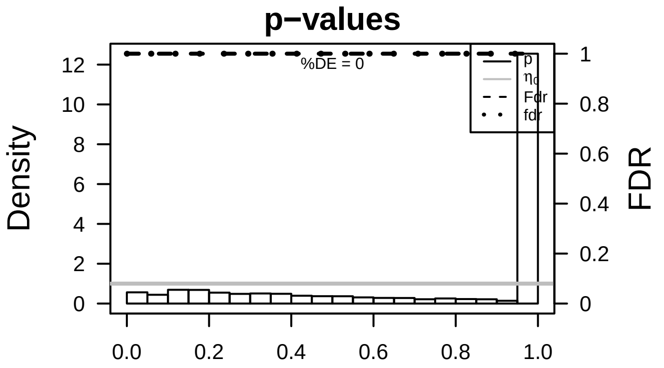


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	VCAN	2.39	−0.1	0.64	VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]
2	SCN2A	1.98	−0.06	0.67	SCN2A	sodium channel, voltage gated, type II alpha subunit [Source:
3	CLHC1	1.96	−0.28	0.35	CLHC1	clathrin heavy chain linker domain containing 1 [Source:HGN
4	CEMIP	1.96	−0.23	0.46	CEMIP	cell migration inducing protein, hyaluronan binding [Source:H
5	OXTR	1.94	−0.06	0.76	OXTR	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]
6	MYL4	1.93	−0.04	0.81	MYL4	myosin, light chain 4, alkali; atrial, embryonic [Source:HGNC
7	PHLDB2	1.91	−0.23	0.46	PHLDB2	pleckstrin homology−like domain, family B, member 2 [Source
8	CHL1	1.89	−0.05	0.73	CHL1	cell adhesion molecule L1−like [Source:HGNC Symbol;Acc:H
9	CCDC81	1.88	−0.05	0.77	CCDC81	coiled−coil domain containing 81 [Source:HGNC Symbol;Acc
10	SDC2	1.85	−0.15	0.51	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
11	GAD1	1.84	−0.07	0.72	GAD1	glutamate decarboxylase 1 (brain, 67kDa) [Source:HGNC Sy
12	SAMD9L	1.83	−0.22	0.3	SAMD9L	sterile alpha motif domain containing 9−like [Source:HGNC S
13	DDX25	1.82	−0.16	0.41	DDX25	DEAD (Asp−Glu−Ala−Asp) box helicase 25 [Source:HGNC S
14	FBXO3	1.81	−0.52	0.27	FBXO3	F−box protein 3 [Source:HGNC Symbol;Acc:HGNC:13582]
15	HIST1H2BH	1.8	−0.08	0.54	HIST1H2BH	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:HGNC:4
16	NEGR1	1.79	−0.04	0.78	NEGR1	neuronal growth regulator 1 [Source:HGNC Symbol;Acc:HGN
17	TPCN1	1.78	−0.2	0.31	TPCN1	two pore segment channel 1 [Source:HGNC Symbol;Acc:HG
18	NFKBIZ	1.76	−0.9	0.29	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B−
19	PLXNB1	1.76	−0.42	0.34	PLXNB1	plexin B1 [Source:HGNC Symbol;Acc:HGNC:9103]
20	HIST1H2BG	1.76	−0.29	0.29	HIST1H2BG	histone cluster 1, H2bg [Source:HGNC Symbol;Acc:HGNC:4

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−08	47 / 1949	Brain	Fetal_TssF
2	1e−05	7 / 72	GSEA	REACTOME_MEIOTIC_RECOMBINATION
3	2e−05	6 / 54	GSEA	REACTOME_RNA_POL_I_PROMOTER_OPENING
4	6e−05	4 / 20	GSEA	MARKS_HDAC_TARGETS_UP
5	6e−05	12 / 283	GSEA	PEREZ_TP63_TARGETS
6	6e−05	6 / 64	GSEA	REACTOME_AMYLOIDS
7	1e−04	7 / 100	GSEA	REACTOME_MEIOSIS
8	2e−04	3 / 11	GSEA	SA_PROGRAMMED_CELL_DEATH
9	2e−04	6 / 78	GSEA	REACTOME_RNA_POL_I_TRANSCRIPTION
10	2e−04	7 / 111	GSEA	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRAN
11	2e−04	6 / 79	CC	nucleosome
12	2e−04	8 / 150	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
13	3e−04	3 / 12	CC	axonal growth cone
14	3e−04	9 / 195	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
15	3e−04	9 / 200	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
16	6e−04	6 / 97	GSEA	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
17	7e−04	13 / 427	Colon	Quies2_Colon
18	8e−04	27 / 1308	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
19	8e−04	9 / 227	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
20	1e−03	7 / 146	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
21	1e−03	16 / 618	GSEA	GOZGIT_ESR1_TARGETS_DN
22	1e−03	4 / 44	GSEA	REACTOME_PACKAGING_OF_TELOMERE_ENDS
23	1e−03	15 / 574	Brain	Overlap_fetal_midbrain_TssP
24	2e−03	7 / 160	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
25	2e−03	4 / 48	BP	JNK cascade
26	2e−03	4 / 49	CC	Golgi lumen
27	2e−03	34 / 1907	Brain	Fetal_TxTrans
28	2e−03	2 / 7	Glio	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
29	2e−03	37 / 2159	Colon	TssP_Colon
30	3e−03	3 / 26	GSEA	MOSERLE_IFNA_RESPONSE
31	3e−03	7 / 173	GSEA	PEREZ_TP53_AND_TP63_TARGETS
32	3e−03	22 / 1079	Colon	ZNF_Colon
33	3e−03	4 / 55	GSEA	GEORGANTAS_HSC_MARKERS
34	3e−03	21 / 1013	Brain	Fetal_TssP
35	3e−03	14 / 564	Brain	Mid_Frontal_Lobe_EnhP
36	3e−03	6 / 133	GSEA	ZHANG_BREAST_CANCER_PROGENITORS_DN
37	3e−03	58 / 3897	Colon	Quies1_Colon
38	3e−03	3 / 28	GSEA	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
39	4e−03	4 / 58	GSEA	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOS
40	4e−03	2 / 9	GSEA	MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	4 / 48	JNK cascade
2	0.005	2 / 10	eyelid development in camera−type eye
3	0.005	2 / 10	maternal behavior
4	0.005	2 / 10	outflow tract septum morphogenesis
5	0.007	2 / 12	positive regulation of synaptic transmission, glutamatergic
6	0.011	4 / 80	response to estradiol
7	0.011	2 / 15	morphogenesis of an epithelium
8	0.013	2 / 16	regulation of protein catabolic process
9	0.014	3 / 47	neuron projection morphogenesis
10	0.016	2 / 18	smooth muscle cell differentiation
11	0.017	6 / 191	brain development
12	0.018	2 / 19	membrane depolarization during action potential
13	0.019	34 / 2210	anatomical structure development
14	0.021	2 / 21	neurotransmitter transport
15	0.022	3 / 56	intrinsic apoptotic signaling pathway
16	0.025	2 / 23	positive regulation of ATPase activity
17	0.025	2 / 23	reciprocal meiotic recombination
18	0.026	3 / 59	epidermis development
19	0.029	4 / 108	nucleosome assembly
20	0.034	2 / 27	cognition

Brain

Rank	p−value	#in/all	Geneset
1	5e−08	47 / 1949	Fetal_TssP
2	1e−03	15 / 574	Overlap_fetal_midbrain_TssP
3	2e−03	34 / 1907	Fetal_TxTrans
4	3e−03	21 / 1013	Fetal_TssP
5	3e−03	14 / 564	Mid_Frontal_Lobe_EnhP
6	9e−03	10 / 383	Fetal_Tx
7	2e−02	19 / 1065	Overlap_fetal_midbrain_Enh
8	3e−02	33 / 2185	Fetal_TssA
9	5e−02	16 / 953	Fetal_Enh
10	6e−02	18 / 1122	Fetal_K9K27me3
11	7e−02	12 / 686	Overlap_fetal_midbrain_TssA
12	1e−01	11 / 656	Overlap_fetal_midbrain_EnhP
13	1e−01	25 / 1845	Fetal_Quies
14	1e−01	13 / 862	Overlap_fetal_midbrain_TxTrans
15	2e−01	103 / 9020	Overlap_fetal_midbrain_ReprPCWk
16	2e−01	8 / 534	Mid_Frontal_Lobe_EnhG
17	2e−01	11 / 786	Fetal_EnhG
18	2e−01	57 304	Fetal_Het
19	2e−01	4 / 229	Mid_Frontal_Lobe_TxTrans
20	2e−01	36 / 2972	Mid_Frontal_Lobe_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	4 / 82	PanCan_TxmisReg_geneset_nanostring
2	0.02	2 / 20	PanCan_ChromMod_geneset_nanostring
3	0.12	3 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.14	3 / 121	PanCan_MAPK_geneset_nanostring
5	0.14	7 / 401	Lembcke_Colonic Inflammation
6	0.15	1 / 15	RHODES_CANCER_META_SIGNATURE
7	0.15	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.15	1 / 15	GENTLES_modul4
9	0.18	1 / 18	PanCan_Notch_geneset_nanostring
10	0.21	1 / 22	PanCan_HH_geneset_nanostring
11	0.37	2 / 120	PanCan_CC+Apop_geneset_nanostring
12	0.45	1 / 55	PanCan_JAK−ST_geneset_nanostring
13	0.48	1 / 61	PanCan_Wnt_geneset_nanostring
14	0.51	0 / 14	LIU_COMMON_CANCER_GENES
15	0.58	2 / 180	SPANG_LPS−index2
16	0.59	0 / 12	LIU_PROSTATE_CANCER_UP
17	0.82	1 / 156	PanCan_PI3K_geneset_nanostring
18	0.90	3 / 489	Lembcke_Normal vs Adenoma
19	0.96	1 / 298	SPANG_BCL6−index2
20	0.99	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 79	nucleosome
2	3e−04	3 / 12	axonal growth cone
3	2e−03	4 / 49	Golgi lumen
4	5e−03	3 / 32	nuclear nucleosome
5	8e−03	2 / 13	TCTN−B9D complex
6	9e−03	4 / 76	extrinsic component of membrane
7	1e−02	2 / 14	clathrin−coated vesicle membrane
8	2e−02	2 / 20	ciliary transition zone
9	2e−02	4 / 102	cytoplasmic vesicle membrane
10	3e−02	3 / 64	anchored component of membrane
11	6e−02	13 / 745	cytoplasmic membrane−bounded vesicle
12	7e−02	3 / 89	tight junction
13	7e−02	4 / 145	endoplasmic reticulum lumen
14	1e−01	134 / 11774	cell
15	1e−01	1 / 10	apical dendrite
16	1e−01	2 / 52	coated pit
17	1e−01	2 / 54	intermediate filament cytoskeleton
18	1e−01	1 / 12	AMP−activated protein kinase complex
19	1e−01	1 / 12	node of Ranvier
20	1e−01	1 / 12	STAGA complex

Chr

Rank	p−value	#in/all	Geneset
1	0.04	14 / 775	Chr 12
2	0.05	17 / 1037	Chr 19
3	0.08	4 / 151	Chr 21
4	0.13	8 / 469	Chr 8
5	0.21	10 / 687	Chr 6
6	0.29	5 / 335	Chr 22
7	0.36	10 / 801	Chr 11
8	0.40	7 / 558	Chr 4
9	0.42	10 / 838	Chr 3
10	0.43	3 / 221	Chr 18
11	0.51	11 / 993	Chr 2
12	0.54	3 / 262	Chr 13
13	0.57	5 / 465	Chr 15
14	0.63	7 / 696	Chr 5
15	0.74	4 / 462	Chr 14
16	0.81	7 / 840	Chr 17
17	0.83	13 / 1500	Chr 1
18	0.85	4 / 551	Chr X
19	0.85	4 / 552	Chr 10
20	0.87	5 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	13 / 427	Quies2_Colon
2	2e−03	37 / 2159	TssP_Colon
3	3e−03	22 / 1079	ZNF_Colon
4	3e−03	58 / 3897	Quies1_Colon
5	1e−02	10 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
6	1e−02	34 / 2142	ReprPC_Colon
7	1e−02	24 / 1386	Het_Colon
8	2e−02	30 / 1889	ReprPCWk_Colon
9	2e−02	6 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
10	4e−02	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
11	5e−02	51 / 3812	TssD1_Colon
12	5e−02	46 / 3383	EnhWk2_Colon
13	8e−02	15 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	9e−02	1 / 9	Budinska_D_Mesenchymal_UP
15	9e−02	119 / 10290	TssWk_Colon
16	9e−02	16 / 1038	HetRpts_Colon
17	1e−01	7 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
18	1e−01	3 / 117	Marisa_CRC−cluster−b
19	1e−01	7 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
20	2e−01	1 / 17	Vilar_hypermutated−in−CRC

Disease

Rank	p−value	#in/all	Geneset
1	0.01	8 / 294	GUDJ_psoriasis down
2	0.33	6 / 435	GUDJ_psoriasis up
3	1.00	0 / 11	BCHETNIA_EBM up
4	1.00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	2 / 7	WILLSCHER_GBM_LTSwt_proteomics−G_UP
2	0.013	3 / 45	Christensen_hypermethylated_in_primary_glioblastoma
3	0.038	3 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
4	0.046	3 / 74	WIRTH_Normal Brain
5	0.049	2 / 33	Christensen_hypomethylated_in_primary_glioblastoma
6	0.049	5 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
7	0.052	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
8	0.083	1 / 8	VERHAAK_PN_Brain
9	0.091	2 / 47	Weller_LGG_gradeII−vs−III_UP
10	0.094	3 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
11	0.101	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
12	0.112	1 / 11	Martinez_Glio_hypermeth
13	0.112	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
14	0.126	2 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
15	0.131	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
16	0.144	2 / 62	cultured astroglia vs. in vivo astrocytes
17	0.168	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
18	0.194	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
19	0.237	1 / 25	Shaw_down_in_1p19q
20	0.246	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−05	7 / 72	REACTOME_MEIOTIC_RECOMBINATION
2	2e−05	6 / 54	REACTOME_RNA_POL_I_PROMOTER_OPENING
3	6e−05	4 / 20	MARKS_HDAC_TARGETS_UP
4	6e−05	12 / 283	PEREZ_TP63_TARGETS
5	6e−05	6 / 64	REACTOME_AMYLOIDS
6	1e−04	7 / 100	REACTOME_MEIOSIS
7	2e−04	3 / 11	SA_PROGRAMMED_CELL_DEATH
8	2e−04	6 / 78	REACTOME_RNA_POL_I_TRANSCRIPTION
9	2e−04	7 / 111	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSC
10	2e−04	8 / 150	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
11	3e−04	9 / 195	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
12	3e−04	9 / 200	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
13	6e−04	6 / 97	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	8e−04	27 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	8e−04	9 / 227	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
16	1e−03	7 / 146	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
17	1e−03	16 / 618	GOZGIT_ESR1_TARGETS_DN
18	1e−03	4 / 44	REACTOME_PACKAGING_OF_TELOMERE_ENDS
19	2e−03	7 / 160	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
20	3e−03	3 / 26	MOSERLE_IFNA_RESPONSE

HM

Rank	p−value	#in/all	Geneset
1	0.06	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
2	0.07	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.08	3 / 95	HALLMARK_SPERMATOGENESIS
4	0.11	4 / 167	HALLMARK_APICAL_JUNCTION
5	0.11	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
6	0.11	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	0.11	3 / 107	HALLMARK_COAGULATION
8	0.11	2 / 53	HALLMARK_TGF_BETA_SIGNALING
9	0.12	4 / 176	HALLMARK_HYPOXIA
10	0.16	3 / 127	HALLMARK_KRAS_SIGNALING_DN
11	0.21	3 / 146	HALLMARK_UV_RESPONSE_UP
12	0.25	1 / 26	HALLMARK_ANGIOGENESIS
13	0.27	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.27	3 / 169	HALLMARK_XENOBIOTIC_METABOLISM
15	0.29	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
16	0.29	3 / 174	HALLMARK_HEME_METABOLISM
17	0.31	3 / 181	HALLMARK_P53_PATHWAY
18	0.45	2 / 140	HALLMARK_APOPTOSIS
19	0.45	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
20	0.52	2 / 162	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	DUMEAUX_Smoking literature genes up
2	0.3	1 / 32	DUMEAUX_Fasting enriched genes
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.02	48 / 3396	HOPP_Repressed
2	0.03	33 / 2188	HOPP_Poised_promoter
3	0.03	3 / 61	SPANG_LPS 6hrs DN
4	0.03	33 / 2211	HOPP_Repetitive
5	0.05	6 / 247	ZHANG_DLBCL mutated
6	0.06	6 / 256	SPANG_IL21 DN
7	0.08	5 / 212	LENZ_Stromal signature 1
8	0.10	17 / 1128	SPANG_BCR DN
9	0.11	34 / 2563	HOPP_Heterochrom
10	0.28	6 / 410	SPANG_CD40 6hrs DN
11	0.30	1 / 33	LEE_Developmental_regulators
12	0.32	2 / 107	SPANG_LPS 6hrs UP
13	0.36	4 / 280	SPANG_CD40 6hrs UP
14	0.37	1 / 43	LENZ_Stromal signature 2
15	0.39	80 / 7209	HOPP_Weak_promoter
16	0.40	1 / 47	Subero_FL_hyper_meth
17	0.42	1 / 50	SPANG_BAFF 9hrs DN
18	0.48	1 / 60	Subero_T−ALL_hyper_meth
19	0.51	1 / 66	TARTE_Plasma cell signature
20	0.59	1 / 81	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 10	hedgehog receptor activity
2	0.006	34 / 2037	DNA binding
3	0.011	2 / 15	hyaluronic acid binding
4	0.020	9 / 373	protein heterodimerization activity
5	0.024	10 / 450	sequence−specific DNA binding
6	0.025	2 / 23	MAP kinase kinase kinase activity
7	0.027	2 / 24	cation channel activity
8	0.031	15 / 820	sequence−specific DNA binding transcription factor activity
9	0.034	2 / 27	RNA polymerase II repressing transcription factor binding
10	0.045	10 / 501	identical protein binding
11	0.052	3 / 78	Rab GTPase binding
12	0.055	7 / 316	protein kinase binding
13	0.060	4 / 136	lyase activity
14	0.062	9 / 461	transferase activity, transferring phosphorus−containing groups
15	0.064	14 / 830	nucleic acid binding transcription factor activity
16	0.067	8 / 398	protein tyrosine kinase activity
17	0.084	14 / 866	signal transducer activity
18	0.088	4 / 156	protein C−terminus binding
19	0.103	1 / 10	FAD binding
20	0.103	1 / 10	guanylate kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	4 / 97	hsa−miR−624
2	0.03	3 / 61	hsa−miR−514
3	0.04	3 / 70	hsa−miR−628−3p
4	0.04	11 / 569	hsa−miR−20b
5	0.05	57 180	hsa−miR−302e
6	0.05	5 / 182	hsa−miR−573
7	0.05	6 / 250	hsa−miR−520a−3p
8	0.05	7 / 314	hsa−miR−520c−3p
9	0.05	2 / 35	hsa−miR−1269
10	0.06	2 / 36	hsa−miR−769−5p
11	0.06	2 / 37	hsa−miR−215
12	0.07	10 / 541	hsa−miR−17
13	0.07	6 / 272	hsa−miR−520b
14	0.08	2 / 42	hsa−miR−192
15	0.08	5 / 209	hsa−miR−196a
16	0.08	3 / 92	hsa−miR−425
17	0.08	5 / 214	hsa−miR−548m
18	0.08	1 / 8	hsa−miR−886−3p
19	0.09	3 / 97	hsa−miR−1303
20	0.09	5 / 222	hsa−miR−185

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	BENTINK_e2f3.2
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	19 / 1139	HEBENSTREIT_low expression TF
2	0.15	66 / 5495	ICGC_Yy1_targets
3	0.16	37 / 2927	ICGC_Rad21_targets
4	0.18	72 / 6114	ICGC_Runx3_targets
5	0.19	1 / 19	MYC_Metabolism UP
6	0.21	10 / 690	ICGC_Atf3_targets
7	0.25	47 / 3966	ICGC_Pu1_targets
8	0.29	16 / 1266	ICGC_NrsfPcr1_targets
9	0.30	51 / 4414	ICGC_Bclaf101388_targets
10	0.31	43 / 3700	ICGC_Nfatc1_targets
11	0.32	32 / 2714	ICGC_Irf4_targets
12	0.36	49 / 4314	ICGC_Ebfsc137065_targets
13	0.37	22 / 1878	ICGC_Cebpbsc150_targets
14	0.38	53 / 4706	ICGC_Sp1_targets
15	0.39	55 / 4909	ICGC_Stat5_targets
16	0.43	65 / 5890	ICGC_Elf1_targets
17	0.47	57 / 5200	ICGC_Mta3_targets
18	0.47	1 / 59	MYC_Targets UP
19	0.50	51 / 4689	ICGC_Taf1_targets
20	0.50	53 / 4879	ICGC_Pmlsc71910_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.01	2 / 14	VAQUERIZAS_Ovary
2	0.01	3 / 45	VAQUERIZAS_Uterus
3	0.03	2 / 23	VAQUERIZAS_Adrenal cortex
4	0.09	1 / 9	VAQUERIZAS_Kidney
5	0.16	1 / 16	VAQUERIZAS_Adrenal gland
6	0.17	1 / 17	VAQUERIZAS_Heart
7	0.22	1 / 23	VAQUERIZAS_Spinal cord
8	0.22	1 / 23	VAQUERIZAS_Trachea
9	0.25	1 / 27	VAQUERIZAS_Lymph node
10	0.27	1 / 29	VAQUERIZAS_Smooth muscle
11	0.27	1 / 29	VAQUERIZAS_Fetal lung
12	0.32	1 / 36	VAQUERIZAS_Fetal brain
13	0.34	1 / 38	VAQUERIZAS_Whole brain
14	0.35	1 / 40	VAQUERIZAS_Thyroid
15	0.47	1 / 58	VAQUERIZAS_Lung
16	0.47	1 / 59	VAQUERIZAS_Whole blood
17	1.00	0 / 41	VAQUERIZAS_Placenta
18	1.00	0 / 26	VAQUERIZAS_Liver
19	1.00	0 / 33	VAQUERIZAS_Prostate
20	1.00	0 / 143	VAQUERIZAS_General

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	8 / 350	WIRTH_Nervous System
2	0.05	1 / 5	WIRTH_Bone marrow
3	0.11	3 / 107	WIRTH_Testis
4	0.12	1 / 12	WIRTH_Lymphocytes
5	0.29	1 / 32	WIRTH_Pancreas
6	0.35	2 / 114	PALMER_T−Cell signature up
7	0.36	1 / 41	WIRTH_Homeostasis
8	0.39	1 / 46	WIRTH_Liver
9	0.70	2 / 225	PALMER_Granulocytes signature up
10	0.73	3 / 350	WIRTH_Immune system
11	0.88	1 / 194	PALMER_B−Cell signature up
12	1.00	0 / 11	WIRTH_Sec. lymphoid organs
13	1.00	0 / 11	WIRTH_Prim. lymphoid organs
14	1.00	0 / 13	WIRTH_B−cells
15	1.00	0 / 8	WIRTH_Tonsil
16	1.00	0 / 12	WIRTH_Thymus
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	40 / 3682	LU_BPDE 0.005 DN
2	1.0	7 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

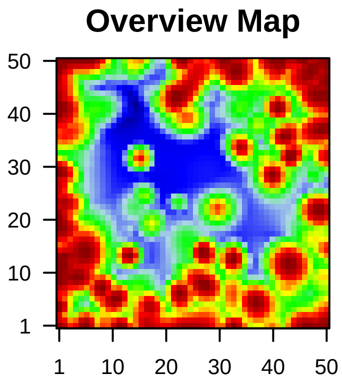
Overexpression Spots

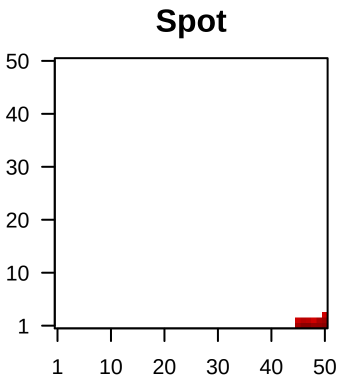
Spot Summary: H1

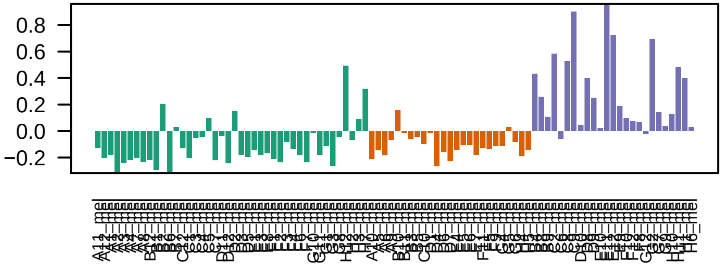
metagenes = 13
genes = 260

<r> metagenes = 0.97
<r> genes = 0.2
beta: r2= 4.71 / log p= −Inf

samples with spot = 16 (17.4 %)
MSC1 : 3 (7.1 %)
MSC3 : 13 (52 %)





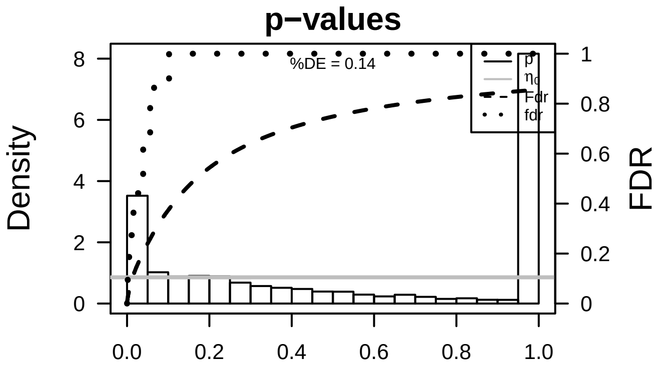


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	DKK1	2.85	−0.31	0.63	DKK1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Sy
2	IL24	2.78	−0.11	0.59	IL24	interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
3	HBEGF	2.46	−0.25	0.53	HBEGF	heparin−binding EGF−like growth factor [Source:HGNC Symb
4	ANXA1	2.44	−0.5	0.78	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
5	PTPRZ1	2.31	−0.37	0.7	PTPRZ1	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
6	NAV3	2.3	−0.23	0.73	NAV3	neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998
7	RGS4	2.3	−0.3	0.4	RGS4	regulator of G−protein signaling 4 [Source:HGNC Symbol;Acc
8	A2M	2.29	−0.9	0.52	A2M	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
9	RGS2	2.26	−0.52	0.33	RGS2	regulator of G−protein signaling 2 [Source:HGNC Symbol;Acc
10	KCNJ2	2.26	−0.25	0.68	KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2
11	HIST1H3D	2.25	−0.35	0.37	HIST1H3D	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
12	FN1	2.23	−1.04	0.4	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
13	SERPINI1	2.21	−0.56	0.39	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
14	LMCD1	2.2	−0.68	0.32	LMCD1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
15	VTN	2.14	−0.36	0.67	VTN	vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
16	ARRDC3	2.09	−0.76	0.5	ARRDC3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:HG
17	CAV1	2.08	−0.76	0.44	CAV1	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
18	MAP2	2.07	−0.14	0.6	MAP2	microtubule−associated protein 2 [Source:HGNC Symbol;Acc
19	S100A4	2.07	−0.2	0.62	S100A4	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:
20	EFNA1	2.04	−0.24	0.37	EFNA1	ephrin−A1 [Source:HGNC Symbol;Acc:HGNC:3221]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−27	42 / 286	GSEA	PASINI_SUZ12_TARGETS_DN
2	9e−26	56 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
3	2e−24	49 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	6e−22	30 / 168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	2e−20	62 / 930	GSEA	NUYTTEN_EZH2_TARGETS_UP
6	2e−19	54 / 749	GSEA	CUI_TCF21_TARGETS_2_DN
7	6e−19	40 / 410	GSEA	LIM_MAMMARY_STEM_CELL_UP
8	6e−19	30 / 212	Lympl	LENZ_Stromal signature 1
9	2e−18	40 / 425	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
10	3e−18	38 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
11	4e−18	33 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
12	1e−17	42 / 494	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
13	3e−17	33 / 302	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
14	3e−15	35 / 401	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
15	1e−14	50 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
16	7e−14	21 / 143	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
17	1e−13	46 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
18	2e−13	25 / 227	GSEA	ONDER_CDH1_TARGETS_2_UP
19	6e−13	40 / 616	GSEA	NABA_MATRISOME
20	7e−13	31 / 377	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
21	9e−13	21 / 163	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
22	2e−12	1 / 14	Cance	LIU_PROSTATE_CANCER_DN
23	2e−12	20 / 153	GSEA	WU_CELL_MIGRATION
24	5e−12	35 / 512	GSEA	SMID_BREAST_CANCER_BASAL_UP
25	6e−12	27 / 308	CC	focal adhesion
26	9e−12	24 / 245	GSEA	WANG_SMARCE1_TARGETS_UP
27	1e−11	14 / 68	GSEA	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
28	1e−11	18 / 131	Colon	Marisa_CRC−cluster−a
29	2e−11	18 / 132	GSEA	NABA_ECM_GLYCOPROTEINS
30	2e−11	21 / 189	GSEA	NABA_CORE_MATRISOME
31	2e−11	50 / 1013	Brain	Fetal_TssP
32	2e−11	23 / 234	GSEA	LU_AGING_BRAIN_UP
33	3e−11	22 / 215	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
34	4e−11	24 / 263	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
35	5e−11	15 / 91	GSEA	BROWNE_HCMV_INFECTION_20HR_DN
36	5e−11	19 / 161	GSEA	ELVIDGE_HYPOXIA_UP
37	9e−11	29 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
38	1e−10	25 / 303	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
39	2e−10	16 / 117	Colon	Marisa_CRC−cluster−b
40	3e−10	17 / 137	HM	HALLMARK_UV_RESPONSE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.05	5 / 111	HORVATH_aging_genes meth UP
2	0.10	4 / 100	HORVATH_aging_genes meth DOWN
3	0.14	2 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−10	36 / 626	cell adhesion
2	1e−08	74 / 2210	anatomical structure development
3	6e−07	10 / 74	wound healing
4	3e−06	52 / 1556	cell differentiation
5	2e−05	29 / 705	locomotion
6	2e−05	16 / 269	extracellular matrix organization
7	2e−05	11 / 134	cell junction organization
8	3e−05	18 / 336	negative regulation of cell proliferation
9	3e−05	5 / 22	actin filament bundle assembly
10	3e−05	5 / 22	negative regulation of endothelial cell proliferation
11	4e−05	21 / 443	anatomical structure formation involved in morphogenesis
12	9e−05	24 / 581	cytoskeleton organization
13	1e−04	11 / 156	cell migration
14	1e−04	8 / 83	muscle contraction
15	1e−04	12 / 187	angiogenesis
16	2e−04	5 / 30	response to progesterone
17	2e−04	6 / 47	response to calcium ion
18	3e−04	5 / 33	substrate adhesion−dependent cell spreading
19	3e−04	4 / 19	peripheral nervous system development
20	3e−04	18 / 409	cell motility

Brain

Rank	p−value	#in/all	Geneset
1	2e−11	50 / 1013	Fetal_TssP
2	3e−06	27 / 574	Overlap_fetal_midbrain_TssP
3	4e−06	66 / 2185	Fetal_TssA
4	7e−06	59 / 1907	Fetal_TxTrans
5	1e−04	56 / 1949	Fetal_TssF
6	3e−03	22 / 668	Mid_Frontal_Lobe_Enh
7	4e−03	32 / 1122	Fetal_K9K27me3
8	6e−03	24 / 786	Fetal_EnhG
9	6e−03	183 / 9330	Overlap_fetal_midbrain_ReprPC
10	1e−02	176 / 9020	Overlap_fetal_midbrain_ReprPCWk
11	2e−02	12 / 349	Fetal_ZNF
12	3e−02	182 / 9528	Overlap_fetal_midbrain_Quies
13	3e−02	27 / 1050	Fetal_EnhP
14	6e−02	6 / 158	Overlap_fetal_midbrain_Het
15	7e−02	116 / 5940	Overlap_fetal_midbrain_HetRpts
16	7e−02	23 / 953	Fetal_Enh
17	7e−02	11 / 383	Fetal_Tx
18	9e−02	97 304	Fetal_Het
19	1e−01	12 / 468	Mid_Frontal_Lobe_TssF
20	1e−01	27 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	1 / 14	LIU_PROSTATE_CANCER_DN
2	2e−05	12 / 156	PanCan_PI3K_geneset_nanostring
3	3e−05	20 / 401	Lembcke_Colonic Inflammation
4	7e−03	4 / 44	PanCan_TGF−B_geneset_nanostring
5	1e−02	6 / 111	PanCan_RAS_geneset_nanostring
6	2e−02	2 / 11	GENTLES_modul17
7	2e−02	4 / 61	PanCan_Wnt_geneset_nanostring
8	5e−02	1 / 3	ZHANG_MGUS up
9	8e−02	9 / 298	SPANG_BCL6−index2
10	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
11	1e−01	3 / 70	SHAUGHNESSY_MM high risk
12	2e−01	4 / 120	PanCan_CC+Apop_geneset_nanostring
13	2e−01	1 / 10	GENTLES_modul13
14	2e−01	3 / 82	PanCan_TXmisReg_geneset_nanostring
15	2e−01	1 / 13	GENTLES_modul12
16	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	2e−01	1 / 15	GENTLES_modul4
18	2e−01	1 / 15	GENTLES_modul10
19	2e−01	1 / 16	GENTLES_modul16
20	3e−01	2 / 55	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−12	27 / 308	focal adhesion
2	3e−09	19 / 202	actin cytoskeleton
3	4e−08	19 / 239	proteinaceous extracellular matrix
4	6e−08	23 / 352	cell surface
5	6e−08	91 / 3088	plasma membrane
6	5e−07	89 / 3132	extracellular region
7	8e−07	14 / 159	extracellular matrix
8	2e−06	33 / 775	extracellular space
9	4e−06	66 / 2193	extracellular exosome
10	9e−06	10 / 99	cell cortex
11	1e−05	48 / 1465	cytoskeleton
12	2e−05	7 / 48	stress fiber
13	4e−05	6 / 37	platelet alpha granule lumen
14	7e−05	10 / 125	lamellipodium
15	2e−04	8 / 89	Z disc
16	3e−04	6 / 52	caveola
17	3e−04	7 / 73	basement membrane
18	3e−04	4 / 19	filamentous actin
19	1e−03	9 / 144	membrane raft
20	2e−03	4 / 31	microtubule associated complex

Chr

Rank	p−value	#in/all	Geneset
1	0.003	23 / 696	Chr 5
2	0.019	17 / 558	Chr 4
3	0.022	23 / 838	Chr 3
4	0.058	18 / 687	Chr 6
5	0.140	32 / 1500	Chr 1
6	0.228	15 / 689	Chr 7
7	0.262	12 / 552	Chr 10
8	0.290	20 / 993	Chr 2
9	0.299	10 / 465	Chr 15
10	0.345	5 / 221	Chr 18
11	0.421	9 / 462	Chr 14
12	0.438	9 / 469	Chr 8
13	0.495	3 / 151	Chr 21
14	0.677	4 / 262	Chr 13
15	0.701	6 / 398	Chr 20
16	0.711	12 / 775	Chr 12
17	0.882	7 / 576	Chr 9
18	0.924	6 / 551	Chr X
19	0.936	3 / 335	Chr 22
20	0.973	8 / 801	Chr 11

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−11	18 / 131	Marisa_CRC−cluster−a
2	4e−11	24 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	2e−10	16 / 117	Marisa_CRC−cluster−b
4	9e−10	23 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	2e−08	219 / 10290	TssWk_Colon
6	2e−07	104 / 3812	TssD1_Colon
7	5e−05	97 / 3897	Quies1_Colon
8	4e−04	15 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
9	7e−04	82 / 3383	EnhWk2_Colon
10	9e−04	5 / 43	Marisa_CRC−cluster−f
11	3e−03	3 / 17	Vilar_mutated−in−CRC−CamP
12	4e−03	15 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
13	4e−03	54 / 2159	TssP_Colon
14	8e−03	4 / 45	Ang_CRC−CIMPH−vs−L_hyper
15	8e−03	15 / 427	Quies2_Colon
16	1e−02	14 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
17	1e−02	4 / 50	Ang_CRC_Hypermethylated
18	1e−02	8 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
19	2e−02	14 / 436	K9acLow_Colon
20	3e−02	7 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	4e−06	18 / 294	GUDJ_psoriasis down
2	6e−01	7 / 435	GUDJ_psoriasis up
3	1e+00	0 / 11	BCHETNIA_EBM up
4	1e+00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1e−06	9 / 62	cultured astroglia vs. in vivo astrocytes
2	8e−05	9 / 103	GIEZELT_GBM_WT_up_VS_mut
3	4e−04	11 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
4	5e−04	4 / 22	KIM prognostic signature LTS vs. STS
5	1e−03	7 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	2e−03	4 / 32	Colman_survival_associated
7	3e−03	3 / 16	KIM deleted & downregulated in LTS
8	5e−03	14 / 365	Down_b
9	6e−03	13 / 332	Up
10	2e−02	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
11	2e−02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
12	2e−02	6 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	2e−02	4 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
14	2e−02	6 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
15	3e−02	2 / 15	VERHAAK_CL subtype
16	3e−02	3 / 39	OPC
17	3e−02	5 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
18	4e−02	3 / 45	Christensen_hypermethylated_in_primary_glioblastoma
19	5e−02	3 / 47	Vishal_subnetwork signature of survival in GBM
20	5e−02	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−27	42 / 286	PASINI_SUZ12_TARGETS_DN
2	9e−26	56 / 594	WONG_ADULT_TISSUE_STEM_MODULE
3	2e−24	49 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	2e−20	62 / 930	NUYTTEN_EZH2_TARGETS_UP
5	2e−19	54 / 749	CUI_TCF21_TARGETS_2_DN
6	6e−19	40 / 410	LIM_MAMMARY_STEM_CELL_UP
7	2e−18	40 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
8	3e−18	38 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
9	4e−18	33 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	1e−17	42 / 494	CHICAS_RB1_TARGETS_CONFLUENT
11	3e−17	33 / 302	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
12	3e−15	35 / 401	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
13	1e−14	50 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
14	7e−14	21 / 143	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
15	1e−13	46 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
16	2e−13	25 / 227	ONDER_CDH1_TARGETS_2_UP
17	6e−13	40 / 616	NABA_MATRISOME
18	7e−13	31 / 377	SMID_BREAST_CANCER_LUMINAL_B_DN
19	9e−13	21 / 163	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
20	2e−12	1 / 14	LIU_PROSTATE_CANCER_DN

HM

Rank	p−value	#in/all	Geneset
1	6e−22	30 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	3e−10	17 / 137	HALLMARK_UV_RESPONSE_DN
3	2e−09	18 / 176	HALLMARK_HYPOXIA
4	1e−08	17 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	4e−06	14 / 181	HALLMARK_P53_PATHWAY
6	8e−05	5 / 26	HALLMARK_ANGIOGENESIS
7	2e−04	10 / 140	HALLMARK_APOPTOSIS
8	7e−04	10 / 165	HALLMARK_MYOGENESIS
9	2e−03	5 / 53	HALLMARK_TGF_BETA_SIGNALING
10	3e−03	7 / 107	HALLMARK_COAGULATION
11	4e−03	4 / 37	HALLMARK_APICAL_SURFACE
12	7e−03	9 / 195	HALLMARK_MITOTIC_SPINDLE
13	9e−03	4 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	9e−03	8 / 167	HALLMARK_APICAL_JUNCTION
15	9e−03	8 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	2e−02	5 / 94	HALLMARK_ANDROGEN_RESPONSE
17	3e−02	7 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	4e−02	6 / 140	HALLMARK_INFLAMMATORY_RESPONSE
19	4e−02	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	5e−02	6 / 148	HALLMARK_KRAS_SIGNALING_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	2 / 18	DUMEAUX_High bmi enriched genes
2	0.07	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
3	0.67	1 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−19	30 / 212	LENZ_Stromal signature 1
2	7e−09	74 / 2188	HOPP_Poised_promoter
3	2e−08	99 / 3396	HOPP_Repressed
4	2e−06	137 / 5693	HOPP_Weak_enhancer
5	4e−06	74 / 2563	HOPP_Heterochrom
6	9e−06	7 / 43	LENZ_Stromal signature 2
7	4e−04	124 / 5538	HOPP_Weak_txn
8	4e−04	4 / 20	SPANG_BAFF 9hrs UP
9	7e−04	8 / 109	ROSOLOWSKI_green total
10	9e−04	13 / 268	SPANG_IL21 UP
11	3e−03	6 / 82	ROSOLOWSKI_green UP
12	3e−03	12 / 275	TARTE_Mature plasma cell signature
13	4e−03	55 / 2211	HOPP_Repetitive
14	4e−03	12 / 280	SPANG_CD40 6hrs UP
15	4e−03	3 / 19	Subero_MM_hyper_meth
16	7e−03	6 / 96	Subero_DLBCL_hyper_meth
17	1e−02	6 / 107	SPANG_LPS 6hrs UP
18	1e−02	5 / 81	Subero_INT_hyper_meth
19	2e−02	144 / 7209	HOPP_Weak_promoter
20	2e−02	31 / 1218	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	2e−09	34 / 609	cytoskeletal protein binding
2	5e−07	195 / 8984	protein binding
3	8e−07	11 / 95	heparin binding
4	2e−06	26 / 530	calcium ion binding
5	6e−06	5 / 16	extracellular matrix binding
6	8e−06	5 / 17	insulin−like growth factor binding
7	2e−05	9 / 86	integrin binding
8	2e−05	16 / 271	actin binding
9	4e−04	17 / 378	structural molecule activity
10	4e−04	6 / 55	serine−type endopeptidase inhibitor activity
11	1e−03	10 / 174	transcription corepressor activity
12	1e−03	4 / 26	endopeptidase inhibitor activity
13	1e−03	19 / 501	identical protein binding
14	2e−03	4 / 29	structural constituent of muscle
15	2e−03	5 / 49	collagen binding
16	2e−03	3 / 14	G−protein alpha−subunit binding
17	2e−03	20 / 550	protein homodimerization activity
18	2e−03	12 / 255	receptor binding
19	2e−03	7 / 102	actin filament binding
20	2e−03	7 / 104	growth factor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−06	12 / 129	hsa−miR−576−3p
2	4e−06	14 / 183	hsa−miR−1283
3	1e−04	14 / 250	hsa−miR−524−5p
4	2e−04	12 / 195	hsa−miR−206
5	3e−04	97 120	hsa−miR−579
6	3e−04	13 / 238	hsa−miR−1252
7	3e−04	17 / 376	hsa−miR−373
8	4e−04	8 / 102	hsa−miR−600
9	4e−04	10 / 157	hsa−miR−450b−5p
10	5e−04	11 / 187	hsa−miR−944
11	7e−04	13 / 261	hsa−miR−548p
12	1e−03	22 / 607	hsa−miR−20a
13	1e−03	87 120	hsa−miR−105
14	1e−03	11 / 215	hsa−miR−29b
15	2e−03	97 157	hsa−miR−512−3p
16	2e−03	11 / 222	hsa−miR−185
17	2e−03	8 / 129	hsa−miR−1272
18	2e−03	5 / 53	hsa−miR−337−3p
19	2e−03	17 / 447	hsa−miR−130b
20	3e−03	5 / 55	hsa−miR−191

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_ras.1
2	0.2	1 / 14	BENTINK_e2f3.1
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	GUSTAFSON_PI3K_DN
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.03	29 / 1139	HEBENSTREIT_low expression TF
2	0.23	26 / 1273	ICGC_P300_targets
3	0.25	56 / 2927	ICGC_Rad21_targets
4	0.31	23 / 1171	KIM_MYC targets
5	0.37	24 / 1266	ICGC_NrsfPcr1_targets
6	0.59	32 / 1872	ICGC_Mef2_targets
7	0.60	10 / 595	ICGC_NrsfPcr2_targets
8	0.64	9 / 553	ICGC_RxraPcr1_targets
9	0.69	33 / 2013	ICGC_Bcl11_targets
10	0.71	10 / 653	ICGC_SrfPcr2_targets
11	0.74	39 / 2416	ICGC_Bcl3_targets
12	0.80	64 / 3966	ICGC_Pu1_targets
13	0.85	28 / 1878	ICGC_Cebpbsc150_targets
14	0.87	43 / 2836	ICGC_BatfPcr1_targets
15	0.88	63 / 4054	ICGC_Egr1_targets
16	0.89	24 / 1701	HEBENSTREIT_high expression TF
17	0.90	67 / 4314	ICGC_Ebfsc137065_targets
18	0.93	17 / 1314	ICGC_Usf1_targets
19	0.95	95 / 6114	ICGC_Runx3_targets
20	0.96	57 / 3924	ICGC_Zeb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.01	3 / 29	VAQUERIZAS_Smooth muscle
2	0.03	3 / 41	VAQUERIZAS_Placenta
3	0.06	2 / 23	VAQUERIZAS_Trachea
4	0.08	3 / 58	VAQUERIZAS_Lung
5	0.09	2 / 29	VAQUERIZAS_Fetal lung
6	0.12	1 / 7	VAQUERIZAS_Appendix
7	0.12	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
8	0.19	2 / 45	VAQUERIZAS_Uterus
9	0.19	1 / 12	VAQUERIZAS_Skin
10	0.22	1 / 14	VAQUERIZAS_Ovary
11	0.23	1 / 15	VAQUERIZAS_Fetal thyroid
12	0.25	1 / 16	VAQUERIZAS_Pancreas
13	0.28	2 / 59	VAQUERIZAS_Whole blood
14	0.29	1 / 19	VAQUERIZAS_Tonsil
15	0.46	3 / 143	VAQUERIZAS_General
16	0.47	1 / 36	VAQUERIZAS_Fetal brain
17	0.48	1 / 37	VAQUERIZAS_Thymus
18	0.49	1 / 38	VAQUERIZAS_Whole brain
19	0.51	1 / 40	VAQUERIZAS_Thyroid
20	1.00	0 / 26	VAQUERIZAS_Liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	WIRTH_Sec. lymphoid organs
2	0.02	2 / 12	WIRTH_Thymus
3	0.02	2 / 14	WIRTH_Telencephalon
4	0.05	7 / 194	PALMER_B−Cell signature up
5	0.09	10 / 350	WIRTH_Nervous System
6	0.14	4 / 114	PALMER_T−Cell signature up
7	0.15	1 / 9	PALMER_CD8+ T−Cell signature up
8	0.18	1 / 11	WIRTH_Cortex cerebri
9	0.20	6 / 225	PALMER_Granulocytes signature up
10	0.21	1 / 13	WIRTH_B−cells
11	0.23	3 / 95	WIRTH_Muscle
12	0.43	1 / 32	WIRTH_Placenta
13	0.56	1 / 46	WIRTH_Liver
14	0.73	1 / 74	WIRTH_Mucosa
15	0.74	5 / 350	WIRTH_Immune system
16	1.00	0 / 32	WIRTH_Pancreas
17	1.00	0 / 11	WIRTH_Prim. lymphoid organs
18	1.00	0 / 8	WIRTH_Tonsil
19	1.00	0 / 12	WIRTH_Lymphocytes
20	1.00	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.04	77 / 3682	LU_BPDE 0.005 DN
2	0.58	19 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

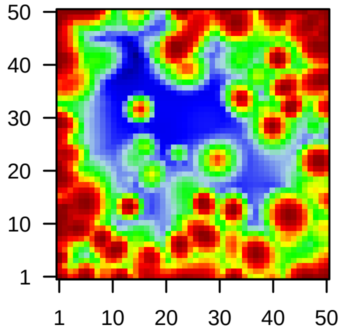
Spot Summary: I1

metagenes = 7
genes = 95

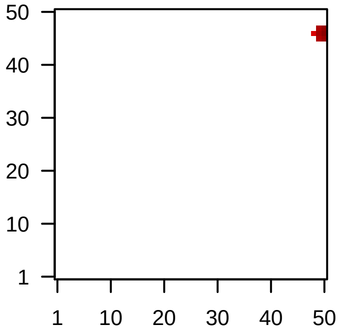
<r> metagenes = 0.97
<r> genes = 0.1
beta: r2= 1.64 / log p= −Inf

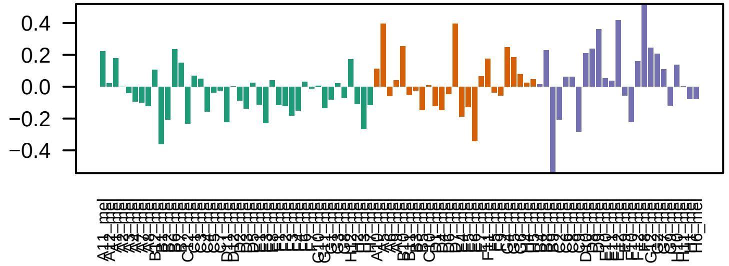
samples with spot = 15 (16.3 %)
MSC1 : 2 (4.8 %)
MSC2 : 5 (20 %)
MSC3 : 8 (32 %)

Overview Map



Spot





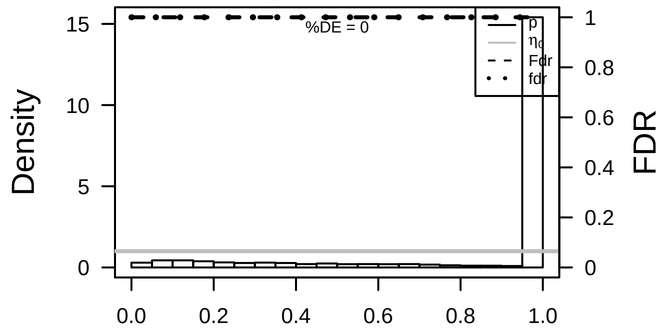
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PIBF1	1.97	−0.47	0.28	PIBF1	progesterone immunomodulatory binding factor 1 [Source:HG
2	CC2D2A	1.84	−0.51	0.36	CC2D2A	coiled−coil and C2 domain containing 2A [Source:HGNC Sym
3	GSDMB	1.8	−0.19	0.37	GSDMB	gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]
4	GORAB	1.77	−0.45	0.34	GORAB	golgin, RAB6−interacting [Source:HGNC Symbol;Acc:HGNC:
5	C1S	1.74	−0.17	0.44	C1S	complement component 1, s subcomponent [Source:HGNC S
6	TMEM53	1.71	−0.39	0.29	TMEM53	transmembrane protein 53 [Source:HGNC Symbol;Acc:HGNC
7	ZNF420	1.68	−0.43	0.28	ZNF420	zinc finger protein 420 [Source:HGNC Symbol;Acc:HGNC:20
8	PHOSPHO2	1.62	−0.32	0.36	PHOSPHO2	phosphatase, orphan 2 [Source:HGNC Symbol;Acc:HGNC:28
9	MFSD8	1.6	−0.35	0.36	MFSD8	major facilitator superfamily domain containing 8 [Source:HGI
10	DCAF10	1.58	−0.65	0.26	DCAF10	DDB1 and CUL4 associated factor 10 [Source:HGNC Symbo
11	TRO	1.57	−0.73	0.41	TRO	trophinin [Source:HGNC Symbol;Acc:HGNC:12326]
12	AMPD2	1.56	−0.6	0.41	AMPD2	adenosine monophosphate deaminase 2 [Source:HGNC Sym
13	TSC2	1.55	−0.53	0.4	TSC2	tuberous sclerosis 2 [Source:HGNC Symbol;Acc:HGNC:1236
14	PHF8	1.55	−0.41	0.26	PHF8	PHD finger protein 8 [Source:HGNC Symbol;Acc:HGNC:2067
15	DNHD1	1.54	−0.23	0.3	DNHD1	dynein heavy chain domain 1 [Source:HGNC Symbol;Acc:HG
16	PHYKPL	1.52	−0.43	0.29	PHYKPL	5−phosphohydroxy−L−lysine phospho−lyase [Source:HGNC
17	ZNF668	1.52	−0.23	0.28	ZNF668	zinc finger protein 668 [Source:HGNC Symbol;Acc:HGNC:25
18	HIST3H2A	1.51	−0.86	0.44	HIST3H2A	histone cluster 3, H2a [Source:HGNC Symbol;Acc:HGNC:205
19	DPH7	1.48	−0.35	0.33	DPH7	diphthamide biosynthesis 7 [Source:HGNC Symbol;Acc:HGN
20	ZUFSP	1.45	−0.68	0.21	ZUFSP	zinc finger with UFM1−specific peptidase domain [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−10	83 / 8580	Colon	TxWk_Colon
2	2e−09	84 / 9027	Colon	Tx_Colon
3	3e−07	82 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
4	7e−07	72 / 7592	Lympl	HOPP_Active_promoter
5	7e−07	68 / 6929	Lympl	HOPP_Txn_elongation
6	3e−05	79 / 9482	Colon	TssA_Colon
7	1e−04	75 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
8	2e−04	64 / 7203	Colon	TssF_Colon
9	2e−04	71 / 8415	Colon	Quies3_Colon
10	6e−04	49 / 5184	Lympl	HOPP_Txn_transition
11	7e−04	54 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
12	7e−04	31 / 2755	BP	transport
13	2e−03	3 / 37	miRN	hsa−miR−760
14	2e−03	3 / 38	GSEA	IRITANI_MAD1_TARGETS_DN
15	2e−03	2 / 11	BP	activation of mitophagy in response to mitochondrial depolarization
16	2e−03	2 / 11	BP	posttranscriptional regulation of gene expression
17	2e−03	5 / 142	GSEA	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
18	2e−03	75 / 9653	Colon	Enh_Colon
19	3e−03	2 / 12	MF	protein methyltransferase activity
20	3e−03	80 / 10605	CC	intracellular
21	3e−03	74 / 9528	Brain	Overlap_fetal_midbrain_Quies
22	3e−03	60 / 7209	Lympl	HOPP_Weak_promoter
23	3e−03	2 / 13	BP	cAMP catabolic process
24	4e−03	2 / 14	BP	protein ADP−ribosylation
25	4e−03	24 / 2136	TF	ICGC_GabpPcr2_targets
26	4e−03	29 / 2798	Colon	TxEnhG1_Colon
27	4e−03	3 / 51	miRN	hsa−miR−508−5p
28	4e−03	4 / 104	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_UP
29	5e−03	2 / 16	GSEA	MEISSNER_NPC_ICP_WITH_H3K4ME3
30	5e−03	3 / 54	CC	transport vesicle
31	5e−03	8 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
32	5e−03	13 / 911	GSEA	BENPORATH_NANOG_TARGETS
33	6e−03	3 / 59	BP	cilium morphogenesis
34	7e−03	12 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
35	7e−03	2 / 20	CC	dynein complex
36	7e−03	2 / 20	MF	NAD+ ADP−ribosyltransferase activity
37	7e−03	2 / 20	BP	regulation of sequence−specific DNA binding transcription factor activity
38	8e−03	2 / 21	GSEA	BIOCARTA_MTOR_PATHWAY
39	8e−03	2 / 21	GSEA	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP
40	8e−03	3 / 64	GSEA	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−04	31 / 2755	transport
2	2e−03	2 / 11	activation of mitophagy in response to mitochondrial depolarization
3	2e−03	2 / 11	posttranscriptional regulation of gene expression
4	3e−03	2 / 13	cAMP catabolic process
5	4e−03	2 / 14	protein ADP−ribosylation
6	6e−03	3 / 59	cilium morphogenesis
7	7e−03	2 / 20	regulation of sequence−specific DNA binding transcription factor activity
8	9e−03	2 / 22	mitotic spindle organization
9	9e−03	3 / 68	microtubule−based movement
10	1e−02	2 / 25	protein methylation
11	2e−02	2 / 31	lysosome organization
12	2e−02	2 / 38	base−excision repair
13	3e−02	14 / 1237	metabolic process
14	3e−02	7 / 478	protein transport
15	3e−02	2 / 45	regulation of cyclin−dependent protein serine/threonine kinase activity
16	5e−02	2 / 56	translational initiation
17	5e−02	2 / 57	response to hormone
18	5e−02	3 / 131	ribonucleoprotein complex assembly
19	5e−02	2 / 59	smoothened signaling pathway
20	6e−02	2 / 60	mRNA transport

Brain

Rank	p−value	#in/all	Geneset
1	3e−07	82 / 9330	Overlap_fetal_midbrain_ReprPC
2	1e−04	75 / 9013	Overlap_fetal_midbrain_K9K27me3
3	7e−04	54 / 5940	Overlap_fetal_midbrain_HetRpts
4	3e−03	74 / 9528	Overlap_fetal_midbrain_Quies
5	1e−02	11 / 786	Fetal_EnhG
6	2e−02	12 / 953	Fetal_Enh
7	8e−02	65 / 9020	Overlap_fetal_midbrain_ReprPCWk
8	8e−02	13 / 1333	Fetal_ReprPCWk
9	8e−02	9 / 831	Fetal_HetRpts
10	1e−01	8 / 769	Overlap_fetal_midbrain_ZNF
11	1e−01	4 / 304	Fetal_Het
12	2e−01	9 / 1050	Fetal_EnhP
13	3e−01	22 / 3081	Mid_Frontal_Lobe_ZNF
14	4e−01	9 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	4e−01	17 / 2462	Mid_Frontal_Lobe_HetRpts
16	4e−01	5 / 656	Overlap_fetal_midbrain_EnhP
17	6e−01	7 / 1122	Fetal_K9K27me3
18	6e−01	1 / 158	Overlap_fetal_midbrain_Het
19	7e−01	1 / 166	Mid_Frontal_Lobe_Tx
20	7e−01	3 / 534	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 16	GENTLES_modul6
2	0.2	1 / 29	KUIPER_MM good survival
3	0.3	2 / 180	SPANG_LPS−index2
4	0.3	0 / 14	LIU_COMMON_CANCER_GENES
5	0.4	0 / 12	LIU_PROSTATE_CANCER_UP
6	0.5	0 / 14	LIU_PROSTATE_CANCER_DN
7	0.6	2 / 298	SPANG_BCL6−index2
8	0.9	1 / 401	Lembcke_Colonic Inflammation
9	1.0	1 / 489	Lembcke_Normal vs Adenoma
10	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1.0	0 / 12	LIU_BREAST_CANCER
15	1.0	0 / 14	LIU_LIVER_CANCER
16	1.0	0 / 15	WANG_ER_UP
17	1.0	0 / 5	WANG_ER_DN
18	1.0	0 / 16	WOLFER_overlap genes
19	1.0	0 / 12	BEN−PORATH_DN
20	1.0	0 / 13	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	0.003	80 / 10605	intracellular
2	0.005	3 / 54	transport vesicle
3	0.007	2 / 20	dynein complex
4	0.011	64 / 8205	cytoplasm
5	0.027	29 / 3214	protein complex
6	0.028	2 / 41	ciliary tip
7	0.039	90 / 13191	cellular_component
8	0.054	82 / 11774	cell
9	0.056	2 / 60	nuclear pore
10	0.057	12 / 1132	Golgi apparatus
11	0.062	1 / 10	mRNA cap binding complex
12	0.062	1 / 10	WASH complex
13	0.067	2 / 66	integral component of endoplasmic reticulum membrane
14	0.074	2 / 70	primary cilium
15	0.074	1 / 12	holo TFIIH complex
16	0.074	1 / 12	STAGA complex
17	0.080	1 / 13	COPI vesicle coat
18	0.080	1 / 13	TCTN−B9D complex
19	0.086	1 / 14	Cul4−RING E3 ubiquitin ligase complex
20	0.086	1 / 14	cytoplasmic dynein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.1	7 / 649	Chr 16
2	0.2	5 / 465	Chr 15
3	0.2	5 / 469	Chr 8
4	0.3	5 / 551	Chr X
5	0.3	7 / 838	Chr 3
6	0.3	4 / 462	Chr 14
7	0.4	6 / 801	Chr 11
8	0.5	7 / 993	Chr 2
9	0.5	3 / 398	Chr 20
10	0.5	4 / 558	Chr 4
11	0.5	10 / 1500	Chr 1
12	0.5	2 / 262	Chr 13
13	0.5	4 / 576	Chr 9
14	0.6	4 / 689	Chr 7
15	0.7	4 / 696	Chr 5
16	0.7	6 / 1037	Chr 19
17	0.7	3 / 552	Chr 10
18	0.7	4 / 775	Chr 12
19	0.8	3 / 687	Chr 6
20	1.0	2 / 840	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−10	83 / 8580	TxWk_Colon
2	2e−09	84 / 9027	Tx_Colon
3	3e−05	79 / 9482	TssA_Colon
4	2e−04	64 / 7203	TssF_Colon
5	2e−04	71 / 8415	Quies3_Colon
6	2e−03	75 / 9653	Enh_Colon
7	4e−03	29 / 2798	TxEnhG1_Colon
8	1e−02	76 / 10290	TssWk_Colon
9	2e−02	43 / 5155	EnhWk1_Colon
10	4e−02	3 / 117	Marisa_CRC−cluster−b
11	5e−02	9 / 739	TxEnhG2_Colon
12	7e−02	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	8e−02	31 / 3812	TssD1_Colon
14	9e−02	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
15	9e−02	1 / 15	Juehling_HNPCC−mutated−in−4
16	1e−01	44 / 5880	TssD2_Colon
17	1e−01	22 / 2698	EnhA_Colon
18	1e−01	30 / 3897	Quies1_Colon
19	2e−01	10 / 1079	ZNF_Colon
20	2e−01	7 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN

Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 435	GUDJ_psoriasis up
2	1	0 / 294	GUDJ_psoriasis down
3	1	0 / 11	BCHETNIA_EBM up
4	1	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.07	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
2	0.08	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
3	0.08	5 / 365	Down_b
4	0.09	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.11	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
6	0.11	1 / 18	Shinawi_with_increased_methylation_in_STS
7	0.13	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
8	0.27	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
9	0.34	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
10	0.35	1 / 68	GIEZELT_GBM_WT_down_VS_mut
11	0.35	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.38	1 / 75	Weller_LGG_A_vs_O_DOWN
13	0.48	1 / 103	GIEZELT_GBM_WT_up_VS_mut
14	0.63	2 / 332	Up
15	0.64	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
16	0.70	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
17	1.00	0 / 15	VERHAAK_CL subtype
18	1.00	0 / 15	VERHAAK_MES subtype
19	1.00	0 / 16	VERHAAK_NL subtype
20	1.00	0 / 14	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	3 / 38	IRITANI_MAD1_TARGETS_DN
2	0.002	5 / 142	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
3	0.004	4 / 104	LAIHO_COLORECTAL_CANCER_SERRATED_UP
4	0.005	2 / 16	MEISSNER_NPC_ICP_WITH_H3K4ME3
5	0.005	8 / 416	SHEN_SMARCA2_TARGETS_UP
6	0.005	13 / 911	BENPORATH_NANOG_TARGETS
7	0.007	12 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
8	0.008	2 / 21	BIOCARTA_MTOR_PATHWAY
9	0.008	2 / 21	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP
10	0.008	3 / 64	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES
11	0.011	10 / 675	BENPORATH_SOX2_TARGETS
12	0.011	3 / 73	TOOKER_GEMCITABINE_RESISTANCE_UP
13	0.012	3 / 74	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN
14	0.012	3 / 74	NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER
15	0.013	2 / 27	MEISSNER_ES_ICP_WITH_H3K4ME3
16	0.014	2 / 28	MEISSNER_BRAIN_ICP_WITH_H3K4ME3
17	0.016	4 / 150	WHITFIELD_CELL_CYCLE_S
18	0.017	3 / 85	ZAMORA_NOS2_TARGETS_DN
19	0.017	4 / 155	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
20	0.018	2 / 32	MURAKAMI_UV_RESPONSE_6HR_UP

HM

Rank	p−value	#in/all	Geneset
1	0.07	3 / 146	HALLMARK_DNA_REPAIR
2	0.09	3 / 162	HALLMARK_COMPLEMENT
3	0.12	2 / 91	HALLMARK_BILE_ACID_METABOLISM
4	0.15	2 / 107	HALLMARK_COAGULATION
5	0.29	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
6	0.31	2 / 174	HALLMARK_HEME_METABOLISM
7	0.31	1 / 57	HALLMARK_MYC_TARGETS_V2
8	0.36	2 / 195	HALLMARK_MITOTIC_SPINDLE
9	0.43	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.44	1 / 91	HALLMARK_PROTEIN_SECRETION
11	0.45	1 / 93	HALLMARK_PEROXISOME
12	0.46	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	0.56	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
14	0.60	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
15	0.66	1 / 165	HALLMARK_MYOGENESIS
16	0.66	1 / 167	HALLMARK_APICAL_JUNCTION
17	0.66	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	0.67	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	0.68	1 / 176	HALLMARK_HYPOXIA
20	0.69	1 / 181	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−07	72 / 7592	HOPP_Active_promoter
2	7e−07	68 / 6929	HOPP_Txn_elongation
3	6e−04	49 / 5184	HOPP_Txn_transition
4	3e−03	60 / 7209	HOPP_Weak_promoter
5	2e−02	53 / 6564	HOPP_Strong_enhancer
6	3e−02	1 / 5	WRIGHT_custom ABC−DLBCL UP
7	7e−02	43 / 5538	HOPP_Weak_txn
8	1e−01	1 / 16	DAVE_BL Inter
9	1e−01	5 / 410	SPANG_CD40 6hrs DN
10	1e−01	42 / 5693	HOPP_Weak_enhancer
11	2e−01	3 / 268	SPANG_IL21 UP
12	3e−01	3 / 294	TARTE_Plasmablast signature
13	3e−01	1 / 61	SPANG_LPS 6hrs DN
14	4e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
15	4e−01	1 / 89	ROSOLOWSKI_blue total
16	5e−01	2 / 247	ZHANG_DLBCL mutated
17	5e−01	2 / 256	SPANG_IL21 DN
18	5e−01	2 / 275	TARTE_Mature plasma cell signature
19	6e−01	14 / 2211	HOPP_Repetitive
20	7e−01	1 / 212	LENZ_Stromal signature 1

MF

Rank	p−value	#in/all	Geneset
1	0.003	2 / 12	protein methyltransferase activity
2	0.007	2 / 20	NAD+ ADP−ribosyltransferase activity
3	0.009	2 / 22	3',5'−cyclic−nucleotide phosphodiesterase activity
4	0.012	2 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductic
5	0.021	2 / 35	clathrin binding
6	0.022	3 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
7	0.028	2 / 41	phosphatase binding
8	0.042	2 / 51	translation initiation factor activity
9	0.046	4 / 210	transferase activity, transferring glycosyl groups
10	0.062	1 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
11	0.062	1 / 10	transaminase activity
12	0.063	7 / 550	protein homodimerization activity
13	0.068	1 / 11	antiporter activity
14	0.068	1 / 11	glutathione peroxidase activity
15	0.068	1 / 11	protein deacetylase activity
16	0.068	1 / 11	protein kinase B binding
17	0.072	2 / 69	microtubule motor activity
18	0.074	2 / 70	phospholipid binding
19	0.074	1 / 12	endodeoxyribonuclease activity
20	0.074	1 / 12	MAP kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 37	hsa−miR−760
2	0.004	3 / 51	hsa−miR−508−5p
3	0.011	2 / 25	hsa−miR−941
4	0.017	2 / 31	hsa−miR−296−5p
5	0.025	2 / 38	hsa−miR−1277
6	0.045	3 / 124	hsa−miR−646
7	0.050	2 / 56	hsa−miR−665
8	0.062	1 / 10	hsa−miR−1249
9	0.076	3 / 154	hsa−miR−139−5p
10	0.083	2 / 75	hsa−miR−877
11	0.115	1 / 19	hsa−miR−542−5p
12	0.124	3 / 191	hsa−miR−330−3p
13	0.126	1 / 21	hsa−miR−554
14	0.126	1 / 21	hsa−miR−662
15	0.126	1 / 21	hsa−miR−1282
16	0.134	2 / 100	hsa−miR−574−5p
17	0.137	1 / 23	hsa−miR−943
18	0.147	4 / 318	hsa−miR−98
19	0.148	5 / 437	hsa−miR−19b
20	0.154	5 / 443	hsa−miR−19a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 9	BENTINK_ras.4
2	1.00	0 / 12	GUSTAFSON_PI3K_UP
3	1.00	0 / 13	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	BENTINK_e2f3.1
5	1.00	0 / 12	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.004	24 / 2136	ICGC_GabpPcr2_targets
2	0.019	40 / 4689	ICGC_Taf1_targets
3	0.021	38 / 4414	ICGC_Bclaf101388_targets
4	0.023	41 / 4879	ICGC_Pmlsc71910_targets
5	0.026	40 / 4774	ICGC_Foxm1_targets
6	0.028	34 / 3924	ICGC_Zeb1_targets
7	0.031	37 / 4385	ICGC_Atf2_targets
8	0.040	40 / 4909	ICGC_Stat5_targets
9	0.041	17 / 1701	HEBENSTREIT_high expression TF
10	0.050	38 / 4682	ICGC_Pol24_targets
11	0.055	31 / 3700	ICGC_Nfatc1_targets
12	0.057	14 / 1383	ICGC_Six5_targets
13	0.060	43 / 5495	ICGC_Yy1_targets
14	0.061	41 / 5200	ICGC_Mta3_targets
15	0.087	17 / 1878	ICGC_Cebpbsc150_targets
16	0.096	41 / 5374	ICGC_Pax5_targets
17	0.105	41 / 5408	ICGC_Pou2_targets
18	0.110	13 / 1400	ICGC_Myc_targets
19	0.110	37 / 4829	ICGC_Nficsc81335_targets
20	0.118	36 / 4706	ICGC_Sp1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.7	2 / 350	WIRTH_Immune system
2	0.7	1 / 194	PALMER_B−Cell signature up
3	0.8	1 / 225	PALMER_Granulocytes signature up
4	1.0	0 / 32	WIRTH_Pancreas
5	1.0	0 / 11	WIRTH_Sec. lymphoid organs
6	1.0	0 / 11	WIRTH_Prim. lymphoid organs
7	1.0	0 / 13	WIRTH_B−cells
8	1.0	0 / 8	WIRTH_Tonsil
9	1.0	0 / 12	WIRTH_Thymus
10	1.0	0 / 12	WIRTH_Lymphocytes
11	1.0	0 / 5	WIRTH_Bone marrow
12	1.0	0 / 350	WIRTH_Nervous System
13	1.0	0 / 11	WIRTH_Globus pallidus
14	1.0	0 / 14	WIRTH_Telencephalon
15	1.0	0 / 11	WIRTH_Cortex cerebri
16	1.0	0 / 10	WIRTH_Hippocampus
17	1.0	0 / 10	WIRTH_Thalamus
18	1.0	0 / 12	WIRTH_Cerebellum
19	1.0	0 / 107	WIRTH_Testis
20	1.0	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	8 / 1115	LU_BPDE 1n DN
2	0.6	23 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

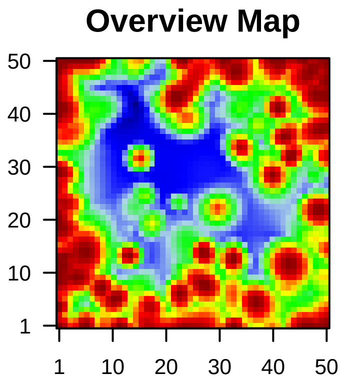
Overexpression Spots

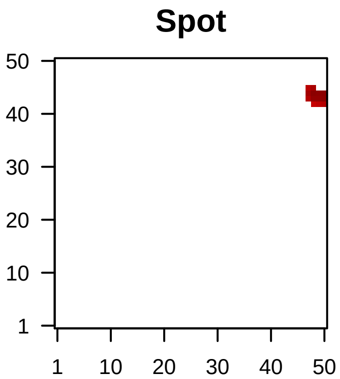
Spot Summary: J1

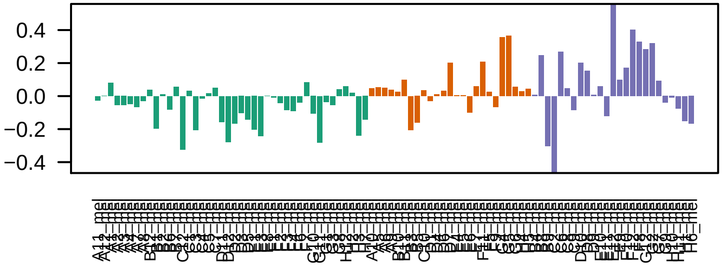
metagenes = 13
genes = 118

<r> metagenes = 0.94
<r> genes = 0.09
beta: r2= 1.47 / log p= −Inf

samples with spot = 12 (13 %)
MSC2 : 4 (16 %)
MSC3 : 8 (32 %)





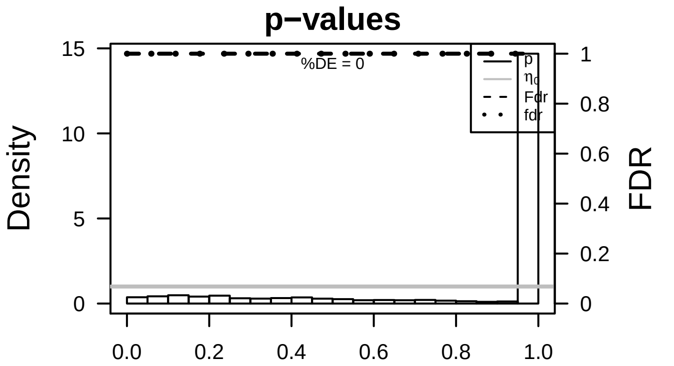


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	NECAB2	1.9	−0.43	0.35	NECAB2	N−terminal EF−hand calcium binding protein 2 [Source:HGN
2	LIN37	1.83	−0.13	0.35	LIN37	lin−37 DREAM MuvB core complex component [Source:HGN
3	PACRGL	1.76	−0.36	0.23	PACRGL	PARK2 co−regulated−like [Source:HGNC Symbol;Acc:HGNC
4	USP19	1.74	−0.4	0.29	USP19	ubiquitin specific peptidase 19 [Source:HGNC Symbol;Acc:H
5	STYXL1	1.73	−0.64	0.39	STYXL1	serine/threonine/tyrosine interacting−like 1 [Source:HGNC Sy
6	ING4	1.73	−0.36	0.37	ING4	inhibitor of growth family, member 4 [Source:HGNC Symbol;A
7	RNF146	1.7	−0.34	0.33	RNF146	ring finger protein 146 [Source:HGNC Symbol;Acc:HGNC:21
8	VASP	1.69	−0.36	0.28	VASP	vasodilator−stimulated phosphoprotein [Source:HGNC Symb
9	LRRC23	1.64	−0.21	0.33	LRRC23	leucine rich repeat containing 23 [Source:HGNC Symbol;Acc
10	LZTR1	1.57	−0.45	0.26	LZTR1	leucine−zipper−like transcription regulator 1 [Source:HGNC
11	BCAS3	1.55	−0.48	0.37	BCAS3	breast carcinoma amplified sequence 3 [Source:HGNC Symb
12	PARP6	1.54	−0.61	0.24	PARP6	poly (ADP−ribose) polymerase family, member 6 [Source:HG
13	CDC16	1.54	−0.74	0.25	CDC16	cell division cycle 16 [Source:HGNC Symbol;Acc:HGNC:172
14	LRRC39	1.52	−0.38	0.35	LRRC39	leucine rich repeat containing 39 [Source:HGNC Symbol;Acc
15	RUFY1	1.52	−0.52	0.24	RUFY1	RUN and FYVE domain containing 1 [Source:HGNC Symbol;
16	RAB4B	1.51	−0.49	0.28	RAB4B	RAB4B, member RAS oncogene family [Source:HGNC Symb
17	CCT6B	1.51	−0.23	0.23	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2) [Source:HG
18	FAM219B	1.51	−0.68	0.23	FAM219B	family with sequence similarity 219, member B [Source:HGN
19	CDAN1	1.49	−0.14	0.31	CDAN1	codanin 1 [Source:HGNC Symbol;Acc:HGNC:1713]
20	ZNF189	1.47	−0.25	0.33	ZNF189	zinc finger protein 189 [Source:HGNC Symbol;Acc:HGNC:12

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	6e−10	88 / 6929	Lympl	HOPP_Txn_elongation
2	1e−08	97 / 8580	Colon	TxWk_Colon
3	4e−08	101 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
4	1e−07	98 / 9027	Colon	Tx_Colon
5	1e−07	88 / 7592	Lympl	HOPP_Active_promoter
6	1e−06	99 / 9482	Colon	TssA_Colon
7	2e−06	66 / 5184	Lympl	HOPP_Txn_transition
8	4e−06	4 / 14	BP	nucleotide metabolic process
9	2e−05	93 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
10	4e−05	69 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
11	9e−05	100 / 10290	Colon	TssWk_Colon
12	1e−04	13 / 478	BP	protein transport
13	4e−04	76 / 7209	Lympl	HOPP_Weak_promoter
14	4e−04	3 / 19	GSEA	TOMLINS_METASTASIS_DN
15	5e−04	23 / 1383	TF	ICGC_Six5_targets
16	7e−04	5 / 89	Lympl	ROSOLOWSKI_blue total
17	8e−04	84 / 8415	Colon	Quies3_Colon
18	2e−03	3 / 30	BP	termination of RNA polymerase I transcription
19	2e−03	3 / 30	BP	transcription elongation from RNA polymerase I promoter
20	2e−03	3 / 33	BP	transcription from RNA polymerase I promoter
21	2e−03	3 / 33	BP	transcription initiation from RNA polymerase I promoter
22	2e−03	3 / 34	BP	histone acetylation
23	3e−03	6 / 176	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
24	3e−03	2 / 11	BP	positive regulation of protein sumoylation
25	3e−03	8 / 310	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
26	3e−03	14 / 775	Chr	Chr 12
27	4e−03	60 / 5693	Lympl	HOPP_Weak_enhancer
28	4e−03	2 / 12	MF	RNA polymerase I activity
29	5e−03	2 / 13	CC	DNA−directed RNA polymerase I complex
30	5e−03	4 / 87	GSEA	BROWNE_HCMV_INFECTION_10HR_UP
31	5e−03	2 / 14	BP	negative regulation of endoplasmic reticulum stress−induced intrinsic apop
32	5e−03	3 / 45	GSEA	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN
33	6e−03	7 / 271	GSEA	ZHANG_TLX_TARGETS_60HR_UP
34	6e−03	45 / 4032	TF	ICGC_Creb1_targets
35	6e−03	13 / 748	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
36	7e−03	6 / 213	BP	chromatin organization
37	8e−03	2 / 17	BP	positive regulation of intracellular protein transport
38	8e−03	2 / 17	GSEA	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER
39	8e−03	20 / 1418	TF	ICGC_Ets1_targets
40	8e−03	3 / 52	GSEA	SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	0 / 14	LIU_COMMON_CANCER_GENES
2	0.1	1 / 15	GENTLES_modul10
3	0.1	1 / 16	GENTLES_modul14
4	0.2	3 / 180	SPANG_LPS−index2
5	0.2	1 / 29	KUIPER_MM good survival
6	0.2	4 / 298	SPANG_BCL6−index2
7	0.3	1 / 47	PanCan_DNARepair_geneset_nanostring
8	0.5	0 / 12	LIU_PROSTATE_CANCER_UP
9	0.5	4 / 489	Lembcke_Normal vs Adenoma
10	0.6	1 / 113	PanCan_Driver_Gene_geneset_nanostring
11	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
12	1.0	1 / 401	Lembcke_Colonic Inflammation
13	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	1.0	0 / 12	LIU_BREAST_CANCER
18	1.0	0 / 14	LIU_LIVER_CANCER
19	1.0	0 / 15	WANG_ER_UP
20	1.0	0 / 5	WANG_ER_DN

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−08	97 / 8580	TxWk_Colon
2	1e−07	98 / 9027	Tx_Colon
3	1e−06	99 / 9482	TssA_Colon
4	9e−05	100 / 10290	TssWk_Colon
5	8e−04	84 / 8415	Quies3_Colon
6	6e−03	13 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
7	7e−02	9 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	9e−02	65 / 7203	TssF_Colon
9	1e−01	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
10	2e−01	3 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	2e−01	1 / 29	Marisa_CRC−cluster−c
12	2e−01	5 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	2e−01	25 / 2698	EnhA_Colon
14	3e−01	1 / 43	Marisa_CRC−cluster−f
15	3e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
16	3e−01	80 / 9653	Enh_Colon
17	3e−01	10 / 1038	HetRpts_Colon
18	4e−01	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
19	4e−01	3 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
20	4e−01	12 / 1386	Het_Colon

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 19	TOMLINS_METASTASIS_DN
2	3e−03	6 / 176	TIEN_INTESTINE_PROBIOTICS_24HR_DN
3	3e−03	8 / 310	DAZARD_RESPONSE_TO_UV_NHEK_DN
4	5e−03	4 / 87	BROWNE_HCMV_INFECTION_10HR_UP
5	5e−03	3 / 45	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN
6	6e−03	7 / 271	ZHANG_TLX_TARGETS_60HR_UP
7	8e−03	2 / 17	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER
8	8e−03	3 / 52	SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN
9	8e−03	3 / 52	IKEDA_MIR1_TARGETS_UP
10	9e−03	7 / 293	DOUGLAS_BMI1_TARGETS_DN
11	9e−03	12 / 696	NUYTTEN_NIPP1_TARGETS_UP
12	1e−02	3 / 55	KYNG_DNA_DAMAGE_BY_UV
13	1e−02	3 / 56	AKL_HTLV1_INFECTION_DN
14	1e−02	3 / 56	CASTELLANO_NRAS_TARGETS_UP
15	1e−02	9 / 453	WEST_ADRENOCORTICAL_TUMOR_DN
16	1e−02	11 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
17	1e−02	2 / 20	REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION
18	1e−02	2 / 20	NAKAJIMA_EOSINOPHIL
19	1e−02	2 / 20	MCCABE_HOXC6_TARGETS_CANCER_DN
20	1e−02	5 / 169	PENG_RAPAMYCIN_RESPONSE_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−10	88 / 6929	HOPP_Txn_elongation
2	1e−07	88 / 7592	HOPP_Active_promoter
3	2e−06	66 / 5184	HOPP_Txn_transition
4	4e−04	76 / 7209	HOPP_Weak_promoter
5	7e−04	5 / 89	ROSOLOWSKI_blue total
6	4e−03	60 / 5693	HOPP_Weak_enhancer
7	2e−02	55 / 5538	HOPP_Weak_txn
8	3e−02	63 / 6564	HOPP_Strong_enhancer
9	5e−02	7 / 410	SPANG_CD40 6hrs DN
10	6e−02	2 / 50	SPANG_BAFF 9hrs DN
11	7e−02	5 / 275	TARTE_Mature plasma cell signature
12	8e−02	2 / 61	SPANG_LPS 6hrs DN
13	9e−02	1 / 12	BENTINK_mBL DOWN
14	1e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
15	1e−01	2 / 82	ROSOLOWSKI_green UP
16	2e−01	1 / 25	Subero_T−PLL_hypo_meth
17	2e−01	4 / 280	SPANG_CD40 6hrs UP
18	2e−01	2 / 109	ROSOLOWSKI_green total
19	3e−01	11 / 1128	SPANG_BCR DN
20	3e−01	1 / 43	LENZ_Stromal signature 2

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_src.10
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 15	BENTINK_ras.6
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	4 / 194	PALMER_B−Cell signature up
2	0.10	4 / 225	PALMER_Granulocytes signature up
3	0.21	2 / 107	WIRTH_Testis
4	0.53	1 / 95	WIRTH_Muscle
5	0.77	2 / 350	WIRTH_Immune system
6	1.00	0 / 32	WIRTH_Pancreas
7	1.00	0 / 11	WIRTH_Sec. lymphoid organs
8	1.00	0 / 11	WIRTH_Prim. lymphoid organs
9	1.00	0 / 13	WIRTH_B−cells
10	1.00	0 / 8	WIRTH_Tonsil
11	1.00	0 / 12	WIRTH_Thymus
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 350	WIRTH_Nervous System
15	1.00	0 / 11	WIRTH_Globus pallidus
16	1.00	0 / 14	WIRTH_Telencephalon
17	1.00	0 / 11	WIRTH_Cortex cerebri
18	1.00	0 / 10	WIRTH_Hippocampus
19	1.00	0 / 10	WIRTH_Thalamus
20	1.00	0 / 12	WIRTH_Cerebellum

BP

Rank	p−value	#in/all	Geneset
1	4e−06	4 / 14	nucleotide metabolic process
2	1e−04	13 / 478	protein transport
3	2e−03	3 / 30	termination of RNA polymerase I transcription
4	2e−03	3 / 30	transcription elongation from RNA polymerase I promoter
5	2e−03	3 / 33	transcription from RNA polymerase I promoter
6	2e−03	3 / 33	transcription initiation from RNA polymerase I promoter
7	2e−03	3 / 34	histone acetylation
8	3e−03	2 / 11	positive regulation of protein sumoylation
9	5e−03	2 / 14	negative regulation of endoplasmic reticulum stress−induced intrinsic apoptoti
10	7e−03	6 / 213	chromatin organization
11	8e−03	2 / 17	positive regulation of intracellular protein transport
12	9e−03	2 / 18	nucleotide−excision repair, DNA damage removal
13	1e−02	2 / 19	positive regulation of filopodium assembly
14	1e−02	2 / 21	melanosome transport
15	2e−02	2 / 24	response to starvation
16	2e−02	2 / 25	regulation of mitochondrial membrane potential
17	2e−02	2 / 27	regulation of endocytosis
18	2e−02	6 / 276	nucleobase−containing compound catabolic process
19	3e−02	2 / 31	regulation of protein stability
20	3e−02	2 / 34	regulation of actin cytoskeleton organization

CC

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	DNA−directed RNA polymerase I complex
2	0.042	18 / 1468	mitochondrion
3	0.069	2 / 54	intermediate filament cytoskeleton
4	0.077	1 / 10	WASH complex
5	0.080	6 / 377	centrosome
6	0.090	2 / 63	mitochondrial intermembrane space
7	0.091	1 / 12	holo TFIIH complex
8	0.091	1 / 12	mitochondrial respiratory chain
9	0.091	1 / 12	U4/U6 x U5 tri−snRNP complex
10	0.099	1 / 13	COPI vesicle coat
11	0.099	1 / 13	filopodium membrane
12	0.099	1 / 13	TCTN−B9D complex
13	0.106	1 / 14	Cul4−RING E3 ubiquitin ligase complex
14	0.106	1 / 14	exocyst
15	0.113	1 / 15	BLOC−1 complex
16	0.113	1 / 15	centriolar satellite
17	0.120	1 / 16	lamellipodium membrane
18	0.121	72 / 8205	cytoplasm
19	0.127	1 / 17	integral component of mitochondrial outer membrane
20	0.127	1 / 17	transcriptionally active chromatin

Disease

Rank	p−value	#in/all	Geneset
1	0.9	2 / 435	GUDJ_psoriasis up
2	0.9	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
2	0.1	3 / 146	HALLMARK_DNA_REPAIR
3	0.2	2 / 93	HALLMARK_PEROXISOME
4	0.2	3 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	0.2	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	0.4	2 / 167	HALLMARK_APICAL_JUNCTION
7	0.5	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.5	1 / 91	HALLMARK_PROTEIN_SECRETION
9	0.5	1 / 94	HALLMARK_ANDROGEN_RESPONSE
10	0.5	1 / 95	HALLMARK_SPERMATOGENESIS
11	0.5	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.6	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
13	0.7	1 / 146	HALLMARK_UV_RESPONSE_UP
14	0.7	1 / 162	HALLMARK_COMPLEMENT
15	0.7	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	0.7	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
17	0.7	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
18	0.8	1 / 174	HALLMARK_HEME_METABOLISM
19	0.8	1 / 183	HALLMARK_GLYCOLYSIS
20	0.8	1 / 196	HALLMARK_MTORC1_SIGNALING

MF

Rank	p−value	#in/all	Geneset
1	0.004	2 / 12	RNA polymerase I activity
2	0.009	3 / 54	damaged DNA binding
3	0.018	2 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductic
4	0.025	3 / 79	protein transporter activity
5	0.035	2 / 37	DNA−directed RNA polymerase activity
6	0.035	2 / 37	histone acetyltransferase activity
7	0.040	3 / 95	hydrolase activity, acting on glycosyl bonds
8	0.052	2 / 46	methylated histone binding
9	0.077	1 / 10	cAMP response element binding protein binding
10	0.077	1 / 10	semaphorin receptor binding
11	0.084	1 / 11	acetyltransferase activity
12	0.084	1 / 11	SUMO transferase activity
13	0.091	1 / 12	lysophospholipase activity
14	0.091	1 / 12	Notch binding
15	0.099	1 / 13	NAD+ binding
16	0.099	1 / 13	Ral GTPase binding
17	0.099	8 / 592	oxidoreductase activity
18	0.104	6 / 405	ligase activity
19	0.106	1 / 14	endoribonuclease activity
20	0.109	2 / 71	single−stranded DNA binding

TF

Rank	p−value	#in/all	Geneset
1	5e−04	23 / 1383	ICGC_Six5_targets
2	6e−03	45 / 4032	ICGC_Creb1_targets
3	8e−03	20 / 1418	ICGC_Ets1_targets
4	1e−02	49 / 4689	ICGC_Taf1_targets
5	2e−02	18 / 1314	ICGC_Usf1_targets
6	2e−02	26 / 2136	ICGC_GabpPcr2_targets
7	2e−02	46 / 4414	ICGC_Bclaf101388_targets
8	2e−02	31 / 2714	ICGC_Irf4_targets
9	3e−02	54 / 5495	ICGC_Yy1_targets
10	4e−02	53 / 5408	ICGC_Pou2_targets
11	4e−02	47 / 4706	ICGC_Sp1_targets
12	4e−02	46 / 4617	ICGC_Tcf12_targets
13	4e−02	48 / 4879	ICGC_Pmlsc71910_targets
14	5e−02	52 / 5374	ICGC_Pax5_targets
15	6e−02	26 / 2416	ICGC_Bcl3_targets
16	7e−02	37 / 3700	ICGC_Nfatc1_targets
17	7e−02	47 / 4909	ICGC_Stat5_targets
18	7e−02	39 / 3966	ICGC_Pu1_targets
19	8e−02	45 / 4682	ICGC_Pol24_targets
20	8e−02	15 / 1266	ICGC_NrsfPcr1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	10 / 1115	LU_BPDE 1n DN
2	1.0	21 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	4e−08	101 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−05	93 / 9013	Overlap_fetal_midbrain_K9K27me3
3	4e−05	69 / 5940	Overlap_fetal_midbrain_HetRpts
4	2e−02	83 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	4e−02	33 / 3081	Mid_Frontal_Lobe_ZNF
6	7e−02	84 / 9528	Overlap_fetal_midbrain_Quies
7	7e−02	26 / 2462	Mid_Frontal_Lobe_HetRpts
8	1e−01	15 / 1333	Fetal_ReprPCWk
9	2e−01	8 / 656	Overlap_fetal_midbrain_EnhP
10	2e−01	9 / 769	Overlap_fetal_midbrain_ZNF
11	2e−01	11 / 989	Mid_Frontal_Lobe_Quies
12	2e−01	4 / 304	Fetal_Het
13	3e−01	8 / 765	Mid_Frontal_Lobe_Het
14	3e−01	10 / 1050	Fetal_EnhP
15	4e−01	2 / 158	Overlap_fetal_midbrain_Het
16	4e−01	11 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	4e−01	7 / 786	Fetal_EnhG
18	5e−01	3 / 349	Fetal_ZNF
19	6e−01	15 / 1907	Fetal_TxTrans
20	6e−01	7 / 884	Overlap_fetal_midbrain_EnhG

Chr

Rank	p−value	#in/all	Geneset
1	0.003	14 / 775	Chr 12
2	0.047	10 / 687	Chr 6
3	0.050	18 / 1500	Chr 1
4	0.284	6 / 558	Chr 4
5	0.346	3 / 262	Chr 13
6	0.447	5 / 551	Chr X
7	0.448	5 / 552	Chr 10
8	0.469	6 / 689	Chr 7
9	0.485	5 / 576	Chr 9
10	0.505	7 / 840	Chr 17
11	0.508	4 / 465	Chr 15
12	0.537	8 / 993	Chr 2
13	0.662	6 / 838	Chr 3
14	0.702	1 / 151	Chr 21
15	0.726	7 / 1037	Chr 19
16	0.749	2 / 335	Chr 22
17	0.764	4 / 649	Chr 16
18	0.886	2 / 462	Chr 14
19	0.919	3 / 696	Chr 5
20	0.960	1 / 398	Chr 20

Glio

Rank	p−value	#in/all	Geneset
1	0.09	2 / 63	Stuehler_Proteins_up_in_STS
2	0.12	2 / 75	Weller_LGG_A_vs_O_DOWN
3	0.12	1 / 16	VERHAAK_NL subtype
4	0.15	5 / 356	Down_a
5	0.16	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
6	0.24	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.36	8 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.40	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	0.41	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
10	0.42	1 / 68	GIEZELT_GBM_WT_down_VS_mut
11	0.42	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.42	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
13	0.45	1 / 74	WIRTH_Normal Brain
14	0.45	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
15	0.55	1 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
16	0.72	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
17	0.93	1 / 332	Up
18	0.95	1 / 365	Down_b
19	1.00	0 / 15	VERHAAK_CL subtype
20	1.00	0 / 15	VERHAAK_MES subtype

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	5 / 166	hsa−miR−580
2	0.01	4 / 109	hsa−miR−499−5p
3	0.02	7 / 327	hsa−miR−590−3p
4	0.02	4 / 132	hsa−miR−194
5	0.03	2 / 33	hsa−miR−1274b
6	0.03	2 / 34	hsa−miR−517b
7	0.03	2 / 35	hsa−miR−1287
8	0.03	5 / 224	hsa−miR−181b
9	0.03	3 / 89	hsa−miR−10b
10	0.03	2 / 37	hsa−miR−1274a
11	0.04	2 / 38	hsa−miR−1258
12	0.04	2 / 39	hsa−miR−516a−3p
13	0.04	3 / 95	hsa−miR−888
14	0.04	3 / 97	hsa−miR−1259
15	0.05	1 / 6	hsa−miR−886−5p
16	0.05	1 / 7	hsa−miR−611
17	0.06	6 / 343	hsa−miR−548b−5p
18	0.06	3 / 110	hsa−miR−491−3p
19	0.06	2 / 49	hsa−miR−208b
20	0.06	3 / 112	hsa−miR−875−3p

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 16	VAQUERIZAS_Adrenal gland
2	0.2	1 / 23	VAQUERIZAS_Adrenal cortex
3	0.3	1 / 38	VAQUERIZAS_Testis
4	0.3	2 / 143	VAQUERIZAS_General
5	1.0	0 / 36	VAQUERIZAS_Fetal brain
6	1.0	0 / 41	VAQUERIZAS_Placenta
7	1.0	0 / 26	VAQUERIZAS_Liver
8	1.0	0 / 33	VAQUERIZAS_Prostate
9	1.0	0 / 29	VAQUERIZAS_Smooth muscle
10	1.0	0 / 45	VAQUERIZAS_Uterus
11	1.0	0 / 9	VAQUERIZAS_Kidney
12	1.0	0 / 23	VAQUERIZAS_Spinal cord
13	1.0	0 / 38	VAQUERIZAS_Whole brain
14	1.0	0 / 37	VAQUERIZAS_Thymus
15	1.0	0 / 40	VAQUERIZAS_Thyroid
16	1.0	0 / 59	VAQUERIZAS_Whole blood
17	1.0	0 / 7	VAQUERIZAS_Appendix
18	1.0	0 / 29	VAQUERIZAS_Fetal lung
19	1.0	0 / 58	VAQUERIZAS_Lung
20	1.0	0 / 16	VAQUERIZAS_Pancreas

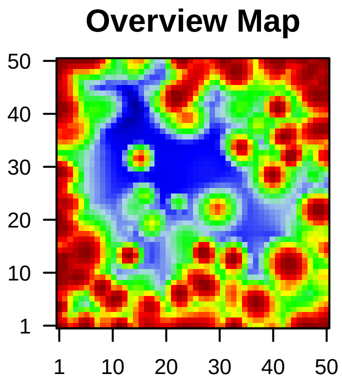
Overexpression Spots

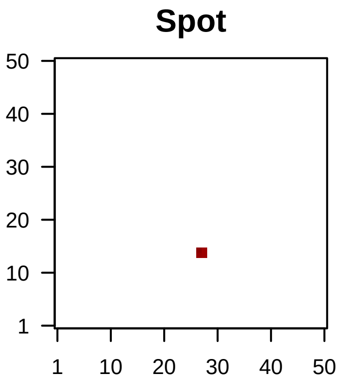
Spot Summary: K1

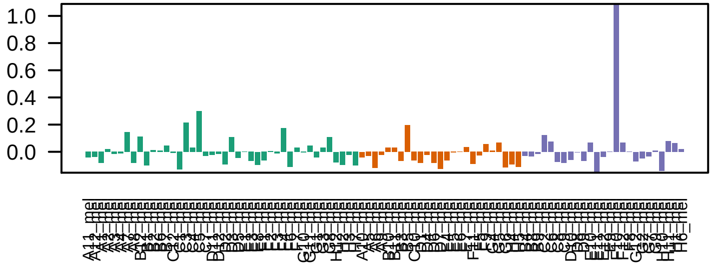
metagenes = 4
genes = 26

<r> metagenes = 0.99
<r> genes = 0.23
beta: r2= 0.4 / log p= −10.74

samples with spot = 4 (4.3 %)
MSC1 : 2 (4.8 %)
MSC2 : 1 (4 %)
MSC3 : 1 (4 %)





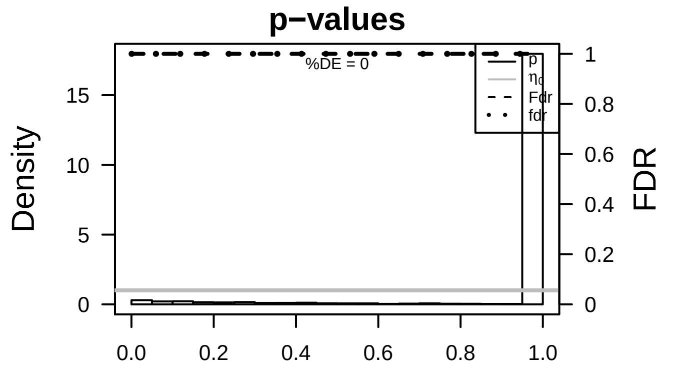


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TMEM135	2.05	−0.37	0.32	TMEM135	transmembrane protein 135 [Source:HGNC Symbol;Acc:HGN
2	GDA	1.99	−0.03	0.68	GDA	guanine deaminase [Source:HGNC Symbol;Acc:HGNC:4212
3	OR52H1	1.86	−0.02	0.69	OR52H1	olfactory receptor, family 52, subfamily H, member 1 [Source:
4	CELF4	1.57	−0.07	0.37	CELF4	CUGBP, Elav−like family member 4 [Source:HGNC Symbol;A
5	RRP9	1.51	−0.53	0.26	RRP9	ribosomal RNA processing 9, small subunit (SSU) processom
6	LIMK2	1.5	−0.23	0.31	LIMK2	LIM domain kinase 2 [Source:HGNC Symbol;Acc:HGNC:661
7	FAM212A	1.5	−0.03	0.53	FAM212A	family with sequence similarity 212, member A [Source:HGN
8	NID2	1.47	−0.09	0.34	NID2	nidogen 2 (osteonidogen) [Source:HGNC Symbol;Acc:HGNC
9	ZNF41	1.45	−0.16	0.25	ZNF41	zinc finger protein 41 [Source:HGNC Symbol;Acc:HGNC:131
10	EML2	1.41	−0.1	0.42	EML2	echinoderm microtubule associated protein like 2 [Source:HG
11	CDON	1.39	−0.12	0.45	CDON	cell adhesion associated, oncogene regulated [Source:HGNC
12	CDRT4	1.38	−0.1	0.5	CDRT4	CMT1A duplicated region transcript 4 [Source:HGNC Symbol
13	KIAA1549L	1.31	−0.21	0.33	KIAA1549L	KIAA1549−like [Source:HGNC Symbol;Acc:HGNC:24836]
14	SLC51A	1.3	−0.09	0.31	SLC51A	solute carrier family 51, alpha subunit [Source:HGNC Symbol
15	ARG1	1.25	−0.08	0.65	ARG1	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]
16	C8orf37	1.25	−0.11	0.43	C8orf37	chromosome 8 open reading frame 37 [Source:HGNC Symbo
17	GCHFR	1.25	−0.09	0.33	GCHFR	GTP cyclohydrolase I feedback regulator [Source:HGNC Sym
18	CLASP2	1.2	−0.93	0.3	CLASP2	cytoplasmic linker associated protein 2 [Source:HGNC Symb
19	PTK7	1.08	−0.1	0.42	PTK7	protein tyrosine kinase 7 (inactive) [Source:HGNC Symbol;Ac
20	TLR5	1.06	−0.04	0.46	TLR5	toll−like receptor 5 [Source:HGNC Symbol;Acc:HGNC:11851]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−04	9 / 1308	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
2	3e−03	2 / 50	GSEA	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
3	4e−03	4 / 371	Colon	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
4	4e−03	4 / 391	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2
5	5e−03	2 / 59	GSEA	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
6	5e−03	2 / 61	GSEA	COATES_MACROPHAGE_M1_VS_M2_DN
7	6e−03	2 / 66	GSEA	LINDVALL_IMMORTALIZED_BY_TERT_DN
8	8e−03	2 / 75	BP	cellular response to lipopolysaccharide
9	8e−03	11 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
10	9e−03	2 / 83	GSEA	WESTON_VEGFA_TARGETS
11	1e−02	1 / 6	GSEA	ZIRN_TRETINOIN_RESPONSE_WT1_DN
12	1e−02	2 / 94	MF	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
13	1e−02	3 / 291	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
14	2e−02	1 / 9	GSEA	REACTOME_PURINE_CATABOLISM
15	2e−02	1 / 10	BP	alternative mRNA splicing, via spliceosome
16	2e−02	1 / 10	BP	establishment of planar polarity
17	2e−02	1 / 10	MF	microtubule plus−end binding
18	2e−02	1 / 10	BP	nitrogen cycle metabolic process
19	2e−02	1 / 10	BP	purine nucleotide catabolic process
20	2e−02	1 / 10	BP	response to vitamin E
21	2e−02	1 / 10	MF	ubiquitin−ubiquitin ligase activity
22	2e−02	1 / 10	BP	urea cycle
23	2e−02	3 / 317	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38
24	2e−02	1 / 11	BP	activation of innate immune response
25	2e−02	1 / 11	BP	cell fate specification
26	2e−02	1 / 11	BP	planar cell polarity pathway involved in neural tube closure
27	2e−02	1 / 11	BP	positive regulation of mRNA splicing, via spliceosome
28	2e−02	1 / 11	BP	response to amine
29	2e−02	1 / 11	BP	response to methylmercury
30	2e−02	1 / 11	GSEA	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLIN
31	2e−02	1 / 11	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G12_DN
32	2e−02	2 / 123	MF	nucleotidyltransferase activity
33	2e−02	1 / 12	BP	cyclic nucleotide biosynthetic process
34	2e−02	1 / 12	MF	MAP kinase tyrosine/serine/threonine phosphatase activity
35	2e−02	1 / 12	BP	microtubule anchoring
36	2e−02	1 / 12	BP	regulation of microtubule−based process
37	2e−02	1 / 12	BP	striated muscle cell differentiation
38	2e−02	1 / 12	GSEA	NIKOLSKY_BREAST_CANCER_14Q22_AMPLICON
39	2e−02	3 / 342	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
40	2e−02	1 / 13	BP	embryonic morphogenesis



Aging

Rank	p−value	#in/all	Geneset
1	0.08	1 / 38	TESCHENDORFF_age_hypermethylated
2	1.00	0 / 100	HORVATH_aging_genes meth DOWN
3	1.00	0 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.008	2 / 75	cellular response to lipopolysaccharide
2	0.017	1 / 10	alternative mRNA splicing, via spliceosome
3	0.017	1 / 10	establishment of planar polarity
4	0.017	1 / 10	nitrogen cycle metabolic process
5	0.017	1 / 10	purine nucleotide catabolic process
6	0.017	1 / 10	response to vitamin E
7	0.017	1 / 10	urea cycle
8	0.019	1 / 11	activation of innate immune response
9	0.019	1 / 11	cell fate specification
10	0.019	1 / 11	planar cell polarity pathway involved in neural tube closure
11	0.019	1 / 11	positive regulation of mRNA splicing, via spliceosome
12	0.019	1 / 11	response to amine
13	0.019	1 / 11	response to methylmercury
14	0.021	1 / 12	cyclic nucleotide biosynthetic process
15	0.021	1 / 12	microtubule anchoring
16	0.021	1 / 12	regulation of microtubule−based process
17	0.021	1 / 12	striated muscle cell differentiation
18	0.023	1 / 13	embryonic morphogenesis
19	0.023	1 / 13	microtubule nucleation
20	0.023	1 / 13	nitric oxide biosynthetic process

Brain

Rank	p−value	#in/all	Geneset
1	0.008	11 / 2972	Mid_Frontal_Lobe_ReprPC
2	0.029	8 / 2185	Fetal_TssA
3	0.055	4 / 831	Fetal_HetRpts
4	0.060	5 / 1236	Mid_Frontal_Lobe_ReprPCWk
5	0.107	6 / 1907	Fetal_TxTrans
6	0.112	4 / 1065	Overlap_fetal_midbrain_Enh
7	0.116	6 / 1949	Fetal_TssF
8	0.128	5 / 1548	Mid_Frontal_Lobe_K9K27me3
9	0.200	3 / 884	Overlap_fetal_midbrain_EnhG
10	0.260	3 / 1013	Fetal_TssP
11	0.278	3 / 1050	Fetal_EnhP
12	0.377	18 / 9528	Overlap_fetal_midbrain_Quies
13	0.394	17 / 9020	Overlap_fetal_midbrain_ReprPCWk
14	0.437	5 / 2462	Mid_Frontal_Lobe_HetRpts
15	0.462	1 / 349	Fetal_ZNF
16	0.493	1 / 383	Fetal_Tx
17	0.595	2 / 1122	Fetal_K9K27me3
18	0.635	1 / 564	Mid_Frontal_Lobe_EnhP
19	0.636	2 / 1207	Overlap_fetal_midbrain_TssF
20	0.642	1 / 574	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	2 / 489	Lembcke_Normal vs Adenoma
2	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
3	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	1.0	0 / 12	LIU_BREAST_CANCER
7	1.0	0 / 14	LIU_COMMON_CANCER_GENES
8	1.0	0 / 14	LIU_LIVER_CANCER
9	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
10	1.0	0 / 12	LIU_PROSTATE_CANCER_UP
11	1.0	0 / 15	WANG_ER_UP
12	1.0	0 / 5	WANG_ER_DN
13	1.0	0 / 16	WOLFER_overlap genes
14	1.0	0 / 12	BEN−PORATH_DN
15	1.0	0 / 13	BEN−PORATH_UP
16	1.0	0 / 15	GENTLES_modul1
17	1.0	0 / 16	GENTLES_modul2
18	1.0	0 / 10	GENTLES_modul3
19	1.0	0 / 15	GENTLES_modul4
20	1.0	0 / 10	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	0.03	2 / 159	extracellular matrix
2	0.05	1 / 30	small−subunit processome
3	0.05	1 / 31	microtubule associated complex
4	0.06	1 / 35	mitotic spindle
5	0.06	1 / 36	nuclear body
6	0.06	1 / 38	cis−Golgi network
7	0.07	2 / 250	microtubule
8	0.07	1 / 43	cytoplasmic microtubule
9	0.10	1 / 63	mitochondrial intermembrane space
10	0.11	1 / 64	ruffle membrane
11	0.12	1 / 73	basement membrane
12	0.12	1 / 75	condensed chromosome kinetochore
13	0.13	8 / 2984	integral component of membrane
14	0.15	1 / 94	melanosome
15	0.16	1 / 99	cell cortex
16	0.17	1 / 106	trans−Golgi network
17	0.17	1 / 109	peroxisome
18	0.19	1 / 120	mitochondrial outer membrane
19	0.22	1 / 138	cell−cell junction
20	0.22	1 / 144	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	0.05	4 / 801	Chr 11
2	0.06	4 / 838	Chr 3
3	0.12	2 / 335	Chr 22
4	0.12	3 / 687	Chr 6
5	0.32	1 / 221	Chr 18
6	0.50	3 / 1500	Chr 1
7	0.51	1 / 398	Chr 20
8	0.56	1 / 462	Chr 14
9	0.56	1 / 465	Chr 15
10	0.57	1 / 469	Chr 8
11	0.63	1 / 551	Chr X
12	0.64	1 / 576	Chr 9
13	0.71	1 / 689	Chr 7
14	0.78	1 / 840	Chr 17
15	0.85	1 / 1037	Chr 19
16	1.00	0 / 552	Chr 10
17	1.00	0 / 775	Chr 12
18	1.00	0 / 262	Chr 13
19	1.00	0 / 649	Chr 16
20	1.00	0 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.004	4 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
2	0.073	1 / 43	Marisa_CRC−cluster−f
3	0.164	1 / 102	Marisa_CRC−cluster−d
4	0.171	2 / 427	Quies2_Colon
5	0.188	13 / 5880	TssD2_Colon
6	0.244	17 / 8415	Quies3_Colon
7	0.263	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
8	0.264	2 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	0.277	2 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
10	0.292	3 / 1079	ZNF_Colon
11	0.296	1 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
12	0.315	2 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	0.330	6 / 2698	EnhA_Colon
14	0.357	1 / 250	K9K27me3_Colon
15	0.379	7 / 3383	EnhWk2_Colon
16	0.392	1 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
17	0.409	3 / 1317	EnhP_Colon
18	0.415	10 / 5155	EnhWk1_Colon
19	0.426	4 / 1889	ReprPCWk_Colon
20	0.432	1 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.2	2 / 435	GUDJ_psoriasis up
2	0.4	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	3 / 365	Down_b
2	0.03	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
3	0.04	1 / 23	WIRTH_PN subtype
4	0.05	1 / 32	Donson−innate immunity−associated with LTS in HGA
5	0.06	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
6	0.10	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	0.12	1 / 71	Weller_LGG_A_vs_O_UP
8	0.16	1 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
9	0.24	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	0.28	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
11	1.00	0 / 15	VERHAAK_CL subtype
12	1.00	0 / 15	VERHAAK_MES subtype
13	1.00	0 / 16	VERHAAK_NL subtype
14	1.00	0 / 14	VERHAAK_PN subtype
15	1.00	0 / 74	WIRTH_Normal Brain
16	1.00	0 / 9	VERHAAK_Brain
17	1.00	0 / 8	VERHAAK_PN_Brain
18	1.00	0 / 11	Martinez_Glio_hypermeth
19	1.00	0 / 3	Martinez_Glio_hypometh
20	1.00	0 / 2	laffaire_hypometh_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
2	3e−03	2 / 50	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
3	4e−03	4 / 391	MEISSNER_NPC_HCP_WITH_H3K4ME2
4	5e−03	2 / 59	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
5	5e−03	2 / 61	COATES_MACROPHAGE_M1_VS_M2_DN
6	6e−03	2 / 66	LINDVALL_IMMORTALIZED_BY_TERT_DN
7	9e−03	2 / 83	WESTON_VEGFA_TARGETS
8	1e−02	1 / 6	ZIRN_TRETINOIN_RESPONSE_WT1_DN
9	1e−02	3 / 291	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
10	2e−02	1 / 9	REACTOME_PURINE_CATABOLISM
11	2e−02	3 / 317	PHONG_TNF_RESPONSE_NOT_VIA_P38
12	2e−02	1 / 11	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLING_S
13	2e−02	1 / 11	BOYAULT_LIVER_CANCER_SUBCLASS_G12_DN
14	2e−02	1 / 12	NIKOLSKY_BREAST_CANCER_14Q22_AMPLICON
15	2e−02	3 / 342	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
16	2e−02	1 / 13	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
17	2e−02	3 / 354	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
18	2e−02	2 / 139	RODWELL_AGING_KIDNEY_NO_BLOOD_DN
19	3e−02	1 / 15	ZHAN_MULTIPLE_MYELOMA_SPIKED
20	3e−02	1 / 15	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP

HM

Rank	p−value	#in/all	Geneset
1	0.04	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
2	0.10	1 / 57	HALLMARK_MYC_TARGETS_V2
3	0.17	1 / 107	HALLMARK_COAGULATION
4	0.17	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	0.21	1 / 137	HALLMARK_UV_RESPONSE_DN
6	0.23	1 / 148	HALLMARK_KRAS_SIGNALING_UP
7	0.26	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	0.26	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.28	1 / 188	HALLMARK_MYC_TARGETS_V1
10	0.29	1 / 196	HALLMARK_MTORC1_SIGNALING
11	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	1.00	0 / 176	HALLMARK_HYPOXIA
13	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	1.00	0 / 195	HALLMARK_MITOTIC_SPINDLE
15	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
16	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
17	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
18	1.00	0 / 146	HALLMARK_DNA_REPAIR
19	1.00	0 / 196	HALLMARK_G2M_CHECKPOINT
20	1.00	0 / 140	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.03	1 / 15	DAVE_Immune response 2
2	0.09	2 / 280	SPANG_CD40 6hrs UP
3	0.23	8 / 3396	HOPP_Repressed
4	0.23	15 / 7209	HOPP_Weak_promoter
5	0.27	12 / 5693	HOPP_Weak_enhancer
6	0.34	5 / 2188	HOPP_Poised_promoter
7	0.38	1 / 268	SPANG_IL21 UP
8	0.68	4 / 2563	HOPP_Heterochrom
9	0.68	9 / 5538	HOPP_Weak_txn
10	0.77	3 / 2211	HOPP_Repetitive
11	0.78	10 / 6564	HOPP_Strong_enhancer
12	0.85	10 / 6929	HOPP_Txn_elongation
13	0.86	7 / 5184	HOPP_Txn_transition
14	0.86	11 / 7592	HOPP_Active_promoter
15	0.89	1 / 1218	SPANG_BCR UP
16	1.00	0 / 13	BENTINK_mBL UP
17	1.00	0 / 12	BENTINK_mBL DOWN
18	1.00	0 / 129	DAVE_BL−vs−DLBCL
19	1.00	0 / 10	DAVE_BL_DN
20	1.00	0 / 16	DAVE_BL_Inter

MF

Rank	p−value	#in/all	Geneset
1	0.01	2 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
2	0.02	1 / 10	microtubule plus−end binding
3	0.02	1 / 10	ubiquitin−ubiquitin ligase activity
4	0.02	2 / 123	nucleotidyltransferase activity
5	0.02	1 / 12	MAP kinase tyrosine/serine/threonine phosphatase activity
6	0.03	1 / 15	amino acid binding
7	0.03	1 / 17	GTP−dependent protein binding
8	0.03	2 / 156	microtubule binding
9	0.04	1 / 24	snoRNA binding
10	0.04	1 / 26	enzyme inhibitor activity
11	0.04	1 / 26	olfactory receptor activity
12	0.06	1 / 36	tubulin binding
13	0.06	1 / 37	DNA−directed RNA polymerase activity
14	0.08	1 / 45	protein tyrosine/serine/threonine phosphatase activity
15	0.08	1 / 46	manganese ion binding
16	0.08	2 / 265	hydrolase activity
17	0.08	1 / 49	collagen binding
18	0.11	2 / 325	protein serine/threonine kinase activity
19	0.14	2 / 373	protein heterodimerization activity
20	0.14	1 / 85	transmembrane signaling receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	2 / 181	hsa−miR−196b
2	0.05	2 / 209	hsa−miR−196a
3	0.07	1 / 43	hsa−miR−423−3p
4	0.07	1 / 44	hsa−miR−885−3p
5	0.10	1 / 61	hsa−miR−612
6	0.10	1 / 63	hsa−miR−1285
7	0.11	1 / 65	hsa−miR−326
8	0.12	1 / 70	hsa−miR−876−3p
9	0.12	1 / 70	hsa−miR−489
10	0.14	1 / 83	hsa−miR−576−5p
11	0.15	1 / 90	hsa−miR−216b
12	0.15	1 / 93	hsa−miR−299−3p
13	0.15	1 / 95	hsa−miR−125a−3p
14	0.16	1 / 97	hsa−miR−544
15	0.17	1 / 107	hsa−miR−501−5p
16	0.18	1 / 116	hsa−miR−376c
17	0.19	1 / 118	hsa−miR−509−3p
18	0.19	1 / 120	hsa−miR−579
19	0.20	1 / 129	hsa−miR−576−3p
20	0.21	1 / 133	hsa−miR−485−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	5 / 1139	HEBENSTREIT_low expression TF
2	0.28	2 / 595	ICGC_NrsfPcr2_targets
3	0.34	3 / 1171	KIM_MYC targets
4	0.53	5 / 2714	ICGC_Irf4_targets
5	0.56	7 / 3966	ICGC_Pu1_targets
6	0.57	5 / 2836	ICGC_BatfPcr1_targets
7	0.60	5 / 2927	ICGC_Rad21_targets
8	0.65	3 / 1872	ICGC_Mef2_targets
9	0.66	2 / 1266	ICGC_NrsfPcr1_targets
10	0.67	7 / 4314	ICGC_Ebfsc137065_targets
11	0.71	2 / 1383	ICGC_Six5_targets
12	0.75	6 / 4054	ICGC_Egr1_targets
13	0.76	9 / 5890	ICGC_Elf1_targets
14	0.79	7 / 4829	ICGC_Nficsc81335_targets
15	0.80	7 / 4879	ICGC_Pmlsc71910_targets
16	0.81	9 / 6114	ICGC_Runx3_targets
17	0.82	2 / 1701	HEBENSTREIT_high expression TF
18	0.82	3 / 2416	ICGC_Bcl3_targets
19	0.82	6 / 4385	ICGC_Atf2_targets
20	0.87	6 / 4617	ICGC_Tcf12_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 350	WIRTH_Nervous System
2	0.33	1 / 225	PALMER_Granulocytes signature up
3	1.00	0 / 32	WIRTH_Pancreas
4	1.00	0 / 350	WIRTH_Immune system
5	1.00	0 / 11	WIRTH_Sec. lymphoid organs
6	1.00	0 / 11	WIRTH_Prim. lymphoid organs
7	1.00	0 / 13	WIRTH_B−cells
8	1.00	0 / 8	WIRTH_Tonsil
9	1.00	0 / 12	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 5	WIRTH_Bone marrow
12	1.00	0 / 11	WIRTH_Globus pallidus
13	1.00	0 / 14	WIRTH_Telencephalon
14	1.00	0 / 11	WIRTH_Cortex cerebri
15	1.00	0 / 10	WIRTH_Hippocampus
16	1.00	0 / 10	WIRTH_Thalamus
17	1.00	0 / 12	WIRTH_Cerebellum
18	1.00	0 / 107	WIRTH_Testis
19	1.00	0 / 41	WIRTH_Homeostasis
20	1.00	0 / 46	WIRTH_Liver

Toxic

Rank	p−value	#in/all	Geneset
1	0.04	11 / 3682	LU_BPDE 0.005 DN
2	0.87	1 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

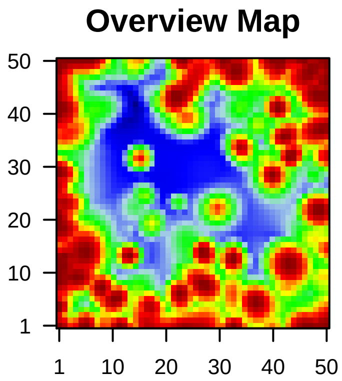
Overexpression Spots

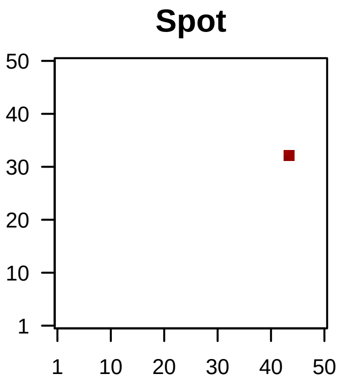
Spot Summary: L1

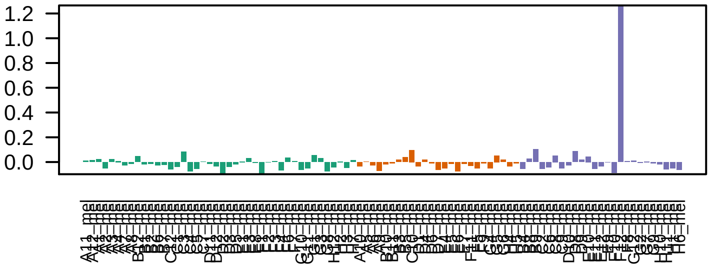
metagenes = 4
genes = 78

<r> metagenes = 0.99
<r> genes = 0.39
beta: r2= 0.4 / log p= −10.87

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)





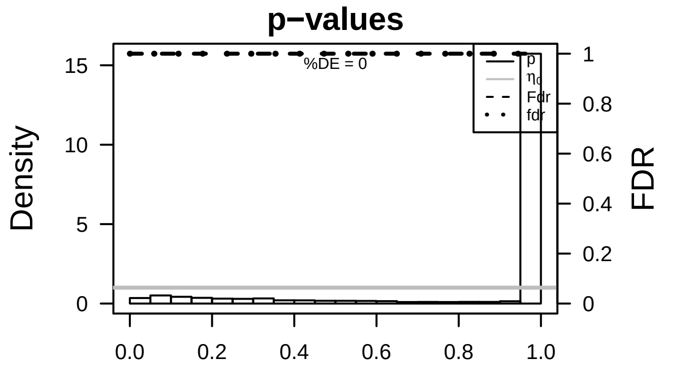


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	GSG1L	1.94	−0.03	0.75	GSG1L	GSG1−like [Source:HGNC Symbol;Acc:HGNC:28283]
2	CD33	1.91	−0.17	0.46	CD33	CD33 molecule [Source:HGNC Symbol;Acc:HGNC:1659]
3	OR10A2	1.85	−0.02	0.78	OR10A2	olfactory receptor, family 10, subfamily A, member 2 [Source:
4	ALOX12B	1.84	−0.08	0.66	ALOX12B	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
5	KLRG1	1.83	−0.25	0.3	KLRG1	killer cell lectin−like receptor subfamily G, member 1 [Source:
6	THSD7A	1.8	−0.15	0.46	THSD7A	thrombospondin, type I, domain containing 7A [Source:HGNC
7	PHF11	1.78	−0.21	0.47	PHF11	PHD finger protein 11 [Source:HGNC Symbol;Acc:HGNC:17
8	TOX	1.77	−0.11	0.43	TOX	thymocyte selection−associated high mobility group box [Sou
9	KLK6	1.74	−0.04	0.58	KLK6	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:HG
10	SART1	1.71	−0.29	0.38	SART1	squamous cell carcinoma antigen recognized by T cells [Sour
11	HIST1H4D	1.69	−0.02	0.77	HIST1H4D	histone cluster 1, H4d [Source:HGNC Symbol;Acc:HGNC:47
12	LARGE	1.67	−0.23	0.26	LARGE	like−glycosyltransferase [Source:HGNC Symbol;Acc:HGNC:6
13	DNER	1.67	−0.06	0.59	DNER	delta/notch−like EGF repeat containing [Source:HGNC Symb
14	ZNF69	1.65	−0.19	0.37	ZNF69	zinc finger protein 69 [Source:HGNC Symbol;Acc:HGNC:131
15	MX2	1.65	−0.04	0.53	MX2	MX dynamin−like GTPase 2 [Source:HGNC Symbol;Acc:HGN
16	MYBPHL	1.64	−0.03	0.64	MYBPHL	myosin binding protein H−like [Source:HGNC Symbol;Acc:HG
17	C1orf61	1.62	−0.08	0.5	C1orf61	chromosome 1 open reading frame 61 [Source:HGNC Symbo
18	RBKS	1.58	−0.08	0.32	RBKS	ribokinase [Source:HGNC Symbol;Acc:HGNC:30325]
19	LGI1	1.57	−0.02	0.76	LGI1	leucine−rich, glioma inactivated 1 [Source:HGNC Symbol;Acc
20	AKAP5	1.56	−0.12	0.43	AKAP5	A kinase (PRKA) anchor protein 5 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−05	5 / 72	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_A
2	5e−04	8 / 350	Tissu	WIRTH_Nervous System
3	7e−04	2 / 8	GSEA	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
4	1e−03	2 / 9	GSEA	KORKOLA_EMBRYONAL_CARCINOMA
5	1e−03	11 / 720	GSEA	BENPORATH_ES_WITH_H3K27ME3
6	2e−03	7 / 338	BP	G−protein coupled receptor signaling pathway
7	2e−03	14 / 1139	TF	HEBENSTREIT_low expression TF
8	3e−03	3 / 52	MF	hormone activity
9	3e−03	6 / 269	BP	extracellular matrix organization
10	3e−03	2 / 16	MF	acetylglucosaminyltransferase activity
11	3e−03	2 / 16	BP	ceramide biosynthetic process
12	3e−03	3 / 56	GSEA	WONG_ENDMETRIUM_CANCER_DN
13	3e−03	3 / 56	GSEA	FURUKAWA_DUSP6_TARGETS_PCI35_UP
14	4e−03	14 / 1207	Brain	Overlap_fetal_midbrain_TssF
15	4e−03	4 / 124	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
16	4e−03	4 / 125	BP	growth
17	4e−03	10 / 724	GSEA	BENPORATH_EED_TARGETS
18	5e−03	2 / 20	GSEA	PID_GLYPICAN_1PATHWAY
19	5e−03	2 / 20	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
20	5e−03	6 / 300	GSEA	REACTOME_GPCR_DOWNSTREAM_SIGNALING
21	5e−03	3 / 67	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
22	6e−03	5 / 217	MF	G−protein coupled receptor activity
23	6e−03	7 / 410	GSEA	LIM_MAMMARY_STEM_CELL_UP
24	6e−03	4 / 138	GSEA	DURAND_STROMA_NS_UP
25	6e−03	12 / 1013	Brain	Fetal_TssP
26	6e−03	2 / 23	BP	eye development
27	6e−03	2 / 23	GSEA	REACTOME_OLFACTORY_SIGNALING_PATHWAY
28	7e−03	8 / 530	MF	calcium ion binding
29	7e−03	2 / 24	GSEA	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN
30	7e−03	4 / 147	GSEA	CAIRO_LIVER_DEVELOPMENT_UP
31	8e−03	4 / 150	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
32	8e−03	18 / 1889	Colon	ReprPCWk_Colon
33	8e−03	2 / 26	BP	detection of chemical stimulus involved in sensory perception of smell
34	8e−03	2 / 26	BP	excretion
35	8e−03	2 / 26	MF	olfactory receptor activity
36	9e−03	25 / 2984	CC	integral component of membrane
37	9e−03	6 / 342	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
38	9e−03	4 / 157	GSEA	OKUMURA_INFLAMMATORY_RESPONSE_LPS
39	9e−03	2 / 28	BP	sperm motility
40	9e−03	2 / 28	GSEA	NEWMAN_ERCC6_TARGETS_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	7 / 338	G−protein coupled receptor signaling pathway
2	0.003	6 / 269	extracellular matrix organization
3	0.003	2 / 16	ceramide biosynthetic process
4	0.004	4 / 125	growth
5	0.006	2 / 23	eye development
6	0.008	2 / 26	detection of chemical stimulus involved in sensory perception of smell
7	0.008	2 / 26	excretion
8	0.009	2 / 28	sperm motility
9	0.011	2 / 30	neutrophil chemotaxis
10	0.011	3 / 87	calcium ion transmembrane transport
11	0.011	3 / 89	kidney development
12	0.011	2 / 31	cellular defense response
13	0.012	25 / 3068	signal transduction
14	0.012	2 / 32	fertilization
15	0.012	2 / 32	protein heterotetramerization
16	0.013	2 / 33	dorsal/ventral pattern formation
17	0.014	2 / 34	arachidonic acid metabolic process
18	0.017	2 / 38	cellular response to cAMP
19	0.018	2 / 39	hair follicle development
20	0.018	2 / 39	ureteric bud development

Brain

Rank	p−value	#in/all	Geneset
1	0.004	14 / 1207	Overlap_fetal_midbrain_TssF
2	0.006	12 / 1013	Fetal_TssP
3	0.016	19 / 2185	Fetal_TssA
4	0.019	17 / 1907	Fetal_TxTrans
5	0.027	20 / 2462	Mid_Frontal_Lobe_HetRpts
6	0.029	7 / 564	Mid_Frontal_Lobe_EnhP
7	0.029	23 / 2972	Mid_Frontal_Lobe_ReprPC
8	0.036	9 / 862	Overlap_fetal_midbrain_TxTrans
9	0.045	16 / 1949	Fetal_TssF
10	0.052	10 / 1065	Overlap_fetal_midbrain_Enh
11	0.118	7 / 786	Fetal_EnhG
12	0.146	7 / 831	Fetal_HetRpts
13	0.149	5 / 534	Mid_Frontal_Lobe_EnhG
14	0.151	6 / 686	Overlap_fetal_midbrain_TssA
15	0.184	5 / 574	Overlap_fetal_midbrain_TssP
16	0.232	4 / 468	Mid_Frontal_Lobe_TssF
17	0.254	6 / 812	Mid_Frontal_Lobe_TssP
18	0.305	1 / 69	Overlap_fetal_midbrain_Tx
19	0.320	6 / 884	Overlap_fetal_midbrain_EnhG
20	0.323	8 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	2 / 156	PanCan_PI3K_geneset_nanostring
2	0.2	1 / 44	PanCan_TGF−B_geneset_nanostring
3	0.3	1 / 55	PanCan_JAK−STAT_geneset_nanostring
4	0.3	0 / 12	LIU_PROSTATE_CANCER_UP
5	0.4	1 / 82	PanCan_TXmisReg_geneset_nanostring
6	0.4	1 / 113	PanCan_Driver_Gene_geneset_nanostring
7	0.5	1 / 120	PanCan_CC+Apop_geneset_nanostring
8	0.5	1 / 121	PanCan_MAPK_geneset_nanostring
9	0.6	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.6	2 / 401	Lembcke_Colonic Inflammation
11	0.8	1 / 298	SPANG_BCL6−index2
12	0.9	1 / 489	Lembcke_Normal vs Adenoma
13	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	1.0	0 / 12	LIU_BREAST_CANCER
18	1.0	0 / 14	LIU_COMMON_CANCER_GENES
19	1.0	0 / 14	LIU_LIVER_CANCER
20	1.0	0 / 15	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	0.009	25 / 2984	integral component of membrane
2	0.011	2 / 31	dendritic shaft
3	0.025	24 / 3088	plasma membrane
4	0.025	3 / 119	external side of plasma membrane
5	0.032	3 / 132	basolateral plasma membrane
6	0.042	4 / 249	neuronal cell body
7	0.051	3 / 159	extracellular matrix
8	0.055	74 / 13191	cellular_component
9	0.061	1 / 12	dendrite membrane
10	0.061	1 / 12	Golgi−associated vesicle
11	0.061	1 / 12	U4/U6 x U5 tri−snRNP complex
12	0.066	1 / 13	filopodium membrane
13	0.066	1 / 13	nBAF complex
14	0.066	1 / 13	synaptic membrane
15	0.081	1 / 16	anchored component of plasma membrane
16	0.086	1 / 17	I band
17	0.091	1 / 18	NuRD complex
18	0.095	1 / 19	calcium channel complex
19	0.114	1 / 23	integrin complex
20	0.119	2 / 113	postsynaptic density

Chr

Rank	p−value	#in/all	Geneset
1	0.07	6 / 558	Chr 4
2	0.13	6 / 649	Chr 16
3	0.24	6 / 801	Chr 11
4	0.35	3 / 398	Chr 20
5	0.40	2 / 262	Chr 13
6	0.44	3 / 462	Chr 14
7	0.45	3 / 469	Chr 8
8	0.45	5 / 840	Chr 17
9	0.47	6 / 1037	Chr 19
10	0.49	4 / 687	Chr 6
11	0.49	4 / 689	Chr 7
12	0.53	2 / 335	Chr 22
13	0.55	1 / 151	Chr 21
14	0.56	3 / 551	Chr X
15	0.60	5 / 993	Chr 2
16	0.69	1 / 221	Chr 18
17	0.71	3 / 696	Chr 5
18	0.82	3 / 838	Chr 3
19	0.91	5 / 1500	Chr 1
20	0.92	1 / 465	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.008	18 / 1889	ReprPCWk_Colon
2	0.012	14 / 1386	Het_Colon
3	0.023	2 / 45	Ang_CRC−CIMPH−vs−L_hyper
4	0.027	18 / 2142	ReprPC_Colon
5	0.028	2 / 50	Ang_CRC_Hypermethylated
6	0.029	18 / 2159	TssP_Colon
7	0.041	1 / 8	Juehling−MSI−enriched−in−7
8	0.045	10 / 1038	HetRpts_Colon
9	0.045	4 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	0.056	9 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
11	0.083	11 / 1317	EnhP_Colon
12	0.086	1 / 17	Vilar_mutated−in−CRC−CamP
13	0.089	5 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
14	0.091	1 / 18	Ang_CRC−CIMPH−vs−L_hypo
15	0.123	1 / 25	Ang_CRC_Hypomethylated
16	0.150	25 / 3897	Quies1_Colon
17	0.153	4 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
18	0.181	5 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
19	0.196	4 / 436	K9acLow_Colon
20	0.235	3 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.02	5 / 294	GUDJ_psoriasis down
2	0.06	1 / 11	BCHETNIA_EBM up
3	0.08	5 / 435	GUDJ_psoriasis up
4	0.10	1 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	3 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
2	0.03	3 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
3	0.04	2 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
4	0.05	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−A_UP
5	0.06	2 / 72	laffaire_hypermeth_LGG_vs_control
6	0.06	1 / 11	Martinez_Glio_hypermeth
7	0.06	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
8	0.08	1 / 16	KIM deleted & downregulated in LTS
9	0.09	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.10	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.11	1 / 22	KIM prognostic signature LTS vs. STS
12	0.14	1 / 29	shaw_responders_down_in_oligo_glioma
13	0.16	1 / 32	Donson−innate immunity−associated with LTS in HGA
14	0.18	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	0.21	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
16	0.22	1 / 47	mature astrocytes
17	0.23	1 / 49	developing astrocytes
18	0.23	1 / 49	OL vs. MOG− OL
19	0.28	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
20	0.29	3 / 356	Down_a

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	5 / 72	RICKMAN_HEAD_AND_NECK_CANCER_A
2	7e−04	2 / 8	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
3	1e−03	2 / 9	KORKOLA_EMBRYONAL_CARCINOMA
4	1e−03	11 / 720	BENPORATH_ES_WITH_H3K27ME3
5	3e−03	3 / 56	WONG_ENDMETRIUM_CANCER_DN
6	3e−03	3 / 56	FURUKAWA_DUSP6_TARGETS_PCI35_UP
7	4e−03	4 / 124	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
8	4e−03	10 / 724	BENPORATH_EED_TARGETS
9	5e−03	2 / 20	PID_GLYPICAN_1PATHWAY
10	5e−03	2 / 20	FARMER_BREAST_CANCER_CLUSTER_1
11	5e−03	6 / 300	REACTOME_GPCR_DOWNSTREAM_SIGNALING
12	5e−03	3 / 67	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
13	6e−03	7 / 410	LIM_MAMMARY_STEM_CELL_UP
14	6e−03	4 / 138	DURAND_STROMA_NS_UP
15	6e−03	2 / 23	REACTOME_OLFACTORY_SIGNALING_PATHWAY
16	7e−03	2 / 24	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN
17	7e−03	4 / 147	CAIRO_LIVER_DEVELOPMENT_UP
18	8e−03	4 / 150	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
19	9e−03	6 / 342	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
20	9e−03	4 / 157	OKUMURA_INFLAMMATORY_RESPONSE_LPS

HM

Rank	p−value	#in/all	Geneset
1	0.01	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.14	2 / 127	HALLMARK_KRAS_SIGNALING_DN
3	0.18	1 / 37	HALLMARK_APICAL_SURFACE
4	0.22	2 / 165	HALLMARK_MYOGENESIS
5	0.22	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	0.22	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.22	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
8	0.23	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.38	1 / 91	HALLMARK_BILE_ACID_METABOLISM
10	0.43	1 / 107	HALLMARK_COAGULATION
11	0.49	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
12	0.52	1 / 140	HALLMARK_APOPTOSIS
13	0.52	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
14	0.58	1 / 162	HALLMARK_COMPLEMENT
15	0.59	1 / 167	HALLMARK_APICAL_JUNCTION
16	0.61	1 / 176	HALLMARK_HYPOXIA
17	0.64	1 / 195	HALLMARK_MITOTIC_SPINDLE
18	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 62	DUMEAUX_Smoking enriched genes
2	1.0	0 / 10	DUMEAUX_Smoking literature genes up
3	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	27 / 3396	HOPP_Repressed
2	0.05	1 / 10	DAVE_BL_DN
3	0.07	1 / 13	WRIGHT_GCB UP
4	0.10	1 / 20	SPANG_BAFF 9hrs UP
5	0.15	1 / 30	TARTE_B−cell signature
6	0.17	15 / 2188	HOPP_Poised_promoter
7	0.22	1 / 47	Subero_FL_hyper_meth
8	0.27	1 / 60	Subero_T−ALL_hyper_meth
9	0.35	1 / 81	Subero_INT_hyper_meth
10	0.35	1 / 82	ROSOLOWSKI_green UP
11	0.37	3 / 410	SPANG_CD40 6hrs DN
12	0.37	15 / 2563	HOPP_Heterochrom
13	0.40	1 / 96	Subero_DLBCL_hyper_meth
14	0.41	2 / 268	SPANG_IL21 UP
15	0.43	2 / 275	TARTE_Mature plasma cell signature
16	0.43	1 / 107	SPANG_LPS 6hrs UP
17	0.43	2 / 280	SPANG_CD40 6hrs UP
18	0.44	1 / 109	ROSOLOWSKI_green total
19	0.73	1 / 247	ZHANG_DLBCL mutated
20	0.74	1 / 256	SPANG_IL21 DN

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 52	hormone activity
2	0.003	2 / 16	acetylglucosaminyltransferase activity
3	0.006	5 / 217	G−protein coupled receptor activity
4	0.007	8 / 530	calcium ion binding
5	0.008	2 / 26	olfactory receptor activity
6	0.015	10 / 866	signal transducer activity
7	0.031	16 / 1859	metal ion binding
8	0.045	4 / 255	receptor binding
9	0.051	1 / 10	aromatase activity
10	0.051	1 / 10	oxidoreductase activity, acting on paired donors, with incorporation or reductic
11	0.056	1 / 11	C2H2 zinc finger domain binding
12	0.056	1 / 11	steroid hydroxylase activity
13	0.057	3 / 166	receptor activity
14	0.061	1 / 12	Notch binding
15	0.061	1 / 12	RNA polymerase II core promoter proximal region sequence−specific DNA bir
16	0.066	1 / 13	GABA receptor binding
17	0.066	1 / 13	glucuronosyltransferase activity
18	0.066	1 / 13	protein kinase A binding
19	0.066	1 / 13	protein kinase A regulatory subunit binding
20	0.071	1 / 14	apolipoprotein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.1	1 / 20	hsa−miR−1288
2	0.1	2 / 105	hsa−miR−1271
3	0.1	1 / 29	hsa−miR−193a−5p
4	0.2	2 / 143	hsa−miR−338−5p
5	0.2	1 / 37	hsa−miR−1274a
6	0.2	1 / 40	hsa−miR−182*
7	0.2	2 / 162	hsa−miR−96
8	0.2	1 / 46	hsa−miR−581
9	0.2	1 / 47	hsa−miR−575
10	0.2	1 / 50	hsa−miR−549
11	0.2	1 / 53	hsa−miR−337−3p
12	0.2	1 / 54	hsa−miR−513a−5p
13	0.3	1 / 57	hsa−miR−891b
14	0.3	1 / 57	hsa−miR−193a−3p
15	0.3	1 / 68	hsa−miR−649
16	0.3	1 / 68	hsa−miR−193b
17	0.3	2 / 214	hsa−miR−182
18	0.3	1 / 74	hsa−miR−1254
19	0.3	1 / 75	hsa−miR−592
20	0.4	1 / 83	hsa−miR−582−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.002	14 / 1139	HEBENSTREIT_low expression TF
2	0.382	4 / 595	ICGC_NrsfPcr2_targets
3	0.450	12 / 2137	ICGC_SrfV0416101_targets
4	0.475	16 / 2927	ICGC_Rad21_targets
5	0.502	7 / 1266	ICGC_NrsfPcr1_targets
6	0.508	7 / 1273	ICGC_P300_targets
7	0.560	3 / 553	ICGC_RxraPcr1_targets
8	0.744	11 / 2416	ICGC_Bcl3_targets
9	0.747	5 / 1171	KIM_MYC targets
10	0.748	9 / 2013	ICGC_Bcl11_targets
11	0.787	28 / 5890	ICGC_Elf1_targets
12	0.831	5 / 1314	ICGC_Usf1_targets
13	0.842	21 / 4682	ICGC_Pol24_targets
14	0.857	28 / 6114	ICGC_Runx3_targets
15	0.863	2 / 653	ICGC_SrfPcr2_targets
16	0.868	17 / 3966	ICGC_Pu1_targets
17	0.879	7 / 1878	ICGC_Cebpbsc150_targets
18	0.880	23 / 5219	ICGC_Tcf3_targets
19	0.883	2 / 690	ICGC_Atf3_targets
20	0.892	17 / 4054	ICGC_Egr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 14	VAQUERIZAS_Ovary
2	0.09	1 / 17	VAQUERIZAS_Pituitary
3	0.11	1 / 23	VAQUERIZAS_Spinal cord
4	0.18	1 / 38	VAQUERIZAS_Whole brain
5	0.18	1 / 38	VAQUERIZAS_Testis
6	0.19	1 / 41	VAQUERIZAS_Placenta
7	0.21	1 / 45	VAQUERIZAS_Uterus
8	1.00	0 / 36	VAQUERIZAS_Fetal brain
9	1.00	0 / 26	VAQUERIZAS_Liver
10	1.00	0 / 33	VAQUERIZAS_Prostate
11	1.00	0 / 29	VAQUERIZAS_Smooth muscle
12	1.00	0 / 143	VAQUERIZAS_General
13	1.00	0 / 9	VAQUERIZAS_Kidney
14	1.00	0 / 37	VAQUERIZAS_Thymus
15	1.00	0 / 40	VAQUERIZAS_Thyroid
16	1.00	0 / 59	VAQUERIZAS_Whole blood
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 29	VAQUERIZAS_Fetal lung
19	1.00	0 / 58	VAQUERIZAS_Lung
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	5e−04	8 / 350	WIRTH_Nervous System
2	5e−02	1 / 9	PALMER_CD8+ T−Cell signature up
3	5e−02	1 / 10	WIRTH_Hippocampus
4	1e−01	3 / 225	PALMER_Granulocytes signature up
5	2e−01	1 / 41	WIRTH_Homeostasis
6	3e−01	1 / 74	WIRTH_Mucosa
7	4e−01	1 / 95	WIRTH_Muscle
8	4e−01	1 / 107	WIRTH_Testis
9	5e−01	1 / 114	PALMER_T−Cell signature up
10	8e−01	1 / 350	WIRTH_Immune system
11	1e+00	0 / 32	WIRTH_Pancreas
12	1e+00	0 / 11	WIRTH_Sec. lymphoid organs
13	1e+00	0 / 11	WIRTH_Prim. lymphoid organs
14	1e+00	0 / 13	WIRTH_B−cells
15	1e+00	0 / 8	WIRTH_Tonsil
16	1e+00	0 / 12	WIRTH_Thymus
17	1e+00	0 / 12	WIRTH_Lymphocytes
18	1e+00	0 / 5	WIRTH_Bone marrow
19	1e+00	0 / 11	WIRTH_Globus pallidus
20	1e+00	0 / 14	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	23 / 3682	LU_BPDE 0.005 DN
2	0.8	4 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

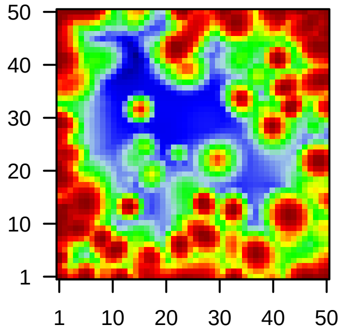
Overexpression Spots

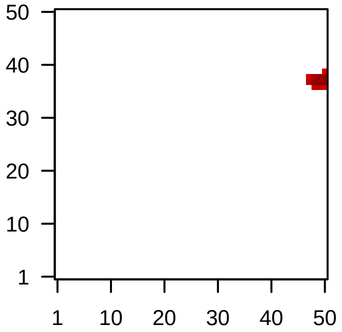
Spot Summary: M1

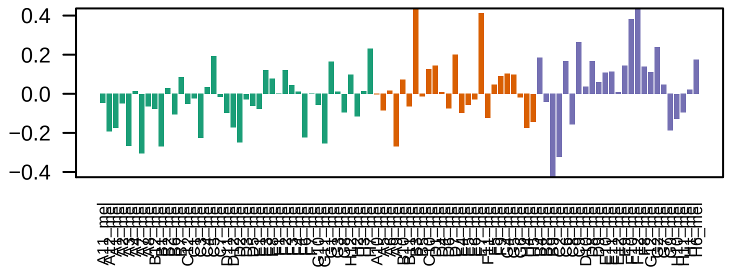
metagenes = 12
genes = 120

<r> metagenes = 0.96
<r> genes = 0.09
beta: r2= 1.25 / log p= −Inf

samples with spot = 10 (10.9 %)
MSC1 : 2 (4.8 %)
MSC2 : 3 (12 %)
MSC3 : 5 (20 %)


Overview Map


Spot

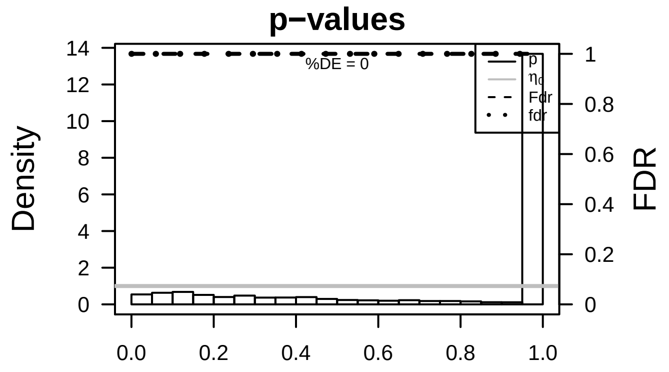


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	P2RX7	2.1	−0.56	0.41	P2RX7	purinergic receptor P2X, ligand gated ion channel, 7 [Source:
2	ZNF35	1.72	−0.24	0.27	ZNF35	zinc finger protein 35 [Source:HGNC Symbol;Acc:HGNC:130
3	CAPS2	1.67	−0.27	0.3	CAPS2	calcyphosine 2 [Source:HGNC Symbol;Acc:HGNC:16471]
4	SLC26A6	1.63	−0.39	0.28	SLC26A6	solute carrier family 26 (anion exchanger), member 6 [Source
5	RNF217	1.62	−0.31	0.24	RNF217	ring finger protein 217 [Source:HGNC Symbol;Acc:HGNC:21
6	SEC61A2	1.62	−0.43	0.21	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae) [Source:HGNC Symbol
7	FBXO32	1.62	−0.54	0.35	FBXO32	F−box protein 32 [Source:HGNC Symbol;Acc:HGNC:16731]
8	ATP10D	1.61	−0.52	0.4	ATP10D	ATPase, class V, type 10D [Source:HGNC Symbol;Acc:HGNC
9	ZFC3H1	1.61	−0.58	0.29	ZFC3H1	zinc finger, C3H1−type containing [Source:HGNC Symbol;Ac
10	ZNF75A	1.6	−0.61	0.35	ZNF75A	zinc finger protein 75a [Source:HGNC Symbol;Acc:HGNC:13
11	GLS2	1.59	−0.14	0.29	GLS2	glutaminase 2 (liver, mitochondrial) [Source:HGNC Symbol;A
12	KPNA5	1.56	−0.35	0.26	KPNA5	karyopherin alpha 5 (importin alpha 6) [Source:HGNC Symbo
13	YBX3	1.54	−0.25	0.31	YBX3	Y box binding protein 3 [Source:HGNC Symbol;Acc:HGNC:2
14	KHDRBS3	1.53	−0.72	0.3	KHDRBS3	KH domain containing, RNA binding, signal transduction ass
15	PROCR	1.53	−0.13	0.43	PROCR	protein C receptor, endothelial [Source:HGNC Symbol;Acc:H
16	RUFY3	1.52	−0.78	0.43	RUFY3	RUN and FYVE domain containing 3 [Source:HGNC Symbol;
17	PDK3	1.52	−0.47	0.39	PDK3	pyruvate dehydrogenase kinase, isozyme 3 [Source:HGNC S
18	MYOM1	1.51	−0.07	0.36	MYOM1	myomesin 1 [Source:HGNC Symbol;Acc:HGNC:7613]
19	TMEM173	1.5	−0.52	0.25	TMEM173	transmembrane protein 173 [Source:HGNC Symbol;Acc:HGN
20	NRIP3	1.5	−0.33	0.32	NRIP3	nuclear receptor interacting protein 3 [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−07	83 / 6929	Lympl	HOPP_Txn_elongation
2	3e−07	101 / 9482	Colon	TssA_Colon
3	3e−07	75 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
4	5e−06	85 / 7592	Lympl	HOPP_Active_promoter
5	1e−05	81 / 7209	Lympl	HOPP_Weak_promoter
6	5e−05	95 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
7	7e−05	17 / 729	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
8	9e−05	92 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
9	1e−04	25 / 1418	TF	ICGC_Ets1_targets
10	2e−04	88 / 8580	Colon	TxWk_Colon
11	2e−04	91 / 9027	Colon	Tx_Colon
12	2e−04	13 / 510	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
13	3e−04	86 / 8415	Colon	Quies3_Colon
14	5e−04	4 / 47	GSEA	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
15	6e−04	8 / 236	GSEA	KOYAMA_SEMA3B_TARGETS_UP
16	7e−04	59 / 5184	Lympl	HOPP_Txn_transition
17	7e−04	93 / 9528	Brain	Overlap_fetal_midbrain_Quies
18	1e−03	3 / 27	BP	histone H4 acetylation
19	1e−03	22 / 1383	TF	ICGC_Six5_targets
20	2e−03	88 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
21	2e−03	4 / 67	BP	microtubule cytoskeleton organization
22	2e−03	3 / 33	GSEA	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY
23	2e−03	60 / 5538	Lympl	HOPP_Weak_txn
24	3e−03	4 / 72	BP	response to organic substance
25	3e−03	3 / 35	GSEA	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
26	3e−03	94 / 9988	CC	organelle
27	3e−03	2 / 11	BP	activation of innate immune response
28	4e−03	24 / 1693	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
29	4e−03	9 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
30	4e−03	20 / 1314	TF	ICGC_Usf1_targets
31	4e−03	8 / 316	MF	protein kinase binding
32	4e−03	2 / 12	BP	histone H2A acetylation
33	4e−03	2 / 12	BP	regulation of release of sequestered calcium ion into cytosol
34	4e−03	6 / 188	BP	regulation of apoptotic process
35	5e−03	2 / 13	miRN	hsa−miR−574−3p
36	5e−03	3 / 43	BP	neurotransmitter secretion
37	5e−03	11 / 555	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
38	5e−03	28 / 2136	TF	ICGC_GabpPcr2_targets
39	5e−03	6 / 198	miRN	hsa−miR−448
40	5e−03	6 / 199	GSEA	RAMALHO_STEMNESS_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 27	histone H4 acetylation
2	0.002	4 / 67	microtubule cytoskeleton organization
3	0.003	4 / 72	response to organic substance
4	0.003	2 / 11	activation of innate immune response
5	0.004	2 / 12	histone H2A acetylation
6	0.004	2 / 12	regulation of release of sequestered calcium ion into cytosol
7	0.004	6 / 188	regulation of apoptotic process
8	0.005	3 / 43	neurotransmitter secretion
9	0.007	2 / 16	female gamete generation
10	0.007	2 / 16	membrane depolarization
11	0.008	2 / 17	cellular response to nitrogen starvation
12	0.008	2 / 17	negative regulation of axonogenesis
13	0.008	3 / 52	regulation of growth
14	0.009	2 / 18	phospholipid translocation
15	0.011	2 / 20	glutamine metabolic process
16	0.012	2 / 21	nucleophagy
17	0.012	2 / 21	regulation of reactive oxygen species metabolic process
18	0.013	2 / 22	response to bacterium
19	0.013	3 / 62	positive regulation of type I interferon production
20	0.016	2 / 24	negative regulation of protein catabolic process

Brain

Rank	p−value	#in/all	Geneset
1	3e−07	75 / 5940	Overlap_fetal_midbrain_HetRpts
2	5e−05	95 / 9330	Overlap_fetal_midbrain_ReprPC
3	9e−05	92 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	7e−04	93 / 9528	Overlap_fetal_midbrain_Quies
5	2e−03	88 / 9013	Overlap_fetal_midbrain_K9K27me3
6	4e−02	10 / 656	Overlap_fetal_midbrain_EnhP
7	4e−02	13 / 953	Fetal_Enh
8	6e−02	14 / 1122	Fetal_K9K27me3
9	2e−01	9 / 786	Fetal_EnhG
10	3e−01	4 / 349	Fetal_ZNF
11	3e−01	8 / 831	Fetal_HetRpts
12	4e−01	5 / 534	Mid_Frontal_Lobe_EnhG
13	5e−01	5 / 564	Mid_Frontal_Lobe_EnhP
14	5e−01	8 / 989	Mid_Frontal_Lobe_Quies
15	6e−01	3 / 383	Fetal_Tx
16	6e−01	24 / 3081	Mid_Frontal_Lobe_ZNF
17	6e−01	19 / 2462	Mid_Frontal_Lobe_HetRpts
18	6e−01	5 / 668	Mid_Frontal_Lobe_Enh
19	6e−01	14 / 1845	Fetal_Quies
20	7e−01	9 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	1 / 15	RHODES_CANCER_META_SIGNATURE
2	0.12	1 / 16	GENTLES_modul16
3	0.15	1 / 20	PanCan_ChromMod_geneset_nanostring
4	0.28	1 / 40	ZHANG_MM up
5	0.28	1 / 40	PanCan_HK_geneset_nanostring
6	0.43	3 / 298	SPANG_BCL6−index2
7	0.48	1 / 82	PanCan_TXmisReg_geneset_nanostring
8	0.59	1 / 111	PanCan_RAS_geneset_nanostring
9	0.60	1 / 113	PanCan_Driver_Gene_geneset_nanostring
10	0.61	0 / 14	LIU_PROSTATE_CANCER_DN
11	0.62	1 / 120	PanCan_CC+Apop_geneset_nanostring
12	0.62	1 / 121	PanCan_MAPK_geneset_nanostring
13	0.72	1 / 156	PanCan_PI3K_geneset_nanostring
14	0.91	2 / 489	Lembcke_Normal vs Adenoma
15	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
16	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.00	0 / 12	LIU_BREAST_CANCER
19	1.00	0 / 14	LIU_COMMON_CANCER_GENES
20	1.00	0 / 14	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.003	94 / 9988	organelle
2	0.005	2 / 14	NuA4 histone acetyltransferase complex
3	0.006	2 / 15	pre−autophagosomal structure membrane
4	0.007	2 / 16	M band
5	0.008	3 / 51	filopodium
6	0.010	2 / 19	inclusion body
7	0.011	3 / 58	neuronal postsynaptic density
8	0.014	96 / 10605	intracellular
9	0.014	78 / 8205	cytoplasm
10	0.016	2 / 24	U12−type spliceosomal complex
11	0.020	2 / 27	aggresome
12	0.022	4 / 132	basolateral plasma membrane
13	0.024	2 / 30	sarcomere
14	0.024	2 / 30	small−subunit processome
15	0.025	4 / 138	cell−cell junction
16	0.025	2 / 31	microtubule associated complex
17	0.029	2 / 33	cell leading edge
18	0.032	7 / 377	centrosome
19	0.044	8 / 491	perinuclear region of cytoplasm
20	0.045	18 / 1468	mitochondrion

Chr

Rank	p−value	#in/all	Geneset
1	0.08	8 / 551	Chr X
2	0.17	9 / 775	Chr 12
3	0.17	6 / 469	Chr 8
4	0.23	9 / 838	Chr 3
5	0.27	10 / 993	Chr 2
6	0.31	5 / 462	Chr 14
7	0.32	7 / 696	Chr 5
8	0.36	8 / 840	Chr 17
9	0.40	4 / 398	Chr 20
10	0.43	13 / 1500	Chr 1
11	0.46	5 / 552	Chr 10
12	0.46	5 / 558	Chr 4
13	0.51	3 / 335	Chr 22
14	0.63	6 / 801	Chr 11
15	0.65	5 / 687	Chr 6
16	0.71	1 / 151	Chr 21
17	0.81	4 / 689	Chr 7
18	0.83	1 / 221	Chr 18
19	0.89	2 / 465	Chr 15
20	0.95	2 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−07	101 / 9482	TssA_Colon
2	2e−04	88 / 8580	TxWk_Colon
3	2e−04	91 / 9027	Tx_Colon
4	3e−04	86 / 8415	Quies3_Colon
5	3e−02	92 / 10290	TssWk_Colon
6	7e−02	1 / 9	KIM_MSI−in−EC
7	7e−02	1 / 9	Budinska_D_Mesenchymal_UP
8	1e−01	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
9	1e−01	64 / 7203	TssF_Colon
10	2e−01	1 / 29	Marisa_CRC−cluster−c
11	2e−01	2 / 117	Marisa_CRC−cluster−b
12	3e−01	8 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
13	3e−01	7 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
14	3e−01	1 / 43	Marisa_CRC−cluster−f
15	3e−01	3 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
16	4e−01	10 / 1079	ZNF_Colon
17	4e−01	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
18	4e−01	1 / 71	Marisa_CRC−cluster−g
19	4e−01	4 / 427	Quies2_Colon
20	6e−01	1 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.7	3 / 435	GUDJ_psoriasis up
2	0.7	2 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.007	4 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
2	0.014	2 / 23	Donson−Misc immune function−associated with LTS in HGA
3	0.055	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
4	0.070	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
5	0.077	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
6	0.091	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	0.103	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	0.114	1 / 15	VERHAAK_CL subtype
9	0.114	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	0.128	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
11	0.136	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	0.139	10 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.169	1 / 23	WIRTH_PN subtype
14	0.191	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
15	0.200	2 / 103	GIEZELT_GBM_WT_up_VS_mut
16	0.246	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	0.258	1 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
18	0.315	1 / 47	WILLSCHER_GBM_Verhaak=PNwt_up
19	0.319	4 / 356	Down_a
20	0.332	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−05	17 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
2	2e−04	13 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
3	5e−04	4 / 47	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
4	6e−04	8 / 236	KOYAMA_SEMA3B_TARGETS_UP
5	2e−03	3 / 33	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY
6	3e−03	3 / 35	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
7	4e−03	24 / 1693	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
8	4e−03	9 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
9	5e−03	11 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
10	5e−03	6 / 199	RAMALHO_STEMNESS_UP
11	5e−03	2 / 14	ZEMBUTSU_SENSITIVITY_TO_METHOTREXATE
12	7e−03	2 / 16	BIOCARTA_HCMV_PATHWAY
13	8e−03	10 / 508	MARTINEZ_TP53_TARGETS_UP
14	9e−03	19 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
15	1e−02	3 / 55	REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BET
16	1e−02	5 / 163	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
17	1e−02	5 / 165	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
18	1e−02	2 / 20	BIOCARTA_NTHI_PATHWAY
19	1e−02	2 / 20	WU_HBX_TARGETS_1_DN
20	1e−02	12 / 706	BENPORATH_MYC_MAX_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	0.006	4 / 91	HALLMARK_PROTEIN_SECRETION
2	0.072	4 / 195	HALLMARK_MITOTIC_SPINDLE
3	0.119	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
4	0.170	3 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	0.174	2 / 94	HALLMARK_ANDROGEN_RESPONSE
6	0.178	3 / 181	HALLMARK_P53_PATHWAY
7	0.180	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	0.182	3 / 183	HALLMARK_GLYCOLYSIS
9	0.208	3 / 196	HALLMARK_MTORC1_SIGNALING
10	0.309	2 / 140	HALLMARK_APOPTOSIS
11	0.309	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
12	0.368	1 / 57	HALLMARK_MYC_TARGETS_V2
13	0.394	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
14	0.505	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	0.520	1 / 91	HALLMARK_BILE_ACID_METABOLISM
16	0.585	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
17	0.639	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
18	0.670	1 / 137	HALLMARK_UV_RESPONSE_DN
19	0.737	1 / 165	HALLMARK_MYOGENESIS
20	0.741	1 / 167	HALLMARK_APICAL_JUNCTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−07	83 / 6929	HOPP_Txn_elongation
2	5e−06	85 / 7592	HOPP_Active_promoter
3	1e−05	81 / 7209	HOPP_Weak_promoter
4	7e−04	59 / 5184	HOPP_Txn_transition
5	2e−03	60 / 5538	HOPP_Weak_txn
6	1e−02	58 / 5693	HOPP_Weak_enhancer
7	9e−02	1 / 12	BENTINK_mBL DOWN
8	1e−01	60 / 6564	HOPP_Strong_enhancer
9	2e−01	2 / 86	ROSOLOWSKI_red total
10	2e−01	12 / 1128	SPANG_BCR DN
11	2e−01	4 / 294	TARTE_Plasmablast signature
12	3e−01	1 / 39	ROSOLOWSKI_blue DOWN
13	3e−01	1 / 43	LENZ_Stromal signature 2
14	3e−01	3 / 247	ZHANG_DLBCL mutated
15	3e−01	1 / 50	SPANG_BAFF 9hrs DN
16	3e−01	3 / 256	SPANG_IL21 DN
17	4e−01	1 / 61	SPANG_LPS 6hrs DN
18	4e−01	4 / 410	SPANG_CD40 6hrs DN
19	5e−01	21 / 2563	HOPP_Heterochrom
20	5e−01	2 / 212	LENZ_Stromal signature 1

MF

Rank	p−value	#in/all	Geneset
1	0.004	8 / 316	protein kinase binding
2	0.008	2 / 17	RNA polymerase II core binding
3	0.012	2 / 21	polyubiquitin binding
4	0.017	2 / 25	aminopeptidase activity
5	0.022	2 / 29	mRNA 3'−UTR binding
6	0.025	5 / 205	ubiquitin protein ligase binding
7	0.025	2 / 31	beta−tubulin binding
8	0.031	14 / 1007	poly(A) RNA binding
9	0.034	2 / 36	SNAP receptor activity
10	0.039	2 / 39	cell adhesion molecule binding
11	0.041	15 / 1149	enzyme binding
12	0.043	2 / 41	ATPase binding
13	0.045	4 / 166	receptor activity
14	0.060	3 / 111	protein binding, bridging
15	0.063	2 / 51	ubiquitin binding
16	0.070	4 / 193	protein complex binding
17	0.072	111 / 13179	molecular_function
18	0.077	1 / 10	gamma−catenin binding
19	0.078	80 / 8984	protein binding
20	0.079	16 / 1365	RNA binding

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	hsa−miR−574−3p
2	0.005	6 / 198	hsa−miR−448
3	0.006	3 / 46	hsa−miR−875−5p
4	0.006	5 / 146	hsa−miR−142−3p
5	0.009	4 / 101	hsa−miR−613
6	0.009	7 / 291	hsa−miR−34c−5p
7	0.011	4 / 108	hsa−miR−449b
8	0.014	3 / 63	hsa−miR−455−3p
9	0.015	5 / 179	hsa−miR−520f
10	0.015	5 / 181	hsa−miR−29c
11	0.017	3 / 67	hsa−miR−1826
12	0.029	5 / 215	hsa−miR−29b
13	0.030	5 / 217	hsa−miR−203
14	0.031	3 / 85	hsa−miR−510
15	0.032	4 / 149	hsa−miR−633
16	0.034	3 / 88	hsa−miR−505
17	0.035	2 / 37	hsa−miR−501−3p
18	0.039	2 / 39	hsa−miR−502−3p
19	0.039	1 / 5	hsa−miR−1268
20	0.039	1 / 5	hsa−miR−585

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	GUSTAFSON_PI3K_DN
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 14	BENTINK_e2f3.1
4	1.0	0 / 12	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−04	25 / 1418	ICGC_Ets1_targets
2	1e−03	22 / 1383	ICGC_Six5_targets
3	4e−03	20 / 1314	ICGC_Usf1_targets
4	5e−03	28 / 2136	ICGC_GabpPcr2_targets
5	7e−03	48 / 4385	ICGC_Atf2_targets
6	1e−02	44 / 4032	ICGC_Creb1_targets
7	1e−02	47 / 4414	ICGC_Bclaf101388_targets
8	2e−02	22 / 1701	HEBENSTREIT_high expression TF
9	2e−02	50 / 4879	ICGC_Pmlsc71910_targets
10	2e−02	23 / 1878	ICGC_Cebpbsc150_targets
11	3e−02	49 / 4829	ICGC_Nficsc81335_targets
12	3e−02	41 / 3924	ICGC_Zeb1_targets
13	4e−02	47 / 4689	ICGC_Taf1_targets
14	4e−02	22 / 1872	ICGC_Mef2_targets
15	5e−02	51 / 5200	ICGC_Mta3_targets
16	5e−02	52 / 5355	ICGC_Pol2_targets
17	6e−02	46 / 4682	ICGC_Pol24_targets
18	6e−02	26 / 2391	ICGC_Pbx3_targets
19	6e−02	52 / 5408	ICGC_Pou2_targets
20	6e−02	46 / 4706	ICGC_Sp1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
2	0.05	1 / 7	VAQUERIZAS_Tongue
3	0.26	1 / 38	VAQUERIZAS_Testis
4	0.69	1 / 143	VAQUERIZAS_General
5	1.00	0 / 36	VAQUERIZAS_Fetal brain
6	1.00	0 / 41	VAQUERIZAS_Placenta
7	1.00	0 / 26	VAQUERIZAS_Liver
8	1.00	0 / 33	VAQUERIZAS_Prostate
9	1.00	0 / 29	VAQUERIZAS_Smooth muscle
10	1.00	0 / 45	VAQUERIZAS_Uterus
11	1.00	0 / 9	VAQUERIZAS_Kidney
12	1.00	0 / 23	VAQUERIZAS_Spinal cord
13	1.00	0 / 38	VAQUERIZAS_Whole brain
14	1.00	0 / 37	VAQUERIZAS_Thymus
15	1.00	0 / 40	VAQUERIZAS_Thyroid
16	1.00	0 / 59	VAQUERIZAS_Whole blood
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 29	VAQUERIZAS_Fetal lung
19	1.00	0 / 58	VAQUERIZAS_Lung
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 8	WIRTH_Tonsil
2	0.08	1 / 11	WIRTH_Sec. lymphoid organs
3	0.11	1 / 14	WIRTH_Telencephalon
4	0.21	2 / 107	WIRTH_Testis
5	0.31	4 / 350	WIRTH_Immune system
6	0.54	1 / 95	WIRTH_Muscle
7	0.54	2 / 225	PALMER_Granulocytes signature up
8	0.77	2 / 350	WIRTH_Nervous System
9	1.00	0 / 32	WIRTH_Pancreas
10	1.00	0 / 11	WIRTH_Prim. lymphoid organs
11	1.00	0 / 13	WIRTH_B−cells
12	1.00	0 / 12	WIRTH_Thymus
13	1.00	0 / 12	WIRTH_Lymphocytes
14	1.00	0 / 5	WIRTH_Bone marrow
15	1.00	0 / 11	WIRTH_Globus pallidus
16	1.00	0 / 11	WIRTH_Cortex cerebri
17	1.00	0 / 10	WIRTH_Hippocampus
18	1.00	0 / 10	WIRTH_Thalamus
19	1.00	0 / 12	WIRTH_Cerebellum
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	12 / 1115	LU_BPDE 1h DN
2	0.5	30 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

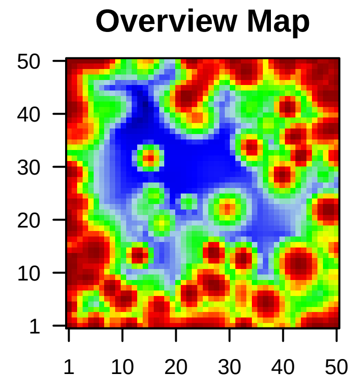
Overexpression Spots

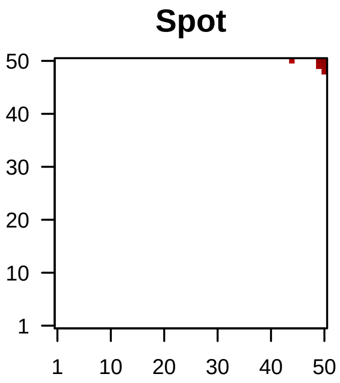
Spot Summary: N1

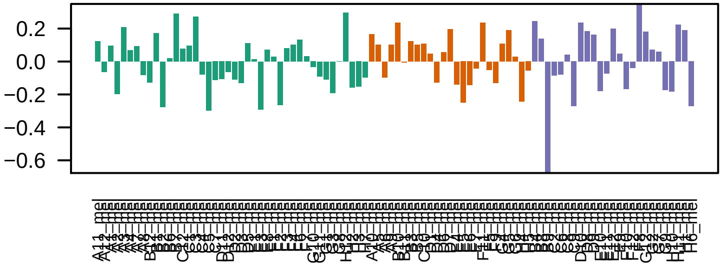
metagenes = 6
genes = 130

<r> metagenes = 0.89
<r> genes = 0.08
beta: r2= 1.95 / log p= −Inf

samples with spot = 16 (17.4 %)
MSC1 : 4 (9.5 %)
MSC2 : 4 (16 %)
MSC3 : 8 (32 %)


Overview Map


Spot

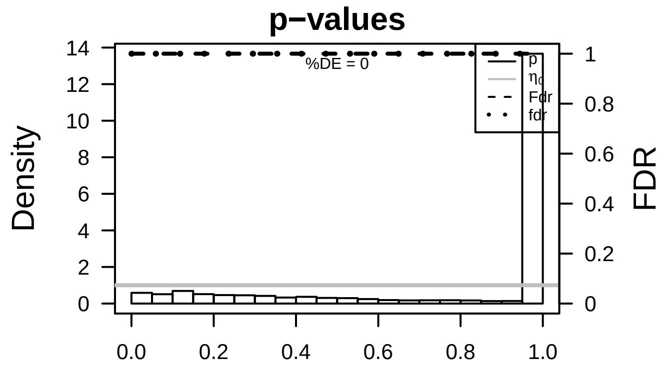


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ITIH3	2.03	−0.28	0.21	ITIH3	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
2	LUZP6	1.88	−1.03	0.3	LUZP6	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
3	ZFP62	1.82	−0.44	0.25	ZFP62	ZFP62 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:
4	C1orf109	1.77	−0.59	0.29	C1orf109	chromosome 1 open reading frame 109 [Source:HGNC Symb
5	AP4M1	1.75	−0.28	0.24	AP4M1	adaptor−related protein complex 4, mu 1 subunit [Source:HG
6	UGP2	1.7	−1.72	0.24	UGP2	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;
7	NLRC5	1.7	−0.18	0.25	NLRC5	NLR family, CARD domain containing 5 [Source:HGNC Symb
8	SRXN1	1.67	−0.81	0.3	SRXN1	sulfiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:16132]
9	ICA1	1.66	−0.29	0.3	ICA1	islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:H
10	RFT1	1.6	−0.52	0.29	RFT1	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
11	IMMP2L	1.59	−0.86	0.29	IMMP2L	IMP2 inner mitochondrial membrane peptidase−like (S. cerev
12	SPATA20	1.59	−0.29	0.29	SPATA20	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
13	LETMD1	1.52	−0.56	0.19	LETMD1	LETM1 domain containing 1 [Source:HGNC Symbol;Acc:HG
14	ASL	1.51	−0.56	0.28	ASL	argininosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:7
15	TRAPPC8	1.51	−0.98	0.27	TRAPPC8	trafficking protein particle complex 8 [Source:HGNC Symbol;
16	TMEM143	1.49	−0.18	0.36	TMEM143	transmembrane protein 143 [Source:HGNC Symbol;Acc:HG
17	MTG2	1.45	−0.44	0.25	MTG2	mitochondrial ribosome−associated GTPase 2 [Source:HGN
18	ZMYM2	1.44	−0.7	0.41	ZMYM2	zinc finger, MYM−type 2 [Source:HGNC Symbol;Acc:HGNC:1
19	ZNF184	1.43	−0.29	0.27	ZNF184	zinc finger protein 184 [Source:HGNC Symbol;Acc:HGNC:12
20	TMEM63A	1.42	−0.27	0.25	TMEM63A	transmembrane protein 63A [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−09	113 / 9482	Colon	TssA_Colon
2	8e−09	109 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	9e−08	107 / 9027	Colon	Tx_Colon
4	1e−06	107 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	1e−06	88 / 6929	Lympl	HOPP_Txn_elongation
6	2e−06	108 / 9528	Brain	Overlap_fetal_midbrain_Quies
7	9e−06	99 / 8580	Colon	TxWk_Colon
8	9e−06	96 / 8205	CC	cytoplasm
9	9e−06	91 / 7592	Lympl	HOPP_Active_promoter
10	3e−05	25 / 1171	TF	KIM_MYC targets
11	4e−05	24 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
12	8e−05	43 / 2798	Colon	TxEnhG1_Colon
13	9e−05	13 / 424	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
14	1e−04	13 / 435	GSEA	GARY_CD5_TARGETS_UP
15	1e−04	66 / 5155	Colon	EnhWk1_Colon
16	1e−04	27 / 1468	CC	mitochondrion
17	3e−04	3 / 15	CC	BLOC−1 complex
18	3e−04	3 / 15	BP	nucleoside metabolic process
19	3e−04	103 / 9653	Colon	Enh_Colon
20	3e−04	13 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
21	4e−04	8 / 200	GSEA	LINSLEY_MIR16_TARGETS
22	5e−04	20 / 1008	GSEA	BRUINS_UVC_RESPONSE_LATE
23	5e−04	71 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
24	6e−04	82 / 7203	Colon	TssF_Colon
25	6e−04	82 / 7209	Lympl	HOPP_Weak_promoter
26	7e−04	9 / 274	miRN	hsa−miR−1244
27	1e−03	33 / 2193	CC	extracellular exosome
28	1e−03	15 / 689	Chr	Chr 7
29	1e−03	4 / 52	miRN	hsa−miR−345
30	2e−03	62 / 5184	Lympl	HOPP_Txn_transition
31	2e−03	4 / 60	GSEA	SESTO_RESPONSE_TO_UV_C7
32	2e−03	4 / 62	GSEA	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
33	2e−03	7 / 206	GSEA	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4
34	3e−03	14 / 683	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
35	3e−03	3 / 32	GSEA	LEE_CALORIE_RESTRICTION_MUSCLE_UP
36	3e−03	8 / 277	BP	translation
37	3e−03	2 / 10	CC	WASH complex
38	3e−03	7 / 222	GSEA	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
39	4e−03	2 / 11	BP	barbed−end actin filament capping
40	4e−03	4 / 75	miRN	hsa−miR−651


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 111	HORVATH_aging_genes meth UP
2	1.0	0 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 15	nucleoside metabolic process
2	3e−03	8 / 277	translation
3	4e−03	2 / 11	barbed−end actin filament capping
4	7e−03	2 / 15	lipid particle organization
5	8e−03	3 / 46	response to unfolded protein
6	9e−03	2 / 17	superoxide metabolic process
7	1e−02	2 / 20	oligodendrocyte development
8	1e−02	24 / 1730	small molecule metabolic process
9	2e−02	2 / 22	negative regulation of JNK cascade
10	2e−02	3 / 62	negative regulation of catalytic activity
11	2e−02	2 / 23	carbohydrate transport
12	2e−02	2 / 23	endoplasmic reticulum organization
13	2e−02	2 / 24	positive regulation of mitotic cell cycle
14	2e−02	3 / 66	activation of signaling protein activity involved in unfolded protein response
15	2e−02	3 / 67	Ras protein signal transduction
16	2e−02	2 / 26	cellular response to glucose starvation
17	2e−02	2 / 26	negative regulation of protein kinase B signaling
18	2e−02	3 / 69	movement of cell or subcellular component
19	2e−02	117 / 12397	biological_process
20	2e−02	6 / 255	cellular amino acid metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	8e−09	109 / 9013	Overlap_fetal_midbrain_K9K27me3
2	1e−06	107 / 9330	Overlap_fetal_midbrain_ReprPC
3	2e−06	108 / 9528	Overlap_fetal_midbrain_Quies
4	5e−04	71 / 5940	Overlap_fetal_midbrain_HetRpts
5	1e−02	8 / 349	Fetal_ZNF
6	3e−02	11 / 656	Overlap_fetal_midbrain_EnhP
7	6e−02	88 / 9020	Overlap_fetal_midbrain_ReprPCWk
8	2e−01	32 / 3081	Mid_Frontal_Lobe_ZNF
9	2e−01	9 / 765	Mid_Frontal_Lobe_Het
10	3e−01	9 / 831	Fetal_HetRpts
11	4e−01	9 / 884	Overlap_fetal_midbrain_EnhG
12	4e−01	2 / 158	Overlap_fetal_midbrain_Het
13	4e−01	10 / 1050	Fetal_EnhP
14	5e−01	3 / 304	Fetal_Het
15	5e−01	12 / 1333	Fetal_ReprPCWk
16	5e−01	10 / 1122	Fetal_K9K27me3
17	7e−01	3 / 383	Fetal_Tx
18	7e−01	6 / 769	Overlap_fetal_midbrain_ZNF
19	7e−01	8 / 1065	Overlap_fetal_midbrain_Enh
20	8e−01	1 / 163	Fetal_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	LIU_PROSTATE_CANCER_UP
2	0.1	1 / 16	GENTLES_modul7
3	0.2	1 / 29	KUIPER_MM good survival
4	0.5	1 / 70	SHAUGHNESSY_MM high risk
5	0.5	1 / 82	PanCan_TXmisReg_geneset_nanostring
6	0.7	1 / 120	PanCan_CC+Apop_geneset_nanostring
7	0.7	1 / 121	PanCan_MAPK_geneset_nanostring
8	0.7	2 / 298	SPANG_BCL6−index2
9	0.8	1 / 180	SPANG_LPS−index2
10	0.8	3 / 489	Lembcke_Normal vs Adenoma
11	1.0	1 / 401	Lembcke_Colonic Inflammation
12	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
13	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	1.0	0 / 12	LIU_BREAST_CANCER
17	1.0	0 / 14	LIU_COMMON_CANCER_GENES
18	1.0	0 / 14	LIU_LIVER_CANCER
19	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
20	1.0	0 / 15	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−06	96 / 8205	cytoplasm
2	1e−04	27 / 1468	mitochondrion
3	3e−04	3 / 15	BLOC−1 complex
4	1e−03	33 / 2193	extracellular exosome
5	3e−03	2 / 10	WASH complex
6	5e−03	5 / 128	ribosome
7	9e−03	9 / 401	mitochondrial inner membrane
8	9e−03	2 / 17	integral component of mitochondrial outer membrane
9	1e−02	2 / 21	clathrin adaptor complex
10	2e−02	32 / 2507	cytosol
11	2e−02	2 / 22	pre−autophagosomal structure
12	2e−02	2 / 24	mitochondrial ribosome
13	3e−02	103 / 10605	intracellular
14	4e−02	2 / 37	chromosome, telomeric region
15	4e−02	36 / 3132	extracellular region
16	5e−02	2 / 42	synaptic vesicle membrane
17	7e−02	7 / 412	lysosome
18	8e−02	2 / 53	acrosomal vesicle
19	8e−02	2 / 54	transport vesicle
20	9e−02	95 / 9988	organelle

Chr

Rank	p−value	#in/all	Geneset
1	0.001	15 / 689	Chr 7
2	0.017	12 / 687	Chr 6
3	0.044	4 / 151	Chr 21
4	0.078	11 / 775	Chr 12
5	0.270	5 / 398	Chr 20
6	0.306	3 / 221	Chr 18
7	0.380	5 / 462	Chr 14
8	0.505	6 / 649	Chr 16
9	0.585	4 / 465	Chr 15
10	0.606	7 / 838	Chr 3
11	0.672	2 / 262	Chr 13
12	0.673	12 / 1500	Chr 1
13	0.709	6 / 801	Chr 11
14	0.717	4 / 552	Chr 10
15	0.725	4 / 558	Chr 4
16	0.748	4 / 576	Chr 9
17	0.751	6 / 840	Chr 17
18	0.775	7 / 993	Chr 2
19	0.795	2 / 335	Chr 22
20	0.864	4 / 696	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−09	113 / 9482	TssA_Colon
2	9e−08	107 / 9027	Tx_Colon
3	9e−06	99 / 8580	TxWk_Colon
4	8e−05	43 / 2798	TxEnhG1_Colon
5	1e−04	66 / 5155	EnhWk1_Colon
6	3e−04	103 / 9653	Enh_Colon
7	6e−04	82 / 7203	TssF_Colon
8	3e−02	85 / 8415	Quies3_Colon
9	5e−02	61 / 5880	TssD2_Colon
10	6e−02	1 / 7	Marisa_CRC−C5
11	7e−02	1 / 8	KIM_CRC−MSI−regulated_DN
12	7e−02	1 / 8	Juehling−MSI−enriched−in−7
13	1e−01	97 / 10290	TssWk_Colon
14	2e−01	3 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	2e−01	11 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
16	2e−01	8 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
17	2e−01	9 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
18	3e−01	5 / 427	Quies2_Colon
19	3e−01	8 / 739	TxEnhG2_Colon
20	3e−01	26 / 2698	EnhA_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.7	3 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.04	1 / 5	Phillips Prolif up vs PN & MES
2	0.04	2 / 38	OL vs. OPC
3	0.06	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.07	12 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.09	2 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
6	0.09	1 / 11	astrocytes_glio
7	0.09	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
8	0.09	6 / 356	Down_a
9	0.13	2 / 72	laffaire_hypermeth_LGG_vs_control
10	0.13	1 / 16	VERHAAK_NL subtype
11	0.20	2 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	0.21	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
13	0.22	5 / 365	Down_b
14	0.22	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	0.28	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
16	0.28	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
17	0.30	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
18	0.33	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
19	0.34	1 / 47	Vishal_subnetwork signature of survival in GBM
20	0.39	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	24 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
2	9e−05	13 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
3	1e−04	13 / 435	GARY_CD5_TARGETS_UP
4	3e−04	13 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
5	4e−04	8 / 200	LINSLEY_MIR16_TARGETS
6	5e−04	20 / 1008	BRUINS_UVC_RESPONSE_LATE
7	2e−03	4 / 60	SESTO_RESPONSE_TO_UV_C7
8	2e−03	4 / 62	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
9	2e−03	7 / 206	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4
10	3e−03	14 / 683	MARTENS_TRETINOIN_RESPONSE_DN
11	3e−03	3 / 32	LEE_CALORIE_RESTRICTION_MUSCLE_UP
12	3e−03	7 / 222	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
13	4e−03	8 / 293	DOUGLAS_BMI1_TARGETS_DN
14	5e−03	4 / 80	SASSON_RESPONSE_TO_FORSKOLIN_UP
15	6e−03	5 / 129	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP
16	7e−03	15 / 843	LOPEZ_MBD_TARGETS
17	7e−03	3 / 45	CHIBA_RESPONSE_TO_TSA
18	7e−03	16 / 930	NUYTTEN_EZH2_TARGETS_UP
19	8e−03	9 / 393	MITSIADES_RESPONSE_TO_APLIDIN_UP
20	8e−03	3 / 47	TONG_INTERACT_WITH_PTTG1

HM

Rank	p−value	#in/all	Geneset
1	0.02	5 / 174	HALLMARK_HEME_METABOLISM
2	0.05	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.06	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	0.06	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
5	0.07	4 / 176	HALLMARK_HYPOXIA
6	0.09	2 / 57	HALLMARK_MYC_TARGETS_V2
7	0.09	4 / 196	HALLMARK_MTORC1_SIGNALING
8	0.12	3 / 137	HALLMARK_UV_RESPONSE_DN
9	0.14	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	0.19	2 / 91	HALLMARK_PROTEIN_SECRETION
11	0.21	3 / 181	HALLMARK_P53_PATHWAY
12	0.24	2 / 107	HALLMARK_COAGULATION
13	0.25	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.30	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
15	0.35	2 / 140	HALLMARK_APOPTOSIS
16	0.42	2 / 162	HALLMARK_COMPLEMENT
17	0.43	2 / 165	HALLMARK_MYOGENESIS
18	0.43	2 / 167	HALLMARK_APICAL_JUNCTION
19	0.44	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	0.48	2 / 183	HALLMARK_GLYCOLYSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−06	88 / 6929	HOPP_Txn_elongation
2	9e−06	91 / 7592	HOPP_Active_promoter
3	6e−04	82 / 7209	HOPP_Weak_promoter
4	2e−03	62 / 5184	HOPP_Txn_transition
5	7e−03	2 / 15	DAVE_Immune response 2
6	3e−02	61 / 5693	HOPP_Weak_enhancer
7	7e−02	16 / 1218	SPANG_BCR UP
8	7e−02	15 / 1128	SPANG_BCR DN
9	8e−02	1 / 10	DAVE_BL_DN
10	1e−01	56 / 5538	HOPP_Weak_txn
11	1e−01	1 / 13	Subero_MCL_hypo_meth
12	1e−01	1 / 14	Subero_mBL_hypo_meth
13	1e−01	64 / 6564	HOPP_Strong_enhancer
14	2e−01	2 / 80	Aukema_BCL2 DN_BCL6 UP
15	2e−01	1 / 20	SPANG_BAFF 9hrs UP
16	2e−01	4 / 268	SPANG_IL21 UP
17	2e−01	1 / 29	Subero_DLBCL_hypo_meth
18	2e−01	1 / 30	TARTE_B−cell signature
19	2e−01	1 / 30	Subero_INT_hypo_meth
20	3e−01	4 / 294	TARTE_Plasmablast signature

MF

Rank	p−value	#in/all	Geneset
1	0.01	10 / 501	identical protein binding
2	0.02	2 / 26	protein kinase inhibitor activity
3	0.02	8 / 394	catalytic activity
4	0.02	3 / 71	structural constituent of ribosome
5	0.03	4 / 136	lyase activity
6	0.05	3 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
7	0.05	3 / 95	hydrolase activity, acting on glycosyl bonds
8	0.08	2 / 53	transferase activity
9	0.08	1 / 10	cAMP response element binding protein binding
10	0.08	1 / 10	leucine zipper domain binding
11	0.08	1 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
12	0.08	1 / 10	lipid transporter activity
13	0.08	1 / 10	protein−lysine N−methyltransferase activity
14	0.09	9 / 609	cytoskeletal protein binding
15	0.09	1 / 11	acetyltransferase activity
16	0.09	1 / 11	ATPase activity, coupled
17	0.09	1 / 11	methyl−CpG binding
18	0.10	1 / 12	low−density lipoprotein particle receptor binding
19	0.10	1 / 12	MAP kinase activity
20	0.11	1 / 13	fatty acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	9 / 274	hsa−miR−1244
2	1e−03	4 / 52	hsa−miR−345
3	4e−03	4 / 75	hsa−miR−651
4	5e−03	6 / 178	hsa−miR−34b
5	5e−03	6 / 179	hsa−miR−520f
6	5e−03	5 / 126	hsa−miR−335
7	6e−03	3 / 42	hsa−miR−129−3p
8	7e−03	4 / 85	hsa−miR−423−5p
9	8e−03	7 / 261	hsa−miR−548p
10	9e−03	3 / 48	hsa−miR−628−5p
11	1e−02	4 / 100	hsa−miR−574−5p
12	1e−02	3 / 56	hsa−miR−384
13	2e−02	3 / 60	hsa−miR−526b*
14	2e−02	7 / 303	hsa−miR−18b
15	2e−02	5 / 175	hsa−miR−548k
16	3e−02	5 / 189	hsa−miR−513a−3p
17	3e−02	4 / 127	hsa−miR−323−3p
18	3e−02	8 / 408	hsa−miR−497
19	3e−02	4 / 130	hsa−miR−383
20	3e−02	2 / 30	hsa−miR−1293

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_myc.1
2	0.1	1 / 15	BENTINK_ras.6
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	GUSTAFSON_PI3K_DN
5	1.0	0 / 14	BENTINK_e2f3.1
6	1.0	0 / 12	BENTINK_e2f3.2
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−05	25 / 1171	KIM_MYC targets
2	3e−02	27 / 2137	ICGC_SrfV0416101_targets
3	4e−02	19 / 1400	ICGC_Myc_targets
4	4e−02	51 / 4689	ICGC_Taf1_targets
5	4e−02	19 / 1418	ICGC_Ets1_targets
6	5e−02	26 / 2136	ICGC_GabpPcr2_targets
7	5e−02	44 / 4032	ICGC_Creb1_targets
8	6e−02	47 / 4385	ICGC_Atf2_targets
9	7e−02	21 / 1701	HEBENSTREIT_high expression TF
10	7e−02	17 / 1314	ICGC_Usf1_targets
11	8e−02	10 / 690	ICGC_Atf3_targets
12	1e−01	48 / 4706	ICGC_Sp1_targets
13	1e−01	49 / 4829	ICGC_Nficsc81335_targets
14	2e−01	49 / 4909	ICGC_Stat5_targets
15	2e−01	53 / 5408	ICGC_Pou2_targets
16	2e−01	53 / 5495	ICGC_Yy1_targets
17	2e−01	40 / 4054	ICGC_Egr1_targets
18	2e−01	8 / 653	ICGC_SrfPcr2_targets
19	2e−01	43 / 4414	ICGC_Bclaf101388_targets
20	2e−01	50 / 5219	ICGC_Tcf3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.4	1 / 59	VAQUERIZAS_Whole blood
2	0.7	1 / 143	VAQUERIZAS_General
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 26	VAQUERIZAS_Liver
6	1.0	0 / 33	VAQUERIZAS_Prostate
7	1.0	0 / 29	VAQUERIZAS_Smooth muscle
8	1.0	0 / 45	VAQUERIZAS_Uterus
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 29	VAQUERIZAS_Fetal lung
16	1.0	0 / 58	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 23	VAQUERIZAS_Trachea
19	1.0	0 / 11	VAQUERIZAS_Fetal liver
20	1.0	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.09	1 / 11	WIRTH_Sec. lymphoid organs
2	0.09	1 / 11	WIRTH_Cortex cerebri
3	0.14	4 / 225	PALMER_Granulocytes signature up
4	0.57	1 / 95	WIRTH_Muscle
5	0.60	3 / 350	WIRTH_Immune system
6	0.60	3 / 350	WIRTH_Nervous System
7	0.63	1 / 114	PALMER_T−Cell signature up
8	0.82	1 / 194	PALMER_B−Cell signature up
9	1.00	0 / 32	WIRTH_Pancreas
10	1.00	0 / 11	WIRTH_Prim. lymphoid organs
11	1.00	0 / 13	WIRTH_B−cells
12	1.00	0 / 8	WIRTH_Tonsil
13	1.00	0 / 12	WIRTH_Thymus
14	1.00	0 / 12	WIRTH_Lymphocytes
15	1.00	0 / 5	WIRTH_Bone marrow
16	1.00	0 / 11	WIRTH_Globus pallidus
17	1.00	0 / 14	WIRTH_Telencephalon
18	1.00	0 / 10	WIRTH_Hippocampus
19	1.00	0 / 10	WIRTH_Thalamus
20	1.00	0 / 12	WIRTH_Cerebellum

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	31 / 3682	LU_BPDE 0.005 DN
2	0.8	8 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: O1

metagenes = 6
genes = 148

<r> metagenes = 0.99
<r> genes = 0.29
beta: r2= 0.75 / log p= −Inf

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

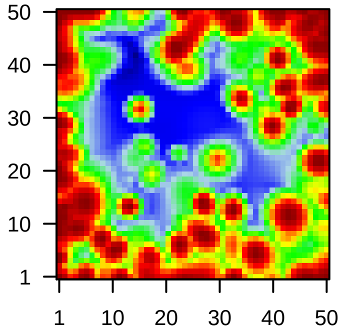
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PRDM6	2.01	−0.06	0.5	PRDM6	PR domain containing 6 [Source:HGNC Symbol;Acc:HGNC:9
2	ZNF221	1.83	−0.1	0.43	ZNF221	zinc finger protein 221 [Source:HGNC Symbol;Acc:HGNC:13
3	SLC22A1	1.81	−0.09	0.66	SLC22A1	solute carrier family 22 (organic cation transporter), member
4	THBS3	1.78	−0.1	0.52	THBS3	thrombospondin 3 [Source:HGNC Symbol;Acc:HGNC:11787]
5	TBC1D19	1.77	−0.25	0.44	TBC1D19	TBC1 domain family, member 19 [Source:HGNC Symbol;Acc
6	SPTLC3	1.76	−0.07	0.57	SPTLC3	serine palmitoyltransferase, long chain base subunit 3 [Sourc
7	SLC25A42	1.76	−0.06	0.63	SLC25A42	solute carrier family 25, member 42 [Source:HGNC Symbol;A
8	PFKFB4	1.74	−0.13	0.5	PFKFB4	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 4 [S
9	PFKP	1.73	−0.4	0.4	PFKP	phosphofructokinase, platelet [Source:HGNC Symbol;Acc:HG
10	RNASET2	1.72	−0.12	0.51	RNASET2	ribonuclease T2 [Source:HGNC Symbol;Acc:HGNC:21686]
11	ZNF34	1.71	−0.21	0.29	ZNF34	zinc finger protein 34 [Source:HGNC Symbol;Acc:HGNC:130
12	HIP1	1.71	−0.31	0.32	HIP1	huntingtin interacting protein 1 [Source:HGNC Symbol;Acc:H
13	ZACN	1.7	−0.24	0.45	ZACN	zinc activated ligand−gated ion channel [Source:HGNC Symb
14	TLCD1	1.7	−0.09	0.49	TLCD1	TLC domain containing 1 [Source:HGNC Symbol;Acc:HGNC:
15	DEPDC7	1.7	−0.22	0.3	DEPDC7	DEP domain containing 7 [Source:HGNC Symbol;Acc:HGNC
16	STAP2	1.7	−0.09	0.64	STAP2	signal transducing adaptor family member 2 [Source:HGNC S
17	PLA2G1B	1.69	−0.02	0.92	PLA2G1B	phospholipase A2, group IB (pancreas) [Source:HGNC Symb
18	GTF2A1L	1.67	−0.02	0.92	GTF2A1L	general transcription factor IIA, 1−like [Source:HGNC Symbol
19	ROPN1L	1.67	−0.06	0.55	ROPN1L	rhophilin associated tail protein 1−like [Source:HGNC Symbol
20	CDKL3	1.67	−0.29	0.26	CDKL3	cyclin−dependent kinase−like 3 [Source:HGNC Symbol;Acc:H

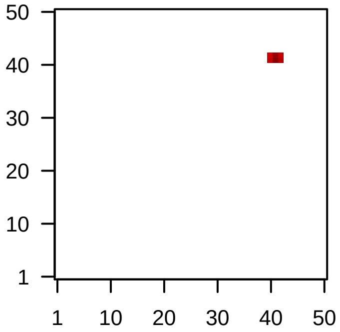
Geneset Overrepresentation

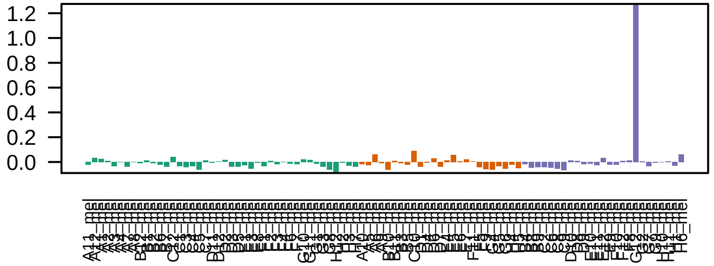
Rank	p−value	#in/all	Geneset	
1	2e−04	42 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
2	2e−04	35 / 1907	Brain	Fetal_TxTrans
3	4e−04	47 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
4	7e−04	51 / 3396	Lymph	HOPP_Repressed
5	9e−04	9 / 250	Colon	K9K27me3_Colon
6	1e−03	4 / 46	MF	manganese ion binding
7	2e−03	3 / 27	GSEA	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN
8	2e−03	4 / 57	GSEA	REACTOME_GLUCOSE_METABOLISM
9	3e−03	34 / 2142	Colon	ReprPC_Colon
10	3e−03	3 / 30	GSEA	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
11	3e−03	2 / 9	GSEA	HASEGAWA_TUMORIGENESIS_BY_RET_C634R
12	4e−03	5 / 104	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
13	4e−03	2 / 10	GSEA	REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT
14	4e−03	4 / 67	GSEA	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
15	5e−03	3 / 34	BP	cellular response to glucose stimulus
16	5e−03	31 / 1949	Brain	Fetal_TssF
17	5e−03	10 / 383	Brain	Fetal_Tx
18	5e−03	4 / 69	Glio	GIEZELT_GBM_STSwt_up_VS_LTSwt
19	5e−03	4 / 70	GSEA	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
20	6e−03	30 / 1889	Colon	ReprPCWk_Colon
21	6e−03	3 / 37	GSEA	ROSS_AML_WITH_CBFB_MYH11_FUSION
22	6e−03	2 / 12	CC	basal part of cell
23	6e−03	2 / 12	BP	embryonic digestive tract morphogenesis
24	7e−03	2 / 13	BP	embryonic morphogenesis
25	7e−03	2 / 13	BP	positive regulation of chondrocyte differentiation
26	7e−03	2 / 13	GSEA	PID_CONE_PATHWAY
27	7e−03	3 / 40	GSEA	ELLWOOD_MYC_TARGETS_DN
28	8e−03	3 / 41	BP	positive regulation of MAP kinase activity
29	8e−03	33 / 2188	Lymph	HOPP_Poised_promoter
30	8e−03	2 / 14	BP	drug transmembrane transport
31	8e−03	2 / 14	GSEA	PID_RHODOPSIN_PATHWAY
32	9e−03	6 / 180	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
33	1e−02	5 / 133	GSEA	ZHANG_BREAST_CANCER_PROGENITORS_DN
34	1e−02	3 / 47	GSEA	WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN
35	1e−02	3 / 47	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_D
36	1e−02	16 / 884	Brain	Overlap_fetal_midbrain_EnhG
37	1e−02	3 / 52	CC	secretory granule
38	1e−02	2 / 19	CC	ciliary base
39	1e−02	2 / 19	MF	ion transmembrane transporter activity
40	2e−02	4 / 96	GSEA	XU_GH1_EXOGENOUS_TARGETS_DN

Overview Map

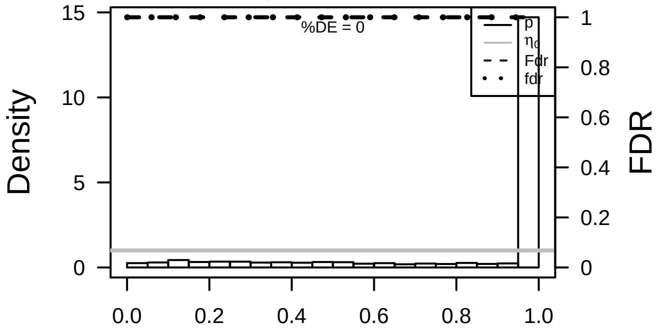


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	3 / 111	HORVATH_aging_genes meth UP
2	0.3	1 / 38	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 100	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.005	3 / 34	cellular response to glucose stimulus
2	0.006	2 / 12	embryonic digestive tract morphogenesis
3	0.007	2 / 13	embryonic morphogenesis
4	0.007	2 / 13	positive regulation of chondrocyte differentiation
5	0.008	3 / 41	positive regulation of MAP kinase activity
6	0.008	2 / 14	drug transmembrane transport
7	0.016	2 / 20	carbohydrate phosphorylation
8	0.018	2 / 21	regulation of rhodopsin mediated signaling pathway
9	0.020	2 / 22	rhodopsin mediated signaling pathway
10	0.020	4 / 104	glucose metabolic process
11	0.022	2 / 23	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion m
12	0.024	3 / 62	phototransduction, visible light
13	0.025	2 / 25	positive regulation of BMP signaling pathway
14	0.028	3 / 66	female pregnancy
15	0.029	2 / 27	photoreceptor cell maintenance
16	0.033	2 / 29	glycogen metabolic process
17	0.035	5 / 182	dephosphorylation
18	0.035	2 / 30	activation of JUN kinase activity
19	0.038	4 / 128	visual perception
20	0.047	2 / 35	glycolytic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−04	42 / 2462	Mid_Frontal_Lobe_HetRpts
2	2e−04	35 / 1907	Fetal_TxTrans
3	4e−04	47 / 2972	Mid_Frontal_Lobe_ReprPC
4	5e−03	31 / 1949	Fetal_TssF
5	5e−03	10 / 383	Fetal_Tx
6	1e−02	16 / 884	Overlap_fetal_midbrain_EnhG
7	2e−02	20 / 1207	Overlap_fetal_midbrain_TssF
8	2e−02	31 / 2185	Fetal_TssA
9	3e−02	23 / 1548	Mid_Frontal_Lobe_K9K27me3
10	3e−02	17 / 1065	Overlap_fetal_midbrain_Enh
11	4e−02	26 / 1845	Fetal_Quies
12	8e−02	15 / 1013	Fetal_TssP
13	8e−02	11 / 686	Overlap_fetal_midbrain_TssA
14	9e−02	13 / 862	Overlap_fetal_midbrain_TxTrans
15	1e−01	9 / 564	Mid_Frontal_Lobe_EnhP
16	1e−01	10 / 668	Mid_Frontal_Lobe_Enh
17	2e−01	16 / 1236	Mid_Frontal_Lobe_ReprPCWk
18	2e−01	3 / 156	Mid_Frontal_Lobe_TssA
19	2e−01	9 / 656	Overlap_fetal_midbrain_EnhP
20	2e−01	8 / 574	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	GENTLES_modul17
2	0.1	1 / 13	GENTLES_modul12
3	0.1	1 / 15	RHODES_CANCER_META_SIGNATURE
4	0.1	1 / 15	GENTLES_modul11
5	0.2	2 / 82	PanCan_TXmisReg_geneset_nanostring
6	0.2	1 / 22	PanCan_HH_geneset_nanostring
7	0.2	3 / 156	PanCan_PI3K_geneset_nanostring
8	0.3	4 / 298	SPANG_BCL6−index2
9	0.4	6 / 489	Lembcke_Normal vs Adenoma
10	0.4	1 / 55	PanCan_JAK−ST_geneset_nanostring
11	0.5	0 / 14	LIU_COMMON_CANCER_GENES
12	0.5	2 / 180	SPANG_LPS−index2
13	0.5	0 / 14	LIU_PROSTATE_CANCER_DN
14	0.6	0 / 12	LIU_PROSTATE_CANCER_UP
15	0.7	1 / 111	PanCan_RAS_geneset_nanostring
16	0.7	1 / 121	PanCan_MAPK_geneset_nanostring
17	0.8	3 / 401	Lembcke_Colonic Inflammation
18	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
19	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	0.006	2 / 12	basal part of cell
2	0.015	3 / 52	secretory granule
3	0.015	2 / 19	ciliary base
4	0.027	2 / 26	basal plasma membrane
5	0.030	5 / 175	early endosome
6	0.031	2 / 28	SCF ubiquitin ligase complex
7	0.032	5 / 178	apical plasma membrane
8	0.055	3 / 87	recycling endosome
9	0.065	2 / 42	photoreceptor outer segment
10	0.079	2 / 47	endocytic vesicle
11	0.092	3 / 108	late endosome
12	0.095	1 / 10	cell−cell contact zone
13	0.095	1 / 10	MHC class I protein complex
14	0.095	1 / 10	myosin filament
15	0.100	2 / 54	transport vesicle
16	0.104	1 / 11	photoreceptor outer segment membrane
17	0.113	1 / 12	actomyosin
18	0.121	1 / 13	microvillus membrane
19	0.130	1 / 14	clathrin−coated vesicle membrane
20	0.132	3 / 127	cytoplasmic vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.02	13 / 689	Chr 7
2	0.08	11 / 687	Chr 6
3	0.08	11 / 696	Chr 5
4	0.09	15 / 1037	Chr 19
5	0.18	8 / 551	Chr X
6	0.31	6 / 462	Chr 14
7	0.31	8 / 649	Chr 16
8	0.32	17 / 1500	Chr 1
9	0.32	10 / 840	Chr 17
10	0.48	6 / 558	Chr 4
11	0.48	3 / 262	Chr 13
12	0.50	5 / 469	Chr 8
13	0.65	2 / 221	Chr 18
14	0.76	3 / 398	Chr 20
15	0.84	6 / 838	Chr 3
16	0.89	5 / 775	Chr 12
17	0.90	5 / 801	Chr 11
18	0.93	3 / 576	Chr 9
19	0.95	2 / 465	Chr 15
20	0.97	5 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	9 / 250	K9K27me3_Colon
2	3e−03	34 / 2142	ReprPC_Colon
3	6e−03	30 / 1889	ReprPCWk_Colon
4	3e−02	21 / 1386	Het_Colon
5	5e−02	8 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
6	5e−02	29 / 2159	TssP_Colon
7	6e−02	19 / 1317	EnhP_Colon
8	7e−02	2 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
9	9e−02	6 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
10	1e−01	45 / 3812	TssD1_Colon
11	1e−01	1 / 11	Budinska_B_Lower crypt−like_DOWN
12	1e−01	9 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	1e−01	1 / 13	TCGA−CRC_less−agressive−disease−markers
14	1e−01	7 / 427	Quies2_Colon
15	1e−01	1 / 15	Budinska_B_Lower crypt−like_UP
16	2e−01	32 / 2698	EnhA_Colon
17	2e−01	13 / 1038	HetRpts_Colon
18	2e−01	43 / 3897	Quies1_Colon
19	2e−01	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
20	3e−01	5 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	0.9	2 / 435	GUDJ_psoriasis up
2	0.9	1 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.005	4 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
2	0.029	1 / 3	Donson−migration tethering and rolling−associated with LTS in HGA
3	0.039	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
4	0.044	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
5	0.064	7 / 356	Down_a
6	0.086	1 / 9	VERHAAK_Brain
7	0.139	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
8	0.160	2 / 72	laffaire_hypermeth_LGG_vs_control
9	0.167	2 / 74	WIRTH_Normal Brain
10	0.170	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
11	0.250	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
12	0.251	1 / 29	shaw_responders_down_in_oligo_glioma
13	0.261	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
14	0.308	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
15	0.315	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
16	0.326	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	0.352	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
18	0.374	1 / 47	mature astrocytes
19	0.374	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
20	0.405	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	3 / 27	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN
2	0.002	4 / 57	REACTOME_GLUCOSE_METABOLISM
3	0.003	3 / 30	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
4	0.003	2 / 9	HASEGAWA_TUMORIGENESIS_BY_RET_C634R
5	0.004	5 / 104	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
6	0.004	2 / 10	REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT
7	0.004	4 / 67	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
8	0.005	4 / 70	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
9	0.006	3 / 37	ROSS_AML_WITH_CBFB_MYH11_FUSION
10	0.007	2 / 13	PID_CONE_PATHWAY
11	0.007	3 / 40	ELLWOOD_MYC_TARGETS_DN
12	0.008	2 / 14	PID_RHODOPSIN_PATHWAY
13	0.009	6 / 180	COLDREN_GEFITINIB_RESISTANCE_DN
14	0.010	5 / 133	ZHANG_BREAST_CANCER_PROGENITORS_DN
15	0.011	3 / 47	WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN
16	0.011	3 / 47	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN
17	0.015	4 / 96	XU_GH1_EXOGENOUS_TARGETS_DN
18	0.016	2 / 20	RICKMAN_HEAD_AND_NECK_CANCER_D
19	0.018	8 / 333	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
20	0.018	3 / 56	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP

HM

Rank	p−value	#in/all	Geneset
1	0.09	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	0.09	3 / 107	HALLMARK_COAGULATION
3	0.21	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	0.23	3 / 167	HALLMARK_APICAL_JUNCTION
5	0.25	3 / 176	HALLMARK_HYPOXIA
6	0.37	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	0.43	2 / 148	HALLMARK_KRAS_SIGNALING_UP
8	0.45	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	0.48	2 / 162	HALLMARK_COMPLEMENT
10	0.49	2 / 165	HALLMARK_MYOGENESIS
11	0.49	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.50	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.52	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.52	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	0.54	2 / 183	HALLMARK_GLYCOLYSIS
16	0.62	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
17	0.75	1 / 137	HALLMARK_UV_RESPONSE_DN
18	0.76	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
19	0.77	1 / 146	HALLMARK_DNA_REPAIR
20	0.77	1 / 146	HALLMARK_UV_RESPONSE_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−04	51 / 3396	HOPP_Repressed
2	8e−03	33 / 2188	HOPP_Poised_promoter
3	4e−02	1 / 4	Shaknovich_ABC_hyper_meth
4	8e−02	1 / 8	MASCQUE_ABC UP
5	9e−02	3 / 107	SPANG_LPS 6hrs UP
6	9e−02	1 / 10	DAVE_BL_DN
7	1e−01	1 / 13	YAMANE_AICDA_targets_recruited
8	1e−01	1 / 14	Subero_mBL_hypo_meth
9	1e−01	1 / 15	WRIGHT_ABC UP
10	2e−01	1 / 17	DAVE_NFkB BL DN
11	2e−01	30 / 2563	HOPP_Heterochrom
12	2e−01	62 / 5693	HOPP_Weak_enhancer
13	2e−01	60 / 5538	HOPP_Weak_txn
14	3e−01	1 / 30	Subero_INT_hypo_meth
15	3e−01	1 / 33	LEE_Developmental_regulators
16	3e−01	1 / 34	Subero_B−ALL_hyper_meth
17	3e−01	4 / 280	SPANG_CD40 6hrs UP
18	4e−01	3 / 247	ZHANG_DLBCL mutated
19	5e−01	3 / 268	SPANG_IL21 UP
20	5e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 46	manganese ion binding
2	0.015	2 / 19	ion transmembrane transporter activity
3	0.016	8 / 325	protein serine/threonine kinase activity
4	0.018	9 / 398	protein tyrosine kinase activity
5	0.020	13 / 691	kinase activity
6	0.023	2 / 24	snoRNA binding
7	0.024	6 / 223	phosphatase activity
8	0.031	4 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activit
9	0.032	3 / 70	phospholipid binding
10	0.035	9 / 451	protein kinase activity
11	0.040	9 / 461	transferase activity, transferring phosphorus−containing groups
12	0.040	60 / 4992	ion binding
13	0.081	9 / 530	calcium ion binding
14	0.085	2 / 49	pyridoxal phosphate binding
15	0.094	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
16	0.095	1 / 10	oxidoreductase activity, acting on paired donors, with incorporation or reductic
17	0.095	1 / 10	Rac guanyl−nucleotide exchange factor activity
18	0.095	1 / 10	ribosomal small subunit binding
19	0.095	1 / 10	transaminase activity
20	0.098	3 / 111	protein binding, bridging

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	2 / 28	hsa−miR−1292
2	0.05	1 / 5	hsa−miR−585
3	0.06	1 / 6	hsa−miR−937
4	0.06	2 / 41	hsa−miR−532−3p
5	0.14	1 / 15	hsa−miR−551a
6	0.18	3 / 146	hsa−miR−655
7	0.18	3 / 147	hsa−miR−506
8	0.19	4 / 228	hsa−miR−124
9	0.20	3 / 157	hsa−miR−548o
10	0.20	1 / 23	hsa−miR−1250
11	0.21	2 / 85	hsa−miR−567
12	0.21	2 / 85	hsa−miR−510
13	0.22	1 / 25	hsa−miR−941
14	0.25	1 / 29	hsa−miR−486−5p
15	0.25	4 / 258	hsa−miR−520e
16	0.26	3 / 180	hsa−miR−302e
17	0.27	1 / 31	hsa−miR−296−5p
18	0.28	2 / 104	hsa−miR−210
19	0.30	2 / 112	hsa−miR−875−3p
20	0.30	5 / 370	hsa−miR−144

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	GUSTAFSON_PI3K_UP
2	1.0	0 / 13	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	BENTINK_e2f3.1
4	1.0	0 / 12	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	19 / 1139	HEBENSTREIT_low expression TF
2	0.07	10 / 595	ICGC_NrsfPcr2_targets
3	0.53	29 / 2927	ICGC_Rad21_targets
4	0.54	13 / 1314	ICGC_Usf1_targets
5	0.63	19 / 2013	ICGC_Bcl11_targets
6	0.63	6 / 653	ICGC_SrfPcr2_targets
7	0.65	41 / 4314	ICGC_Ebfsc137065_targets
8	0.68	6 / 690	ICGC_Atf3_targets
9	0.69	17 / 1872	ICGC_Mef2_targets
10	0.72	11 / 1266	ICGC_NrsfPcr1_targets
11	0.73	36 / 3924	ICGC_Zeb1_targets
12	0.75	44 / 4774	ICGC_Foxm1_targets
13	0.75	57 / 6114	ICGC_Runx3_targets
14	0.81	47 / 5200	ICGC_Mta3_targets
15	0.83	11 / 1400	ICGC_Myc_targets
16	0.85	15 / 1878	ICGC_Cebpbsc150_targets
17	0.87	47 / 5355	ICGC_Pol2_targets
18	0.88	47 / 5374	ICGC_Pax5_targets
19	0.88	31 / 3700	ICGC_Nfatc1_targets
20	0.88	48 / 5495	ICGC_Yy1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 17	VAQUERIZAS_Heart
2	0.2	3 / 143	VAQUERIZAS_General
3	0.2	1 / 23	VAQUERIZAS_Spinal cord
4	0.3	1 / 38	VAQUERIZAS_Whole brain
5	0.3	1 / 38	VAQUERIZAS_Testis
6	0.4	1 / 45	VAQUERIZAS_Uterus
7	1.0	0 / 36	VAQUERIZAS_Fetal brain
8	1.0	0 / 41	VAQUERIZAS_Placenta
9	1.0	0 / 26	VAQUERIZAS_Liver
10	1.0	0 / 33	VAQUERIZAS_Prostate
11	1.0	0 / 29	VAQUERIZAS_Smooth muscle
12	1.0	0 / 9	VAQUERIZAS_Kidney
13	1.0	0 / 37	VAQUERIZAS_Thymus
14	1.0	0 / 40	VAQUERIZAS_Thyroid
15	1.0	0 / 59	VAQUERIZAS_Whole blood
16	1.0	0 / 7	VAQUERIZAS_Appendix
17	1.0	0 / 29	VAQUERIZAS_Fetal lung
18	1.0	0 / 58	VAQUERIZAS_Lung
19	1.0	0 / 16	VAQUERIZAS_Pancreas
20	1.0	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	3 / 95	WIRTH_Muscle
2	0.09	1 / 10	WIRTH_Hippocampus
3	0.10	1 / 11	WIRTH_Prim. lymphoid organs
4	0.27	5 / 350	WIRTH_Nervous System
5	0.27	1 / 32	WIRTH_Pancreas
6	0.27	1 / 32	WIRTH_Placenta
7	0.29	2 / 107	WIRTH_Testis
8	0.31	2 / 114	PALMER_T−Cell signature up
9	0.37	1 / 46	WIRTH_Liver
10	0.66	2 / 225	PALMER_Granulocytes signature up
11	0.68	3 / 350	WIRTH_Immune system
12	1.00	0 / 11	WIRTH_Sec. lymphoid organs
13	1.00	0 / 13	WIRTH_B−cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 12	WIRTH_Lymphocytes
17	1.00	0 / 5	WIRTH_Bone marrow
18	1.00	0 / 11	WIRTH_Globus pallidus
19	1.00	0 / 14	WIRTH_Telencephalon
20	1.00	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	45 / 3682	LU_BPDE 0.005 DN
2	0.93	7 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

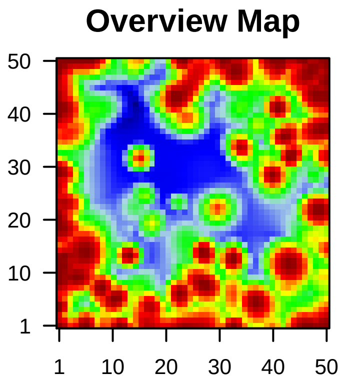
Overexpression Spots

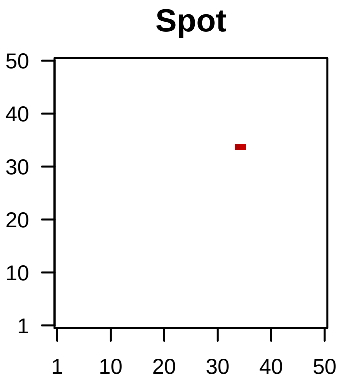
Spot Summary: P1

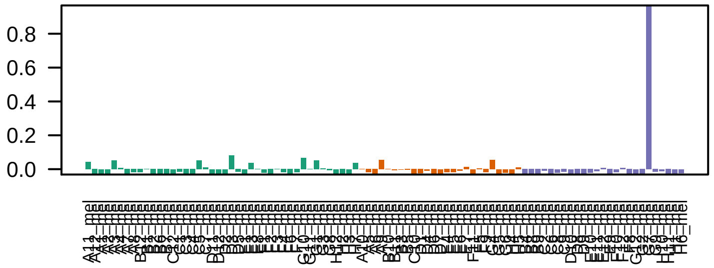
metagenes = 2
genes = 36

<r> metagenes = 0.99
<r> genes = 0.56
beta: r2= 0.05 / log p= −1.53

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)


Overview Map


Spot

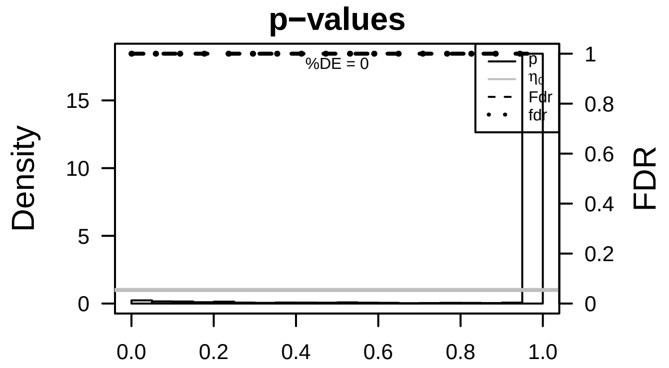


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	HIST3H3	1.77	−0.04	0.57	HIST3H3	histone cluster 3, H3 [Source:HGNC Symbol;Acc:HGNC:477
2	EBLN2	1.67	−0.1	0.33	EBLN2	endogenous Bornavirus−like nucleoprotein 2 [Source:HGNC
3	MAGEA3	1.66	−0.03	0.64	MAGEA3	melanoma antigen family A3 [Source:HGNC Symbol;Acc:HG
4	HECW2	1.53	−0.02	0.78	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein lig
5	C9orf153	1.47	−0.04	0.7	C9orf153	chromosome 9 open reading frame 153 [Source:HGNC Sym
6	JAKMIP2	1.47	−0.07	0.33	JAKMIP2	janus kinase and microtubule interacting protein 2 [Source:H
7	PYGM	1.43	−0.02	0.79	PYGM	phosphorylase, glycogen, muscle [Source:HGNC Symbol;Ac
8	MGST1	1.42	−0.04	0.57	MGST1	microsomal glutathione S−transferase 1 [Source:HGNC Sym
9	TRPM8	1.39	−0.08	0.51	TRPM8	transient receptor potential cation channel, subfamily M, mem
10	PEX11G	1.29	−0.02	0.79	PEX11G	peroxisomal biogenesis factor 11 gamma [Source:HGNC Syn
11	CXorf65	1.27	−0.04	0.43	CXorf65	chromosome X open reading frame 65 [Source:HGNC Symb
12	SUSD4	1.24	−0.04	0.43	SUSD4	sushi domain containing 4 [Source:HGNC Symbol;Acc:HGN
13	PRPH	1.24	−0.02	0.8	PRPH	peripherin [Source:HGNC Symbol;Acc:HGNC:9461]
14	MAGEA6	1.21	−0.03	0.81	MAGEA6	melanoma antigen family A6 [Source:HGNC Symbol;Acc:HG
15	OR14I1	1.2	−0.03	0.59	OR14I1	olfactory receptor, family 14, subfamily I, member 1 [Source:
16	SCCPDH	1.18	−0.02	0.41	SCCPDH	saccharopine dehydrogenase (putative) [Source:HGNC Sym
17	ZNF792	1.11	−0.04	0.51	ZNF792	zinc finger protein 792 [Source:HGNC Symbol;Acc:HGNC:24
18	PIK3AP1	1.09	−0.02	0.77	PIK3AP1	phosphoinositide−3−kinase adaptor protein 1 [Source:HGNC
19	HIST1H2AK	1.08	−0.03	0.58	HIST1H2AK	histone cluster 1, H2ak [Source:HGNC Symbol;Acc:HGNC:47
20	SEPT3	1.08	−0.04	0.38	SEPT3	septin 3 [Source:HGNC Symbol;Acc:HGNC:10750]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−05	15 / 2159	Colon	TssP_Colon
2	6e−04	2 / 15	BP	protein homotrimerization
3	6e−04	2 / 15	GSEA	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
4	7e−04	10 / 1317	Colon	EnhP_Colon
5	8e−04	3 / 79	CC	nucleosome
6	9e−04	7 / 686	Brain	Overlap_fetal_midbrain_TssA
7	1e−03	2 / 22	GSEA	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP
8	2e−03	3 / 97	GSEA	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	2e−03	3 / 98	GSEA	CERVERA_SDHB_TARGETS_1_UP
10	2e−03	3 / 104	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
11	2e−03	2 / 28	GSEA	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
12	2e−03	5 / 391	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2
13	2e−03	5 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
14	2e−03	16 / 3396	Lymp	HOPP_Repressed
15	3e−03	2 / 32	CC	nuclear nucleosome
16	3e−03	2 / 32	BP	protein heterotetramerization
17	3e−03	12 / 2142	Colon	ReprPC_Colon
18	4e−03	2 / 40	GSEA	JAEGER_METASTASIS_UP
19	5e−03	2 / 43	GSEA	YU_MYC_TARGETS_DN
20	5e−03	2 / 45	GSEA	ZHAN_MULTIPLE_MYELOMA_PR_UP
21	6e−03	2 / 48	Canc	KUIPER_MM poor survival
22	6e−03	4 / 312	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
23	7e−03	1 / 3	GSEA	BAFNA_MUC4_TARGETS_DN
24	8e−03	2 / 58	BP	cellular calcium ion homeostasis
25	9e−03	2 / 62	GSEA	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP
26	1e−02	5 / 574	Brain	Overlap_fetal_midbrain_TssP
27	1e−02	2 / 67	GSEA	HILLION_HMGA1B_TARGETS
28	1e−02	3 / 197	GSEA	BENPORATH_MYC_TARGETS_WITH_EBOX
29	1e−02	4 / 373	MF	protein heterodimerization activity
30	1e−02	1 / 5	GSEA	CHOI_ATL_ACUTE_STAGE
31	1e−02	2 / 72	GSEA	REACTOME_MEIOTIC_RECOMBINATION
32	2e−02	2 / 82	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
33	2e−02	1 / 8	Colon	Marisa_CRC−C1
34	2e−02	1 / 8	Colon	Marisa_CRC−C2
35	2e−02	1 / 8	GSEA	BIOCARTA_FEEDER_PATHWAY
36	2e−02	3 / 250	Colon	K9K27me3_Colon
37	2e−02	1 / 9	GSEA	REACTOME_ROLE_OF_DCC_IN_REGULATING_APOPTOSIS
38	2e−02	1 / 9	GSEA	VANDESLUIS_COMMD1_TARGETS_GROUP_4_DN
39	2e−02	2 / 100	Glio	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
40	2e−02	2 / 100	GSEA	REACTOME_MEIOSIS


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	6e−04	2 / 15	protein homotrimerization
2	3e−03	2 / 32	protein heterotetramerization
3	8e−03	2 / 58	cellular calcium ion homeostasis
4	2e−02	1 / 10	cellular response to electrical stimulus
5	2e−02	1 / 10	Leydig cell differentiation
6	2e−02	1 / 10	regulation of gene silencing
7	3e−02	1 / 11	intermediate filament cytoskeleton organization
8	3e−02	2 / 108	nucleosome assembly
9	3e−02	1 / 12	lipid glycosylation
10	3e−02	1 / 13	neuromuscular synaptic transmission
11	3e−02	1 / 13	skeletal muscle contraction
12	4e−02	1 / 16	skeletal muscle fiber development
13	4e−02	1 / 17	complement activation, classical pathway
14	4e−02	1 / 17	glycogen catabolic process
15	4e−02	1 / 17	negative regulation of adenylate cyclase activity
16	4e−02	1 / 17	regulation of complement activation
17	4e−02	1 / 19	positive regulation of filopodium assembly
18	4e−02	1 / 19	protein targeting to plasma membrane
19	4e−02	1 / 19	response to organonitrogen compound
20	5e−02	1 / 21	lipid storage

Brain

Rank	p−value	#in/all	Geneset
1	9e−04	7 / 686	Overlap_fetal_midbrain_TssA
2	1e−02	5 / 574	Overlap_fetal_midbrain_TssP
3	4e−02	5 / 812	Mid_Frontal_Lobe_TssP
4	5e−02	5 / 862	Overlap_fetal_midbrain_TxTrans
5	5e−02	2 / 156	Mid_Frontal_Lobe_TssA
6	7e−02	11 / 2972	Mid_Frontal_Lobe_ReprPC
7	1e−01	3 / 468	Mid_Frontal_Lobe_TssF
8	1e−01	2 / 229	Mid_Frontal_Lobe_TxTrans
9	1e−01	4 / 786	Fetal_EnhG
10	2e−01	5 / 1207	Overlap_fetal_midbrain_TssF
11	2e−01	3 / 668	Mid_Frontal_Lobe_Enh
12	4e−01	2 / 564	Mid_Frontal_Lobe_EnhP
13	4e−01	3 / 953	Fetal_Enh
14	4e−01	3 / 989	Mid_Frontal_Lobe_Quies
15	5e−01	3 / 1122	Fetal_K9K27me3
16	5e−01	4 / 1548	Mid_Frontal_Lobe_K9K27me3
17	6e−01	2 / 831	Fetal_HetRpts
18	7e−01	1 / 534	Mid_Frontal_Lobe_EnhG
19	8e−01	4 / 2185	Fetal_TssA
20	8e−01	1 / 656	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	2 / 48	KUIPER_MM poor survival
2	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
3	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	1.000	0 / 12	LIU_BREAST_CANCER
7	1.000	0 / 14	LIU_COMMON_CANCER_GENES
8	1.000	0 / 14	LIU_LIVER_CANCER
9	1.000	0 / 14	LIU_PROSTATE_CANCER_DN
10	1.000	0 / 12	LIU_PROSTATE_CANCER_UP
11	1.000	0 / 15	WANG_ER_UP
12	1.000	0 / 5	WANG_ER_DN
13	1.000	0 / 16	WOLFER_overlap genes
14	1.000	0 / 12	BEN−PORATH_DN
15	1.000	0 / 13	BEN−PORATH_UP
16	1.000	0 / 15	GENTLES_modul1
17	1.000	0 / 16	GENTLES_modul2
18	1.000	0 / 10	GENTLES_modul3
19	1.000	0 / 15	GENTLES_modul4
20	1.000	0 / 10	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	8e−04	3 / 79	nucleosome
2	3e−03	2 / 32	nuclear nucleosome
3	3e−02	1 / 11	photoreceptor outer segment membrane
4	3e−02	2 / 109	peroxisome
5	3e−02	1 / 12	dendrite membrane
6	3e−02	1 / 13	filopodium membrane
7	3e−02	1 / 14	integral component of peroxisomal membrane
8	8e−02	1 / 33	sarcoplasmic reticulum
9	8e−02	1 / 35	integral component of Golgi membrane
10	8e−02	2 / 200	axon
11	9e−02	1 / 42	photoreceptor outer segment
12	1e−01	1 / 47	lipid particle
13	1e−01	1 / 48	peroxisomal membrane
14	1e−01	1 / 51	filopodium
15	1e−01	1 / 53	intermediate filament
16	1e−01	1 / 58	neuronal postsynaptic density
17	2e−01	1 / 81	apical part of cell
18	2e−01	2 / 331	nuclear chromosome
19	2e−01	3 / 663	chromosome
20	2e−01	1 / 115	midbody

Chr

Rank	p−value	#in/all	Geneset
1	0.03	5 / 775	Chr 12
2	0.14	3 / 551	Chr X
3	0.20	4 / 993	Chr 2
4	0.23	4 / 1037	Chr 19
5	0.38	2 / 552	Chr 10
6	0.41	1 / 221	Chr 18
7	0.48	4 / 1500	Chr 1
8	0.49	2 / 687	Chr 6
9	0.49	2 / 696	Chr 5
10	0.55	1 / 335	Chr 22
11	0.60	2 / 838	Chr 3
12	0.60	2 / 840	Chr 17
13	0.74	1 / 558	Chr 4
14	0.75	1 / 576	Chr 9
15	0.86	1 / 801	Chr 11
16	1.00	0 / 262	Chr 13
17	1.00	0 / 462	Chr 14
18	1.00	0 / 465	Chr 15
19	1.00	0 / 649	Chr 16
20	1.00	0 / 398	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−05	15 / 2159	TssP_Colon
2	7e−04	10 / 1317	EnhP_Colon
3	3e−03	12 / 2142	ReprPC_Colon
4	2e−02	1 / 8	Marisa_CRC−C1
5	2e−02	1 / 8	Marisa_CRC−C2
6	2e−02	3 / 250	K9K27me3_Colon
7	3e−02	9 / 1889	ReprPCWk_Colon
8	4e−02	4 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	6e−02	2 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
10	2e−01	1 / 71	Marisa_CRC−cluster−g
11	2e−01	2 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
12	3e−01	2 / 427	Quies2_Colon
13	4e−01	2 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	5e−01	1 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
15	6e−01	1 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
16	6e−01	1 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
17	7e−01	2 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	7e−01	1 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
19	8e−01	1 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
20	8e−01	6 / 3383	EnhWk2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.5	1 / 294	GUDJ_psoriasis down
2	1.0	0 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
2	0.09	1 / 40	in vivo astrocytes vs. cultured astroglia
3	0.11	1 / 47	mature astrocytes
4	0.35	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
5	0.60	2 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	1.00	0 / 15	VERHAAK_CL subtype
7	1.00	0 / 15	VERHAAK_MES subtype
8	1.00	0 / 16	VERHAAK_NL subtype
9	1.00	0 / 14	VERHAAK_PN subtype
10	1.00	0 / 23	WIRTH_PN subtype
11	1.00	0 / 74	WIRTH_Normal Brain
12	1.00	0 / 9	VERHAAK_Brain
13	1.00	0 / 8	VERHAAK_PN_Brain
14	1.00	0 / 11	Martinez_Glio_hypermeth
15	1.00	0 / 3	Martinez_Glio_hypometh
16	1.00	0 / 2	laffaire_hypometh_LGG_vs_control
17	1.00	0 / 72	laffaire_hypermeth_LGG_vs_control
18	1.00	0 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
19	1.00	0 / 4	Donson−adaptive−immunity−associated with LTS in HGA
20	1.00	0 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	2 / 15	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
2	1e−03	2 / 22	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP
3	2e−03	3 / 97	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
4	2e−03	3 / 98	CERVERA_SDHB_TARGETS_1_UP
5	2e−03	3 / 104	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
6	2e−03	2 / 28	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
7	2e−03	5 / 391	MEISSNER_NPC_HCP_WITH_H3K4ME2
8	2e−03	5 / 400	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
9	4e−03	2 / 40	JAEGER_METASTASIS_UP
10	5e−03	2 / 43	YU_MYC_TARGETS_DN
11	5e−03	2 / 45	ZHAN_MULTIPLE_MYELOMA_PR_UP
12	6e−03	4 / 312	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
13	7e−03	1 / 3	BAFNA_MUC4_TARGETS_DN
14	9e−03	2 / 62	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP
15	1e−02	2 / 67	HILLION_HMGA1B_TARGETS
16	1e−02	3 / 197	BENPORATH_MYC_TARGETS_WITH_EBOX
17	1e−02	1 / 5	CHOI_ATL_ACUTE_STAGE
18	1e−02	2 / 72	REACTOME_MEIOTIC_RECOMBINATION
19	2e−02	2 / 82	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
20	2e−02	1 / 8	BIOCARTA_FEEDER_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.1	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.2	1 / 91	HALLMARK_BILE_ACID_METABOLISM
3	0.3	1 / 165	HALLMARK_MYOGENESIS
4	0.3	1 / 176	HALLMARK_HYPOXIA
5	1.0	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	1.0	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	1.0	0 / 195	HALLMARK_MITOTIC_SPINDLE
8	1.0	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1.0	0 / 53	HALLMARK_TGF_BETA_SIGNALING
10	1.0	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	1.0	0 / 146	HALLMARK_DNA_REPAIR
12	1.0	0 / 196	HALLMARK_G2M_CHECKPOINT
13	1.0	0 / 140	HALLMARK_APOPTOSIS
14	1.0	0 / 29	HALLMARK_NOTCH_SIGNALING
15	1.0	0 / 188	HALLMARK_ADIPOGENESIS
16	1.0	0 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
17	1.0	0 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
18	1.0	0 / 94	HALLMARK_ANDROGEN_RESPONSE
19	1.0	0 / 91	HALLMARK_PROTEIN_SECRETION
20	1.0	0 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	16 / 3396	HOPP_Repressed
2	0.063	9 / 2188	HOPP_Poised_promoter
3	0.401	7 / 2563	HOPP_Heterochrom
4	0.445	1 / 247	ZHANG_DLBCL mutated
5	0.481	1 / 275	TARTE_Mature plasma cell signature
6	0.794	2 / 1218	SPANG_BCR UP
7	0.911	3 / 2211	HOPP_Repetitive
8	0.937	1 / 1128	SPANG_BCR DN
9	0.999	7 / 6564	HOPP_Strong_enhancer
10	1.000	8 / 7209	HOPP_Weak_promoter
11	1.000	4 / 5693	HOPP_Weak_enhancer
12	1.000	3 / 5538	HOPP_Weak_txn
13	1.000	5 / 6929	HOPP_Txn_elongation
14	1.000	6 / 7592	HOPP_Active_promoter
15	1.000	2 / 5184	HOPP_Txn_transition
16	1.000	0 / 13	BENTINK_mBL UP
17	1.000	0 / 12	BENTINK_mBL DOWN
18	1.000	0 / 129	DAVE_BL−vs−DLBCL
19	1.000	0 / 10	DAVE_BL_DN
20	1.000	0 / 16	DAVE_BL Inter

MF

Rank	p−value	#in/all	Geneset
1	0.01	4 / 373	protein heterodimerization activity
2	0.02	1 / 10	acetylgalactosaminyltransferase activity
3	0.02	1 / 10	glutathione binding
4	0.03	1 / 11	glutathione peroxidase activity
5	0.03	1 / 15	hyaluronic acid binding
6	0.04	1 / 18	glutathione transferase activity
7	0.05	2 / 152	histone binding
8	0.05	1 / 22	transferase activity, transferring hexosyl groups
9	0.06	1 / 25	protein phosphatase inhibitor activity
10	0.06	1 / 26	olfactory receptor activity
11	0.08	1 / 36	calcium channel activity
12	0.09	2 / 210	transferase activity, transferring glycosyl groups
13	0.09	3 / 450	sequence−specific DNA binding
14	0.09	1 / 40	extracellular matrix structural constituent
15	0.09	1 / 41	phosphatase binding
16	0.10	1 / 46	transferase activity, transferring alkyl or aryl (other than methyl) groups
17	0.11	1 / 49	drug binding
18	0.11	1 / 49	pyridoxal phosphate binding
19	0.11	3 / 501	identical protein binding
20	0.12	1 / 53	transferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.09	1 / 40	hsa−miR−182*
2	0.12	1 / 52	hsa−miR−431
3	0.14	1 / 63	hsa−miR−1285
4	0.17	1 / 77	hsa−miR−1305
5	0.18	1 / 84	hsa−miR−486−3p
6	0.18	1 / 84	hsa−miR−220c
7	0.19	1 / 88	hsa−miR−505
8	0.19	1 / 91	hsa−miR−378
9	0.21	1 / 98	hsa−miR−147
10	0.21	1 / 100	hsa−miR−574−5p
11	0.23	1 / 108	hsa−miR−449b
12	0.25	1 / 120	hsa−miR−421
13	0.25	1 / 121	hsa−miR−543
14	0.27	2 / 428	hsa−let−7b
15	0.27	1 / 133	hsa−miR−198
16	0.28	1 / 136	hsa−miR−155
17	0.31	1 / 157	hsa−miR−450b−5p
18	0.36	1 / 189	hsa−miR−128
19	0.37	1 / 195	hsa−miR−206
20	0.38	1 / 198	hsa−miR−181c

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	1 / 19	MYC_Metabolism UP
2	0.13	1 / 59	MYC_Targets UP
3	0.51	3 / 1139	HEBENSTREIT_low expression TF
4	0.66	4 / 1872	ICGC_Mef2_targets
5	0.71	6 / 2927	ICGC_Rad21_targets
6	0.76	1 / 595	ICGC_NrsfPcr2_targets
7	0.78	3 / 1701	HEBENSTREIT_high expression TF
8	0.81	1 / 690	ICGC_Atf3_targets
9	0.83	2 / 1314	ICGC_Usf1_targets
10	0.84	4 / 2416	ICGC_Bcl3_targets
11	0.90	8 / 4682	ICGC_Pol24_targets
12	0.93	9 / 5355	ICGC_Pol2_targets
13	0.93	6 / 3924	ICGC_Zeb1_targets
14	0.93	9 / 5374	ICGC_Pax5_targets
15	0.93	8 / 4909	ICGC_Stat5_targets
16	0.94	6 / 3966	ICGC_Pu1_targets
17	0.94	9 / 5408	ICGC_Pou2_targets
18	0.94	10 / 5890	ICGC_Elf1_targets
19	0.94	6 / 4054	ICGC_Egr1_targets
20	0.95	2 / 1878	ICGC_Cebpbsc150_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 36	VAQUERIZAS_Fetal brain
2	1	0 / 41	VAQUERIZAS_Placenta
3	1	0 / 26	VAQUERIZAS_Liver
4	1	0 / 33	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 45	VAQUERIZAS_Uterus
7	1	0 / 143	VAQUERIZAS_General
8	1	0 / 9	VAQUERIZAS_Kidney
9	1	0 / 23	VAQUERIZAS_Spinal cord
10	1	0 / 38	VAQUERIZAS_Whole brain
11	1	0 / 37	VAQUERIZAS_Thymus
12	1	0 / 40	VAQUERIZAS_Thyroid
13	1	0 / 59	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 29	VAQUERIZAS_Fetal lung
16	1	0 / 58	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 23	VAQUERIZAS_Trachea
19	1	0 / 11	VAQUERIZAS_Fetal liver
20	1	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	2 / 194	PALMER_B−Cell signature up
2	0.20	1 / 95	WIRTH_Muscle
3	0.57	1 / 350	WIRTH_Nervous System
4	1.00	0 / 32	WIRTH_Pancreas
5	1.00	0 / 350	WIRTH_Immune system
6	1.00	0 / 11	WIRTH_Sec. lymphoid organs
7	1.00	0 / 11	WIRTH_Prim. lymphoid organs
8	1.00	0 / 13	WIRTH_B−cells
9	1.00	0 / 8	WIRTH_Tonsil
10	1.00	0 / 12	WIRTH_Thymus
11	1.00	0 / 12	WIRTH_Lymphocytes
12	1.00	0 / 5	WIRTH_Bone marrow
13	1.00	0 / 11	WIRTH_Globus pallidus
14	1.00	0 / 14	WIRTH_Telencephalon
15	1.00	0 / 11	WIRTH_Cortex cerebri
16	1.00	0 / 10	WIRTH_Hippocampus
17	1.00	0 / 10	WIRTH_Thalamus
18	1.00	0 / 12	WIRTH_Cerebellum
19	1.00	0 / 107	WIRTH_Testis
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	8 / 3682	LU_BPDE 0.005 DN
2	0.8	2 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Overexpression Spots

Spot Summary: Q1

metagenes = 13
genes = 95

<r> metagenes = 0.93
<r> genes = 0.12
beta: r2= 0.93 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 4 (9.5 %)
MSC2 : 1 (4 %)
MSC3 : 4 (16 %)

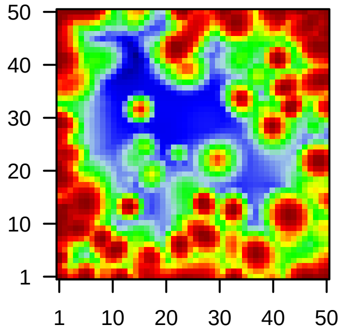
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CEBPZOS	2.03	−0.32	0.44	CEBPZOS	CEBPZ opposite strand [Source:HGNC Symbol;Acc:HGNC:4
2	PTPLA	1.83	−0.81	0.36		
3	CRYBA1	1.75	−0.08	0.38	CRYBA1	crystallin, beta A1 [Source:HGNC Symbol;Acc:HGNC:2394]
4	STX19	1.74	−0.05	0.44	STX19	syntaxin 19 [Source:HGNC Symbol;Acc:HGNC:19300]
5	MED17	1.72	−0.38	0.47	MED17	mediator complex subunit 17 [Source:HGNC Symbol;Acc:HG
6	DNAJC25−GN	1.69	−0.22	0.44	DNAJC25−GNG10	DNAJC25−GNG10 readthrough [Source:HGNC Symbol;Acc:
7	BBS7	1.69	−0.86	0.24	BBS7	Bardet−Biedl syndrome 7 [Source:HGNC Symbol;Acc:HGNC
8	ZNF436	1.67	−0.09	0.31	ZNF436	zinc finger protein 436 [Source:HGNC Symbol;Acc:HGNC:20
9	TAF1	1.65	−0.46	0.2	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)−as
10	UBE2Q1	1.64	−1.07	0.23	UBE2Q1	ubiquitin−conjugating enzyme E2Q family member 1 [Source:
11	STON1−GTF	1.64	−0.1	0.44	STON1−GTF2A1L	STON1−GTF2A1L readthrough [Source:HGNC Symbol;Acc:
12	CDK17	1.63	−0.39	0.23	CDK17	cyclin−dependent kinase 17 [Source:HGNC Symbol;Acc:HG
13	TIAM2	1.62	−0.27	0.38	TIAM2	T−cell lymphoma invasion and metastasis 2 [Source:HGNC
14	NFS1	1.6	−0.79	0.35	NFS1	NFS1 cysteine desulfurase [Source:HGNC Symbol;Acc:HGN
15	OGN	1.59	−0.17	0.36	OGN	osteoglycin [Source:HGNC Symbol;Acc:HGNC:8126]
16	C10orf131	1.59	−0.08	0.42	C10orf131	chromosome 10 open reading frame 131 [Source:HGNC Sym
17	PMP2	1.57	−0.02	0.53	PMP2	peripheral myelin protein 2 [Source:HGNC Symbol;Acc:HGN
18	SPPL2A	1.56	−0.76	0.42	SPPL2A	signal peptide peptidase like 2A [Source:HGNC Symbol;Acc:
19	WDR19	1.54	−0.49	0.28	WDR19	WD repeat domain 19 [Source:HGNC Symbol;Acc:HGNC:18
20	ASAP2	1.53	−0.23	0.24	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 [

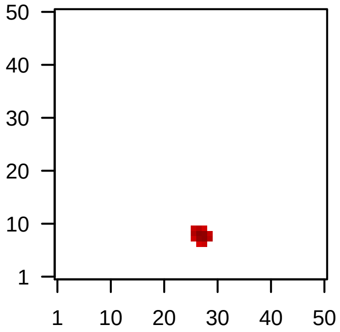
Geneset Overrepresentation

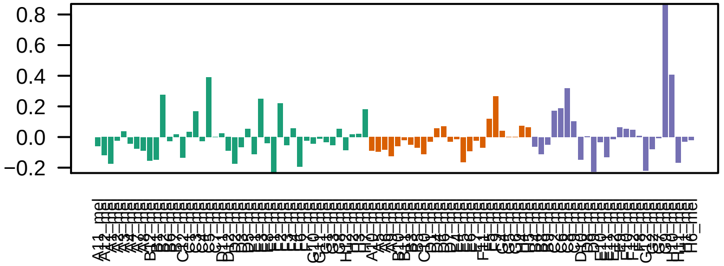
Rank	p−value	#in/all	Geneset	
1	2e−06	76 / 8580	Colon	TxWk_Colon
2	4e−06	9 / 196	miRN	hsa−miR−9
3	8e−06	65 / 6929	Lymp	HOPP_Txn_elongation
4	2e−05	58 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
5	2e−05	76 / 9027	Colon	Tx_Colon
6	4e−05	12 / 473	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
7	4e−05	72 / 8415	Colon	Quies3_Colon
8	9e−05	51 / 5184	Lymp	HOPP_Txn_transition
9	1e−04	11 / 459	miRN	hsa−miR−195
10	2e−04	11 / 479	miRN	hsa−miR−16
11	2e−04	15 / 833	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
12	2e−04	9 / 327	miRN	hsa−miR−590−3p
13	3e−04	65 / 7592	Lymp	HOPP_Active_promoter
14	3e−04	6 / 143	miRN	hsa−miR−338−5p
15	3e−04	8 / 268	miRN	hsa−miR−363
16	3e−04	7 / 203	miRN	hsa−miR−33a
17	4e−04	10 / 427	GSE	PILON_KLF1_TARGETS_UP
18	5e−04	7 / 217	MF	transcription coactivator activity
19	5e−04	4 / 58	GSE	JI_RESPONSE_TO_FSH_DN
20	6e−04	52 / 5693	Lymp	HOPP_Weak_enhancer
21	6e−04	11 / 541	miRN	hsa−miR−17
22	7e−04	3 / 28	MF	ubiquitin conjugating enzyme activity
23	8e−04	10 / 471	miRN	hsa−miR−15b
24	9e−04	4 / 67	miRN	hsa−miR−1826
25	9e−04	7 / 242	miRN	hsa−miR−26b
26	9e−04	29 / 2577	CC	nucleoplasm
27	1e−03	61 / 7209	Lymp	HOPP_Weak_promoter
28	1e−03	3 / 33	miRN	hsa−miR−934
29	1e−03	10 / 507	miRN	hsa−miR−15a
30	2e−03	78 / 10290	Colon	TssWk_Colon
31	2e−03	3 / 40	BP	androgen receptor signaling pathway
32	2e−03	8 / 370	miRN	hsa−miR−144
33	2e−03	50 / 5696	CC	nucleus
34	2e−03	6 / 215	miRN	hsa−miR−199a−3p
35	3e−03	5 / 150	miRN	hsa−miR−338−3p
36	3e−03	12 / 748	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
37	3e−03	7 / 296	miRN	hsa−miR−25
38	3e−03	73 / 9482	Colon	TssA_Colon
39	3e−03	10 / 569	miRN	hsa−miR−20b
40	3e−03	5 / 157	miRN	hsa−miR−450b−5p

Overview Map

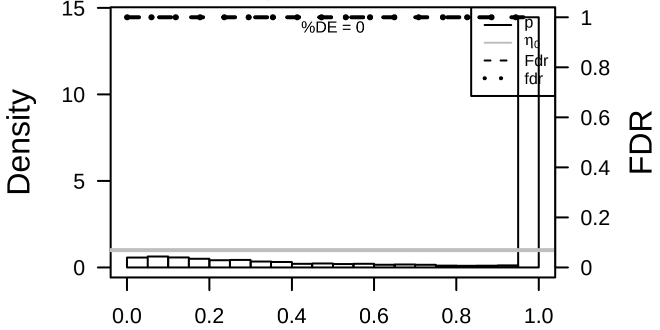


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 100	HORVATH_aging_genes meth DOWN
2	1	0 / 111	HORVATH_aging_genes meth UP
3	1	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	3 / 40	androgen receptor signaling pathway
2	0.004	2 / 15	intracellular steroid hormone receptor signaling pathway
3	0.006	3 / 59	cilium morphogenesis
4	0.008	2 / 21	negative regulation of apoptotic signaling pathway
5	0.008	2 / 22	vasculature development
6	0.009	2 / 23	limb development
7	0.018	17 / 1565	regulation of transcription, DNA−templated
8	0.018	2 / 33	protein K63−linked ubiquitination
9	0.020	2 / 34	positive regulation of interleukin−6 production
10	0.021	2 / 35	skeletal muscle cell differentiation
11	0.024	6 / 352	multicellular organismal development
12	0.028	3 / 103	cilium assembly
13	0.028	2 / 41	negative regulation of phosphatase activity
14	0.029	34 / 3980	cellular nitrogen compound metabolic process
15	0.029	2 / 42	camera−type eye development
16	0.033	2 / 45	defense response
17	0.034	2 / 46	embryonic digit morphogenesis
18	0.037	2 / 48	positive regulation of proteasomal ubiquitin−dependent protein catabolic proce
19	0.048	3 / 128	visual perception
20	0.049	2 / 56	stem cell maintenance

Brain

Rank	p−value	#in/all	Geneset
1	2e−05	58 / 5940	Overlap_fetal_midbrain_HetRpts
2	6e−03	71 / 9330	Overlap_fetal_midbrain_ReprPC
3	1e−02	68 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	5e−02	9 / 769	Overlap_fetal_midbrain_ZNF
5	6e−02	68 / 9528	Overlap_fetal_midbrain_Quies
6	1e−01	11 / 1122	Fetal_K9K27me3
7	1e−01	7 / 656	Overlap_fetal_midbrain_EnhP
8	1e−01	10 / 1050	Fetal_EnhP
9	2e−01	62 / 9013	Overlap_fetal_midbrain_K9K27me3
10	2e−01	4 / 349	Fetal_ZNF
11	3e−01	8 / 953	Fetal_Enh
12	3e−01	7 / 831	Fetal_HetRpts
13	4e−01	6 / 786	Fetal_EnhG
14	5e−01	13 / 1949	Fetal_TssF
15	5e−01	4 / 564	Mid_Frontal_Lobe_EnhP
16	5e−01	6 / 884	Overlap_fetal_midbrain_EnhG
17	5e−01	7 / 1065	Overlap_fetal_midbrain_Enh
18	6e−01	2 / 304	Fetal_Het
19	6e−01	19 / 3081	Mid_Frontal_Lobe_ZNF
20	6e−01	4 / 668	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	2 / 40	ZHANG_MM up
2	0.03	3 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.26	1 / 48	KUIPER_MM poor survival
4	0.27	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.30	1 / 55	PanCan_JAK−ST_geneset_nanostring
6	0.32	1 / 61	PanCan_Wnt_geneset_nanostring
7	0.34	0 / 14	LIU_COMMON_CANCER_GENES
8	0.36	1 / 70	SHAUGHNESSY_MM high risk
9	0.53	1 / 120	PanCan_CC+Apop_geneset_nanostring
10	0.63	1 / 156	PanCan_PI3K_geneset_nanostring
11	0.68	1 / 180	SPANG_LPS−index2
12	0.73	2 / 401	Lembcke_Colonic Inflammation
13	0.85	1 / 298	SPANG_BCL6−index2
14	0.96	1 / 489	Lembcke_Normal vs Adenoma
15	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
16	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
17	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.00	0 / 12	LIU_BREAST_CANCER
19	1.00	0 / 14	LIU_LIVER_CANCER
20	1.00	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	9e−04	29 / 2577	nucleoplasm
2	2e−03	50 / 5696	nucleus
3	2e−02	2 / 37	lateral plasma membrane
4	2e−02	3 / 99	cell cortex
5	3e−02	6 / 377	centrosome
6	4e−02	2 / 51	axoneme
7	4e−02	2 / 51	filopodium
8	5e−02	71 / 9988	organelle
9	6e−02	1 / 10	beta−catenin destruction complex
10	6e−02	1 / 10	DNA replication factor A complex
11	6e−02	1 / 10	fascia adherens
12	7e−02	1 / 11	Golgi−associated vesicle membrane
13	7e−02	1 / 11	nonmotile primary cilium
14	7e−02	1 / 12	apical junction complex
15	7e−02	1 / 12	PRC1 complex
16	8e−02	1 / 13	microvillus membrane
17	8e−02	1 / 13	SWI/SNF complex
18	9e−02	1 / 15	Ino80 complex
19	9e−02	3 / 169	transcription factor complex
20	9e−02	3 / 170	nuclear speck

Chr

Rank	p−value	#in/all	Geneset
1	0.01	9 / 576	Chr 9
2	0.10	10 / 993	Chr 2
3	0.15	13 / 1500	Chr 1
4	0.28	6 / 696	Chr 5
5	0.28	7 / 838	Chr 3
6	0.28	7 / 840	Chr 17
7	0.35	4 / 469	Chr 8
8	0.46	4 / 552	Chr 10
9	0.50	2 / 262	Chr 13
10	0.55	5 / 775	Chr 12
11	0.57	3 / 465	Chr 15
12	0.64	4 / 687	Chr 6
13	0.72	2 / 398	Chr 20
14	0.82	3 / 689	Chr 7
15	0.87	2 / 551	Chr X
16	0.87	2 / 558	Chr 4
17	0.89	3 / 801	Chr 11
18	0.92	2 / 649	Chr 16
19	0.95	1 / 462	Chr 14
20	0.96	3 / 1037	Chr 19

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	76 / 8580	TxWk_Colon
2	2e−05	76 / 9027	Tx_Colon
3	4e−05	72 / 8415	Quies3_Colon
4	2e−03	78 / 10290	TssWk_Colon
5	3e−03	12 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
6	3e−03	73 / 9482	TssA_Colon
7	2e−02	9 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	3e−02	1 / 5	Juehling−MSI−enriched−in−8−to−9
9	6e−02	1 / 9	KIM_MSI−in−EC
10	1e−01	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
11	1e−01	1 / 16	Vilar_non−hypermutated−in−CRC
12	1e−01	10 / 1079	ZNF_Colon
13	2e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
14	3e−01	8 / 1038	HetRpts_Colon
15	3e−01	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
16	4e−01	26 / 3812	TssD1_Colon
17	4e−01	47 / 7203	TssF_Colon
18	5e−01	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
19	5e−01	4 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
20	5e−01	3 / 436	K9acLow_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.6	2 / 294	GUDJ_psoriasis down
2	1.0	0 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.009	3 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	0.017	11 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
3	0.036	2 / 47	Vishal_subnetwork signature of survival in GBM
4	0.056	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
5	0.056	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
6	0.056	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
7	0.062	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
8	0.062	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−A_UP
9	0.068	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
10	0.102	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
11	0.136	1 / 23	Donson−Misc immune function−associated with LTS in HGA
12	0.152	1 / 26	Christensen_hypomethylated_in_ependymoma
13	0.189	1 / 33	Christensen_hypomethylated_in_primary_glioblastoma
14	0.210	1 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
15	0.210	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
16	0.220	1 / 39	OPC
17	0.225	1 / 40	in vivo astrocytes vs. cultured astroglia
18	0.272	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
19	0.282	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
20	0.309	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	12 / 473	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
2	2e−04	15 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
3	4e−04	10 / 427	PILON_KLF1_TARGETS_UP
4	5e−04	4 / 58	JI_RESPONSE_TO_FSH_DN
5	3e−03	5 / 157	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
6	4e−03	7 / 310	DAZARD_RESPONSE_TO_UV_NHEK_DN
7	4e−03	13 / 890	ACEVEDO_LIVER_CANCER_UP
8	5e−03	13 / 911	BENPORATH_NANOG_TARGETS
9	5e−03	3 / 54	MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_DN
10	7e−03	12 / 840	GEORGES_TARGETS_OF_MIR192_AND_MIR215
11	7e−03	4 / 118	DAZARD_RESPONSE_TO_UV_SCC_DN
12	7e−03	2 / 20	NABA_PROTEOGLYCANS
13	7e−03	4 / 121	PID_P53_DOWNSTREAM_PATHWAY
14	8e−03	2 / 21	HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_UP
15	1e−02	10 / 675	BENPORATH_SOX2_TARGETS
16	1e−02	2 / 25	TSENG_ADIPOGENIC_POTENTIAL_UP
17	1e−02	14 / 1123	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
18	1e−02	2 / 26	RIZ_ERYTHROID_DIFFERENTIATION_HEMGN
19	1e−02	4 / 141	WHITFIELD_CELL_CYCLE_M_G1
20	1e−02	8 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.05	2 / 57	HALLMARK_MYC_TARGETS_V2
2	0.06	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
3	0.11	3 / 181	HALLMARK_P53_PATHWAY
4	0.20	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.22	2 / 137	HALLMARK_UV_RESPONSE_DN
6	0.29	1 / 53	HALLMARK_TGF_BETA_SIGNALING
7	0.29	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	0.29	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	0.29	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.35	2 / 195	HALLMARK_MITOTIC_SPINDLE
11	0.38	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	0.44	1 / 91	HALLMARK_PROTEIN_SECRETION
13	0.45	1 / 94	HALLMARK_ANDROGEN_RESPONSE
14	0.45	1 / 95	HALLMARK_SPERMATOGENESIS
15	0.50	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
16	0.59	1 / 140	HALLMARK_APOPTOSIS
17	0.61	1 / 148	HALLMARK_KRAS_SIGNALING_UP
18	0.65	1 / 165	HALLMARK_MYOGENESIS
19	0.66	1 / 167	HALLMARK_APICAL_JUNCTION
20	0.67	1 / 174	HALLMARK_HEME_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−06	65 / 6929	HOPP_Txn_elongation
2	9e−05	51 / 5184	HOPP_Txn_transition
3	3e−04	65 / 7592	HOPP_Active_promoter
4	6e−04	52 / 5693	HOPP_Weak_enhancer
5	1e−03	61 / 7209	HOPP_Weak_promoter
6	4e−03	48 / 5538	HOPP_Weak_txn
7	3e−02	24 / 2563	HOPP_Heterochrom
8	4e−02	13 / 1218	SPANG_BCR UP
9	7e−02	1 / 11	Subero_T−ALL_hypo_meth
10	7e−02	49 / 6564	HOPP_Strong_enhancer
11	1e−01	1 / 25	Subero_T−PLL_hypo_meth
12	2e−01	18 / 2211	HOPP_Repetitive
13	2e−01	3 / 268	SPANG_IL21 UP
14	4e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
15	5e−01	2 / 256	SPANG_IL21 DN
16	6e−01	2 / 294	TARTE_Plasmablast signature
17	6e−01	7 / 1128	SPANG_BCR DN
18	7e−01	1 / 212	LENZ_Stromal signature 1
19	8e−01	1 / 280	SPANG_CD40 6hrs UP
20	9e−01	1 / 410	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	5e−04	7 / 217	transcription coactivator activity
2	7e−04	3 / 28	ubiquitin conjugating enzyme activity
3	4e−03	2 / 15	lysine−acetylated histone binding
4	8e−03	8 / 456	protein binding transcription factor activity
5	1e−02	68 / 8984	protein binding
6	1e−02	7 / 386	nucleotide binding
7	1e−02	2 / 27	thyroid hormone receptor binding
8	1e−02	2 / 28	RNA polymerase II activating transcription factor binding
9	1e−02	2 / 29	ubiquitin−like protein transferase activity
10	2e−02	2 / 33	estrogen receptor binding
11	3e−02	2 / 39	androgen receptor binding
12	3e−02	20 / 2037	DNA binding
13	4e−02	2 / 47	ligand−dependent nuclear receptor transcription coactivator activity
14	4e−02	6 / 397	transcription factor binding
15	4e−02	3 / 123	ubiquitin protein ligase activity
16	5e−02	4 / 217	GTPase activator activity
17	5e−02	2 / 56	transcription cofactor activity
18	6e−02	2 / 62	protein phosphatase binding
19	6e−02	11 / 1033	nucleic acid binding
20	6e−02	1 / 10	histone methyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−06	9 / 196	hsa−miR−9
2	1e−04	11 / 459	hsa−miR−195
3	2e−04	11 / 479	hsa−miR−16
4	2e−04	9 / 327	hsa−miR−590−3p
5	3e−04	6 / 143	hsa−miR−338−5p
6	3e−04	8 / 268	hsa−miR−363
7	3e−04	7 / 203	hsa−miR−33a
8	6e−04	11 / 541	hsa−miR−17
9	8e−04	10 / 471	hsa−miR−15b
10	9e−04	4 / 67	hsa−miR−1826
11	9e−04	7 / 242	hsa−miR−26b
12	1e−03	3 / 33	hsa−miR−934
13	1e−03	10 / 507	hsa−miR−15a
14	2e−03	8 / 370	hsa−miR−144
15	2e−03	6 / 215	hsa−miR−199a−3p
16	3e−03	5 / 150	hsa−miR−338−3p
17	3e−03	7 / 296	hsa−miR−25
18	3e−03	10 / 569	hsa−miR−20b
19	3e−03	5 / 157	hsa−miR−450b−5p
20	3e−03	4 / 97	hsa−miR−544

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	1 / 13	GUSTAFSON_PI3K_DN
2	0.09	1 / 14	BENTINK_src.2
3	0.09	1 / 15	BENTINK_ras.6
4	1.00	0 / 12	GUSTAFSON_PI3K_UP
5	1.00	0 / 14	BENTINK_e2f3.1
6	1.00	0 / 12	BENTINK_e2f3.2
7	1.00	0 / 13	BENTINK_myc.1
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 9	BENTINK_ras.4
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	26 / 2714	ICGC_Irf4_targets
2	0.03	15 / 1400	ICGC_Myc_targets
3	0.05	19 / 2013	ICGC_Bcl11_targets
4	0.05	8 / 653	ICGC_SrfPcr2_targets
5	0.06	7 / 553	ICGC_RxraPcr1_targets
6	0.07	37 / 4706	ICGC_Sp1_targets
7	0.08	7 / 595	ICGC_NrsfPcr2_targets
8	0.10	13 / 1383	ICGC_Six5_targets
9	0.10	12 / 1266	ICGC_NrsfPcr1_targets
10	0.11	12 / 1273	ICGC_P300_targets
11	0.12	18 / 2137	ICGC_SrfV0416101_targets
12	0.14	30 / 3924	ICGC_Zeb1_targets
13	0.14	35 / 4682	ICGC_Pol24_targets
14	0.14	33 / 4385	ICGC_Atf2_targets
15	0.14	35 / 4689	ICGC_Taf1_targets
16	0.16	36 / 4879	ICGC_Pmlsc71910_targets
17	0.16	28 / 3700	ICGC_Nfatc1_targets
18	0.17	34 / 4617	ICGC_Tcf12_targets
19	0.18	14 / 1701	HEBENSTREIT_high expression TF
20	0.19	17 / 2136	ICGC_GabpPcr2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.6	1 / 143	VAQUERIZAS_General
2	1.0	0 / 36	VAQUERIZAS_Fetal brain
3	1.0	0 / 41	VAQUERIZAS_Placenta
4	1.0	0 / 26	VAQUERIZAS_Liver
5	1.0	0 / 33	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 45	VAQUERIZAS_Uterus
8	1.0	0 / 9	VAQUERIZAS_Kidney
9	1.0	0 / 23	VAQUERIZAS_Spinal cord
10	1.0	0 / 38	VAQUERIZAS_Whole brain
11	1.0	0 / 37	VAQUERIZAS_Thymus
12	1.0	0 / 40	VAQUERIZAS_Thyroid
13	1.0	0 / 59	VAQUERIZAS_Whole blood
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 29	VAQUERIZAS_Fetal lung
16	1.0	0 / 58	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 23	VAQUERIZAS_Trachea
19	1.0	0 / 11	VAQUERIZAS_Fetal liver
20	1.0	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 11	WIRTH_Prim. lymphoid organs
2	0.25	1 / 46	WIRTH_Liver
3	0.38	1 / 74	WIRTH_Mucosa
4	0.42	2 / 225	PALMER_Granulocytes signature up
5	0.49	1 / 107	WIRTH_Testis
6	0.52	1 / 114	PALMER_T−Cell signature up
7	0.65	2 / 350	WIRTH_Immune system
8	0.65	2 / 350	WIRTH_Nervous System
9	0.71	1 / 194	PALMER_B−Cell signature up
10	1.00	0 / 32	WIRTH_Pancreas
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 13	WIRTH_B−cells
13	1.00	0 / 8	WIRTH_Tonsil
14	1.00	0 / 12	WIRTH_Thymus
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	23 / 3682	LU_BPDE 0.005 DN
2	0.7	6 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

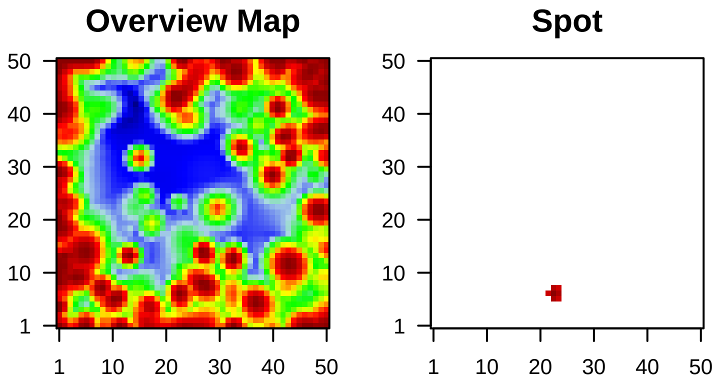
Overexpression Spots

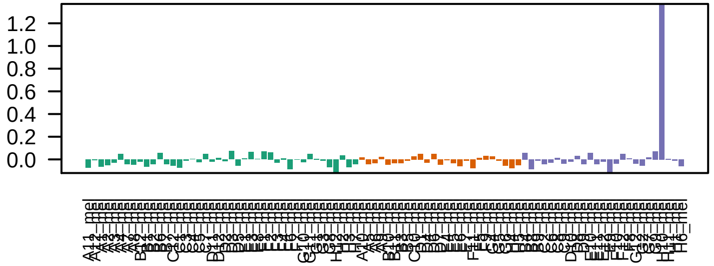
Spot Summary: R1

metagenes = 7
genes = 116

<r> metagenes = 0.98
<r> genes = 0.26
beta: r2= 0.88 / log p= −Inf

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)



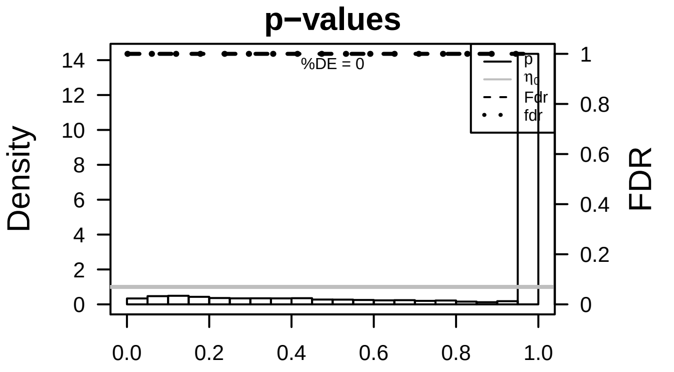


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	MDGA1	2.66	−0.09	0.7	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor
2	UCN	2.09	−0.09	0.57	UCN	urocortin [Source:HGNC Symbol;Acc:HGNC:12516]
3	FAM214A	2.08	−0.56	0.27	FAM214A	family with sequence similarity 214, member A [Source:HGN
4	LACE1	1.9	−0.39	0.28	LACE1	lactation elevated 1 [Source:HGNC Symbol;Acc:HGNC:1641
5	BEND7	1.89	−0.18	0.51	BEND7	BEN domain containing 7 [Source:HGNC Symbol;Acc:HGNC
6	MFSD9	1.89	−0.22	0.46	MFSD9	major facilitator superfamily domain containing 9 [Source:HG
7	PCOLCE	1.89	−0.09	0.58	PCOLCE	procollagen C−endopeptidase enhancer [Source:HGNC Sym
8	PPP1R3E	1.88	−0.08	0.55	PPP1R3E	protein phosphatase 1, regulatory subunit 3E [Source:HGNC
9	ZNF625−ZNF	1.87	−0.15	0.35	ZNF625−ZNF20	ZNF625−ZNF20 readthrough (NMD candidate) [Source:HGN
10	GAB3	1.85	−0.1	0.46	GAB3	GRB2−associated binding protein 3 [Source:HGNC Symbol;
11	LAT	1.85	−0.11	0.49	LAT	linker for activation of T cells [Source:HGNC Symbol;Acc:HG
12	AGO2	1.83	−0.49	0.27	AGO2	argonaute RISC catalytic component 2 [Source:HGNC Symb
13	LRP5L	1.81	−0.12	0.47	LRP5L	low density lipoprotein receptor−related protein 5−like [Sourc
14	SOX9	1.79	−0.07	0.66	SOX9	SRY (sex determining region Y)−box 9 [Source:HGNC Symb
15	ENGASE	1.77	−0.15	0.45	ENGASE	endo−beta−N−acetylglucosaminidase [Source:HGNC Symbo
16	CHAC1	1.75	−0.08	0.65	CHAC1	ChaC glutathione−specific gamma−glutamylcyclotransferase
17	PBX3	1.71	−0.1	0.48	PBX3	pre−B−cell leukemia homeobox 3 [Source:HGNC Symbol;Ac
18	CDK3	1.7	−0.08	0.61	CDK3	cyclin−dependent kinase 3 [Source:HGNC Symbol;Acc:HGN
19	HYDIN	1.68	−0.04	0.73	HYDIN	HYDIN, axonemal central pair apparatus protein [Source:HG
20	PIM2	1.68	−0.31	0.37	PIM2	Pim−2 proto−oncogene, serine/threonine kinase [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	0.001	3 / 27	GSEA	ZHAN_MULTIPLE_MYELOMA_DN
2	0.002	3 / 30	BP	epithelial to mesenchymal transition
3	0.002	37 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
4	0.002	4 / 66	GSEA	BAELDE_DIABETIC_NEPHROPATHY_UP
5	0.002	6 / 167	GSEA	BROWNE_HCMV_INFECTION_18HR_UP
6	0.003	2 / 10	GSEA	FRASOR_TAMOXIFEN_RESPONSE_DN
7	0.003	8 / 304	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
8	0.003	3 / 36	GSEA	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN
9	0.003	6 / 180	miRN	hsa−miR−302e
10	0.003	16 / 966	GSEA	PEREZ_TP53_TARGETS
11	0.004	2 / 12	MF	enhancer sequence−specific DNA binding
12	0.004	2 / 12	MF	Notch binding
13	0.004	2 / 12	MF	Wnt−activated receptor activity
14	0.004	2 / 13	BP	embryonic camera−type eye morphogenesis
15	0.004	2 / 13	BP	positive regulation of chondrocyte differentiation
16	0.004	2 / 13	GSEA	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
17	0.005	2 / 14	BP	homeostasis of number of cells
18	0.006	4 / 91	BP	protein stabilization
19	0.007	2 / 16	BP	cilium movement
20	0.007	2 / 16	GSEA	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
21	0.007	2 / 16	GSEA	ZEMBUTSU_SENSITIVITY_TO_CISPLATIN
22	0.007	4 / 98	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
23	0.007	3 / 51	miRN	hsa−miR−556−3p
24	0.008	12 / 689	Chr	Chr 7
25	0.008	3 / 52	MF	hormone activity
26	0.008	3 / 52	CC	perikaryon
27	0.008	6 / 222	miRN	hsa−miR−520g
28	0.009	9 / 453	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
29	0.010	4 / 107	GSEA	SANSOM_APC_TARGETS_UP
30	0.010	7 / 307	miRN	hsa−miR−302b
31	0.010	5 / 169	CC	transcription factor complex
32	0.012	2 / 21	BP	negative regulation of Notch signaling pathway
33	0.012	7 / 314	miRN	hsa−miR−520c−3p
34	0.012	13 / 820	MF	sequence−specific DNA binding transcription factor activity
35	0.012	3 / 61	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP
36	0.012	3 / 61	GSEA	HUANG_GATA2_TARGETS_DN
37	0.012	5 / 176	miRN	hsa−miR−199b−3p
38	0.012	7 / 318	miRN	hsa−miR−302a
39	0.013	12 / 737	BP	positive regulation of transcription from RNA polymerase II promoter
40	0.013	3 / 62	BP	canonical Wnt signaling pathway



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 100	HORVATH_aging_genes meth DOWN
2	0.6	1 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	3 / 30	epithelial to mesenchymal transition
2	0.004	2 / 13	embryonic camera−type eye morphogenesis
3	0.004	2 / 13	positive regulation of chondrocyte differentiation
4	0.005	2 / 14	homeostasis of number of cells
5	0.006	4 / 91	protein stabilization
6	0.007	2 / 16	cilium movement
7	0.012	2 / 21	negative regulation of Notch signaling pathway
8	0.013	12 / 737	positive regulation of transcription from RNA polymerase II promoter
9	0.013	3 / 62	canonical Wnt signaling pathway
10	0.014	2 / 23	positive regulation of epithelial cell migration
11	0.017	2 / 26	cellular response to organic substance
12	0.021	2 / 29	glycogen metabolic process
13	0.021	2 / 29	protein localization to nucleus
14	0.022	8 / 441	negative regulation of transcription, DNA−templated
15	0.023	2 / 30	dendrite development
16	0.026	2 / 32	chondrocyte differentiation
17	0.026	2 / 32	tight junction assembly
18	0.027	2 / 33	calcium−mediated signaling
19	0.029	2 / 34	positive regulation of interleukin−6 production
20	0.035	2 / 38	cellular response to cAMP

Brain

Rank	p−value	#in/all	Geneset
1	0.002	37 / 2972	Mid_Frontal_Lobe_ReprPC
2	0.036	9 / 574	Overlap_fetal_midbrain_TssP
3	0.039	27 / 2462	Mid_Frontal_Lobe_HetRpts
4	0.094	17 / 1548	Mid_Frontal_Lobe_K9K27me3
5	0.141	8 / 656	Overlap_fetal_midbrain_EnhP
6	0.144	9 / 765	Mid_Frontal_Lobe_Het
7	0.161	9 / 786	Fetal_EnhG
8	0.168	8 / 686	Overlap_fetal_midbrain_TssA
9	0.279	6 / 564	Mid_Frontal_Lobe_EnhP
10	0.284	27 / 3081	Mid_Frontal_Lobe_ZNF
11	0.305	10 / 1050	Fetal_EnhP
12	0.328	9 / 953	Fetal_Enh
13	0.365	2 / 163	Fetal_ReprPC
14	0.368	9 / 989	Mid_Frontal_Lobe_Quies
15	0.372	11 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	0.381	10 / 1122	Fetal_K9K27me3
17	0.472	10 / 1207	Overlap_fetal_midbrain_TssF
18	0.514	7 / 862	Overlap_fetal_midbrain_TxTrans
19	0.537	2 / 229	Mid_Frontal_Lobe_TxTrans
20	0.579	3 / 383	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	1 / 7	GENTLES_modul18
2	0.09	6 / 401	Lembcke_Colonic Inflammation
3	0.11	1 / 15	GENTLES_modul1
4	0.12	1 / 16	GENTLES_modul14
5	0.13	0 / 12	LIU_PROSTATE_CANCER_UP
6	0.16	1 / 22	PanCan_HH_geneset_nanostring
7	0.38	1 / 61	PanCan_Wnt_geneset_nanostring
8	0.48	1 / 82	PanCan_TXmisReg_geneset_nanostring
9	0.58	1 / 111	PanCan_RAS_geneset_nanostring
10	0.59	1 / 113	PanCan_Driver_Gene_geneset_nanostring
11	0.61	1 / 120	PanCan_CC+Apop_geneset_nanostring
12	0.68	2 / 298	SPANG_BCL6−index2
13	0.98	1 / 489	Lembcke_Normal vs Adenoma
14	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
15	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
16	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.00	0 / 12	LIU_BREAST_CANCER
19	1.00	0 / 14	LIU_COMMON_CANCER_GENES
20	1.00	0 / 14	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.008	3 / 52	perikaryon
2	0.010	5 / 169	transcription factor complex
3	0.033	3 / 89	tight junction
4	0.043	2 / 42	intercellular bridge
5	0.075	1 / 10	mRNA cap binding complex
6	0.083	1 / 11	Golgi−associated vesicle membrane
7	0.083	1 / 11	RISC complex
8	0.104	1 / 14	cytoplasmic dynein complex
9	0.111	1 / 15	mast cell granule
10	0.118	1 / 16	anchored component of plasma membrane
11	0.124	2 / 78	dendritic spine
12	0.125	1 / 17	cytoplasmic ribonucleoprotein granule
13	0.128	3 / 159	extracellular matrix
14	0.132	1 / 18	protein phosphatase type 2A complex
15	0.145	1 / 20	exon−exon junction complex
16	0.152	1 / 21	immunological synapse
17	0.159	1 / 22	integral component of lumenal side of endoplasmic reticulum membrane
18	0.172	1 / 24	cortical actin cytoskeleton
19	0.172	1 / 24	polysome
20	0.178	1 / 25	clathrin−coated endocytic vesicle membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.008	12 / 689	Chr 7
2	0.048	6 / 335	Chr 22
3	0.145	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
4	0.187	11 / 1037	Chr 19
5	0.208	9 / 838	Chr 3
6	0.263	6 / 552	Chr 10
7	0.403	7 / 775	Chr 12
8	0.450	6 / 687	Chr 6
9	0.517	8 / 993	Chr 2
10	0.610	2 / 262	Chr 13
11	0.629	4 / 551	Chr X
12	0.664	4 / 576	Chr 9
13	0.709	3 / 465	Chr 15
14	0.714	3 / 469	Chr 8
15	0.747	10 / 1500	Chr 1
16	0.752	4 / 649	Chr 16
17	0.757	5 / 801	Chr 11
18	0.793	5 / 840	Chr 17
19	0.826	1 / 221	Chr 18
20	0.914	3 / 696	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.03	11 / 739	TxEnhG2_Colon
2	0.04	1 / 5	Budinska_A_Surface crypt−like_UP
3	0.04	2 / 43	Marisa_CRC−cluster−f
4	0.06	1 / 8	Marisa_CRC−C3
5	0.08	2 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
6	0.12	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
7	0.12	1 / 16	Vilar_non−hypermutated−in−CRC
8	0.17	21 / 2159	TssP_Colon
9	0.19	2 / 102	Marisa_CRC−cluster−d
10	0.19	5 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
11	0.20	5 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
12	0.20	3 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	0.22	11 / 1079	ZNF_Colon
14	0.23	1 / 33	Marisa_CRC−cluster−e
15	0.27	2 / 131	Marisa_CRC−cluster−a
16	0.29	3 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
17	0.31	9 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	0.31	3 / 250	K9K27me3_Colon
19	0.33	4 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
20	0.38	3 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.4	4 / 435	GUDJ_psoriasis up
2	0.7	2 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	3 / 75	GIEZELT_GBM_STS_down_VS_LTS
2	0.03	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
3	0.05	1 / 7	WILLSCHER_GBM_LTSwt_proteomics−G_UP
4	0.11	1 / 15	VERHAAK_CL subtype
5	0.12	10 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.13	1 / 18	Barbus_GBM_STS_vs._LTS
7	0.26	1 / 38	OL vs. OPC
8	0.32	1 / 49	developing astrocytes
9	0.34	1 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
10	0.41	1 / 68	GIEZELT_GBM_WT_down_VS_mut
11	0.42	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
12	0.42	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
13	0.43	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
14	0.43	1 / 72	laffaire_hypermeth_LGG_vs_control
15	0.44	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
16	0.44	1 / 74	WIRTH_Normal Brain
17	0.44	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
18	0.45	1 / 75	Weller_LGG_A_vs_O_DOWN
19	0.52	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
20	0.53	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	3 / 27	ZHAN_MULTIPLE_MYELOMA_DN
2	0.002	4 / 66	BAELDE_DIABETIC_NEPHROPATHY_UP
3	0.002	6 / 167	BROWNE_HCMV_INFECTION_18HR_UP
4	0.003	2 / 10	FRASOR_TAMOXIFEN_RESPONSE_DN
5	0.003	8 / 304	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
6	0.003	3 / 36	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN
7	0.003	16 / 966	PEREZ_TP53_TARGETS
8	0.004	2 / 13	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
9	0.007	2 / 16	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
10	0.007	2 / 16	ZEMBUTSU_SENSITIVITY_TO_CISPLATIN
11	0.007	4 / 98	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
12	0.009	9 / 453	WEST_ADRENOCORTICAL_TUMOR_DN
13	0.010	4 / 107	SANSOM_APC_TARGETS_UP
14	0.012	3 / 61	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP
15	0.012	3 / 61	HUANG_GATA2_TARGETS_DN
16	0.013	5 / 178	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
17	0.014	2 / 23	VALK_AML_CLUSTER_8
18	0.014	7 / 327	DELACROIX_RARG_BOUND_MEF
19	0.015	2 / 24	CERIBELLI_GENES_INACTIVE_AND_BOUND_BY_NFY
20	0.016	3 / 67	KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3

HM

Rank	p−value	#in/all	Geneset
1	0.03	2 / 37	HALLMARK_APICAL_SURFACE
2	0.11	3 / 148	HALLMARK_KRAS_SIGNALING_UP
3	0.14	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	0.18	1 / 26	HALLMARK_ANGIOGENESIS
5	0.20	1 / 29	HALLMARK_NOTCH_SIGNALING
6	0.32	2 / 146	HALLMARK_UV_RESPONSE_UP
7	0.36	1 / 57	HALLMARK_MYC_TARGETS_V2
8	0.38	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	0.38	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.40	2 / 174	HALLMARK_HEME_METABOLISM
11	0.42	2 / 183	HALLMARK_GLYCOLYSIS
12	0.43	2 / 188	HALLMARK_ADIPOGENESIS
13	0.50	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
14	0.51	1 / 91	HALLMARK_BILE_ACID_METABOLISM
15	0.52	1 / 94	HALLMARK_ANDROGEN_RESPONSE
16	0.58	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
17	0.66	1 / 137	HALLMARK_UV_RESPONSE_DN
18	0.67	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
19	0.73	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
20	0.74	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 18	DUMEAUX_High bmi enriched genes
11	1	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.03	1 / 4	Shaknovich_ABC_hyper_meth
2	0.05	5 / 256	SPANG_IL21 DN
3	0.06	5 / 275	TARTE_Mature plasma cell signature
4	0.08	1 / 10	DAVE_BL_DN
5	0.08	1 / 10	Shaknovich_ABC_hypo_meth
6	0.08	51 / 5538	HOPP_Weak_txn
7	0.11	1 / 15	WRIGHT_ABC UP
8	0.13	2 / 80	Aukema_BCL2 DN_BCL6 UP
9	0.23	1 / 34	Subero_B−ALL_hyper_meth
10	0.29	1 / 43	LENZ_Stromal signature 2
11	0.31	1 / 47	Subero_FL_hyper_meth
12	0.35	19 / 2188	HOPP_Poised_promoter
13	0.38	1 / 60	Subero_T−ALL_hyper_meth
14	0.38	1 / 61	SPANG_LPS 6hrs DN
15	0.42	46 / 5693	HOPP_Weak_enhancer
16	0.48	10 / 1218	SPANG_BCR UP
17	0.50	2 / 212	LENZ_Stromal signature 1
18	0.52	9 / 1128	SPANG_BCR DN
19	0.58	2 / 247	ZHANG_DLBCL mutated
20	0.58	26 / 3396	HOPP_Repressed

MF

Rank	p−value	#in/all	Geneset
1	0.004	2 / 12	enhancer sequence−specific DNA binding
2	0.004	2 / 12	Notch binding
3	0.004	2 / 12	Wnt−activated receptor activity
4	0.008	3 / 52	hormone activity
5	0.012	13 / 820	sequence−specific DNA binding transcription factor activity
6	0.013	2 / 22	Wnt−protein binding
7	0.013	13 / 830	nucleic acid binding transcription factor activity
8	0.023	2 / 30	cyclin−dependent protein serine/threonine kinase activity
9	0.029	2 / 34	calcium−dependent phospholipid binding
10	0.035	2 / 38	protein serine/threonine phosphatase activity
11	0.038	3 / 95	heparin binding
12	0.041	2 / 41	G−protein coupled receptor binding
13	0.049	4 / 176	transcription regulatory region DNA binding
14	0.071	2 / 56	phosphoprotein phosphatase activity
15	0.075	1 / 10	armadillo repeat domain binding
16	0.075	1 / 10	deoxyribonuclease activity
17	0.075	1 / 10	neutral amino acid transmembrane transporter activity
18	0.075	1 / 10	peptidase activator activity
19	0.075	1 / 10	tropomyosin binding
20	0.083	1 / 11	RNA polymerase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	6 / 180	hsa−miR−302e
2	0.007	3 / 51	hsa−miR−556−3p
3	0.008	6 / 222	hsa−miR−520g
4	0.010	7 / 307	hsa−miR−302b
5	0.012	7 / 314	hsa−miR−520c−3p
6	0.012	5 / 176	hsa−miR−199b−3p
7	0.012	7 / 318	hsa−miR−302a
8	0.014	6 / 250	hsa−miR−520a−3p
9	0.015	4 / 120	hsa−miR−579
10	0.015	7 / 329	hsa−miR−302d
11	0.015	2 / 24	hsa−miR−602
12	0.016	6 / 258	hsa−miR−520e
13	0.020	4 / 132	hsa−miR−199b−5p
14	0.020	6 / 272	hsa−miR−520b
15	0.021	3 / 75	hsa−miR−651
16	0.023	6 / 280	hsa−miR−30c
17	0.034	2 / 37	hsa−miR−197
18	0.035	6 / 310	hsa−miR−548i
19	0.037	6 / 315	hsa−miR−302c
20	0.043	2 / 42	hsa−miR−541

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 12	GUSTAFSON_PI3K_UP
2	1	0 / 13	GUSTAFSON_PI3K_DN
3	1	0 / 14	BENTINK_e2f3.1
4	1	0 / 12	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 9	BENTINK_ras.4
8	1	0 / 15	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.3	35 / 4054	ICGC_Egr1_targets
2	0.3	7 / 690	ICGC_Atf3_targets
3	0.3	6 / 595	ICGC_NrsfPcr2_targets
4	0.4	43 / 5219	ICGC_Tcf3_targets
5	0.4	50 / 6114	ICGC_Runx3_targets
6	0.4	44 / 5355	ICGC_Pol2_targets
7	0.4	48 / 5890	ICGC_Elf1_targets
8	0.4	33 / 4032	ICGC_Creb1_targets
9	0.4	12 / 1400	ICGC_Myc_targets
10	0.4	20 / 2416	ICGC_Bcl3_targets
11	0.4	42 / 5200	ICGC_Mta3_targets
12	0.5	43 / 5374	ICGC_Pax5_targets
13	0.5	43 / 5408	ICGC_Pou2_targets
14	0.5	39 / 4909	ICGC_Stat5_targets
15	0.5	37 / 4689	ICGC_Taf1_targets
16	0.5	34 / 4314	ICGC_Ebfsc137065_targets
17	0.5	16 / 2013	ICGC_Bcl11_targets
18	0.5	38 / 4829	ICGC_Nficsc81335_targets
19	0.6	37 / 4774	ICGC_Foxm1_targets
20	0.6	5 / 653	ICGC_SrfPcr2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 36	VAQUERIZAS_Fetal brain
2	0.04	2 / 38	VAQUERIZAS_Whole brain
3	0.10	1 / 14	VAQUERIZAS_Ovary
4	0.11	1 / 15	VAQUERIZAS_Fetal thyroid
5	0.12	1 / 16	VAQUERIZAS_Pancreas
6	0.12	1 / 16	VAQUERIZAS_Adrenal gland
7	0.12	1 / 16	VAQUERIZAS_Salivary gland
8	0.12	1 / 17	VAQUERIZAS_Pituitary
9	0.17	1 / 23	VAQUERIZAS_Spinal cord
10	0.17	1 / 23	VAQUERIZAS_Trachea
11	0.17	1 / 23	VAQUERIZAS_Adrenal cortex
12	0.20	1 / 29	VAQUERIZAS_Fetal lung
13	0.23	1 / 33	VAQUERIZAS_Prostate
14	0.26	1 / 38	VAQUERIZAS_Testis
15	0.27	1 / 40	VAQUERIZAS_Thyroid
16	0.28	1 / 41	VAQUERIZAS_Placenta
17	0.30	1 / 45	VAQUERIZAS_Uterus
18	0.37	1 / 58	VAQUERIZAS_Lung
19	0.37	1 / 59	VAQUERIZAS_Whole blood
20	0.68	1 / 143	VAQUERIZAS_General

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	1 / 11	WIRTH_Globus pallidus
2	0.22	1 / 32	WIRTH_Pancreas
3	0.22	2 / 114	PALMER_T−Cell signature up
4	0.26	3 / 225	PALMER_Granulocytes signature up
5	0.28	1 / 41	WIRTH_Homeostasis
6	0.53	1 / 95	WIRTH_Muscle
7	0.57	1 / 107	WIRTH_Testis
8	0.76	2 / 350	WIRTH_Immune system
9	0.78	1 / 194	PALMER_B−Cell signature up
10	0.94	1 / 350	WIRTH_Nervous System
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 13	WIRTH_B−cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 12	WIRTH_Lymphocytes
17	1.00	0 / 5	WIRTH_Bone marrow
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	10 / 1115	LU_BPDE 1n DN
2	0.8	25 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

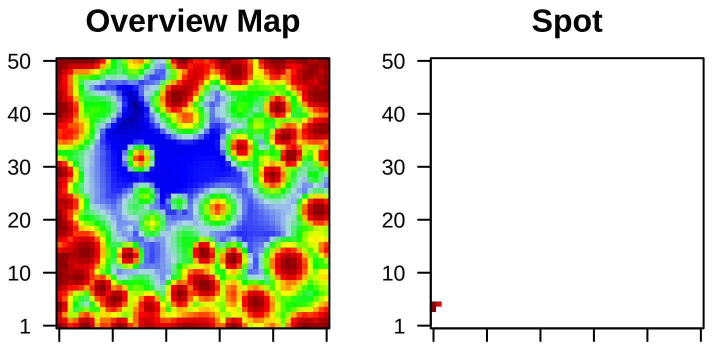
Overexpression Spots

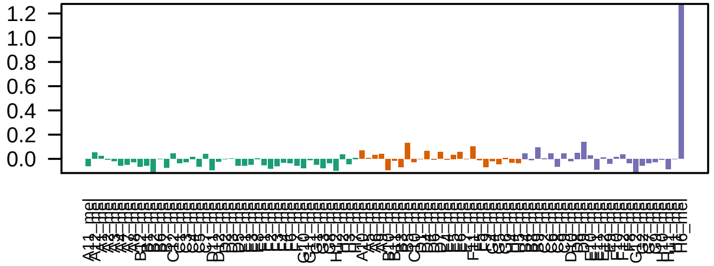
Spot Summary: S1

metagenes = 3
genes = 129

<r> metagenes = 0.99
<r> genes = 0.26
beta: r2= 1.3 / log p= −Inf

samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)



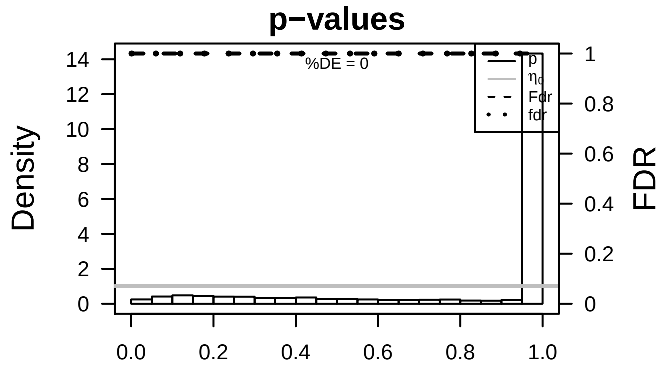


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	HORMAD1	2.38	−0.23	0.34	HORMAD1	HORMA domain containing 1 [Source:HGNC Symbol;Acc:HG
2	SCHIP1	2.29	−0.1	0.48	SCHIP1	schwannomin interacting protein 1 [Source:HGNC Symbol;Ac
3	MAGEA1	2.11	−0.1	0.48	MAGEA1	melanoma antigen family A1 [Source:HGNC Symbol;Acc:HGI
4	GARNL3	2.01	−0.2	0.26	GARNL3	GTPase activating Rap/RanGAP domain−like 3 [Source:HGN
5	THNSL2	1.98	−0.03	0.7	THNSL2	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
6	IFI44	1.95	−0.25	0.34	IFI44	interferon−induced protein 44 [Source:HGNC Symbol;Acc:HG
7	LPHN1	1.9	−0.17	0.32		
8	PORCN	1.88	−0.18	0.38	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
9	BMP1	1.79	−0.12	0.44	BMP1	bone morphogenetic protein 1 [Source:HGNC Symbol;Acc:H
10	ZNF253	1.78	−0.15	0.24	ZNF253	zinc finger protein 253 [Source:HGNC Symbol;Acc:HGNC:13
11	CHRNA5	1.75	−0.07	0.48	CHRNA5	cholinergic receptor, nicotinic, alpha 5 (neuronal) [Source:HG
12	DNAH12	1.73	−0.08	0.53	DNAH12	dynein, axonemal, heavy chain 12 [Source:HGNC Symbol;Ac
13	CD79B	1.71	−0.06	0.5	CD79B	CD79b molecule, immunoglobulin−associated beta [Source:H
14	UBASH3B	1.7	−0.05	0.56	UBASH3B	ubiquitin associated and SH3 domain containing B [Source:H
15	IFIT1	1.69	−0.13	0.35	IFIT1	interferon−induced protein with tetratricopeptide repeats 1 [Sc
16	TTLL4	1.68	−0.73	0.31	TTLL4	tubulin tyrosine ligase−like family member 4 [Source:HGNC S
17	ZNF14	1.68	−0.14	0.38	ZNF14	zinc finger protein 14 [Source:HGNC Symbol;Acc:HGNC:129
18	TMED7−TICA	1.66	−0.04	0.7	TMED7−TICAM2	TMED7−TICAM2 readthrough [Source:HGNC Symbol;Acc:H
19	ADHFE1	1.66	−0.24	0.33	ADHFE1	alcohol dehydrogenase, iron containing, 1 [Source:HGNC Sy
20	RHBDF2	1.65	−0.35	0.37	RHBDF2	rhomboid 5 homolog 2 (Drosophila) [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−04	2 / 5	GSEA	KREPPEL_CD99_TARGETS_UP
2	8e−04	8 / 231	GSEA	DURAND_STROMA_S_UP
3	1e−03	3 / 26	BP	negative regulation of GTPase activity
4	1e−03	3 / 26	GSEA	MOSERLE_IFNA_RESPONSE
5	3e−03	2 / 9	GSEA	THILLAINADESAN_ZNF217_TARGETS_DN
6	3e−03	4 / 67	GSEA	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
7	3e−03	4 / 70	GSEA	BORCZUK_MALIGNANT_MESOTHELIOMA_DN
8	3e−03	2 / 10	BP	regulation of cytokine production
9	3e−03	4 / 71	GSEA	BOSCO_TH1_CYTOTOXIC_MODULE
10	3e−03	15 / 801	Chr	Chr 11
11	4e−03	2 / 11	GSEA	ROETH_TERT_TARGETS_UP
12	5e−03	2 / 12	GSEA	GRANDVAUX_IRF3_TARGETS_UP
13	5e−03	2 / 13	CC	integrator complex
14	5e−03	2 / 13	BP	snRNA processing
15	5e−03	2 / 13	MF	ubiquitin conjugating enzyme binding
16	5e−03	2 / 13	GSEA	HOWLIN_CITED1_TARGETS_2_UP
17	6e−03	2 / 14	BP	positive regulation of blood pressure
18	6e−03	2 / 14	GSEA	PID_ERB_GENOMIC_PATHWAY
19	7e−03	3 / 45	GSEA	BECKER_TAMOXIFEN_RESISTANCE_UP
20	7e−03	2 / 15	BP	cellular response to lithium ion
21	7e−03	2 / 15	BP	keratinization
22	7e−03	3 / 46	GSEA	CROMER_TUMORIGENESIS_UP
23	8e−03	4 / 92	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
24	8e−03	2 / 16	BP	calcium ion import
25	8e−03	2 / 16	BP	tRNA methylation
26	9e−03	2 / 17	GSEA	YIH_RESPONSE_TO_ARSENITE_C4
27	9e−03	38 / 3081	Brain	Mid_Frontal_Lobe_ZNF
28	1e−02	3 / 53	GSEA	LEE_LIVER_CANCER_E2F1_UP
29	1e−02	2 / 20	CC	dynein complex
30	1e−02	2 / 20	BP	meiotic nuclear division
31	1e−02	2 / 20	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
32	1e−02	2 / 20	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_D
33	1e−02	2 / 20	GSEA	ZHANG_INTERFERON_RESPONSE
34	1e−02	3 / 58	GSEA	LUCAS_HNF4A_TARGETS_UP
35	1e−02	31 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
36	2e−02	25 / 1872	TF	ICGC_Mef2_targets
37	2e−02	4 / 111	GSEA	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
38	2e−02	3 / 61	GSEA	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
39	2e−02	5 / 172	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP
40	2e−02	2 / 23	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 100	HORVATH_aging_genes meth DOWN
2	0.6	1 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 26	negative regulation of GTPase activity
2	0.003	2 / 10	regulation of cytokine production
3	0.005	2 / 13	snRNA processing
4	0.006	2 / 14	positive regulation of blood pressure
5	0.007	2 / 15	cellular response to lithium ion
6	0.007	2 / 15	keratinization
7	0.008	2 / 16	calcium ion import
8	0.008	2 / 16	tRNA methylation
9	0.012	2 / 20	meiotic nuclear division
10	0.019	2 / 25	cell projection organization
11	0.019	2 / 25	negative regulation of insulin receptor signaling pathway
12	0.024	2 / 28	extrinsic apoptotic signaling pathway in absence of ligand
13	0.024	2 / 28	mitotic cell cycle checkpoint
14	0.025	3 / 73	cation transport
15	0.032	3 / 81	muscle organ development
16	0.046	2 / 40	negative regulation of protein binding
17	0.059	2 / 46	response to hydrogen peroxide
18	0.080	2 / 55	positive regulation of endothelial cell proliferation
19	0.082	1 / 10	cell−cell junction assembly
20	0.082	1 / 10	locomotor rhythm

Brain

Rank	p−value	#in/all	Geneset
1	0.009	38 / 3081	Mid_Frontal_Lobe_ZNF
2	0.015	31 / 2462	Mid_Frontal_Lobe_HetRpts
3	0.041	24 / 1949	Fetal_TssF
4	0.046	7 / 383	Fetal_Tx
5	0.052	12 / 831	Fetal_HetRpts
6	0.170	17 / 1548	Mid_Frontal_Lobe_K9K27me3
7	0.195	20 / 1907	Fetal_TxTrans
8	0.258	13 / 1236	Mid_Frontal_Lobe_ReprPCWk
9	0.292	85 / 9528	Overlap_fetal_midbrain_Quies
10	0.307	6 / 534	Mid_Frontal_Lobe_EnhG
11	0.313	83 / 9330	Overlap_fetal_midbrain_ReprPC
12	0.330	7 / 656	Overlap_fetal_midbrain_EnhP
13	0.337	12 / 1207	Overlap_fetal_midbrain_TssF
14	0.337	80 / 9020	Overlap_fetal_midbrain_ReprPCWk
15	0.353	6 / 564	Mid_Frontal_Lobe_EnhP
16	0.411	17 / 1845	Fetal_Quies
17	0.459	8 / 862	Overlap_fetal_midbrain_TxTrans
18	0.471	12 / 1333	Fetal_ReprPCWk
19	0.474	9 / 989	Mid_Frontal_Lobe_Quies
20	0.485	26 / 2972	Mid_Frontal_Lobe_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	BEN−PORATH_DN
2	0.1	0 / 15	RHODES_CANCER_META_SIGNATURE
3	0.1	0 / 14	LIU_COMMON_CANCER_GENES
4	0.1	1 / 16	GENTLES_modul16
5	0.1	3 / 156	PanCan_PI3K_geneset_nanostring
6	0.2	3 / 180	SPANG_LPS−index2
7	0.2	0 / 14	LIU_LIVER_CANCER
8	0.2	2 / 111	PanCan_RAS_geneset_nanostring
9	0.3	5 / 401	Lembcke_Colonic Inflammation
10	0.3	2 / 121	PanCan_MAPK_geneset_nanostring
11	0.5	3 / 298	SPANG_BCL6−index2
12	0.5	0 / 12	LIU_PROSTATE_CANCER_UP
13	0.6	4 / 489	Lembcke_Normal vs Adenoma
14	0.6	1 / 113	PanCan_Driver_Gene_geneset_nanostring
15	0.6	1 / 120	PanCan_CC+Apop_geneset_nanostring
16	0.8	0 / 14	LIU_PROSTATE_CANCER_DN
17	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
18	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
19	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.0	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	integrator complex
2	0.012	2 / 20	dynein complex
3	0.023	11 / 649	endoplasmic reticulum membrane
4	0.032	3 / 81	late endosome membrane
5	0.057	2 / 45	transcriptional repressor complex
6	0.061	2 / 47	lipid particle
7	0.071	2 / 51	axoneme
8	0.082	3 / 119	external side of plasma membrane
9	0.082	1 / 10	beta−catenin destruction complex
10	0.088	5 / 276	cilium
11	0.089	15 / 1201	endoplasmic reticulum
12	0.090	1 / 11	acetylcholine−gated channel complex
13	0.094	32 / 2984	integral component of membrane
14	0.098	1 / 12	axonal growth cone
15	0.098	1 / 12	npBAF complex
16	0.106	1 / 13	nBAF complex
17	0.106	1 / 13	Sin3 complex
18	0.106	1 / 13	SWI/SNF complex
19	0.113	1 / 14	gap junction
20	0.121	1 / 15	alpha−amino−3−hydroxy−5−methyl−4−isoxazolepropionic acid selective gluta

Chr

Rank	p−value	#in/all	Geneset
1	0.003	15 / 801	Chr 11
2	0.052	10 / 649	Chr 16
3	0.100	8 / 551	Chr X
4	0.106	13 / 1037	Chr 19
5	0.187	4 / 262	Chr 13
6	0.208	6 / 465	Chr 15
7	0.211	16 / 1500	Chr 1
8	0.292	9 / 840	Chr 17
9	0.334	6 / 552	Chr 10
10	0.343	6 / 558	Chr 4
11	0.427	8 / 838	Chr 3
12	0.549	3 / 335	Chr 22
13	0.561	4 / 462	Chr 14
14	0.573	4 / 469	Chr 8
15	0.729	1 / 151	Chr 21
16	0.731	4 / 576	Chr 9
17	0.941	3 / 696	Chr 5
18	0.974	4 / 993	Chr 2
19	0.998	1 / 687	Chr 6
20	0.998	1 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.03	2 / 33	Marisa_CRC−cluster−e
2	0.03	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
3	0.05	7 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
4	0.06	71 / 7203	TssF_Colon
5	0.07	1 / 8	Boland_CRC−MSI−TGC
6	0.07	30 / 2698	EnhA_Colon
7	0.08	14 / 1079	ZNF_Colon
8	0.08	40 / 3812	TssD1_Colon
9	0.11	2 / 66	Marisa_CRC−cluster−h
10	0.13	6 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	0.17	3 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	0.19	6 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
13	0.22	4 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
14	0.25	92 / 10290	TssWk_Colon
15	0.26	48 / 5155	EnhWk1_Colon
16	0.29	4 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
17	0.34	3 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
18	0.35	26 / 2798	TxEnhG1_Colon
19	0.36	31 / 3383	EnhWk2_Colon
20	0.37	20 / 2142	ReprPC_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.03	8 / 435	GUDJ_psoriasis up
2	1.00	0 / 294	GUDJ_psoriasis down
3	1.00	0 / 11	BCHETNIA_EBM up
4	1.00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	3 / 72	laffaire_hypermeth_LGG_vs_control
2	0.06	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
3	0.06	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
4	0.07	1 / 9	VERHAAK_Brain
5	0.09	1 / 11	astrocytes_glio
6	0.12	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.12	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	0.12	2 / 71	Weller_LGG_A_vs_O_UP
9	0.13	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
10	0.18	1 / 23	Donson−Misc immune function−associated with LTS in HGA
11	0.20	1 / 26	Christensen_hypomethylated_in_ependymoma
12	0.20	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
13	0.21	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
14	0.21	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	0.25	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
16	0.27	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	0.28	1 / 38	OL vs. OPC
18	0.29	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
19	0.33	1 / 47	mature astrocytes
20	0.34	1 / 49	OL vs. MOG− OL

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 5	KREPPEL_CD99_TARGETS_UP
2	8e−04	8 / 231	DURAND_STROMA_S_UP
3	1e−03	3 / 26	MOSERLE_IFNA_RESPONSE
4	3e−03	2 / 9	THILLAINADESAN_ZNF217_TARGETS_DN
5	3e−03	4 / 67	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
6	3e−03	4 / 70	BORCZUK_MALIGNANT_MESOTHELIOMA_DN
7	3e−03	4 / 71	BOSCO_TH1_CYTOTOXIC_MODULE
8	4e−03	2 / 11	ROETH_TERT_TARGETS_UP
9	5e−03	2 / 12	GRANDVAUX_IRF3_TARGETS_UP
10	5e−03	2 / 13	HOWLIN_CITED1_TARGETS_2_UP
11	6e−03	2 / 14	PID_ERB_GENOMIC_PATHWAY
12	7e−03	3 / 45	BECKER_TAMOXIFEN_RESISTANCE_UP
13	7e−03	3 / 46	CROMER_TUMORIGENESIS_UP
14	8e−03	4 / 92	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
15	9e−03	2 / 17	YIH_RESPONSE_TO_ARSENITE_C4
16	1e−02	3 / 53	LEE_LIVER_CANCER_E2F1_UP
17	1e−02	2 / 20	FARMER_BREAST_CANCER_CLUSTER_1
18	1e−02	2 / 20	RICKMAN_HEAD_AND_NECK_CANCER_D
19	1e−02	2 / 20	ZHANG_INTERFERON_RESPONSE
20	1e−02	3 / 58	LUCAS_HNF4A_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.06	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	0.17	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.17	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	0.20	3 / 181	HALLMARK_P53_PATHWAY
5	0.23	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
6	0.30	2 / 127	HALLMARK_KRAS_SIGNALING_DN
7	0.33	2 / 137	HALLMARK_UV_RESPONSE_DN
8	0.34	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
9	0.36	2 / 146	HALLMARK_UV_RESPONSE_UP
10	0.40	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	0.41	2 / 165	HALLMARK_MYOGENESIS
12	0.43	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
13	0.44	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.51	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
15	0.54	1 / 91	HALLMARK_PROTEIN_SECRETION
16	0.54	1 / 91	HALLMARK_BILE_ACID_METABOLISM
17	0.60	1 / 107	HALLMARK_COAGULATION
18	0.61	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
19	0.66	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
20	0.70	1 / 140	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
2	0.24	1 / 32	DUMEAUX_Fasting enriched genes
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.02	6 / 256	SPANG_IL21 DN
2	0.04	2 / 39	ROSOLOWSKI_blue DOWN
3	0.05	1 / 6	MASCQUE_mBL UP
4	0.10	2 / 61	SPANG_LPS 6hrs DN
5	0.11	1 / 13	BENTINK_mBL UP
6	0.11	1 / 13	Subero_MCL_hypo_meth
7	0.17	23 / 2188	HOPP_Poised_promoter
8	0.24	2 / 109	ROSOLOWSKI_green total
9	0.24	13 / 1218	SPANG_BCR UP
10	0.25	1 / 34	Subero_B−ALL_hyper_meth
11	0.27	5 / 410	SPANG_CD40 6hrs DN
12	0.30	2 / 129	DAVE_BL−vs−DLBCL
13	0.35	1 / 50	SPANG_BAFF 9hrs DN
14	0.37	31 / 3396	HOPP_Repressed
15	0.40	1 / 60	Subero_T−ALL_hyper_meth
16	0.42	3 / 275	TARTE_Mature plasma cell signature
17	0.53	19 / 2211	HOPP_Repetitive
18	0.62	21 / 2563	HOPP_Heterochrom
19	0.67	2 / 268	SPANG_IL21 UP
20	0.76	44 / 5538	HOPP_Weak_txn

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	ubiquitin conjugating enzyme binding
2	0.026	3 / 75	metallopeptidase activity
3	0.030	3 / 79	ion channel binding
4	0.048	2 / 41	ATPase activity, coupled to transmembrane movement of substances
5	0.060	3 / 104	growth factor activity
6	0.066	2 / 49	pyridoxal phosphate binding
7	0.070	22 / 1859	metal ion binding
8	0.072	51 / 4992	ion binding
9	0.079	4 / 189	methyltransferase activity
10	0.082	1 / 10	acetylcholine−activated cation−selective channel activity
11	0.082	1 / 10	cholesterol transporter activity
12	0.082	1 / 10	lipid transporter activity
13	0.082	1 / 10	protein−lysine N−methyltransferase activity
14	0.082	1 / 10	semaphorin receptor activity
15	0.082	1 / 10	sodium channel activity
16	0.082	1 / 10	transaminase activity
17	0.090	1 / 11	glutathione peroxidase activity
18	0.098	1 / 12	channel activity
19	0.098	1 / 12	protein kinase A catalytic subunit binding
20	0.098	1 / 12	tau−protein kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	3 / 82	hsa−miR−365
2	0.06	4 / 169	hsa−miR−374b
3	0.07	4 / 182	hsa−miR−573
4	0.07	4 / 182	hsa−miR−374a
5	0.08	2 / 54	hsa−miR−518d−5p
6	0.08	2 / 54	hsa−miR−520c−5p
7	0.08	2 / 56	hsa−miR−892a
8	0.09	1 / 11	hsa−miR−1180
9	0.11	2 / 66	hsa−miR−140−3p
10	0.11	1 / 14	hsa−miR−891a
11	0.11	1 / 14	hsa−miR−671−3p
12	0.13	2 / 73	hsa−miR−184
13	0.13	2 / 74	hsa−miR−1827
14	0.15	1 / 19	hsa−miR−645
15	0.17	1 / 21	hsa−miR−662
16	0.17	3 / 164	hsa−miR−323b−5p
17	0.18	1 / 23	hsa−miR−1250
18	0.18	1 / 23	hsa−miR−1228
19	0.19	1 / 24	hsa−miR−483−3p
20	0.19	1 / 24	hsa−miR−1225−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_src.10
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 15	BENTINK_ras.6
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	25 / 1872	ICGC_Mef2_targets
2	0.04	47 / 4385	ICGC_Atf2_targets
3	0.06	42 / 3924	ICGC_Zeb1_targets
4	0.07	10 / 690	ICGC_Atf3_targets
5	0.08	16 / 1273	ICGC_P300_targets
6	0.08	30 / 2714	ICGC_Irf4_targets
7	0.10	60 / 6114	ICGC_Runx3_targets
8	0.11	31 / 2927	ICGC_Rad21_targets
9	0.12	48 / 4829	ICGC_Nficsc81335_targets
10	0.12	26 / 2416	ICGC_Bcl3_targets
11	0.14	43 / 4314	ICGC_Ebfsc137065_targets
12	0.14	51 / 5219	ICGC_Tcf3_targets
13	0.14	47 / 4774	ICGC_Foxm1_targets
14	0.15	15 / 1314	ICGC_Usf1_targets
15	0.16	25 / 2391	ICGC_Pbx3_targets
16	0.17	45 / 4617	ICGC_Tcf12_targets
17	0.18	43 / 4414	ICGC_Bclaf101388_targets
18	0.19	21 / 2013	ICGC_Bcl11_targets
19	0.20	51 / 5374	ICGC_Pax5_targets
20	0.21	45 / 4706	ICGC_Sp1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.3	1 / 38	VAQUERIZAS_Testis
2	0.3	2 / 143	VAQUERIZAS_General
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 41	VAQUERIZAS_Placenta
5	1.0	0 / 26	VAQUERIZAS_Liver
6	1.0	0 / 33	VAQUERIZAS_Prostate
7	1.0	0 / 29	VAQUERIZAS_Smooth muscle
8	1.0	0 / 45	VAQUERIZAS_Uterus
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 37	VAQUERIZAS_Thymus
13	1.0	0 / 40	VAQUERIZAS_Thyroid
14	1.0	0 / 59	VAQUERIZAS_Whole blood
15	1.0	0 / 7	VAQUERIZAS_Appendix
16	1.0	0 / 29	VAQUERIZAS_Fetal lung
17	1.0	0 / 58	VAQUERIZAS_Lung
18	1.0	0 / 16	VAQUERIZAS_Pancreas
19	1.0	0 / 23	VAQUERIZAS_Trachea
20	1.0	0 / 11	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	7 / 350	WIRTH_Nervous System
2	0.06	3 / 107	WIRTH_Testis
3	0.20	2 / 95	WIRTH_Muscle
4	0.24	1 / 32	WIRTH_Placenta
5	0.50	2 / 194	PALMER_B−Cell signature up
6	0.58	3 / 350	WIRTH_Immune system
7	0.63	1 / 114	PALMER_T−Cell signature up
8	0.86	1 / 225	PALMER_Granulocytes signature up
9	1.00	0 / 32	WIRTH_Pancreas
10	1.00	0 / 11	WIRTH_Sec. lymphoid organs
11	1.00	0 / 11	WIRTH_Prim. lymphoid organs
12	1.00	0 / 13	WIRTH_B−cells
13	1.00	0 / 8	WIRTH_Tonsil
14	1.00	0 / 12	WIRTH_Thymus
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	13 / 1115	LU_BPDE 1h DN
2	0.7	29 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

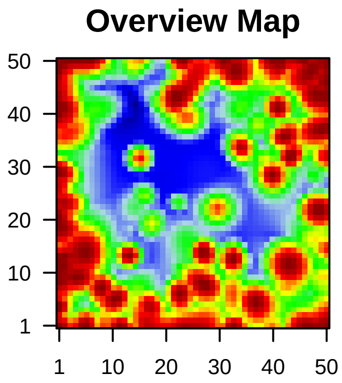
Overexpression Spots

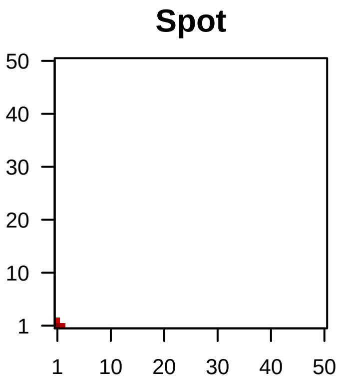
Spot Summary: T1

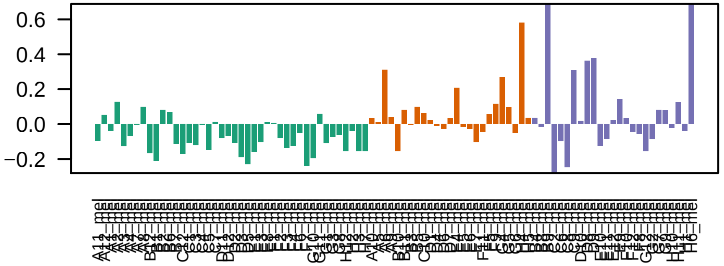
metagenes = 3
genes = 103

<r> metagenes = 0.99
<r> genes = 0.12
beta: r2= 1.36 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC2 : 4 (16 %)
MSC3 : 5 (20 %)





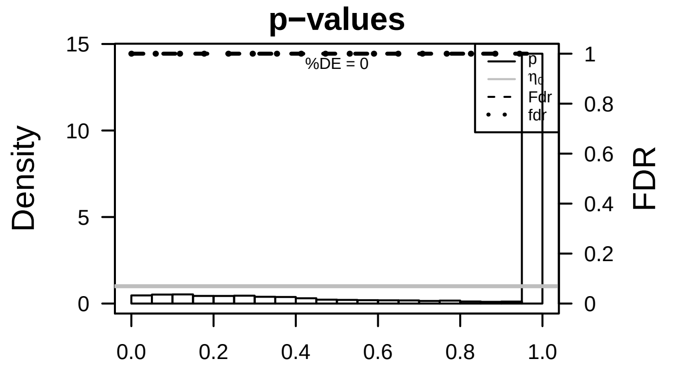


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	GPR107	2.16	−0.36	0.34	GPR107	G protein−coupled receptor 107 [Source:HGNC Symbol;Acc:
2	PCDHGC3	1.86	−0.36	0.29	PCDHGC3	protocadherin gamma subfamily C, 3 [Source:HGNC Symbol;
3	PCNX	1.8	−0.45	0.4	PCNX	pecanex homolog (Drosophila) [Source:HGNC Symbol;Acc:H
4	APBB1	1.74	−0.25	0.51	APBB1	amyloid beta (A4) precursor protein−binding, family B, membe
5	GPD1L	1.69	−0.25	0.28	GPD1L	glycerol−3−phosphate dehydrogenase 1−like [Source:HGNC
6	ZNF513	1.6	−0.11	0.36	ZNF513	zinc finger protein 513 [Source:HGNC Symbol;Acc:HGNC:26
7	ERCC2	1.6	−0.22	0.36	ERCC2	excision repair cross−complementation group 2 [Source:HGN
8	CRELD1	1.58	−0.42	0.36	CRELD1	cysteine−rich with EGF−like domains 1 [Source:HGNC Symb
9	ADAM23	1.57	−0.36	0.42	ADAM23	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
10	CYHR1	1.54	−0.41	0.29	CYHR1	cysteine/histidine−rich 1 [Source:HGNC Symbol;Acc:HGNC:1
11	CRKL	1.52	−0.36	0.35	CRKL	v−crk avian sarcoma virus CT10 oncogene homolog−like [So
12	C10orf88	1.52	−0.43	0.41	C10orf88	chromosome 10 open reading frame 88 [Source:HGNC Symb
13	CCDC126	1.52	−0.57	0.3	CCDC126	coiled−coil domain containing 126 [Source:HGNC Symbol;Ac
14	ARHGAP18	1.51	−0.22	0.45	ARHGAP18	Rho GTPase activating protein 18 [Source:HGNC Symbol;Ac
15	ANKRD29	1.51	−0.23	0.43	ANKRD29	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:HGNC
16	PTPN13	1.5	−0.41	0.27	PTPN13	protein tyrosine phosphatase, non−receptor type 13 (APO−1/
17	NLN	1.5	−0.62	0.28	NLN	neurolysin (metallopeptidase M3 family) [Source:HGNC Symb
18	SMG9	1.5	−0.41	0.21	SMG9	SMG9 nonsense mediated mRNA decay factor [Source:HGN
19	GABPB2	1.5	−0.54	0.37	GABPB2	GA binding protein transcription factor, beta subunit 2 [Source
20	AKAP1	1.47	−0.5	0.44	AKAP1	A kinase (PRKA) anchor protein 1 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−06	65 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
2	1e−06	82 / 8580	Colon	TxWk_Colon
3	2e−06	84 / 9027	Colon	Tx_Colon
4	7e−05	6 / 101	BP	RNA processing
5	9e−05	83 / 9482	Colon	TssA_Colon
6	1e−04	4 / 36	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
7	1e−04	83 / 9528	Brain	Overlap_fetal_midbrain_Quies
8	2e−04	17 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
9	2e−04	81 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
10	2e−04	3 / 18	GSEA	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP
11	4e−04	65 / 6929	Lymph	HOPP_Txn_elongation
12	5e−04	15 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
13	6e−04	21 / 1418	TF	ICGC_Ets1_targets
14	6e−04	7 / 210	MF	transferase activity, transferring glycosyl groups
15	6e−04	3 / 25	MF	ATP−dependent helicase activity
16	7e−04	5 / 102	miRN	hsa−miR−224
17	8e−04	19 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
18	9e−04	13 / 696	Chr	Chr 5
19	1e−03	6 / 167	MF	helicase activity
20	1e−03	6 / 168	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
21	1e−03	4 / 68	miRN	hsa−miR−606
22	1e−03	3 / 31	GSEA	KAAB_FAILED_HEART_ATRIUM_UP
23	1e−03	5 / 120	GSEA	ALCALAY_AML_BY_NPM1_LOCALIZATION_UP
24	1e−03	8 / 315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
25	2e−03	6 / 183	miRN	hsa−miR−1283
26	2e−03	4 / 74	miRN	hsa−miR−422a
27	2e−03	8 / 325	GSEA	WANG_LMO4_TARGETS_UP
28	2e−03	3 / 36	GSEA	XU_CREBBP_TARGETS_DN
29	2e−03	4 / 77	miRN	hsa−miR−1305
30	2e−03	4 / 79	miRN	hsa−miR−569
31	2e−03	9 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
32	2e−03	2 / 11	GSEA	HOLLEMAN_DAUNORUBICIN_B_ALL_DN
33	3e−03	72 / 8415	Colon	Quies3_Colon
34	3e−03	6 / 203	miRN	hsa−miR−33a
35	3e−03	7 / 276	BP	nucleobase−containing compound catabolic process
36	3e−03	5 / 145	GSEA	VERHAAK_GLIOBLASTOMA_CLASSICAL
37	3e−03	2 / 13	Pathw	BENTINK_myc.1
38	3e−03	2 / 13	GSEA	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
39	4e−03	15 / 1007	MF	poly(A) RNA binding
40	4e−03	18 / 1325	BP	catabolic process



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 100	HORVATH_aging_genes meth DOWN
2	1.0	0 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−05	6 / 101	RNA processing
2	1e−04	4 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
3	3e−03	7 / 276	nucleobase−containing compound catabolic process
4	4e−03	18 / 1325	catabolic process
5	5e−03	2 / 16	NAD metabolic process
6	7e−03	3 / 56	protein O−linked glycosylation
7	7e−03	3 / 56	stem cell maintenance
8	7e−03	23 / 1975	cellular protein modification process
9	1e−02	4 / 130	protein dephosphorylation
10	2e−02	3 / 80	peptidyl−serine phosphorylation
11	2e−02	10 / 687	gene expression
12	4e−02	2 / 44	DNA duplex unwinding
13	4e−02	4 / 182	dephosphorylation
14	4e−02	2 / 46	fatty acid biosynthetic process
15	5e−02	7 / 478	protein transport
16	5e−02	2 / 53	retina development in camera−type eye
17	5e−02	4 / 204	in utero embryonic development
18	6e−02	35 / 3980	cellular nitrogen compound metabolic process
19	6e−02	2 / 58	ER to Golgi vesicle−mediated transport
20	6e−02	3 / 132	regulation of gene expression

Brain

Rank	p−value	#in/all	Geneset
1	1e−06	65 / 5940	Overlap_fetal_midbrain_HetRpts
2	1e−04	83 / 9528	Overlap_fetal_midbrain_Quies
3	2e−04	81 / 9330	Overlap_fetal_midbrain_ReprPC
4	4e−03	75 / 9013	Overlap_fetal_midbrain_K9K27me3
5	2e−02	72 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	4e−02	10 / 769	Overlap_fetal_midbrain_ZNF
7	2e−01	8 / 765	Mid_Frontal_Lobe_Het
8	2e−01	8 / 786	Fetal_EnhG
9	2e−01	25 / 3081	Mid_Frontal_Lobe_ZNF
10	2e−01	10 / 1122	Fetal_K9K27me3
11	3e−01	9 / 1050	Fetal_EnhP
12	3e−01	2 / 158	Overlap_fetal_midbrain_Het
13	3e−01	6 / 656	Overlap_fetal_midbrain_EnhP
14	3e−01	3 / 304	Fetal_Het
15	4e−01	3 / 349	Fetal_ZNF
16	5e−01	7 / 953	Fetal_Enh
17	5e−01	4 / 564	Mid_Frontal_Lobe_EnhP
18	6e−01	9 / 1333	Fetal_ReprPCWk
19	7e−01	1 / 156	Mid_Frontal_Lobe_TssA
20	7e−01	5 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	4 / 298	SPANG_BCL6−index2
2	0.3	1 / 47	PanCan_DNARepair_geneset_nanostring
3	0.3	1 / 48	KUIPER_MM poor survival
4	0.4	2 / 180	SPANG_LPS−index2
5	0.4	0 / 14	LIU_COMMON_CANCER_GENES
6	0.6	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	0.7	3 / 489	Lembcke_Normal vs Adenoma
8	0.9	0 / 14	LIU_PROSTATE_CANCER_DN
9	0.9	1 / 401	Lembcke_Colonic Inflammation
10	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1.0	0 / 12	LIU_BREAST_CANCER
14	1.0	0 / 14	LIU_LIVER_CANCER
15	1.0	0 / 12	LIU_PROSTATE_CANCER_UP
16	1.0	0 / 15	WANG_ER_UP
17	1.0	0 / 5	WANG_ER_DN
18	1.0	0 / 16	WOLFER_overlap genes
19	1.0	0 / 12	BEN−PORATH_DN
20	1.0	0 / 13	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	0.02	3 / 78	ubiquitin ligase complex
2	0.02	2 / 30	small−subunit processome
3	0.02	2 / 35	mediator complex
4	0.03	82 / 10605	intracellular
5	0.03	10 / 747	nucleolus
6	0.03	66 / 8205	cytoplasm
7	0.05	4 / 205	neuron projection
8	0.05	3 / 125	lamellipodium
9	0.07	2 / 61	cytoplasmic mRNA processing body
10	0.07	24 / 2577	nucleoplasm
11	0.08	1 / 12	basal part of cell
12	0.08	1 / 12	holo TFIIH complex
13	0.08	1 / 12	HOPS complex
14	0.09	1 / 13	proteasome regulatory particle
15	0.09	1 / 14	Cul4−RING E3 ubiquitin ligase complex
16	0.09	1 / 14	ER to Golgi transport vesicle
17	0.09	2 / 75	condensed chromosome kinetochore
18	0.10	1 / 15	centriolar satellite
19	0.10	1 / 15	dendrite cytoplasm
20	0.10	1 / 15	eukaryotic 43S preinitiation complex

Chr

Rank	p−value	#in/all	Geneset
1	9e−04	13 / 696	Chr 5
2	9e−02	7 / 552	Chr 10
3	2e−01	6 / 558	Chr 4
4	2e−01	8 / 840	Chr 17
5	3e−01	6 / 649	Chr 16
6	3e−01	4 / 398	Chr 20
7	4e−01	5 / 576	Chr 9
8	4e−01	4 / 469	Chr 8
9	5e−01	6 / 838	Chr 3
10	5e−01	7 / 993	Chr 2
11	7e−01	2 / 335	Chr 22
12	7e−01	4 / 687	Chr 6
13	7e−01	6 / 1037	Chr 19
14	8e−01	1 / 221	Chr 18
15	8e−01	8 / 1500	Chr 1
16	8e−01	2 / 465	Chr 15
17	8e−01	1 / 262	Chr 13
18	9e−01	3 / 689	Chr 7
19	9e−01	3 / 801	Chr 11
20	1e+00	1 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−06	82 / 8580	TxWk_Colon
2	2e−06	84 / 9027	Tx_Colon
3	9e−05	83 / 9482	TssA_Colon
4	3e−03	72 / 8415	Quies3_Colon
5	8e−03	62 / 7203	TssF_Colon
6	3e−02	50 / 5880	TssD2_Colon
7	5e−02	44 / 5155	EnhWk1_Colon
8	5e−02	1 / 8	Marisa_CRC−C1
9	7e−02	25 / 2698	EnhA_Colon
10	1e−01	1 / 15	Budinska_B_Lower crypt−like_UP
11	1e−01	77 / 10290	TssWk_Colon
12	1e−01	72 / 9653	Enh_Colon
13	2e−01	2 / 102	Marisa_CRC−cluster−d
14	2e−01	1 / 29	Marisa_CRC−cluster−c
15	3e−01	4 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
16	3e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
17	3e−01	22 / 2798	TxEnhG1_Colon
18	4e−01	6 / 739	TxEnhG2_Colon
19	4e−01	2 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
20	5e−01	8 / 1079	ZNF_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.4	4 / 435	GUDJ_psoriasis up
2	1.0	0 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.001	8 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.041	2 / 47	mature astrocytes
3	0.073	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
4	0.073	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
5	0.079	5 / 332	Up
6	0.080	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.098	1 / 15	VERHAAK_CL subtype
8	0.147	1 / 23	WIRTH_PN subtype
9	0.181	1 / 29	shaw_responders_down_in_oligo_glioma
10	0.231	1 / 38	OL vs. OPC
11	0.242	4 / 365	Down_b
12	0.277	1 / 47	Vishal_subnetwork signature of survival in GBM
13	0.287	1 / 49	developing astrocytes
14	0.353	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	0.362	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
16	0.396	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
17	0.405	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
18	0.452	1 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
19	0.478	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
20	0.510	1 / 103	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	17 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	2e−04	3 / 18	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP
3	5e−04	15 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
4	8e−04	19 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	1e−03	6 / 168	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
6	1e−03	3 / 31	KAAB_FAILED_HEART_ATRIUM_UP
7	1e−03	5 / 120	ALCALAY_AML_BY_NPM1_LOCALIZATION_UP
8	2e−03	8 / 325	WANG_LMO4_TARGETS_UP
9	2e−03	3 / 36	XU_CREBBP_TARGETS_DN
10	2e−03	9 / 416	SHEN_SMARCA2_TARGETS_UP
11	2e−03	2 / 11	HOLLEMAN_DAUNORUBICIN_B_ALL_DN
12	3e−03	5 / 145	VERHAAK_GLIOBLASTOMA_CLASSICAL
13	3e−03	2 / 13	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
14	4e−03	7 / 291	HORIUCHI_WTAP_TARGETS_DN
15	4e−03	3 / 48	STARK_HYPPOCAMPUS_22Q11_DELETION_UP
16	5e−03	5 / 158	BENPORATH_NOS_TARGETS
17	5e−03	3 / 51	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_UP
18	7e−03	2 / 18	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP
19	9e−03	6 / 258	BENPORATH_OCT4_TARGETS
20	1e−02	4 / 127	REACTOME_METABOLISM_OF_MRNA

HM

Rank	p−value	#in/all	Geneset
1	0.02	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	0.11	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.14	3 / 188	HALLMARK_MYC_TARGETS_V1
4	0.15	3 / 195	HALLMARK_MITOTIC_SPINDLE
5	0.18	1 / 29	HALLMARK_NOTCH_SIGNALING
6	0.25	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
7	0.27	2 / 146	HALLMARK_DNA_REPAIR
8	0.28	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.34	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.35	2 / 181	HALLMARK_P53_PATHWAY
11	0.47	1 / 91	HALLMARK_BILE_ACID_METABOLISM
12	0.47	1 / 93	HALLMARK_PEROXISOME
13	0.48	1 / 94	HALLMARK_ANDROGEN_RESPONSE
14	0.53	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	0.58	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
16	0.64	1 / 148	HALLMARK_KRAS_SIGNALING_UP
17	0.69	1 / 167	HALLMARK_APICAL_JUNCTION
18	0.69	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
19	0.69	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
20	0.72	1 / 183	HALLMARK_GLYCOLYSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−04	65 / 6929	HOPP_Txn_elongation
2	4e−03	49 / 5184	HOPP_Txn_transition
3	7e−03	58 / 6564	HOPP_Strong_enhancer
4	7e−03	65 / 7592	HOPP_Active_promoter
5	2e−02	49 / 5538	HOPP_Weak_txn
6	3e−02	49 / 5693	HOPP_Weak_enhancer
7	3e−02	5 / 256	SPANG_IL21 DN
8	4e−02	59 / 7209	HOPP_Weak_promoter
9	9e−02	1 / 13	BENTINK_mBL UP
10	1e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
11	1e−01	1 / 19	Subero_MM_hyper_meth
12	2e−01	19 / 2211	HOPP_Repetitive
13	2e−01	1 / 33	LEE_Developmental_regulators
14	2e−01	11 / 1218	SPANG_BCR UP
15	2e−01	3 / 247	ZHANG_DLBCL mutated
16	2e−01	10 / 1128	SPANG_BCR DN
17	3e−01	3 / 294	TARTE_Plasmablast signature
18	3e−01	1 / 60	Subero_T−ALL_hyper_meth
19	4e−01	1 / 66	TARTE_Plasma cell signature
20	4e−01	1 / 81	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	6e−04	7 / 210	transferase activity, transferring glycosyl groups
2	6e−04	3 / 25	ATP−dependent helicase activity
3	1e−03	6 / 167	helicase activity
4	4e−03	15 / 1007	poly(A) RNA binding
5	8e−03	2 / 20	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anhyd
6	1e−02	7 / 364	ATPase activity
7	1e−02	2 / 27	four−way junction helicase activity
8	1e−02	2 / 27	ribosome binding
9	2e−02	2 / 29	ATP−dependent DNA helicase activity
10	2e−02	2 / 32	Rac GTPase binding
11	2e−02	2 / 34	ATP−dependent RNA helicase activity
12	2e−02	16 / 1365	RNA binding
13	3e−02	3 / 104	iron ion binding
14	6e−02	4 / 217	transcription coactivator activity
15	7e−02	1 / 10	proteasome binding
16	7e−02	1 / 10	ribosomal small subunit binding
17	7e−02	4 / 223	phosphatase activity
18	7e−02	1 / 11	acetyltransferase activity
19	7e−02	1 / 11	ATPase activity, coupled
20	8e−02	2 / 67	phosphotransferase activity, alcohol group as acceptor

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	5 / 102	hsa−miR−224
2	1e−03	4 / 68	hsa−miR−606
3	2e−03	6 / 183	hsa−miR−1283
4	2e−03	4 / 74	hsa−miR−422a
5	2e−03	4 / 77	hsa−miR−1305
6	2e−03	4 / 79	hsa−miR−569
7	3e−03	6 / 203	hsa−miR−33a
8	4e−03	3 / 46	hsa−miR−874
9	5e−03	2 / 16	hsa−miR−220a
10	6e−03	7 / 318	hsa−miR−340
11	6e−03	6 / 242	hsa−miR−26b
12	7e−03	4 / 109	hsa−miR−499−5p
13	8e−03	4 / 113	hsa−miR−507
14	8e−03	2 / 20	hsa−miR−1288
15	8e−03	5 / 181	hsa−miR−29c
16	9e−03	3 / 63	hsa−miR−1278
17	1e−02	6 / 269	hsa−miR−101
18	1e−02	5 / 197	hsa−miR−222
19	1e−02	7 / 358	hsa−let−7d
20	1e−02	5 / 198	hsa−miR−181c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.003	2 / 13	BENTINK_myc.1
2	0.079	1 / 12	BENTINK_e2f3.2
3	0.079	1 / 12	BENTINK_ras.1
4	1.000	0 / 12	GUSTAFSON_PI3K_UP
5	1.000	0 / 13	GUSTAFSON_PI3K_DN
6	1.000	0 / 14	BENTINK_e2f3.1
7	1.000	0 / 9	BENTINK_ras.4
8	1.000	0 / 15	BENTINK_ras.6
9	1.000	0 / 13	BENTINK_src.10
10	1.000	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−04	21 / 1418	ICGC_Ets1_targets
2	6e−03	18 / 1383	ICGC_Six5_targets
3	9e−03	24 / 2137	ICGC_SrfV0416101_targets
4	1e−02	38 / 3924	ICGC_Zeb1_targets
5	2e−02	43 / 4689	ICGC_Taf1_targets
6	3e−02	43 / 4829	ICGC_Nficsc81335_targets
7	3e−02	15 / 1266	ICGC_NrsfPcr1_targets
8	3e−02	15 / 1314	ICGC_Usf1_targets
9	4e−02	39 / 4414	ICGC_Bclaf101388_targets
10	5e−02	42 / 4879	ICGC_Pmlsc71910_targets
11	5e−02	40 / 4617	ICGC_Tcf12_targets
12	7e−02	50 / 6114	ICGC_Runx3_targets
13	7e−02	45 / 5408	ICGC_Pou2_targets
14	7e−02	35 / 4032	ICGC_Creb1_targets
15	8e−02	41 / 4909	ICGC_Stat5_targets
16	8e−02	40 / 4774	ICGC_Foxm1_targets
17	8e−02	43 / 5200	ICGC_Mta3_targets
18	8e−02	43 / 5219	ICGC_Tcf3_targets
19	9e−02	7 / 553	ICGC_RxraPcr1_targets
20	9e−02	18 / 1872	ICGC_Mef2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 33	VAQUERIZAS_Prostate
2	1.0	0 / 36	VAQUERIZAS_Fetal brain
3	1.0	0 / 41	VAQUERIZAS_Placenta
4	1.0	0 / 26	VAQUERIZAS_Liver
5	1.0	0 / 29	VAQUERIZAS_Smooth muscle
6	1.0	0 / 45	VAQUERIZAS_Uterus
7	1.0	0 / 143	VAQUERIZAS_General
8	1.0	0 / 9	VAQUERIZAS_Kidney
9	1.0	0 / 23	VAQUERIZAS_Spinal cord
10	1.0	0 / 38	VAQUERIZAS_Whole brain
11	1.0	0 / 37	VAQUERIZAS_Thymus
12	1.0	0 / 40	VAQUERIZAS_Thyroid
13	1.0	0 / 59	VAQUERIZAS_Whole blood
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 29	VAQUERIZAS_Fetal lung
16	1.0	0 / 58	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 23	VAQUERIZAS_Trachea
19	1.0	0 / 11	VAQUERIZAS_Fetal liver
20	1.0	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.08	1 / 12	WIRTH_Thymus
2	0.22	4 / 350	WIRTH_Nervous System
3	0.55	1 / 114	PALMER_T−Cell signature up
4	0.70	2 / 350	WIRTH_Immune system
5	0.74	1 / 194	PALMER_B−Cell signature up
6	0.79	1 / 225	PALMER_Granulocytes signature up
7	1.00	0 / 32	WIRTH_Pancreas
8	1.00	0 / 11	WIRTH_Sec. lymphoid organs
9	1.00	0 / 11	WIRTH_Prim. lymphoid organs
10	1.00	0 / 13	WIRTH_B−cells
11	1.00	0 / 8	WIRTH_Tonsil
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 11	WIRTH_Globus pallidus
15	1.00	0 / 14	WIRTH_Telencephalon
16	1.00	0 / 11	WIRTH_Cortex cerebri
17	1.00	0 / 10	WIRTH_Hippocampus
18	1.00	0 / 10	WIRTH_Thalamus
19	1.00	0 / 12	WIRTH_Cerebellum
20	1.00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	11 / 1115	LU_BPDE 1h DN
2	0.8	22 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	