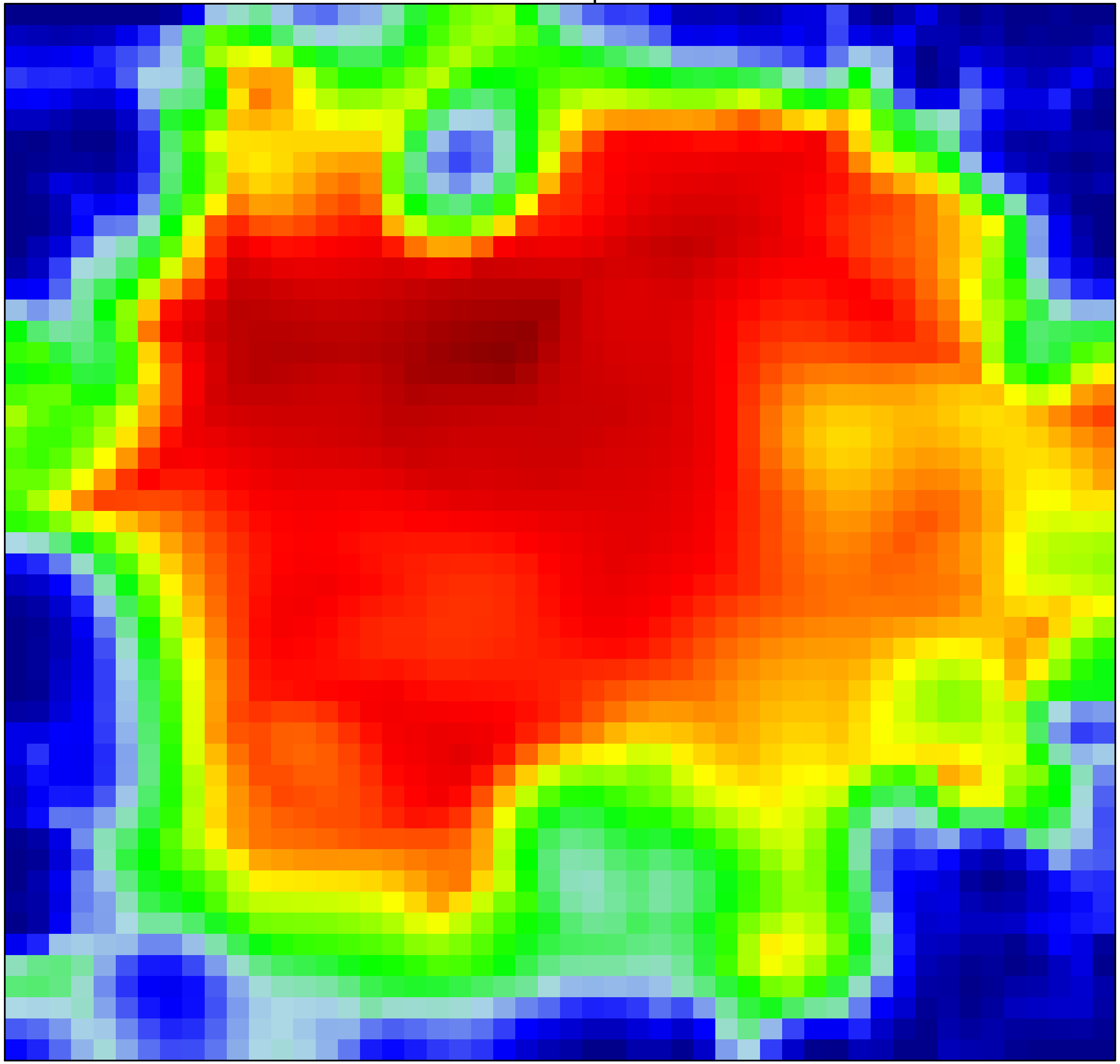
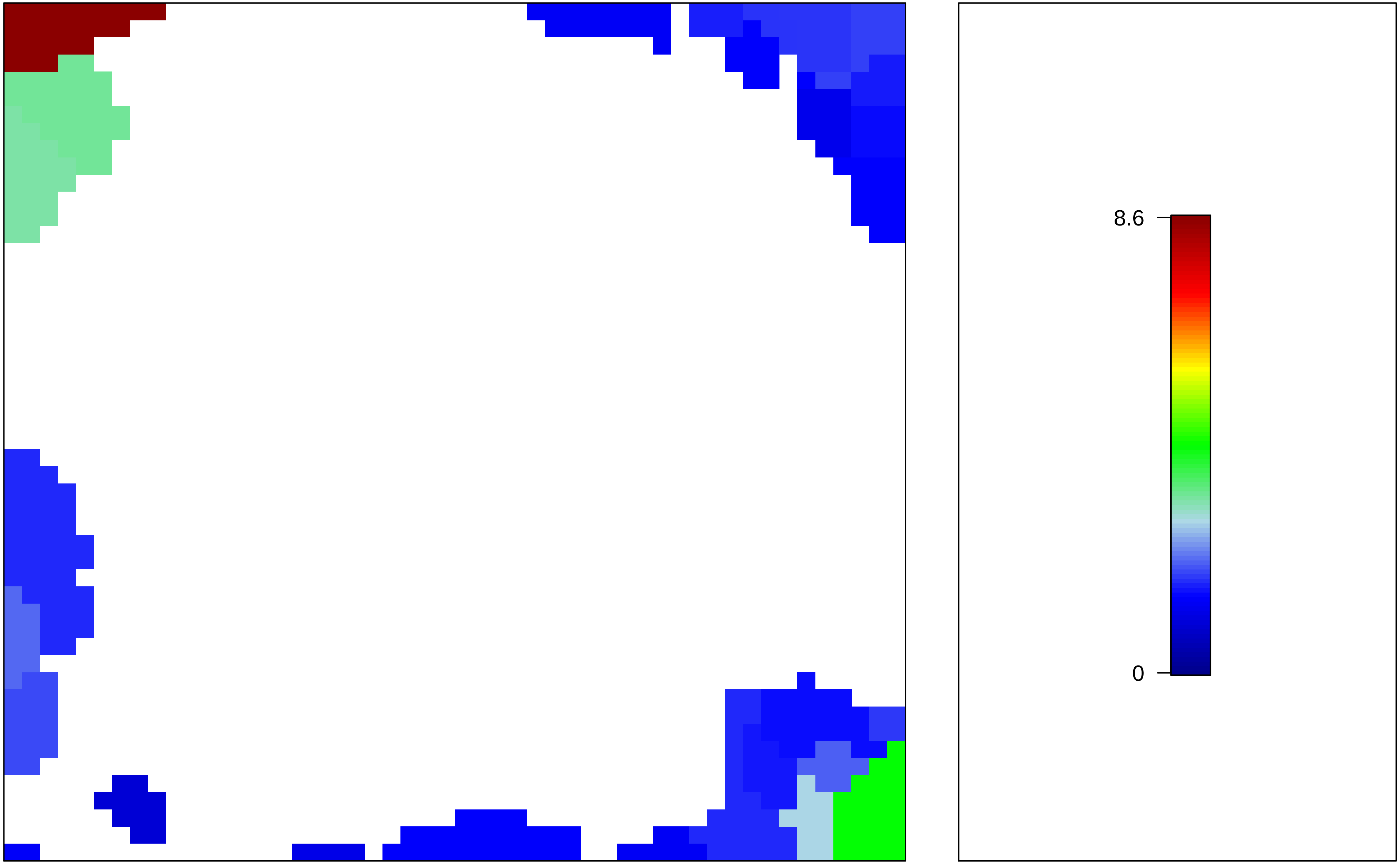
Underexpression Spots

landscape



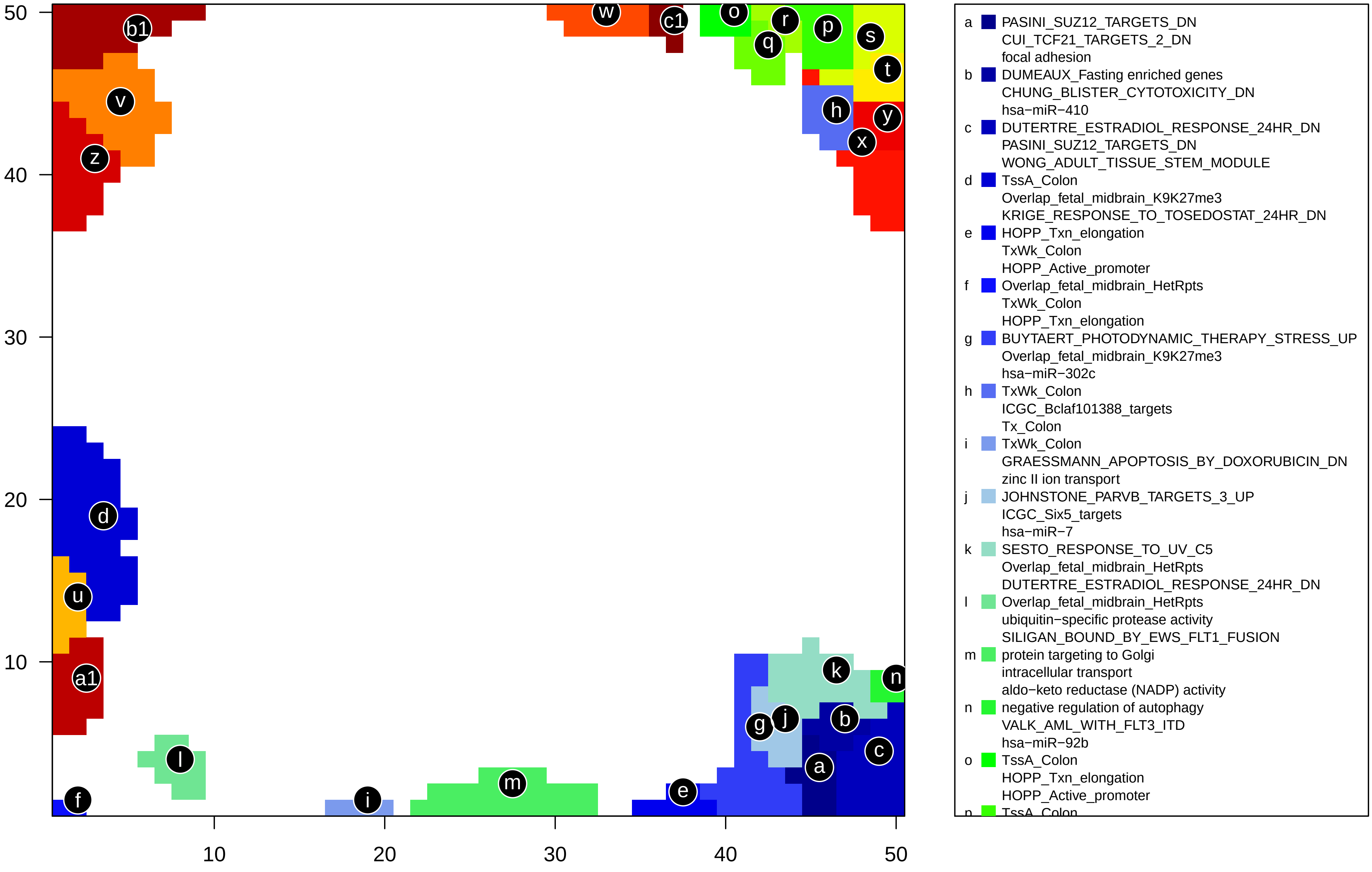
Underexpression Spots

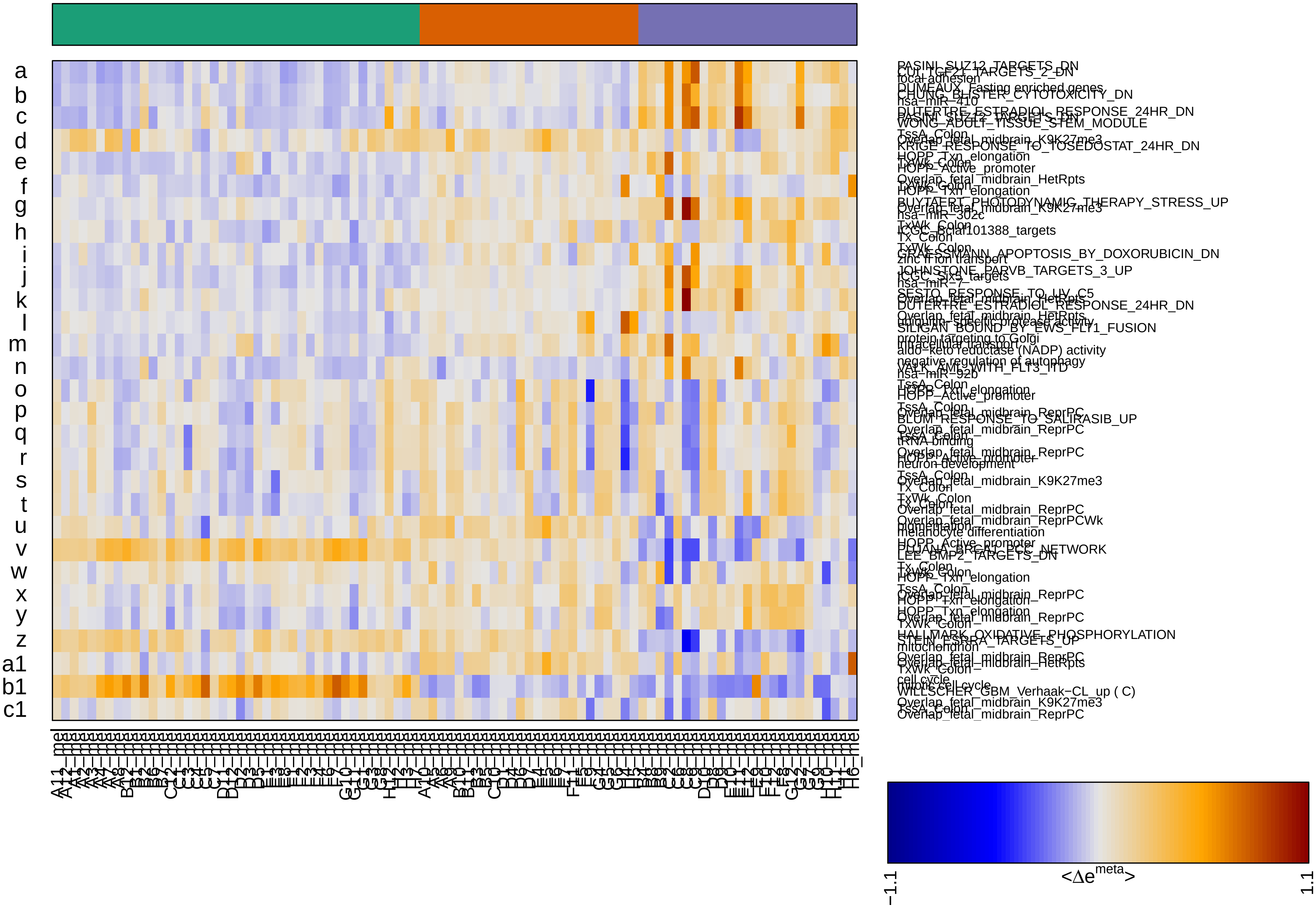
beta−scores



Underexpression Spots

annotation

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a1
b1
c1
PASINI_SUZ12_TARGETS_DN
CUI_TCF21_TARGETS_2_DN
focal adhesion
DUMEAUX_Fasting enriched genes
CHUNG_BLISTER_CYTOTOXICITY_DN
hsa−miR−410
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
PASINI_SUZ12_TARGETS_DN
WONG_ADULT_TISSUE_STEM_MODULE
TssA_Colon
Overlap_fetal_midbrain_K9K27me3
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
HOPP_Txn_elongation
TxWk_Colon
HOPP_Active_promoter
Overlap_fetal_midbrain_HetRpts
TxWk_Colon
HOPP_Txn_elongation
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
Overlap_fetal_midbrain_K9K27me3
hsa−miR−302c
TxWk_Colon
ICGC_Fetal101388_targets
Tx_Colon
TxWk_Colon
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
zinc II ion transport
JOHNSTONE_PARVB_TARGETS_3_UP
ICGC_Six5_targets
hsa−miR−7
SESTO_RESPONSE_TO_UV_C5
Overlap_fetal_midbrain_HetRpts
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
Overlap_fetal_midbrain_HetRpts
ubiquitin−specific protease activity
SILIGAN_BOUND_BY_EWS_FLT1_FUSION
protein targeting to Golgi
intracellular transport
aldo−keto reductase (NADP) activity
negative regulation of autophagy
VALK_AML_WITH_FLT3_ITD
hsa−miR−92b
TssA_Colon
HOPP_Txn_elongation
HOPP_Active_promoter
TssA_Colon
Overlap_fetal_midbrain_ReprPC
BLUM_RESPONSE_TO_SALIRASIB_UP
Overlap_fetal_midbrain_ReprPC
TssA_Colon
tRNA binding
Overlap_fetal_midbrain_ReprPC
HOPP_Active_promoter
neuron development
TssA_Colon
Overlap_fetal_midbrain_K9K27me3
Tx_Colon
TxWk_Colon
Tx_Colon
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_ReprPCWk
pigmentation
melanocyte differentiation
HOPP_Active_promoter
BUDHU_LIVER_CANCER_NETWORK
LEE_BMP2_TARGETS_DN
Tx_Colon
TxWk_Colon
HOPP_Txn_elongation
TssA_Colon
Overlap_fetal_midbrain_ReprPC
HOPP_Txn_elongation
HOPP_Txn_elongation
Overlap_fetal_midbrain_ReprPC
TxWk_Colon
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
mitochondrion
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_HetRpts
TxWk_Colon
cell cycle
mitotic cell cycle
WILLSCHER_GBM_Verhaak−CL_up (C)
Overlap_fetal_midbrain_K9K27me3
TssA_Colon
Overlap_fetal_midbrain_ReprPC
−1.1
<Δe^meta>
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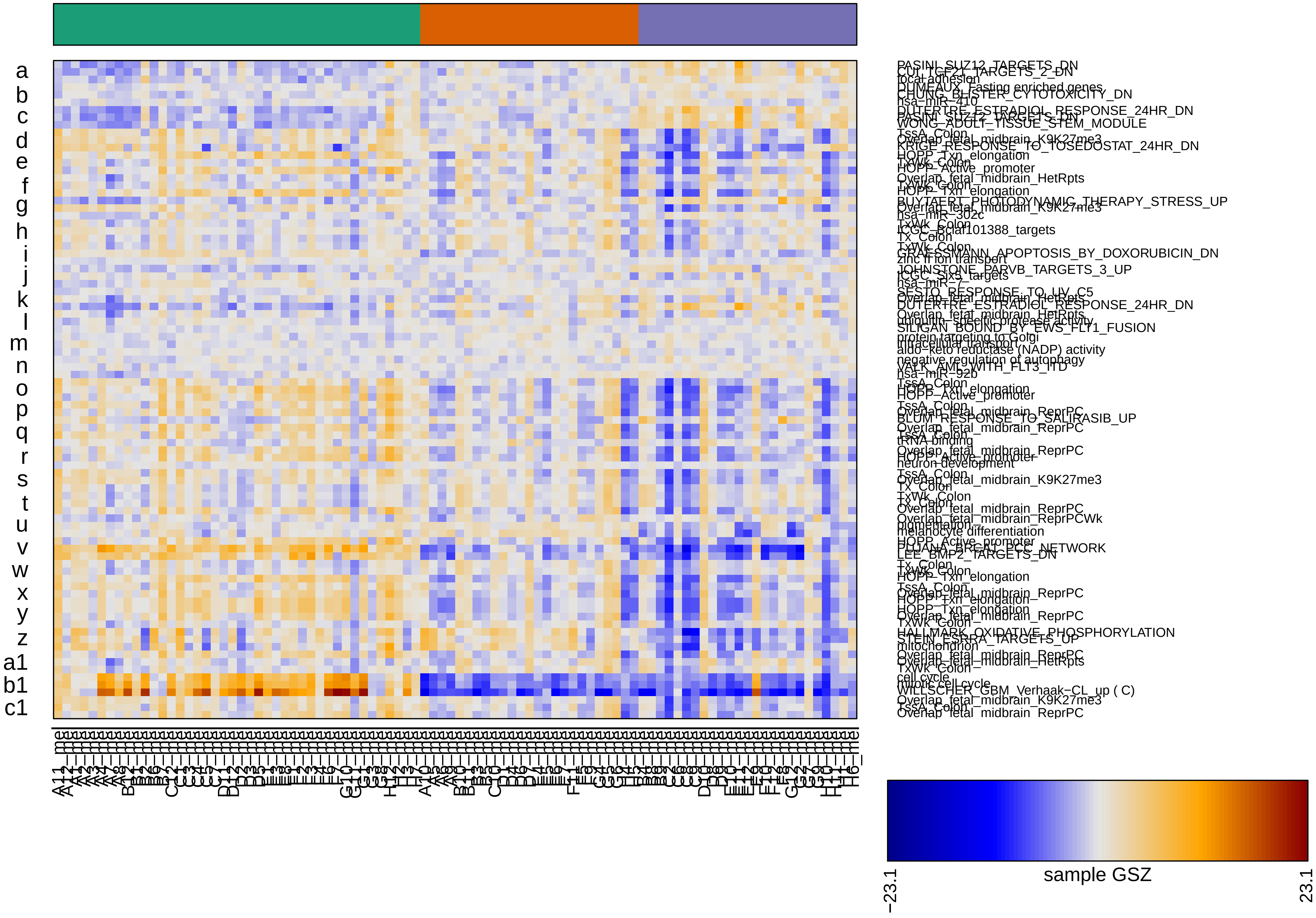
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PASINI_SUZ12_TARGETS_DN
CUI_TCF21_TARGETS_2_DN
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DUMEAUX_Fasting enriched genes
CHUNG_BLISTER_CYTOTOXICITY_DN
hsa−miR−410
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HOPP_Txn_elongation
TxWk_Colon
HOPP_Active_promoter
Overlap_fetal_midbrain_HetRpts
TxWk_Colon
HOPP_Txn_elongation
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
Overlap_fetal_midbrain_K9K27me3
hsa−miR−302c
TxWk_Colon
ICGC_Brd4i101388_targets
Tx_Colon
TxWk_Colon
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
zinc II ion transport
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Overlap_fetal_midbrain_ReprPC
BLUM_RESPONSE_TO_SALIRASIB_UP
Overlap_fetal_midbrain_ReprPC
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Tx_Colon
TxWk_Colon
Tx_Colon
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_ReprPCWk
pigmentation
melanocyte differentiation
HOPP_Active_promoter
PUJANA_BRCA2_PCC_NETWORK
LEE_BMP2_TARGETS_DN
Tx_Colon
TxWk_Colon
HOPP_Txn_elongation
TssA_Colon
Overlap_fetal_midbrain_ReprPC
HOPP_Txn_elongation
HOPP_Txn_elongation
Overlap_fetal_midbrain_ReprPC
TxWk_Colon
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
mitochondrion
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_HetRpts
TxWk_Colon
cell cycle
mitotic cell cycle
WILLSCHER_GBM_Verhaak−CL_up (C)
Overlap_fetal_midbrain_K9K27me3
TssA_Colon
Overlap_fetal_midbrain_ReprPC
sample GSZ
−23.1
23.1

Underexpression Spots

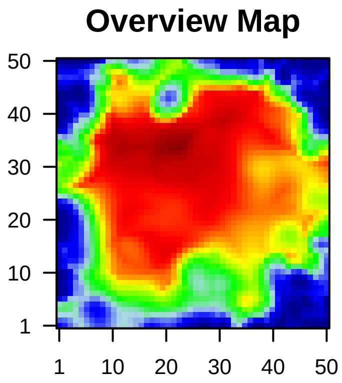
Spot Summary: a

\# metagenes = 10
\# genes = 115

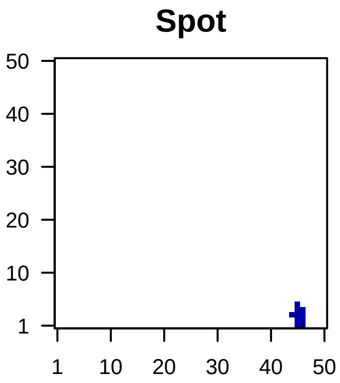
<r> metagenes = 0.98
<r> genes = 0.17
beta: r2= 2.87 / log p= −Inf

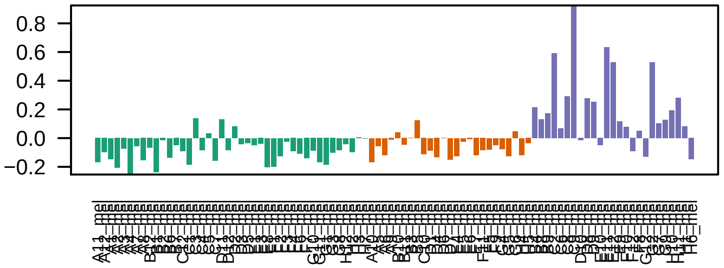
\# samples with spot = 11 (12 %)
MSC3 : 11 (44 %)

Overview Map



Spot





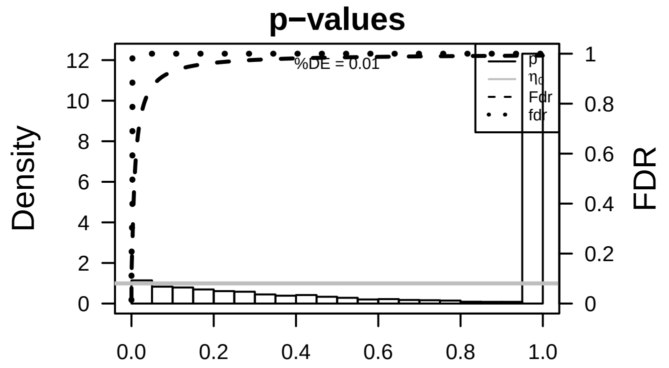
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	METTL8	2.02	−0.64	0.29	METTL8	methyltransferase like 8 [Source:HGNC Symbol;Acc:HGNC:2
2	PRICKLE2	1.91	−0.42	0.54	PRICKLE2	prickle homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:H
3	NCKIPSD	1.86	−0.24	0.36	NCKIPSD	NCK interacting protein with SH3 domain [Source:HGNC Syn
4	PEG10	1.83	−0.45	0.45	PEG10	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:1
5	CDH6	1.82	−0.11	0.47	CDH6	cadherin 6, type 2, K−cadherin (fetal kidney) [Source:HGNC
6	HIST1H2BF	1.82	−0.29	0.39	HIST1H2BF	histone cluster 1, H2bf [Source:HGNC Symbol;Acc:HGNC:47
7	TLE4	1.76	−0.24	0.48	TLE4	transducin−like enhancer of split 4 [Source:HGNC Symbol;Ac
8	PRRG1	1.74	−0.59	0.47	PRRG1	proline rich Gla (G−carboxyglutamic acid) 1 [Source:HGNC S
9	KIF13A	1.73	−0.39	0.38	KIF13A	kinesin family member 13A [Source:HGNC Symbol;Acc:HGN
10	OLR1	1.73	−0.06	0.66	OLR1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
11	NTN4	1.72	−0.1	0.76	NTN4	netrin 4 [Source:HGNC Symbol;Acc:HGNC:13658]
12	FLNB	1.72	−0.52	0.34	FLNB	filamin B, beta [Source:HGNC Symbol;Acc:HGNC:3755]
13	FAM171B	1.72	−0.76	0.36	FAM171B	family with sequence similarity 171, member B [Source:HGN
14	MCAM	1.68	−0.82	0.3	MCAM	melanoma cell adhesion molecule [Source:HGNC Symbol;Ac
15	ACOT12	1.68	−0.17	0.52	ACOT12	acyl−CoA thioesterase 12 [Source:HGNC Symbol;Acc:HGNC
16	GZF1	1.66	−0.57	0.42	GZF1	GDNF−inducible zinc finger protein 1 [Source:HGNC Symbol;
17	PTPN12	1.65	−0.76	0.24	PTPN12	protein tyrosine phosphatase, non−receptor type 12 [Source:
18	ARHGAP29	1.64	−0.16	0.48	ARHGAP29	Rho GTPase activating protein 29 [Source:HGNC Symbol;Ac
19	CTTNBP2NL	1.64	−0.57	0.44	CTTNBP2NL	CTTNBP2 N−terminal like [Source:HGNC Symbol;Acc:HGNC
20	RAPH1	1.64	−0.49	0.46	RAPH1	Ras association (RalGDS/AF−6) and pleckstrin homology dor

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−06	12 / 286	GSEA	PASINI_SUZ12_TARGETS_DN
2	5e−06	19 / 749	GSEA	CUI_TCF21_TARGETS_2_DN
3	5e−06	12 / 308	CC	focal adhesion
4	9e−06	19 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
5	2e−05	14 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
6	2e−05	13 / 425	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
7	3e−05	9 / 202	CC	actin cytoskeleton
8	4e−05	8 / 163	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
9	6e−05	7 / 129	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_U
10	7e−05	15 / 609	MF	cytoskeletal protein binding
11	8e−05	7 / 134	BP	cell junction organization
12	8e−05	5 / 58	GSEA	PID_AP1_PATHWAY
13	1e−04	6 / 98	GSEA	REACTOME_CELL_CELL_COMMUNICATION
14	1e−04	12 / 426	GSEA	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
15	1e−04	25 / 1465	CC	cytoskeleton
16	1e−04	6 / 102	MF	actin filament binding
17	2e−04	14 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
18	3e−04	16 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
19	3e−04	8 / 215	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
20	3e−04	3 / 17	CC	protein−DNA complex
21	3e−04	7 / 166	GSEA	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
22	3e−04	9 / 278	GSEA	GABRIELY_MIR21_TARGETS
23	3e−04	3 / 18	GSEA	BIOCARTA_CALCINEURIN_PATHWAY
24	3e−04	3 / 18	GSEA	AMIT_DELAYED_EARLY_GENES
25	4e−04	8 / 227	GSEA	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
26	4e−04	6 / 125	CC	lamellipodium
27	4e−04	87 / 8984	MF	protein binding
28	5e−04	5 / 83	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN
29	5e−04	3 / 20	GSEA	PID_ECADHERIN_KERATINOCYTE_PATHWAY
30	5e−04	4 / 47	GSEA	BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_DN
31	5e−04	6 / 129	miRN	hsa−miR−1272
32	5e−04	15 / 730	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
33	5e−04	6 / 130	GSEA	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2
34	5e−04	5 / 86	MF	integrin binding
35	6e−04	3 / 22	BP	actin filament bundle assembly
36	7e−04	7 / 189	GSEA	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN
37	7e−04	6 / 138	CC	cell−cell junction
38	8e−04	4 / 54	GSEA	BOYLAN_MULTIPLE_MYELOMA_C_DN
39	8e−04	3 / 24	GSEA	REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_
40	8e−04	3 / 24	GSEA	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 100	HORVATH_aging_genes meth DOWN
2	0.2	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	8e−05	7 / 134	cell junction organization
2	6e−04	3 / 22	actin filament bundle assembly
3	1e−03	3 / 26	hippo signaling
4	1e−03	13 / 626	cell adhesion
5	1e−03	8 / 271	positive regulation of apoptotic process
6	2e−03	4 / 64	cell junction assembly
7	2e−03	12 / 581	negative regulation of transcription from RNA polymerase II promoter
8	2e−03	3 / 34	adherens junction organization
9	2e−03	3 / 34	negative regulation of fat cell differentiation
10	2e−03	3 / 35	skeletal muscle cell differentiation
11	3e−03	2 / 10	hemidesmosome assembly
12	4e−03	2 / 12	negative regulation of organ growth
13	4e−03	2 / 12	regulation of cell motility
14	5e−03	2 / 14	centrosome duplication
15	5e−03	2 / 14	generation of neurons
16	5e−03	11 / 581	cytoskeleton organization
17	6e−03	3 / 48	cellular protein localization
18	7e−03	2 / 16	skeletal muscle fiber development
19	8e−03	12 / 705	locomotion
20	1e−02	8 / 382	positive regulation of GTPase activity

Brain

Rank	p−value	#in/all	Geneset
1	0.003	61 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.005	11 / 574	Overlap_fetal_midbrain_TssP
3	0.013	16 / 1122	Fetal_K9K27me3
4	0.015	14 / 953	Fetal_Enh
5	0.019	81 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	0.022	83 / 9330	Overlap_fetal_midbrain_ReprPC
7	0.025	14 / 1013	Fetal_TssP
8	0.032	14 / 1050	Fetal_EnhP
9	0.034	10 / 668	Mid_Frontal_Lobe_Enh
10	0.041	11 / 786	Fetal_EnhG
11	0.074	23 / 2185	Fetal_TssA
12	0.102	4 / 229	Mid_Frontal_Lobe_TxTrans
13	0.124	3 / 158	Overlap_fetal_midbrain_Het
14	0.133	80 / 9528	Overlap_fetal_midbrain_Quies
15	0.216	15 / 1548	Mid_Frontal_Lobe_K9K27me3
16	0.247	18 / 1949	Fetal_TssF
17	0.282	7 / 686	Overlap_fetal_midbrain_TssA
18	0.286	4 / 349	Fetal_ZNF
19	0.345	4 / 383	Fetal_Tx
20	0.361	2 / 163	Fetal_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	1 / 14	LIU_PROSTATE_CANCER_DN
2	5e−02	2 / 44	PanCan_TGF−B_geneset_nanostring
3	5e−02	2 / 48	KUIPER_MM poor survival
4	6e−02	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	7e−02	3 / 120	PanCan_CC+Apop_geneset_nanostring
6	1e−01	2 / 70	SHAUGHNESSY_MM high risk
7	2e−01	5 / 401	Lembcke_Colonic Inflammation
8	2e−01	2 / 113	PanCan_Driver_Gene_geneset_nanostring
9	3e−01	2 / 156	PanCan_PI3K_geneset_nanostring
10	3e−01	1 / 55	PanCan_JAK−ST_geneset_nanostring
11	4e−01	1 / 61	PanCan_Wnt_geneset_nanostring
12	4e−01	0 / 14	LIU_COMMON_CANCER_GENES
13	5e−01	0 / 12	LIU_PROSTATE_CANCER_UP
14	5e−01	1 / 82	PanCan_TXmisReg_geneset_nanostring
15	6e−01	1 / 111	PanCan_RAS_geneset_nanostring
16	6e−01	1 / 121	PanCan_MAPK_geneset_nanostring
17	7e−01	2 / 298	SPANG_BCL6−index2
18	9e−01	2 / 489	Lembcke_Normal vs Adenoma
19	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
20	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	5e−06	12 / 308	focal adhesion
2	3e−05	9 / 202	actin cytoskeleton
3	1e−04	25 / 1465	cytoskeleton
4	3e−04	3 / 17	protein−DNA complex
5	4e−04	6 / 125	lamellipodium
6	7e−04	6 / 138	cell−cell junction
7	4e−03	2 / 13	phagocytic cup
8	5e−03	4 / 89	Z disc
9	5e−03	2 / 14	gap junction
10	5e−03	36 / 3088	plasma membrane
11	7e−03	4 / 99	cell cortex
12	8e−03	3 / 53	intermediate filament
13	1e−02	6 / 239	proteinaceous extracellular matrix
14	2e−02	3 / 73	basement membrane
15	2e−02	2 / 29	cell−cell adherens junction
16	2e−02	100 / 11774	cell
17	3e−02	2 / 33	cell leading edge
18	3e−02	2 / 35	trans−Golgi network membrane
19	4e−02	2 / 39	intercalated disc
20	4e−02	4 / 164	endosome membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.04	10 / 696	Chr 5
2	0.15	4 / 262	Chr 13
3	0.15	6 / 462	Chr 14
4	0.16	7 / 576	Chr 9
5	0.20	9 / 838	Chr 3
6	0.26	6 / 552	Chr 10
7	0.27	14 / 1500	Chr 1
8	0.44	6 / 687	Chr 6
9	0.44	6 / 689	Chr 7
10	0.56	6 / 775	Chr 12
11	0.60	3 / 398	Chr 20
12	0.63	4 / 558	Chr 4
13	0.66	7 / 993	Chr 2
14	0.69	1 / 151	Chr 21
15	0.75	5 / 801	Chr 11
16	0.81	3 / 551	Chr X
17	0.82	1 / 221	Chr 18
18	0.88	2 / 465	Chr 15
19	0.88	2 / 469	Chr 8
20	0.88	3 / 649	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	46 / 3897	Oules1_Colon
2	1e−03	8 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	6e−03	2 / 15	TCGA_Mutated−in−CRC_hypermutated
4	7e−03	2 / 16	TCGA_Mutated−in−CRC_non−hypermutated
5	7e−03	2 / 16	Vilar_non−hypermutated−in−CRC
6	7e−03	2 / 17	Vilar_mutated−in−CRC−CamP
7	7e−03	2 / 17	Vilar_hypermutated−in−CRC
8	1e−02	41 / 3812	TssD1_Colon
9	1e−02	91 / 10290	TssWk_Colon
10	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
11	2e−02	1 / 2	Budinska_A_Surface crypt−like_DOWN
12	2e−02	6 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
13	2e−02	25 / 2159	TssP_Colon
14	3e−02	77 / 8580	TxWk_Colon
15	3e−02	80 / 9027	Tx_Colon
16	4e−02	4 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
17	5e−02	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
18	5e−02	1 / 7	Juehling_HNPCC−mutated−in−5
19	8e−02	3 / 131	Marisa_CRC−cluster−a
20	1e−01	5 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	0.08	5 / 294	GUDJ_psoriasis down
2	0.66	3 / 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	0.006	3 / 49	OL vs. MOG− OL
2	0.036	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.037	2 / 39	OPC
4	0.051	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
5	0.074	2 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
6	0.082	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
7	0.090	2 / 65	GIEZELT_GBM_STS_up_VS_LTS
8	0.098	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.107	2 / 72	laffaire_hypermeth_LGG_vs_control
10	0.110	1 / 15	VERHAAK_CL subtype
11	0.117	1 / 16	KIM deleted & downregulated in LTS
12	0.131	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
13	0.157	1 / 22	KIM prognostic signature LTS vs. STS
14	0.173	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
15	0.182	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	0.190	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
17	0.232	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
18	0.252	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
19	0.256	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
20	0.296	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	12 / 286	PASINI_SUZ12_TARGETS_DN
2	5e−06	19 / 749	CUI_TCF21_TARGETS_2_DN
3	9e−06	19 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
4	2e−05	14 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
5	2e−05	13 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	4e−05	8 / 163	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	6e−05	7 / 129	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP
8	8e−05	5 / 58	PID_AP1_PATHWAY
9	1e−04	6 / 98	REACTOME_CELL_CELL_COMMUNICATION
10	1e−04	12 / 426	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
11	2e−04	14 / 594	WONG_ADULT_TISSUE_STEM_MODULE
12	3e−04	16 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
13	3e−04	8 / 215	BILD_HRAS_ONCOGENIC_SIGNATURE
14	3e−04	7 / 166	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
15	3e−04	9 / 278	GABRIELY_MIR21_TARGETS
16	3e−04	3 / 18	BIOCARTA_CALCINEURIN_PATHWAY
17	3e−04	3 / 18	AMIT_DELAYED_EARLY_GENES
18	4e−04	8 / 227	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
19	5e−04	5 / 83	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN
20	5e−04	3 / 20	PID_ECADHERIN_KERATINOCYTE_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.004	6 / 195	HALLMARK_MITOTIC_SPINDLE
2	0.010	5 / 167	HALLMARK_APICAL_JUNCTION
3	0.012	5 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	0.013	5 / 181	HALLMARK_P53_PATHWAY
5	0.131	3 / 162	HALLMARK_COMPLEMENT
6	0.136	3 / 165	HALLMARK_MYOGENESIS
7	0.142	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	0.157	2 / 91	HALLMARK_PROTEIN_SECRETION
9	0.183	1 / 26	HALLMARK_ANGIOGENESIS
10	0.202	1 / 29	HALLMARK_NOTCH_SIGNALING
11	0.214	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
12	0.307	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
13	0.313	2 / 146	HALLMARK_UV_RESPONSE_UP
14	0.338	1 / 53	HALLMARK_TGF_BETA_SIGNALING
15	0.372	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	0.380	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
17	0.391	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	0.397	2 / 176	HALLMARK_HYPOXIA
19	0.438	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	0.508	1 / 91	HALLMARK_BILE_ACID_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	30 / 2211	HOPP_Repetitive
2	0.002	29 / 2188	HOPP_Poised_promoter
3	0.003	18 / 1128	SPANG_BCR DN
4	0.009	57 / 5693	HOPP_Weak_enhancer
5	0.023	36 / 3396	HOPP_Repressed
6	0.032	3 / 89	ROSOLOWSKI_blue total
7	0.044	2 / 43	LENZ_Stromal signature 2
8	0.057	5 / 268	SPANG_IL21 UP
9	0.083	4 / 212	LENZ_Stromal signature 1
10	0.096	1 / 13	WRIGHT_GCB UP
11	0.103	1 / 14	Subero_MCL_hyper_meth
12	0.106	63 / 7209	HOPP_Weak_promoter
13	0.139	49 / 5538	HOPP_Weak_txn
14	0.143	57 / 6564	HOPP_Strong_enhancer
15	0.164	1 / 23	DAVE_Immune response 1
16	0.165	4 / 275	TARTE_Mature plasma cell signature
17	0.233	1 / 34	Subero_B−ALL_hyper_meth
18	0.236	58 / 6929	HOPP_Txn_elongation
19	0.245	63 / 7592	HOPP_Active_promoter
20	0.251	23 / 2563	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	7e−05	15 / 609	cytoskeletal protein binding
2	1e−04	6 / 102	actin filament binding
3	4e−04	87 / 8984	protein binding
4	5e−04	5 / 86	integrin binding
5	2e−03	15 / 830	nucleic acid binding transcription factor activity
6	2e−03	7 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
7	2e−03	6 / 174	transcription corepressor activity
8	3e−03	2 / 10	gamma−catenin binding
9	4e−03	14 / 820	sequence−specific DNA binding transcription factor activity
10	7e−03	4 / 97	SH3 domain binding
11	8e−03	110 / 13179	molecular_function
12	1e−02	2 / 20	nuclear hormone receptor binding
13	1e−02	2 / 21	retinoic acid receptor binding
14	1e−02	5 / 176	transcription regulatory region DNA binding
15	1e−02	4 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activity
16	1e−02	3 / 66	Rho guanyl−nucleotide exchange factor activity
17	2e−02	2 / 27	RNA polymerase II repressing transcription factor binding
18	2e−02	6 / 271	actin binding
19	3e−02	2 / 33	core promoter sequence−specific DNA binding
20	3e−02	3 / 84	RNA polymerase II core promoter proximal region sequence−specific DNA bir

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−04	6 / 129	hsa−miR−1272
2	1e−03	4 / 60	hsa−miR−650
3	1e−03	4 / 61	hsa−miR−324−5p
4	2e−03	5 / 110	hsa−miR−491−3p
5	2e−03	4 / 68	hsa−miR−299−5p
6	2e−03	5 / 115	hsa−miR−515−5p
7	5e−03	10 / 488	hsa−miR−103
8	5e−03	10 / 488	hsa−miR−107
9	6e−03	9 / 432	hsa−miR−424
10	7e−03	4 / 98	hsa−miR−147
11	8e−03	6 / 222	hsa−miR−185
12	8e−03	9 / 447	hsa−miR−130b
13	8e−03	4 / 102	hsa−miR−377
14	8e−03	5 / 161	hsa−miR−511
15	9e−03	5 / 164	hsa−miR−323b−5p
16	1e−02	5 / 170	hsa−miR−183
17	1e−02	4 / 116	hsa−miR−498
18	1e−02	5 / 182	hsa−miR−374a
19	1e−02	4 / 119	hsa−miR−1248
20	1e−02	3 / 66	hsa−miR−648

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	2 / 9	MYC_Targets DOWN
2	0.015	1 / 2	MYC_Cell cycle DOWN
3	0.036	31 / 2927	ICGC_Rad21_targets
4	0.038	1 / 5	MYC_TF and cofactors
5	0.093	21 / 2013	ICGC_Bcl11_targets
6	0.143	37 / 4054	ICGC_Egr1_targets
7	0.164	17 / 1701	HEBENSTREIT_high expression TF
8	0.171	12 / 1139	HEBENSTREIT_low expression TF
9	0.196	18 / 1872	ICGC_Mef2_targets
10	0.198	26 / 2836	ICGC_BatfPcr1_targets
11	0.210	35 / 3966	ICGC_Pu1_targets
12	0.216	46 / 5355	ICGC_Pol2_targets
13	0.258	6 / 553	ICGC_RxraPcr1_targets
14	0.294	19 / 2137	ICGC_SrfV0416101_targets
15	0.330	36 / 4314	ICGC_Ebfsc137065_targets
16	0.351	45 / 5495	ICGC_Yy1_targets
17	0.402	32 / 3924	ICGC_Zeb1_targets
18	0.450	43 / 5408	ICGC_Pou2_targets
19	0.491	41 / 5219	ICGC_Tcf3_targets
20	0.507	42 / 5374	ICGC_Pax5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.001	4 / 58	VAQUERIZAS_Lung
2	0.001	2 / 7	VAQUERIZAS_Appendix
3	0.001	2 / 7	VAQUERIZAS_Tongue
4	0.004	3 / 41	VAQUERIZAS_Placenta
5	0.005	2 / 14	VAQUERIZAS_Ovary
6	0.007	2 / 16	VAQUERIZAS_Pancreas
7	0.014	2 / 23	VAQUERIZAS_Trachea
8	0.027	2 / 33	VAQUERIZAS_Prostate
9	0.047	2 / 45	VAQUERIZAS_Uterus
10	0.089	1 / 12	VAQUERIZAS_Skin
11	0.124	1 / 17	VAQUERIZAS_Heart
12	0.137	1 / 19	VAQUERIZAS_Tonsil
13	0.164	1 / 23	VAQUERIZAS_Adrenal cortex
14	0.202	1 / 29	VAQUERIZAS_Fetal lung
15	0.268	1 / 40	VAQUERIZAS_Thyroid
16	0.304	2 / 143	VAQUERIZAS_General
17	0.369	1 / 59	VAQUERIZAS_Whole blood
18	1.000	0 / 36	VAQUERIZAS_Fetal brain
19	1.000	0 / 26	VAQUERIZAS_Liver
20	1.000	0 / 29	VAQUERIZAS_Smooth muscle

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	4 / 194	PALMER_B−Cell signature up
2	0.08	1 / 11	WIRTH_Cortex cerebri
3	0.09	1 / 12	WIRTH_Thymus
4	0.11	2 / 74	WIRTH_Mucosa
5	0.29	4 / 350	WIRTH_Immune system
6	0.30	1 / 46	WIRTH_Liver
7	0.51	3 / 350	WIRTH_Nervous System
8	0.52	2 / 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_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	0.04	37 / 3682	LU_BPDE 0.005 DN
2	0.15	12 / 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	

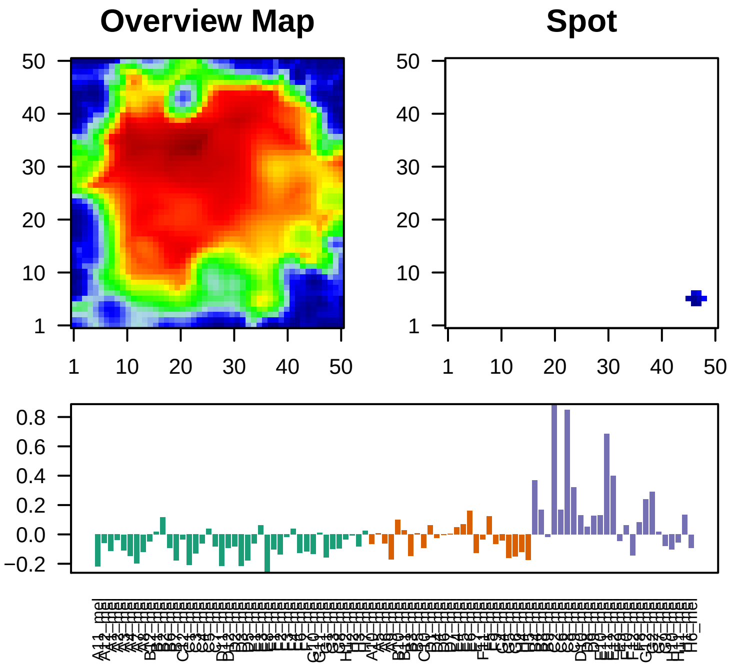
Underexpression Spots

Spot Summary: b

\# metagenes = 8
\# genes = 44

<r> metagenes = 0.98
<r> genes = 0.19
beta: r2= 2.07 / log p= −Inf

\# samples with spot = 8 (8.7 %)
MSC3 : 8 (32 %)

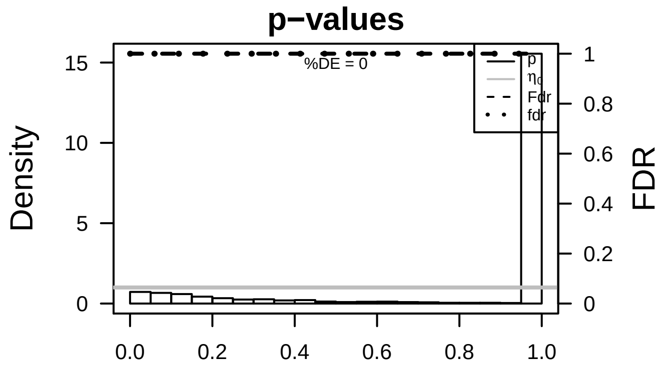


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CYTH3	1.9	−0.46	0.64	CYTH3	cytohesin 3 [Source:HGNC Symbol;Acc:HGNC:9504]
2	RIC8A	1.83	−0.33	0.32	RIC8A	RIC8 guanine nucleotide exchange factor A [Source:HGNC S
3	LEAP2	1.81	−0.18	0.35	LEAP2	liver expressed antimicrobial peptide 2 [Source:HGNC Symbo
4	ZNF383	1.77	−0.16	0.55	ZNF383	zinc finger protein 383 [Source:HGNC Symbol;Acc:HGNC:18
5	PLCD3	1.75	−0.26	0.49	PLCD3	phospholipase C, delta 3 [Source:HGNC Symbol;Acc:HGNC:
6	FAM65B	1.73	−0.09	0.75	FAM65B	family with sequence similarity 65, member B [Source:HGNC
7	EXOC6B	1.66	−0.54	0.38	EXOC6B	exocyst complex component 6B [Source:HGNC Symbol;Acc:
8	LIN7A	1.57	−0.45	0.43	LIN7A	lin−7 homolog A (C. elegans) [Source:HGNC Symbol;Acc:HG
9	PIAS3	1.51	−0.37	0.3	PIAS3	protein inhibitor of activated STAT, 3 [Source:HGNC Symbol;
10	KLF13	1.49	−0.43	0.46	KLF13	Kruppel−like factor 13 [Source:HGNC Symbol;Acc:HGNC:13
11	HSPB7	1.46	−0.16	0.62	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular) [
12	HEG1	1.41	−0.34	0.44	HEG1	heart development protein with EGF−like domains 1 [Source:
13	FAT4	1.4	−0.06	0.76	FAT4	FAT atypical cadherin 4 [Source:HGNC Symbol;Acc:HGNC:2
14	BDNF	1.4	−0.09	0.74	BDNF	brain−derived neurotrophic factor [Source:HGNC Symbol;Acc
15	ATXN1	1.35	−0.33	0.46	ATXN1	ataxin 1 [Source:HGNC Symbol;Acc:HGNC:10548]
16	CDC42BPB	1.34	−0.37	0.44	CDC42BPB	CDC42 binding protein kinase beta (DMPK−like) [Source:HG
17	BAZ2A	1.3	−0.95	0.24	BAZ2A	bromodomain adjacent to zinc finger domain, 2A [Source:HG
18	RAD50	1.29	−1.07	0.31	RAD50	RAD50 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:
19	MYH9	1.29	−1.04	0.45	MYH9	myosin, heavy chain 9, non−muscle [Source:HGNC Symbol;
20	PBX1	1.27	−0.16	0.54	PBX1	pre−B−cell leukemia homeobox 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−04	3 / 32	Lifesty	DUMEAUX_Fasting enriched genes
2	1e−04	3 / 35	GSEA	CHUNG_BLISTER_CYTOTOXICITY_DN
3	2e−04	4 / 102	miRN	hsa−miR−410
4	3e−04	4 / 111	Aging	HORVATH_aging_genes meth UP
5	5e−04	3 / 51	GSEA	CORRE_MULTIPLE_MYELOMA_UP
6	5e−04	26 / 4992	MF	ion binding
7	6e−04	2 / 12	CC	actomyosin
8	8e−04	2 / 14	GSEA	REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1
9	1e−03	2 / 17	BP	actomyosin structure organization
10	1e−03	2 / 17	GSEA	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LK
11	1e−03	4 / 156	MF	protein C−terminus binding
12	1e−03	2 / 19	GSEA	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN
13	2e−03	2 / 20	BP	response to light stimulus
14	2e−03	2 / 21	BP	glutamate secretion
15	2e−03	37 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
16	2e−03	2 / 22	BP	vasculature development
17	2e−03	3 / 88	miRN	hsa−miR−149
18	2e−03	2 / 25	miRN	hsa−miR−99b
19	3e−03	2 / 26	GSEA	REACTOME_PKB_MEDIATED_EVENTS
20	3e−03	3 / 95	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_UP
21	3e−03	4 / 200	GSEA	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
22	3e−03	4 / 200	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
23	3e−03	9 / 1050	Brain	Fetal_EnhP
24	3e−03	2 / 29	BP	regulation of excitatory postsynaptic membrane potential
25	4e−03	7 / 682	GSEA	KRIEG_HYPOXIA_NOT_VIA_KDM3A
26	4e−03	2 / 31	BP	inner ear development
27	4e−03	2 / 31	BP	visual learning
28	4e−03	2 / 33	CC	cell leading edge
29	4e−03	2 / 33	CC	Golgi stack
30	4e−03	2 / 33	GSEA	COWLING_MYCN_TARGETS
31	4e−03	3 / 111	GSEA	ZHU_CMV_ALL_DN
32	5e−03	2 / 35	BP	branching involved in ureteric bud morphogenesis
33	5e−03	2 / 37	BP	termination of G−protein coupled receptor signaling pathway
34	6e−03	3 / 122	BP	plasma membrane organization
35	6e−03	2 / 38	BP	actin cytoskeleton reorganization
36	6e−03	2 / 39	GSEA	ZHAN_MULTIPLE_MYELOMA_MS_UP
37	6e−03	3 / 128	GSEA	RASHI_RESPONSE_TO_IONIZING_RADIATION_5
38	7e−03	2 / 41	CC	cleavage furrow
39	7e−03	10 / 1394	GSEA	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
40	7e−03	2 / 43	BP	neurotransmitter secretion



Aging

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 111	HORVATH_aging_genes meth UP
2	3e−01	1 / 100	HORVATH_aging_genes meth DOWN
3	1e+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	0.001	2 / 17	actomyosin structure organization
2	0.002	2 / 20	response to light stimulus
3	0.002	2 / 21	glutamate secretion
4	0.002	2 / 22	vasculature development
5	0.003	2 / 29	regulation of excitatory postsynaptic membrane potential
6	0.004	2 / 31	inner ear development
7	0.004	2 / 31	visual learning
8	0.005	2 / 35	branching involved in ureteric bud morphogenesis
9	0.005	2 / 37	termination of G−protein coupled receptor signaling pathway
10	0.006	3 / 122	plasma membrane organization
11	0.006	2 / 38	actin cytoskeleton reorganization
12	0.007	2 / 43	neurotransmitter secretion
13	0.007	2 / 43	rhythmic process
14	0.008	2 / 45	regulation of circadian rhythm
15	0.008	2 / 46	chondroitin sulfate metabolic process
16	0.009	2 / 48	positive regulation of protein catabolic process
17	0.010	3 / 150	Wnt signaling pathway
18	0.012	2 / 55	vasculogenesis
19	0.012	2 / 57	response to hormone
20	0.015	2 / 63	negative regulation of transforming growth factor beta receptor signaling pathw

Brain

Rank	p−value	#in/all	Geneset
1	0.002	37 / 9330	Overlap_fetal_midbrain_ReprPC
2	0.003	9 / 1050	Fetal_EnhP
3	0.025	6 / 769	Overlap_fetal_midbrain_ZNF
4	0.034	33 / 9013	Overlap_fetal_midbrain_K9K27me3
5	0.061	3 / 304	Fetal_Het
6	0.067	23 / 5940	Overlap_fetal_midbrain_HetRpts
7	0.084	3 / 349	Fetal_ZNF
8	0.231	4 / 831	Fetal_HetRpts
9	0.308	3 / 656	Overlap_fetal_midbrain_EnhP
10	0.312	4 / 953	Fetal_Enh
11	0.376	1 / 158	Overlap_fetal_midbrain_Het
12	0.428	4 / 1122	Fetal_K9K27me3
13	0.432	10 / 3081	Mid_Frontal_Lobe_ZNF
14	0.471	6 / 1845	Fetal_Quies
15	0.473	29 / 9528	Overlap_fetal_midbrain_Quies
16	0.512	2 / 574	Overlap_fetal_midbrain_TssP
17	0.533	27 / 9020	Overlap_fetal_midbrain_ReprPCWk
18	0.566	4 / 1333	Fetal_ReprPCWk
19	0.569	3 / 989	Mid_Frontal_Lobe_Quies
20	0.620	3 / 1065	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 11	GENTLES_modul17
2	0.04	1 / 13	GENTLES_modul12
3	0.05	1 / 18	PanCan_Notch_geneset_nanostring
4	0.06	1 / 20	PanCan_ChromMod_geneset_nanostring
5	0.08	1 / 29	KUIPER_MM good survival
6	0.12	1 / 44	PanCan_TGF−B_geneset_nanostring
7	0.13	1 / 47	PanCan_DNARepair_geneset_nanostring
8	0.15	1 / 55	PanCan_JAK−ST_geneset_nanostring
9	0.17	1 / 61	PanCan_Wnt_geneset_nanostring
10	0.22	1 / 82	PanCan_TXmisReg_geneset_nanostring
11	0.22	2 / 298	SPANG_BCL6−index2
12	0.29	1 / 113	PanCan_Driver_Gene_geneset_nanostring
13	0.30	1 / 120	PanCan_CC+Apop_geneset_nanostring
14	0.30	1 / 121	PanCan_MAPK_geneset_nanostring
15	0.33	2 / 401	Lembcke_Colonic Inflammation
16	0.37	1 / 156	PanCan_PI3K_geneset_nanostring
17	0.43	2 / 489	Lembcke_Normal vs Adenoma
18	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
19	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
20	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−04	2 / 12	actomyosin
2	4e−03	2 / 33	cell leading edge
3	4e−03	2 / 33	Golgi stack
4	7e−03	2 / 41	cleavage furrow
5	8e−03	3 / 138	cell−cell junction
6	3e−02	2 / 85	ruffle
7	3e−02	1 / 10	pronucleus
8	4e−02	1 / 12	AMP−activated protein kinase complex
9	4e−02	2 / 105	ribonucleoprotein complex
10	4e−02	1 / 14	exocyst
11	4e−02	2 / 113	postsynaptic density
12	5e−02	1 / 18	voltage−gated calcium channel complex
13	5e−02	1 / 19	nuclear chromosome, telomeric region
14	5e−02	1 / 19	site of double−strand break
15	6e−02	1 / 21	immunological synapse
16	6e−02	1 / 22	cortical cytoskeleton
17	6e−02	1 / 22	histone acetyltransferase complex
18	7e−02	1 / 23	integrin complex
19	7e−02	3 / 331	nuclear chromosome
20	8e−02	1 / 29	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	0.05	5 / 687	Chr 6
2	0.06	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
3	0.26	2 / 335	Chr 22
4	0.30	3 / 649	Chr 16
5	0.34	4 / 993	Chr 2
6	0.36	1 / 151	Chr 21
7	0.37	4 / 1037	Chr 19
8	0.40	2 / 462	Chr 14
9	0.46	3 / 838	Chr 3
10	0.46	5 / 1500	Chr 1
11	0.50	2 / 558	Chr 4
12	0.62	2 / 696	Chr 5
13	0.68	2 / 775	Chr 12
14	0.69	2 / 801	Chr 11
15	0.70	1 / 398	Chr 20
16	0.88	1 / 689	Chr 7
17	0.92	1 / 840	Chr 17
18	1.00	0 / 552	Chr 10
19	1.00	0 / 262	Chr 13
20	1.00	0 / 465	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
2	0.04	4 / 436	K9acLow_Colon
3	0.04	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
4	0.05	1 / 18	Boland_CRC−MSI−A6−A10
5	0.06	6 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	0.07	3 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	0.13	1 / 45	Ang_CRC−CIMPH−vs−L_hyper
8	0.14	1 / 50	Ang_CRC_Hypermethylated
9	0.16	11 / 2698	EnhA_Colon
10	0.17	4 / 739	TxEnhG2_Colon
11	0.17	2 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
12	0.18	2 / 263	Pentrack_CRC_TCGA_corr_J_msi=h_UP_mss_DN
13	0.23	31 / 9482	TssA_Colon
14	0.29	1 / 117	Marisa_CRC−cluster−b
15	0.30	29 / 9027	Tx_Colon
16	0.31	10 / 2798	TxEnhG1_Colon
17	0.32	1 / 131	Marisa_CRC−cluster−a
18	0.34	17 / 5155	EnhWk1_Colon
19	0.36	2 / 427	Quies2_Colon
20	0.37	27 / 8580	TxWk_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	0.03	2 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
2	0.14	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
3	0.17	1 / 63	Stuehler_Proteins_up_in_STS
4	0.18	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
5	0.63	1 / 332	Up
6	0.66	1 / 356	Down_a
7	0.67	1 / 365	Down_b
8	1.00	0 / 15	VERHAAK_CL subtype
9	1.00	0 / 15	VERHAAK_MES subtype
10	1.00	0 / 16	VERHAAK_NL subtype
11	1.00	0 / 14	VERHAAK_PN subtype
12	1.00	0 / 23	WIRTH_PN subtype
13	1.00	0 / 74	WIRTH_Normal Brain
14	1.00	0 / 9	VERHAAK_Brain
15	1.00	0 / 8	VERHAAK_PN_Brain
16	1.00	0 / 11	Martinez_Glio_hypermeth
17	1.00	0 / 3	Martinez_Glio_hypometh
18	1.00	0 / 2	laffaire_hypometh_LGG_vs_control
19	1.00	0 / 72	laffaire_hypermeth_LGG_vs_control
20	1.00	0 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 35	CHUNG_BLISTER_CYTOTOXICITY_DN
2	5e−04	3 / 51	CORRE_MULTIPLE_MYELOMA_UP
3	8e−04	2 / 14	REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1
4	1e−03	2 / 17	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1
5	1e−03	2 / 19	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN
6	3e−03	2 / 26	REACTOME_PKB_MEDIATED_EVENTS
7	3e−03	3 / 95	KOBAYASHI_EGFR_SIGNALING_24HR_UP
8	3e−03	4 / 200	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
9	3e−03	4 / 200	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
10	4e−03	7 / 682	KRIEG_HYPOXIA_NOT_VIA_KDM3A
11	4e−03	2 / 33	COWLING_MYCN_TARGETS
12	4e−03	3 / 111	ZHU_CMV_ALL_DN
13	6e−03	2 / 39	ZHAN_MULTIPLE_MYELOMA_MS_UP
14	6e−03	3 / 128	RASHI_RESPONSE_TO_IONIZING_RADIATION_5
15	7e−03	10 / 1394	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
16	8e−03	2 / 45	PID_HEDGEHOG_GLI_PATHWAY
17	8e−03	5 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
18	8e−03	2 / 46	PID_FOXO_PATHWAY
19	8e−03	2 / 46	PID_AJDISS_2PATHWAY
20	8e−03	4 / 272	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN

HM

Rank	p−value	#in/all	Geneset
1	0.008	3 / 137	HALLMARK_UV_RESPONSE_DN
2	0.088	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
3	0.089	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	0.094	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.096	2 / 176	HALLMARK_HYPOXIA
6	0.101	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	0.107	2 / 188	HALLMARK_ADIPOGENESIS
8	0.114	2 / 195	HALLMARK_MITOTIC_SPINDLE
9	0.130	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	0.146	1 / 53	HALLMARK_TGF_BETA_SIGNALING
11	0.237	1 / 91	HALLMARK_BILE_ACID_METABOLISM
12	0.242	1 / 93	HALLMARK_PEROXISOME
13	0.249	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.341	1 / 140	HALLMARK_APOPTOSIS
15	0.353	1 / 146	HALLMARK_UV_RESPONSE_UP
16	0.389	1 / 165	HALLMARK_MYOGENESIS
17	0.393	1 / 167	HALLMARK_APICAL_JUNCTION
18	0.394	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
19	0.411	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	0.421	1 / 183	HALLMARK_GLYCOLYSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 32	DUMEAUX_Fasting enriched genes
2	4e−02	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	2e−01	1 / 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 / 7	DUMEAUX_Women normal BMI 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	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.04	3 / 247	ZHANG_DLBCL mutated
2	0.04	1 / 15	WRIGHT_ABC UP
3	0.18	2 / 256	SPANG_IL21 DN
4	0.21	1 / 81	Subero_INT_hyper_meth
5	0.22	1 / 82	ROSOLOWSKI_green UP
6	0.22	10 / 2563	HOPP_Heterochrom
7	0.25	1 / 96	Subero_DLBCL_hyper_meth
8	0.28	23 / 6929	HOPP_Txn_elongation
9	0.28	1 / 109	ROSOLOWSKI_green total
10	0.32	1 / 129	DAVE_BL−vs−DLBCL
11	0.34	2 / 410	SPANG_CD40 6hrs DN
12	0.37	21 / 6564	HOPP_Strong_enhancer
13	0.47	1 / 212	LENZ_Stromal signature 1
14	0.48	7 / 2188	HOPP_Poised_promoter
15	0.49	4 / 1218	SPANG_BCR UP
16	0.54	17 / 5693	HOPP_Weak_enhancer
17	0.55	1 / 268	SPANG_IL21 UP
18	0.56	1 / 275	TARTE_Mature plasma cell signature
19	0.59	1 / 294	TARTE_Plasmablast signature
20	0.66	3 / 1128	SPANG_BCR DN

MF

Rank	p−value	#in/all	Geneset
1	5e−04	26 / 4992	ion binding
2	1e−03	4 / 156	protein C−terminus binding
3	2e−02	11 / 1859	metal ion binding
4	3e−02	1 / 10	acetylgalactosaminyltransferase activity
5	3e−02	1 / 10	actin−dependent ATPase activity
6	3e−02	1 / 10	type I transforming growth factor beta receptor binding
7	3e−02	2 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
8	3e−02	1 / 11	acetyltransferase activity
9	3e−02	1 / 11	SUMO transferase activity
10	4e−02	1 / 12	core promoter proximal region sequence−specific DNA binding
11	4e−02	1 / 12	poly(U) RNA binding
12	4e−02	1 / 14	enhancer binding
13	4e−02	1 / 14	G−protein alpha−subunit binding
14	4e−02	1 / 15	ARF guanyl−nucleotide exchange factor activity
15	4e−02	1 / 15	lysine−acetylated histone binding
16	4e−02	1 / 15	microfilament motor activity
17	5e−02	1 / 16	calcium−dependent cysteine−type endopeptidase activity
18	5e−02	4 / 461	transferase activity, transferring phosphorus−containing groups
19	5e−02	1 / 17	syntaxin−1 binding
20	5e−02	1 / 18	3'−5' exonuclease activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 102	hsa−miR−410
2	2e−03	3 / 88	hsa−miR−149
3	2e−03	2 / 25	hsa−miR−99b
4	8e−03	2 / 46	hsa−miR−346
5	8e−03	2 / 46	hsa−miR−874
6	9e−03	2 / 49	hsa−miR−1224−3p
7	1e−02	5 / 447	hsa−miR−130b
8	1e−02	4 / 289	hsa−miR−186
9	1e−02	3 / 154	hsa−miR−139−5p
10	1e−02	5 / 456	hsa−miR−130a
11	1e−02	4 / 294	hsa−miR−561
12	1e−02	3 / 157	hsa−miR−512−3p
13	1e−02	2 / 55	hsa−miR−629
14	1e−02	2 / 58	hsa−miR−627
15	1e−02	2 / 58	hsa−miR−328
16	2e−02	2 / 65	hsa−miR−9*
17	2e−02	2 / 73	hsa−miR−657
18	2e−02	3 / 197	hsa−miR−222
19	2e−02	3 / 204	hsa−miR−221
20	2e−02	2 / 82	hsa−miR−188−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	1 / 12	GUSTAFSON_PI3K_UP
2	0.04	1 / 13	GUSTAFSON_PI3K_DN
3	0.04	1 / 13	BENTINK_src.10
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 / 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	11 / 2013	ICGC_Bcl11_targets
2	0.06	21 / 5219	ICGC_Tcf3_targets
3	0.06	13 / 2836	ICGC_BatfPcr1_targets
4	0.08	13 / 2927	ICGC_Rad21_targets
5	0.09	10 / 2137	ICGC_SrfV0416101_targets
6	0.10	16 / 3966	ICGC_Pu1_targets
7	0.12	16 / 4032	ICGC_Creb1_targets
8	0.12	8 / 1701	HEBENSTREIT_high expression TF
9	0.13	18 / 4706	ICGC_Sp1_targets
10	0.17	6 / 1266	ICGC_NrsfPcr1_targets
11	0.17	18 / 4909	ICGC_Stat5_targets
12	0.17	21 / 5890	ICGC_Elf1_targets
13	0.18	17 / 4617	ICGC_Tcf12_targets
14	0.19	8 / 1878	ICGC_Cebpbsc150_targets
15	0.23	21 / 6114	ICGC_Runx3_targets
16	0.24	17 / 4829	ICGC_Nficsc81335_targets
17	0.25	18 / 5200	ICGC_Mta3_targets
18	0.26	14 / 3924	ICGC_Zeb1_targets
19	0.27	9 / 2391	ICGC_Pbx3_targets
20	0.29	13 / 3700	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.3	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	0.1	2 / 225	PALMER_Granulocytes signature up
2	0.2	1 / 95	WIRTH_Muscle
3	0.3	2 / 350	WIRTH_Nervous System
4	0.4	1 / 194	PALMER_B−Cell signature up
5	1.0	0 / 32	WIRTH_Pancreas
6	1.0	0 / 350	WIRTH_Immune system
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	0.9	8 / 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	

Underexpression Spots

Spot Summary: c

metagenes = 22
genes = 348

<r> metagenes = 0.97
<r> genes = 0.17
beta: r2= 4.29 / log p= −Inf

samples with spot = 15 (16.3 %)
MSC1 : 3 (7.1 %)
MSC3 : 12 (48 %)

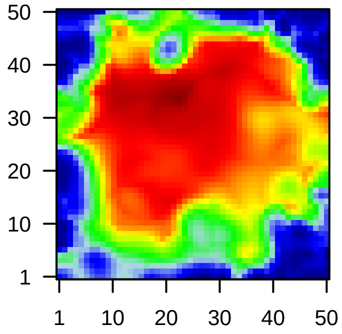
Spot Genelist

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 Sym
4	ANXA1	2.44	−0.5	0.78	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
5	FADS3	2.35	−0.24	0.56	FADS3	fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35
6	PTPRZ1	2.31	−0.37	0.7	PTPRZ1	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
7	NAV3	2.3	−0.23	0.73	NAV3	neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998
8	RGS4	2.3	−0.3	0.4	RGS4	regulator of G−protein signaling 4 [Source:HGNC Symbol;Ac
9	A2M	2.29	−0.9	0.52	A2M	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
10	RGS2	2.26	−0.52	0.33	RGS2	regulator of G−protein signaling 2 [Source:HGNC Symbol;Ac
11	KCNJ2	2.26	−0.25	0.68	KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2
12	HIST1H3D	2.25	−0.35	0.37	HIST1H3D	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
13	FN1	2.23	−1.04	0.4	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
14	SERPINI1	2.21	−0.56	0.39	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
15	LMCD1	2.2	−0.68	0.32	LMCD1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
16	VTN	2.14	−0.36	0.67	VTN	vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
17	SLC40A1	2.11	−0.56	0.38	SLC40A1	solute carrier family 40 (iron−regulated transporter), member
18	ARRDC3	2.09	−0.76	0.5	ARRDC3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:HG
19	CAV1	2.08	−0.76	0.44	CAV1	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
20	MAP2	2.07	−0.14	0.6	MAP2	microtubule−associated protein 2 [Source:HGNC Symbol;Acc

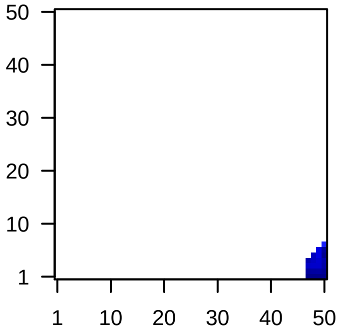
Geneset Overrepresentation

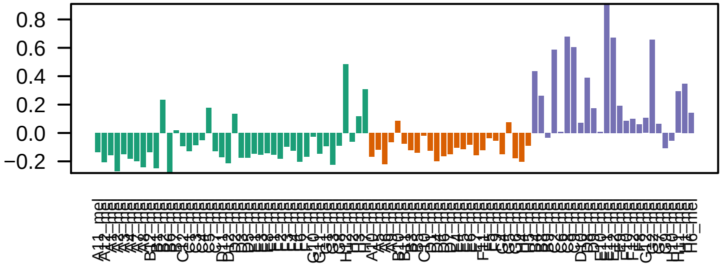
Rank	p−value	#in/all	Geneset	
1	1e−27	60 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	1e−26	47 / 286	GSEA	PASINI_SUZ12_TARGETS_DN
3	5e−23	61 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
4	5e−23	38 / 212	Lymph	LENZ_Stromal signature 1
5	1e−22	44 / 302	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	3e−21	66 / 749	GSEA	CUI_TCF21_TARGETS_2_DN
7	1e−20	73 / 930	GSEA	NUYTTEN_EZH2_TARGETS_UP
8	2e−20	32 / 168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
9	2e−18	44 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
10	2e−18	46 / 425	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
11	8e−18	44 / 401	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
12	3e−15	41 / 410	GSEA	LIM_MAMMARY_STEM_CELL_UP
13	4e−15	45 / 494	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
14	1e−14	59 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	2e−14	31 / 245	GSEA	WANG_SMARCE1_TARGETS_UP
16	2e−14	33 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
17	3e−14	30 / 234	GSEA	LU_AGING_BRAIN_UP
18	5e−14	55 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
19	6e−14	39 / 406	GSEA	BAELDE_DIABETIC_NEPHROPATHY_DN
20	2e−13	19 / 91	GSEA	BROWNE_HCMV_INFECTION_20HR_DN
21	3e−13	1 / 14	Canc	LIU_PROSTATE_CANCER_DN
22	3e−13	22 / 131	Colon	Marisa_CRC−cluster−a
23	9e−13	22 / 137	HM	HALLMARK_UV_RESPONSE_DN
24	3e−12	20 / 117	Colon	Marisa_CRC−cluster−b
25	4e−12	27 / 227	GSEA	ONDER_CDH1_TARGETS_2_UP
26	4e−12	25 / 195	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
27	5e−12	23 / 164	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
28	8e−12	39 / 475	GSEA	ONKEN_UVEAL_MELANOMA_DN
29	1e−11	45 / 616	GSEA	NABA_MATRISOME
30	2e−11	60 / 1013	Brain	Fetal_TssP
31	2e−11	30 / 303	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
32	8e−11	34 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
33	8e−11	25 / 222	GSEA	UDAYAKUMAR_MED1_TARGETS_DN
34	1e−10	43 / 618	GSEA	GOZGIT_ESR1_TARGETS_DN
35	2e−10	21 / 163	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
36	2e−10	31 / 352	CC	cell surface
37	2e−10	24 / 215	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
38	2e−10	27 / 272	GSEA	LEI_MYB_TARGETS
39	3e−10	22 / 181	HM	HALLMARK_P53_PATHWAY
40	3e−10	17 / 104	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_UP

Overview Map

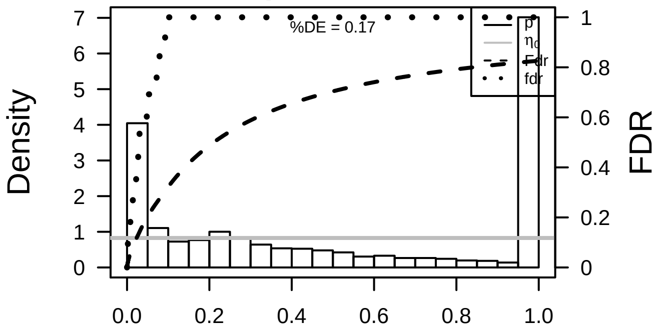


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	5 / 111	HORVATH_aging_genes meth UP
2	0.2	2 / 38	TESCHENDORFF_age_hypermethylated
3	0.4	3 / 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	

Cancer

Rank	p−value	#in/all	Geneset
1	3e−13	1 / 14	LIU_PROSTATE_CANCER_DN
2	2e−05	14 / 156	PanCan_PI3K_geneset_nanostring
3	2e−04	22 / 401	Lembcke_Colonic Inflammation
4	2e−03	2 / 3	ZHANG_MGUS up
5	5e−03	8 / 111	PanCan_RAS_geneset_nanostring
6	1e−02	5 / 61	PanCan_Wnt_geneset_nanostring
7	2e−02	4 / 44	PanCan_TGF−B_geneset_nanostring
8	2e−02	2 / 10	GENTLES_modul13
9	3e−02	2 / 11	GENTLES_modul17
10	4e−02	5 / 82	PanCan_TXmisReg_geneset_nanostring
11	5e−02	12 / 298	SPANG_BCL6−index2
12	2e−01	1 / 14	LIU_LIVER_CANCER
13	2e−01	0 / 14	LIU_COMMON_CANCER_GENES
14	2e−01	2 / 40	ZHANG_MM up
15	2e−01	1 / 12	LIU_BREAST_CANCER
16	2e−01	1 / 12	LIU_PROSTATE_CANCER_UP
17	3e−01	1 / 13	GENTLES_modul12
18	3e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
19	3e−01	1 / 15	GENTLES_modul4
20	3e−01	1 / 15	GENTLES_modul10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−13	22 / 131	Marisa_CRC−cluster−a
2	3e−12	20 / 117	Marisa_CRC−cluster−b
3	6e−10	290 / 10290	TssWk_Colon
4	3e−09	25 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	1e−07	133 / 3812	TssD1_Colon
6	8e−07	22 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
7	1e−06	118 / 3383	EnhWk2_Colon
8	1e−06	131 / 3897	Quies1_Colon
9	3e−05	257 / 9482	TssA_Colon
10	2e−04	229 / 8415	Quies3_Colon
11	3e−04	21 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
12	4e−04	151 / 5155	EnhWk1_Colon
13	7e−04	87 / 2698	EnhA_Colon
14	1e−03	229 / 8580	TxWk_Colon
15	1e−03	3 / 9	Budinska_D_Mesenchymal_UP
16	1e−03	252 / 9653	Enh_Colon
17	1e−03	238 / 9027	Tx_Colon
18	3e−03	5 / 43	Marisa_CRC−cluster−f
19	3e−03	20 / 436	K9acLow_Colon
20	8e−03	10 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−27	60 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	1e−26	47 / 286	PASINI_SUZ12_TARGETS_DN
3	5e−23	61 / 594	WONG_ADULT_TISSUE_STEM_MODULE
4	1e−22	44 / 302	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
5	3e−21	66 / 749	CUI_TCF21_TARGETS_2_DN
6	1e−20	73 / 930	NUYTTEN_EZH2_TARGETS_UP
7	2e−18	44 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
8	2e−18	46 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
9	8e−18	44 / 401	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
10	3e−15	41 / 410	LIM_MAMMARY_STEM_CELL_UP
11	4e−15	45 / 494	CHICAS_RB1_TARGETS_CONFLUENT
12	1e−14	59 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
13	2e−14	31 / 245	WANG_SMARCE1_TARGETS_UP
14	2e−14	33 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
15	3e−14	30 / 234	LU_AGING_BRAIN_UP
16	5e−14	55 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
17	6e−14	39 / 406	BAELDE_DIABETIC_NEPHROPATHY_DN
18	2e−13	19 / 91	BROWNE_HCMV_INFECTION_20HR_DN
19	3e−13	1 / 14	LIU_PROSTATE_CANCER_DN
20	4e−12	27 / 227	ONDER_CDH1_TARGETS_2_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−23	38 / 212	LENZ_Stromal signature 1
2	5e−10	95 / 2188	HOPP_Poised_promoter
3	2e−08	101 / 2563	HOPP_Heterochrom
4	5e−08	123 / 3396	HOPP_Repressed
5	5e−07	178 / 5693	HOPP_Weak_enhancer
6	2e−06	13 / 109	ROSOLOWSKI_green total
7	3e−06	21 / 280	SPANG_CD40 6hrs UP
8	2e−05	10 / 82	ROSOLOWSKI_green UP
9	4e−04	200 / 7209	HOPP_Weak_promoter
10	7e−04	6 / 47	Subero_FL_hyper_meth
11	9e−04	4 / 19	Subero_MM_hyper_meth
12	9e−04	158 / 5538	HOPP_Weak_txn
13	1e−03	4 / 20	SPANG_BAFF 9hrs UP
14	2e−03	181 / 6564	HOPP_Strong_enhancer
15	2e−03	8 / 96	Subero_DLBCL_hyper_meth
16	2e−03	72 / 2211	HOPP_Repetitive
17	2e−03	44 / 1218	SPANG_BCR UP
18	3e−03	7 / 81	Subero_INT_hyper_meth
19	3e−03	5 / 43	LENZ_Stromal signature 2
20	4e−03	8 / 107	SPANG_LPS 6hrs UP

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_ras.1
2	0.3	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	

Tissue

Rank	p−value	#in/all	Geneset
1	9e−05	4 / 11	WIRTH_Sec. lymphoid organs
2	5e−03	8 / 114	PALMER_T−Cell signature up
3	4e−02	9 / 194	PALMER_B−Cell signature up
4	4e−02	2 / 14	WIRTH_Telencephalon
5	2e−01	4 / 95	WIRTH_Muscle
6	2e−01	1 / 9	PALMER_CD8+ T−Cell signature up
7	2e−01	1 / 11	WIRTH_Cortex cerebri
8	2e−01	1 / 12	WIRTH_Thymus
9	3e−01	1 / 13	WIRTH_B−cells
10	4e−01	9 / 350	WIRTH_Nervous System
11	5e−01	1 / 32	WIRTH_Placenta
12	6e−01	5 / 225	PALMER_Granulocytes signature up
13	7e−01	1 / 46	WIRTH_Liver
14	8e−01	6 / 350	WIRTH_Immune system
15	1e+00	0 / 32	WIRTH_Pancreas
16	1e+00	0 / 11	WIRTH_Prim. lymphoid organs
17	1e+00	0 / 8	WIRTH_Tonsil
18	1e+00	0 / 12	WIRTH_Lymphocytes
19	1e+00	0 / 5	WIRTH_Bone marrow
20	1e+00	0 / 11	WIRTH_Globus pallidus

BP

Rank	p−value	#in/all	Geneset
1	4e−09	93 / 2210	anatomical structure development
2	8e−09	40 / 626	cell adhesion
3	1e−07	12 / 74	wound healing
4	5e−07	12 / 83	muscle contraction
5	8e−07	34 / 581	cytoskeleton organization
6	2e−06	28 / 443	anatomical structure formation involved in morphogenesis
7	5e−06	20 / 269	extracellular matrix organization
8	7e−06	106 / 3068	signal transduction
9	9e−06	63 / 1556	cell differentiation
10	1e−05	22 / 336	negative regulation of cell proliferation
11	2e−05	53 / 1255	cellular component assembly
12	2e−05	35 / 705	locomotion
13	2e−05	31 / 590	cell morphogenesis
14	6e−05	5 / 19	peripheral nervous system development
15	7e−05	12 / 134	cell junction organization
16	8e−05	11 / 115	cell cycle arrest
17	9e−05	77 / 2172	response to stress
18	1e−04	10 / 98	neuron projection development
19	1e−04	19 / 312	axon guidance
20	2e−04	4 / 13	retinal ganglion cell axon guidance

CC

Rank	p−value	#in/all	Geneset
1	2e−10	31 / 352	cell surface
2	8e−10	28 / 308	focal adhesion
3	6e−09	92 / 2193	extracellular exosome
4	2e−08	117 / 3132	extracellular region
5	2e−06	40 / 775	extracellular space
6	4e−06	19 / 239	proteinaceous extracellular matrix
7	5e−06	17 / 202	actin cytoskeleton
8	1e−05	106 / 3088	plasma membrane
9	2e−05	14 / 159	extracellular matrix
10	4e−05	10 / 89	Z disc
11	8e−05	57 / 1465	cytoskeleton
12	1e−04	7 / 48	stress fiber
13	2e−04	5 / 23	integrin complex
14	2e−04	7 / 52	caveola
15	9e−04	4 / 19	filamentous actin
16	1e−03	7 / 70	sarcolemma
17	1e−03	9 / 113	postsynaptic density
18	2e−03	10 / 138	cell−cell junction
19	2e−03	7 / 73	basement membrane
20	2e−03	5 / 37	platelet alpha granule lumen

Disease

Rank	p−value	#in/all	Geneset
1	2e−04	18 / 294	GUDJ_psoriasis down
2	6e−01	10 / 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	

HM

Rank	p−value	#in/all	Geneset
1	2e−20	32 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	9e−13	22 / 137	HALLMARK_UV_RESPONSE_DN
3	3e−10	22 / 181	HALLMARK_P53_PATHWAY
4	5e−09	20 / 176	HALLMARK_HYPOXIA
5	9e−07	17 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	1e−04	13 / 165	HALLMARK_MYOGENESIS
7	3e−04	5 / 26	HALLMARK_ANGIOGENESIS
8	4e−04	11 / 140	HALLMARK_APOPTOSIS
9	2e−03	11 / 167	HALLMARK_IL2_STAT5_SIGNALING
10	3e−03	10 / 148	HALLMARK_KRAS_SIGNALING_UP
11	4e−03	8 / 107	HALLMARK_COAGULATION
12	5e−03	5 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
13	6e−03	10 / 167	HALLMARK_APICAL_JUNCTION
14	6e−03	7 / 94	HALLMARK_ANDROGEN_RESPONSE
15	8e−03	5 / 53	HALLMARK_TGF_BETA_SIGNALING
16	1e−02	4 / 37	HALLMARK_APICAL_SURFACE
17	1e−02	10 / 183	HALLMARK_GLYCOLYSIS
18	2e−02	10 / 196	HALLMARK_MTORC1_SIGNALING
19	2e−02	9 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	5e−02	7 / 140	HALLMARK_INFLAMMATORY_RESPONSE

MF

Rank	p−value	#in/all	Geneset
1	1e−09	41 / 609	cytoskeletal protein binding
2	9e−08	13 / 86	integrin binding
3	3e−07	13 / 95	heparin binding
4	1e−06	252 / 8984	protein binding
5	2e−06	6 / 17	insulin−like growth factor binding
6	2e−06	21 / 271	actin binding
7	2e−05	29 / 530	calcium ion binding
8	5e−05	5 / 18	laminin binding
9	1e−04	7 / 49	collagen binding
10	2e−04	4 / 14	G−protein alpha−subunit binding
11	4e−04	4 / 16	extracellular matrix binding
12	5e−04	5 / 29	structural constituent of muscle
13	6e−04	20 / 378	structural molecule activity
14	7e−04	9 / 104	growth factor activity
15	8e−04	7 / 65	protease binding
16	1e−03	3 / 10	peptidase activator activity
17	1e−03	5 / 36	chromatin DNA binding
18	3e−03	20 / 430	lipid binding
19	4e−03	22 / 501	identical protein binding
20	4e−03	4 / 29	insulin receptor binding

TF

Rank	p−value	#in/all	Geneset
1	0.02	38 / 1139	HEBENSTREIT_low expression TF
2	0.05	1 / 2	MYC_ECM cell adhesion DOWN
3	0.08	35 / 1171	KIM_MYC targets
4	0.09	37 / 1266	ICGC_NrsfPcr1_targets
5	0.13	36 / 1273	ICGC_P300_targets
6	0.17	76 / 2927	ICGC_Rad21_targets
7	0.19	1 / 9	MYC_Targets DOWN
8	0.22	49 / 1872	ICGC_Mef2_targets
9	0.30	1 / 15	NOWICK_TF
10	0.32	16 / 595	ICGC_NrsfPcr2_targets
11	0.58	55 / 2391	ICGC_Pbx3_targets
12	0.60	91 / 3966	ICGC_Pu1_targets
13	0.67	14 / 653	ICGC_SrfPcr2_targets
14	0.71	41 / 1878	ICGC_Cebpbsc150_targets
15	0.72	53 / 2416	ICGC_Bcl3_targets
16	0.74	87 / 3924	ICGC_Zeb1_targets
17	0.76	104 / 4682	ICGC_Pol24_targets
18	0.83	60 / 2836	ICGC_BatfPcr1_targets
19	0.84	117 / 5355	ICGC_Pol2_targets
20	0.84	10 / 553	ICGC_RxraPcr1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	89 / 3682	LU_BPDE 0.005 DN
2	0.8	23 / 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	2e−11	60 / 1013	Fetal_TssP
2	2e−07	79 / 1907	Fetal_TxTrans
3	2e−06	259 / 9330	Overlap_fetal_midbrain_ReprPC
4	6e−06	250 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	1e−05	81 / 2185	Fetal_TssA
6	7e−05	256 / 9528	Overlap_fetal_midbrain_Quies
7	8e−05	71 / 1949	Fetal_TssF
8	8e−05	29 / 574	Overlap_fetal_midbrain_TssP
9	4e−04	170 / 5940	Overlap_fetal_midbrain_HetRpts
10	1e−03	18 / 349	Fetal_ZNF
11	5e−03	38 / 1050	Fetal_EnhP
12	1e−02	14 / 304	Fetal_Het
13	1e−02	25 / 668	Mid_Frontal_Lobe_Enh
14	2e−02	16 / 383	Fetal_Tx
15	3e−02	30 / 884	Overlap_fetal_midbrain_EnhG
16	5e−02	17 / 468	Mid_Frontal_Lobe_TssF
17	9e−02	32 / 1065	Overlap_fetal_midbrain_Enh
18	1e−01	44 / 1548	Mid_Frontal_Lobe_K9K27me3
19	1e−01	24 / 786	Fetal_EnhG
20	1e−01	23 / 769	Overlap_fetal_midbrain_ZNF

Chr

Rank	p−value	#in/all	Geneset
1	0.001	25 / 558	Chr 4
2	0.004	32 / 838	Chr 3
3	0.010	49 / 1500	Chr 1
4	0.054	23 / 687	Chr 6
5	0.060	23 / 696	Chr 5
6	0.147	8 / 221	Chr 18
7	0.222	16 / 552	Chr 10
8	0.294	13 / 465	Chr 15
9	0.379	25 / 993	Chr 2
10	0.449	19 / 775	Chr 12
11	0.508	19 / 801	Chr 11
12	0.588	9 / 398	Chr 20
13	0.649	15 / 689	Chr 7
14	0.661	10 / 469	Chr 8
15	0.689	3 / 151	Chr 21
16	0.865	4 / 262	Chr 13
17	0.919	7 / 462	Chr 14
18	0.931	14 / 840	Chr 17
19	0.970	9 / 649	Chr 16
20	0.976	7 / 551	Chr X

Glio

Rank	p−value	#in/all	Geneset
1	2e−08	12 / 62	cultured astroglia vs. in vivo astrocytes
2	1e−07	14 / 103	GIEZELT_GBM_WT_up_VS_mut
3	7e−06	7 / 32	Colman_survival_associated
4	1e−04	14 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
5	3e−04	9 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	5e−03	5 / 47	Vishal_subnetwork signature of survival in GBM
7	1e−02	15 / 332	Up
8	1e−02	3 / 22	KIM prognostic signature LTS vs. STS
9	2e−02	7 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
10	3e−02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
11	3e−02	4 / 49	OL vs. MOG− OL
12	3e−02	4 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
13	3e−02	7 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	3e−02	6 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	4e−02	2 / 14	VERHAAK_PN subtype
16	5e−02	4 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
17	5e−02	14 / 365	Down_b
18	5e−02	2 / 16	KIM deleted & downregulated in LTS
19	5e−02	3 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
20	7e−02	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	2 / 18	DUMEAUX_High bmi enriched genes
2	0.09	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
3	0.43	2 / 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	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−07	37 / 607	hsa−miR−20a
2	5e−07	34 / 569	hsa−miR−20b
3	8e−07	22 / 282	hsa−miR−570
4	1e−06	32 / 541	hsa−miR−17
5	2e−06	17 / 187	hsa−miR−944
6	3e−06	27 / 426	hsa−miR−519d
7	6e−06	16 / 183	hsa−miR−1283
8	9e−06	24 / 376	hsa−miR−373
9	1e−05	22 / 328	hsa−miR−18a
10	1e−05	13 / 129	hsa−miR−576−3p
11	2e−05	30 / 552	hsa−miR−93
12	2e−05	24 / 391	hsa−miR−519a
13	3e−05	8 / 53	hsa−miR−337−3p
14	3e−05	28 / 517	hsa−miR−106b
15	4e−05	24 / 411	hsa−miR−372
16	4e−05	14 / 168	hsa−miR−520h
17	5e−05	14 / 170	hsa−miR−183
18	6e−05	14 / 175	hsa−miR−548k
19	7e−05	16 / 222	hsa−miR−520g
20	7e−05	20 / 321	hsa−miR−32

TF Tissue

Rank	p−value	#in/all	Geneset
1	5e−04	5 / 29	VAQUERIZAS_Smooth muscle
2	5e−03	3 / 15	VAQUERIZAS_Fetal thyroid
3	1e−02	5 / 59	VAQUERIZAS_Whole blood
4	2e−02	4 / 45	VAQUERIZAS_Uterus
5	4e−02	2 / 14	VAQUERIZAS_Ovary
6	5e−02	3 / 36	VAQUERIZAS_Fetal brain
7	7e−02	3 / 40	VAQUERIZAS_Thyroid
8	7e−02	3 / 41	VAQUERIZAS_Placenta
9	1e−01	2 / 23	VAQUERIZAS_Trachea
10	1e−01	2 / 29	VAQUERIZAS_Fetal lung
11	2e−01	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
12	2e−01	3 / 58	VAQUERIZAS_Lung
13	2e−01	2 / 37	VAQUERIZAS_Thymus
14	2e−01	2 / 38	VAQUERIZAS_Whole brain
15	2e−01	1 / 12	VAQUERIZAS_Skin
16	3e−01	1 / 16	VAQUERIZAS_Salivary gland
17	4e−01	1 / 19	VAQUERIZAS_Tonsil
18	4e−01	1 / 23	VAQUERIZAS_Adrenal cortex
19	5e−01	1 / 27	VAQUERIZAS_Lymph node
20	5e−01	1 / 33	VAQUERIZAS_Prostate

Underexpression Spots

Spot Summary: d

metagenes = 43
genes = 418

<r> metagenes = 0.72
<r> genes = 0.08
beta: r2= 1.71 / log p= −Inf

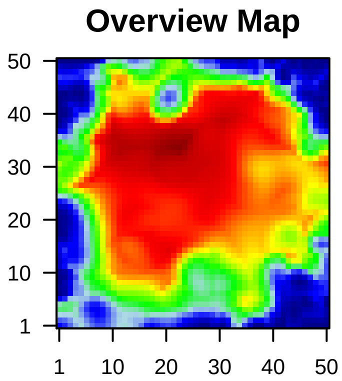
samples with spot = 15 (16.3 %)
MSC1 : 10 (23.8 %)
MSC2 : 3 (12 %)
MSC3 : 2 (8 %)

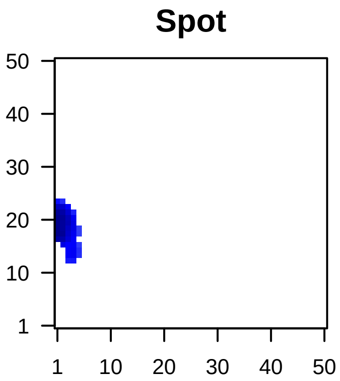
Spot Genelist

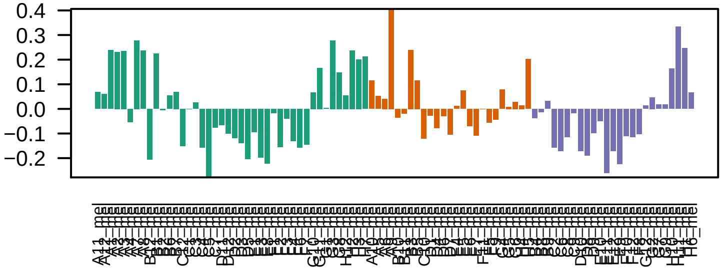
Rank	ID	max e	min e	r	Symbol	Description
1	FZD3	2.09	−0.27	0.28	FZD3	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4
2	SLC25A14	2.08	−0.21	0.26	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member
3	RAB40B	1.91	−0.31	0.29	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
4	TKTL1	1.87	−0.19	0.27	TKTL1	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
5	ARRDC1	1.83	−0.36	0.26	ARRDC1	arrestin domain containing 1 [Source:HGNC Symbol;Acc:HG
6	TAPBPL	1.83	−0.08	0.34	TAPBPL	TAP binding protein−like [Source:HGNC Symbol;Acc:HGNC:
7	NSMCE4A	1.83	−0.38	0.29	NSMCE4A	non−SMC element 4 homolog A (S. cerevisiae) [Source:HGN
8	FAM131A	1.78	−0.18	0.29	FAM131A	family with sequence similarity 131, member A [Source:HGN
9	DBNDD2	1.77	−0.24	0.33	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing
10	LCMT2	1.75	−0.37	0.3	LCMT2	leucine carboxyl methyltransferase 2 [Source:HGNC Symbol;
11	TTC7B	1.74	−0.65	0.19	TTC7B	tetratricopeptide repeat domain 7B [Source:HGNC Symbol;A
12	GSTA1	1.74	−0.45	0.3	GSTA1	glutathione S−transferase alpha 1 [Source:HGNC Symbol;Ac
13	ELAC2	1.72	−0.93	0.27	ELAC2	elaC ribonuclease Z 2 [Source:HGNC Symbol;Acc:HGNC:14
14	IFNAR2	1.71	−0.41	0.45	IFNAR2	interferon (alpha, beta and omega) receptor 2 [Source:HGNC
15	STAT6	1.71	−0.38	0.29	STAT6	signal transducer and activator of transcription 6, interleukin−
16	NECAB3	1.7	−0.22	0.25	NECAB3	N−terminal EF−hand calcium binding protein 3 [Source:HGN
17	LMLN	1.68	−0.37	0.26	LMLN	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
18	SCRN2	1.68	−0.18	0.3	SCRN2	secernin 2 [Source:HGNC Symbol;Acc:HGNC:30381]
19	CPS1	1.65	−0.46	0.24	CPS1	carbamoyl−phosphate synthase 1, mitochondrial [Source:HG
20	MIOS	1.64	−0.23	0.29	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila) [Sou

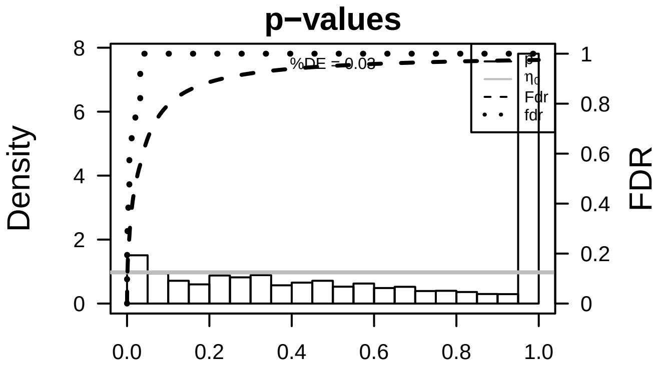
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−21	353 / 9482	Colon	TssA_Colon
2	4e−15	327 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	6e−14	69 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	2e−13	302 / 8205	CC	cytoplasm
5	9e−12	318 / 9027	Colon	Tx_Colon
6	4e−11	268 / 7203	Colon	TssF_Colon
7	1e−10	58 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
8	2e−10	352 / 10605	CC	intracellular
9	3e−09	137 / 3081	Brain	Mid_Frontal_Lobe_ZNF
10	9e−09	79 / 1468	CC	mitochondrion
11	1e−08	332 / 9988	CC	organelle
12	1e−08	320 / 9528	Brain	Overlap_fetal_midbrain_Quies
13	7e−08	218 / 5880	Colon	TssD2_Colon
14	9e−08	66 / 1201	CC	endoplasmic reticulum
15	3e−07	69 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
16	9e−07	32 / 440	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
17	1e−06	19 / 188	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_UP
18	1e−06	307 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
19	2e−06	117 / 2798	Colon	TxEnhG1_Colon
20	5e−06	313 / 9653	Colon	Enh_Colon
21	1e−05	30 / 447	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_UP
22	1e−05	256 / 7592	Lymph	HOPP_Active_promoter
23	2e−05	282 / 8580	Colon	TxWk_Colon
24	2e−05	186 / 5184	Lymph	HOPP_Txn_transition
25	4e−05	30 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
26	4e−05	25 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
27	4e−05	170 / 4689	TF	ICGC_Taf1_targets
28	4e−05	362 / 11774	CC	cell
29	4e−05	8 / 47	GSEA	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
30	4e−05	19 / 238	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
31	6e−05	10 / 78	GSEA	SCHUHMACHER_MYC_TARGETS_UP
32	8e−05	36 / 649	CC	endoplasmic reticulum membrane
33	8e−05	54 / 1132	CC	Golgi apparatus
34	1e−04	23 / 340	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
35	1e−04	22 / 321	GSEA	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
36	1e−04	26 / 416	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
37	2e−04	34 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
38	2e−04	173 / 4909	TF	ICGC_Stat5_targets
39	2e−04	22 / 332	Glio	Up
40	2e−04	147 / 4054	TF	ICGC_Egr1_targets









Aging

Rank	p−value	#in/all	Geneset
1	0.5	3 / 100	HORVATH_aging_genes meth DOWN
2	0.7	1 / 38	TESCHENDORFF_age_hypermethylated
3	1.0	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	3e−04	4 / 12	oxidative phosphorylation
2	6e−04	11 / 120	transforming growth factor beta receptor signaling pathway
3	7e−04	6 / 39	membrane fusion
4	8e−04	5 / 27	platelet aggregation
5	8e−04	5 / 27	positive regulation of DNA replication
6	1e−03	70 / 1730	small molecule metabolic process
7	2e−03	32 / 653	homeostatic process
8	2e−03	4 / 19	negative regulation of proteolysis
9	2e−03	5 / 32	mitochondrion degradation
10	2e−03	13 / 182	dephosphorylation
11	2e−03	8 / 81	MAPK cascade
12	2e−03	3 / 10	regulation of cell death
13	3e−03	4 / 21	aerobic respiration
14	3e−03	29 / 598	membrane organization
15	3e−03	10 / 129	insulin receptor signaling pathway
16	4e−03	4 / 23	osteoclast differentiation
17	4e−03	4 / 23	protein export from nucleus
18	4e−03	5 / 38	actin cytoskeleton reorganization
19	5e−03	7 / 74	nucleobase−containing small molecule metabolic process
20	5e−03	6 / 56	cellular iron ion homeostasis

Brain

Rank	p−value	#in/all	Geneset
1	4e−15	327 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−09	137 / 3081	Mid_Frontal_Lobe_ZNF
3	1e−08	320 / 9528	Overlap_fetal_midbrain_Quies
4	1e−06	307 / 9330	Overlap_fetal_midbrain_ReprPC
5	9e−04	37 / 765	Mid_Frontal_Lobe_Het
6	6e−03	53 / 1333	Fetal_ReprPCWk
7	3e−02	186 / 5940	Overlap_fetal_midbrain_HetRpts
8	2e−01	59 / 1845	Fetal_Quies
9	2e−01	27 / 831	Fetal_HetRpts
10	3e−01	25 / 769	Overlap_fetal_midbrain_ZNF
11	3e−01	12 / 349	Fetal_ZNF
12	4e−01	17 / 564	Mid_Frontal_Lobe_EnhP
13	4e−01	71 / 2462	Mid_Frontal_Lobe_HetRpts
14	4e−01	85 / 2972	Mid_Frontal_Lobe_ReprPC
15	6e−01	8 / 304	Fetal_Het
16	7e−01	25 / 953	Fetal_Enh
17	7e−01	4 / 166	Mid_Frontal_Lobe_Tx
18	7e−01	249 / 9020	Overlap_fetal_midbrain_ReprPCWk
19	7e−01	20 / 786	Fetal_EnhG
20	8e−01	3 / 158	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	3 / 12	LIU_PROSTATE_CANCER_UP
2	0.005	12 / 180	SPANG_LPS−index2
3	0.009	3 / 16	GENTLES_modul16
4	0.050	2 / 13	GENTLES_modul12
5	0.073	2 / 16	GENTLES_modul7
6	0.102	3 / 40	PanCan_HK_geneset_nanostring
7	0.201	3 / 55	PanCan_JAK−ST_geneset_nanostring
8	0.245	3 / 61	PanCan_Wnt_geneset_nanostring
9	0.254	5 / 121	PanCan_MAPK_geneset_nanostring
10	0.297	0 / 14	LIU_PROSTATE_CANCER_DN
11	0.310	1 / 13	BEN−PORATH_UP
12	0.310	2 / 40	ZHANG_MM up
13	0.314	3 / 70	SHAUGHNESSY_MM high risk
14	0.348	1 / 15	GENTLES_modul1
15	0.348	1 / 15	GENTLES_modul4
16	0.352	2 / 44	PanCan_TGF−B_geneset_nanostring
17	0.366	1 / 16	GENTLES_modul2
18	0.366	1 / 16	GENTLES_modul14
19	0.392	4 / 113	PanCan_Driver_Gene_geneset_nanostring
20	0.402	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−13	302 / 8205	cytoplasm
2	2e−10	352 / 10605	intracellular
3	9e−09	79 / 1468	mitochondrion
4	1e−08	332 / 9988	organelle
5	9e−08	66 / 1201	endoplasmic reticulum
6	4e−05	362 / 11774	cell
7	8e−05	36 / 649	endoplasmic reticulum membrane
8	8e−05	54 / 1132	Golgi apparatus
9	5e−04	7 / 51	endoplasmic reticulum−Golgi intermediate compartment
10	7e−04	86 / 2193	extracellular exosome
11	7e−04	390 / 13191	cellular_component
12	1e−03	36 / 745	cytoplasmic membrane−bounded vesicle
13	2e−03	6 / 47	lipid particle
14	2e−03	93 / 2507	cytosol
15	3e−03	5 / 35	cell periphery
16	5e−03	29 / 616	endosome
17	5e−03	21 / 401	mitochondrial inner membrane
18	5e−03	7 / 76	extrinsic component of membrane
19	8e−03	3 / 15	integral component of mitochondrial inner membrane
20	8e−03	6 / 63	mitochondrial intermembrane space

Chr

Rank	p−value	#in/all	Geneset
1	0.001	39 / 840	Chr 17
2	0.007	27 / 576	Chr 9
3	0.094	10 / 221	Chr 18
4	0.096	16 / 398	Chr 20
5	0.103	24 / 649	Chr 16
6	0.158	20 / 558	Chr 4
7	0.251	6 / 151	Chr 21
8	0.321	25 / 801	Chr 11
9	0.342	11 / 335	Chr 22
10	0.447	14 / 469	Chr 8
11	0.456	8 / 262	Chr 13
12	0.473	20 / 689	Chr 7
13	0.491	24 / 838	Chr 3
14	0.547	13 / 465	Chr 15
15	0.590	15 / 552	Chr 10
16	0.756	26 / 1037	Chr 19
17	0.814	16 / 687	Chr 6
18	0.829	18 / 775	Chr 12
19	0.859	23 / 993	Chr 2
20	0.910	11 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−21	353 / 9482	TssA_Colon
2	9e−12	318 / 9027	Tx_Colon
3	4e−11	268 / 7203	TssF_Colon
4	7e−08	218 / 5880	TssD2_Colon
5	2e−06	117 / 2798	TxEnhG1_Colon
6	5e−06	313 / 9653	Enh_Colon
7	2e−05	282 / 8580	TxWk_Colon
8	1e−03	175 / 5155	EnhWk1_Colon
9	1e−03	32 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	2e−03	35 / 739	TxEnhG2_Colon
11	7e−03	33 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
12	8e−03	261 / 8415	Quies3_Colon
13	1e−02	38 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	3e−02	91 / 2698	EnhA_Colon
15	6e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
16	6e−02	2 / 15	TCGA_Mutated−in−CRC_hypermutated
17	8e−02	2 / 17	Vilar_hypermutated−in−CRC
18	1e−01	8 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
19	1e−01	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
20	2e−01	1 / 6	Marisa_CRC−C4

Disease

Rank	p−value	#in/all	Geneset
1	0.2	11 / 294	GUDJ_psoriasis down
2	0.4	1 / 20	BCHETNIA_EBM−DM up
3	0.9	9 / 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	2e−04	22 / 332	Up
2	8e−03	6 / 63	Stuehler_Proteins_up_in_STS
3	4e−02	6 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	4e−02	9 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	4e−02	2 / 11	Christensen_hypermethylated_in_ependymoma
6	4e−02	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
7	9e−02	15 / 365	Down_b
8	1e−01	2 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
9	2e−01	12 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	2e−01	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
11	2e−01	5 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
12	3e−01	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
13	3e−01	4 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	3e−01	2 / 38	OL vs. OPC
15	3e−01	3 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
16	3e−01	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
17	3e−01	4 / 103	GIEZELT_GBM_WT_up_VS_mut
18	3e−01	1 / 14	VERHAAK_PN subtype
19	3e−01	26 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
20	3e−01	1 / 15	VERHAAK_CL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−14	69 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	1e−10	58 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	3e−07	69 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	9e−07	32 / 440	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
5	1e−06	19 / 188	DAZARD_RESPONSE_TO_UV_NHEK_UP
6	1e−05	30 / 447	ENK_UV_RESPONSE_KERATINOCYTE_UP
7	4e−05	30 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
8	4e−05	25 / 363	RUTELLA_RESPONSE_TO_HGF_UP
9	4e−05	8 / 47	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
10	4e−05	19 / 238	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
11	6e−05	10 / 78	SCHUHMACHER_MYC_TARGETS_UP
12	1e−04	23 / 340	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
13	1e−04	22 / 321	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
14	1e−04	26 / 416	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
15	2e−04	34 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
16	2e−04	24 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
17	3e−04	19 / 274	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
18	4e−04	20 / 303	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
19	4e−04	64 / 1495	BLALOCK_ALZHEIMERS_DISEASE_UP
20	4e−04	41 / 842	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP

HM

Rank	p−value	#in/all	Geneset
1	0.003	11 / 146	HALLMARK_UV_RESPONSE_UP
2	0.014	7 / 91	HALLMARK_PROTEIN_SECRETION
3	0.016	5 / 53	HALLMARK_TGF_BETA_SIGNALING
4	0.018	7 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	0.026	5 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.028	10 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.034	7 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.040	8 / 137	HALLMARK_UV_RESPONSE_DN
9	0.040	10 / 188	HALLMARK_ADIPOGENESIS
10	0.040	10 / 188	HALLMARK_MYC_TARGETS_V1
11	0.049	6 / 94	HALLMARK_ANDROGEN_RESPONSE
12	0.053	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	0.054	8 / 146	HALLMARK_DNA_REPAIR
14	0.102	9 / 196	HALLMARK_MTORC1_SIGNALING
15	0.118	8 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
16	0.118	8 / 174	HALLMARK_HEME_METABOLISM
17	0.144	8 / 183	HALLMARK_GLYCOLYSIS
18	0.145	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
19	0.202	7 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
20	0.215	3 / 57	HALLMARK_MYC_TARGETS_V2

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.35	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	1e−05	256 / 7592	HOPP_Active_promoter
2	2e−05	186 / 5184	HOPP_Txn_transition
3	1e−03	226 / 6929	HOPP_Txn_elongation
4	3e−03	22 / 410	SPANG_CD40 6hrs DN
5	4e−03	47 / 1128	SPANG_BCR DN
6	9e−03	227 / 7209	HOPP_Weak_promoter
7	9e−03	3 / 16	DAVE_BL Inter
8	1e−02	207 / 6564	HOPP_Strong_enhancer
9	3e−02	7 / 109	ROSOLOWSKI_green total
10	4e−02	5 / 66	TARTE_Plasma cell signature
11	5e−02	2 / 13	YAMANE_AICDA_targets_recruited
12	7e−02	3 / 34	Subero_B−ALL_hyper_meth
13	9e−02	5 / 86	ROSOLOWSKI_red total
14	1e−01	2 / 19	DAVE_c−myc BL UP
15	1e−01	2 / 19	Subero_MM_hyper_meth
16	2e−01	40 / 1218	SPANG_BCR UP
17	2e−01	4 / 80	Aukema_BCL2 DN_BCL6 UP
18	2e−01	4 / 82	ROSOLOWSKI_green UP
19	2e−01	11 / 294	TARTE_Plasmablast signature
20	2e−01	1 / 9	Subero_B−ALL_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	0.001	6 / 42	protein kinase C binding
2	0.002	3 / 10	receptor signaling protein tyrosine kinase activity
3	0.003	6 / 51	ubiquitin binding
4	0.003	3 / 11	protein kinase B binding
5	0.003	3 / 11	proton−transporting ATP synthase activity, rotational mechanism
6	0.004	14 / 223	phosphatase activity
7	0.007	28 / 609	cytoskeletal protein binding
8	0.011	7 / 86	ubiquitin−like protein binding
9	0.011	41 / 1007	poly(A) RNA binding
10	0.011	3 / 17	glycosaminoglycan binding
11	0.013	3 / 18	2 iron, 2 sulfur cluster binding
12	0.013	4 / 33	peptide binding
13	0.014	52 / 1365	RNA binding
14	0.017	19 / 397	transcription factor binding
15	0.018	4 / 36	phosphatidylinositol−4,5−bisphosphate binding
16	0.022	24 / 550	protein homodimerization activity
17	0.026	3 / 23	proton−transporting ATPase activity, rotational mechanism
18	0.027	7 / 104	iron ion binding
19	0.031	2 / 10	actin−dependent ATPase activity
20	0.031	2 / 10	proteasome binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	23 / 358	hsa−let−7d
2	6e−04	8 / 68	hsa−miR−342−3p
3	2e−03	9 / 97	hsa−miR−624
4	2e−03	9 / 101	hsa−miR−325
5	4e−03	17 / 291	hsa−miR−34c−5p
6	4e−03	7 / 73	hsa−miR−657
7	6e−03	5 / 41	hsa−miR−1308
8	6e−03	10 / 141	hsa−miR−138
9	6e−03	20 / 386	hsa−let−7c
10	8e−03	16 / 288	hsa−miR−34a
11	8e−03	12 / 191	hsa−miR−520d−5p
12	9e−03	16 / 294	hsa−miR−561
13	9e−03	15 / 269	hsa−miR−449a
14	9e−03	4 / 30	hsa−miR−371−3p
15	9e−03	8 / 105	hsa−miR−1271
16	1e−02	21 / 428	hsa−let−7b
17	1e−02	14 / 250	hsa−miR−524−5p
18	1e−02	11 / 179	hsa−miR−381
19	1e−02	5 / 50	hsa−miR−487a
20	1e−02	3 / 18	hsa−miR−380*

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 12	GUSTAFSON_PI3K_UP
2	0.3	1 / 13	GUSTAFSON_PI3K_DN
3	0.3	1 / 13	BENTINK_myc.1
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	4e−05	170 / 4689	ICGC_Taf1_targets
2	2e−04	173 / 4909	ICGC_Stat5_targets
3	2e−04	147 / 4054	ICGC_Egr1_targets
4	3e−04	154 / 4314	ICGC_Ebfsc137065_targets
5	4e−04	199 / 5890	ICGC_Elf1_targets
6	9e−04	183 / 5408	ICGC_Pou2_targets
7	1e−03	132 / 3700	ICGC_Nfatc1_targets
8	1e−03	203 / 6114	ICGC_Runx3_targets
9	1e−03	177 / 5219	ICGC_Tcf3_targets
10	1e−03	51 / 1171	KIM_MYC targets
11	1e−03	184 / 5495	ICGC_Yy1_targets
12	2e−03	165 / 4879	ICGC_Pmlsc71910_targets
13	4e−03	89 / 2416	ICGC_Bcl3_targets
14	4e−03	80 / 2136	ICGC_GabpPcr2_targets
15	4e−03	160 / 4774	ICGC_Foxm1_targets
16	4e−03	157 / 4682	ICGC_Pol24_targets
17	4e−03	155 / 4617	ICGC_Tcf12_targets
18	5e−03	137 / 4032	ICGC_Creb1_targets
19	6e−03	56 / 1418	ICGC_Ets1_targets
20	6e−03	171 / 5200	ICGC_Mta3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.07	2 / 16	VAQUERIZAS_Pancreas
2	0.08	4 / 59	VAQUERIZAS_Whole blood
3	0.10	2 / 19	VAQUERIZAS_Tonsil
4	0.10	3 / 40	VAQUERIZAS_Thyroid
5	0.24	2 / 33	VAQUERIZAS_Prostate
6	0.36	2 / 45	VAQUERIZAS_Uterus
7	0.37	1 / 16	VAQUERIZAS_Salivary gland
8	0.37	5 / 143	VAQUERIZAS_General
9	0.38	1 / 17	VAQUERIZAS_Heart
10	0.49	2 / 58	VAQUERIZAS_Lung
11	0.54	1 / 27	VAQUERIZAS_Lymph node
12	0.56	1 / 29	VAQUERIZAS_Smooth muscle
13	0.56	1 / 29	VAQUERIZAS_Fetal lung
14	0.64	1 / 36	VAQUERIZAS_Fetal brain
15	0.65	1 / 37	VAQUERIZAS_Thymus
16	0.66	1 / 38	VAQUERIZAS_Whole brain
17	1.00	0 / 41	VAQUERIZAS_Placenta
18	1.00	0 / 26	VAQUERIZAS_Liver
19	1.00	0 / 9	VAQUERIZAS_Kidney
20	1.00	0 / 23	VAQUERIZAS_Spinal cord

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	8 / 194	PALMER_B−Cell signature up
2	0.2	9 / 225	PALMER_Granulocytes signature up
3	0.3	1 / 11	WIRTH_Cortex cerebri
4	0.3	1 / 12	WIRTH_Cerebellum
5	0.3	1 / 13	WIRTH_B−cells
6	0.3	1 / 14	WIRTH_Telencephalon
7	0.4	1 / 16	PALMER_Lymphocytes signature up
8	0.4	4 / 114	PALMER_T−Cell signature up
9	0.5	10 / 350	WIRTH_Immune system
10	0.7	1 / 41	WIRTH_Homeostasis
11	0.7	1 / 46	WIRTH_Liver
12	1.0	1 / 107	WIRTH_Testis
13	1.0	4 / 350	WIRTH_Nervous System
14	1.0	0 / 32	WIRTH_Pancreas
15	1.0	0 / 11	WIRTH_Sec. lymphoid organs
16	1.0	0 / 11	WIRTH_Prim. lymphoid organs
17	1.0	0 / 8	WIRTH_Tonsil
18	1.0	0 / 12	WIRTH_Thymus
19	1.0	0 / 12	WIRTH_Lymphocytes
20	1.0	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.09	39 / 1115	LU_BPDE 1h DN
2	0.93	91 / 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	

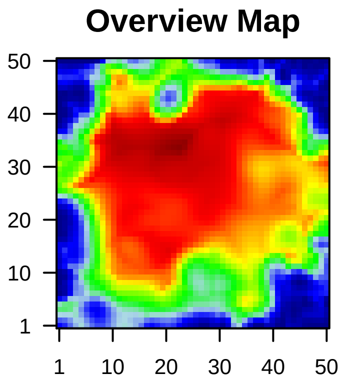
Underexpression Spots

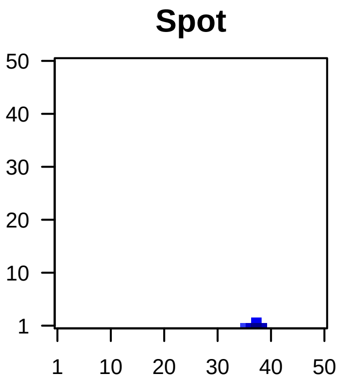
Spot Summary: e

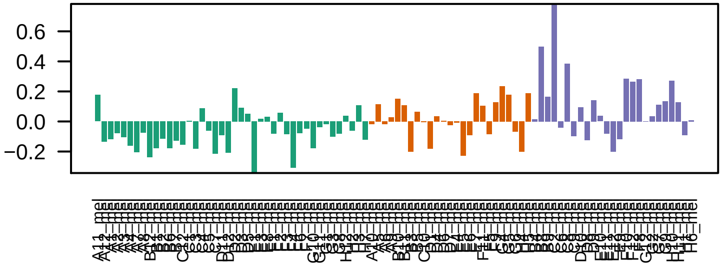
metagenes = 7
genes = 84

<r> metagenes = 0.95
<r> genes = 0.11
beta: r2= 1.33 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 1 (2.4 %)
MSC2 : 1 (4 %)
MSC3 : 7 (28 %)





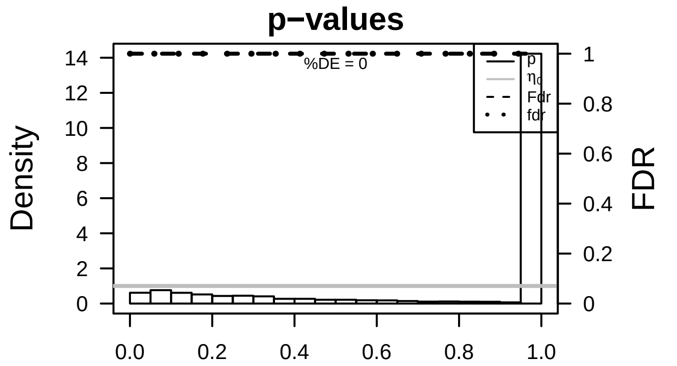


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	MYO5B	2.19	−0.18	0.41	MYO5B	myosin VB [Source:HGNC Symbol;Acc:HGNC:7603]
2	KLHDC8B	2.08	−0.34	0.35	KLHDC8B	kelch domain containing 8B [Source:HGNC Symbol;Acc:HGN
3	CDK8	1.64	−0.46	0.32	CDK8	cyclin−dependent kinase 8 [Source:HGNC Symbol;Acc:HGN
4	CHKB	1.6	−0.43	0.31	CHKB	choline kinase beta [Source:HGNC Symbol;Acc:HGNC:1938]
5	CTSH	1.59	−0.45	0.26	CTSH	cathepsin H [Source:HGNC Symbol;Acc:HGNC:2535]
6	ALDH1A2	1.58	−0.25	0.32	ALDH1A2	aldehyde dehydrogenase 1 family, member A2 [Source:HGN
7	ANKRD6	1.57	−0.2	0.36	ANKRD6	ankyrin repeat domain 6 [Source:HGNC Symbol;Acc:HGNC:
8	CETN3	1.57	−0.48	0.31	CETN3	centrin, EF−hand protein, 3 [Source:HGNC Symbol;Acc:HGN
9	ABCB1	1.55	−0.2	0.46	ABCB1	ATP−binding cassette, sub−family B (MDR/TAP), member 1 [
10	YIPF2	1.54	−0.56	0.33	YIPF2	Yip1 domain family, member 2 [Source:HGNC Symbol;Acc:H
11	CCBL1	1.52	−0.33	0.43	CCBL1	cysteine conjugate−beta lyase, cytoplasmic [Source:HGNC S
12	ANO10	1.48	−0.73	0.34	ANO10	anoctamin 10 [Source:HGNC Symbol;Acc:HGNC:25519]
13	NAA35	1.48	−0.36	0.34	NAA35	N(alpha)−acetyltransferase 35, NatC auxiliary subunit [Sourc
14	AVIL	1.47	−0.18	0.41	AVIL	advillin [Source:HGNC Symbol;Acc:HGNC:14188]
15	ZSCAN29	1.46	−0.19	0.41	ZSCAN29	zinc finger and SCAN domain containing 29 [Source:HGNC S
16	ACSS2	1.44	−0.76	0.28	ACSS2	acyl−CoA synthetase short−chain family member 2 [Source:H
17	AHR	1.44	−0.34	0.37	AHR	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:HGNC
18	VPS13A	1.42	−0.97	0.25	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae) [Source
19	ALDH3B1	1.41	−0.56	0.44	ALDH3B1	aldehyde dehydrogenase 3 family, member B1 [Source:HGN
20	MINPP1	1.41	−0.57	0.33	MINPP1	multiple inositol−polyphosphate phosphatase 1 [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−06	61 / 6929	Lympl	HOPP_Txn_elongation
2	6e−06	68 / 8580	Colon	TxWk_Colon
3	6e−06	63 / 7592	Lympl	HOPP_Active_promoter
4	2e−05	69 / 9027	Colon	Tx_Colon
5	3e−05	9 / 281	Colon	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	4e−05	52 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
7	4e−05	59 / 7209	Lympl	HOPP_Weak_promoter
8	6e−05	68 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
9	6e−05	65 / 8415	Colon	Quies3_Colon
10	6e−05	15 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
11	7e−05	4 / 40	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
12	2e−04	74 / 10605	CC	intracellular
13	3e−04	68 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
14	4e−04	6 / 173	Colon	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	5e−04	3 / 28	GSEA	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOL
16	5e−04	5 / 118	GSEA	DAZARD_RESPONSE_TO_UV_SCC_DN
17	6e−04	3 / 29	GSEA	ZWANG_EGF_PERSISTENTLY_UP
18	6e−04	5 / 121	GSEA	ONDER_CDH1_TARGETS_1_UP
19	7e−04	3 / 31	miRN	hsa−miR−892b
20	7e−04	7 / 263	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
21	7e−04	7 / 263	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
22	7e−04	44 / 5184	Lympl	HOPP_Txn_transition
23	8e−04	46 / 5538	Lympl	HOPP_Weak_txn
24	9e−04	6 / 199	GSEA	RAMALHO_STEMNESS_UP
25	1e−03	9 / 457	GSEA	SENESE_HDAC3_TARGETS_UP
26	1e−03	67 / 9482	Colon	TssA_Colon
27	1e−03	3 / 38	GSEA	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1
28	1e−03	7 / 294	GSEA	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
29	1e−03	9 / 473	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
30	2e−03	5 / 148	GSEA	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN
31	2e−03	8 / 386	BP	regulation of transcription from RNA polymerase II promoter
32	2e−03	2 / 11	BP	negative regulation of intracellular estrogen receptor signaling pathway
33	2e−03	2 / 11	Glio	Mukasa_UP_in_Astroglioma
34	2e−03	3 / 42	MF	RNA polymerase II core promoter sequence−specific DNA binding
35	2e−03	3 / 43	GSEA	KEGG_N_GLYCAN_BIOSYNTHESIS
36	2e−03	77 / 11774	CC	cell
37	2e−03	4 / 95	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_UP
38	2e−03	9 / 503	GSEA	MARTINEZ_RB1_AND_TP53_TARGETS_UP
39	2e−03	9 / 508	GSEA	MARTINEZ_TP53_TARGETS_UP
40	2e−03	9 / 510	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP



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	0.002	8 / 386	regulation of transcription from RNA polymerase II promoter
2	0.002	2 / 11	negative regulation of intracellular estrogen receptor signaling pathway
3	0.003	2 / 15	lipid biosynthetic process
4	0.004	26 / 2755	transport
5	0.005	2 / 18	cellular amino acid biosynthetic process
6	0.005	2 / 18	phospholipid translocation
7	0.005	3 / 63	dolichol−linked oligosaccharide biosynthetic process
8	0.012	11 / 897	vesicle−mediated transport
9	0.012	2 / 30	phospholipid transport
10	0.012	2 / 30	positive regulation of apoptotic signaling pathway
11	0.018	7 / 478	protein transport
12	0.021	13 / 1237	metabolic process
13	0.024	6 / 394	cell proliferation
14	0.027	3 / 115	protein N−linked glycosylation via asparagine
15	0.028	2 / 46	hippocampus development
16	0.029	2 / 47	protein targeting to mitochondrion
17	0.031	3 / 120	transforming growth factor beta receptor signaling pathway
18	0.034	2 / 51	cellular response to retinoic acid
19	0.034	2 / 51	circadian regulation of gene expression
20	0.036	2 / 53	blood vessel development

Brain

Rank	p−value	#in/all	Geneset
1	4e−05	52 / 5940	Overlap_fetal_midbrain_HetRpts
2	6e−05	68 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	3e−04	68 / 9330	Overlap_fetal_midbrain_ReprPC
4	1e−02	13 / 1122	Fetal_K9K27me3
5	2e−02	63 / 9528	Overlap_fetal_midbrain_Quies
6	6e−02	10 / 1013	Fetal_TssP
7	7e−02	58 / 9013	Overlap_fetal_midbrain_K9K27me3
8	1e−01	8 / 831	Fetal_HetRpts
9	1e−01	9 / 989	Mid_Frontal_Lobe_Quies
10	1e−01	7 / 769	Overlap_fetal_midbrain_ZNF
11	2e−01	7 / 786	Fetal_EnhG
12	2e−01	6 / 656	Overlap_fetal_midbrain_EnhP
13	2e−01	8 / 953	Fetal_Enh
14	2e−01	8 / 1050	Fetal_EnhP
15	4e−01	8 / 1207	Overlap_fetal_midbrain_TssF
16	4e−01	4 / 564	Mid_Frontal_Lobe_EnhP
17	4e−01	12 / 1949	Fetal_TssF
18	4e−01	5 / 765	Mid_Frontal_Lobe_Het
19	5e−01	2 / 304	Fetal_Het
20	5e−01	9 / 1548	Mid_Frontal_Lobe_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	5 / 180	SPANG_LPS−index2
2	0.021	2 / 40	ZHANG_MM up
3	0.082	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	0.082	1 / 15	WANG_ER_UP
5	0.089	4 / 298	SPANG_BCL6−index2
6	0.117	1 / 22	PanCan_HH_geneset_nanostring
7	0.293	1 / 61	PanCan_Wnt_geneset_nanostring
8	0.369	0 / 12	LIU_PROSTATE_CANCER_UP
9	0.397	3 / 401	Lembcke_Colonic Inflammation
10	0.495	1 / 120	PanCan_CC+Apop_geneset_nanostring
11	0.498	1 / 121	PanCan_MAPK_geneset_nanostring
12	0.589	1 / 156	PanCan_PI3K_geneset_nanostring
13	0.769	2 / 489	Lembcke_Normal vs Adenoma
14	0.893	0 / 14	LIU_PROSTATE_CANCER_DN
15	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
16	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.000	0 / 12	LIU_BREAST_CANCER
19	1.000	0 / 14	LIU_COMMON_CANCER_GENES
20	1.000	0 / 14	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−04	74 / 10605	intracellular
2	2e−03	77 / 11774	cell
3	3e−03	59 / 8205	cytoplasm
4	5e−03	24 / 2507	cytosol
5	2e−02	6 / 377	centrosome
6	3e−02	12 / 1132	Golgi apparatus
7	3e−02	65 / 9988	organelle
8	3e−02	2 / 50	cell body
9	5e−02	2 / 60	nuclear pore
10	5e−02	40 / 5696	nucleus
11	6e−02	1 / 10	beta−catenin destruction complex
12	7e−02	2 / 76	cell projection
13	7e−02	6 / 512	microtubule organizing center
14	7e−02	2 / 77	ciliary basal body
15	7e−02	3 / 169	transcription factor complex
16	7e−02	1 / 13	COPI vesicle coat
17	8e−02	11 / 1201	endoplasmic reticulum
18	8e−02	1 / 14	exocyst
19	8e−02	2 / 81	centriole
20	8e−02	20 / 2576	membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.04	7 / 551	Chr X
2	0.11	9 / 993	Chr 2
3	0.19	4 / 398	Chr 20
4	0.19	6 / 689	Chr 7
5	0.23	5 / 576	Chr 9
6	0.30	6 / 801	Chr 11
7	0.34	6 / 838	Chr 3
8	0.44	2 / 262	Chr 13
9	0.49	3 / 465	Chr 15
10	0.55	4 / 687	Chr 6
11	0.56	4 / 696	Chr 5
12	0.61	3 / 552	Chr 10
13	0.62	8 / 1500	Chr 1
14	0.65	4 / 775	Chr 12
15	0.72	1 / 221	Chr 18
16	0.74	2 / 462	Chr 14
17	0.75	2 / 469	Chr 8
18	0.83	2 / 558	Chr 4
19	0.85	1 / 335	Chr 22
20	0.86	3 / 840	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−06	68 / 8580	TxWk_Colon
2	2e−05	69 / 9027	Tx_Colon
3	3e−05	9 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	6e−05	65 / 8415	Quies3_Colon
5	4e−04	6 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	7e−04	7 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
7	1e−03	67 / 9482	TssA_Colon
8	1e−02	32 / 3897	Quies1_Colon
9	1e−02	68 / 10290	TssWk_Colon
10	4e−02	11 / 1079	ZNF_Colon
11	4e−02	1 / 8	Juehting−MSI−enriched−in−7
12	5e−02	26 / 3383	EnhWk2_Colon
13	6e−02	2 / 71	Marisa_CRC−cluster−g
14	2e−01	20 / 2798	TxEnhG1_Colon
15	2e−01	4 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
16	3e−01	44 / 7203	TssF_Colon
17	3e−01	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
18	3e−01	24 / 3812	TssD1_Colon
19	3e−01	57 / 9653	Enh_Colon
20	4e−01	31 / 5155	EnhWk1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.4	3 / 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	0.002	2 / 11	Mukasa_UP_in_Astroglioma
2	0.003	2 / 15	VERHAAK_MES subtype
3	0.048	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
4	0.052	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
5	0.060	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
6	0.061	1 / 11	Martinez_Glio_hypermeth
7	0.061	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
8	0.061	2 / 71	Weller_LGG_A_vs_O_UP
9	0.087	1 / 16	VERHAAK_NL subtype
10	0.097	1 / 18	Barbus_GBM_STS_vs._LTS
11	0.158	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	0.190	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
13	0.227	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
14	0.234	1 / 47	Vishal_subnetwork signature of survival in GBM
15	0.247	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
16	0.277	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
17	0.321	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
18	0.325	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
19	0.347	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
20	0.347	1 / 75	Weller_LGG_A_vs_O_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−05	15 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	7e−05	4 / 40	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
3	5e−04	3 / 28	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLIC
4	5e−04	5 / 118	DAZARD_RESPONSE_TO_UV_SCC_DN
5	6e−04	3 / 29	ZWANG_EGF_PERSISTENTLY_UP
6	6e−04	5 / 121	ONDER_CDH1_TARGETS_1_UP
7	7e−04	7 / 263	IVANOVA_HEMATOPOIESIS_MATURE_CELL
8	9e−04	6 / 199	RAMALHO_STEMNESS_UP
9	1e−03	9 / 457	SENESE_HDAC3_TARGETS_UP
10	1e−03	3 / 38	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1
11	1e−03	7 / 294	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
12	1e−03	9 / 473	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
13	2e−03	5 / 148	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN
14	2e−03	3 / 43	KEGG_N_GLYCAN_BIOSYNTHESIS
15	2e−03	4 / 95	KOBAYASHI_EGFR_SIGNALING_24HR_UP
16	2e−03	9 / 503	MARTINEZ_RB1_AND_TP53_TARGETS_UP
17	2e−03	9 / 508	MARTINEZ_TP53_TARGETS_UP
18	2e−03	9 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
19	3e−03	7 / 329	WANG_LMO4_TARGETS_DN
20	3e−03	2 / 15	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRAI

HM

Rank	p−value	#in/all	Geneset
1	0.01	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
2	0.05	3 / 148	HALLMARK_KRAS_SIGNALING_UP
3	0.08	3 / 181	HALLMARK_P53_PATHWAY
4	0.10	2 / 93	HALLMARK_PEROXISOME
5	0.19	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
6	0.19	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
7	0.23	2 / 162	HALLMARK_COMPLEMENT
8	0.25	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.26	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	0.34	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	0.40	1 / 91	HALLMARK_PROTEIN_SECRETION
12	0.40	1 / 91	HALLMARK_BILE_ACID_METABOLISM
13	0.42	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.46	1 / 107	HALLMARK_COAGULATION
15	0.46	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
16	0.54	1 / 137	HALLMARK_UV_RESPONSE_DN
17	0.57	1 / 146	HALLMARK_DNA_REPAIR
18	0.57	1 / 146	HALLMARK_UV_RESPONSE_UP
19	0.61	1 / 165	HALLMARK_MYOGENESIS
20	0.61	1 / 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	1e−06	61 / 6929	HOPP_Txn_elongation
2	6e−06	63 / 7592	HOPP_Active_promoter
3	4e−05	59 / 7209	HOPP_Weak_promoter
4	7e−04	44 / 5184	HOPP_Txn_transition
5	8e−04	46 / 5538	HOPP_Weak_txn
6	2e−02	42 / 5693	HOPP_Weak_enhancer
7	2e−02	1 / 4	MASCOUE_mBL DOWN
8	4e−02	1 / 8	YAMANE_AICDA_targets_nonrecruited
9	5e−02	45 / 6564	HOPP_Strong_enhancer
10	7e−02	1 / 12	BENTINK_mBL DOWN
11	7e−02	18 / 2211	HOPP_Repetitive
12	1e−01	1 / 23	DAVE_Immune response 1
13	2e−01	1 / 30	TARTE_B−cell signature
14	2e−01	3 / 247	ZHANG_DLBCL mutated
15	2e−01	2 / 129	DAVE_BL−vs−DLBCL
16	2e−01	9 / 1128	SPANG_BCR DN
17	2e−01	4 / 410	SPANG_CD40 6hrs DN
18	3e−01	2 / 212	LENZ_Stromal signature 1
19	4e−01	2 / 268	SPANG_IL21 UP
20	5e−01	1 / 107	SPANG_LPS 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 42	RNA polymerase II core promoter sequence−specific DNA binding
2	0.003	2 / 15	phospholipid−translocating ATPase activity
3	0.004	2 / 16	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD o
4	0.004	3 / 58	cysteine−type peptidase activity
5	0.009	2 / 26	NF−kappaB binding
6	0.018	2 / 36	G−protein beta/gamma−subunit complex binding
7	0.034	80 / 13179	molecular_function
8	0.041	59 / 8984	protein binding
9	0.055	1 / 10	armadillo repeat domain binding
10	0.055	1 / 10	transaminase activity
11	0.061	1 / 11	co−SMAD binding
12	0.061	1 / 11	poly(A)−specific ribonuclease activity
13	0.061	2 / 71	cysteine−type endopeptidase activity
14	0.066	1 / 12	AU−rich element binding
15	0.066	1 / 12	GTPase inhibitor activity
16	0.066	1 / 12	lysophospholipase activity
17	0.066	1 / 12	MAP kinase tyrosine/serine/threonine phosphatase activity
18	0.066	1 / 12	poly(A) binding
19	0.066	1 / 12	protein kinase A catalytic subunit binding
20	0.066	1 / 12	RNA polymerase II transcription factor binding transcription factor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 31	hsa−miR−892b
2	3e−03	6 / 246	hsa−miR−27b
3	3e−03	6 / 251	hsa−miR−548l
4	3e−03	5 / 177	hsa−miR−548e
5	4e−03	3 / 54	hsa−miR−518d−5p
6	4e−03	3 / 54	hsa−miR−520c−5p
7	4e−03	3 / 57	hsa−miR−889
8	5e−03	3 / 61	hsa−miR−219−5p
9	6e−03	4 / 127	hsa−miR−323−3p
10	6e−03	5 / 208	hsa−miR−432
11	7e−03	7 / 395	hsa−miR−301b
12	7e−03	5 / 214	hsa−miR−548m
13	8e−03	7 / 405	hsa−miR−519c−3p
14	9e−03	4 / 144	hsa−miR−548f
15	1e−02	4 / 149	hsa−miR−518a−5p
16	1e−02	5 / 233	hsa−miR−27a
17	1e−02	4 / 154	hsa−miR−527
18	1e−02	3 / 83	hsa−miR−576−5p
19	1e−02	2 / 29	hsa−miR−193a−5p
20	1e−02	3 / 88	hsa−miR−10a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	1 / 12	GUSTAFSON_PI3K_UP
2	0.08	1 / 14	BENTINK_src.2
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	0.03	16 / 1701	HEBENSTREIT_high expression TF
2	0.08	1 / 15	NOWICK_TF
3	0.12	10 / 1171	KIM_MYC targets
4	0.26	26 / 4054	ICGC_Egr1_targets
5	0.28	10 / 1418	ICGC_Ets1_targets
6	0.37	15 / 2391	ICGC_Pbx3_targets
7	0.38	4 / 553	ICGC_RxraPcr1_targets
8	0.43	8 / 1273	ICGC_P300_targets
9	0.44	13 / 2137	ICGC_SrfV0416101_targets
10	0.52	23 / 4032	ICGC_Creb1_targets
11	0.55	16 / 2836	ICGC_BatfPcr1_targets
12	0.56	12 / 2136	ICGC_GabpPcr2_targets
13	0.59	29 / 5219	ICGC_Tcf3_targets
14	0.60	30 / 5408	ICGC_Pou2_targets
15	0.60	11 / 2013	ICGC_Bcl11_targets
16	0.63	10 / 1872	ICGC_Mef2_targets
17	0.64	25 / 4617	ICGC_Tcf12_targets
18	0.68	7 / 1383	ICGC_Six5_targets
19	0.69	14 / 2714	ICGC_Irf4_targets
20	0.72	23 / 4414	ICGC_Bclaf101388_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 29	VAQUERIZAS_Smooth muscle
2	0.2	1 / 38	VAQUERIZAS_Whole brain
3	0.2	1 / 41	VAQUERIZAS_Placenta
4	0.6	1 / 143	VAQUERIZAS_General
5	1.0	0 / 36	VAQUERIZAS_Fetal brain
6	1.0	0 / 26	VAQUERIZAS_Liver
7	1.0	0 / 33	VAQUERIZAS_Prostate
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	0.1	3 / 225	PALMER_Granulocytes signature up
2	0.3	2 / 194	PALMER_B−Cell signature up
3	0.3	3 / 350	WIRTH_Immune system
4	0.3	1 / 74	WIRTH_Mucosa
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 / 350	WIRTH_Nervous System
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	0.01	13 / 1115	LU_BPDE 1h DN
2	0.02	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	

Underexpression Spots

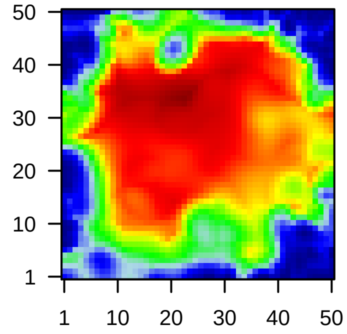
Spot Summary: f

metagenes = 2
genes = 79

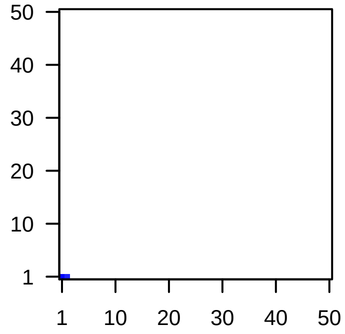
<r> metagenes = 1
<r> genes = 0.13
beta: r2= 1.37 / log p= −Inf

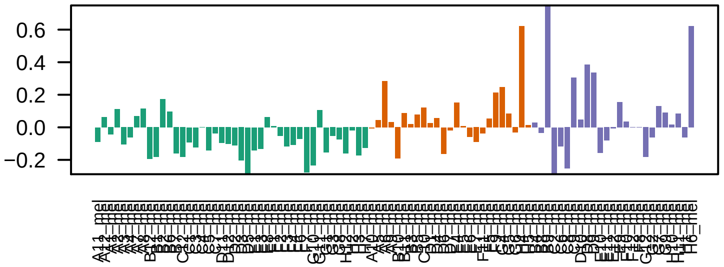
samples with spot = 9 (9.8 %)
MSC2 : 4 (16 %)
MSC3 : 5 (20 %)

Overview Map



Spot





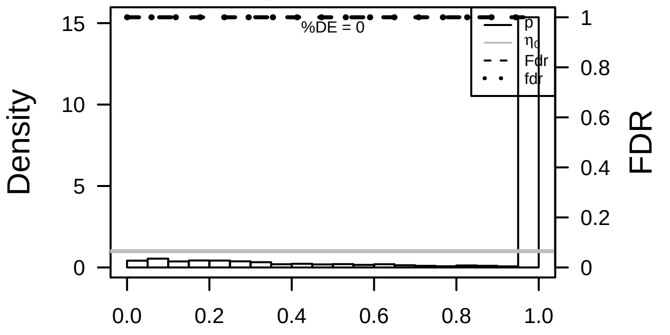
Spot Genelist

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	APBB1	1.74	−0.25	0.51	APBB1	amyloid beta (A4) precursor protein−binding, family B, membe
3	ZNF513	1.6	−0.11	0.36	ZNF513	zinc finger protein 513 [Source:HGNC Symbol;Acc:HGNC:26
4	CRELD1	1.58	−0.42	0.36	CRELD1	cysteine−rich with EGF−like domains 1 [Source:HGNC Symb
5	CCDC126	1.52	−0.57	0.3	CCDC126	coiled−coil domain containing 126 [Source:HGNC Symbol;Ac
6	ARHGAP18	1.51	−0.22	0.45	ARHGAP18	Rho GTPase activating protein 18 [Source:HGNC Symbol;Ac
7	ANKRD29	1.51	−0.23	0.43	ANKRD29	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:HGNC
8	PTPN13	1.5	−0.41	0.27	PTPN13	protein tyrosine phosphatase, non−receptor type 13 (APO−1/
9	NLN	1.5	−0.62	0.28	NLN	neurolysin (metallopeptidase M3 family) [Source:HGNC Sym
10	SMG9	1.5	−0.41	0.21	SMG9	SMG9 nonsense mediated mRNA decay factor [Source:HGN
11	GABPB2	1.5	−0.54	0.37	GABPB2	GA binding protein transcription factor, beta subunit 2 [Source
12	AKAP1	1.47	−0.5	0.44	AKAP1	A kinase (PRKA) anchor protein 1 [Source:HGNC Symbol;Ac
13	HOOK3	1.46	−0.47	0.37	HOOK3	hook microtubule−tethering protein 3 [Source:HGNC Symbol;
14	NAALAD2	1.44	−0.15	0.35	NAALAD2	N−acetylated alpha−linked acidic dipeptidase 2 [Source:HGN
15	POFUT1	1.43	−0.5	0.28	POFUT1	protein O−fucosyltransferase 1 [Source:HGNC Symbol;Acc:H
16	CCDC94	1.43	−0.33	0.33	CCDC94	coiled−coil domain containing 94 [Source:HGNC Symbol;Acc
17	BTBD2	1.42	−0.22	0.42	BTBD2	BTB (POZ) domain containing 2 [Source:HGNC Symbol;Acc:
18	AIF1L	1.4	−0.2	0.53	AIF1L	allograft inflammatory factor 1−like [Source:HGNC Symbol;Ac
19	TBL2	1.4	−0.5	0.41	TBL2	transducin (beta)−like 2 [Source:HGNC Symbol;Acc:HGNC:1
20	AASDHPPT	1.4	−0.89	0.32	AASDHPPT	aminoadipate−semialdehyde dehydrogenase−phosphopantet

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	50 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
2	1e−05	63 / 8580	Colon	TxWk_Colon
3	2e−05	55 / 6929	Lymph	HOPP_Txn_elongation
4	3e−05	20 / 1418	TF	ICGC_Ets1_targets
5	4e−05	64 / 9027	Colon	Tx_Colon
6	6e−05	65 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
7	1e−04	65 / 9482	Colon	TssA_Colon
8	2e−04	65 / 9528	Brain	Overlap_fetal_midbrain_Quies
9	2e−04	5 / 101	BP	RNA processing
10	2e−04	43 / 5184	Lymph	HOPP_Txn_transition
11	7e−04	6 / 203	miRN	hsa−miR−33a
12	8e−04	6 / 210	MF	transferase activity, transferring glycosyl groups
13	9e−04	3 / 36	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	9e−04	54 / 7592	Lymph	HOPP_Active_promoter
15	1e−03	11 / 696	Chr	Chr 5
16	1e−03	13 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	1e−03	21 / 1975	BP	cellular protein modification process
18	1e−03	12 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
19	1e−03	7 / 315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
20	1e−03	5 / 158	GSEA	BENPORATH_NOS_TARGETS
21	1e−03	2 / 11	GSEA	HOLLEMAN_DAUNORUBICIN_B_ALL_DN
22	2e−03	8 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
23	2e−03	48 / 6564	Lymph	HOPP_Strong_enhancer
24	2e−03	3 / 46	miRN	hsa−miR−874
25	2e−03	5 / 168	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
26	2e−03	15 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
27	2e−03	16 / 1383	TF	ICGC_Six5_targets
28	2e−03	51 / 7209	Lymph	HOPP_Weak_promoter
29	2e−03	57 / 8415	Colon	Quies3_Colon
30	2e−03	4 / 102	miRN	hsa−miR−224
31	2e−03	13 / 1007	MF	poly(A) RNA binding
32	2e−03	15 / 1266	TF	ICGC_NrsfPcr1_targets
33	2e−03	6 / 258	GSEA	BENPORATH_OCT4_TARGETS
34	2e−03	3 / 51	GSEA	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_UP
35	3e−03	5 / 183	miRN	hsa−miR−1283
36	3e−03	4 / 113	miRN	hsa−miR−507
37	3e−03	3 / 56	BP	protein O−linked glycosylation
38	3e−03	3 / 56	BP	stem cell maintenance
39	4e−03	5 / 197	miRN	hsa−miR−222
40	4e−03	59 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3

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	2e−04	5 / 101	RNA processing
2	9e−04	3 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
3	1e−03	21 / 1975	cellular protein modification process
4	3e−03	3 / 56	protein O−linked glycosylation
5	3e−03	3 / 56	stem cell maintenance
6	5e−03	4 / 130	protein dephosphorylation
7	9e−03	3 / 80	peptidyl−serine phosphorylation
8	2e−02	5 / 276	nucleobase−containing compound catabolic process
9	3e−02	5 / 316	small GTPase mediated signal transduction
10	3e−02	8 / 687	gene expression
11	3e−02	2 / 53	retina development in camera−type eye
12	4e−02	2 / 58	ER to Golgi vesicle−mediated transport
13	4e−02	6 / 478	protein transport
14	4e−02	2 / 62	hematopoietic progenitor cell differentiation
15	4e−02	12 / 1325	catabolic process
16	5e−02	28 / 3980	cellular nitrogen compound metabolic process
17	5e−02	1 / 10	endothelial cell morphogenesis
18	5e−02	1 / 10	nuclear−transcribed mRNA catabolic process
19	5e−02	1 / 10	pantothenate metabolic process
20	5e−02	1 / 10	positive regulation of T cell differentiation

Brain

Rank	p−value	#in/all	Geneset
1	1e−05	50 / 5940	Overlap_fetal_midbrain_HetRpts
2	6e−05	65 / 9330	Overlap_fetal_midbrain_ReprPC
3	2e−04	65 / 9528	Overlap_fetal_midbrain_Quies
4	4e−03	59 / 9013	Overlap_fetal_midbrain_K9K27me3
5	5e−02	55 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	1e−01	7 / 769	Overlap_fetal_midbrain_ZNF
7	2e−01	20 / 3081	Mid_Frontal_Lobe_ZNF
8	2e−01	6 / 765	Mid_Frontal_Lobe_Het
9	2e−01	3 / 304	Fetal_Het
10	2e−01	6 / 786	Fetal_EnhG
11	2e−01	7 / 953	Fetal_Enh
12	2e−01	8 / 1122	Fetal_K9K27me3
13	3e−01	7 / 1050	Fetal_EnhP
14	3e−01	4 / 564	Mid_Frontal_Lobe_EnhP
15	4e−01	8 / 1333	Fetal_ReprPCWk
16	4e−01	6 / 1013	Fetal_TssP
17	5e−01	4 / 656	Overlap_fetal_midbrain_EnhP
18	6e−01	1 / 158	Overlap_fetal_midbrain_Het
19	6e−01	10 / 1949	Fetal_TssF
20	6e−01	4 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	4 / 298	SPANG_BCL6−index2
2	0.22	1 / 48	KUIPER_MM poor survival
3	0.24	2 / 180	SPANG_LPS−index2
4	0.29	0 / 14	LIU_COMMON_CANCER_GENES
5	0.48	3 / 489	Lembcke_Normal vs Adenoma
6	0.88	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_LIVER_CANCER
13	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
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	0.008	3 / 78	ubiquitin ligase complex
2	0.011	65 / 10605	intracellular
3	0.014	2 / 35	mediator complex
4	0.016	9 / 747	nucleolus
5	0.028	3 / 125	lamellipodium
6	0.045	51 / 8205	cytoplasm
7	0.059	2 / 75	condensed chromosome kinetochore
8	0.061	1 / 12	basal part of cell
9	0.061	1 / 12	HOPS complex
10	0.066	1 / 13	proteasome regulatory particle
11	0.071	1 / 14	Cul4−RING E3 ubiquitin ligase complex
12	0.071	1 / 14	ER to Golgi transport vesicle
13	0.072	2 / 84	growth cone
14	0.073	19 / 2577	nucleoplasm
15	0.076	1 / 15	centriolar satellite
16	0.076	1 / 15	dendrite cytoplasm
17	0.076	1 / 15	eukaryotic 43S preinitiation complex
18	0.076	1 / 15	pericentriolar material
19	0.086	1 / 17	proteasome accessory complex
20	0.091	1 / 18	DNA−directed RNA polymerase III complex

Chr

Rank	p−value	#in/all	Geneset
1	0.001	11 / 696	Chr 5
2	0.073	6 / 558	Chr 4
3	0.073	8 / 840	Chr 17
4	0.157	4 / 398	Chr 20
5	0.164	5 / 552	Chr 10
6	0.359	4 / 576	Chr 9
7	0.449	3 / 469	Chr 8
8	0.604	5 / 993	Chr 2
9	0.649	4 / 838	Chr 3
10	0.685	7 / 1500	Chr 1
11	0.691	1 / 221	Chr 18
12	0.706	3 / 687	Chr 6
13	0.708	3 / 689	Chr 7
14	0.800	3 / 801	Chr 11
15	0.803	4 / 1037	Chr 19
16	0.861	2 / 649	Chr 16
17	0.917	1 / 465	Chr 15
18	0.948	1 / 551	Chr X
19	0.985	1 / 775	Chr 12
20	1.000	0 / 262	Chr 13

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−05	63 / 8580	TxWk_Colon
2	4e−05	64 / 9027	Tx_Colon
3	1e−04	65 / 9482	TssA_Colon
4	2e−03	57 / 8415	Quies3_Colon
5	7e−02	45 / 7203	TssF_Colon
6	9e−02	60 / 10290	TssWk_Colon
7	1e−01	33 / 5155	EnhWk1_Colon
8	1e−01	1 / 29	Marisa_CRC−cluster−c
9	1e−01	36 / 5880	TssD2_Colon
10	2e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
11	2e−01	17 / 2698	EnhA_Colon
12	3e−01	54 / 9653	Enh_Colon
13	3e−01	17 / 2798	TxEnhG1_Colon
14	3e−01	3 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
15	4e−01	5 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	4e−01	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
17	4e−01	1 / 102	Marisa_CRC−cluster−d
18	4e−01	2 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
19	4e−01	21 / 3812	TssD1_Colon
20	5e−01	1 / 131	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.2	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	7 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.030	5 / 332	Up
3	0.056	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
4	0.076	1 / 15	VERHAAK_CL subtype
5	0.114	1 / 23	WIRTH_PN subtype
6	0.142	1 / 29	shaw_responders_down_in_oligo_glioma
7	0.220	1 / 47	Vishal_subnetwork signature of survival in GBM
8	0.220	1 / 47	mature astrocytes
9	0.228	1 / 49	developing astrocytes
10	0.283	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	0.290	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
12	0.302	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	0.327	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
14	0.392	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	0.420	1 / 103	GIEZELT_GBM_WT_up_VS_mut
16	0.457	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
17	0.569	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
18	0.575	2 / 365	Down_b
19	0.623	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
20	0.850	1 / 356	Down_a

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	13 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	0.001	12 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	0.001	5 / 158	BENPORATH_NOS_TARGETS
4	0.001	2 / 11	HOLLEMAN_DAUNORUBICIN_B_ALL_DN
5	0.002	8 / 416	SHEN_SMARCA2_TARGETS_UP
6	0.002	5 / 168	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
7	0.002	15 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	0.002	6 / 258	BENPORATH_OCT4_TARGETS
9	0.002	3 / 51	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_UP
10	0.004	2 / 18	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP
11	0.004	2 / 18	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP
12	0.004	6 / 291	HORIUCHI_WTAP_TARGETS_DN
13	0.004	5 / 203	SANSOM_APC_MYC_TARGETS
14	0.005	4 / 132	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
15	0.007	4 / 145	VERHAAK_GLIOBLASTOMA_CLASSICAL
16	0.008	2 / 26	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
17	0.009	9 / 675	BENPORATH_SOX2_TARGETS
18	0.011	3 / 88	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEP
19	0.012	7 / 469	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP
20	0.013	4 / 172	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP

HM

Rank	p−value	#in/all	Geneset
1	0.08	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	0.08	3 / 195	HALLMARK_MITOTIC_SPINDLE
3	0.14	1 / 29	HALLMARK_NOTCH_SIGNALING
4	0.22	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	0.23	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	0.25	2 / 181	HALLMARK_P53_PATHWAY
7	0.26	2 / 188	HALLMARK_MYC_TARGETS_V1
8	0.38	1 / 91	HALLMARK_BILE_ACID_METABOLISM
9	0.39	1 / 93	HALLMARK_PEROXISOME
10	0.49	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
11	0.52	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
12	0.54	1 / 146	HALLMARK_DNA_REPAIR
13	0.54	1 / 148	HALLMARK_KRAS_SIGNALING_UP
14	0.59	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	0.59	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
16	0.62	1 / 183	HALLMARK_GLYCOLYSIS
17	0.65	1 / 196	HALLMARK_G2M_CHECKPOINT
18	0.65	1 / 196	HALLMARK_MTORC1_SIGNALING
19	0.65	1 / 197	HALLMARK_E2F_TARGETS
20	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB

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	2e−05	55 / 6929	HOPP_Txn_elongation
2	2e−04	43 / 5184	HOPP_Txn_transition
3	9e−04	54 / 7592	HOPP_Active_promoter
4	2e−03	48 / 6564	HOPP_Strong_enhancer
5	2e−03	51 / 7209	HOPP_Weak_promoter
6	4e−03	41 / 5538	HOPP_Weak_txn
7	1e−02	5 / 256	SPANG_IL21 DN
8	1e−02	40 / 5693	HOPP_Weak_enhancer
9	7e−02	1 / 13	BENTINK_mBL UP
10	9e−02	1 / 17	Aukema_BCL2 UP_BCL6 DN
11	1e−01	1 / 19	Subero_MM_hyper_meth
12	1e−01	3 / 247	ZHANG_DLBCL mutated
13	2e−01	1 / 33	LEE_Developmental_regulators
14	2e−01	15 / 2211	HOPP_Repetitive
15	2e−01	9 / 1218	SPANG_BCR UP
16	2e−01	3 / 294	TARTE_Plasmablast signature
17	2e−01	8 / 1128	SPANG_BCR DN
18	3e−01	1 / 60	Subero_T−ALL_hyper_meth
19	3e−01	1 / 66	TARTE_Plasma cell signature
20	3e−01	1 / 81	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	8e−04	6 / 210	transferase activity, transferring glycosyl groups
2	2e−03	13 / 1007	poly(A) RNA binding
3	8e−03	2 / 25	ATP−dependent helicase activity
4	9e−03	2 / 27	ribosome binding
5	1e−02	14 / 1365	RNA binding
6	1e−02	2 / 32	Rac GTPase binding
7	1e−02	2 / 34	ATP−dependent RNA helicase activity
8	2e−02	3 / 104	iron ion binding
9	3e−02	4 / 217	transcription coactivator activity
10	4e−02	4 / 248	GTPase activity
11	5e−02	2 / 67	phosphotransferase activity, alcohol group as acceptor
12	5e−02	1 / 10	ribosomal small subunit binding
13	6e−02	1 / 11	acetyltransferase activity
14	6e−02	3 / 167	helicase activity
15	7e−02	1 / 13	mannose binding
16	7e−02	1 / 13	protein kinase A regulatory subunit binding
17	7e−02	2 / 83	translation factor activity, RNA binding
18	7e−02	1 / 14	enhancer binding
19	8e−02	1 / 15	dioxygenase activity
20	8e−02	1 / 15	L−ascorbic acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	6 / 203	hsa−miR−33a
2	2e−03	3 / 46	hsa−miR−874
3	2e−03	4 / 102	hsa−miR−224
4	3e−03	5 / 183	hsa−miR−1283
5	3e−03	4 / 113	hsa−miR−507
6	4e−03	5 / 197	hsa−miR−222
7	4e−03	5 / 204	hsa−miR−221
8	5e−03	3 / 68	hsa−miR−606
9	6e−03	3 / 70	hsa−miR−548b−3p
10	7e−03	6 / 321	hsa−miR−32
11	8e−03	3 / 77	hsa−miR−1305
12	8e−03	3 / 79	hsa−miR−569
13	1e−02	4 / 159	hsa−miR−298
14	1e−02	3 / 88	hsa−miR−496
15	1e−02	6 / 358	hsa−let−7d
16	1e−02	4 / 169	hsa−miR−369−3p
17	1e−02	4 / 172	hsa−miR−29a
18	1e−02	3 / 96	hsa−miR−125b
19	1e−02	3 / 96	hsa−miR−125a−5p
20	2e−02	4 / 181	hsa−miR−29c

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	0.07	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	3e−05	20 / 1418	ICGC_Ets1_targets
2	2e−03	16 / 1383	ICGC_Six5_targets
3	2e−03	15 / 1266	ICGC_NrsfPcr1_targets
4	2e−02	29 / 3924	ICGC_Zeb1_targets
5	3e−02	18 / 2137	ICGC_SrfV0416101_targets
6	3e−02	16 / 1872	ICGC_Mef2_targets
7	3e−02	16 / 1878	ICGC_Cebpbsc150_targets
8	4e−02	32 / 4617	ICGC_Tcf12_targets
9	4e−02	12 / 1314	ICGC_Usf1_targets
10	5e−02	32 / 4689	ICGC_Taf1_targets
11	6e−02	26 / 3700	ICGC_Nfatc1_targets
12	6e−02	30 / 4414	ICGC_Bclaf101388_targets
13	6e−02	32 / 4774	ICGC_Foxm1_targets
14	7e−02	6 / 553	ICGC_RxraPcr1_targets
15	8e−02	27 / 3966	ICGC_Pu1_targets
16	8e−02	1 / 15	NOWICK_TF
17	9e−02	32 / 4909	ICGC_Stat5_targets
18	9e−02	27 / 4032	ICGC_Creb1_targets
19	1e−01	31 / 4829	ICGC_Nficsc81335_targets
20	1e−01	31 / 4879	ICGC_Pmlsc71910_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	0.06	1 / 12	WIRTH_Thymus
2	0.45	1 / 114	PALMER_T−Cell signature up
3	0.55	2 / 350	WIRTH_Immune system
4	0.55	2 / 350	WIRTH_Nervous System
5	0.64	1 / 194	PALMER_B−Cell signature up
6	0.70	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	0.07	10 / 1115	LU_BPDE 1h DN
2	0.84	16 / 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	

Underexpression Spots

Spot Summary: g

metagenes = 25
genes = 196

<r> metagenes = 0.81
<r> genes = 0.11
beta: r2= 1.71 / log p= −Inf

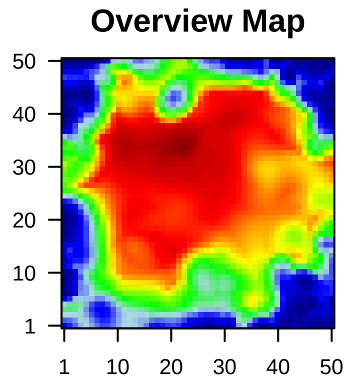
samples with spot = 7 (7.6 %)
MSC3 : 7 (28 %)

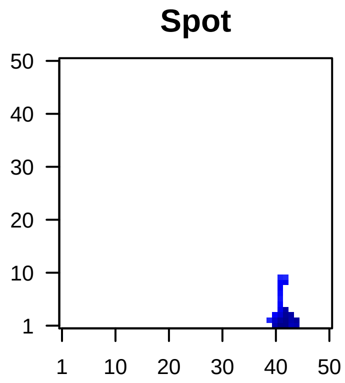
Spot Genelist

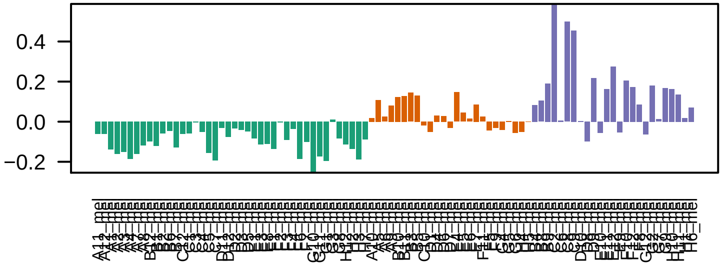
Rank	ID	max e	min e	r	Symbol	Description
1	PLA2G4C	2.46	−0.18	0.51	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium−independer
2	FOLR3	2.37	−0.05	0.84	FOLR3	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:HGNC
3	HIST1H4H	2.16	−0.25	0.44	HIST1H4H	histone cluster 1, H4h [Source:HGNC Symbol;Acc:HGNC:478
4	ABCB9	1.97	−0.21	0.43	ABCB9	ATP−binding cassette, sub−family B (MDR/TAP), member 9 [S
5	RFTN1	1.87	−0.37	0.29	RFTN1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:HGNC:30
6	ABCA4	1.81	−0.14	0.63	ABCA4	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
7	ALKBH3	1.81	−0.44	0.29	ALKBH3	alkB, alkylation repair homolog 3 (E. coli) [Source:HGNC Sym
8	ZNF280D	1.8	−0.69	0.33	ZNF280D	zinc finger protein 280D [Source:HGNC Symbol;Acc:HGNC:2
9	RNF41	1.76	−0.51	0.38	RNF41	ring finger protein 41, E3 ubiquitin protein ligase [Source:HGN
10	CCS	1.76	−0.44	0.31	CCS	copper chaperone for superoxide dismutase [Source:HGNC S
11	AFAP1	1.75	−0.15	0.56	AFAP1	actin filament associated protein 1 [Source:HGNC Symbol;Ac
12	HIVEP1	1.7	−0.3	0.36	HIVEP1	human immunodeficiency virus type I enhancer binding protei
13	ZBTB20	1.7	−0.33	0.3	ZBTB20	zinc finger and BTB domain containing 20 [Source:HGNC Syı
14	CTSF	1.68	−0.32	0.28	CTSF	cathepsin F [Source:HGNC Symbol;Acc:HGNC:2531]
15	TNIK	1.64	−0.11	0.56	TNIK	TRAF2 and NCK interacting kinase [Source:HGNC Symbol;A
16	ABCC10	1.61	−0.35	0.27	ABCC10	ATP−binding cassette, sub−family C (CFTR/MRP), member 1
17	JDP2	1.6	−0.17	0.48	JDP2	Jun dimerization protein 2 [Source:HGNC Symbol;Acc:HGNC
18	ACAD8	1.6	−0.29	0.33	ACAD8	acyl−CoA dehydrogenase family, member 8 [Source:HGNC S
19	HDAC5	1.59	−0.46	0.42	HDAC5	histone deacetylase 5 [Source:HGNC Symbol;Acc:HGNC:14(
20	CUL2	1.59	−0.6	0.31	CUL2	cullin 2 [Source:HGNC Symbol;Acc:HGNC:2552]

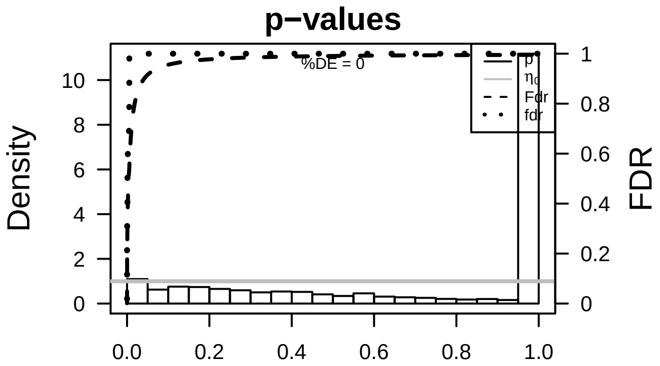
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−07	30 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
2	2e−06	149 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	2e−05	15 / 315	miRN	hsa−miR−302c
4	3e−05	15 / 329	miRN	hsa−miR−302d
5	3e−05	106 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	9e−05	23 / 730	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
7	2e−04	149 / 9528	Brain	Overlap_fetal_midbrain_Quies
8	2e−04	13 / 307	miRN	hsa−miR−302b
9	2e−04	12 / 268	miRN	hsa−miR−363
10	2e−04	8 / 124	GSEA	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN
11	2e−04	24 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
12	3e−04	5 / 45	TF Tis	VAQUERIZAS_Uterus
13	3e−04	13 / 318	miRN	hsa−miR−302a
14	3e−04	19 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
15	4e−04	13 / 327	miRN	hsa−miR−367
16	4e−04	3 / 12	GSEA	GERHOLD_RESPONSE_TO_TZD_DN
17	5e−04	22 / 765	Brain	Mid_Frontal_Lobe_Het
18	5e−04	4 / 29	miRN	hsa−miR−486−5p
19	6e−04	6 / 78	CC	ubiquitin ligase complex
20	7e−04	14 / 392	GSEA	HAN_SATB1_TARGETS_DN
21	7e−04	3 / 14	BP	neural tube formation
22	7e−04	3 / 14	GSEA	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP
23	8e−04	140 / 9027	Colon	Tx_Colon
24	8e−04	5 / 56	GSEA	MARSON_FOXP3_TARGETS_UP
25	9e−04	4 / 33	BP	negative regulation of osteoblast differentiation
26	9e−04	12 / 314	miRN	hsa−miR−520c−3p
27	9e−04	11 / 271	GSEA	ZHANG_TLX_TARGETS_60HR_UP
28	9e−04	8 / 153	miRN	hsa−miR−583
29	1e−03	9 / 196	GSEA	CHANG_CORE_SERUM_RESPONSE_DN
30	1e−03	143 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
31	1e−03	4 / 37	miRN	hsa−miR−197
32	1e−03	8 / 163	miRN	hsa−miR−495
33	2e−03	14 / 426	miRN	hsa−miR−519d
34	2e−03	7 / 130	GSEA	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
35	2e−03	8 / 168	GSEA	RIZKI_TUMOR_INVASIVENESS_3D_UP
36	2e−03	9 / 208	GSEA	ZHANG_TLX_TARGETS_36HR_UP
37	2e−03	10 / 250	miRN	hsa−miR−524−5p
38	2e−03	11 / 294	miRN	hsa−miR−561
39	2e−03	12 / 340	miRN	hsa−miR−142−5p
40	2e−03	3 / 19	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_M


Overview Map


Spot




p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.4	2 / 111	HORVATH_aging_genes meth UP
3	0.7	1 / 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	7e−04	3 / 14	neural tube formation
2	9e−04	4 / 33	negative regulation of osteoblast differentiation
3	2e−03	5 / 69	negative regulation of cell migration
4	3e−03	57 / 3068	signal transduction
5	4e−03	7 / 155	ubiquitin−dependent protein catabolic process
6	6e−03	13 / 441	negative regulation of transcription, DNA−templated
7	7e−03	4 / 58	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
8	7e−03	2 / 10	cell−cell junction assembly
9	7e−03	2 / 10	positive regulation of macrophage derived foam cell differentiation
10	9e−03	2 / 11	relaxation of cardiac muscle
11	1e−02	15 / 581	negative regulation of transcription from RNA polymerase II promoter
12	1e−02	3 / 34	somitogenesis
13	1e−02	2 / 12	regulation of N−methyl−D−aspartate selective glutamate receptor activity
14	1e−02	2 / 13	chromatin silencing
15	1e−02	2 / 13	positive regulation of cellular protein metabolic process
16	1e−02	2 / 13	regulation of bone mineralization
17	1e−02	3 / 37	nucleotide−binding domain, leucine rich repeat containing receptor signaling p
18	1e−02	10 / 336	protein ubiquitination
19	1e−02	2 / 14	acyl−CoA metabolic process
20	1e−02	2 / 14	tRNA aminoacylation

Brain

Rank	p−value	#in/all	Geneset
1	2e−06	149 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−05	106 / 5940	Overlap_fetal_midbrain_HetRpts
3	2e−04	149 / 9528	Overlap_fetal_midbrain_Quies
4	5e−04	22 / 765	Mid_Frontal_Lobe_Het
5	1e−03	143 / 9330	Overlap_fetal_midbrain_ReprPC
6	5e−03	136 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	2e−02	53 / 3081	Mid_Frontal_Lobe_ZNF
8	7e−02	12 / 564	Mid_Frontal_Lobe_EnhP
9	8e−02	15 / 769	Overlap_fetal_midbrain_ZNF
10	9e−02	8 / 349	Fetal_ZNF
11	2e−01	14 / 786	Fetal_EnhG
12	2e−01	4 / 158	Overlap_fetal_midbrain_Het
13	2e−01	30 / 1949	Fetal_TssF
14	2e−01	6 / 304	Fetal_Het
15	2e−01	17 / 1065	Overlap_fetal_midbrain_Enh
16	4e−01	19 / 1333	Fetal_ReprPCWk
17	4e−01	12 / 831	Fetal_HetRpts
18	5e−01	8 / 574	Overlap_fetal_midbrain_TssP
19	5e−01	13 / 953	Fetal_Enh
20	6e−01	28 / 2185	Fetal_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	0 / 12	LIU_PROSTATE_CANCER_UP
2	0.10	2 / 40	ZHANG_MM_up
3	0.10	7 / 298	SPANG_BCL6−index2
4	0.13	2 / 47	PanCan_DNARepair_geneset_nanostring
5	0.15	1 / 12	BEN−PORATH_DN
6	0.17	1 / 14	LIU_PROSTATE_CANCER_DN
7	0.18	3 / 111	PanCan_RAS_geneset_nanostring
8	0.19	2 / 61	PanCan_Wnt_geneset_nanostring
9	0.23	1 / 20	PanCan_ChromMod_geneset_nanostring
10	0.23	2 / 70	SHAUGHNESSY_MM high risk
11	0.31	8 / 489	Lembcke_Normal vs Adenoma
12	0.42	3 / 180	SPANG_LPS−index2
13	0.43	6 / 401	Lembcke_Colonic Inflammation
14	0.47	2 / 121	PanCan_MAPK_geneset_nanostring
15	0.48	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	0.56	0 / 15	RHODES_CANCER_META_SIGNATURE
17	0.58	0 / 14	LIU_COMMON_CANCER_GENES
18	0.78	1 / 113	PanCan_Driver−Gene_geneset_nanostring
19	0.86	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	0.87	1 / 156	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−04	6 / 78	ubiquitin ligase complex
2	7e−03	2 / 10	beta−catenin destruction complex
3	9e−03	2 / 11	integral component of nuclear inner membrane
4	1e−02	5 / 99	cell cortex
5	1e−02	47 / 2577	nucleoplasm
6	1e−02	2 / 12	cullin−RING ubiquitin ligase complex
7	2e−02	12 / 456	vacuole
8	2e−02	11 / 412	lysosome
9	2e−02	9 / 308	focal adhesion
10	3e−02	7 / 223	lysosomal membrane
11	5e−02	150 / 10605	intracellular
12	6e−02	2 / 29	cell−cell adherens junction
13	6e−02	2 / 31	histone deacetylase complex
14	7e−02	2 / 33	Golgi stack
15	8e−02	3 / 76	extrinsic component of membrane
16	8e−02	2 / 36	nuclear body
17	9e−02	4 / 127	cytoplasmic vesicle
18	9e−02	2 / 39	autophagic vacuole
19	1e−01	3 / 84	PML body
20	1e−01	84 / 5696	nucleus

Chr

Rank	p−value	#in/all	Geneset
1	0.09	16 / 840	Chr 17
2	0.15	7 / 335	Chr 22
3	0.19	10 / 552	Chr 10
4	0.20	12 / 689	Chr 7
5	0.25	23 / 1500	Chr 1
6	0.31	13 / 838	Chr 3
7	0.32	3 / 151	Chr 21
8	0.40	7 / 462	Chr 14
9	0.41	7 / 465	Chr 15
10	0.42	10 / 687	Chr 6
11	0.42	6 / 398	Chr 20
12	0.43	14 / 993	Chr 2
13	0.48	11 / 801	Chr 11
14	0.49	8 / 576	Chr 9
15	0.67	3 / 262	Chr 13
16	0.80	8 / 775	Chr 12
17	0.81	7 / 696	Chr 5
18	0.85	5 / 551	Chr X
19	0.86	5 / 558	Chr 4
20	0.95	1 / 221	Chr 18

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−04	140 / 9027	Tx_Colon
2	3e−03	143 / 9482	TssA_Colon
3	4e−03	19 / 739	TxEnhG2_Colon
4	6e−03	85 / 5155	EnhWk1_Colon
5	6e−03	3 / 29	Marisa_CRC−cluster−c
6	1e−02	127 / 8415	Quies3_Colon
7	1e−02	129 / 8580	TxWk_Colon
8	2e−02	2 / 15	Juehling_HNPCC−mutated−in−4
9	2e−02	7 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
10	2e−02	149 / 10290	TssWk_Colon
11	2e−02	49 / 2798	TxEnhG1_Colon
12	2e−02	2 / 16	Juehling−MSI−enriched−in−6
13	2e−02	2 / 17	Vilar_mutated−in−CRC−CamP
14	3e−02	62 / 3812	TssD1_Colon
15	3e−02	8 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
16	5e−02	89 / 5880	TssD2_Colon
17	6e−02	1 / 5	Juehling−MSI−enriched−in−8−to−9
18	8e−02	53 / 3383	EnhWk2_Colon
19	9e−02	1 / 7	Kaneda_CIMP−group2
20	9e−02	4 / 131	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.2	6 / 294	GUDJ_psoriasis down
2	0.7	5 / 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	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
2	0.012	5 / 103	GIEZELT_GBM_WT_up_VS_mut
3	0.023	10 / 365	Down_b
4	0.057	8 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	0.060	3 / 68	GIEZELT_GBM_WT_down_VS_mut
6	0.076	1 / 6	shaw_responders_up_in_oligo_glioma
7	0.112	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
8	0.112	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
9	0.112	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
10	0.124	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
11	0.169	1 / 14	VERHAAK_PN subtype
12	0.172	2 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
13	0.201	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
14	0.212	1 / 18	Barbus_GBM_STS_vs._LTS
15	0.212	1 / 18	Shinawi_with_increased_methylation_in_STS
16	0.225	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
17	0.239	2 / 71	Weller_LGG_gradeII−vs−III_DOWN
18	0.291	1 / 26	Christensen_hypomethylated_in_ependymoma
19	0.354	1 / 33	Christensen_hypomethylated_in_primary_glioblastoma
20	0.365	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−07	30 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
2	9e−05	23 / 730	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
3	2e−04	8 / 124	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN
4	2e−04	24 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	3e−04	19 / 594	WONG_ADULT_TISSUE_STEM_MODULE
6	4e−04	3 / 12	GERHOLD_RESPONSE_TO_TZD_DN
7	7e−04	14 / 392	HAN_SATB1_TARGETS_DN
8	7e−04	3 / 14	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP
9	8e−04	5 / 56	MARSON_FOXP3_TARGETS_UP
10	9e−04	11 / 271	ZHANG_TLX_TARGETS_60HR_UP
11	1e−03	9 / 196	CHANG_CORE_SERUM_RESPONSE_DN
12	2e−03	7 / 130	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
13	2e−03	8 / 168	RIZKI_TUMOR_INVASIVENESS_3D_UP
14	2e−03	9 / 208	ZHANG_TLX_TARGETS_36HR_UP
15	2e−03	3 / 19	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MON
16	2e−03	3 / 19	JEON_SMAD6_TARGETS_UP
17	2e−03	5 / 67	LEIN_MIDBRAIN_MARKERS
18	2e−03	11 / 302	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
19	2e−03	8 / 175	MCBRYAN_PUBERTAL_BREAST_6_7WK_UP
20	3e−03	12 / 361	LU_EZH2_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.005	4 / 53	HALLMARK_TGF_BETA_SIGNALING
2	0.012	3 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.046	5 / 148	HALLMARK_KRAS_SIGNALING_UP
4	0.069	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
5	0.074	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.084	5 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.180	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	0.196	4 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.291	1 / 26	HALLMARK_ANGIOGENESIS
10	0.360	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.376	3 / 167	HALLMARK_APICAL_JUNCTION
12	0.474	3 / 195	HALLMARK_MITOTIC_SPINDLE
13	0.495	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
14	0.540	2 / 137	HALLMARK_UV_RESPONSE_DN
15	0.548	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
16	0.551	2 / 140	HALLMARK_APOPTOSIS
17	0.551	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
18	0.555	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
19	0.574	2 / 146	HALLMARK_UV_RESPONSE_UP
20	0.641	2 / 165	HALLMARK_MYOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	2 / 32	DUMEAUX_Fasting 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 / 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 / 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	0.003	10 / 268	SPANG_IL21 UP
2	0.011	116 / 7592	HOPP_Active_promoter
3	0.014	3 / 39	ROSOLOWSKI_blue DOWN
4	0.018	106 / 6929	HOPP_Txn_elongation
5	0.030	24 / 1218	SPANG_BCR UP
6	0.032	8 / 280	SPANG_CD40 6hrs UP
7	0.047	38 / 2211	HOPP_Repetitive
8	0.060	106 / 7209	HOPP_Weak_promoter
9	0.066	21 / 1128	SPANG_BCR DN
10	0.097	2 / 40	Subero_mBL_hyper_meth
11	0.104	3 / 86	ROSOLOWSKI_red total
12	0.124	1 / 10	DAVE_BL_DN
13	0.124	1 / 10	Shaknovich_ABC_hypo_meth
14	0.157	80 / 5538	HOPP_Weak_txn
15	0.158	1 / 13	Subero_MCL_hypo_meth
16	0.166	3 / 107	SPANG_LPS 6hrs UP
17	0.169	1 / 14	Subero_MCL_hyper_meth
18	0.201	1 / 17	Aukema_BCL2 UP_BCL6 DN
19	0.206	74 / 5184	HOPP_Txn_transition
20	0.215	2 / 66	TARTE_Plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	0.006	9 / 248	GTPase activity
2	0.007	2 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
3	0.014	2 / 14	ferrous iron binding
4	0.015	8 / 244	ubiquitin−protein transferase activity
5	0.016	2 / 15	L−ascorbic acid binding
6	0.016	3 / 41	ATPase activity, coupled to transmembrane movement of substances
7	0.018	11 / 405	ligase activity
8	0.019	3 / 43	SMAD binding
9	0.021	2 / 17	mitogen−activated protein kinase binding
10	0.021	2 / 17	protein disulfide isomerase activity
11	0.023	5 / 123	ubiquitin protein ligase activity
12	0.024	3 / 47	GDP binding
13	0.027	9 / 322	GTP binding
14	0.027	6 / 174	transcription corepressor activity
15	0.031	2 / 21	histone deacetylase activity
16	0.031	2 / 21	RNA polymerase II transcription corepressor activity
17	0.033	2 / 22	calmodulin−dependent protein kinase activity
18	0.033	2 / 22	RNA polymerase II transcription coactivator activity
19	0.036	78 / 4992	ion binding
20	0.036	2 / 23	MAP kinase kinase kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	15 / 315	hsa−miR−302c
2	3e−05	15 / 329	hsa−miR−302d
3	2e−04	13 / 307	hsa−miR−302b
4	2e−04	12 / 268	hsa−miR−363
5	3e−04	13 / 318	hsa−miR−302a
6	4e−04	13 / 327	hsa−miR−367
7	5e−04	4 / 29	hsa−miR−486−5p
8	9e−04	12 / 314	hsa−miR−520c−3p
9	9e−04	8 / 153	hsa−miR−583
10	1e−03	4 / 37	hsa−miR−197
11	1e−03	8 / 163	hsa−miR−495
12	2e−03	14 / 426	hsa−miR−519d
13	2e−03	10 / 250	hsa−miR−524−5p
14	2e−03	11 / 294	hsa−miR−561
15	2e−03	12 / 340	hsa−miR−142−5p
16	2e−03	11 / 296	hsa−miR−25
17	2e−03	6 / 101	hsa−miR−603
18	3e−03	10 / 263	hsa−miR−92b
19	3e−03	16 / 552	hsa−miR−93
20	3e−03	9 / 222	hsa−miR−520g

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	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	0.003	82 / 4829	ICGC_Nficsc81335_targets
2	0.007	68 / 3966	ICGC_Pu1_targets
3	0.016	86 / 5408	ICGC_Pou2_targets
4	0.018	43 / 2391	ICGC_Pbx3_targets
5	0.018	76 / 4706	ICGC_Sp1_targets
6	0.019	39 / 2137	ICGC_SrfV0416101_targets
7	0.024	75 / 4689	ICGC_Taf1_targets
8	0.032	34 / 1878	ICGC_Cebpbsc150_targets
9	0.032	36 / 2013	ICGC_Bcl11_targets
10	0.038	90 / 5890	ICGC_Elf1_targets
11	0.047	41 / 2416	ICGC_Bcl3_targets
12	0.047	72 / 4617	ICGC_Tcf12_targets
13	0.061	12 / 553	ICGC_RxraPcr1_targets
14	0.062	72 / 4682	ICGC_Pol24_targets
15	0.067	73 / 4774	ICGC_Foxm1_targets
16	0.068	46 / 2836	ICGC_BatfPcr1_targets
17	0.068	68 / 4414	ICGC_Bclaf101388_targets
18	0.073	23 / 1273	ICGC_P300_targets
19	0.076	74 / 4879	ICGC_Pmlsc71910_targets
20	0.085	62 / 4032	ICGC_Creb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 45	VAQUERIZAS_Uterus
2	6e−03	3 / 29	VAQUERIZAS_Smooth muscle
3	9e−03	3 / 33	VAQUERIZAS_Prostate
4	2e−02	2 / 17	VAQUERIZAS_Pituitary
5	4e−02	2 / 23	VAQUERIZAS_Trachea
6	6e−02	2 / 29	VAQUERIZAS_Fetal lung
7	8e−02	2 / 36	VAQUERIZAS_Fetal brain
8	9e−02	2 / 38	VAQUERIZAS_Testis
9	1e−01	2 / 41	VAQUERIZAS_Placenta
10	2e−01	2 / 58	VAQUERIZAS_Lung
11	2e−01	1 / 15	VAQUERIZAS_Fetal thyroid
12	2e−01	1 / 16	VAQUERIZAS_Salivary gland
13	3e−01	1 / 23	VAQUERIZAS_Spinal cord
14	3e−01	1 / 23	VAQUERIZAS_Adrenal cortex
15	4e−01	1 / 37	VAQUERIZAS_Thymus
16	4e−01	1 / 40	VAQUERIZAS_Thyroid
17	5e−01	1 / 59	VAQUERIZAS_Whole blood
18	6e−01	2 / 143	VAQUERIZAS_General
19	1e+00	0 / 26	VAQUERIZAS_Liver
20	1e+00	0 / 9	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.009	2 / 11	WIRTH_Cortex cerebri
2	0.158	1 / 13	WIRTH_B−cells
3	0.158	1 / 13	WIRTH_Thyroid gland
4	0.169	1 / 14	WIRTH_Telencephalon
5	0.625	1 / 74	WIRTH_Mucosa
6	0.727	2 / 194	PALMER_B−Cell signature up
7	0.780	1 / 114	PALMER_T−Cell signature up
8	0.950	1 / 225	PALMER_Granulocytes signature up
9	0.991	1 / 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 / 8	WIRTH_Tonsil
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 / 350	WIRTH_Nervous System
18	1.000	0 / 11	WIRTH_Globus pallidus
19	1.000	0 / 10	WIRTH_Hippocampus
20	1.000	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	16 / 1115	LU_BPDE 1h DN
2	0.6	48 / 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	

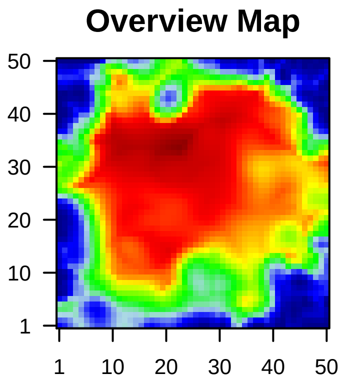
Underexpression Spots

Spot Summary: h

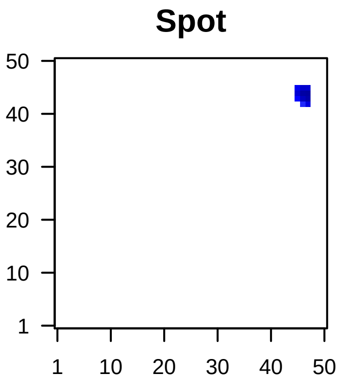
metagenes = 11
genes = 67

<r> metagenes = 0.95
<r> genes = 0.1
beta: r2= 1.21 / log p= −Inf

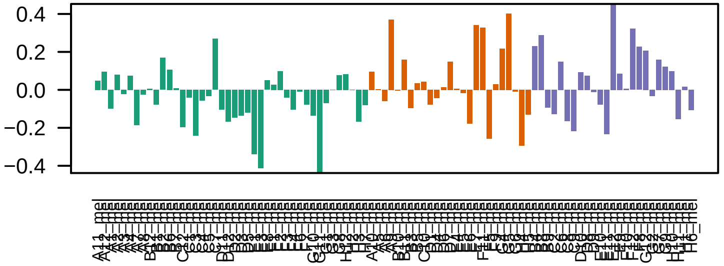
samples with spot = 12 (13 %)
MSC1 : 1 (2.4 %)
MSC2 : 5 (20 %)
MSC3 : 6 (24 %)



Overview Map



Spot

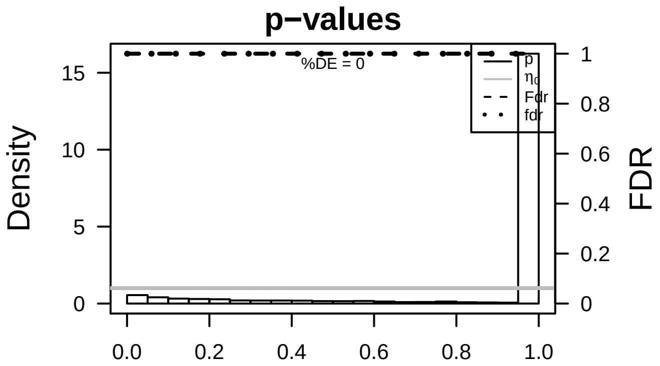


Spot Genelist

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:HGNC
2	PACRGL	1.76	−0.36	0.23	PACRGL	PARK2 co−regulated−like [Source:HGNC Symbol;Acc:HGNC
3	ING4	1.73	−0.36	0.37	ING4	inhibitor of growth family, member 4 [Source:HGNC Symbol;A
4	CNOT10	1.64	−1.42	0.27	CNOT10	CCR4−NOT transcription complex, subunit 10 [Source:HGNC
5	IL18R1	1.62	−0.08	0.34	IL18R1	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:HGNC:5
6	DENND2D	1.53	−0.17	0.22	DENND2D	DENN/MADD domain containing 2D [Source:HGNC Symbol;
7	HARS2	1.52	−0.54	0.29	HARS2	histidyl−tRNA synthetase 2, mitochondrial [Source:HGNC Sy
8	ATP13A2	1.52	−0.41	0.33	ATP13A2	ATPase type 13A2 [Source:HGNC Symbol;Acc:HGNC:30213
9	LRRC39	1.52	−0.38	0.35	LRRC39	leucine rich repeat containing 39 [Source:HGNC Symbol;Acc:
10	DPP10	1.49	−0.21	0.3	DPP10	dipeptidyl−peptidase 10 (non−functional) [Source:HGNC Sym
11	DCP1B	1.48	−0.35	0.33	DCP1B	decapping mRNA 1B [Source:HGNC Symbol;Acc:HGNC:244
12	UBR1	1.44	−0.77	0.26	UBR1	ubiquitin protein ligase E3 component n−recognin 1 [Source:
13	POLR1B	1.44	−0.88	0.35	POLR1B	polymerase (RNA) I polypeptide B, 128kDa [Source:HGNC S
14	TOMM40L	1.43	−0.16	0.25	TOMM40L	translocase of outer mitochondrial membrane 40 homolog (ye
15	MFSD10	1.42	−0.48	0.37	MFSD10	major facilitator superfamily domain containing 10 [Source:HG
16	HELB	1.42	−0.2	0.37	HELB	helicase (DNA) B [Source:HGNC Symbol;Acc:HGNC:17196]
17	TSC22D3	1.4	−0.56	0.21	TSC22D3	TSC22 domain family, member 3 [Source:HGNC Symbol;Acc
18	PXYLP1	1.4	−0.2	0.25	PXYLP1	2−phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc
19	RAD17	1.39	−0.6	0.39	RAD17	RAD17 homolog (S. pombe) [Source:HGNC Symbol;Acc:HG
20	RBBP9	1.39	−0.61	0.34	RBBP9	retinoblastoma binding protein 9 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−05	54 / 8580	Colon	TxWk_Colon
2	6e−05	35 / 4414	TF	ICGC_Bclaf101388_targets
3	6e−05	55 / 9027	Colon	Tx_Colon
4	8e−05	17 / 1383	TF	ICGC_Six5_targets
5	1e−04	32 / 3924	TF	ICGC_Zeb1_targets
6	1e−04	49 / 7592	Lymph	HOPP_Active_promoter
7	1e−04	20 / 1878	TF	ICGC_Cebpbsc150_targets
8	1e−04	38 / 5184	Lymph	HOPP_Txn_transition
9	1e−04	25 / 2714	TF	ICGC_Irf4_targets
10	2e−04	5 / 127	GSEA	REACTOME_METABOLISM_OF_MRNA
11	3e−04	5 / 134	GSEA	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
12	6e−04	35 / 4879	TF	ICGC_Pmlsc71910_targets
13	6e−04	34 / 4689	TF	ICGC_Taf1_targets
14	6e−04	35 / 4909	TF	ICGC_Stat5_targets
15	7e−04	3 / 39	GSEA	GENTILE_UV_RESPONSE_CLUSTER_D5
16	7e−04	20 / 2136	TF	ICGC_GabpPcr2_targets
17	7e−04	20 / 2137	TF	ICGC_SrfV0416101_targets
18	8e−04	37 / 5374	TF	ICGC_Pax5_targets
19	8e−04	34 / 4774	TF	ICGC_Foxm1_targets
20	9e−04	10 / 687	BP	gene expression
21	9e−04	3 / 43	GSEA	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY
22	1e−03	5 / 171	GSEA	REACTOME_METABOLISM_OF_RNA
23	1e−03	34 / 4829	TF	ICGC_Nficsc81335_targets
24	1e−03	42 / 6564	Lymph	HOPP_Strong_enhancer
25	1e−03	15 / 1418	TF	ICGC_Ets1_targets
26	1e−03	3 / 47	GSEA	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC
27	1e−03	2 / 12	MF	RNA polymerase I activity
28	1e−03	12 / 990	GSEA	DANG_BOUND_BY_MYC
29	1e−03	3 / 48	BP	regulation of cellular amino acid metabolic process
30	1e−03	2 / 13	CC	DNA−directed RNA polymerase I complex
31	2e−03	7 / 385	GSEA	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
32	2e−03	5 / 191	GSEA	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOM
33	2e−03	3 / 52	BP	nuclear−transcribed mRNA catabolic process, deadenylation−dependent de
34	2e−03	36 / 5355	TF	ICGC_Pol2_targets
35	2e−03	8 / 502	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
36	2e−03	2 / 14	GSEA	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE
37	2e−03	43 / 6929	Lymph	HOPP_Txn_elongation
38	2e−03	3 / 56	GSEA	KEGG_RNA_DEGRADATION
39	2e−03	35 / 5200	TF	ICGC_Mta3_targets
40	2e−03	31 / 4385	TF	ICGC_Atf2_targets



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	9e−04	10 / 687	gene expression
2	1e−03	3 / 48	regulation of cellular amino acid metabolic process
3	2e−03	3 / 52	nuclear−transcribed mRNA catabolic process, deadenylation−dependent deca
4	3e−03	3 / 61	regulation of translation
5	7e−03	2 / 29	exonucleolytic nuclear−transcribed mRNA catabolic process involved in deade
6	8e−03	5 / 277	translation
7	8e−03	2 / 30	termination of RNA polymerase I transcription
8	8e−03	2 / 30	transcription elongation from RNA polymerase I promoter
9	9e−03	2 / 32	protein catabolic process
10	9e−03	2 / 33	transcription from RNA polymerase I promoter
11	9e−03	2 / 33	transcription initiation from RNA polymerase I promoter
12	1e−02	2 / 40	ER−associated ubiquitin−dependent protein catabolic process
13	2e−02	2 / 44	tRNA aminoacylation for protein translation
14	2e−02	2 / 48	positive regulation of protein catabolic process
15	2e−02	3 / 131	ribonucleoprotein complex assembly
16	2e−02	3 / 139	DNA replication
17	3e−02	2 / 56	spermatid development
18	3e−02	11 / 1325	catabolic process
19	3e−02	2 / 62	DNA damage response, signal transduction by p53 class mediator resulting in
20	3e−02	2 / 64	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy

Brain

Rank	p−value	#in/all	Geneset
1	0.003	10 / 831	Fetal_HetRpts
2	0.004	52 / 9330	Overlap_fetal_midbrain_ReprPC
3	0.023	21 / 3081	Mid_Frontal_Lobe_ZNF
4	0.028	48 / 9013	Overlap_fetal_midbrain_K9K27me3
5	0.055	49 / 9528	Overlap_fetal_midbrain_Quies
6	0.101	32 / 5940	Overlap_fetal_midbrain_HetRpts
7	0.238	8 / 1333	Fetal_ReprPCWk
8	0.265	1 / 69	Overlap_fetal_midbrain_Tx
9	0.271	5 / 786	Fetal_EnhG
10	0.324	6 / 1050	Fetal_EnhP
11	0.383	8 / 1548	Mid_Frontal_Lobe_K9K27me3
12	0.393	2 / 304	Fetal_Het
13	0.419	5 / 953	Fetal_Enh
14	0.448	4 / 769	Overlap_fetal_midbrain_ZNF
15	0.503	1 / 156	Mid_Frontal_Lobe_TssA
16	0.506	9 / 1949	Fetal_TssF
17	0.564	40 / 9020	Overlap_fetal_midbrain_ReprPCWk
18	0.642	1 / 229	Mid_Frontal_Lobe_TxTrans
19	0.649	4 / 989	Mid_Frontal_Lobe_Quies
20	0.668	3 / 765	Mid_Frontal_Lobe_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	2 / 40	PanCan_HK_geneset_nanostring
2	0.03	1 / 14	LIU_COMMON_CANCER_GENES
3	0.06	1 / 13	GENTLES_modul12
4	0.07	1 / 16	GENTLES_modul14
5	0.12	1 / 29	KUIPER_MM good survival
6	0.15	3 / 298	SPANG_BCL6−index2
7	0.16	1 / 40	ZHANG_MM up
8	0.19	2 / 180	SPANG_LPS−index2
9	0.24	0 / 15	RHODES_CANCER_META_SIGNATURE
10	0.37	3 / 489	Lembcke_Normal vs Adenoma
11	0.83	0 / 14	LIU_PROSTATE_CANCER_DN
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 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.00	0 / 12	LIU_BREAST_CANCER
16	1.00	0 / 14	LIU_LIVER_CANCER
17	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
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	0.001	2 / 13	DNA−directed RNA polymerase I complex
2	0.002	3 / 57	proteasome complex
3	0.019	3 / 128	ribosome
4	0.024	4 / 246	mitochondrial matrix
5	0.024	2 / 54	intermediate filament cytoskeleton
6	0.030	2 / 61	cytoplasmic mRNA processing body
7	0.044	17 / 2507	cytosol
8	0.048	1 / 11	RISC complex
9	0.056	1 / 13	COPI vesicle coat
10	0.056	1 / 13	proteasome regulatory particle
11	0.061	1 / 14	ER to Golgi transport vesicle
12	0.065	1 / 15	CCR4−NOT complex
13	0.073	1 / 17	integral component of mitochondrial outer membrane
14	0.073	1 / 17	proteasome accessory complex
15	0.081	1 / 19	inclusion body
16	0.081	1 / 19	site of double−strand break
17	0.089	1 / 21	mitochondrial small ribosomal subunit
18	0.089	1 / 21	vesicle membrane
19	0.093	1 / 22	histone acetyltransferase complex
20	0.101	1 / 24	Cul3−RING ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	8 / 775	Chr 12
2	0.08	7 / 838	Chr 3
3	0.10	5 / 551	Chr X
4	0.31	6 / 1037	Chr 19
5	0.33	4 / 649	Chr 16
6	0.35	8 / 1500	Chr 1
7	0.52	4 / 840	Chr 17
8	0.59	3 / 687	Chr 6
9	0.60	3 / 689	Chr 7
10	0.62	2 / 465	Chr 15
11	0.65	4 / 993	Chr 2
12	0.72	2 / 558	Chr 4
13	0.82	2 / 696	Chr 5
14	0.83	1 / 398	Chr 20
15	0.88	1 / 462	Chr 14
16	0.88	2 / 801	Chr 11
17	0.88	1 / 469	Chr 8
18	0.92	1 / 552	Chr 10
19	0.93	1 / 576	Chr 9
20	1.00	0 / 262	Chr 13

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	54 / 8580	TxWk_Colon
2	6e−05	55 / 9027	Tx_Colon
3	3e−03	53 / 9482	TssA_Colon
4	2e−02	46 / 8415	Quies3_Colon
5	2e−02	7 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	3e−02	53 / 10290	TssWk_Colon
7	3e−02	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
8	5e−02	7 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	6e−02	1 / 13	TCGA−CRC_less−agressive−disease−markers
10	8e−02	17 / 2698	EnhA_Colon
11	1e−01	37 / 7203	TssF_Colon
12	2e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
13	3e−01	4 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	4e−01	2 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
15	5e−01	5 / 1038	HetRpts_Colon
16	5e−01	5 / 1079	ZNF_Colon
17	5e−01	23 / 5155	EnhWk1_Colon
18	5e−01	43 / 9653	Enh_Colon
19	6e−01	6 / 1386	Het_Colon
20	6e−01	3 / 739	TxEnhG2_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	0.03	8 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.04	2 / 74	WIRTH_Normal Brain
3	0.05	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	0.07	1 / 16	VERHAAK_NL subtype
5	0.08	1 / 18	Shinawi_with_increased_methylation_in_STS
6	0.16	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	0.16	3 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	0.19	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
9	0.20	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	0.21	3 / 356	Down_a
11	0.25	1 / 63	Stuehler_Proteins_up_in_STS
12	0.81	1 / 365	Down_b
13	1.00	0 / 15	VERHAAK_CL subtype
14	1.00	0 / 15	VERHAAK_MES subtype
15	1.00	0 / 14	VERHAAK_PN subtype
16	1.00	0 / 23	WIRTH_PN subtype
17	1.00	0 / 9	VERHAAK_Brain
18	1.00	0 / 8	VERHAAK_PN_Brain
19	1.00	0 / 11	Martinez_Glio_hypermeth
20	1.00	0 / 3	Martinez_Glio_hypometh

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 127	REACTOME_METABOLISM_OF_MRNA
2	3e−04	5 / 134	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
3	7e−04	3 / 39	GENTILE_UV_RESPONSE_CLUSTER_D5
4	9e−04	3 / 43	REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY
5	1e−03	5 / 171	REACTOME_METABOLISM_OF_RNA
6	1e−03	3 / 47	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC
7	1e−03	12 / 990	DANG_BOUND_BY_MYC
8	2e−03	7 / 385	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
9	2e−03	5 / 191	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_
10	2e−03	8 / 502	KIM_ALL_DISORDERS_CALB1_CORR_UP
11	2e−03	2 / 14	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE
12	2e−03	3 / 56	KEGG_RNA_DEGRADATION
13	3e−03	3 / 64	VANASSE_BCL2_TARGETS_DN
14	3e−03	5 / 223	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRES
15	3e−03	7 / 439	RAO_BOUND_BY_SALL4_ISOFORM_B
16	5e−03	3 / 77	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_
17	7e−03	3 / 90	NIELSEN_GIST
18	8e−03	2 / 30	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
19	9e−03	2 / 33	KEGG_BASE_EXCISION_REPAIR
20	1e−02	8 / 683	MARTENS_TRETINOIN_RESPONSE_DN

HM

Rank	p−value	#in/all	Geneset
1	0.05	3 / 188	HALLMARK_MYC_TARGETS_V1
2	0.06	3 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	0.14	2 / 146	HALLMARK_DNA_REPAIR
4	0.22	1 / 57	HALLMARK_MYC_TARGETS_V2
5	0.24	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.33	1 / 91	HALLMARK_PROTEIN_SECRETION
7	0.34	1 / 94	HALLMARK_ANDROGEN_RESPONSE
8	0.35	1 / 95	HALLMARK_SPERMATOGENESIS
9	0.35	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	0.38	1 / 107	HALLMARK_COAGULATION
11	0.39	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	0.43	1 / 127	HALLMARK_KRAS_SIGNALING_DN
13	0.47	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
14	0.47	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
15	0.53	1 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	0.56	1 / 181	HALLMARK_P53_PATHWAY
17	0.56	1 / 183	HALLMARK_GLYCOLYSIS
18	0.58	1 / 196	HALLMARK_MTORC1_SIGNALING
19	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
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	1e−04	49 / 7592	HOPP_Active_promoter
2	1e−04	38 / 5184	HOPP_Txn_transition
3	1e−03	42 / 6564	HOPP_Strong_enhancer
4	2e−03	43 / 6929	HOPP_Txn_elongation
5	4e−02	4 / 280	SPANG_CD40 6hrs UP
6	5e−02	1 / 12	BENTINK_mBL DOWN
7	6e−02	39 / 7209	HOPP_Weak_promoter
8	8e−02	1 / 19	DAVE_c−myc BL UP
9	1e−01	8 / 1128	SPANG_BCR DN
10	2e−01	1 / 50	SPANG_BAFF 9hrs DN
11	2e−01	29 / 5693	HOPP_Weak_enhancer
12	2e−01	1 / 61	SPANG_LPS 6hrs DN
13	3e−01	3 / 410	SPANG_CD40 6hrs DN
14	3e−01	27 / 5538	HOPP_Weak_txn
15	3e−01	1 / 89	ROSOLOWSKI_blue total
16	3e−01	2 / 268	SPANG_IL21 UP
17	4e−01	1 / 107	SPANG_LPS 6hrs UP
18	4e−01	1 / 129	DAVE_BL−vs−DLBCL
19	7e−01	1 / 247	ZHANG_DLBCL mutated
20	7e−01	1 / 256	SPANG_IL21 DN

MF

Rank	p−value	#in/all	Geneset
1	0.001	2 / 12	RNA polymerase I activity
2	0.006	2 / 27	four−way junction helicase activity
3	0.006	4 / 167	helicase activity
4	0.011	2 / 35	aminoacyl−tRNA ligase activity
5	0.012	2 / 37	DNA−directed RNA polymerase activity
6	0.013	2 / 39	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
7	0.029	11 / 1309	ATP binding
8	0.040	2 / 71	structural constituent of ribosome
9	0.044	1 / 10	ribosomal small subunit binding
10	0.048	1 / 11	RNA helicase activity
11	0.052	1 / 12	miRNA binding
12	0.056	1 / 13	NAD+ binding
13	0.069	1 / 16	ferrous iron transmembrane transporter activity
14	0.078	10 / 1365	RNA binding
15	0.079	4 / 364	ATPase activity
16	0.085	1 / 20	NAD+ ADP−ribosyltransferase activity
17	0.089	1 / 21	exonuclease activity
18	0.097	1 / 23	rRNA binding
19	0.098	4 / 394	catalytic activity
20	0.104	2 / 123	nucleotidyltransferase activity

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.004	3 / 69	hsa−miR−518c
2	0.004	3 / 70	hsa−miR−375
3	0.006	3 / 83	hsa−miR−1265
4	0.008	2 / 31	hsa−miR−617
5	0.010	4 / 189	hsa−miR−513a−3p
6	0.010	2 / 34	hsa−miR−517b
7	0.014	2 / 40	hsa−miR−518d−3p
8	0.014	2 / 41	hsa−miR−518b
9	0.015	3 / 116	hsa−miR−498
10	0.016	6 / 459	hsa−miR−195
11	0.017	3 / 122	hsa−miR−515−3p
12	0.019	6 / 479	hsa−miR−16
13	0.020	3 / 129	hsa−miR−218
14	0.021	2 / 50	hsa−miR−518f
15	0.021	3 / 132	hsa−miR−508−3p
16	0.025	6 / 507	hsa−miR−15a
17	0.026	3 / 143	hsa−miR−338−5p
18	0.027	3 / 145	hsa−miR−922
19	0.029	2 / 60	hsa−miR−296−3p
20	0.032	4 / 270	hsa−miR−30b

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−05	35 / 4414	ICGC_Bclaf101388_targets
2	8e−05	17 / 1383	ICGC_Six5_targets
3	1e−04	32 / 3924	ICGC_Zeb1_targets
4	1e−04	20 / 1878	ICGC_Cebpbsc150_targets
5	1e−04	25 / 2714	ICGC_Irf4_targets
6	6e−04	35 / 4879	ICGC_Pmlsc71910_targets
7	6e−04	34 / 4689	ICGC_Taf1_targets
8	6e−04	35 / 4909	ICGC_Stat5_targets
9	7e−04	20 / 2136	ICGC_GabpPcr2_targets
10	7e−04	20 / 2137	ICGC_SrfV0416101_targets
11	8e−04	37 / 5374	ICGC_Pax5_targets
12	8e−04	34 / 4774	ICGC_Foxm1_targets
13	1e−03	34 / 4829	ICGC_Nficsc81335_targets
14	1e−03	15 / 1418	ICGC_Ets1_targets
15	2e−03	36 / 5355	ICGC_Pol2_targets
16	2e−03	35 / 5200	ICGC_Mta3_targets
17	2e−03	31 / 4385	ICGC_Atf2_targets
18	3e−03	36 / 5495	ICGC_Yy1_targets
19	3e−03	32 / 4706	ICGC_Sp1_targets
20	4e−03	35 / 5408	ICGC_Pou2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 29	VAQUERIZAS_Fetal lung
2	0.2	1 / 58	VAQUERIZAS_Lung
3	0.5	1 / 143	VAQUERIZAS_General
4	1.0	0 / 36	VAQUERIZAS_Fetal brain
5	1.0	0 / 41	VAQUERIZAS_Placenta
6	1.0	0 / 26	VAQUERIZAS_Liver
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 / 9	VAQUERIZAS_Kidney
11	1.0	0 / 23	VAQUERIZAS_Spinal cord
12	1.0	0 / 38	VAQUERIZAS_Whole brain
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 / 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	0.05	1 / 12	WIRTH_Cerebellum
2	0.06	1 / 13	WIRTH_B−cells
3	0.21	2 / 194	PALMER_B−Cell signature up
4	0.35	1 / 95	WIRTH_Muscle
5	0.40	1 / 114	PALMER_T−Cell signature up
6	0.46	2 / 350	WIRTH_Immune 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 / 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 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	5 / 1115	LU_BPDE 1h DN
2	0.7	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	

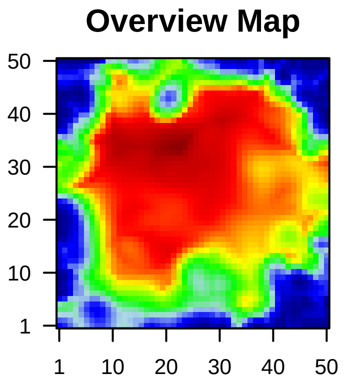
Underexpression Spots

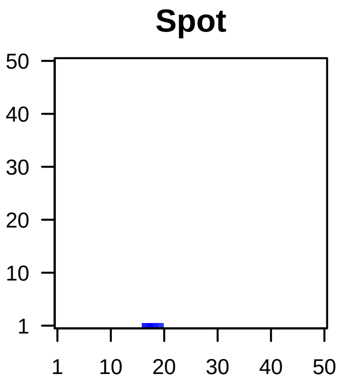
Spot Summary: i

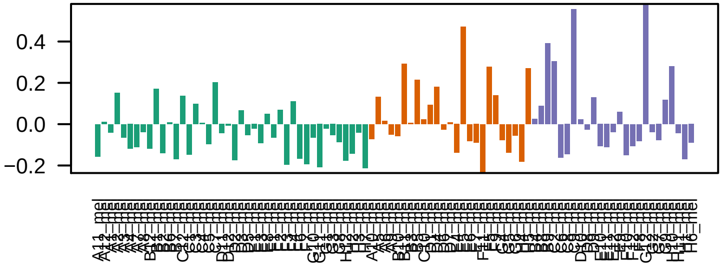
metagenes = 4
genes = 72

<r> metagenes = 0.96
<r> genes = 0.13
beta: r2= 1.16 / log p= −Inf

samples with spot = 11 (12 %)
MSC1 : 1 (2.4 %)
MSC2 : 5 (20 %)
MSC3 : 5 (20 %)





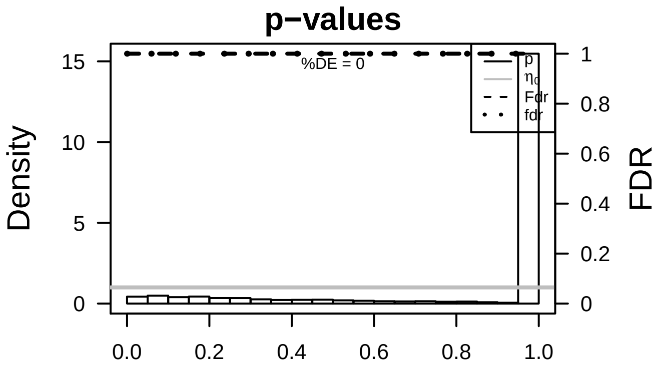


Spot Genelist

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	PRDM4	1.67	−0.36	0.35	PRDM4	PR domain containing 4 [Source:HGNC Symbol;Acc:HGNC:
3	SLC39A3	1.61	−0.35	0.41	SLC39A3	solute carrier family 39 (zinc transporter), member 3 [Source:
4	AC004381.6	1.6	−0.22	0.34		
5	SARS2	1.6	−0.55	0.31	SARS2	seryl−tRNA synthetase 2, mitochondrial [Source:HGNC Sym
6	NFIX	1.57	−0.33	0.44	NFIX	nuclear factor I/X (CCAAT−binding transcription factor) [Sour
7	ABCA7	1.54	−0.2	0.44	ABCA7	ATP−binding cassette, sub−family A (ABC1), member 7 [Sou
8	MPDZ	1.54	−0.52	0.36	MPDZ	multiple PDZ domain protein [Source:HGNC Symbol;Acc:HG
9	ACP5	1.53	−0.12	0.48	ACP5	acid phosphatase 5, tartrate resistant [Source:HGNC Symbol
10	ADCK1	1.53	−0.23	0.3	ADCK1	aarF domain containing kinase 1 [Source:HGNC Symbol;Acc
11	PRMT9	1.48	−0.3	0.25	PRMT9	protein arginine methyltransferase 9 [Source:HGNC Symbol;
12	KIAA0586	1.48	−0.54	0.33	KIAA0586	KIAA0586 [Source:HGNC Symbol;Acc:HGNC:19960]
13	AREL1	1.46	−0.72	0.31	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1 [Source:HGN
14	RDH13	1.45	−0.46	0.24	RDH13	retinol dehydrogenase 13 (all−trans/9−cis) [Source:HGNC Sy
15	SFXN5	1.45	−0.18	0.34	SFXN5	sideroflexin 5 [Source:HGNC Symbol;Acc:HGNC:16073]
16	RGMB	1.44	−0.5	0.26	RGMB	repulsive guidance molecule family member b [Source:HGNC
17	ANKS3	1.42	−0.39	0.41	ANKS3	ankyrin repeat and sterile alpha motif domain containing 3 [S
18	ANKRD37	1.42	−0.26	0.33	ANKRD37	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:HGNC
19	AHSA2	1.41	−0.46	0.22	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolo
20	SLC30A6	1.41	−0.59	0.29	SLC30A6	solute carrier family 30 (zinc transporter), member 6 [Source:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	58 / 8580	Colon	TxWk_Colon
2	3e−05	21 / 1693	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
3	7e−05	3 / 17	BP	zinc II ion transport
4	1e−04	58 / 9027	Colon	Tx_Colon
5	4e−04	3 / 31	CC	membrane coat
6	1e−03	4 / 92	GSEA	JAZAG_TGFB1_SIGNALING_UP
7	1e−03	2 / 10	BP	positive regulation of cellular metabolic process
8	1e−03	4 / 102	miRN	hsa−miR−1301
9	1e−03	2 / 12	GSEA	IVANOV_MUTATED_IN_COLON_CANCER
10	2e−03	46 / 6929	Lymp	HOPP_Txn_elongation
11	2e−03	2 / 13	BP	zinc II ion transmembrane transport
12	2e−03	2 / 13	MF	zinc ion transmembrane transporter activity
13	2e−03	5 / 186	miRN	hsa−miR−586
14	2e−03	2 / 14	MF	ferrous iron binding
15	2e−03	4 / 112	GSEA	KEGG_LYSOSOME
16	2e−03	3 / 54	miRN	hsa−miR−518d−5p
17	2e−03	3 / 54	miRN	hsa−miR−520c−5p
18	2e−03	2 / 15	MF	cation transmembrane transporter activity
19	3e−03	6 / 288	GSEA	WEST_ADRENOCORTICAL_TUMOR_UP
20	3e−03	7 / 391	miRN	hsa−miR−519a
21	3e−03	8 / 506	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
22	3e−03	52 / 8415	Colon	Quies3_Colon
23	3e−03	4 / 124	GSEA	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN
24	3e−03	2 / 17	CC	costamere
25	3e−03	2 / 17	GSEA	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURF
26	3e−03	3 / 60	miRN	hsa−miR−296−3p
27	4e−03	3 / 65	miRN	hsa−miR−30e*
28	4e−03	40 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
29	4e−03	7 / 424	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
30	4e−03	2 / 21	CC	clathrin adaptor complex
31	5e−03	2 / 22	BP	regulation of defense response to virus by virus
32	5e−03	2 / 22	GSEA	REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISE
33	5e−03	2 / 23	BP	positive regulation of ATPase activity
34	5e−03	13 / 1237	BP	metabolic process
35	6e−03	4 / 155	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
36	7e−03	2 / 27	BP	phospholipid biosynthetic process
37	7e−03	3 / 83	miRN	hsa−miR−30a*
38	7e−03	3 / 83	GSEA	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
39	8e−03	2 / 28	GSEA	BILANGES_RAPAMYCIN_SENSITIVE_GENES
40	8e−03	2 / 29	GSEA	DANG_MYC_TARGETS_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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	1 / 14	LIU_COMMON_CANCER_GENES
2	0.07	1 / 16	GENTLES_modul16
3	0.13	1 / 29	KUIPER_MM good survival
4	0.21	1 / 48	KUIPER_MM poor survival
5	0.42	2 / 298	SPANG_BCL6−index2
6	0.42	1 / 113	PanCan_Driver_Gene_geneset_nanostring
7	0.58	2 / 401	Lembcke_Colonic Inflammation
8	0.58	1 / 180	SPANG_LPS−index2
9	0.68	2 / 489	Lembcke_Normal vs Adenoma
10	0.85	0 / 14	LIU_PROSTATE_CANCER_DN
11	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
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 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.00	0 / 12	LIU_BREAST_CANCER
16	1.00	0 / 14	LIU_LIVER_CANCER
17	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
18	1.00	0 / 15	WANG_ER_UP
19	1.00	0 / 5	WANG_ER_DN
20	1.00	0 / 16	WOLFER_overlap genes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	58 / 8580	TxWk_Colon
2	1e−04	58 / 9027	Tx_Colon
3	3e−03	52 / 8415	Quies3_Colon
4	2e−02	54 / 9482	TssA_Colon
5	6e−02	1 / 13	TCGA−CRC_less−agressive−disease−markers
6	7e−02	1 / 15	Budinska_B_Lower crypt−like_UP
7	7e−02	41 / 7203	TssF_Colon
8	2e−01	3 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
9	2e−01	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
10	2e−01	16 / 2698	EnhA_Colon
11	3e−01	16 / 2798	TxEnhG1_Colon
12	3e−01	3 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	3e−01	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
14	3e−01	31 / 5880	TssD2_Colon
15	4e−01	6 / 1079	ZNF_Colon
16	4e−01	1 / 117	Marisa_CRC−cluster−b
17	5e−01	19 / 3812	TssD1_Colon
18	5e−01	4 / 739	TxEnhG2_Colon
19	5e−01	50 / 10290	TssWk_Colon
20	5e−01	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	21 / 1693	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
2	1e−03	4 / 92	JAZAG_TGFB1_SIGNALING_UP
3	1e−03	2 / 12	IVANOV_MUTATED_IN_COLON_CANCER
4	2e−03	4 / 112	KEGG_LYSOSOME
5	3e−03	6 / 288	WEST_ADRENOCORTICAL_TUMOR_UP
6	3e−03	8 / 506	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
7	3e−03	4 / 124	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN
8	3e−03	2 / 17	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFAC
9	4e−03	7 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
10	5e−03	2 / 22	REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEAS
11	6e−03	4 / 155	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
12	7e−03	3 / 83	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
13	8e−03	2 / 28	BILANGES_RAPAMYCIN_SENSITIVE_GENES
14	8e−03	2 / 29	DANG_MYC_TARGETS_DN
15	9e−03	6 / 372	FOSTER_TOLERANT_MACROPHAGE_DN
16	1e−02	2 / 32	APPEL_IMATINIB_RESPONSE
17	1e−02	6 / 386	DELACROIX_RAR_BOUND_ES
18	1e−02	3 / 96	MARKEY_RB1_CHRONIC_LOF_UP
19	1e−02	2 / 34	SPIRA_SMOKERS_LUNG_CANCER_UP
20	1e−02	2 / 36	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	46 / 6929	HOPP_Txn_elongation
2	0.009	35 / 5184	HOPP_Txn_transition
3	0.014	46 / 7592	HOPP_Active_promoter
4	0.044	34 / 5538	HOPP_Weak_txn
5	0.047	42 / 7209	HOPP_Weak_promoter
6	0.074	1 / 16	ROSOLOWSKI_red UP
7	0.093	2 / 107	SPANG_LPS 6hrs UP
8	0.148	32 / 5693	HOPP_Weak_enhancer
9	0.150	3 / 280	SPANG_CD40 6hrs UP
10	0.228	35 / 6564	HOPP_Strong_enhancer
11	0.339	1 / 86	ROSOLOWSKI_red total
12	0.348	1 / 89	ROSOLOWSKI_blue total
13	0.494	11 / 2211	HOPP_Repetitive
14	0.532	6 / 1218	SPANG_BCR UP
15	0.581	12 / 2563	HOPP_Heterochrom
16	0.635	5 / 1128	SPANG_BCR DN
17	0.697	1 / 247	ZHANG_DLBCL mutated
18	0.710	1 / 256	SPANG_IL21 DN
19	0.727	1 / 268	SPANG_IL21 UP
20	0.759	1 / 294	TARTE_Plasmablast signature

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	1 / 11	WIRTH_Globus pallidus
2	0.06	1 / 13	WIRTH_B−cells
3	0.50	2 / 350	WIRTH_Immune system
4	0.66	1 / 225	PALMER_Granulocytes signature up
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

BP

Rank	p−value	#in/all	Geneset
1	7e−05	3 / 17	zinc II ion transport
2	1e−03	2 / 10	positive regulation of cellular metabolic process
3	2e−03	2 / 13	zinc II ion transmembrane transport
4	5e−03	2 / 22	regulation of defense response to virus by virus
5	5e−03	2 / 23	positive regulation of ATPase activity
6	5e−03	13 / 1237	metabolic process
7	7e−03	2 / 27	phospholipid biosynthetic process
8	1e−02	2 / 37	intracellular receptor signaling pathway
9	1e−02	2 / 37	triglyceride biosynthetic process
10	2e−02	2 / 41	protein peptidyl−prolyl isomerization
11	2e−02	2 / 43	cellular response to growth factor stimulus
12	2e−02	2 / 43	rhythmic process
13	2e−02	2 / 45	regulation of circadian rhythm
14	2e−02	2 / 50	steroid hormone mediated signaling pathway
15	3e−02	2 / 53	protein homotetramerization
16	3e−02	2 / 56	response to glucose
17	3e−02	2 / 58	cation transmembrane transport
18	3e−02	2 / 58	protein ubiquitination involved in ubiquitin−dependent protein catabolic process
19	3e−02	2 / 59	smoothened signaling pathway
20	4e−02	2 / 63	dolichol−linked oligosaccharide biosynthetic process

CC

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 31	membrane coat
2	3e−03	2 / 17	costamere
3	4e−03	2 / 21	clathrin adaptor complex
4	3e−02	3 / 144	postsynaptic membrane
5	5e−02	5 / 412	lysosome
6	6e−02	1 / 12	node of Ranvier
7	6e−02	1 / 13	COPI vesicle coat
8	6e−02	1 / 13	dystrophin−associated glycoprotein complex
9	6e−02	1 / 13	phagocytic cup
10	6e−02	1 / 14	clathrin−coated vesicle membrane
11	7e−02	7 / 747	nucleolus
12	7e−02	1 / 16	anchored component of plasma membrane
13	8e−02	1 / 18	protein phosphatase type 2A complex
14	9e−02	1 / 19	calcium channel complex
15	9e−02	1 / 19	inclusion body
16	9e−02	3 / 223	lysosomal membrane
17	9e−02	2 / 106	trans−Golgi network
18	1e−01	17 / 2576	membrane
19	1e−01	1 / 24	polysome
20	1e−01	1 / 25	clathrin−coated endocytic vesicle membrane

Disease

Rank	p−value	#in/all	Geneset
1	0.3	3 / 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	

HM

Rank	p−value	#in/all	Geneset
1	0.02	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.05	3 / 174	HALLMARK_HEME_METABOLISM
3	0.06	3 / 188	HALLMARK_ADIPOGENESIS
4	0.07	3 / 196	HALLMARK_MTORC1_SIGNALING
5	0.07	2 / 91	HALLMARK_PROTEIN_SECRETION
6	0.19	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
7	0.21	2 / 176	HALLMARK_HYPOXIA
8	0.21	2 / 181	HALLMARK_P53_PATHWAY
9	0.25	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	0.36	1 / 94	HALLMARK_ANDROGEN_RESPONSE
11	0.37	1 / 95	HALLMARK_SPERMATOGENESIS
12	0.37	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	0.48	1 / 137	HALLMARK_UV_RESPONSE_DN
14	0.49	1 / 140	HALLMARK_APOPTOSIS
15	0.54	1 / 162	HALLMARK_COMPLEMENT
16	0.57	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
17	0.59	1 / 183	HALLMARK_GLYCOLYSIS
18	0.61	1 / 196	HALLMARK_G2M_CHECKPOINT
19	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS

MF

Rank	p−value	#in/all	Geneset
1	0.002	2 / 13	zinc ion transmembrane transporter activity
2	0.002	2 / 14	ferrous iron binding
3	0.002	2 / 15	cation transmembrane transporter activity
4	0.012	2 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
5	0.016	2 / 41	peptidyl−prolyl cis−trans isomerase activity
6	0.020	2 / 46	steroid hormone receptor activity
7	0.037	5 / 386	nucleotide binding
8	0.044	5 / 405	ligase activity
9	0.045	2 / 71	chaperone binding
10	0.047	1 / 10	cholesterol transporter activity
11	0.048	7 / 695	transmembrane transporter activity
12	0.051	1 / 11	metal ion transmembrane transporter activity
13	0.051	1 / 11	vinculin binding
14	0.055	2 / 79	protein transporter activity
15	0.056	1 / 12	alpha−actinin binding
16	0.056	1 / 12	poly(A) binding
17	0.056	1 / 12	protein methyltransferase activity
18	0.060	1 / 13	ATPase activator activity
19	0.060	1 / 13	mannosyltransferase activity
20	0.062	3 / 189	methyltransferase activity

TF

Rank	p−value	#in/all	Geneset
1	0.04	1 / 9	MYC_Targets DOWN
2	0.18	12 / 1878	ICGC_Cebpbsc150_targets
3	0.19	11 / 1701	HEBENSTREIT_high expression TF
4	0.22	13 / 2137	ICGC_SrfV0416101_targets
5	0.23	22 / 3924	ICGC_Zeb1_targets
6	0.23	5 / 690	ICGC_Atf3_targets
7	0.25	12 / 2013	ICGC_Bcl11_targets
8	0.28	22 / 4054	ICGC_Egr1_targets
9	0.32	12 / 2136	ICGC_GabpPcr2_targets
10	0.33	7 / 1171	KIM_MYC targets
11	0.34	8 / 1383	ICGC_Six5_targets
12	0.35	24 / 4617	ICGC_Tcf12_targets
13	0.37	8 / 1418	ICGC_Ets1_targets
14	0.38	24 / 4682	ICGC_Pol24_targets
15	0.39	24 / 4689	ICGC_Taf1_targets
16	0.39	25 / 4909	ICGC_Stat5_targets
17	0.39	24 / 4706	ICGC_Sp1_targets
18	0.40	22 / 4314	ICGC_Ebfsc137065_targets
19	0.42	14 / 2714	ICGC_Irf4_targets
20	0.43	15 / 2927	ICGC_Rad21_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	14 / 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	

Brain

Rank	p−value	#in/all	Geneset
1	0.004	40 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.011	9 / 769	Overlap_fetal_midbrain_ZNF
3	0.019	52 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	0.024	53 / 9330	Overlap_fetal_midbrain_ReprPC
5	0.053	6 / 564	Mid_Frontal_Lobe_EnhP
6	0.093	49 / 9013	Overlap_fetal_midbrain_K9K27me3
7	0.110	8 / 1013	Fetal_TssP
8	0.165	50 / 9528	Overlap_fetal_midbrain_Quies
9	0.175	2 / 158	Overlap_fetal_midbrain_Het
10	0.206	18 / 3081	Mid_Frontal_Lobe_ZNF
11	0.235	7 / 1050	Fetal_EnhP
12	0.282	14 / 2462	Mid_Frontal_Lobe_HetRpts
13	0.300	2 / 229	Mid_Frontal_Lobe_TxTrans
14	0.303	5 / 765	Mid_Frontal_Lobe_Het
15	0.304	6 / 953	Fetal_Enh
16	0.326	11 / 1949	Fetal_TssF
17	0.384	4 / 656	Overlap_fetal_midbrain_EnhP
18	0.451	6 / 1122	Fetal_K9K27me3
19	0.473	3 / 534	Mid_Frontal_Lobe_EnhG
20	0.500	2 / 349	Fetal_ZNF

Chr

Rank	p−value	#in/all	Geneset
1	0.09	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
2	0.13	5 / 558	Chr 4
3	0.18	4 / 462	Chr 14
4	0.19	4 / 469	Chr 8
5	0.21	6 / 838	Chr 3
6	0.30	4 / 576	Chr 9
7	0.38	3 / 465	Chr 15
8	0.52	1 / 151	Chr 21
9	0.52	5 / 993	Chr 2
10	0.54	4 / 801	Chr 11
11	0.56	5 / 1037	Chr 19
12	0.61	3 / 649	Chr 16
13	0.64	3 / 687	Chr 6
14	0.65	3 / 696	Chr 5
15	0.66	1 / 221	Chr 18
16	0.72	1 / 262	Chr 13
17	0.77	3 / 840	Chr 17
18	0.80	1 / 335	Chr 22
19	0.85	2 / 689	Chr 7
20	0.89	2 / 775	Chr 12

Glio

Rank	p−value	#in/all	Geneset
1	0.02	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.04	2 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
3	0.11	1 / 25	Shaw_down_in_1p19q
4	0.13	1 / 29	shaw_responders_down_in_oligo_glioma
5	0.16	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	0.20	1 / 47	mature astrocytes
7	0.21	1 / 49	OL vs. MOG− OL
8	0.22	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
9	0.28	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.28	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	0.29	1 / 71	Weller_LGG_gradeII−vs−III_DOWN
12	0.30	1 / 75	Weller_LGG_A_vs_O_DOWN
13	0.39	1 / 103	GIEZELT_GBM_WT_up_VS_mut
14	0.47	2 / 332	Up
15	0.78	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
16	0.82	1 / 356	Down_a
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

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	0.001	4 / 102	hsa−miR−1301
2	0.002	5 / 186	hsa−miR−586
3	0.002	3 / 54	hsa−miR−518d−5p
4	0.002	3 / 54	hsa−miR−520c−5p
5	0.003	7 / 391	hsa−miR−519a
6	0.003	3 / 60	hsa−miR−296−3p
7	0.004	3 / 65	hsa−miR−30e*
8	0.007	3 / 83	hsa−miR−30a*
9	0.009	6 / 378	hsa−miR−454
10	0.010	3 / 94	hsa−miR−526a
11	0.011	4 / 179	hsa−miR−582−5p
12	0.011	3 / 96	hsa−miR−513b
13	0.013	6 / 405	hsa−miR−519c−3p
14	0.016	6 / 426	hsa−miR−519d
15	0.018	5 / 318	hsa−miR−340
16	0.019	7 / 569	hsa−miR−20b
17	0.019	3 / 118	hsa−miR−509−3p
18	0.019	6 / 443	hsa−miR−19a
19	0.020	6 / 447	hsa−miR−130b
20	0.020	4 / 217	hsa−miR−181d

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 11	VAQUERIZAS_Fetal liver
2	0.08	1 / 17	VAQUERIZAS_Pituitary
3	0.12	1 / 26	VAQUERIZAS_Liver
4	0.17	1 / 40	VAQUERIZAS_Thyroid
5	0.19	1 / 45	VAQUERIZAS_Uterus
6	0.50	1 / 143	VAQUERIZAS_General
7	1.00	0 / 36	VAQUERIZAS_Fetal brain
8	1.00	0 / 41	VAQUERIZAS_Placenta
9	1.00	0 / 33	VAQUERIZAS_Prostate
10	1.00	0 / 29	VAQUERIZAS_Smooth muscle
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 / 59	VAQUERIZAS_Whole blood
16	1.00	0 / 7	VAQUERIZAS_Appendix
17	1.00	0 / 29	VAQUERIZAS_Fetal lung
18	1.00	0 / 58	VAQUERIZAS_Lung
19	1.00	0 / 16	VAQUERIZAS_Pancreas
20	1.00	0 / 23	VAQUERIZAS_Trachea

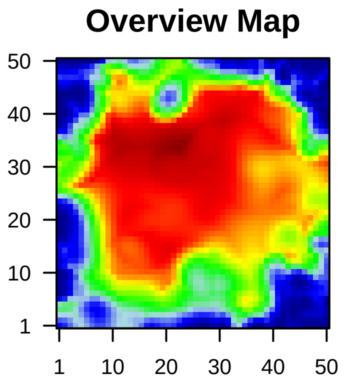
Underexpression Spots

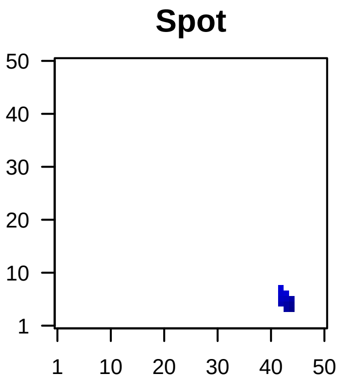
Spot Summary: j

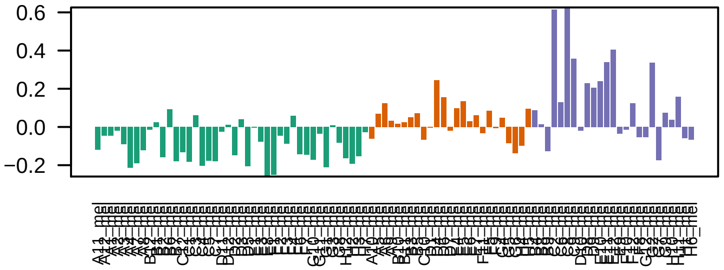
metagenes = 11
genes = 79

<r> metagenes = 0.95
<r> genes = 0.17
beta: r2= 1.59 / log p= −Inf

samples with spot = 10 (10.9 %)
MSC2 : 1 (4 %)
MSC3 : 9 (36 %)


Overview Map


Spot

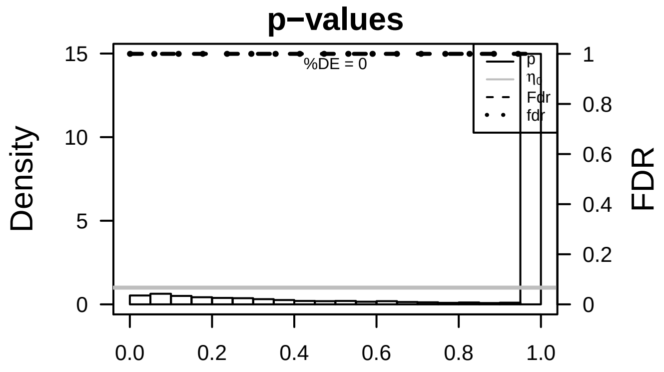


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	AP2A2	1.86	−0.65	0.42	AP2A2	adaptor−related protein complex 2, alpha 2 subunit [Source:H
2	TIGD6	1.81	−0.15	0.51	TIGD6	tigger transposable element derived 6 [Source:HGNC Symbo
3	HSPG2	1.69	−0.27	0.33	HSPG2	heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:H
4	PNPLA3	1.68	−0.22	0.36	PNPLA3	patatin−like phospholipase domain containing 3 [Source:HGN
5	USP45	1.66	−0.5	0.31	USP45	ubiquitin specific peptidase 45 [Source:HGNC Symbol;Acc:H
6	TNIP1	1.59	−0.28	0.43	TNIP1	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:HG
7	EHD2	1.48	−0.17	0.56	EHD2	EH−domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
8	RUNX1	1.45	−0.83	0.41	RUNX1	runt−related transcription factor 1 [Source:HGNC Symbol;Acc
9	HIST2H2AA4	1.39	−0.5	0.47	HIST2H2AA4	histone cluster 2, H2aa4 [Source:HGNC Symbol;Acc:HGNC:
10	LRRK1	1.38	−0.11	0.56	LRRK1	leucine−rich repeat kinase 1 [Source:HGNC Symbol;Acc:HGN
11	PES1	1.38	−0.54	0.31	PES1	pescadillo ribosomal biogenesis factor 1 [Source:HGNC Sym
12	RTN2	1.37	−0.21	0.42	RTN2	reticulon 2 [Source:HGNC Symbol;Acc:HGNC:10468]
13	GATAD1	1.37	−0.48	0.36	GATAD1	GATA zinc finger domain containing 1 [Source:HGNC Symbol
14	INTS6	1.35	−0.71	0.24	INTS6	integrator complex subunit 6 [Source:HGNC Symbol;Acc:HGN
15	KIAA0195	1.34	−0.77	0.25	KIAA0195	KIAA0195 [Source:HGNC Symbol;Acc:HGNC:28983]
16	SMG5	1.31	−0.73	0.41	SMG5	SMG5 nonsense mediated mRNA decay factor [Source:HGN
17	FBXL20	1.29	−0.54	0.49	FBXL20	F−box and leucine−rich repeat protein 20 [Source:HGNC Syn
18	ACBD4	1.27	−0.15	0.4	ACBD4	acyl−CoA binding domain containing 4 [Source:HGNC Symbo
19	ACCS	1.26	−0.14	0.58	ACCS	1−aminocyclopropane−1−carboxylate synthase homolog (Ara
20	B9D1	1.24	−0.85	0.26	B9D1	B9 protein domain 1 [Source:HGNC Symbol;Acc:HGNC:2412

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	9 / 396	GSEA	JOHNSTONE_PARVB_TARGETS_3_UP
2	3e−04	18 / 1383	TF	ICGC_Six5_targets
3	3e−04	6 / 170	miRN	hsa−miR−7
4	4e−04	2 / 6	Lympl	DAVE_MHCCII BL DN
5	6e−04	2 / 7	GSEA	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY
6	8e−04	3 / 35	BP	cellular response to starvation
7	1e−03	2 / 9	GSEA	TURJANSKI_MAPK14_TARGETS
8	1e−03	27 / 2836	TF	ICGC_BatfPcr1_targets
9	1e−03	2 / 10	CC	MHC class I protein complex
10	1e−03	3 / 41	GSEA	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS
11	2e−03	3 / 43	GSEA	CAMPS_COLON_CANCER_COPY_NUMBER_DN
12	2e−03	5 / 169	miRN	hsa−miR−374b
13	2e−03	2 / 13	BP	DNA damage response, signal transduction by p53 class mediator
14	2e−03	3 / 48	Canc	KUIPER_MM poor survival
15	3e−03	2 / 15	GSEA	GALE_APL_WITH_FLT3_MUTATED_DN
16	3e−03	2 / 15	GSEA	GEISS_RESPONSE_TO_DSRNA_DN
17	3e−03	5 / 182	miRN	hsa−miR−374a
18	3e−03	2 / 16	BP	positive regulation of T cell mediated cytotoxicity
19	3e−03	2 / 16	GSEA	KIM_MYCL1_AMPLIFICATION_TARGETS_DN
20	3e−03	2 / 16	GSEA	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP
21	3e−03	3 / 57	GSEA	ROSS_AML_WITH_PML_RARA_FUSION
22	4e−03	4 / 118	MF	carbohydrate binding
23	4e−03	2 / 17	CC	basal lamina
24	4e−03	2 / 17	GSEA	NUMATA_CSF3_SIGNALING_VIA_STAT3
25	4e−03	3 / 59	GSEA	CADWELL_ATG16L1_TARGETS_UP
26	4e−03	2 / 18	Lifesty	DUMEAUX_High bmi enriched genes
27	4e−03	2 / 18	GSEA	KEGG_GRAFT_VERSUS_HOST_DISEASE
28	4e−03	4 / 123	GSEA	JOHNSTONE_PARVB_TARGETS_2_UP
29	4e−03	3 / 61	miRN	hsa−miR−514
30	4e−03	3 / 62	GSEA	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP
31	5e−03	2 / 19	GSEA	KEGG_ALLOGRAFT_REJECTION
32	5e−03	2 / 19	GSEA	REACTOME_HS_GAG_DEGRADATION
33	5e−03	2 / 19	GSEA	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_F
34	5e−03	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
35	5e−03	3 / 64	GSEA	REACTOME_AMYLOIDS
36	5e−03	2 / 20	GSEA	KEGG_AUTOIMMUNE_THYROID_DISEASE
37	5e−03	2 / 20	GSEA	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
38	6e−03	34 / 4314	TF	ICGC_Ebfsc137065_targets
39	6e−03	3 / 68	GSEA	SANA_TNF_SIGNALING_UP
40	6e−03	3 / 69	miRN	hsa−miR−873


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	8e−04	3 / 35	cellular response to starvation
2	2e−03	2 / 13	DNA damage response, signal transduction by p53 class mediator
3	3e−03	2 / 16	positive regulation of T cell mediated cytotoxicity
4	7e−03	2 / 23	glycosaminoglycan catabolic process
5	1e−02	2 / 28	synapse organization
6	1e−02	2 / 29	negative regulation of I−kappaB kinase/NF−kappaB signaling
7	1e−02	4 / 162	ribosome biogenesis
8	1e−02	2 / 34	glycosaminoglycan biosynthetic process
9	2e−02	2 / 39	positive regulation of neuron apoptotic process
10	2e−02	2 / 39	retinoid metabolic process
11	2e−02	2 / 46	chondroitin sulfate metabolic process
12	3e−02	2 / 48	cellular protein localization
13	3e−02	2 / 49	protein deubiquitination
14	3e−02	2 / 49	type I interferon signaling pathway
15	3e−02	2 / 50	antigen processing and presentation
16	3e−02	2 / 53	regulation of immune response
17	4e−02	2 / 57	protein localization
18	4e−02	2 / 59	positive regulation of peptidyl−tyrosine phosphorylation
19	4e−02	8 / 737	positive regulation of transcription from RNA polymerase II promoter
20	4e−02	2 / 62	phototransduction, visible light

Brain

Rank	p−value	#in/all	Geneset
1	0.02	41 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.06	37 / 163	Fetal_ReprPC
3	0.19	20 / 3081	Mid_Frontal_Lobe_ZNF
4	0.22	3 / 304	Fetal_Het
5	0.28	51 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	0.31	1 / 69	Overlap_fetal_midbrain_Tx
7	0.33	3 / 383	Fetal_Tx
8	0.35	4 / 564	Mid_Frontal_Lobe_EnhP
9	0.36	50 / 9013	Overlap_fetal_midbrain_K9K27me3
10	0.45	6 / 1013	Fetal_TssP
11	0.61	49 / 9330	Overlap_fetal_midbrain_ReprPC
12	0.61	5 / 989	Mid_Frontal_Lobe_Quies
13	0.65	6 / 1236	Mid_Frontal_Lobe_ReprPCWk
14	0.67	5 / 1050	Fetal_EnhP
15	0.68	12 / 2462	Mid_Frontal_Lobe_HetRpts
16	0.70	3 / 668	Mid_Frontal_Lobe_Enh
17	0.71	1 / 229	Mid_Frontal_Lobe_TxTrans
18	0.78	2 / 534	Mid_Frontal_Lobe_EnhG
19	0.80	3 / 786	Fetal_EnhG
20	0.83	3 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	3 / 48	KUIPER_MM poor survival
2	0.005	0 / 14	LIU_PROSTATE_CANCER_DN
3	0.022	3 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.028	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.069	0 / 12	LIU_PROSTATE_CANCER_UP
6	0.071	2 / 82	PanCan_TXmisReg_geneset_nanostring
7	0.071	3 / 180	SPANG_LPS−index2
8	0.165	4 / 401	Lembcke_Colonic Inflammation
9	0.192	1 / 40	PanCan_HK_geneset_nanostring
10	0.212	3 / 298	SPANG_BCL6−index2
11	0.278	1 / 61	PanCan_Wnt_geneset_nanostring
12	0.297	0 / 14	LIU_COMMON_CANCER_GENES
13	0.474	1 / 120	PanCan_CC+Apop_geneset_nanostring
14	0.477	1 / 121	PanCan_MAPK_geneset_nanostring
15	0.553	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	0.567	1 / 156	PanCan_PI3K_geneset_nanostring
17	0.739	2 / 489	Lembcke_Normal vs Adenoma
18	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
19	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
20	1.000	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.001	2 / 10	MHC class I protein complex
2	0.004	2 / 17	basal lamina
3	0.006	2 / 22	integral component of lumenal side of endoplasmic reticulum membrane
4	0.007	3 / 73	basement membrane
5	0.014	2 / 34	ER to Golgi transport vesicle membrane
6	0.026	2 / 47	phagocytic vesicle membrane
7	0.028	2 / 49	Golgi lumen
8	0.031	2 / 52	caveola
9	0.039	5 / 352	cell surface
10	0.041	2 / 60	lysosomal lumen
11	0.045	8 / 747	nucleolus
12	0.053	3 / 159	extracellular matrix
13	0.057	1 / 11	interstitial matrix
14	0.066	2 / 79	nucleosome
15	0.067	1 / 13	integrator complex
16	0.067	1 / 13	TCTN−B9D complex
17	0.072	1 / 14	Cul4−RING E3 ubiquitin ligase complex
18	0.074	2 / 84	PML body
19	0.082	1 / 16	excitatory synapse
20	0.086	2 / 92	early endosome membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.02	8 / 649	Chr 16
2	0.08	8 / 840	Chr 17
3	0.16	3 / 262	Chr 13
4	0.17	11 / 1500	Chr 1
5	0.25	6 / 801	Chr 11
6	0.30	5 / 689	Chr 7
7	0.50	4 / 687	Chr 6
8	0.54	2 / 335	Chr 22
9	0.56	1 / 151	Chr 21
10	0.63	2 / 398	Chr 20
11	0.65	5 / 1037	Chr 19
12	0.71	2 / 465	Chr 15
13	0.72	3 / 696	Chr 5
14	0.78	4 / 993	Chr 2
15	0.80	2 / 551	Chr X
16	0.83	3 / 838	Chr 3
17	0.95	1 / 552	Chr 10
18	0.95	1 / 558	Chr 4
19	0.99	1 / 775	Chr 12
20	1.00	0 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.08	34 / 5155	EnhWk1_Colon
2	0.08	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
3	0.08	1 / 16	Vilar_non−hypermutated−in−CRC
4	0.09	1 / 17	Vilar_mutated−in−CRC−CamP
5	0.10	51 / 8415	Quies3_Colon
6	0.10	2 / 102	Marisa_CRC−cluster−d
7	0.13	51 / 8580	TxWk_Colon
8	0.14	1 / 29	Marisa_CRC−cluster−c
9	0.15	53 / 9027	Tx_Colon
10	0.19	5 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	0.20	4 / 436	K9acLow_Colon
12	0.22	2 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
13	0.23	35 / 5880	TssD2_Colon
14	0.26	17 / 2698	EnhA_Colon
15	0.27	9 / 1317	EnhP_Colon
16	0.28	23 / 3812	TssD1_Colon
17	0.31	41 / 7203	TssF_Colon
18	0.32	53 / 9482	TssA_Colon
19	0.36	5 / 739	TxEnhG2_Colon
20	0.36	3 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 20	BCHETNIA_EBM−DM up
2	0.5	2 / 294	GUDJ_psoriasis down
3	1.0	0 / 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	0.05	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
2	0.06	2 / 75	Weller_LGG_A_vs_O_DOWN
3	0.07	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
4	0.22	1 / 47	Vishal_subnetwork signature of survival in GBM
5	0.26	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
6	0.26	3 / 332	Up
7	0.30	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	0.32	1 / 72	laffaire_hypermeth_LGG_vs_control
9	0.32	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	0.33	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
11	0.41	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
12	0.41	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
13	0.49	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	0.82	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
15	0.83	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
16	0.85	1 / 356	Down_a
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	9 / 396	JOHNSTONE_PARVB_TARGETS_3_UP
2	6e−04	2 / 7	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY
3	1e−03	2 / 9	TURJANSKI_MAPK14_TARGETS
4	1e−03	3 / 41	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS
5	2e−03	3 / 43	CAMPS_COLON_CANCER_COPY_NUMBER_DN
6	3e−03	2 / 15	GALE_APL_WITH_FLT3_MUTATED_DN
7	3e−03	2 / 15	GEISS_RESPONSE_TO_DSRNA_DN
8	3e−03	2 / 16	KIM_MYCL1_AMPLIFICATION_TARGETS_DN
9	3e−03	2 / 16	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP
10	3e−03	3 / 57	ROSS_AML_WITH_PML_RARA_FUSION
11	4e−03	2 / 17	NUMATA_CSF3_SIGNALING_VIA_STAT3
12	4e−03	3 / 59	CADWELL_ATG16L1_TARGETS_UP
13	4e−03	2 / 18	KEGG_GRAFT_VERSUS_HOST_DISEASE
14	4e−03	4 / 123	JOHNSTONE_PARVB_TARGETS_2_UP
15	4e−03	3 / 62	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP
16	5e−03	2 / 19	KEGG_ALLOGRAFT_REJECTION
17	5e−03	2 / 19	REACTOME_HS_GAG_DEGRADATION
18	5e−03	2 / 19	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEI
19	5e−03	0 / 14	LIU_PROSTATE_CANCER_DN
20	5e−03	3 / 64	REACTOME_AMYLOIDS

HM

Rank	p−value	#in/all	Geneset
1	0.2	2 / 137	HALLMARK_UV_RESPONSE_DN
2	0.2	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.2	2 / 146	HALLMARK_DNA_REPAIR
4	0.2	2 / 165	HALLMARK_MYOGENESIS
5	0.2	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
6	0.2	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.2	1 / 53	HALLMARK_TGF_BETA_SIGNALING
8	0.3	2 / 181	HALLMARK_P53_PATHWAY
9	0.3	1 / 57	HALLMARK_MYC_TARGETS_V2
10	0.3	2 / 195	HALLMARK_MITOTIC_SPINDLE
11	0.3	2 / 196	HALLMARK_MTORC1_SIGNALING
12	0.4	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	0.4	1 / 91	HALLMARK_BILE_ACID_METABOLISM
14	0.4	1 / 93	HALLMARK_PEROXISOME
15	0.4	1 / 94	HALLMARK_ANDROGEN_RESPONSE
16	0.5	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
17	0.6	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	0.6	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
19	0.6	1 / 176	HALLMARK_HYPOXIA
20	0.6	1 / 183	HALLMARK_GLYCOLYSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.004	2 / 18	DUMEAUX_High bmi enriched genes
2	1.000	0 / 62	DUMEAUX_Smoking enriched genes
3	1.000	0 / 10	DUMEAUX_Smoking literature genes up
4	1.000	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.000	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.000	0 / 5	DUMEAUX_Estrogen related in non 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 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Women normal BMI literature genes up
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	4e−04	2 / 6	DAVE_MHCCII BL DN
2	7e−02	17 / 2211	HOPP_Repetitive
3	8e−02	10 / 1128	SPANG_BCR DN
4	1e−01	43 / 6929	HOPP_Txn_elongation
5	1e−01	1 / 29	Subero_DLBCL_hypo_meth
6	1e−01	1 / 30	Subero_INT_hypo_meth
7	1e−01	40 / 6564	HOPP_Strong_enhancer
8	2e−01	32 / 5184	HOPP_Txn_transition
9	2e−01	3 / 275	TARTE_Mature plasma cell signature
10	2e−01	1 / 43	LENZ_Stromal signature 2
11	3e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
12	4e−01	1 / 89	ROSOLOWSKI_blue total
13	4e−01	2 / 247	ZHANG_DLBCL_mutated
14	5e−01	1 / 129	DAVE_BL−vs−DLBCL
15	6e−01	2 / 410	SPANG_CD40 6hrs DN
16	7e−01	39 / 7592	HOPP_Active_promoter
17	7e−01	28 / 5538	HOPP_Weak_txn
18	7e−01	1 / 212	LENZ_Stromal signature 1
19	8e−01	9 / 2188	HOPP_Poised_promoter
20	9e−01	14 / 3396	HOPP_Repressed

MF

Rank	p−value	#in/all	Geneset
1	0.004	4 / 118	carbohydrate binding
2	0.006	3 / 71	ubiquitin−specific protease activity
3	0.007	2 / 23	rRNA binding
4	0.007	2 / 24	histone acetyltransferase binding
5	0.008	2 / 26	peptide antigen binding
6	0.009	2 / 27	protein phosphatase 2A binding
7	0.011	2 / 30	RNA polymerase II transcription factor binding
8	0.020	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
9	0.031	2 / 52	RNA polymerase II distal enhancer sequence−specific DNA binding transcript
10	0.033	2 / 54	damaged DNA binding
11	0.038	2 / 58	cysteine−type peptidase activity
12	0.043	2 / 62	protein phosphatase binding
13	0.044	2 / 63	RNA polymerase II transcription regulatory region sequence−specific DNA bir
14	0.047	2 / 65	protease binding
15	0.049	5 / 373	protein heterodimerization activity
16	0.052	1 / 10	hedgehog receptor activity
17	0.052	1 / 10	ubiquitin−ubiquitin ligase activity
18	0.057	1 / 11	ribonuclease activity
19	0.062	1 / 12	neurexin family protein binding
20	0.066	2 / 79	protein transporter activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	6 / 170	hsa−miR−7
2	2e−03	5 / 169	hsa−miR−374b
3	3e−03	5 / 182	hsa−miR−374a
4	4e−03	3 / 61	hsa−miR−514
5	6e−03	3 / 69	hsa−miR−873
6	7e−03	4 / 140	hsa−miR−522
7	8e−03	2 / 25	hsa−miR−663
8	9e−03	4 / 153	hsa−miR−200c
9	9e−03	2 / 27	hsa−miR−521
10	1e−02	3 / 82	hsa−miR−630
11	1e−02	4 / 157	hsa−miR−450b−5p
12	1e−02	2 / 29	hsa−miR−1225−3p
13	1e−02	5 / 263	hsa−miR−92b
14	1e−02	5 / 268	hsa−miR−363
15	2e−02	2 / 36	hsa−miR−644
16	2e−02	3 / 100	hsa−miR−574−5p
17	2e−02	4 / 191	hsa−miR−641
18	2e−02	3 / 107	hsa−miR−146b−5p
19	2e−02	5 / 296	hsa−miR−25
20	2e−02	3 / 110	hsa−miR−146a

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	3e−04	18 / 1383	ICGC_Six5_targets
2	1e−03	27 / 2836	ICGC_BatfPcr1_targets
3	6e−03	34 / 4314	ICGC_Ebfsc137065_targets
4	1e−02	39 / 5374	ICGC_Pax5_targets
5	2e−02	1 / 3	MYC_Tumor supressor genes UP
6	2e−02	34 / 4617	ICGC_Tcf12_targets
7	2e−02	34 / 4689	ICGC_Taf1_targets
8	2e−02	37 / 5219	ICGC_Tcf3_targets
9	2e−02	38 / 5408	ICGC_Pou2_targets
10	2e−02	20 / 2391	ICGC_Pbx3_targets
11	2e−02	22 / 2714	ICGC_Irf4_targets
12	2e−02	30 / 4054	ICGC_Egr1_targets
13	3e−02	1 / 5	MYC_Apoptosis UP
14	3e−02	1 / 5	MYC_TF and cofactors
15	3e−02	18 / 2137	ICGC_SrfV0416101_targets
16	3e−02	29 / 3966	ICGC_Pu1_targets
17	3e−02	33 / 4682	ICGC_Pol24_targets
18	4e−02	16 / 1878	ICGC_Cebpbsc150_targets
19	4e−02	1 / 8	MYC_Cell cycle UP
20	5e−02	1 / 9	MYC_DNA repair UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 37	VAQUERIZAS_Thymus
2	0.06	1 / 11	VAQUERIZAS_Fetal liver
3	0.08	1 / 15	VAQUERIZAS_Fetal thyroid
4	0.08	1 / 16	VAQUERIZAS_Pancreas
5	0.13	1 / 26	VAQUERIZAS_Liver
6	0.14	1 / 29	VAQUERIZAS_Smooth muscle
7	0.16	1 / 33	VAQUERIZAS_Prostate
8	0.17	1 / 36	VAQUERIZAS_Fetal brain
9	0.18	1 / 38	VAQUERIZAS_Whole brain
10	0.19	1 / 40	VAQUERIZAS_Thyroid
11	0.27	1 / 59	VAQUERIZAS_Whole blood
12	1.00	0 / 41	VAQUERIZAS_Placenta
13	1.00	0 / 45	VAQUERIZAS_Uterus
14	1.00	0 / 143	VAQUERIZAS_General
15	1.00	0 / 9	VAQUERIZAS_Kidney
16	1.00	0 / 23	VAQUERIZAS_Spinal cord
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 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 14	WIRTH_Telencephalon
2	0.44	1 / 107	WIRTH_Testis
3	0.56	2 / 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	0.9	3 / 1115	LU_BPDE 1n DN
2	1.0	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	

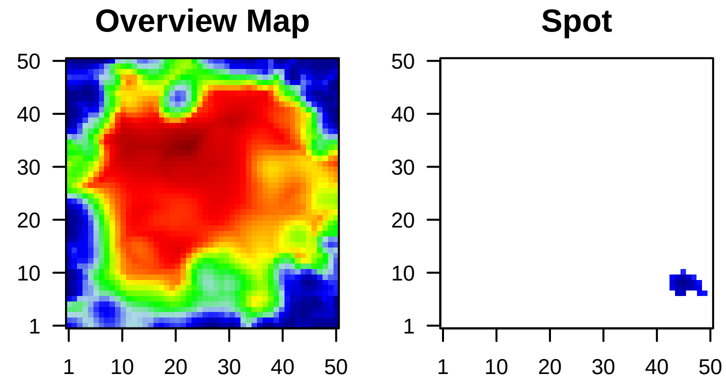
Underexpression Spots

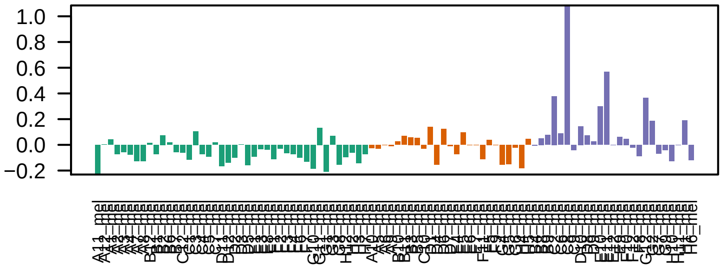
Spot Summary: k

metagenes = 22
genes = 117

<r> metagenes = 0.91
<r> genes = 0.14
beta: r2= 1.52 / log p= −Inf

samples with spot = 5 (5.4 %)
MSC3 : 5 (20 %)



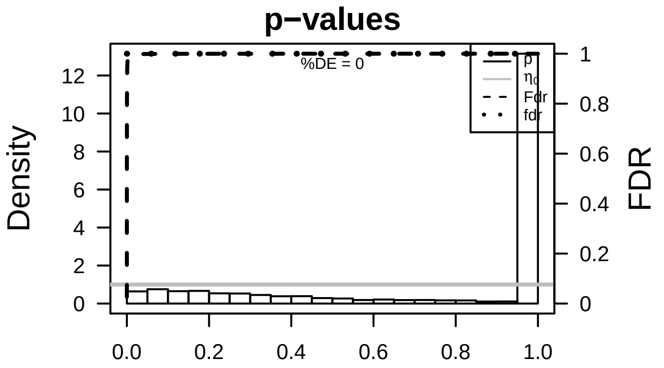


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LUM	3.07	−0.63	0.39	LUM	lumican [Source:HGNC Symbol;Acc:HGNC:6724]
2	CADM1	2.03	−0.14	0.49	CADM1	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:
3	RTN1	2	−0.05	0.87	RTN1	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]
4	MYH3	1.9	−0.09	0.63	MYH3	myosin, heavy chain 3, skeletal muscle, embryonic [Source:H
5	ZSCAN31	1.86	−0.22	0.4	ZSCAN31	zinc finger and SCAN domain containing 31 [Source:HGNC
6	CTC1	1.84	−0.21	0.34	CTC1	CTS telomere maintenance complex component 1 [Source:H
7	EXT1	1.78	−0.36	0.4	EXT1	exostosin glycosyltransferase 1 [Source:HGNC Symbol;Acc:
8	FST	1.77	−0.31	0.4	FST	follistatin [Source:HGNC Symbol;Acc:HGNC:3971]
9	PICALM	1.74	−0.64	0.45	PICALM	phosphatidylinositol binding clathrin assembly protein [Source
10	IGFBP7	1.71	−0.16	0.54	IGFBP7	insulin−like growth factor binding protein 7 [Source:HGNC Sy
11	PTCHD4	1.7	−0.23	0.59	PTCHD4	patched domain containing 4 [Source:HGNC Symbol;Acc:HG
12	CALCOCO1	1.7	−0.37	0.48	CALCOCO1	calcium binding and coiled−coil domain 1 [Source:HGNC Syn
13	HEMK1	1.68	−0.19	0.47	HEMK1	HemK methyltransferase family member 1 [Source:HGNC Sy
14	BMI1	1.67	−0.81	0.21	BMI1	BMI1 proto−oncogene, polycomb ring finger [Source:HGNC
15	PDE5A	1.66	−0.76	0.32	PDE5A	phosphodiesterase 5A, cGMP−specific [Source:HGNC Symb
16	PPP2R5B	1.65	−0.11	0.51	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta [Source:H
17	MANBA	1.64	−0.29	0.46	MANBA	mannosidase, beta A, lysosomal [Source:HGNC Symbol;Acc:
18	SLC41A2	1.63	−0.37	0.3	SLC41A2	solute carrier family 41 (magnesium transporter), member 2 [
19	NFIL3	1.62	−0.45	0.35	NFIL3	nuclear factor, interleukin 3 regulated [Source:HGNC Symbol
20	ZNF81	1.61	−0.16	0.41	ZNF81	zinc finger protein 81 [Source:HGNC Symbol;Acc:HGNC:131

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−06	6 / 46	GSE	SESTO_RESPONSE_TO_UV_C5
2	1e−05	70 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
3	2e−05	14 / 472	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	5e−05	5 / 52	CC	coated pit
5	6e−05	78 / 7209	Lymp	HOPP_Weak_promoter
6	6e−05	88 / 8580	Colon	TxWk_Colon
7	9e−05	13 / 473	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
8	2e−04	90 / 9027	Colon	Tx_Colon
9	2e−04	16 / 741	GSE	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
10	5e−04	7 / 179	miRN	hsa−miR−582−5p
11	5e−04	6 / 129	miRN	hsa−miR−576−3p
12	5e−04	4 / 48	GSE	HOWLIN_PUBERTAL_MAMMARY_GLAND
13	7e−04	88 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
14	8e−04	3 / 23	miRN	hsa−miR−1227
15	8e−04	16 / 833	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
16	1e−03	3 / 25	BP	activation of GTPase activity
17	1e−03	5 / 97	GSE	SENESE_HDAC2_TARGETS_DN
18	1e−03	83 / 8415	Colon	Quies3_Colon
19	1e−03	6 / 146	miRN	hsa−miR−140−5p
20	1e−03	7 / 206	GSE	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS
21	1e−03	4 / 60	BP	regulation of GTPase activity
22	1e−03	4 / 61	GSE	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP
23	1e−03	3 / 28	BP	vesicle organization
24	2e−03	4 / 63	GSE	LINDVALL_IMMORTALIZED_BY_TERT_UP
25	2e−03	71 / 6929	Lymp	HOPP_Txn_elongation
26	2e−03	89 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
27	2e−03	76 / 7592	Lymp	HOPP_Active_promoter
28	2e−03	10 / 426	GSE	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
29	2e−03	3 / 32	BP	regulation of synaptic plasticity
30	2e−03	12 / 581	BP	negative regulation of transcription from RNA polymerase II promoter
31	2e−03	4 / 69	GSE	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
32	2e−03	113 / 13179	MF	molecular_function
33	2e−03	5 / 116	GSE	FIGUEROA_AML_METHYLATION_CLUSTER_6_UP
34	3e−03	4 / 73	BP	cation transport
35	3e−03	7 / 238	GSE	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN
36	3e−03	2 / 11	BP	relaxation of cardiac muscle
37	3e−03	10 / 458	GSE	ENK_UV_RESPONSE_EPIDERMIS_DN
38	3e−03	7 / 246	CC	dendrite
39	3e−03	9 / 385	GSE	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
40	4e−03	17 / 1050	Brain	Fetal_EnhP



Aging

Rank	p−value	#in/all	Geneset
1	1.0	0 / 11	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	0.001	3 / 25	activation of GTPase activity
2	0.001	4 / 60	regulation of GTPase activity
3	0.001	3 / 28	vesicle organization
4	0.002	3 / 32	regulation of synaptic plasticity
5	0.002	12 / 581	negative regulation of transcription from RNA polymerase II promoter
6	0.003	4 / 73	cation transport
7	0.003	2 / 11	relaxation of cardiac muscle
8	0.004	4 / 81	ephrin receptor signaling pathway
9	0.004	2 / 12	clathrin−mediated endocytosis
10	0.005	2 / 13	actin filament−based movement
11	0.005	3 / 43	cellular response to growth factor stimulus
12	0.005	5 / 142	phosphorylation
13	0.008	2 / 17	actomyosin structure organization
14	0.008	2 / 17	regulation of cytokinesis
15	0.009	2 / 18	cellular response to interleukin−4
16	0.014	2 / 23	DNA methylation
17	0.014	2 / 23	endoderm development
18	0.014	2 / 23	gastrulation
19	0.016	2 / 25	bone mineralization
20	0.016	2 / 25	lipoprotein metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	1e−05	70 / 5940	Overlap_fetal_midbrain_HetRpts
2	7e−04	88 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	2e−03	89 / 9330	Overlap_fetal_midbrain_ReprPC
4	4e−03	17 / 1050	Fetal_EnhP
5	4e−03	89 / 9528	Overlap_fetal_midbrain_Quies
6	7e−02	9 / 656	Overlap_fetal_midbrain_EnhP
7	8e−02	79 / 9013	Overlap_fetal_midbrain_K9K27me3
8	1e−01	12 / 1013	Fetal_TssP
9	1e−01	30 / 3081	Mid_Frontal_Lobe_ZNF
10	1e−01	10 / 831	Fetal_HetRpts
11	1e−01	12 / 1065	Overlap_fetal_midbrain_Enh
12	1e−01	5 / 349	Fetal_ZNF
13	2e−01	7 / 564	Mid_Frontal_Lobe_EnhP
14	2e−01	10 / 884	Overlap_fetal_midbrain_EnhG
15	2e−01	9 / 786	Fetal_EnhG
16	3e−01	8 / 765	Mid_Frontal_Lobe_Het
17	3e−01	11 / 1122	Fetal_K9K27me3
18	6e−01	12 / 1548	Mid_Frontal_Lobe_K9K27me3
19	6e−01	6 / 769	Overlap_fetal_midbrain_ZNF
20	6e−01	3 / 383	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.009	7 / 298	SPANG_BCL6−index2
2	0.091	1 / 12	LIU_PROSTATE_CANCER_UP
3	0.112	1 / 15	GENTLES_modul4
4	0.112	1 / 15	GENTLES_modul11
5	0.119	1 / 16	GENTLES_modul14
6	0.272	1 / 40	ZHANG_MM_up
7	0.294	1 / 44	PanCan_TGF−B_geneset_nanostring
8	0.349	2 / 156	PanCan_PI3K_geneset_nanostring
9	0.388	0 / 15	RHODES_CANCER_META_SIGNATURE
10	0.389	4 / 401	Lembcke_Colonic Inflammation
11	0.412	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	0.416	2 / 180	SPANG_LPS−index2
13	0.618	1 / 121	PanCan_MAPK_geneset_nanostring
14	0.902	2 / 489	Lembcke_Normal vs Adenoma
15	0.955	0 / 14	LIU_PROSTATE_CANCER_DN
16	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.000	0 / 12	LIU_BREAST_CANCER
19	1.000	0 / 14	LIU_COMMON_CANCER_GENES
20	1.000	0 / 14	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 52	coated pit
2	3e−03	7 / 246	dendrite
3	4e−03	3 / 39	intercalated disc
4	5e−03	4 / 85	ruffle
5	5e−03	10 / 487	intracellular membrane−bounded organelle
6	5e−03	9 / 412	lysosome
7	6e−03	3 / 48	clathrin−coated vesicle
8	9e−03	2 / 18	protein phosphatase type 2A complex
9	1e−02	9 / 456	vacuole
10	1e−02	2 / 21	vesicle membrane
11	1e−02	6 / 249	neuronal cell body
12	2e−02	3 / 66	integral component of endoplasmic reticulum membrane
13	2e−02	3 / 78	dendritic spine
14	2e−02	2 / 31	histone deacetylase complex
15	3e−02	2 / 33	sarcoplasmic reticulum
16	3e−02	93 / 10605	intracellular
17	3e−02	2 / 35	myosin complex
18	3e−02	101 / 11774	cell
19	5e−02	54 / 5696	nucleus
20	6e−02	2 / 49	extrinsic component of cytoplasmic side of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	13 / 801	Chr 11
2	0.03	19 / 1500	Chr 1
3	0.04	11 / 775	Chr 12
4	0.04	10 / 687	Chr 6
5	0.15	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
6	0.30	5 / 462	Chr 14
7	0.34	8 / 840	Chr 17
8	0.61	2 / 262	Chr 13
9	0.65	4 / 558	Chr 4
10	0.65	5 / 696	Chr 5
11	0.65	6 / 838	Chr 3
12	0.67	7 / 993	Chr 2
13	0.70	1 / 151	Chr 21
14	0.81	3 / 551	Chr X
15	0.82	3 / 552	Chr 10
16	0.83	6 / 1037	Chr 19
17	0.84	3 / 576	Chr 9
18	0.89	2 / 465	Chr 15
19	0.89	2 / 469	Chr 8
20	0.91	3 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−05	88 / 8580	TxWk_Colon
2	2e−04	90 / 9027	Tx_Colon
3	1e−03	83 / 8415	Quies3_Colon
4	6e−03	88 / 9482	TssA_Colon
5	7e−03	9 / 427	Quies2_Colon
6	1e−02	7 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	1e−02	42 / 3897	Quies1_Colon
8	2e−02	92 / 10290	TssWk_Colon
9	2e−02	27 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
10	2e−02	15 / 1079	ZNF_Colon
11	3e−02	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
12	5e−02	1 / 7	Marisa_CRC−C5
13	5e−02	1 / 7	Juehling_HNPCC−mutated−in−5
14	6e−02	1 / 8	Marisa_CRC−C3
15	8e−02	65 / 7203	TssF_Colon
16	8e−02	3 / 131	Marisa_CRC−cluster−a
17	9e−02	37 / 3812	TssD1_Colon
18	9e−02	6 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
19	1e−01	53 / 5880	TssD2_Colon
20	1e−01	9 / 739	TxEnhG2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.7	2 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	12 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.06	1 / 8	Colman_survival_robust
3	0.09	2 / 65	GIEZELT_GBM_STS_up_VS_LTS
4	0.09	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
5	0.10	2 / 68	GIEZELT_GBM_WT_down_VS_mut
6	0.10	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.12	1 / 16	VERHAAK_NL subtype
8	0.15	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	0.15	5 / 356	Down_a
10	0.16	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
11	0.22	1 / 32	Donson−innate immunity−associated with LTS in HGA
12	0.22	1 / 32	Colman_survival_associated
13	0.24	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	0.27	1 / 39	OPC
15	0.30	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
16	0.31	1 / 47	Vishal_subnetwork signature of survival in GBM
17	0.32	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
18	0.33	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
19	0.36	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
20	0.43	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	6 / 46	SESTO_RESPONSE_TO_UV_C5
2	2e−05	14 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
3	9e−05	13 / 473	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
4	2e−04	16 / 741	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
5	5e−04	4 / 48	HOWLIN_PUBERTAL_MAMMARY_GLAND
6	8e−04	16 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
7	1e−03	5 / 97	SENESE_HDAC2_TARGETS_DN
8	1e−03	7 / 206	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS
9	1e−03	4 / 61	SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP
10	2e−03	4 / 63	LINDVALL_IMMORTALIZED_BY_TERT_UP
11	2e−03	10 / 426	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
12	2e−03	4 / 69	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
13	2e−03	5 / 116	FIGUEROA_AML_METHYLATION_CLUSTER_6_UP
14	3e−03	7 / 238	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN
15	3e−03	10 / 458	ENK_UV_RESPONSE_EPIDERMIS_DN
16	3e−03	9 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
17	4e−03	3 / 39	GENTILE_UV_RESPONSE_CLUSTER_D8
18	4e−03	5 / 131	GROSS_HYPOXIA_VIA_ELK3_DN
19	4e−03	3 / 40	PARK_HSC_MARKERS
20	4e−03	3 / 40	ZHAN_MULTIPLE_MYELOMA_CD1_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	4 / 137	HALLMARK_UV_RESPONSE_DN
2	0.02	2 / 31	HALLMARK_HEDGEHOG_SIGNALING
3	0.04	4 / 165	HALLMARK_MYOGENESIS
4	0.05	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
5	0.10	3 / 140	HALLMARK_APOPTOSIS
6	0.12	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	0.14	3 / 162	HALLMARK_COMPLEMENT
8	0.15	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
9	0.17	2 / 93	HALLMARK_PEROXISOME
10	0.19	1 / 26	HALLMARK_ANGIOGENESIS
11	0.20	3 / 196	HALLMARK_MTORC1_SIGNALING
12	0.21	2 / 107	HALLMARK_COAGULATION
13	0.25	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	0.30	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
15	0.34	1 / 53	HALLMARK_TGF_BETA_SIGNALING
16	0.38	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
17	0.40	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	0.40	2 / 174	HALLMARK_HEME_METABOLISM
19	0.41	2 / 176	HALLMARK_HYPOXIA
20	0.41	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	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	6e−05	78 / 7209	HOPP_Weak_promoter
2	2e−03	71 / 6929	HOPP_Txn_elongation
3	2e−03	76 / 7592	HOPP_Active_promoter
4	2e−02	6 / 268	SPANG_IL21 UP
5	5e−02	3 / 107	SPANG_LPS 6hrs UP
6	5e−02	3 / 109	ROSOLOWSKI_green total
7	7e−02	52 / 5538	HOPP_Weak_txn
8	7e−02	53 / 5693	HOPP_Weak_enhancer
9	7e−02	60 / 6564	HOPP_Strong_enhancer
10	1e−01	2 / 66	TARTE_Plasma cell signature
11	1e−01	14 / 1218	SPANG_BCR UP
12	1e−01	48 / 5184	HOPP_Txn_transition
13	1e−01	1 / 14	Subero_MCL_hyper_meth
14	1e−01	1 / 15	WRIGHT_ABC UP
15	1e−01	2 / 81	Subero_INT_hyper_meth
16	1e−01	2 / 82	ROSOLOWSKI_green UP
17	2e−01	2 / 96	Subero_DLBCL_hyper_meth
18	2e−01	21 / 2188	HOPP_Poised_promoter
19	2e−01	3 / 212	LENZ_Stromal signature 1
20	3e−01	1 / 40	Subero_mBL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	0.002	113 / 13179	molecular_function
2	0.004	3 / 42	glycoprotein binding
3	0.006	2 / 15	cation transmembrane transporter activity
4	0.007	84 / 8984	protein binding
5	0.010	2 / 19	protein phosphatase type 2A regulator activity
6	0.012	5 / 174	transcription corepressor activity
7	0.014	5 / 180	protein domain specific binding
8	0.014	2 / 23	ephrin receptor binding
9	0.023	2 / 30	hydrolase activity, hydrolyzing O−glycosyl compounds
10	0.028	8 / 456	protein binding transcription factor activity
11	0.035	10 / 657	enzyme regulator activity
12	0.059	2 / 50	motor activity
13	0.063	2 / 52	p53 binding
14	0.072	2 / 56	transcription cofactor activity
15	0.075	22 / 2037	DNA binding
16	0.076	1 / 10	armadillo repeat domain binding
17	0.076	1 / 10	glucocorticoid receptor binding
18	0.076	1 / 10	hedgehog receptor activity
19	0.076	1 / 10	protein−lysine N−methyltransferase activity
20	0.076	1 / 10	Rac guanyl−nucleotide exchange factor activity

miRNA Target

Rank	p−value	#in/all	Geneset
1	5e−04	7 / 179	hsa−miR−582−5p
2	5e−04	6 / 129	hsa−miR−576−3p
3	8e−04	3 / 23	hsa−miR−1227
4	1e−03	6 / 146	hsa−miR−140−5p
5	5e−03	5 / 140	hsa−miR−522
6	7e−03	4 / 96	hsa−miR−513b
7	1e−02	3 / 56	hsa−miR−208a
8	2e−02	7 / 328	hsa−miR−520d−3p
9	2e−02	4 / 121	hsa−miR−664
10	2e−02	5 / 190	hsa−miR−548d−3p
11	2e−02	6 / 264	hsa−miR−30a
12	2e−02	5 / 198	hsa−miR−181c
13	2e−02	6 / 272	hsa−miR−520b
14	2e−02	6 / 274	hsa−miR−548h
15	2e−02	5 / 203	hsa−miR−545
16	2e−02	4 / 137	hsa−miR−656
17	2e−02	5 / 208	hsa−miR−432
18	2e−02	4 / 140	hsa−miR−409−3p
19	3e−02	5 / 217	hsa−miR−181d
20	3e−02	5 / 218	hsa−miR−181a

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	0.02	23 / 1878	ICGC_Cebpbsc150_targets
2	0.07	15 / 1266	ICGC_NrsfPcr1_targets
3	0.15	7 / 553	ICGC_RxraPcr1_targets
4	0.15	19 / 1872	ICGC_Mef2_targets
5	0.15	14 / 1314	ICGC_Usf1_targets
6	0.16	27 / 2836	ICGC_BatfPcr1_targets
7	0.19	7 / 595	ICGC_NrsfPcr2_targets
8	0.21	27 / 2927	ICGC_Rad21_targets
9	0.21	39 / 4385	ICGC_Atf2_targets
10	0.22	36 / 4032	ICGC_Creb1_targets
11	0.22	25 / 2714	ICGC_Irf4_targets
12	0.23	19 / 2013	ICGC_Bcl11_targets
13	0.23	33 / 3700	ICGC_Nfatc1_targets
14	0.25	22 / 2391	ICGC_Pbx3_targets
15	0.26	16 / 1701	HEBENSTREIT_high expression TF
16	0.27	42 / 4879	ICGC_Pmlsc71910_targets
17	0.29	34 / 3924	ICGC_Zeb1_targets
18	0.32	19 / 2137	ICGC_SrfV0416101_targets
19	0.35	40 / 4774	ICGC_Foxm1_targets
20	0.37	39 / 4682	ICGC_Pol24_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 45	VAQUERIZAS_Uterus
2	0.09	1 / 12	VAQUERIZAS_Skin
3	0.10	3 / 143	VAQUERIZAS_General
4	0.10	1 / 14	VAQUERIZAS_Ovary
5	0.17	1 / 23	VAQUERIZAS_Adrenal cortex
6	0.21	1 / 29	VAQUERIZAS_Smooth muscle
7	0.21	1 / 29	VAQUERIZAS_Fetal lung
8	0.28	1 / 41	VAQUERIZAS_Placenta
9	0.37	1 / 58	VAQUERIZAS_Lung
10	0.37	1 / 59	VAQUERIZAS_Whole blood
11	1.00	0 / 36	VAQUERIZAS_Fetal brain
12	1.00	0 / 26	VAQUERIZAS_Liver
13	1.00	0 / 33	VAQUERIZAS_Prostate
14	1.00	0 / 9	VAQUERIZAS_Kidney
15	1.00	0 / 23	VAQUERIZAS_Spinal cord
16	1.00	0 / 38	VAQUERIZAS_Whole brain
17	1.00	0 / 37	VAQUERIZAS_Thymus
18	1.00	0 / 40	VAQUERIZAS_Thyroid
19	1.00	0 / 7	VAQUERIZAS_Appendix
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 95	WIRTH_Muscle
2	0.5	3 / 350	WIRTH_Nervous System
3	0.8	1 / 114	PALMER_T−Cell signature up
4	0.8	1 / 194	PALMER_B−Cell signature up
5	0.8	1 / 225	PALMER_Granulocytes signature up
6	0.8	1 / 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 / 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	0.01	40 / 3682	LU_BPDE 0.005 DN
2	0.52	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	

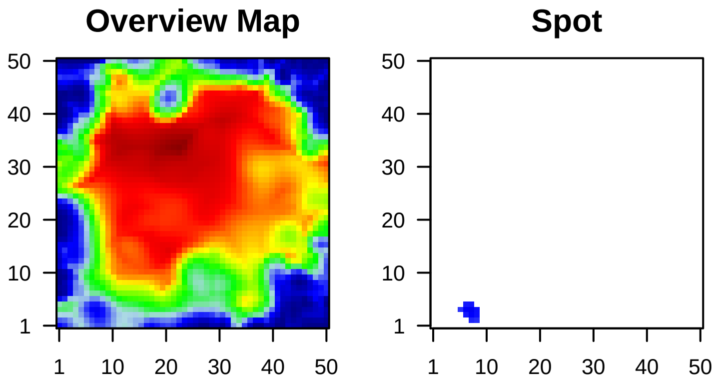
Underexpression Spots

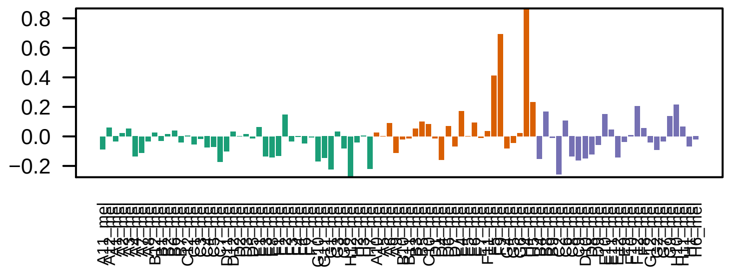
Spot Summary: I

metagenes = 11
genes = 63

<r> metagenes = 0.93
<r> genes = 0.13
beta: r2= 0.93 / log p= −Inf

samples with spot = 6 (6.5 %)
MSC2 : 4 (16 %)
MSC3 : 2 (8 %)



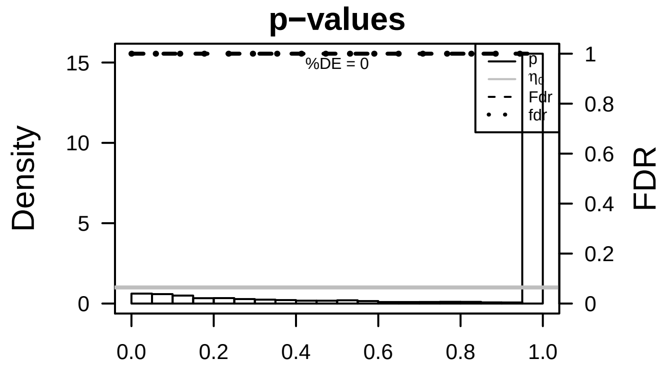


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LYSMD2	1.8	−0.24	0.55	LYSMD2	LysM, putative peptidoglycan−binding, domain containing 2 [S
2	C5	1.65	−0.12	0.42	C5	complement component 5 [Source:HGNC Symbol;Acc:HGNC
3	TBC1D2B	1.65	−0.13	0.36	TBC1D2B	TBC1 domain family, member 2B [Source:HGNC Symbol;Acc
4	ZNF462	1.64	−0.44	0.46	ZNF462	zinc finger protein 462 [Source:HGNC Symbol;Acc:HGNC:21
5	ELAC1	1.52	−0.56	0.28	ELAC1	elaC ribonuclease Z 1 [Source:HGNC Symbol;Acc:HGNC:14
6	SLC2A10	1.49	−0.29	0.42	SLC2A10	solute carrier family 2 (facilitated glucose transporter), membe
7	ZSCAN2	1.48	−0.17	0.42	ZSCAN2	zinc finger and SCAN domain containing 2 [Source:HGNC Sy
8	PTPN4	1.47	−0.66	0.36	PTPN4	protein tyrosine phosphatase, non−receptor type 4 (megakar
9	ZNF236	1.45	−0.61	0.35	ZNF236	zinc finger protein 236 [Source:HGNC Symbol;Acc:HGNC:13
10	MTCL1	1.45	−0.21	0.33	MTCL1	microtubule crosslinking factor 1 [Source:HGNC Symbol;Acc:
11	RAP1A	1.44	−0.41	0.32	RAP1A	RAP1A, member of RAS oncogene family [Source:HGNC Sy
12	ZFAT	1.42	−0.4	0.38	ZFAT	zinc finger and AT hook domain containing [Source:HGNC Sy
13	OBSCN	1.39	−0.31	0.32	OBSCN	obscurin, cytoskeletal calmodulin and titin−interacting RhoGE
14	KCNAB1	1.34	−0.16	0.49	KCNAB1	potassium channel, voltage gated subfamily A regulatory beta
15	NUMB	1.33	−0.72	0.31	NUMB	numb homolog (Drosophila) [Source:HGNC Symbol;Acc:HGN
16	ZNF432	1.33	−0.35	0.37	ZNF432	zinc finger protein 432 [Source:HGNC Symbol;Acc:HGNC:20
17	FAM78A	1.3	−0.11	0.36	FAM78A	family with sequence similarity 78, member A [Source:HGNC
18	MEGF8	1.28	−0.14	0.42	MEGF8	multiple EGF−like−domains 8 [Source:HGNC Symbol;Acc:HG
19	PTPRJ	1.27	−0.63	0.44	PTPRJ	protein tyrosine phosphatase, receptor type, J [Source:HGNC
20	STRBP	1.27	−0.67	0.36	STRBP	spermatid perinuclear RNA binding protein [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	42 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
2	2e−04	4 / 71	MF	ubiquitin−specific protease activity
3	6e−04	3 / 38	GSEA	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
4	7e−04	3 / 41	GSEA	KEGG_NOTCH_SIGNALING_PATHWAY
5	8e−04	4 / 97	miRN	hsa−miR−544
6	8e−04	2 / 10	BP	positive regulation of astrocyte differentiation
7	9e−04	5 / 176	BP	heart development
8	1e−03	2 / 11	BP	negative regulation of oligodendrocyte differentiation
9	1e−03	5 / 183	miRN	hsa−miR−1283
10	1e−03	3 / 49	BP	protein deubiquitination
11	2e−03	2 / 14	BP	positive regulation of JAK−STAT cascade
12	2e−03	2 / 14	GSEA	FUKUSHIMA_TNFSF11_TARGETS
13	2e−03	8 / 527	GSEA	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
14	2e−03	2 / 15	CC	extrinsic component of plasma membrane
15	2e−03	2 / 15	MF	lysine−acetylated histone binding
16	2e−03	2 / 15	GSEA	LUND_SILENCED_BY_METHYLATION
17	2e−03	2 / 17	BP	neuronal stem cell maintenance
18	2e−03	2 / 17	BP	protein K48−linked deubiquitination
19	2e−03	3 / 63	miRN	hsa−miR−659
20	2e−03	5 / 221	Chr	Chr 18
21	3e−03	2 / 18	BP	regulation of neurogenesis
22	3e−03	2 / 18	Canc	PanCan_Notch_geneset_nanostring
23	3e−03	2 / 19	BP	labyrinthine layer blood vessel development
24	3e−03	5 / 233	miRN	hsa−miR−26a
25	3e−03	6 / 340	miRN	hsa−miR−142−5p
26	3e−03	49 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
27	3e−03	2 / 20	BP	ventricular septum morphogenesis
28	3e−03	2 / 20	GSEA	BARRIER_COLON_CANCER_RECURRENCE_DN
29	3e−03	5 / 239	miRN	hsa−miR−152
30	4e−03	17 / 2013	TF	ICGC_Bcl11_targets
31	4e−03	5 / 242	miRN	hsa−miR−26b
32	4e−03	2 / 23	GSEA	SCHRAMM_INHBA_TARGETS_DN
33	4e−03	3 / 77	GSEA	PID_MET_PATHWAY
34	5e−03	2 / 24	BP	mitotic cytokinesis
35	5e−03	4 / 160	miRN	hsa−miR−1297
36	5e−03	2 / 25	BP	positive regulation of BMP signaling pathway
37	5e−03	40 / 6929	Lymp	HOPP_Txn_elongation
38	5e−03	2 / 26	GSEA	KEGG_PRION_DISEASES
39	5e−03	46 / 8415	Colon	Quies3_Colon
40	6e−03	9 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_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	8e−04	2 / 10	positive regulation of astrocyte differentiation
2	9e−04	5 / 176	heart development
3	1e−03	2 / 11	negative regulation of oligodendrocyte differentiation
4	1e−03	3 / 49	protein deubiquitination
5	2e−03	2 / 14	positive regulation of JAK−STAT cascade
6	2e−03	2 / 17	neuronal stem cell maintenance
7	2e−03	2 / 17	protein K48−linked deubiquitination
8	3e−03	2 / 18	regulation of neurogenesis
9	3e−03	2 / 19	labyrinthine layer blood vessel development
10	3e−03	2 / 20	ventricular septum morphogenesis
11	5e−03	2 / 24	mitotic cytokinesis
12	5e−03	2 / 25	positive regulation of BMP signaling pathway
13	6e−03	6 / 386	regulation of transcription from RNA polymerase II promoter
14	6e−03	2 / 27	oligodendrocyte differentiation
15	6e−03	3 / 88	peptidyl−tyrosine dephosphorylation
16	1e−02	2 / 35	negative regulation of cell differentiation
17	1e−02	2 / 37	neural tube development
18	1e−02	4 / 204	in utero embryonic development
19	1e−02	2 / 38	DNA−templated transcription, initiation
20	1e−02	2 / 38	embryonic skeletal system morphogenesis

Brain

Rank	p−value	#in/all	Geneset
1	2e−05	42 / 5940	Overlap_fetal_midbrain_HetRpts
2	3e−03	49 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	2e−02	8 / 786	Fetal_EnhG
4	3e−02	6 / 564	Mid_Frontal_Lobe_EnhP
5	5e−02	47 / 9528	Overlap_fetal_midbrain_Quies
6	8e−02	8 / 1050	Fetal_EnhP
7	8e−02	7 / 884	Overlap_fetal_midbrain_EnhG
8	8e−02	8 / 1065	Overlap_fetal_midbrain_Enh
9	9e−02	44 / 9013	Overlap_fetal_midbrain_K9K27me3
10	1e−01	45 / 9330	Overlap_fetal_midbrain_ReprPC
11	1e−01	3 / 304	Fetal_Het
12	1e−01	5 / 656	Overlap_fetal_midbrain_EnhP
13	2e−01	5 / 769	Overlap_fetal_midbrain_ZNF
14	3e−01	6 / 1013	Fetal_TssP
15	3e−01	4 / 668	Mid_Frontal_Lobe_Enh
16	3e−01	15 / 3081	Mid_Frontal_Lobe_ZNF
17	4e−01	3 / 534	Mid_Frontal_Lobe_EnhG
18	4e−01	2 / 349	Fetal_ZNF
19	4e−01	9 / 1949	Fetal_TssF
20	5e−01	1 / 156	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	2 / 18	PanCan_Notch_geneset_nanostring
2	0.036	2 / 70	SHAUGHNESSY_MM high risk
3	0.066	1 / 16	GENTLES_modul2
4	0.083	2 / 113	PanCan_Driver_Gene_geneset_nanostring
5	0.493	0 / 14	LIU_PROSTATE_CANCER_DN
6	0.511	2 / 401	Lembcke_Colonic Inflammation
7	0.537	1 / 180	SPANG_LPS−index2
8	0.879	1 / 489	Lembcke_Normal vs Adenoma
9	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
10	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.000	0 / 12	LIU_BREAST_CANCER
14	1.000	0 / 14	LIU_COMMON_CANCER_GENES
15	1.000	0 / 14	LIU_LIVER_CANCER
16	1.000	0 / 12	LIU_PROSTATE_CANCER_UP
17	1.000	0 / 15	WANG_ER_UP
18	1.000	0 / 5	WANG_ER_DN
19	1.000	0 / 16	WOLFER_overlap genes
20	1.000	0 / 12	BEN−PORATH_DN

CC

Rank	p−value	#in/all	Geneset
1	0.002	2 / 15	extrinsic component of plasma membrane
2	0.006	2 / 28	myofibril
3	0.006	4 / 175	early endosome
4	0.018	2 / 48	clathrin−coated vesicle
5	0.021	2 / 53	acrosomal vesicle
6	0.042	1 / 10	myosin filament
7	0.042	1 / 10	perinuclear endoplasmic reticulum
8	0.050	1 / 12	npBAF complex
9	0.050	1 / 12	XY body
10	0.054	1 / 13	DNA−directed RNA polymerase I complex
11	0.054	1 / 13	nBAF complex
12	0.054	1 / 13	SWI/SNF complex
13	0.058	1 / 14	clathrin−coated vesicle membrane
14	0.060	2 / 94	melanosome
15	0.062	1 / 15	BAF−type complex
16	0.062	1 / 15	dendrite cytoplasm
17	0.066	1 / 16	M band
18	0.084	30 / 5696	nucleus
19	0.085	1 / 21	histone methyltransferase complex
20	0.085	1 / 21	immunological synapse

Chr

Rank	p−value	#in/all	Geneset
1	0.002	5 / 221	Chr 18
2	0.035	6 / 576	Chr 9
3	0.047	5 / 465	Chr 15
4	0.082	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
5	0.244	6 / 993	Chr 2
6	0.424	3 / 558	Chr 4
7	0.507	2 / 398	Chr 20
8	0.588	2 / 462	Chr 14
9	0.596	2 / 469	Chr 8
10	0.623	6 / 1500	Chr 1
11	0.675	1 / 262	Chr 13
12	0.685	2 / 552	Chr 10
13	0.700	3 / 840	Chr 17
14	0.763	1 / 335	Chr 22
15	0.769	2 / 649	Chr 16
16	0.797	2 / 689	Chr 7
17	0.802	2 / 696	Chr 5
18	0.826	3 / 1037	Chr 19
19	0.848	2 / 775	Chr 12
20	0.878	2 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.005	46 / 8415	Quies3_Colon
2	0.009	46 / 8580	TxWk_Colon
3	0.013	49 / 9482	TssA_Colon
4	0.015	10 / 1079	ZNF_Colon
5	0.015	47 / 9027	Tx_Colon
6	0.032	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
7	0.033	1 / 8	Marisa_CRC−C3
8	0.037	2 / 71	Marisa_CRC−cluster−g
9	0.065	20 / 3383	EnhWk2_Colon
10	0.168	20 / 3812	TssD1_Colon
11	0.175	45 / 9653	Enh_Colon
12	0.221	47 / 10290	TssWk_Colon
13	0.232	8 / 1386	Het_Colon
14	0.241	25 / 5155	EnhWk1_Colon
15	0.277	6 / 1038	HetRpts_Colon
16	0.282	19 / 3897	Quies1_Colon
17	0.287	2 / 250	K9K27me3_Colon
18	0.353	1 / 102	Marisa_CRC−cluster−d
19	0.384	4 / 739	TxEnhG2_Colon
20	0.470	2 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

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	0.05	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
2	0.07	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
3	0.17	3 / 332	Up
4	0.19	3 / 356	Down_a
5	0.25	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	0.25	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	0.27	1 / 74	WIRTH_Normal Brain
8	0.27	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
9	0.36	1 / 103	GIEZELT_GBM_WT_up_VS_mut
10	0.39	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	0.48	4 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.49	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	0.54	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
14	1.00	0 / 15	VERHAAK_CL subtype
15	1.00	0 / 15	VERHAAK_MES subtype
16	1.00	0 / 16	VERHAAK_NL subtype
17	1.00	0 / 14	VERHAAK_PN subtype
18	1.00	0 / 23	WIRTH_PN subtype
19	1.00	0 / 9	VERHAAK_Brain
20	1.00	0 / 8	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 38	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
2	7e−04	3 / 41	KEGG_NOTCH_SIGNALING_PATHWAY
3	2e−03	2 / 14	FUKUSHIMA_TNFSF11_TARGETS
4	2e−03	8 / 527	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
5	2e−03	2 / 15	LUND_SILENCED_BY_METHYLATION
6	3e−03	2 / 20	BARRIER_COLON_CANCER_RECURRENCE_DN
7	4e−03	2 / 23	SCHRAMM_INHBA_TARGETS_DN
8	4e−03	3 / 77	PID_MET_PATHWAY
9	5e−03	2 / 26	KEGG_PRION_DISEASES
10	6e−03	9 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
11	6e−03	2 / 27	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_DN
12	6e−03	4 / 172	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_UP
13	6e−03	2 / 28	BURTON_ADIPOGENESIS_10
14	7e−03	2 / 30	PID_MAPK_TRK_PATHWAY
15	9e−03	6 / 422	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
16	9e−03	2 / 34	YIH_RESPONSE_TO_ARSENITE_C3
17	1e−02	2 / 35	LIU_TARGETS_OF_VMYB_VS_CMYB_DN
18	1e−02	2 / 35	ZHAN_MULTIPLE_MYELOMA_CD2_UP
19	1e−02	3 / 105	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
20	1e−02	2 / 37	RIZ_ERYTHROID_DIFFERENTIATION_CCNE1

HM

Rank	p−value	#in/all	Geneset
1	0.007	2 / 29	HALLMARK_NOTCH_SIGNALING
2	0.010	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.062	2 / 95	HALLMARK_SPERMATOGENESIS
4	0.101	2 / 127	HALLMARK_KRAS_SIGNALING_DN
5	0.146	1 / 37	HALLMARK_APICAL_SURFACE
6	0.155	2 / 165	HALLMARK_MYOGENESIS
7	0.464	1 / 146	HALLMARK_DNA_REPAIR
8	0.464	1 / 146	HALLMARK_UV_RESPONSE_UP
9	0.500	1 / 162	HALLMARK_COMPLEMENT
10	0.515	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	0.525	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.531	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	0.539	1 / 181	HALLMARK_P53_PATHWAY
14	0.553	1 / 188	HALLMARK_ADIPOGENESIS
15	0.568	1 / 196	HALLMARK_MTORC1_SIGNALING
16	1.000	0 / 176	HALLMARK_HYPOXIA
17	1.000	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
18	1.000	0 / 195	HALLMARK_MITOTIC_SPINDLE
19	1.000	0 / 53	HALLMARK_TGF_BETA_SIGNALING
20	1.000	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	0.005	40 / 6929	HOPP_Txn_elongation
2	0.007	32 / 5184	HOPP_Txn_transition
3	0.011	3 / 107	SPANG_LPS 6hrs UP
4	0.017	3 / 129	DAVE_BL−vs−DLBCL
5	0.041	15 / 2211	HOPP_Repetitive
6	0.046	35 / 6564	HOPP_Strong_enhancer
7	0.048	9 / 1128	SPANG_BCR DN
8	0.054	1 / 13	Subero_MCL_hypo_meth
9	0.058	1 / 14	Subero_mBL_hypo_meth
10	0.091	38 / 7592	HOPP_Active_promoter
11	0.116	3 / 280	SPANG_CD40 6hrs UP
12	0.116	1 / 29	Subero_DLBCL_hypo_meth
13	0.120	1 / 30	Subero_INT_hypo_meth
14	0.135	1 / 34	Subero_B−ALL_hyper_meth
15	0.227	2 / 212	LENZ_Stromal signature 1
16	0.252	3 / 410	SPANG_CD40 6hrs DN
17	0.282	2 / 247	ZHANG_DLBCL mutated
18	0.296	2 / 256	SPANG_IL21 DN
19	0.298	26 / 5538	HOPP_Weak_txn
20	0.461	25 / 5693	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 71	ubiquitin−specific protease activity
2	2e−03	2 / 15	lysine−acetylated histone binding
3	6e−03	3 / 89	protein tyrosine phosphatase activity
4	7e−03	2 / 29	structural constituent of muscle
5	1e−02	16 / 2037	DNA binding
6	1e−02	10 / 1033	nucleic acid binding
7	2e−02	3 / 123	nucleotidyltransferase activity
8	2e−02	2 / 45	protein tyrosine/serine/threonine phosphatase activity
9	2e−02	2 / 51	ubiquitinyl hydrolase activity
10	2e−02	14 / 1859	metal ion binding
11	3e−02	5 / 397	transcription factor binding
12	3e−02	2 / 64	beta−catenin binding
13	3e−02	2 / 67	phosphatidylinositol binding
14	4e−02	2 / 71	cysteine−type endopeptidase activity
15	4e−02	1 / 10	gamma−catenin binding
16	5e−02	1 / 11	aldo−keto reductase (NADP) activity
17	5e−02	1 / 11	SUMO transferase activity
18	5e−02	1 / 11	titin binding
19	5e−02	1 / 12	NADPH binding
20	5e−02	1 / 12	RNA polymerase I activity

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 97	hsa−miR−544
2	1e−03	5 / 183	hsa−miR−1283
3	2e−03	3 / 63	hsa−miR−659
4	3e−03	5 / 233	hsa−miR−26a
5	3e−03	6 / 340	hsa−miR−142−5p
6	3e−03	5 / 239	hsa−miR−152
7	4e−03	5 / 242	hsa−miR−26b
8	5e−03	4 / 160	hsa−miR−1297
9	7e−03	4 / 176	hsa−miR−23b
10	7e−03	4 / 179	hsa−miR−582−5p
11	7e−03	4 / 182	hsa−miR−23a
12	1e−02	3 / 107	hsa−miR−33b
13	1e−02	2 / 41	hsa−miR−525−3p
14	1e−02	2 / 41	hsa−miR−532−3p
15	1e−02	6 / 467	hsa−miR−301a
16	2e−02	2 / 49	hsa−miR−519b−5p
17	2e−02	2 / 49	hsa−miR−519c−5p
18	2e−02	2 / 53	hsa−miR−552
19	2e−02	4 / 251	hsa−miR−548l
20	2e−02	2 / 54	hsa−miR−518d−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	0.004	17 / 2013	ICGC_Bcl11_targets
2	0.015	31 / 5219	ICGC_Tcf3_targets
3	0.017	1 / 4	MYC_TFs
4	0.021	17 / 2416	ICGC_Bcl3_targets
5	0.038	27 / 4682	ICGC_Pol24_targets
6	0.040	6 / 595	ICGC_NrsfPcr2_targets
7	0.040	24 / 4054	ICGC_Egr1_targets
8	0.041	10 / 1273	ICGC_P300_targets
9	0.045	25 / 4314	ICGC_Ebfsc137065_targets
10	0.052	12 / 1701	HEBENSTREIT_high expression TF
11	0.057	17 / 2714	ICGC_Irf4_targets
12	0.058	18 / 2927	ICGC_Rad21_targets
13	0.066	29 / 5355	ICGC_Pol2_targets
14	0.072	15 / 2391	ICGC_Pbx3_targets
15	0.084	21 / 3700	ICGC_Nfatc1_targets
16	0.089	29 / 5495	ICGC_Yy1_targets
17	0.094	22 / 3966	ICGC_Pu1_targets
18	0.096	24 / 4414	ICGC_Bclaf101388_targets
19	0.110	28 / 5374	ICGC_Pax5_targets
20	0.111	25 / 4706	ICGC_Sp1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 143	VAQUERIZAS_General
2	0.03	1 / 7	VAQUERIZAS_Tongue
3	0.05	1 / 12	VAQUERIZAS_Skin
4	0.06	1 / 15	VAQUERIZAS_Fetal thyroid
5	0.13	1 / 33	VAQUERIZAS_Prostate
6	0.16	1 / 40	VAQUERIZAS_Thyroid
7	0.16	1 / 41	VAQUERIZAS_Placenta
8	0.22	1 / 58	VAQUERIZAS_Lung
9	1.00	0 / 36	VAQUERIZAS_Fetal brain
10	1.00	0 / 26	VAQUERIZAS_Liver
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 / 37	VAQUERIZAS_Thymus
17	1.00	0 / 59	VAQUERIZAS_Whole blood
18	1.00	0 / 7	VAQUERIZAS_Appendix
19	1.00	0 / 29	VAQUERIZAS_Fetal lung
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 32	WIRTH_Pancreas
2	0.2	3 / 350	WIRTH_Immune system
3	0.3	1 / 95	WIRTH_Muscle
4	0.6	1 / 194	PALMER_B−Cell signature up
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	0.9	3 / 1115	LU_BPDE 1n DN
2	0.9	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	

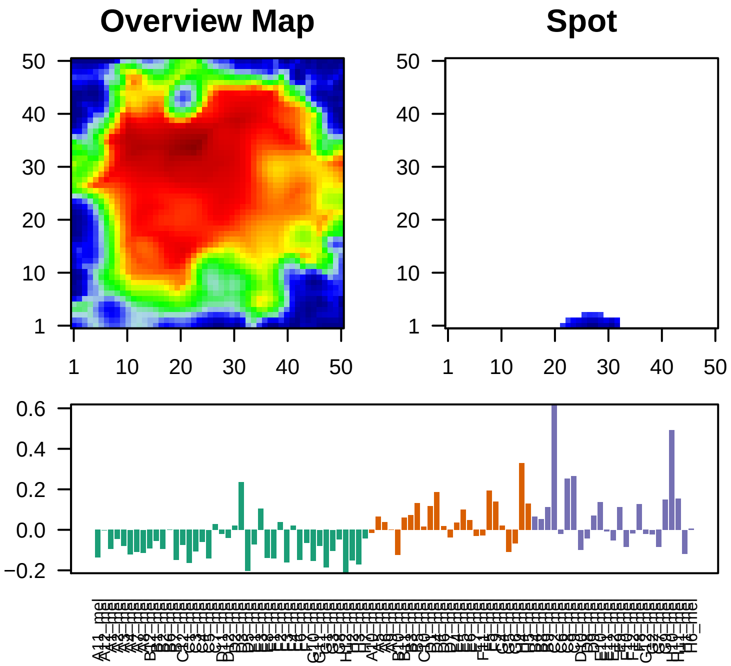
Underexpression Spots

Spot Summary: m

metagenes = 25
genes = 335

<r> metagenes = 0.9
<r> genes = 0.17
beta: r2= 1.41 / log p= −Inf

samples with spot = 7 (7.6 %)
MSC1 : 1 (2.4 %)
MSC2 : 2 (8 %)
MSC3 : 4 (16 %)

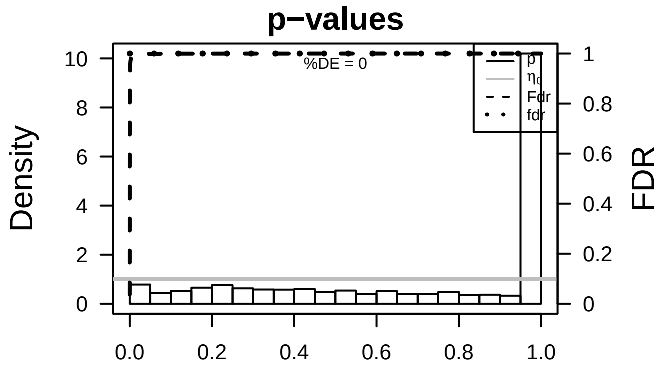


Spot Genelist

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
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	AKR1C2	1.81	−0.32	0.34	AKR1C2	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
5	BBS10	1.74	−0.2	0.49	BBS10	Bardet−Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGN
6	ATG2B	1.7	−0.32	0.46	ATG2B	autophagy related 2B [Source:HGNC Symbol;Acc:HGNC:201
7	ZNF264	1.67	−0.28	0.42	ZNF264	zinc finger protein 264 [Source:HGNC Symbol;Acc:HGNC:13
8	SSX5	1.66	−0.14	0.38	SSX5	synovial sarcoma, X breakpoint 5 [Source:HGNC Symbol;Acc
9	ATG4A	1.64	−0.6	0.24	ATG4A	autophagy related 4A, cysteine peptidase [Source:HGNC Sy
10	GALK2	1.64	−0.44	0.28	GALK2	galactokinase 2 [Source:HGNC Symbol;Acc:HGNC:4119]
11	ZNF525	1.63	−0.32	0.36	ZNF525	zinc finger protein 525 [Source:HGNC Symbol;Acc:HGNC:29
12	ITSN2	1.62	−0.64	0.33	ITSN2	intersectin 2 [Source:HGNC Symbol;Acc:HGNC:6184]
13	ABHD2	1.62	−0.46	0.29	ABHD2	abhydrolase domain containing 2 [Source:HGNC Symbol;Acc
14	IKBKE	1.62	−0.27	0.43	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B−cells,
15	TSPAN31	1.62	−0.77	0.34	TSPAN31	tetraspanin 31 [Source:HGNC Symbol;Acc:HGNC:10539]
16	ZNF28	1.61	−0.51	0.35	ZNF28	zinc finger protein 28 [Source:HGNC Symbol;Acc:HGNC:130
17	RNF25	1.6	−0.33	0.28	RNF25	ring finger protein 25 [Source:HGNC Symbol;Acc:HGNC:146
18	AKR1C3	1.59	−0.15	0.54	AKR1C3	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
19	FBXO36	1.58	−0.24	0.35	FBXO36	F−box protein 36 [Source:HGNC Symbol;Acc:HGNC:27020]
20	STYX	1.58	−0.53	0.4	STYX	serine/threonine/tyrosine interacting protein [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−06	6 / 19	BP	protein targeting to Golgi
2	3e−05	6 / 28	BP	intracellular transport
3	7e−05	4 / 11	MF	aldo−keto reductase (NADP) activity
4	3e−04	5 / 27	BP	retina homeostasis
5	3e−04	9 / 99	GSE	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
6	3e−04	9 / 100	miRN	hsa−miR−1299
7	4e−04	11 / 146	miRN	hsa−miR−655
8	6e−04	16 / 287	GSE	GRESHOCK_CANCER_COPY_NUMBER_UP
9	7e−04	6 / 49	miRN	hsa−miR−1224−3p
10	7e−04	7 / 68	GSE	KEGG_RENAL_CELL_CARCINOMA
11	7e−04	9 / 111	BP	Notch signaling pathway
12	8e−04	10 / 136	GSE	KEGG_CHEMOKINE_SIGNALING_PATHWAY
13	9e−04	8 / 92	GSE	REACTOME_SIGNALING_BY_NOTCH
14	9e−04	6 / 52	GSE	PID_NOTCH_PATHWAY
15	1e−03	8 / 93	GSE	REACTOME_SIGNALING_BY_FGFR
16	1e−03	14 / 244	MF	ubiquitin−protein transferase activity
17	1e−03	5 / 37	miRN	hsa−miR−197
18	1e−03	4 / 23	BP	secondary metabolic process
19	1e−03	4 / 23	BP	spliceosomal complex assembly
20	1e−03	3 / 11	CC	Gemini of coiled bodies
21	2e−03	5 / 41	GSE	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING
22	2e−03	3 / 12	CC	SMN complex
23	2e−03	3 / 12	GSE	PID_LPA4_PATHWAY
24	2e−03	3 / 12	GSE	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
25	2e−03	3 / 12	GSE	REACTOME_TRAF3_DEPENDENT_IRF_ACTIVATION_PATHWAY
26	2e−03	7 / 83	GSE	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR
27	2e−03	155 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
28	2e−03	5 / 43	BP	autophagic vacuole assembly
29	2e−03	5 / 43	GSE	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES
30	2e−03	8 / 107	GSE	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
31	2e−03	7 / 84	GSE	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION
32	3e−03	3 / 13	MF	GABA receptor binding
33	3e−03	29 / 761	GSE	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
34	3e−03	5 / 44	GSE	PID_HES_HEY_PATHWAY
35	3e−03	4 / 27	GSE	REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION
36	3e−03	4 / 27	GSE	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
37	3e−03	4 / 27	GSE	NOJIMA_SFRP2_TARGETS_UP
38	3e−03	16 / 336	BP	protein ubiquitination
39	3e−03	53 / 1664	BP	transcription, DNA−templated
40	3e−03	4 / 28	GSE	KEGG_STEROID_HORMONE_BIOSYNTHESIS



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 100	HORVATH_aging_genes meth DOWN
2	0.9	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	0.007	3 / 18	PanCan_Notch_geneset_nanostring
2	0.012	7 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.044	8 / 180	SPANG_LPS−index2
4	0.205	9 / 298	SPANG_BCL6−index2
5	0.233	1 / 12	LIU_PROSTATE_CANCER_UP
6	0.249	2 / 44	PanCan_TGF−B_geneset_nanostring
7	0.249	1 / 13	BEN−PORATH_UP
8	0.249	1 / 13	GENTLES_modul12
9	0.266	1 / 14	LIU_COMMON_CANCER_GENES
10	0.282	1 / 15	GENTLES_modul4
11	0.298	1 / 16	GENTLES_modul6
12	0.298	1 / 16	GENTLES_modul16
13	0.338	2 / 55	PanCan_JAK−ST_geneset_nanostring
14	0.357	1 / 20	PanCan_ChromMod_geneset_nanostring
15	0.371	0 / 12	LIU_BREAST_CANCER
16	0.385	1 / 22	PanCan_HH_geneset_nanostring
17	0.489	3 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.494	3 / 121	PanCan_MAPK_geneset_nanostring
19	0.654	1 / 48	KUIPER_MM poor survival
20	0.701	2 / 111	PanCan_RAS_geneset_nanostring

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.04	74 / 2798	TxEnhG1_Colon
2	0.05	202 / 8580	TxWk_Colon
3	0.12	9 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	0.13	2 / 29	Marisa_CRC−cluster−c
5	0.14	207 / 9027	Tx_Colon
6	0.14	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
7	0.16	1 / 8	KIM_CRC−MSI−regulated_DN
8	0.17	66 / 2698	EnhA_Colon
9	0.17	25 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	0.18	4 / 102	Marisa_CRC−cluster−d
11	0.28	1 / 15	TCGA_Mutated−in−CRC_hypermutated
12	0.30	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
13	0.30	1 / 16	Vilar_non−hypermutated−in−CRC
14	0.31	1 / 17	Vilar_mutated−in−CRC−CamP
15	0.31	1 / 17	Vilar_hypermutated−in−CRC
16	0.32	117 / 5155	EnhWk1_Colon
17	0.33	1 / 18	Ang_CRC−CIMPH−vs−L_hypo
18	0.42	9 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
19	0.42	1 / 25	Ang_CRC_Hypomethylated
20	0.45	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	9 / 99	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
2	6e−04	16 / 287	GRESHOCK_CANCER_COPY_NUMBER_UP
3	7e−04	7 / 68	KEGG_RENAL_CELL_CARCINOMA
4	8e−04	10 / 136	KEGG_CHEMOKINE_SIGNALING_PATHWAY
5	9e−04	8 / 92	REACTOME_SIGNALING_BY_NOTCH
6	9e−04	6 / 52	PID_NOTCH_PATHWAY
7	1e−03	8 / 93	REACTOME_SIGNALING_BY_FGFR
8	2e−03	5 / 41	REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING
9	2e−03	3 / 12	PID_LPA4_PATHWAY
10	2e−03	3 / 12	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
11	2e−03	3 / 12	REACTOME_TRAF3_DEPENDENT_IRF_ACTIVATION_PATHWAY
12	2e−03	7 / 83	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR
13	2e−03	5 / 43	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES
14	2e−03	8 / 107	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
15	2e−03	7 / 84	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION
16	3e−03	29 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
17	3e−03	5 / 44	PID_HES_HEY_PATHWAY
18	3e−03	4 / 27	REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION
19	3e−03	4 / 27	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
20	3e−03	4 / 27	NOJIMA_SFRP2_TARGETS_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.07	3 / 43	LENZ_Stromal signature 2
2	0.08	32 / 1128	SPANG_BCR DN
3	0.12	1 / 6	DAVE_MHCCII BL DN
4	0.13	9 / 268	SPANG_IL21 UP
5	0.16	122 / 5184	HOPP_Txn_transition
6	0.17	8 / 247	ZHANG_DLBCL mutated
7	0.25	1 / 13	BENTINK_mBL UP
8	0.28	1 / 15	WRIGHT_ABC UP
9	0.31	1 / 17	Aukema_BCL2 UP_BCL6 DN
10	0.34	29 / 1218	SPANG_BCR UP
11	0.43	3 / 109	ROSOLOWSKI_green total
12	0.48	49 / 2211	HOPP_Repetitive
13	0.52	1 / 33	LEE_Developmental_regulators
14	0.54	3 / 129	DAVE_BL−vs−DLBCL
15	0.54	2 / 82	ROSOLOWSKI_green UP
16	0.56	120 / 5538	HOPP_Weak_txn
17	0.58	123 / 5693	HOPP_Weak_enhancer
18	0.58	2 / 89	ROSOLOWSKI_blue total
19	0.60	1 / 42	CARO_OxPhos_in_DLBCL_UP
20	0.62	149 / 6929	HOPP_Txn_elongation

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	0.2	1 / 9	PALMER_CD8+ T−Cell signature up
2	0.2	1 / 12	WIRTH_Cerebellum
3	0.2	1 / 13	WIRTH_Thyroid gland
4	0.4	3 / 107	WIRTH_Testis
5	0.5	3 / 114	PALMER_T−Cell signature up
6	0.5	1 / 32	WIRTH_Placenta
7	0.6	4 / 194	PALMER_B−Cell signature up
8	0.6	1 / 46	WIRTH_Liver
9	0.6	7 / 350	WIRTH_Immune system
10	0.6	7 / 350	WIRTH_Nervous System
11	1.0	2 / 225	PALMER_Granulocytes signature up
12	1.0	0 / 32	WIRTH_Pancreas
13	1.0	0 / 11	WIRTH_Sec. lymphoid organs
14	1.0	0 / 11	WIRTH_Prim. lymphoid organs
15	1.0	0 / 13	WIRTH_B−cells
16	1.0	0 / 8	WIRTH_Tonsil
17	1.0	0 / 12	WIRTH_Thymus
18	1.0	0 / 12	WIRTH_Lymphocytes
19	1.0	0 / 5	WIRTH_Bone marrow
20	1.0	0 / 11	WIRTH_Globus pallidus

BP

Rank	p−value	#in/all	Geneset
1	2e−06	6 / 19	protein targeting to Golgi
2	3e−05	6 / 28	intracellular transport
3	3e−04	5 / 27	retina homeostasis
4	7e−04	9 / 111	Notch signaling pathway
5	1e−03	4 / 23	secondary metabolic process
6	1e−03	4 / 23	spliceosomal complex assembly
7	2e−03	5 / 43	autophagic vacuole assembly
8	3e−03	16 / 336	protein ubiquitination
9	3e−03	53 / 1664	transcription, DNA−templated
10	4e−03	10 / 166	epidermal growth factor receptor signaling pathway
11	4e−03	4 / 30	cellular response to calcium ion
12	4e−03	32 / 897	vesicle−mediated transport
13	5e−03	13 / 259	protein targeting
14	5e−03	3 / 16	renal system development
15	6e−03	3 / 17	cellular response to nitrogen starvation
16	6e−03	5 / 54	retrograde transport, endosome to Golgi
17	8e−03	3 / 19	positive regulation of erythrocyte differentiation
18	1e−02	8 / 136	fibroblast growth factor receptor signaling pathway
19	1e−02	4 / 39	retinoid metabolic process
20	1e−02	3 / 21	nucleophagy

CC

Rank	p−value	#in/all	Geneset
1	0.001	3 / 11	Gemini of coiled bodies
2	0.002	3 / 12	SMN complex
3	0.004	12 / 223	lysosomal membrane
4	0.005	5 / 52	coated pit
5	0.006	3 / 17	SMN−Sm protein complex
6	0.008	146 / 5696	nucleus
7	0.015	3 / 24	Cul3−RING ubiquitin ligase complex
8	0.020	4 / 48	peroxisomal membrane
9	0.027	2 / 12	U4/U6 x U5 tri−snRNP complex
10	0.041	2 / 15	pre−autophagosomal structure membrane
11	0.051	5 / 92	spliceosomal complex
12	0.066	244 / 10605	intracellular
13	0.066	67 / 2577	nucleoplasm
14	0.083	3 / 47	Cajal body
15	0.090	5 / 109	peroxisome
16	0.091	4 / 78	ubiquitin ligase complex
17	0.095	22 / 747	nucleolus
18	0.096	16 / 512	microtubule organizing center
19	0.103	2 / 25	MLL1 complex
20	0.114	3 / 54	intermediate filament cytoskeleton

Disease

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	BCHETNIA_EBM up
2	0.36	1 / 20	BCHETNIA_EBM−DM up
3	0.62	6 / 294	GUDJ_psoriasis down
4	1.00	2 / 435	GUDJ_psoriasis 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	0.004	7 / 94	HALLMARK_ANDROGEN_RESPONSE
2	0.025	3 / 29	HALLMARK_NOTCH_SIGNALING
3	0.031	7 / 137	HALLMARK_UV_RESPONSE_DN
4	0.128	3 / 57	HALLMARK_MYC_TARGETS_V2
5	0.138	4 / 91	HALLMARK_PROTEIN_SECRETION
6	0.181	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	0.319	3 / 91	HALLMARK_BILE_ACID_METABOLISM
8	0.322	2 / 53	HALLMARK_TGF_BETA_SIGNALING
9	0.340	5 / 176	HALLMARK_HYPOXIA
10	0.343	3 / 95	HALLMARK_SPERMATOGENESIS
11	0.344	5 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.365	4 / 140	HALLMARK_INFLAMMATORY_RESPONSE
13	0.378	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	0.395	4 / 146	HALLMARK_DNA_REPAIR
15	0.411	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
16	0.426	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
17	0.483	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
18	0.496	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
19	0.510	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
20	0.521	3 / 126	HALLMARK_ALLOGRAFT_REJECTION

MF

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 11	aldo−keto reductase (NADP) activity
2	1e−03	14 / 244	ubiquitin−protein transferase activity
3	3e−03	3 / 13	GABA receptor binding
4	6e−03	3 / 17	receptor signaling complex scaffold activity
5	8e−03	17 / 405	ligase activity
6	1e−02	3 / 21	RNA polymerase II transcription corepressor activity
7	1e−02	3 / 22	ribonucleoprotein complex binding
8	1e−02	4 / 41	ATPase activity, coupled to transmembrane movement of substances
9	1e−02	14 / 325	protein serine/threonine kinase activity
10	1e−02	4 / 43	SMAD binding
11	2e−02	2 / 10	adenylate cyclase activity
12	2e−02	2 / 10	glucocorticoid receptor binding
13	2e−02	2 / 11	insulin−like growth factor receptor binding
14	2e−02	3 / 29	ubiquitin−like protein transferase activity
15	2e−02	17 / 461	transferase activity, transferring phosphorus−containing groups
16	3e−02	4 / 52	p53 binding
17	3e−02	3 / 30	RNA polymerase II transcription factor binding
18	3e−02	2 / 12	phosphorus−oxygen lyase activity
19	3e−02	23 / 691	kinase activity
20	3e−02	2 / 13	long−chain fatty acid−CoA ligase activity

TF

Rank	p−value	#in/all	Geneset
1	0.04	2 / 15	NOWICK_TF
2	0.15	16 / 553	ICGC_RxraPcr1_targets
3	0.21	68 / 2836	ICGC_BatfPcr1_targets
4	0.40	89 / 3966	ICGC_Pu1_targets
5	0.43	14 / 595	ICGC_NrsfPcr2_targets
6	0.48	60 / 2714	ICGC_Irf4_targets
7	0.56	113 / 5219	ICGC_Tcf3_targets
8	0.59	27 / 1273	ICGC_P300_targets
9	0.61	36 / 1701	HEBENSTREIT_high expression TF
10	0.66	26 / 1266	ICGC_NrsfPcr1_targets
11	0.66	115 / 5408	ICGC_Pou2_targets
12	0.71	113 / 5374	ICGC_Pax5_targets
13	0.72	98 / 4689	ICGC_Taf1_targets
14	0.75	13 / 690	ICGC_Atf3_targets
15	0.77	37 / 1872	ICGC_Mef2_targets
16	0.77	111 / 5355	ICGC_Pol2_targets
17	0.77	97 / 4706	ICGC_Sp1_targets
18	0.77	37 / 1878	ICGC_Cebpbsc150_targets
19	0.78	95 / 4617	ICGC_Tcf12_targets
20	0.81	47 / 2391	ICGC_Pbx3_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	21 / 1115	LU_BPDE 1h DN
2	0.9	71 / 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	155 / 5940	Overlap_fetal_midbrain_HetRpts
2	0.031	25 / 769	Overlap_fetal_midbrain_ZNF
3	0.043	13 / 349	Fetal_ZNF
4	0.079	78 / 3081	Mid_Frontal_Lobe_ZNF
5	0.132	6 / 158	Overlap_fetal_midbrain_Het
6	0.157	28 / 1050	Fetal_EnhP
7	0.256	28 / 1122	Fetal_K9K27me3
8	0.278	14 / 534	Mid_Frontal_Lobe_EnhG
9	0.451	18 / 786	Fetal_EnhG
10	0.464	15 / 656	Overlap_fetal_midbrain_EnhP
11	0.493	15 / 668	Mid_Frontal_Lobe_Enh
12	0.497	7 / 304	Fetal_Het
13	0.536	29 / 1333	Fetal_ReprPCWk
14	0.607	16 / 765	Mid_Frontal_Lobe_Het
15	0.666	3 / 156	Mid_Frontal_Lobe_TssA
16	0.686	200 / 9330	Overlap_fetal_midbrain_ReprPC
17	0.694	3 / 163	Fetal_ReprPC
18	0.732	192 / 9020	Overlap_fetal_midbrain_ReprPCWk
19	0.838	17 / 953	Fetal_Enh
20	0.839	200 / 9528	Overlap_fetal_midbrain_Quies

Chr

Rank	p−value	#in/all	Geneset
1	0.02	20 / 552	Chr 10
2	0.10	13 / 398	Chr 20
3	0.10	28 / 993	Chr 2
4	0.14	39 / 1500	Chr 1
5	0.24	18 / 687	Chr 6
6	0.25	18 / 689	Chr 7
7	0.33	25 / 1037	Chr 19
8	0.35	7 / 262	Chr 13
9	0.56	14 / 649	Chr 16
10	0.66	11 / 551	Chr X
11	0.69	9 / 465	Chr 15
12	0.71	4 / 221	Chr 18
13	0.75	16 / 840	Chr 17
14	0.76	13 / 696	Chr 5
15	0.81	10 / 576	Chr 9
16	0.82	15 / 838	Chr 3
17	0.86	5 / 335	Chr 22
18	0.88	7 / 462	Chr 14
19	0.92	8 / 558	Chr 4
20	0.96	1 / 151	Chr 21

Glio

Rank	p−value	#in/all	Geneset
1	0.04	1 / 2	laffaire_hypometh_LGG_vs_control
2	0.11	24 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
3	0.14	1 / 7	KIM amplified & overexpressed in LTS
4	0.14	1 / 7	Shaw_up_in_1p19qdel
5	0.16	3 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	0.18	11 / 365	Down_b
7	0.18	1 / 9	VERHAAK_Brain
8	0.18	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
9	0.18	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
10	0.18	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
11	0.19	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
12	0.19	2 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
13	0.20	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
14	0.20	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
15	0.22	1 / 11	astrocytes_glio
16	0.22	2 / 40	in vivo astrocytes vs. cultured astroglia
17	0.27	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
18	0.30	1 / 16	VERHAAK_NL subtype
19	0.31	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
20	0.33	1 / 18	Shinawi_with_increased_methylation_in_STS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.15	2 / 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 / 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 / 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	3e−04	9 / 100	hsa−miR−1299
2	4e−04	11 / 146	hsa−miR−655
3	7e−04	6 / 49	hsa−miR−1224−3p
4	1e−03	5 / 37	hsa−miR−197
5	4e−03	4 / 30	hsa−miR−654−5p
6	6e−03	15 / 328	hsa−miR−18a
7	6e−03	5 / 53	hsa−miR−337−3p
8	6e−03	10 / 181	hsa−miR−1
9	7e−03	10 / 183	hsa−miR−129−5p
10	7e−03	6 / 78	hsa−miR−890
11	7e−03	7 / 103	hsa−miR−1284
12	8e−03	3 / 19	hsa−miR−645
13	8e−03	3 / 19	hsa−miR−563
14	9e−03	10 / 189	hsa−miR−513a−3p
15	1e−02	13 / 284	hsa−miR−320a
16	1e−02	5 / 60	hsa−miR−1200
17	1e−02	5 / 61	hsa−miR−324−5p
18	1e−02	9 / 170	hsa−miR−320b
19	1e−02	3 / 23	hsa−miR−517a
20	1e−02	7 / 116	hsa−miR−498

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 27	VAQUERIZAS_Lymph node
2	0.2	1 / 9	VAQUERIZAS_Kidney
3	0.2	1 / 12	VAQUERIZAS_Skin
4	0.3	1 / 15	VAQUERIZAS_Bone marrow
5	0.3	1 / 16	VAQUERIZAS_Pancreas
6	0.4	2 / 58	VAQUERIZAS_Lung
7	0.4	1 / 26	VAQUERIZAS_Liver
8	0.5	1 / 33	VAQUERIZAS_Prostate
9	0.6	1 / 45	VAQUERIZAS_Uterus
10	0.7	1 / 59	VAQUERIZAS_Whole blood
11	1.0	1 / 143	VAQUERIZAS_General
12	1.0	0 / 36	VAQUERIZAS_Fetal brain
13	1.0	0 / 41	VAQUERIZAS_Placenta
14	1.0	0 / 29	VAQUERIZAS_Smooth muscle
15	1.0	0 / 23	VAQUERIZAS_Spinal cord
16	1.0	0 / 38	VAQUERIZAS_Whole brain
17	1.0	0 / 37	VAQUERIZAS_Thymus
18	1.0	0 / 40	VAQUERIZAS_Thyroid
19	1.0	0 / 7	VAQUERIZAS_Appendix
20	1.0	0 / 29	VAQUERIZAS_Fetal lung

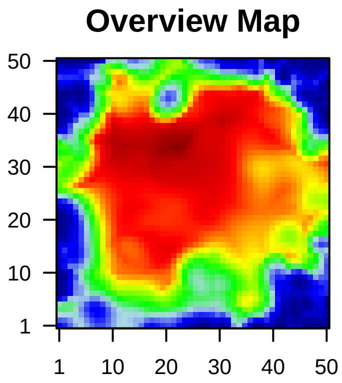
Underexpression Spots

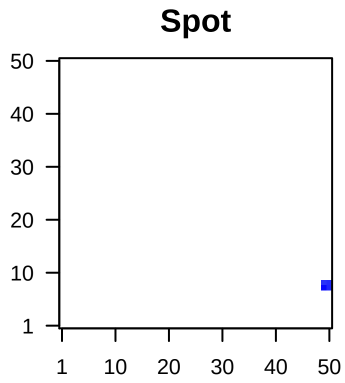
Spot Summary: n

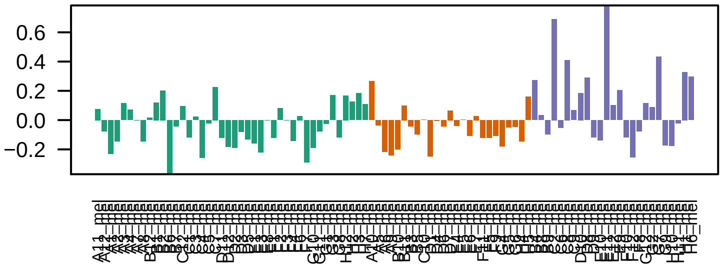
metagenes = 4
genes = 28

<r> metagenes = 0.99
<r> genes = 0.13
beta: r2= 1.82 / log p= −Inf

samples with spot = 12 (13 %)
MSC1 : 2 (4.8 %)
MSC2 : 1 (4 %)
MSC3 : 9 (36 %)





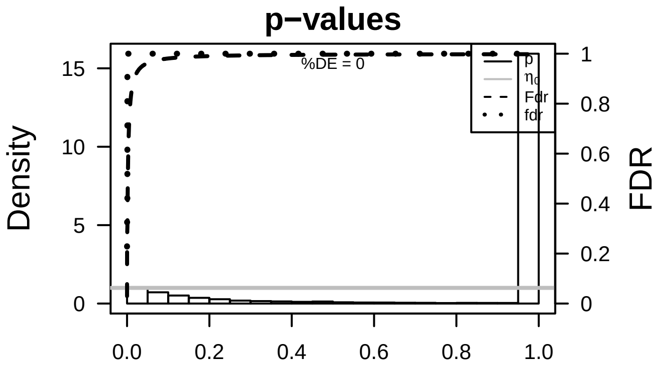


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	SOCS2	1.83	−0.58	0.29	SOCS2	suppressor of cytokine signaling 2 [Source:HGNC Symbol;Ac
2	LIPT2	1.75	−0.15	0.39	LIPT2	lipoyl(octanoyl) transferase 2 (putative) [Source:HGNC Symb
3	GPR176	1.6	−0.15	0.48	GPR176	G protein−coupled receptor 176 [Source:HGNC Symbol;Acc:
4	RAB8B	1.49	−0.43	0.42	RAB8B	RAB8B, member RAS oncogene family [Source:HGNC Symb
5	FBXO46	1.47	−0.33	0.26	FBXO46	F−box protein 46 [Source:HGNC Symbol;Acc:HGNC:25069]
6	RUNX1T1	1.45	−0.12	0.42	RUNX1T1	runt−related transcription factor 1; translocated to, 1 (cyclin D
7	VPS8	1.45	−0.89	0.28	VPS8	vacuolar protein sorting 8 homolog (S. cerevisiae) [Source:H
8	IRF2	1.37	−0.71	0.28	IRF2	interferon regulatory factor 2 [Source:HGNC Symbol;Acc:HG
9	CDC42EP3	1.36	−0.65	0.27	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3 [Source:HG
10	ZNF621	1.36	−0.57	0.26	ZNF621	zinc finger protein 621 [Source:HGNC Symbol;Acc:HGNC:24
11	C17orf51	1.36	−0.29	0.33	C17orf51	chromosome 17 open reading frame 51 [Source:HGNC Symb
12	SENP7	1.34	−0.51	0.32	SENP7	SUMO1/sentrin specific peptidase 7 [Source:HGNC Symbol;
13	ACTN1	1.3	−0.99	0.37	ACTN1	actinin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:163]
14	ZMYND11	1.29	−0.51	0.22	ZMYND11	zinc finger, MYND−type containing 11 [Source:HGNC Symbo
15	GOLGA8B	1.21	−0.71	0.3	GOLGA8B	golgin A8 family, member B [Source:HGNC Symbol;Acc:HGN
16	TCF3	1.18	−0.66	0.25	TCF3	transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:116
17	PTPRA	1.11	−0.72	0.25	PTPRA	protein tyrosine phosphatase, receptor type, A [Source:HGN
18	AKT1	1.04	−0.77	0.25	AKT1	v−akt murine thymoma viral oncogene homolog 1 [Source:H
19	DRAM2	1.04	−1.33	0.2	DRAM2	DNA−damage regulated autophagy modulator 2 [Source:HG
20	BCL2L1	1.01	−0.73	0.27	BCL2L1	BCL2−like 1 [Source:HGNC Symbol;Acc:HGNC:992]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−06	3 / 16	BP	negative regulation of autophagy
2	3e−05	3 / 32	GSEA	VALK_AML_WITH_FLT3_ITD
3	1e−04	5 / 263	miRN	hsa−miR−92b
4	1e−04	5 / 268	miRN	hsa−miR−363
5	1e−04	5 / 271	miRN	hsa−miR−92a
6	1e−04	3 / 55	Canc	PanCan_JAK−ST_geneset_nanostring
7	2e−04	5 / 296	miRN	hsa−miR−25
8	3e−04	5 / 321	miRN	hsa−miR−32
9	3e−04	5 / 327	miRN	hsa−miR−367
10	4e−04	2 / 15	BP	negative regulation of release of cytochrome c from mitochondria
11	4e−04	6 / 522	BP	apoptotic process
12	4e−04	3 / 75	GSEA	KANG_IMMORTALIZED_BY_TERT_UP
13	4e−04	3 / 79	miRN	hsa−miR−569
14	5e−04	3 / 82	Canc	PanCan_TXmisReg_geneset_nanostring
15	5e−04	9 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
16	7e−04	3 / 92	GSEA	KEGG_JAK_STAT_SIGNALING_PATHWAY
17	7e−04	2 / 21	GSEA	BIOCARTA_BAD_PATHWAY
18	7e−04	3 / 94	HM	HALLMARK_ANDROGEN_RESPONSE
19	8e−04	5 / 394	BP	cell proliferation
20	8e−04	2 / 22	BP	negative regulation of JNK cascade
21	8e−04	2 / 22	GSEA	BIOCARTA_CHEMICAL_PATHWAY
22	8e−04	2 / 22	GSEA	BIOCARTA_RAS_PATHWAY
23	8e−04	2 / 22	GSEA	VALK_AML_CLUSTER_2
24	8e−04	2 / 23	GSEA	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
25	8e−04	2 / 23	GSEA	GOLUB_ALL_VS_AML_UP
26	9e−04	2 / 24	BP	apoptotic mitochondrial changes
27	9e−04	2 / 24	BP	germ cell development
28	1e−03	2 / 26	BP	negative regulation of extrinsic apoptotic signaling pathway in absence of li
29	1e−03	2 / 26	GSEA	PID_CD40_PATHWAY
30	1e−03	2 / 26	GSEA	ONO_AML1_TARGETS_DN
31	1e−03	2 / 27	GSEA	ST_WNT_BETA_CATENIN_PATHWAY
32	1e−03	2 / 27	GSEA	SHIN_B_CELL_LYMPHOMA_CLUSTER_2
33	1e−03	2 / 28	GSEA	PID_IL2_PI3K_PATHWAY
34	1e−03	2 / 28	GSEA	PID_RETINOIC_ACID_PATHWAY
35	1e−03	2 / 28	GSEA	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
36	1e−03	5 / 456	MF	protein binding transcription factor activity
37	1e−03	15 / 3812	Colon	TssD1_Colon
38	2e−03	2 / 32	BP	fertilization
39	2e−03	2 / 32	GSEA	BIOCARTA_IL2RB_PATHWAY
40	2e−03	2 / 34	GSEA	PID_PI3KCI_AKT_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	

BP

Rank	p−value	#in/all	Geneset
1	3e−06	3 / 16	negative regulation of autophagy
2	4e−04	2 / 15	negative regulation of release of cytochrome c from mitochondria
3	4e−04	6 / 522	apoptotic process
4	8e−04	5 / 394	cell proliferation
5	8e−04	2 / 22	negative regulation of JNK cascade
6	9e−04	2 / 24	apoptotic mitochondrial changes
7	9e−04	2 / 24	germ cell development
8	1e−03	2 / 26	negative regulation of extrinsic apoptotic signaling pathway in absence of ligar
9	2e−03	2 / 32	fertilization
10	4e−03	6 / 815	cell death
11	5e−03	2 / 56	intrinsic apoptotic signaling pathway
12	6e−03	2 / 63	cellular response to insulin stimulus
13	8e−03	2 / 71	negative regulation of protein kinase activity
14	1e−02	2 / 81	positive regulation of sequence−specific DNA binding transcription factor activ
15	2e−02	1 / 10	cellular response to peptide
16	2e−02	1 / 10	endothelial cell morphogenesis
17	2e−02	1 / 10	maternal placenta development
18	2e−02	1 / 11	positive regulation of glycogen biosynthetic process
19	2e−02	1 / 11	regulation of G1/S transition of mitotic cell cycle
20	2e−02	1 / 11	response to food

Brain

Rank	p−value	#in/all	Geneset
1	0.004	24 / 9013	Overlap_fetal_midbrain_K9K27me3
2	0.004	24 / 9020	Overlap_fetal_midbrain_ReprPCWk
3	0.023	23 / 9330	Overlap_fetal_midbrain_ReprPC
4	0.050	16 / 5940	Overlap_fetal_midbrain_HetRpts
5	0.126	6 / 1845	Fetal_Quies
6	0.173	3 / 765	Mid_Frontal_Lobe_Het
7	0.183	3 / 786	Fetal_EnhG
8	0.205	3 / 831	Fetal_HetRpts
9	0.267	3 / 953	Fetal_Enh
10	0.270	1 / 166	Mid_Frontal_Lobe_Tx
11	0.278	20 / 9528	Overlap_fetal_midbrain_Quies
12	0.295	2 / 574	Overlap_fetal_midbrain_TssP
13	0.303	5 / 1949	Fetal_TssF
14	0.318	3 / 1050	Fetal_EnhP
15	0.353	2 / 656	Overlap_fetal_midbrain_EnhP
16	0.353	1 / 229	Mid_Frontal_Lobe_TxTrans
17	0.361	2 / 668	Mid_Frontal_Lobe_Enh
18	0.396	5 / 2185	Fetal_TssA
19	0.430	2 / 769	Overlap_fetal_midbrain_ZNF
20	0.440	1 / 304	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 55	PanCan_JAK−ST_geneset_nanostring
2	5e−04	3 / 82	PanCan_TXmisReg_geneset_nanostring
3	2e−03	4 / 298	SPANG_BCL6−index2
4	2e−02	2 / 111	PanCan_RAS_geneset_nanostring
5	2e−02	2 / 120	PanCan_CC+Apop_geneset_nanostring
6	3e−02	2 / 156	PanCan_PI3K_geneset_nanostring
7	2e−01	0 / 14	LIU_PROSTATE_CANCER_DN
8	2e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
9	2e−01	1 / 121	PanCan_MAPK_geneset_nanostring
10	5e−01	1 / 401	Lembcke_Colonic Inflammation
11	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1e+00	0 / 12	LIU_BREAST_CANCER
16	1e+00	0 / 14	LIU_COMMON_CANCER_GENES
17	1e+00	0 / 14	LIU_LIVER_CANCER
18	1e+00	0 / 12	LIU_PROSTATE_CANCER_UP
19	1e+00	0 / 15	WANG_ER_UP
20	1e+00	0 / 5	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	0.005	8 / 1468	mitochondrion
2	0.006	2 / 64	Golgi cisterna membrane
3	0.013	2 / 91	nuclear matrix
4	0.019	1 / 10	fascia adherens
5	0.019	2 / 113	spindle
6	0.022	1 / 12	holo TFIIH complex
7	0.024	1 / 13	pseudopodium
8	0.026	1 / 14	trans−Golgi network transport vesicle
9	0.028	2 / 138	cell−cell junction
10	0.028	2 / 138	microtubule cytoskeleton
11	0.028	1 / 15	RNA polymerase II transcription factor complex
12	0.039	1 / 21	secretory granule membrane
13	0.049	4 / 745	cytoplasmic membrane−bounded vesicle
14	0.055	2 / 202	actin cytoskeleton
15	0.059	1 / 32	chloride channel complex
16	0.059	1 / 32	nuclear nucleosome
17	0.064	3 / 491	perinuclear region of cytoplasm
18	0.066	1 / 36	microvillus
19	0.066	1 / 36	phagocytic vesicle
20	0.068	1 / 37	platelet alpha granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.01	4 / 465	Chr 15
2	0.14	3 / 696	Chr 5
3	0.17	2 / 398	Chr 20
4	0.21	3 / 838	Chr 3
5	0.22	2 / 462	Chr 14
6	0.43	2 / 775	Chr 12
7	0.59	2 / 1037	Chr 19
8	0.59	1 / 469	Chr 8
9	0.65	1 / 551	Chr X
10	0.65	1 / 552	Chr 10
11	0.66	1 / 558	Chr 4
12	0.79	1 / 801	Chr 11
13	0.79	2 / 1500	Chr 1
14	0.80	1 / 840	Chr 17
15	0.86	1 / 993	Chr 2
16	1.00	0 / 262	Chr 13
17	1.00	0 / 649	Chr 16
18	1.00	0 / 221	Chr 18
19	1.00	0 / 151	Chr 21
20	1.00	0 / 335	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	15 / 3812	TssD1_Colon
2	0.003	12 / 2798	TxEnhG1_Colon
3	0.015	3 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	0.030	23 / 9482	TssA_Colon
5	0.037	11 / 3383	EnhWk2_Colon
6	0.042	12 / 3897	Quies1_Colon
7	0.087	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	0.093	22 / 9653	Enh_Colon
9	0.100	20 / 8580	TxWk_Colon
10	0.121	8 / 2698	EnhA_Colon
11	0.121	3 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	0.165	3 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
13	0.169	20 / 9027	Tx_Colon
14	0.198	2 / 436	K9acLow_Colon
15	0.199	1 / 117	Marisa_CRC−cluster−b
16	0.220	1 / 131	Marisa_CRC−cluster−a
17	0.234	16 / 7203	TssF_Colon
18	0.263	4 / 1386	Het_Colon
19	0.280	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	0.280	5 / 1889	ReprPCWk_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 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
2	0.02	1 / 9	Mukasa_UP_in_GBM
3	0.02	3 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.03	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
5	0.06	1 / 32	Colman_survival_associated
6	0.09	1 / 49	developing astrocytes
7	0.10	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
8	0.12	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	0.17	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.17	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.18	1 / 103	GIEZELT_GBM_WT_up_VS_mut
12	0.21	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	0.29	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
14	0.47	1 / 332	Up
15	0.48	2 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
16	1.00	0 / 15	VERHAAK_CL subtype
17	1.00	0 / 15	VERHAAK_MES subtype
18	1.00	0 / 16	VERHAAK_NL subtype
19	1.00	0 / 14	VERHAAK_PN subtype
20	1.00	0 / 23	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	3 / 32	VALK_AML_WITH_FLT3_ITD
2	4e−04	3 / 75	KANG_IMMORTALIZED_BY_TERT_UP
3	5e−04	9 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	7e−04	3 / 92	KEGG_JAK_STAT_SIGNALING_PATHWAY
5	7e−04	2 / 21	BIOCARTA_BAD_PATHWAY
6	8e−04	2 / 22	BIOCARTA_CHEMICAL_PATHWAY
7	8e−04	2 / 22	BIOCARTA_RAS_PATHWAY
8	8e−04	2 / 22	VALK_AML_CLUSTER_2
9	8e−04	2 / 23	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
10	8e−04	2 / 23	GOLUB_ALL_VS_AML_UP
11	1e−03	2 / 26	PID_CD40_PATHWAY
12	1e−03	2 / 26	ONO_AML1_TARGETS_DN
13	1e−03	2 / 27	ST_WNT_BETA_CATENIN_PATHWAY
14	1e−03	2 / 27	SHIN_B_CELL_LYMPHOMA_CLUSTER_2
15	1e−03	2 / 28	PID_IL2_PI3K_PATHWAY
16	1e−03	2 / 28	PID_RETINOIC_ACID_PATHWAY
17	1e−03	2 / 28	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
18	2e−03	2 / 32	BIOCARTA_IL2RB_PATHWAY
19	2e−03	2 / 34	PID_PI3KCI_AKT_PATHWAY
20	2e−03	2 / 34	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP

HM

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 94	HALLMARK_ANDROGEN_RESPONSE
2	3e−02	2 / 140	HALLMARK_APOPTOSIS
3	4e−02	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
4	2e−01	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	2e−01	1 / 93	HALLMARK_PEROXISOME
6	2e−01	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	2e−01	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
8	3e−01	1 / 162	HALLMARK_COMPLEMENT
9	3e−01	1 / 167	HALLMARK_APICAL_JUNCTION
10	3e−01	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	3e−01	1 / 188	HALLMARK_ADIPOGENESIS
12	1e+00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	1e+00	0 / 176	HALLMARK_HYPOXIA
14	1e+00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1e+00	0 / 195	HALLMARK_MITOTIC_SPINDLE
16	1e+00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	1e+00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
18	1e+00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	1e+00	0 / 146	HALLMARK_DNA_REPAIR
20	1e+00	0 / 196	HALLMARK_G2M_CHECKPOINT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	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	0.009	21 / 7592	HOPP_Active_promoter
2	0.011	1 / 6	MASCQUE_mBL UP
3	0.013	16 / 5184	HOPP_Txn_transition
4	0.024	1 / 13	BENTINK_mBL UP
5	0.043	1 / 23	DAVE_Immune response 1
6	0.046	18 / 6929	HOPP_Txn_elongation
7	0.059	17 / 6564	HOPP_Strong_enhancer
8	0.060	2 / 212	LENZ_Stromal signature 1
9	0.084	2 / 256	SPANG_IL21 DN
10	0.160	4 / 1128	SPANG_BCR DN
11	0.217	1 / 129	DAVE_BL−vs−DLBCL
12	0.366	15 / 7209	HOPP_Weak_promoter
13	0.375	1 / 247	ZHANG_DLBCL mutated
14	0.400	1 / 268	SPANG_IL21 UP
15	0.408	1 / 275	TARTE_Mature plasma cell signature
16	0.467	7 / 3396	HOPP_Repressed
17	0.608	4 / 2188	HOPP_Poised_promoter
18	0.617	4 / 2211	HOPP_Repetitive
19	0.638	10 / 5538	HOPP_Weak_txn
20	0.682	2 / 1218	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	0.001	5 / 456	protein binding transcription factor activity
2	0.019	1 / 10	voltage−gated ion channel activity
3	0.021	1 / 11	insulin−like growth factor receptor binding
4	0.021	1 / 11	vinculin binding
5	0.024	1 / 13	GTP−Rho binding
6	0.026	1 / 14	enhancer binding
7	0.026	1 / 14	regulatory region DNA binding
8	0.026	1 / 14	transmembrane receptor protein tyrosine phosphatase activity
9	0.030	1 / 16	phosphatidylinositol−3,4−bisphosphate binding
10	0.030	1 / 16	RNA polymerase II carboxy−terminal domain kinase activity
11	0.033	1 / 18	14−3−3 protein binding
12	0.033	1 / 18	mitogen−activated protein kinase kinase kinase binding
13	0.039	1 / 21	E−box binding
14	0.041	1 / 22	amino acid transmembrane transporter activity
15	0.042	2 / 174	transcription corepressor activity
16	0.043	1 / 23	bHLH transcription factor binding
17	0.046	1 / 25	protein serine/threonine/tyrosine kinase activity
18	0.048	1 / 26	chloride channel activity
19	0.048	1 / 26	protein kinase inhibitor activity
20	0.050	1 / 27	protein phosphatase 2A binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	5 / 263	hsa−miR−92b
2	1e−04	5 / 268	hsa−miR−363
3	1e−04	5 / 271	hsa−miR−92a
4	2e−04	5 / 296	hsa−miR−25
5	3e−04	5 / 321	hsa−miR−32
6	3e−04	5 / 327	hsa−miR−367
7	4e−04	3 / 79	hsa−miR−569
8	2e−03	3 / 132	hsa−miR−199b−5p
9	2e−03	2 / 37	hsa−miR−501−3p
10	3e−03	3 / 146	hsa−miR−655
11	3e−03	3 / 147	hsa−miR−143
12	3e−03	3 / 149	hsa−miR−518a−5p
13	3e−03	3 / 153	hsa−miR−200c
14	3e−03	2 / 43	hsa−miR−331−5p
15	3e−03	3 / 154	hsa−miR−527
16	3e−03	3 / 157	hsa−miR−141
17	4e−03	2 / 47	hsa−miR−1291
18	4e−03	3 / 165	hsa−miR−153
19	4e−03	2 / 50	hsa−miR−1201
20	4e−03	2 / 50	hsa−miR−610

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	1 / 13	BENTINK_src.10
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 / 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	2 / 553	ICGC_RxraPcr1_targets
2	0.4	2 / 690	ICGC_Atf3_targets
3	0.5	6 / 2836	ICGC_BatfPcr1_targets
4	0.6	9 / 4706	ICGC_Sp1_targets
5	0.6	7 / 3700	ICGC_Nfatc1_targets
6	0.6	4 / 2136	ICGC_GabpPcr2_targets
7	0.6	9 / 4879	ICGC_Pmlsc71910_targets
8	0.6	8 / 4385	ICGC_Atf2_targets
9	0.6	8 / 4414	ICGC_Bclaf101388_targets
10	0.6	3 / 1701	HEBENSTREIT_high expression TF
11	0.6	7 / 3924	ICGC_Zeb1_targets
12	0.6	2 / 1139	HEBENSTREIT_low expression TF
13	0.7	7 / 3966	ICGC_Pu1_targets
14	0.7	1 / 595	ICGC_NrsfPcr2_targets
15	0.7	8 / 4689	ICGC_Taf1_targets
16	0.7	3 / 1872	ICGC_Mef2_targets
17	0.7	3 / 1878	ICGC_Cebpbsc150_targets
18	0.7	9 / 5355	ICGC_Pol2_targets
19	0.7	8 / 4829	ICGC_Nficsc81335_targets
20	0.8	8 / 4909	ICGC_Stat5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	1 / 15	VAQUERIZAS_Bone marrow
2	0.03	1 / 16	VAQUERIZAS_Adrenal gland
3	0.05	1 / 27	VAQUERIZAS_Lymph node
4	0.11	1 / 59	VAQUERIZAS_Whole blood
5	0.24	1 / 143	VAQUERIZAS_General
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 / 29	VAQUERIZAS_Smooth muscle
11	1.00	0 / 45	VAQUERIZAS_Uterus
12	1.00	0 / 9	VAQUERIZAS_Kidney
13	1.00	0 / 23	VAQUERIZAS_Spinal cord
14	1.00	0 / 38	VAQUERIZAS_Whole brain
15	1.00	0 / 37	VAQUERIZAS_Thymus
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	0.2	1 / 114	PALMER_T−Cell signature up
2	0.3	1 / 194	PALMER_B−Cell signature up
3	0.3	1 / 225	PALMER_Granulocytes signature up
4	0.5	1 / 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 / 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 / 350	WIRTH_Nervous System
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	0.6	7 / 3682	LU_BPDE 0.005 DN
2	0.6	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	

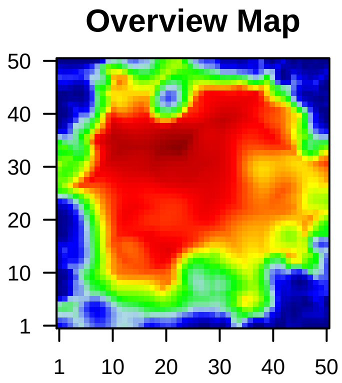
Underexpression Spots

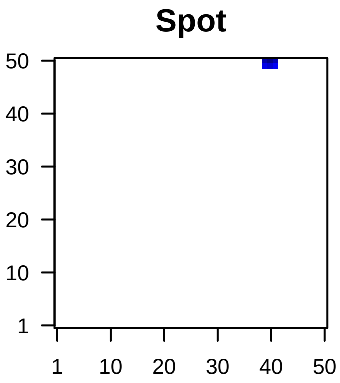
Spot Summary: o

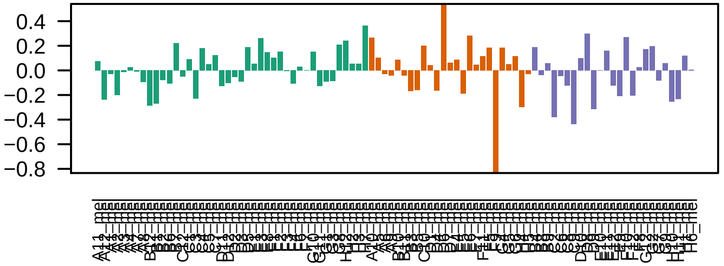
metagenes = 6
genes = 84

<r> metagenes = 0.98
<r> genes = 0.11
beta: r2= 1.65 / log p= −Inf

samples with spot = 12 (13 %)
MSC1 : 5 (11.9 %)
MSC2 : 4 (16 %)
MSC3 : 3 (12 %)





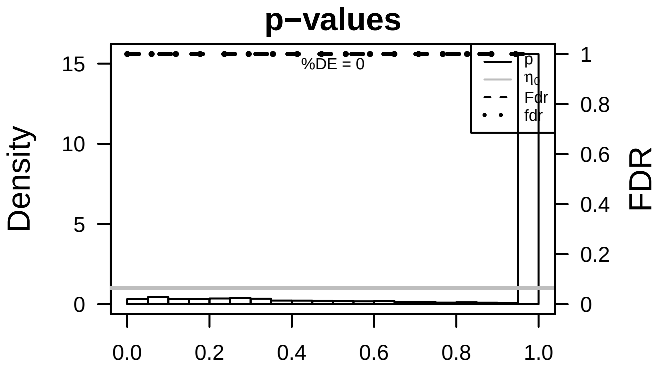


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	EMC1	1.82	−0.59	0.33	EMC1	ER membrane protein complex subunit 1 [Source:HGNC Syn
2	SELL	1.69	−0.16	0.33	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
3	LIPT1	1.57	−0.38	0.29	LIPT1	lipoyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:29569]
4	FUCA1	1.57	−0.24	0.34	FUCA1	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:H
5	GPX8	1.56	−0.72	0.32	GPX8	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Ac
6	FAM114A2	1.56	−0.67	0.26	FAM114A2	family with sequence similarity 114, member A2 [Source:HGN
7	PLA2G4A	1.54	−0.31	0.29	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium−dependent)
8	PEX13	1.54	−0.59	0.25	PEX13	peroxisomal biogenesis factor 13 [Source:HGNC Symbol;Acc
9	INSIG2	1.46	−0.73	0.36	INSIG2	insulin induced gene 2 [Source:HGNC Symbol;Acc:HGNC:20
10	ETFDH	1.46	−0.74	0.32	ETFDH	electron−transferring−flavoprotein dehydrogenase [Source:H
11	IFITM2	1.41	−0.89	0.28	IFITM2	interferon induced transmembrane protein 2 [Source:HGNC
12	MVK	1.37	−0.38	0.26	MVK	mevalonate kinase [Source:HGNC Symbol;Acc:HGNC:7530]
13	TRMT61B	1.36	−0.96	0.32	TRMT61B	tRNA methyltransferase 61B [Source:HGNC Symbol;Acc:HG
14	JMJD4	1.33	−0.48	0.24	JMJD4	jumonji domain containing 4 [Source:HGNC Symbol;Acc:HGN
15	MED20	1.33	−0.62	0.29	MED20	mediator complex subunit 20 [Source:HGNC Symbol;Acc:HG
16	GOLGA2	1.32	−0.82	0.37	GOLGA2	golgin A2 [Source:HGNC Symbol;Acc:HGNC:4425]
17	BRE	1.31	−0.94	0.37	BRE	brain and reproductive organ−expressed (TNFRSF1A modula
18	VPS37A	1.3	−0.54	0.38	VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae) [Source
19	C1GALT1C1	1.29	−0.93	0.38	C1GALT1C1	C1GALT1−specific chaperone 1 [Source:HGNC Symbol;Acc:
20	ZFP90	1.27	−0.47	0.31	ZFP90	ZFP90 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−09	77 / 9482	Colon	TssA_Colon
2	3e−08	64 / 6929	Lympl	HOPP_Txn_elongation
3	5e−08	67 / 7592	Lympl	HOPP_Active_promoter
4	8e−07	73 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	2e−06	69 / 8580	Colon	TxWk_Colon
6	2e−06	55 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
7	7e−06	70 / 9027	Colon	Tx_Colon
8	6e−05	68 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
9	1e−04	46 / 5184	Lympl	HOPP_Txn_transition
10	2e−04	64 / 8415	Colon	Quies3_Colon
11	3e−04	57 / 7209	Lympl	HOPP_Weak_promoter
12	4e−04	47 / 5538	Lympl	HOPP_Weak_txn
13	4e−04	21 / 1701	TF	HEBENSTREIT_high expression TF
14	6e−04	3 / 30	BP	negative regulation of viral genome replication
15	1e−03	16 / 1218	Lympl	SPANG_BCR UP
16	1e−03	8 / 379	GSEA	LIM_MAMMARY_STEM_CELL_DN
17	1e−03	13 / 890	GSEA	ACEVEDO_LIVER_CANCER_UP
18	2e−03	2 / 12	BP	negative regulation of DNA damage response, signal transduction by p53 c
19	2e−03	7 / 315	Glio	WILLSCHER_GBM_Verhaak−PNwt & CL_up
20	2e−03	8 / 408	GSEA	ZHANG_BREAST_CANCER_PROGENITORS_UP
21	2e−03	4 / 98	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
22	2e−03	4 / 100	GSEA	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER
23	3e−03	8 / 422	BP	viral process
24	3e−03	2 / 14	GSEA	KEGG_OTHER_GLYCAN_DEGRADATION
25	3e−03	2 / 14	GSEA	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS
26	3e−03	45 / 5693	Lympl	HOPP_Weak_enhancer
27	3e−03	59 / 8205	CC	cytoplasm
28	4e−03	3 / 57	CC	proteasome complex
29	4e−03	16 / 1383	TF	ICGC_Six5_targets
30	5e−03	16 / 1400	TF	ICGC_Myc_targets
31	6e−03	69 / 10290	Colon	TssWk_Colon
32	6e−03	2 / 21	BP	adipose tissue development
33	7e−03	2 / 22	GSEA	PETRETTO_HEART_MASS_QTL_CIS_DN
34	7e−03	2 / 23	BP	glycosaminoglycan catabolic process
35	8e−03	2 / 24	GSEA	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TF
36	8e−03	4 / 140	miRN	hsa−miR−409−3p
37	9e−03	2 / 25	MF	cytochrome−c oxidase activity
38	1e−02	5 / 230	GSEA	ROZANOV_MMP14_TARGETS_UP
39	1e−02	2 / 27	GSEA	BEIER_GLIOMA_STEM_CELL_UP
40	1e−02	3 / 81	BP	positive regulation of sequence−specific DNA binding transcription factor ac



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	6e−04	3 / 30	negative regulation of viral genome replication
2	2e−03	2 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
3	3e−03	8 / 422	viral process
4	6e−03	2 / 21	adipose tissue development
5	7e−03	2 / 23	glycosaminoglycan catabolic process
6	1e−02	3 / 81	positive regulation of sequence−specific DNA binding transcription factor activ
7	1e−02	2 / 30	cholesterol biosynthetic process
8	2e−02	8 / 570	symbiosis, encompassing mutualism through parasitism
9	2e−02	2 / 34	arachidonic acid metabolic process
10	2e−02	3 / 110	defense response to virus
11	3e−02	2 / 48	positive regulation of proteasomal ubiquitin−dependent protein catabolic proce
12	3e−02	16 / 1730	small molecule metabolic process
13	3e−02	13 / 1325	catabolic process
14	4e−02	5 / 322	mitochondrion organization
15	4e−02	9 / 815	lipid metabolic process
16	5e−02	2 / 61	palate development
17	5e−02	3 / 143	protein homooligomerization
18	5e−02	2 / 62	endosomal transport
19	5e−02	2 / 62	viral life cycle
20	6e−02	1 / 10	cellular response to antibiotic

Brain

Rank	p−value	#in/all	Geneset
1	8e−07	73 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−06	55 / 5940	Overlap_fetal_midbrain_HetRpts
3	6e−05	68 / 9013	Overlap_fetal_midbrain_K9K27me3
4	3e−02	11 / 1050	Fetal_EnhP
5	5e−02	59 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	5e−02	10 / 989	Mid_Frontal_Lobe_Quies
7	6e−02	61 / 9528	Overlap_fetal_midbrain_Quies
8	2e−01	8 / 953	Fetal_Enh
9	2e−01	2 / 158	Overlap_fetal_midbrain_Het
10	4e−01	3 / 383	Fetal_Tx
11	5e−01	5 / 786	Fetal_EnhG
12	5e−01	18 / 3081	Mid_Frontal_Lobe_ZNF
13	5e−01	8 / 1333	Fetal_ReprPCWk
14	5e−01	4 / 656	Overlap_fetal_midbrain_EnhP
15	6e−01	6 / 1065	Overlap_fetal_midbrain_Enh
16	6e−01	2 / 349	Fetal_ZNF
17	6e−01	1 / 163	Fetal_ReprPC
18	6e−01	10 / 1845	Fetal_Quies
19	6e−01	6 / 1122	Fetal_K9K27me3
20	6e−01	3 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	2 / 70	SHAUGHNESSY_MM high risk
2	0.09	1 / 16	GENTLES_modul6
3	0.24	3 / 298	SPANG_BCL6−index2
4	0.31	0 / 14	LIU_COMMON_CANCER_GENES
5	0.38	0 / 14	LIU_PROSTATE_CANCER_DN
6	0.47	1 / 111	PanCan_RAS_geneset_nanostring
7	0.50	1 / 121	PanCan_MAPK_geneset_nanostring
8	0.67	2 / 401	Lembcke_Colonic Inflammation
9	0.77	2 / 489	Lembcke_Normal vs Adenoma
10	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
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	59 / 8205	cytoplasm
2	0.004	3 / 57	proteasome complex
3	0.015	3 / 92	spliceosomal complex
4	0.019	2 / 38	cytoplasmic side of plasma membrane
5	0.026	6 / 401	mitochondrial inner membrane
6	0.030	26 / 3214	protein complex
7	0.035	14 / 1468	mitochondrion
8	0.054	67 / 10605	intracellular
9	0.055	1 / 10	ER membrane protein complex
10	0.055	1 / 10	WASH complex
11	0.061	1 / 11	CD40 receptor complex
12	0.066	1 / 12	STAGA complex
13	0.066	1 / 12	XY body
14	0.071	2 / 77	ciliary basal body
15	0.071	1 / 13	proteasome regulatory particle
16	0.071	1 / 13	transcription factor TFTC complex
17	0.074	2 / 79	catalytic step 2 spliceosome
18	0.075	2 / 80	mitochondrial membrane
19	0.076	1 / 14	ER to Golgi transport vesicle
20	0.076	1 / 14	integral component of peroxisomal membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.02	7 / 462	Chr 14
2	0.02	11 / 993	Chr 2
3	0.08	13 / 1500	Chr 1
4	0.19	6 / 687	Chr 6
5	0.20	6 / 696	Chr 5
6	0.27	4 / 469	Chr 8
7	0.29	3 / 335	Chr 22
8	0.30	6 / 801	Chr 11
9	0.36	2 / 221	Chr 18
10	0.52	5 / 838	Chr 3
11	0.66	2 / 398	Chr 20
12	0.72	3 / 649	Chr 16
13	0.82	2 / 551	Chr X
14	0.84	2 / 576	Chr 9
15	0.86	3 / 840	Chr 17
16	0.91	2 / 689	Chr 7
17	0.93	1 / 465	Chr 15
18	0.94	2 / 775	Chr 12
19	0.96	1 / 552	Chr 10
20	0.96	1 / 558	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−09	77 / 9482	TssA_Colon
2	2e−06	69 / 8580	TxWk_Colon
3	7e−06	70 / 9027	Tx_Colon
4	2e−04	64 / 8415	Quies3_Colon
5	6e−03	69 / 10290	TssWk_Colon
6	5e−02	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
7	6e−02	1 / 11	Budinska_B_Lower crypt−like_DOWN
8	6e−02	8 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	8e−02	10 / 1079	ZNF_Colon
10	2e−01	6 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	2e−01	45 / 7203	TssF_Colon
12	3e−01	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
13	3e−01	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	3e−01	1 / 66	Marisa_CRC−cluster−h
15	4e−01	23 / 3812	TssD1_Colon
16	4e−01	56 / 9653	Enh_Colon
17	4e−01	2 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
18	4e−01	6 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
19	4e−01	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
20	4e−01	1 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.9	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	0.002	7 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.033	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
3	0.082	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	0.117	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
5	0.132	1 / 25	Shaw_down_in_1p19q
6	0.194	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	0.227	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.301	1 / 63	Stuehler_Proteins_up_in_STS
9	0.321	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	0.332	1 / 71	Weller_LGG_A_vs_O_UP
11	0.444	1 / 103	GIEZELT_GBM_WT_up_VS_mut
12	0.523	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.564	2 / 332	Up
14	0.650	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
15	0.877	1 / 365	Down_b
16	1.000	0 / 15	VERHAAK_CL subtype
17	1.000	0 / 15	VERHAAK_MES subtype
18	1.000	0 / 16	VERHAAK_NL subtype
19	1.000	0 / 14	VERHAAK_PN subtype
20	1.000	0 / 23	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	8 / 379	LIM_MAMMARY_STEM_CELL_DN
2	0.001	13 / 890	ACEVEDO_LIVER_CANCER_UP
3	0.002	8 / 408	ZHANG_BREAST_CANCER_PROGENITORS_UP
4	0.002	4 / 98	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
5	0.002	4 / 100	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER
6	0.003	2 / 14	KEGG_OTHER_GLYCAN_DEGRADATION
7	0.003	2 / 14	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS
8	0.007	2 / 22	PETRETTO_HEART_MASS_QTL_CIS_DN
9	0.008	2 / 24	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRAI
10	0.010	5 / 230	ROZANOV_MMP14_TARGETS_UP
11	0.010	2 / 27	BEIER_GLIOMA_STEM_CELL_UP
12	0.011	2 / 28	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
13	0.013	6 / 343	THUM_SYSTOLIC_HEART_FAILURE_UP
14	0.015	9 / 681	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
15	0.015	18 / 1858	PILON_KLF1_TARGETS_DN
16	0.015	2 / 33	PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY
17	0.015	7 / 460	ACEVEDO_LIVER_CANCER_DN
18	0.016	2 / 34	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_4HR
19	0.016	2 / 34	SPIRA_SMOKERS_LUNG_CANCER_UP
20	0.016	2 / 34	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP

HM

Rank	p−value	#in/all	Geneset
1	0.03	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.07	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
3	0.07	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
4	0.07	3 / 169	HALLMARK_XENOBIOTIC_METABOLISM
5	0.09	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	0.23	2 / 162	HALLMARK_COMPLEMENT
7	0.25	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	0.29	2 / 188	HALLMARK_ADIPOGENESIS
9	0.40	1 / 91	HALLMARK_PROTEIN_SECRETION
10	0.40	1 / 91	HALLMARK_BILE_ACID_METABOLISM
11	0.41	1 / 93	HALLMARK_PEROXISOME
12	0.41	1 / 94	HALLMARK_ANDROGEN_RESPONSE
13	0.46	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.51	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
15	0.55	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	0.55	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
17	0.57	1 / 146	HALLMARK_DNA_REPAIR
18	0.57	1 / 148	HALLMARK_KRAS_SIGNALING_UP
19	0.62	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
20	0.62	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	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	3e−08	64 / 6929	HOPP_Txn_elongation
2	5e−08	67 / 7592	HOPP_Active_promoter
3	1e−04	46 / 5184	HOPP_Txn_transition
4	3e−04	57 / 7209	HOPP_Weak_promoter
5	4e−04	47 / 5538	HOPP_Weak_txn
6	1e−03	16 / 1218	SPANG_BCR UP
7	3e−03	45 / 5693	HOPP_Weak_enhancer
8	2e−02	1 / 4	Shaknovich_ABC_hyper_meth
9	4e−02	1 / 7	CARO_OxPhos_vs_BCR_UP
10	4e−02	1 / 8	MASCQUE_GCB UP
11	1e−01	2 / 107	SPANG_LPS 6hrs UP
12	2e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
13	2e−01	41 / 6564	HOPP_Strong_enhancer
14	3e−01	17 / 2563	HOPP_Heterochrom
15	3e−01	1 / 61	SPANG_LPS 6hrs DN
16	4e−01	1 / 82	ROSOLOWSKI_green UP
17	4e−01	1 / 89	ROSOLOWSKI_blue total
18	5e−01	1 / 109	ROSOLOWSKI_green total
19	5e−01	2 / 275	TARTE_Mature plasma cell signature
20	5e−01	2 / 280	SPANG_CD40 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.009	2 / 25	cytochrome−c oxidase activity
2	0.019	2 / 37	histone acetyltransferase activity
3	0.019	8 / 592	oxidoreductase activity
4	0.024	4 / 193	transferase activity, transferring acyl groups
5	0.024	6 / 394	catalytic activity
6	0.055	1 / 10	cAMP response element binding protein binding
7	0.055	1 / 10	glutathione binding
8	0.061	1 / 11	cAMP response element binding
9	0.061	1 / 11	glutathione peroxidase activity
10	0.061	1 / 11	quinone binding
11	0.066	1 / 12	enhancer sequence−specific DNA binding
12	0.066	1 / 12	low−density lipoprotein particle receptor binding
13	0.066	1 / 12	lysophospholipase activity
14	0.066	1 / 12	phospholipase activity
15	0.066	1 / 12	RNA polymerase II transcription factor binding transcription factor activity
16	0.071	1 / 13	Ral GTPase binding
17	0.071	1 / 13	thioesterase binding
18	0.076	1 / 14	endoribonuclease activity
19	0.076	1 / 14	peroxidase activity
20	0.076	1 / 14	phospholipase A2 activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	4 / 140	hsa−miR−409−3p
2	0.028	2 / 46	hsa−miR−1256
3	0.045	3 / 140	hsa−miR−522
4	0.052	2 / 65	hsa−miR−9*
5	0.055	2 / 67	hsa−miR−1246
6	0.066	2 / 74	hsa−miR−1827
7	0.066	1 / 12	hsa−miR−369−5p
8	0.077	3 / 175	hsa−miR−548k
9	0.084	2 / 85	hsa−miR−567
10	0.114	2 / 102	hsa−miR−500
11	0.125	3 / 217	hsa−miR−203
12	0.145	3 / 233	hsa−miR−26a
13	0.150	2 / 121	hsa−miR−664
14	0.152	2 / 122	hsa−miR−515−3p
15	0.156	2 / 124	hsa−miR−223
16	0.157	3 / 242	hsa−miR−26b
17	0.161	1 / 31	hsa−miR−617
18	0.166	2 / 129	hsa−miR−218
19	0.171	1 / 33	hsa−miR−1274b
20	0.174	2 / 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	4e−04	21 / 1701	HEBENSTREIT_high expression TF
2	4e−03	16 / 1383	ICGC_Six5_targets
3	5e−03	16 / 1400	ICGC_Myc_targets
4	1e−02	8 / 553	ICGC_RxraPcr1_targets
5	7e−02	11 / 1171	KIM_MYC targets
6	9e−02	17 / 2136	ICGC_GabpPcr2_targets
7	9e−02	37 / 5408	ICGC_Pou2_targets
8	1e−01	20 / 2714	ICGC_Irf4_targets
9	2e−01	27 / 3966	ICGC_Pu1_targets
10	2e−01	31 / 4682	ICGC_Pol24_targets
11	2e−01	31 / 4689	ICGC_Taf1_targets
12	2e−01	17 / 2391	ICGC_Pbx3_targets
13	2e−01	29 / 4414	ICGC_Bclaf101388_targets
14	2e−01	15 / 2137	ICGC_SrfV0416101_targets
15	2e−01	31 / 4829	ICGC_Nficsc81335_targets
16	2e−01	31 / 4879	ICGC_Pmlsc71910_targets
17	3e−01	26 / 4032	ICGC_Creb1_targets
18	3e−01	13 / 1878	ICGC_Cebpbsc150_targets
19	3e−01	26 / 4054	ICGC_Egr1_targets
20	3e−01	36 / 5890	ICGC_Elf1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
2	0.18	1 / 36	VAQUERIZAS_Fetal brain
3	0.20	1 / 40	VAQUERIZAS_Thyroid
4	0.56	1 / 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	0.07	1 / 13	WIRTH_B−cells
2	0.14	3 / 225	PALMER_Granulocytes signature up
3	0.32	3 / 350	WIRTH_Immune system
4	0.67	1 / 194	PALMER_B−Cell signature up
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 / 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	0.8	5 / 1115	LU_BPDE 1h DN
2	1.0	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	

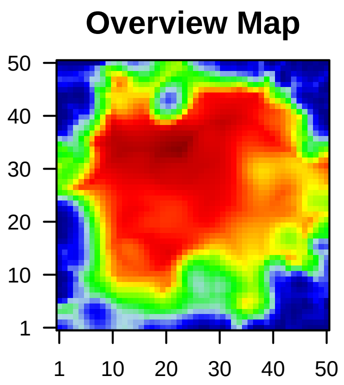
Underexpression Spots

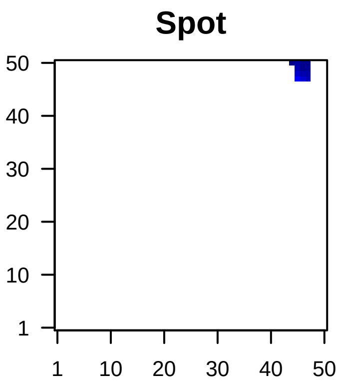
Spot Summary: p

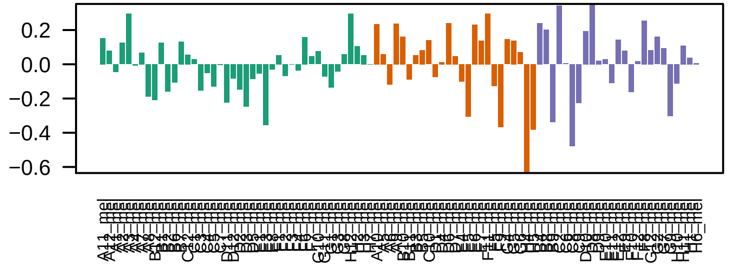
metagenes = 13
genes = 148

<r> metagenes = 0.95
<r> genes = 0.11
beta: r2= 1.79 / log p= −Inf

samples with spot = 13 (14.1 %)
MSC1 : 2 (4.8 %)
MSC2 : 5 (20 %)
MSC3 : 6 (24 %)





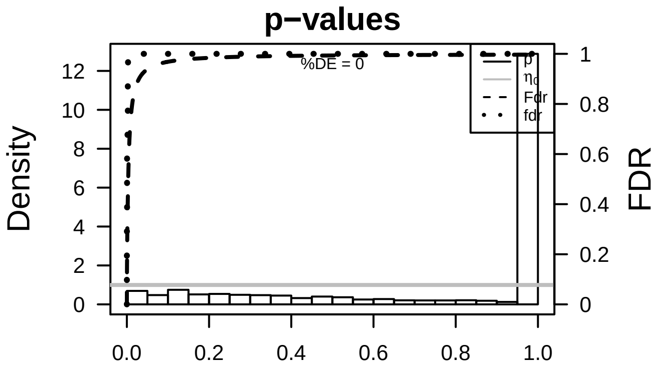


Spot Genelist

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	AP4M1	1.75	−0.28	0.24	AP4M1	adaptor−related protein complex 4, mu 1 subunit [Source:HG
3	PPCDC	1.72	−0.42	0.2	PPCDC	phosphopantothenoylcysteine decarboxylase [Source:HGNC
4	BBS4	1.71	−0.53	0.31	BBS4	Bardet−Biedl syndrome 4 [Source:HGNC Symbol;Acc:HGNC
5	PISD	1.67	−0.46	0.24	PISD	phosphatidylserine decarboxylase [Source:HGNC Symbol;Ac
6	MXI1	1.66	−0.86	0.23	MXI1	MAX interactor 1, dimerization protein [Source:HGNC Symbo
7	TRIB3	1.65	−0.81	0.34	TRIB3	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:1
8	RNF170	1.65	−0.21	0.3	RNF170	ring finger protein 170 [Source:HGNC Symbol;Acc:HGNC:25
9	PTPRR	1.65	−0.28	0.31	PTPRR	protein tyrosine phosphatase, receptor type, R [Source:HGN
10	C2orf74	1.63	−0.75	0.24	C2orf74	chromosome 2 open reading frame 74 [Source:HGNC Symb
11	ORMDL3	1.56	−0.27	0.34	ORMDL3	ORMDL sphingolipid biosynthesis regulator 3 [Source:HGNC
12	PKN1	1.55	−0.45	0.28	PKN1	protein kinase N1 [Source:HGNC Symbol;Acc:HGNC:9405]
13	ELOVL6	1.55	−0.58	0.26	ELOVL6	ELOVL fatty acid elongase 6 [Source:HGNC Symbol;Acc:HG
14	MED29	1.51	−0.56	0.37	MED29	mediator complex subunit 29 [Source:HGNC Symbol;Acc:HG
15	GATSL3	1.49	−0.08	0.28	GATSL3	GATS protein−like 3 [Source:HGNC Symbol;Acc:HGNC:3442
16	COG5	1.49	−0.47	0.24	COG5	component of oligomeric golgi complex 5 [Source:HGNC Sym
17	MARCH9	1.49	−0.56	0.26	MARCH9	membrane−associated ring finger (C3HC4) 9 [Source:HGNC
18	TSEN2	1.47	−0.64	0.17	TSEN2	TSEN2 tRNA splicing endonuclease subunit [Source:HGNC
19	ARHGEF2	1.47	−0.64	0.32	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Sourc
20	POC5	1.43	−0.71	0.27	POC5	POC5 centriolar protein [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−13	133 / 9482	Colon	TssA_Colon
2	7e−09	124 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	9e−08	14 / 235	GSEA	BLUM_RESPONSE_TO_SALIRASIB_UP
4	8e−07	117 / 9027	Colon	Tx_Colon
5	9e−07	80 / 5184	Lymph	HOPP_Txn_transition
6	5e−06	102 / 7592	Lymph	HOPP_Active_promoter
7	1e−05	10 / 176	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
8	1e−05	8 / 108	GSEA	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
9	2e−05	12 / 273	GSEA	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
10	2e−05	113 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
11	3e−05	109 / 8580	Colon	TxWk_Colon
12	9e−05	28 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	1e−04	8 / 147	BP	tRNA metabolic process
14	1e−04	7 / 111	GSEA	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
15	1e−04	4 / 26	GSEA	KRIGE_AMINO_ACID_DEPRIVATION
16	1e−04	91 / 6929	Lymph	HOPP_Txn_elongation
17	3e−04	7 / 126	GSEA	PENG_LEUCINE_DEPRIVATION_UP
18	3e−04	102 / 8205	CC	cytoplasm
19	3e−04	3 / 14	CC	exosome (RNase complex)
20	4e−04	4 / 35	MF	aminoacyl−tRNA ligase activity
21	4e−04	7 / 135	GSEA	KAAB_FAILED_HEART_ATRIUM_DN
22	4e−04	92 / 7203	Colon	TssF_Colon
23	5e−04	4 / 37	GSEA	KAAB_FAILED_HEART_VENTRICLE_DN
24	5e−04	3 / 16	GSEA	TOMIDA_METASTASIS_DN
25	5e−04	28 / 1468	CC	mitochondrion
26	7e−04	3 / 18	GSEA	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN
27	7e−04	4 / 41	GSEA	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
28	8e−04	4 / 42	GSEA	REACTOME_TRNA_AMINOACYLATION
29	8e−04	14 / 532	GSEA	PARENT_MTOR_SIGNALING_UP
30	9e−04	4 / 44	BP	tRNA aminoacylation for protein translation
31	9e−04	18 / 800	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
32	1e−03	9 / 260	GSEA	ENK_UV_RESPONSE_EPIDERMIS_UP
33	1e−03	15 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
34	1e−03	0 / 12	Cance	LIU_PROSTATE_CANCER_UP
35	1e−03	15 / 620	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
36	1e−03	19 / 890	GSEA	ACEVEDO_LIVER_CANCER_UP
37	1e−03	4 / 49	GSEA	PRAMOONJAGO_SOX4_TARGETS_UP
38	1e−03	2 / 6	GSEA	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS
39	1e−03	30 / 1730	BP	small molecule metabolic process
40	2e−03	11 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN



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	1e−04	8 / 147	tRNA metabolic process
2	9e−04	4 / 44	tRNA aminoacylation for protein translation
3	1e−03	30 / 1730	small molecule metabolic process
4	2e−03	9 / 277	translation
5	2e−03	4 / 55	tRNA processing
6	4e−03	8 / 255	cellular amino acid metabolic process
7	4e−03	2 / 10	negative regulation of viral transcription
8	4e−03	2 / 10	protein localization to Golgi apparatus
9	5e−03	2 / 11	negative regulation of B cell proliferation
10	8e−03	2 / 14	RNA phosphodiester bond hydrolysis
11	8e−03	2 / 14	tRNA aminoacylation
12	9e−03	4 / 83	mitochondrial translational elongation
13	9e−03	4 / 83	mitochondrial translational initiation
14	9e−03	4 / 83	mitochondrial translational termination
15	9e−03	2 / 15	nucleoside metabolic process
16	9e−03	2 / 15	protein localization to organelle
17	1e−02	2 / 16	ceramide metabolic process
18	1e−02	3 / 47	proton transport
19	1e−02	8 / 309	intracellular protein transport
20	1e−02	2 / 17	zinc II ion transport

Brain

Rank	p−value	#in/all	Geneset
1	7e−09	124 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−05	113 / 9013	Overlap_fetal_midbrain_K9K27me3
3	4e−03	75 / 5940	Overlap_fetal_midbrain_HetRpts
4	3e−02	106 / 9528	Overlap_fetal_midbrain_Quies
5	4e−02	40 / 3081	Mid_Frontal_Lobe_ZNF
6	8e−02	98 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	1e−01	11 / 765	Mid_Frontal_Lobe_Het
8	2e−01	13 / 989	Mid_Frontal_Lobe_Quies
9	2e−01	8 / 564	Mid_Frontal_Lobe_EnhP
10	2e−01	11 / 831	Fetal_HetRpts
11	3e−01	5 / 349	Fetal_ZNF
12	3e−01	18 / 1548	Mid_Frontal_Lobe_K9K27me3
13	3e−01	14 / 1236	Mid_Frontal_Lobe_ReprPCWk
14	3e−01	11 / 953	Fetal_Enh
15	4e−01	4 / 304	Fetal_Het
16	5e−01	11 / 1050	Fetal_EnhP
17	6e−01	18 / 1845	Fetal_Quies
18	6e−01	13 / 1333	Fetal_ReprPCWk
19	6e−01	7 / 769	Overlap_fetal_midbrain_ZNF
20	8e−01	9 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	0 / 12	LIU_PROSTATE_CANCER_UP
2	0.010	8 / 298	SPANG_BCL6−index2
3	0.104	4 / 180	SPANG_LPS−index2
4	0.121	1 / 13	GENTLES_modul12
5	0.139	1 / 15	WANG_ER_UP
6	0.139	1 / 15	GENTLES_modul1
7	0.147	1 / 16	GENTLES_modul6
8	0.147	1 / 16	GENTLES_modul14
9	0.195	2 / 82	PanCan_TXmisReg_geneset_nanostring
10	0.251	1 / 29	KUIPER_MM good survival
11	0.308	2 / 113	PanCan_Driver_Gene_geneset_nanostring
12	0.329	1 / 40	PanCan_HK_geneset_nanostring
13	0.355	1 / 44	PanCan_TGF−B_geneset_nanostring
14	0.374	1 / 47	PanCan_DNARepair_geneset_nanostring
15	0.380	1 / 48	KUIPER_MM poor survival
16	0.482	0 / 14	LIU_COMMON_CANCER_GENES
17	0.487	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
18	0.503	1 / 70	SHAUGHNESSY_MM high risk
19	0.699	1 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.702	1 / 121	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−04	102 / 8205	cytoplasm
2	3e−04	3 / 14	exosome (RNase complex)
3	5e−04	28 / 1468	mitochondrion
4	3e−03	14 / 616	endosome
5	3e−03	12 / 487	intracellular membrane−bounded organelle
6	4e−03	5 / 106	trans−Golgi network
7	4e−03	2 / 10	nuclear exosome (RNase complex)
8	5e−03	34 / 2193	extracellular exosome
9	6e−03	2 / 12	Golgi transport complex
10	7e−03	7 / 223	lysosomal membrane
11	7e−03	113 / 9988	organelle
12	7e−03	3 / 40	recycling endosome membrane
13	8e−03	20 / 1132	Golgi apparatus
14	9e−03	2 / 15	BLOC−1 complex
15	2e−02	2 / 21	clathrin adaptor complex
16	2e−02	2 / 21	mitochondrial small ribosomal subunit
17	2e−02	9 / 412	lysosome
18	2e−02	5 / 164	endosome membrane
19	2e−02	116 / 10605	intracellular
20	3e−02	12 / 649	endoplasmic reticulum membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.09	8 / 469	Chr 8
2	0.13	12 / 840	Chr 17
3	0.15	10 / 689	Chr 7
4	0.18	4 / 221	Chr 18
5	0.18	8 / 552	Chr 10
6	0.19	3 / 151	Chr 21
7	0.38	8 / 696	Chr 5
8	0.45	11 / 1037	Chr 19
9	0.46	7 / 649	Chr 16
10	0.47	6 / 551	Chr X
11	0.48	5 / 462	Chr 14
12	0.56	4 / 398	Chr 20
13	0.65	7 / 775	Chr 12
14	0.66	9 / 993	Chr 2
15	0.68	4 / 465	Chr 15
16	0.69	7 / 801	Chr 11
17	0.73	7 / 838	Chr 3
18	0.74	2 / 262	Chr 13
19	0.82	5 / 687	Chr 6
20	0.83	4 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−13	133 / 9482	TssA_Colon
2	8e−07	117 / 9027	Tx_Colon
3	3e−05	109 / 8580	TxWk_Colon
4	4e−04	92 / 7203	TssF_Colon
5	8e−03	98 / 8415	Quies3_Colon
6	1e−02	109 / 9653	Enh_Colon
7	2e−02	114 / 10290	TssWk_Colon
8	2e−02	63 / 5155	EnhWk1_Colon
9	3e−02	70 / 5880	TssD2_Colon
10	5e−02	35 / 2698	EnhA_Colon
11	7e−02	1 / 7	Marisa_CRC−C5
12	8e−02	1 / 8	Marisa_CRC−C2
13	8e−02	1 / 8	Juehling−MSI−enriched−in−7
14	9e−02	7 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
15	1e−01	11 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	1e−01	1 / 16	Vilar_non−hypermutated−in=CRC
17	2e−01	33 / 2798	TxEnhG1_Colon
18	2e−01	12 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
19	2e−01	3 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	3e−01	2 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.6	4 / 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	0.04	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
2	0.05	7 / 332	Up
3	0.05	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
4	0.10	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
5	0.11	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
6	0.15	6 / 365	Down_b
7	0.21	11 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.24	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
9	0.37	1 / 47	Vishal_subnetwork signature of survival in GBM
10	0.37	1 / 47	mature astrocytes
11	0.37	1 / 47	Weller_LGG_gradeII−vs−III_UP
12	0.37	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
13	0.39	1 / 49	OL vs. MOG−_OL
14	0.43	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
15	0.46	1 / 62	cultured astroglia vs. in vivo astrocytes
16	0.48	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
17	0.48	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
18	0.49	1 / 68	GIEZELT_GBM_WT_down_VS_mut
19	0.51	1 / 71	Weller_LGG_A_vs_O_UP
20	0.52	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−08	14 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
2	1e−05	10 / 176	TIEN_INTESTINE_PROBIOTICS_24HR_DN
3	1e−05	8 / 108	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
4	2e−05	12 / 273	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
5	9e−05	28 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	1e−04	7 / 111	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
7	1e−04	4 / 26	KRIGE_AMINO_ACID_DEPRIVATION
8	3e−04	7 / 126	PENG_LEUCINE_DEPRIVATION_UP
9	4e−04	7 / 135	KAAB_FAILED_HEART_ATRIUM_DN
10	5e−04	4 / 37	KAAB_FAILED_HEART_VENTRICLE_DN
11	5e−04	3 / 16	TOMIDA_METASTASIS_DN
12	7e−04	3 / 18	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN
13	7e−04	4 / 41	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
14	8e−04	4 / 42	REACTOME_TRNA_AMINOACYLATION
15	8e−04	14 / 532	PARENT_MTOR_SIGNALING_UP
16	9e−04	18 / 800	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
17	1e−03	9 / 260	ENK_UV_RESPONSE_EPIDERMIS_UP
18	1e−03	15 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
19	1e−03	0 / 12	LIU_PROSTATE_CANCER_UP
20	1e−03	15 / 620	MILI_PSEUDOPODIA_HAPTOTAXIS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.003	7 / 188	HALLMARK_ADIPOGENESIS
2	0.005	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	0.029	5 / 174	HALLMARK_HEME_METABOLISM
4	0.045	5 / 196	HALLMARK_MTORC1_SIGNALING
5	0.055	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	0.057	4 / 146	HALLMARK_DNA_REPAIR
7	0.070	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	0.098	4 / 176	HALLMARK_HYPOXIA
9	0.108	4 / 183	HALLMARK_GLYCOLYSIS
10	0.119	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	0.134	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	0.162	3 / 140	HALLMARK_APOPTOSIS
13	0.167	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	0.213	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
15	0.230	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	0.235	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
17	0.301	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
18	0.355	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
19	0.410	1 / 53	HALLMARK_TGF_BETA_SIGNALING
20	0.425	2 / 146	HALLMARK_UV_RESPONSE_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	DUMEAUX_Red blood cells in non smokers 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 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 5	DUMEAUX_Monocytes in 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	9e−07	80 / 5184	HOPP_Txn_transition
2	5e−06	102 / 7592	HOPP_Active_promoter
3	1e−04	91 / 6929	HOPP_Txn_elongation
4	3e−03	82 / 6564	HOPP_Strong_enhancer
5	4e−03	22 / 1218	SPANG_BCR UP
6	2e−02	84 / 7209	HOPP_Weak_promoter
7	3e−02	7 / 294	TARTE_Plasmablast signature
8	8e−02	1 / 8	YAMANE_AICDA_targets_nonrecruited
9	9e−02	3 / 107	SPANG_LPS 6hrs UP
10	1e−01	2 / 61	SPANG_LPS 6hrs DN
11	1e−01	5 / 268	SPANG_IL21 UP
12	1e−01	2 / 66	TARTE_Plasma cell signature
13	2e−01	1 / 20	SPANG_BAFF 9hrs UP
14	2e−01	2 / 82	ROSOLOWSKI_green UP
15	3e−01	1 / 30	TARTE_B−cell signature
16	3e−01	2 / 109	ROSOLOWSKI_green total
17	3e−01	4 / 280	SPANG_CD40 6hrs UP
18	4e−01	1 / 47	Subero_FL_hyper_meth
19	4e−01	5 / 410	SPANG_CD40 6hrs DN
20	4e−01	12 / 1128	SPANG_BCR DN

MF

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 35	aminoacyl−tRNA ligase activity
2	2e−03	3 / 27	RNA polymerase II repressing transcription factor binding
3	5e−03	2 / 11	metal ion transmembrane transporter activity
4	7e−03	3 / 39	androgen receptor binding
5	7e−03	10 / 405	ligase activity
6	9e−03	2 / 15	hydrolase activity, acting on acid anhydrides
7	2e−02	2 / 23	proton−transporting ATPase activity, rotational mechanism
8	3e−02	2 / 25	transferase activity, transferring acyl groups other than amino−acyl groups
9	3e−02	5 / 168	magnesium ion binding
10	3e−02	2 / 26	protein kinase inhibitor activity
11	3e−02	2 / 26	transforming growth factor beta receptor binding
12	3e−02	5 / 181	transporter activity
13	4e−02	2 / 32	Rac GTPase binding
14	5e−02	2 / 36	tRNA binding
15	6e−02	19 / 1309	ATP binding
16	6e−02	4 / 149	protein dimerization activity
17	8e−02	2 / 47	GDP binding
18	8e−02	3 / 104	growth factor activity
19	9e−02	1 / 10	deoxyribonuclease activity
20	9e−02	1 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	4 / 51	hsa−miR−571
2	0.003	4 / 60	hsa−miR−671−5p
3	0.005	5 / 111	hsa−miR−361−5p
4	0.005	9 / 328	hsa−miR−18a
5	0.007	6 / 168	hsa−miR−520h
6	0.011	3 / 46	hsa−miR−874
7	0.017	6 / 208	hsa−miR−432
8	0.019	7 / 272	hsa−miR−520b
9	0.019	10 / 471	hsa−miR−15b
10	0.022	2 / 23	hsa−miR−1227
11	0.022	2 / 23	hsa−miR−609
12	0.023	6 / 222	hsa−miR−520g
13	0.029	10 / 507	hsa−miR−15a
14	0.031	7 / 303	hsa−miR−18b
15	0.037	7 / 314	hsa−miR−520c−3p
16	0.037	3 / 74	hsa−miR−708
17	0.038	2 / 31	hsa−miR−296−5p
18	0.038	6 / 250	hsa−miR−520a−3p
19	0.038	3 / 75	hsa−miR−939
20	0.039	9 / 459	hsa−miR−195

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	57 / 4385	ICGC_Atf2_targets
2	0.02	59 / 4689	ICGC_Taf1_targets
3	0.03	60 / 4909	ICGC_Stat5_targets
4	0.04	59 / 4879	ICGC_Pmlsc71910_targets
5	0.04	18 / 1171	KIM_MYC targets
6	0.05	48 / 3924	ICGC_Zeb1_targets
7	0.06	52 / 4314	ICGC_Ebfsc137065_targets
8	0.06	56 / 4706	ICGC_Sp1_targets
9	0.06	20 / 1400	ICGC_Myc_targets
10	0.08	52 / 4414	ICGC_Bclaf101388_targets
11	0.08	48 / 4032	ICGC_Creb1_targets
12	0.08	63 / 5495	ICGC_Yy1_targets
13	0.09	35 / 2836	ICGC_BatfPcr1_targets
14	0.10	1 / 11	MYC_Protein synthesis degradation UP
15	0.12	55 / 4829	ICGC_Nficsc81335_targets
16	0.12	47 / 4054	ICGC_Egr1_targets
17	0.14	54 / 4774	ICGC_Foxm1_targets
18	0.14	18 / 1383	ICGC_Six5_targets
19	0.15	65 / 5890	ICGC_Elf1_targets
20	0.15	58 / 5200	ICGC_Mta3_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	0.4	1 / 45	VAQUERIZAS_Uterus
4	0.4	1 / 59	VAQUERIZAS_Whole blood
5	1.0	0 / 36	VAQUERIZAS_Fetal brain
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 / 143	VAQUERIZAS_General
10	1.0	0 / 9	VAQUERIZAS_Kidney
11	1.0	0 / 23	VAQUERIZAS_Spinal cord
12	1.0	0 / 38	VAQUERIZAS_Whole brain
13	1.0	0 / 37	VAQUERIZAS_Thymus
14	1.0	0 / 40	VAQUERIZAS_Thyroid
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	0.02	6 / 225	PALMER_Granulocytes signature up
2	0.11	1 / 12	WIRTH_Lymphocytes
3	0.11	1 / 12	WIRTH_Cerebellum
4	0.13	1 / 14	WIRTH_Telencephalon
5	0.31	2 / 114	PALMER_T−Cell signature up
6	0.86	1 / 194	PALMER_B−Cell signature up
7	0.97	1 / 350	WIRTH_Immune 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 / 5	WIRTH_Bone marrow
15	1.00	0 / 350	WIRTH_Nervous System
16	1.00	0 / 11	WIRTH_Globus pallidus
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	0.01	19 / 1115	LU_BPDE 1n DN
2	0.83	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	

Underexpression Spots

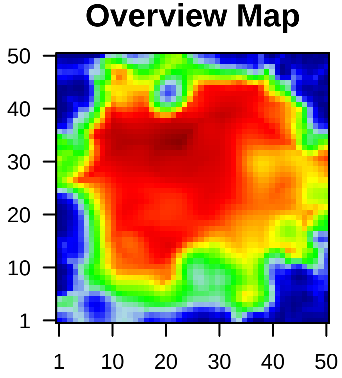
Spot Summary: q

metagenes = 9
genes = 43

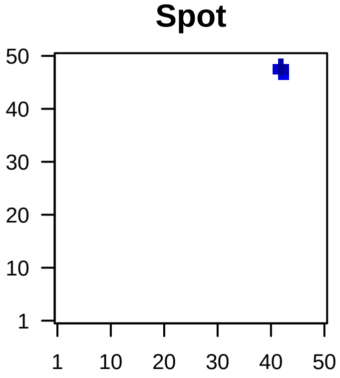
<r> metagenes = 0.96
<r> genes = 0.11
beta: r2= 1.42 / log p= −Inf

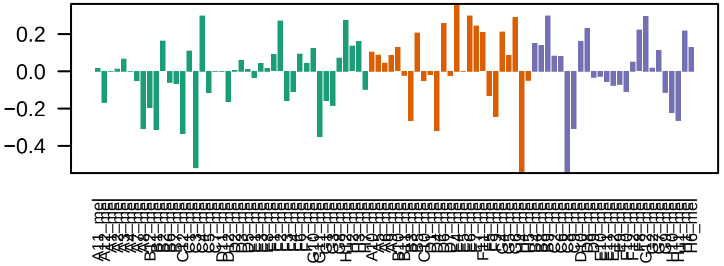
samples with spot = 16 (17.4 %)
MSC1 : 3 (7.1 %)
MSC2 : 8 (32 %)
MSC3 : 5 (20 %)

Overview Map



Spot





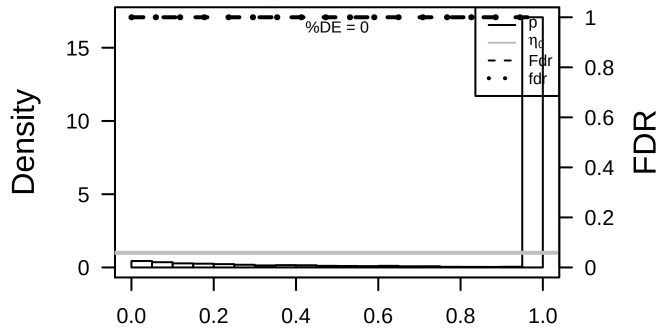
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	EARS2	1.77	−0.56	0.34	EARS2	glutamyl−tRNA synthetase 2, mitochondrial [Source:HGNC S
2	SEC24D	1.59	−0.54	0.31	SEC24D	SEC24 family member D [Source:HGNC Symbol;Acc:HGNC:
3	TMEM254	1.55	−0.6	0.34	TMEM254	transmembrane protein 254 [Source:HGNC Symbol;Acc:HGN
4	PEX3	1.48	−0.66	0.34	PEX3	peroxisomal biogenesis factor 3 [Source:HGNC Symbol;Acc:
5	TMED9	1.47	−0.8	0.28	TMED9	transmembrane emp24 protein transport domain containing 9
6	POMT1	1.44	−0.58	0.22	POMT1	protein−O−mannosyltransferase 1 [Source:HGNC Symbol;Ac
7	GEMIN7	1.44	−0.94	0.27	GEMIN7	gem (nuclear organelle) associated protein 7 [Source:HGNC
8	SPA17	1.43	−0.31	0.34	SPA17	sperm autoantigenic protein 17 [Source:HGNC Symbol;Acc:
9	SNAPC2	1.4	−0.41	0.32	SNAPC2	small nuclear RNA activating complex, polypeptide 2, 45kDa
10	GEMIN5	1.39	−0.64	0.28	GEMIN5	gem (nuclear organelle) associated protein 5 [Source:HGNC
11	SC5D	1.28	−1.43	0.35	SC5D	sterol−C5−desaturase [Source:HGNC Symbol;Acc:HGNC:10
12	TMEM68	1.27	−0.78	0.31	TMEM68	transmembrane protein 68 [Source:HGNC Symbol;Acc:HGN
13	ABHD10	1.21	−0.94	0.29	ABHD10	abhydrolase domain containing 10 [Source:HGNC Symbol;Ac
14	SETDB2	1.2	−0.57	0.26	SETDB2	SET domain, bifurcated 2 [Source:HGNC Symbol;Acc:HGNC
15	SDE2	1.2	−0.45	0.29	SDE2	SDE2 telomere maintenance homolog (S. pombe) [Source:H
16	LAS1L	1.19	−0.74	0.29	LAS1L	LAS1−like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:
17	BCAP29	1.18	−1.78	0.4	BCAP29	B−cell receptor−associated protein 29 [Source:HGNC Symbo
18	PTCD1	1.11	−0.26	0.26	PTCD1	pentatricopeptide repeat domain 1 [Source:HGNC Symbol;Ac
19	PEX6	1.09	−0.16	0.28	PEX6	peroxisomal biogenesis factor 6 [Source:HGNC Symbol;Acc:
20	SWI5	1.07	−1.04	0.26	SWI5	SWI5 recombination repair homolog (yeast) [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−06	40 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	6e−05	39 / 9482	Colon	TssA_Colon
3	2e−04	3 / 36	MF	tRNA binding
4	3e−04	37 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
5	4e−04	9 / 805	GSEA	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_8D
6	4e−04	2 / 11	CC	Gemini of coiled bodies
7	5e−04	33 / 7592	Lympl	HOPP_Active_promoter
8	5e−04	2 / 12	CC	SMN complex
9	6e−04	25 / 4879	TF	ICGC_Pmlsc71910_targets
10	6e−04	26 / 5200	TF	ICGC_Mta3_targets
11	9e−04	24 / 4689	TF	ICGC_Taf1_targets
12	9e−04	23 / 4385	TF	ICGC_Atf2_targets
13	9e−04	23 / 4414	TF	ICGC_Bclaf101388_targets
14	1e−03	2 / 17	CC	SMN−Sm protein complex
15	1e−03	2 / 18	BP	peroxisome organization
16	1e−03	5 / 288	GSEA	WEST_ADRENOCORTICAL_TUMOR_UP
17	1e−03	31 / 7209	Lympl	HOPP_Weak_promoter
18	1e−03	3 / 78	GSEA	ROVERSI_GLIOMA_COPY_NUMBER_UP
19	2e−03	10 / 1171	TF	KIM_MYC targets
20	2e−03	24 / 4909	TF	ICGC_Stat5_targets
21	2e−03	30 / 6929	Lympl	HOPP_Txn_elongation
22	2e−03	23 / 4617	TF	ICGC_Tcf12_targets
23	2e−03	2 / 23	BP	ncRNA metabolic process
24	2e−03	23 / 4682	TF	ICGC_Pol24_targets
25	2e−03	8 / 831	Brain	Fetal_HetRpts
26	2e−03	3 / 92	GSEA	BRUINS_UVC_RESPONSE_MIDDLE
27	2e−03	4 / 196	GSEA	AMUNDSON_RESPONSE_TO_ARSENITE
28	2e−03	3 / 93	GSEA	HELLER_SILENCED_BY_METHYLATION_DN
29	3e−03	2 / 26	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENT
30	3e−03	3 / 97	GSEA	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
31	3e−03	6 / 494	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
32	3e−03	25 / 5408	TF	ICGC_Pou2_targets
33	3e−03	6 / 502	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
34	3e−03	2 / 29	BP	spliceosomal snRNP assembly
35	3e−03	35 / 9027	Colon	Tx_Colon
36	3e−03	6 / 510	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
37	4e−03	2 / 31	miRN	hsa−miR−17*
38	4e−03	2 / 31	GSEA	JIANG_AGING_CEREBRAL_CORTEX_UP
39	4e−03	3 / 107	GSEA	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS
40	4e−03	25 / 5495	TF	ICGC_Yy1_targets

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	0.001	2 / 18	peroxisome organization
2	0.002	2 / 23	ncRNA metabolic process
3	0.003	2 / 29	spliceosomal snRNP assembly
4	0.007	2 / 44	tRNA aminoacylation for protein translation
5	0.009	3 / 147	tRNA metabolic process
6	0.012	2 / 58	ER to Golgi vesicle−mediated transport
7	0.014	6 / 687	gene expression
8	0.029	1 / 10	negative regulation of JUN kinase activity
9	0.034	1 / 12	epithelial cilium movement
10	0.034	1 / 12	mitochondrial genome maintenance
11	0.034	1 / 12	protein O−linked mannosylation
12	0.037	1 / 13	COPI coating of Golgi vesicle
13	0.037	1 / 13	left/right axis specification
14	0.037	1 / 13	mannosylation
15	0.037	1 / 13	snRNA processing
16	0.040	1 / 14	COPII vesicle coating
17	0.040	1 / 14	tRNA aminoacylation
18	0.048	1 / 17	iron−sulfur cluster assembly
19	0.048	1 / 17	protein K63−linked deubiquitination
20	0.048	1 / 17	protein refolding

Brain

Rank	p−value	#in/all	Geneset
1	6e−06	40 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−04	37 / 9013	Overlap_fetal_midbrain_K9K27me3
3	2e−03	8 / 831	Fetal_HetRpts
4	5e−03	26 / 5940	Overlap_fetal_midbrain_HetRpts
5	2e−02	15 / 3081	Mid_Frontal_Lobe_ZNF
6	6e−02	33 / 9528	Overlap_fetal_midbrain_Quies
7	9e−02	7 / 1333	Fetal_ReprPCWk
8	2e−01	2 / 304	Fetal_Het
9	3e−01	28 / 9020	Overlap_fetal_midbrain_ReprPCWk
10	4e−01	1 / 163	Fetal_ReprPC
11	4e−01	4 / 1122	Fetal_K9K27me3
12	6e−01	3 / 989	Mid_Frontal_Lobe_Quies
13	6e−01	2 / 668	Mid_Frontal_Lobe_Enh
14	6e−01	5 / 1845	Fetal_Quies
15	6e−01	1 / 349	Fetal_ZNF
16	7e−01	2 / 765	Mid_Frontal_Lobe_Het
17	7e−01	2 / 769	Overlap_fetal_midbrain_ZNF
18	7e−01	3 / 1236	Mid_Frontal_Lobe_ReprPCWk
19	7e−01	1 / 468	Mid_Frontal_Lobe_TssF
20	8e−01	1 / 534	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	1 / 70	SHAUGHNESSY_MM high risk
2	0.3	0 / 14	LIU_PROSTATE_CANCER_DN
3	0.4	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	0.4	1 / 180	SPANG_LPS−index2
5	0.4	2 / 489	Lembcke_Normal vs Adenoma
6	0.6	1 / 298	SPANG_BCL6−index2
7	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
8	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
9	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
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	4e−04	2 / 11	Gemini of coiled bodies
2	5e−04	2 / 12	SMN complex
3	1e−03	2 / 17	SMN−Sm protein complex
4	5e−03	37 / 9988	organelle
5	5e−03	2 / 36	nuclear body
6	7e−03	9 / 1201	endoplasmic reticulum
7	7e−03	3 / 135	myelin sheath
8	7e−03	38 / 10605	intracellular
9	8e−03	32 / 8205	cytoplasm
10	8e−03	2 / 48	peroxisomal membrane
11	1e−02	14 / 2576	membrane
12	1e−02	16 / 3214	protein complex
13	3e−02	13 / 2577	nucleoplasm
14	3e−02	2 / 94	melanosome
15	3e−02	1 / 12	dendrite membrane
16	4e−02	1 / 13	dystrophin−associated glycoprotein complex
17	4e−02	1 / 13	integrator complex
18	4e−02	1 / 13	sperm principal piece
19	4e−02	5 / 649	endoplasmic reticulum membrane
20	4e−02	2 / 109	peroxisome

Chr

Rank	p−value	#in/all	Geneset
1	0.05	5 / 689	Chr 7
2	0.14	4 / 687	Chr 6
3	0.23	3 / 576	Chr 9
4	0.29	3 / 649	Chr 16
5	0.33	3 / 696	Chr 5
6	0.36	1 / 151	Chr 21
7	0.40	2 / 469	Chr 8
8	0.41	3 / 801	Chr 11
9	0.48	1 / 221	Chr 18
10	0.48	2 / 558	Chr 4
11	0.54	1 / 262	Chr 13
12	0.59	3 / 1037	Chr 19
13	0.64	4 / 1500	Chr 1
14	0.69	1 / 398	Chr 20
15	0.80	1 / 551	Chr X
16	0.80	1 / 552	Chr 10
17	0.90	1 / 775	Chr 12
18	0.92	1 / 838	Chr 3
19	0.92	1 / 840	Chr 17
20	0.95	1 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−05	39 / 9482	TssA_Colon
2	3e−03	35 / 9027	Tx_Colon
3	2e−02	32 / 8580	TxWk_Colon
4	4e−02	27 / 7203	TssF_Colon
5	9e−02	2 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	1e−01	29 / 8415	Quies3_Colon
7	1e−01	34 / 10290	TssWk_Colon
8	1e−01	1 / 45	Ang_CRC−CIMPH−vs−L_hyper
9	1e−01	1 / 50	Ang_CRC_Hypermethylated
10	2e−01	11 / 2798	TxEnhG1_Colon
11	2e−01	2 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	2e−01	3 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	3e−01	19 / 5880	TssD2_Colon
14	5e−01	15 / 5155	EnhWk1_Colon
15	6e−01	2 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
16	6e−01	2 / 739	TxEnhG2_Colon
17	7e−01	1 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
18	8e−01	2 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
19	8e−01	26 / 9653	Enh_Colon
20	8e−01	2 / 1079	ZNF_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.7	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	0.006	1 / 2	WILLSCHER_GBM_LTSmut_proteomics−E_UP
2	0.009	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
3	0.012	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
4	0.014	2 / 63	Stuehler_Proteins_up_in_STS
5	0.031	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
6	0.043	1 / 15	VERHAAK_MES subtype
7	0.077	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.094	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
9	0.194	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
10	0.232	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	0.445	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.622	1 / 332	Up
13	0.648	1 / 356	Down_a
14	0.658	1 / 365	Down_b
15	1.000	0 / 15	VERHAAK_CL subtype
16	1.000	0 / 16	VERHAAK_NL subtype
17	1.000	0 / 14	VERHAAK_PN subtype
18	1.000	0 / 23	WIRTH_PN subtype
19	1.000	0 / 74	WIRTH_Normal Brain
20	1.000	0 / 9	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	9 / 805	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_8D
2	1e−03	5 / 288	WEST_ADRENOCORTICAL_TUMOR_UP
3	1e−03	3 / 78	ROVERSI_GLIOMA_COPY_NUMBER_UP
4	2e−03	3 / 92	BRUINS_UVC_RESPONSE_MIDDLE
5	2e−03	4 / 196	AMUNDSON_RESPONSE_TO_ARSENITE
6	2e−03	3 / 93	HELLER_SILENCED_BY_METHYLATION_DN
7	3e−03	2 / 26	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_
8	3e−03	3 / 97	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
9	3e−03	6 / 494	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
10	3e−03	6 / 502	KIM_ALL_DISORDERS_CALB1_CORR_UP
11	3e−03	6 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
12	4e−03	2 / 31	JIANG_AGING_CEREBRAL_CORTEX_UP
13	4e−03	3 / 107	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS
14	4e−03	3 / 115	YAGI_AML_SURVIVAL
15	6e−03	2 / 39	CHANDRAN_METASTASIS_TOP50_DN
16	6e−03	2 / 41	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
17	7e−03	2 / 42	REACTOME_TRNA_AMINOACYLATION
18	7e−03	2 / 42	APRELIKOVA_BRCA1_TARGETS
19	7e−03	3 / 136	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
20	8e−03	3 / 142	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20M

HM

Rank	p−value	#in/all	Geneset
1	0.009	3 / 146	HALLMARK_UV_RESPONSE_UP
2	0.019	3 / 196	HALLMARK_MTORC1_SIGNALING
3	0.020	3 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	0.030	2 / 93	HALLMARK_PEROXISOME
5	0.062	2 / 140	HALLMARK_APOPTOSIS
6	0.128	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	0.153	1 / 57	HALLMARK_MYC_TARGETS_V2
8	0.194	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.233	1 / 91	HALLMARK_PROTEIN_SECRETION
10	0.233	1 / 91	HALLMARK_BILE_ACID_METABOLISM
11	0.239	1 / 94	HALLMARK_ANDROGEN_RESPONSE
12	0.244	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	0.382	1 / 165	HALLMARK_MYOGENESIS
14	0.386	1 / 167	HALLMARK_APICAL_JUNCTION
15	0.422	1 / 188	HALLMARK_ADIPOGENESIS
16	0.436	1 / 196	HALLMARK_G2M_CHECKPOINT
17	1.000	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
18	1.000	0 / 176	HALLMARK_HYPOXIA
19	1.000	0 / 195	HALLMARK_MITOTIC_SPINDLE
20	1.000	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	5e−04	33 / 7592	HOPP_Active_promoter
2	1e−03	31 / 7209	HOPP_Weak_promoter
3	2e−03	30 / 6929	HOPP_Txn_elongation
4	2e−02	22 / 5184	HOPP_Txn_transition
5	3e−02	2 / 86	ROSOLOWSKI_red total
6	8e−02	21 / 5538	HOPP_Weak_txn
7	1e−01	6 / 1128	SPANG_BCR DN
8	1e−01	1 / 39	ROSOLOWSKI_blue DOWN
9	1e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
10	1e−01	3 / 410	SPANG_CD40 6hrs DN
11	2e−01	1 / 82	ROSOLOWSKI_green UP
12	2e−01	1 / 89	ROSOLOWSKI_blue total
13	3e−01	19 / 5693	HOPP_Weak_enhancer
14	3e−01	1 / 109	ROSOLOWSKI_green total
15	3e−01	5 / 1218	SPANG_BCR UP
16	5e−01	1 / 268	SPANG_IL21 UP
17	6e−01	1 / 275	TARTE_Mature plasma cell signature
18	6e−01	19 / 6564	HOPP_Strong_enhancer
19	6e−01	6 / 2211	HOPP_Repetitive
20	1e+00	3 / 2563	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 36	tRNA binding
2	1e−02	9 / 1309	ATP binding
3	3e−02	1 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
4	3e−02	1 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
5	3e−02	1 / 11	ATPase activity, coupled
6	3e−02	1 / 11	quinone binding
7	3e−02	1 / 12	low−density lipoprotein particle receptor binding
8	3e−02	1 / 12	oxidoreductase activity, acting on NAD(P)H
9	4e−02	1 / 13	mannosyltransferase activity
10	6e−02	1 / 22	amino acid transmembrane transporter activity
11	6e−02	1 / 22	histone−lysine N−methyltransferase activity
12	6e−02	2 / 142	calmodulin binding
13	6e−02	1 / 23	Hsp70 protein binding
14	6e−02	1 / 23	proton−transporting ATPase activity, rotational mechanism
15	8e−02	1 / 28	hydrogen ion transmembrane transporter activity
16	8e−02	1 / 30	hydrolase activity, hydrolyzing O−glycosyl compounds
17	8e−02	2 / 167	helicase activity
18	1e−01	7 / 1365	RNA binding
19	1e−01	2 / 181	transporter activity
20	1e−01	1 / 35	4 iron, 4 sulfur cluster binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	2 / 31	hsa−miR−17*
2	0.020	2 / 75	hsa−miR−509−5p
3	0.020	2 / 76	hsa−miR−509−3−5p
4	0.026	1 / 9	hsa−miR−373*
5	0.026	3 / 222	hsa−miR−185
6	0.027	2 / 88	hsa−miR−505
7	0.029	2 / 91	hsa−miR−378
8	0.036	2 / 104	hsa−miR−210
9	0.048	2 / 121	hsa−miR−543
10	0.051	1 / 18	hsa−miR−564
11	0.052	4 / 488	hsa−miR−103
12	0.056	2 / 132	hsa−miR−508−3p
13	0.056	1 / 20	hsa−miR−1288
14	0.059	1 / 21	hsa−miR−554
15	0.059	1 / 21	hsa−miR−596
16	0.064	3 / 318	hsa−miR−340
17	0.065	1 / 23	hsa−miR−1227
18	0.069	2 / 149	hsa−miR−518a−5p
19	0.070	1 / 25	hsa−miR−1273
20	0.073	2 / 154	hsa−miR−527

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	6e−04	25 / 4879	ICGC_Pmlsc71910_targets
2	6e−04	26 / 5200	ICGC_Mta3_targets
3	9e−04	24 / 4689	ICGC_Taf1_targets
4	9e−04	23 / 4385	ICGC_Atf2_targets
5	9e−04	23 / 4414	ICGC_Bclaf101388_targets
6	2e−03	10 / 1171	KIM_MYC targets
7	2e−03	24 / 4909	ICGC_Stat5_targets
8	2e−03	23 / 4617	ICGC_Tcf12_targets
9	2e−03	23 / 4682	ICGC_Pol24_targets
10	3e−03	25 / 5408	ICGC_Pou2_targets
11	4e−03	25 / 5495	ICGC_Yy1_targets
12	6e−03	13 / 2137	ICGC_SrfV0416101_targets
13	6e−03	22 / 4706	ICGC_Sp1_targets
14	7e−03	22 / 4774	ICGC_Foxm1_targets
15	8e−03	26 / 6114	ICGC_Runx3_targets
16	9e−03	22 / 4829	ICGC_Nficsc81335_targets
17	1e−02	25 / 5890	ICGC_Elf1_targets
18	1e−02	19 / 4032	ICGC_Creb1_targets
19	1e−02	23 / 5355	ICGC_Pol2_targets
20	2e−02	12 / 2136	ICGC_GabpPcr2_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	0.04	1 / 13	WIRTH_B−cells
2	0.14	2 / 225	PALMER_Granulocytes signature up
3	0.64	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 / 8	WIRTH_Tonsil
8	1.00	0 / 12	WIRTH_Thymus
9	1.00	0 / 12	WIRTH_Lymphocytes
10	1.00	0 / 5	WIRTH_Bone marrow
11	1.00	0 / 350	WIRTH_Nervous System
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	0.3	13 / 3682	LU_BPDE 0.005 DN
2	0.4	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	

Underexpression Spots

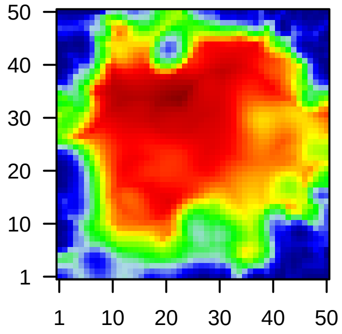
Spot Summary: r

metagenes = 5
genes = 60

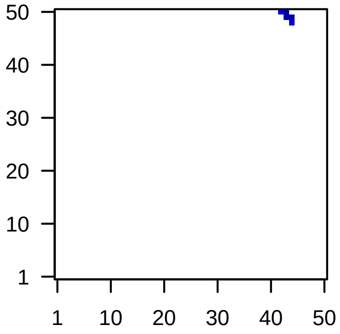
<r> metagenes = 0.97
<r> genes = 0.11
beta: r2= 1.79 / log p= −Inf

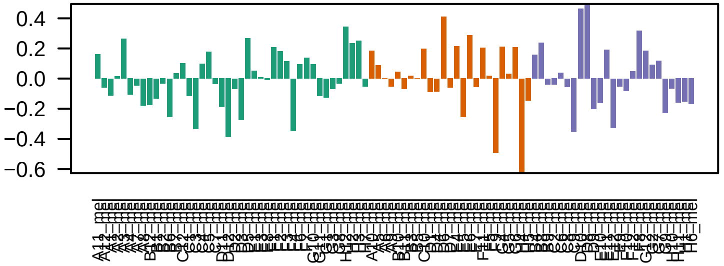
samples with spot = 17 (18.5 %)
MSC1 : 6 (14.3 %)
MSC2 : 7 (28 %)
MSC3 : 4 (16 %)

Overview Map



Spot





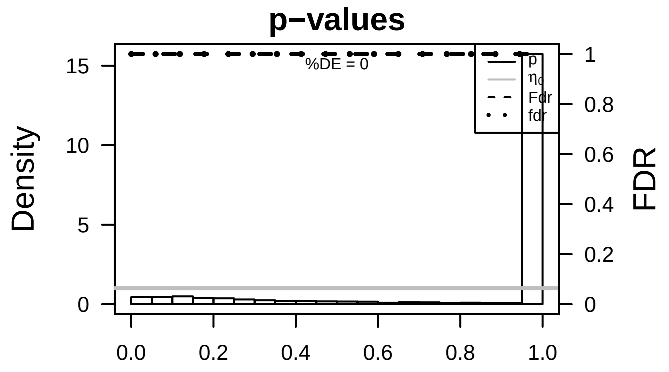
Spot Genelist

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	GABRA5	1.67	−0.18	0.24	GABRA5	gamma−aminobutyric acid (GABA) A receptor, alpha 5 [Sour
3	GULP1	1.65	−0.53	0.26	GULP1	GULP, engulfment adaptor PTB domain containing 1 [Source
4	PGBD2	1.63	−0.39	0.31	PGBD2	piggyBac transposable element derived 2 [Source:HGNC Sy
5	STK11IP	1.61	−0.17	0.35	STK11IP	serine/threonine kinase 11 interacting protein [Source:HGNC
6	SIL1	1.56	−0.68	0.35	SIL1	SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:
7	PDLIM2	1.55	−0.27	0.24	PDLIM2	PDZ and LIM domain 2 (mystique) [Source:HGNC Symbol;A
8	ATG13	1.55	−0.73	0.39	ATG13	autophagy related 13 [Source:HGNC Symbol;Acc:HGNC:290
9	PJA1	1.53	−0.56	0.36	PJA1	praja ring finger 1, E3 ubiquitin protein ligase [Source:HGNC
10	DNAJB9	1.51	−0.61	0.28	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9 [Source:HG
11	PARP11	1.51	−0.34	0.23	PARP11	poly (ADP−ribose) polymerase family, member 11 [Source:H
12	CFH	1.5	−0.41	0.31	CFH	complement factor H [Source:HGNC Symbol;Acc:HGNC:488
13	DDX19B	1.48	−0.89	0.3	DDX19B	DEAD (Asp−Glu−Ala−Asp) box polypeptide 19B [Source:HG
14	CCDC93	1.46	−0.78	0.33	CCDC93	coiled−coil domain containing 93 [Source:HGNC Symbol;Acc
15	GSS	1.46	−0.89	0.33	GSS	glutathione synthetase [Source:HGNC Symbol;Acc:HGNC:46
16	FLYWCH1	1.44	−0.29	0.31	FLYWCH1	FLYWCH−type zinc finger 1 [Source:HGNC Symbol;Acc:HG
17	PSEN1	1.42	−0.9	0.34	PSEN1	presenilin 1 [Source:HGNC Symbol;Acc:HGNC:9508]
18	TRMT2B	1.39	−0.31	0.28	TRMT2B	tRNA methyltransferase 2 homolog B (S. cerevisiae) [Source:
19	MUS81	1.39	−0.32	0.3	MUS81	MUS81 structure−specific endonuclease subunit [Source:HG
20	FAM172A	1.37	−0.84	0.23	FAM172A	family with sequence similarity 172, member A [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−06	53 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	4e−04	44 / 7592	Lymp	HOPP_Active_promoter
3	6e−04	3 / 41	BP	neuron development
4	6e−04	3 / 42	GSE	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
5	7e−04	5 / 175	miRN	hsa−miR−548k
6	9e−04	8 / 507	miRN	hsa−miR−15a
7	1e−03	4 / 115	miRN	hsa−miR−515−5p
8	1e−03	2 / 13	GSE	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
9	2e−03	3 / 61	GSE	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS
10	2e−03	4 / 132	miRN	hsa−miR−320d
11	2e−03	49 / 9482	Colon	TssA_Colon
12	2e−03	6 / 341	GSE	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
13	3e−03	5 / 235	GSE	BLUM_RESPONSE_TO_SALIRASIB_UP
14	3e−03	4 / 146	miRN	hsa−miR−320c
15	3e−03	4 / 147	miRN	hsa−miR−143
16	3e−03	39 / 6929	Lymp	HOPP_Txn_elongation
17	4e−03	6 / 366	miRN	hsa−miR−519b−3p
18	5e−03	4 / 167	HM	HALLMARK_IL2_STAT5_SIGNALING
19	5e−03	4 / 170	miRN	hsa−miR−320b
20	5e−03	2 / 27	GSE	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
21	6e−03	6 / 405	miRN	hsa−miR−519c−3p
22	7e−03	5 / 294	GSE	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
23	7e−03	43 / 8205	CC	cytoplasm
24	7e−03	7 / 555	GSE	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
25	7e−03	2 / 31	CC	dendritic shaft
26	7e−03	3 / 98	GSE	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
27	8e−03	6 / 432	miRN	hsa−miR−424
28	8e−03	2 / 33	MF	estrogen receptor binding
29	8e−03	3 / 101	miRN	hsa−miR−603
30	8e−03	1 / 2	TF	MYC_ECM cell adhesion DOWN
31	8e−03	2 / 34	BP	response to nutrient levels
32	8e−03	2 / 34	GSE	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
33	9e−03	3 / 106	GSE	WIERENGA_STAT5A_TARGETS_GROUP1
34	9e−03	3 / 107	GSE	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS
35	9e−03	2 / 36	GSE	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION
36	1e−02	3 / 109	MF	RNA polymerase II regulatory region sequence−specific DNA binding
37	1e−02	3 / 114	BP	negative regulation of neuron apoptotic process
38	1e−02	6 / 471	miRN	hsa−miR−15b
39	1e−02	3 / 117	BP	regulation of mitochondrion degradation
40	1e−02	2 / 41	BP	positive regulation of MAP kinase activity

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	3 / 41	neuron development
2	8e−03	2 / 34	response to nutrient levels
3	1e−02	3 / 114	negative regulation of neuron apoptotic process
4	1e−02	3 / 117	regulation of mitochondrion degradation
5	1e−02	2 / 41	positive regulation of MAP kinase activity
6	1e−02	2 / 43	autophagic vacuole assembly
7	1e−02	2 / 43	determination of left/right symmetry
8	1e−02	2 / 45	embryonic limb morphogenesis
9	2e−02	3 / 129	autophagy
10	2e−02	4 / 255	cellular amino acid metabolic process
11	3e−02	2 / 66	activation of signaling protein activity involved in unfolded protein response
12	3e−02	5 / 431	negative regulation of apoptotic process
13	3e−02	2 / 68	positive regulation of MAPK cascade
14	3e−02	2 / 71	negative regulation of protein kinase activity
15	4e−02	1 / 10	beta−amyloid metabolic process
16	4e−02	1 / 10	cellular response to antibiotic
17	4e−02	1 / 10	establishment or maintenance of epithelial cell apical/basal polarity
18	4e−02	1 / 10	extracellular fibril organization
19	4e−02	1 / 10	L−glutamate transport
20	4e−02	1 / 10	negative regulation of cardiac muscle cell apoptotic process

Brain

Rank	p−value	#in/all	Geneset
1	9e−06	53 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−02	44 / 9013	Overlap_fetal_midbrain_K9K27me3
3	3e−02	13 / 1845	Fetal_Quies
4	5e−02	7 / 831	Fetal_HetRpts
5	6e−02	7 / 884	Overlap_fetal_midbrain_EnhG
6	8e−02	8 / 1122	Fetal_K9K27me3
7	1e−01	7 / 1065	Overlap_fetal_midbrain_Enh
8	1e−01	41 / 9020	Overlap_fetal_midbrain_ReprPCWk
9	2e−01	5 / 769	Overlap_fetal_midbrain_ZNF
10	2e−01	6 / 1013	Fetal_TssP
11	3e−01	27 / 5940	Overlap_fetal_midbrain_HetRpts
12	3e−01	2 / 304	Fetal_Het
13	4e−01	9 / 1949	Fetal_TssF
14	5e−01	4 / 953	Fetal_Enh
15	6e−01	12 / 3081	Mid_Frontal_Lobe_ZNF
16	6e−01	2 / 534	Mid_Frontal_Lobe_EnhG
17	7e−01	2 / 574	Overlap_fetal_midbrain_TssP
18	7e−01	9 / 2462	Mid_Frontal_Lobe_HetRpts
19	7e−01	37 / 9528	Overlap_fetal_midbrain_Quies
20	7e−01	4 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 29	KUIPER_MM good survival
2	0.1	3 / 298	SPANG_BCL6−index2
3	0.2	1 / 47	PanCan_DNARepair_geneset_nanostring
4	0.2	0 / 14	LIU_COMMON_CANCER_GENES
5	0.2	1 / 70	SHAUGHNESSY_MM high risk
6	0.5	1 / 180	SPANG_LPS−index2
7	0.9	1 / 489	Lembcke_Normal vs Adenoma
8	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
9	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
10	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	1.0	0 / 12	LIU_BREAST_CANCER
13	1.0	0 / 14	LIU_LIVER_CANCER
14	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
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	0.007	43 / 8205	cytoplasm
2	0.007	2 / 31	dendritic shaft
3	0.016	2 / 48	stress fiber
4	0.029	2 / 66	integral component of endoplasmic reticulum membrane
5	0.047	1 / 12	holo TFIIH complex
6	0.048	3 / 202	actin cytoskeleton
7	0.051	1 / 13	integrator complex
8	0.051	1 / 13	neuronal cell body membrane
9	0.067	1 / 17	costamere
10	0.067	1 / 17	nuclear outer membrane
11	0.071	15 / 2507	cytosol
12	0.080	3 / 249	neuronal cell body
13	0.080	6 / 747	nucleolus
14	0.085	1 / 22	pre−autophagosomal structure
15	0.085	1 / 22	smooth endoplasmic reticulum
16	0.091	2 / 125	lamellipodium
17	0.093	1 / 24	cortical actin cytoskeleton
18	0.107	2 / 138	cell−cell junction
19	0.115	1 / 30	endoplasmic reticulum−Golgi intermediate compartment membrane
20	0.115	1 / 30	sarcomere

Chr

Rank	p−value	#in/all	Geneset
1	0.04	5 / 462	Chr 14
2	0.05	8 / 993	Chr 2
3	0.12	4 / 465	Chr 15
4	0.15	5 / 689	Chr 7
5	0.15	5 / 696	Chr 5
6	0.22	5 / 801	Chr 11
7	0.29	3 / 469	Chr 8
8	0.38	4 / 775	Chr 12
9	0.39	3 / 551	Chr X
10	0.46	1 / 151	Chr 21
11	0.49	3 / 649	Chr 16
12	0.59	1 / 221	Chr 18
13	0.74	5 / 1500	Chr 1
14	0.75	1 / 335	Chr 22
15	0.80	1 / 398	Chr 20
16	0.86	2 / 838	Chr 3
17	0.86	2 / 840	Chr 17
18	0.90	1 / 558	Chr 4
19	0.94	1 / 687	Chr 6
20	1.00	0 / 552	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	49 / 9482	TssA_Colon
2	0.032	1 / 8	Juehling−MSI−enriched−in−7
3	0.040	1 / 10	KIM_MSI−in−CRC
4	0.081	47 / 10290	TssWk_Colon
5	0.111	1 / 29	Marisa_CRC−cluster−c
6	0.128	34 / 7203	TssF_Colon
7	0.174	6 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
8	0.182	38 / 8415	Quies3_Colon
9	0.209	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
10	0.235	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
11	0.266	4 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	0.299	39 / 9027	Tx_Colon
13	0.358	4 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
14	0.417	36 / 8580	TxWk_Colon
15	0.461	12 / 2798	TxEnhG1_Colon
16	0.484	2 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
17	0.506	1 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
18	0.518	2 / 427	Quies2_Colon
19	0.530	2 / 436	K9acLow_Colon
20	0.597	15 / 3812	TssD1_Colon

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	

Glio

Rank	p−value	#in/all	Geneset
1	0.02	1 / 6	neurons_glio
2	0.03	2 / 65	GIEZELT_GBM_STS_up_VS_LTS
3	0.06	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	0.12	1 / 32	Donson−innate immunity−associated with LTS in HGA
5	0.14	1 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
6	0.14	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
7	0.14	1 / 38	OL vs. OPC
8	0.18	1 / 49	OL vs. MOG− OL
9	0.21	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
10	0.22	1 / 62	cultured astroglia vs. in vivo astrocytes
11	0.25	5 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.26	1 / 74	WIRTH_Normal Brain
13	0.36	2 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	0.74	1 / 332	Up
15	1.00	0 / 15	VERHAAK_CL subtype
16	1.00	0 / 15	VERHAAK_MES subtype
17	1.00	0 / 16	VERHAAK_NL subtype
18	1.00	0 / 14	VERHAAK_PN subtype
19	1.00	0 / 23	WIRTH_PN subtype
20	1.00	0 / 9	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 42	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
2	1e−03	2 / 13	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
3	2e−03	3 / 61	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS
4	2e−03	6 / 341	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
5	3e−03	5 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
6	5e−03	2 / 27	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
7	7e−03	5 / 294	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
8	7e−03	7 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
9	7e−03	3 / 98	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
10	8e−03	2 / 34	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
11	9e−03	3 / 106	WIERENGA_STAT5A_TARGETS_GROUP1
12	9e−03	3 / 107	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS
13	9e−03	2 / 36	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION
14	1e−02	2 / 41	KEGG_GLUTATHIONE_METABOLISM
15	1e−02	2 / 42	PID_ILK_PATHWAY
16	1e−02	2 / 44	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S
17	1e−02	2 / 45	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_UP
18	1e−02	6 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
19	2e−02	2 / 47	SUNG_METASTASIS_STROMA_DN
20	2e−02	4 / 245	WANG_SMARCE1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.005	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
2	0.031	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.045	3 / 196	HALLMARK_MTORC1_SIGNALING
4	0.072	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	0.139	2 / 162	HALLMARK_COMPLEMENT
6	0.149	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
7	0.176	2 / 188	HALLMARK_ADIPOGENESIS
8	0.260	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.317	1 / 94	HALLMARK_ANDROGEN_RESPONSE
10	0.320	1 / 95	HALLMARK_SPERMATOGENESIS
11	0.353	1 / 107	HALLMARK_COAGULATION
12	0.403	1 / 127	HALLMARK_KRAS_SIGNALING_DN
13	0.434	1 / 140	HALLMARK_APOPTOSIS
14	0.434	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
15	0.448	1 / 146	HALLMARK_DNA_REPAIR
16	0.452	1 / 148	HALLMARK_KRAS_SIGNALING_UP
17	0.493	1 / 167	HALLMARK_APICAL_JUNCTION
18	0.500	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
19	0.508	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	0.548	1 / 195	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	DUMEAUX_Monocytes in 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 / 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−04	44 / 7592	HOPP_Active_promoter
2	3e−03	39 / 6929	HOPP_Txn_elongation
3	4e−02	9 / 1128	SPANG_BCR DN
4	5e−02	36 / 7209	HOPP_Weak_promoter
5	2e−01	1 / 43	LENZ_Stromal signature 2
6	2e−01	25 / 5184	HOPP_Txn_transition
7	3e−01	26 / 5693	HOPP_Weak_enhancer
8	4e−01	24 / 5538	HOPP_Weak_txn
9	4e−01	10 / 2211	HOPP_Repetitive
10	6e−01	5 / 1218	SPANG_BCR UP
11	6e−01	1 / 212	LENZ_Stromal signature 1
12	6e−01	10 / 2563	HOPP_Heterochrom
13	6e−01	1 / 247	ZHANG_DLBCL mutated
14	7e−01	1 / 280	SPANG_CD40 6hrs UP
15	7e−01	1 / 294	TARTE_Plasmablast signature
16	8e−01	24 / 6564	HOPP_Strong_enhancer
17	1e+00	5 / 3396	HOPP_Repressed
18	1e+00	1 / 2188	HOPP_Poised_promoter
19	1e+00	0 / 13	BENTINK_mBL UP
20	1e+00	0 / 12	BENTINK_mBL DOWN

MF

Rank	p−value	#in/all	Geneset
1	0.008	2 / 33	estrogen receptor binding
2	0.010	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
3	0.017	2 / 50	motor activity
4	0.023	6 / 550	protein homodimerization activity
5	0.039	4 / 316	protein kinase binding
6	0.040	1 / 10	glutathione binding
7	0.040	1 / 10	glycine binding
8	0.044	1 / 11	ATPase activity, coupled
9	0.044	1 / 11	telomeric DNA binding
10	0.047	1 / 12	alpha−actinin binding
11	0.047	1 / 12	dynein binding
12	0.047	1 / 12	enhancer sequence−specific DNA binding
13	0.047	1 / 12	misfolded protein binding
14	0.051	1 / 13	5'−nucleotidase activity
15	0.051	1 / 13	GABA receptor binding
16	0.055	1 / 14	heparan sulfate proteoglycan binding
17	0.059	1 / 15	microfilament motor activity
18	0.063	1 / 16	RNA polymerase II carboxy−terminal domain kinase activity
19	0.067	1 / 17	aspartic−type endopeptidase activity
20	0.078	1 / 20	NAD+ ADP−ribosyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−04	5 / 175	hsa−miR−548k
2	9e−04	8 / 507	hsa−miR−15a
3	1e−03	4 / 115	hsa−miR−515−5p
4	2e−03	4 / 132	hsa−miR−320d
5	3e−03	4 / 146	hsa−miR−320c
6	3e−03	4 / 147	hsa−miR−143
7	4e−03	6 / 366	hsa−miR−519b−3p
8	5e−03	4 / 170	hsa−miR−320b
9	6e−03	6 / 405	hsa−miR−519c−3p
10	8e−03	6 / 432	hsa−miR−424
11	8e−03	3 / 101	hsa−miR−603
12	1e−02	6 / 471	hsa−miR−15b
13	1e−02	6 / 479	hsa−miR−16
14	2e−02	3 / 136	hsa−miR−155
15	2e−02	6 / 517	hsa−miR−106b
16	2e−02	3 / 137	hsa−miR−656
17	2e−02	2 / 51	hsa−miR−556−3p
18	2e−02	2 / 53	hsa−miR−552
19	2e−02	5 / 395	hsa−miR−301b
20	2e−02	2 / 57	hsa−miR−891b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 14	BENTINK_e2f3.1
2	1.00	0 / 12	GUSTAFSON_PI3K_UP
3	1.00	0 / 13	GUSTAFSON_PI3K_DN
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	

TF

Rank	p−value	#in/all	Geneset
1	0.008	1 / 2	MYC_ECM cell adhesion DOWN
2	0.036	1 / 9	MYC_Targets DOWN
3	0.077	11 / 1701	HEBENSTREIT_high expression TF
4	0.146	12 / 2136	ICGC_GabpPcr2_targets
5	0.211	8 / 1418	ICGC_Ets1_targets
6	0.336	7 / 1400	ICGC_Myc_targets
7	0.346	9 / 1878	ICGC_Cebpbsc150_targets
8	0.517	5 / 1171	KIM_MYC targets
9	0.623	5 / 1314	ICGC_Usf1_targets
10	0.660	2 / 553	ICGC_RxraPcr1_targets
11	0.661	14 / 3700	ICGC_Nfatc1_targets
12	0.669	5 / 1383	ICGC_Six5_targets
13	0.686	4 / 1139	HEBENSTREIT_low expression TF
14	0.764	4 / 1266	ICGC_NrsfPcr1_targets
15	0.810	16 / 4617	ICGC_Tcf12_targets
16	0.838	13 / 3924	ICGC_Zeb1_targets
17	0.870	14 / 4314	ICGC_Ebfsc137065_targets
18	0.879	16 / 4879	ICGC_Pmlsc71910_targets
19	0.880	6 / 2137	ICGC_SrfV0416101_targets
20	0.885	16 / 4909	ICGC_Stat5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 16	VAQUERIZAS_Salivary gland
2	0.07	1 / 17	VAQUERIZAS_Heart
3	0.09	1 / 23	VAQUERIZAS_Trachea
4	0.10	1 / 26	VAQUERIZAS_Liver
5	0.13	1 / 33	VAQUERIZAS_Prostate
6	0.44	1 / 143	VAQUERIZAS_General
7	1.00	0 / 36	VAQUERIZAS_Fetal brain
8	1.00	0 / 41	VAQUERIZAS_Placenta
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	0.5	1 / 194	PALMER_B−Cell signature up
2	0.6	1 / 225	PALMER_Granulocytes signature up
3	1.0	0 / 32	WIRTH_Pancreas
4	1.0	0 / 350	WIRTH_Immune system
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	13 / 3682	LU_BPDE 0.005 DN
2	0.8	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	

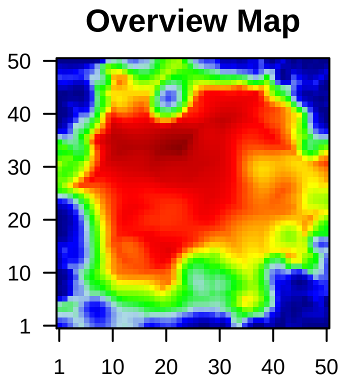
Underexpression Spots

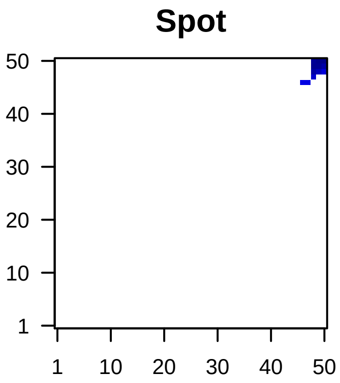
Spot Summary: s

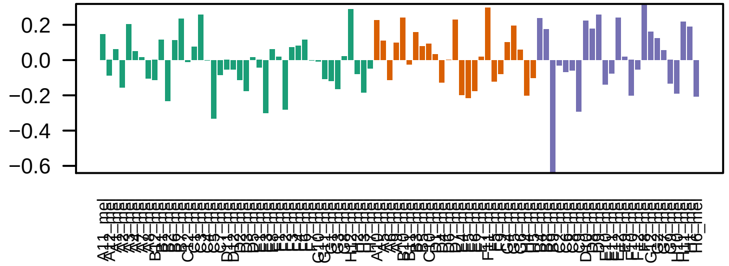
metagenes = 12
genes = 179

<r> metagenes = 0.94
<r> genes = 0.09
beta: r2= 1.87 / log p= −Inf

samples with spot = 15 (16.3 %)
MSC1 : 4 (9.5 %)
MSC2 : 5 (20 %)
MSC3 : 6 (24 %)





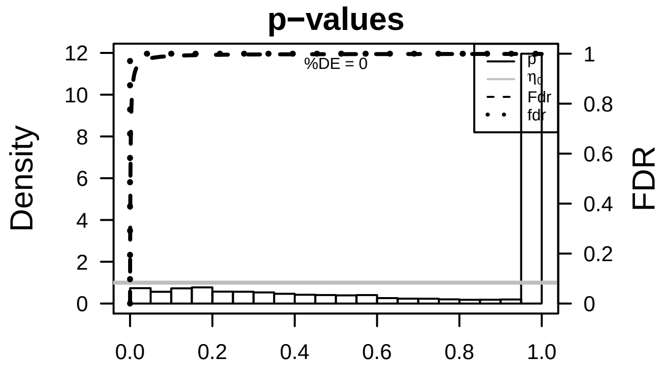


Spot Genelist

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	OAS1	1.86	−0.2	0.37	OAS1	2'−5'−oligoadenylate synthetase 1, 40/46kDa [Source:HGNC
4	ZFP62	1.82	−0.44	0.25	ZFP62	ZFP62 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:
5	C1orf109	1.77	−0.59	0.29	C1orf109	chromosome 1 open reading frame 109 [Source:HGNC Symb
6	CYP19A1	1.7	−0.37	0.31	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1 [Sour
7	UGP2	1.7	−1.72	0.24	UGP2	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
8	NLRC5	1.7	−0.18	0.25	NLRC5	NLR family, CARD domain containing 5 [Source:HGNC Symb
9	SRXN1	1.67	−0.81	0.3	SRXN1	sulfiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:16132]
10	ICA1	1.66	−0.29	0.3	ICA1	islet cell autoantigen 1, 69kDa [Source:HGNC Symbol;Acc:H
11	RFT1	1.6	−0.52	0.29	RFT1	RFT1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
12	IMMP2L	1.59	−0.86	0.29	IMMP2L	IMP2 inner mitochondrial membrane peptidase−like (S. cerev
13	SPATA20	1.59	−0.29	0.29	SPATA20	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
14	METTL1	1.57	−1.04	0.29	METTL1	methyltransferase like 1 [Source:HGNC Symbol;Acc:HGNC:7
15	WDR27	1.54	−0.32	0.21	WDR27	WD repeat domain 27 [Source:HGNC Symbol;Acc:HGNC:21
16	LETMD1	1.52	−0.56	0.19	LETMD1	LETM1 domain containing 1 [Source:HGNC Symbol;Acc:HG
17	ASL	1.51	−0.56	0.28	ASL	argininosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:7
18	CYB561A3	1.51	−1.09	0.25	CYB561A3	cytochrome b561 family, member A3 [Source:HGNC Symbol;
19	TRAPPC8	1.51	−0.98	0.27	TRAPPC8	trafficking protein particle complex 8 [Source:HGNC Symbol;
20	PIGV	1.49	−0.28	0.34	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V [Sou

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−12	155 / 9482	Colon	TssA_Colon
2	1e−09	146 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	1e−08	144 / 9027	Colon	Tx_Colon
4	2e−08	135 / 8205	CC	cytoplasm
5	3e−08	43 / 1468	CC	mitochondrion
6	3e−08	120 / 6929	Lymp	HOPP_Txn_elongation
7	3e−08	146 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
8	5e−08	37 / 1171	TF	KIM_MYC targets
9	2e−07	136 / 8580	Colon	TxWk_Colon
10	5e−06	19 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
11	1e−05	17 / 424	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
12	3e−05	30 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
13	4e−05	118 / 7592	Lymp	HOPP_Active_promoter
14	4e−05	56 / 2798	Colon	TxEnhG1_Colon
15	6e−05	88 / 5184	Lymp	HOPP_Txn_transition
16	1e−04	23 / 800	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
17	1e−04	20 / 649	CC	endoplasmic reticulum membrane
18	1e−04	138 / 9528	Brain	Overlap_fetal_midbrain_Quies
19	2e−04	26 / 1008	GSEA	BRUINS_UVC_RESPONSE_LATE
20	2e−04	16 / 476	GSEA	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
21	3e−04	138 / 9653	Colon	Enh_Colon
22	3e−04	9 / 179	miRN	hsa−miR−520f
23	3e−04	37 / 1730	BP	small molecule metabolic process
24	5e−04	6 / 83	GSEA	LI_DCP2_BOUND_MRNA
25	6e−04	147 / 10605	CC	intracellular
26	7e−04	9 / 200	GSEA	LINSLEY_MIR16_TARGETS
27	8e−04	8 / 162	BP	ribosome biogenesis
28	8e−04	83 / 5155	Colon	EnhWk1_Colon
29	8e−04	14 / 435	GSEA	GARY_CD5_TARGETS_UP
30	9e−04	19 / 706	GSEA	BENPORATH_MYC_MAX_TARGETS
31	9e−04	7 / 128	CC	ribosome
32	9e−04	108 / 7203	Colon	TssF_Colon
33	1e−03	13 / 393	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_UP
34	1e−03	13 / 401	CC	mitochondrial inner membrane
35	1e−03	27 / 1201	CC	endoplasmic reticulum
36	2e−03	9 / 222	GSEA	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
37	2e−03	9 / 223	GSEA	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP
38	2e−03	10 / 277	BP	translation
39	2e−03	11 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
40	2e−03	4 / 45	GSEA	CHIBA_RESPONSE_TO_TSA



Aging

Rank	p−value	#in/all	Geneset
1	0.4	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	3e−04	37 / 1730	small molecule metabolic process
2	8e−04	8 / 162	ribosome biogenesis
3	2e−03	10 / 277	translation
4	7e−03	12 / 435	cellular protein metabolic process
5	7e−03	3 / 32	proteolysis involved in cellular protein catabolic process
6	7e−03	4 / 62	negative regulation of catalytic activity
7	7e−03	5 / 98	toll−like receptor signaling pathway
8	7e−03	4 / 63	dolichol−linked oligosaccharide biosynthetic process
9	7e−03	4 / 63	response to ethanol
10	7e−03	2 / 11	barbed−end actin filament capping
11	7e−03	11 / 388	proteolysis
12	9e−03	4 / 67	Ras protein signal transduction
13	9e−03	2 / 12	ubiquinone biosynthetic process
14	1e−02	2 / 13	mannosylation
15	1e−02	7 / 204	post−translational protein modification
16	1e−02	2 / 15	lipid particle organization
17	1e−02	2 / 15	nucleoside metabolic process
18	1e−02	3 / 43	autophagic vacuole assembly
19	2e−02	2 / 16	preassembly of GPI anchor in ER membrane
20	2e−02	3 / 45	memory

Brain

Rank	p−value	#in/all	Geneset
1	1e−09	146 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−08	146 / 9330	Overlap_fetal_midbrain_ReprPC
3	1e−04	138 / 9528	Overlap_fetal_midbrain_Quies
4	5e−03	89 / 5940	Overlap_fetal_midbrain_HetRpts
5	1e−02	10 / 349	Fetal_ZNF
6	4e−02	15 / 765	Mid_Frontal_Lobe_Het
7	5e−02	13 / 656	Overlap_fetal_midbrain_EnhP
8	1e−01	21 / 1333	Fetal_ReprPCWk
9	1e−01	116 / 9020	Overlap_fetal_midbrain_ReprPCWk
10	3e−01	41 / 3081	Mid_Frontal_Lobe_ZNF
11	3e−01	33 / 2462	Mid_Frontal_Lobe_HetRpts
12	3e−01	15 / 1050	Fetal_EnhP
13	3e−01	3 / 163	Fetal_ReprPC
14	3e−01	11 / 769	Overlap_fetal_midbrain_ZNF
15	4e−01	12 / 884	Overlap_fetal_midbrain_EnhG
16	5e−01	5 / 383	Fetal_Tx
17	5e−01	4 / 304	Fetal_Het
18	5e−01	12 / 989	Mid_Frontal_Lobe_Quies
19	5e−01	10 / 831	Fetal_HetRpts
20	6e−01	2 / 158	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	GENTLES_modul3
2	0.1	1 / 12	LIU_BREAST_CANCER
3	0.1	1 / 12	LIU_PROSTATE_CANCER_UP
4	0.2	0 / 15	RHODES_CANCER_META_SIGNATURE
5	0.2	1 / 16	GENTLES_modul7
6	0.3	1 / 29	KUIPER_MM good survival
7	0.4	1 / 40	ZHANG_MM up
8	0.4	2 / 120	PanCan_CC+Apop_geneset_nanostring
9	0.4	2 / 121	PanCan_MAPK_geneset_nanostring
10	0.4	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.5	1 / 55	PanCan_JAK−ST_geneset_nanostring
12	0.5	1 / 61	PanCan_Wnt_geneset_nanostring
13	0.6	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	0.6	2 / 156	PanCan_PI3K_geneset_nanostring
15	0.6	1 / 70	SHAUGHNESSY_MM high risk
16	0.6	1 / 82	PanCan_TXmisReg_geneset_nanostring
17	0.6	2 / 180	SPANG_LPS−index2
18	0.7	3 / 298	SPANG_BCL6−index2
19	0.7	5 / 489	Lembcke_Normal vs Adenoma
20	0.7	1 / 111	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−08	135 / 8205	cytoplasm
2	3e−08	43 / 1468	mitochondrion
3	1e−04	20 / 649	endoplasmic reticulum membrane
4	6e−04	147 / 10605	intracellular
5	9e−04	7 / 128	ribosome
6	1e−03	13 / 401	mitochondrial inner membrane
7	1e−03	27 / 1201	endoplasmic reticulum
8	2e−03	3 / 22	pre−autophagosomal structure
9	2e−03	138 / 9988	organelle
10	3e−03	3 / 24	mitochondrial ribosome
11	6e−03	2 / 10	WASH complex
12	9e−03	17 / 747	nucleolus
13	1e−02	38 / 2193	extracellular exosome
14	1e−02	4 / 75	blood microparticle
15	1e−02	2 / 15	BLOC−1 complex
16	2e−02	2 / 17	integral component of mitochondrial outer membrane
17	2e−02	153 / 11774	cell
18	3e−02	2 / 22	mitochondrial large ribosomal subunit
19	3e−02	40 / 2507	cytosol
20	5e−02	10 / 456	vacuole

Chr

Rank	p−value	#in/all	Geneset
1	0.009	16 / 687	Chr 6
2	0.039	14 / 689	Chr 7
3	0.048	15 / 775	Chr 12
4	0.060	15 / 801	Chr 11
5	0.110	4 / 151	Chr 21
6	0.195	8 / 462	Chr 14
7	0.216	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
8	0.258	10 / 649	Chr 16
9	0.492	6 / 465	Chr 15
10	0.500	3 / 221	Chr 18
11	0.526	5 / 398	Chr 20
12	0.546	7 / 576	Chr 9
13	0.615	3 / 262	Chr 13
14	0.690	9 / 840	Chr 17
15	0.773	3 / 335	Chr 22
16	0.800	5 / 552	Chr 10
17	0.808	5 / 558	Chr 4
18	0.813	15 / 1500	Chr 1
19	0.821	4 / 469	Chr 8
20	0.885	7 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−12	155 / 9482	TssA_Colon
2	1e−08	144 / 9027	Tx_Colon
3	2e−07	136 / 8580	TxWk_Colon
4	4e−05	56 / 2798	TxEnhG1_Colon
5	3e−04	138 / 9653	Enh_Colon
6	8e−04	83 / 5155	EnhWk1_Colon
7	9e−04	108 / 7203	TssF_Colon
8	5e−02	82 / 5880	TssD2_Colon
9	6e−02	134 / 10290	TssWk_Colon
10	6e−02	112 / 8415	Quies3_Colon
11	9e−02	1 / 8	KIM_CRC−MSI−regulated_DN
12	1e−01	39 / 2698	EnhA_Colon
13	2e−01	11 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
14	2e−01	12 / 739	TxEnhG2_Colon
15	2e−01	2 / 66	Marisa_CRC−cluster−h
16	2e−01	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
17	2e−01	12 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
18	3e−01	7 / 427	Quies2_Colon
19	3e−01	13 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	3e−01	3 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.8	4 / 435	GUDJ_psoriasis up
2	1.0	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	9 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.03	4 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
3	0.06	1 / 5	Phillips Prolif up vs PN & MES
4	0.07	8 / 356	Down_a
5	0.08	2 / 38	OL vs. OPC
6	0.08	15 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
7	0.12	1 / 11	astrocytes_glio
8	0.12	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
9	0.15	2 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
10	0.17	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
11	0.18	1 / 16	VERHAAK_NL subtype
12	0.20	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
13	0.22	2 / 72	laffaire_hypermeth_LGG_vs_control
14	0.28	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
15	0.28	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
16	0.32	1 / 32	Colman_survival_associated
17	0.33	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
18	0.34	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
19	0.38	1 / 39	OPC
20	0.42	2 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−06	19 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	1e−05	17 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
3	3e−05	30 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
4	1e−04	23 / 800	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
5	2e−04	26 / 1008	BRUINS_UVC_RESPONSE_LATE
6	2e−04	16 / 476	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
7	5e−04	6 / 83	LI_DCP2_BOUND_MRNA
8	7e−04	9 / 200	LINSLEY_MIR16_TARGETS
9	8e−04	14 / 435	GARY_CD5_TARGETS_UP
10	9e−04	19 / 706	BENPORATH_MYC_MAX_TARGETS
11	1e−03	13 / 393	MITSIADES_RESPONSE_TO_APLIDIN_UP
12	2e−03	9 / 222	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
13	2e−03	9 / 223	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP
14	2e−03	11 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
15	2e−03	4 / 45	CHIBA_RESPONSE_TO_TSA
16	3e−03	3 / 23	KEGG_PROTEIN_EXPORT
17	3e−03	11 / 338	DAIRKEE_TERT_TARGETS_UP
18	3e−03	5 / 80	SASSON_RESPONSE_TO_FORSKOLIN_UP
19	3e−03	20 / 843	LOPEZ_MBD_TARGETS
20	3e−03	10 / 293	DOUGLAS_BMI1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.04	4 / 107	HALLMARK_COAGULATION
3	0.05	5 / 169	HALLMARK_XENOBIOTIC_METABOLISM
4	0.06	5 / 174	HALLMARK_HEME_METABOLISM
5	0.06	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.08	4 / 137	HALLMARK_UV_RESPONSE_DN
7	0.15	2 / 57	HALLMARK_MYC_TARGETS_V2
8	0.16	4 / 176	HALLMARK_HYPOXIA
9	0.19	4 / 188	HALLMARK_ADIPOGENESIS
10	0.19	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
11	0.21	4 / 196	HALLMARK_MTORC1_SIGNALING
12	0.24	3 / 140	HALLMARK_APOPTOSIS
13	0.30	1 / 29	HALLMARK_NOTCH_SIGNALING
14	0.31	3 / 162	HALLMARK_COMPLEMENT
15	0.31	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
16	0.32	3 / 165	HALLMARK_MYOGENESIS
17	0.32	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	0.33	3 / 167	HALLMARK_APICAL_JUNCTION
19	0.37	3 / 181	HALLMARK_P53_PATHWAY
20	0.38	3 / 183	HALLMARK_GLYCOLYSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.5	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 / 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−08	120 / 6929	HOPP_Txn_elongation
2	4e−05	118 / 7592	HOPP_Active_promoter
3	6e−05	88 / 5184	HOPP_Txn_transition
4	1e−02	103 / 7209	HOPP_Weak_promoter
5	1e−02	2 / 15	DAVE_Immune response 2
6	2e−02	23 / 1218	SPANG_BCR UP
7	5e−02	20 / 1128	SPANG_BCR DN
8	1e−01	6 / 268	SPANG_IL21 UP
9	1e−01	1 / 10	DAVE_BL_DN
10	1e−01	87 / 6564	HOPP_Strong_enhancer
11	1e−01	1 / 13	Subero_MCL_hypo_meth
12	2e−01	1 / 14	Subero_mBL_hypo_meth
13	2e−01	2 / 66	TARTE_Plasma cell signature
14	2e−01	1 / 20	SPANG_BAFF 9hrs UP
15	3e−01	2 / 80	Aukema_BCL2 DN_BCL6 UP
16	3e−01	1 / 29	Subero_DLBCL_hypo_meth
17	3e−01	1 / 30	TARTE_B−cell signature
18	3e−01	1 / 30	Subero_INT_hypo_meth
19	4e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
20	4e−01	4 / 280	SPANG_CD40 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 24	snoRNA binding
2	0.006	2 / 10	ribosomal small subunit binding
3	0.006	12 / 433	peptidase activity
4	0.011	4 / 71	structural constituent of ribosome
5	0.011	3 / 39	SNARE binding
6	0.014	4 / 77	electron carrier activity
7	0.021	10 / 394	catalytic activity
8	0.022	2 / 19	MAP kinase kinase activity
9	0.024	5 / 136	lyase activity
10	0.026	3 / 53	transferase activity
11	0.029	2 / 22	transferase activity, transferring hexosyl groups
12	0.033	13 / 609	cytoskeletal protein binding
13	0.039	24 / 1365	RNA binding
14	0.039	2 / 26	endopeptidase inhibitor activity
15	0.039	2 / 26	protein kinase inhibitor activity
16	0.042	6 / 210	transferase activity, transferring glycosyl groups
17	0.054	2 / 31	beta−tubulin binding
18	0.054	3 / 71	cysteine−type endopeptidase activity
19	0.055	12 / 592	oxidoreductase activity
20	0.061	18 / 1007	poly(A) RNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	9 / 179	hsa−miR−520f
2	4e−03	4 / 52	hsa−miR−345
3	5e−03	5 / 91	hsa−miR−378
4	7e−03	5 / 100	hsa−miR−574−5p
5	8e−03	9 / 288	hsa−miR−34a
6	1e−02	8 / 261	hsa−miR−548p
7	1e−02	3 / 42	hsa−miR−129−3p
8	2e−02	4 / 82	hsa−miR−630
9	2e−02	8 / 274	hsa−miR−1244
10	2e−02	5 / 126	hsa−miR−335
11	2e−02	3 / 47	hsa−miR−1291
12	2e−02	4 / 85	hsa−miR−423−5p
13	2e−02	4 / 85	hsa−miR−510
14	2e−02	3 / 48	hsa−miR−628−5p
15	2e−02	6 / 178	hsa−miR−34b
16	2e−02	5 / 133	hsa−miR−485−5p
17	3e−02	8 / 293	hsa−miR−202
18	3e−02	6 / 187	hsa−miR−382
19	3e−02	3 / 56	hsa−miR−384
20	3e−02	5 / 144	hsa−miR−135b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	BENTINK_myc.1
2	0.17	1 / 15	BENTINK_ras.6
3	1.00	0 / 12	GUSTAFSON_PI3K_UP
4	1.00	0 / 13	GUSTAFSON_PI3K_DN
5	1.00	0 / 14	BENTINK_e2f3.1
6	1.00	0 / 12	BENTINK_e2f3.2
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 9	BENTINK_ras.4
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	5e−08	37 / 1171	KIM_MYC targets
2	5e−03	39 / 2136	ICGC_GabpPcr2_targets
3	2e−02	36 / 2137	ICGC_SrfV0416101_targets
4	3e−02	25 / 1400	ICGC_Myc_targets
5	5e−02	59 / 4032	ICGC_Creb1_targets
6	9e−02	23 / 1418	ICGC_Ets1_targets
7	1e−01	65 / 4689	ICGC_Taf1_targets
8	1e−01	61 / 4385	ICGC_Atf2_targets
9	1e−01	26 / 1701	HEBENSTREIT_high expression TF
10	1e−01	12 / 690	ICGC_Atf3_targets
11	2e−01	21 / 1383	ICGC_Six5_targets
12	2e−01	20 / 1314	ICGC_Usf1_targets
13	2e−01	59 / 4414	ICGC_Bclaf101388_targets
14	2e−01	65 / 4909	ICGC_Stat5_targets
15	2e−01	64 / 4829	ICGC_Nficsc81335_targets
16	2e−01	1 / 19	MYC_Metabolism UP
17	3e−01	61 / 4706	ICGC_Sp1_targets
18	3e−01	25 / 1878	ICGC_Cebpbsc150_targets
19	4e−01	17 / 1266	ICGC_NrsfPcr1_targets
20	4e−01	68 / 5408	ICGC_Pou2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.5	1 / 59	VAQUERIZAS_Whole blood
2	0.8	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	0.1	1 / 11	WIRTH_Sec. lymphoid organs
2	0.1	1 / 11	WIRTH_Cortex cerebri
3	0.1	5 / 225	PALMER_Granulocytes signature up
4	0.1	1 / 13	WIRTH_B−cells
5	0.2	4 / 194	PALMER_B−Cell signature up
6	0.3	1 / 32	WIRTH_Placenta
7	0.6	4 / 350	WIRTH_Immune system
8	0.7	1 / 95	WIRTH_Muscle
9	0.8	1 / 114	PALMER_T−Cell signature up
10	0.8	3 / 350	WIRTH_Nervous System
11	1.0	0 / 32	WIRTH_Pancreas
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 8	WIRTH_Tonsil
14	1.0	0 / 12	WIRTH_Thymus
15	1.0	0 / 12	WIRTH_Lymphocytes
16	1.0	0 / 5	WIRTH_Bone marrow
17	1.0	0 / 11	WIRTH_Globus pallidus
18	1.0	0 / 14	WIRTH_Telencephalon
19	1.0	0 / 10	WIRTH_Hippocampus
20	1.0	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	46 / 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	

Underexpression Spots

Spot Summary: t

metagenes = 8
genes = 103

<r> metagenes = 0.97
<r> genes = 0.1
beta: r2= 1.62 / log p= −Inf

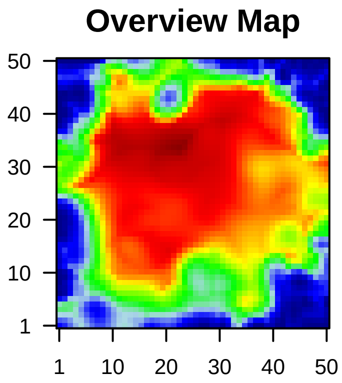
samples with spot = 16 (17.4 %)
MSC1 : 2 (4.8 %)
MSC2 : 5 (20 %)
MSC3 : 9 (36 %)

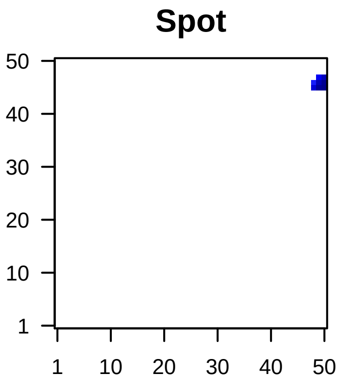
Spot Genelist

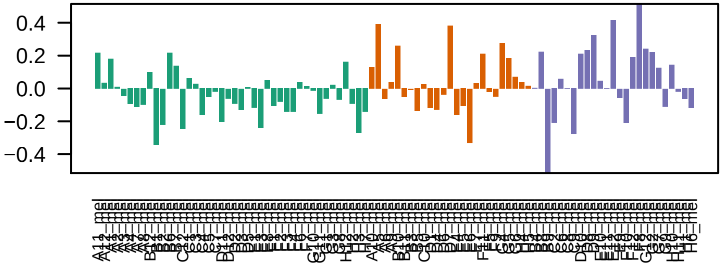
Rank	ID	max e	min e	r	Symbol	Description
1	PIBF1	1.97	−0.47	0.28	PIBF1	progesterone immunomodulatory binding factor 1 [Source:HG
2	CC2D2A	1.84	−0.51	0.36	CC2D2A	coiled−coil and C2 domain containing 2A [Source:HGNC Syn
3	GSDMB	1.8	−0.19	0.37	GSDMB	gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]
4	GORAB	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	VASP	1.69	−0.36	0.28	VASP	vasodilator−stimulated phosphoprotein [Source:HGNC Symbo
8	ZNF420	1.68	−0.43	0.28	ZNF420	zinc finger protein 420 [Source:HGNC Symbol;Acc:HGNC:20
9	PHOSPHO2	1.62	−0.32	0.36	PHOSPHO2	phosphatase, orphan 2 [Source:HGNC Symbol;Acc:HGNC:28
10	MFSD8	1.6	−0.35	0.36	MFSD8	major facilitator superfamily domain containing 8 [Source:HGI
11	DCAF10	1.58	−0.65	0.26	DCAF10	DDB1 and CUL4 associated factor 10 [Source:HGNC Symbo
12	TRO	1.57	−0.73	0.41	TRO	trophinin [Source:HGNC Symbol;Acc:HGNC:12326]
13	AMPD2	1.56	−0.6	0.41	AMPD2	adenosine monophosphate deaminase 2 [Source:HGNC Syn
14	TSC2	1.55	−0.53	0.4	TSC2	tuberous sclerosis 2 [Source:HGNC Symbol;Acc:HGNC:1236
15	PHF8	1.55	−0.41	0.26	PHF8	PHD finger protein 8 [Source:HGNC Symbol;Acc:HGNC:2067
16	DNHD1	1.54	−0.23	0.3	DNHD1	dynein heavy chain domain 1 [Source:HGNC Symbol;Acc:HG
17	PHYKPL	1.52	−0.43	0.29	PHYKPL	5−phosphohydroxy−L−lysine phospho−lyase [Source:HGNC
18	ZNF668	1.52	−0.23	0.28	ZNF668	zinc finger protein 668 [Source:HGNC Symbol;Acc:HGNC:25
19	HIST3H2A	1.51	−0.86	0.44	HIST3H2A	histone cluster 3, H2a [Source:HGNC Symbol;Acc:HGNC:205
20	DPH7	1.48	−0.35	0.33	DPH7	diphthamide biosynthesis 7 [Source:HGNC Symbol;Acc:HGN

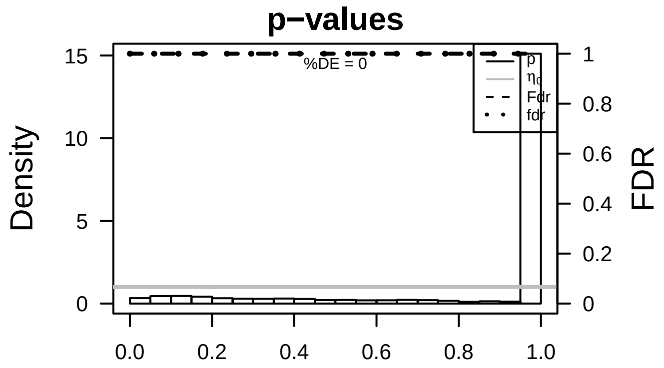
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−11	90 / 8580	Colon	TxWk_Colon
2	5e−10	91 / 9027	Colon	Tx_Colon
3	9e−08	89 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
4	5e−07	73 / 6929	Lympl	HOPP_Txn_elongation
5	2e−06	76 / 7592	Lympl	HOPP_Active_promoter
6	2e−05	37 / 2755	BP	transport
7	7e−05	84 / 9482	Colon	TssA_Colon
8	8e−05	81 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
9	1e−04	77 / 8415	Colon	Quies3_Colon
10	2e−04	54 / 5184	Lympl	HOPP_Txn_transition
11	3e−04	59 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
12	5e−04	28 / 2136	TF	ICGC_GabpPcr2_targets
13	5e−04	4 / 54	CC	transport vesicle
14	1e−03	66 / 7203	Colon	TssF_Colon
15	1e−03	6 / 176	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
16	2e−03	3 / 35	GSEA	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN
17	2e−03	2 / 10	CC	WASH complex
18	2e−03	3 / 37	miRN	hsa−miR−760
19	2e−03	3 / 38	GSEA	IRITANI_MAD1_TARGETS_DN
20	3e−03	2 / 11	BP	activation of mitophagy in response to mitochondrial depolarization
21	3e−03	2 / 11	BP	posttranscriptional regulation of gene expression
22	3e−03	2 / 12	MF	protein methyltransferase activity
23	3e−03	5 / 142	GSEA	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
24	4e−03	2 / 13	BP	cAMP catabolic process
25	4e−03	64 / 7209	Lympl	HOPP_Weak_promoter
26	4e−03	31 / 2798	Colon	TxEnhG1_Colon
27	4e−03	2 / 14	BP	protein ADP−ribosylation
28	4e−03	79 / 9528	Brain	Overlap_fetal_midbrain_Quies
29	5e−03	2 / 15	CC	BLOC−1 complex
30	5e−03	3 / 51	miRN	hsa−miR−508−5p
31	5e−03	2 / 16	GSEA	MEISSNER_NPC_ICP_WITH_H3K4ME3
32	6e−03	4 / 104	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_UP
33	6e−03	45 / 4689	TF	ICGC_Taf1_targets
34	7e−03	85 / 10605	CC	intracellular
35	7e−03	83 / 10290	Colon	TssWk_Colon
36	7e−03	11 / 675	GSEA	BENPORATH_SOX2_TARGETS
37	7e−03	39 / 3924	TF	ICGC_Zeb1_targets
38	7e−03	79 / 9653	Colon	Enh_Colon
39	8e−03	3 / 59	BP	cilium morphogenesis
40	8e−03	46 / 4879	TF	ICGC_Pmlsc71910_targets









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	2e-05	37 / 2755	transport
2	3e-03	2 / 11	activation of mitophagy in response to mitochondrial depolarization
3	3e-03	2 / 11	posttranscriptional regulation of gene expression
4	4e-03	2 / 13	cAMP catabolic process
5	4e-03	2 / 14	protein ADP-ribosylation
6	8e-03	3 / 59	cilium morphogenesis
7	8e-03	2 / 20	heme biosynthetic process
8	8e-03	2 / 20	regulation of sequence-specific DNA binding transcription factor activity
9	1e-02	2 / 22	mitotic spindle organization
10	1e-02	3 / 68	microtubule-based movement
11	1e-02	2 / 25	protein methylation
12	2e-02	12 / 863	transmembrane transport
13	2e-02	8 / 478	protein transport
14	2e-02	3 / 81	cytoskeleton-dependent intracellular transport
15	2e-02	2 / 31	lysosome organization
16	3e-02	2 / 38	base-excision repair
17	4e-02	2 / 45	regulation of cyclin-dependent protein serine/threonine kinase activity
18	5e-02	14 / 1237	metabolic process
19	5e-02	2 / 53	protein homotetramerization
20	6e-02	2 / 56	translational initiation

Brain

Rank	p-value	#in/all	Geneset
1	9e-08	89 / 9330	Overlap_fetal_midbrain_ReprPC
2	8e-05	81 / 9013	Overlap_fetal_midbrain_K9K27me3
3	3e-04	59 / 5940	Overlap_fetal_midbrain_HetRpts
4	4e-03	79 / 9528	Overlap_fetal_midbrain_Quies
5	8e-03	12 / 786	Fetal_EnhG
6	1e-02	13 / 953	Fetal_Enh
7	4e-02	15 / 1333	Fetal_ReprPCWk
8	8e-02	70 / 9020	Overlap_fetal_midbrain_ReprPCWk
9	1e-01	9 / 831	Fetal_HetRpts
10	2e-01	4 / 304	Fetal_Het
11	2e-01	8 / 769	Overlap_fetal_midbrain_ZNF
12	2e-01	25 / 3081	Mid_Frontal_Lobe_ZNF
13	3e-01	20 / 2462	Mid_Frontal_Lobe_HetRpts
14	3e-01	9 / 1050	Fetal_EnhP
15	4e-01	10 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	5e-01	5 / 656	Overlap_fetal_midbrain_EnhP
17	5e-01	8 / 1122	Fetal_K9K27me3
18	5e-01	7 / 989	Mid_Frontal_Lobe_Quies
19	7e-01	1 / 158	Overlap_fetal_midbrain_Het
20	7e-01	1 / 166	Mid_Frontal_Lobe_Tx

Cancer

Rank	p-value	#in/all	Geneset
1	0.08	0 / 14	LIU_COMMON_CANCER_GENES
2	0.11	1 / 16	GENTLES_modul6
3	0.18	1 / 29	KUIPER_MM good survival
4	0.34	3 / 298	SPANG_BCL6-index2
5	0.36	2 / 180	SPANG_LPS-index2
6	0.43	0 / 12	LIU_PROSTATE_CANCER_UP
7	0.51	0 / 14	LIU_PROSTATE_CANCER_DN
8	0.94	1 / 401	Lembcke_Colonic Inflammation
9	0.97	1 / 489	Lembcke_Normal vs Adenoma
10	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1.00	0 / 12	LIU_BREAST_CANCER
15	1.00	0 / 14	LIU_LIVER_CANCER
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	5e-04	4 / 54	transport vesicle
2	2e-03	2 / 10	WASH complex
3	5e-03	2 / 15	BLOC-1 complex
4	7e-03	85 / 10605	intracellular
5	8e-03	2 / 20	dynein complex
6	1e-02	69 / 8205	cytoplasm
7	2e-02	32 / 3214	protein complex
8	2e-02	98 / 13191	cellular_component
9	3e-02	2 / 41	ciliary tip
10	5e-02	2 / 51	filopodium
11	5e-02	13 / 1132	Golgi apparatus
12	5e-02	7 / 487	intracellular membrane-bounded organelle
13	7e-02	2 / 60	nuclear pore
14	7e-02	1 / 10	mRNA cap binding complex
15	7e-02	4 / 223	lysosomal membrane
16	7e-02	9 / 745	cytoplasmic membrane-bounded vesicle
17	7e-02	88 / 11774	cell
18	8e-02	2 / 66	integral component of endoplasmic reticulum membrane
19	8e-02	27 / 2984	integral component of membrane
20	8e-02	1 / 12	holo TFIIH complex

Chr

Rank	p-value	#in/all	Geneset
1	0.2	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	5 / 552	Chr 10
6	0.4	7 / 838	Chr 3
7	0.4	4 / 462	Chr 14
8	0.4	8 / 1037	Chr 19
9	0.5	6 / 775	Chr 12
10	0.5	6 / 801	Chr 11
11	0.5	3 / 398	Chr 20
12	0.5	7 / 993	Chr 2
13	0.5	4 / 558	Chr 4
14	0.5	2 / 262	Chr 13
15	0.6	4 / 576	Chr 9
16	0.6	10 / 1500	Chr 1
17	0.7	4 / 687	Chr 6
18	0.7	4 / 689	Chr 7
19	0.7	4 / 696	Chr 5
20	0.9	3 / 840	Chr 17

Colon Cancer

Rank	p-value	#in/all	Geneset
1	6e-11	90 / 8580	TxWk_Colon
2	5e-10	91 / 9027	Tx_Colon
3	7e-05	84 / 9482	TssA_Colon
4	1e-04	77 / 8415	Quies3_Colon
5	1e-03	66 / 7203	TssF_Colon
6	4e-03	31 / 2798	TxEnhG1_Colon
7	7e-03	83 / 10290	TssWk_Colon
8	7e-03	79 / 9653	Enh_Colon
9	2e-02	46 / 5155	EnhWk1_Colon
10	3e-02	10 / 739	TxEnhG2_Colon
11	5e-02	3 / 117	Marisa_CRC-cluster-b
12	6e-02	34 / 3812	TssD1_Colon
13	8e-02	2 / 66	Pentrack_CRC_TCGA_corr_N_msi-h_DN
14	9e-02	1 / 14	Hewish_dMMR-secondary-mutations_DNA-repair
15	1e-01	1 / 15	Juehling_HNPCC-mutated-in-4
16	2e-01	23 / 2698	EnhA_Colon
17	2e-01	46 / 5880	TssD2_Colon
18	2e-01	10 / 1079	ZNF_Colon
19	2e-01	31 / 3897	Quies1_Colon
20	3e-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	0.01	2 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
2	0.08	2 / 70	Weller_LGG_1p19qDel-vs-intact_UP
3	0.09	1 / 13	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (I)
4	0.11	5 / 365	Down_b
5	0.12	1 / 18	Shinawi_with_increased_methylation_in_STS
6	0.12	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.13	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.29	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
9	0.36	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
10	0.36	1 / 65	Weller_LGG_1p19qDel-vs-intact_DOWN
11	0.38	1 / 68	GIEZELT_GBM_WT_down_VS_mut
12	0.38	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	0.41	1 / 75	Weller_LGG_A_vs_O_DOWN
14	0.50	1 / 100	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up_(MES&CL down)
15	0.51	1 / 103	GIEZELT_GBM_WT_up_VS_mut
16	0.67	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
17	0.67	2 / 332	Up
18	0.72	1 / 184	WILLSCHER_GBM_Verhaak-CL & MES_up
19	0.92	1 / 356	Down_a
20	1.00	0 / 15	VERHAAK_CL subtype

GSEA C2

Rank	p-value	#in/all	Geneset
1	0.001	6 / 176	TIEN_INTESTINE_PROBIOTICS_24HR_DN
2	0.002	3 / 35	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN
3	0.002	3 / 38	IRITANI_MAD1_TARGETS_DN
4	0.003	5 / 142	IWANAGA_CARCINOGENESIS_BY_KRAS_UP
5	0.005	2 / 16	MEISSNER_NPC_ICP_WITH_H3K4ME3
6	0.006	4 / 104	LAIHO_COLORECTAL_CANCER_SERRATED_UP
7	0.007	11 / 675	BENPORATH_SOX2_TARGETS
8	0.008	8 / 416	SHEN_SMARCA2_TARGETS_UP
9	0.009	2 / 21	BIOCARTA_MTOR_PATHWAY
10	0.009	2 / 21	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP
11	0.010	6 / 261	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
12	0.010	3 / 64	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES
13	0.010	13 / 911	BENPORATH_NANOG_TARGETS
14	0.013	12 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	0.014	3 / 73	TOOKER_GEMCITABINE_RESISTANCE_UP
16	0.015	3 / 74	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_DN
17	0.015	3 / 74	NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER
18	0.015	2 / 27	MEISSNER_ES_ICP_WITH_H3K4ME3
19	0.016	4 / 139	RUIZ_TNC_TARGETS_UP
20	0.016	2 / 28	MEISSNER_BRAIN_ICP_WITH_H3K4ME3

HM

Rank	p-value	#in/all	Geneset
1	0.08	3 / 146	HALLMARK_DNA_REPAIR
2	0.10	3 / 162	HALLMARK_COMPLEMENT
3	0.13	2 / 91	HALLMARK_BILE_ACID_METABOLISM
4	0.17	2 / 107	HALLMARK_COAGULATION
5	0.32	2 / 167	HALLMARK_APICAL_JUNCTION
6	0.33	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
7	0.33	1 / 57	HALLMARK_MYC_TARGETS_V2
8	0.34	2 / 174	HALLMARK_HEME_METABOLISM
9	0.39	2 / 195	HALLMARK_MITOTIC_SPINDLE
10	0.46	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
11	0.47	1 / 91	HALLMARK_PROTEIN_SECRETION
12	0.48	1 / 93	HALLMARK_PEROXISOME
13	0.49	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.59	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
15	0.63	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
16	0.69	1 / 165	HALLMARK_MYOGENESIS
17	0.69	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	0.70	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	0.71	1 / 176	HALLMARK_HYPOXIA
20	0.72	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	5e-07	73 / 6929	HOPP_Txn_elongation
2	2e-06	76 / 7592	HOPP_Active_promoter
3	2e-04	54 / 5184	HOPP_Txn_transition
4	4e-03	64 / 7209	HOPP_Weak_promoter
5	9e-03	58 / 6564	HOPP_Strong_enhancer
6	2e-02	7 / 410	SPANG_CD40 6hrs DN
7	2e-02	3 / 89	ROSOLOWSKI_blue total
8	3e-02	1 / 5	WRIGHT_custom ABC-DLBCL UP
9	1e-01	1 / 16	DAVE_BL_Inter
10	1e-01	44 / 5538	HOPP_Weak_txn
11	3e-01	43 / 5693	HOPP_Weak_enhancer
12	3e-01	3 / 268	SPANG_IL21 UP
13	3e-01	3 / 275	TARTE_Mature plasma cell signature
14	3e-01	3 / 294	TARTE_Plasmablast signature
15	3e-01	1 / 61	SPANG_LPS 6hrs DN
16	4e-01	1 / 80	Aukema_BCL2 DN_BCL6 UP
17	5e-01	16 / 2211	HOPP_Repetitive
18	5e-01	2 / 247	ZHANG_DLBCL mutated
19	5e-01	2 / 256	SPANG_IL21 DN
20	7e-01	7 / 1128	SPANG_BCR DN

MF

Rank	p-value	#in/all	Geneset
1	0.003	2 / 12	protein methyltransferase activity
2	0.008	2 / 20	NAD+ ADP-ribosyltransferase activity
3	0.010	2 / 22	3',5'-cyclic-nucleotide phosphodiesterase activity
4	0.014	2 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductic
5	0.024	2 / 35	clathrin binding
6	0.028	3 / 94	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
7	0.033	2 / 41	phosphatase binding
8	0.049	2 / 51	translation initiation factor activity
9	0.052	9 / 695	transmembrane transporter activity
10	0.058	4 / 210	transferase activity, transferring glycosyl groups
11	0.067	1 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
12	0.067	1 / 10	transaminase activity
13	0.074	1 / 11	antiporter activity
14	0.074	1 / 11	glutathione peroxidase activity
15	0.074	1 / 11	protein deacetylase activity
16	0.074	1 / 11	protein kinase B binding
17	0.080	1 / 12	endodeoxyribonuclease activity
18	0.080	1 / 12	MAP kinase activity
19	0.083	2 / 69	microtubule motor activity
20	0.085	2 / 70	phospholipid binding

miRNA target

Rank	p-value	#in/all	Geneset
1	0.002	3 / 37	hsa-miR-760
2	0.005	3 / 51	hsa-miR-508-5p
3	0.013	2 / 25	hsa-miR-941
4	0.019	2 / 31	hsa-miR-296-5p
5	0.028	2 / 38	hsa-miR-1277
6	0.055	3 / 124	hsa-miR-646
7	0.058	2 / 56	hsa-miR-665
8	0.067	1 / 10	hsa-miR-1249
9	0.083	6 / 437	hsa-miR-19b
10	0.088	6 / 443	hsa-miR-19a
11	0.092	3 / 154	hsa-miR-139-5p
12	0.096	2 / 75	hsa-miR-877
13	0.124	1 / 19	hsa-miR-542-5p
14	0.125	2 / 88	hsa-miR-10a
15	0.127	2 / 89	hsa-miR-10b
16	0.133	4 / 282	hsa-miR-570
17	0.136	1 / 21	hsa-miR-554
18	0.136	1 / 21	hsa-miR-662
19	0.136	1 / 21	hsa-miR-1282
20	0.147	3 / 191	hsa-miR-330-3p

PathwAct

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	5e-04	28 / 2136	ICGC_GabpPcr2_targets
2	6e-03	45 / 4689	ICGC_Taf1_targets
3	7e-03	39 / 3924	ICGC_Zeb1_targets
4	8e-03	46 / 4879	ICGC_Pmlsc71910_targets
5	1e-02	42 / 4414	ICGC_Bclaf101388_targets
6	1e-02	20 / 1701	HEBENSTREIT_high expression TF
7	2e-02	44 / 4774	ICGC_Foxm1_targets
8	2e-02	41 / 4385	ICGC_Atf2_targets
9	2e-02	35 / 3700	ICGC_Nfatc1_targets
10	3e-02	44 / 4909	ICGC_Stat5_targets
11	3e-02	46 / 5200	ICGC_Mta3_targets
12	3e-02	16 / 1383	ICGC_Six5_targets
13	3e-02	48 / 5495	ICGC_Yy1_targets
14	3e-02	42 / 4682	ICGC_Pol24_targets
15	5e-02	46 / 5374	ICGC_Pax5_targets
16	5e-02	41 / 4706	ICGC_Sp1_targets
17	5e-02	46 / 5408	ICGC_Pou2_targets
18	7e-02	45 / 5355	ICGC_Pol2_targets
19	7e-02	41 / 4829	ICGC_Nficsc81335_targets
20	9e-02	48 / 5890	ICGC_Elf1_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	0.2	10 / 1115	LU_BPDE 1h DN
2	0.7	24 / 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	

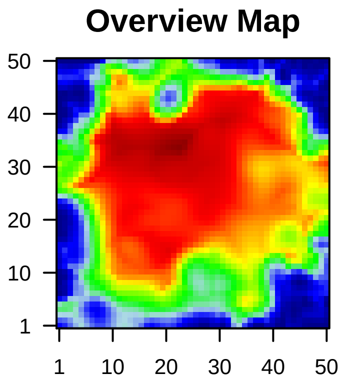
Underexpression Spots

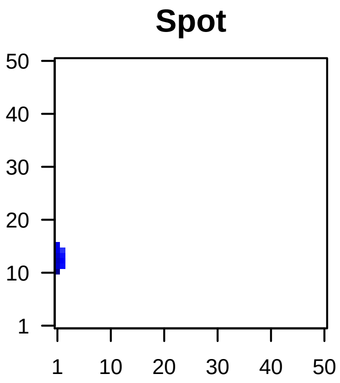
Spot Summary: u

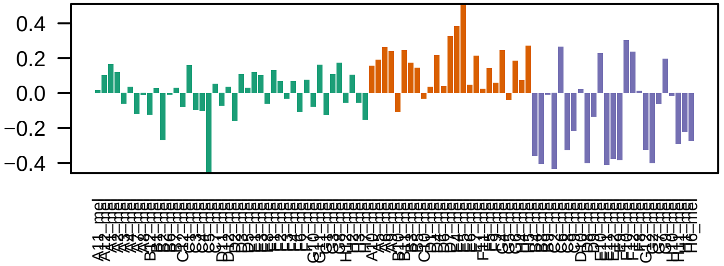
metagenes = 10
genes = 177

<r> metagenes = 0.92
<r> genes = 0.14
beta: r2= 2.14 / log p= −Inf

samples with spot = 15 (16.3 %)
MSC2 : 10 (40 %)
MSC3 : 5 (20 %)





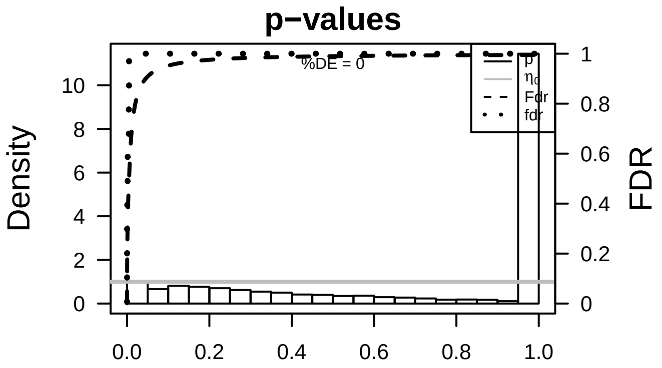


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	EGLN3	1.89	−0.41	0.36	EGLN3	egl−9 family hypoxia−inducible factor 3 [Source:HGNC Symbo
2	CFAP61	1.86	−0.52	0.45	CFAP61	cilia and flagella associated protein 61 [Source:HGNC Symbo
3	LYRM9	1.85	−0.31	0.28	LYRM9	LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
4	SLC26A4	1.8	−0.16	0.43	SLC26A4	solute carrier family 26 (anion exchanger), member 4 [Source
5	BBS5	1.74	−0.64	0.36	BBS5	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
6	STARD3	1.71	−0.69	0.23	STARD3	StAR−related lipid transfer (START) domain containing 3 [Sou
7	C1orf54	1.7	−0.3	0.41	C1orf54	chromosome 1 open reading frame 54 [Source:HGNC Symbo
8	SUOX	1.69	−0.67	0.27	SUOX	sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
9	VAV3	1.65	−0.26	0.39	VAV3	vav 3 guanine nucleotide exchange factor [Source:HGNC Syr
10	PRKCH	1.63	−0.39	0.32	PRKCH	protein kinase C, eta [Source:HGNC Symbol;Acc:HGNC:940
11	BID	1.61	−0.75	0.4	BID	BH3 interacting domain death agonist [Source:HGNC Symbo
12	TGDS	1.58	−0.72	0.45	TGDS	TDP−glucose 4,6−dehydratase [Source:HGNC Symbol;Acc:H
13	ANKRD44	1.57	−0.71	0.34	ANKRD44	ankyrin repeat domain 44 [Source:HGNC Symbol;Acc:HGNC
14	DGKI	1.57	−0.49	0.35	DGKI	diacylglycerol kinase, iota [Source:HGNC Symbol;Acc:HGNC
15	SCIN	1.52	−0.65	0.27	SCIN	scinderin [Source:HGNC Symbol;Acc:HGNC:21695]
16	GALNT3	1.52	−0.97	0.57	GALNT3	polypeptide N−acetylgalactosaminyltransferase 3 [Source:HG
17	ERCC8	1.5	−0.53	0.22	ERCC8	excision repair cross−complementation group 8 [Source:HGN
18	MYO1D	1.5	−0.5	0.31	MYO1D	myosin ID [Source:HGNC Symbol;Acc:HGNC:7598]
19	BCAT2	1.5	−0.51	0.38	BCAT2	branched chain amino−acid transaminase 2, mitochondrial [S
20	KIF3C	1.5	−0.28	0.27	KIF3C	kinesin family member 3C [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−08	139 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
2	1e−06	8 / 67	BP	pigmentation
3	2e−06	5 / 18	BP	melanocyte differentiation
4	3e−06	140 / 9528	Brain	Overlap_fetal_midbrain_Quies
5	6e−06	134 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
6	1e−05	4 / 13	BP	melanin biosynthetic process
7	2e−05	4 / 15	BP	developmental pigmentation
8	2e−05	4 / 15	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
9	3e−05	135 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
10	6e−05	17 / 482	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
11	9e−05	25 / 930	GSEA	NUYTTEN_EZH2_TARGETS_UP
12	1e−04	4 / 21	BP	melanosome transport
13	2e−04	68 / 3897	Colon	Quies1_Colon
14	2e−04	10 / 212	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
15	2e−04	101 / 6564	Lympl	HOPP_Strong_enhancer
16	3e−04	13 / 353	GSEA	ONDER_CDH1_TARGETS_2_DN
17	3e−04	6 / 79	GSEA	NELSON_RESPONSE_TO_ANDROGEN_UP
18	4e−04	13 / 364	GSEA	REACTOME_HEMOSTASIS
19	4e−04	3 / 13	GSEA	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
20	5e−04	121 / 8415	Colon	Quies3_Colon
21	5e−04	5 / 55	GSEA	BILBAN_B_CLL_LPL_UP
22	5e−04	6 / 84	miRN	hsa−miR−339−5p
23	5e−04	5 / 57	BP	response to hormone
24	7e−04	3 / 15	Colon	Budinska_B_Lower crypt−like_UP
25	7e−04	14 / 436	Colon	K9acLow_Colon
26	7e−04	13 / 388	BP	blood coagulation
27	8e−04	12 / 346	GSEA	RIGGI_EWING_SARCOMA_PROGENITOR_UP
28	9e−04	64 / 3812	Colon	TssD1_Colon
29	9e−04	10 / 256	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
30	9e−04	5 / 64	GSEA	CHANG_IMMORTALIZED_BY_HPV31_UP
31	1e−03	81 / 5155	Colon	EnhWk1_Colon
32	1e−03	58 / 3383	Colon	EnhWk2_Colon
33	1e−03	12 / 356	GSEA	DELYS_THYROID_CANCER_UP
34	1e−03	14 / 458	GSEA	ENK_UV_RESPONSE_EPIDERMIS_DN
35	1e−03	4 / 40	GSEA	ZHAN_MULTIPLE_MYELOMA_CD1_DN
36	1e−03	7 / 139	GSEA	PUIFFE_INVASION_INHIBITED_BY_ASCITES_DN
37	1e−03	9 / 223	GSEA	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
38	1e−03	2 / 5	GSEA	TSAI_DNAJB4_TARGETS_DN
39	1e−03	3 / 19	BP	positive regulation of erythrocyte differentiation
40	1e−03	11 / 317	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 100	HORVATH_aging_genes meth DOWN
2	0.7	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	1e−06	8 / 67	pigmentation
2	2e−06	5 / 18	melanocyte differentiation
3	1e−05	4 / 13	melanin biosynthetic process
4	2e−05	4 / 15	developmental pigmentation
5	1e−04	4 / 21	melanosome transport
6	5e−04	5 / 57	response to hormone
7	7e−04	13 / 388	blood coagulation
8	1e−03	3 / 19	positive regulation of erythrocyte differentiation
9	3e−03	3 / 25	amino acid transmembrane transport
10	3e−03	9 / 255	cellular amino acid metabolic process
11	4e−03	4 / 54	positive regulation of neuron differentiation
12	4e−03	3 / 27	metanephros development
13	4e−03	17 / 705	locomotion
14	4e−03	3 / 28	amino acid transport
15	4e−03	15 / 590	cell morphogenesis
16	6e−03	5 / 96	leukocyte migration
17	6e−03	2 / 10	negative regulation of smooth muscle cell migration
18	6e−03	2 / 10	response to vitamin E
19	7e−03	2 / 11	regulation of G1/S transition of mitotic cell cycle
20	7e−03	3 / 34	response to nutrient levels

Brain

Rank	p−value	#in/all	Geneset
1	9e−08	139 / 9020	Overlap_fetal_midbrain_ReprPCWk
2	3e−06	140 / 9528	Overlap_fetal_midbrain_Quies
3	6e−06	134 / 9013	Overlap_fetal_midbrain_K9K27me3
4	3e−05	135 / 9330	Overlap_fetal_midbrain_ReprPC
5	4e−03	22 / 1013	Fetal_TssP
6	6e−03	87 / 5940	Overlap_fetal_midbrain_HetRpts
7	3e−02	14 / 668	Mid_Frontal_Lobe_Enh
8	3e−02	35 / 2185	Fetal_TssA
9	4e−02	31 / 1907	Fetal_TxTrans
10	5e−02	19 / 1065	Overlap_fetal_midbrain_Enh
11	5e−02	3 / 69	Overlap_fetal_midbrain_Tx
12	6e−02	17 / 953	Fetal_Enh
13	6e−02	16 / 884	Overlap_fetal_midbrain_EnhG
14	7e−02	37 / 2462	Mid_Frontal_Lobe_HetRpts
15	1e−01	19 / 1207	Overlap_fetal_midbrain_TssF
16	1e−01	13 / 786	Fetal_EnhG
17	2e−01	28 / 1949	Fetal_TssF
18	2e−01	12 / 769	Overlap_fetal_midbrain_ZNF
19	2e−01	41 / 3081	Mid_Frontal_Lobe_ZNF
20	2e−01	9 / 574	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	6 / 180	SPANG_LPS−index2
2	0.02	10 / 401	Lembcke_Colonic Inflammation
3	0.02	1 / 2	GENTLES_modul8
4	0.04	0 / 14	LIU_PROSTATE_CANCER_DN
5	0.06	7 / 298	SPANG_BCL6−index2
6	0.07	0 / 12	LIU_PROSTATE_CANCER_UP
7	0.09	2 / 44	PanCan_TGF−B_geneset_nanostring
8	0.11	1 / 10	GENTLES_modul13
9	0.16	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	0.16	1 / 15	GENTLES_modul4
11	0.17	1 / 16	WOLFER_overlap genes
12	0.25	2 / 82	PanCan_TXmisReg_geneset_nanostring
13	0.29	1 / 29	KUIPER_MM good survival
14	0.36	7 / 489	Lembcke_Normal vs Adenoma
15	0.38	2 / 111	PanCan_RAS_geneset_nanostring
16	0.38	1 / 40	ZHANG_MM up
17	0.38	1 / 40	PanCan_HK_geneset_nanostring
18	0.39	2 / 113	PanCan_Driver_Gene_geneset_nanostring
19	0.41	2 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.43	1 / 48	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	0.005	5 / 94	melanosome
2	0.005	51 / 3088	plasma membrane
3	0.007	4 / 64	Golgi cisterna membrane
4	0.009	43 / 2576	membrane
5	0.010	2 / 13	axolemma
6	0.018	6 / 175	early endosome
7	0.018	47 / 2984	integral component of membrane
8	0.023	4 / 91	nuclear matrix
9	0.023	3 / 52	secretory granule
10	0.025	2 / 21	immunological synapse
11	0.027	2 / 22	smooth endoplasmic reticulum
12	0.039	4 / 108	late endosome
13	0.044	10 / 456	vacuole
14	0.046	2 / 29	cell−cell adherens junction
15	0.049	6 / 223	lysosomal membrane
16	0.049	108 / 8205	cytoplasm
17	0.055	9 / 412	lysosome
18	0.057	38 / 2507	cytosol
19	0.060	5 / 178	apical plasma membrane
20	0.061	12 / 616	endosome

Chr

Rank	p−value	#in/all	Geneset
1	0.003	15 / 576	Chr 9
2	0.022	11 / 465	Chr 15
3	0.023	11 / 469	Chr 8
4	0.036	7 / 262	Chr 13
5	0.047	10 / 462	Chr 14
6	0.204	12 / 775	Chr 12
7	0.264	4 / 221	Chr 18
8	0.282	14 / 993	Chr 2
9	0.488	7 / 558	Chr 4
10	0.534	2 / 151	Chr 21
11	0.637	6 / 552	Chr 10
12	0.661	9 / 838	Chr 3
13	0.694	4 / 398	Chr 20
14	0.706	7 / 687	Chr 6
15	0.719	7 / 696	Chr 5
16	0.782	6 / 649	Chr 16
17	0.786	15 / 1500	Chr 1
18	0.828	6 / 689	Chr 7
19	0.872	7 / 840	Chr 17
20	0.894	4 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	68 / 3897	Quies1_Colon
2	5e−04	121 / 8415	Quies3_Colon
3	7e−04	3 / 15	Budinska_B_Lower crypt−like_UP
4	7e−04	14 / 436	K9acLow_Colon
5	9e−04	64 / 3812	TssD1_Colon
6	1e−03	81 / 5155	EnhWk1_Colon
7	1e−03	58 / 3383	EnhWk2_Colon
8	3e−03	138 / 10290	TssWk_Colon
9	5e−03	2 / 9	KIM_MSI−in−EC
10	5e−03	12 / 427	Quies2_Colon
11	1e−02	128 / 9653	Enh_Colon
12	2e−02	125 / 9482	TssA_Colon
13	3e−02	35 / 2159	TssP_Colon
14	3e−02	4 / 102	Marisa_CRC−cluster−d
15	4e−02	118 / 9027	Tx_Colon
16	4e−02	9 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
17	6e−02	1 / 5	Budinska_C_CIMP−H−like_UP
18	6e−02	33 / 2142	ReprPC_Colon
19	6e−02	18 / 1038	HetRpts_Colon
20	7e−02	4 / 131	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.1	6 / 294	GUDJ_psoriasis down
2	0.3	7 / 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	2 / 29	shaw_responders_down_in_oligo_glioma
2	0.05	3 / 68	GIEZELT_GBM_WT_down_VS_mut
3	0.06	3 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
4	0.06	1 / 5	oligodendrocytes_glio
5	0.07	2 / 38	OL vs. OPC
6	0.10	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
7	0.11	2 / 47	mature astrocytes
8	0.11	2 / 49	OL vs. MOG−_OL
9	0.12	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	0.17	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	0.19	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	0.19	1 / 18	Barbus_GBM_STS_vs._LTS
13	0.21	2 / 72	laffaire_hypermeth_LGG_vs_control
14	0.22	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
15	0.26	6 / 365	Down_b
16	0.29	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
17	0.31	5 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
18	0.32	2 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
19	0.33	2 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
20	0.34	2 / 103	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 15	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
2	6e−05	17 / 482	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
3	9e−05	25 / 930	NUYTTEN_EZH2_TARGETS_UP
4	2e−04	10 / 212	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
5	3e−04	13 / 353	ONDER_CDH1_TARGETS_2_DN
6	3e−04	6 / 79	NELSON_RESPONSE_TO_ANDROGEN_UP
7	4e−04	13 / 364	REACTOME_HEMOSTASIS
8	4e−04	3 / 13	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
9	5e−04	5 / 55	BILBAN_B_CLL_LPL_UP
10	8e−04	12 / 346	RIGGI_EWING_SARCOMA_PROGENITOR_UP
11	9e−04	10 / 256	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
12	9e−04	5 / 64	CHANG_IMMORTALIZED_BY_HPV31_UP
13	1e−03	12 / 356	DELYS_THYROID_CANCER_UP
14	1e−03	14 / 458	ENK_UV_RESPONSE_EPIDERMIS_DN
15	1e−03	4 / 40	ZHAN_MULTIPLE_MYELOMA_CD1_DN
16	1e−03	7 / 139	PUIFFE_INVASION_INHIBITED_BY_ASCITES_DN
17	1e−03	9 / 223	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
18	1e−03	2 / 5	TSAI_DNAJB4_TARGETS_DN
19	1e−03	11 / 317	PHONG_TNF_RESPONSE_NOT_VIA_P38
20	1e−03	4 / 42	PID_RHOA_REG_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.004	7 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.005	5 / 94	HALLMARK_ANDROGEN_RESPONSE
3	0.017	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	0.029	6 / 196	HALLMARK_MTORC1_SIGNALING
5	0.046	5 / 165	HALLMARK_MYOGENESIS
6	0.055	5 / 174	HALLMARK_HEME_METABOLISM
7	0.057	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	0.098	4 / 148	HALLMARK_KRAS_SIGNALING_UP
9	0.135	4 / 167	HALLMARK_APICAL_JUNCTION
10	0.137	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
11	0.138	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	0.145	2 / 57	HALLMARK_MYC_TARGETS_V2
13	0.157	4 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	0.199	4 / 195	HALLMARK_MITOTIC_SPINDLE
15	0.219	3 / 137	HALLMARK_UV_RESPONSE_DN
16	0.229	3 / 140	HALLMARK_APOPTOSIS
17	0.232	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
18	0.248	3 / 146	HALLMARK_UV_RESPONSE_UP
19	0.291	1 / 29	HALLMARK_NOTCH_SIGNALING
20	0.313	2 / 96	HALLMARK_PI3K_AKT_MTOR_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	2e−04	101 / 6564	HOPP_Strong_enhancer
2	6e−03	39 / 2211	HOPP_Repetitive
3	1e−02	105 / 7592	HOPP_Active_promoter
4	1e−02	2 / 15	DAVE_Immune response 2
5	1e−02	4 / 80	Aukema_BCL2 DN_BCL6 UP
6	2e−02	2 / 17	DAVE_NFkB BL DN
7	2e−02	36 / 2188	HOPP_Poised_promoter
8	2e−02	10 / 410	SPANG_CD40 6hrs DN
9	2e−02	21 / 1128	SPANG_BCR DN
10	3e−02	80 / 5693	HOPP_Weak_enhancer
11	5e−02	2 / 30	Subero_INT_hypo_meth
12	5e−02	93 / 6929	HOPP_Txn_elongation
13	5e−02	72 / 5184	HOPP_Txn_transition
14	6e−02	1 / 5	WRIGHT_custom ABC−DLBCL UP
15	7e−02	49 / 3396	HOPP_Repressed
16	7e−02	95 / 7209	HOPP_Weak_promoter
17	9e−02	1 / 8	Subero_MM_hypo_meth
18	1e−01	74 / 5538	HOPP_Weak_txn
19	1e−01	1 / 10	DAVE_BL DN
20	1e−01	1 / 13	BENTINK_mBL UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 22	amino acid transmembrane transporter activity
2	0.003	3 / 26	protein kinase inhibitor activity
3	0.004	3 / 28	cholesterol binding
4	0.006	2 / 10	neutral amino acid transmembrane transporter activity
5	0.006	2 / 10	Rac guanyl−nucleotide exchange factor activity
6	0.006	2 / 10	semaphorin receptor binding
7	0.011	2 / 14	polypeptide N−acetylgalactosaminyltransferase activity
8	0.013	11 / 430	lipid binding
9	0.013	2 / 15	microfilament motor activity
10	0.017	2 / 17	Ras GTPase binding
11	0.021	2 / 19	1−phosphatidylinositol binding
12	0.021	3 / 50	motor activity
13	0.023	2 / 20	peptide hormone binding
14	0.035	2 / 25	phosphatidylinositol−3−phosphate binding
15	0.035	2 / 25	protein serine/threonine/tyrosine kinase activity
16	0.037	2 / 26	peptide antigen binding
17	0.043	3 / 66	Rho guanyl−nucleotide exchange factor activity
18	0.057	12 / 609	cytoskeletal protein binding
19	0.069	6 / 244	ubiquitin−protein transferase activity
20	0.077	3 / 84	guanyl−nucleotide exchange factor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−04	6 / 84	hsa−miR−339−5p
2	2e−03	8 / 196	hsa−miR−9
3	3e−03	4 / 50	hsa−miR−518f
4	4e−03	5 / 87	hsa−miR−134
5	4e−03	7 / 170	hsa−miR−183
6	5e−03	9 / 274	hsa−miR−1244
7	6e−03	4 / 61	hsa−miR−612
8	8e−03	9 / 294	hsa−miR−561
9	9e−03	5 / 108	hsa−miR−449b
10	9e−03	3 / 37	hsa−miR−501−3p
11	1e−02	3 / 38	hsa−miR−1224−5p
12	1e−02	5 / 112	hsa−miR−297
13	1e−02	9 / 312	hsa−miR−30e
14	1e−02	3 / 42	hsa−miR−129−3p
15	1e−02	9 / 318	hsa−miR−340
16	1e−02	4 / 78	hsa−miR−1321
17	1e−02	5 / 120	hsa−miR−105
18	1e−02	8 / 269	hsa−miR−30d
19	1e−02	8 / 269	hsa−miR−449a
20	1e−02	11 / 437	hsa−miR−19b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	BENTINK_ras.4
2	0.1	1 / 12	BENTINK_ras.1
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 / 13	BENTINK_myc.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	45 / 2714	ICGC_Irf4_targets
2	0.011	62 / 4054	ICGC_Egr1_targets
3	0.014	66 / 4414	ICGC_Bclaf101388_targets
4	0.018	34 / 2013	ICGC_Bcl11_targets
5	0.032	31 / 1878	ICGC_Cebpbsc150_targets
6	0.039	62 / 4314	ICGC_Ebfsc137065_targets
7	0.043	43 / 2836	ICGC_BatfPcr1_targets
8	0.047	66 / 4682	ICGC_Pol24_targets
9	0.049	30 / 1872	ICGC_Mef2_targets
10	0.063	11 / 553	ICGC_RxraPcr1_targets
11	0.064	75 / 5495	ICGC_Yy1_targets
12	0.067	65 / 4689	ICGC_Taf1_targets
13	0.079	55 / 3924	ICGC_Zeb1_targets
14	0.083	67 / 4909	ICGC_Stat5_targets
15	0.093	42 / 2927	ICGC_Rad21_targets
16	0.093	55 / 3966	ICGC_Pu1_targets
17	0.096	70 / 5200	ICGC_Mta3_targets
18	0.098	60 / 4385	ICGC_Atf2_targets
19	0.099	66 / 4879	ICGC_Pmlsc71910_targets
20	0.099	72 / 5374	ICGC_Pax5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 27	VAQUERIZAS_Lymph node
2	0.08	2 / 40	VAQUERIZAS_Thyroid
3	0.18	1 / 17	VAQUERIZAS_Pituitary
4	0.20	1 / 19	VAQUERIZAS_Tonsil
5	0.24	1 / 23	VAQUERIZAS_Spinal cord
6	0.29	1 / 29	VAQUERIZAS_Smooth muscle
7	0.29	1 / 29	VAQUERIZAS_Fetal lung
8	0.32	1 / 33	VAQUERIZAS_Prostate
9	0.36	1 / 38	VAQUERIZAS_Whole brain
10	0.39	1 / 41	VAQUERIZAS_Placenta
11	0.41	1 / 45	VAQUERIZAS_Uterus
12	0.50	1 / 58	VAQUERIZAS_Lung
13	0.50	2 / 143	VAQUERIZAS_General
14	1.00	0 / 36	VAQUERIZAS_Fetal brain
15	1.00	0 / 26	VAQUERIZAS_Liver
16	1.00	0 / 9	VAQUERIZAS_Kidney
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	0.1	7 / 350	WIRTH_Immune system
2	0.1	1 / 12	WIRTH_Thymus
3	0.1	1 / 13	WIRTH_Thyroid gland
4	0.3	4 / 225	PALMER_Granulocytes signature up
5	0.3	2 / 95	WIRTH_Muscle
6	0.6	1 / 74	WIRTH_Mucosa
7	0.6	4 / 350	WIRTH_Nervous System
8	0.7	1 / 107	WIRTH_Testis
9	0.7	1 / 114	PALMER_T−Cell signature up
10	0.9	1 / 194	PALMER_B−Cell signature up
11	1.0	0 / 32	WIRTH_Pancreas
12	1.0	0 / 11	WIRTH_Sec. lymphoid organs
13	1.0	0 / 11	WIRTH_Prim. lymphoid organs
14	1.0	0 / 13	WIRTH_B−cells
15	1.0	0 / 8	WIRTH_Tonsil
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	0.2	48 / 3682	LU_BPDE 0.005 DN
2	0.7	12 / 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	

Underexpression Spots

Spot Summary: v

metagenes = 30
genes = 257

<r> metagenes = 0.9
<r> genes = 0.12
beta: r2= 3.37 / log p= −Inf

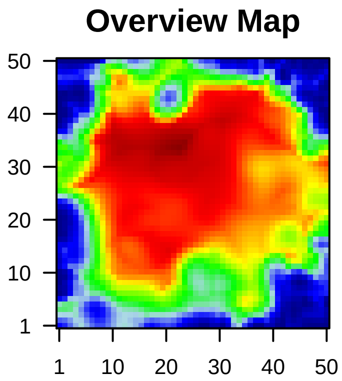
samples with spot = 13 (14.1 %)
MSC1 : 13 (31 %)

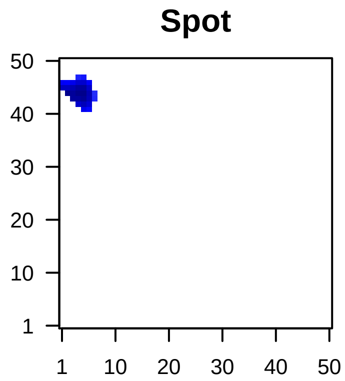
Spot Genelist

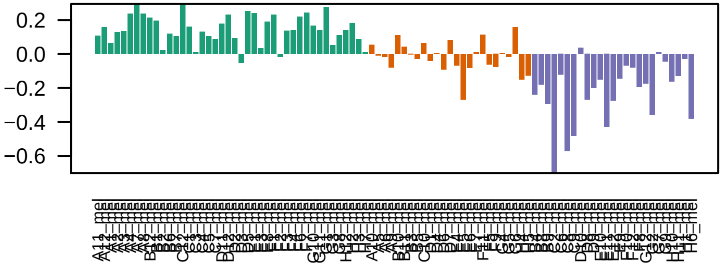
Rank	ID	max e	min e	r	Symbol	Description
1	C4orf33	1.97	−0.26	0.29	C4orf33	chromosome 4 open reading frame 33 [Source:HGNC Symb
2	GINS4	1.81	−0.28	0.4	GINS4	GINS complex subunit 4 (Sld5 homolog) [Source:HGNC Sym
3	MARCH3	1.72	−0.43	0.33	MARCH3	membrane−associated ring finger (C3HC4) 3, E3 ubiquitin pr
4	THUMPD2	1.71	−1.04	0.28	THUMPD2	THUMP domain containing 2 [Source:HGNC Symbol;Acc:HG
5	ERI1	1.67	−0.32	0.35	ERI1	exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:23994]
6	MTBP	1.64	−0.38	0.33	MTBP	MDM2 binding protein [Source:HGNC Symbol;Acc:HGNC:74
7	MCCC1	1.64	−0.58	0.24	MCCC1	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
8	FAM81A	1.62	−0.21	0.22	FAM81A	family with sequence similarity 81, member A [Source:HGNC
9	MED24	1.62	−0.74	0.24	MED24	mediator complex subunit 24 [Source:HGNC Symbol;Acc:HG
10	NT5DC2	1.62	−0.98	0.28	NT5DC2	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
11	MUC7	1.61	−0.26	0.44	MUC7	mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]
12	HMGN4	1.6	−1.21	0.25	HMGN4	high mobility group nucleosomal binding domain 4 [Source:H
13	FANCG	1.6	−0.28	0.37	FANCG	Fanconi anemia, complementation group G [Source:HGNC S
14	SCAPER	1.59	−0.91	0.31	SCAPER	S−phase cyclin A−associated protein in the ER [Source:HGN
15	RBM10	1.58	−0.51	0.3	RBM10	RNA binding motif protein 10 [Source:HGNC Symbol;Acc:HG
16	C1orf21	1.56	−0.91	0.34	C1orf21	chromosome 1 open reading frame 21 [Source:HGNC Symb
17	MIPEP	1.55	−0.46	0.29	MIPEP	mitochondrial intermediate peptidase [Source:HGNC Symbol
18	CAD	1.54	−0.51	0.28	CAD	carbamoyl−phosphate synthetase 2, aspartate transcarbamyl
19	TMEM243	1.54	−0.76	0.45	TMEM243	transmembrane protein 243, mitochondrial [Source:HGNC Sy
20	REPS1	1.53	−0.63	0.24	REPS1	RALBP1 associated Eps domain containing 1 [Source:HGNC

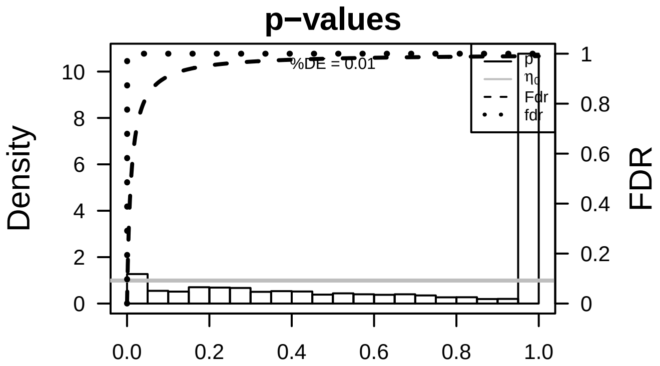
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−16	193 / 7592	Lymp	HOPP_Active_promoter
2	2e−15	69 / 1460	GSE	PUJANA_BRCA1_PCC_NETWORK
3	1e−12	46 / 834	GSE	LEE_BMP2_TARGETS_DN
4	2e−12	211 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	2e−12	174 / 6929	Lymp	HOPP_Txn_elongation
6	6e−12	59 / 1326	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	7e−12	212 / 9482	Colon	TssA_Colon
8	9e−12	55 / 1192	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	1e−11	42 / 756	GSE	WEI_MYCN_TARGETS_WITH_E_BOX
10	8e−11	24 / 278	GSE	MANALO_HYPOXIA_DN
11	2e−10	216 / 9988	CC	organelle
12	5e−10	51 / 1171	TF	KIM_MYC targets
13	9e−10	200 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
14	1e−09	19 / 197	HM	HALLMARK_E2F_TARGETS
15	1e−09	171 / 7209	Lymp	HOPP_Weak_promoter
16	2e−09	67 / 1858	GSE	PILON_KLF1_TARGETS_DN
17	2e−09	37 / 724	GSE	PUJANA_CHEK2_PCC_NETWORK
18	7e−09	21 / 268	GSE	FOURNIER_ACINAR_DEVELOPMENT_LATE_2
19	8e−09	26 / 405	GSE	MOOTHA_HUMAN_MITODB_6_2002
20	1e−08	31 / 562	GSE	CAIRO_HEPATOBLASTOMA_CLASSES_UP
21	3e−08	219 / 10605	CC	intracellular
22	1e−07	25 / 436	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
23	3e−07	52 / 1468	CC	mitochondrion
24	5e−07	21 / 341	GSE	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
25	7e−07	9 / 59	TF	MYC_Targets UP
26	7e−07	136 / 5696	CC	nucleus
27	7e−07	21 / 351	GSE	BENPORATH_ES_1
28	7e−07	16 / 211	GSE	BIDUS_METASTASIS_UP
29	9e−07	7 / 32	GSE	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PRO
30	1e−06	25 / 485	GSE	CHICAS_RB1_TARGETS_SENESCENT
31	1e−06	126 / 5184	Lymp	HOPP_Txn_transition
32	1e−06	31 / 700	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
33	1e−06	39 / 1008	GSE	BRUINS_UVC_RESPONSE_LATE
34	1e−06	45 / 1251	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
35	2e−06	20 / 338	GSE	DAIRKEE_TERT_TARGETS_UP
36	2e−06	35 / 862	GSE	JOHNSTONE_PARVB_TARGETS_3_DN
37	2e−06	26 / 536	GSE	TIEN_INTESTINE_PROBIOTICS_24HR_UP
38	2e−06	19 / 312	GSE	WONG_EMBRYONIC_STEM_CELL_CORE
39	2e−06	37 / 944	GSE	NUYTTEN_EZH2_TARGETS_DN
40	2e−06	15 / 202	GSE	CHANG_CORE_SERUM_RESPONSE_UP









Aging

Rank	p−value	#in/all	Geneset
1	0.8	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−06	100 / 3980	cellular nitrogen compound metabolic process
2	4e−05	17 / 322	mitochondrion organization
3	8e−05	6 / 42	mitotic nuclear envelope disassembly
4	1e−04	5 / 29	regulation of glucose transport
5	1e−04	5 / 29	viral transcription
6	1e−04	28 / 768	DNA metabolic process
7	2e−04	5 / 33	hexose transport
8	3e−04	7 / 75	water−soluble vitamin metabolic process
9	3e−04	4 / 20	DNA−dependent DNA replication
10	5e−04	7 / 81	vitamin metabolic process
11	5e−04	48 / 1730	small molecule metabolic process
12	6e−04	13 / 259	protein targeting
13	6e−04	86 / 3644	biosynthetic process
14	8e−04	24 / 687	gene expression
15	8e−04	17 / 412	mitotic cell cycle
16	1e−03	33 / 1110	cell cycle
17	2e−03	5 / 52	glucose transport
18	3e−03	8 / 139	DNA replication
19	4e−03	4 / 37	transcription from RNA polymerase III promoter
20	4e−03	5 / 62	viral life cycle

Brain

Rank	p−value	#in/all	Geneset
1	2e−12	211 / 9330	Overlap_fetal_midbrain_ReprPC
2	9e−10	200 / 9013	Overlap_fetal_midbrain_K9K27me3
3	5e−05	193 / 9528	Overlap_fetal_midbrain_Quies
4	2e−04	130 / 5940	Overlap_fetal_midbrain_HetRpts
5	2e−02	33 / 1333	Fetal_ReprPCWk
6	7e−02	19 / 765	Mid_Frontal_Lobe_Het
7	9e−02	166 / 9020	Overlap_fetal_midbrain_ReprPCWk
8	1e−01	23 / 1050	Fetal_EnhP
9	2e−01	12 / 534	Mid_Frontal_Lobe_EnhG
10	3e−01	8 / 349	Fetal_ZNF
11	4e−01	16 / 831	Fetal_HetRpts
12	4e−01	15 / 786	Fetal_EnhG
13	4e−01	6 / 304	Fetal_Het
14	5e−01	43 / 2462	Mid_Frontal_Lobe_HetRpts
15	6e−01	21 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	6e−01	17 / 1013	Fetal_TssP
17	6e−01	31 / 1845	Fetal_Quies
18	6e−01	67 / 383	Fetal_Tx
19	7e−01	15 / 953	Fetal_Enh
20	7e−01	10 / 668	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	5 / 47	PanCan_DNARepair_geneset_nanostring
2	0.002	3 / 16	GENTLES_modul2
3	0.022	0 / 15	RHODES_CANCER_META_SIGNATURE
4	0.030	2 / 16	GENTLES_modul7
5	0.056	5 / 120	PanCan_CC+Apop_geneset_nanostring
6	0.090	6 / 180	SPANG_LPS−index2
7	0.117	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.150	2 / 40	ZHANG_MM up
9	0.159	1 / 10	GENTLES_modul5
10	0.202	1 / 13	BEN−PORATH_UP
11	0.215	1 / 14	LIU_PROSTATE_CANCER_DN
12	0.229	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	0.229	1 / 15	GENTLES_modul4
14	0.242	1 / 16	WOLFER_overlap genes
15	0.242	1 / 16	GENTLES_modul6
16	0.268	1 / 18	PanCan_Notch_geneset_nanostring
17	0.280	4 / 156	PanCan_PI3K_geneset_nanostring
18	0.293	1 / 20	PanCan_ChromMod_geneset_nanostring
19	0.406	0 / 14	LIU_LIVER_CANCER
20	0.407	0 / 12	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−10	216 / 9988	organelle
2	3e−08	219 / 10605	intracellular
3	3e−07	52 / 1468	mitochondrion
4	7e−07	136 / 5696	nucleus
5	2e−06	177 / 8205	cytoplasm
6	6e−05	226 / 11774	cell
7	9e−05	14 / 246	mitochondrial matrix
8	1e−04	81 / 3214	protein complex
9	2e−04	67 / 2577	nucleoplasm
10	5e−04	64 / 2507	cytosol
11	6e−04	6 / 60	nuclear pore
12	6e−04	17 / 401	mitochondrial inner membrane
13	1e−03	25 / 747	nucleolus
14	1e−03	7 / 97	chromatin
15	4e−03	3 / 19	site of double−strand break
16	1e−02	20 / 663	chromosome
17	1e−02	5 / 80	mitochondrial membrane
18	1e−02	51 / 2193	extracellular exosome
19	1e−02	3 / 30	COP9 signalosome
20	1e−02	2 / 11	Arp2/3 protein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.03	14 / 469	Chr 8
2	0.06	24 / 993	Chr 2
3	0.07	15 / 576	Chr 9
4	0.09	14 / 551	Chr X
5	0.13	16 / 687	Chr 6
6	0.18	6 / 221	Chr 18
7	0.26	16 / 775	Chr 12
8	0.32	13 / 649	Chr 16
9	0.54	8 / 462	Chr 14
10	0.58	14 / 838	Chr 3
11	0.59	14 / 840	Chr 17
12	0.61	9 / 552	Chr 10
13	0.62	13 / 801	Chr 11
14	0.74	2 / 151	Chr 21
15	0.75	8 / 558	Chr 4
16	0.75	23 / 1500	Chr 1
17	0.83	4 / 335	Chr 22
18	0.83	3 / 262	Chr 13
19	0.84	9 / 689	Chr 7
20	0.91	5 / 465	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−12	212 / 9482	TssA_Colon
2	5e−06	179 / 8415	Quies3_Colon
3	8e−06	181 / 8580	TxWk_Colon
4	3e−05	186 / 9027	Tx_Colon
5	2e−04	202 / 10290	TssWk_Colon
6	1e−03	25 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
7	9e−03	143 / 7203	TssF_Colon
8	2e−02	19 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	3e−02	4 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
10	3e−02	2 / 16	Juehling−MSI−enriched−in−6
11	5e−02	16 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
12	8e−02	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
13	1e−01	175 / 9653	Enh_Colon
14	1e−01	1 / 9	KIM_MSI−in−EC
15	2e−01	1 / 15	Juehling_HNPCC−mutated−in−4
16	2e−01	1 / 15	Budinska_B_Lower crypt−like_UP
17	3e−01	106 / 5880	TssD2_Colon
18	5e−01	1 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
19	5e−01	16 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	6e−01	65 / 3812	TssD1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.07	12 / 435	GUDJ_psoriasis up
2	0.88	3 / 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	2e−05	18 / 332	Up
2	2e−02	4 / 63	Stuehler_Proteins_up_in_STS
3	3e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
4	4e−02	2 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
5	5e−02	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	6e−02	6 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	7e−02	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
8	9e−02	20 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
9	9e−02	9 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	1e−01	1 / 6	shaw_responders_up_in_oligo_glioma
11	1e−01	10 / 365	Down_b
12	1e−01	1 / 8	Colman_survival_robust
13	1e−01	1 / 9	Mukasa_UP_in_GBM
14	2e−01	1 / 11	Mukasa_UP_in_Astroglioma
15	3e−01	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
16	3e−01	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
17	3e−01	1 / 23	WIRTH_PN subtype
18	3e−01	2 / 71	Weller_LGG_A_vs_O_UP
19	4e−01	1 / 29	shaw_responders_down_in_oligo_glioma
20	4e−01	1 / 32	Donson−innate immunity−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−15	69 / 1460	PUJANA_BRCA1_PCC_NETWORK
2	1e−12	46 / 834	LEE_BMP2_TARGETS_DN
3	6e−12	59 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	9e−12	55 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	1e−11	42 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
6	8e−11	24 / 278	MANALO_HYPOXIA_DN
7	2e−09	67 / 1858	PILON_KLF1_TARGETS_DN
8	2e−09	37 / 724	PUJANA_CHEK2_PCC_NETWORK
9	7e−09	21 / 268	FOURNIER_ACINAR_DEVELOPMENT_LATE_2
10	8e−09	26 / 405	MOOTHA_HUMAN_MITODB_6_2002
11	1e−08	31 / 562	CAIRO_HEPATOBLASTOMA_CLASSES_UP
12	1e−07	25 / 436	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
13	5e−07	21 / 341	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
14	7e−07	21 / 351	BENPORATH_ES_1
15	7e−07	16 / 211	BIDUS_METASTASIS_UP
16	9e−07	7 / 32	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTE
17	1e−06	25 / 485	CHICAS_RB1_TARGETS_SENESCENT
18	1e−06	31 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
19	1e−06	39 / 1008	BRUINS_UVC_RESPONSE_LATE
20	1e−06	45 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−09	19 / 197	HALLMARK_E2F_TARGETS
2	2e−03	10 / 188	HALLMARK_MYC_TARGETS_V1
3	2e−03	10 / 196	HALLMARK_G2M_CHECKPOINT
4	2e−03	10 / 196	HALLMARK_MTORC1_SIGNALING
5	2e−03	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	1e−02	7 / 146	HALLMARK_UV_RESPONSE_UP
7	2e−02	8 / 188	HALLMARK_ADIPOGENESIS
8	3e−02	7 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
9	3e−02	6 / 141	HALLMARK_FATTY_ACID_METABOLISM
10	5e−02	7 / 195	HALLMARK_MITOTIC_SPINDLE
11	8e−02	4 / 94	HALLMARK_ANDROGEN_RESPONSE
12	1e−01	5 / 146	HALLMARK_DNA_REPAIR
13	2e−01	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	2e−01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	2e−01	4 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	2e−01	3 / 95	HALLMARK_SPERMATOGENESIS
17	2e−01	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	3e−01	4 / 162	HALLMARK_COMPLEMENT
19	3e−01	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	3e−01	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 10	DUMEAUX_Smoking literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
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	4e−16	193 / 7592	HOPP_Active_promoter
2	2e−12	174 / 6929	HOPP_Txn_elongation
3	1e−09	171 / 7209	HOPP_Weak_promoter
4	1e−06	126 / 5184	HOPP_Txn_transition
5	2e−04	15 / 294	TARTE_Plasmablast signature
6	4e−04	7 / 80	Aukema_BCL2 DN_BCL6 UP
7	6e−04	139 / 6564	HOPP_Strong_enhancer
8	4e−03	116 / 5538	HOPP_Weak_txn
9	6e−03	4 / 42	CARO_OxPhos_in_DLBCL_UP
10	8e−03	117 / 5693	HOPP_Weak_enhancer
11	3e−02	28 / 1128	SPANG_BCR DN
12	7e−02	5 / 129	DAVE_BL−vs−DLBCL
13	2e−01	1 / 10	Shaknovich_ABC_hypo_meth
14	2e−01	3 / 86	ROSOLOWSKI_red total
15	2e−01	1 / 12	BENTINK_mBL DOWN
16	2e−01	1 / 13	YAMANE_AICDA_targets_recruited
17	2e−01	2 / 50	SPANG_BAFF 9hrs DN
18	3e−01	1 / 17	DAVE_NFkB BL DN
19	3e−01	24 / 1218	SPANG_BCR UP
20	3e−01	1 / 19	DAVE_c−myc BL UP

MF

Rank	p−value	#in/all	Geneset
1	8e−04	9 / 142	isomerase activity
2	2e−03	16 / 405	ligase activity
3	2e−03	9 / 164	nuclease activity
4	3e−03	4 / 35	4 iron, 4 sulfur cluster binding
5	5e−03	4 / 40	heat shock protein binding
6	5e−03	7 / 123	nucleotidyltransferase activity
7	7e−03	3 / 23	protein disulfide oxidoreductase activity
8	7e−03	14 / 386	nucleotide binding
9	1e−02	3 / 29	ATP−dependent DNA helicase activity
10	1e−02	3 / 29	DNA−directed DNA polymerase activity
11	1e−02	27 / 1007	poly(A) RNA binding
12	1e−02	2 / 11	nucleosome binding
13	2e−02	2 / 13	nucleocytoplasmic transporter activity
14	2e−02	2 / 13	thioesterase binding
15	2e−02	5 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
16	2e−02	2 / 14	endoribonuclease activity
17	2e−02	3 / 36	enzyme activator activity
18	3e−02	3 / 37	DNA−directed RNA polymerase activity
19	3e−02	2 / 15	amino acid binding
20	3e−02	33 / 1365	RNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−06	8 / 60	hsa−miR−126*
2	4e−04	10 / 157	hsa−miR−548o
3	2e−03	7 / 102	hsa−miR−1301
4	4e−03	3 / 19	hsa−miR−645
5	4e−03	9 / 181	hsa−miR−548a−3p
6	5e−03	4 / 40	hsa−miR−647
7	6e−03	4 / 43	hsa−miR−661
8	7e−03	8 / 163	hsa−miR−495
9	9e−03	10 / 243	hsa−miR−122
10	1e−02	11 / 289	hsa−miR−186
11	1e−02	8 / 177	hsa−miR−548e
12	1e−02	7 / 149	hsa−miR−633
13	2e−02	4 / 56	hsa−miR−665
14	2e−02	6 / 118	hsa−miR−509−3p
15	2e−02	9 / 228	hsa−miR−124
16	2e−02	10 / 269	hsa−miR−449a
17	2e−02	11 / 321	hsa−miR−32
18	2e−02	6 / 130	hsa−miR−383
19	3e−02	11 / 328	hsa−miR−548a−5p
20	3e−02	8 / 208	hsa−miR−432

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 14	BENTINK_src.2
2	0.19	1 / 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	5e−10	51 / 1171	KIM_MYC targets
2	7e−07	9 / 59	MYC_Targets UP
3	3e−04	4 / 19	MYC_Metabolism UP
4	1e−02	2 / 9	MYC_RNA processing binding UP
5	1e−02	42 / 1701	HEBENSTREIT_high expression TF
6	1e−02	50 / 2137	ICGC_SrfV0416101_targets
7	6e−02	17 / 653	ICGC_SrfPcr2_targets
8	7e−02	29 / 1266	ICGC_NrsfPcr1_targets
9	9e−02	40 / 1878	ICGC_Cebpbsc150_targets
10	1e−01	30 / 1400	ICGC_Myc_targets
11	1e−01	1 / 8	MYC_Cell cycle UP
12	1e−01	1 / 9	MYC_DNA repair UP
13	2e−01	1 / 11	MYC_Protein synthesis degradation UP
14	2e−01	28 / 1383	ICGC_Six5_targets
15	2e−01	46 / 2391	ICGC_Pbx3_targets
16	2e−01	75 / 4032	ICGC_Creb1_targets
17	2e−01	12 / 553	ICGC_RxraPcr1_targets
18	2e−01	86 / 4689	ICGC_Taf1_targets
19	3e−01	85 / 4682	ICGC_Pol24_targets
20	3e−01	80 / 4414	ICGC_Bclaf101388_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	VAQUERIZAS_Fetal thyroid
2	0.3	1 / 23	VAQUERIZAS_Spinal cord
3	0.5	1 / 36	VAQUERIZAS_Fetal brain
4	0.5	1 / 38	VAQUERIZAS_Whole brain
5	0.5	1 / 38	VAQUERIZAS_Testis
6	0.5	1 / 40	VAQUERIZAS_Thyroid
7	0.5	1 / 45	VAQUERIZAS_Uterus
8	0.6	1 / 58	VAQUERIZAS_Lung
9	1.0	0 / 41	VAQUERIZAS_Placenta
10	1.0	0 / 26	VAQUERIZAS_Liver
11	1.0	0 / 33	VAQUERIZAS_Prostate
12	1.0	0 / 29	VAQUERIZAS_Smooth muscle
13	1.0	0 / 143	VAQUERIZAS_General
14	1.0	0 / 9	VAQUERIZAS_Kidney
15	1.0	0 / 37	VAQUERIZAS_Thymus
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 / 16	VAQUERIZAS_Pancreas
20	1.0	0 / 23	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	PALMER_CD8+ T−Cell signature up
2	0.2	1 / 13	WIRTH_B−cells
3	0.2	5 / 194	PALMER_B−Cell signature up
4	0.2	1 / 16	PALMER_Lymphocytes signature up
5	0.4	1 / 32	WIRTH_Pancreas
6	0.5	2 / 95	WIRTH_Muscle
7	0.6	2 / 107	WIRTH_Testis
8	0.7	5 / 350	WIRTH_Immune system
9	0.9	1 / 114	PALMER_T−Cell signature up
10	0.9	2 / 225	PALMER_Granulocytes signature up
11	1.0	2 / 350	WIRTH_Nervous System
12	1.0	0 / 11	WIRTH_Sec. lymphoid organs
13	1.0	0 / 11	WIRTH_Prim. lymphoid organs
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	0.04	27 / 1115	LU_BPDE 1n DN
2	0.80	58 / 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	

Underexpression Spots

Spot Summary: w

metagenes = 11
genes = 162

<r> metagenes = 0.91
<r> genes = 0.08
beta: r2= 1.33 / log p= −Inf

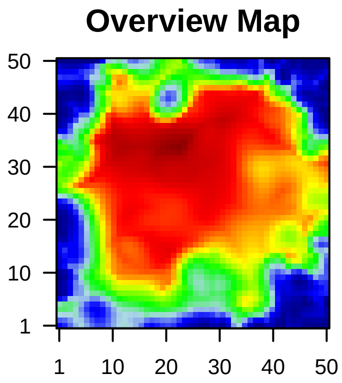
samples with spot = 9 (9.8 %)
MSC1 : 2 (4.8 %)
MSC2 : 3 (12 %)
MSC3 : 4 (16 %)

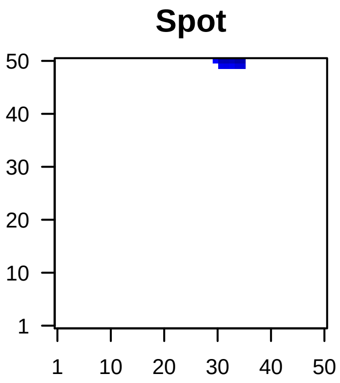
Spot Genelist

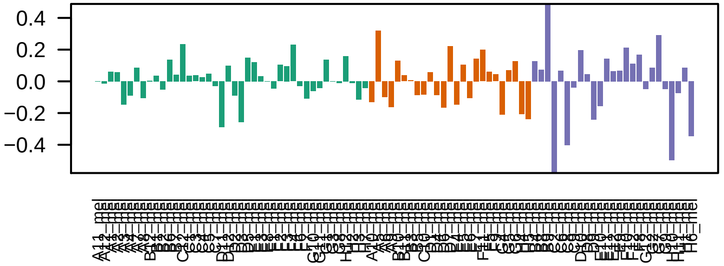
Rank	ID	max e	min e	r	Symbol	Description
1	TYK2	2.19	−0.38	0.23	TYK2	tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:12440]
2	BAAT	1.99	−0.45	0.28	BAAT	bile acid CoA:amino acid N−acyltransferase [Source:HGNC S
3	FAM179B	1.85	−0.27	0.24	FAM179B	family with sequence similarity 179, member B [Source:HGN
4	PLCG1	1.83	−0.72	0.36	PLCG1	phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
5	FBXW4	1.8	−0.4	0.22	FBXW4	F−box and WD repeat domain containing 4 [Source:HGNC Sy
6	RAD51B	1.8	−0.76	0.28	RAD51B	RAD51 paralog B [Source:HGNC Symbol;Acc:HGNC:9822]
7	PCK2	1.77	−0.36	0.39	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial) [Sourc
8	PLD6	1.73	−0.29	0.35	PLD6	phospholipase D family, member 6 [Source:HGNC Symbol;Ac
9	TRIM68	1.72	−0.24	0.3	TRIM68	tripartite motif containing 68 [Source:HGNC Symbol;Acc:HGN
10	DMWD	1.7	−0.24	0.22	DMWD	dystrophia myotonica, WD repeat containing [Source:HGNC S
11	DAK	1.69	−0.31	0.33	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae) [Source:H
12	POLR3F	1.67	−0.67	0.28	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa [S
13	POLI	1.67	−0.5	0.34	POLI	polymerase (DNA directed) iota [Source:HGNC Symbol;Acc:H
14	MTRF1	1.66	−0.48	0.25	MTRF1	mitochondrial translational release factor 1 [Source:HGNC Sy
15	COG3	1.64	−0.54	0.39	COG3	component of oligomeric golgi complex 3 [Source:HGNC Sym
16	DHRS12	1.62	−0.43	0.27	DHRS12	dehydrogenase/reductase (SDR family) member 12 [Source:H
17	APPL2	1.58	−0.55	0.35	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and
18	ZNF561	1.55	−0.49	0.27	ZNF561	zinc finger protein 561 [Source:HGNC Symbol;Acc:HGNC:28
19	BCHE	1.54	−0.55	0.27	BCHE	butyrylcholinesterase [Source:HGNC Symbol;Acc:HGNC:983
20	CPT1B	1.54	−0.41	0.35	CPT1B	carnitine palmitoyltransferase 1B (muscle) [Source:HGNC Sy

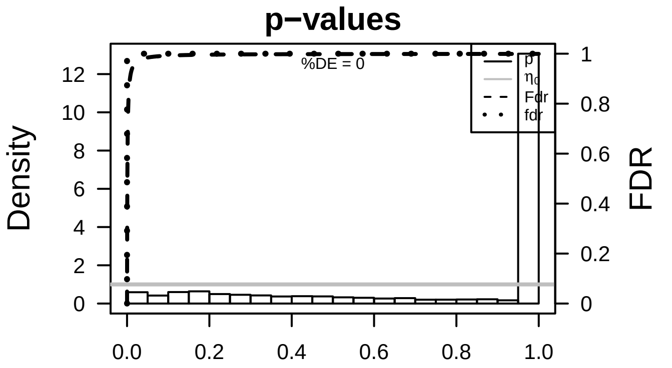
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−13	140 / 9027	Colon	Tx_Colon
2	7e−13	136 / 8580	Colon	TxWk_Colon
3	3e−10	115 / 6929	Lympl	HOPP_Txn_elongation
4	3e−10	139 / 9482	Colon	TssA_Colon
5	1e−09	103 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	3e−09	133 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
7	1e−08	118 / 7592	Lympl	HOPP_Active_promoter
8	2e−08	134 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
9	5e−08	90 / 5184	Lympl	HOPP_Txn_transition
10	1e−06	35 / 1365	MF	RNA binding
11	1e−05	139 / 10605	CC	intracellular
12	1e−05	27 / 1007	MF	poly(A) RNA binding
13	6e−05	127 / 9528	Brain	Overlap_fetal_midbrain_Quies
14	2e−04	47 / 2577	CC	nucleoplasm
15	2e−04	19 / 687	BP	gene expression
16	2e−04	29 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
17	3e−04	22 / 890	GSEA	ACEVEDO_LIVER_CANCER_UP
18	3e−04	20 / 775	Chr	Chr 12
19	3e−04	15 / 493	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
20	5e−04	8 / 167	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
21	7e−04	13 / 422	BP	viral process
22	8e−04	3 / 17	MF	RNA polymerase II core binding
23	9e−04	25 / 1171	TF	KIM_MYC targets
24	1e−03	10 / 278	GSEA	MANALO_HYPOXIA_DN
25	1e−03	109 / 8205	CC	cytoplasm
26	1e−03	19 / 800	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
27	1e−03	127 / 9988	CC	organelle
28	1e−03	36 / 1975	BP	cellular protein modification process
29	1e−03	12 / 393	BP	mRNA processing
30	1e−03	98 / 7209	Lympl	HOPP_Weak_promoter
31	2e−03	4 / 47	Glio	Vishal_subnetwork signature of survival in GBM
32	2e−03	5 / 79	MF	protein transporter activity
33	2e−03	3 / 23	BP	ncRNA metabolic process
34	2e−03	14 / 532	GSEA	PARENT_MTOR_SIGNALING_UP
35	2e−03	10 / 309	GSEA	REACTOME_METABOLISM_OF_PROTEINS
36	2e−03	110 / 8415	Colon	Quies3_Colon
37	2e−03	3 / 24	MF	histone acetyltransferase binding
38	2e−03	116 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
39	3e−03	3 / 26	GSEA	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS
40	3e−03	14 / 555	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 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	19 / 687	gene expression
2	7e−04	13 / 422	viral process
3	1e−03	36 / 1975	cellular protein modification process
4	1e−03	12 / 393	mRNA processing
5	2e−03	3 / 23	ncRNA metabolic process
6	3e−03	6 / 131	ribonucleoprotein complex assembly
7	3e−03	6 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
8	3e−03	9 / 277	translation
9	4e−03	3 / 29	spliceosomal snRNP assembly
10	4e−03	14 / 570	symbiosis, encompassing mutualism through parasitism
11	5e−03	3 / 31	7−methylguanosine mRNA capping
12	5e−03	3 / 32	RNA phosphodiester bond hydrolysis, endonucleolytic
13	6e−03	2 / 11	DNA methylation involved in gamete generation
14	6e−03	2 / 11	negative regulation of growth
15	7e−03	4 / 69	transcription elongation from RNA polymerase II promoter
16	7e−03	2 / 12	histone H2A monoubiquitination
17	7e−03	2 / 12	mitochondrial fusion
18	8e−03	3 / 37	regulation of translational initiation
19	8e−03	3 / 37	transcription from RNA polymerase III promoter
20	8e−03	8 / 259	protein targeting

Brain

Rank	p−value	#in/all	Geneset
1	1e−09	103 / 5940	Overlap_fetal_midbrain_HetRpts
2	3e−09	133 / 9013	Overlap_fetal_midbrain_K9K27me3
3	2e−08	134 / 9330	Overlap_fetal_midbrain_ReprPC
4	6e−05	127 / 9528	Overlap_fetal_midbrain_Quies
5	2e−03	116 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	4e−02	43 / 3081	Mid_Frontal_Lobe_ZNF
7	7e−02	10 / 534	Mid_Frontal_Lobe_EnhG
8	1e−01	4 / 163	Fetal_ReprPC
9	1e−01	13 / 831	Fetal_HetRpts
10	1e−01	12 / 769	Overlap_fetal_midbrain_ZNF
11	2e−01	18 / 1333	Fetal_ReprPCWk
12	4e−01	13 / 1050	Fetal_EnhP
13	4e−01	4 / 304	Fetal_Het
14	5e−01	2 / 156	Mid_Frontal_Lobe_TssA
15	6e−01	7 / 656	Overlap_fetal_midbrain_EnhP
16	6e−01	6 / 564	Mid_Frontal_Lobe_EnhP
17	7e−01	7 / 765	Mid_Frontal_Lobe_Het
18	7e−01	3 / 349	Fetal_ZNF
19	8e−01	9 / 989	Mid_Frontal_Lobe_Quies
20	8e−01	7 / 786	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	8 / 298	SPANG_BCL6−index2
2	0.05	1 / 5	WANG_ER_DN
3	0.10	1 / 10	GENTLES_modul5
4	0.14	1 / 14	LIU_LIVER_CANCER
5	0.15	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.15	1 / 15	GENTLES_modul1
7	0.15	1 / 15	GENTLES_modul4
8	0.16	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	0.16	1 / 16	GENTLES_modul6
10	0.16	1 / 16	GENTLES_modul14
11	0.27	1 / 29	KUIPER_MM good survival
12	0.49	0 / 15	RHODES_CANCER_META_SIGNATURE
13	0.52	0 / 14	LIU_COMMON_CANCER_GENES
14	0.54	1 / 70	SHAUGHNESSY_MM high risk
15	0.59	0 / 12	LIU_PROSTATE_CANCER_UP
16	0.59	1 / 82	PanCan_TXmisReg_geneset_nanostring
17	0.74	1 / 121	PanCan_MAPK_geneset_nanostring
18	0.79	4 / 489	Lembcke_Normal vs Adenoma
19	0.99	0 / 14	LIU_PROSTATE_CANCER_DN
20	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	1e−05	139 / 10605	intracellular
2	2e−04	47 / 2577	nucleoplasm
3	1e−03	109 / 8205	cytoplasm
4	1e−03	127 / 9988	organelle
5	4e−03	79 / 5696	nucleus
6	6e−03	49 / 3214	protein complex
7	7e−03	141 / 11774	cell
8	8e−03	3 / 38	cis−Golgi network
9	1e−02	2 / 14	Cul4−RING E3 ubiquitin ligase complex
10	1e−02	6 / 170	nuclear speck
11	1e−02	2 / 17	transcriptionally active chromatin
12	2e−02	21 / 1201	endoplasmic reticulum
13	2e−02	2 / 21	clathrin adaptor complex
14	2e−02	2 / 22	mitochondrial large ribosomal subunit
15	3e−02	4 / 108	late endosome
16	3e−02	4 / 109	peroxisome
17	4e−02	2 / 30	peroxisomal matrix
18	4e−02	4 / 120	mitochondrial outer membrane
19	4e−02	10 / 491	perinuclear region of cytoplasm
20	4e−02	151 / 13191	cellular_component

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	20 / 775	Chr 12
2	3e−02	10 / 462	Chr 14
3	2e−01	5 / 262	Chr 13
4	3e−01	6 / 398	Chr 20
5	3e−01	9 / 687	Chr 6
6	3e−01	13 / 1037	Chr 19
7	4e−01	12 / 993	Chr 2
8	5e−01	8 / 696	Chr 5
9	5e−01	2 / 151	Chr 21
10	5e−01	4 / 335	Chr 22
11	5e−01	9 / 801	Chr 11
12	6e−01	16 / 1500	Chr 1
13	6e−01	6 / 576	Chr 9
14	6e−01	7 / 689	Chr 7
15	7e−01	2 / 221	Chr 18
16	8e−01	4 / 465	Chr 15
17	8e−01	4 / 469	Chr 8
18	9e−01	4 / 552	Chr 10
19	9e−01	4 / 649	Chr 16
20	9e−01	3 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−13	140 / 9027	Tx_Colon
2	7e−13	136 / 8580	TxWk_Colon
3	3e−10	139 / 9482	TssA_Colon
4	2e−03	110 / 8415	Quies3_Colon
5	1e−02	93 / 7203	TssF_Colon
6	4e−02	39 / 2698	EnhA_Colon
7	4e−02	123 / 10290	TssWk_Colon
8	5e−02	67 / 5155	EnhWk1_Colon
9	8e−02	1 / 8	KIM_CRC−MSI−regulated_DN
10	1e−01	113 / 9653	Enh_Colon
11	2e−01	36 / 2798	TxEnhG1_Colon
12	2e−01	2 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	2e−01	11 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
14	2e−01	46 / 3812	TssD1_Colon
15	2e−01	69 / 5880	TssD2_Colon
16	4e−01	1 / 43	Marisa_CRC−cluster−f
17	4e−01	13 / 1079	ZNF_Colon
18	4e−01	8 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
19	4e−01	11 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	4e−01	5 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	1	2 / 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	0.002	4 / 47	Vishal_subnetwork signature of survival in GBM
2	0.011	17 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
3	0.029	8 / 332	Up
4	0.043	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
5	0.074	1 / 7	KIM amplified & overexpressed in LTS
6	0.096	4 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	0.151	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	0.152	1 / 15	VERHAAK_CL subtype
9	0.152	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	0.215	1 / 22	KIM prognostic signature LTS vs. STS
11	0.310	2 / 103	GIEZELT_GBM_WT_up_VS_mut
12	0.334	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
13	0.397	2 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	0.423	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	0.466	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
16	0.500	1 / 63	Stuehler_Proteins_up_in_STS
17	0.511	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
18	0.527	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
19	0.527	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
20	0.532	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	29 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	3e−04	22 / 890	ACEVEDO_LIVER_CANCER_UP
3	3e−04	15 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
4	5e−04	8 / 167	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
5	1e−03	10 / 278	MANALO_HYPOXIA_DN
6	1e−03	19 / 800	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
7	2e−03	14 / 532	PARENT_MTOR_SIGNALING_UP
8	2e−03	10 / 309	REACTOME_METABOLISM_OF_PROTEINS
9	3e−03	3 / 26	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_
10	3e−03	14 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
11	3e−03	3 / 27	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN
12	3e−03	3 / 28	ST_ERK1_ERK2_MAPK_PATHWAY
13	3e−03	3 / 28	REACTOME_MRNA_CAPPING
14	3e−03	3 / 28	KIM_TIAL1_TARGETS
15	3e−03	14 / 562	CAIRO_HEPATOBLASTOMA_CLASSES_UP
16	4e−03	2 / 9	QUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
17	4e−03	4 / 60	SESTO_RESPONSE_TO_UV_C7
18	4e−03	3 / 30	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
19	4e−03	7 / 185	WELCSH_BRCA1_TARGETS_UP
20	5e−03	5 / 100	SESTO_RESPONSE_TO_UV_C0

HM

Rank	p−value	#in/all	Geneset
1	0.02	5 / 146	HALLMARK_DNA_REPAIR
2	0.06	5 / 188	HALLMARK_ADIPOGENESIS
3	0.11	3 / 107	HALLMARK_COAGULATION
4	0.11	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
5	0.14	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.15	4 / 188	HALLMARK_MYC_TARGETS_V1
7	0.17	4 / 196	HALLMARK_MTORC1_SIGNALING
8	0.19	3 / 137	HALLMARK_UV_RESPONSE_DN
9	0.19	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	0.28	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.40	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
12	0.46	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
13	0.47	1 / 57	HALLMARK_MYC_TARGETS_V2
14	0.48	2 / 148	HALLMARK_KRAS_SIGNALING_UP
15	0.53	2 / 162	HALLMARK_COMPLEMENT
16	0.55	2 / 167	HALLMARK_APICAL_JUNCTION
17	0.58	2 / 176	HALLMARK_HYPOXIA
18	0.63	2 / 196	HALLMARK_G2M_CHECKPOINT
19	0.64	2 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
20	0.64	1 / 93	HALLMARK_PEROXISOME

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	DUMEAUX_Smoking literature genes up
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
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	3e−10	115 / 6929	HOPP_Txn_elongation
2	1e−08	118 / 7592	HOPP_Active_promoter
3	5e−08	90 / 5184	HOPP_Txn_transition
4	1e−03	98 / 7209	HOPP_Weak_promoter
5	8e−02	1 / 8	MASCQUE_ABC UP
6	1e−01	2 / 50	SPANG_BAFF 9hrs DN
7	1e−01	80 / 6564	HOPP_Strong_enhancer
8	2e−01	1 / 16	ROSOLOWSKI_red UP
9	2e−01	16 / 1128	SPANG_BCR DN
10	2e−01	1 / 19	DAVE_c−myc BL UP
11	3e−01	4 / 247	ZHANG_DLBCL mutated
12	3e−01	6 / 410	SPANG_CD40 6hrs DN
13	4e−01	4 / 280	SPANG_CD40 6hrs UP
14	4e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
15	4e−01	4 / 294	TARTE_Plasmablast signature
16	4e−01	2 / 129	DAVE_BL−vs−DLBCL
17	5e−01	1 / 61	SPANG_LPS 6hrs DN
18	5e−01	1 / 66	TARTE_Plasma cell signature
19	5e−01	3 / 256	SPANG_IL21 DN
20	5e−01	62 / 5693	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	1e−06	35 / 1365	RNA binding
2	1e−05	27 / 1007	poly(A) RNA binding
3	8e−04	3 / 17	RNA polymerase II core binding
4	2e−03	5 / 79	protein transporter activity
5	2e−03	3 / 24	histone acetyltransferase binding
6	3e−03	115 / 8984	protein binding
7	4e−03	154 / 13179	molecular_function
8	5e−03	2 / 10	protein phosphatase type 1 regulator activity
9	6e−03	2 / 11	cAMP response element binding
10	7e−03	3 / 36	tRNA binding
11	8e−03	3 / 37	endonuclease activity
12	9e−03	2 / 13	mannosyltransferase activity
13	1e−02	4 / 83	translation factor activity, RNA binding
14	1e−02	21 / 1149	enzyme binding
15	3e−02	2 / 23	rRNA binding
16	3e−02	9 / 386	nucleotide binding
17	3e−02	5 / 164	nuclease activity
18	4e−02	2 / 29	mRNA 3'−UTR binding
19	5e−02	2 / 33	receptor tyrosine kinase binding
20	5e−02	2 / 34	DNA−dependent ATPase activity

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.008	3 / 37	hsa−miR−1274a
2	0.018	4 / 92	hsa−miR−425
3	0.027	4 / 104	hsa−miR−210
4	0.034	5 / 164	hsa−miR−323b−5p
5	0.034	3 / 65	hsa−miR−9*
6	0.038	3 / 68	hsa−miR−193b
7	0.041	4 / 119	hsa−miR−217
8	0.042	4 / 120	hsa−miR−105
9	0.047	5 / 179	hsa−miR−582−5p
10	0.047	3 / 74	hsa−miR−1254
11	0.049	3 / 75	hsa−miR−877
12	0.049	5 / 182	hsa−miR−374a
13	0.054	5 / 187	hsa−miR−382
14	0.059	4 / 134	hsa−miR−488
15	0.062	3 / 83	hsa−miR−582−3p
16	0.069	4 / 141	hsa−miR−138
17	0.072	3 / 88	hsa−miR−587
18	0.075	3 / 90	hsa−miR−216a
19	0.077	2 / 42	hsa−miR−769−3p
20	0.086	2 / 45	hsa−miR−411

PathwAct

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	BENTINK_e2f3.2
2	0.1	1 / 12	BENTINK_ras.1
3	0.1	1 / 13	BENTINK_myc.1
4	1.0	0 / 12	GUSTAFSON_PI3K_UP
5	1.0	0 / 13	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
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	9e−04	25 / 1171	KIM_MYC targets
2	9e−03	25 / 1400	ICGC_Myc_targets
3	1e−02	34 / 2136	ICGC_GabpPcr2_targets
4	2e−02	12 / 553	ICGC_RxraPcr1_targets
5	2e−02	33 / 2137	ICGC_SrfV0416101_targets
6	7e−02	53 / 4032	ICGC_Creb1_targets
7	8e−02	60 / 4689	ICGC_Taf1_targets
8	1e−01	24 / 1701	HEBENSTREIT_high expression TF
9	1e−01	32 / 2391	ICGC_Pbx3_targets
10	1e−01	55 / 4385	ICGC_Atf2_targets
11	2e−01	1 / 19	MYC_Metabolism UP
12	2e−01	34 / 2714	ICGC_Irf4_targets
13	2e−01	17 / 1266	ICGC_NrsfPcr1_targets
14	2e−01	10 / 690	ICGC_Atf3_targets
15	2e−01	58 / 4879	ICGC_Pmlsc71910_targets
16	3e−01	58 / 4909	ICGC_Stat5_targets
17	3e−01	44 / 3700	ICGC_Nfatc1_targets
18	3e−01	63 / 5408	ICGC_Pou2_targets
19	3e−01	18 / 1418	ICGC_Ets1_targets
20	3e−01	23 / 1872	ICGC_Mef2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 7	VAQUERIZAS_Appendix
2	0.16	1 / 16	VAQUERIZAS_Pancreas
3	0.27	1 / 29	VAQUERIZAS_Smooth muscle
4	0.33	1 / 37	VAQUERIZAS_Thymus
5	0.34	1 / 38	VAQUERIZAS_Whole brain
6	0.34	1 / 38	VAQUERIZAS_Testis
7	0.48	1 / 59	VAQUERIZAS_Whole blood
8	0.79	1 / 143	VAQUERIZAS_General
9	1.00	0 / 36	VAQUERIZAS_Fetal brain
10	1.00	0 / 41	VAQUERIZAS_Placenta
11	1.00	0 / 26	VAQUERIZAS_Liver
12	1.00	0 / 33	VAQUERIZAS_Prostate
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 / 40	VAQUERIZAS_Thyroid
17	1.00	0 / 29	VAQUERIZAS_Fetal lung
18	1.00	0 / 58	VAQUERIZAS_Lung
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 / 14	WIRTH_Telencephalon
2	0.2	6 / 350	WIRTH_Immune system
3	0.3	1 / 32	WIRTH_Placenta
4	0.6	2 / 194	PALMER_B−Cell signature up
5	0.7	2 / 225	PALMER_Granulocytes signature up
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 / 350	WIRTH_Nervous System
15	1.0	0 / 11	WIRTH_Globus pallidus
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 / 1115	LU_BPDE 1n DN
2	0.7	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	

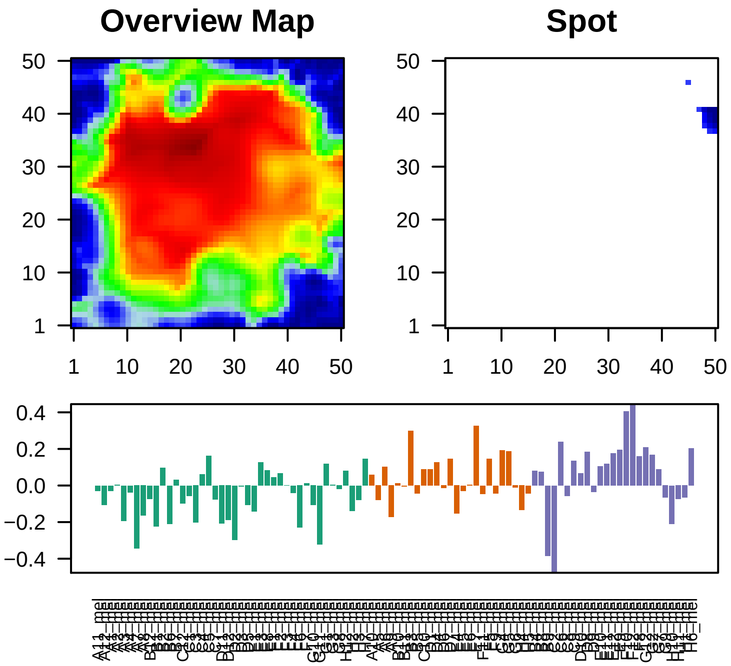
Underexpression Spots

Spot Summary: x

metagenes = 16
genes = 178

<r> metagenes = 0.89
<r> genes = 0.09
beta: r2= 1.43 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC2 : 3 (12 %)
MSC3 : 6 (24 %)

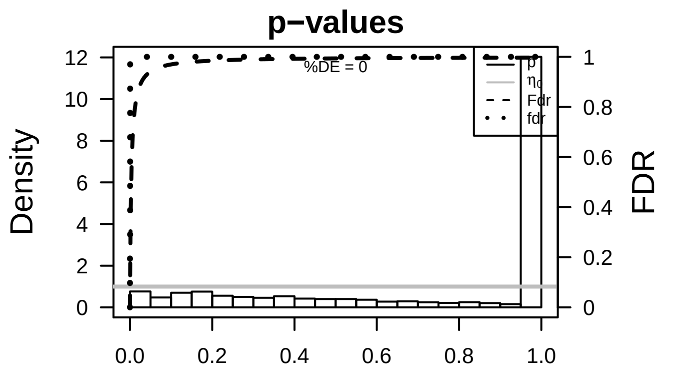


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CCL18	2.45	−0.48	0.42	CCL18	chemokine (C−C motif) ligand 18 (pulmonary and activation−ı
2	P2RX7	2.1	−0.56	0.41	P2RX7	purinergic receptor P2X, ligand gated ion channel, 7 [Source:
3	CTSK	1.72	−0.29	0.38	CTSK	cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536]
4	ZNF35	1.72	−0.24	0.27	ZNF35	zinc finger protein 35 [Source:HGNC Symbol;Acc:HGNC:130
5	SYNPR	1.68	−0.63	0.31	SYNPR	synaptoporin [Source:HGNC Symbol;Acc:HGNC:16507]
6	CAPS2	1.67	−0.27	0.3	CAPS2	calcyphosine 2 [Source:HGNC Symbol;Acc:HGNC:16471]
7	SLC26A6	1.63	−0.39	0.28	SLC26A6	solute carrier family 26 (anion exchanger), member 6 [Source
8	RNF217	1.62	−0.31	0.24	RNF217	ring finger protein 217 [Source:HGNC Symbol;Acc:HGNC:21
9	FBXO32	1.62	−0.54	0.35	FBXO32	F−box protein 32 [Source:HGNC Symbol;Acc:HGNC:16731]
10	CES2	1.61	−0.39	0.25	CES2	carboxylesterase 2 [Source:HGNC Symbol;Acc:HGNC:1864]
11	ATP10D	1.61	−0.52	0.4	ATP10D	ATPase, class V, type 10D [Source:HGNC Symbol;Acc:HGNC
12	WDR59	1.61	−0.74	0.43	WDR59	WD repeat domain 59 [Source:HGNC Symbol;Acc:HGNC:25
13	ZFC3H1	1.61	−0.58	0.29	ZFC3H1	zinc finger, C3H1−type containing [Source:HGNC Symbol;Ac
14	ZFP1	1.6	−0.33	0.3	ZFP1	ZFP1 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:2
15	ZNF75A	1.6	−0.61	0.35	ZNF75A	zinc finger protein 75a [Source:HGNC Symbol;Acc:HGNC:13
16	GLS2	1.59	−0.14	0.29	GLS2	glutaminase 2 (liver, mitochondrial) [Source:HGNC Symbol;A
17	HSPBAP1	1.58	−0.39	0.36	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1 [Source:HGN
18	DEPDC5	1.58	−0.65	0.28	DEPDC5	DEP domain containing 5 [Source:HGNC Symbol;Acc:HGNC
19	KPNA5	1.56	−0.35	0.26	KPNA5	karyopherin alpha 5 (importin alpha 6) [Source:HGNC Symbo
20	SMOX	1.56	−0.19	0.27	SMOX	spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	8e−13	155 / 9482	Colon	TssA_Colon
2	3e−11	151 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	6e−10	123 / 6929	Lympl	HOPP_Txn_elongation
4	2e−09	140 / 8580	Colon	TxWk_Colon
5	6e−09	137 / 8415	Colon	Quies3_Colon
6	8e−09	143 / 9027	Colon	Tx_Colon
7	3e−08	107 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
8	9e−08	125 / 7592	Lympl	HOPP_Active_promoter
9	5e−07	94 / 5184	Lympl	HOPP_Txn_transition
10	8e−07	38 / 1383	TF	ICGC_Six5_targets
11	1e−05	79 / 4385	TF	ICGC_Atf2_targets
12	2e−05	150 / 10605	CC	intracellular
13	3e−05	113 / 7209	Lympl	HOPP_Weak_promoter
14	3e−05	73 / 4032	TF	ICGC_Creb1_targets
15	3e−05	133 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
16	4e−05	124 / 8205	CC	cytoplasm
17	4e−05	18 / 510	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
18	5e−05	4 / 18	BP	phospholipid translocation
19	9e−05	142 / 9988	CC	organelle
20	1e−04	131 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
21	2e−04	81 / 4829	TF	ICGC_Nficsc81335_targets
22	2e−04	31 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	2e−04	75 / 4414	TF	ICGC_Bclaf101388_targets
24	3e−04	47 / 2391	TF	ICGC_Pbx3_targets
25	3e−04	68 / 3924	TF	ICGC_Zeb1_targets
26	3e−04	43 / 2136	TF	ICGC_GabpPcr2_targets
27	3e−04	32 / 1418	TF	ICGC_Ets1_targets
28	3e−04	78 / 4689	TF	ICGC_Taf1_targets
29	3e−04	16 / 503	GSEA	MARTINEZ_RB1_AND_TP53_TARGETS_UP
30	4e−04	16 / 508	GSEA	MARTINEZ_TP53_TARGETS_UP
31	4e−04	80 / 4879	TF	ICGC_Pmlsc71910_targets
32	4e−04	4 / 30	BP	phospholipid transport
33	6e−04	7 / 121	miRN	hsa−miR−212
34	6e−04	11 / 285	BP	organelle organization
35	6e−04	134 / 9528	Brain	Overlap_fetal_midbrain_Quies
36	7e−04	3 / 15	MF	phospholipid−translocating ATPase activity
37	7e−04	142 / 10290	Colon	TssWk_Colon
38	8e−04	4 / 35	GSEA	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
39	8e−04	79 / 4909	TF	ICGC_Stat5_targets
40	9e−04	15 / 494	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 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	5e−05	4 / 18	phospholipid translocation
2	4e−04	4 / 30	phospholipid transport
3	6e−04	11 / 285	organelle organization
4	1e−03	5 / 67	microtubule cytoskeleton organization
5	2e−03	5 / 72	response to organic substance
6	2e−03	3 / 22	homeostasis of number of cells within a tissue
7	3e−03	161 / 12397	biological_process
8	6e−03	4 / 62	positive regulation of type I interferon production
9	7e−03	2 / 11	activation of innate immune response
10	9e−03	2 / 12	histone H2A acetylation
11	9e−03	2 / 12	regulation of release of sequestered calcium ion into cytosol
12	1e−02	2 / 13	positive regulation of transcription elongation from RNA polymerase II promote
13	1e−02	2 / 14	COPII vesicle coating
14	1e−02	2 / 14	positive regulation of calcium ion transport into cytosol
15	1e−02	14 / 598	membrane organization
16	1e−02	25 / 1325	catabolic process
17	1e−02	3 / 43	neurotransmitter secretion
18	2e−02	2 / 16	female gamete generation
19	2e−02	9 / 322	mitochondrion organization
20	2e−02	2 / 17	cellular response to nitrogen starvation

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	151 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−08	107 / 5940	Overlap_fetal_midbrain_HetRpts
3	3e−05	133 / 9013	Overlap_fetal_midbrain_K9K27me3
4	1e−04	131 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	6e−04	134 / 9528	Overlap_fetal_midbrain_Quies
6	7e−03	51 / 3081	Mid_Frontal_Lobe_ZNF
7	3e−02	14 / 656	Overlap_fetal_midbrain_EnhP
8	5e−02	20 / 1122	Fetal_K9K27me3
9	6e−02	17 / 953	Fetal_Enh
10	1e−01	14 / 831	Fetal_HetRpts
11	1e−01	13 / 786	Fetal_EnhG
12	2e−01	6 / 349	Fetal_ZNF
13	2e−01	19 / 1333	Fetal_ReprPCWk
14	3e−01	10 / 668	Mid_Frontal_Lobe_Enh
15	3e−01	3 / 158	Overlap_fetal_midbrain_Het
16	3e−01	5 / 304	Fetal_Het
17	3e−01	11 / 769	Overlap_fetal_midbrain_ZNF
18	4e−01	31 / 2462	Mid_Frontal_Lobe_HetRpts
19	4e−01	10 / 765	Mid_Frontal_Lobe_Het
20	5e−01	22 / 1845	Fetal_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	3 / 70	SHAUGHNESSY_MM high risk
2	0.16	1 / 15	RHODES_CANCER_META_SIGNATURE
3	0.17	1 / 16	GENTLES_modul14
4	0.17	1 / 16	GENTLES_modul16
5	0.21	1 / 20	PanCan_ChromMod_geneset_nanostring
6	0.28	5 / 298	SPANG_BCL6−index2
7	0.38	1 / 40	ZHANG_MM up
8	0.38	2 / 111	PanCan_RAS_geneset_nanostring
9	0.42	2 / 121	PanCan_MAPK_geneset_nanostring
10	0.55	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	0.56	2 / 156	PanCan_PI3K_geneset_nanostring
12	0.63	1 / 82	PanCan_TXmisReg_geneset_nanostring
13	0.74	1 / 113	PanCan_Driver_Gene_geneset_nanostring
14	0.76	1 / 120	PanCan_CC+Apop_geneset_nanostring
15	0.84	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	0.85	0 / 14	LIU_PROSTATE_CANCER_DN
17	0.93	3 / 489	Lembcke_Normal vs Adenoma
18	0.95	2 / 401	Lembcke_Colonic Inflammation
19	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	1.00	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−05	150 / 10605	intracellular
2	4e−05	124 / 8205	cytoplasm
3	9e−05	142 / 9988	organelle
4	3e−03	155 / 11774	cell
5	4e−03	3 / 27	aggresome
6	4e−03	44 / 2507	cytosol
7	8e−03	23 / 1132	Golgi apparatus
8	8e−03	28 / 1468	mitochondrion
9	1e−02	2 / 14	ER to Golgi transport vesicle
10	1e−02	2 / 14	NuA4 histone acetyltransferase complex
11	1e−02	2 / 15	pre−autophagosomal structure membrane
12	2e−02	2 / 16	M band
13	2e−02	3 / 45	SNARE complex
14	2e−02	2 / 19	inclusion body
15	3e−02	7 / 246	mitochondrial matrix
16	3e−02	2 / 24	polysome
17	4e−02	3 / 65	kinetochore
18	5e−02	2 / 30	peroxisomal matrix
19	5e−02	2 / 30	sarcomere
20	5e−02	2 / 30	small−subunit processome

Chr

Rank	p−value	#in/all	Geneset
1	0.02	27 / 1500	Chr 1
2	0.02	17 / 838	Chr 3
3	0.13	12 / 696	Chr 5
4	0.21	9 / 551	Chr X
5	0.31	7 / 462	Chr 14
6	0.35	8 / 558	Chr 4
7	0.49	10 / 801	Chr 11
8	0.51	8 / 649	Chr 16
9	0.55	10 / 840	Chr 17
10	0.58	8 / 687	Chr 6
11	0.58	9 / 775	Chr 12
12	0.65	5 / 465	Chr 15
13	0.66	5 / 469	Chr 8
14	0.70	4 / 398	Chr 20
15	0.75	10 / 993	Chr 2
16	0.77	3 / 335	Chr 22
17	0.80	10 / 1037	Chr 19
18	0.84	1 / 151	Chr 21
19	0.90	4 / 552	Chr 10
20	0.92	4 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−13	155 / 9482	TssA_Colon
2	2e−09	140 / 8580	TxWk_Colon
3	6e−09	137 / 8415	Quies3_Colon
4	8e−09	143 / 9027	Tx_Colon
5	7e−04	142 / 10290	TssWk_Colon
6	3e−02	20 / 1079	ZNF_Colon
7	4e−02	98 / 7203	TssF_Colon
8	5e−02	2 / 29	Marisa_CRC−cluster−c
9	6e−02	5 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
10	6e−02	1 / 5	Budinska_C_CIMP−H−like_UP
11	9e−02	41 / 2798	TxEnhG1_Colon
12	9e−02	1 / 8	Juehling−MSI−enriched−in−7
13	1e−01	1 / 9	KIM_MSI−in−EC
14	1e−01	1 / 9	Budinska_D_Mesenchymal_UP
15	1e−01	53 / 3812	TssD1_Colon
16	1e−01	1 / 10	KIM_MSI−in−CRC
17	2e−01	3 / 117	Marisa_CRC−cluster−b
18	2e−01	1 / 15	Juehling_HNPCC−mutated−in−4
19	2e−01	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
20	2e−01	1 / 16	Vilar_non−hypermutated−in−CRC

Disease

Rank	p−value	#in/all	Geneset
1	0.7	3 / 294	GUDJ_psoriasis down
2	0.8	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	

Glio

Rank	p−value	#in/all	Geneset
1	9e−04	6 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
2	5e−02	3 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	8e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
4	1e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
5	1e−01	7 / 332	Up
6	1e−01	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
7	1e−01	3 / 100	WILLSCHER_GBM_Verhaak=PN (mut&wt)_up_(MES&CL down)
8	1e−01	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
9	2e−01	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
10	2e−01	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
11	2e−01	1 / 18	Shinawi_with_increased_methylation_in_STS
12	2e−01	13 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
13	2e−01	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
14	2e−01	1 / 23	WIRTH_PN subtype
15	2e−01	1 / 23	Donson−Misc immune function−associated with LTS in HGA
16	3e−01	2 / 103	GIEZELT_GBM_WT_up_VS_mut
17	4e−01	1 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
18	4e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
19	4e−01	1 / 40	in vivo astrocytes vs. cultured astroglia
20	4e−01	5 / 356	Down_a

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	18 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
2	2e−04	31 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
3	3e−04	16 / 503	MARTINEZ_RB1_AND_TP53_TARGETS_UP
4	4e−04	16 / 508	MARTINEZ_TP53_TARGETS_UP
5	8e−04	4 / 35	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
6	9e−04	15 / 494	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
7	1e−03	9 / 213	WONG_MITOCHONDRIA_GENE_MODULE
8	1e−03	9 / 214	CHEN_HOXA5_TARGETS_9HR_UP
9	2e−03	16 / 579	MARTINEZ_RB1_TARGETS_UP
10	2e−03	14 / 471	ENK_UV_RESPONSE_KERATINOCYTE_DN
11	2e−03	3 / 21	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP
12	2e−03	18 / 706	BENPORATH_MYC_MAX_TARGETS
13	2e−03	7 / 150	UEDA_PERIFERAL_CLOCK
14	2e−03	17 / 659	SCHLOSSER_SERUM_RESPONSE_DN
15	2e−03	4 / 47	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
16	3e−03	15 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
17	3e−03	18 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
18	3e−03	17 / 683	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
19	4e−03	3 / 28	LANG_MYB_FAMILY_TARGETS
20	5e−03	13 / 475	ONKEN_UVEAL_MELANOMA_DN

HM

Rank	p−value	#in/all	Geneset
1	0.005	5 / 91	HALLMARK_PROTEIN_SECRETION
2	0.057	5 / 174	HALLMARK_HEME_METABOLISM
3	0.084	5 / 195	HALLMARK_MITOTIC_SPINDLE
4	0.143	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
5	0.221	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.253	3 / 146	HALLMARK_DNA_REPAIR
7	0.296	2 / 91	HALLMARK_BILE_ACID_METABOLISM
8	0.318	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.354	3 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	0.366	2 / 107	HALLMARK_COAGULATION
11	0.374	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	0.415	3 / 196	HALLMARK_MTORC1_SIGNALING
13	0.431	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.499	2 / 140	HALLMARK_APOPTOSIS
15	0.499	2 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	0.639	2 / 181	HALLMARK_P53_PATHWAY
17	0.645	2 / 183	HALLMARK_GLYCOLYSIS
18	0.659	2 / 188	HALLMARK_MYC_TARGETS_V1
19	0.673	1 / 93	HALLMARK_PEROXISOME
20	0.677	1 / 94	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	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	6e−10	123 / 6929	HOPP_Txn_elongation
2	9e−08	125 / 7592	HOPP_Active_promoter
3	5e−07	94 / 5184	HOPP_Txn_transition
4	3e−05	113 / 7209	HOPP_Weak_promoter
5	2e−03	85 / 5538	HOPP_Weak_txn
6	5e−03	85 / 5693	HOPP_Weak_enhancer
7	1e−01	1 / 12	BENTINK_mBL DOWN
8	1e−01	86 / 6564	HOPP_Strong_enhancer
9	2e−01	1 / 16	DAVE_BL Inter
10	2e−01	4 / 212	LENZ_Stromal signature 1
11	3e−01	34 / 2563	HOPP_Heterochrom
12	3e−01	2 / 86	ROSOLOWSKI_red total
13	3e−01	1 / 33	LEE_Developmental_regulators
14	3e−01	4 / 247	ZHANG_DLBCL mutated
15	4e−01	2 / 107	SPANG_LPS 6hrs UP
16	4e−01	4 / 268	SPANG_IL21 UP
17	5e−01	1 / 50	SPANG_BAFF 9hrs DN
18	5e−01	4 / 294	TARTE_Plasmablast signature
19	5e−01	1 / 61	SPANG_LPS 6hrs DN
20	5e−01	5 / 410	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 15	phospholipid−translocating ATPase activity
2	5e−03	3 / 29	mRNA 3'−UTR binding
3	9e−03	3 / 36	SNAP receptor activity
4	1e−02	122 / 8984	protein binding
5	2e−02	2 / 17	fatty−acyl−CoA binding
6	3e−02	2 / 21	polyubiquitin binding
7	3e−02	165 / 13179	molecular_function
8	4e−02	8 / 316	protein kinase binding
9	4e−02	2 / 27	chemokine activity
10	4e−02	2 / 27	four−way junction helicase activity
11	4e−02	3 / 65	protease binding
12	4e−02	4 / 111	protein binding, bridging
13	5e−02	2 / 29	carboxylic ester hydrolase activity
14	5e−02	2 / 30	hydrolase activity, hydrolyzing O−glycosyl compounds
15	5e−02	5 / 168	magnesium ion binding
16	5e−02	2 / 31	beta−tubulin binding
17	5e−02	3 / 71	cysteine−type endopeptidase activity
18	5e−02	9 / 405	ligase activity
19	6e−02	2 / 33	RNA polymerase II transcription cofactor activity
20	7e−02	2 / 35	phosphoprotein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	7 / 121	hsa−miR−212
2	1e−03	6 / 98	hsa−miR−147
3	1e−03	7 / 139	hsa−miR−132
4	2e−03	3 / 23	hsa−miR−24−1*
5	5e−03	6 / 132	hsa−miR−199b−5p
6	1e−02	7 / 198	hsa−miR−448
7	1e−02	4 / 70	hsa−miR−628−3p
8	1e−02	6 / 153	hsa−miR−200c
9	1e−02	2 / 13	hsa−miR−574−3p
10	1e−02	5 / 112	hsa−miR−875−3p
11	1e−02	4 / 75	hsa−miR−877
12	1e−02	4 / 77	hsa−miR−205
13	2e−02	4 / 80	hsa−miR−584
14	2e−02	8 / 269	hsa−miR−449a
15	2e−02	6 / 170	hsa−miR−452
16	2e−02	9 / 328	hsa−miR−548a−5p
17	2e−02	3 / 46	hsa−miR−875−5p
18	2e−02	4 / 88	hsa−miR−505
19	2e−02	8 / 289	hsa−miR−186
20	2e−02	6 / 186	hsa−miR−586

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	8e−07	38 / 1383	ICGC_Six5_targets
2	1e−05	79 / 4385	ICGC_Atf2_targets
3	3e−05	73 / 4032	ICGC_Creb1_targets
4	2e−04	81 / 4829	ICGC_Nficsc81335_targets
5	2e−04	75 / 4414	ICGC_Bclaf101388_targets
6	3e−04	47 / 2391	ICGC_Pbx3_targets
7	3e−04	68 / 3924	ICGC_Zeb1_targets
8	3e−04	43 / 2136	ICGC_GabpPcr2_targets
9	3e−04	32 / 1418	ICGC_Ets1_targets
10	3e−04	78 / 4689	ICGC_Taf1_targets
11	4e−04	80 / 4879	ICGC_Pmlsc71910_targets
12	8e−04	79 / 4909	ICGC_Stat5_targets
13	9e−04	63 / 3700	ICGC_Nfatc1_targets
14	1e−03	77 / 4774	ICGC_Foxm1_targets
15	1e−03	76 / 4706	ICGC_Sp1_targets
16	1e−03	37 / 1878	ICGC_Cebpbsc150_targets
17	2e−03	81 / 5200	ICGC_Mta3_targets
18	2e−03	74 / 4682	ICGC_Pol24_targets
19	3e−03	73 / 4617	ICGC_Tcf12_targets
20	4e−03	82 / 5408	ICGC_Pou2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.08	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
2	0.08	1 / 7	VAQUERIZAS_Tongue
3	0.13	1 / 12	VAQUERIZAS_Skin
4	0.16	1 / 15	VAQUERIZAS_Fetal thyroid
5	0.17	1 / 16	VAQUERIZAS_Salivary gland
6	0.29	1 / 29	VAQUERIZAS_Smooth muscle
7	0.37	1 / 38	VAQUERIZAS_Testis
8	0.38	1 / 40	VAQUERIZAS_Thyroid
9	0.39	1 / 41	VAQUERIZAS_Placenta
10	0.51	2 / 143	VAQUERIZAS_General
11	1.00	0 / 36	VAQUERIZAS_Fetal brain
12	1.00	0 / 26	VAQUERIZAS_Liver
13	1.00	0 / 33	VAQUERIZAS_Prostate
14	1.00	0 / 45	VAQUERIZAS_Uterus
15	1.00	0 / 9	VAQUERIZAS_Kidney
16	1.00	0 / 23	VAQUERIZAS_Spinal cord
17	1.00	0 / 38	VAQUERIZAS_Whole brain
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	0.007	2 / 11	WIRTH_Globus pallidus
2	0.015	2 / 16	PALMER_Lymphocytes signature up
3	0.092	1 / 8	WIRTH_Tonsil
4	0.124	1 / 11	WIRTH_Sec. lymphoid organs
5	0.155	1 / 14	WIRTH_Telencephalon
6	0.281	4 / 225	PALMER_Granulocytes signature up
7	0.589	1 / 74	WIRTH_Mucosa
8	0.681	1 / 95	WIRTH_Muscle
9	0.724	1 / 107	WIRTH_Testis
10	0.791	3 / 350	WIRTH_Immune system
11	0.791	3 / 350	WIRTH_Nervous System
12	1.000	0 / 32	WIRTH_Pancreas
13	1.000	0 / 11	WIRTH_Prim. lymphoid organs
14	1.000	0 / 13	WIRTH_B−cells
15	1.000	0 / 12	WIRTH_Thymus
16	1.000	0 / 12	WIRTH_Lymphocytes
17	1.000	0 / 5	WIRTH_Bone marrow
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	0.6	13 / 1115	LU_BPDE 1n DN
2	1.0	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	

Underexpression Spots

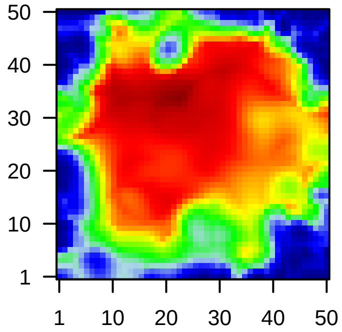
Spot Summary: y

metagenes = 9
genes = 89

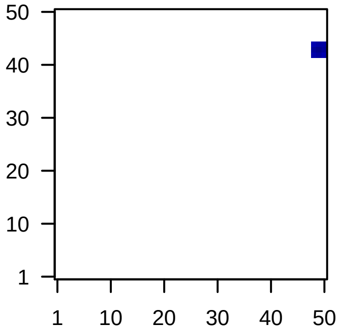
<r> metagenes = 0.97
<r> genes = 0.1
beta: r2= 1.51 / log p= −Inf

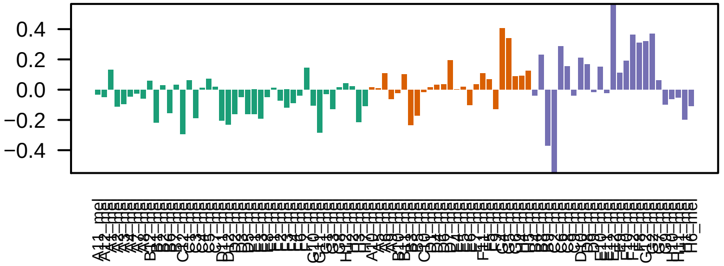
samples with spot = 11 (12 %)
MSC2 : 3 (12 %)
MSC3 : 8 (32 %)

Overview Map



Spot





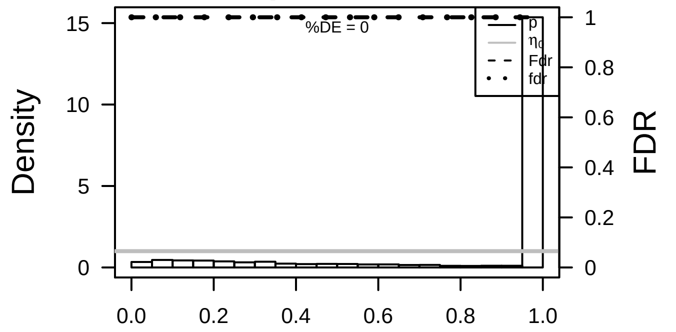
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LIN37	1.83	−0.13	0.35	LIN37	lin−37 DREAM MuvB core complex component [Source:HGN
2	USP19	1.74	−0.4	0.29	USP19	ubiquitin specific peptidase 19 [Source:HGNC Symbol;Acc:H
3	STYXL1	1.73	−0.64	0.39	STYXL1	serine/threonine/tyrosine interacting−like 1 [Source:HGNC Sy
4	RNF146	1.7	−0.34	0.33	RNF146	ring finger protein 146 [Source:HGNC Symbol;Acc:HGNC:21
5	LRRC23	1.64	−0.21	0.33	LRRC23	leucine rich repeat containing 23 [Source:HGNC Symbol;Acc
6	LZTR1	1.57	−0.45	0.26	LZTR1	leucine−zipper−like transcription regulator 1 [Source:HGNC
7	BCAS3	1.55	−0.48	0.37	BCAS3	breast carcinoma amplified sequence 3 [Source:HGNC Symb
8	PARP6	1.54	−0.61	0.24	PARP6	poly (ADP−ribose) polymerase family, member 6 [Source:HG
9	CDC16	1.54	−0.74	0.25	CDC16	cell division cycle 16 [Source:HGNC Symbol;Acc:HGNC:172
10	RUFY1	1.52	−0.52	0.24	RUFY1	RUN and FYVE domain containing 1 [Source:HGNC Symbol;
11	RAB4B	1.51	−0.49	0.28	RAB4B	RAB4B, member RAS oncogene family [Source:HGNC Symb
12	CCT6B	1.51	−0.23	0.23	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2) [Source:HG
13	FAM219B	1.51	−0.68	0.23	FAM219B	family with sequence similarity 219, member B [Source:HGN
14	CDAN1	1.49	−0.14	0.31	CDAN1	codanin 1 [Source:HGNC Symbol;Acc:HGNC:1713]
15	ZNF189	1.47	−0.25	0.33	ZNF189	zinc finger protein 189 [Source:HGNC Symbol;Acc:HGNC:12
16	ZNF10	1.46	−0.32	0.22	ZNF10	zinc finger protein 10 [Source:HGNC Symbol;Acc:HGNC:128
17	GMPR	1.45	−0.32	0.35	GMPR	guanosine monophosphate reductase [Source:HGNC Symbo
18	HMGCL	1.45	−0.6	0.32	HMGCL	3−hydroxymethyl−3−methylglutaryl−CoA lyase [Source:HGN
19	NKRF	1.44	−0.3	0.23	NKRF	NFKB repressing factor [Source:HGNC Symbol;Acc:HGNC:1
20	KDM5C	1.44	−0.73	0.3	KDM5C	lysine (K)−specific demethylase 5C [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−08	67 / 6929	Lymp	HOPP_Txn_elongation
2	2e−07	78 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	3e−07	74 / 8580	Colon	TxWk_Colon
4	4e−07	78 / 9482	Colon	TssA_Colon
5	8e−07	68 / 7592	Lymp	HOPP_Active_promoter
6	1e−06	4 / 14	BP	nucleotide metabolic process
7	1e−06	75 / 9027	Colon	Tx_Colon
8	3e−05	72 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
9	6e−05	54 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
10	1e−04	11 / 478	BP	protein transport
11	1e−04	77 / 10290	Colon	TssWk_Colon
12	2e−04	48 / 5184	Lymp	HOPP_Txn_transition
13	2e−04	60 / 7209	Lymp	HOPP_Weak_promoter
14	5e−04	8 / 310	GSE	DAZARD_RESPONSE_TO_UV_NHEK_DN
15	1e−03	65 / 8415	Colon	Quies3_Colon
16	2e−03	4 / 87	GSE	BROWNE_HCMV_INFECTION_10HR_UP
17	2e−03	2 / 11	BP	positive regulation of protein sumoylation
18	3e−03	2 / 14	BP	negative regulation of endoplasmic reticulum stress−induced intrinsic apop
19	3e−03	5 / 166	miRN	hsa−miR−580
20	4e−03	3 / 52	GSE	IKEDA_MIR1_TARGETS_UP
21	4e−03	4 / 109	miRN	hsa−miR−499−5p
22	4e−03	36 / 4032	TF	ICGC_Creb1_targets
23	5e−03	2 / 17	BP	positive regulation of intracellular protein transport
24	5e−03	2 / 17	GSE	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER
25	5e−03	3 / 56	GSE	CASTELLANO_NRAS_TARGETS_UP
26	5e−03	2 / 18	BP	nucleotide−excision repair, DNA damage removal
27	6e−03	2 / 19	BP	positive regulation of filopodium assembly
28	6e−03	2 / 19	GSE	TOMLINS_METASTASIS_DN
29	6e−03	6 / 271	GSE	ZHANG_TLX_TARGETS_60HR_UP
30	6e−03	9 / 555	GSE	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
31	6e−03	3 / 62	GSE	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP
32	6e−03	2 / 20	GSE	NAKAJIMA_EOSINOPHIL
33	6e−03	2 / 20	GSE	MCCABE_HOXC6_TARGETS_CANCER_DN
34	7e−03	46 / 5693	Lymp	HOPP_Weak_enhancer
35	8e−03	16 / 1383	TF	ICGC_Six5_targets
36	8e−03	5 / 206	GSE	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS
37	8e−03	4 / 132	miRN	hsa−miR−194
38	8e−03	3 / 69	GSE	MORI_PRE_BI_LYMPHOCYTE_DN
39	9e−03	3 / 70	GSE	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP
40	9e−03	3 / 71	GSE	KAYO_CALORIE_RESTRICTION_MUSCLE_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	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	1e−06	4 / 14	nucleotide metabolic process
2	1e−04	11 / 478	protein transport
3	2e−03	2 / 11	positive regulation of protein sumoylation
4	3e−03	2 / 14	negative regulation of endoplasmic reticulum stress−induced intrinsic apoptoti
5	5e−03	2 / 17	positive regulation of intracellular protein transport
6	5e−03	2 / 18	nucleotide−excision repair, DNA damage removal
7	6e−03	2 / 19	positive regulation of filopodium assembly
8	9e−03	2 / 24	response to starvation
9	9e−03	5 / 213	chromatin organization
10	1e−02	2 / 25	regulation of mitochondrial membrane potential
11	1e−02	2 / 27	regulation of endocytosis
12	1e−02	2 / 31	regulation of protein stability
13	2e−02	2 / 34	histone acetylation
14	2e−02	2 / 34	regulation of actin cytoskeleton organization
15	2e−02	5 / 254	spermatogenesis
16	2e−02	3 / 98	chromatin modification
17	3e−02	2 / 45	transcription−coupled nucleotide−excision repair
18	3e−02	2 / 49	negative regulation of cysteine−type endopeptidase activity involved in apopto
19	3e−02	2 / 49	protein deubiquitination
20	4e−02	2 / 51	circadian regulation of gene expression

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	78 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−05	72 / 9013	Overlap_fetal_midbrain_K9K27me3
3	6e−05	54 / 5940	Overlap_fetal_midbrain_HetRpts
4	1e−02	65 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	4e−02	9 / 769	Overlap_fetal_midbrain_ZNF
6	9e−02	20 / 2462	Mid_Frontal_Lobe_HetRpts
7	1e−01	24 / 3081	Mid_Frontal_Lobe_ZNF
8	1e−01	7 / 656	Overlap_fetal_midbrain_EnhP
9	1e−01	4 / 304	Fetal_Het
10	1e−01	9 / 989	Mid_Frontal_Lobe_Quies
11	2e−01	62 / 9528	Overlap_fetal_midbrain_Quies
12	2e−01	7 / 765	Mid_Frontal_Lobe_Het
13	2e−01	2 / 158	Overlap_fetal_midbrain_Het
14	3e−01	10 / 1333	Fetal_ReprPCWk
15	3e−01	8 / 1050	Fetal_EnhP
16	3e−01	9 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	3e−01	3 / 349	Fetal_ZNF
18	4e−01	6 / 884	Overlap_fetal_midbrain_EnhG
19	5e−01	12 / 1907	Fetal_TxTrans
20	6e−01	6 / 1065	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	1 / 15	GENTLES_modul10
2	0.09	1 / 16	GENTLES_modul14
3	0.25	1 / 47	PanCan_DNARepair_geneset_nanostring
4	0.27	3 / 298	SPANG_BCL6−index2
5	0.39	0 / 12	LIU_PROSTATE_CANCER_UP
6	0.49	1 / 113	PanCan_Driver_Gene_geneset_nanostring
7	0.66	1 / 180	SPANG_LPS−index2
8	0.80	2 / 489	Lembcke_Normal vs Adenoma
9	0.91	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.91	1 / 401	Lembcke_Colonic Inflammation
11	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
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 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.00	0 / 12	LIU_BREAST_CANCER
16	1.00	0 / 14	LIU_COMMON_CANCER_GENES
17	1.00	0 / 14	LIU_LIVER_CANCER
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	6 / 377	centrosome
2	0.06	42 / 5696	nucleus
3	0.06	57 / 8205	cytoplasm
4	0.07	1 / 12	holo TFIIH complex
5	0.07	1 / 12	U4/U6 x U5 tri−snRNP complex
6	0.08	1 / 13	COPI vesicle coat
7	0.08	1 / 13	TCTN−B9D complex
8	0.08	1 / 14	Cul4−RING E3 ubiquitin ligase complex
9	0.08	1 / 14	exocyst
10	0.09	1 / 15	centriolar satellite
11	0.09	6 / 512	microtubule organizing center
12	0.09	2 / 83	endomembrane system
13	0.10	1 / 17	integral component of mitochondrial outer membrane
14	0.10	1 / 17	transcriptionally active chromatin
15	0.11	20 / 2507	cytosol
16	0.11	1 / 19	calcium channel complex
17	0.11	1 / 19	nuclear chromosome, telomeric region
18	0.11	1 / 19	site of double−strand break
19	0.11	1 / 20	ciliary transition zone
20	0.11	1 / 20	dynein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	10 / 775	Chr 12
2	0.06	14 / 1500	Chr 1
3	0.12	7 / 687	Chr 6
4	0.21	3 / 262	Chr 13
5	0.24	5 / 551	Chr X
6	0.39	7 / 993	Chr 2
7	0.40	5 / 689	Chr 7
8	0.43	4 / 558	Chr 4
9	0.46	4 / 576	Chr 9
10	0.53	3 / 465	Chr 15
11	0.60	1 / 151	Chr 21
12	0.60	2 / 335	Chr 22
13	0.65	3 / 552	Chr 10
14	0.75	4 / 840	Chr 17
15	0.75	5 / 1037	Chr 19
16	0.77	2 / 462	Chr 14
17	0.79	3 / 696	Chr 5
18	0.89	3 / 838	Chr 3
19	0.91	2 / 649	Chr 16
20	0.91	1 / 398	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−07	74 / 8580	TxWk_Colon
2	4e−07	78 / 9482	TssA_Colon
3	1e−06	75 / 9027	Tx_Colon
4	1e−04	77 / 10290	TssWk_Colon
5	1e−03	65 / 8415	Quies3_Colon
6	1e−02	10 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
7	4e−02	52 / 7203	TssF_Colon
8	9e−02	3 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	9e−02	5 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	2e−01	63 / 9653	Enh_Colon
11	2e−01	1 / 29	Marisa_CRC−cluster−c
12	2e−01	6 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	2e−01	1 / 43	Marisa_CRC−cluster−f
14	2e−01	3 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
15	3e−01	8 / 1038	HetRpts_Colon
16	3e−01	1 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
17	3e−01	19 / 2798	TxEnhG1_Colon
18	3e−01	1 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
19	3e−01	1 / 71	Marisa_CRC−cluster−g
20	4e−01	3 / 390	Pentrack_CRC_TCGA_corr_C_normal_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	2 / 63	Stuehler_Proteins_up_in_STS
2	0.07	2 / 75	Weller_LGG_A_vs_O_DOWN
3	0.12	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.24	7 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.32	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	0.34	1 / 68	GIEZELT_GBM_WT_down_VS_mut
7	0.34	1 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	0.34	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
9	0.36	3 / 356	Down_a
10	0.36	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
11	0.62	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	0.87	1 / 332	Up
13	0.89	1 / 365	Down_b
14	1.00	0 / 15	VERHAAK_CL subtype
15	1.00	0 / 15	VERHAAK_MES subtype
16	1.00	0 / 16	VERHAAK_NL subtype
17	1.00	0 / 14	VERHAAK_PN subtype
18	1.00	0 / 23	WIRTH_PN subtype
19	1.00	0 / 74	WIRTH_Normal Brain
20	1.00	0 / 9	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	8 / 310	DAZARD_RESPONSE_TO_UV_NHEK_DN
2	2e−03	4 / 87	BROWNE_HCMV_INFECTION_10HR_UP
3	4e−03	3 / 52	IKEDA_MIR1_TARGETS_UP
4	5e−03	2 / 17	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER
5	5e−03	3 / 56	CASTELLANO_NRAS_TARGETS_UP
6	6e−03	2 / 19	TOMLINS_METASTASIS_DN
7	6e−03	6 / 271	ZHANG_TLX_TARGETS_60HR_UP
8	6e−03	9 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
9	6e−03	3 / 62	NATSUME_RESPONSE_TO_INTERFERON_BETA_UP
10	6e−03	2 / 20	NAKAJIMA_EOSINOPHIL
11	6e−03	2 / 20	MCCABE_HOXC6_TARGETS_CANCER_DN
12	8e−03	5 / 206	VANOEVELEN_MYOGENESIS_SIN3A_TARGETS
13	8e−03	3 / 69	MORI_PRE_BI_LYMPHOCYTE_DN
14	9e−03	3 / 70	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP
15	9e−03	3 / 71	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
16	9e−03	2 / 24	CHO_NR4A1_TARGETS
17	1e−02	4 / 140	ELVIDGE_HYPOXIA_DN
18	1e−02	4 / 148	DAZARD_UV_RESPONSE_CLUSTER_G6
19	1e−02	2 / 28	REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NE
20	1e−02	2 / 28	MATZUK_SPERMATID_DIFFERENTIATION

HM

Rank	p−value	#in/all	Geneset
1	0.05	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
2	0.11	2 / 93	HALLMARK_PEROXISOME
3	0.14	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.22	2 / 146	HALLMARK_DNA_REPAIR
5	0.41	1 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	0.42	1 / 91	HALLMARK_PROTEIN_SECRETION
7	0.44	1 / 95	HALLMARK_SPERMATOGENESIS
8	0.44	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.53	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
10	0.59	1 / 146	HALLMARK_UV_RESPONSE_UP
11	0.62	1 / 162	HALLMARK_COMPLEMENT
12	0.64	1 / 167	HALLMARK_APICAL_JUNCTION
13	0.64	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.64	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
15	0.64	1 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
16	0.65	1 / 174	HALLMARK_HEME_METABOLISM
17	0.67	1 / 183	HALLMARK_GLYCOLYSIS
18	0.69	1 / 196	HALLMARK_MTORC1_SIGNALING
19	0.70	1 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
20	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	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	3e−08	67 / 6929	HOPP_Txn_elongation
2	8e−07	68 / 7592	HOPP_Active_promoter
3	2e−04	48 / 5184	HOPP_Txn_transition
4	2e−04	60 / 7209	HOPP_Weak_promoter
5	7e−03	46 / 5693	HOPP_Weak_enhancer
6	1e−02	44 / 5538	HOPP_Weak_txn
7	8e−02	4 / 275	TARTE_Mature plasma cell signature
8	9e−02	2 / 82	ROSOLOWSKI_green UP
9	9e−02	46 / 6564	HOPP_Strong_enhancer
10	1e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
11	1e−01	2 / 89	ROSOLOWSKI_blue total
12	1e−01	2 / 109	ROSOLOWSKI_green total
13	1e−01	1 / 25	Subero_T−PLL_hypo_meth
14	2e−01	10 / 1218	SPANG_BCR UP
15	2e−01	3 / 256	SPANG_IL21 DN
16	2e−01	1 / 43	LENZ_Stromal signature 2
17	3e−01	3 / 294	TARTE_Plasmablast signature
18	3e−01	1 / 50	SPANG_BAFF 9hrs DN
19	3e−01	1 / 61	SPANG_LPS 6hrs DN
20	4e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP

MF

Rank	p−value	#in/all	Geneset
1	0.01	2 / 26	oxidoreductase activity, acting on paired donors, with incorporation or reductio
2	0.01	3 / 79	protein transporter activity
3	0.02	2 / 37	histone acetyltransferase activity
4	0.04	2 / 54	damaged DNA binding
5	0.06	1 / 10	cAMP response element binding protein binding
6	0.06	1 / 10	semaphorin receptor binding
7	0.06	1 / 11	acetyltransferase activity
8	0.06	1 / 11	SUMO transferase activity
9	0.06	7 / 592	oxidoreductase activity
10	0.07	2 / 71	single−stranded DNA binding
11	0.07	2 / 71	ubiquitin−specific protease activity
12	0.07	1 / 12	lysophospholipase activity
13	0.07	1 / 12	Notch binding
14	0.08	1 / 13	Ral GTPase binding
15	0.08	2 / 77	electron carrier activity
16	0.08	1 / 14	endoribonuclease activity
17	0.08	2 / 81	protein N−terminus binding
18	0.09	1 / 15	cytokine binding
19	0.09	1 / 15	dioxygenase activity
20	0.09	1 / 15	spectrin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	5 / 166	hsa−miR−580
2	0.004	4 / 109	hsa−miR−499−5p
3	0.008	4 / 132	hsa−miR−194
4	0.017	2 / 33	hsa−miR−1274b
5	0.019	2 / 35	hsa−miR−1287
6	0.019	3 / 95	hsa−miR−888
7	0.021	2 / 37	hsa−miR−1274a
8	0.030	3 / 112	hsa−miR−875−3p
9	0.034	4 / 204	hsa−miR−221
10	0.035	2 / 49	hsa−miR−208b
11	0.035	1 / 6	hsa−miR−886−5p
12	0.041	1 / 7	hsa−miR−611
13	0.044	2 / 56	hsa−miR−208a
14	0.046	2 / 57	hsa−miR−1302
15	0.053	1 / 9	hsa−miR−615−3p
16	0.056	3 / 145	hsa−miR−135a
17	0.061	5 / 353	hsa−let−7i
18	0.068	2 / 71	hsa−miR−1290
19	0.071	2 / 73	hsa−miR−657
20	0.083	4 / 275	hsa−miR−577

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	1 / 13	BENTINK_src.10
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 / 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	36 / 4032	ICGC_Creb1_targets
2	0.008	16 / 1383	ICGC_Six5_targets
3	0.010	16 / 1418	ICGC_Ets1_targets
4	0.024	14 / 1314	ICGC_Usf1_targets
5	0.030	37 / 4689	ICGC_Taf1_targets
6	0.046	12 / 1171	KIM_MYC targets
7	0.053	34 / 4414	ICGC_Bclaf101388_targets
8	0.060	40 / 5408	ICGC_Pou2_targets
9	0.076	40 / 5495	ICGC_Yy1_targets
10	0.085	38 / 5219	ICGC_Tcf3_targets
11	0.092	34 / 4617	ICGC_Tcf12_targets
12	0.115	34 / 4706	ICGC_Sp1_targets
13	0.118	35 / 4879	ICGC_Pmlsc71910_targets
14	0.120	7 / 690	ICGC_Atf3_targets
15	0.124	21 / 2714	ICGC_Irf4_targets
16	0.133	17 / 2136	ICGC_GabpPcr2_targets
17	0.135	11 / 1266	ICGC_NrsfPcr1_targets
18	0.136	14 / 1701	HEBENSTREIT_high expression TF
19	0.145	27 / 3700	ICGC_Nfatc1_targets
20	0.151	34 / 4829	ICGC_Nficsc81335_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.09	1 / 16	VAQUERIZAS_Adrenal gland
2	0.13	1 / 23	VAQUERIZAS_Adrenal cortex
3	0.20	1 / 38	VAQUERIZAS_Testis
4	0.21	2 / 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	0.05	4 / 225	PALMER_Granulocytes signature up
2	0.11	3 / 194	PALMER_B−Cell signature up
3	0.13	2 / 107	WIRTH_Testis
4	0.62	2 / 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 / 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 / 350	WIRTH_Nervous System
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

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	8 / 1115	LU_BPDE 1n DN
2	0.8	19 / 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	

Underexpression Spots

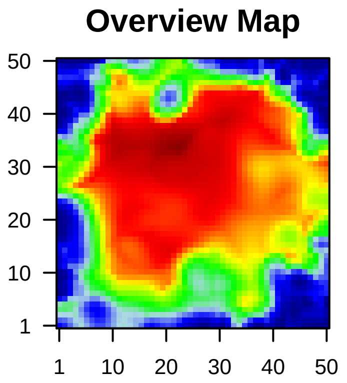
Spot Summary: z

\# metagenes = 22
\# genes = 331

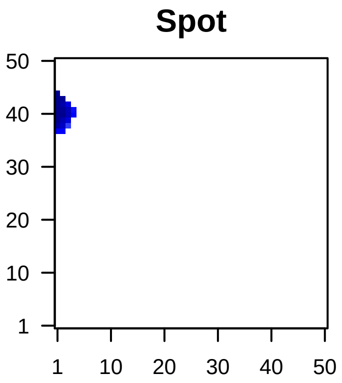
<r> metagenes = 0.96
<r> genes = 0.16
beta: r2= 3.28 / log p= −Inf

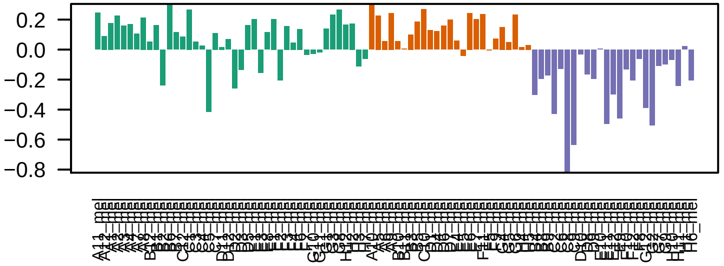
\# samples with spot = 18 (19.6 %)
MSC1 : 9 (21.4 %)
MSC2 : 9 (36 %)

Overview Map



Spot





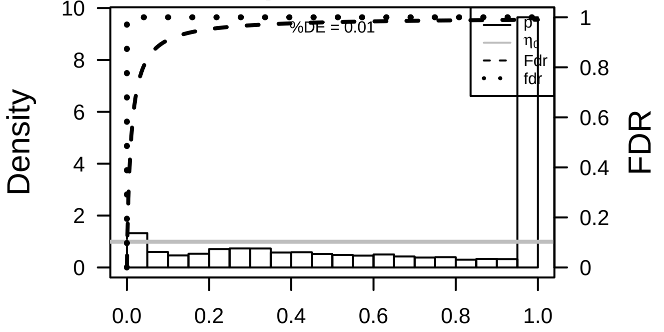
Spot Genelist

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	BCS1L	1.71	−0.91	0.27	BCS1L	BC1 (ubiquinol−cytochrome c reductase) synthesis−like [Sou
3	GAPDHS	1.71	−1.17	0.59	GAPDHS	glyceraldehyde−3−phosphate dehydrogenase, spermatogeni
4	ST6GALNAC	1.69	−0.39	0.32	ST6GALNAC3	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
5	TRMT1	1.65	−0.71	0.36	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:H
6	NMRK2	1.63	−1.2	0.71	NMRK2	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
7	NT5DC1	1.63	−0.93	0.28	NT5DC1	5'−nucleotidase domain containing 1 [Source:HGNC Symbol;
8	SEPSECS	1.63	−0.31	0.32	SEPSECS	Sep (O−phosphoserine) tRNA:Sec (selenocysteine) tRNA sy
9	WIPF3	1.62	−0.29	0.33	WIPF3	WAS/WASL interacting protein family, member 3 [Source:HG
10	ANO2	1.61	−0.48	0.34	ANO2	anoctamin 2, calcium activated chloride channel [Source:HG
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	ISY1	1.53	−0.64	0.24	ISY1	ISY1 splicing factor homolog (S. cerevisiae) [Source:HGNC S
15	SNX8	1.52	−0.75	0.39	SNX8	sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
16	TOE1	1.52	−0.48	0.26	TOE1	target of EGR1, member 1 (nuclear) [Source:HGNC Symbol;
17	FAM193B	1.52	−0.7	0.27	FAM193B	family with sequence similarity 193, member B [Source:HGN
18	IFI35	1.51	−0.5	0.32	IFI35	interferon−induced protein 35 [Source:HGNC Symbol;Acc:HG
19	MAP3K6	1.5	−0.36	0.35	MAP3K6	mitogen−activated protein kinase kinase kinase 6 [Source:HG
20	NENF	1.49	−0.83	0.33	NENF	neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−19	32 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	7e−17	40 / 368	GSEA	STEIN_ESRRA_TARGETS_UP
3	2e−16	84 / 1468	CC	mitochondrion
4	1e−15	231 / 7203	Colon	TssF_Colon
5	7e−15	39 / 401	CC	mitochondrial inner membrane
6	2e−14	43 / 500	GSEA	STEIN_ESRRA_TARGETS
7	6e−12	35 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
8	4e−11	48 / 756	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
9	7e−11	239 / 8205	CC	cytoplasm
10	7e−11	33 / 398	GSEA	MOOTHA_PGC
11	8e−11	34 / 421	GSEA	MOOTHA_MITOCHONDRIA
12	9e−11	264 / 9482	Colon	TssA_Colon
13	9e−10	28 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
14	1e−09	51 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
15	8e−09	33 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
16	1e−08	22 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
17	2e−08	74 / 1730	BP	small molecule metabolic process
18	4e−08	10 / 45	MF	NAD binding
19	5e−08	34 / 541	BP	oxidation−reduction process
20	6e−08	54 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
21	6e−08	246 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
22	7e−08	246 / 9027	Colon	Tx_Colon
23	8e−08	31 / 475	GSEA	ONKEN_UVEAL_MELANOMA_DN
24	1e−07	8 / 28	BP	tricarboxylic acid cycle
25	1e−07	8 / 28	GSEA	KEGG_CITRATE_CYCLE_TCA_CYCLE
26	4e−07	10 / 57	HM	HALLMARK_MYC_TARGETS_V2
27	5e−07	6 / 15	GSEA	MOOTHA_TCA
28	5e−07	42 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
29	5e−07	37 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
30	6e−07	25 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
31	9e−07	9 / 48	GSEA	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
32	1e−06	17 / 188	HM	HALLMARK_ADIPOGENESIS
33	1e−06	59 / 1400	TF	ICGC_Myc_targets
34	1e−06	10 / 63	Glio	Stuehler_Proteins_up_in_STS
35	1e−06	6 / 17	BP	mitochondrial respiratory chain complex I assembly
36	2e−06	81 / 2193	CC	extracellular exosome
37	2e−06	22 / 312	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
38	2e−06	14 / 136	GSEA	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
39	2e−06	23 / 338	GSEA	DAIRKEE_TERT_TARGETS_UP
40	2e−06	272 / 10605	CC	intracellular

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	3 / 100	HORVATH_aging_genes meth DOWN
2	0.7	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	2e−08	74 / 1730	small molecule metabolic process
2	5e−08	34 / 541	oxidation−reduction process
3	1e−07	8 / 28	tricarboxylic acid cycle
4	1e−06	6 / 17	mitochondrial respiratory chain complex I assembly
5	6e−06	5 / 13	melanin biosynthetic process
6	1e−05	21 / 322	mitochondrion organization
7	4e−05	5 / 18	melanocyte differentiation
8	7e−05	19 / 311	generation of precursor metabolites and energy
9	7e−05	7 / 47	protein targeting to mitochondrion
10	1e−04	6 / 37	gluconeogenesis
11	2e−04	16 / 255	cellular amino acid metabolic process
12	5e−04	7 / 63	response to ethanol
13	5e−04	9 / 104	glucose metabolic process
14	6e−04	4 / 18	2−oxoglutarate metabolic process
15	6e−04	4 / 18	cellular amino acid biosynthetic process
16	7e−04	45 / 1237	metabolic process
17	7e−04	7 / 67	pigmentation
18	9e−04	10 / 135	cellular metabolic process
19	1e−03	15 / 277	translation
20	2e−03	4 / 23	secondary metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	6e−08	246 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−05	242 / 9330	Overlap_fetal_midbrain_ReprPC
3	1e−04	97 / 3081	Mid_Frontal_Lobe_ZNF
4	1e−03	238 / 9528	Overlap_fetal_midbrain_Quies
5	2e−03	30 / 765	Mid_Frontal_Lobe_Het
6	1e−02	42 / 1333	Fetal_ReprPCWk
7	4e−02	148 / 5940	Overlap_fetal_midbrain_HetRpts
8	1e−01	63 / 2462	Mid_Frontal_Lobe_HetRpts
9	2e−01	23 / 831	Fetal_HetRpts
10	3e−01	10 / 349	Fetal_ZNF
11	3e−01	5 / 156	Mid_Frontal_Lobe_TssA
12	3e−01	44 / 1845	Fetal_Quies
13	5e−01	2 / 69	Overlap_fetal_midbrain_Tx
14	5e−01	202 / 9020	Overlap_fetal_midbrain_ReprPCWk
15	5e−01	17 / 769	Overlap_fetal_midbrain_ZNF
16	7e−01	23 / 1122	Fetal_K9K27me3
17	7e−01	3 / 163	Fetal_ReprPC
18	7e−01	19 / 953	Fetal_Enh
19	7e−01	20 / 1013	Fetal_TssP
20	8e−01	61 / 2972	Mid_Frontal_Lobe_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 10	GENTLES_modul5
2	0.04	2 / 15	GENTLES_modul1
3	0.05	1 / 15	RHODES_CANCER_META_SIGNATURE
4	0.06	3 / 40	ZHANG_MM up
5	0.08	16 / 489	Lembcke_Normal vs Adenoma
6	0.11	7 / 180	SPANG_LPS−index2
7	0.18	1 / 14	LIU_COMMON_CANCER_GENES
8	0.20	3 / 70	SHAUGHNESSY_MM high risk
9	0.22	9 / 298	SPANG_BCL6−index2
10	0.24	1 / 12	LIU_BREAST_CANCER
11	0.25	1 / 13	BEN−PORATH_UP
12	0.25	1 / 13	GENTLES_modul12
13	0.27	5 / 156	PanCan_PI3K_geneset_nanostring
14	0.28	4 / 120	PanCan_CC+Apop_geneset_nanostring
15	0.29	1 / 15	GENTLES_modul10
16	0.29	1 / 15	GENTLES_modul11
17	0.29	2 / 48	KUIPER_MM poor survival
18	0.30	1 / 16	WOLFER_overlap genes
19	0.30	1 / 16	GENTLES_modul2
20	0.30	1 / 16	GENTLES_modul7

CC

Rank	p−value	#in/all	Geneset
1	2e−16	84 / 1468	mitochondrion
2	7e−15	39 / 401	mitochondrial inner membrane
3	7e−11	239 / 8205	cytoplasm
4	2e−06	81 / 2193	extracellular exosome
5	2e−06	272 / 10605	intracellular
6	2e−06	260 / 9988	organelle
7	7e−06	11 / 94	melanosome
8	1e−05	13 / 135	myelin sheath
9	5e−05	23 / 412	lysosome
10	9e−05	24 / 456	vacuole
11	3e−04	10 / 120	mitochondrial outer membrane
12	4e−04	80 / 2507	cytosol
13	1e−03	14 / 246	mitochondrial matrix
14	2e−03	283 / 11774	cell
15	6e−03	89 / 3132	extracellular region
16	9e−03	27 / 745	cytoplasmic membrane−bounded vesicle
17	1e−02	5 / 60	lysosomal lumen
18	1e−02	23 / 616	endosome
19	1e−02	5 / 63	mitochondrial intermembrane space
20	2e−02	3 / 24	mitochondrial ribosome

Chr

Rank	p−value	#in/all	Geneset
1	0.01	22 / 576	Chr 9
2	0.02	32 / 993	Chr 2
3	0.08	30 / 1037	Chr 19
4	0.11	17 / 552	Chr 10
5	0.12	8 / 221	Chr 18
6	0.21	10 / 335	Chr 22
7	0.28	20 / 775	Chr 12
8	0.29	18 / 696	Chr 5
9	0.35	12 / 469	Chr 8
10	0.41	20 / 840	Chr 17
11	0.43	4 / 151	Chr 21
12	0.46	11 / 465	Chr 15
13	0.48	15 / 649	Chr 16
14	0.57	15 / 687	Chr 6
15	0.69	11 / 551	Chr X
16	0.84	4 / 262	Chr 13
17	0.86	14 / 801	Chr 11
18	0.90	14 / 838	Chr 3
19	0.94	5 / 398	Chr 20
20	0.95	10 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−15	231 / 7203	TssF_Colon
2	9e−11	264 / 9482	TssA_Colon
3	7e−08	246 / 9027	Tx_Colon
4	2e−05	227 / 8580	TxWk_Colon
5	1e−04	164 / 5880	TssD2_Colon
6	7e−04	86 / 2798	TxEnhG1_Colon
7	1e−03	30 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
8	2e−03	140 / 5155	EnhWk1_Colon
9	3e−03	26 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	4e−03	28 / 739	TxEnhG2_Colon
11	7e−03	236 / 9653	Enh_Colon
12	1e−02	247 / 10290	TssWk_Colon
13	7e−02	201 / 8415	Quies3_Colon
14	1e−01	13 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
15	1e−01	68 / 2698	EnhA_Colon
16	2e−01	1 / 8	Boland_CRC−MSI−TGC
17	2e−01	1 / 8	Marisa_CRC−C6
18	2e−01	2 / 33	Marisa_CRC−cluster−e
19	2e−01	3 / 71	Marisa_CRC−cluster−g
20	3e−01	15 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	14 / 435	GUDJ_psoriasis up
2	0.4	1 / 20	BCHETNIA_EBM−DM up
3	0.8	5 / 294	GUDJ_psoriasis down
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	1e−06	10 / 63	Stuehler_Proteins_up_in_STS
2	1e−02	29 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−02	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
4	3e−02	14 / 365	Down_b
5	4e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
6	5e−02	3 / 38	OL vs. OPC
7	6e−02	5 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	1e−01	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
9	1e−01	2 / 26	Christensen_hypomethylated_in_ependymoma
10	1e−01	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
11	2e−01	2 / 32	Donson−innate immunity−associated with LTS in HGA
12	2e−01	1 / 8	Colman_survival_robust
13	2e−01	11 / 356	Down_a
14	2e−01	1 / 9	VERHAAK_Brain
15	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
16	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
17	2e−01	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
18	2e−01	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
19	2e−01	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
20	2e−01	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−17	40 / 368	STEIN_ESRRA_TARGETS_UP
2	2e−14	43 / 500	STEIN_ESRRA_TARGETS
3	6e−12	35 / 405	MOOTHA_HUMAN_MITODB_6_2002
4	4e−11	48 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
5	7e−11	33 / 398	MOOTHA_PGC
6	8e−11	34 / 421	MOOTHA_MITOCHONDRIA
7	9e−10	28 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
8	1e−09	51 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
9	8e−09	33 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
10	1e−08	22 / 233	PENG_RAPAMYCIN_RESPONSE_DN
11	6e−08	54 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
12	8e−08	31 / 475	ONKEN_UVEAL_MELANOMA_DN
13	1e−07	8 / 28	KEGG_CITRATE_CYCLE_TCA_CYCLE
14	5e−07	6 / 15	MOOTHA_TCA
15	5e−07	42 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
16	5e−07	37 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
17	6e−07	25 / 363	RUTELLA_RESPONSE_TO_HGF_UP
18	9e−07	9 / 48	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
19	2e−06	22 / 312	WONG_EMBRYONIC_STEM_CELL_CORE
20	2e−06	14 / 136	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR

HM

Rank	p−value	#in/all	Geneset
1	9e−19	32 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	4e−07	10 / 57	HALLMARK_MYC_TARGETS_V2
3	1e−06	17 / 188	HALLMARK_ADIPOGENESIS
4	7e−05	12 / 141	HALLMARK_FATTY_ACID_METABOLISM
5	3e−03	11 / 183	HALLMARK_GLYCOLYSIS
6	4e−03	7 / 91	HALLMARK_PROTEIN_SECRETION
7	1e−02	10 / 196	HALLMARK_MTORC1_SIGNALING
8	1e−02	9 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	2e−02	5 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	2e−02	9 / 188	HALLMARK_MYC_TARGETS_V1
11	3e−02	8 / 162	HALLMARK_COMPLEMENT
12	1e−01	6 / 146	HALLMARK_UV_RESPONSE_UP
13	2e−01	4 / 93	HALLMARK_PEROXISOME
14	2e−01	6 / 174	HALLMARK_HEME_METABOLISM
15	2e−01	4 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
16	3e−01	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
17	3e−01	5 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	3e−01	3 / 91	HALLMARK_BILE_ACID_METABOLISM
19	3e−01	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	3e−01	3 / 94	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
2	0.29	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.33	1 / 18	DUMEAUX_High bmi enriched genes
4	0.40	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	3e−06	8 / 42	CARO_OxPhos_in_DLBCL_UP
2	9e−06	193 / 6929	HOPP_Txn_elongation
3	1e−04	202 / 7592	HOPP_Active_promoter
4	4e−04	191 / 7209	HOPP_Weak_promoter
5	5e−04	8 / 82	ROSOLOWSKI_green UP
6	7e−04	9 / 109	ROSOLOWSKI_green total
7	1e−03	142 / 5184	HOPP_Txn_transition
8	2e−03	15 / 294	TARTE_Plasmablast signature
9	8e−03	168 / 6564	HOPP_Strong_enhancer
10	9e−03	13 / 275	TARTE_Mature plasma cell signature
11	1e−02	17 / 410	SPANG_CD40 6hrs DN
12	7e−02	1 / 3	WRIGHT_custom GCB−DLBCL UP
13	1e−01	4 / 80	Aukema_BCL2 DN_BCL6 UP
14	2e−01	3 / 61	SPANG_LPS 6hrs DN
15	2e−01	1 / 8	MASCQUE_GCB UP
16	2e−01	1 / 8	MASCQUE_ABC UP
17	2e−01	1 / 8	Subero_B−CLL_hypo_meth
18	2e−01	30 / 1128	SPANG_BCR DN
19	2e−01	131 / 5538	HOPP_Weak_txn
20	2e−01	2 / 40	Subero_mBL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	4e−08	10 / 45	NAD binding
2	9e−06	31 / 592	oxidoreductase activity
3	9e−04	48 / 1365	RNA binding
4	2e−03	5 / 39	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
5	3e−03	3 / 13	NAD+ binding
6	3e−03	4 / 28	hydrogen ion transmembrane transporter activity
7	6e−03	3 / 17	aspartic−type endopeptidase activity
8	6e−03	3 / 17	fatty−acyl−CoA binding
9	6e−03	3 / 17	sialyltransferase activity
10	7e−03	17 / 394	catalytic activity
11	1e−02	3 / 23	proton−transporting ATPase activity, rotational mechanism
12	2e−02	305 / 13179	molecular_function
13	2e−02	3 / 25	aminopeptidase activity
14	2e−02	2 / 10	estradiol 17−beta−dehydrogenase activity
15	2e−02	2 / 10	FAD binding
16	2e−02	3 / 27	ribosome binding
17	2e−02	20 / 550	protein homodimerization activity
18	2e−02	4 / 49	pyridoxal phosphate binding
19	2e−02	2 / 11	protein deacetylase activity
20	3e−02	32 / 1007	poly(A) RNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	5 / 68	hsa−miR−361−3p
2	0.02	2 / 11	hsa−miR−604
3	0.04	4 / 58	hsa−miR−409−5p
4	0.05	3 / 36	hsa−miR−518e
5	0.05	3 / 37	hsa−miR−760
6	0.06	4 / 65	hsa−miR−518c*
7	0.06	5 / 96	hsa−miR−513b
8	0.07	2 / 19	hsa−miR−645
9	0.09	3 / 48	hsa−miR−524−3p
10	0.10	5 / 110	hsa−miR−146a
11	0.10	5 / 112	hsa−miR−297
12	0.11	6 / 147	hsa−miR−506
13	0.12	4 / 84	hsa−miR−220c
14	0.13	1 / 6	hsa−miR−937
15	0.13	3 / 56	hsa−miR−384
16	0.13	3 / 56	hsa−miR−892a
17	0.14	4 / 89	hsa−miR−608
18	0.14	8 / 228	hsa−miR−124
19	0.15	1 / 7	hsa−miR−339−3p
20	0.15	4 / 92	hsa−miR−362−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	BENTINK_src.10
2	0.3	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 / 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	1e−06	59 / 1400	ICGC_Myc_targets
2	1e−05	122 / 3924	ICGC_Zeb1_targets
3	1e−05	56 / 1418	ICGC_Ets1_targets
4	2e−05	140 / 4689	ICGC_Taf1_targets
5	5e−05	143 / 4909	ICGC_Stat5_targets
6	6e−05	62 / 1701	HEBENSTREIT_high expression TF
7	1e−04	149 / 5219	ICGC_Tcf3_targets
8	1e−04	164 / 5890	ICGC_Elf1_targets
9	1e−04	136 / 4706	ICGC_Sp1_targets
10	2e−04	151 / 5355	ICGC_Pol2_targets
11	2e−04	139 / 4879	ICGC_Pmlsc71910_targets
12	4e−04	118 / 4054	ICGC_Egr1_targets
13	6e−04	151 / 5495	ICGC_Yy1_targets
14	6e−04	132 / 4682	ICGC_Pol24_targets
15	7e−04	148 / 5374	ICGC_Pax5_targets
16	8e−04	47 / 1314	ICGC_Usf1_targets
17	8e−04	125 / 4414	ICGC_Bclaf101388_targets
18	1e−03	129 / 4617	ICGC_Tcf12_targets
19	1e−03	147 / 5408	ICGC_Pou2_targets
20	1e−03	132 / 4774	ICGC_Foxm1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.01	3 / 23	VAQUERIZAS_Adrenal cortex
2	0.05	2 / 16	VAQUERIZAS_Pancreas
3	0.05	2 / 16	VAQUERIZAS_Adrenal gland
4	0.09	2 / 23	VAQUERIZAS_Trachea
5	0.15	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
6	0.18	1 / 9	VAQUERIZAS_Kidney
7	0.20	2 / 37	VAQUERIZAS_Thymus
8	0.22	1 / 11	VAQUERIZAS_Fetal liver
9	0.30	1 / 16	VAQUERIZAS_Salivary gland
10	0.32	1 / 17	VAQUERIZAS_Pituitary
11	0.39	4 / 143	VAQUERIZAS_General
12	0.40	1 / 23	VAQUERIZAS_Spinal cord
13	0.44	1 / 26	VAQUERIZAS_Liver
14	0.46	1 / 27	VAQUERIZAS_Lymph node
15	0.48	1 / 29	VAQUERIZAS_Fetal lung
16	0.56	1 / 36	VAQUERIZAS_Fetal brain
17	0.57	1 / 38	VAQUERIZAS_Whole brain
18	0.64	1 / 45	VAQUERIZAS_Uterus
19	0.73	1 / 58	VAQUERIZAS_Lung
20	1.00	0 / 41	VAQUERIZAS_Placenta

Tissue

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

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	33 / 1115	LU_BPDE 1n DN
2	0.95	70 / 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	

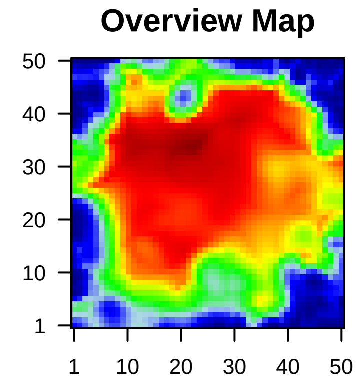
Underexpression Spots

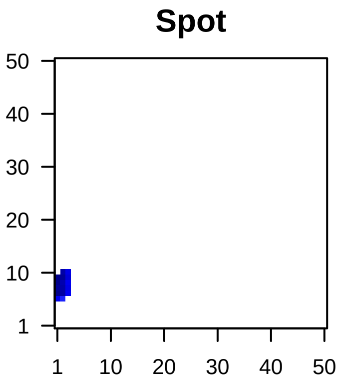
Spot Summary: a1

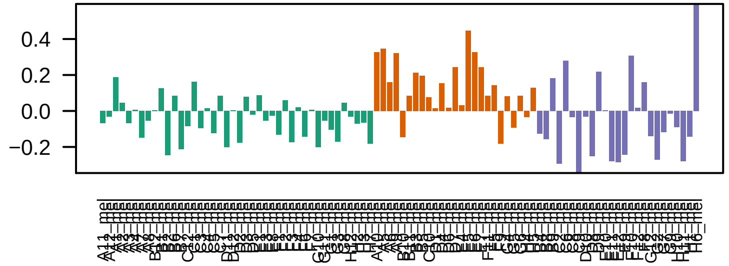
metagenes = 16
genes = 202

<r> metagenes = 0.91
<r> genes = 0.11
beta: r2= 1.93 / log p= −Inf

samples with spot = 13 (14.1 %)
MSC2 : 9 (36 %)
MSC3 : 4 (16 %)


Overview Map


Spot

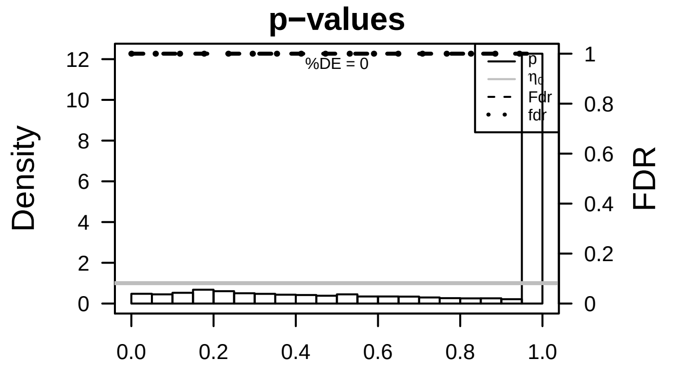


Spot Genelist

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:HGN
2	RNF40	1.97	−0.54	0.27	RNF40	ring finger protein 40, E3 ubiquitin protein ligase [Source:HGN
3	KCNQ5	1.87	−0.46	0.35	KCNQ5	potassium channel, voltage gated KQT−like subfamily Q, mer
4	FLVCR2	1.85	−0.18	0.36	FLVCR2	feline leukemia virus subgroup C cellular receptor family, men
5	CC2D1B	1.84	−0.41	0.22	CC2D1B	coiled−coil and C2 domain containing 1B [Source:HGNC Sym
6	PLA2G4B	1.82	−0.16	0.33	PLA2G4B	phospholipase A2, group IVB (cytosolic) [Source:HGNC Syml
7	HESX1	1.78	−0.08	0.46	HESX1	HESX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:4877]
8	KRTAP19−1	1.78	−0.78	0.4	KRTAP19−1	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:H
9	TRMT2A	1.77	−0.13	0.32	TRMT2A	tRNA methyltransferase 2 homolog A (S. cerevisiae) [Source:
10	HS1BP3	1.76	−0.38	0.28	HS1BP3	HCLS1 binding protein 3 [Source:HGNC Symbol;Acc:HGNC:
11	GAS8	1.75	−0.56	0.29	GAS8	growth arrest−specific 8 [Source:HGNC Symbol;Acc:HGNC:4
12	PRDM10	1.72	−0.23	0.39	PRDM10	PR domain containing 10 [Source:HGNC Symbol;Acc:HGNC:
13	E4F1	1.71	−0.16	0.32	E4F1	E4F transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:
14	C1orf145	1.69	−0.19	0.38	C1orf145	chromosome 1 open reading frame 145 [Source:HGNC Symb
15	TXNDC16	1.69	−0.35	0.28	TXNDC16	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc
16	IFI30	1.68	−0.18	0.35	IFI30	interferon, gamma−inducible protein 30 [Source:HGNC Symb
17	PLA1A	1.68	−0.26	0.34	PLA1A	phospholipase A1 member A [Source:HGNC Symbol;Acc:HG
18	CTC−534A2.2	1.67	−0.37	0.26		
19	ARMCX5	1.66	−0.33	0.31	ARMCX5	armadillo repeat containing, X−linked 5 [Source:HGNC Symb
20	FUBP3	1.66	−0.52	0.3	FUBP3	far upstream element (FUSE) binding protein 3 [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−07	160 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	4e−06	112 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
3	6e−05	143 / 8580	Colon	TxWk_Colon
4	2e−04	5 / 41	MF	ATPase binding
5	3e−04	146 / 9027	Colon	Tx_Colon
6	3e−04	36 / 1468	CC	mitochondrion
7	4e−04	3 / 11	BP	fatty acid oxidation
8	4e−04	7 / 100	miRN	hsa−miR−574−5p
9	5e−04	3 / 12	GSEA	REACTOME_HYALURONAN_METABOLISM
10	7e−04	144 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−03	33 / 1394	GSEA	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
12	1e−03	2 / 4	GSEA	KERLEY_RESPONSE_TO_CISPLATIN_DN
13	1e−03	101 / 5880	Colon	TssD2_Colon
14	2e−03	115 / 6929	Lympl	HOPP_Txn_elongation
15	2e−03	3 / 18	BP	peroxisome organization
16	2e−03	3 / 18	BP	phosphatidylinositol metabolic process
17	2e−03	3 / 19	MF	cAMP binding
18	3e−03	8 / 174	HM	HALLMARK_HEME_METABOLISM
19	3e−03	7 / 140	GSEA	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN
20	3e−03	9 / 220	BP	cofactor metabolic process
21	4e−03	3 / 23	BP	hyaluronan metabolic process
22	4e−03	6 / 109	CC	peroxisome
23	4e−03	4 / 48	CC	peroxisomal membrane
24	4e−03	8 / 188	HM	HALLMARK_ADIPOGENESIS
25	5e−03	5 / 81	CC	late endosome membrane
26	5e−03	5 / 81	MF	protein N−terminus binding
27	5e−03	146 / 9482	Colon	TssA_Colon
28	5e−03	140 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
29	5e−03	4 / 52	BP	fatty acid metabolic process
30	6e−03	132 / 8415	Colon	Quies3_Colon
31	6e−03	3 / 27	GSEA	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
32	6e−03	3 / 27	GSEA	WANG_RESPONSE_TO_ANDROGEN_UP
33	6e−03	5 / 85	GSEA	HUMMERICH_SKIN_CANCER_PROGRESSION_DN
34	6e−03	8 / 200	GSEA	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
35	6e−03	146 / 9528	Brain	Overlap_fetal_midbrain_Quies
36	7e−03	49 / 2576	CC	membrane
37	7e−03	4 / 56	GSEA	MARSON_FOXP3_TARGETS_UP
38	7e−03	14 / 494	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
39	8e−03	2 / 10	BP	cellular response to electrical stimulus
40	8e−03	2 / 10	BP	cellular response to epinephrine stimulus


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 100	HORVATH_aging_genes meth DOWN
2	0.8	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	4e−04	3 / 11	fatty acid oxidation
2	2e−03	3 / 18	peroxisome organization
3	2e−03	3 / 18	phosphatidylinositol metabolic process
4	3e−03	9 / 220	cofactor metabolic process
5	4e−03	3 / 23	hyaluronan metabolic process
6	5e−03	4 / 52	fatty acid metabolic process
7	8e−03	2 / 10	cellular response to electrical stimulus
8	8e−03	2 / 10	cellular response to epinephrine stimulus
9	8e−03	2 / 10	temperature homeostasis
10	9e−03	2 / 11	protein import into peroxisome matrix
11	9e−03	4 / 61	lipid transport
12	1e−02	4 / 63	response to ethanol
13	1e−02	2 / 12	regulation of acetyl−CoA biosynthetic process from pyruvate
14	1e−02	3 / 35	positive regulation of smooth muscle cell proliferation
15	1e−02	3 / 36	erythrocyte differentiation
16	1e−02	3 / 36	toxin transport
17	1e−02	2 / 13	phospholipid catabolic process
18	1e−02	2 / 13	positive regulation of smooth muscle cell migration
19	1e−02	2 / 13	response to arsenic−containing substance
20	1e−02	2 / 14	homeostasis of number of cells

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	160 / 9330	Overlap_fetal_midbrain_ReprPC
2	4e−06	112 / 5940	Overlap_fetal_midbrain_HetRpts
3	7e−04	144 / 9013	Overlap_fetal_midbrain_K9K27me3
4	5e−03	140 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	6e−03	146 / 9528	Overlap_fetal_midbrain_Quies
6	1e−02	56 / 3081	Mid_Frontal_Lobe_ZNF
7	2e−01	14 / 765	Mid_Frontal_Lobe_Het
8	2e−01	18 / 1050	Fetal_EnhP
9	2e−01	13 / 769	Overlap_fetal_midbrain_ZNF
10	3e−01	7 / 383	Fetal_Tx
11	3e−01	6 / 349	Fetal_ZNF
12	3e−01	20 / 1333	Fetal_ReprPCWk
13	4e−01	17 / 1122	Fetal_K9K27me3
14	4e−01	12 / 786	Fetal_EnhG
15	4e−01	5 / 304	Fetal_Het
16	4e−01	10 / 656	Overlap_fetal_midbrain_EnhP
17	4e−01	28 / 1949	Fetal_TssF
18	4e−01	27 / 1907	Fetal_TxTrans
19	5e−01	25 / 1845	Fetal_Quies
20	6e−01	13 / 989	Mid_Frontal_Lobe_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	3 / 40	PanCan_HK_geneset_nanostring
2	0.13	1 / 10	GENTLES_modul5
3	0.17	1 / 14	LIU_COMMON_CANCER_GENES
4	0.19	1 / 15	GENTLES_modul4
5	0.19	3 / 111	PanCan_RAS_geneset_nanostring
6	0.20	1 / 16	GENTLES_modul16
7	0.24	1 / 20	PanCan_ChromMod_geneset_nanostring
8	0.42	1 / 40	ZHANG_MM up
9	0.44	3 / 180	SPANG_LPS−index2
10	0.47	1 / 47	PanCan_DNARepair_geneset_nanostring
11	0.48	1 / 48	KUIPER_MM poor survival
12	0.49	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	0.53	1 / 55	PanCan_JAK−ST_geneset_nanostring
14	0.60	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	0.61	0 / 14	LIU_PROSTATE_CANCER_DN
16	0.62	1 / 70	SHAUGHNESSY_MM high risk
17	0.77	3 / 298	SPANG_BCL6−index2
18	0.80	5 / 489	Lembcke_Normal vs Adenoma
19	0.88	1 / 156	PanCan_PI3K_geneset_nanostring
20	0.97	2 / 401	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	3e−04	36 / 1468	mitochondrion
2	4e−03	6 / 109	peroxisome
3	4e−03	4 / 48	peroxisomal membrane
4	5e−03	5 / 81	late endosome membrane
5	7e−03	49 / 2576	membrane
6	8e−03	3 / 31	brush border membrane
7	1e−02	2 / 12	HOPS complex
8	2e−02	13 / 487	intracellular membrane−bounded organelle
9	2e−02	8 / 246	mitochondrial matrix
10	3e−02	3 / 47	actin filament
11	3e−02	6 / 178	apical plasma membrane
12	5e−02	123 / 8205	cytoplasm
13	6e−02	4 / 108	late endosome
14	6e−02	2 / 30	peroxisomal matrix
15	7e−02	51 / 3088	plasma membrane
16	8e−02	4 / 120	mitochondrial outer membrane
17	8e−02	2 / 35	adherens junction
18	8e−02	2 / 35	axon terminus
19	8e−02	2 / 35	condensed nuclear chromosome
20	8e−02	3 / 76	extrinsic component of membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.04	18 / 840	Chr 17
2	0.04	9 / 335	Chr 22
3	0.05	5 / 151	Chr 21
4	0.06	17 / 838	Chr 3
5	0.19	9 / 469	Chr 8
6	0.27	16 / 993	Chr 2
7	0.30	8 / 465	Chr 15
8	0.38	22 / 1500	Chr 1
9	0.47	8 / 551	Chr X
10	0.48	4 / 262	Chr 13
11	0.49	8 / 558	Chr 4
12	0.53	11 / 801	Chr 11
13	0.60	6 / 462	Chr 14
14	0.60	9 / 696	Chr 5
15	0.66	8 / 649	Chr 16
16	0.79	4 / 398	Chr 20
17	0.80	2 / 221	Chr 18
18	0.87	5 / 552	Chr 10
19	0.89	5 / 576	Chr 9
20	0.95	6 / 775	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−05	143 / 8580	TxWk_Colon
2	3e−04	146 / 9027	Tx_Colon
3	1e−03	101 / 5880	TssD2_Colon
4	5e−03	146 / 9482	TssA_Colon
5	6e−03	132 / 8415	Quies3_Colon
6	4e−02	110 / 7203	TssF_Colon
7	6e−02	3 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
8	7e−02	3 / 71	Marisa_CRC−cluster−g
9	7e−02	55 / 3383	EnhWk2_Colon
10	8e−02	18 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
11	9e−02	46 / 2798	TxEnhG1_Colon
12	1e−01	79 / 5155	EnhWk1_Colon
13	1e−01	44 / 2698	EnhA_Colon
14	1e−01	1 / 8	Marisa_CRC−C1
15	1e−01	147 / 10290	TssWk_Colon
16	2e−01	8 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
17	2e−01	3 / 102	Marisa_CRC−cluster−d
18	2e−01	9 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
19	2e−01	1 / 15	Juehling_HNPCC−mutated−in−4
20	2e−01	57 / 3812	TssD1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.4	5 / 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	3 / 63	Stuehler_Proteins_up_in_STS
2	0.13	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
3	0.13	3 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
4	0.14	1 / 11	Martinez_Glio_hypermeth
5	0.14	2 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
6	0.17	4 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	0.21	7 / 356	Down_a
8	0.21	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	0.24	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
10	0.26	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	0.29	1 / 25	Shaw_down_in_1p19q
12	0.33	1 / 29	shaw_responders_down_in_oligo_glioma
13	0.35	13 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
14	0.40	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
15	0.40	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
16	0.46	1 / 45	Christensen_hypermethylated_in_primary_glioblastoma
17	0.47	1 / 47	Vishal_subnetwork signature of survival in GBM
18	0.55	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
19	0.57	1 / 62	cultured astroglia vs. in vivo astrocytes
20	0.59	1 / 65	GIEZELT_GBM_STS_up_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 12	REACTOME_HYALURONAN_METABOLISM
2	1e−03	33 / 1394	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
3	1e−03	2 / 4	KERLEY_RESPONSE_TO_CISPLATIN_DN
4	3e−03	7 / 140	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN
5	6e−03	3 / 27	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
6	6e−03	3 / 27	WANG_RESPONSE_TO_ANDROGEN_UP
7	6e−03	5 / 85	HUMMERICH_SKIN_CANCER_PROGRESSION_DN
8	6e−03	8 / 200	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
9	7e−03	4 / 56	MARSON_FOXP3_TARGETS_UP
10	7e−03	14 / 494	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
11	8e−03	2 / 10	DAZARD_UV_RESPONSE_CLUSTER_G5
12	8e−03	3 / 31	HAN_JNK_SINGALING_DN
13	8e−03	3 / 31	DORN_ADENOVIRUS_INFECTION_12HR_DN
14	9e−03	2 / 11	KEGG_ALPHA_LINOLENIC_ACID_METABOLISM
15	9e−03	8 / 216	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
16	1e−02	5 / 96	LENAOUR_DENDRITIC_CELL_MATURATION_UP
17	1e−02	6 / 134	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
18	1e−02	3 / 33	PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY
19	1e−02	4 / 63	SANA_RESPONSE_TO_IFNG_UP
20	1e−02	2 / 12	BIOCARTA_IL10_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.003	8 / 174	HALLMARK_HEME_METABOLISM
2	0.004	8 / 188	HALLMARK_ADIPOGENESIS
3	0.031	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	0.038	4 / 93	HALLMARK_PEROXISOME
5	0.039	4 / 94	HALLMARK_ANDROGEN_RESPONSE
6	0.042	5 / 140	HALLMARK_APOPTOSIS
7	0.053	6 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	0.100	5 / 181	HALLMARK_P53_PATHWAY
9	0.125	4 / 141	HALLMARK_FATTY_ACID_METABOLISM
10	0.126	5 / 195	HALLMARK_MITOTIC_SPINDLE
11	0.126	3 / 91	HALLMARK_BILE_ACID_METABOLISM
12	0.128	5 / 196	HALLMARK_MTORC1_SIGNALING
13	0.185	4 / 165	HALLMARK_MYOGENESIS
14	0.196	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
15	0.216	4 / 176	HALLMARK_HYPOXIA
16	0.279	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
17	0.330	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
18	0.345	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
19	0.374	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
20	0.397	1 / 37	HALLMARK_APICAL_SURFACE

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	115 / 6929	HOPP_Txn_elongation
2	0.013	2 / 13	BENTINK_mBL UP
3	0.034	83 / 5184	HOPP_Txn_transition
4	0.046	87 / 5538	HOPP_Weak_txn
5	0.053	1 / 4	MASCQUE_mBL DOWN
6	0.053	22 / 1128	SPANG_BCR DN
7	0.065	88 / 5693	HOPP_Weak_enhancer
8	0.079	1 / 6	MASCQUE_mBL UP
9	0.084	113 / 7592	HOPP_Active_promoter
10	0.094	3 / 80	Aukema_BCL2 DN_BCL6 UP
11	0.103	42 / 2563	HOPP_Heterochrom
12	0.111	3 / 86	ROSOLOWSKI_red total
13	0.151	1 / 12	BENTINK_mBL DOWN
14	0.164	105 / 7209	HOPP_Weak_promoter
15	0.196	1 / 16	ROSOLOWSKI_red UP
16	0.228	1 / 19	DAVE_c−myc BL UP
17	0.298	5 / 268	SPANG_IL21 UP
18	0.323	4 / 212	LENZ_Stromal signature 1
19	0.336	1 / 30	TARTE_B−cell signature
20	0.371	1 / 34	Subero_B−ALL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 41	ATPase binding
2	2e−03	3 / 19	cAMP binding
3	5e−03	5 / 81	protein N−terminus binding
4	8e−03	2 / 10	semaphorin receptor activity
5	1e−02	2 / 12	lysophospholipase activity
6	2e−02	2 / 16	acetylglucosaminyltransferase activity
7	2e−02	2 / 17	Ras GTPase binding
8	3e−02	2 / 19	1−phosphatidylinositol binding
9	3e−02	2 / 19	acyl−CoA dehydrogenase activity
10	3e−02	2 / 20	ligand−dependent nuclear receptor binding
11	3e−02	11 / 430	lipid binding
12	4e−02	2 / 22	oxidoreductase activity, acting on the CH−CH group of donors
13	4e−02	2 / 22	ribonucleoprotein complex binding
14	4e−02	5 / 136	lyase activity
15	4e−02	2 / 23	ephrin receptor binding
16	5e−02	2 / 26	growth factor binding
17	5e−02	4 / 104	iron ion binding
18	5e−02	2 / 28	hydrogen ion transmembrane transporter activity
19	6e−02	3 / 64	flavin adenine dinucleotide binding
20	6e−02	3 / 66	Rho guanyl−nucleotide exchange factor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	7 / 100	hsa−miR−574−5p
2	9e−03	4 / 60	hsa−miR−532−5p
3	2e−02	2 / 15	hsa−miR−191*
4	3e−02	8 / 263	hsa−miR−92b
5	3e−02	5 / 129	hsa−miR−218
6	4e−02	4 / 93	hsa−miR−299−3p
7	4e−02	2 / 23	hsa−miR−323−5p
8	4e−02	2 / 23	hsa−miR−943
9	4e−02	5 / 138	hsa−miR−136
10	4e−02	3 / 56	hsa−miR−665
11	5e−02	5 / 145	hsa−miR−922
12	5e−02	8 / 296	hsa−miR−25
13	5e−02	5 / 147	hsa−miR−143
14	5e−02	4 / 104	hsa−miR−605
15	6e−02	4 / 107	hsa−miR−190b
16	6e−02	3 / 66	hsa−miR−648
17	6e−02	2 / 30	hsa−miR−371−3p
18	7e−02	2 / 31	hsa−miR−342−5p
19	7e−02	3 / 70	hsa−miR−548b−3p
20	7e−02	5 / 164	hsa−miR−323b−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	BENTINK_ras.4
2	0.2	1 / 12	BENTINK_e2f3.2
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 / 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	0.01	89 / 5408	ICGC_Pou2_targets
2	0.02	98 / 6114	ICGC_Runx3_targets
3	0.03	43 / 2391	ICGC_Pbx3_targets
4	0.03	32 / 1701	HEBENSTREIT_high expression TF
5	0.03	78 / 4829	ICGC_Nficsc81335_targets
6	0.05	78 / 4909	ICGC_Stat5_targets
7	0.06	64 / 3966	ICGC_Pu1_targets
8	0.06	74 / 4682	ICGC_Pol24_targets
9	0.07	63 / 3924	ICGC_Zeb1_targets
10	0.07	26 / 1418	ICGC_Ets1_targets
11	0.07	85 / 5495	ICGC_Yy1_targets
12	0.09	74 / 4774	ICGC_Foxm1_targets
13	0.10	89 / 5890	ICGC_Elf1_targets
14	0.10	67 / 4314	ICGC_Ebfsc137065_targets
15	0.10	63 / 4032	ICGC_Creb1_targets
16	0.11	44 / 2714	ICGC_Irf4_targets
17	0.11	47 / 2927	ICGC_Rad21_targets
18	0.12	72 / 4706	ICGC_Sp1_targets
19	0.12	24 / 1383	ICGC_Six5_targets
20	0.13	35 / 2136	ICGC_GabpPcr2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	4 / 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	0.009	2 / 11	WIRTH_Prim. lymphoid organs
2	0.124	5 / 194	PALMER_B−Cell signature up
3	0.151	1 / 12	WIRTH_Lymphocytes
4	0.151	1 / 12	WIRTH_Cerebellum
5	0.363	4 / 225	PALMER_Granulocytes signature up
6	0.426	2 / 107	WIRTH_Testis
7	0.429	1 / 41	WIRTH_Homeostasis
8	0.459	2 / 114	PALMER_T−Cell signature up
9	0.857	3 / 350	WIRTH_Nervous System
10	0.992	1 / 350	WIRTH_Immune system
11	1.000	0 / 32	WIRTH_Pancreas
12	1.000	0 / 11	WIRTH_Sec. lymphoid organs
13	1.000	0 / 13	WIRTH_B−cells
14	1.000	0 / 8	WIRTH_Tonsil
15	1.000	0 / 12	WIRTH_Thymus
16	1.000	0 / 5	WIRTH_Bone marrow
17	1.000	0 / 11	WIRTH_Globus pallidus
18	1.000	0 / 14	WIRTH_Telencephalon
19	1.000	0 / 11	WIRTH_Cortex cerebri
20	1.000	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	14 / 1115	LU_BPDE 1n DN
2	0.9	43 / 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	

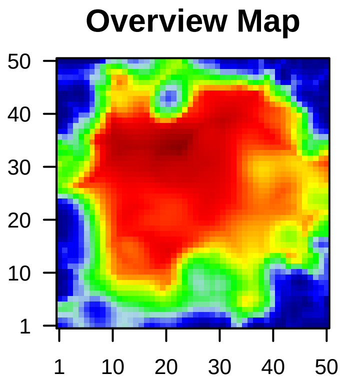
Underexpression Spots

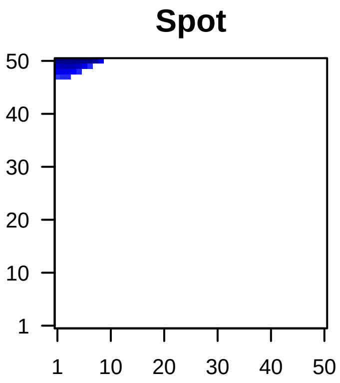
Spot Summary: b1

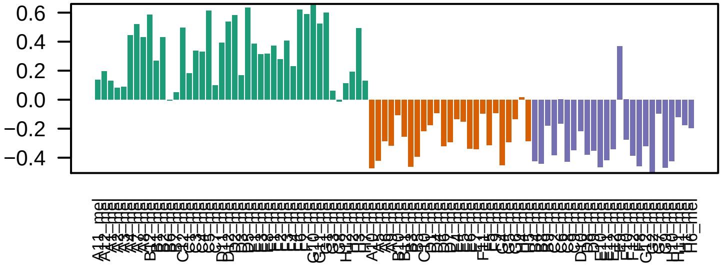
metagenes = 24
genes = 395

<r> metagenes = 0.91
<r> genes = 0.26
beta: r2= 8.63 / log p= −Inf

samples with spot = 29 (31.5 %)
MSC1 : 28 (66.7 %)
MSC3 : 1 (4 %)





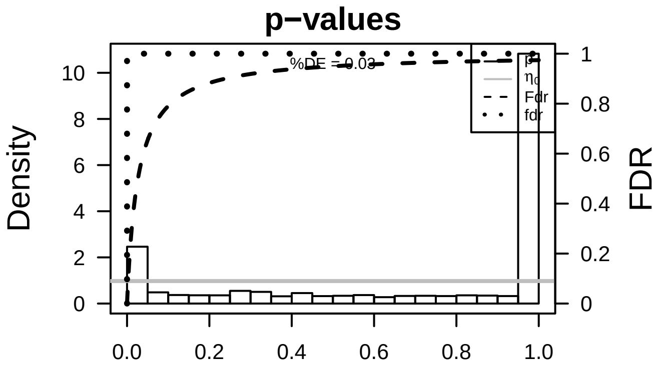


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CEP97	2.41	−1.21	0.26	CEP97	centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGN
2	UBE2C	2.22	−1.05	0.87	UBE2C	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
3	NUF2	2.2	−0.57	0.84	NUF2	NUF2, NDC80 kinetochore complex component [Source:HGN
4	CDK1	2.16	−1.11	0.84	CDK1	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
5	CCNB1	2.14	−1.08	0.66	CCNB1	cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
6	NEK2	2.14	−0.38	0.68	NEK2	NIMA−related kinase 2 [Source:HGNC Symbol;Acc:HGNC:77
7	SMCO4	2.1	−0.21	0.34	SMCO4	single−pass membrane protein with coiled−coil domains 4 [S
8	PLK1	2.09	−0.46	0.65	PLK1	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
9	AURKB	2.03	−0.61	0.79	AURKB	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
10	CKAP2L	2.01	−0.57	0.84	CKAP2L	cytoskeleton associated protein 2−like [Source:HGNC Symbo
11	CDC20	2	−0.67	0.71	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
12	KIF20A	1.98	−0.39	0.74	KIF20A	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
13	NDC80	1.96	−0.62	0.87	NDC80	NDC80 kinetochore complex component [Source:HGNC Sym
14	DLGAP5	1.93	−0.47	0.78	DLGAP5	discs, large (Drosophila) homolog−associated protein 5 [Sour
15	PRR11	1.93	−0.5	0.75	PRR11	proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
16	RRM2	1.92	−0.76	0.86	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
17	SGOL1	1.91	−0.72	0.75	SGOL1	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
18	HIST1H4E	1.9	−0.46	0.45	HIST1H4E	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
19	CDCA3	1.88	−0.49	0.83	CDCA3	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H
20	RHEBL1	1.86	−0.2	0.55	RHEBL1	Ras homolog enriched in brain like 1 [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	207 / 1110	BP	cell cycle
2	1e−99	130 / 412	BP	mitotic cell cycle
3	1e−99	122 / 142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	1e−99	108 / 197	HM	HALLMARK_E2F_TARGETS
5	1e−99	12 / 16	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	1e−99	250 / 1192	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	1e−99	219 / 1251	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	1e−99	98 / 139	GSE	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	1e−99	128 / 390	GSE	PUJANA_BRCA2_PCC_NETWORK
10	1e−99	180 / 944	GSE	NUYTTEN_EZH2_TARGETS_DN
11	1e−99	166 / 616	GSE	BENPORATH_CYCLING_GENES
12	1e−99	189 / 700	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
13	1e−99	120 / 327	GSE	BLUM_RESPONSE_TO_SALIRASIB_DN
14	1e−99	94 / 145	GSE	CHANG_CYCLING_GENES
15	1e−99	143 / 436	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	1e−99	121 / 267	GSE	ZHANG_TLX_TARGETS_60HR_DN
17	1e−99	140 / 242	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
18	1e−99	171 / 305	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
19	1e−99	227 / 550	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
20	1e−97	132 / 505	GSE	BERENJENO_TRANSFORMED_BY_RHOA_UP
21	9e−94	86 / 162	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
22	3e−93	127 / 489	Canc	Lembcke_Normal vs Adenoma
23	4e−93	78 / 124	GSE	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
24	2e−92	116 / 388	GSE	REACTOME_CELL_CYCLE
25	8e−91	83 / 155	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
26	9e−91	70 / 96	GSE	CROONQUIST_IL6_DEPRIVATION_DN
27	3e−88	103 / 301	GSE	REACTOME_CELL_CYCLE_MITOTIC
28	8e−88	72 / 110	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
29	1e−86	110 / 373	GSE	VECCHI_GASTRIC_CANCER_EARLY_UP
30	8e−86	100 / 291	GSE	HORIUCHI_WTAP_TARGETS_DN
31	2e−85	97 / 270	GSE	BASAKI_YBX1_TARGETS_UP
32	4e−84	66 / 93	GSE	KONG_E2F3_TARGETS
33	8e−84	122 / 517	GSE	FEVR_CTNNB1_TARGETS_DN
34	9e−84	139 / 724	GSE	PUJANA_CHEK2_PCC_NETWORK
35	4e−83	67 / 99	GSE	BURTON_ADIPOGENESIS_3
36	1e−82	62 / 81	GSE	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
37	3e−81	66 / 99	GSE	LEE_EARLY_T_LYMPHOCYTE_UP
38	8e−81	84 / 198	GSE	FUJII_YBX1_TARGETS_DN
39	9e−80	83 / 196	HM	HALLMARK_G2M_CHECKPOINT
40	1e−79	79 / 171	GSE	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.2	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	

Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	12 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	3e−93	127 / 489	Lembcke_Normal vs Adenoma
3	4e−36	8 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	8e−15	24 / 120	PanCan_CC+Apop_geneset_nanostring
5	1e−11	14 / 47	PanCan_DNARepair_geneset_nanostring
6	2e−09	8 / 16	WOLFER_overlap genes
7	4e−08	9 / 29	KUIPER_MM good survival
8	6e−08	6 / 10	GENTLES_modul3
9	7e−08	2 / 15	RHODES_CANCER_META_SIGNATURE
10	4e−07	10 / 48	KUIPER_MM poor survival
11	2e−06	11 / 70	SHAUGHNESSY_MM high risk
12	1e−05	5 / 13	BEN−PORATH_UP
13	8e−03	3 / 16	GENTLES_modul2
14	5e−02	2 / 14	LIU_COMMON_CANCER_GENES
15	6e−02	2 / 15	GENTLES_modul1
16	7e−02	2 / 16	GENTLES_modul6
17	1e−01	2 / 20	PanCan_ChromMod_geneset_nanostring
18	2e−01	5 / 113	PanCan_Driver_Gene_geneset_nanostring
19	3e−01	1 / 12	LIU_BREAST_CANCER
20	3e−01	2 / 40	PanCan_HK_geneset_nanostring

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−20	64 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	1e−13	58 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
3	4e−08	320 / 10290	TssWk_Colon
4	1e−07	299 / 9482	TssA_Colon
5	4e−04	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
6	9e−04	254 / 8415	Quies3_Colon
7	3e−03	219 / 7203	TssF_Colon
8	1e−02	3 / 18	Boland_CRC−MSI−A6−A10
9	1e−02	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
10	2e−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	8e−02	114 / 3812	TssD1_Colon
15	1e−01	1 / 5	Budinska_C_CIMP−H−like_UP
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	3e−01	4 / 102	Marisa_CRC−cluster−d
20	3e−01	3 / 71	Marisa_CRC−cluster−g

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	12 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	1e−99	250 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	1e−99	219 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	1e−99	98 / 139	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e−99	128 / 390	PUJANA_BRCA2_PCC_NETWORK
6	1e−99	180 / 944	NUYTTEN_EZH2_TARGETS_DN
7	1e−99	166 / 616	BENPORATH_CYCLING_GENES
8	1e−99	189 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	1e−99	120 / 327	BLUM_RESPONSE_TO_SALIRASIB_DN
10	1e−99	94 / 145	CHANG_CYCLING_GENES
11	1e−99	143 / 436	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	1e−99	121 / 267	ZHANG_TLX_TARGETS_60HR_DN
13	1e−99	140 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
14	1e−99	171 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
15	1e−99	227 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
16	1e−97	132 / 505	BERENJENO_TRANSFORMED_BY_RHOA_UP
17	9e−94	86 / 162	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	4e−93	78 / 124	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
19	2e−92	116 / 388	REACTOME_CELL_CYCLE
20	8e−91	83 / 155	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−38	307 / 6929	HOPP_Txn_elongation
2	3e−35	59 / 294	TARTE_Plasmablast signature
3	3e−22	294 / 7592	HOPP_Active_promoter
4	6e−22	230 / 5184	HOPP_Txn_transition
5	3e−12	22 / 129	DAVE_BL−vs−DLBCL
6	7e−09	67 / 1218	SPANG_BCR UP
7	9e−08	14 / 89	ROSOLOWSKI_blue total
8	3e−06	236 / 7209	HOPP_Weak_promoter
9	3e−05	214 / 6564	HOPP_Strong_enhancer
10	1e−02	2 / 6	MASCQUE_mBL UP
11	4e−02	12 / 256	SPANG_IL21 DN
12	7e−02	2 / 16	DAVE_BL Inter
13	9e−02	2 / 19	DAVE_c−myc BL UP
14	1e−01	162 / 5693	HOPP_Weak_enhancer
15	2e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
16	2e−01	2 / 30	TARTE_B−cell signature
17	2e−01	1 / 8	MASCQUE_GCB UP
18	3e−01	1 / 13	WRIGHT_GCB UP
19	3e−01	1 / 13	YAMANE_AICDA_targets_recruited
20	3e−01	1 / 14	Subero_mBL_hypo_meth

Pathw Act

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 15	BENTINK_ras.6
2	3e−03	3 / 12	GUSTAFSON_PI3K_UP
3	4e−02	2 / 12	BENTINK_e2f3.2
4	4e−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	

Tissue

Rank	p−value	#in/all	Geneset
1	0.003	3 / 12	WIRTH_Thymus
2	0.039	2 / 12	WIRTH_Cerebellum
3	0.256	1 / 11	WIRTH_Prim. lymphoid organs
4	0.359	4 / 114	PALMER_T−Cell signature up
5	0.411	6 / 194	PALMER_B−Cell signature up
6	0.586	9 / 350	WIRTH_Immune system
7	0.984	2 / 225	PALMER_Granulocytes signature up
8	0.985	4 / 350	WIRTH_Nervous System
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

BP

Rank	p−value	#in/all	Geneset
1	1e−99	207 / 1110	cell cycle
2	1e−99	130 / 412	mitotic cell cycle
3	7e−76	135 / 768	DNA metabolic process
4	4e−69	90 / 312	mitotic nuclear division
5	1e−64	96 / 409	cell division
6	1e−46	55 / 160	chromosome segregation
7	7e−46	101 / 721	chromosome organization
8	4e−42	49 / 139	DNA replication
9	2e−29	22 / 29	DNA strand elongation involved in DNA replication
10	5e−26	50 / 298	DNA repair
11	1e−24	35 / 139	G1/S transition of mitotic cell cycle
12	7e−21	31 / 133	G2/M transition of mitotic cell cycle
13	2e−20	15 / 20	telomere maintenance via semi−conservative replication
14	8e−20	189 / 3980	cellular nitrogen compound metabolic process
15	7e−19	15 / 23	DNA replication initiation
16	2e−18	15 / 24	telomere maintenance via recombination
17	3e−17	56 / 581	cytoskeleton organization
18	1e−16	17 / 41	CENP−A containing nucleosome assembly
19	2e−16	13 / 20	mitotic sister chromatid segregation
20	3e−15	19 / 65	telomere maintenance

CC

Rank	p−value	#in/all	Geneset
1	1e−74	126 / 663	chromosome
2	3e−44	286 / 5696	nucleus
3	2e−42	184 / 2577	nucleoplasm
4	7e−29	28 / 59	chromosome, centromeric region
5	5e−28	30 / 75	condensed chromosome kinetochore
6	8e−25	30 / 93	spindle pole
7	2e−24	109 / 1465	cytoskeleton
8	5e−23	49 / 331	nuclear chromosome
9	3e−22	170 / 3214	protein complex
10	6e−22	59 / 512	microtubule organizing center
11	9e−22	358 / 10605	intracellular
12	1e−21	24 / 65	kinetochore
13	4e−21	345 / 9988	organelle
14	1e−20	49 / 377	centrosome
15	2e−15	24 / 113	spindle
16	3e−13	22 / 115	midbody
17	8e−12	13 / 38	spindle microtubule
18	1e−11	361 / 11774	cell
19	6e−11	118 / 2507	cytosol
20	6e−10	17 / 97	chromatin

Disease

Rank	p−value	#in/all	Geneset
1	3e−35	70 / 435	GUDJ_psoriasis up
2	1e+00	3 / 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	

HM

Rank	p−value	#in/all	Geneset
1	1e−99	108 / 197	HALLMARK_E2F_TARGETS
2	9e−80	83 / 196	HALLMARK_G2M_CHECKPOINT
3	2e−25	41 / 195	HALLMARK_MITOTIC_SPINDLE
4	1e−07	20 / 188	HALLMARK_MYC_TARGETS_V1
5	2e−06	16 / 146	HALLMARK_DNA_REPAIR
6	8e−06	12 / 95	HALLMARK_SPERMATOGENESIS
7	2e−03	12 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
8	2e−03	13 / 196	HALLMARK_MTORC1_SIGNALING
9	4e−03	6 / 57	HALLMARK_MYC_TARGETS_V2
10	3e−02	8 / 140	HALLMARK_APOPTOSIS
11	1e−01	5 / 93	HALLMARK_PEROXISOME
12	2e−01	6 / 146	HALLMARK_UV_RESPONSE_UP
13	2e−01	7 / 183	HALLMARK_GLYCOLYSIS
14	3e−01	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	3e−01	5 / 141	HALLMARK_FATTY_ACID_METABOLISM
16	3e−01	4 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
17	4e−01	5 / 162	HALLMARK_COMPLEMENT
18	5e−01	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
19	5e−01	5 / 174	HALLMARK_HEME_METABOLISM
20	5e−01	5 / 181	HALLMARK_P53_PATHWAY

MF

Rank	p−value	#in/all	Geneset
1	9e−16	312 / 8984	protein binding
2	2e−11	77 / 1309	ATP binding
3	2e−10	34 / 364	ATPase activity
4	1e−09	21 / 156	microtubule binding
5	1e−09	98 / 2037	DNA binding
6	4e−09	14 / 71	single−stranded DNA binding
7	3e−08	13 / 69	microtubule motor activity
8	3e−07	29 / 376	chromatin binding
9	6e−07	8 / 29	DNA−directed DNA polymerase activity
10	2e−06	17 / 167	helicase activity
11	3e−06	16 / 152	histone binding
12	1e−05	9 / 54	damaged DNA binding
13	1e−05	23 / 316	protein kinase binding
14	2e−05	6 / 23	DNA helicase activity
15	3e−05	15 / 164	nuclease activity
16	4e−05	34 / 609	cytoskeletal protein binding
17	4e−05	5 / 16	ATP−dependent microtubule motor activity, plus−end−directed
18	1e−04	6 / 29	ATP−dependent DNA helicase activity
19	2e−04	6 / 34	DNA−dependent ATPase activity
20	3e−04	6 / 35	4 iron, 4 sulfur cluster binding

TF

Rank	p−value	#in/all	Geneset
1	1e−07	62 / 1171	KIM_MYC targets
2	1e−07	177 / 4829	ICGC_Nficsc81335_targets
3	7e−07	170 / 4689	ICGC_Taf1_targets
4	2e−05	64 / 1418	ICGC_Ets1_targets
5	2e−05	144 / 4032	ICGC_Creb1_targets
6	1e−04	164 / 4879	ICGC_Pmlsc71910_targets
7	2e−04	8 / 59	MYC_Targets UP
8	2e−04	158 / 4706	ICGC_Sp1_targets
9	5e−04	158 / 4774	ICGC_Foxm1_targets
10	5e−04	155 / 4682	ICGC_Pol24_targets
11	8e−04	174 / 5408	ICGC_Pou2_targets
12	9e−04	66 / 1701	HEBENSTREIT_high expression TF
13	1e−03	186 / 5890	ICGC_Elf1_targets
14	1e−03	3 / 9	MYC_DNA repair UP
15	2e−03	157 / 4909	ICGC_Stat5_targets
16	3e−03	142 / 4385	ICGC_Atf2_targets
17	3e−03	69 / 1878	ICGC_Cebpbsc150_targets
18	5e−03	147 / 4617	ICGC_Tcf12_targets
19	5e−03	188 / 6114	ICGC_Runx3_targets
20	7e−03	170 / 5495	ICGC_Yy1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	33 / 1115	LU_BPDE 1h DN
2	1.0	72 / 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	2e−18	326 / 9330	Overlap_fetal_midbrain_ReprPC
2	5e−14	103 / 1845	Fetal_Quies
3	3e−07	48 / 831	Fetal_HetRpts
4	1e−06	284 / 9013	Overlap_fetal_midbrain_K9K27me3
5	1e−04	51 / 1122	Fetal_K9K27me3
6	1e−02	49 / 1333	Fetal_ReprPCWk
7	1e−01	7 / 163	Fetal_ReprPC
8	4e−01	35 / 1236	Mid_Frontal_Lobe_ReprPCWk
9	4e−01	7 / 229	Mid_Frontal_Lobe_TxTrans
10	5e−01	13 / 468	Mid_Frontal_Lobe_TssF
11	5e−01	240 / 9020	Overlap_fetal_midbrain_ReprPCWk
12	6e−01	26 / 989	Mid_Frontal_Lobe_Quies
13	7e−01	25 / 1050	Fetal_EnhP
14	8e−01	22 / 953	Fetal_Enh
15	8e−01	3 / 158	Overlap_fetal_midbrain_Het
16	8e−01	3 / 166	Mid_Frontal_Lobe_Tx
17	8e−01	6 / 304	Fetal_Het
18	9e−01	6 / 349	Fetal_ZNF
19	9e−01	10 / 534	Mid_Frontal_Lobe_EnhG
20	9e−01	2 / 156	Mid_Frontal_Lobe_TssA

Chr

Rank	p−value	#in/all	Geneset
1	0.004	26 / 558	Chr 4
2	0.007	22 / 465	Chr 15
3	0.023	13 / 262	Chr 13
4	0.034	11 / 221	Chr 18
5	0.090	27 / 775	Chr 12
6	0.111	13 / 335	Chr 22
7	0.260	13 / 398	Chr 20
8	0.298	24 / 801	Chr 11
9	0.344	14 / 462	Chr 14
10	0.367	20 / 687	Chr 6
11	0.373	5 / 151	Chr 21
12	0.483	19 / 696	Chr 5
13	0.500	15 / 552	Chr 10
14	0.553	22 / 838	Chr 3
15	0.725	20 / 840	Chr 17
16	0.746	15 / 649	Chr 16
17	0.764	36 / 1500	Chr 1
18	0.820	15 / 689	Chr 7
19	0.842	12 / 576	Chr 9
20	0.870	11 / 551	Chr X

Glio

Rank	p−value	#in/all	Geneset
1	1e−99	122 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	3e−30	27 / 49	developing astrocytes
3	2e−27	29 / 71	Weller_LGG_gradeII−vs−III_DOWN
4	6e−07	11 / 62	cultured astroglia vs. in vivo astrocytes
5	2e−06	4 / 5	Phillips Prolif up vs PN & MES
6	3e−05	43 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
7	1e−02	6 / 75	Weller_LGG_A_vs_O_DOWN
8	2e−02	4 / 39	OPC
9	6e−02	6 / 103	GIEZELT_GBM_WT_up_VS_mut
10	6e−02	14 / 332	Up
11	2e−01	1 / 9	Mukasa_UP_in_GBM
12	3e−01	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
13	3e−01	1 / 14	VERHAAK_PN subtype
14	3e−01	1 / 16	KIM deleted & downregulated in LTS
15	4e−01	2 / 49	OL vs. MOG− OL
16	4e−01	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
17	4e−01	5 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
18	4e−01	1 / 22	KIM prognostic signature LTS vs. STS
19	5e−01	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
20	6e−01	2 / 70	Weller_LGG_1p19qDel−vs−intact_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	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	21 / 327	hsa−miR−590−3p
2	3e−04	12 / 135	hsa−miR−28−5p
3	4e−04	10 / 103	hsa−miR−1284
4	5e−04	20 / 328	hsa−miR−18a
5	9e−04	20 / 344	hsa−miR−548d−5p
6	1e−03	10 / 115	hsa−miR−154
7	1e−03	8 / 77	hsa−miR−1261
8	1e−03	13 / 179	hsa−miR−582−5p
9	1e−03	19 / 328	hsa−miR−520d−3p
10	2e−03	9 / 104	hsa−miR−210
11	3e−03	20 / 376	hsa−miR−373
12	3e−03	22 / 433	hsa−miR−548n
13	3e−03	18 / 328	hsa−miR−548a−5p
14	3e−03	17 / 303	hsa−miR−18b
15	3e−03	18 / 329	hsa−miR−302d
16	3e−03	7 / 74	hsa−miR−708
17	4e−03	17 / 310	hsa−miR−548i
18	4e−03	7 / 76	hsa−miR−619
19	4e−03	10 / 140	hsa−miR−522
20	4e−03	9 / 119	hsa−miR−217

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 11	VAQUERIZAS_Fetal liver
2	0.07	3 / 37	VAQUERIZAS_Thymus
3	0.08	3 / 38	VAQUERIZAS_Testis
4	0.15	2 / 26	VAQUERIZAS_Liver
5	0.33	1 / 15	VAQUERIZAS_Bone marrow
6	0.80	1 / 59	VAQUERIZAS_Whole blood
7	0.90	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

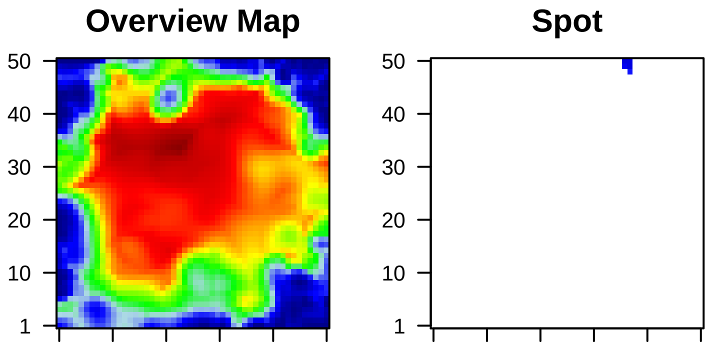
Underexpression Spots

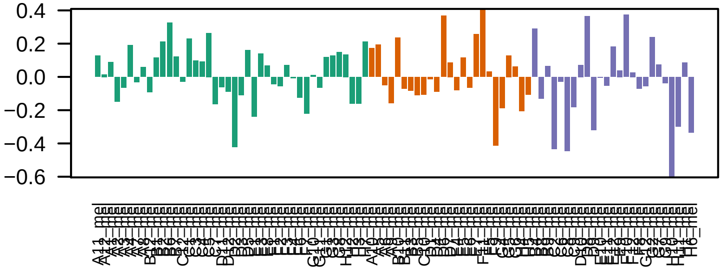
Spot Summary: c1

metagenes = 5
genes = 51

<r> metagenes = 0.99
<r> genes = 0.11
beta: r2= 1.35 / log p= −Inf

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



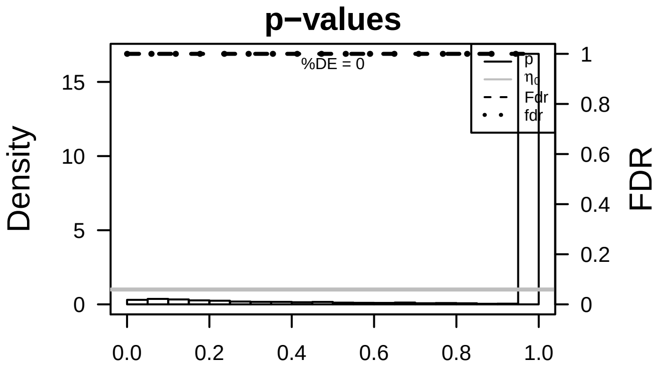


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PTPN21	2	−0.19	0.26	PTPN21	protein tyrosine phosphatase, non−receptor type 21 [Source:I
2	SLC44A2	1.9	−0.2	0.28	SLC44A2	solute carrier family 44 (choline transporter), member 2 [Sour
3	PABPC1L	1.68	−0.4	0.26	PABPC1L	poly(A) binding protein, cytoplasmic 1−like [Source:HGNC Sy
4	GLYCTK	1.67	−0.22	0.29	GLYCTK	glycerate kinase [Source:HGNC Symbol;Acc:HGNC:24247]
5	TRAM1L1	1.61	−0.29	0.32	TRAM1L1	translocation associated membrane protein 1−like 1 [Source:I
6	KDM4A	1.56	−0.44	0.26	KDM4A	lysine (K)−specific demethylase 4A [Source:HGNC Symbol;A
7	METTL18	1.56	−0.63	0.26	METTL18	methyltransferase like 18 [Source:HGNC Symbol;Acc:HGNC:
8	TRMT1L	1.55	−0.46	0.22	TRMT1L	tRNA methyltransferase 1 homolog (S. cerevisiae)−like [Sourc
9	LOH12CR1	1.53	−0.31	0.27	LOH12CR1	loss of heterozygosity, 12, chromosomal region 1 [Source:HG
10	TRPA1	1.47	−0.46	0.18	TRPA1	transient receptor potential cation channel, subfamily A, mem
11	DMAP1	1.45	−0.55	0.35	DMAP1	DNA methyltransferase 1 associated protein 1 [Source:HGNC
12	PXK	1.43	−0.35	0.19	PXK	PX domain containing serine/threonine kinase [Source:HGNC
13	GMPR2	1.41	−1.09	0.38	GMPR2	guanosine monophosphate reductase 2 [Source:HGNC Symb
14	COA7	1.4	−0.45	0.29	COA7	cytochrome c oxidase assembly factor 7 (putative) [Source:H
15	ERCC6	1.4	−0.79	0.35	ERCC6	excision repair cross−complementation group 6 [Source:HGN
16	PIGN	1.39	−1.17	0.29	PIGN	phosphatidylinositol glycan anchor biosynthesis, class N [Sou
17	CDK10	1.38	−0.52	0.29	CDK10	cyclin−dependent kinase 10 [Source:HGNC Symbol;Acc:HGN
18	TRAPPC11	1.36	−0.63	0.35	TRAPPC11	trafficking protein particle complex 11 [Source:HGNC Symbol
19	SMC5	1.31	−0.83	0.2	SMC5	structural maintenance of chromosomes 5 [Source:HGNC Sy
20	MECR	1.31	−0.74	0.38	MECR	mitochondrial trans−2−enoyl−CoA reductase [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−06	46 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
2	3e−06	47 / 9482	Colon	TssA_Colon
3	1e−05	46 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
4	5e−05	40 / 7592	Lympl	HOPP_Active_promoter
5	2e−04	42 / 8580	Colon	TxWk_Colon
6	2e−04	43 / 9027	Colon	Tx_Colon
7	4e−04	37 / 7209	Lympl	HOPP_Weak_promoter
8	1e−03	2 / 14	BP	nucleotide biosynthetic process
9	1e−03	29 / 5184	Lympl	HOPP_Txn_transition
10	1e−03	4 / 136	GSEA	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
11	1e−03	4 / 137	GSEA	JISON_SICKLE_CELL_DISEASE_DN
12	1e−03	35 / 6929	Lympl	HOPP_Txn_elongation
13	2e−03	2 / 17	miRN	hsa−miR−1298
14	2e−03	3 / 70	GSEA	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
15	2e−03	3 / 71	MF	structural constituent of ribosome
16	2e−03	10 / 1008	GSEA	BRUINS_UVC_RESPONSE_LATE
17	2e−03	15 / 1975	BP	cellular protein modification process
18	2e−03	2 / 20	GSEA	DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
19	2e−03	2 / 21	CC	transcription elongation factor complex
20	3e−03	22 / 3644	BP	biosynthetic process
21	3e−03	3 / 82	miRN	hsa−miR−767−5p
22	3e−03	3 / 83	BP	mitochondrial translational elongation
23	3e−03	3 / 83	BP	mitochondrial translational initiation
24	3e−03	3 / 83	BP	mitochondrial translational termination
25	3e−03	2 / 24	CC	mitochondrial ribosome
26	3e−03	6 / 424	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
27	3e−03	12 / 1468	CC	mitochondrion
28	4e−03	2 / 27	CC	aggresome
29	4e−03	44 / 10290	Colon	TssWk_Colon
30	4e−03	3 / 96	BP	mitochondrial translation
31	4e−03	4 / 195	miRN	hsa−miR−206
32	5e−03	2 / 30	BP	mitotic metaphase plate congression
33	5e−03	2 / 30	GSEA	WONG_IFNA2_RESISTANCE_DN
34	5e−03	8 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
35	5e−03	30 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
36	5e−03	2 / 32	miRN	hsa−miR−631
37	6e−03	2 / 34	GSEA	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP
38	6e−03	38 / 8415	Colon	Quies3_Colon
39	7e−03	2 / 36	GSEA	BURTON_ADIPOGENESIS_PEAK_AT_8HR
40	7e−03	2 / 37	GSEA	BROWNE_HCMV_INFECTION_8HR_DN



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 / 14	nucleotide biosynthetic process
2	0.002	15 / 1975	cellular protein modification process
3	0.003	22 / 3644	biosynthetic process
4	0.003	3 / 83	mitochondrial translational elongation
5	0.003	3 / 83	mitochondrial translational initiation
6	0.003	3 / 83	mitochondrial translational termination
7	0.004	3 / 96	mitochondrial translation
8	0.005	2 / 30	mitotic metaphase plate congression
9	0.010	2 / 44	protein autoubiquitination
10	0.010	2 / 45	cell growth
11	0.011	7 / 721	chromosome organization
12	0.014	2 / 52	regulation of growth
13	0.015	2 / 54	nucleobase−containing compound metabolic process
14	0.015	4 / 277	translation
15	0.016	4 / 285	organelle organization
16	0.022	4 / 312	mitotic nuclear division
17	0.027	2 / 74	nucleobase−containing small molecule metabolic process
18	0.034	1 / 10	positive regulation of DNA−templated transcription, elongation
19	0.034	1 / 10	response to pain
20	0.037	3 / 213	chromatin organization

Brain

Rank	p−value	#in/all	Geneset
1	3e−06	46 / 9013	Overlap_fetal_midbrain_K9K27me3
2	1e−05	46 / 9330	Overlap_fetal_midbrain_ReprPC
3	5e−03	30 / 5940	Overlap_fetal_midbrain_HetRpts
4	9e−03	41 / 9528	Overlap_fetal_midbrain_Quies
5	3e−02	38 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	1e−01	5 / 769	Overlap_fetal_midbrain_ZNF
7	1e−01	4 / 564	Mid_Frontal_Lobe_EnhP
8	2e−01	5 / 831	Fetal_HetRpts
9	2e−01	14 / 3081	Mid_Frontal_Lobe_ZNF
10	4e−01	8 / 1949	Fetal_TssF
11	4e−01	1 / 163	Fetal_ReprPC
12	5e−01	5 / 1333	Fetal_ReprPCWk
13	5e−01	3 / 765	Mid_Frontal_Lobe_Het
14	6e−01	6 / 1845	Fetal_Quies
15	6e−01	3 / 953	Fetal_Enh
16	7e−01	2 / 656	Overlap_fetal_midbrain_EnhP
17	7e−01	1 / 349	Fetal_ZNF
18	7e−01	3 / 1065	Overlap_fetal_midbrain_Enh
19	7e−01	1 / 383	Fetal_Tx
20	8e−01	3 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	0 / 14	LIU_COMMON_CANCER_GENES
2	0.10	1 / 29	KUIPER_MM good survival
3	0.15	1 / 47	PanCan_DNARepair_geneset_nanostring
4	0.65	1 / 298	SPANG_BCL6−index2
5	0.82	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_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	0.002	2 / 21	transcription elongation factor complex
2	0.003	2 / 24	mitochondrial ribosome
3	0.003	12 / 1468	mitochondrion
4	0.004	2 / 27	aggresome
5	0.010	3 / 128	ribosome
6	0.018	36 / 8205	cytoplasm
7	0.020	2 / 63	mitochondrial intermembrane space
8	0.040	1 / 12	cullin−RING ubiquitin ligase complex
9	0.047	1 / 14	NuA4 histone acetyltransferase complex
10	0.048	4 / 401	mitochondrial inner membrane
11	0.050	1 / 15	ESC/E(Z) complex
12	0.053	42 / 10605	intracellular
13	0.057	1 / 17	multivesicular body
14	0.057	1 / 17	replication fork
15	0.057	40 / 9988	organelle
16	0.070	1 / 21	anaphase−promoting complex
17	0.070	1 / 21	mitochondrial small ribosomal subunit
18	0.073	1 / 22	histone acetyltransferase complex
19	0.079	1 / 24	Cul3−RING ubiquitin ligase complex
20	0.115	7 / 1201	endoplasmic reticulum

Chr

Rank	p−value	#in/all	Geneset
1	0.1	4 / 552	Chr 10
2	0.1	4 / 558	Chr 4
3	0.1	5 / 775	Chr 12
4	0.1	8 / 1500	Chr 1
5	0.2	3 / 398	Chr 20
6	0.2	2 / 221	Chr 18
7	0.2	3 / 462	Chr 14
8	0.3	3 / 576	Chr 9
9	0.3	4 / 838	Chr 3
10	0.6	1 / 262	Chr 13
11	0.7	2 / 687	Chr 6
12	0.7	2 / 689	Chr 7
13	0.8	2 / 801	Chr 11
14	0.8	1 / 465	Chr 15
15	0.8	1 / 469	Chr 8
16	0.9	1 / 551	Chr X
17	0.9	2 / 993	Chr 2
18	0.9	1 / 649	Chr 16
19	0.9	1 / 840	Chr 17
20	1.0	1 / 1037	Chr 19

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	47 / 9482	TssA_Colon
2	2e−04	42 / 8580	TxWk_Colon
3	2e−04	43 / 9027	Tx_Colon
4	4e−03	44 / 10290	TssWk_Colon
5	6e−03	38 / 8415	Quies3_Colon
6	5e−02	31 / 7203	TssF_Colon
7	9e−02	14 / 2798	TxEnhG1_Colon
8	1e−01	5 / 739	TxEnhG2_Colon
9	3e−01	1 / 102	Marisa_CRC−cluster−d
10	5e−01	34 / 9653	Enh_Colon
11	5e−01	1 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
12	6e−01	13 / 3812	TssD1_Colon
13	6e−01	1 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
14	6e−01	20 / 5880	TssD2_Colon
15	6e−01	9 / 2698	EnhA_Colon
16	6e−01	2 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
17	6e−01	3 / 934	Lembcke_TCGA=expr_kmeans_N_CIMP.H_DN
18	7e−01	2 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
19	7e−01	1 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
20	7e−01	3 / 1079	ZNF_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	0.05	2 / 103	GIEZELT_GBM_WT_up_VS_mut
2	0.09	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
3	0.16	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
4	0.18	1 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
5	0.18	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
6	0.20	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
7	0.21	1 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	0.23	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
9	0.28	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.29	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.32	2 / 332	Up
12	0.33	4 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.33	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	0.35	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
15	0.42	1 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
16	0.67	1 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	0.71	1 / 356	Down_a
18	0.72	1 / 365	Down_b
19	1.00	0 / 15	VERHAAK_CL subtype
20	1.00	0 / 15	VERHAAK_MES subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	4 / 136	IVANOVA_HEMATOPOIESIS_INTERMEDIATE_PROGENITOR
2	0.001	4 / 137	JISON_SICKLE_CELL_DISEASE_DN
3	0.002	3 / 70	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
4	0.002	10 / 1008	BRUINS_UVC_RESPONSE_LATE
5	0.002	2 / 20	DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
6	0.003	6 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
7	0.005	2 / 30	WONG_IFNA2_RESISTANCE_DN
8	0.005	8 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
9	0.006	2 / 34	HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP
10	0.007	2 / 36	BURTON_ADIPOGENESIS_PEAK_AT_8HR
11	0.007	2 / 37	BROWNE_HCMV_INFECTION_8HR_DN
12	0.012	7 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
13	0.012	2 / 49	FAELT_B_CLL_WITH_VH3_21_DN
14	0.014	1 / 4	YANG_MUC2_TARGETS_COLON_3MO_DN
15	0.014	5 / 416	SHEN_SMARCA2_TARGETS_UP
16	0.014	5 / 421	MOOTHA_MITOCHONDRIA
17	0.016	5 / 435	GARY_CD5_TARGETS_UP
18	0.019	2 / 62	LIU_NASOPHARYNGEAL_CARCINOMA
19	0.020	4 / 303	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP
20	0.020	2 / 64	LEE_AGING_CEREBELLUM_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.3	1 / 94	HALLMARK_ANDROGEN_RESPONSE
3	0.4	1 / 137	HALLMARK_UV_RESPONSE_DN
4	0.4	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
5	0.4	1 / 146	HALLMARK_DNA_REPAIR
6	0.4	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
7	0.5	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	0.5	1 / 188	HALLMARK_ADIPOGENESIS
9	0.5	1 / 196	HALLMARK_G2M_CHECKPOINT
10	0.5	1 / 196	HALLMARK_MTORC1_SIGNALING
11	0.5	1 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	1.0	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	1.0	0 / 176	HALLMARK_HYPOXIA
14	1.0	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1.0	0 / 195	HALLMARK_MITOTIC_SPINDLE
16	1.0	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	1.0	0 / 53	HALLMARK_TGF_BETA_SIGNALING
18	1.0	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	1.0	0 / 140	HALLMARK_APOPTOSIS
20	1.0	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	5e−05	40 / 7592	HOPP_Active_promoter
2	4e−04	37 / 7209	HOPP_Weak_promoter
3	1e−03	29 / 5184	HOPP_Txn_transition
4	1e−03	35 / 6929	HOPP_Txn_elongation
5	6e−02	3 / 268	SPANG_IL21 UP
6	1e−01	7 / 1218	SPANG_BCR UP
7	1e−01	27 / 6564	HOPP_Strong_enhancer
8	2e−01	23 / 5538	HOPP_Weak_txn
9	2e−01	2 / 247	ZHANG_DLBCL mutated
10	3e−01	22 / 5693	HOPP_Weak_enhancer
11	5e−01	1 / 212	LENZ_Stromal signature 1
12	5e−01	4 / 1128	SPANG_BCR DN
13	6e−01	1 / 275	TARTE_Mature plasma cell signature
14	8e−01	1 / 410	SPANG_CD40 6hrs DN
15	8e−01	6 / 2211	HOPP_Repetitive
16	1e+00	5 / 2563	HOPP_Heterochrom
17	1e+00	1 / 2188	HOPP_Poised_promoter
18	1e+00	3 / 3396	HOPP_Repressed
19	1e+00	0 / 13	BENTINK_mBL UP
20	1e+00	0 / 12	BENTINK_mBL DOWN

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 71	structural constituent of ribosome
2	0.015	6 / 592	oxidoreductase activity
3	0.027	3 / 189	methyltransferase activity
4	0.033	3 / 205	ubiquitin protein ligase binding
5	0.040	1 / 12	channel activity
6	0.040	1 / 12	GTPase inhibitor activity
7	0.040	1 / 12	protein methyltransferase activity
8	0.044	1 / 13	FMN binding
9	0.044	1 / 13	myosin V binding
10	0.051	3 / 244	ubiquitin−protein transferase activity
11	0.057	1 / 17	RNA polymerase II core binding
12	0.057	1 / 17	sulfuric ester hydrolase activity
13	0.060	1 / 18	cyclin binding
14	0.067	1 / 20	WW domain binding
15	0.070	1 / 21	exonuclease activity
16	0.076	1 / 23	protein disulfide oxidoreductase activity
17	0.076	1 / 23	rRNA binding
18	0.076	1 / 23	tumor necrosis factor receptor binding
19	0.089	1 / 27	RNA polymerase II repressing transcription factor binding
20	0.092	1 / 28	cholesterol binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	2 / 17	hsa−miR−1298
2	0.003	3 / 82	hsa−miR−767−5p
3	0.004	4 / 195	hsa−miR−206
4	0.005	2 / 32	hsa−miR−631
5	0.008	3 / 120	hsa−miR−579
6	0.015	3 / 150	hsa−miR−338−3p
7	0.019	2 / 61	hsa−miR−514
8	0.027	3 / 189	hsa−miR−513a−3p
9	0.030	3 / 198	hsa−miR−448
10	0.040	1 / 12	hsa−miR−639
11	0.047	2 / 101	hsa−miR−613
12	0.048	2 / 102	hsa−miR−377
13	0.054	2 / 109	hsa−miR−499−5p
14	0.062	2 / 118	hsa−miR−509−3p
15	0.063	4 / 437	hsa−miR−19b
16	0.063	1 / 19	hsa−miR−563
17	0.065	2 / 121	hsa−miR−212
18	0.065	4 / 443	hsa−miR−19a
19	0.065	3 / 270	hsa−miR−30b
20	0.068	2 / 124	hsa−miR−223

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	14 / 2136	ICGC_GabpPcr2_targets
2	0.04	5 / 553	ICGC_RxraPcr1_targets
3	0.08	22 / 4879	ICGC_Pmlsc71910_targets
4	0.09	22 / 4909	ICGC_Stat5_targets
5	0.09	20 / 4385	ICGC_Atf2_targets
6	0.09	21 / 4689	ICGC_Taf1_targets
7	0.10	8 / 1400	ICGC_Myc_targets
8	0.10	7 / 1171	KIM_MYC targets
9	0.11	21 / 4774	ICGC_Foxm1_targets
10	0.12	21 / 4829	ICGC_Nficsc81335_targets
11	0.13	23 / 5408	ICGC_Pou2_targets
12	0.13	19 / 4314	ICGC_Ebfsc137065_targets
13	0.14	22 / 5200	ICGC_Mta3_targets
14	0.15	19 / 4414	ICGC_Bclaf101388_targets
15	0.18	17 / 3966	ICGC_Pu1_targets
16	0.18	16 / 3700	ICGC_Nfatc1_targets
17	0.19	9 / 1878	ICGC_Cebpbsc150_targets
18	0.19	10 / 2137	ICGC_SrfV0416101_targets
19	0.19	7 / 1383	ICGC_Six5_targets
20	0.21	17 / 4054	ICGC_Egr1_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	0.04	1 / 11	WIRTH_Cortex cerebri
2	0.31	1 / 107	WIRTH_Testis
3	0.34	2 / 350	WIRTH_Immune system
4	0.54	1 / 225	PALMER_Granulocytes signature up
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 / 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 / 350	WIRTH_Nervous System
14	1.00	0 / 11	WIRTH_Globus pallidus
15	1.00	0 / 14	WIRTH_Telencephalon
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 / 41	WIRTH_Homeostasis
20	1.00	0 / 46	WIRTH_Liver

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	6 / 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	