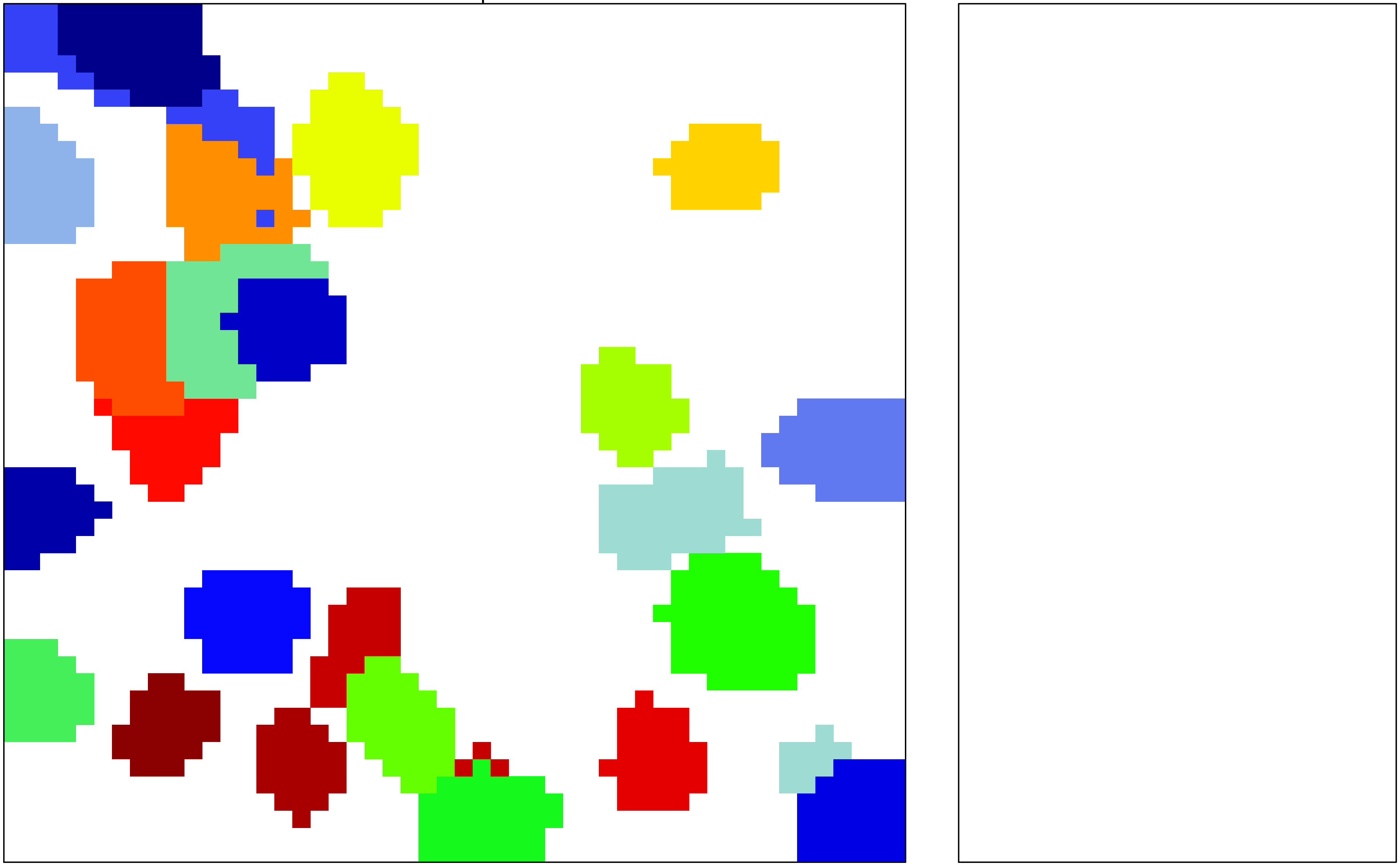
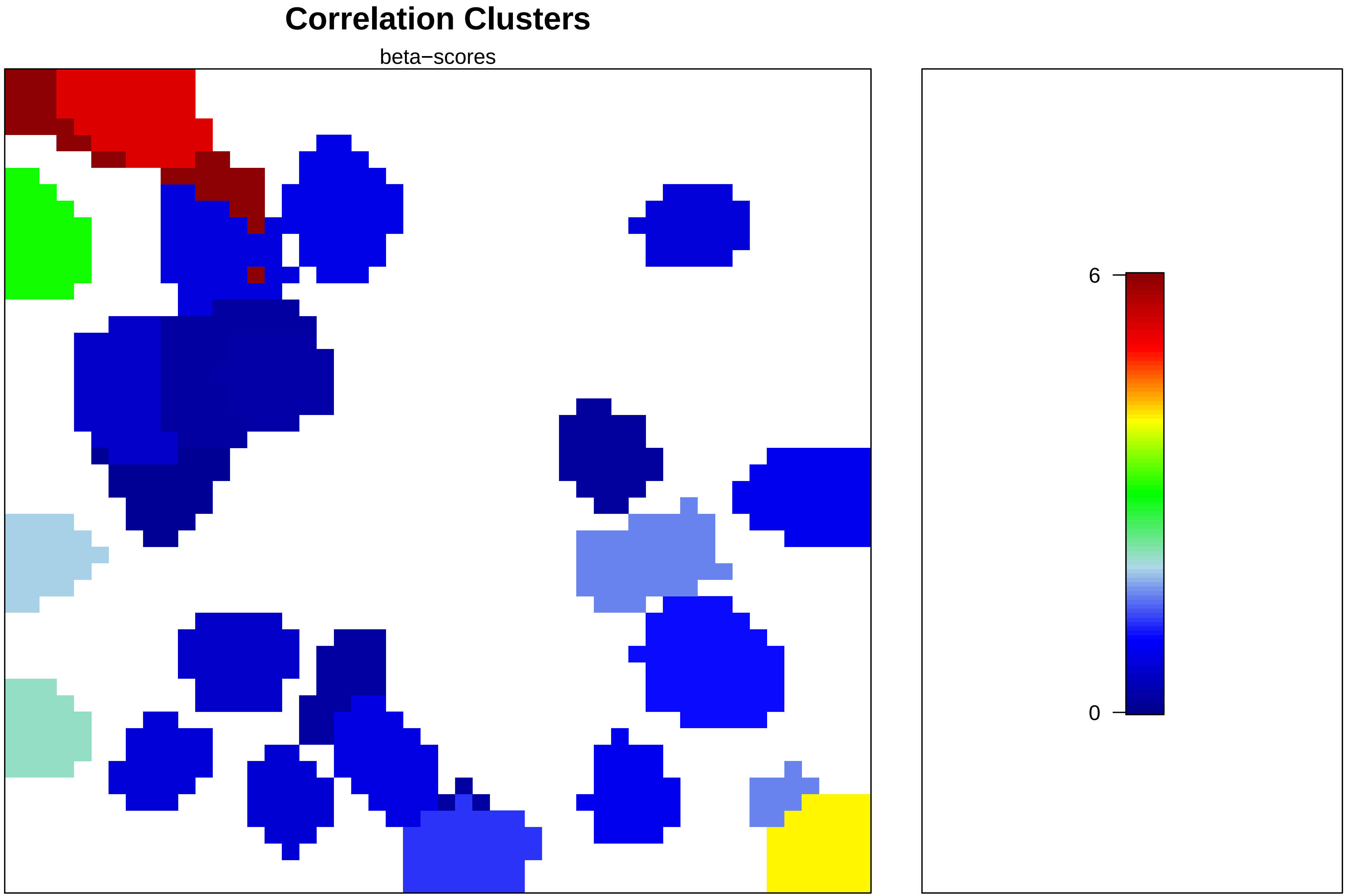
Correlation Clusters

landscape




Correlation Clusters
beta−scores
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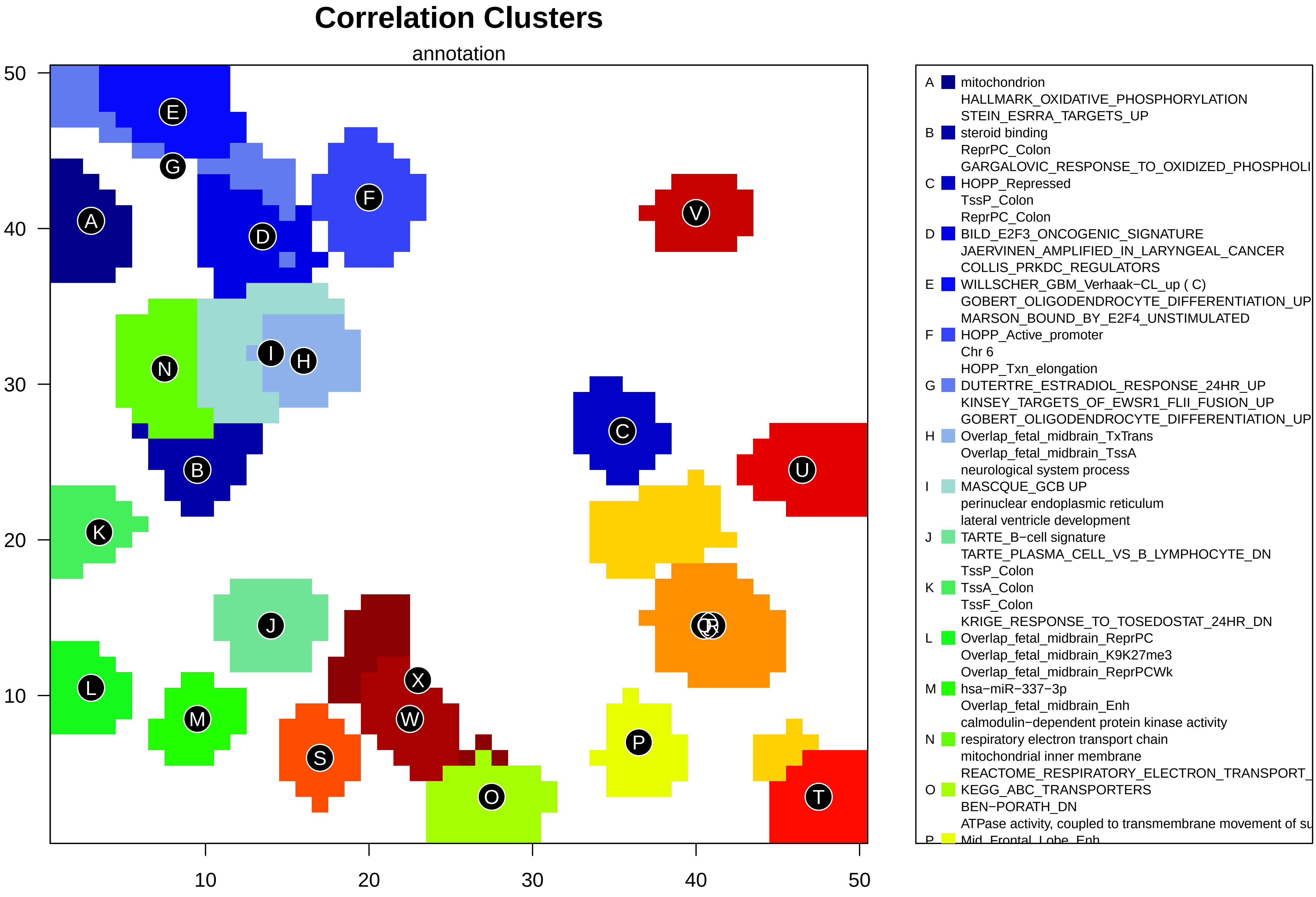
Correlation Clusters
annotation
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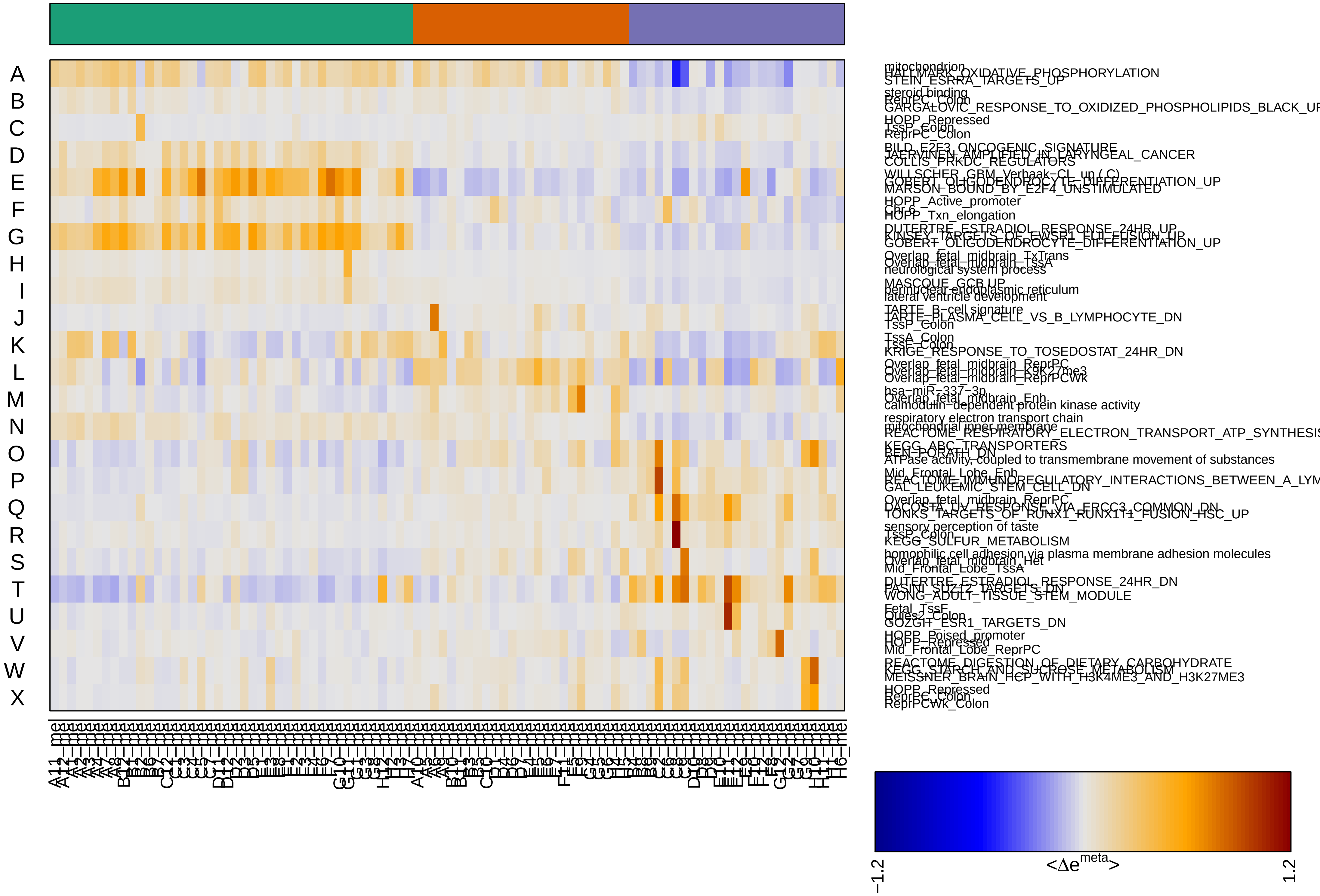
X
A mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
B steroid binding
ReprPC_Colon
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLI
C HOPP_Repressed
TssP_Colon
ReprPC_Colon
D BILD_E2F3_ONCOGENIC_SIGNATURE
JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
COLLIS_PRKDC_REGULATORS
E WILLSCHER_GBM_Verhaak−CL_up (C)
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
MARSON_BOUND_BY_E2F4_UNSTIMULATED
F HOPP_Active_promoter
Chr 6
HOPP_Txn_elongation
G DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
H Overlap_fetal_midbrain_TxTrans
Overlap_fetal_midbrain_TssA
neurological system process
I MASCQUE_GCB UP
perinuclear endoplasmic reticulum
lateral ventricle development
J TARTE_B−cell signature
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
TssP_Colon
K TssA_Colon
TssF_Colon
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
L Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_ReprPCWk
M hsa−miR−337−3p
Overlap_fetal_midbrain_Enh
calmodulin−dependent protein kinase activity
N respiratory electron transport chain
mitochondrial inner membrane
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_
O KEGG_ABC_TRANSPORTERS
BEN−PORATH_DN
ATPase activity, coupled to transmembrane movement of su
P Mid_Frontal_Lobe_Enh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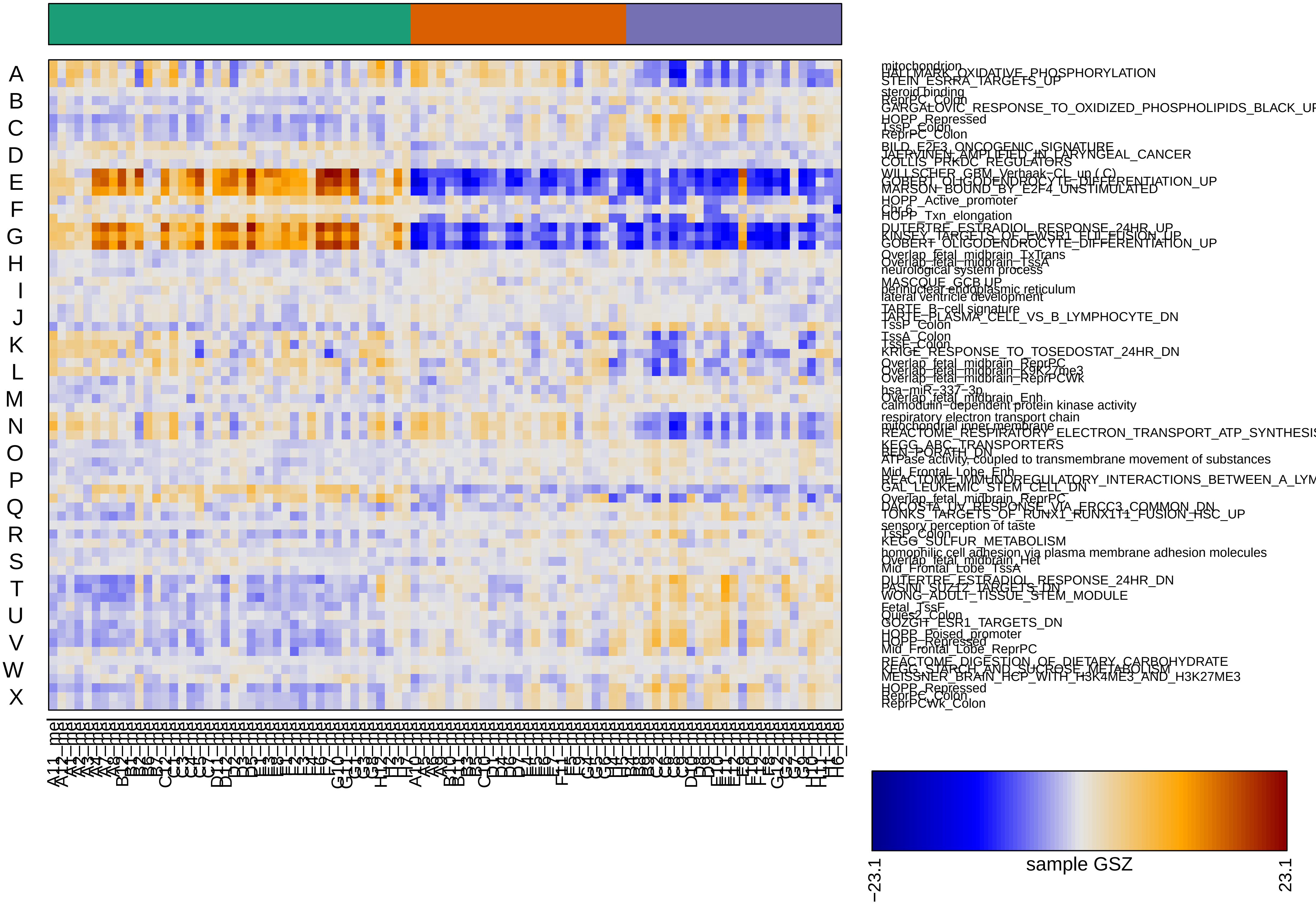
X
mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
steroid binding
ReprPC_Colon
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP
HOPP_Repressed
TssP_Colon
ReprPC_Colon
BILD_E2F3_ONCOGENIC_SIGNATURE
JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
COLLIS_PRKDC_REGULATORS
WILLSCHER_GBM_Verhaak−CL_up (C)
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
MARSON_BOUND_BY_E2F4_UNSTIMULATED
HOPP_Active_promoter
Chr 6
HOPP_Txn_elongation
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
Overlap_fetal_midbrain_TxTrans
Overlap_fetal_midbrain_TssA
neurological system process
MASCOUE_GCB UP
perinuclear endoplasmic reticulum
lateral ventricle development
TARTE_B−cell signature
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
TssP_Colon
TssA_Colon
TssF_Colon
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_ReprPCWk
hsa−miR−337−3p
Overlap_fetal_midbrain_Enh
calmodulin−dependent protein kinase activity
respiratory electron transport chain
mitochondrial inner membrane
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
KEGG_ABC_TRANSPORTERS
BEN_PORATH_DN
ATPase activity, coupled to transmembrane movement of substances
Mid_Frontal_Lobe_Enh
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
GAL_LEUKEMIC_STEM_CELL_DN
Overlap_fetal_midbrain_ReprPC
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
sensory perception of taste
TssP_Colon
KEGG_SULFUR_METABOLISM
homophilic cell adhesion via plasma membrane adhesion molecules
Overlap_fetal_midbrain_Het
Mid_Frontal_Lobe_TssA
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
PASINI_SUZ12_TARGETS_DN
WONG_ADULT_TISSUE_STEM_MODULE
Fetal_TssF
Quies2_Colon
GOZGIT_ESR1_TARGETS_DN
HOPP_Poised_promoter
HOPP_Repressed
Mid_Frontal_Lobe_ReprPC
REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
KEGG_STARCH_AND_SUCROSE_METABOLISM
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
HOPP_Repressed
ReprPC_Colon
ReprPCWk_Colon
−1.2
<Δe^{meta}>
1.2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mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
steroid binding
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WILLSCHER_GBM_Verhaak−CL_up (C)
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HOPP_Active_promoter
Chr 6
HOPP_Txn_elongation
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
Overlap_fetal_midbrain_TxTrans
Overlap_fetal_midbrain_TssA
neurological system process
MASCOUE_GCB_UP
perinuclear endoplasmic reticulum
lateral ventricle development
TARTE_B−cell signature
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
TssP_Colon
TssA_Colon
TssF_Colon
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_ReprPCWk
hsa−miR−337−3p
Overlap_fetal_midbrain_Enh
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Overlap_fetal_midbrain_ReprPC
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
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TssP_Colon
KEGG_SULFUR_METABOLISM
homophilic cell adhesion via plasma membrane adhesion molecules
Overlap_fetal_midbrain_Het
Mid_Frontal_Lobe_TssA
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
PASINI_SUZ12_TARGETS_DN
WONG_ADULT_TISSUE_STEM_MODULE
Fetal_TssF
Quies2_Colon
GOZGIT_ESR1_TARGETS_DN
HOPP_Poised_promoter
HOPP_Repressed
Mid_Frontal_Lobe_ReprPC
REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
KEGG_STARCH_AND_SUCROSE_METABOLISM
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
HOPP_Repressed
ReprPC_Colon
ReprPCWk_Colon
−23.1
sample GSZ
23.1

Correlation Clusters

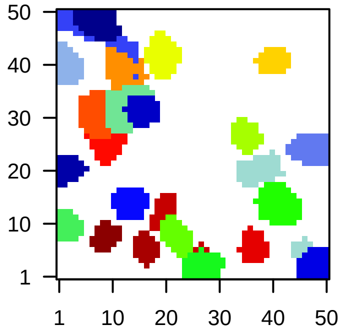
Spot Summary: A

metagenes = 33
genes = 404

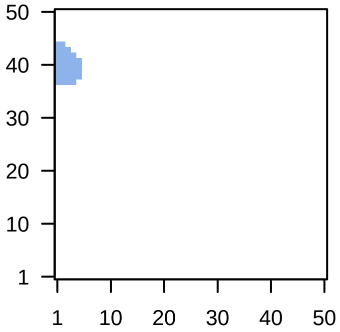
<r> metagenes = 0.94
<r> genes = 0.15
beta: r2= 3.06 / log p= −Inf

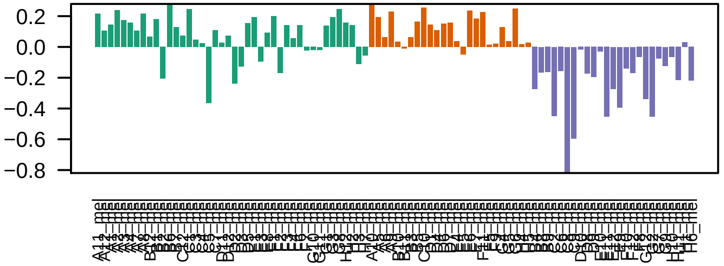
samples with spot = 23 (25 %)
MSC1 : 13 (31 %)
MSC2 : 10 (40 %)

Overview Map



Spot





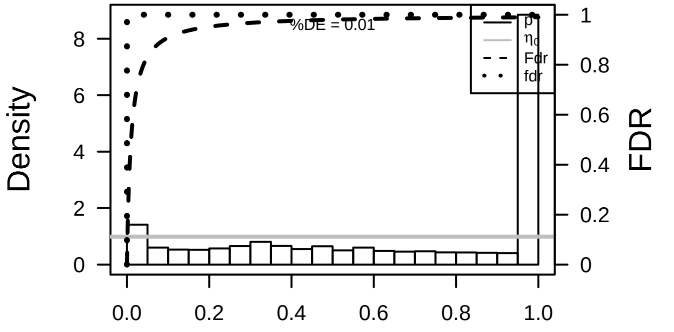
Spot Genelist

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	ZNF30	1.71	−0.15	0.26	ZNF30	zinc finger protein 30 [Source:HGNC Symbol;Acc:HGNC:130
4	GAPDHS	1.71	−1.17	0.59	GAPDHS	glyceraldehyde−3−phosphate dehydrogenase, spermatogeni
5	ST6GALNAC	1.69	−0.39	0.32	ST6GALNAC3	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
6	TRMT1	1.65	−0.71	0.36	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:H
7	NMRK2	1.63	−1.2	0.71	NMRK2	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
8	NT5DC1	1.63	−0.93	0.28	NT5DC1	5'−nucleotidase domain containing 1 [Source:HGNC Symbol;
9	SEPSECS	1.63	−0.31	0.32	SEPSECS	Sep (O−phosphoserine) tRNA:Sec (selenocysteine) tRNA sy
10	WIPF3	1.62	−0.29	0.33	WIPF3	WAS/WASL interacting protein family, member 3 [Source:HG
11	ANO2	1.61	−0.48	0.34	ANO2	anoctamin 2, calcium activated chloride channel [Source:HG
12	CPN1	1.59	−0.23	0.33	CPN1	carboxypeptidase N, polypeptide 1 [Source:HGNC Symbol;A
13	CAPG	1.58	−0.72	0.39	CAPG	capping protein (actin filament), gelsolin−like [Source:HGNC
14	NPAS2	1.58	−0.27	0.28	NPAS2	neuronal PAS domain protein 2 [Source:HGNC Symbol;Acc:
15	TM2D2	1.57	−1.01	0.27	TM2D2	TM2 domain containing 2 [Source:HGNC Symbol;Acc:HGNC
16	MAPK10	1.57	−0.69	0.44	MAPK10	mitogen−activated protein kinase 10 [Source:HGNC Symbol;
17	SNAP29	1.56	−0.44	0.3	SNAP29	synaptosomal−associated protein, 29kDa [Source:HGNC Sy
18	C1orf21	1.56	−0.91	0.34	C1orf21	chromosome 1 open reading frame 21 [Source:HGNC Symb
19	PEX2	1.56	−0.83	0.18	PEX2	peroxisomal biogenesis factor 2 [Source:HGNC Symbol;Acc:
20	HTRA2	1.56	−0.39	0.28	HTRA2	HtrA serine peptidase 2 [Source:HGNC Symbol;Acc:HGNC:1

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−22	107 / 1468	CC	mitochondrion
2	8e−22	38 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	5e−19	47 / 368	GSE	STEIN_ESRRA_TARGETS_UP
4	3e−18	48 / 401	CC	mitochondrial inner membrane
5	2e−17	47 / 405	GSE	MOOTHA_HUMAN_MITODB_6_2002
6	2e−16	276 / 7203	Colon	TssF_Colon
7	2e−16	51 / 500	GSE	STEIN_ESRRA_TARGETS
8	1e−14	44 / 421	GSE	MOOTHA_MITOCHONDRIA
9	5e−14	60 / 756	GSE	WEI_MYCN_TARGETS_WITH_E_BOX
10	9e−14	294 / 8205	CC	cytoplasm
11	2e−13	324 / 9482	Colon	TssA_Colon
12	2e−13	41 / 398	GSE	MOOTHA_PGC
13	1e−12	44 / 478	GSE	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	2e−12	73 / 1126	GSE	BLALOCK_ALZHEIMERS_DISEASE_DN
15	5e−11	93 / 1730	BP	small molecule metabolic process
16	2e−10	60 / 925	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	4e−10	303 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
18	5e−10	303 / 9027	Colon	Tx_Colon
19	1e−09	14 / 63	Glio	Stuehler_Proteins_up_in_STS
20	1e−09	8 / 15	GSE	MOOTHA_TCA
21	2e−09	10 / 28	BP	tricarboxylic acid cycle
22	2e−09	10 / 28	GSE	KEGG_CITRATE_CYCLE_TCA_CYCLE
23	3e−09	22 / 177	GSE	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
24	3e−09	31 / 338	GSE	DAIRKEE_TERT_TARGETS_UP
25	5e−09	30 / 325	GSE	PENG_GLUTAMINE_DEPRIVATION_DN
26	8e−09	29 / 312	GSE	WONG_EMBRYONIC_STEM_CELL_CORE
27	1e−08	11 / 42	Lymp	CARO_OxPhos_in_DLBCL_UP
28	1e−08	46 / 685	GSE	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
29	2e−08	8 / 19	GSE	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE
30	2e−08	23 / 213	GSE	WONG_MITOCHONDRIA_GENE_MODULE
31	2e−08	24 / 233	GSE	PENG_RAPAMYCIN_RESPONSE_DN
32	3e−08	36 / 475	GSE	ONKEN_UVEAL_MELANOMA_DN
33	3e−08	242 / 6929	Lymp	HOPP_Txn_elongation
34	6e−08	28 / 322	BP	mitochondrion organization
35	8e−08	38 / 541	BP	oxidation−reduction process
36	1e−07	50 / 831	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
37	2e−07	20 / 188	HM	HALLMARK_ADIPOGENESIS
38	2e−07	68 / 1326	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
39	2e−07	19 / 171	GSE	BURTON_ADIPOGENESIS_6
40	3e−07	10 / 45	MF	NAD binding

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	4 / 111	HORVATH_aging_genes meth UP
2	0.5	3 / 100	HORVATH_aging_genes meth DOWN
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	4 / 40	ZHANG_MM up
2	0.03	2 / 15	RHODES_CANCER_META_SIGNATURE
3	0.03	2 / 10	GENTLES_modul5
4	0.06	9 / 180	SPANG_LPS−index2
5	0.06	2 / 15	GENTLES_modul1
6	0.06	2 / 15	GENTLES_modul10
7	0.07	2 / 16	GENTLES_modul2
8	0.12	18 / 489	Lembcke_Normal vs Adenoma
9	0.27	1 / 14	LIU_COMMON_CANCER_GENES
10	0.28	1 / 12	LIU_BREAST_CANCER
11	0.29	10 / 298	SPANG_BCL6−index2
12	0.30	3 / 70	SHAUGHNESSY_MM high risk
13	0.30	1 / 13	BEN−PORATH_UP
14	0.30	1 / 13	GENTLES_modul12
15	0.34	1 / 15	GENTLES_modul11
16	0.36	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	0.36	1 / 16	WOLFER_overlap genes
18	0.36	1 / 16	GENTLES_modul7
19	0.37	2 / 47	PanCan_DNARepair_geneset_nanostring
20	0.38	2 / 48	KUIPER_MM poor survival

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−16	276 / 7203	TssF_Colon
2	2e−13	324 / 9482	TssA_Colon
3	5e−10	303 / 9027	Tx_Colon
4	2e−06	278 / 8580	TxWk_Colon
5	2e−04	195 / 5880	TssD2_Colon
6	3e−04	37 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
7	4e−04	33 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	5e−04	36 / 739	TxEnhG2_Colon
9	7e−04	102 / 2798	TxEnhG1_Colon
10	2e−03	168 / 5155	EnhWk1_Colon
11	3e−03	288 / 9653	Enh_Colon
12	7e−03	253 / 8415	Quies3_Colon
13	1e−02	300 / 10290	TssWk_Colon
14	7e−02	85 / 2698	EnhA_Colon
15	1e−01	21 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
16	1e−01	15 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
17	2e−01	1 / 8	Boland_CRC−MSI−TGC
18	2e−01	1 / 8	Marisa_CRC−C6
19	2e−01	3 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
20	2e−01	2 / 33	Marisa_CRC−cluster−e

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−19	47 / 368	STEIN_ESRRA_TARGETS_UP
2	2e−17	47 / 405	MOOTHA_HUMAN_MITODB_6_2002
3	2e−16	51 / 500	STEIN_ESRRA_TARGETS
4	1e−14	44 / 421	MOOTHA_MITOCHONDRIA
5	5e−14	60 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
6	2e−13	41 / 398	MOOTHA_PGC
7	1e−12	44 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
8	2e−12	73 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
9	2e−10	60 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
10	1e−09	8 / 15	MOOTHA_TCA
11	2e−09	10 / 28	KEGG_CITRATE_CYCLE_TCA_CYCLE
12	3e−09	22 / 177	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
13	3e−09	31 / 338	DAIRKEE_TERT_TARGETS_UP
14	5e−09	30 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
15	8e−09	29 / 312	WONG_EMBRYONIC_STEM_CELL_CORE
16	1e−08	46 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
17	2e−08	8 / 19	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE
18	2e−08	23 / 213	WONG_MITOCHONDRIA_GENE_MODULE
19	2e−08	24 / 233	PENG_RAPAMYCIN_RESPONSE_DN
20	3e−08	36 / 475	ONKEN_UVEAL_MELANOMA_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−08	11 / 42	CARO_OxPhos_in_DLBCL_UP
2	3e−08	242 / 6929	HOPP_Txn_elongation
3	5e−06	250 / 7592	HOPP_Active_promoter
4	2e−05	181 / 5184	HOPP_Txn_transition
5	4e−05	235 / 7209	HOPP_Weak_promoter
6	2e−04	20 / 294	TARTE_Plasmablast signature
7	1e−03	209 / 6564	HOPP_Strong_enhancer
8	2e−03	8 / 82	ROSOLOWSKI_green UP
9	3e−03	9 / 109	ROSOLOWSKI_green total
10	9e−03	20 / 410	SPANG_CD40 6hrs DN
11	4e−02	13 / 275	TARTE_Mature plasma cell signature
12	7e−02	5 / 80	Aukema_BCL2 DN_BCL6 UP
13	8e−02	1 / 3	WRIGHT_custom GCB−DLBCL UP
14	8e−02	4 / 61	SPANG_LPS 6hrs DN
15	2e−01	159 / 5538	HOPP_Weak_txn
16	2e−01	1 / 8	MASCQUE_GCB UP
17	2e−01	1 / 8	MASCQUE_ABC UP
18	2e−01	1 / 8	Subero_B−CLL_hypo_meth
19	2e−01	1 / 10	Shaknovich_ABC_hypo_meth
20	3e−01	2 / 40	Subero_mBL_hyper_meth

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	

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	PALMER_CD8+ T−Cell signature up
2	0.3	4 / 95	WIRTH_Muscle
3	0.3	1 / 11	WIRTH_Cortex cerebri
4	0.3	7 / 194	PALMER_B−Cell signature up
5	0.3	1 / 13	WIRTH_B−cells
6	0.3	1 / 13	WIRTH_Thyroid gland
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_Nervous System
10	0.6	6 / 225	PALMER_Granulocytes signature up
11	0.6	1 / 32	WIRTH_Pancreas
12	0.9	6 / 350	WIRTH_Immune system
13	0.9	1 / 107	WIRTH_Testis
14	1.0	0 / 11	WIRTH_Sec. lymphoid organs
15	1.0	0 / 11	WIRTH_Prim. lymphoid organs
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	5e−11	93 / 1730	small molecule metabolic process
2	2e−09	10 / 28	tricarboxylic acid cycle
3	6e−08	28 / 322	mitochondrion organization
4	8e−08	38 / 541	oxidation−reduction process
5	4e−07	26 / 311	generation of precursor metabolites and energy
6	4e−06	6 / 17	mitochondrial respiratory chain complex I assembly
7	4e−06	15 / 135	cellular metabolic process
8	5e−06	8 / 37	gluconeogenesis
9	2e−05	5 / 13	melanin biosynthetic process
10	3e−05	8 / 47	protein targeting to mitochondrion
11	7e−05	19 / 255	cellular amino acid metabolic process
12	7e−05	20 / 277	translation
13	9e−05	5 / 18	melanocyte differentiation
14	1e−04	11 / 104	glucose metabolic process
15	3e−04	9 / 80	rRNA processing
16	4e−04	8 / 67	pigmentation
17	7e−04	12 / 147	tRNA metabolic process
18	8e−04	18 / 285	organelle organization
19	1e−03	52 / 1237	metabolic process
20	1e−03	4 / 18	2−oxoglutarate metabolic process

CC

Rank	p−value	#in/all	Geneset
1	3e−22	107 / 1468	mitochondrion
2	3e−18	48 / 401	mitochondrial inner membrane
3	9e−14	294 / 8205	cytoplasm
4	3e−07	331 / 10605	intracellular
5	4e−07	316 / 9988	organelle
6	4e−07	97 / 2193	extracellular exosome
7	1e−05	20 / 246	mitochondrial matrix
8	2e−05	101 / 2507	cytosol
9	2e−05	14 / 135	myelin sheath
10	5e−05	11 / 94	melanosome
11	4e−04	24 / 412	lysosome
12	4e−04	346 / 11774	cell
13	4e−04	5 / 24	mitochondrial ribosome
14	7e−04	25 / 456	vacuole
15	1e−03	8 / 80	mitochondrial membrane
16	2e−03	7 / 63	mitochondrial intermembrane space
17	2e−03	10 / 120	mitochondrial outer membrane
18	2e−03	109 / 3132	extracellular region
19	3e−03	10 / 128	ribosome
20	1e−02	31 / 745	cytoplasmic membrane−bounded vesicle

Disease

Rank	p−value	#in/all	Geneset
1	0.09	17 / 435	GUDJ_psoriasis up
2	0.42	1 / 20	BCHETNIA_EBM−DM up
3	0.81	6 / 294	GUDJ_psoriasis down
4	1.00	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	8e−22	38 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	2e−07	20 / 188	HALLMARK_ADIPOGENESIS
3	3e−07	11 / 57	HALLMARK_MYC_TARGETS_V2
4	1e−06	16 / 141	HALLMARK_FATTY_ACID_METABOLISM
5	9e−05	16 / 196	HALLMARK_MTORC1_SIGNALING
6	1e−02	11 / 183	HALLMARK_GLYCOLYSIS
7	1e−02	7 / 91	HALLMARK_PROTEIN_SECRETION
8	1e−02	10 / 162	HALLMARK_COMPLEMENT
9	1e−02	11 / 188	HALLMARK_MYC_TARGETS_V1
10	4e−02	9 / 169	HALLMARK_XENOBIOTIC_METABOLISM
11	5e−02	9 / 174	HALLMARK_HEME_METABOLISM
12	5e−02	5 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	1e−01	7 / 146	HALLMARK_UV_RESPONSE_UP
14	1e−01	5 / 93	HALLMARK_PEROXISOME
15	1e−01	5 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
16	2e−01	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
17	3e−01	6 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	4e−01	5 / 146	HALLMARK_DNA_REPAIR
19	4e−01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
20	4e−01	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE

MF

Rank	p−value	#in/all	Geneset
1	3e−07	10 / 45	NAD binding
2	1e−05	35 / 592	oxidoreductase activity
3	4e−05	62 / 1365	RNA binding
4	6e−04	6 / 39	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
5	8e−04	5 / 28	hydrogen ion transmembrane transporter activity
6	1e−03	22 / 394	catalytic activity
7	2e−03	43 / 1007	poly(A) RNA binding
8	5e−03	3 / 13	NAD+ binding
9	9e−03	3 / 16	nucleoside diphosphate kinase activity
10	1e−02	3 / 17	aspartic−type endopeptidase activity
11	1e−02	3 / 17	fatty−acyl−CoA binding
12	1e−02	3 / 17	sialyltransferase activity
13	1e−02	6 / 71	structural constituent of ribosome
14	1e−02	3 / 19	3'−5'−exoribonuclease activity
15	1e−02	4 / 35	aminoacyl−tRNA ligase activity
16	1e−02	29 / 695	transmembrane transporter activity
17	2e−02	4 / 36	tRNA binding
18	2e−02	4 / 37	coenzyme binding
19	2e−02	371 / 13179	molecular_function
20	2e−02	6 / 79	protein transporter activity

TF

Rank	p−value	#in/all	Geneset
1	3e−07	70 / 1400	ICGC_Myc_targets
2	1e−05	168 / 4689	ICGC_Taf1_targets
3	2e−05	144 / 3924	ICGC_Zeb1_targets
4	2e−05	74 / 1701	HEBENSTREIT_high expression TF
5	4e−05	171 / 4909	ICGC_Stat5_targets
6	6e−05	63 / 1418	ICGC_Ets1_targets
7	7e−05	145 / 4054	ICGC_Egr1_targets
8	2e−04	195 / 5890	ICGC_Elf1_targets
9	2e−04	176 / 5219	ICGC_Tcf3_targets
10	2e−04	161 / 4706	ICGC_Sp1_targets
11	3e−04	57 / 1314	ICGC_Usf1_targets
12	4e−04	151 / 4414	ICGC_Bclaf101388_targets
13	6e−04	181 / 5495	ICGC_Yy1_targets
14	6e−04	177 / 5355	ICGC_Pol2_targets
15	7e−04	163 / 4879	ICGC_Pmlsc71910_targets
16	9e−04	155 / 4617	ICGC_Tcf12_targets
17	1e−03	176 / 5408	ICGC_Pou2_targets
18	1e−03	175 / 5374	ICGC_Pax5_targets
19	2e−03	157 / 4774	ICGC_Foxm1_targets
20	2e−03	32 / 690	ICGC_Atf3_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	41 / 1115	LU_BPDE 1h DN
2	0.97	85 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	4e−10	303 / 9013	Overlap_fetal_midbrain_K9K27me3
2	5e−06	295 / 9330	Overlap_fetal_midbrain_ReprPC
3	2e−05	118 / 3081	Mid_Frontal_Lobe_ZNF
4	3e−04	291 / 9528	Overlap_fetal_midbrain_Quies
5	5e−04	37 / 765	Mid_Frontal_Lobe_Het
6	9e−03	185 / 5940	Overlap_fetal_midbrain_HetRpts
7	2e−02	49 / 1333	Fetal_ReprPCWk
8	1e−01	77 / 2462	Mid_Frontal_Lobe_HetRpts
9	1e−01	29 / 831	Fetal_HetRpts
10	2e−01	12 / 349	Fetal_ZNF
11	2e−01	55 / 1845	Fetal_Quies
12	4e−01	5 / 156	Mid_Frontal_Lobe_TssA
13	4e−01	247 / 9020	Overlap_fetal_midbrain_ReprPCWk
14	6e−01	2 / 69	Overlap_fetal_midbrain_Tx
15	6e−01	33 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	6e−01	4 / 163	Fetal_ReprPC
17	7e−01	19 / 769	Overlap_fetal_midbrain_ZNF
18	7e−01	77 / 2972	Mid_Frontal_Lobe_ReprPC
19	8e−01	27 / 1122	Fetal_K9K27me3
20	8e−01	6 / 304	Fetal_Het

Chr

Rank	p−value	#in/all	Geneset
1	0.008	40 / 993	Chr 2
2	0.042	23 / 576	Chr 9
3	0.047	22 / 552	Chr 10
4	0.139	17 / 469	Chr 8
5	0.148	9 / 221	Chr 18
6	0.155	26 / 775	Chr 12
7	0.192	33 / 1037	Chr 19
8	0.201	12 / 335	Chr 22
9	0.228	6 / 151	Chr 21
10	0.346	25 / 840	Chr 17
11	0.384	14 / 465	Chr 15
12	0.524	19 / 696	Chr 5
13	0.596	17 / 649	Chr 16
14	0.639	14 / 551	Chr X
15	0.757	9 / 398	Chr 20
16	0.828	18 / 801	Chr 11
17	0.841	15 / 687	Chr 6
18	0.843	5 / 262	Chr 13
19	0.899	14 / 689	Chr 7
20	0.919	17 / 838	Chr 3

Glio

Rank	p−value	#in/all	Geneset
1	1e−09	14 / 63	Stuehler_Proteins_up_in_STS
2	5e−03	36 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
3	3e−02	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
4	4e−02	16 / 365	Down_b
5	5e−02	4 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	6e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
7	8e−02	3 / 38	OL vs. OPC
8	1e−01	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
9	1e−01	5 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
10	1e−01	7 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	2e−01	2 / 26	Christensen_hypomethylated_in_ependymoma
12	2e−01	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
13	2e−01	1 / 8	Colman_survival_robust
14	2e−01	2 / 32	Donson−innate immunity−associated with LTS in HGA
15	2e−01	1 / 9	VERHAAK_Brain
16	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
17	2e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
18	2e−01	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
19	2e−01	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
20	3e−01	1 / 11	Christensen_hypermethylated_in_ependymoma

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
2	0.2	3 / 62	DUMEAUX_Smoking enriched genes
3	0.3	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.4	1 / 18	DUMEAUX_High bmi enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
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 / 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	0.02	5 / 56	hsa−miR−892a
2	0.03	2 / 11	hsa−miR−604
3	0.04	5 / 68	hsa−miR−361−3p
4	0.07	4 / 58	hsa−miR−409−5p
5	0.07	3 / 36	hsa−miR−518e
6	0.08	3 / 37	hsa−miR−760
7	0.09	2 / 19	hsa−miR−645
8	0.09	5 / 89	hsa−miR−608
9	0.10	4 / 65	hsa−miR−518c*
10	0.11	5 / 94	hsa−miR−219−2−3p
11	0.12	3 / 44	hsa−miR−658
12	0.12	5 / 96	hsa−miR−513b
13	0.14	3 / 48	hsa−miR−524−3p
14	0.14	5 / 102	hsa−miR−224
15	0.15	11 / 284	hsa−miR−503
16	0.15	1 / 6	hsa−miR−937
17	0.15	1 / 6	hsa−miR−886−5p
18	0.15	6 / 133	hsa−miR−198
19	0.16	6 / 134	hsa−miR−488
20	0.16	3 / 51	hsa−miR−508−5p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 23	VAQUERIZAS_Adrenal cortex
2	0.07	2 / 16	VAQUERIZAS_Pancreas
3	0.07	2 / 16	VAQUERIZAS_Adrenal gland
4	0.07	2 / 16	VAQUERIZAS_Salivary gland
5	0.13	2 / 23	VAQUERIZAS_Trachea
6	0.18	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
7	0.22	1 / 9	VAQUERIZAS_Kidney
8	0.26	1 / 11	VAQUERIZAS_Fetal liver
9	0.27	2 / 37	VAQUERIZAS_Thymus
10	0.28	2 / 38	VAQUERIZAS_Whole brain
11	0.37	1 / 17	VAQUERIZAS_Pituitary
12	0.47	1 / 23	VAQUERIZAS_Spinal cord
13	0.51	1 / 26	VAQUERIZAS_Liver
14	0.52	1 / 27	VAQUERIZAS_Lymph node
15	0.55	4 / 143	VAQUERIZAS_General
16	0.55	1 / 29	VAQUERIZAS_Smooth muscle
17	0.55	1 / 29	VAQUERIZAS_Fetal lung
18	0.63	1 / 36	VAQUERIZAS_Fetal brain
19	0.71	1 / 45	VAQUERIZAS_Uterus
20	0.80	1 / 58	VAQUERIZAS_Lung

Correlation Clusters

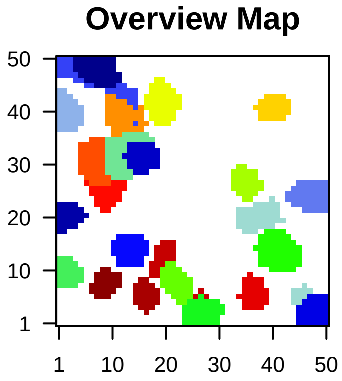
Spot Summary: B

\# metagenes = 28
\# genes = 19

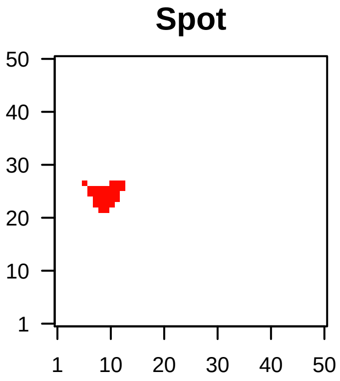
<r> metagenes = 0.94
<r> genes = 0.42
beta: r2= 0.1 / log p= −2.76

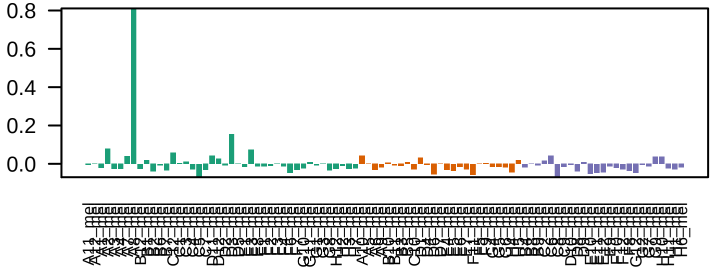
\# samples with spot = 1 (1.1 %)
MSC1 : 1 (2.4 %)

Overview Map



Spot





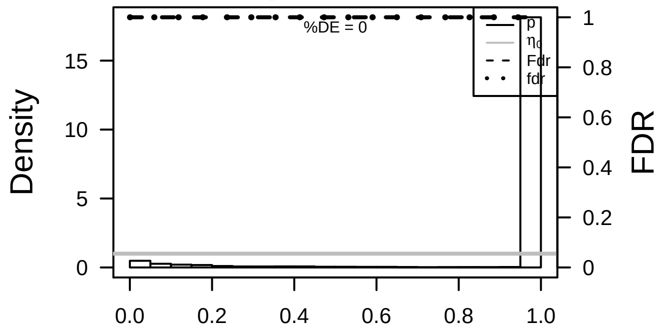
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CD247	1.67	−0.03	0.44	CD247	CD247 molecule [Source:HGNC Symbol;Acc:HGNC:1677]
2	DNAH11	1.55	−0.08	0.34	DNAH11	dynein, axonemal, heavy chain 11 [Source:HGNC Symbol;Ac
3	CDC42EP2	1.34	−0.07	0.3	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2 [Source:HGN
4	ZNF713	1.33	−0.05	0.18	ZNF713	zinc finger protein 713 [Source:HGNC Symbol;Acc:HGNC:22
5	PVRL1	1.3	−0.05	0.27	PVRL1	poliovirus receptor−related 1 (herpesvirus entry mediator C) [
6	CARNS1	1.3	−0.03	0.42	CARNS1	carnosine synthase 1 [Source:HGNC Symbol;Acc:HGNC:292
7	ST8SIA5	1.15	−0.01	0.43	ST8SIA5	ST8 alpha−N−acetyl−neuraminide alpha−2,8−sialyltransferas
8	PAQR5	1.13	−0.04	0.34	PAQR5	progestin and adipoQ receptor family member V [Source:HGN
9	ESR2	1.13	−0.05	0.42	ESR2	estrogen receptor 2 (ER beta) [Source:HGNC Symbol;Acc:H
10	SYT8	0.99	−0.01	0.45	SYT8	synaptotagmin VIII [Source:HGNC Symbol;Acc:HGNC:19264
11	CHST13	0.94	−0.02	0.45	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13 [Source:HGN
12	GCM1	0.91	−0.02	0.26	GCM1	glial cells missing homolog 1 (Drosophila) [Source:HGNC Sy
13	CTD−2006C1	0.77	−0.02	0.44		
14	PM20D1	0.77	−0.03	0.34	PM20D1	peptidase M20 domain containing 1 [Source:HGNC Symbol;
15	MIP	0.59	−0.04	0.4	MIP	major intrinsic protein of lens fiber [Source:HGNC Symbol;Ac
16	EIF1	0.43	−0.43	0.19	EIF1	eukaryotic translation initiation factor 1 [Source:HGNC Symb
17	IKZF1	0.37	0	0.42	IKZF1	IKAROS family zinc finger 1 (Ikaros) [Source:HGNC Symbol;
18	SET	0.35	−0.42	0.31	SET	SET nuclear proto−oncogene [Source:HGNC Symbol;Acc:HG
19	HNRNPC	0.35	−0.55	0.31	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2) [Source:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	2 / 17	MF	steroid binding
2	4e−04	9 / 2142	Colon	ReprPC_Colon
3	7e−04	2 / 33	GSE	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_
4	9e−04	8 / 1889	Colon	ReprPCWk_Colon
5	2e−03	2 / 53	BP	retina development in camera−type eye
6	2e−03	6 / 1199	GSE	PUJANA_ATM_PCC_NETWORK
7	2e−03	2 / 58	GSE	PID_ERA_GENOMIC_PATHWAY
8	3e−03	10 / 3396	Lymp	HOPP_Repressed
9	3e−03	5 / 892	GSE	YOSHIMURA_MAPK8_TARGETS_UP
10	4e−03	2 / 74	GSE	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
11	4e−03	2 / 75	miRN	hsa−miR−939
12	5e−03	1 / 4	GSE	BIOCARTA_TCAPOPTOSIS_PATHWAY
13	6e−03	1 / 5	GSE	BIOCARTA_TCRA_PATHWAY
14	6e−03	1 / 5	GSE	BIOCARTA_NO2IL12_PATHWAY
15	6e−03	3 / 316	GSE	HSIAO_HOUSEKEEPING_GENES
16	7e−03	1 / 6	GSE	BIOCARTA_CTL_PATHWAY
17	7e−03	1 / 6	GSE	BIOCARTA_IL17_PATHWAY
18	7e−03	1 / 6	GSE	BIOCARTA_TCYTOTOXIC_PATHWAY
19	8e−03	3 / 350	Tissu	WIRTH_Immune system
20	8e−03	1 / 7	GSE	BIOCARTA_THELPER_PATHWAY
21	8e−03	1 / 7	GSE	REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_S
22	8e−03	1 / 7	GSE	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
23	8e−03	1 / 7	GSE	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
24	8e−03	1 / 7	GSE	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
25	9e−03	8 / 2698	Colon	EnhA_Colon
26	1e−02	1 / 8	GSE	BIOCARTA_SET_PATHWAY
27	1e−02	7 / 2159	Colon	TssP_Colon
28	1e−02	9 / 3383	Colon	EnhWk2_Colon
29	1e−02	7 / 2185	Brain	Fetal_TssA
30	1e−02	7 / 2188	Lymp	HOPP_Poised_promoter
31	1e−02	1 / 9	GSE	BIOCARTA_CTLA4_PATHWAY
32	1e−02	1 / 9	GSE	MATZUK_PREOVULATORY_FOLLICLE
33	1e−02	2 / 132	GSE	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP
34	1e−02	2 / 132	GSE	SENGUPTA_EBNA1_ANTICORRELATED
35	1e−02	1 / 10	BP	lymph node development
36	1e−02	1 / 10	CC	pericentric heterochromatin
37	1e−02	1 / 10	CC	viral nucleocapsid
38	1e−02	1 / 10	Lymp	Shaknovich_ABC_hypo_meth
39	1e−02	1 / 10	GSE	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS
40	1e−02	5 / 1207	Brain	Overlap_fetal_midbrain_TssF

p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	0.002	2 / 53	retina development in camera−type eye
2	0.012	1 / 10	lymph node development
3	0.013	1 / 11	3'−UTR−mediated mRNA stabilization
4	0.013	1 / 11	acrosome reaction
5	0.013	1 / 11	positive regulation of B cell differentiation
6	0.014	1 / 12	iron ion transport
7	0.014	1 / 12	lens morphogenesis in camera−type eye
8	0.016	1 / 13	natural killer cell differentiation
9	0.016	1 / 13	positive regulation of protein complex assembly
10	0.017	1 / 14	nucleosome disassembly
11	0.017	9 / 3644	biosynthetic process
12	0.019	1 / 16	cilium movement
13	0.020	1 / 17	intracellular estrogen receptor signaling pathway
14	0.020	1 / 17	sialylation
15	0.020	1 / 17	synaptic vesicle endocytosis
16	0.022	1 / 18	camera−type eye morphogenesis
17	0.024	1 / 20	calcium ion−dependent exocytosis of neurotransmitter
18	0.024	1 / 20	oogenesis
19	0.026	1 / 22	regulation of defense response to virus by virus
20	0.028	1 / 23	ATP−dependent chromatin remodeling

Brain

Rank	p−value	#in/all	Geneset
1	0.01	7 / 2185	Fetal_TssA
2	0.01	5 / 1207	Overlap_fetal_midbrain_TssF
3	0.02	4 / 862	Overlap_fetal_midbrain_TxTrans
4	0.02	6 / 1949	Fetal_TssF
5	0.05	7 / 2972	Mid_Frontal_Lobe_ReprPC
6	0.07	3 / 812	Mid_Frontal_Lobe_TssP
7	0.14	2 / 534	Mid_Frontal_Lobe_EnhG
8	0.15	2 / 574	Overlap_fetal_midbrain_TssP
9	0.18	1 / 158	Overlap_fetal_midbrain_Het
10	0.19	4 / 1907	Fetal_TxTrans
11	0.19	2 / 668	Mid_Frontal_Lobe_Enh
12	0.20	2 / 686	Overlap_fetal_midbrain_TssA
13	0.24	2 / 769	Overlap_fetal_midbrain_ZNF
14	0.29	3 / 1548	Mid_Frontal_Lobe_K9K27me3
15	0.33	13 / 9528	Overlap_fetal_midbrain_Quies
16	0.35	1 / 349	Fetal_ZNF
17	0.35	2 / 1013	Fetal_TssP
18	0.40	2 / 1122	Fetal_K9K27me3
19	0.40	12 / 9020	Overlap_fetal_midbrain_ReprPCWk
20	0.44	1 / 468	Mid_Frontal_Lobe_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	1 / 12	LIU_BREAST_CANCER
2	0.08	2 / 401	Lembcke_Colonic Inflammation
3	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
4	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
5	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	1.00	0 / 14	LIU_COMMON_CANCER_GENES
8	1.00	0 / 14	LIU_LIVER_CANCER
9	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
10	1.00	0 / 12	LIU_PROSTATE_CANCER_UP
11	1.00	0 / 15	WANG_ER_UP
12	1.00	0 / 5	WANG_ER_DN
13	1.00	0 / 16	WOLFER_overlap genes
14	1.00	0 / 12	BEN−PORATH_DN
15	1.00	0 / 13	BEN−PORATH_UP
16	1.00	0 / 15	GENTLES_modul1
17	1.00	0 / 16	GENTLES_modul2
18	1.00	0 / 10	GENTLES_modul3
19	1.00	0 / 15	GENTLES_modul4
20	1.00	0 / 10	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	0.01	1 / 10	pericentric heterochromatin
2	0.01	1 / 10	viral nucleocapsid
3	0.02	1 / 14	gap junction
4	0.02	1 / 17	membrane−bounded vesicle
5	0.02	1 / 20	dynein complex
6	0.03	1 / 29	cell−cell adherens junction
7	0.04	1 / 35	adherens junction
8	0.04	1 / 35	integral component of Golgi membrane
9	0.05	1 / 41	presynaptic membrane
10	0.05	1 / 42	synaptic vesicle membrane
11	0.06	1 / 53	acrosomal vesicle
12	0.08	6 / 2576	membrane
13	0.09	1 / 79	catalytic step 2 spliceosome
14	0.10	1 / 83	endomembrane system
15	0.10	1 / 83	synaptic vesicle
16	0.10	2 / 438	Golgi membrane
17	0.11	1 / 92	spliceosomal complex
18	0.12	2 / 487	intracellular membrane−bounded organelle
19	0.12	18 / 13191	cellular_component
20	0.12	1 / 105	ribonucleoprotein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.01	4 / 801	Chr 11
2	0.05	3 / 689	Chr 7
3	0.11	2 / 462	Chr 14
4	0.24	1 / 221	Chr 18
5	0.44	1 / 465	Chr 15
6	0.51	1 / 576	Chr 9
7	0.56	2 / 1500	Chr 1
8	0.57	1 / 687	Chr 6
9	0.62	1 / 775	Chr 12
10	0.65	1 / 838	Chr 3
11	0.65	1 / 840	Chr 17
12	1.00	0 / 552	Chr 10
13	1.00	0 / 262	Chr 13
14	1.00	0 / 649	Chr 16
15	1.00	0 / 1037	Chr 19
16	1.00	0 / 993	Chr 2
17	1.00	0 / 398	Chr 20
18	1.00	0 / 151	Chr 21
19	1.00	0 / 335	Chr 22
20	1.00	0 / 558	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	9 / 2142	ReprPC_Colon
2	9e−04	8 / 1889	ReprPCWk_Colon
3	9e−03	8 / 2698	EnhA_Colon
4	1e−02	7 / 2159	TssP_Colon
5	1e−02	9 / 3383	EnhWk2_Colon
6	2e−02	12 / 5880	TssD2_Colon
7	2e−02	16 / 9653	Enh_Colon
8	3e−02	9 / 3897	Quies1_Colon
9	7e−02	4 / 1317	EnhP_Colon
10	1e−01	2 / 436	K9acLow_Colon
11	1e−01	2 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
12	1e−01	9 / 5155	EnhWk1_Colon
13	1e−01	3 / 1079	ZNF_Colon
14	2e−01	2 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
15	2e−01	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
16	3e−01	1 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
17	3e−01	6 / 3812	TssD1_Colon
18	3e−01	1 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
19	4e−01	1 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
20	4e−01	1 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.01	1 / 11	BCHETNIA_EBM up
2	0.02	1 / 20	BCHETNIA_EBM−DM up
3	0.05	2 / 294	GUDJ_psoriasis down
4	1.00	0 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	1 / 38	OL vs. OPC
2	0.06	1 / 49	OL vs. MOG− OL
3	0.07	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
4	0.07	2 / 365	Down_b
5	0.08	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
6	0.08	1 / 71	Weller_LGG_A_vs_O_UP
7	0.09	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
8	0.10	1 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	0.11	1 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.11	1 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.13	1 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
12	0.14	1 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	0.20	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
14	0.33	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 / 74	WIRTH_Normal Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 33	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_UP
2	2e−03	6 / 1199	PUJANA_ATM_PCC_NETWORK
3	2e−03	2 / 58	PID_ERA_GENOMIC_PATHWAY
4	3e−03	5 / 892	YOSHIMURA_MAPK8_TARGETS_UP
5	4e−03	2 / 74	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
6	5e−03	1 / 4	BIOCARTA_TCAPOPTOSIS_PATHWAY
7	6e−03	1 / 5	BIOCARTA_TCRA_PATHWAY
8	6e−03	1 / 5	BIOCARTA_NO2IL12_PATHWAY
9	6e−03	3 / 316	HSIAO_HOUSEKEEPING_GENES
10	7e−03	1 / 6	BIOCARTA_CTL_PATHWAY
11	7e−03	1 / 6	BIOCARTA_IL17_PATHWAY
12	7e−03	1 / 6	BIOCARTA_TCYTOTOXIC_PATHWAY
13	8e−03	1 / 7	BIOCARTA_THELPER_PATHWAY
14	8e−03	1 / 7	REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYN
15	8e−03	1 / 7	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
16	8e−03	1 / 7	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
17	8e−03	1 / 7	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
18	1e−02	1 / 8	BIOCARTA_SET_PATHWAY
19	1e−02	1 / 9	BIOCARTA_CTLA4_PATHWAY
20	1e−02	1 / 9	MATZUK_PREOVULATORY_FOLLICLE

HM

Rank	p−value	#in/all	Geneset
1	0.02	2 / 188	HALLMARK_MYC_TARGETS_V1
2	0.11	1 / 93	HALLMARK_PEROXISOME
3	0.14	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
4	0.17	1 / 148	HALLMARK_KRAS_SIGNALING_UP
5	0.18	1 / 167	HALLMARK_APICAL_JUNCTION
6	0.19	1 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.21	1 / 195	HALLMARK_MITOTIC_SPINDLE
8	1.00	0 / 176	HALLMARK_HYPOXIA
9	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
12	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	1.00	0 / 146	HALLMARK_DNA_REPAIR
14	1.00	0 / 196	HALLMARK_G2M_CHECKPOINT
15	1.00	0 / 140	HALLMARK_APOPTOSIS
16	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING
17	1.00	0 / 188	HALLMARK_ADIPOGENESIS
18	1.00	0 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	1.00	0 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
20	1.00	0 / 94	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	10 / 3396	HOPP_Repressed
2	0.011	7 / 2188	HOPP_Poised_promoter
3	0.012	1 / 10	Shaknovich_ABC_hypo_meth
4	0.152	3 / 1128	SPANG_BCR DN
5	0.269	1 / 256	SPANG_IL21 DN
6	0.286	1 / 275	TARTE_Mature plasma cell signature
7	0.303	1 / 294	TARTE_Plasmablast signature
8	0.396	1 / 410	SPANG_CD40 6hrs DN
9	0.515	3 / 2211	HOPP_Repetitive
10	0.544	9 / 7209	HOPP_Weak_promoter
11	0.582	8 / 6564	HOPP_Strong_enhancer
12	0.623	3 / 2563	HOPP_Heterochrom
13	0.630	9 / 7592	HOPP_Active_promoter
14	0.786	1 / 1218	SPANG_BCR UP
15	0.810	5 / 5184	HOPP_Txn_transition
16	0.880	5 / 5693	HOPP_Weak_enhancer
17	0.917	6 / 6929	HOPP_Txn_elongation
18	0.947	4 / 5538	HOPP_Weak_txn
19	1.000	0 / 13	BENTINK_mBL UP
20	1.000	0 / 12	BENTINK_mBL DOWN

MF

Rank	p−value	#in/all	Geneset
1	2e−04	2 / 17	steroid binding
2	1e−02	1 / 11	structural constituent of eye lens
3	1e−02	1 / 12	poly(U) RNA binding
4	2e−02	1 / 13	GTP−Rho binding
5	2e−02	2 / 166	receptor activity
6	2e−02	1 / 16	coreceptor activity
7	2e−02	2 / 181	transporter activity
8	2e−02	1 / 17	sialyltransferase activity
9	2e−02	1 / 19	protein phosphatase type 2A regulator activity
10	3e−02	1 / 23	virus receptor activity
11	3e−02	6 / 2037	DNA binding
12	3e−02	1 / 25	protein phosphatase inhibitor activity
13	3e−02	2 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
14	3e−02	1 / 29	mRNA 3'−UTR binding
15	3e−02	1 / 29	nucleosomal DNA binding
16	4e−02	1 / 33	core promoter sequence−specific DNA binding
17	4e−02	1 / 35	clathrin binding
18	4e−02	1 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
19	4e−02	1 / 37	sulfotransferase activity
20	5e−02	1 / 39	cell adhesion molecule binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	2 / 75	hsa−miR−939
2	0.013	1 / 11	hsa−miR−1180
3	0.038	1 / 32	hsa−miR−1231
4	0.039	1 / 33	hsa−miR−589
5	0.043	1 / 36	hsa−miR−769−5p
6	0.044	1 / 37	hsa−miR−760
7	0.045	1 / 38	hsa−miR−1258
8	0.047	1 / 40	hsa−miR−450a
9	0.049	2 / 294	hsa−miR−561
10	0.050	1 / 42	hsa−miR−642
11	0.052	1 / 44	hsa−miR−658
12	0.053	1 / 45	hsa−miR−411
13	0.054	1 / 46	hsa−miR−1256
14	0.056	1 / 47	hsa−miR−623
15	0.058	1 / 49	hsa−miR−654−3p
16	0.064	1 / 54	hsa−miR−330−5p
17	0.065	1 / 55	hsa−miR−629
18	0.070	1 / 60	hsa−miR−1200
19	0.071	1 / 61	hsa−miR−514
20	0.071	1 / 61	hsa−miR−324−5p

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.04	4 / 1139	HEBENSTREIT_low expression TF
2	0.18	4 / 1872	ICGC_Mef2_targets
3	0.24	3 / 1400	ICGC_Myc_targets
4	0.33	4 / 2416	ICGC_Bcl3_targets
5	0.40	3 / 1878	ICGC_Cebpbsc150_targets
6	0.43	6 / 4314	ICGC_Ebfsc137065_targets
7	0.48	2 / 1314	ICGC_Usf1_targets
8	0.52	6 / 4682	ICGC_Pol24_targets
9	0.55	5 / 3966	ICGC_Pu1_targets
10	0.57	3 / 2391	ICGC_Pbx3_targets
11	0.70	3 / 2836	ICGC_BatfPcr1_targets
12	0.70	5 / 4617	ICGC_Tcf12_targets
13	0.72	2 / 2013	ICGC_Bcl11_targets
14	0.77	4 / 4054	ICGC_Egr1_targets
15	0.80	1 / 1273	ICGC_P300_targets
16	0.82	5 / 5219	ICGC_Tcf3_targets
17	0.83	4 / 4385	ICGC_Atf2_targets
18	0.84	5 / 5355	ICGC_Pol2_targets
19	0.84	1 / 1418	ICGC_Ets1_targets
20	0.84	5 / 5408	ICGC_Pou2_targets

TF_Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.008	3 / 350	WIRTH_Immune system
2	0.038	1 / 32	WIRTH_Pancreas
3	0.038	1 / 32	WIRTH_Placenta
4	0.349	1 / 350	WIRTH_Nervous System
5	1.000	0 / 11	WIRTH_Sec. lymphoid organs
6	1.000	0 / 11	WIRTH_Prim. lymphoid organs
7	1.000	0 / 13	WIRTH_B−cells
8	1.000	0 / 8	WIRTH_Tonsil
9	1.000	0 / 12	WIRTH_Thymus
10	1.000	0 / 12	WIRTH_Lymphocytes
11	1.000	0 / 5	WIRTH_Bone marrow
12	1.000	0 / 11	WIRTH_Globus pallidus
13	1.000	0 / 14	WIRTH_Telencephalon
14	1.000	0 / 11	WIRTH_Cortex cerebri
15	1.000	0 / 10	WIRTH_Hippocampus
16	1.000	0 / 10	WIRTH_Thalamus
17	1.000	0 / 12	WIRTH_Cerebellum
18	1.000	0 / 107	WIRTH_Testis
19	1.000	0 / 41	WIRTH_Homeostasis
20	1.000	0 / 46	WIRTH_Liver

Toxic

Rank	p−value	#in/all	Geneset
1	0.02	9 / 3682	LU_BPDE 0.005 DN
2	0.75	1 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

Spot Summary: C

metagenes = 30
genes = 92

<r> metagenes = 0.94
<r> genes = 0.37
beta: r2= 0.16 / log p= −4.04

samples with spot = 1 (1.1 %)
MSC1 : 1 (2.4 %)

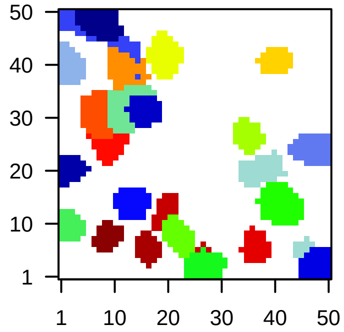
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	OPHN1	2.4	−0.43	0.41	OPHN1	oligophrenin 1 [Source:HGNC Symbol;Acc:HGNC:8148]
2	RORA	2.04	−0.07	0.7	RORA	RAR−related orphan receptor A [Source:HGNC Symbol;Acc:
3	FBLN5	2.02	−0.06	0.46	FBLN5	fibulin 5 [Source:HGNC Symbol;Acc:HGNC:3602]
4	S100A6	1.89	−0.08	0.64	S100A6	S100 calcium binding protein A6 [Source:HGNC Symbol;Acc:
5	PLA2G7	1.77	−0.08	0.38	PLA2G7	phospholipase A2, group VII (platelet−activating factor acetyl
6	IGF2BP1	1.75	−0.03	0.86	IGF2BP1	insulin−like growth factor 2 mRNA binding protein 1 [Source:
7	SPATA9	1.74	−0.06	0.62	SPATA9	spermatogenesis associated 9 [Source:HGNC Symbol;Acc:H
8	NUDT7	1.72	−0.03	0.53	NUDT7	nudix (nucleoside diphosphate linked moiety X)−type motif 7
9	ILDR2	1.72	−0.08	0.39	ILDR2	immunoglobulin−like domain containing receptor 2 [Source:H
10	RNF31	1.69	−0.25	0.33	RNF31	ring finger protein 31 [Source:HGNC Symbol;Acc:HGNC:160
11	CCNA1	1.64	−0.04	0.83	CCNA1	cyclin A1 [Source:HGNC Symbol;Acc:HGNC:1577]
12	ZNF570	1.59	−0.11	0.5	ZNF570	zinc finger protein 570 [Source:HGNC Symbol;Acc:HGNC:26
13	GNG2	1.58	−0.12	0.43	GNG2	guanine nucleotide binding protein (G protein), gamma 2 [So
14	PPIL6	1.54	−0.06	0.42	PPIL6	peptidylprolyl isomerase (cyclophilin)−like 6 [Source:HGNC S
15	CTPS2	1.53	−0.05	0.66	CTPS2	CTP synthase 2 [Source:HGNC Symbol;Acc:HGNC:2520]
16	TRAF3IP3	1.51	−0.04	0.72	TRAF3IP3	TRAF3 interacting protein 3 [Source:HGNC Symbol;Acc:HG
17	MAPK4	1.48	−0.12	0.32	MAPK4	mitogen−activated protein kinase 4 [Source:HGNC Symbol;A
18	DPF1	1.48	−0.06	0.38	DPF1	D4, zinc and double PHD fingers family 1 [Source:HGNC Syn
19	AMDHD1	1.44	−0.18	0.44	AMDHD1	amidohydrolase domain containing 1 [Source:HGNC Symbol;
20	RNF180	1.41	−0.2	0.37	RNF180	ring finger protein 180 [Source:HGNC Symbol;Acc:HGNC:27

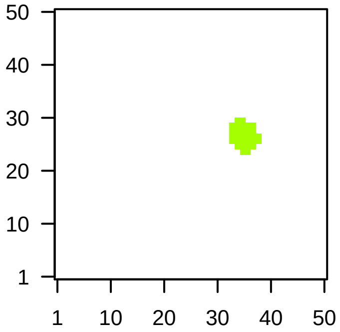
Geneset Overrepresentation

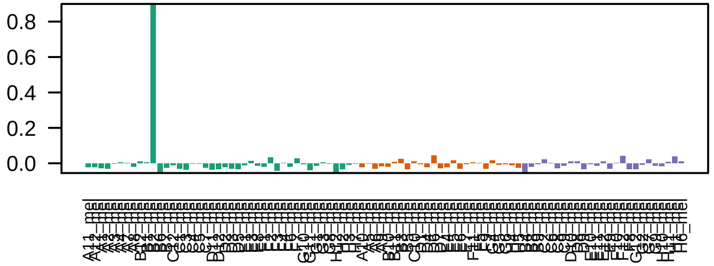
Rank	p−value	#in/all	Geneset	
1	8e−11	49 / 3396	Lympl	HOPP_Repressed
2	3e−09	36 / 2159	Colon	TssP_Colon
3	4e−08	34 / 2142	Colon	ReprPC_Colon
4	7e−07	24 / 1317	Colon	EnhP_Colon
5	4e−06	28 / 1889	Colon	ReprPCWk_Colon
6	1e−05	15 / 674	GSEA	BENPORATH_SUZ12_TARGETS
7	3e−05	15 / 720	GSEA	BENPORATH_ES_WITH_H3K27ME3
8	1e−04	15 / 812	Brain	Mid_Frontal_Lobe_TssP
9	1e−04	10 / 396	GSEA	BENPORATH_PRC2_TARGETS
10	1e−04	18 / 1139	TF	HEBENSTREIT_low expression TF
11	2e−04	27 / 2185	Brain	Fetal_TssA
12	2e−04	7 / 199	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
13	3e−04	3 / 21	GSEA	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
14	4e−04	13 / 724	GSEA	BENPORATH_EED_TARGETS
15	8e−04	7 / 250	Colon	K9K27me3_Colon
16	9e−04	12 / 686	Brain	Overlap_fetal_midbrain_TssA
17	1e−03	10 / 519	BP	cell−cell signaling
18	1e−03	2 / 9	GSEA	BIOCARTA_ERYTH_PATHWAY
19	1e−03	2 / 9	GSEA	BIOCARTA_AHSP_PATHWAY
20	1e−03	4 / 80	BP	anterior/posterior pattern specification
21	2e−03	3 / 39	GSEA	MEISSNER_NPC_HCP_WITH_H3K27ME3
22	2e−03	4 / 85	GSEA	KEEN_RESPONSE_TO_ROSIGLITAZONE_DN
23	2e−03	3 / 40	GSEA	ZHENG_IL22_SIGNALING_UP
24	2e−03	13 / 862	Brain	Overlap_fetal_midbrain_TxTrans
25	2e−03	30 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
26	2e−03	3 / 42	GSEA	JIANG_AGING_HYPOTHALAMUS_UP
27	2e−03	3 / 43	BP	substantia nigra development
28	2e−03	24 / 2188	Lympl	HOPP_Poised_promoter
29	2e−03	16 / 1207	Brain	Overlap_fetal_midbrain_TssF
30	2e−03	2 / 12	CC	endocytic vesicle lumen
31	2e−03	2 / 12	BP	monocyte chemotaxis
32	2e−03	2 / 12	GSEA	PID_THROMBIN_PAR4_PATHWAY
33	3e−03	7 / 313	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
34	3e−03	14 / 1013	Brain	Fetal_TssP
35	3e−03	2 / 14	MF	peroxidase activity
36	3e−03	3 / 50	GSEA	LEIN_NEURON_MARKERS
37	4e−03	2 / 15	BP	hydrogen peroxide catabolic process
38	4e−03	2 / 16	GSEA	SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_IN_CAN
39	5e−03	3 / 55	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_C
40	5e−03	2 / 17	CC	cytoplasmic ribonucleoprotein granule

Overview Map

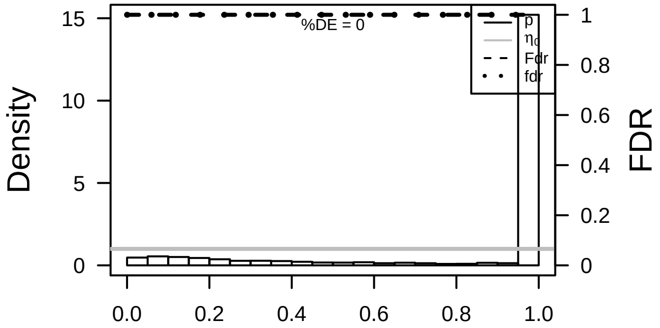


Spot





p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	0.001	10 / 519	cell−cell signaling
2	0.001	4 / 80	anterior/posterior pattern specification
3	0.002	3 / 43	substantia nigra development
4	0.002	2 / 12	monocyte chemotaxis
5	0.004	2 / 15	hydrogen peroxide catabolic process
6	0.005	2 / 17	negative regulation of myeloid cell differentiation
7	0.005	2 / 17	synaptic vesicle endocytosis
8	0.005	18 / 1556	cell differentiation
9	0.006	7 / 352	multicellular organismal development
10	0.006	2 / 20	adult behavior
11	0.006	2 / 20	bicarbonate transport
12	0.007	2 / 21	neurotransmitter transport
13	0.009	2 / 24	actin filament polymerization
14	0.009	2 / 24	insulin secretion
15	0.011	4 / 141	actin cytoskeleton organization
16	0.011	2 / 26	response to interleukin−1
17	0.011	3 / 76	cell−matrix adhesion
18	0.011	22 / 2210	anatomical structure development
19	0.012	2 / 27	regulation of endocytosis
20	0.012	7 / 409	cell motility

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	15 / 812	Mid_Frontal_Lobe_TssP
2	2e−04	27 / 2185	Fetal_TssA
3	9e−04	12 / 686	Overlap_fetal_midbrain_TssA
4	2e−03	13 / 862	Overlap_fetal_midbrain_TxTrans
5	2e−03	30 / 2972	Mid_Frontal_Lobe_ReprPC
6	2e−03	16 / 1207	Overlap_fetal_midbrain_TssF
7	3e−03	14 / 1013	Fetal_TssP
8	6e−03	20 / 1845	Fetal_Quies
9	7e−03	15 / 1236	Mid_Frontal_Lobe_ReprPCWk
10	9e−03	20 / 1907	Fetal_TxTrans
11	2e−02	19 / 1949	Fetal_TssF
12	3e−02	6 / 383	Fetal_Tx
13	6e−02	21 / 2462	Mid_Frontal_Lobe_HetRpts
14	6e−02	6 / 468	Mid_Frontal_Lobe_TssF
15	1e−01	6 / 534	Mid_Frontal_Lobe_EnhG
16	1e−01	10 / 1065	Overlap_fetal_midbrain_Enh
17	1e−01	7 / 668	Mid_Frontal_Lobe_Enh
18	1e−01	6 / 574	Overlap_fetal_midbrain_TssP
19	2e−01	3 / 229	Mid_Frontal_Lobe_TxTrans
20	2e−01	8 / 884	Overlap_fetal_midbrain_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	6 / 401	Lembcke_Colonic Inflammation
2	0.25	1 / 48	KUIPER_MM poor survival
3	0.28	1 / 55	PanCan_JAK−ST_geneset_nanostring
4	0.39	1 / 82	PanCan_TXmisReg_geneset_nanostring
5	0.42	0 / 14	LIU_PROSTATE_CANCER_DN
6	0.52	1 / 120	PanCan_CC+Apop_geneset_nanostring
7	0.61	1 / 156	PanCan_PI3K_geneset_nanostring
8	0.67	1 / 180	SPANG_LPS−index2
9	0.80	2 / 489	Lembcke_Normal vs Adenoma
10	0.84	1 / 298	SPANG_BCL6−index2
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 / 12	LIU_PROSTATE_CANCER_UP
19	1.00	0 / 15	WANG_ER_UP
20	1.00	0 / 5	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	endocytic vesicle lumen
2	0.005	2 / 17	cytoplasmic ribonucleoprotein granule
3	0.006	7 / 352	cell surface
4	0.007	11 / 775	extracellular space
5	0.011	3 / 75	blood microparticle
6	0.017	5 / 246	dendrite
7	0.022	86 / 13191	cellular_component
8	0.029	2 / 44	terminal bouton
9	0.049	25 / 2984	integral component of membrane
10	0.051	5 / 332	cell junction
11	0.059	1 / 10	beta−catenin destruction complex
12	0.059	1 / 10	low−density lipoprotein particle
13	0.065	1 / 11	CD40 receptor complex
14	0.070	25 / 3088	plasma membrane
15	0.070	1 / 12	axonal growth cone
16	0.072	2 / 73	basement membrane
17	0.076	1 / 13	nBAF complex
18	0.080	25 / 3132	extracellular region
19	0.081	2 / 78	dendritic spine
20	0.082	1 / 14	NuA4 histone acetyltransferase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.1	7 / 649	Chr 16
2	0.1	7 / 689	Chr 7
3	0.1	5 / 462	Chr 14
4	0.2	3 / 221	Chr 18
5	0.2	6 / 687	Chr 6
6	0.2	5 / 551	Chr X
7	0.2	6 / 696	Chr 5
8	0.4	3 / 398	Chr 20
9	0.5	4 / 576	Chr 9
10	0.5	3 / 465	Chr 15
11	0.5	3 / 469	Chr 8
12	0.6	5 / 840	Chr 17
13	0.6	1 / 151	Chr 21
14	0.7	3 / 552	Chr 10
15	0.7	5 / 993	Chr 2
16	0.8	5 / 1037	Chr 19
17	0.8	1 / 262	Chr 13
18	0.9	2 / 558	Chr 4
19	0.9	1 / 335	Chr 22
20	0.9	3 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−09	36 / 2159	TssP_Colon
2	4e−08	34 / 2142	ReprPC_Colon
3	7e−07	24 / 1317	EnhP_Colon
4	4e−06	28 / 1889	ReprPCWk_Colon
5	8e−04	7 / 250	K9K27me3_Colon
6	1e−02	34 / 3897	Quies1_Colon
7	2e−02	7 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	3e−02	2 / 45	Ang_CRC−CIMPH−vs−L_hyper
9	3e−02	4 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
10	3e−02	6 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	4e−02	2 / 50	Ang_CRC_Hypermethylated
12	5e−02	6 / 427	Quies2_Colon
13	6e−02	7 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	6e−02	4 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	7e−02	4 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
16	7e−02	13 / 1386	Het_Colon
17	8e−02	1 / 13	TCGA−CRC_less−agressive−disease−markers
18	1e−01	4 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	1e−01	1 / 25	Ang_CRC_Hypomethylated
20	2e−01	2 / 131	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.3	3 / 294	GUDJ_psoriasis down
2	0.9	1 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.005	2 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
2	0.023	2 / 39	OPC
3	0.026	4 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
4	0.054	2 / 62	cultured astroglia vs. in vivo astrocytes
5	0.065	1 / 11	astrocytes_glio
6	0.067	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
7	0.074	2 / 74	WIRTH_Normal Brain
8	0.104	1 / 18	Shinawi_with_increased_methylation_in_STS
9	0.177	1 / 32	Donson−innate immunity−associated with LTS in HGA
10	0.187	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
11	0.202	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
12	0.207	1 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
13	0.258	1 / 49	developing astrocytes
14	0.263	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	0.298	1 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
16	0.351	1 / 71	Weller_LGG_A_vs_O_UP
17	0.355	1 / 72	laffaire_hypermeth_LGG_vs_control
18	0.363	1 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
19	0.367	3 / 356	Down_a
20	0.367	1 / 75	GIEZELT_GBM_STS_down_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−05	15 / 674	BENPORATH_SUZ12_TARGETS
2	3e−05	15 / 720	BENPORATH_ES_WITH_H3K27ME3
3	1e−04	10 / 396	BENPORATH_PRC2_TARGETS
4	2e−04	7 / 199	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
5	3e−04	3 / 21	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
6	4e−04	13 / 724	BENPORATH_EED_TARGETS
7	1e−03	2 / 9	BIOCARTA_ERYTH_PATHWAY
8	1e−03	2 / 9	BIOCARTA_AHSP_PATHWAY
9	2e−03	3 / 39	MEISSNER_NPC_HCP_WITH_H3K27ME3
10	2e−03	4 / 85	KEEN_RESPONSE_TO_ROSIGLITAZONE_DN
11	2e−03	3 / 40	ZHENG_IL22_SIGNALING_UP
12	2e−03	3 / 42	JIANG_AGING_HYPOTHALAMUS_UP
13	2e−03	2 / 12	PID_THROMBIN_PAR4_PATHWAY
14	3e−03	7 / 313	SMID_BREAST_CANCER_NORMAL_LIKE_UP
15	3e−03	3 / 50	LEIN_NEURON_MARKERS
16	4e−03	2 / 16	SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_IN_CANCE
17	5e−03	3 / 55	RICKMAN_HEAD_AND_NECK_CANCER_C
18	5e−03	3 / 57	BRUNO_HEMATOPOIESIS
19	5e−03	3 / 58	DARWICHE_PAPILLOMA_PROGRESSION_RISK
20	6e−03	6 / 266	VECCHI_GASTRIC_CANCER_EARLY_DN

HM

Rank	p−value	#in/all	Geneset
1	0.08	3 / 162	HALLMARK_COMPLEMENT
2	0.10	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.11	2 / 93	HALLMARK_PEROXISOME
4	0.14	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
5	0.14	2 / 107	HALLMARK_COAGULATION
6	0.16	1 / 29	HALLMARK_NOTCH_SIGNALING
7	0.17	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
8	0.20	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	0.27	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
10	0.27	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	0.31	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	0.33	2 / 195	HALLMARK_MITOTIC_SPINDLE
13	0.43	1 / 91	HALLMARK_BILE_ACID_METABOLISM
14	0.44	1 / 95	HALLMARK_SPERMATOGENESIS
15	0.54	1 / 127	HALLMARK_KRAS_SIGNALING_DN
16	0.57	1 / 137	HALLMARK_UV_RESPONSE_DN
17	0.57	1 / 140	HALLMARK_APOPTOSIS
18	0.57	1 / 140	HALLMARK_INFLAMMATORY_RESPONSE
19	0.64	1 / 165	HALLMARK_MYOGENESIS
20	0.64	1 / 167	HALLMARK_APICAL_JUNCTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	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	8e−11	49 / 3396	HOPP_Repressed
2	2e−03	24 / 2188	HOPP_Poised_promoter
3	5e−02	2 / 60	Subero_T−ALL_hyper_meth
4	8e−02	1 / 13	YAMANE_AICDA_targets_recruited
5	9e−02	2 / 81	Subero_INT_hyper_meth
6	1e−01	2 / 89	ROSOLOWSKI_blue total
7	1e−01	1 / 20	SPANG_BAFF 9hrs UP
8	1e−01	2 / 96	Subero_DLBCL_hyper_meth
9	2e−01	1 / 33	LEE_Developmental_regulators
10	2e−01	1 / 40	Subero_mBL_hyper_meth
11	2e−01	3 / 275	TARTE_Mature plasma cell signature
12	3e−01	16 / 2211	HOPP_Repetitive
13	4e−01	1 / 86	ROSOLOWSKI_red total
14	4e−01	2 / 247	ZHANG_DLBCL mutated
15	5e−01	1 / 107	SPANG_LPS 6hrs UP
16	7e−01	14 / 2563	HOPP_Heterochrom
17	7e−01	2 / 410	SPANG_CD40 6hrs DN
18	7e−01	31 / 5538	HOPP_Weak_txn
19	8e−01	1 / 268	SPANG_IL21 UP
20	8e−01	1 / 280	SPANG_CD40 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.003	2 / 14	peroxidase activity
2	0.008	2 / 22	oxygen binding
3	0.009	3 / 70	phospholipid binding
4	0.009	3 / 71	PDZ domain binding
5	0.015	3 / 85	transmembrane signaling receptor activity
6	0.016	2 / 32	Rac GTPase binding
7	0.016	2 / 32	Rho GTPase binding
8	0.022	5 / 265	hydrolase activity
9	0.023	2 / 39	cell adhesion molecule binding
10	0.024	5 / 271	actin binding
11	0.025	3 / 104	growth factor activity
12	0.040	2 / 52	hormone activity
13	0.050	2 / 59	syntaxin binding
14	0.058	2 / 64	beta−catenin binding
15	0.059	1 / 10	armadillo repeat domain binding
16	0.059	1 / 10	metalloendopeptidase inhibitor activity
17	0.059	1 / 10	sodium channel activity
18	0.059	1 / 10	tropomyosin binding
19	0.065	1 / 11	3−beta−hydroxy−delta5−steroid dehydrogenase activity
20	0.065	1 / 11	S100 protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	2 / 62	hsa−miR−1236
2	0.06	1 / 11	hsa−miR−1180
3	0.09	1 / 15	hsa−miR−598
4	0.13	1 / 23	hsa−miR−609
5	0.17	1 / 30	hsa−miR−371−3p
6	0.17	1 / 31	hsa−miR−892b
7	0.18	1 / 33	hsa−miR−589
8	0.19	1 / 35	hsa−miR−1229
9	0.20	1 / 36	hsa−miR−1226
10	0.20	1 / 37	hsa−miR−1274a
11	0.21	1 / 38	hsa−miR−1277
12	0.21	2 / 140	hsa−miR−522
13	0.23	1 / 42	hsa−miR−642
14	0.23	1 / 42	hsa−miR−769−3p
15	0.23	3 / 274	hsa−miR−548h
16	0.24	1 / 44	hsa−miR−658
17	0.25	1 / 48	hsa−miR−553
18	0.26	1 / 50	hsa−miR−1201
19	0.26	1 / 50	hsa−miR−549
20	0.28	1 / 54	hsa−miR−513a−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	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	1e−04	18 / 1139	HEBENSTREIT_low expression TF
2	2e−01	22 / 2927	ICGC_Rad21_targets
3	3e−01	57 595	ICGC_NrsfPcr2_targets
4	5e−01	8 / 1273	ICGC_P300_targets
5	7e−01	7 / 1266	ICGC_NrsfPcr1_targets
6	7e−01	27 / 4682	ICGC_Pol24_targets
7	7e−01	7 / 1314	ICGC_Usf1_targets
8	7e−01	10 / 1872	ICGC_Mef2_targets
9	7e−01	24 / 4314	ICGC_Ebfsc137065_targets
10	8e−01	15 / 2836	ICGC_BatfPcr1_targets
11	8e−01	14 / 2714	ICGC_Irf4_targets
12	8e−01	30 / 5495	ICGC_Yy1_targets
13	8e−01	29 / 5355	ICGC_Pol2_targets
14	8e−01	5 / 1171	KIM_MYC targets
15	9e−01	2 / 553	ICGC_RxraPcr1_targets
16	9e−01	6 / 1400	ICGC_Myc_targets
17	9e−01	9 / 2013	ICGC_Bcl11_targets
18	9e−01	24 / 4774	ICGC_Foxm1_targets
19	9e−01	8 / 1878	ICGC_Cebpbsc150_targets
20	9e−01	27 / 5374	ICGC_Pax5_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	0.005	7 / 350	WIRTH_Nervous System
2	0.020	6 / 350	WIRTH_Immune system
3	0.076	1 / 13	WIRTH_B−cells
4	0.152	2 / 114	PALMER_T−Cell signature up
5	0.244	1 / 46	WIRTH_Liver
6	0.397	2 / 225	PALMER_Granulocytes signature up
7	0.440	1 / 95	WIRTH_Muscle
8	0.480	1 / 107	WIRTH_Testis
9	1.000	0 / 32	WIRTH_Pancreas
10	1.000	0 / 11	WIRTH_Sec. lymphoid organs
11	1.000	0 / 11	WIRTH_Prim. lymphoid organs
12	1.000	0 / 8	WIRTH_Tonsil
13	1.000	0 / 12	WIRTH_Thymus
14	1.000	0 / 12	WIRTH_Lymphocytes
15	1.000	0 / 5	WIRTH_Bone marrow
16	1.000	0 / 11	WIRTH_Globus pallidus
17	1.000	0 / 14	WIRTH_Telencephalon
18	1.000	0 / 11	WIRTH_Cortex cerebri
19	1.000	0 / 10	WIRTH_Hippocampus
20	1.000	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.008	33 / 3682	LU_BPDE 0.005 DN
2	0.678	6 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

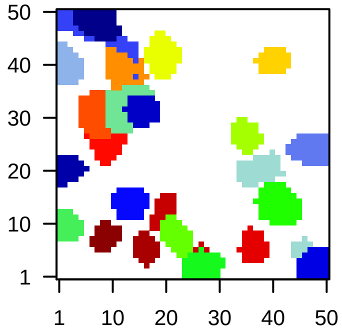
Spot Summary: D

metagenes = 41
genes = 112

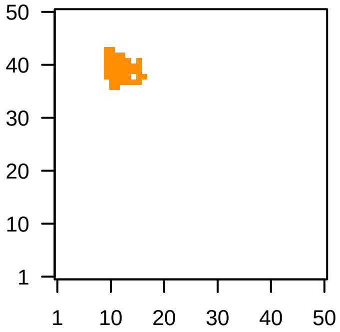
<r> metagenes = 0.93
<r> genes = 0.1
beta: r2= 0.7 / log p= −Inf

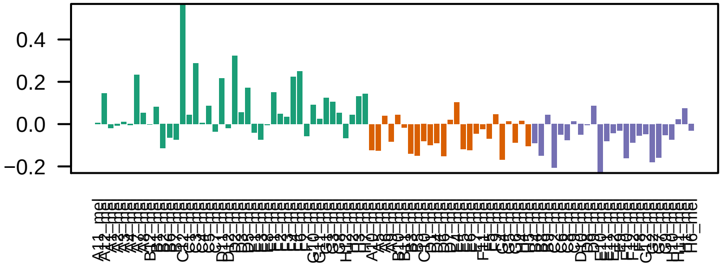
samples with spot = 8 (8.7 %)
MSC1 : 8 (19 %)

Overview Map



Spot





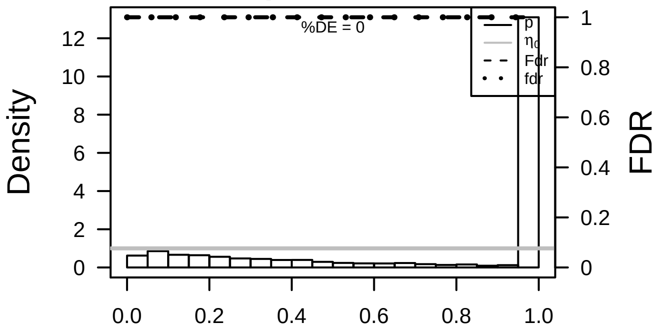
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	KLHL32	1.89	−0.06	0.37	KLHL32	kelch−like family member 32 [Source:HGNC Symbol;Acc:HG
2	HSD17B6	1.83	−0.06	0.33	HSD17B6	hydroxysteroid (17−beta) dehydrogenase 6 [Source:HGNC S
3	ASH2L	1.79	−0.43	0.38	ASH2L	ash2 (absent, small, or homeotic)−like (Drosophila) [Source:
4	STRA6	1.68	−0.03	0.39	STRA6	stimulated by retinoic acid 6 [Source:HGNC Symbol;Acc:HG
5	S100B	1.66	−0.6	0.29	S100B	S100 calcium binding protein B [Source:HGNC Symbol;Acc:
6	CMPK2	1.65	−0.03	0.36	CMPK2	cytidine monophosphate (UMP−CMP) kinase 2, mitochondria
7	TEX15	1.65	−0.25	0.33	TEX15	testis expressed 15 [Source:HGNC Symbol;Acc:HGNC:1173
8	LETM2	1.64	−0.08	0.36	LETM2	leucine zipper−EF−hand containing transmembrane protein 2
9	GLRB	1.63	−0.2	0.3	GLRB	glycine receptor, beta [Source:HGNC Symbol;Acc:HGNC:432
10	PTGR2	1.62	−0.38	0.31	PTGR2	prostaglandin reductase 2 [Source:HGNC Symbol;Acc:HGNC
11	MORN1	1.62	−0.12	0.29	MORN1	MORN repeat containing 1 [Source:HGNC Symbol;Acc:HGN
12	ZNF566	1.6	−0.4	0.3	ZNF566	zinc finger protein 566 [Source:HGNC Symbol;Acc:HGNC:25
13	PLCL2	1.6	−0.12	0.4	PLCL2	phospholipase C−like 2 [Source:HGNC Symbol;Acc:HGNC:9
14	PTGES3L	1.6	−0.06	0.32	PTGES3L	prostaglandin E synthase 3 (cytosolic)−like [Source:HGNC S
15	HAUS3	1.57	−0.34	0.41	HAUS3	HAUS augmin−like complex, subunit 3 [Source:HGNC Symb
16	HSBP1L1	1.56	−0.25	0.26	HSBP1L1	heat shock factor binding protein 1−like 1 [Source:HGNC Sy
17	FGD6	1.56	−0.11	0.28	FGD6	FYVE, RhoGEF and PH domain containing 6 [Source:HGNC
18	F3	1.55	−0.16	0.37	F3	coagulation factor III (thromboplastin, tissue factor) [Source:H
19	GPR98	1.54	−0.17	0.28		
20	PLAUR	1.54	−0.14	0.25	PLAUR	plasminogen activator, urokinase receptor [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−07	11 / 218	GSEA	BILD_E2F3_ONCOGENIC_SIGNATURE
2	1e−04	4 / 36	GSEA	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
3	2e−04	3 / 15	GSEA	COLLIS_PRKDC_REGULATORS
4	2e−04	3 / 16	GSEA	BIOCARTA_EIF_PATHWAY
5	3e−04	3 / 17	GSEA	REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA
6	4e−04	4 / 47	GSEA	SUNG_METASTASIS_STROMA_DN
7	5e−04	4 / 49	GSEA	SANSOM_WNT_PATHWAY_REQUIRE_MYC
8	5e−04	6 / 135	GSEA	WHITFIELD_CELL_CYCLE_G1_S
9	7e−04	3 / 24	GSEA	REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING
10	8e−04	3 / 25	GSEA	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAM
11	9e−04	33 / 2577	CC	nucleoplasm
12	1e−03	19 / 1192	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	1e−03	83 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
14	1e−03	4 / 65	GSEA	REACTOME_OPIOID_SIGNALLING
15	1e−03	3 / 30	GSEA	WONG_IFNA2_RESISTANCE_DN
16	2e−03	2 / 8	GSEA	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
17	2e−03	3 / 32	GSEA	DOANE_BREAST_CANCER_ESR1_DN
18	2e−03	6 / 171	GSEA	REACTOME_METABOLISM_OF_RNA
19	2e−03	2 / 9	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYE
20	2e−03	21 / 1460	GSEA	PUJANA_BRCA1_PCC_NETWORK
21	3e−03	2 / 12	GSEA	HASINA_NOL7_TARGETS_DN
22	3e−03	2 / 12	GSEA	DISTECHE_ESCAPED_FROM_X_INACTIVATION
23	4e−03	13 / 747	CC	nucleolus
24	4e−03	6 / 199	Colon	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
25	4e−03	14 / 840	GSEA	GEORGES_TARGETS_OF_MIR192_AND_MIR215
26	4e−03	2 / 13	GSEA	HASINA_NOL7_TARGETS_UP
27	5e−03	9 / 425	GSEA	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C
28	5e−03	3 / 45	GSEA	PID_TXA2PATHWAY
29	5e−03	3 / 45	GSEA	ABRAMSON_INTERACT_WITH_AIRE
30	5e−03	2 / 14	BP	digestive tract morphogenesis
31	5e−03	2 / 14	GSEA	LEE_LIVER_CANCER_HEPATOBLAST
32	5e−03	4 / 92	CC	early endosome membrane
33	5e−03	3 / 47	GSEA	REACTOME_METABOLISM_OF_NON_CODING_RNA
34	5e−03	12 / 687	BP	gene expression
35	5e−03	2 / 15	CC	U1 snRNP
36	5e−03	2 / 15	GSEA	PID_INTEGRIN5_PATHWAY
37	5e−03	2 / 15	GSEA	REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCL
38	5e−03	2 / 15	GSEA	MAINA_VHL_TARGETS_DN
39	6e−03	3 / 48	BP	activation of phospholipase C activity
40	6e−03	4 / 96	GSEA	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOW

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 111	HORVATH_aging_genes meth UP
2	0.5	1 / 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	0.005	2 / 14	digestive tract morphogenesis
2	0.005	12 / 687	gene expression
3	0.006	3 / 48	activation of phospholipase C activity
4	0.006	4 / 97	central nervous system development
5	0.008	13 / 815	lipid metabolic process
6	0.008	2 / 18	histone lysine methylation
7	0.008	39 / 3644	biosynthetic process
8	0.009	2 / 19	histone H3−K4 methylation
9	0.010	2 / 20	neuromuscular process
10	0.011	4 / 114	positive regulation of protein phosphorylation
11	0.011	3 / 61	mRNA export from nucleus
12	0.011	3 / 62	phototransduction, visible light
13	0.013	2 / 23	ncRNA metabolic process
14	0.013	3 / 65	double−strand break repair via homologous recombination
15	0.016	4 / 128	endocytosis
16	0.020	2 / 29	glycogen metabolic process
17	0.020	2 / 29	spliceosomal snRNP assembly
18	0.022	5 / 213	chromatin organization
19	0.022	2 / 31	negative regulation of nucleic acid−templated transcription
20	0.023	3 / 81	muscle organ development

Brain

Rank	p−value	#in/all	Geneset
1	0.001	83 / 9020	Overlap_fetal_midbrain_ReprPCWk
2	0.006	84 / 9528	Overlap_fetal_midbrain_Quies
3	0.016	81 / 9330	Overlap_fetal_midbrain_ReprPC
4	0.023	78 / 9013	Overlap_fetal_midbrain_K9K27me3
5	0.030	4 / 156	Mid_Frontal_Lobe_TssA
6	0.052	12 / 953	Fetal_Enh
7	0.092	10 / 831	Fetal_HetRpts
8	0.119	51 / 5940	Overlap_fetal_midbrain_HetRpts
9	0.121	5 / 349	Fetal_ZNF
10	0.130	7 / 564	Mid_Frontal_Lobe_EnhP
11	0.134	9 / 786	Fetal_EnhG
12	0.154	9 / 812	Mid_Frontal_Lobe_TssP
13	0.217	11 / 1122	Fetal_K9K27me3
14	0.273	5 / 468	Mid_Frontal_Lobe_TssF
15	0.353	2 / 166	Mid_Frontal_Lobe_Tx
16	0.372	13 / 1548	Mid_Frontal_Lobe_K9K27me3
17	0.405	1 / 69	Overlap_fetal_midbrain_Tx
18	0.479	19 / 2462	Mid_Frontal_Lobe_HetRpts
19	0.489	8 / 1013	Fetal_TssP
20	0.513	2 / 229	Mid_Frontal_Lobe_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 10	GENTLES_modul13
2	0.09	1 / 14	LIU_COMMON_CANCER_GENES
3	0.10	1 / 14	LIU_PROSTATE_CANCER_DN
4	0.11	1 / 15	RHODES_CANCER_META_SIGNATURE
5	0.11	1 / 15	WANG_ER_UP
6	0.11	1 / 15	GENTLES_modul10
7	0.11	1 / 15	GENTLES_modul11
8	0.11	1 / 16	GENTLES_modul7
9	0.20	2 / 111	PanCan_RAS_geneset_nanostring
10	0.20	0 / 14	LIU_LIVER_CANCER
11	0.30	1 / 47	PanCan_DNARepair_geneset_nanostring
12	0.30	1 / 48	KUIPER_MM poor survival
13	0.33	2 / 156	PanCan_PI3K_geneset_nanostring
14	0.46	1 / 82	PanCan_TXmisReg_geneset_nanostring
15	0.57	1 / 113	PanCan_Driver_Gene_geneset_nanostring
16	0.58	3 / 401	Lembcke_Colonic Inflammation
17	0.60	1 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.60	1 / 121	PanCan_MAPK_geneset_nanostring
19	0.66	2 / 298	SPANG_BCL6−index2
20	0.68	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−04	33 / 2577	nucleoplasm
2	4e−03	13 / 747	nucleolus
3	5e−03	4 / 92	early endosome membrane
4	5e−03	2 / 15	U1 snRNP
5	6e−03	56 / 5696	nucleus
6	7e−03	2 / 17	SMN−Sm protein complex
7	7e−03	91 / 10605	intracellular
8	9e−03	5 / 170	nuclear speck
9	1e−02	5 / 175	early endosome
10	1e−02	2 / 21	histone methyltransferase complex
11	1e−02	2 / 25	MLL1 complex
12	2e−02	34 / 3214	protein complex
13	3e−02	72 / 8205	cytoplasm
14	3e−02	6 / 308	focal adhesion
15	3e−02	3 / 92	spliceosomal complex
16	3e−02	96 / 11774	cell
17	4e−02	2 / 41	cleavage furrow
18	4e−02	9 / 616	endosome
19	6e−02	9 / 663	chromosome
20	7e−02	2 / 59	chromosome, centromeric region

Chr

Rank	p−value	#in/all	Geneset
1	0.1	3 / 151	Chr 21
2	0.1	6 / 465	Chr 15
3	0.1	6 / 469	Chr 8
4	0.2	8 / 775	Chr 12
5	0.2	6 / 551	Chr X
6	0.3	9 / 993	Chr 2
7	0.3	4 / 398	Chr 20
8	0.4	6 / 687	Chr 6
9	0.4	6 / 689	Chr 7
10	0.4	7 / 840	Chr 17
11	0.5	3 / 335	Chr 22
12	0.5	2 / 221	Chr 18
13	0.5	5 / 649	Chr 16
14	0.6	2 / 262	Chr 13
15	0.6	4 / 558	Chr 4
16	0.7	7 / 1037	Chr 19
17	0.7	3 / 462	Chr 14
18	0.7	5 / 801	Chr 11
19	0.8	5 / 838	Chr 3
20	0.8	9 / 1500	Chr 1

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.004	6 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
2	0.007	76 / 8415	Quies3_Colon
3	0.027	81 / 9482	TssA_Colon
4	0.036	86 / 10290	TssWk_Colon
5	0.053	7 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	0.058	37 / 3897	Quies1_Colon
7	0.058	1 / 8	Boland_CRC−MMR−system
8	0.091	5 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	0.099	2 / 71	Marisa_CRC−cluster−g
10	0.112	8 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	0.120	31 / 3383	EnhWk2_Colon
12	0.124	4 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
13	0.126	1 / 18	Boland_CRC−MSI−A6−A10
14	0.136	7 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
15	0.143	78 / 9653	Enh_Colon
16	0.177	2 / 102	Marisa_CRC−cluster−d
17	0.201	69 / 8580	TxWk_Colon
18	0.213	43 / 5155	EnhWk1_Colon
19	0.220	1 / 33	Marisa_CRC−cluster−e
20	0.254	32 / 3812	TssD1_Colon

Disease

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

Glio

Rank	p−value	#in/all	Geneset
1	0.006	4 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
2	0.007	4 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
3	0.007	4 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
4	0.009	3 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
5	0.014	4 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	0.017	3 / 72	laffaire_hypermeth_LGG_vs_control
7	0.018	3 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
8	0.019	3 / 75	Weller_LGG_A_vs_O_DOWN
9	0.036	2 / 40	in vivo astrocytes vs. cultured astroglia
10	0.045	2 / 45	Christensen_hypermethylated_in_primary_glioblastoma
11	0.059	3 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
12	0.072	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−A_UP
13	0.079	1 / 11	Martinez_Glio_hypermeth
14	0.086	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
15	0.096	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
16	0.126	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
17	0.179	9 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
18	0.243	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
19	0.243	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
20	0.291	4 / 365	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−07	11 / 218	BILD_E2F3_ONCOGENIC_SIGNATURE
2	1e−04	4 / 36	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
3	2e−04	3 / 15	COLLIS_PRKDC_REGULATORS
4	2e−04	3 / 16	BIOCARTA_EIF_PATHWAY
5	3e−04	3 / 17	REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PLC_BETA
6	4e−04	4 / 47	SUNG_METASTASIS_STROMA_DN
7	5e−04	4 / 49	SANSOM_WNT_PATHWAY_REQUIRE_MYC
8	5e−04	6 / 135	WHITFIELD_CELL_CYCLE_G1_S
9	7e−04	3 / 24	REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING
10	8e−04	3 / 25	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMAT
11	1e−03	19 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	1e−03	4 / 65	REACTOME_OPIOID_SIGNALLING
13	1e−03	3 / 30	WONG_IFNA2_RESISTANCE_DN
14	2e−03	2 / 8	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
15	2e−03	3 / 32	DOANE_BREAST_CANCER_ESR1_DN
16	2e−03	6 / 171	REACTOME_METABOLISM_OF_RNA
17	2e−03	2 / 9	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELL
18	2e−03	21 / 1460	PUJANA_BRCA1_PCC_NETWORK
19	3e−03	2 / 12	HASINA_NOL7_TARGETS_DN
20	3e−03	2 / 12	DISTECHE_ESCAPED_FROM_X_INACTIVATION

HM

Rank	p−value	#in/all	Geneset
1	0.04	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
2	0.04	4 / 176	HALLMARK_HYPOXIA
3	0.05	4 / 183	HALLMARK_GLYCOLYSIS
4	0.05	4 / 188	HALLMARK_MYC_TARGETS_V1
5	0.09	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
6	0.15	3 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.16	2 / 95	HALLMARK_SPERMATOGENESIS
8	0.18	3 / 197	HALLMARK_E2F_TARGETS
9	0.24	1 / 37	HALLMARK_APICAL_SURFACE
10	0.24	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
11	0.27	2 / 137	HALLMARK_UV_RESPONSE_DN
12	0.28	2 / 140	HALLMARK_APOPTOSIS
13	0.30	2 / 146	HALLMARK_DNA_REPAIR
14	0.34	2 / 162	HALLMARK_COMPLEMENT
15	0.35	1 / 57	HALLMARK_MYC_TARGETS_V2
16	0.36	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
17	0.36	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
18	0.36	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
19	0.39	2 / 181	HALLMARK_P53_PATHWAY
20	0.43	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 18	DUMEAUX_High bmi enriched genes
2	0.2	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 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.02	3 / 81	Subero_INT_hyper_meth
2	0.04	3 / 96	Subero_DLBCL_hyper_meth
3	0.04	2 / 40	Subero_mBL_hyper_meth
4	0.05	66 / 7592	HOPP_Active_promoter
5	0.05	2 / 47	Subero_FL_hyper_meth
6	0.07	1 / 10	DAVE_BL_DN
7	0.07	2 / 60	Subero_T−ALL_hyper_meth
8	0.09	1 / 12	BENTINK_mBL_DOWN
9	0.09	1 / 13	Subero_MCL_hypo_meth
10	0.10	59 / 6929	HOPP_Txn_elongation
11	0.11	1 / 16	ROSOLOWSKI_red UP
12	0.12	1 / 17	DAVE_NFkB BL DN
13	0.12	1 / 17	Aukema_BCL2 UP_BCL6 DN
14	0.12	13 / 1218	SPANG_BCR UP
15	0.13	4 / 256	SPANG_IL21 DN
16	0.14	60 / 7209	HOPP_Weak_promoter
17	0.15	55 / 6564	HOPP_Strong_enhancer
18	0.15	4 / 275	TARTE_Mature plasma cell signature
19	0.17	44 / 5184	HOPP_Txn_transition
20	0.23	1 / 34	Subero_B−ALL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	0.007	2 / 17	histone methyltransferase activity (H3−K4 specific)
2	0.007	4 / 102	mRNA binding
3	0.010	2 / 20	phosphatidylinositol phospholipase C activity
4	0.010	5 / 176	transcription regulatory region DNA binding
5	0.012	2 / 22	histone−lysine N−methyltransferase activity
6	0.013	2 / 23	phosphoric diester hydrolase activity
7	0.015	2 / 25	transferase activity, transferring acyl groups other than amino−acyl groups
8	0.022	4 / 142	calmodulin binding
9	0.024	3 / 83	translation factor activity, RNA binding
10	0.030	4 / 156	protein C−terminus binding
11	0.042	7 / 430	lipid binding
12	0.047	16 / 1365	RNA binding
13	0.047	14 / 1149	enzyme binding
14	0.053	4 / 189	methyltransferase activity
15	0.056	2 / 51	translation initiation factor activity
16	0.072	1 / 10	estradiol 17−beta−dehydrogenase activity
17	0.072	1 / 10	glycine binding
18	0.072	1 / 10	histone methyltransferase activity
19	0.072	1 / 10	receptor signaling protein tyrosine kinase activity
20	0.075	45 / 4992	ion binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	6 / 233	hsa−miR−27a
2	0.010	6 / 246	hsa−miR−27b
3	0.011	7 / 327	hsa−miR−367
4	0.013	3 / 66	hsa−miR−643
5	0.014	5 / 189	hsa−miR−128
6	0.014	3 / 67	hsa−miR−1246
7	0.014	3 / 68	hsa−miR−649
8	0.015	3 / 69	hsa−miR−873
9	0.016	5 / 198	hsa−miR−448
10	0.020	2 / 29	hsa−miR−1225−3p
11	0.021	6 / 288	hsa−miR−34a
12	0.024	3 / 83	hsa−miR−582−3p
13	0.028	2 / 35	hsa−miR−770−5p
14	0.030	3 / 90	hsa−miR−216b
15	0.030	4 / 157	hsa−miR−141
16	0.036	2 / 40	hsa−miR−182*
17	0.039	3 / 100	hsa−miR−574−5p
18	0.039	2 / 42	hsa−miR−769−3p
19	0.040	3 / 101	hsa−miR−516b
20	0.041	3 / 102	hsa−miR−410

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.03	1 / 4	MYC_TFs
2	0.03	44 / 4617	ICGC_Tcf12_targets
3	0.04	38 / 3924	ICGC_Zeb1_targets
4	0.05	48 / 5219	ICGC_Tcf3_targets
5	0.05	53 / 5890	ICGC_Elf1_targets
6	0.05	45 / 4879	ICGC_Pmlsc71910_targets
7	0.07	43 / 4689	ICGC_Taf1_targets
8	0.07	48 / 5355	ICGC_Pol2_targets
9	0.08	8 / 595	ICGC_NrsfPcr2_targets
10	0.09	37 / 4054	ICGC_Egr1_targets
11	0.10	53 / 6114	ICGC_Runx3_targets
12	0.10	42 / 4706	ICGC_Sp1_targets
13	0.13	39 / 4414	ICGC_Bclaf101388_targets
14	0.13	45 / 5200	ICGC_Mta3_targets
15	0.14	38 / 4314	ICGC_Ebfsc137065_targets
16	0.14	47 / 5495	ICGC_Yy1_targets
17	0.16	14 / 1400	ICGC_Myc_targets
18	0.17	42 / 4909	ICGC_Stat5_targets
19	0.17	20 / 2136	ICGC_GabpPcr2_targets
20	0.20	32 / 3700	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 29	VAQUERIZAS_Fetal lung
2	0.2	1 / 38	VAQUERIZAS_Whole brain
3	0.3	1 / 40	VAQUERIZAS_Thyroid
4	0.3	2 / 143	VAQUERIZAS_General
5	0.4	1 / 58	VAQUERIZAS_Lung
6	1.0	0 / 36	VAQUERIZAS_Fetal brain
7	1.0	0 / 41	VAQUERIZAS_Placenta
8	1.0	0 / 26	VAQUERIZAS_Liver
9	1.0	0 / 33	VAQUERIZAS_Prostate
10	1.0	0 / 29	VAQUERIZAS_Smooth muscle
11	1.0	0 / 45	VAQUERIZAS_Uterus
12	1.0	0 / 9	VAQUERIZAS_Kidney
13	1.0	0 / 23	VAQUERIZAS_Spinal cord
14	1.0	0 / 37	VAQUERIZAS_Thymus
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	6 / 350	WIRTH_Nervous System
2	0.06	1 / 8	WIRTH_Tonsil
3	0.07	1 / 9	PALMER_CD8+ T−Cell signature up
4	0.11	2 / 74	WIRTH_Mucosa
5	0.49	3 / 350	WIRTH_Immune system
6	0.58	1 / 114	PALMER_T−Cell 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 / 12	WIRTH_Thymus
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 11	WIRTH_Globus pallidus
15	1.00	0 / 14	WIRTH_Telencephalon
16	1.00	0 / 11	WIRTH_Cortex cerebri
17	1.00	0 / 10	WIRTH_Hippocampus
18	1.00	0 / 10	WIRTH_Thalamus
19	1.00	0 / 12	WIRTH_Cerebellum
20	1.00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	9 / 1115	LU_BPDE 1h DN
2	0.7	26 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

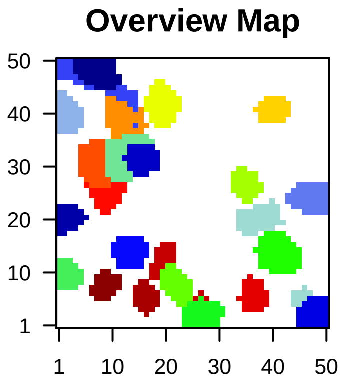
Correlation Clusters

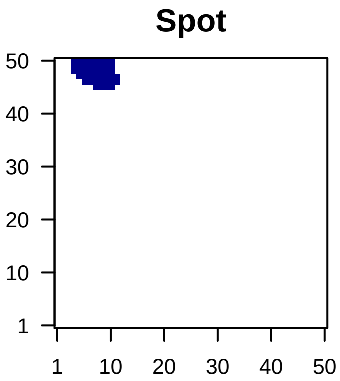
Spot Summary: E

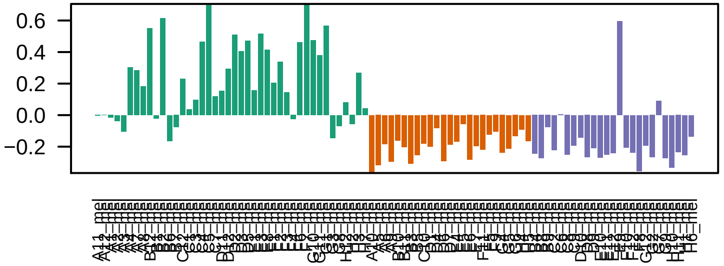
metagenes = 43
genes = 442

<r> metagenes = 0.94
<r> genes = 0.21
beta: r2= 5.25 / log p= −Inf

samples with spot = 24 (26.1 %)
MSC1 : 23 (54.8 %)
MSC3 : 1 (4 %)





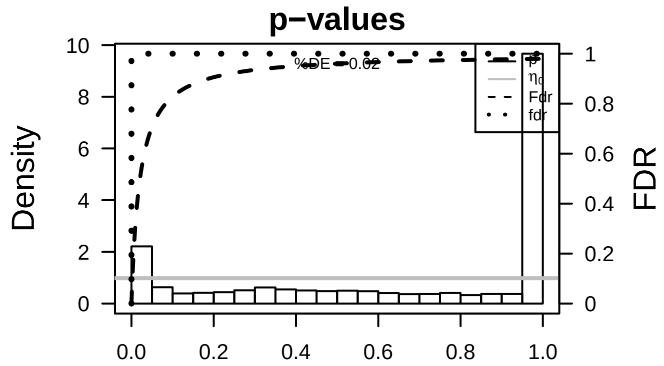


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	HTN1	2.69	−0.09	0.35	HTN1	histatin 1 [Source:HGNC Symbol;Acc:HGNC:5283]
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	PLK1	2.09	−0.46	0.65	PLK1	polo−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
8	TMEM71	2.04	−0.12	0.25	TMEM71	transmembrane protein 71 [Source:HGNC Symbol;Acc:HGN
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	ITGA6	1.91	−0.26	0.33	ITGA6	integrin, alpha 6 [Source:HGNC Symbol;Acc:HGNC:6142]
18	SGOL1	1.91	−0.72	0.75	SGOL1	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
19	HIST1H4E	1.9	−0.46	0.45	HIST1H4E	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
20	FCGR2A	1.9	−0.23	0.29	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32) [Source:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	95 / 142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−99	161 / 550	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	1e−93	153 / 700	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
4	2e−87	140 / 616	GSEA	BENPORATH_CYCLING_GENES
5	5e−85	79 / 139	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	1e−84	181 / 1192	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	5e−83	11 / 16	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	1e−79	116 / 436	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	7e−77	99 / 305	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
10	9e−76	90 / 242	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
11	3e−75	96 / 291	GSEA	HORIUCHI_WTAP_TARGETS_DN
12	9e−72	162 / 1110	BP	cell cycle
13	1e−71	72 / 145	GSEA	CHANG_CYCLING_GENES
14	6e−71	150 / 944	GSEA	NUYTTEN_EZH2_TARGETS_DN
15	6e−71	170 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
16	2e−70	73 / 155	GSEA	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
17	2e−69	94 / 312	BP	mitotic nuclear division
18	2e−66	102 / 409	BP	cell division
19	2e−66	100 / 390	GSEA	PUJANA_BRCA2_PCC_NETWORK
20	1e−62	74 / 196	HM	HALLMARK_G2M_CHECKPOINT
21	1e−60	97 / 412	BP	mitotic cell cycle
22	4e−58	67 / 170	GSEA	WHITFIELD_CELL_CYCLE_G2
23	5e−58	57 / 110	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
24	1e−57	71 / 201	GSEA	WHITFIELD_CELL_CYCLE_G2_M
25	4e−57	59 / 124	GSEA	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
26	6e−57	79 / 270	GSEA	BASAKI_YBX1_TARGETS_UP
27	4e−55	127 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
28	6e−55	53 / 99	GSEA	LEE_EARLY_T_LYMPHOCYTE_UP
29	2e−54	68 / 197	HM	HALLMARK_E2F_TARGETS
30	3e−53	97 / 489	Canc	Lembcke_Normal vs Adenoma
31	3e−52	62 / 165	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
32	4e−52	81 / 327	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
33	1e−51	48 / 84	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
34	3e−51	68 / 216	GSEA	MARKEY_RB1_ACUTE_LOF_DN
35	5e−51	50 / 96	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
36	3e−50	112 / 724	GSEA	PUJANA_CHEK2_PCC_NETWORK
37	4e−50	85 / 388	GSEA	REACTOME_CELL_CYCLE
38	1e−48	59 / 162	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
39	2e−48	82 / 373	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
40	4e−48	52 / 118	GSEA	ODONNELL_TFRC_TARGETS_DN



Aging

Rank	p-value	#in/all	Geneset
1	0.1	6 / 111	HORVATH_aging_genes meth UP
2	1.0	1 / 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	5e-83	11 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	3e-53	97 / 489	Lembcke_Normal vs Adenoma
3	7e-30	8 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	2e-06	2 / 15	RHODES_CANCER_META_SIGNATURE
5	4e-05	10 / 70	SHAUGHNESSY_MM high risk
6	8e-05	5 / 16	WOLFER_overlap genes
7	4e-04	4 / 13	BEN-PORATH_UP
8	5e-04	7 / 48	KUIPER_MM poor survival
9	1e-03	5 / 29	KUIPER_MM good survival
10	3e-03	3 / 10	GENTLES_modul3
11	3e-03	10 / 120	PanCan_CC+Apop_geneset_nanostring
12	1e-02	3 / 16	GENTLES_modul16
13	1e-02	1 / 14	LIU_COMMON_CANCER_GENES
14	7e-02	2 / 15	GENTLES_modul4
15	8e-02	2 / 16	GENTLES_modul6
16	1e-01	3 / 40	PanCan_HK_geneset_nanostring
17	2e-01	4 / 82	PanCan_TXmisReg_geneset_nanostring
18	3e-01	1 / 12	LIU_BREAST_CANCER
19	3e-01	1 / 12	LIU_PROSTATE_CANCER_UP
20	3e-01	1 / 13	GENTLES_modul12

Colon Cancer

Rank	p-value	#in/all	Geneset
1	1e-14	59 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	1e-10	343 / 9482	TssA_Colon
3	4e-10	55 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
4	9e-10	361 / 10290	TssWk_Colon
5	2e-03	280 / 8415	Quies3_Colon
6	1e-02	134 / 3812	TssD1_Colon
7	2e-02	2 / 8	Marisa_CRC-C6
8	3e-02	234 / 7203	TssF_Colon
9	6e-02	1 / 2	Hewish_dMMR-secondary-mutations_Cell-motility
10	8e-02	2 / 16	Juehling-MSI-enriched-in-6
11	1e-01	2 / 18	Boland_CRC-MSI-A6-A10
12	1e-01	1 / 4	Juehling_HNPCC-mutated-in-6-to-8
13	1e-01	187 / 5880	TssD2_Colon
14	1e-01	1 / 5	Budinska_C_CIMP-H-like_UP
15	1e-01	266 / 8580	TxWk_Colon
16	2e-01	5 / 102	Marisa_CRC-cluster-d
17	2e-01	2 / 29	Marisa_CRC-cluster-c
18	2e-01	1 / 8	Marisa_CRC-C1
19	2e-01	1 / 8	Juehling-MSI-enriched-in-7
20	2e-01	21 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

GSEA C2

Rank	p-value	#in/all	Geneset
1	1e-99	161 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	1e-93	153 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
3	2e-87	140 / 616	BENPORATH_CYCLING_GENES
4	5e-85	79 / 139	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e-84	181 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
6	5e-83	11 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	1e-79	116 / 436	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	7e-77	99 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	9e-76	90 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
10	3e-75	96 / 291	HORIUCHI_WTAP_TARGETS_DN
11	1e-71	72 / 145	CHANG_CYCLING_GENES
12	6e-71	150 / 944	NUYTTEN_EZH2_TARGETS_DN
13	6e-71	170 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	2e-70	73 / 155	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
15	2e-66	100 / 390	PUJANA_BRCA2_PCC_NETWORK
16	4e-58	67 / 170	WHITFIELD_CELL_CYCLE_G2
17	5e-58	57 / 110	WHITEFORD_PEDIATRIC_CANCER_MARKERS
18	1e-57	71 / 201	WHITFIELD_CELL_CYCLE_G2_M
19	4e-57	59 / 124	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
20	6e-57	79 / 270	BASAKI_YBX1_TARGETS_UP

Lymphoma

Rank	p-value	#in/all	Geneset
1	4e-31	324 / 6929	HOPP_Txn_elongation
2	1e-30	341 / 7592	HOPP_Active_promoter
3	2e-21	47 / 294	TARTE_Plasmablast signature
4	4e-16	236 / 5184	HOPP_Txn_transition
5	6e-11	281 / 7209	HOPP_Weak_promoter
6	5e-08	18 / 129	DAVE_BL-vs-DLBCL
7	1e-07	69 / 1218	SPANG_BCR UP
8	1e-05	12 / 89	ROSOLOWSKI_blue total
9	4e-05	236 / 6564	HOPP_Strong_enhancer
10	5e-04	203 / 5693	HOPP_Weak_enhancer
11	2e-03	4 / 19	DAVE_c-myc BL UP
12	3e-03	193 / 5538	HOPP_Weak_txn
13	8e-02	2 / 16	DAVE_BL Inter
14	9e-02	1 / 3	WRIGHT_custom GCB-DLBCL UP
15	2e-01	11 / 280	SPANG_CD40 6hrs UP
16	2e-01	1 / 8	MASCQUE_GCB UP
17	2e-01	1 / 8	YAMANE_AICDA_targets_nonrecruited
18	2e-01	5 / 109	ROSOLOWSKI_green total
19	2e-01	4 / 82	ROSOLOWSKI_green UP
20	3e-01	70 / 2211	HOPP_Repetitive

Pathw Act

Rank	p-value	#in/all	Geneset
1	0.07	2 / 15	BENTINK_ras.6
2	0.30	1 / 12	BENTINK_e2f3.2
3	0.30	1 / 12	BENTINK_ras.1
4	0.32	1 / 13	BENTINK_src.10
5	1.00	0 / 12	GUSTAFSON_PI3K_UP
6	1.00	0 / 13	GUSTAFSON_PI3K_DN
7	1.00	0 / 14	BENTINK_e2f3.1
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 9	BENTINK_ras.4
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p-value	#in/all	Geneset
1	0.05	2 / 12	WIRTH_Lymphocytes
2	0.06	16 / 350	WIRTH_Immune system
3	0.12	6 / 114	PALMER_T-Cell signature up
4	0.26	1 / 10	WIRTH_Thalamus
5	0.28	1 / 11	WIRTH_Globus pallidus
6	0.30	1 / 12	WIRTH_Cerebellum
7	0.35	8 / 225	PALMER_Granulocytes signature up
8	0.83	4 / 194	PALMER_B-Cell signature up
9	0.98	5 / 350	WIRTH_Nervous System
10	1.00	0 / 32	WIRTH_Pancreas
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 13	WIRTH_B-cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 14	WIRTH_Telencephalon
18	1.00	0 / 11	WIRTH_Cortex cerebri
19	1.00	0 / 10	WIRTH_Hippocampus
20	1.00	0 / 107	WIRTH_Testis

BP

Rank	p-value	#in/all	Geneset
1	9e-72	162 / 1110	cell cycle
2	2e-69	94 / 312	mitotic nuclear division
3	2e-66	102 / 409	cell division
4	1e-60	97 / 412	mitotic cell cycle
5	2e-46	57 / 160	chromosome segregation
6	3e-30	87 / 721	chromosome organization
7	4e-24	81 / 768	DNA metabolic process
8	2e-20	32 / 133	G2/M transition of mitotic cell cycle
9	5e-20	64 / 581	cytoskeleton organization
10	1e-17	14 / 20	mitotic sister chromatid segregation
11	8e-15	24 / 108	nucleosome assembly
12	3e-13	15 / 41	CENP-A containing nucleosome assembly
13	8e-13	58 / 694	protein complex assembly
14	1e-10	16 / 68	microtubule-based movement
15	3e-10	8 / 12	mitotic chromosome condensation
16	5e-10	11 / 30	mitotic metaphase plate congression
17	6e-10	59 / 843	macromolecular complex assembly
18	7e-10	10 / 24	mitotic cytokinesis
19	1e-09	76 / 1255	cellular component assembly
20	6e-09	9 / 22	mitotic spindle organization

CC

Rank	p-value	#in/all	Geneset
1	3e-45	102 / 663	chromosome
2	1e-32	291 / 5696	nucleus
3	4e-27	122 / 1465	cytoskeleton
4	2e-24	26 / 59	chromosome, centromeric region
5	6e-24	28 / 75	condensed chromosome kinetochore
6	3e-23	26 / 65	kinetochore
7	4e-23	162 / 2577	nucleoplasm
8	3e-22	63 / 512	microtubule organizing center
9	4e-22	29 / 93	spindle pole
10	7e-20	393 / 10605	intracellular
11	3e-19	50 / 377	centrosome
12	2e-18	28 / 113	spindle
13	1e-16	372 / 9988	organelle
14	1e-16	17 / 38	spindle microtubule
15	2e-16	170 / 3214	protein complex
16	1e-13	34 / 250	microtubule
17	9e-13	134 / 2507	cytosol
18	4e-12	37 / 331	nuclear chromosome
19	4e-12	15 / 48	kinesin complex
20	2e-11	21 / 115	midbody

Disease

Rank	p-value	#in/all	Geneset
1	8e-24	60 / 435	GUDJ_psoriasis up
2	3e-01	1 / 11	BCHETNIA_EBM up
3	5e-01	1 / 20	BCHETNIA_EBM-DM up
4	1e+00	3 / 294	GUDJ_psoriasis down
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-62	74 / 196	HALLMARK_G2M_CHECKPOINT
2	2e-54	68 / 197	HALLMARK_E2F_TARGETS
3	2e-24	42 / 195	HALLMARK_MITOTIC_SPINDLE
4	4e-06	13 / 95	HALLMARK_SPERMATOGENESIS
5	2e-02	11 / 183	HALLMARK_GLYCOLYSIS
6	2e-02	11 / 188	HALLMARK_MYC_TARGETS_V1
7	6e-02	6 / 93	HALLMARK_PEROXISOME
8	1e-01	8 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
9	2e-01	8 / 196	HALLMARK_MTORC1_SIGNALING
10	2e-01	3 / 57	HALLMARK_MYC_TARGETS_V2
11	2e-01	6 / 141	HALLMARK_FATTY_ACID_METABOLISM
12	3e-01	7 / 174	HALLMARK_HEME_METABOLISM
13	3e-01	4 / 91	HALLMARK_BILE_ACID_METABOLISM
14	4e-01	6 / 167	HALLMARK_IL2_STAT5_SIGNALING
15	4e-01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
16	4e-01	5 / 146	HALLMARK_DNA_REPAIR
17	6e-01	1 / 29	HALLMARK_NOTCH_SIGNALING
18	6e-01	4 / 140	HALLMARK_APOPTOSIS
19	6e-01	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
20	6e-01	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

MF

Rank	p-value	#in/all	Geneset
1	3e-17	31 / 156	microtubule binding
2	5e-12	334 / 8984	protein binding
3	1e-10	16 / 69	microtubule motor activity
4	4e-09	21 / 152	histone binding
5	3e-07	42 / 609	cytoskeletal protein binding
6	9e-07	27 / 316	protein kinase binding
7	4e-06	6 / 16	ATP-dependent microtubule motor activity, plus-end-directed
8	2e-04	6 / 29	nucleosomal DNA binding
9	2e-04	24 / 364	ATPase activity
10	4e-04	7 / 46	methylated histone binding
11	5e-04	60 / 1309	ATP binding
12	6e-04	4 / 14	DNA binding, bending
13	9e-04	53 / 1149	enzyme binding
14	1e-03	84 / 2037	DNA binding
15	1e-03	8 / 71	single-stranded DNA binding
16	2e-03	22 / 373	protein heterodimerization activity
17	2e-03	22 / 376	chromatin binding
18	3e-03	409 / 13179	molecular_function
19	3e-03	58 / 1365	RNA binding
20	4e-03	5 / 36	tubulin binding

TF

Rank	p-value	#in/all	Geneset
1	7e-06	71 / 1418	ICGC_Ets1_targets
2	4e-05	59 / 1171	KIM_MYC targets
3	4e-04	152 / 4032	ICGC_Creb1_targets
4	4e-04	63 / 1383	ICGC_Six5_targets
5	7e-04	73 / 1701	HEBENSTREIT_high expression TF
6	1e-03	170 / 4689	ICGC_Taf1_targets
7	4e-03	170 / 4829	ICGC_Nficsc81335_targets
8	4e-03	168 / 4774	ICGC_Foxm1_targets
9	6e-03	170 / 4879	ICGC_Pmlsc71910_targets
10	6e-03	74 / 1878	ICGC_Cebpbsc150_targets
11	7e-03	164 / 4706	ICGC_Sp1_targets
12	8e-03	163 / 4682	ICGC_Pol24_targets
13	1e-02	183 / 5408	ICGC_Pou2_targets
14	6e-02	179 / 5495	ICGC_Yy1_targets
15	7e-02	83 / 2391	ICGC_Pbx3_targets
16	8e-02	190 / 5890	ICGC_Elf1_targets
17	8e-02	145 / 4414	ICGC_Bclaf101388_targets
18	1e-01	4 / 59	MYC_Targets UP
19	1e-01	22 / 553	ICGC_RxraPcr1_targets
20	1e-01	167 / 5200	ICGC_Mta3_targets

Toxic

Rank	p-value	#in/all	Geneset
1	0.3	36 / 1115	LU_BPDE 1n DN
2	1.0	83 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p-value	#in/all	Geneset
1	4e-21	366 / 9330	Overlap_fetal_midbrain_ReprPC
2	1e-09	327 / 9013	Overlap_fetal_midbrain_K9K27me3
3	5e-07	91 / 1845	Fetal_Quies
4	7e-05	45 / 831	Fetal_HetRpts
5	2e-02	45 / 1122	Fetal_K9K27me3
6	4e-02	51 / 1333	Fetal_ReprPCWk
7	5e-02	9 / 163	Fetal_ReprPC
8	6e-02	193 / 5940	Overlap_fetal_midbrain_HetRpts
9	2e-01	7 / 158	Overlap_fetal_midbrain_Het
10	4e-01	31 / 989	Mid_Frontal_Lobe_Quies
11	4e-01	24 / 769	Overlap_fetal_midbrain_ZNF
12	5e-01	11 / 349	Fetal_ZNF
13	5e-01	32 / 1050	Fetal_EnhP
14	5e-01	37 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	5e-01	7 / 229	Mid_Frontal_Lobe_TxTrans
16	7e-01	263 / 9020	Overlap_fetal_midbrain_ReprPCWk
17	8e-01	25 / 953	Fetal_Enh
18	8e-01	20 / 786	Fetal_EnhG
19	8e-01	7 / 304	Fetal_Het
20	8e-01	19 / 765	Mid_Frontal_Lobe_Het

Chr

Rank	p-value	#in/all	Geneset
1	0.02	33 / 775	Chr 12
2	0.04	21 / 469	Chr 8
3	0.06	20 / 462	Chr 14
4	0.07	23 / 558	Chr 4
5	0.10	19 / 465	Chr 15
6	0.10	53 / 1500	Chr 1
7	0.23	24 / 687	Chr 6
8	0.25	10 / 262	Chr 13
9	0.33	23 / 696	Chr 5
10	0.38	18 / 552	Chr 10
11	0.41	31 / 993	Chr 2
12	0.45	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
13	0.64	11 / 398	Chr 20
14	0.65	16 / 576	Chr 9
15	0.65	6 / 221	Chr 18
16	0.66	4 / 151	Chr 21
17	0.78	8 / 335	Chr 22
18	0.82	21 / 838	Chr 3
19	0.82	21 / 840	Chr 17
20	0.87	19 / 801	Chr 11

Glio

Rank	p-value	#in/all	Geneset
1	1e-99	95 / 142	WILLSCHER_GBM_Verhaak-CL_up (C)
2	2e-30	28 / 49	developing astrocytes
3	5e-17	22 / 71	Weller_LGG_gradeII-vs-III_DOWN
4	2e-06	11 / 62	cultured astroglia vs. in vivo astrocytes
5	2e-03	40 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	3e-03	19 / 315	WILLSCHER_GBM_Verhaak-PNwt & CL_up
7	6e-03	5 / 39	OPC
8	8e-03	2 / 5	Phillips Prolif up vs PN & MES
9	2e-02	6 / 75	Weller_LGG_A_vs_O_DOWN
10	3e-02	2 / 10	WILLSCHER_GBM_LTSmut_proteomics-A_UP
11	4e-02	2 / 11	WILLSCHER_GBM_LTSmut_proteomics-B_UP
12	1e-01	1 / 4	WILLSCHER_GBM_STSwt_proteomics-L_UP
13	2e-01	2 / 25	Shaw_down_in_1p19q
14	2e-01	2 / 29	shaw_responders_down_in_oligo_glioma
15	3e-01	1 / 11	WILLSCHER__GBM_LTSwt_proteomics-C_UP
16	3e-01	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
17	3e-01	3 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
18	3e-01	1 / 14	VERHAAK_PN subtype
19	4e-01	1 / 15	VERHAAK_MES subtype
20	4e-01	11 / 332	Up

Lifestyle

Rank	p-value	#in/all	Geneset
1	0.1	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
2	0.6	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 / 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	

miRNA target

Rank	p-value	#in/all	Geneset
1	3e-06	16 / 135	hsa-miR-28-5p
2	3e-04	11 / 105	hsa-miR-376b
3	3e-04	9 / 74	hsa-miR-708
4	4e-04	18 / 243	hsa-miR-122
5	4e-04	14 / 166	hsa-miR-548g
6	6e-04	14 / 170	hsa-miR-7
7	6e-04	6 / 36	hsa-miR-518e
8	9e-04	8 / 68	hsa-miR-1184
9	1e-03	25 / 433	hsa-miR-548n
10	1e-03	13 / 164	hsa-miR-323b-5p
11	2e-03	7 / 59	hsa-miR-492
12	2e-03	9 / 93	hsa-miR-299-3p
13	2e-03	20 / 327	hsa-miR-590-3p
14	2e-03	20 / 328	hsa-miR-548a-5p
15	2e-03	10 / 115	hsa-miR-154
16	2e-03	13 / 176	hsa-miR-23b
17	2e-03	18 / 288	hsa-miR-34a
18	3e-03	8 / 80	hsa-miR-876-5p
19	3e-03	18 / 289	hsa-miR-186
20	3e-03	10 / 118	hsa-miR-509-3p

TF Tissue

Rank	p-value	#in/all	Geneset
1	0.1	3 / 37	VAQUERIZAS_Thymus
2	0.1	4 / 59	VAQUERIZAS_Whole blood
3	0.1	3 / 38	VAQUERIZAS_Testis
4	0.1	2 / 19	VAQUERIZAS_Tonsil
5	0.3	1 / 11	VAQUERIZAS_Fetal liver
6	0.3	1 / 12	VAQUERIZAS_Skin
7	0.4	1 / 17	VAQUERIZAS_Heart
8	0.5	2 / 58	VAQUERIZAS_Lung
9	0.5	1 / 26	VAQUERIZAS_Liver
10	0.6	1 / 27	VAQUERIZAS_Lymph node
11	0.6	1 / 29	VAQUERIZAS_Smooth muscle
12	0.6	1 / 33	VAQUERIZAS_Prostate
13	0.7	1 / 40	VAQUERIZAS_Thyroid
14	0.7	1 / 45	VAQUERIZAS_Uterus
15	0.8	3 / 143	VAQUERIZAS_General
16	1.0	0 / 36	VAQUERIZAS_Fetal brain
17	1.0	0 / 41	VAQUERIZAS_Placenta
18	1.0	0 / 9	VAQUERIZAS_Kidney
19	1.0	0 / 23	VAQUERIZAS_Spinal cord
20	1.0	0 / 38	VAQUERIZAS_Whole brain

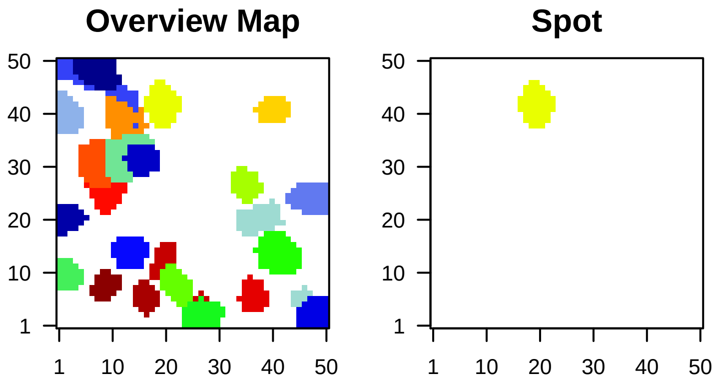
Correlation Clusters

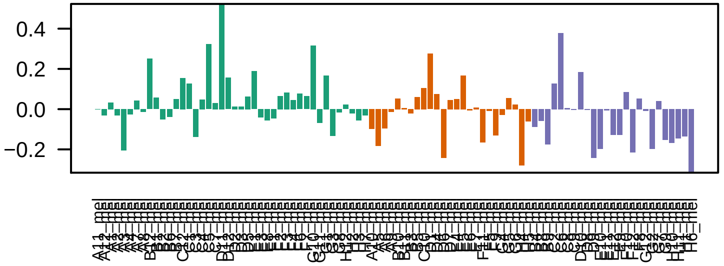
Spot Summary: F

metagenes = 45
genes = 157

<r> metagenes = 0.93
<r> genes = 0.09
beta: r2= 0.79 / log p= −Inf

samples with spot = 10 (10.9 %)
MSC1 : 6 (14.3 %)
MSC2 : 2 (8 %)
MSC3 : 2 (8 %)



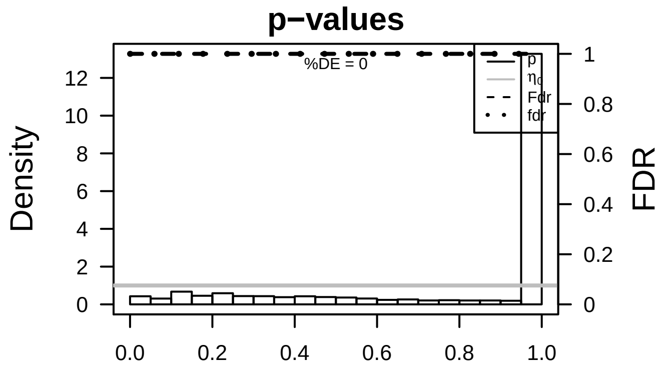


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ERI2	1.89	−0.37	0.35	ERI2	ERI1 exoribonuclease family member 2 [Source:HGNC Symb
2	SHQ1	1.79	−0.67	0.29	SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor [Source:HG
3	USP41	1.78	−0.26	0.29	USP41	ubiquitin specific peptidase 41 [Source:HGNC Symbol;Acc:H
4	RFX2	1.78	−0.41	0.34	RFX2	regulatory factor X, 2 (influences HLA class II expression) [Sc
5	AURKC	1.77	−0.17	0.31	AURKC	aurora kinase C [Source:HGNC Symbol;Acc:HGNC:11391]
6	FAXC	1.75	−0.16	0.43	FAXC	failed axon connections homolog (Drosophila) [Source:HGNC
7	AP3M2	1.69	−0.65	0.34	AP3M2	adaptor−related protein complex 3, mu 2 subunit [Source:HG
8	LPAR2	1.66	−0.05	0.33	LPAR2	lysophosphatidic acid receptor 2 [Source:HGNC Symbol;Acc:
9	UCN2	1.65	−0.02	0.37	UCN2	urocortin 2 [Source:HGNC Symbol;Acc:HGNC:18414]
10	DISP1	1.64	−0.17	0.29	DISP1	dispatched homolog 1 (Drosophila) [Source:HGNC Symbol;A
11	ZNF823	1.63	−0.26	0.26	ZNF823	zinc finger protein 823 [Source:HGNC Symbol;Acc:HGNC:30
12	MGAT1	1.62	−0.49	0.22	MGAT1	mannosyl (alpha−1,3−)−glycoprotein beta−1,2−N−acetylgluc
13	CCDC101	1.62	−0.38	0.44	CCDC101	coiled−coil domain containing 101 [Source:HGNC Symbol;Ac
14	DCLK3	1.59	−0.03	0.39	DCLK3	doublecortin−like kinase 3 [Source:HGNC Symbol;Acc:HGNC
15	SPINK4	1.57	−0.02	0.37	SPINK4	serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symb
16	C11orf74	1.56	−0.37	0.35	C11orf74	chromosome 11 open reading frame 74 [Source:HGNC Symb
17	NDUFAF7	1.56	−0.7	0.33	NDUFAF7	NADH dehydrogenase (ubiquinone) complex I, assembly fact
18	ZBTB17	1.53	−0.51	0.2	ZBTB17	zinc finger and BTB domain containing 17 [Source:HGNC Sy
19	HDX	1.53	−0.3	0.3	HDX	highly divergent homeobox [Source:HGNC Symbol;Acc:HGN
20	COQ3	1.5	−0.41	0.38	COQ3	coenzyme Q3 methyltransferase [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−07	112 / 7592	Lympl	HOPP_Active_promoter
2	2e−07	24 / 687	Chr	Chr 6
3	5e−07	104 / 6929	Lympl	HOPP_Txn_elongation
4	8e−06	90 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
5	9e−06	117 / 8580	Colon	TxWk_Colon
6	9e−06	124 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
7	2e−05	80 / 5184	Lympl	HOPP_Txn_transition
8	3e−05	124 / 9482	Colon	TssA_Colon
9	5e−05	14 / 376	GSEA	OSMAN_BLADDER_CANCER_UP
10	5e−05	119 / 9027	Colon	Tx_Colon
11	7e−05	12 / 294	miRN	hsa−miR−561
12	1e−04	4 / 25	MF	ATP−dependent helicase activity
13	2e−04	99 / 7209	Lympl	HOPP_Weak_promoter
14	5e−04	3 / 15	BP	Golgi to plasma membrane transport
15	6e−04	11 / 322	BP	mitochondrion organization
16	7e−04	4 / 38	TF Tis	VAQUERIZAS_Testis
17	9e−04	80 / 5696	CC	nucleus
18	1e−03	36 / 2037	MF	DNA binding
19	1e−03	3 / 21	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
20	2e−03	12 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
21	2e−03	3 / 23	BP	spliceosomal complex assembly
22	2e−03	88 / 6564	Lympl	HOPP_Strong_enhancer
23	2e−03	19 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
24	2e−03	113 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
25	2e−03	42 / 2577	CC	nucleoplasm
26	2e−03	4 / 53	GSEA	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_UP
27	2e−03	30 / 1664	BP	transcription, DNA−templated
28	2e−03	78 / 5693	Lympl	HOPP_Weak_enhancer
29	3e−03	3 / 26	BP	positive regulation of intrinsic apoptotic signaling pathway
30	3e−03	4 / 56	GSEA	GUO_HEX_TARGETS_DN
31	3e−03	3 / 28	GSEA	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP
32	3e−03	10 / 337	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
33	3e−03	8 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
34	3e−03	18 / 840	GSEA	GEORGES_TARGETS_OF_MIR192_AND_MIR215
35	3e−03	3 / 29	BP	sphingolipid biosynthetic process
36	4e−03	112 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
37	4e−03	127 / 10605	CC	intracellular
38	5e−03	4 / 64	GSEA	SESTO_RESPONSE_TO_UV_C1
39	5e−03	12 / 476	GSEA	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
40	5e−03	3 / 33	GSEA	DORSAM_HOXA9_TARGETS_UP



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 15	Golgi to plasma membrane transport
2	6e−04	11 / 322	mitochondrion organization
3	2e−03	3 / 23	spliceosomal complex assembly
4	2e−03	30 / 1664	transcription, DNA−templated
5	3e−03	3 / 26	positive regulation of intrinsic apoptotic signaling pathway
6	3e−03	3 / 29	sphingolipid biosynthetic process
7	7e−03	2 / 12	mitochondrial fusion
8	8e−03	2 / 13	positive regulation of transcription elongation from RNA polymerase II promot
9	8e−03	2 / 13	rRNA methylation
10	8e−03	4 / 75	regulation of catalytic activity
11	9e−03	10 / 393	mRNA processing
12	1e−02	2 / 15	triglyceride catabolic process
13	1e−02	7 / 229	RNA splicing
14	1e−02	3 / 44	DNA duplex unwinding
15	1e−02	6 / 177	mRNA splicing, via spliceosome
16	1e−02	5 / 131	ribonucleoprotein complex assembly
17	1e−02	5 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
18	1e−02	3 / 47	protein targeting to mitochondrion
19	2e−02	12 / 570	symbiosis, encompassing mutualism through parasitism
20	2e−02	50 / 3644	biosynthetic process

Brain

Rank	p−value	#in/all	Geneset
1	8e−06	90 / 5940	Overlap_fetal_midbrain_HetRpts
2	9e−06	124 / 9330	Overlap_fetal_midbrain_ReprPC
3	2e−03	113 / 9013	Overlap_fetal_midbrain_K9K27me3
4	4e−03	112 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	7e−03	20 / 1050	Fetal_EnhP
6	1e−02	115 / 9528	Overlap_fetal_midbrain_Quies
7	2e−02	44 / 3081	Mid_Frontal_Lobe_ZNF
8	3e−02	5 / 158	Overlap_fetal_midbrain_Het
9	2e−01	8 / 564	Mid_Frontal_Lobe_EnhP
10	3e−01	14 / 1122	Fetal_K9K27me3
11	3e−01	12 / 953	Fetal_Enh
12	3e−01	5 / 349	Fetal_ZNF
13	4e−01	10 / 831	Fetal_HetRpts
14	4e−01	4 / 304	Fetal_Het
15	4e−01	9 / 769	Overlap_fetal_midbrain_ZNF
16	5e−01	11 / 989	Mid_Frontal_Lobe_Quies
17	5e−01	20 / 1845	Fetal_Quies
18	6e−01	11 / 1065	Overlap_fetal_midbrain_Enh
19	7e−01	6 / 656	Overlap_fetal_midbrain_EnhP
20	7e−01	8 / 884	Overlap_fetal_midbrain_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 7	GENTLES_modul18
2	0.09	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.15	1 / 15	GENTLES_modul10
4	0.15	1 / 15	GENTLES_modul11
5	0.21	1 / 22	PanCan_HH_geneset_nanostring
6	0.21	0 / 12	LIU_PROSTATE_CANCER_UP
7	0.33	2 / 111	PanCan_RAS_geneset_nanostring
8	0.35	1 / 40	PanCan_HK_geneset_nanostring
9	0.37	2 / 121	PanCan_MAPK_geneset_nanostring
10	0.39	1 / 47	PanCan_DNARepair_geneset_nanostring
11	0.40	1 / 48	KUIPER_MM poor survival
12	0.48	1 / 61	PanCan_Wnt_geneset_nanostring
13	0.51	0 / 14	LIU_COMMON_CANCER_GENES
14	0.57	2 / 180	SPANG_LPS−index2
15	0.58	1 / 82	PanCan_TXmisReg_geneset_nanostring
16	0.62	4 / 401	Lembcke_Colonic Inflammation
17	0.70	1 / 113	PanCan_Driver_Gene_geneset_nanostring
18	0.72	1 / 120	PanCan_CC+Apop_geneset_nanostring
19	0.76	4 / 489	Lembcke_Normal vs Adenoma
20	0.80	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−04	80 / 5696	nucleus
2	2e−03	42 / 2577	nucleoplasm
3	4e−03	127 / 10605	intracellular
4	7e−03	2 / 12	transcription export complex
5	8e−03	120 / 9988	organelle
6	1e−02	2 / 15	BAF−type complex
7	1e−02	2 / 17	integral component of mitochondrial outer membrane
8	2e−02	2 / 21	transcription factor TFIID complex
9	3e−02	2 / 25	MLL1 complex
10	5e−02	2 / 33	cell leading edge
11	6e−02	97 / 8205	cytoplasm
12	9e−02	2 / 47	endocytic vesicle
13	1e−01	1 / 10	very−low−density lipoprotein particle
14	1e−01	1 / 10	viral nucleocapsid
15	1e−01	41 / 3214	protein complex
16	1e−01	4 / 170	nuclear speck
17	1e−01	3 / 109	peroxisome
18	1e−01	1 / 11	nuclear periphery
19	1e−01	1 / 11	spindle pole centrosome
20	1e−01	1 / 12	endocytic vesicle lumen

Chr

Rank	p−value	#in/all	Geneset
1	2e−07	24 / 687	Chr 6
2	6e−02	14 / 838	Chr 3
3	7e−02	7 / 335	Chr 22
4	7e−02	13 / 775	Chr 12
5	1e−01	8 / 469	Chr 8
6	2e−01	14 / 993	Chr 2
7	2e−01	7 / 462	Chr 14
8	4e−01	8 / 689	Chr 7
9	5e−01	3 / 262	Chr 13
10	5e−01	6 / 552	Chr 10
11	5e−01	5 / 465	Chr 15
12	6e−01	4 / 398	Chr 20
13	7e−01	2 / 221	Chr 18
14	8e−01	1 / 151	Chr 21
15	9e−01	4 / 649	Chr 16
16	9e−01	7 / 1037	Chr 19
17	9e−01	3 / 551	Chr X
18	9e−01	3 / 558	Chr 4
19	9e−01	4 / 696	Chr 5
20	9e−01	3 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−06	117 / 8580	TxWk_Colon
2	3e−05	124 / 9482	TssA_Colon
3	5e−05	119 / 9027	Tx_Colon
4	7e−03	123 / 10290	TssWk_Colon
5	1e−02	91 / 7203	TssF_Colon
6	1e−02	103 / 8415	Quies3_Colon
7	3e−02	51 / 3812	TssD1_Colon
8	7e−02	50 / 3897	Quies1_Colon
9	9e−02	1 / 9	TCGA−CRC_agressive−disease−markers
10	2e−01	14 / 1038	HetRpts_Colon
11	2e−01	34 / 2798	TxEnhG1_Colon
12	2e−01	18 / 1386	Het_Colon
13	3e−01	10 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
14	3e−01	1 / 33	Marisa_CRC−cluster−e
15	4e−01	1 / 45	Ang_CRC−CIMPH−vs−L_hyper
16	4e−01	2 / 131	Marisa_CRC−cluster−a
17	4e−01	104 / 9653	Enh_Colon
18	4e−01	1 / 50	Ang_CRC_Hypermethylated
19	4e−01	4 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
20	4e−01	7 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.3	6 / 435	GUDJ_psoriasis up
2	0.8	2 / 294	GUDJ_psoriasis down
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.04	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
2	0.06	7 / 332	Up
3	0.07	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
4	0.11	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
5	0.12	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
6	0.14	2 / 63	Stuehler_Proteins_up_in_STS
7	0.14	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	0.16	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.21	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
10	0.22	1 / 23	WIRTH_PN subtype
11	0.24	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	0.25	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
13	0.40	10 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
14	0.41	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
15	0.43	4 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
16	0.50	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
17	0.52	1 / 68	GIEZELT_GBM_WT_down_VS_mut
18	0.54	1 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
19	0.55	1 / 75	Weller_LGG_A_vs_O_DOWN
20	0.63	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−05	14 / 376	OSMAN_BLADDER_CANCER_UP
2	1e−03	3 / 21	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
3	2e−03	12 / 416	SHEN_SMARCA2_TARGETS_UP
4	2e−03	19 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
5	2e−03	4 / 53	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_UP
6	3e−03	4 / 56	GUO_HEX_TARGETS_DN
7	3e−03	3 / 28	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP
8	3e−03	10 / 337	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
9	3e−03	8 / 233	PENG_RAPAMYCIN_RESPONSE_DN
10	3e−03	18 / 840	GEORGES_TARGETS_OF_MIR192_AND_MIR215
11	5e−03	4 / 64	SESTO_RESPONSE_TO_UV_C1
12	5e−03	12 / 476	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
13	5e−03	3 / 33	DORSAM_HOXA9_TARGETS_UP
14	6e−03	2 / 11	BIOCARTA_AKAP13_PATHWAY
15	6e−03	10 / 373	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
16	7e−03	4 / 71	WALLACE_PROSTATE_CANCER_RACE_DN
17	7e−03	7 / 209	BROWNE_HCMV_INFECTION_16HR_UP
18	7e−03	3 / 37	RIZ_ERYTHROID_DIFFERENTIATION_CCNE1
19	7e−03	9 / 323	JOHNSTONE_PARVB_TARGETS_2_DN
20	8e−03	3 / 39	REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PRO

HM

Rank	p−value	#in/all	Geneset
1	0.06	4 / 140	HALLMARK_INFLAMMATORY_RESPONSE
2	0.06	4 / 141	HALLMARK_FATTY_ACID_METABOLISM
3	0.11	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.15	4 / 195	HALLMARK_MITOTIC_SPINDLE
5	0.16	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	0.23	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	0.24	1 / 26	HALLMARK_ANGIOGENESIS
8	0.26	2 / 93	HALLMARK_PEROXISOME
9	0.32	3 / 188	HALLMARK_MYC_TARGETS_V1
10	0.39	2 / 126	HALLMARK_ALLOGRAFT_REJECTION
11	0.39	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
12	0.46	2 / 146	HALLMARK_DNA_REPAIR
13	0.46	2 / 146	HALLMARK_UV_RESPONSE_UP
14	0.52	2 / 165	HALLMARK_MYOGENESIS
15	0.55	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
16	0.55	2 / 174	HALLMARK_HEME_METABOLISM
17	0.59	2 / 188	HALLMARK_ADIPOGENESIS
18	0.62	1 / 91	HALLMARK_BILE_ACID_METABOLISM
19	0.64	1 / 95	HALLMARK_SPERMATOGENESIS
20	0.64	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−07	112 / 7592	HOPP_Active_promoter
2	5e−07	104 / 6929	HOPP_Txn_elongation
3	2e−05	80 / 5184	HOPP_Txn_transition
4	2e−04	99 / 7209	HOPP_Weak_promoter
5	2e−03	88 / 6564	HOPP_Strong_enhancer
6	2e−03	78 / 5693	HOPP_Weak_enhancer
7	2e−02	20 / 1128	SPANG_BCR DN
8	4e−02	70 / 5538	HOPP_Weak_txn
9	5e−02	3 / 80	Aukema_BCL2 DN_BCL6 UP
10	6e−02	19 / 1218	SPANG_BCR UP
11	1e−01	3 / 107	SPANG_LPS 6hrs UP
12	1e−01	1 / 13	WRIGHT_GCB UP
13	1e−01	2 / 60	Subero_T−ALL_hyper_meth
14	1e−01	2 / 61	SPANG_LPS 6hrs DN
15	1e−01	1 / 14	Subero_MCL_hyper_meth
16	2e−01	5 / 268	SPANG_IL21 UP
17	2e−01	5 / 280	SPANG_CD40 6hrs UP
18	2e−01	2 / 89	ROSOLOWSKI_blue total
19	3e−01	2 / 96	Subero_DLBCL_hyper_meth
20	3e−01	1 / 34	Subero_B−ALL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 25	ATP−dependent helicase activity
2	1e−03	36 / 2037	DNA binding
3	7e−03	2 / 12	poly(A) binding
4	7e−03	8 / 265	hydrolase activity
5	8e−03	2 / 13	protein kinase C activity
6	9e−03	6 / 167	helicase activity
7	1e−02	19 / 1007	poly(A) RNA binding
8	2e−02	2 / 20	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anhyd
9	2e−02	2 / 21	exonuclease activity
10	2e−02	18 / 1033	nucleic acid binding
11	3e−02	6 / 217	transcription coactivator activity
12	3e−02	147 / 13179	molecular_function
13	4e−02	2 / 29	ATP−dependent DNA helicase activity
14	4e−02	6 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
15	4e−02	106 / 8984	protein binding
16	5e−02	2 / 34	ATP−dependent RNA helicase activity
17	5e−02	9 / 456	protein binding transcription factor activity
18	5e−02	6 / 255	receptor binding
19	6e−02	2 / 37	DNA−directed RNA polymerase activity
20	7e−02	2 / 41	phosphatase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−05	12 / 294	hsa−miR−561
2	7e−03	3 / 38	hsa−miR−1258
3	1e−02	5 / 133	hsa−miR−485−5p
4	1e−02	4 / 87	hsa−miR−595
5	1e−02	7 / 239	hsa−miR−152
6	1e−02	7 / 243	hsa−miR−122
7	2e−02	4 / 94	hsa−miR−219−2−3p
8	2e−02	4 / 98	hsa−miR−590−5p
9	2e−02	2 / 23	hsa−miR−1250
10	3e−02	3 / 60	hsa−miR−1200
11	3e−02	5 / 157	hsa−miR−512−3p
12	3e−02	3 / 63	hsa−miR−1278
13	3e−02	4 / 110	hsa−miR−491−3p
14	3e−02	4 / 113	hsa−miR−507
15	3e−02	3 / 67	hsa−miR−1246
16	4e−02	2 / 31	hsa−miR−342−5p
17	4e−02	2 / 31	hsa−miR−17*
18	4e−02	5 / 182	hsa−miR−374a
19	5e−02	5 / 183	hsa−miR−1283
20	5e−02	2 / 33	hsa−miR−1296

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.09	1 / 9	MYC_RNA processing binding UP
2	0.25	9 / 653	ICGC_SrfPcr2_targets
3	0.34	20 / 1701	HEBENSTREIT_high expression TF
4	0.36	14 / 1171	KIM_MYC targets
5	0.52	15 / 1400	ICGC_Myc_targets
6	0.53	6 / 553	ICGC_RxraPcr1_targets
7	0.64	24 / 2391	ICGC_Pbx3_targets
8	0.68	21 / 2136	ICGC_GabpPcr2_targets
9	0.74	12 / 1314	ICGC_Usf1_targets
10	0.75	13 / 1418	ICGC_Ets1_targets
11	0.76	5 / 595	ICGC_NrsfPcr2_targets
12	0.79	17 / 1878	ICGC_Cebpbsc150_targets
13	0.80	12 / 1383	ICGC_Six5_targets
14	0.81	25 / 2714	ICGC_Irf4_targets
15	0.86	9 / 1139	HEBENSTREIT_low expression TF
16	0.86	5 / 690	ICGC_Atf3_targets
17	0.88	18 / 2137	ICGC_SrfV0416101_targets
18	0.90	36 / 4032	ICGC_Creb1_targets
19	0.90	48 / 5219	ICGC_Tcf3_targets
20	0.91	20 / 2416	ICGC_Bcl3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	7e−04	4 / 38	VAQUERIZAS_Testis
2	9e−03	3 / 40	VAQUERIZAS_Thyroid
3	2e−02	3 / 59	VAQUERIZAS_Whole blood
4	5e−02	2 / 33	VAQUERIZAS_Prostate
5	1e−01	1 / 11	VAQUERIZAS_Fetal liver
6	1e−01	2 / 58	VAQUERIZAS_Lung
7	1e−01	1 / 15	VAQUERIZAS_Bone marrow
8	1e−01	1 / 15	VAQUERIZAS_Fetal thyroid
9	2e−01	1 / 23	VAQUERIZAS_Spinal cord
10	2e−01	1 / 26	VAQUERIZAS_Liver
11	2e−01	1 / 27	VAQUERIZAS_Lymph node
12	3e−01	1 / 29	VAQUERIZAS_Smooth muscle
13	3e−01	1 / 29	VAQUERIZAS_Fetal lung
14	3e−01	1 / 36	VAQUERIZAS_Fetal brain
15	3e−01	1 / 37	VAQUERIZAS_Thymus
16	4e−01	1 / 41	VAQUERIZAS_Placenta
17	4e−01	2 / 143	VAQUERIZAS_General
18	1e+00	0 / 45	VAQUERIZAS_Uterus
19	1e+00	0 / 9	VAQUERIZAS_Kidney
20	1e+00	0 / 38	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	WIRTH_Cortex cerebri
2	0.1	1 / 12	WIRTH_Cerebellum
3	0.3	2 / 114	PALMER_T−Cell signature up
4	0.6	2 / 194	PALMER_B−Cell signature up
5	0.6	1 / 95	WIRTH_Muscle
6	0.7	1 / 107	WIRTH_Testis
7	0.9	2 / 350	WIRTH_Nervous System
8	0.9	1 / 225	PALMER_Granulocytes signature up
9	1.0	1 / 350	WIRTH_Immune system
10	1.0	0 / 32	WIRTH_Pancreas
11	1.0	0 / 11	WIRTH_Sec. lymphoid organs
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 13	WIRTH_B−cells
14	1.0	0 / 8	WIRTH_Tonsil
15	1.0	0 / 12	WIRTH_Thymus
16	1.0	0 / 12	WIRTH_Lymphocytes
17	1.0	0 / 5	WIRTH_Bone marrow
18	1.0	0 / 11	WIRTH_Globus pallidus
19	1.0	0 / 14	WIRTH_Telencephalon
20	1.0	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	42 / 3682	LU_BPDE 0.005 DN
2	0.8	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	

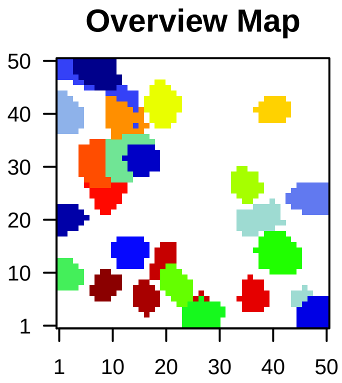
Correlation Clusters

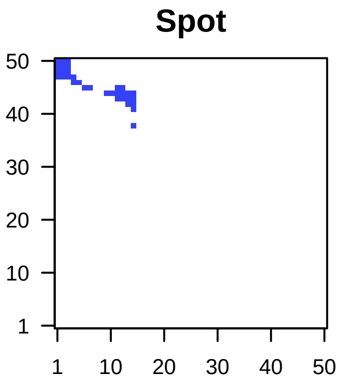
Spot Summary: G

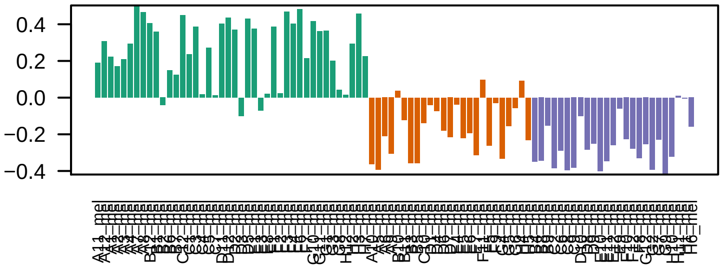
metagenes = 33
genes = 290

<r> metagenes = 0.92
<r> genes = 0.21
beta: r2= 5.98 / log p= −Inf

samples with spot = 31 (33.7 %)
MSC1 : 31 (73.8 %)





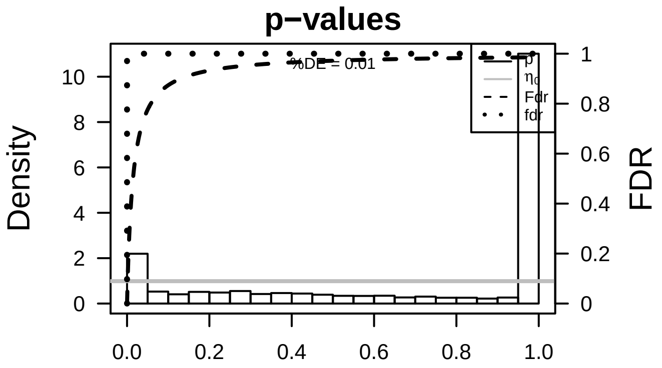


Spot Genelist

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	SMCO4	2.1	−0.21	0.34	SMCO4	single−pass membrane protein with coiled−coil domains 4 [S
3	JMJD7	2.04	−0.18	0.24	JMJD7	jumonji domain containing 7 [Source:HGNC Symbol;Acc:HGN
4	C4orf33	1.97	−0.26	0.29	C4orf33	chromosome 4 open reading frame 33 [Source:HGNC Symb
5	RNASEH2B	1.84	−0.73	0.47	RNASEH2B	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
6	RAD51	1.81	−0.59	0.62	RAD51	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
7	KNTC1	1.78	−1.13	0.64	KNTC1	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
8	ZNF519	1.76	−0.35	0.39	ZNF519	zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30
9	POLE	1.73	−0.5	0.57	POLE	polymerase (DNA directed), epsilon, catalytic subunit [Source
10	ZNF101	1.71	−0.32	0.24	ZNF101	zinc finger protein 101 [Source:HGNC Symbol;Acc:HGNC:12
11	NCAPH2	1.68	−0.47	0.42	NCAPH2	non−SMC condensin II complex, subunit H2 [Source:HGNC
12	ORC1	1.67	−0.3	0.59	ORC1	origin recognition complex, subunit 1 [Source:HGNC Symbol;
13	TIFA	1.66	−0.19	0.52	TIFA	TRAF−interacting protein with forkhead−associated domain [
14	DTL	1.66	−0.94	0.84	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
15	CCNE2	1.65	−0.54	0.71	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
16	MTBP	1.64	−0.38	0.33	MTBP	MDM2 binding protein [Source:HGNC Symbol;Acc:HGNC:74
17	BRIP1	1.64	−0.35	0.57	BRIP1	BRCA1 interacting protein C−terminal helicase 1 [Source:HG
18	CHEK1	1.64	−0.5	0.56	CHEK1	checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925
19	TAF1A	1.63	−0.49	0.34	TAF1A	TATA box binding protein (TBP)−associated factor, RNA polyn
20	BARD1	1.62	−1.09	0.73	BARD1	BRCA1 associated RING domain 1 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−91	95 / 305	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	1e−86	149 / 1192	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	5e−82	109 / 550	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	1e−64	131 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	6e−63	72 / 267	GSEA	ZHANG_TLX_TARGETS_60HR_DN
6	1e−62	89 / 485	GSEA	CHICAS_RB1_TARGETS_SENESCENT
7	1e−60	68 / 242	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
8	4e−60	63 / 197	HM	HALLMARK_E2F_TARGETS
9	4e−59	99 / 700	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	7e−57	117 / 1110	BP	cell cycle
11	3e−56	77 / 390	GSEA	PUJANA_BRCA2_PCC_NETWORK
12	4e−51	95 / 768	BP	DNA metabolic process
13	5e−51	68 / 327	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
14	8e−51	80 / 505	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
15	1e−48	72 / 412	BP	mitotic cell cycle
16	4e−48	70 / 388	GSEA	REACTOME_CELL_CYCLE
17	7e−48	78 / 517	GSEA	FEVR_CTNNB1_TARGETS_DN
18	1e−46	65 / 335	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
19	4e−46	62 / 301	GSEA	REACTOME_CELL_CYCLE_MITOTIC
20	8e−46	119 / 1460	GSEA	PUJANA_BRCA1_PCC_NETWORK
21	4e−45	92 / 834	GSEA	LEE_BMP2_TARGETS_DN
22	2e−44	46 / 139	BP	DNA replication
23	2e−44	86 / 724	GSEA	PUJANA_CHEK2_PCC_NETWORK
24	3e−42	35 / 68	GSEA	VERNELL_RETINOBLASTOMA_PATHWAY_UP
25	3e−39	48 / 198	GSEA	FUJII_YBX1_TARGETS_DN
26	1e−38	44 / 160	GSEA	PUJANA_XPRSS_INT_NETWORK
27	2e−37	144 / 2577	CC	nucleoplasm
28	3e−37	45 / 181	GSEA	REACTOME_DNA_REPLICATION
29	1e−36	72 / 609	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
30	6e−36	34 / 87	GSEA	ZHANG_TLX_TARGETS_UP
31	1e−35	37 / 113	GSEA	PUJANA_BRCA_CENTERED_NETWORK
32	2e−35	71 / 616	GSEA	BENPORATH_CYCLING_GENES
33	2e−35	43 / 175	GSEA	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
34	3e−35	51 / 278	GSEA	MANALO_HYPOXIA_DN
35	4e−35	39 / 135	GSEA	WHITFIELD_CELL_CYCLE_G1_S
36	1e−34	42 / 171	GSEA	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
37	1e−34	85 / 944	GSEA	NUYTTEN_EZH2_TARGETS_DN
38	3e−34	72 / 663	CC	chromosome
39	4e−34	81 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
40	5e−34	32 / 81	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	7e−57	117 / 1110	cell cycle
2	4e−51	95 / 768	DNA metabolic process
3	1e−48	72 / 412	mitotic cell cycle
4	2e−44	46 / 139	DNA replication
5	1e−32	22 / 29	DNA strand elongation involved in DNA replication
6	1e−29	168 / 3980	cellular nitrogen compound metabolic process
7	2e−22	40 / 298	DNA repair
8	6e−21	15 / 23	DNA replication initiation
9	3e−20	14 / 20	telomere maintenance via semi−conservative replication
10	1e−19	27 / 139	G1/S transition of mitotic cell cycle
11	1e−18	55 / 721	chromosome organization
12	1e−18	14 / 24	telomere maintenance via recombination
13	4e−15	17 / 65	telomere maintenance
14	6e−13	24 / 195	cellular response to DNA damage stimulus
15	4e−12	9 / 16	nucleotide−excision repair, DNA gap filling
16	1e−11	14 / 63	double−strand break repair
17	2e−11	122 / 3644	biosynthetic process
18	1e−10	10 / 30	DNA damage checkpoint
19	2e−09	29 / 409	cell division
20	1e−08	24 / 312	mitotic nuclear division

Brain

Rank	p−value	#in/all	Geneset
1	3e−15	242 / 9330	Overlap_fetal_midbrain_ReprPC
2	4e−05	60 / 1845	Fetal_Quies
3	1e−04	206 / 9013	Overlap_fetal_midbrain_K9K27me3
4	6e−04	38 / 1122	Fetal_K9K27me3
5	9e−04	142 / 5940	Overlap_fetal_midbrain_HetRpts
6	5e−03	197 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	1e−02	26 / 831	Fetal_HetRpts
8	1e−01	24 / 953	Fetal_Enh
9	1e−01	26 / 1050	Fetal_EnhP
10	2e−01	5 / 163	Fetal_ReprPC
11	2e−01	192 / 9528	Overlap_fetal_midbrain_Quies
12	2e−01	8 / 304	Fetal_Het
13	3e−01	27 / 1236	Mid_Frontal_Lobe_ReprPCWk
14	3e−01	17 / 769	Overlap_fetal_midbrain_ZNF
15	4e−01	28 / 1333	Fetal_ReprPCWk
16	7e−01	14 / 786	Fetal_EnhG
17	7e−01	9 / 534	Mid_Frontal_Lobe_EnhG
18	7e−01	17 / 989	Mid_Frontal_Lobe_Quies
19	8e−01	18 / 1065	Overlap_fetal_midbrain_Enh
20	8e−01	2 / 166	Mid_Frontal_Lobe_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	6e−21	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	6e−20	47 / 489	Lembcke_Normal vs Adenoma
3	7e−15	15 / 47	PanCan_DNARepair_geneset_nanostring
4	2e−12	19 / 120	PanCan_CC+Apop_geneset_nanostring
5	4e−07	6 / 16	WOLFER_overlap genes
6	6e−07	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
7	3e−05	4 / 10	GENTLES_modul3
8	2e−04	4 / 15	GENTLES_modul1
9	2e−04	1 / 15	RHODES_CANCER_META_SIGNATURE
10	2e−04	5 / 29	KUIPER_MM good survival
11	3e−03	3 / 16	GENTLES_modul2
12	1e−02	5 / 70	SHAUGHNESSY_MM high risk
13	1e−02	4 / 48	KUIPER_MM poor survival
14	2e−02	6 / 113	PanCan_Driver_Gene_geneset_nanostring
15	6e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
16	2e−01	1 / 13	BEN−PORATH_UP
17	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
18	3e−01	1 / 15	WANG_ER_UP
19	3e−01	1 / 15	GENTLES_modul4
20	3e−01	1 / 16	GENTLES_modul6

CC

Rank	p−value	#in/all	Geneset
1	2e−37	144 / 2577	nucleoplasm
2	3e−34	72 / 663	chromosome
3	4e−29	204 / 5696	nucleus
4	1e−14	33 / 331	nuclear chromosome
5	3e−14	250 / 9988	organelle
6	1e−12	256 / 10605	intracellular
7	5e−11	111 / 3214	protein complex
8	2e−08	26 / 377	centrosome
9	5e−08	38 / 747	nucleolus
10	8e−07	260 / 11774	cell
11	2e−06	10 / 75	condensed chromosome kinetochore
12	2e−06	9 / 59	chromosome, centromeric region
13	3e−06	27 / 512	microtubule organizing center
14	4e−06	7 / 35	condensed nuclear chromosome
15	8e−06	20 / 332	nuclear envelope
16	2e−05	10 / 97	chromatin
17	4e−05	8 / 65	kinetochore
18	8e−05	9 / 93	spindle pole
19	9e−05	4 / 13	Fanconi anaemia nuclear complex
20	1e−04	49 / 1465	cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.007	20 / 558	Chr 4
2	0.029	9 / 221	Chr 18
3	0.033	10 / 262	Chr 13
4	0.120	10 / 335	Chr 22
5	0.152	20 / 801	Chr 11
6	0.249	10 / 398	Chr 20
7	0.278	19 / 838	Chr 3
8	0.282	16 / 696	Chr 5
9	0.297	11 / 465	Chr 15
10	0.339	4 / 151	Chr 21
11	0.361	15 / 687	Chr 6
12	0.365	15 / 689	Chr 7
13	0.510	11 / 551	Chr X
14	0.573	16 / 840	Chr 17
15	0.614	12 / 649	Chr 16
16	0.681	8 / 462	Chr 14
17	0.752	9 / 552	Chr 10
18	0.812	7 / 469	Chr 8
19	0.831	12 / 775	Chr 12
20	0.877	8 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−12	238 / 9482	TssA_Colon
2	3e−07	238 / 10290	TssWk_Colon
3	1e−06	203 / 8415	Quies3_Colon
4	7e−05	28 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
5	1e−04	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
6	3e−04	29 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
7	2e−03	165 / 7203	TssF_Colon
8	7e−03	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
9	1e−02	2 / 8	Boland_CRC−MMR−system
10	3e−02	183 / 8580	TxWk_Colon
11	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
12	5e−02	190 / 9027	Tx_Colon
13	1e−01	1 / 8	Marisa_CRC−C3
14	2e−01	1 / 9	KIM_MSI−in−EC
15	2e−01	1 / 13	TCGA−CRC_less−agressive−disease−markers
16	3e−01	1 / 15	Juehling_HNPCC−mutated−in−4
17	3e−01	79 / 3812	TssD1_Colon
18	3e−01	1 / 18	Boland_CRC−MSI−A6−A10
19	5e−01	1 / 33	Marisa_CRC−cluster−e
20	6e−01	11 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	3e−04	20 / 435	GUDJ_psoriasis up
2	1e+00	2 / 294	GUDJ_psoriasis down
3	1e+00	0 / 11	BCHETNIA_EBM up
4	1e+00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−25	32 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	9e−06	9 / 71	Weller_LGG_gradeII−vs−III_DOWN
3	9e−05	18 / 332	Up
4	4e−03	2 / 5	Phillips Prolif up vs PN & MES
5	4e−03	28 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	7e−02	2 / 22	KIM prognostic signature LTS vs. STS
7	7e−02	3 / 49	developing astrocytes
8	1e−01	1 / 7	KIM amplified & overexpressed in LTS
9	2e−01	1 / 9	Mukasa_UP_in_GBM
10	3e−01	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	3e−01	1 / 16	KIM deleted & downregulated in LTS
12	3e−01	3 / 103	GIEZELT_GBM_WT_up_VS_mut
13	3e−01	2 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	4e−01	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
15	4e−01	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
16	4e−01	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
17	4e−01	1 / 29	shaw_responders_down_in_oligo_glioma
18	5e−01	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
19	5e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
20	6e−01	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−91	95 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	1e−86	149 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	5e−82	109 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	1e−64	131 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	6e−63	72 / 267	ZHANG_TLX_TARGETS_60HR_DN
6	1e−62	89 / 485	CHICAS_RB1_TARGETS_SENESCENT
7	1e−60	68 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
8	4e−59	99 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	3e−56	77 / 390	PUJANA_BRCA2_PCC_NETWORK
10	5e−51	68 / 327	BLUM_RESPONSE_TO_SALIRASIB_DN
11	8e−51	80 / 505	BERENJENO_TRANSFORMED_BY_RHOA_UP
12	4e−48	70 / 388	REACTOME_CELL_CYCLE
13	7e−48	78 / 517	FEVR_CTNNB1_TARGETS_DN
14	1e−46	65 / 335	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
15	4e−46	62 / 301	REACTOME_CELL_CYCLE_MITOTIC
16	8e−46	119 / 1460	PUJANA_BRCA1_PCC_NETWORK
17	4e−45	92 / 834	LEE_BMP2_TARGETS_DN
18	2e−44	86 / 724	PUJANA_CHEK2_PCC_NETWORK
19	3e−42	35 / 68	VERNELL_RETINOBLASTOMA_PATHWAY_UP
20	3e−39	48 / 198	FUJII_YBX1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−60	63 / 197	HALLMARK_E2F_TARGETS
2	1e−17	29 / 196	HALLMARK_G2M_CHECKPOINT
3	2e−11	22 / 188	HALLMARK_MYC_TARGETS_V1
4	4e−09	17 / 146	HALLMARK_DNA_REPAIR
5	4e−04	12 / 195	HALLMARK_MITOTIC_SPINDLE
6	5e−04	12 / 196	HALLMARK_MTORC1_SIGNALING
7	5e−03	5 / 57	HALLMARK_MYC_TARGETS_V2
8	2e−02	8 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
9	6e−02	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	7e−02	6 / 146	HALLMARK_UV_RESPONSE_UP
11	1e−01	4 / 93	HALLMARK_PEROXISOME
12	1e−01	6 / 167	HALLMARK_IL2_STAT5_SIGNALING
13	1e−01	5 / 140	HALLMARK_APOPTOSIS
14	2e−01	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
15	2e−01	5 / 162	HALLMARK_COMPLEMENT
16	3e−01	5 / 181	HALLMARK_P53_PATHWAY
17	3e−01	3 / 95	HALLMARK_SPERMATOGENESIS
18	3e−01	4 / 141	HALLMARK_FATTY_ACID_METABOLISM
19	4e−01	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	4e−01	4 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	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	4e−22	215 / 6929	HOPP_Txn_elongation
2	7e−19	36 / 294	TARTE_Plasmablast signature
3	2e−14	164 / 5184	HOPP_Txn_transition
4	5e−11	202 / 7592	HOPP_Active_promoter
5	2e−06	167 / 6564	HOPP_Strong_enhancer
6	8e−06	12 / 129	DAVE_BL−vs−DLBCL
7	4e−04	169 / 7209	HOPP_Weak_promoter
8	5e−03	2 / 6	MASCQUE_mBL UP
9	8e−03	36 / 1218	SPANG_BCR UP
10	1e−02	11 / 256	SPANG_IL21 DN
11	7e−02	3 / 50	SPANG_BAFF 9hrs DN
12	1e−01	4 / 89	ROSOLOWSKI_blue total
13	1e−01	2 / 30	TARTE_B−cell signature
14	1e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
15	1e−01	1 / 8	MASCQUE_GCB UP
16	2e−01	27 / 1128	SPANG_BCR DN
17	2e−01	119 / 5693	HOPP_Weak_enhancer
18	2e−01	2 / 39	ROSOLOWSKI_blue DOWN
19	2e−01	1 / 13	WRIGHT_GCB UP
20	2e−01	1 / 13	YAMANE_AICDA_targets_recruited

MF

Rank	p−value	#in/all	Geneset
1	9e−14	88 / 2037	DNA binding
2	5e−10	224 / 8984	protein binding
3	1e−08	12 / 71	single−stranded DNA binding
4	3e−08	17 / 167	helicase activity
5	6e−08	8 / 29	DNA−directed DNA polymerase activity
6	2e−07	7 / 23	DNA helicase activity
7	1e−06	23 / 376	chromatin binding
8	3e−06	22 / 364	ATPase activity
9	4e−06	14 / 164	nuclease activity
10	9e−06	13 / 152	histone binding
11	9e−06	8 / 54	damaged DNA binding
12	1e−05	22 / 405	ligase activity
13	2e−05	6 / 29	ATP−dependent DNA helicase activity
14	2e−05	5 / 18	3'−5' exonuclease activity
15	6e−05	46 / 1309	ATP binding
16	9e−05	4 / 13	nucleocytoplasmic transporter activity
17	5e−04	5 / 34	DNA−dependent ATPase activity
18	5e−04	5 / 35	4 iron, 4 sulfur cluster binding
19	6e−04	4 / 21	exonuclease activity
20	7e−04	9 / 123	nucleotidyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−10	28 / 344	hsa−miR−548d−5p
2	1e−08	24 / 314	hsa−miR−548c−5p
3	3e−07	23 / 343	hsa−miR−548b−5p
4	3e−07	21 / 293	hsa−miR−548j
5	8e−07	21 / 310	hsa−miR−548i
6	1e−06	25 / 433	hsa−miR−548n
7	2e−06	21 / 328	hsa−miR−548a−5p
8	4e−06	20 / 315	hsa−miR−559
9	7e−06	18 / 274	hsa−miR−548h
10	3e−04	11 / 157	hsa−miR−548o
11	3e−04	5 / 31	hsa−miR−626
12	3e−04	8 / 88	hsa−miR−505
13	6e−04	7 / 75	hsa−miR−651
14	7e−04	16 / 328	hsa−miR−520d−3p
15	9e−04	8 / 103	hsa−miR−653
16	9e−04	4 / 23	hsa−miR−517a
17	1e−03	14 / 275	hsa−miR−577
18	1e−03	16 / 340	hsa−miR−142−5p
19	1e−03	7 / 83	hsa−miR−576−5p
20	1e−03	4 / 25	hsa−miR−517c

Pathw Act

Rank	p−value	#in/all	Geneset
1	6e−05	4 / 12	GUSTAFSON_PI3K_UP
2	2e−04	4 / 15	BENTINK_ras.6
3	2e−02	2 / 12	BENTINK_ras.1
4	3e−02	2 / 14	BENTINK_src.2
5	2e−01	1 / 9	BENTINK_ras.4
6	2e−01	1 / 12	BENTINK_e2f3.2
7	2e−01	1 / 13	BENTINK_myc.1
8	1e+00	0 / 13	GUSTAFSON_PI3K_DN
9	1e+00	0 / 14	BENTINK_e2f3.1
10	1e+00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−05	126 / 4689	ICGC_Taf1_targets
2	5e−05	126 / 4829	ICGC_Nficsc81335_targets
3	8e−05	108 / 4032	ICGC_Creb1_targets
4	1e−04	7 / 59	MYC_Targets UP
5	6e−04	3 / 9	MYC_DNA repair UP
6	7e−04	39 / 1171	KIM_MYC targets
7	1e−03	22 / 553	ICGC_RxraPcr1_targets
8	1e−03	95 / 3700	ICGC_Nfatc1_targets
9	1e−03	110 / 4414	ICGC_Bclaf101388_targets
10	1e−03	114 / 4617	ICGC_Tcf12_targets
11	2e−03	115 / 4706	ICGC_Sp1_targets
12	2e−03	119 / 4909	ICGC_Stat5_targets
13	2e−03	129 / 5408	ICGC_Pou2_targets
14	3e−03	118 / 4879	ICGC_Pmlsc71910_targets
15	3e−03	138 / 5890	ICGC_Elf1_targets
16	3e−03	107 / 4385	ICGC_Atf2_targets
17	5e−03	141 / 6114	ICGC_Runx3_targets
18	5e−03	112 / 4682	ICGC_Pol24_targets
19	6e−03	122 / 5200	ICGC_Mta3_targets
20	7e−03	125 / 5355	ICGC_Pol2_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.001	3 / 12	WIRTH_Thymus
2	0.147	10 / 350	WIRTH_Immune system
3	0.195	1 / 11	WIRTH_Prim. lymphoid organs
4	0.210	1 / 12	WIRTH_Cerebellum
5	0.226	1 / 13	WIRTH_Thyroid gland
6	0.524	4 / 194	PALMER_B−Cell signature up
7	0.936	2 / 225	PALMER_Granulocytes signature up
8	0.992	2 / 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

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	22 / 1115	LU_BPDE 1n DN
2	1.0	54 / 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	

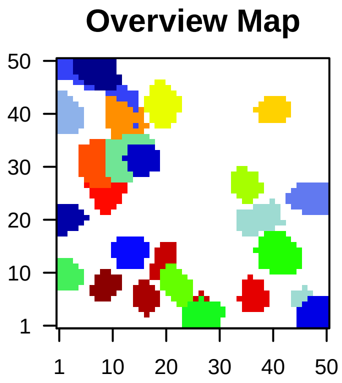
Correlation Clusters

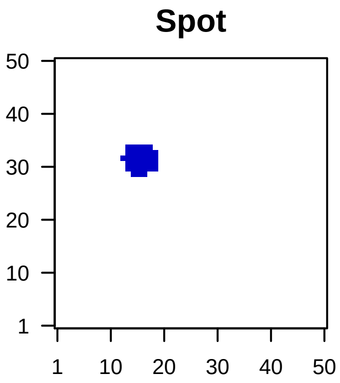
Spot Summary: H

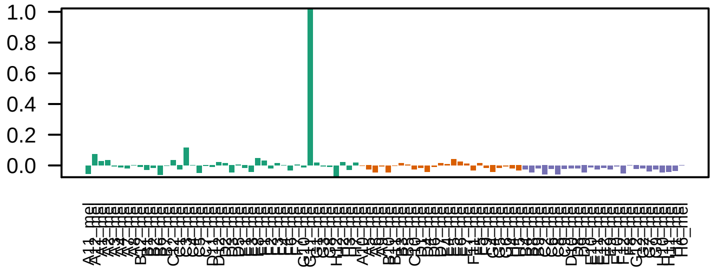
metagenes = 33
genes = 112

<r> metagenes = 0.97
<r> genes = 0.27
beta: r2= 0.23 / log p= −5.89

samples with spot = 1 (1.1 %)
MSC1 : 1 (2.4 %)


Overview Map


Spot

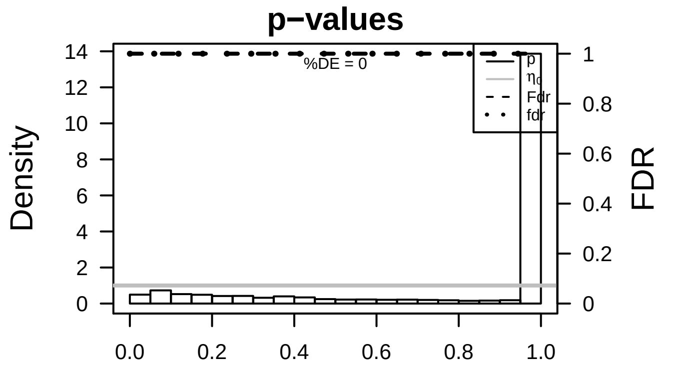


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CACNA2D1	2.14	−0.28	0.44	CACNA2D1	calcium channel, voltage−dependent, alpha 2/delta subunit 1
2	RDH12	2.07	−0.08	0.56	RDH12	retinol dehydrogenase 12 (all−trans/9−cis/11−cis) [Source:HG
3	ZNF239	1.83	−0.02	0.92	ZNF239	zinc finger protein 239 [Source:HGNC Symbol;Acc:HGNC:13
4	PCDH8	1.81	−0.03	0.85	PCDH8	protocadherin 8 [Source:HGNC Symbol;Acc:HGNC:8660]
5	ACP2	1.74	−0.18	0.38	ACP2	acid phosphatase 2, lysosomal [Source:HGNC Symbol;Acc:H
6	ARHGAP28	1.72	−0.12	0.51	ARHGAP28	Rho GTPase activating protein 28 [Source:HGNC Symbol;Ac
7	ZNF555	1.68	−0.17	0.38	ZNF555	zinc finger protein 555 [Source:HGNC Symbol;Acc:HGNC:28
8	TRPM3	1.67	−0.18	0.32	TRPM3	transient receptor potential cation channel, subfamily M, mem
9	CSNK1G2	1.66	−0.29	0.39	CSNK1G2	casein kinase 1, gamma 2 [Source:HGNC Symbol;Acc:HGNC
10	KDM4C	1.65	−0.19	0.42	KDM4C	lysine (K)−specific demethylase 4C [Source:HGNC Symbol;A
11	CTD−3214H1	1.64	−0.14	0.43		
12	DDIT4L	1.61	−0.06	0.7	DDIT4L	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
13	ST3GAL5	1.6	−0.33	0.38	ST3GAL5	ST3 beta−galactoside alpha−2,3−sialyltransferase 5 [Source:
14	MROH8	1.59	−0.06	0.49	MROH8	maestro heat−like repeat family member 8 [Source:HGNC Sy
15	HOXA1	1.58	−0.05	0.67	HOXA1	homeobox A1 [Source:HGNC Symbol;Acc:HGNC:5099]
16	ITGA9	1.56	−0.14	0.5	ITGA9	integrin, alpha 9 [Source:HGNC Symbol;Acc:HGNC:6145]
17	SAMD13	1.56	−0.05	0.72	SAMD13	sterile alpha motif domain containing 13 [Source:HGNC Syml
18	ZNF675	1.55	−0.17	0.32	ZNF675	zinc finger protein 675 [Source:HGNC Symbol;Acc:HGNC:30
19	TGFA	1.54	−0.07	0.62	TGFA	transforming growth factor, alpha [Source:HGNC Symbol;Acc
20	N6AMT2	1.53	−0.2	0.4	N6AMT2	N−6 adenine−specific DNA methyltransferase 2 (putative) [Sc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−06	20 / 862	Brain	Overlap_fetal_midbrain_TxTrans
2	1e−05	17 / 686	Brain	Overlap_fetal_midbrain_TssA
3	4e−05	11 / 336	BP	neurological system process
4	8e−05	14 / 571	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	8e−05	16 / 724	GSEA	BENPORATH_EED_TARGETS
6	1e−04	17 / 823	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
7	2e−04	22 / 1317	Colon	EnhP_Colon
8	2e−04	5 / 75	GSEA	KANG_IMMORTALIZED_BY_TERT_UP
9	2e−04	4 / 41	BP	heart looping
10	3e−04	15 / 720	GSEA	BENPORATH_ES_WITH_H3K27ME3
11	3e−04	4 / 45	Glio	Christensen_hypermethylated_in_primary_glioblastoma
12	4e−04	30 / 2159	Colon	TssP_Colon
13	4e−04	14 / 674	GSEA	BENPORATH_SUZ12_TARGETS
14	5e−04	6 / 134	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K27ME3
15	5e−04	11 / 450	MF	sequence−specific DNA binding
16	5e−04	9 / 312	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
17	7e−04	4 / 54	BP	positive regulation of epithelial cell proliferation
18	7e−04	7 / 199	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
19	7e−04	3 / 24	BP	neural crest cell migration
20	1e−03	3 / 27	BP	positive regulation of interferon−gamma production
21	1e−03	6 / 156	Canc	PanCan_PI3K_geneset_nanostring
22	1e−03	4 / 66	GSEA	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM
23	2e−03	3 / 31	BP	inner ear development
24	2e−03	28 / 2142	Colon	ReprPC_Colon
25	2e−03	7 / 233	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
26	2e−03	39 / 3396	Lymph	HOPP_Repressed
27	2e−03	3 / 33	BP	positive regulation of T cell proliferation
28	2e−03	4 / 72	GSEA	KEGG_DILATED_CARDIOMYOPATHY
29	2e−03	3 / 34	BP	positive regulation of interleukin−6 production
30	2e−03	2 / 10	BP	negative regulation of JUN kinase activity
31	2e−03	2 / 10	BP	positive regulation of nitric−oxide synthase biosynthetic process
32	2e−03	2 / 10	BP	regulation of respiratory gaseous exchange by neurological system process
33	3e−03	14 / 812	Brain	Mid_Frontal_Lobe_TssP
34	3e−03	9 / 396	GSEA	BENPORATH_PRC2_TARGETS
35	3e−03	2 / 11	BP	central nervous system neuron differentiation
36	3e−03	5 / 132	BP	regulation of gene expression
37	3e−03	3 / 40	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_F
38	3e−03	2 / 12	GSEA	MATZUK_EARLY_ANTRAL_FOLLICLE
39	4e−03	3 / 42	GSEA	KEGG_HEDGEHOG_SIGNALING_PATHWAY
40	4e−03	4 / 88	BP	activation of MAPK activity


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.03	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.53	1 / 100	HORVATH_aging_genes meth DOWN
3	0.56	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	4e−05	11 / 336	neurological system process
2	2e−04	4 / 41	heart looping
3	7e−04	4 / 54	positive regulation of epithelial cell proliferation
4	7e−04	3 / 24	neural crest cell migration
5	1e−03	3 / 27	positive regulation of interferon−gamma production
6	2e−03	3 / 31	inner ear development
7	2e−03	3 / 33	positive regulation of T cell proliferation
8	2e−03	3 / 34	positive regulation of interleukin−6 production
9	2e−03	2 / 10	negative regulation of JUN kinase activity
10	2e−03	2 / 10	positive regulation of nitric−oxide synthase biosynthetic process
11	2e−03	2 / 10	regulation of respiratory gaseous exchange by neurological system process
12	3e−03	2 / 11	central nervous system neuron differentiation
13	3e−03	5 / 132	regulation of gene expression
14	4e−03	4 / 88	activation of MAPK activity
15	4e−03	8 / 346	positive regulation of cell proliferation
16	5e−03	2 / 14	digestive tract morphogenesis
17	5e−03	2 / 14	negative regulation of interferon−gamma production
18	5e−03	2 / 14	positive regulation of chemokine production
19	5e−03	3 / 46	heart morphogenesis
20	5e−03	2 / 15	morphogenesis of an epithelium

Brain

Rank	p−value	#in/all	Geneset
1	5e−06	20 / 862	Overlap_fetal_midbrain_TxTrans
2	1e−05	17 / 686	Overlap_fetal_midbrain_TssA
3	3e−03	14 / 812	Mid_Frontal_Lobe_TssP
4	3e−02	21 / 1845	Fetal_Quies
5	3e−02	15 / 1207	Overlap_fetal_midbrain_TssF
6	6e−02	8 / 574	Overlap_fetal_midbrain_TssP
7	6e−02	29 / 2972	Mid_Frontal_Lobe_ReprPC
8	7e−02	6 / 383	Fetal_Tx
9	9e−02	10 / 831	Fetal_HetRpts
10	1e−01	3 / 158	Overlap_fetal_midbrain_Het
11	1e−01	14 / 1333	Fetal_ReprPCWk
12	1e−01	3 / 163	Fetal_ReprPC
13	1e−01	13 / 1236	Mid_Frontal_Lobe_ReprPCWk
14	2e−01	11 / 1065	Overlap_fetal_midbrain_Enh
15	2e−01	11 / 1122	Fetal_K9K27me3
16	3e−01	4 / 349	Fetal_ZNF
17	3e−01	5 / 468	Mid_Frontal_Lobe_TssF
18	3e−01	21 / 2462	Mid_Frontal_Lobe_HetRpts
19	3e−01	2 / 156	Mid_Frontal_Lobe_TssA
20	4e−01	5 / 534	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	6 / 156	PanCan_PI3K_geneset_nanostring
2	0.011	2 / 22	PanCan_HH_geneset_nanostring
3	0.075	2 / 61	PanCan_Wnt_geneset_nanostring
4	0.124	2 / 82	PanCan_TXmisReg_geneset_nanostring
5	0.199	2 / 111	PanCan_RAS_geneset_nanostring
6	0.200	0 / 14	LIU_LIVER_CANCER
7	0.204	2 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.226	2 / 121	PanCan_MAPK_geneset_nanostring
9	0.295	1 / 47	PanCan_DNARepair_geneset_nanostring
10	0.336	1 / 55	PanCan_JAK−ST_geneset_nanostring
11	0.346	4 / 401	Lembcke_Colonic Inflammation
12	0.380	3 / 298	SPANG_BCL6−index2
13	0.386	2 / 180	SPANG_LPS−index2
14	0.393	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	0.407	1 / 70	SHAUGHNESSY_MM high risk
16	0.492	4 / 489	Lembcke_Normal vs Adenoma
17	0.592	1 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.674	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	0.946	0 / 14	LIU_PROSTATE_CANCER_DN
20	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	0.01	2 / 23	integrin complex
2	0.02	2 / 28	myofibril
3	0.02	3 / 83	endomembrane system
4	0.04	6 / 332	cell junction
5	0.04	2 / 41	presynaptic membrane
6	0.07	1 / 10	fascia adherens
7	0.07	7 / 491	perinuclear region of cytoplasm
8	0.09	1 / 12	Golgi transport complex
9	0.09	1 / 12	XY body
10	0.09	3 / 144	postsynaptic membrane
11	0.09	1 / 13	contractile fiber
12	0.10	2 / 70	primary cilium
13	0.10	29 / 3088	plasma membrane
14	0.10	1 / 14	exocyst
15	0.10	1 / 14	male germ cell nucleus
16	0.10	9 / 751	integral component of plasma membrane
17	0.11	1 / 16	excitatory synapse
18	0.12	2 / 79	nucleosome
19	0.12	1 / 17	replication fork
20	0.12	3 / 164	endosome membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.02	14 / 1037	Chr 19
2	0.11	7 / 551	Chr X
3	0.14	7 / 576	Chr 9
4	0.26	5 / 465	Chr 15
5	0.31	3 / 262	Chr 13
6	0.35	7 / 775	Chr 12
7	0.39	5 / 552	Chr 10
8	0.46	8 / 993	Chr 2
9	0.56	11 / 1500	Chr 1
10	0.57	3 / 398	Chr 20
11	0.58	5 / 687	Chr 6
12	0.68	1 / 151	Chr 21
13	0.71	4 / 649	Chr 16
14	0.71	5 / 801	Chr 11
15	0.75	5 / 838	Chr 3
16	0.76	4 / 689	Chr 7
17	0.76	4 / 696	Chr 5
18	0.81	1 / 221	Chr 18
19	0.86	2 / 462	Chr 14
20	0.87	2 / 469	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−05	14 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
2	2e−04	22 / 1317	EnhP_Colon
3	4e−04	30 / 2159	TssP_Colon
4	2e−03	28 / 2142	ReprPC_Colon
5	5e−03	24 / 1889	ReprPCWk_Colon
6	9e−03	7 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
7	9e−03	14 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
8	3e−02	5 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
9	7e−02	6 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
10	8e−02	6 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	8e−02	1 / 11	Budinska_B_Lower crypt−like_DOWN
12	2e−01	3 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	3e−01	6 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	3e−01	10 / 1079	ZNF_Colon
15	3e−01	1 / 45	Ang_CRC−CIMPH−vs−L_hyper
16	3e−01	31 / 3812	TssD1_Colon
17	3e−01	1 / 50	Ang_CRC_Hypermethylated
18	3e−01	12 / 1386	Het_Colon
19	3e−01	2 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	3e−01	74 / 9653	Enh_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.2	5 / 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	3e−04	4 / 45	Christensen_hypermethylated_in_primary_glioblastoma
2	4e−02	3 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
3	4e−02	3 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
4	5e−02	2 / 47	Weller_LGG_gradeII−vs−III_UP
5	5e−02	1 / 7	WILLSCHER_GBM_LTSwt_proteomics−G_UP
6	6e−02	3 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	7e−02	3 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	7e−02	2 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
9	8e−02	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
10	9e−02	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
11	1e−01	1 / 14	VERHAAK_PN subtype
12	1e−01	2 / 74	WIRTH_Normal Brain
13	1e−01	1 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
14	2e−01	3 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
15	2e−01	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
16	2e−01	1 / 33	Christensen_hypomethylated_in_primary_glioblastoma
17	2e−01	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
18	2e−01	1 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
19	2e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
20	3e−01	1 / 40	in vivo astrocytes vs. cultured astroglia

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−05	16 / 724	BENPORATH_EED_TARGETS
2	1e−04	17 / 823	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
3	2e−04	5 / 75	KANG_IMMORTALIZED_BY_TERT_UP
4	3e−04	15 / 720	BENPORATH_ES_WITH_H3K27ME3
5	4e−04	14 / 674	BENPORATH_SUZ12_TARGETS
6	5e−04	6 / 134	MEISSNER_BRAIN_HCP_WITH_H3K27ME3
7	5e−04	9 / 312	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
8	7e−04	7 / 199	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
9	1e−03	4 / 66	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM
10	2e−03	7 / 233	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
11	2e−03	4 / 72	KEGG_DILATED_CARDIOMYOPATHY
12	3e−03	9 / 396	BENPORATH_PRC2_TARGETS
13	3e−03	3 / 40	RICKMAN_HEAD_AND_NECK_CANCER_F
14	3e−03	2 / 12	MATZUK_EARLY_ANTRAL_FOLLICLE
15	4e−03	3 / 42	KEGG_HEDGEHOG_SIGNALING_PATHWAY
16	5e−03	3 / 46	PID_FOXO_PATHWAY
17	6e−03	4 / 97	KEGG_CELL_ADHESION_MOLECULES_CAMS
18	6e−03	2 / 16	LEE_DOUBLE_POLAR_THYMOCYTE
19	7e−03	3 / 54	RASHI_RESPONSE_TO_IONIZING_RADIATION_4
20	8e−03	2 / 18	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 167	HALLMARK_APICAL_JUNCTION
2	0.2	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.2	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
4	0.2	1 / 29	HALLMARK_NOTCH_SIGNALING
5	0.2	2 / 127	HALLMARK_KRAS_SIGNALING_DN
6	0.3	2 / 165	HALLMARK_MYOGENESIS
7	0.4	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
8	0.4	2 / 196	HALLMARK_G2M_CHECKPOINT
9	0.4	2 / 197	HALLMARK_E2F_TARGETS
10	0.5	1 / 95	HALLMARK_SPERMATOGENESIS
11	0.6	1 / 107	HALLMARK_COAGULATION
12	0.6	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	0.6	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
14	0.6	1 / 137	HALLMARK_UV_RESPONSE_DN
15	0.6	1 / 140	HALLMARK_APOPTOSIS
16	0.7	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
17	0.7	1 / 146	HALLMARK_DNA_REPAIR
18	0.7	1 / 146	HALLMARK_UV_RESPONSE_UP
19	0.7	1 / 148	HALLMARK_KRAS_SIGNALING_UP
20	0.7	1 / 162	HALLMARK_COMPLEMENT

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	0.002	39 / 3396	HOPP_Repressed
2	0.019	2 / 29	Subero_DLBCL_hypo_meth
3	0.029	24 / 2188	HOPP_Poised_promoter
4	0.034	3 / 96	Subero_DLBCL_hyper_meth
5	0.035	2 / 40	Subero_mBL_hyper_meth
6	0.047	2 / 47	Subero_FL_hyper_meth
7	0.058	1 / 8	Subero_B−CLL_hypo_meth
8	0.058	1 / 8	Subero_MM_hypo_meth
9	0.073	2 / 60	Subero_T−ALL_hyper_meth
10	0.092	1 / 13	YAMANE_AICDA_targets_recruited
11	0.092	1 / 13	Subero_MCL_hypo_meth
12	0.099	1 / 14	Subero_MCL_hyper_meth
13	0.119	2 / 80	Aukema_BCL2 DN_BCL6 UP
14	0.121	2 / 81	Subero_INT_hyper_meth
15	0.138	1 / 20	SPANG_BAFF 9hrs UP
16	0.170	1 / 25	Subero_T−PLL_hypo_meth
17	0.200	1 / 30	TARTE_B−cell signature
18	0.200	1 / 30	Subero_INT_hypo_meth
19	0.224	1 / 34	Subero_B−ALL_hyper_meth
20	0.252	1 / 39	ROSOLOWSKI_blue DOWN

MF

Rank	p−value	#in/all	Geneset
1	5e−04	11 / 450	sequence−specific DNA binding
2	6e−03	2 / 16	cysteine−type endopeptidase activator activity involved in apoptotic process
3	2e−02	2 / 26	olfactory receptor activity
4	2e−02	2 / 28	RNA polymerase II activating transcription factor binding
5	2e−02	5 / 217	G−protein coupled receptor activity
6	2e−02	2 / 32	Rac GTPase binding
7	3e−02	7 / 394	catalytic activity
8	3e−02	5 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
9	3e−02	2 / 37	coenzyme binding
10	4e−02	4 / 171	RNA polymerase II core promoter proximal region sequence−specific DNA bir
11	4e−02	2 / 42	glycoprotein binding
12	6e−02	3 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activit
13	6e−02	2 / 54	damaged DNA binding
14	6e−02	2 / 56	phosphoprotein phosphatase activity
15	7e−02	1 / 10	calcium−activated potassium channel activity
16	7e−02	1 / 10	phosphotyrosine binding
17	8e−02	2 / 62	protein phosphatase binding
18	8e−02	1 / 11	insulin−like growth factor receptor binding
19	8e−02	1 / 11	retinol dehydrogenase activity
20	8e−02	1 / 11	vinculin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	4 / 181	hsa−miR−196b
2	0.07	3 / 127	hsa−miR−323−3p
3	0.08	2 / 63	hsa−miR−455−3p
4	0.09	2 / 66	hsa−miR−643
5	0.10	1 / 14	hsa−miR−891a
6	0.10	2 / 74	hsa−miR−1827
7	0.10	3 / 153	hsa−miR−200c
8	0.11	1 / 15	hsa−miR−191*
9	0.11	3 / 155	hsa−miR−429
10	0.11	2 / 77	hsa−miR−1305
11	0.11	3 / 158	hsa−miR−200b
12	0.13	2 / 84	hsa−miR−486−3p
13	0.13	1 / 19	hsa−miR−645
14	0.16	2 / 95	hsa−miR−125a−3p
15	0.16	1 / 23	hsa−miR−943
16	0.17	1 / 25	hsa−miR−663b
17	0.18	1 / 26	hsa−miR−519e*
18	0.18	1 / 26	hsa−miR−337−5p
19	0.19	1 / 28	hsa−miR−1292
20	0.19	2 / 108	hsa−miR−449b

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.004	17 / 1139	HEBENSTREIT_low expression TF
2	0.015	1 / 2	MYC_Cell cycle DOWN
3	0.065	1 / 9	MYC_Targets DOWN
4	0.087	14 / 1273	ICGC_P300_targets
5	0.427	19 / 2416	ICGC_Bcl3_targets
6	0.528	14 / 1872	ICGC_Mef2_targets
7	0.643	14 / 2013	ICGC_Bcl11_targets
8	0.648	4 / 595	ICGC_NrsfPcr2_targets
9	0.694	20 / 2927	ICGC_Rad21_targets
10	0.695	30 / 4314	ICGC_Ebfsc137065_targets
11	0.731	14 / 2136	ICGC_GabpPcr2_targets
12	0.736	18 / 2714	ICGC_Irf4_targets
13	0.737	25 / 3700	ICGC_Nfatc1_targets
14	0.798	26 / 3966	ICGC_Pu1_targets
15	0.863	28 / 4414	ICGC_Bclaf101388_targets
16	0.868	3 / 653	ICGC_SrfPcr2_targets
17	0.892	34 / 5355	ICGC_Pol2_targets
18	0.903	10 / 1878	ICGC_Cebpbsc150_targets
19	0.914	30 / 4879	ICGC_Pmlsc71910_targets
20	0.918	13 / 2391	ICGC_Pbx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.005	2 / 15	VAQUERIZAS_Bone marrow
2	0.031	2 / 37	VAQUERIZAS_Thymus
3	0.037	2 / 41	VAQUERIZAS_Placenta
4	0.112	1 / 16	VAQUERIZAS_Adrenal gland
5	0.157	1 / 23	VAQUERIZAS_Adrenal cortex
6	0.218	1 / 33	VAQUERIZAS_Prostate
7	0.258	1 / 40	VAQUERIZAS_Thyroid
8	0.351	1 / 58	VAQUERIZAS_Lung
9	0.356	1 / 59	VAQUERIZAS_Whole blood
10	0.657	1 / 143	VAQUERIZAS_General
11	1.000	0 / 36	VAQUERIZAS_Fetal brain
12	1.000	0 / 26	VAQUERIZAS_Liver
13	1.000	0 / 29	VAQUERIZAS_Smooth muscle
14	1.000	0 / 45	VAQUERIZAS_Uterus
15	1.000	0 / 9	VAQUERIZAS_Kidney
16	1.000	0 / 23	VAQUERIZAS_Spinal cord
17	1.000	0 / 38	VAQUERIZAS_Whole brain
18	1.000	0 / 7	VAQUERIZAS_Appendix
19	1.000	0 / 29	VAQUERIZAS_Fetal lung
20	1.000	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.09	1 / 12	WIRTH_Thymus
2	0.19	2 / 107	WIRTH_Testis
3	0.26	4 / 350	WIRTH_Nervous System
4	0.26	1 / 41	WIRTH_Homeostasis
5	0.29	1 / 46	WIRTH_Liver
6	0.42	1 / 74	WIRTH_Mucosa
7	0.50	2 / 225	PALMER_Granulocytes signature up
8	0.51	1 / 95	WIRTH_Muscle
9	0.74	2 / 350	WIRTH_Immune system
10	1.00	0 / 32	WIRTH_Pancreas
11	1.00	0 / 11	WIRTH_Sec. lymphoid organs
12	1.00	0 / 11	WIRTH_Prim. lymphoid organs
13	1.00	0 / 13	WIRTH_B−cells
14	1.00	0 / 8	WIRTH_Tonsil
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	31 / 3682	LU_BPDE 0.005 DN
2	0.4	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	

Correlation Clusters

Spot Summary: I

metagenes = 42
genes = 4

<r> metagenes = 0.92
<r> genes = 0.3
beta: r2= 0.18 / log p= −4.71

samples with spot = 9 (9.8 %)
MSC1 : 8 (19 %)
MSC2 : 1 (4 %)

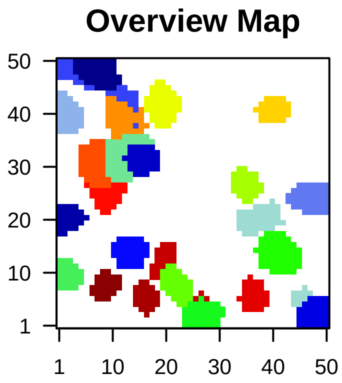
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	IQCC	1.67	−0.08	0.2	IQCC	IQ motif containing C [Source:HGNC Symbol;Acc:HGNC:255
2	TPBGL	0.97	−0.07	0.29	TPBGL	trophoblast glycoprotein−like [Source:HGNC Symbol;Acc:HG
3	MSRA	0.84	−0.07	0.26	MSRA	methionine sulfoxide reductase A [Source:HGNC Symbol;Acc
4	DBI	0.33	−0.61	0.45	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl−C

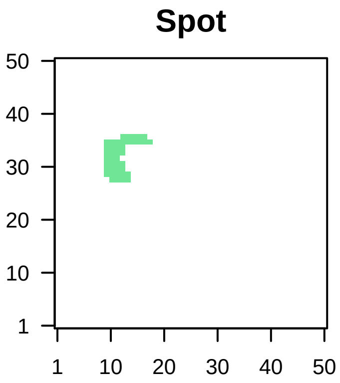
Geneset Overrepresentation

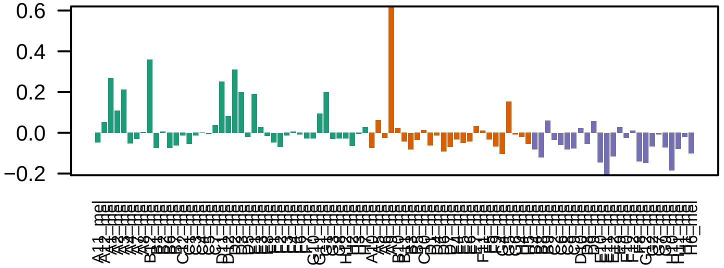
Rank	p−value	#in/all	Geneset	
1	0.002	1 / 8	Lympl	MASCQUE_GCB UP
2	0.003	1 / 10	CC	perinuclear endoplasmic reticulum
3	0.003	1 / 11	BP	lateral ventricle development
4	0.003	1 / 13	GSEA	FU_INTERACT_WITH_ALKBH8
5	0.004	1 / 16	BP	phosphatidylcholine acyl−chain remodeling
6	0.005	1 / 17	MF	fatty−acyl−CoA binding
7	0.005	1 / 20	BP	behavioral fear response
8	0.005	1 / 20	BP	triglyceride metabolic process
9	0.005	2 / 458	GSEA	ENK_UV_RESPONSE_EPIDERMIS_DN
10	0.006	1 / 23	GSEA	RUAN_RESPONSE_TO_TROGLITAZONE_UP
11	0.006	1 / 24	GSEA	MCCABE_HOXC6_TARGETS_CANCER_UP
12	0.007	2 / 527	GSEA	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
13	0.008	1 / 30	BP	long−term synaptic potentiation
14	0.008	1 / 31	GSEA	LEIN_ASTROCYTE_MARKERS
15	0.009	2 / 597	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
16	0.009	1 / 35	BP	learning or memory
17	0.010	1 / 38	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
18	0.010	1 / 39	BP	hair follicle development
19	0.012	1 / 43	BP	skin development
20	0.012	1 / 43	GSEA	NADLER_OBESITY_DN
21	0.013	1 / 47	HM	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
22	0.013	1 / 47	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
23	0.013	1 / 47	GSEA	LEE_LIVER_CANCER_E2F1_DN
24	0.013	1 / 50	GSEA	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
25	0.014	1 / 52	GSEA	KEGG_PPAR_SIGNALING_PATHWAY
26	0.014	1 / 52	GSEA	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_UP
27	0.015	1 / 55	GSEA	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
28	0.017	1 / 64	GSEA	GAVIN_FOXP3_TARGETS_CLUSTER_P2
29	0.019	1 / 71	GSEA	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
30	0.019	1 / 71	GSEA	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
31	0.019	1 / 71	GSEA	GAVIN_FOXP3_TARGETS_CLUSTER_P7
32	0.019	1 / 72	GSEA	MORI_PRE_BI_LYMPHOCYTE_UP
33	0.020	1 / 73	GSEA	RUAN_RESPONSE_TO_TNF_DN
34	0.021	1 / 77	GSEA	MUNSHI_MULTIPLE_MYELOMA_UP
35	0.021	1 / 78	GSEA	CHEN_LIVER_METABOLISM_QTL_CIS
36	0.021	1 / 79	GSEA	NELSON_RESPONSE_TO_ANDROGEN_UP
37	0.022	1 / 83	GSEA	GRADE_COLON_AND_RECTAL_CANCER_DN
38	0.025	1 / 94	HM	HALLMARK_ANDROGEN_RESPONSE
39	0.027	1 / 101	BP	response to oxidative stress
40	0.029	1 / 107	GSEA	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS

Overview Map

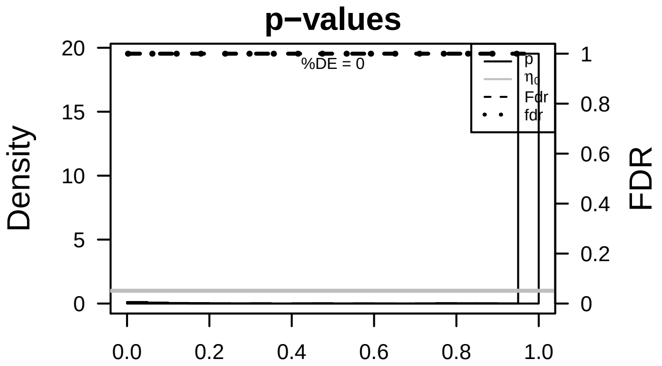


Spot





p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	0.003	1 / 11	lateral ventricle development
2	0.004	1 / 16	phosphatidylcholine acyl−chain remodeling
3	0.005	1 / 20	behavioral fear response
4	0.005	1 / 20	triglyceride metabolic process
5	0.008	1 / 30	long−term synaptic potentiation
6	0.009	1 / 35	learning or memory
7	0.010	1 / 39	hair follicle development
8	0.012	1 / 43	skin development
9	0.027	1 / 101	response to oxidative stress
10	0.067	1 / 255	cellular amino acid metabolic process
11	0.069	1 / 264	sulfur compound metabolic process
12	0.069	2 / 1730	small molecule metabolic process
13	0.138	1 / 541	oxidation−reduction process
14	0.202	1 / 815	lipid metabolic process
15	0.435	1 / 1975	cellular protein modification process
16	0.469	1 / 2172	response to stress
17	0.560	1 / 2755	transport
18	0.713	1 / 3980	cellular nitrogen compound metabolic process
19	0.984	2 / 12397	biological_process
20	1.000	0 / 18	2−oxoglutarate metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.1	2 / 2462	Mid_Frontal_Lobe_HetRpts
2	0.1	1 / 534	Mid_Frontal_Lobe_EnhG
3	0.1	1 / 564	Mid_Frontal_Lobe_EnhP
4	0.2	1 / 668	Mid_Frontal_Lobe_Enh
5	0.2	1 / 765	Mid_Frontal_Lobe_Het
6	0.2	1 / 1013	Fetal_TssP
7	0.3	1 / 1333	Fetal_ReprPCWk
8	0.4	1 / 1548	Mid_Frontal_Lobe_K9K27me3
9	0.4	1 / 1845	Fetal_Quies
10	0.4	1 / 1907	Fetal_TxTrans
11	0.5	1 / 2185	Fetal_TssA
12	0.5	3 / 9013	Overlap_fetal_midbrain_K9K27me3
13	0.6	1 / 2972	Mid_Frontal_Lobe_ReprPC
14	0.6	1 / 3081	Mid_Frontal_Lobe_ZNF
15	0.9	2 / 9330	Overlap_fetal_midbrain_ReprPC
16	0.9	2 / 9528	Overlap_fetal_midbrain_Quies
17	1.0	1 / 9020	Overlap_fetal_midbrain_ReprPCWk
18	1.0	0 / 812	Mid_Frontal_Lobe_TssP
19	1.0	0 / 989	Mid_Frontal_Lobe_Quies
20	1.0	0 / 156	Mid_Frontal_Lobe_TssA

Cancer

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

CC

Rank	p−value	#in/all	Geneset
1	0.003	1 / 10	perinuclear endoplasmic reticulum
2	0.051	2 / 1468	mitochondrion
3	0.053	1 / 202	actin cytoskeleton
4	0.107	2 / 2193	extracellular exosome
5	0.198	2 / 3132	extracellular region
6	0.272	1 / 1132	Golgi apparatus
7	0.286	1 / 1201	endoplasmic reticulum
8	0.340	1 / 1465	cytoskeleton
9	0.533	1 / 2576	membrane
10	0.534	1 / 2577	nucleoplasm
11	0.593	1 / 2984	integral component of membrane
12	0.762	2 / 8205	cytoplasm
13	0.856	1 / 5696	nucleus
14	0.894	2 / 9988	organelle
15	0.927	2 / 10605	intracellular
16	0.936	3 / 13191	cellular_component
17	0.970	2 / 11774	cell
18	1.000	0 / 11	acetylcholine−gated channel complex
19	1.000	0 / 15	acrosomal membrane
20	1.000	0 / 53	acrosomal vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.1	1 / 469	Chr 8
2	0.2	1 / 801	Chr 11
3	0.2	1 / 993	Chr 2
4	0.3	1 / 1500	Chr 1
5	1.0	0 / 552	Chr 10
6	1.0	0 / 775	Chr 12
7	1.0	0 / 262	Chr 13
8	1.0	0 / 462	Chr 14
9	1.0	0 / 465	Chr 15
10	1.0	0 / 649	Chr 16
11	1.0	0 / 840	Chr 17
12	1.0	0 / 221	Chr 18
13	1.0	0 / 1037	Chr 19
14	1.0	0 / 398	Chr 20
15	1.0	0 / 151	Chr 21
16	1.0	0 / 335	Chr 22
17	1.0	0 / 838	Chr 3
18	1.0	0 / 558	Chr 4
19	1.0	0 / 696	Chr 5
20	1.0	0 / 687	Chr 6

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 250	K9K27me3_Colon
2	0.11	1 / 427	Quies2_Colon
3	0.17	3 / 5880	TssD2_Colon
4	0.23	1 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
5	0.29	3 / 7203	TssF_Colon
6	0.32	1 / 1386	Het_Colon
7	0.42	1 / 1889	ReprPCWk_Colon
8	0.46	1 / 2142	ReprPC_Colon
9	0.55	1 / 2698	EnhA_Colon
10	0.57	1 / 2798	TxEnhG1_Colon
11	0.64	1 / 3383	EnhWk2_Colon
12	0.70	1 / 3897	Quies1_Colon
13	0.78	2 / 8415	Quies3_Colon
14	0.82	1 / 5155	EnhWk1_Colon
15	0.86	2 / 9482	TssA_Colon
16	0.87	2 / 9653	Enh_Colon
17	0.91	2 / 10290	TssWk_Colon
18	0.97	1 / 8580	TxWk_Colon
19	0.98	1 / 9027	Tx_Colon
20	1.00	0 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes

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	0.09	1 / 332	Up
2	1.00	0 / 15	VERHAAK_CL subtype
3	1.00	0 / 15	VERHAAK_MES subtype
4	1.00	0 / 16	VERHAAK_NL subtype
5	1.00	0 / 14	VERHAAK_PN subtype
6	1.00	0 / 23	WIRTH_PN subtype
7	1.00	0 / 74	WIRTH_Normal Brain
8	1.00	0 / 9	VERHAAK_Brain
9	1.00	0 / 8	VERHAAK_PN_Brain
10	1.00	0 / 11	Martinez_Glio_hypermeth
11	1.00	0 / 3	Martinez_Glio_hypometh
12	1.00	0 / 2	laffaire_hypometh_LGG_vs_control
13	1.00	0 / 72	laffaire_hypermeth_LGG_vs_control
14	1.00	0 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
15	1.00	0 / 4	Donson−adaptive−immunity−associated with LTS in HGA
16	1.00	0 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
17	1.00	0 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
18	1.00	0 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
19	1.00	0 / 32	Donson−innate immunity−associated with LTS in HGA
20	1.00	0 / 3	Donson−migration tethering and rolling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.003	1 / 13	FU_INTERACT_WITH_ALKBH8
2	0.005	2 / 458	ENK_UV_RESPONSE_EPIDERMIS_DN
3	0.006	1 / 23	RUAN_RESPONSE_TO_TROGLITAZONE_UP
4	0.006	1 / 24	MCCABE_HOXC6_TARGETS_CANCER_UP
5	0.007	2 / 527	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
6	0.008	1 / 31	LEIN_ASTROCYTE_MARKERS
7	0.009	2 / 597	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
8	0.010	1 / 38	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
9	0.012	1 / 43	NADLER_OBESITY_DN
10	0.013	1 / 47	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
11	0.013	1 / 47	LEE_LIVER_CANCER_E2F1_DN
12	0.013	1 / 50	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN
13	0.014	1 / 52	KEGG_PPAR_SIGNALING_PATHWAY
14	0.014	1 / 52	JOHANSSON_GLIOMAGENESIS_BY_PDGFB_UP
15	0.015	1 / 55	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
16	0.017	1 / 64	GAVIN_FOXP3_TARGETS_CLUSTER_P2
17	0.019	1 / 71	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
18	0.019	1 / 71	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
19	0.019	1 / 71	GAVIN_FOXP3_TARGETS_CLUSTER_P7
20	0.019	1 / 72	MORI_PRE_BI_LYMPHOCYTE_UP

HM

Rank	p−value	#in/all	Geneset
1	0.01	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.03	1 / 94	HALLMARK_ANDROGEN_RESPONSE
3	1.00	0 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	1.00	0 / 176	HALLMARK_HYPOXIA
5	1.00	0 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	1.00	0 / 195	HALLMARK_MITOTIC_SPINDLE
7	1.00	0 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	1.00	0 / 53	HALLMARK_TGF_BETA_SIGNALING
9	1.00	0 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	1.00	0 / 146	HALLMARK_DNA_REPAIR
11	1.00	0 / 196	HALLMARK_G2M_CHECKPOINT
12	1.00	0 / 140	HALLMARK_APOPTOSIS
13	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING
14	1.00	0 / 188	HALLMARK_ADIPOGENESIS
15	1.00	0 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
16	1.00	0 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
17	1.00	0 / 165	HALLMARK_MYOGENESIS
18	1.00	0 / 91	HALLMARK_PROTEIN_SECRETION
19	1.00	0 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
20	1.00	0 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	1 / 8	MASCOUE_GCB UP
2	0.077	1 / 294	TARTE_Plasmablast signature
3	0.291	3 / 7209	HOPP_Weak_promoter
4	0.330	3 / 7592	HOPP_Active_promoter
5	0.436	2 / 5184	HOPP_Txn_transition
6	0.472	1 / 2188	HOPP_Poised_promoter
7	0.475	1 / 2211	HOPP_Repetitive
8	0.478	2 / 5538	HOPP_Weak_txn
9	0.496	2 / 5693	HOPP_Weak_enhancer
10	0.596	2 / 6564	HOPP_Strong_enhancer
11	0.636	2 / 6929	HOPP_Txn_elongation
12	0.646	1 / 3396	HOPP_Repressed
13	1.000	0 / 13	BENTINK_mBL UP
14	1.000	0 / 12	BENTINK_mBL DOWN
15	1.000	0 / 129	DAVE_BL−vs−DLBCL
16	1.000	0 / 10	DAVE_BL_DN
17	1.000	0 / 16	DAVE_BL_Inter
18	1.000	0 / 10	DAVE_BL UP
19	1.000	0 / 19	DAVE_c−myc BL UP
20	1.000	0 / 6	DAVE_MHCCII BL DN

MF

Rank	p−value	#in/all	Geneset
1	0.005	1 / 17	fatty−acyl−CoA binding
2	0.040	1 / 149	protein dimerization activity
3	0.111	1 / 430	lipid binding
4	0.150	1 / 592	oxidoreductase activity
5	0.806	1 / 4992	ion binding
6	0.935	3 / 13179	molecular_function
7	0.976	1 / 8984	protein binding
8	1.000	0 / 18	14−3−3 protein binding
9	1.000	0 / 19	1−phosphatidylinositol binding
10	1.000	0 / 18	2 iron, 2 sulfur cluster binding
11	1.000	0 / 22	3',5'−cyclic−nucleotide phosphodiesterase activity
12	1.000	0 / 18	3'−5' exonuclease activity
13	1.000	0 / 19	3'−5'−exoribonuclease activity
14	1.000	0 / 11	3−beta−hydroxy−delta5−steroid dehydrogenase activity
15	1.000	0 / 35	4 iron, 4 sulfur cluster binding
16	1.000	0 / 13	5'−nucleotidase activity
17	1.000	0 / 10	acetylcholine−activated cation−selective channel activity
18	1.000	0 / 10	acetylgalactosaminyltransferase activity
19	1.000	0 / 16	acetylglucosaminyltransferase activity
20	1.000	0 / 11	acetyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1	0 / 408	hsa−miR−497
2	1	0 / 291	hsa−miR−34c−5p
3	1	0 / 300	hsa−miR−548c−3p
4	1	0 / 376	hsa−miR−373
5	1	0 / 179	hsa−miR−520f
6	1	0 / 314	hsa−miR−520c−3p
7	1	0 / 303	hsa−miR−18b
8	1	0 / 92	hsa−miR−425
9	1	0 / 272	hsa−miR−520b
10	1	0 / 155	hsa−miR−31
11	1	0 / 180	hsa−miR−302e
12	1	0 / 179	hsa−miR−582−5p
13	1	0 / 329	hsa−miR−302d
14	1	0 / 318	hsa−miR−302a
15	1	0 / 426	hsa−miR−519d
16	1	0 / 552	hsa−miR−93
17	1	0 / 154	hsa−miR−139−5p
18	1	0 / 569	hsa−miR−20b
19	1	0 / 523	hsa−miR−106a
20	1	0 / 541	hsa−miR−17

PathwAct

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

TF

Rank	p−value	#in/all	Geneset
1	0.07	2 / 1701	HEBENSTREIT_high expression TF
2	0.28	1 / 1171	KIM_MYC targets
3	0.30	1 / 1266	ICGC_NrsfPcr1_targets
4	0.31	1 / 1314	ICGC_Usf1_targets
5	0.42	1 / 1872	ICGC_Mef2_targets
6	0.42	1 / 1878	ICGC_Cebpbsc150_targets
7	0.46	1 / 2137	ICGC_SrfV0416101_targets
8	0.51	1 / 2416	ICGC_Bcl3_targets
9	0.55	1 / 2714	ICGC_Irf4_targets
10	0.68	1 / 3700	ICGC_Nfatc1_targets
11	0.71	1 / 3924	ICGC_Zeb1_targets
12	0.72	1 / 4032	ICGC_Creb1_targets
13	0.72	1 / 4054	ICGC_Egr1_targets
14	0.75	1 / 4314	ICGC_Ebfsc137065_targets
15	0.75	1 / 4385	ICGC_Atf2_targets
16	0.76	1 / 4414	ICGC_Bclaf101388_targets
17	0.77	1 / 4617	ICGC_Tcf12_targets
18	0.78	1 / 4682	ICGC_Pol24_targets
19	0.78	1 / 4689	ICGC_Taf1_targets
20	0.78	1 / 4706	ICGC_Sp1_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 225	PALMER_Granulocytes signature up
2	1.00	0 / 32	WIRTH_Pancreas
3	1.00	0 / 350	WIRTH_Immune system
4	1.00	0 / 11	WIRTH_Sec. lymphoid organs
5	1.00	0 / 11	WIRTH_Prim. lymphoid organs
6	1.00	0 / 13	WIRTH_B−cells
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	0.7	1 / 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	

Correlation Clusters

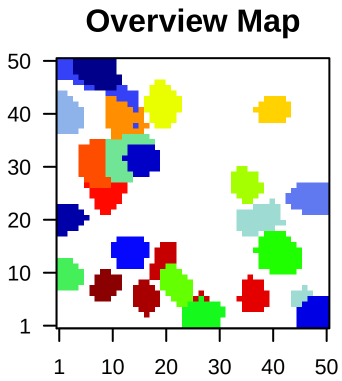
Spot Summary: J

metagenes = 36
genes = 215

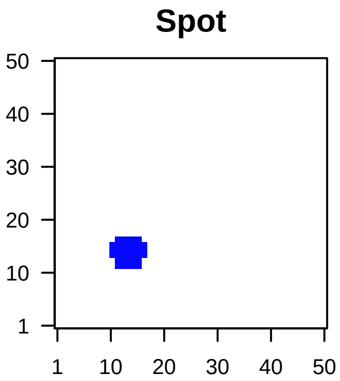
<r> metagenes = 0.95
<r> genes = 0.25
beta: r2= 0.52 / log p= −15.35

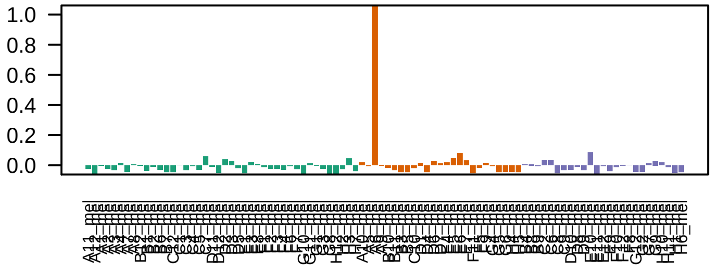
samples with spot = 1 (1.1 %)
MSC2 : 1 (4 %)

Overview Map



Spot





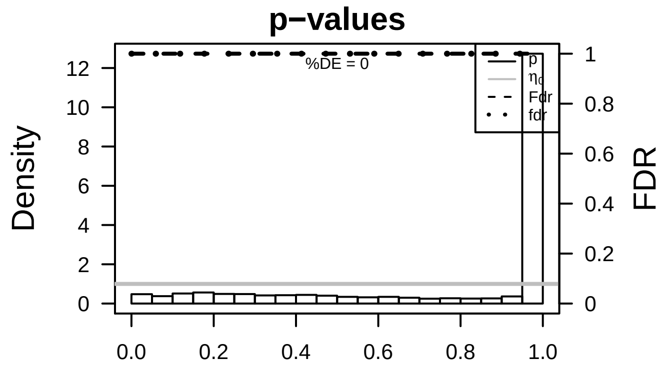
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TPRN	2.31	−0.2	0.44	TPRN	taperin [Source:HGNC Symbol;Acc:HGNC:26894]
2	C3orf14	2.29	−0.16	0.39	C3orf14	chromosome 3 open reading frame 14 [Source:HGNC Symbo
3	MDK	2.02	−0.1	0.54	MDK	midkine (neurite growth−promoting factor 2) [Source:HGNC S
4	C10orf107	1.93	−0.08	0.67	C10orf107	chromosome 10 open reading frame 107 [Source:HGNC Syn
5	ANKS1B	1.88	−0.13	0.64	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B [
6	MEGF10	1.88	−0.23	0.44	MEGF10	multiple EGF−like−domains 10 [Source:HGNC Symbol;Acc:H
7	ZNF442	1.86	−0.19	0.45	ZNF442	zinc finger protein 442 [Source:HGNC Symbol;Acc:HGNC:20
8	GANC	1.84	−0.25	0.37	GANC	glucosidase, alpha; neutral C [Source:HGNC Symbol;Acc:HG
9	NEK3	1.8	−0.27	0.32	NEK3	NIMA−related kinase 3 [Source:HGNC Symbol;Acc:HGNC:77
10	C9orf92	1.79	−0.1	0.62	C9orf92	chromosome 9 open reading frame 92 [Source:HGNC Symbo
11	MDGA2	1.77	−0.23	0.41	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor
12	THAP9	1.76	−0.33	0.34	THAP9	THAP domain containing 9 [Source:HGNC Symbol;Acc:HGN
13	MCU	1.74	−0.18	0.47	MCU	mitochondrial calcium uniporter [Source:HGNC Symbol;Acc:
14	NFKBIE	1.74	−0.22	0.3	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B−
15	SNAP25	1.72	−0.13	0.43	SNAP25	synaptosomal−associated protein, 25kDa [Source:HGNC Sy
16	ZSCAN26	1.72	−0.31	0.26	ZSCAN26	zinc finger and SCAN domain containing 26 [Source:HGNC S
17	GIT2	1.69	−0.46	0.25	GIT2	G protein−coupled receptor kinase interacting ArfGAP 2 [Sou
18	CTIF	1.67	−0.36	0.29	CTIF	CBP80/20−dependent translation initiation factor [Source:HG
19	ALDH1A1	1.65	−0.08	0.91	ALDH1A1	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
20	TTYH2	1.65	−0.14	0.49	TTYH2	tweety family member 2 [Source:HGNC Symbol;Acc:HGNC:1

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−06	6 / 30	Lymp	TARTE_B−cell signature
2	5e−06	6 / 31	GSE	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
3	3e−05	54 / 2159	Colon	TssP_Colon
4	7e−05	37 / 1317	Colon	EnhP_Colon
5	1e−04	3 / 7	Lifest	DUMEAUX_Women normal BMI literature genes up
6	2e−04	14 / 314	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	3e−04	5 / 41	MF	phosphatase binding
8	3e−04	4 / 23	GSE	REACTOME_OLFACTORY_SIGNALING_PATHWAY
9	5e−04	31 / 1139	TF	HEBENSTREIT_low expression TF
10	5e−04	4 / 26	BP	detection of chemical stimulus involved in sensory perception of smell
11	5e−04	4 / 26	MF	olfactory receptor activity
12	6e−04	4 / 27	GSE	HAHTOLA_SEZARY_SYNDROM_DN
13	6e−04	49 / 2142	Colon	ReprPC_Colon
14	8e−04	3 / 13	GSE	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
15	8e−04	13 / 319	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
16	9e−04	44 / 1889	Colon	ReprPCWk_Colon
17	1e−03	5 / 53	BP	response to cytokine
18	1e−03	11 / 249	GSE	BHAT_ESR1_TARGETS_VIA_AKT1_UP
19	1e−03	25 / 884	Brain	Overlap_fetal_midbrain_EnhG
20	1e−03	14 / 379	GSE	REACTOME_SIGNALING_BY_GPCR
21	1e−03	3 / 16	BP	calcium ion−dependent exocytosis
22	2e−03	9 / 185	GSE	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP
23	2e−03	4 / 35	CC	cell periphery
24	2e−03	3 / 17	MF	receptor signaling complex scaffold activity
25	2e−03	4 / 38	GSE	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
26	2e−03	8 / 160	GSE	WIERENGA_STAT5A_TARGETS_DN
27	2e−03	3 / 19	TF Ti	VAQUERIZAS_Tonsil
28	3e−03	4 / 41	CC	cleavage furrow
29	3e−03	4 / 42	GSE	KEGG_OLFACTORY_TRANSDUCTION
30	3e−03	6 / 100	GSE	BROWNE_HCMV_INFECTION_12HR_UP
31	4e−03	5 / 72	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
32	4e−03	7 / 139	GSE	MOHANKUMAR_TLX1_TARGETS_DN
33	4e−03	2 / 7	GSE	DER_IFN_BETA_RESPONSE_DN
34	4e−03	8 / 177	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
35	4e−03	21 / 775	CC	extracellular space
36	4e−03	11 / 300	GSE	REACTOME_GPCR_DOWNSTREAM_SIGNALING
37	5e−03	9 / 218	GSE	SENESE_HDAC1_TARGETS_DN
38	5e−03	8 / 179	GSE	NABA_SECRETED_FACTORS
39	6e−03	3 / 26	GSE	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
40	7e−03	3 / 27	MF	chemokine activity

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.5	2 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 100	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 26	detection of chemical stimulus involved in sensory perception of smell
2	1e−03	5 / 53	response to cytokine
3	1e−03	3 / 16	calcium ion−dependent exocytosis
4	8e−03	5 / 85	response to virus
5	9e−03	2 / 10	DNA integration
6	9e−03	2 / 10	regulation of sodium ion transmembrane transporter activity
7	1e−02	2 / 11	positive regulation of interleukin−2 production
8	1e−02	3 / 35	negative regulation of Wnt signaling pathway
9	1e−02	2 / 13	behavioral response to pain
10	1e−02	2 / 13	negative regulation of viral release from host cell
11	2e−02	2 / 14	negative regulation of interferon−gamma production
12	2e−02	2 / 14	T cell proliferation
13	2e−02	3 / 38	regulation of G−protein coupled receptor protein signaling pathway
14	2e−02	4 / 69	negative regulation of cell migration
15	2e−02	2 / 15	nucleotide phosphorylation
16	2e−02	2 / 15	positive regulation of interleukin−10 production
17	2e−02	4 / 72	calcium ion transport
18	2e−02	2 / 16	cellular response to cytokine stimulus
19	2e−02	2 / 16	positive regulation of interleukin−12 production
20	2e−02	3 / 42	cellular response to transforming growth factor beta stimulus

Brain

Rank	p−value	#in/all	Geneset
1	0.001	25 / 884	Overlap_fetal_midbrain_EnhG
2	0.021	24 / 1065	Overlap_fetal_midbrain_Enh
3	0.026	6 / 156	Mid_Frontal_Lobe_TssA
4	0.027	55 / 2972	Mid_Frontal_Lobe_ReprPC
5	0.039	31 / 1548	Mid_Frontal_Lobe_K9K27me3
6	0.040	14 / 574	Overlap_fetal_midbrain_TssP
7	0.044	25 / 1207	Overlap_fetal_midbrain_TssF
8	0.116	6 / 229	Mid_Frontal_Lobe_TxTrans
9	0.129	38 / 2185	Fetal_TssA
10	0.196	13 / 686	Overlap_fetal_midbrain_TssA
11	0.200	15 / 812	Mid_Frontal_Lobe_TssP
12	0.243	7 / 349	Fetal_ZNF
13	0.243	12 / 656	Overlap_fetal_midbrain_EnhP
14	0.247	10 / 534	Mid_Frontal_Lobe_EnhG
15	0.272	31 / 1907	Fetal_TxTrans
16	0.291	22 / 1333	Fetal_ReprPCWk
17	0.316	13 / 765	Mid_Frontal_Lobe_Het
18	0.335	20 / 1236	Mid_Frontal_Lobe_ReprPCWk
19	0.367	8 / 468	Mid_Frontal_Lobe_TssF
20	0.433	3 / 166	Mid_Frontal_Lobe_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.06	3 / 61	PanCan_Wnt_geneset_nanostring
3	0.11	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.20	1 / 15	GENTLES_modul10
5	0.21	1 / 16	GENTLES_modul14
6	0.26	0 / 12	LIU_BREAST_CANCER
7	0.27	1 / 22	PanCan_HH_geneset_nanostring
8	0.35	0 / 14	LIU_LIVER_CANCER
9	0.47	1 / 44	PanCan_TGF−B_geneset_nanostring
10	0.49	2 / 113	PanCan_Driver_Gene_geneset_nanostring
11	0.50	1 / 47	PanCan_DNARepair_geneset_nanostring
12	0.53	2 / 121	PanCan_MAPK_geneset_nanostring
13	0.55	1 / 55	PanCan_JAK−ST_geneset_nanostring
14	0.57	7 / 489	Lembcke_Normal vs Adenoma
15	0.62	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
16	0.70	1 / 82	PanCan_TXmisReg_geneset_nanostring
17	0.74	2 / 180	SPANG_LPS−index2
18	0.83	1 / 120	PanCan_CC+Apop_geneset_nanostring
19	0.84	4 / 401	Lembcke_Colonic Inflammation
20	0.93	2 / 298	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	0.002	4 / 35	cell periphery
2	0.003	4 / 41	cleavage furrow
3	0.004	21 / 775	extracellular space
4	0.009	11 / 332	cell junction
5	0.021	4 / 73	basement membrane
6	0.023	3 / 42	synaptic vesicle membrane
7	0.025	57 / 3088	plasma membrane
8	0.032	3 / 48	kinesin complex
9	0.034	4 / 84	growth cone
10	0.040	4 / 89	tight junction
11	0.043	5 / 132	basolateral plasma membrane
12	0.050	5 / 138	cell−cell junction
13	0.058	5 / 144	postsynaptic membrane
14	0.072	7 / 250	microtubule
15	0.074	2 / 31	brush border membrane
16	0.078	2 / 32	chloride channel complex
17	0.081	3 / 70	sarcolemma
18	0.082	4 / 113	postsynaptic density
19	0.095	2 / 36	T−tubule
20	0.098	3 / 76	cell projection

Chr

Rank	p−value	#in/all	Geneset
1	0.06	9 / 335	Chr 22
2	0.07	17 / 801	Chr 11
3	0.09	14 / 649	Chr 16
4	0.20	13 / 687	Chr 6
5	0.21	11 / 576	Chr 9
6	0.28	10 / 551	Chr X
7	0.28	10 / 552	Chr 10
8	0.42	23 / 1500	Chr 1
9	0.43	11 / 696	Chr 5
10	0.52	6 / 398	Chr 20
11	0.54	15 / 1037	Chr 19
12	0.54	10 / 689	Chr 7
13	0.65	2 / 151	Chr 21
14	0.78	12 / 993	Chr 2
15	0.80	9 / 775	Chr 12
16	0.80	5 / 462	Chr 14
17	0.82	6 / 558	Chr 4
18	0.83	2 / 221	Chr 18
19	0.86	9 / 840	Chr 17
20	0.91	4 / 465	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	54 / 2159	TssP_Colon
2	7e−05	37 / 1317	EnhP_Colon
3	2e−04	14 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
4	6e−04	49 / 2142	ReprPC_Colon
5	8e−04	13 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	9e−04	44 / 1889	ReprPCWk_Colon
7	3e−02	1 / 2	Hewish_dMMR−secondary−mutations_Immune_surveillance
8	6e−02	59 / 3383	EnhWk2_Colon
9	6e−02	11 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
10	7e−02	27 / 1386	Het_Colon
11	7e−02	3 / 66	Marisa_CRC−cluster−h
12	7e−02	7 / 250	K9K27me3_Colon
13	8e−02	2 / 33	Marisa_CRC−cluster−e
14	9e−02	9 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
15	9e−02	5 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
16	1e−01	65 / 3897	Quies1_Colon
17	1e−01	1 / 8	Marisa_CRC−C6
18	1e−01	20 / 1038	HetRpts_Colon
19	1e−01	18 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	2e−01	147 / 9653	Enh_Colon

Disease

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

Glio

Rank	p−value	#in/all	Geneset
1	0.01	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
2	0.01	4 / 65	GIEZELT_GBM_STS_up_VS_LTS
3	0.07	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
4	0.09	3 / 74	WIRTH_Normal Brain
5	0.10	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
6	0.11	2 / 39	OPC
7	0.11	1 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
8	0.12	1 / 9	Mukasa_UP_in_GBM
9	0.15	2 / 47	mature astrocytes
10	0.15	2 / 47	Weller_LGG_gradeII−vs−III_UP
11	0.16	2 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
12	0.17	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
13	0.18	3 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
14	0.20	1 / 15	VERHAAK_MES subtype
15	0.21	1 / 16	KIM deleted & downregulated in LTS
16	0.23	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
17	0.26	7 / 356	Down_a
18	0.27	1 / 22	KIM prognostic signature LTS vs. STS
19	0.29	1 / 23	WIRTH_PN subtype
20	0.29	1 / 23	Donson−Misc immune function−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−06	6 / 31	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
2	3e−04	4 / 23	REACTOME_OLFACTORY_SIGNALING_PATHWAY
3	6e−04	4 / 27	HAHTOLA_SEZARY_SYNDROM_DN
4	8e−04	3 / 13	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
5	1e−03	11 / 249	BHAT_ESR1_TARGETS_VIA_AKT1_UP
6	1e−03	14 / 379	REACTOME_SIGNALING_BY_GPCR
7	2e−03	9 / 185	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP
8	2e−03	4 / 38	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
9	2e−03	8 / 160	WIERENGA_STAT5A_TARGETS_DN
10	3e−03	4 / 42	KEGG_OLFACTORY_TRANSDUCTION
11	3e−03	6 / 100	BROWNE_HCMV_INFECTION_12HR_UP
12	4e−03	5 / 72	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
13	4e−03	7 / 139	MOHANKUMAR_TLX1_TARGETS_DN
14	4e−03	2 / 7	DER_IFN_BETA_RESPONSE_DN
15	4e−03	11 / 300	REACTOME_GPCR_DOWNSTREAM_SIGNALING
16	5e−03	9 / 218	SENESE_HDAC1_TARGETS_DN
17	5e−03	8 / 179	NABA_SECRETED_FACTORS
18	6e−03	3 / 26	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
19	7e−03	3 / 27	BIOCARTA_MYOSIN_PATHWAY
20	8e−03	9 / 236	KOYAMA_SEMA3B_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.004	8 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	0.037	6 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.037	6 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
4	0.145	3 / 91	HALLMARK_BILE_ACID_METABOLISM
5	0.216	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.245	4 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	0.275	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
8	0.335	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
9	0.360	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.363	3 / 148	HALLMARK_KRAS_SIGNALING_UP
11	0.364	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
12	0.391	2 / 93	HALLMARK_PEROXISOME
13	0.409	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	0.418	1 / 37	HALLMARK_APICAL_SURFACE
15	0.437	3 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	0.440	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
17	0.444	3 / 169	HALLMARK_XENOBIOTIC_METABOLISM
18	0.539	1 / 53	HALLMARK_TGF_BETA_SIGNALING
19	0.593	2 / 137	HALLMARK_UV_RESPONSE_DN
20	0.628	2 / 146	HALLMARK_UV_RESPONSE_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 7	DUMEAUX_Women normal BMI literature genes up
2	4e−01	1 / 32	DUMEAUX_Fasting enriched genes
3	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
5	1e+00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1e+00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1e+00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1e+00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1e+00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1e+00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−06	6 / 30	TARTE_B−cell signature
2	8e−03	45 / 2188	HOPP_Poised_promoter
3	2e−02	63 / 3396	HOPP_Repressed
4	7e−02	2 / 29	Subero_DLBCL_hypo_meth
5	8e−02	10 / 410	SPANG_CD40 6hrs DN
6	1e−01	1 / 8	Subero_MM_hypo_meth
7	1e−01	1 / 10	DAVE_BL UP
8	2e−01	37 / 2211	HOPP_Repetitive
9	2e−01	5 / 212	LENZ_Stromal signature 1
10	2e−01	1 / 15	DAVE_Immune response 2
11	2e−01	2 / 61	SPANG_LPS 6hrs DN
12	3e−01	1 / 20	SPANG_BAFF 9hrs UP
13	3e−01	1 / 25	Subero_T−PLL_hypo_meth
14	4e−01	1 / 30	Subero_INT_hypo_meth
15	4e−01	5 / 275	TARTE_Mature plasma cell signature
16	4e−01	1 / 33	LEE_Developmental_regulators
17	4e−01	39 / 2563	HOPP_Heterochrom
18	4e−01	2 / 96	Subero_DLBCL_hyper_meth
19	5e−01	2 / 107	SPANG_LPS 6hrs UP
20	5e−01	4 / 247	ZHANG_DLBCL mutated

MF

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 41	phosphatase binding
2	5e−04	4 / 26	olfactory receptor activity
3	2e−03	3 / 17	receptor signaling complex scaffold activity
4	7e−03	3 / 27	chemokine activity
5	9e−03	2 / 10	ephrin receptor activity
6	9e−03	2 / 10	guanylate kinase activity
7	9e−03	2 / 10	proteoglycan binding
8	1e−02	4 / 64	beta−catenin binding
9	1e−02	2 / 13	neuropeptide hormone activity
10	1e−02	2 / 13	taste receptor activity
11	2e−02	2 / 14	RNA polymerase II transcription factor binding transcription factor activity invo
12	2e−02	4 / 69	microtubule motor activity
13	2e−02	2 / 15	spectrin binding
14	2e−02	3 / 43	SMAD binding
15	2e−02	2 / 17	steroid binding
16	3e−02	3 / 46	steroid hormone receptor activity
17	3e−02	3 / 49	drug binding
18	4e−02	2 / 21	sodium channel regulator activity
19	4e−02	3 / 51	ubiquitinyl hydrolase activity
20	4e−02	2 / 23	ephrin receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	4 / 90	hsa−miR−216b
2	0.13	4 / 133	hsa−miR−198
3	0.16	1 / 12	hsa−miR−652
4	0.17	1 / 13	hsa−miR−638
5	0.18	2 / 54	hsa−miR−518d−5p
6	0.18	2 / 54	hsa−miR−520c−5p
7	0.24	3 / 118	hsa−miR−509−3p
8	0.26	2 / 68	hsa−miR−1184
9	0.26	2 / 69	hsa−miR−1266
10	0.27	1 / 22	hsa−miR−516a−5p
11	0.30	1 / 24	hsa−miR−220b
12	0.30	2 / 75	hsa−miR−513c
13	0.33	3 / 139	hsa−miR−132
14	0.35	1 / 29	hsa−miR−193a−5p
15	0.35	3 / 146	hsa−miR−142−3p
16	0.37	1 / 32	hsa−miR−631
17	0.37	1 / 32	hsa−miR−1178
18	0.40	2 / 94	hsa−miR−526a
19	0.41	2 / 96	hsa−miR−150
20	0.41	1 / 36	hsa−miR−769−5p

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	5e−04	31 / 1139	HEBENSTREIT_low expression TF
2	2e−01	34 / 2013	ICGC_Bcl11_targets
3	2e−01	47 / 2927	ICGC_Rad21_targets
4	3e−01	44 / 2836	ICGC_BatfPcr1_targets
5	4e−01	9 / 553	ICGC_RxraPcr1_targets
6	5e−01	9 / 595	ICGC_NrsfPcr2_targets
7	6e−01	18 / 1266	ICGC_NrsfPcr1_targets
8	6e−01	18 / 1273	ICGC_P300_targets
9	6e−01	77 / 5408	ICGC_Pou2_targets
10	7e−01	74 / 5374	ICGC_Pax5_targets
11	7e−01	36 / 2714	ICGC_Irf4_targets
12	8e−01	16 / 1314	ICGC_Usf1_targets
13	8e−01	70 / 5219	ICGC_Tcf3_targets
14	8e−01	23 / 1872	ICGC_Mef2_targets
15	8e−01	53 / 4054	ICGC_Egr1_targets
16	8e−01	82 / 6114	ICGC_Runx3_targets
17	9e−01	52 / 4032	ICGC_Creb1_targets
18	9e−01	51 / 3966	ICGC_Pu1_targets
19	9e−01	78 / 5890	ICGC_Elf1_targets
20	9e−01	16 / 1418	ICGC_Ets1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.002	3 / 19	VAQUERIZAS_Tonsil
2	0.016	3 / 37	VAQUERIZAS_Thymus
3	0.054	2 / 26	VAQUERIZAS_Liver
4	0.058	2 / 27	VAQUERIZAS_Lymph node
5	0.097	1 / 7	VAQUERIZAS_Tongue
6	0.197	1 / 15	VAQUERIZAS_Bone marrow
7	0.205	2 / 58	VAQUERIZAS_Lung
8	0.208	1 / 16	VAQUERIZAS_Salivary gland
9	0.220	1 / 17	VAQUERIZAS_Pituitary
10	0.343	3 / 143	VAQUERIZAS_General
11	0.345	1 / 29	VAQUERIZAS_Smooth muscle
12	0.482	1 / 45	VAQUERIZAS_Uterus
13	0.578	1 / 59	VAQUERIZAS_Whole blood
14	1.000	0 / 36	VAQUERIZAS_Fetal brain
15	1.000	0 / 41	VAQUERIZAS_Placenta
16	1.000	0 / 33	VAQUERIZAS_Prostate
17	1.000	0 / 9	VAQUERIZAS_Kidney
18	1.000	0 / 23	VAQUERIZAS_Spinal cord
19	1.000	0 / 38	VAQUERIZAS_Whole brain
20	1.000	0 / 40	VAQUERIZAS_Thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 14	WIRTH_Telencephalon
2	0.06	6 / 194	PALMER_B−Cell signature up
3	0.07	9 / 350	WIRTH_Nervous System
4	0.11	1 / 8	WIRTH_Tonsil
5	0.12	2 / 41	WIRTH_Homeostasis
6	0.40	2 / 95	WIRTH_Muscle
7	0.41	4 / 225	PALMER_Granulocytes signature up
8	0.49	1 / 46	WIRTH_Liver
9	0.66	1 / 74	WIRTH_Mucosa
10	0.75	4 / 350	WIRTH_Immune system
11	1.00	0 / 32	WIRTH_Pancreas
12	1.00	0 / 11	WIRTH_Sec. lymphoid organs
13	1.00	0 / 11	WIRTH_Prim. lymphoid organs
14	1.00	0 / 13	WIRTH_B−cells
15	1.00	0 / 12	WIRTH_Thymus
16	1.00	0 / 12	WIRTH_Lymphocytes
17	1.00	0 / 5	WIRTH_Bone marrow
18	1.00	0 / 11	WIRTH_Globus pallidus
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.05	23 / 1115	LU_BPDE 1n DN
2	0.13	61 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

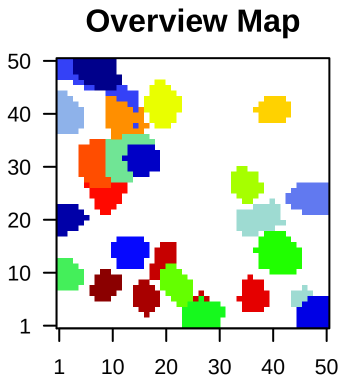
Correlation Clusters

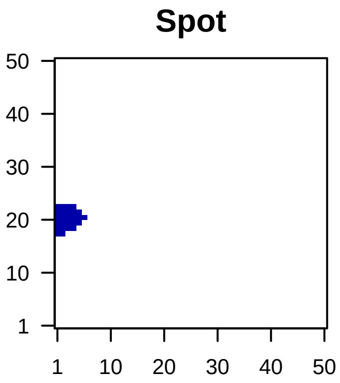
Spot Summary: K

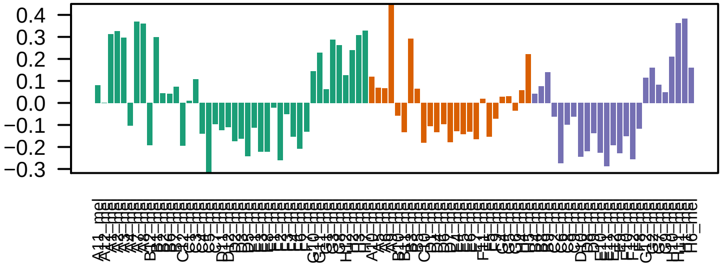
metagenes = 26
genes = 272

<r> metagenes = 0.96
<r> genes = 0.14
beta: r2= 1.96 / log p= −Inf

samples with spot = 20 (21.7 %)
MSC1 : 12 (28.6 %)
MSC2 : 3 (12 %)
MSC3 : 5 (20 %)





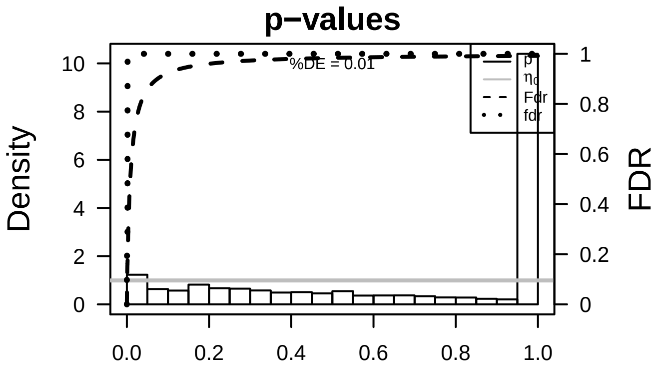


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	RAB40B	1.91	−0.31	0.29	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
2	ARRDC1	1.83	−0.36	0.26	ARRDC1	arrestin domain containing 1 [Source:HGNC Symbol;Acc:HG
3	NSMCE4A	1.83	−0.38	0.29	NSMCE4A	non−SMC element 4 homolog A (S. cerevisiae) [Source:HGN
4	FAM131A	1.78	−0.18	0.29	FAM131A	family with sequence similarity 131, member A [Source:HGN
5	DBNDD2	1.77	−0.24	0.33	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing
6	IFNAR2	1.71	−0.41	0.45	IFNAR2	interferon (alpha, beta and omega) receptor 2 [Source:HGNC
7	NECAB3	1.7	−0.22	0.25	NECAB3	N−terminal EF−hand calcium binding protein 3 [Source:HGN
8	LMLN	1.68	−0.37	0.26	LMLN	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
9	MIOS	1.64	−0.23	0.29	MIOS	missing oocyte, meiosis regulator, homolog (Drosophila) [Sou
10	ORAI3	1.62	−0.39	0.21	ORAI3	ORAI calcium release−activated calcium modulator 3 [Source
11	SDCCAG3	1.61	−0.51	0.35	SDCCAG3	serologically defined colon cancer antigen 3 [Source:HGNC
12	PVR	1.6	−0.17	0.21	PVR	poliovirus receptor [Source:HGNC Symbol;Acc:HGNC:9705]
13	GET4	1.6	−0.28	0.32	GET4	golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:
14	PXMP4	1.59	−0.29	0.33	PXMP4	peroxisomal membrane protein 4, 24kDa [Source:HGNC Sy
15	DNAJC4	1.59	−0.96	0.27	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HG
16	SLC35A3	1.58	−0.48	0.31	SLC35A3	solute carrier family 35 (UDP−N−acetylglucosamine (UDP−G
17	E2F4	1.58	−0.5	0.36	E2F4	E2F transcription factor 4, p107/p130−binding [Source:HGNC
18	TMEM175	1.57	−0.23	0.29	TMEM175	transmembrane protein 175 [Source:HGNC Symbol;Acc:HG
19	RITA1	1.56	−0.34	0.27	RITA1	RBPJ interacting and tubulin associated 1 [Source:HGNC Sy
20	RAD51D	1.55	−0.37	0.23	RAD51D	RAD51 paralog D [Source:HGNC Symbol;Acc:HGNC:9823]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−18	236 / 9482	Colon	TssA_Colon
2	2e−14	193 / 7203	Colon	TssF_Colon
3	3e−12	50 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	4e−12	217 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
5	1e−11	203 / 8205	CC	cytoplasm
6	1e−10	44 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	9e−09	28 / 440	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
8	1e−08	51 / 1201	CC	endoplasmic reticulum
9	2e−08	232 / 10605	CC	intracellular
10	7e−08	206 / 9027	Colon	Tx_Colon
11	9e−08	52 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
12	1e−07	32 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
13	2e−07	55 / 1468	CC	mitochondrion
14	2e−07	26 / 447	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_UP
15	2e−07	92 / 3081	Brain	Mid_Frontal_Lobe_ZNF
16	3e−07	212 / 9528	Brain	Overlap_fetal_midbrain_Quies
17	4e−07	16 / 188	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_UP
18	4e−07	18 / 238	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
19	1e−06	146 / 5880	Colon	TssD2_Colon
20	2e−06	25 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
21	3e−06	31 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
22	3e−06	82 / 2798	Colon	TxEnhG1_Colon
23	8e−06	29 / 649	CC	endoplasmic reticulum membrane
24	9e−06	209 / 9653	Colon	Enh_Colon
25	1e−05	214 / 9988	CC	organelle
26	2e−05	7 / 47	GSEA	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
27	4e−05	19 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
28	4e−05	16 / 274	GSEA	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
29	5e−05	4 / 12	BP	oxidative phosphorylation
30	6e−05	116 / 4689	TF	ICGC_Taf1_targets
31	7e−05	126 / 5219	TF	ICGC_Tcf3_targets
32	9e−05	8 / 78	GSEA	SCHUHMACHER_MYC_TARGETS_UP
33	1e−04	119 / 4909	TF	ICGC_Stat5_targets
34	1e−04	102 / 4054	TF	ICGC_Egr1_targets
35	1e−04	16 / 303	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
36	2e−04	137 / 5890	TF	ICGC_Elf1_targets
37	2e−04	141 / 6114	TF	ICGC_Runx3_targets
38	2e−04	10 / 135	GSEA	WELCSH_BRCA1_TARGETS_DN
39	2e−04	127 / 5408	TF	ICGC_Pou2_targets
40	3e−04	24 / 598	BP	membrane organization



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.5	2 / 100	HORVATH_aging_genes meth DOWN
3	0.9	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	5e−05	4 / 12	oxidative phosphorylation
2	3e−04	24 / 598	membrane organization
3	3e−04	5 / 32	mitochondrion degradation
4	6e−04	9 / 129	insulin receptor signaling pathway
5	1e−03	4 / 27	phospholipid biosynthetic process
6	1e−03	4 / 27	platelet aggregation
7	2e−03	3 / 13	ATP biosynthetic process
8	2e−03	3 / 13	natural killer cell differentiation
9	2e−03	3 / 14	sterol metabolic process
10	2e−03	4 / 30	cholesterol biosynthetic process
11	2e−03	6 / 74	nucleobase−containing small molecule metabolic process
12	2e−03	3 / 15	negative regulation of release of cytochrome c from mitochondria
13	3e−03	4 / 33	negative regulation of epidermal growth factor receptor signaling pathway
14	3e−03	47 / 1730	small molecule metabolic process
15	3e−03	5 / 56	cellular iron ion homeostasis
16	5e−03	3 / 19	negative regulation of proteolysis
17	5e−03	3 / 19	phosphatidylinositol 3−kinase signaling
18	6e−03	7 / 120	transforming growth factor beta receptor signaling pathway
19	6e−03	4 / 41	cellular response to hydrogen peroxide
20	8e−03	25 / 815	cell death

Brain

Rank	p−value	#in/all	Geneset
1	4e−12	217 / 9013	Overlap_fetal_midbrain_K9K27me3
2	2e−07	92 / 3081	Mid_Frontal_Lobe_ZNF
3	3e−07	212 / 9528	Overlap_fetal_midbrain_Quies
4	4e−04	28 / 765	Mid_Frontal_Lobe_Het
5	2e−03	193 / 9330	Overlap_fetal_midbrain_ReprPC
6	3e−02	34 / 1333	Fetal_ReprPCWk
7	6e−02	65 / 2972	Mid_Frontal_Lobe_ReprPC
8	1e−01	41 / 1845	Fetal_Quies
9	3e−01	17 / 831	Fetal_HetRpts
10	4e−01	111 / 5940	Overlap_fetal_midbrain_HetRpts
11	6e−01	3 / 163	Fetal_ReprPC
12	6e−01	3 / 166	Mid_Frontal_Lobe_Tx
13	6e−01	44 / 2462	Mid_Frontal_Lobe_HetRpts
14	6e−01	6 / 349	Fetal_ZNF
15	8e−01	10 / 656	Overlap_fetal_midbrain_EnhP
16	8e−01	25 / 1548	Mid_Frontal_Lobe_K9K27me3
17	8e−01	8 / 564	Mid_Frontal_Lobe_EnhP
18	8e−01	158 / 9020	Overlap_fetal_midbrain_ReprPCWk
19	8e−01	17 / 1122	Fetal_K9K27me3
20	8e−01	14 / 953	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	3 / 16	GENTLES_modul16
2	0.034	2 / 16	GENTLES_modul2
3	0.036	1 / 2	GENTLES_modul8
4	0.036	3 / 40	PanCan_HK_geneset_nanostring
5	0.047	7 / 180	SPANG_LPS−index2
6	0.165	2 / 40	ZHANG_MM up
7	0.184	1 / 12	LIU_PROSTATE_CANCER_UP
8	0.213	1 / 13	BEN−PORATH_UP
9	0.213	1 / 13	GENTLES_modul12
10	0.282	11 / 489	Lembcke_Normal vs Adenoma
11	0.366	2 / 70	SHAUGHNESSY_MM high risk
12	0.414	1 / 29	KUIPER_MM good survival
13	0.462	6 / 298	SPANG_BCL6−index2
14	0.556	1 / 44	PanCan_TGF−B_geneset_nanostring
15	0.588	1 / 48	KUIPER_MM poor survival
16	0.638	1 / 55	PanCan_JAK−ST_geneset_nanostring
17	0.647	2 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.651	2 / 121	PanCan_MAPK_geneset_nanostring
19	0.682	0 / 15	RHODES_CANCER_META_SIGNATURE
20	0.716	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	1e−11	203 / 8205	cytoplasm
2	1e−08	51 / 1201	endoplasmic reticulum
3	2e−08	232 / 10605	intracellular
4	2e−07	55 / 1468	mitochondrion
5	8e−06	29 / 649	endoplasmic reticulum membrane
6	1e−05	214 / 9988	organelle
7	3e−04	237 / 11774	cell
8	3e−04	6 / 51	endoplasmic reticulum−Golgi intermediate compartment
9	4e−04	61 / 2193	extracellular exosome
10	2e−03	5 / 47	lipid particle
11	2e−03	14 / 308	focal adhesion
12	2e−03	4 / 30	endoplasmic reticulum−Golgi intermediate compartment membrane
13	2e−03	22 / 616	endosome
14	3e−03	9 / 164	endosome membrane
15	4e−03	4 / 35	cell periphery
16	4e−03	254 / 13191	cellular_component
17	5e−03	33 / 1132	Golgi apparatus
18	6e−03	5 / 63	mitochondrial intermembrane space
19	7e−03	15 / 401	mitochondrial inner membrane
20	7e−03	3 / 22	pre−autophagosomal structure

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	29 / 840	Chr 17
2	5e−03	20 / 576	Chr 9
3	3e−02	13 / 398	Chr 20
4	1e−01	7 / 221	Chr 18
5	1e−01	24 / 1037	Chr 19
6	1e−01	16 / 649	Chr 16
7	1e−01	5 / 151	Chr 21
8	2e−01	9 / 335	Chr 22
9	3e−01	6 / 262	Chr 13
10	4e−01	11 / 552	Chr 10
11	4e−01	11 / 558	Chr 4
12	5e−01	9 / 465	Chr 15
13	6e−01	15 / 838	Chr 3
14	6e−01	14 / 801	Chr 11
15	6e−01	12 / 689	Chr 7
16	9e−01	9 / 696	Chr 5
17	9e−01	13 / 993	Chr 2
18	9e−01	5 / 469	Chr 8
19	9e−01	6 / 551	Chr X
20	9e−01	9 / 775	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−18	236 / 9482	TssA_Colon
2	2e−14	193 / 7203	TssF_Colon
3	7e−08	206 / 9027	Tx_Colon
4	1e−06	146 / 5880	TssD2_Colon
5	3e−06	82 / 2798	TxEnhG1_Colon
6	9e−06	209 / 9653	Enh_Colon
7	2e−03	180 / 8580	TxWk_Colon
8	5e−03	24 / 739	TxEnhG2_Colon
9	8e−03	21 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	9e−03	65 / 2698	EnhA_Colon
11	3e−02	21 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
12	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
13	6e−02	107 / 5155	EnhWk1_Colon
14	9e−02	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
15	1e−01	1 / 8	Marisa_CRC−C1
16	1e−01	1 / 8	Marisa_CRC−C2
17	1e−01	3 / 71	Marisa_CRC−cluster−g
18	2e−01	14 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
19	2e−01	5 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	2e−01	160 / 8415	Quies3_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 20	BCHETNIA_EBM−DM up
2	0.6	5 / 294	GUDJ_psoriasis down
3	0.7	7 / 435	GUDJ_psoriasis up
4	1.0	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.007	14 / 365	Down_b
2	0.008	13 / 332	Up
3	0.021	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	0.028	4 / 63	Stuehler_Proteins_up_in_STS
5	0.120	4 / 103	GIEZELT_GBM_WT_up_VS_mut
6	0.152	2 / 38	OL vs. OPC
7	0.170	4 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	0.184	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
9	0.184	1 / 11	Christensen_hypermethylated_in_ependymoma
10	0.195	4 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	0.213	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
12	0.242	1 / 15	VERHAAK_CL subtype
13	0.246	3 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	0.255	1 / 16	VERHAAK_NL subtype
15	0.279	2 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
16	0.282	1 / 18	Barbus_GBM_STS_vs._LTS
17	0.313	2 / 62	cultured astroglia vs. in vivo astrocytes
18	0.331	4 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
19	0.333	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
20	0.353	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−12	50 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	1e−10	44 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	9e−09	28 / 440	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
4	9e−08	52 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	1e−07	32 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
6	2e−07	26 / 447	ENK_UV_RESPONSE_KERATINOCYTE_UP
7	4e−07	16 / 188	DAZARD_RESPONSE_TO_UV_NHEK_UP
8	4e−07	18 / 238	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
9	2e−06	25 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
10	3e−06	31 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
11	2e−05	7 / 47	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
12	4e−05	19 / 363	RUTELLA_RESPONSE_TO_HGF_UP
13	4e−05	16 / 274	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
14	9e−05	8 / 78	SCHUHMACHER_MYC_TARGETS_UP
15	1e−04	16 / 303	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
16	2e−04	10 / 135	WELCSH_BRCA1_TARGETS_DN
17	4e−04	7 / 74	SMITH_TERT_TARGETS_DN
18	5e−04	21 / 510	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
19	5e−04	8 / 100	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
20	5e−04	8 / 100	SESTO_RESPONSE_TO_UV_C0

HM

Rank	p−value	#in/all	Geneset
1	3e−04	10 / 146	HALLMARK_UV_RESPONSE_UP
2	4e−03	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	7e−03	6 / 94	HALLMARK_ANDROGEN_RESPONSE
4	2e−02	4 / 53	HALLMARK_TGF_BETA_SIGNALING
5	3e−02	5 / 91	HALLMARK_PROTEIN_SECRETION
6	3e−02	5 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	5e−02	6 / 146	HALLMARK_DNA_REPAIR
8	5e−02	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	7e−02	7 / 196	HALLMARK_MTORC1_SIGNALING
10	8e−02	5 / 126	HALLMARK_ALLOGRAFT_REJECTION
11	9e−02	4 / 93	HALLMARK_PEROXISOME
12	1e−01	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	1e−01	6 / 174	HALLMARK_HEME_METABOLISM
14	1e−01	6 / 188	HALLMARK_ADIPOGENESIS
15	1e−01	6 / 188	HALLMARK_MYC_TARGETS_V1
16	2e−01	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	2e−01	5 / 167	HALLMARK_APICAL_JUNCTION
18	2e−01	5 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
19	3e−01	4 / 140	HALLMARK_APOPTOSIS
20	3e−01	4 / 162	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.24	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	119 / 5184	HOPP_Txn_transition
2	0.007	159 / 7592	HOPP_Active_promoter
3	0.018	144 / 6929	HOPP_Txn_elongation
4	0.019	14 / 410	SPANG_CD40 6hrs DN
5	0.021	5 / 86	ROSOLOWSKI_red total
6	0.032	4 / 66	TARTE_Plasma cell signature
7	0.034	2 / 16	DAVE_BL Inter
8	0.039	29 / 1128	SPANG_BCR DN
9	0.044	10 / 294	TARTE_Plasmablast signature
10	0.059	4 / 80	Aukema_BCL2 DN_BCL6 UP
11	0.127	2 / 34	Subero_B−ALL_hyper_meth
12	0.137	1 / 8	YAMANE_AICDA_targets_nonrecruited
13	0.159	2 / 39	ROSOLOWSKI_blue DOWN
14	0.168	1 / 10	DAVE_BL UP
15	0.198	1 / 12	BENTINK_mBL DOWN
16	0.213	1 / 13	WRIGHT_GCB UP
17	0.213	1 / 13	YAMANE_AICDA_targets_recruited
18	0.227	1 / 14	Subero_MCL_hyper_meth
19	0.255	1 / 16	ROSOLOWSKI_red UP
20	0.282	125 / 6564	HOPP_Strong_enhancer

MF

Rank	p−value	#in/all	Geneset
1	3e−04	6 / 51	ubiquitin binding
2	9e−04	3 / 11	proton−transporting ATP synthase activity, rotational mechanism
3	3e−03	3 / 17	glycosaminoglycan binding
4	4e−03	3 / 18	2 iron, 2 sulfur cluster binding
5	5e−03	6 / 86	ubiquitin−like protein binding
6	7e−03	4 / 42	protein kinase C binding
7	7e−03	3 / 22	ribonucleoprotein complex binding
8	8e−03	3 / 23	proton−transporting ATPase activity, rotational mechanism
9	1e−02	6 / 104	iron ion binding
10	1e−02	18 / 550	protein homodimerization activity
11	1e−02	2 / 10	proteasome binding
12	1e−02	2 / 10	receptor signaling protein tyrosine kinase activity
13	2e−02	3 / 29	beta−amyloid binding
14	2e−02	21 / 691	kinase activity
15	2e−02	2 / 12	misfolded protein binding
16	2e−02	3 / 33	peptide binding
17	2e−02	2 / 13	5'−nucleotidase activity
18	2e−02	7 / 156	protein C−terminus binding
19	3e−02	2 / 14	ferrous iron binding
20	3e−02	14 / 430	lipid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	6 / 68	hsa−miR−342−3p
2	0.002	7 / 96	hsa−miR−133a
3	0.002	7 / 97	hsa−miR−133b
4	0.002	4 / 30	hsa−miR−371−3p
5	0.004	12 / 269	hsa−miR−449a
6	0.004	8 / 141	hsa−miR−138
7	0.006	9 / 179	hsa−miR−381
8	0.006	12 / 282	hsa−miR−570
9	0.007	2 / 7	hsa−miR−611
10	0.007	12 / 288	hsa−miR−34a
11	0.008	5 / 68	hsa−miR−606
12	0.008	5 / 69	hsa−miR−1266
13	0.009	6 / 97	hsa−miR−624
14	0.009	6 / 97	hsa−miR−1303
15	0.009	8 / 161	hsa−miR−511
16	0.011	5 / 73	hsa−miR−657
17	0.011	2 / 9	hsa−miR−202*
18	0.013	6 / 105	hsa−miR−1271
19	0.013	4 / 50	hsa−miR−487a
20	0.014	2 / 10	hsa−miR−487b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	BENTINK_ras.6
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 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−05	116 / 4689	ICGC_Taf1_targets
2	7e−05	126 / 5219	ICGC_Tcf3_targets
3	1e−04	119 / 4909	ICGC_Stat5_targets
4	1e−04	102 / 4054	ICGC_Egr1_targets
5	2e−04	137 / 5890	ICGC_Elf1_targets
6	2e−04	141 / 6114	ICGC_Runx3_targets
7	2e−04	127 / 5408	ICGC_Pou2_targets
8	6e−04	115 / 4879	ICGC_Pmlsc71910_targets
9	8e−04	49 / 1701	HEBENSTREIT_high expression TF
10	1e−03	64 / 2416	ICGC_Bcl3_targets
11	1e−03	125 / 5495	ICGC_Yy1_targets
12	1e−03	90 / 3700	ICGC_Nfatc1_targets
13	1e−03	108 / 4617	ICGC_Tcf12_targets
14	1e−03	119 / 5200	ICGC_Mta3_targets
15	2e−03	94 / 3924	ICGC_Zeb1_targets
16	2e−03	96 / 4032	ICGC_Creb1_targets
17	2e−03	101 / 4314	ICGC_Ebfsc137065_targets
18	4e−03	108 / 4774	ICGC_Foxm1_targets
19	5e−03	119 / 5374	ICGC_Pax5_targets
20	6e−03	39 / 1418	ICGC_Ets1_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	7 / 225	PALMER_Granulocytes signature up
2	0.2	1 / 12	WIRTH_Cerebellum
3	0.2	1 / 13	WIRTH_B−cells
4	0.2	1 / 14	WIRTH_Telencephalon
5	0.6	2 / 114	PALMER_T−Cell signature up
6	0.7	3 / 194	PALMER_B−Cell signature up
7	0.9	4 / 350	WIRTH_Immune system
8	1.0	3 / 350	WIRTH_Nervous System
9	1.0	0 / 32	WIRTH_Pancreas
10	1.0	0 / 11	WIRTH_Sec. lymphoid organs
11	1.0	0 / 11	WIRTH_Prim. lymphoid organs
12	1.0	0 / 8	WIRTH_Tonsil
13	1.0	0 / 12	WIRTH_Thymus
14	1.0	0 / 12	WIRTH_Lymphocytes
15	1.0	0 / 5	WIRTH_Bone marrow
16	1.0	0 / 11	WIRTH_Globus pallidus
17	1.0	0 / 11	WIRTH_Cortex cerebri
18	1.0	0 / 10	WIRTH_Hippocampus
19	1.0	0 / 10	WIRTH_Thalamus
20	1.0	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	25 / 1115	LU_BPDE 1h DN
2	0.9	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	

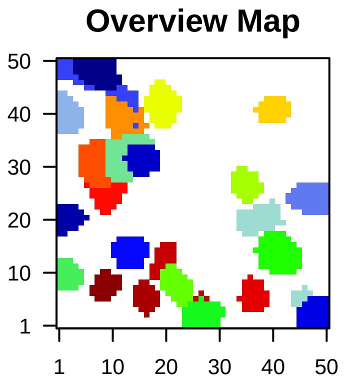
Correlation Clusters

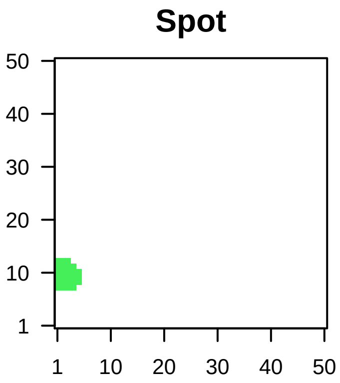
Spot Summary: L

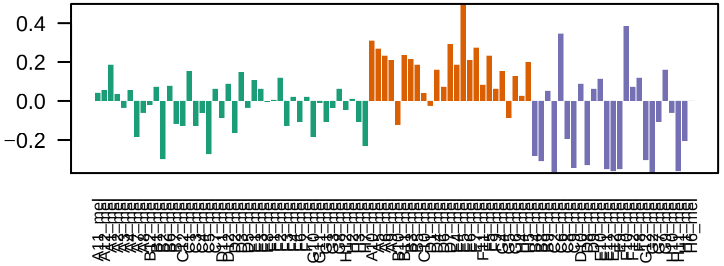
metagenes = 26
genes = 309

<r> metagenes = 0.93
<r> genes = 0.12
beta: r2= 2.15 / log p= −Inf

samples with spot = 19 (20.7 %)
MSC1 : 1 (2.4 %)
MSC2 : 15 (60 %)
MSC3 : 3 (12 %)





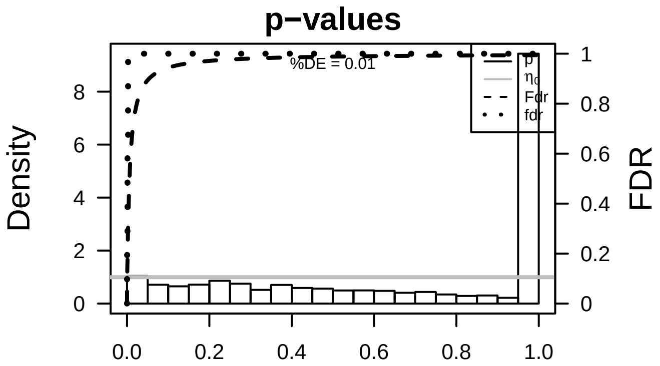


Spot Genelist

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	EGLN3	1.89	−0.41	0.36	EGLN3	egl−9 family hypoxia−inducible factor 3 [Source:HGNC Symbo
3	KCNQ5	1.87	−0.46	0.35	KCNQ5	potassium channel, voltage gated KQT−like subfamily Q, mer
4	CFAP61	1.86	−0.52	0.45	CFAP61	cilia and flagella associated protein 61 [Source:HGNC Symbo
5	LYRM9	1.85	−0.31	0.28	LYRM9	LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
6	CC2D1B	1.84	−0.41	0.22	CC2D1B	coiled−coil and C2 domain containing 1B [Source:HGNC Sym
7	TAPBPL	1.83	−0.08	0.34	TAPBPL	TAP binding protein−like [Source:HGNC Symbol;Acc:HGNC:3
8	PLA2G4B	1.82	−0.16	0.33	PLA2G4B	phospholipase A2, group IVB (cytosolic) [Source:HGNC Symb
9	KRTAP19−1	1.78	−0.78	0.4	KRTAP19−1	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:H
10	LCMT2	1.75	−0.37	0.3	LCMT2	leucine carboxyl methyltransferase 2 [Source:HGNC Symbol;
11	TMEM150A	1.75	−0.24	0.35	TMEM150A	transmembrane protein 150A [Source:HGNC Symbol;Acc:HG
12	RDH14	1.75	−0.43	0.31	RDH14	retinol dehydrogenase 14 (all−trans/9−cis/11−cis) [Source:HG
13	GAS8	1.75	−0.56	0.29	GAS8	growth arrest−specific 8 [Source:HGNC Symbol;Acc:HGNC:4
14	BBS5	1.74	−0.64	0.36	BBS5	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
15	STAT6	1.71	−0.38	0.29	STAT6	signal transducer and activator of transcription 6, interleukin−
16	C1orf54	1.7	−0.3	0.41	C1orf54	chromosome 1 open reading frame 54 [Source:HGNC Symbo
17	SUOX	1.69	−0.67	0.27	SUOX	sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
18	TXNDC16	1.69	−0.35	0.28	TXNDC16	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc
19	PLA1A	1.68	−0.26	0.34	PLA1A	phospholipase A1 member A [Source:HGNC Symbol;Acc:HG
20	CTC−534A2.2	1.67	−0.37	0.26		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−11	245 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	1e−08	233 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	2e−07	229 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
4	2e−07	238 / 9528	Brain	Overlap_fetal_midbrain_Quies
5	3e−07	166 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	1e−06	6 / 18	BP	melanocyte differentiation
7	9e−06	9 / 67	BP	pigmentation
8	9e−06	5 / 15	BP	developmental pigmentation
9	2e−05	7 / 42	GSEA	PID_RHOA_REG_PATHWAY
10	3e−05	171 / 6564	Lympl	HOPP_Strong_enhancer
11	3e−05	4 / 10	MF	semaphorin receptor binding
12	4e−05	208 / 8415	Colon	Quies3_Colon
13	4e−05	10 / 100	miRN	hsa−miR−574−5p
14	6e−05	5 / 21	BP	melanosome transport
15	6e−05	31 / 705	BP	locomotion
16	8e−05	92 / 3088	CC	plasma membrane
17	1e−04	4 / 13	BP	melanin biosynthetic process
18	1e−04	4 / 13	GSEA	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
19	1e−04	9 / 94	CC	melanosome
20	1e−04	19 / 353	GSEA	ONDER_CDH1_TARGETS_2_DN
21	2e−04	12 / 167	GSEA	KIM_MYC_AMPLIFICATION_TARGETS_UP
22	2e−04	107 / 3812	Colon	TssD1_Colon
23	2e−04	4 / 15	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
24	2e−04	25 / 552	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
25	2e−04	97 / 3383	Colon	EnhWk2_Colon
26	2e−04	26 / 590	BP	cell morphogenesis
27	3e−04	17 / 317	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38
28	3e−04	4 / 17	MF	Ras GTPase binding
29	4e−04	7 / 65	BP	regulation of Rho protein signal transduction
30	4e−04	7 / 66	MF	Rho guanyl−nucleotide exchange factor activity
31	4e−04	215 / 9027	Colon	Tx_Colon
32	5e−04	18 / 356	GSEA	DELYS_THYROID_CANCER_UP
33	5e−04	206 / 8580	Colon	TxWk_Colon
34	5e−04	13 / 212	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
35	5e−04	4 / 19	MF	1−phosphatidylinositol binding
36	5e−04	4 / 19	MF	cAMP binding
37	6e−04	18 / 363	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
38	6e−04	76 / 2576	CC	membrane
39	6e−04	223 / 9482	Colon	TssA_Colon
40	6e−04	5 / 34	GSEA	PID_RAC1_REG_PATHWAY



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 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	1e−06	6 / 18	melanocyte differentiation
2	9e−06	9 / 67	pigmentation
3	9e−06	5 / 15	developmental pigmentation
4	6e−05	5 / 21	melanosome transport
5	6e−05	31 / 705	locomotion
6	1e−04	4 / 13	melanin biosynthetic process
7	2e−04	26 / 590	cell morphogenesis
8	4e−04	7 / 65	regulation of Rho protein signal transduction
9	9e−04	3 / 10	negative regulation of smooth muscle cell migration
10	2e−03	3 / 13	positive regulation of smooth muscle cell migration
11	2e−03	15 / 312	axon guidance
12	4e−03	4 / 31	phosphatidylinositol phosphorylation
13	4e−03	7 / 96	leukocyte migration
14	4e−03	8 / 124	regulation of small GTPase mediated signal transduction
15	5e−03	17 / 409	cell motility
16	5e−03	8 / 129	insulin receptor signaling pathway
17	6e−03	4 / 35	positive regulation of smooth muscle cell proliferation
18	6e−03	3 / 18	phosphatidylinositol metabolic process
19	6e−03	7 / 104	apoptotic signaling pathway
20	6e−03	28 / 815	lipid metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	7e−11	245 / 9330	Overlap_fetal_midbrain_ReprPC
2	1e−08	233 / 9013	Overlap_fetal_midbrain_K9K27me3
3	2e−07	229 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	2e−07	238 / 9528	Overlap_fetal_midbrain_Quies
5	3e−07	166 / 5940	Overlap_fetal_midbrain_HetRpts
6	2e−02	31 / 1013	Fetal_TssP
7	2e−02	22 / 668	Mid_Frontal_Lobe_Enh
8	3e−02	78 / 3081	Mid_Frontal_Lobe_ZNF
9	4e−02	50 / 1907	Fetal_TxTrans
10	8e−02	29 / 1065	Overlap_fetal_midbrain_Enh
11	9e−02	54 / 2185	Fetal_TssA
12	1e−01	21 / 786	Fetal_EnhG
13	1e−01	27 / 1050	Fetal_EnhP
14	2e−01	3 / 69	Overlap_fetal_midbrain_Tx
15	2e−01	11 / 383	Fetal_Tx
16	2e−01	15 / 574	Overlap_fetal_midbrain_TssP
17	2e−01	22 / 884	Overlap_fetal_midbrain_EnhG
18	2e−01	29 / 1207	Overlap_fetal_midbrain_TssF
19	2e−01	45 / 1949	Fetal_TssF
20	2e−01	19 / 769	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	5 / 111	PanCan_RAS_geneset_nanostring
2	0.08	7 / 180	SPANG_LPS−index2
3	0.09	10 / 298	SPANG_BCL6−index2
4	0.11	3 / 55	PanCan_JAK−ST_geneset_nanostring
5	0.13	12 / 401	Lembcke_Colonic_Inflammation
6	0.19	1 / 10	GENTLES_modul13
7	0.24	0 / 12	LIU_PROSTATE_CANCER_UP
8	0.24	1 / 13	GENTLES_modul12
9	0.25	1 / 14	LIU_COMMON_CANCER_GENES
10	0.27	1 / 15	GENTLES_modul4
11	0.28	0 / 14	LIU_PROSTATE_CANCER_DN
12	0.31	1 / 18	PanCan_Notch_geneset_nanostring
13	0.34	1 / 20	PanCan_ChromMod_geneset_nanostring
14	0.51	2 / 82	PanCan_TXmisReg_geneset_nanostring
15	0.57	1 / 40	ZHANG_MM up
16	0.57	1 / 40	PanCan_HK_geneset_nanostring
17	0.60	1 / 44	PanCan_TGF−B_geneset_nanostring
18	0.63	1 / 47	PanCan_DNARepair_geneset_nanostring
19	0.63	3 / 156	PanCan_PI3K_geneset_nanostring
20	0.64	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	8e−05	92 / 3088	plasma membrane
2	1e−04	9 / 94	melanosome
3	6e−04	76 / 2576	membrane
4	4e−03	10 / 175	early endosome
5	5e−03	23 / 616	endosome
6	6e−03	69 / 2507	cytosol
7	8e−03	191 / 8205	cytoplasm
8	9e−03	3 / 21	immunological synapse
9	1e−02	9 / 178	apical plasma membrane
10	1e−02	17 / 456	vacuole
11	2e−02	2 / 10	perinuclear endoplasmic reticulum
12	2e−02	4 / 52	secretory granule
13	2e−02	15 / 412	lysosome
14	3e−02	41 / 1465	cytoskeleton
15	3e−02	257 / 11774	cell
16	4e−02	9 / 223	lysosomal membrane
17	5e−02	74 / 2984	integral component of membrane
18	6e−02	3 / 44	motile cilium
19	6e−02	2 / 20	retromer complex
20	7e−02	9 / 246	mitochondrial matrix

Chr

Rank	p−value	#in/all	Geneset
1	0.004	19 / 465	Chr 15
2	0.021	11 / 262	Chr 13
3	0.038	29 / 993	Chr 2
4	0.090	17 / 576	Chr 9
5	0.175	13 / 469	Chr 8
6	0.254	19 / 775	Chr 12
7	0.258	9 / 335	Chr 22
8	0.368	16 / 696	Chr 5
9	0.380	33 / 1500	Chr 1
10	0.381	4 / 151	Chr 21
11	0.469	18 / 838	Chr 3
12	0.473	18 / 840	Chr 17
13	0.483	5 / 221	Chr 18
14	0.487	12 / 558	Chr 4
15	0.487	10 / 462	Chr 14
16	0.583	8 / 398	Chr 20
17	0.888	8 / 551	Chr X
18	0.909	10 / 689	Chr 7
19	0.925	9 / 649	Chr 16
20	0.942	7 / 552	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−05	208 / 8415	Quies3_Colon
2	2e−04	107 / 3812	TssD1_Colon
3	2e−04	97 / 3383	EnhWk2_Colon
4	4e−04	215 / 9027	Tx_Colon
5	5e−04	206 / 8580	TxWk_Colon
6	6e−04	223 / 9482	TssA_Colon
7	7e−04	134 / 5155	EnhWk1_Colon
8	7e−04	106 / 3897	Quies1_Colon
9	2e−03	147 / 5880	TssD2_Colon
10	2e−03	223 / 9653	Enh_Colon
11	4e−03	234 / 10290	TssWk_Colon
12	2e−02	29 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	2e−02	6 / 102	Marisa_CRC−cluster−d
14	3e−02	14 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
15	4e−02	68 / 2698	EnhA_Colon
16	5e−02	10 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
17	5e−02	6 / 131	Marisa_CRC−cluster−a
18	7e−02	10 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
19	7e−02	14 / 436	K9acLow_Colon
20	1e−01	1 / 5	Budinska_C_CIMP−H−like_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.09	10 / 294	GUDJ_psoriasis down
2	0.41	10 / 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	0.02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
2	0.06	11 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.10	1 / 5	oligodendrocytes_glio
4	0.11	6 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	0.12	2 / 29	shaw_responders_down_in_oligo_glioma
6	0.14	3 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	0.19	2 / 38	OL vs. OPC
8	0.19	3 / 72	laffaire_hypermeth_LGG_vs_control
9	0.19	3 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	0.20	3 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
11	0.20	10 / 356	Down_a
12	0.21	1 / 11	Martinez_Glio_hypermeth
13	0.25	2 / 47	mature astrocytes
14	0.27	2 / 49	OL vs. MOG−OL
15	0.27	2 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
16	0.27	1 / 15	VERHAAK_CL subtype
17	0.32	3 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
18	0.34	3 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
19	0.38	1 / 23	Donson−Misc immune function−associated with LTS in HGA
20	0.39	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	7 / 42	PID_RHOA_REG_PATHWAY
2	1e−04	4 / 13	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
3	1e−04	19 / 353	ONDER_CDH1_TARGETS_2_DN
4	2e−04	12 / 167	KIM_MYC_AMPLIFICATION_TARGETS_UP
5	2e−04	4 / 15	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
6	2e−04	25 / 552	HAMAI_APOPTOSIS_VIA_TRAIL_UP
7	3e−04	17 / 317	PHONG_TNF_RESPONSE_NOT_VIA_P38
8	5e−04	18 / 356	DELYS_THYROID_CANCER_UP
9	5e−04	13 / 212	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
10	6e−04	18 / 363	RUTELLA_RESPONSE_TO_HGF_UP
11	6e−04	5 / 34	PID_RAC1_REG_PATHWAY
12	8e−04	6 / 53	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE
13	8e−04	13 / 223	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
14	9e−04	13 / 227	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
15	9e−04	9 / 121	KATSANOU_ELAVL1_TARGETS_DN
16	9e−04	6 / 55	BILBAN_B_CLL_LPL_UP
17	9e−04	3 / 10	REACTOME_SIGNALING_BY_NOTCH4
18	9e−04	3 / 10	REACTOME_SIGNALING_BY_NOTCH2
19	9e−04	3 / 10	REACTOME_SIGNALING_BY_NOTCH3
20	1e−03	4 / 22	WILLIAMS_ESR1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.001	11 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	0.022	3 / 29	HALLMARK_NOTCH_SIGNALING
3	0.028	8 / 174	HALLMARK_HEME_METABOLISM
4	0.042	8 / 188	HALLMARK_ADIPOGENESIS
5	0.045	5 / 94	HALLMARK_ANDROGEN_RESPONSE
6	0.050	8 / 195	HALLMARK_MITOTIC_SPINDLE
7	0.051	8 / 196	HALLMARK_MTORC1_SIGNALING
8	0.056	7 / 165	HALLMARK_MYOGENESIS
9	0.063	7 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.082	7 / 181	HALLMARK_P53_PATHWAY
11	0.161	6 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.178	2 / 37	HALLMARK_APICAL_SURFACE
13	0.193	5 / 148	HALLMARK_KRAS_SIGNALING_UP
14	0.197	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	0.264	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
16	0.315	4 / 137	HALLMARK_UV_RESPONSE_DN
17	0.330	2 / 57	HALLMARK_MYC_TARGETS_V2
18	0.390	5 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
19	0.395	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
20	0.419	1 / 26	HALLMARK_ANGIOGENESIS

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−05	171 / 6564	HOPP_Strong_enhancer
2	1e−03	39 / 1128	SPANG_BCR DN
3	1e−03	133 / 5184	HOPP_Txn_transition
4	2e−03	169 / 6929	HOPP_Txn_elongation
5	3e−03	142 / 5693	HOPP_Weak_enhancer
6	3e−03	181 / 7592	HOPP_Active_promoter
7	4e−03	63 / 2211	HOPP_Repetitive
8	6e−03	6 / 80	Aukema_BCL2 DN_BCL6 UP
9	1e−02	16 / 410	SPANG_CD40 6hrs DN
10	2e−02	132 / 5538	HOPP_Weak_txn
11	3e−02	166 / 7209	HOPP_Weak_promoter
12	3e−02	9 / 212	LENZ_Stromal signature 1
13	3e−02	10 / 247	ZHANG_DLBCL mutated
14	5e−02	2 / 17	DAVE_NFkB BL DN
15	5e−02	56 / 2188	HOPP_Poised_promoter
16	8e−02	1 / 4	MASCQUE_mBL DOWN
17	1e−01	1 / 5	WRIGHT_custom ABC−DLBCL UP
18	1e−01	61 / 2563	HOPP_Heterochrom
19	2e−01	1 / 10	DAVE_BL_DN
20	2e−01	1 / 12	BENTINK_mBL DOWN

MF

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 10	semaphorin receptor binding
2	3e−04	4 / 17	Ras GTPase binding
3	4e−04	7 / 66	Rho guanyl−nucleotide exchange factor activity
4	5e−04	4 / 19	1−phosphatidylinositol binding
5	5e−04	4 / 19	cAMP binding
6	8e−03	6 / 84	guanyl−nucleotide exchange factor activity
7	1e−02	4 / 41	ATPase binding
8	1e−02	7 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activity
9	2e−02	2 / 10	cytoskeletal adaptor activity
10	2e−02	2 / 10	Rac guanyl−nucleotide exchange factor activity
11	2e−02	16 / 430	lipid binding
12	2e−02	2 / 12	lysophospholipase activity
13	2e−02	2 / 12	Ras guanyl−nucleotide exchange factor activity
14	3e−02	5 / 84	RNA polymerase II core promoter proximal region sequence−specific DNA bir
15	3e−02	2 / 14	phosphatidylserine binding
16	3e−02	2 / 14	polypeptide N−acetylgalactosaminyltransferase activity
17	4e−02	2 / 15	microfilament motor activity
18	4e−02	3 / 36	phosphatidylinositol−4,5−bisphosphate binding
19	4e−02	201 / 8984	protein binding
20	4e−02	3 / 37	coenzyme binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−05	10 / 100	hsa−miR−574−5p
2	3e−03	13 / 263	hsa−miR−92b
3	4e−03	14 / 296	hsa−miR−25
4	4e−03	13 / 268	hsa−miR−363
5	5e−03	13 / 274	hsa−miR−1244
6	6e−03	8 / 130	hsa−miR−383
7	8e−03	4 / 38	hsa−miR−490−5p
8	1e−02	3 / 22	hsa−miR−516a−5p
9	1e−02	7 / 120	hsa−miR−105
10	1e−02	10 / 214	hsa−miR−182
11	1e−02	7 / 124	hsa−miR−223
12	2e−02	9 / 187	hsa−miR−382
13	2e−02	17 / 467	hsa−miR−301a
14	2e−02	15 / 395	hsa−miR−301b
15	2e−02	4 / 50	hsa−miR−1201
16	2e−02	10 / 233	hsa−miR−26a
17	2e−02	11 / 269	hsa−miR−30d
18	3e−02	11 / 270	hsa−miR−30b
19	3e−02	8 / 170	hsa−miR−452
20	3e−02	4 / 54	hsa−miR−940

PathwACT

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	BENTINK_ras.4
2	0.2	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	0.005	77 / 2836	ICGC_Batf/cr1_targets
2	0.018	71 / 2714	ICGC_Irf4_targets
3	0.050	49 / 1878	ICGC_Cebpbsc150_targets
4	0.051	52 / 2013	ICGC_Bcl11_targets
5	0.061	102 / 4314	ICGC_Ebfsc137065_targets
6	0.067	48 / 1872	ICGC_Mef2_targets
7	0.073	88 / 3700	ICGC_Nfatc1_targets
8	0.075	109 / 4682	ICGC_Pol24_targets
9	0.100	102 / 4414	ICGC_Bclaf101388_targets
10	0.102	34 / 1314	ICGC_Usf1_targets
11	0.109	92 / 3966	ICGC_Pu1_targets
12	0.124	122 / 5408	ICGC_Pou2_targets
13	0.127	42 / 1701	HEBENSTREIT_high expression TF
14	0.146	92 / 4032	ICGC_Creb1_targets
15	0.161	99 / 4385	ICGC_Atf2_targets
16	0.174	122 / 5495	ICGC_Yy1_targets
17	0.196	17 / 653	ICGC_SrfPcr2_targets
18	0.201	106 / 4774	ICGC_Foxm1_targets
19	0.204	34 / 1418	ICGC_Ets1_targets
20	0.222	118 / 5374	ICGC_Pax5_targets

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	2 / 40	VAQUERIZAS_Thyroid
4	0.3	1 / 17	VAQUERIZAS_Pituitary
5	0.3	1 / 19	VAQUERIZAS_Tonsil
6	0.3	2 / 58	VAQUERIZAS_Lung
7	0.3	4 / 143	VAQUERIZAS_General
8	0.4	1 / 23	VAQUERIZAS_Spinal cord
9	0.4	1 / 23	VAQUERIZAS_Trachea
10	0.5	1 / 29	VAQUERIZAS_Smooth muscle
11	0.5	1 / 29	VAQUERIZAS_Fetal lung
12	0.5	1 / 33	VAQUERIZAS_Prostate
13	0.5	1 / 38	VAQUERIZAS_Whole brain
14	0.5	1 / 38	VAQUERIZAS_Testis
15	0.6	1 / 41	VAQUERIZAS_Placenta
16	0.6	1 / 45	VAQUERIZAS_Uterus
17	0.7	1 / 59	VAQUERIZAS_Whole blood
18	1.0	0 / 36	VAQUERIZAS_Fetal brain
19	1.0	0 / 26	VAQUERIZAS_Liver
20	1.0	0 / 37	VAQUERIZAS_Thymus

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	7 / 194	PALMER_B−Cell signature up
2	0.2	4 / 107	WIRTH_Testis
3	0.2	1 / 11	WIRTH_Prim. lymphoid organs
4	0.2	1 / 12	WIRTH_Thymus
5	0.2	1 / 12	WIRTH_Lymphocytes
6	0.2	1 / 12	WIRTH_Cerebellum
7	0.2	1 / 13	WIRTH_Thyroid gland
8	0.4	3 / 114	PALMER_T−Cell signature up
9	0.5	5 / 225	PALMER_Granulocytes signature up
10	0.6	1 / 41	WIRTH_Homeostasis
11	0.6	2 / 95	WIRTH_Muscle
12	0.6	7 / 350	WIRTH_Immune system
13	0.8	1 / 74	WIRTH_Mucosa
14	0.9	5 / 350	WIRTH_Nervous System
15	1.0	0 / 32	WIRTH_Pancreas
16	1.0	0 / 11	WIRTH_Sec. lymphoid organs
17	1.0	0 / 13	WIRTH_B−cells
18	1.0	0 / 8	WIRTH_Tonsil
19	1.0	0 / 5	WIRTH_Bone marrow
20	1.0	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	73 / 3682	LU_BPDE 0.005 DN
2	0.9	18 / 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	

Correlation Clusters

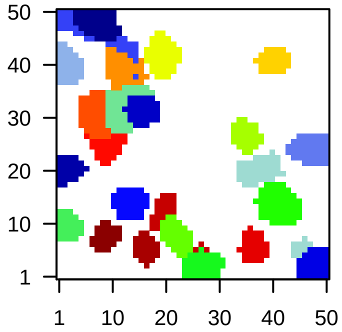
Spot Summary: M

metagenes = 26
genes = 190

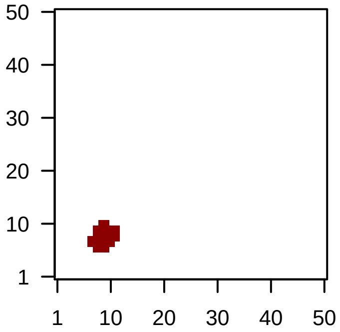
<r> metagenes = 0.93
<r> genes = 0.2
beta: r2= 0.65 / log p= −Inf

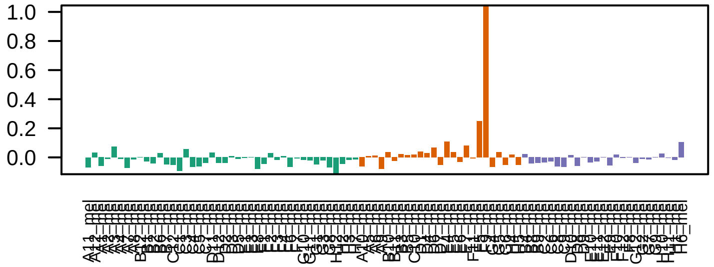
samples with spot = 2 (2.2 %)
MSC2 : 2 (8 %)

Overview Map



Spot





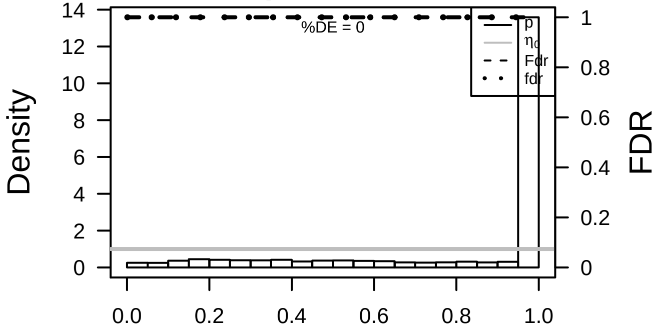
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	METAP1D	2.04	−0.33	0.31	METAP1D	methionyl aminopeptidase type 1D (mitochondrial) [Source:H
2	SLC24A1	1.94	−0.09	0.54	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchange
3	GPR183	1.92	−0.15	0.49	GPR183	G protein−coupled receptor 183 [Source:HGNC Symbol;Acc:
4	RHPN2	1.85	−0.17	0.36	RHPN2	rhophilin, Rho GTPase binding protein 2 [Source:HGNC Sym
5	KCNIP4	1.84	−0.07	0.63	KCNIP4	Kv channel interacting protein 4 [Source:HGNC Symbol;Acc:
6	ACP6	1.8	−0.24	0.32	ACP6	acid phosphatase 6, lysophosphatidic [Source:HGNC Symbo
7	GPR171	1.8	−0.08	0.72	GPR171	G protein−coupled receptor 171 [Source:HGNC Symbol;Acc:
8	JAM3	1.8	−0.24	0.47	JAM3	junctional adhesion molecule 3 [Source:HGNC Symbol;Acc:H
9	TMEM27	1.79	−0.08	0.5	TMEM27	transmembrane protein 27 [Source:HGNC Symbol;Acc:HGN
10	CHAMP1	1.78	−0.27	0.33	CHAMP1	chromosome alignment maintaining phosphoprotein 1 [Sourc
11	ZNF530	1.78	−0.18	0.28	ZNF530	zinc finger protein 530 [Source:HGNC Symbol;Acc:HGNC:29
12	UGT3A2	1.78	−0.08	0.49	UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2 [Source:HG
13	CFAP46	1.73	−0.09	0.51	CFAP46	cilia and flagella associated protein 46 [Source:HGNC Symb
14	ADAM22	1.7	−0.14	0.59	ADAM22	ADAM metallopeptidase domain 22 [Source:HGNC Symbol;A
15	TRPC1	1.7	−0.16	0.36	TRPC1	transient receptor potential cation channel, subfamily C, mem
16	SLC29A3	1.68	−0.08	0.39	SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter),
17	RD3L	1.67	−0.09	0.49	RD3L	retinal degeneration 3−like [Source:HGNC Symbol;Acc:HGN
18	PDCD2L	1.66	−0.43	0.32	PDCD2L	programmed cell death 2−like [Source:HGNC Symbol;Acc:H
19	ZNF546	1.65	−0.15	0.42	ZNF546	zinc finger protein 546 [Source:HGNC Symbol;Acc:HGNC:28
20	AGPAT9	1.65	−0.35	0.3	AGPAT9	1−acylglycerol−3−phosphate O−acyltransferase 9 [Source:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−04	5 / 53	miRN	hsa−miR−337−3p
2	2e−03	25 / 1065	Brain	Overlap_fetal_midbrain_Enh
3	3e−03	3 / 22	MF	calmodulin−dependent protein kinase activity
4	3e−03	3 / 22	MF	delayed rectifier potassium channel activity
5	3e−03	4 / 47	GSEA	LEE_EARLY_T_LYMPHOCYTE_DN
6	3e−03	24 / 1038	Colon	HetRpts_Colon
7	3e−03	3 / 24	MF	N−acetyltransferase activity
8	5e−03	29 / 1386	Colon	Het_Colon
9	6e−03	3 / 30	GSEA	PIONTEK_PKD1_TARGETS_UP
10	7e−03	36 / 1872	TF	ICGC_Mef2_targets
11	7e−03	5 / 94	GSEA	OHGUCHI_LIVER_HNF4A_TARGETS_DN
12	8e−03	11 / 373	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
13	8e−03	2 / 11	BP	DNA methylation involved in gamete generation
14	8e−03	6 / 138	GSEA	LEE_LIVER_CANCER_SURVIVAL_UP
15	8e−03	4 / 63	miRN	hsa−miR−1285
16	9e−03	5 / 101	miRN	hsa−miR−325
17	1e−02	2 / 12	BP	regulation of neurotransmitter secretion
18	1e−02	2 / 12	Glio	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
19	1e−02	4 / 67	GSEA	MCCLUNG_COCAINE_REWARD_5D
20	1e−02	14 / 550	MF	protein homodimerization activity
21	1e−02	6 / 145	miRN	hsa−miR−922
22	1e−02	2 / 13	Lymph	YAMANE_AICDA_targets_recruited
23	1e−02	2 / 13	GSEA	BIOCARTA_CACAM_PATHWAY
24	1e−02	2 / 13	GSEA	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION
25	1e−02	2 / 14	BP	histone H4−K5 acetylation
26	1e−02	2 / 14	BP	histone H4−K8 acetylation
27	1e−02	2 / 14	BP	positive regulation of chemokine production
28	1e−02	2 / 14	miRN	hsa−miR−147b
29	1e−02	15 / 629	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
30	2e−02	2 / 15	BP	peptide hormone processing
31	2e−02	2 / 15	GSEA	SABATES_COLORECTAL_ADENOMA_SIZE_UP
32	2e−02	2 / 15	GSEA	GEISS_RESPONSE_TO_DSRNA_DN
33	2e−02	3 / 42	GSEA	KRASNOSELSKAYA_ILF3_TARGETS_DN
34	2e−02	2 / 16	GSEA	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_
35	2e−02	2 / 16	GSEA	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP
36	2e−02	3 / 44	miRN	hsa−miR−640
37	2e−02	3 / 44	GSEA	MARSON_FOXP3_TARGETS_DN
38	2e−02	14 / 591	Colon	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
39	2e−02	7 / 213	GSEA	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP
40	2e−02	2 / 17	BP	definitive hemopoiesis

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.05	4 / 111	HORVATH_aging_genes meth UP
2	0.13	3 / 100	HORVATH_aging_genes meth DOWN
3	0.38	1 / 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	0.008	2 / 11	DNA methylation involved in gamete generation
2	0.010	2 / 12	regulation of neurotransmitter secretion
3	0.013	2 / 14	histone H4−K5 acetylation
4	0.013	2 / 14	histone H4−K8 acetylation
5	0.013	2 / 14	positive regulation of chemokine production
6	0.015	2 / 15	peptide hormone processing
7	0.019	2 / 17	definitive hemopoiesis
8	0.019	2 / 17	pseudouridine synthesis
9	0.022	3 / 47	negative regulation of neuron differentiation
10	0.025	7 / 225	ion transport
11	0.026	2 / 20	regulation of protein binding
12	0.026	10 / 388	proteolysis
13	0.031	2 / 22	positive regulation of transforming growth factor beta receptor signaling pathw
14	0.034	2 / 23	humoral immune response
15	0.042	3 / 61	lipid transport
16	0.042	3 / 61	palate development
17	0.042	2 / 26	cellular response to organic substance
18	0.046	2 / 27	endosome organization
19	0.047	17 / 863	transmembrane transport
20	0.049	2 / 28	mesoderm development

Brain

Rank	p−value	#in/all	Geneset
1	0.002	25 / 1065	Overlap_fetal_midbrain_Enh
2	0.027	22 / 1122	Fetal_K9K27me3
3	0.039	14 / 656	Overlap_fetal_midbrain_EnhP
4	0.077	18 / 989	Mid_Frontal_Lobe_Quies
5	0.095	16 / 884	Overlap_fetal_midbrain_EnhG
6	0.103	11 / 564	Mid_Frontal_Lobe_EnhP
7	0.158	33 / 2185	Fetal_TssA
8	0.198	13 / 786	Fetal_EnhG
9	0.201	29 / 1949	Fetal_TssF
10	0.237	9 / 534	Mid_Frontal_Lobe_EnhG
11	0.262	119 / 9020	Overlap_fetal_midbrain_ReprPCWk
12	0.329	19 / 1333	Fetal_ReprPCWk
13	0.365	78 / 5940	Overlap_fetal_midbrain_HetRpts
14	0.382	7 / 468	Mid_Frontal_Lobe_TssF
15	0.390	33 / 2462	Mid_Frontal_Lobe_HetRpts
16	0.391	25 / 1845	Fetal_Quies
17	0.432	13 / 953	Fetal_Enh
18	0.454	11 / 812	Mid_Frontal_Lobe_TssP
19	0.459	25 / 1907	Fetal_TxTrans
20	0.473	9 / 668	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	GENTLES_modul13
2	0.1	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.2	2 / 55	PanCan_JAK−ST_geneset_nanostring
4	0.2	1 / 15	GENTLES_modul1
5	0.2	1 / 15	GENTLES_modul4
6	0.2	1 / 15	GENTLES_modul11
7	0.2	1 / 16	GENTLES_modul14
8	0.2	3 / 121	PanCan_MAPK_geneset_nanostring
9	0.2	1 / 20	PanCan_ChromMod_geneset_nanostring
10	0.3	3 / 156	PanCan_PI3K_geneset_nanostring
11	0.4	1 / 40	ZHANG_MM up
12	0.4	1 / 40	PanCan_HK_geneset_nanostring
13	0.4	2 / 111	PanCan_RAS_geneset_nanostring
14	0.4	2 / 113	PanCan_Driver_Gene_geneset_nanostring
15	0.5	1 / 48	KUIPER_MM poor survival
16	0.5	1 / 61	PanCan_Wnt_geneset_nanostring
17	0.6	5 / 401	Lembcke_Colonic Inflammation
18	0.6	6 / 489	Lembcke_Normal vs Adenoma
19	0.6	1 / 82	PanCan_TXmisReg_geneset_nanostring
20	0.9	2 / 298	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	0.03	3 / 51	voltage−gated potassium channel complex
2	0.03	49 / 2984	integral component of membrane
3	0.03	2 / 22	histone acetyltransferase complex
4	0.06	2 / 31	brush border membrane
5	0.09	3 / 83	endomembrane system
6	0.09	2 / 41	presynaptic membrane
7	0.10	2 / 42	intercellular bridge
8	0.10	2 / 43	cytoplasmic microtubule
9	0.11	3 / 91	nuclear matrix
10	0.11	4 / 144	membrane raft
11	0.12	2 / 47	Cajal body
12	0.12	2 / 47	lipid particle
13	0.12	1 / 10	apical dendrite
14	0.12	1 / 10	cell−cell contact zone
15	0.12	1 / 10	neuron projection terminus
16	0.12	2 / 48	peroxisomal membrane
17	0.13	1 / 11	Arp2/3 protein complex
18	0.14	2 / 51	axoneme
19	0.14	1 / 12	XY body
20	0.15	1 / 13	microvillus membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.02	13 / 552	Chr 10
2	0.14	9 / 465	Chr 15
3	0.16	12 / 689	Chr 7
4	0.28	9 / 558	Chr 4
5	0.30	3 / 151	Chr 21
6	0.38	7 / 469	Chr 8
7	0.40	8 / 551	Chr X
8	0.42	5 / 335	Chr 22
9	0.44	14 / 1037	Chr 19
10	0.56	10 / 801	Chr 11
11	0.61	12 / 993	Chr 2
12	0.63	10 / 840	Chr 17
13	0.63	18 / 1500	Chr 1
14	0.65	3 / 262	Chr 13
15	0.74	9 / 838	Chr 3
16	0.74	6 / 576	Chr 9
17	0.77	2 / 221	Chr 18
18	0.78	7 / 696	Chr 5
19	0.84	4 / 462	Chr 14
20	0.87	7 / 775	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.003	24 / 1038	HetRpts_Colon
2	0.005	29 / 1386	Het_Colon
3	0.018	14 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
4	0.028	16 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
5	0.040	7 / 250	K9K27me3_Colon
6	0.055	20 / 1079	ZNF_Colon
7	0.100	8 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
8	0.111	7 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	0.153	56 / 3897	Quies1_Colon
10	0.153	1 / 13	TCGA−CRC_less−agressive−disease−markers
11	0.157	29 / 1889	ReprPCWk_Colon
12	0.175	8 / 427	Quies2_Colon
13	0.179	32 / 2142	ReprPC_Colon
14	0.185	37 / 117	Marisa_CRC−cluster−b
15	0.227	2 / 71	Marisa_CRC−cluster−g
16	0.237	53 / 3812	TssD1_Colon
17	0.291	1 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN
18	0.309	1 / 29	Marisa_CRC−cluster−c
19	0.348	3 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	0.371	2 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	BCHETNIA_EBM up
2	0.5	4 / 294	GUDJ_psoriasis down
3	0.6	5 / 435	GUDJ_psoriasis 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	2 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
2	0.03	1 / 2	WILLSCHER_GBM_LTSwt_proteomics−M_UP
3	0.05	8 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.06	3 / 71	Weller_LGG_A_vs_O_UP
5	0.06	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
6	0.07	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	0.07	1 / 6	neurons_glio
8	0.11	1 / 9	Phillips PN up vs MES & Prolif
9	0.20	2 / 65	GIEZELT_GBM_STS_up_VS_LTS
10	0.20	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
11	0.21	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.21	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
13	0.24	2 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
14	0.24	2 / 74	WIRTH_Normal Brain
15	0.27	1 / 25	Shaw_down_in_1p19q
16	0.29	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
17	0.30	2 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
18	0.36	2 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
19	0.38	2 / 103	GIEZELT_GBM_WT_up_VS_mut
20	0.45	1 / 47	Weller_LGG_gradeII−vs−III_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.003	4 / 47	LEE_EARLY_T_LYMPHOCYTE_DN
2	0.006	3 / 30	PIONTEK_PKD1_TARGETS_UP
3	0.007	5 / 94	OHGUCHI_LIVER_HNF4A_TARGETS_DN
4	0.008	11 / 373	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
5	0.008	6 / 138	LEE_LIVER_CANCER_SURVIVAL_UP
6	0.010	4 / 67	MCCLUNG_COCAINE_REWARD_5D
7	0.011	2 / 13	BIOCARTA_CACAM_PATHWAY
8	0.011	2 / 13	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION
9	0.014	15 / 629	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
10	0.015	2 / 15	SABATES_COLORECTAL_ADENOMA_SIZE_UP
11	0.015	2 / 15	GEISS_RESPONSE_TO_DSRNA_DN
12	0.016	3 / 42	KRASNOSELSKAYA_ILF3_TARGETS_DN
13	0.017	2 / 16	REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_T
14	0.017	2 / 16	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP
15	0.018	3 / 44	MARSON_FOXP3_TARGETS_DN
16	0.019	7 / 213	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP
17	0.019	3 / 45	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
18	0.026	2 / 20	NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
19	0.026	9 / 333	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
20	0.028	5 / 134	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED

HM

Rank	p−value	#in/all	Geneset
1	0.08	4 / 127	HALLMARK_KRAS_SIGNALING_DN
2	0.12	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.26	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
4	0.37	3 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.37	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.52	2 / 137	HALLMARK_UV_RESPONSE_DN
7	0.55	2 / 146	HALLMARK_UV_RESPONSE_UP
8	0.56	2 / 148	HALLMARK_KRAS_SIGNALING_UP
9	0.63	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
10	0.63	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	0.68	2 / 183	HALLMARK_GLYCOLYSIS
12	0.69	1 / 91	HALLMARK_BILE_ACID_METABOLISM
13	0.69	2 / 188	HALLMARK_MYC_TARGETS_V1
14	0.70	1 / 95	HALLMARK_SPERMATOGENESIS
15	0.80	1 / 126	HALLMARK_ALLOGRAFT_REJECTION
16	0.83	1 / 140	HALLMARK_APOPTOSIS
17	0.84	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
18	0.88	1 / 167	HALLMARK_APICAL_JUNCTION
19	0.88	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
20	0.89	1 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	1 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.06	2 / 32	DUMEAUX_Fasting enriched genes
3	0.19	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 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	YAMANE_AICDA_targets_recruited
2	0.17	77 / 5538	HOPP_Weak_txn
3	0.18	1 / 16	DAVE_BL Inter
4	0.22	5 / 256	SPANG_IL21 DN
5	0.36	16 / 1128	SPANG_BCR DN
6	0.37	30 / 2211	HOPP_Repetitive
7	0.41	74 / 5693	HOPP_Weak_enhancer
8	0.42	6 / 410	SPANG_CD40 6hrs DN
9	0.46	4 / 275	TARTE_Mature plasma cell signature
10	0.48	84 / 6564	HOPP_Strong_enhancer
11	0.49	92 / 7209	HOPP_Weak_promoter
12	0.49	2 / 129	DAVE_BL−vs−DLBCL
13	0.57	32 / 2563	HOPP_Heterochrom
14	0.57	1 / 66	TARTE_Plasma cell signature
15	0.61	3 / 247	ZHANG_DLBCL mutated
16	0.65	1 / 82	ROSOLOWSKI_green UP
17	0.69	14 / 1218	SPANG_BCR UP
18	0.69	3 / 280	SPANG_CD40 6hrs UP
19	0.74	25 / 2188	HOPP_Poised_promoter
20	0.75	1 / 109	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 22	calmodulin−dependent protein kinase activity
2	0.003	3 / 22	delayed rectifier potassium channel activity
3	0.003	3 / 24	N−acetyltransferase activity
4	0.010	14 / 550	protein homodimerization activity
5	0.021	21 / 1033	nucleic acid binding
6	0.028	6 / 181	transporter activity
7	0.031	2 / 22	transferase activity, transferring hexosyl groups
8	0.034	2 / 23	hydrolase activity, acting on ester bonds
9	0.036	4 / 98	ion channel activity
10	0.037	2 / 24	cation channel activity
11	0.042	2 / 26	transforming growth factor beta receptor binding
12	0.049	2 / 28	Ran GTPase binding
13	0.059	14 / 695	transmembrane transporter activity
14	0.061	3 / 71	PDZ domain binding
15	0.062	2 / 32	voltage−gated potassium channel activity
16	0.065	2 / 33	symporter activity
17	0.076	2 / 36	calcium channel activity
18	0.093	3 / 85	metalloendopeptidase activity
19	0.095	2 / 41	ATPase activity, coupled to transmembrane movement of substances
20	0.096	3 / 86	integrin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−04	5 / 53	hsa−miR−337−3p
2	8e−03	4 / 63	hsa−miR−1285
3	9e−03	5 / 101	hsa−miR−325
4	1e−02	6 / 145	hsa−miR−922
5	1e−02	2 / 14	hsa−miR−147b
6	2e−02	3 / 44	hsa−miR−640
7	2e−02	3 / 45	hsa−miR−660
8	2e−02	3 / 48	hsa−miR−524−3p
9	4e−02	2 / 24	hsa−miR−632
10	4e−02	3 / 58	hsa−miR−219−1−3p
11	4e−02	3 / 58	hsa−miR−324−3p
12	4e−02	2 / 25	hsa−miR−663
13	4e−02	3 / 61	hsa−miR−612
14	5e−02	8 / 321	hsa−miR−32
15	6e−02	6 / 215	hsa−miR−199a−3p
16	6e−02	5 / 169	hsa−miR−369−3p
17	7e−02	2 / 33	hsa−miR−934
18	7e−02	3 / 76	hsa−miR−620
19	9e−02	3 / 82	hsa−miR−767−5p
20	1e−01	8 / 370	hsa−miR−144

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_src.2
2	1.0	0 / 12	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 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 / 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	0.007	36 / 1872	ICGC_Mef2_targets
2	0.072	13 / 653	ICGC_SrfPcr2_targets
3	0.135	11 / 595	ICGC_NrsfPcr2_targets
4	0.164	36 / 2416	ICGC_Bcl3_targets
5	0.205	42 / 2927	ICGC_Rad21_targets
6	0.232	31 / 2136	ICGC_GabpPcr2_targets
7	0.233	31 / 2137	ICGC_SrfV0416101_targets
8	0.238	21 / 1400	ICGC_Myc_targets
9	0.243	25 / 1701	HEBENSTREIT_high expression TF
10	0.252	19 / 1266	ICGC_NrsfPcr1_targets
11	0.256	21 / 1418	ICGC_Ets1_targets
12	0.269	27 / 1878	ICGC_Cebpbsc150_targets
13	0.285	72 / 5355	ICGC_Pol2_targets
14	0.291	54 / 3966	ICGC_Pu1_targets
15	0.306	19 / 1314	ICGC_Usf1_targets
16	0.321	72 / 5408	ICGC_Pou2_targets
17	0.377	10 / 690	ICGC_Atf3_targets
18	0.402	53 / 4032	ICGC_Creb1_targets
19	0.412	68 / 5219	ICGC_Tcf3_targets
20	0.421	61 / 4682	ICGC_Pol24_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 8	WIRTH_Tonsil
2	0.1	1 / 11	WIRTH_Prim. lymphoid organs
3	0.2	2 / 74	WIRTH_Mucosa
4	0.3	4 / 225	PALMER_Granulocytes signature up
5	0.4	2 / 107	WIRTH_Testis
6	0.4	1 / 41	WIRTH_Homeostasis
7	0.4	1 / 46	WIRTH_Liver
8	0.5	5 / 350	WIRTH_Immune system
9	0.7	2 / 194	PALMER_B−Cell signature up
10	0.8	1 / 114	PALMER_T−Cell signature up
11	1.0	1 / 350	WIRTH_Nervous System
12	1.0	0 / 32	WIRTH_Pancreas
13	1.0	0 / 11	WIRTH_Sec. lymphoid organs
14	1.0	0 / 13	WIRTH_B−cells
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	21 / 1115	LU_BPDE 1h DN
2	0.09	55 / 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	

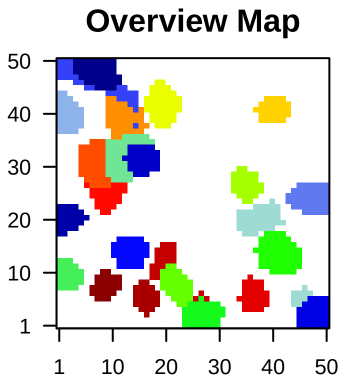
Correlation Clusters

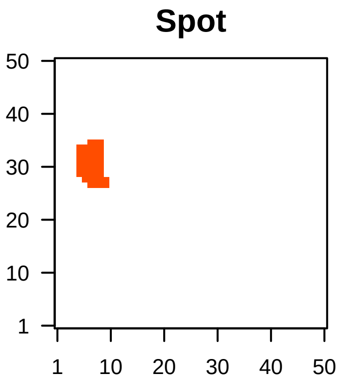
Spot Summary: N

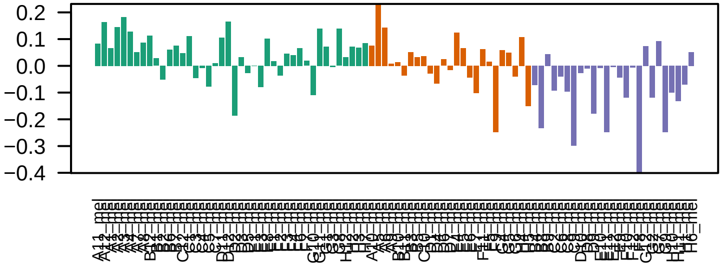
\# metagenes = 42
\# genes = 82

<r> metagenes = 0.93
<r> genes = 0.11
beta: r2= 0.52 / log p= −15.48

\# samples with spot = 4 (4.3 %)
MSC1 : 3 (7.1 %)
MSC2 : 1 (4 %)





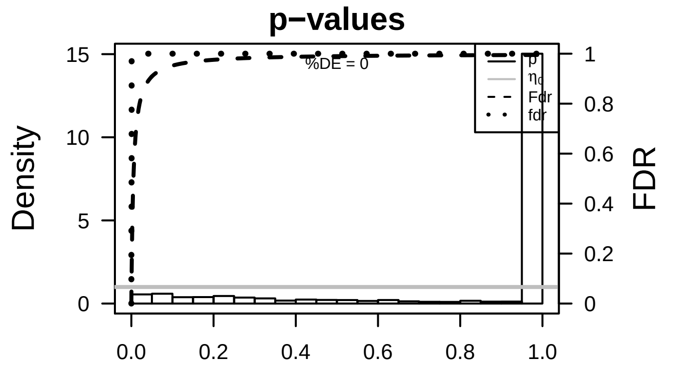


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	GSTA3	1.71	−0.15	0.28	GSTA3	glutathione S−transferase alpha 3 [Source:HGNC Symbol;Ac
2	FOXRED1	1.56	−0.57	0.29	FOXRED1	FAD−dependent oxidoreductase domain containing 1 [Source
3	UNKL	1.51	−0.21	0.29	UNKL	unkempt family zinc finger−like [Source:HGNC Symbol;Acc:H
4	LDLRAD3	1.42	−0.33	0.3	LDLRAD3	low density lipoprotein receptor class A domain containing 3 [
5	HCN3	1.42	−0.08	0.22	HCN3	hyperpolarization activated cyclic nucleotide gated potassium
6	C17orf49	1.41	−0.76	0.36	C17orf49	chromosome 17 open reading frame 49 [Source:HGNC Symb
7	UNC13B	1.38	−0.18	0.29	UNC13B	unc−13 homolog B (C. elegans) [Source:HGNC Symbol;Acc:
8	PRKCD	1.37	−0.24	0.33	PRKCD	protein kinase C, delta [Source:HGNC Symbol;Acc:HGNC:93
9	GFPT2	1.37	−0.14	0.2	GFPT2	glutamine−fructose−6−phosphate transaminase 2 [Source:H
10	FIG4	1.34	−0.7	0.28	FIG4	FIG4 phosphoinositide 5−phosphatase [Source:HGNC Symb
11	CREBL2	1.33	−0.22	0.27	CREBL2	cAMP responsive element binding protein−like 2 [Source:HG
12	HMGXB3	1.27	−0.52	0.26	HMGXB3	HMG box domain containing 3 [Source:HGNC Symbol;Acc:H
13	KATNA1	1.27	−0.94	0.17	KATNA1	katanin p60 (ATPase containing) subunit A 1 [Source:HGNC
14	CRMP1	1.27	−0.11	0.29	CRMP1	collapsin response mediator protein 1 [Source:HGNC Symbo
15	MED9	1.26	−0.63	0.27	MED9	mediator complex subunit 9 [Source:HGNC Symbol;Acc:HGN
16	MOSPD3	1.25	−0.41	0.28	MOSPD3	motile sperm domain containing 3 [Source:HGNC Symbol;Ac
17	DBP	1.22	−0.38	0.34	DBP	D site of albumin promoter (albumin D−box) binding protein [
18	ERCC6L	1.21	−0.12	0.37	ERCC6L	excision repair cross−complementation group 6−like [Source:
19	MCOLN2	1.19	−0.05	0.25	MCOLN2	mucolipin 2 [Source:HGNC Symbol;Acc:HGNC:13357]
20	ETV4	1.19	−0.17	0.36	ETV4	ets variant 4 [Source:HGNC Symbol;Acc:HGNC:3493]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−17	14 / 94	BP	respiratory electron transport chain
2	2e−16	22 / 401	CC	mitochondrial inner membrane
3	3e−16	13 / 78	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
4	6e−16	14 / 107	GSEA	KEGG_OXIDATIVE_PHOSPHORYLATION
5	2e−14	14 / 135	BP	cellular metabolic process
6	3e−14	11 / 62	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
7	5e−14	13 / 114	GSEA	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSP
8	3e−13	12 / 102	GSEA	KEGG_PARKINSONS_DISEASE
9	9e−13	17 / 311	BP	generation of precursor metabolites and energy
10	1e−12	11 / 85	GSEA	MOOTHA_VOXPHOS
11	1e−12	23 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
12	3e−12	13 / 157	GSEA	KEGG_HUNTINGTONS_DISEASE
13	4e−12	14 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
14	2e−11	12 / 142	GSEA	KEGG_ALZHEIMERS_DISEASE
15	1e−10	13 / 213	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
16	2e−09	14 / 316	GSEA	HSIAO_HOUSEKEEPING_GENES
17	2e−09	9 / 93	GSEA	PECE_MAMMARY_STEM_CELL_UP
18	5e−09	18 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
19	8e−09	15 / 421	GSEA	MOOTHA_MITOCHONDRIA
20	3e−08	7 / 58	GSEA	KEGG_CARDIAC_MUSCLE_CONTRACTION
21	4e−08	14 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
22	9e−08	6 / 41	CC	mitochondrial respiratory chain complex I
23	2e−07	25 / 1468	CC	mitochondrion
24	2e−07	6 / 48	BP	hydrogen ion transmembrane transport
25	3e−07	14 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
26	4e−06	25 / 1730	BP	small molecule metabolic process
27	4e−06	6 / 77	GSEA	CHICAS_RB1_TARGETS_LOW_SERUM
28	4e−06	15 / 683	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
29	9e−06	19 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
30	1e−05	4 / 25	MF	cytochrome−c oxidase activity
31	1e−05	7 / 137	GSEA	KIM_ALL_DISORDERS_DURATION_CORR_DN
32	2e−05	4 / 29	GSEA	HONMA_DOCETAXEL_RESISTANCE
33	2e−05	13 / 592	MF	oxidoreductase activity
34	2e−05	5 / 63	GSEA	MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP
35	3e−05	3 / 12	CC	mitochondrial respiratory chain
36	3e−05	3 / 12	BP	oxidative phosphorylation
37	7e−05	4 / 40	BP	mitochondrial electron transport, NADH to ubiquinone
38	7e−05	4 / 40	MF	NADH dehydrogenase (ubiquinone) activity
39	9e−05	4 / 43	GSEA	DAZARD_UV_RESPONSE_CLUSTER_G1
40	2e−04	5 / 96	GSEA	BOUDOUKHA_BOUND_BY_IGF2BP2



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	9e−17	14 / 94	respiratory electron transport chain
2	2e−14	14 / 135	cellular metabolic process
3	9e−13	17 / 311	generation of precursor metabolites and energy
4	2e−07	6 / 48	hydrogen ion transmembrane transport
5	4e−06	25 / 1730	small molecule metabolic process
6	3e−05	3 / 12	oxidative phosphorylation
7	7e−05	4 / 40	mitochondrial electron transport, NADH to ubiquinone
8	3e−03	12 / 863	transmembrane transport
9	4e−03	2 / 17	mitochondrial ATP synthesis coupled proton transport
10	4e−03	6 / 277	translation
11	5e−03	2 / 20	microtubule bundle formation
12	6e−03	3 / 65	Fc−gamma receptor signaling pathway involved in phagocytosis
13	6e−03	2 / 21	aerobic respiration
14	6e−03	25 / 2755	transport
15	1e−02	2 / 28	negative regulation of neuron projection development
16	1e−02	3 / 83	mitochondrial translational elongation
17	1e−02	3 / 83	mitochondrial translational initiation
18	1e−02	3 / 83	mitochondrial translational termination
19	1e−02	3 / 84	osteoblast differentiation
20	2e−02	9 / 705	locomotion

Brain

Rank	p−value	#in/all	Geneset
1	0.001	7 / 304	Fetal_Het
2	0.003	62 / 9013	Overlap_fetal_midbrain_K9K27me3
3	0.018	61 / 9330	Overlap_fetal_midbrain_ReprPC
4	0.044	5 / 349	Fetal_ZNF
5	0.061	3 / 163	Fetal_ReprPC
6	0.071	23 / 3081	Mid_Frontal_Lobe_ZNF
7	0.088	8 / 831	Fetal_HetRpts
8	0.132	7 / 769	Overlap_fetal_midbrain_ZNF
9	0.247	6 / 765	Mid_Frontal_Lobe_Het
10	0.278	16 / 2462	Mid_Frontal_Lobe_HetRpts
11	0.318	12 / 1845	Fetal_Quies
12	0.425	54 / 9528	Overlap_fetal_midbrain_Quies
13	0.432	6 / 953	Fetal_Enh
14	0.458	8 / 1333	Fetal_ReprPCWk
15	0.488	11 / 1907	Fetal_TxTrans
16	0.488	9 / 1548	Mid_Frontal_Lobe_K9K27me3
17	0.519	11 / 1949	Fetal_TssF
18	0.585	1 / 158	Overlap_fetal_midbrain_Het
19	0.603	1 / 166	Mid_Frontal_Lobe_Tx
20	0.607	3 / 564	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	2 / 10	GENTLES_modul5
2	0.003	2 / 15	GENTLES_modul1
3	0.075	1 / 14	LIU_LIVER_CANCER
4	0.080	1 / 15	GENTLES_modul10
5	0.085	1 / 16	GENTLES_modul7
6	0.201	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	0.366	1 / 82	PanCan_TXmisReg_geneset_nanostring
8	0.492	2 / 298	SPANG_BCL6−index2
9	0.510	3 / 489	Lembcke_Normal vs Adenoma
10	0.633	1 / 180	SPANG_LPS−index2
11	0.887	0 / 14	LIU_PROSTATE_CANCER_DN
12	0.895	1 / 401	Lembcke_Colonic Inflammation
13	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1.000	0 / 12	LIU_BREAST_CANCER
17	1.000	0 / 14	LIU_COMMON_CANCER_GENES
18	1.000	0 / 12	LIU_PROSTATE_CANCER_UP
19	1.000	0 / 15	WANG_ER_UP
20	1.000	0 / 5	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−16	22 / 401	mitochondrial inner membrane
2	9e−08	6 / 41	mitochondrial respiratory chain complex I
3	2e−07	25 / 1468	mitochondrion
4	3e−05	3 / 12	mitochondrial respiratory chain
5	3e−04	32 / 3214	protein complex
6	8e−04	76 / 11774	cell
7	1e−03	68 / 9988	organelle
8	1e−03	59 / 8205	cytoplasm
9	2e−03	70 / 10605	intracellular
10	3e−03	22 / 2193	extracellular exosome
11	4e−03	4 / 113	spindle
12	5e−03	2 / 19	mitochondrial proton−transporting ATP synthase complex
13	5e−03	4 / 128	ribosome
14	7e−03	4 / 135	myelin sheath
15	1e−02	5 / 250	microtubule
16	1e−02	3 / 91	nuclear matrix
17	1e−02	79 / 13191	cellular_component
18	3e−02	4 / 202	actin cytoskeleton
19	4e−02	5 / 332	cell junction
20	4e−02	3 / 138	cell−cell junction

Chr

Rank	p−value	#in/all	Geneset
1	0.006	11 / 840	Chr 17
2	0.027	11 / 1037	Chr 19
3	0.036	8 / 687	Chr 6
4	0.086	7 / 689	Chr 7
5	0.149	6 / 649	Chr 16
6	0.340	5 / 696	Chr 5
7	0.456	5 / 801	Chr 11
8	0.476	3 / 465	Chr 15
9	0.482	3 / 469	Chr 8
10	0.569	1 / 151	Chr 21
11	0.591	3 / 551	Chr X
12	0.650	2 / 398	Chr 20
13	0.709	1 / 221	Chr 18
14	0.809	3 / 775	Chr 12
15	0.950	2 / 838	Chr 3
16	0.956	1 / 552	Chr 10
17	0.957	1 / 558	Chr 4
18	0.961	1 / 576	Chr 9
19	0.972	4 / 1500	Chr 1
20	0.997	1 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.004	64 / 9482	TssA_Colon
2	0.021	42 / 5880	TssD2_Colon
3	0.040	58 / 9027	Tx_Colon
4	0.049	1 / 9	TCGA−CRC_agressive−disease−markers
5	0.059	1 / 11	Budinska_B_Lower crypt−like_DOWN
6	0.068	47 / 7203	TssF_Colon
7	0.084	54 / 8580	TxWk_Colon
8	0.109	2 / 102	Marisa_CRC−cluster−d
9	0.224	6 / 739	TxEnhG2_Colon
10	0.374	17 / 2798	TxEnhG1_Colon
11	0.403	2 / 250	K9K27me3_Colon
12	0.413	2 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
13	0.428	2 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
14	0.483	4 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	0.488	54 / 9653	Enh_Colon
16	0.493	29 / 5155	EnhWk1_Colon
17	0.518	1 / 131	Marisa_CRC−cluster−a
18	0.598	4 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
19	0.601	1 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	0.611	2 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	0.8	1 / 294	GUDJ_psoriasis down
2	0.9	1 / 435	GUDJ_psoriasis up
3	1.0	0 / 11	BCHETNIA_EBM up
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.04	3 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	0.05	2 / 63	Stuehler_Proteins_up_in_STS
3	0.05	5 / 365	Down_b
4	0.12	1 / 23	WIRTH_PN subtype
5	0.14	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
6	0.16	1 / 32	Colman_survival_associated
7	0.22	2 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.23	1 / 47	Vishal_subnetwork signature of survival in GBM
9	0.23	1 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
10	0.24	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	0.30	1 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	0.30	1 / 65	GIEZELT_GBM_STS_up_VS_LTS
13	0.30	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
14	0.32	1 / 70	Weller_LGG_1p19qDel−vs−intact_UP
15	0.33	1 / 71	Weller_LGG_A_vs_O_UP
16	0.41	1 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
17	0.44	1 / 103	GIEZELT_GBM_WT_up_VS_mut
18	0.55	2 / 332	Up
19	0.64	1 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
20	0.85	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−16	13 / 78	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
2	6e−16	14 / 107	KEGG_OXIDATIVE_PHOSPHORYLATION
3	3e−14	11 / 62	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
4	5e−14	13 / 114	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
5	3e−13	12 / 102	KEGG_PARKINSONS_DISEASE
6	1e−12	11 / 85	MOOTHA_VOXPHOS
7	1e−12	23 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
8	3e−12	13 / 157	KEGG_HUNTINGTONS_DISEASE
9	2e−11	12 / 142	KEGG_ALZHEIMERS_DISEASE
10	1e−10	13 / 213	WONG_MITOCHONDRIA_GENE_MODULE
11	2e−09	14 / 316	HSIAO_HOUSEKEEPING_GENES
12	2e−09	9 / 93	PECE_MAMMARY_STEM_CELL_UP
13	5e−09	18 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
14	8e−09	15 / 421	MOOTHA_MITOCHONDRIA
15	3e−08	7 / 58	KEGG_CARDIAC_MUSCLE_CONTRACTION
16	4e−08	14 / 405	MOOTHA_HUMAN_MITODB_6_2002
17	3e−07	14 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
18	4e−06	6 / 77	CHICAS_RB1_TARGETS_LOW_SERUM
19	4e−06	15 / 683	MARTENS_TRETINOIN_RESPONSE_DN
20	9e−06	19 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−12	14 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	6e−04	6 / 188	HALLMARK_MYC_TARGETS_V1
3	4e−02	2 / 57	HALLMARK_MYC_TARGETS_V2
4	8e−02	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	1e−01	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	2e−01	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
7	2e−01	2 / 146	HALLMARK_UV_RESPONSE_UP
8	2e−01	2 / 148	HALLMARK_KRAS_SIGNALING_UP
9	2e−01	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
10	2e−01	2 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
11	2e−01	2 / 174	HALLMARK_HEME_METABOLISM
12	3e−01	2 / 183	HALLMARK_GLYCOLYSIS
13	3e−01	2 / 188	HALLMARK_ADIPOGENESIS
14	3e−01	2 / 195	HALLMARK_MITOTIC_SPINDLE
15	5e−01	1 / 127	HALLMARK_KRAS_SIGNALING_DN
16	5e−01	1 / 137	HALLMARK_UV_RESPONSE_DN
17	5e−01	1 / 141	HALLMARK_FATTY_ACID_METABOLISM
18	6e−01	1 / 162	HALLMARK_COMPLEMENT
19	6e−01	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	6e−01	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
2	0.29	1 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 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 / 5184	HOPP_Txn_transition
2	1e−02	49 / 6929	HOPP_Txn_elongation
3	8e−02	4 / 294	TARTE_Plasmablast signature
4	2e−01	3 / 247	ZHANG_DLBCL mutated
5	2e−01	4 / 410	SPANG_CD40 6hrs DN
6	2e−01	1 / 42	CARO_OxPhos_in_DLBCL_UP
7	2e−01	1 / 50	SPANG_BAFF 9hrs DN
8	3e−01	1 / 61	SPANG_LPS 6hrs DN
9	3e−01	2 / 212	LENZ_Stromal signature 1
10	4e−01	1 / 80	Aukema_BCL2 DN_BCL6 UP
11	4e−01	1 / 82	ROSOLOWSKI_green UP
12	4e−01	1 / 86	ROSOLOWSKI_red total
13	4e−01	38 / 6564	HOPP_Strong_enhancer
14	4e−01	2 / 256	SPANG_IL21 DN
15	4e−01	2 / 268	SPANG_IL21 UP
16	4e−01	41 / 7209	HOPP_Weak_promoter
17	4e−01	1 / 107	SPANG_LPS 6hrs UP
18	5e−01	2 / 275	TARTE_Mature plasma cell signature
19	5e−01	43 / 7592	HOPP_Active_promoter
20	5e−01	1 / 109	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 25	cytochrome−c oxidase activity
2	2e−05	13 / 592	oxidoreductase activity
3	7e−05	4 / 40	NADH dehydrogenase (ubiquinone) activity
4	1e−03	11 / 695	transmembrane transporter activity
5	7e−03	3 / 71	structural constituent of ribosome
6	1e−02	4 / 166	receptor activity
7	2e−02	2 / 41	peptidyl−prolyl cis−trans isomerase activity
8	4e−02	3 / 142	isomerase activity
9	5e−02	10 / 1007	poly(A) RNA binding
10	5e−02	1 / 10	lamin binding
11	5e−02	1 / 10	neutral amino acid transmembrane transporter activity
12	6e−02	1 / 11	cAMP response element binding
13	6e−02	1 / 11	hormone binding
14	6e−02	1 / 11	proton−transporting ATP synthase activity, rotational mechanism
15	6e−02	1 / 12	dynein binding
16	6e−02	1 / 12	GTPase inhibitor activity
17	6e−02	1 / 12	insulin receptor substrate binding
18	7e−02	3 / 171	RNA polymerase II core promoter proximal region sequence−specific DNA bir
19	7e−02	1 / 13	protein kinase C activity
20	7e−02	1 / 13	voltage−gated sodium channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	3 / 70	hsa−miR−489
2	0.013	3 / 88	hsa−miR−505
3	0.043	2 / 60	hsa−miR−532−5p
4	0.054	2 / 68	hsa−miR−606
5	0.056	2 / 69	hsa−miR−873
6	0.075	1 / 14	hsa−miR−452*
7	0.088	2 / 90	hsa−miR−216a
8	0.095	1 / 18	hsa−miR−564
9	0.116	3 / 215	hsa−miR−199a−3p
10	0.129	1 / 25	hsa−miR−1273
11	0.129	1 / 25	hsa−miR−432*
12	0.142	2 / 120	hsa−miR−421
13	0.144	1 / 28	hsa−miR−1292
14	0.146	3 / 239	hsa−miR−152
15	0.150	2 / 124	hsa−miR−493
16	0.167	1 / 33	hsa−miR−555
17	0.167	2 / 133	hsa−miR−198
18	0.176	1 / 35	hsa−miR−588
19	0.179	3 / 264	hsa−miR−30a
20	0.186	3 / 269	hsa−miR−30d

PathwAct

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

TF

Rank	p−value	#in/all	Geneset
1	0.002	15 / 1171	KIM_MYC targets
2	0.002	22 / 2136	ICGC_GabpPcr2_targets
3	0.016	1 / 3	MYC_Tumor supressor genes UP
4	0.019	14 / 1383	ICGC_Six5_targets
5	0.027	1 / 5	MYC_Cell growth and proliferation UP
6	0.042	2 / 59	MYC_Targets UP
7	0.047	13 / 1418	ICGC_Ets1_targets
8	0.049	1 / 9	MYC_DNA repair UP
9	0.060	33 / 4689	ICGC_Taf1_targets
10	0.071	31 / 4414	ICGC_Bclaf101388_targets
11	0.074	28 / 3924	ICGC_Zeb1_targets
12	0.087	36 / 5355	ICGC_Pol2_targets
13	0.097	32 / 4706	ICGC_Sp1_targets
14	0.144	35 / 5408	ICGC_Pou2_targets
15	0.151	32 / 4909	ICGC_Stat5_targets
16	0.184	37 / 5890	ICGC_Elf1_targets
17	0.200	31 / 4879	ICGC_Pmlsc71910_targets
18	0.209	26 / 4032	ICGC_Creb1_targets
19	0.227	30 / 4774	ICGC_Foxm1_targets
20	0.234	34 / 5495	ICGC_Yy1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 40	VAQUERIZAS_Thyroid
2	0.04	3 / 143	VAQUERIZAS_General
3	0.08	1 / 16	VAQUERIZAS_Adrenal gland
4	0.09	1 / 17	VAQUERIZAS_Pituitary
5	0.19	1 / 37	VAQUERIZAS_Thymus
6	0.22	1 / 45	VAQUERIZAS_Uterus
7	1.00	0 / 36	VAQUERIZAS_Fetal brain
8	1.00	0 / 41	VAQUERIZAS_Placenta
9	1.00	0 / 26	VAQUERIZAS_Liver
10	1.00	0 / 33	VAQUERIZAS_Prostate
11	1.00	0 / 29	VAQUERIZAS_Smooth muscle
12	1.00	0 / 9	VAQUERIZAS_Kidney
13	1.00	0 / 23	VAQUERIZAS_Spinal cord
14	1.00	0 / 38	VAQUERIZAS_Whole brain
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

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	1 / 12	WIRTH_Lymphocytes
2	0.08	1 / 16	PALMER_Lymphocytes signature up
3	0.72	1 / 225	PALMER_Granulocytes signature up
4	0.86	1 / 350	WIRTH_Immune system
5	0.86	1 / 350	WIRTH_Nervous System
6	1.00	0 / 32	WIRTH_Pancreas
7	1.00	0 / 11	WIRTH_Sec. lymphoid organs
8	1.00	0 / 11	WIRTH_Prim. lymphoid organs
9	1.00	0 / 13	WIRTH_B−cells
10	1.00	0 / 8	WIRTH_Tonsil
11	1.00	0 / 12	WIRTH_Thymus
12	1.00	0 / 5	WIRTH_Bone marrow
13	1.00	0 / 11	WIRTH_Globus pallidus
14	1.00	0 / 14	WIRTH_Telencephalon
15	1.00	0 / 11	WIRTH_Cortex cerebri
16	1.00	0 / 10	WIRTH_Hippocampus
17	1.00	0 / 10	WIRTH_Thalamus
18	1.00	0 / 12	WIRTH_Cerebellum
19	1.00	0 / 107	WIRTH_Testis
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	18 / 3682	LU_BPDE 0.005 DN
2	0.9	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	

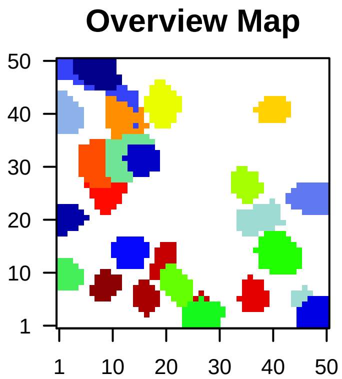
Correlation Clusters

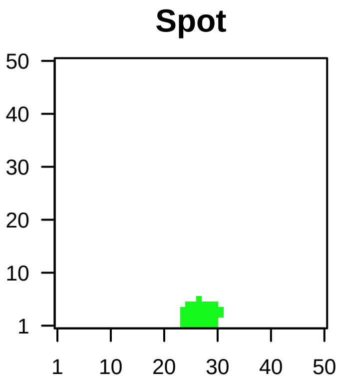
Spot Summary: O

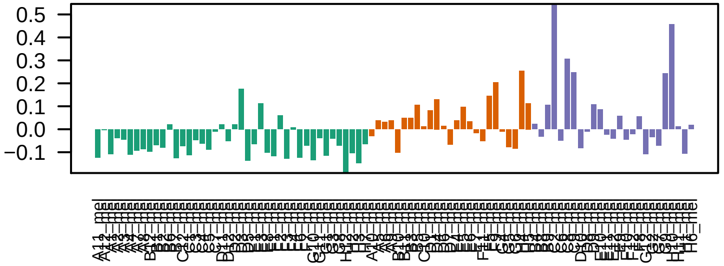
metagenes = 37
genes = 448

<r> metagenes = 0.93
<r> genes = 0.35
beta: r2= 1.24 / log p= −Inf

samples with spot = 8 (8.7 %)
MSC1 : 1 (2.4 %)
MSC2 : 2 (8 %)
MSC3 : 5 (20 %)





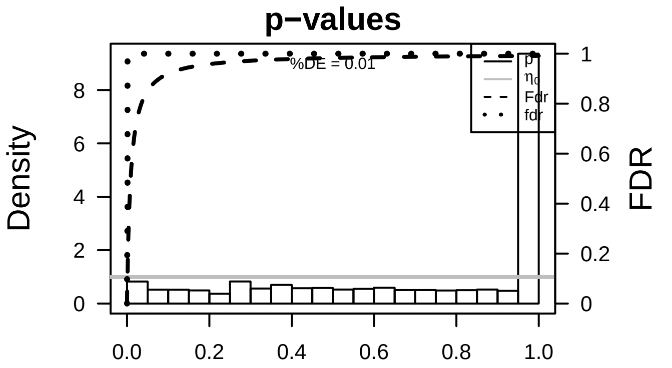


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PELP1	1.9	−0.32	0.55	PELP1	proline, glutamate and leucine rich protein 1 [Source:HGNC S
2	RCBTB2	1.87	−0.27	0.37	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (PC
3	BMP4	1.84	−0.21	0.45	BMP4	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:HG
4	ATG2B	1.7	−0.32	0.46	ATG2B	autophagy related 2B [Source:HGNC Symbol;Acc:HGNC:201
5	ZNF264	1.67	−0.28	0.42	ZNF264	zinc finger protein 264 [Source:HGNC Symbol;Acc:HGNC:13
6	SSX5	1.66	−0.14	0.38	SSX5	synovial sarcoma, X breakpoint 5 [Source:HGNC Symbol;Acc
7	ZNF550	1.66	−0.21	0.31	ZNF550	zinc finger protein 550 [Source:HGNC Symbol;Acc:HGNC:28
8	GALK2	1.64	−0.44	0.28	GALK2	galactokinase 2 [Source:HGNC Symbol;Acc:HGNC:4119]
9	ZNF525	1.63	−0.32	0.36	ZNF525	zinc finger protein 525 [Source:HGNC Symbol;Acc:HGNC:29
10	RNF25	1.6	−0.33	0.28	RNF25	ring finger protein 25 [Source:HGNC Symbol;Acc:HGNC:146
11	ATOH8	1.6	−0.33	0.34	ATOH8	atonal homolog 8 (Drosophila) [Source:HGNC Symbol;Acc:H
12	AKR1C3	1.59	−0.15	0.54	AKR1C3	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
13	DENND1A	1.58	−0.51	0.32	DENND1A	DENN/MADD domain containing 1A [Source:HGNC Symbol;
14	TLE1	1.57	−0.57	0.46	TLE1	transducin−like enhancer of split 1 (E(sp1) homolog, Drosoph
15	ADCY6	1.55	−0.31	0.46	ADCY6	adenylate cyclase 6 [Source:HGNC Symbol;Acc:HGNC:237]
16	AHDC1	1.54	−0.11	0.48	AHDC1	AT hook, DNA binding motif, containing 1 [Source:HGNC Sym
17	PHYH	1.53	−0.43	0.25	PHYH	phytanoyl−CoA 2−hydroxylase [Source:HGNC Symbol;Acc:H
18	CLEC16A	1.51	−0.62	0.38	CLEC16A	C−type lectin domain family 16, member A [Source:HGNC Sy
19	CCDC180	1.51	−0.11	0.45	CCDC180	coiled−coil domain containing 180 [Source:HGNC Symbol;Ac
20	AP000350.10	1.5	−0.11	0.57		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−14	15 / 37	GSEA	KEGG_ABC_TRANSPORTERS
2	2e−12	9 / 12	Canc	BEN−PORATH_DN
3	3e−12	14 / 41	MF	ATPase activity, coupled to transmembrane movement of substances
4	2e−11	18 / 85	MF	metalloendopeptidase activity
5	7e−11	11 / 27	GSEA	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
6	1e−09	8 / 14	BP	cAMP biosynthetic process
7	2e−08	9 / 25	BP	adenylate cyclase−activating G−protein coupled receptor signaling pathway
8	1e−07	6 / 10	MF	adenylate cyclase activity
9	2e−07	18 / 149	GSEA	NABA_ECM_REGULATORS
10	3e−07	12 / 67	GSEA	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
11	4e−07	6 / 12	BP	cyclic nucleotide biosynthetic process
12	4e−07	6 / 12	MF	phosphorus−oxygen lyase activity
13	4e−07	6 / 12	GSEA	PID_LPA4_PATHWAY
14	4e−07	6 / 12	GSEA	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
15	6e−07	13 / 83	GSEA	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION
16	7e−07	6 / 13	MF	transmembrane receptor protein serine/threonine kinase activity
17	7e−07	6 / 13	GSEA	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS
18	1e−06	6 / 14	MF	aldehyde dehydrogenase (NAD) activity
19	2e−06	5 / 9	GSEA	REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY
20	3e−06	17 / 159	CC	extracellular matrix
21	3e−06	6 / 16	MF	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD
22	5e−06	21 / 239	CC	proteinaceous extracellular matrix
23	7e−06	5 / 11	MF	aldo−keto reductase (NADP) activity
24	8e−06	11 / 75	MF	metallopeptidase activity
25	1e−05	12 / 91	HM	HALLMARK_BILE_ACID_METABOLISM
26	1e−05	7 / 28	BP	intracellular transport
27	1e−05	6 / 19	BP	protein targeting to Golgi
28	2e−05	9 / 54	GSEA	PID_ENDOTHELIN_PATHWAY
29	2e−05	12 / 99	GSEA	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
30	3e−05	7 / 32	BP	adenylate cyclase−inhibiting G−protein coupled receptor signaling pathway
31	3e−05	5 / 14	MF	transforming growth factor beta−activated receptor activity
32	3e−05	5 / 14	Canc	LIU_PROSTATE_CANCER_DN
33	4e−05	62 / 1309	MF	ATP binding
34	4e−05	5 / 15	BP	activation of protein kinase A activity
35	4e−05	5 / 15	GSEA	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
36	5e−05	52 / 1040	MF	zinc ion binding
37	5e−05	22 / 300	GSEA	REACTOME_GPCR_DOWNSTREAM_SIGNALING
38	6e−05	11 / 93	GSEA	REACTOME_SIGNALING_BY_FGFR
39	7e−05	7 / 37	GSEA	REACTOME_PLC_BETA_MEDIATED_EVENTS
40	7e−05	7 / 37	GSEA	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS



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	0.8	2 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−09	8 / 14	cAMP biosynthetic process
2	2e−08	9 / 25	adenylate cyclase−activating G−protein coupled receptor signaling pathway
3	4e−07	6 / 12	cyclic nucleotide biosynthetic process
4	1e−05	7 / 28	intracellular transport
5	1e−05	6 / 19	protein targeting to Golgi
6	3e−05	7 / 32	adenylate cyclase−inhibiting G−protein coupled receptor signaling pathway
7	4e−05	5 / 15	activation of protein kinase A activity
8	8e−05	5 / 17	long−chain fatty acid metabolic process
9	9e−05	6 / 27	adenylate cyclase−modulating G−protein coupled receptor signaling pathway
10	2e−04	4 / 11	cellular aldehyde metabolic process
11	3e−04	7 / 45	cholesterol homeostasis
12	3e−04	5 / 22	renal water homeostasis
13	4e−04	7 / 48	activation of phospholipase C activity
14	4e−04	9 / 79	positive regulation of angiogenesis
15	7e−04	5 / 26	positive regulation of cAMP biosynthetic process
16	7e−04	6 / 39	retinoid metabolic process
17	8e−04	23 / 388	proteolysis
18	9e−04	5 / 27	retina homeostasis
19	9e−04	5 / 27	water transport
20	1e−03	4 / 17	activation of adenylate cyclase activity

Brain

Rank	p−value	#in/all	Geneset
1	0.02	33 / 812	Mid_Frontal_Lobe_TssP
2	0.03	12 / 229	Mid_Frontal_Lobe_TxTrans
3	0.03	76 / 2185	Fetal_TssA
4	0.04	99 / 2972	Mid_Frontal_Lobe_ReprPC
5	0.05	5 / 69	Overlap_fetal_midbrain_Tx
6	0.07	43 / 1207	Overlap_fetal_midbrain_TssF
7	0.08	21 / 534	Mid_Frontal_Lobe_EnhG
8	0.10	8 / 166	Mid_Frontal_Lobe_Tx
9	0.12	18 / 468	Mid_Frontal_Lobe_TssF
10	0.15	63 / 1949	Fetal_TssF
11	0.17	41 / 1236	Mid_Frontal_Lobe_ReprPCWk
12	0.18	61 / 1907	Fetal_TxTrans
13	0.19	50 / 1548	Mid_Frontal_Lobe_K9K27me3
14	0.20	29 / 862	Overlap_fetal_midbrain_TxTrans
15	0.29	6 / 158	Overlap_fetal_midbrain_Het
16	0.31	22 / 686	Overlap_fetal_midbrain_TssA
17	0.35	21 / 668	Mid_Frontal_Lobe_Enh
18	0.37	32 / 1050	Fetal_EnhP
19	0.40	32 / 1065	Overlap_fetal_midbrain_Enh
20	0.41	12 / 383	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	9 / 12	BEN−PORATH_DN
2	3e−05	5 / 14	LIU_PROSTATE_CANCER_DN
3	4e−04	4 / 13	BEN−PORATH_UP
4	2e−02	8 / 113	PanCan_Driver_Gene_geneset_nanostring
5	4e−02	4 / 44	PanCan_TGF−B_geneset_nanostring
6	4e−02	2 / 12	LIU_PROSTATE_CANCER_UP
7	7e−02	2 / 15	GENTLES_modul4
8	9e−02	2 / 18	PanCan_Notch_geneset_nanostring
9	2e−01	3 / 55	PanCan_JAK−ST_geneset_nanostring
10	3e−01	1 / 13	GENTLES_modul12
11	3e−01	1 / 14	LIU_COMMON_CANCER_GENES
12	4e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	4e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	4e−01	1 / 16	GENTLES_modul16
15	5e−01	1 / 22	PanCan_HH_geneset_nanostring
16	6e−01	5 / 180	SPANG_LPS−index2
17	7e−01	3 / 120	PanCan_CC+Apop_geneset_nanostring
18	7e−01	3 / 121	PanCan_MAPK_geneset_nanostring
19	7e−01	7 / 298	SPANG_BCL6−index2
20	8e−01	1 / 48	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	3e−06	17 / 159	extracellular matrix
2	5e−06	21 / 239	proteinaceous extracellular matrix
3	2e−04	10 / 87	recycling endosome
4	1e−03	10 / 109	peroxisome
5	1e−02	4 / 30	sarcomere
6	2e−02	6 / 75	blood microparticle
7	2e−02	4 / 39	autophagic vacuole
8	4e−02	2 / 11	Gemini of coiled bodies
9	4e−02	2 / 12	SMN complex
10	4e−02	3 / 28	myofibril
11	5e−02	4 / 48	stress fiber
12	5e−02	5 / 70	sarcolemma
13	5e−02	12 / 246	mitochondrial matrix
14	5e−02	2 / 13	axolemma
15	6e−02	2 / 14	clathrin−coated vesicle membrane
16	6e−02	2 / 14	integral component of peroxisomal membrane
17	6e−02	4 / 52	coated pit
18	7e−02	5 / 78	ubiquitin ligase complex
19	7e−02	2 / 16	Ada2/Gcn5/Ada3 transcription activator complex
20	8e−02	2 / 17	protein−DNA complex

Chr

Rank	p−value	#in/all	Geneset
1	0.008	26 / 552	Chr 10
2	0.079	36 / 993	Chr 2
3	0.114	24 / 649	Chr 16
4	0.131	50 / 1500	Chr 1
5	0.168	17 / 462	Chr 14
6	0.241	23 / 689	Chr 7
7	0.412	31 / 1037	Chr 19
8	0.439	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
9	0.459	12 / 398	Chr 20
10	0.603	6 / 221	Chr 18
11	0.616	9 / 335	Chr 22
12	0.619	7 / 262	Chr 13
13	0.674	15 / 576	Chr 9
14	0.675	12 / 465	Chr 15
15	0.695	18 / 696	Chr 5
16	0.722	14 / 558	Chr 4
17	0.760	21 / 840	Chr 17
18	0.780	19 / 775	Chr 12
19	0.864	12 / 551	Chr X
20	0.878	18 / 801	Chr 11

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.004	54 / 1317	EnhP_Colon
2	0.010	3 / 16	TCGA_Mutated−in−CRC_non−hypermutated
3	0.012	14 / 250	K9K27me3_Colon
4	0.033	4 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	0.038	4 / 45	Ang_CRC−CIMPH−vs−L_hyper
6	0.053	4 / 50	Ang_CRC_Hypermethylated
7	0.054	73 / 2142	ReprPC_Colon
8	0.065	38 / 1038	HetRpts_Colon
9	0.066	2 / 15	Juehling_HNPCC−mutated−in−4
10	0.074	2 / 16	Vilar_non−hypermutated−in−CRC
11	0.078	124 / 3897	Quies1_Colon
12	0.091	2 / 18	Ang_CRC−CIMPH−vs−L_hypo
13	0.098	63 / 1889	ReprPCWk_Colon
14	0.099	8 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	0.102	71 / 2159	TssP_Colon
16	0.115	9 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
17	0.124	13 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
18	0.138	21 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
19	0.158	2 / 25	Ang_CRC_Hypomethylated
20	0.170	6 / 131	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.01	16 / 294	GUDJ_psoriasis down
2	0.04	2 / 11	BCHETNIA_EBM up
3	0.11	2 / 20	BCHETNIA_EBM−DM up
4	0.93	8 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	0.1	15 / 365	Down_b
2	0.1	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.1	3 / 40	in vivo astrocytes vs. cultured astroglia
4	0.1	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
5	0.1	2 / 22	KIM prognostic signature LTS vs. STS
6	0.1	3 / 45	Christensen_hypermethylated_in_primary_glioblastoma
7	0.1	5 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
8	0.2	5 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	0.2	4 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
10	0.2	1 / 7	KIM amplified & overexpressed in LTS
11	0.2	1 / 7	Phillips MES up vs Prolif & PN
12	0.2	3 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
13	0.2	1 / 9	VERHAAK_Brain
14	0.3	3 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	0.3	1 / 11	astrocytes_glio
16	0.3	5 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
17	0.3	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
18	0.3	2 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
19	0.3	3 / 72	laffaire_hypermeth_LGG_vs_control
20	0.3	3 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−14	15 / 37	KEGG_ABC_TRANSPORTERS
2	7e−11	11 / 27	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
3	2e−07	18 / 149	NABA_ECM_REGULATORS
4	3e−07	12 / 67	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
5	4e−07	6 / 12	PID_LPA4_PATHWAY
6	4e−07	6 / 12	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
7	6e−07	13 / 83	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION
8	7e−07	6 / 13	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS
9	2e−06	5 / 9	REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY
10	2e−05	9 / 54	PID_ENDOTHELIN_PATHWAY
11	2e−05	12 / 99	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
12	3e−05	5 / 14	LIU_PROSTATE_CANCER_DN
13	4e−05	5 / 15	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
14	5e−05	22 / 300	REACTOME_GPCR_DOWNSTREAM_SIGNALING
15	6e−05	11 / 93	REACTOME_SIGNALING_BY_FGFR
16	7e−05	7 / 37	REACTOME_PLC_BETA_MEDIATED_EVENTS
17	7e−05	7 / 37	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS
18	9e−05	6 / 27	REACTOME_DAG_AND_IP3_SIGNALING
19	1e−04	6 / 28	KEGG_BUTANOATE_METABOLISM
20	2e−04	12 / 120	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMB

HM

Rank	p−value	#in/all	Geneset
1	1e−05	12 / 91	HALLMARK_BILE_ACID_METABOLISM
2	5e−02	6 / 94	HALLMARK_ANDROGEN_RESPONSE
3	9e−02	4 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	1e−01	7 / 148	HALLMARK_KRAS_SIGNALING_UP
5	1e−01	5 / 95	HALLMARK_SPERMATOGENESIS
6	2e−01	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	2e−01	8 / 188	HALLMARK_ADIPOGENESIS
8	2e−01	6 / 137	HALLMARK_UV_RESPONSE_DN
9	2e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
10	2e−01	6 / 140	HALLMARK_INFLAMMATORY_RESPONSE
11	2e−01	2 / 31	HALLMARK_HEDGEHOG_SIGNALING
12	2e−01	7 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	3e−01	4 / 91	HALLMARK_PROTEIN_SECRETION
14	3e−01	5 / 127	HALLMARK_KRAS_SIGNALING_DN
15	3e−01	6 / 167	HALLMARK_APICAL_JUNCTION
16	3e−01	6 / 169	HALLMARK_XENOBIOTIC_METABOLISM
17	4e−01	5 / 141	HALLMARK_FATTY_ACID_METABOLISM
18	4e−01	6 / 176	HALLMARK_HYPOXIA
19	4e−01	6 / 181	HALLMARK_P53_PATHWAY
20	5e−01	4 / 126	HALLMARK_ALLOGRAFT_REJECTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.10	4 / 62	DUMEAUX_Smoking enriched genes
3	0.23	2 / 32	DUMEAUX_Fasting 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	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−04	125 / 3396	HOPP_Repressed
2	3e−02	77 / 2211	HOPP_Repetitive
3	4e−02	87 / 2563	HOPP_Heterochrom
4	5e−02	3 / 29	Subero_DLBCL_hypo_meth
5	5e−02	12 / 247	ZHANG_DLBCL_mutated
6	5e−02	3 / 30	Subero_INT_hypo_meth
7	6e−02	2 / 14	Subero_mBL_hypo_meth
8	1e−01	5 / 96	Subero_DLBCL_hyper_meth
9	1e−01	3 / 47	Subero_FL_hyper_meth
10	2e−01	1 / 6	DAVE_MHCCII BL DN
11	2e−01	37 / 1128	SPANG_BCR DN
12	3e−01	1 / 13	BENTINK_mBL UP
13	3e−01	1 / 14	Subero_MCL_hyper_meth
14	3e−01	2 / 42	CARO_OxPhos_in_DLBCL_UP
15	3e−01	2 / 43	LENZ_Stromal signature 2
16	4e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
17	4e−01	7 / 212	LENZ_Stromal signature 1
18	4e−01	3 / 81	Subero_INT_hyper_meth
19	5e−01	63 / 2188	HOPP_Poised_promoter
20	5e−01	2 / 60	Subero_T−ALL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	3e−12	14 / 41	ATPase activity, coupled to transmembrane movement of substances
2	2e−11	18 / 85	metalloendopeptidase activity
3	1e−07	6 / 10	adenylate cyclase activity
4	4e−07	6 / 12	phosphorus−oxygen lyase activity
5	7e−07	6 / 13	transmembrane receptor protein serine/threonine kinase activity
6	1e−06	6 / 14	aldehyde dehydrogenase (NAD) activity
7	3e−06	6 / 16	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD o
8	7e−06	5 / 11	aldo−keto reductase (NADP) activity
9	8e−06	11 / 75	metallopeptidase activity
10	3e−05	5 / 14	transforming growth factor beta−activated receptor activity
11	4e−05	62 / 1309	ATP binding
12	5e−05	52 / 1040	zinc ion binding
13	1e−04	4 / 10	cholesterol transporter activity
14	2e−04	177 / 4992	ion binding
15	4e−04	4 / 13	long−chain fatty acid−CoA ligase activity
16	4e−04	6 / 35	receptor signaling protein serine/threonine kinase activity
17	2e−03	3 / 10	transaminase activity
18	3e−03	23 / 433	peptidase activity
19	4e−03	3 / 12	activin binding
20	4e−03	21 / 394	catalytic activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	6 / 54	hsa−miR−513a−5p
2	0.007	3 / 14	hsa−miR−891a
3	0.010	5 / 47	hsa−miR−623
4	0.011	4 / 31	hsa−miR−617
5	0.012	5 / 49	hsa−miR−1224−3p
6	0.013	10 / 154	hsa−miR−527
7	0.023	7 / 99	hsa−miR−376a
8	0.023	6 / 78	hsa−miR−890
9	0.024	9 / 146	hsa−miR−655
10	0.025	2 / 9	hsa−miR−373*
11	0.026	3 / 23	hsa−miR−517a
12	0.027	7 / 103	hsa−miR−1284
13	0.028	4 / 41	hsa−miR−532−3p
14	0.030	3 / 24	hsa−miR−483−3p
15	0.031	4 / 42	hsa−miR−483−5p
16	0.033	3 / 25	hsa−miR−517c
17	0.033	5 / 63	hsa−miR−659
18	0.034	10 / 181	hsa−miR−1
19	0.037	14 / 289	hsa−miR−186
20	0.038	4 / 45	hsa−miR−660

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	GUSTAFSON_PI3K_DN
2	0.3	1 / 14	BENTINK_e2f3.1
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
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	7e−04	4 / 15	NOWICK_TF
2	3e−01	36 / 1139	HEBENSTREIT_low expression TF
3	5e−01	17 / 595	ICGC_NrsfPcr2_targets
4	6e−01	79 / 2836	ICGC_BatfPcr1_targets
5	6e−01	15 / 553	ICGC_RxraPcr1_targets
6	7e−01	73 / 2714	ICGC_Irf4_targets
7	7e−01	33 / 1273	ICGC_P300_targets
8	8e−01	52 / 2013	ICGC_Bcl11_targets
9	9e−01	14 / 653	ICGC_SrfPcr2_targets
10	9e−01	102 / 3966	ICGC_Pu1_targets
11	9e−01	57 / 2391	ICGC_Pbx3_targets
12	1e+00	43 / 1878	ICGC_Cebpbsc150_targets
13	1e+00	57 / 2416	ICGC_Bcl3_targets
14	1e+00	70 / 2927	ICGC_Rad21_targets
15	1e+00	27 / 1266	ICGC_NrsfPcr1_targets
16	1e+00	116 / 4682	ICGC_Pol24_targets
17	1e+00	36 / 1701	HEBENSTREIT_high expression TF
18	1e+00	40 / 1872	ICGC_Mef2_targets
19	1e+00	127 / 5219	ICGC_Tcf3_targets
20	1e+00	131 / 5374	ICGC_Pax5_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	VAQUERIZAS_Kidney
2	0.3	1 / 12	VAQUERIZAS_Skin
3	0.4	1 / 16	VAQUERIZAS_Pancreas
4	0.5	2 / 59	VAQUERIZAS_Whole blood
5	0.5	1 / 26	VAQUERIZAS_Liver
6	0.5	1 / 27	VAQUERIZAS_Lymph node
7	0.6	1 / 33	VAQUERIZAS_Prostate
8	0.6	1 / 36	VAQUERIZAS_Fetal brain
9	0.7	1 / 38	VAQUERIZAS_Testis
10	0.7	1 / 45	VAQUERIZAS_Uterus
11	0.8	1 / 58	VAQUERIZAS_Lung
12	1.0	1 / 143	VAQUERIZAS_General
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

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	4 / 41	WIRTH_Homeostasis
2	0.04	4 / 46	WIRTH_Liver
3	0.08	6 / 107	WIRTH_Testis
4	0.16	4 / 74	WIRTH_Mucosa
5	0.23	1 / 9	PALMER_CD8+ T−Cell signature up
6	0.23	2 / 32	WIRTH_Placenta
7	0.25	1 / 10	WIRTH_Hippocampus
8	0.28	4 / 95	WIRTH_Muscle
9	0.29	1 / 12	WIRTH_Cerebellum
10	0.31	1 / 13	WIRTH_Thyroid gland
11	0.37	1 / 16	PALMER_Lymphocytes signature up
12	0.41	11 / 350	WIRTH_Immune system
13	0.54	10 / 350	WIRTH_Nervous System
14	0.62	6 / 225	PALMER_Granulocytes signature up
15	0.63	3 / 114	PALMER_T−Cell signature up
16	0.65	5 / 194	PALMER_B−Cell signature up
17	1.00	0 / 32	WIRTH_Pancreas
18	1.00	0 / 11	WIRTH_Sec. lymphoid organs
19	1.00	0 / 11	WIRTH_Prim. lymphoid organs
20	1.00	0 / 13	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	29 / 1115	LU_BPDE 1h DN
2	0.8	98 / 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	

Correlation Clusters

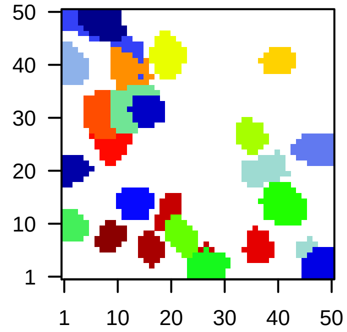
Spot Summary: P

metagenes = 29
genes = 310

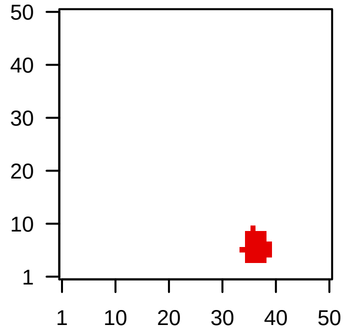
<r> metagenes = 0.93
<r> genes = 0.25
beta: r2= 0.87 / log p= −Inf

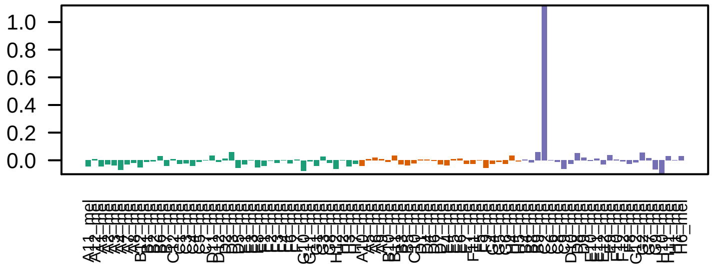
samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

Overview Map



Spot





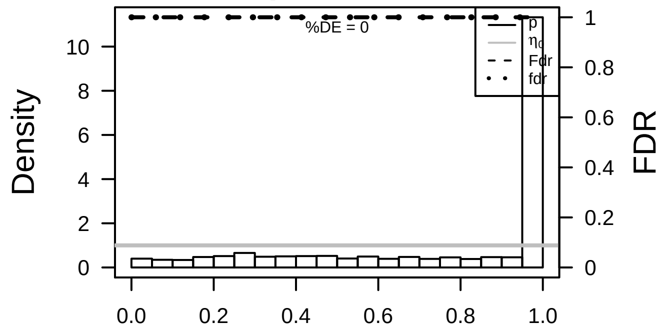
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	FAP	2.68	−0.06	0.83	FAP	fibroblast activation protein, alpha [Source:HGNC Symbol;Ac
2	CLU	2.35	−0.13	0.5	CLU	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
3	CPNE7	2.15	−0.03	0.94	CPNE7	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
4	WDR90	2.04	−0.35	0.29	WDR90	WD repeat domain 90 [Source:HGNC Symbol;Acc:HGNC:26
5	HSF4	1.98	−0.15	0.42	HSF4	heat shock transcription factor 4 [Source:HGNC Symbol;Acc:
6	CLDN15	1.9	−0.12	0.65	CLDN15	claudin 15 [Source:HGNC Symbol;Acc:HGNC:2036]
7	SLC10A7	1.89	−0.17	0.4	SLC10A7	solute carrier family 10, member 7 [Source:HGNC Symbol;Ac
8	SNX16	1.89	−0.17	0.26	SNX16	sorting nexin 16 [Source:HGNC Symbol;Acc:HGNC:14980]
9	STAMBPL1	1.85	−0.35	0.41	STAMBPL1	STAM binding protein−like 1 [Source:HGNC Symbol;Acc:HGN
10	BBS1	1.84	−0.26	0.32	BBS1	Bardet−Biedl syndrome 1 [Source:HGNC Symbol;Acc:HGNC
11	FHL3	1.83	−0.11	0.6	FHL3	four and a half LIM domains 3 [Source:HGNC Symbol;Acc:HG
12	PPP1R12B	1.81	−0.43	0.28	PPP1R12B	protein phosphatase 1, regulatory subunit 12B [Source:HGN
13	ARL6	1.79	−0.24	0.4	ARL6	ADP−ribosylation factor−like 6 [Source:HGNC Symbol;Acc:HG
14	C15orf65	1.79	−0.07	0.65	C15orf65	chromosome 15 open reading frame 65 [Source:HGNC Symb
15	GPRC5A	1.78	−0.07	0.48	GPRC5A	G protein−coupled receptor, class C, group 5, member A [Sou
16	MRAS	1.78	−0.21	0.43	MRAS	muscle RAS oncogene homolog [Source:HGNC Symbol;Acc:
17	TMEM140	1.78	−0.21	0.44	TMEM140	transmembrane protein 140 [Source:HGNC Symbol;Acc:HGN
18	FAM149A	1.78	−0.07	0.59	FAM149A	family with sequence similarity 149, member A [Source:HGN
19	ZNF350	1.76	−0.62	0.27	ZNF350	zinc finger protein 350 [Source:HGNC Symbol;Acc:HGNC:16
20	TEP1	1.75	−0.14	0.46	TEP1	telomerase−associated protein 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	31 / 668	Brain	Mid_Frontal_Lobe_Enh
2	8e−05	6 / 36	GSE	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LY
3	9e−05	13 / 180	GSE	GAL_LEUKEMIC_STEM_CELL_DN
4	4e−04	45 / 1317	Colon	EnhP_Colon
5	5e−04	85 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
6	5e−04	17 / 332	GSE	PEDRIOLI_MIR31_TARGETS_DN
7	5e−04	5 / 33	GSE	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
8	9e−04	3 / 10	BP	activation of transmembrane receptor protein tyrosine kinase activity
9	9e−04	4 / 22	GSE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE
10	2e−03	4 / 25	GSE	VALK_AML_CLUSTER_5
11	2e−03	4 / 28	GSE	CUI_TCF21_TARGETS_UP
12	3e−03	5 / 49	GSE	DELASERNA_MYOD_TARGETS_DN
13	3e−03	3 / 15	GSE	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROT
14	4e−03	6 / 73	Glio	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
15	4e−03	3 / 16	BP	regulation of neuronal synaptic plasticity
16	4e−03	5 / 53	BP	regulation of immune response
17	5e−03	3 / 17	GSE	REACTOME_BOTULINUM_NEUROTOXICITY
18	5e−03	3 / 17	GSE	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1B
19	5e−03	6 / 77	GSE	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP
20	5e−03	5 / 55	GSE	GEORGANTAS_HSC_MARKERS
21	6e−03	3 / 18	Glio	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
22	6e−03	3 / 18	GSE	BIOCARTA_RAC1_PATHWAY
23	6e−03	5 / 56	GSE	FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN
24	6e−03	36 / 1139	TF	HEBENSTREIT_low expression TF
25	6e−03	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
26	6e−03	3 / 19	GSE	PLASARI_NFIC_TARGETS_BASAL_UP
27	7e−03	61 / 2188	Lymp	HOPP_Poised_promoter
28	7e−03	8 / 136	GSE	DARWICHE_PAPILLOMA_RISK_LOW_DN
29	7e−03	4 / 38	BP	cellular response to amino acid stimulus
30	7e−03	3 / 20	BP	negative regulation of T cell proliferation
31	8e−03	8 / 138	GSE	DURAND_STROMA_NS_UP
32	8e−03	17 / 430	MF	lipid binding
33	8e−03	2 / 7	GSE	OXFORD_RALB_TARGETS_UP
34	8e−03	2 / 7	GSE	MIKKELSEN_DEDIFFERENTIATED_STATE_DN
35	9e−03	3 / 21	GSE	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
36	9e−03	3 / 21	GSE	GENTLES_LEUKEMIC_STEM_CELL_UP
37	9e−03	5 / 63	GSE	HECKER_IFNB1_TARGETS
38	1e−02	60 / 2185	Brain	Fetal_TssA
39	1e−02	13 / 304	GSE	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
40	1e−02	4 / 42	GSE	REACTOME_HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.08	5 / 111	HORVATH_aging_genes meth UP
2	0.87	1 / 100	HORVATH_aging_genes meth DOWN
3	1.00	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 10	activation of transmembrane receptor protein tyrosine kinase activity
2	4e−03	3 / 16	regulation of neuronal synaptic plasticity
3	4e−03	5 / 53	regulation of immune response
4	7e−03	4 / 38	cellular response to amino acid stimulus
5	7e−03	3 / 20	negative regulation of T cell proliferation
6	2e−02	3 / 26	cellular response to organic substance
7	2e−02	2 / 10	cellular response to electrical stimulus
8	2e−02	2 / 10	positive regulation of interleukin−4 production
9	2e−02	2 / 10	regulation of cell size
10	2e−02	2 / 10	response to lipid
11	2e−02	2 / 11	cellular response to gonadotropin stimulus
12	2e−02	4 / 52	fat cell differentiation
13	2e−02	7 / 137	cell surface receptor signaling pathway
14	2e−02	2 / 12	negative regulation of interleukin−6 production
15	2e−02	2 / 12	positive regulation of protein export from nucleus
16	2e−02	2 / 12	protein localization to cilium
17	3e−02	3 / 31	cellular defense response
18	3e−02	4 / 56	intrinsic apoptotic signaling pathway
19	3e−02	2 / 13	actin filament−based movement
20	3e−02	2 / 13	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion

Brain

Rank	p−value	#in/all	Geneset
1	2e−05	31 / 668	Mid_Frontal_Lobe_Enh
2	5e−04	85 / 2972	Mid_Frontal_Lobe_ReprPC
3	1e−02	60 / 2185	Fetal_TssA
4	1e−02	28 / 862	Overlap_fetal_midbrain_TxTrans
5	1e−02	30 / 953	Fetal_Enh
6	2e−02	36 / 1236	Mid_Frontal_Lobe_ReprPCWk
7	3e−02	30 / 1013	Fetal_TssP
8	5e−02	28 / 989	Mid_Frontal_Lobe_Quies
9	5e−02	75 / 3081	Mid_Frontal_Lobe_ZNF
10	5e−02	23 / 786	Fetal_EnhG
11	1e−01	48 / 1949	Fetal_TssF
12	1e−01	39 / 1548	Mid_Frontal_Lobe_K9K27me3
13	1e−01	14 / 468	Mid_Frontal_Lobe_TssF
14	1e−01	31 / 1207	Overlap_fetal_midbrain_TssF
15	1e−01	15 / 534	Mid_Frontal_Lobe_EnhG
16	2e−01	57 / 2462	Mid_Frontal_Lobe_HetRpts
17	2e−01	22 / 884	Overlap_fetal_midbrain_EnhG
18	2e−01	15 / 574	Overlap_fetal_midbrain_TssP
19	2e−01	19 / 765	Mid_Frontal_Lobe_Het
20	3e−01	5 / 166	Mid_Frontal_Lobe_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	0 / 14	LIU_PROSTATE_CANCER_DN
2	0.098	1 / 5	WANG_ER_DN
3	0.201	11 / 401	Lembcke_Colonic Inflammation
4	0.204	1 / 11	GENTLES_modul17
5	0.236	1 / 13	GENTLES_modul12
6	0.265	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.267	1 / 15	RHODES_CANCER_META_SIGNATURE
8	0.268	8 / 298	SPANG_BCL6−index2
9	0.667	2 / 111	PanCan_RAS_geneset_nanostring
10	0.680	1 / 55	PanCan_JAK−ST_geneset_nanostring
11	0.713	2 / 121	PanCan_MAPK_geneset_nanostring
12	0.718	1 / 61	PanCan_Wnt_geneset_nanostring
13	0.751	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	0.766	1 / 70	SHAUGHNESSY_MM high risk
15	0.833	2 / 156	PanCan_PI3K_geneset_nanostring
16	0.904	1 / 113	PanCan_Driver_Gene_geneset_nanostring
17	0.917	1 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.938	6 / 489	Lembcke_Normal vs Adenoma
19	0.976	1 / 180	SPANG_LPS−index2
20	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	0.01	6 / 91	nuclear matrix
2	0.01	6 / 92	early endosome membrane
3	0.02	2 / 10	apical dendrite
4	0.02	2 / 10	neuron projection terminus
5	0.02	2 / 10	WASH complex
6	0.03	33 / 1132	Golgi apparatus
7	0.03	5 / 83	synaptic vesicle
8	0.04	3 / 37	lateral plasma membrane
9	0.04	2 / 16	vacuolar membrane
10	0.05	3 / 42	synaptic vesicle membrane
11	0.06	5 / 102	cytoplasmic vesicle membrane
12	0.06	3 / 45	SNARE complex
13	0.07	2 / 21	clathrin adaptor complex
14	0.07	7 / 177	synapse
15	0.07	2 / 22	presynaptic active zone
16	0.07	3 / 48	stress fiber
17	0.09	3 / 51	axoneme
18	0.09	3 / 51	voltage−gated potassium channel complex
19	0.09	2 / 25	PcG protein complex
20	0.11	2 / 28	SCF ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.03	30 / 1037	Chr 19
2	0.08	19 / 649	Chr 16
3	0.12	12 / 398	Chr 20
4	0.16	15 / 552	Chr 10
5	0.17	8 / 262	Chr 13
6	0.25	17 / 689	Chr 7
7	0.26	12 / 469	Chr 8
8	0.30	6 / 221	Chr 18
9	0.34	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
10	0.38	18 / 801	Chr 11
11	0.60	3 / 151	Chr 21
12	0.61	9 / 462	Chr 14
13	0.62	9 / 465	Chr 15
14	0.64	11 / 576	Chr 9
15	0.70	10 / 551	Chr X
16	0.79	27 / 1500	Chr 1
17	0.81	13 / 775	Chr 12
18	0.81	9 / 558	Chr 4
19	0.82	14 / 840	Chr 17
20	0.87	16 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	45 / 1317	EnhP_Colon
2	1e−02	59 / 2159	TssP_Colon
3	1e−02	58 / 2142	ReprPC_Colon
4	2e−02	11 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
5	3e−02	12 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
6	3e−02	23 / 739	TxEnhG2_Colon
7	4e−02	1 / 2	Budinska_A_Surface crypt−like_DOWN
8	5e−02	93 / 3897	Quies1_Colon
9	5e−02	30 / 1079	ZNF_Colon
10	6e−02	4 / 71	Marisa_CRC−cluster−g
11	6e−02	5 / 102	Marisa_CRC−cluster−d
12	7e−02	14 / 436	K9acLow_Colon
13	8e−02	36 / 1386	Het_Colon
14	8e−02	14 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
15	9e−02	9 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
16	1e−01	1 / 5	Budinska_A_Surface crypt−like_UP
17	1e−01	27 / 1038	HetRpts_Colon
18	1e−01	46 / 1889	ReprPCWk_Colon
19	2e−01	1 / 8	Marisa_CRC−C3
20	2e−01	12 / 427	Quies2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.3	8 / 294	GUDJ_psoriasis down
2	0.9	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	0.004	6 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
2	0.006	3 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
3	0.029	4 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
4	0.051	4 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
5	0.052	2 / 18	Barbus_GBM_STS_vs._LTS
6	0.063	12 / 356	Down_a
7	0.065	4 / 74	WIRTH_Normal Brain
8	0.071	3 / 47	Weller_LGG_gradeII−vs−III_UP
9	0.071	3 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
10	0.080	2 / 23	WIRTH_PN subtype
11	0.098	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
12	0.118	2 / 29	shaw_responders_down_in_oligo_glioma
13	0.139	2 / 32	Donson−innate immunity−associated with LTS in HGA
14	0.149	4 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
15	0.177	6 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
16	0.197	2 / 40	in vivo astrocytes vs. cultured astroglia
17	0.204	1 / 11	Mukasa_UP_in_Astroglioma
18	0.204	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
19	0.236	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
20	0.267	1 / 15	VERHAAK_CL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−05	6 / 36	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
2	9e−05	13 / 180	GAL_LEUKEMIC_STEM_CELL_DN
3	5e−04	17 / 332	PEDRIOLI_MIR31_TARGETS_DN
4	5e−04	5 / 33	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
5	9e−04	4 / 22	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE
6	2e−03	4 / 25	VALK_AML_CLUSTER_5
7	2e−03	4 / 28	CUI_TCF21_TARGETS_UP
8	3e−03	5 / 49	DELASERNA_MYOD_TARGETS_DN
9	3e−03	3 / 15	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEI
10	5e−03	3 / 17	REACTOME_BOTULINUM_NEUROTOXICITY
11	5e−03	3 / 17	SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1B
12	5e−03	6 / 77	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP
13	5e−03	5 / 55	GEORGANTAS_HSC_MARKERS
14	6e−03	3 / 18	BIOCARTA_RAC1_PATHWAY
15	6e−03	5 / 56	FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN
16	6e−03	0 / 14	LIU_PROSTATE_CANCER_DN
17	6e−03	3 / 19	PLASARI_NFIC_TARGETS_BASAL_UP
18	7e−03	8 / 136	DARWICHE_PAPILLOMA_RISK_LOW_DN
19	8e−03	8 / 138	DURAND_STROMA_NS_UP
20	8e−03	2 / 7	OXFORD_RALB_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.1	5 / 126	HALLMARK_ALLOGRAFT_REJECTION
2	0.2	5 / 162	HALLMARK_COMPLEMENT
3	0.3	5 / 165	HALLMARK_MYOGENESIS
4	0.3	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	0.3	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	0.3	3 / 93	HALLMARK_PEROXISOME
7	0.4	4 / 167	HALLMARK_APICAL_JUNCTION
8	0.4	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.5	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	0.5	3 / 127	HALLMARK_KRAS_SIGNALING_DN
11	0.5	4 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.5	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	0.6	2 / 91	HALLMARK_BILE_ACID_METABOLISM
14	0.6	3 / 148	HALLMARK_KRAS_SIGNALING_UP
15	0.6	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
16	0.6	2 / 107	HALLMARK_COAGULATION
17	0.7	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
18	0.7	3 / 183	HALLMARK_GLYCOLYSIS
19	0.8	2 / 140	HALLMARK_APOPTOSIS
20	0.8	2 / 146	HALLMARK_UV_RESPONSE_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	1 / 32	DUMEAUX_Fasting enriched genes
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.007	61 / 2188	HOPP_Poised_promoter
2	0.011	87 / 3396	HOPP_Repressed
3	0.113	9 / 275	TARTE_Mature plasma cell signature
4	0.146	7 / 212	LENZ_Stromal signature 1
5	0.146	2 / 33	LEE_Developmental_regulators
6	0.190	2 / 39	ROSOLOWSKI_blue DOWN
7	0.217	8 / 280	SPANG_CD40 6hrs UP
8	0.243	50 / 2211	HOPP_Repetitive
9	0.250	2 / 47	Subero_FL_hyper_meth
10	0.272	7 / 256	SPANG_IL21 DN
11	0.272	4 / 129	DAVE_BL−vs−DLBCL
12	0.273	2 / 50	SPANG_BAFF 9hrs DN
13	0.297	1 / 17	Aukema_BCL2 UP_BCL6 DN
14	0.376	3 / 107	SPANG_LPS 6hrs UP
15	0.393	2 / 66	TARTE_Plasma cell signature
16	0.404	1 / 25	Subero_T−PLL_hypo_meth
17	0.463	1 / 30	TARTE_B−cell signature
18	0.471	6 / 268	SPANG_IL21 UP
19	0.497	2 / 81	Subero_INT_hyper_meth
20	0.529	2 / 86	ROSOLOWSKI_red total

MF

Rank	p−value	#in/all	Geneset
1	0.008	17 / 430	lipid binding
2	0.037	2 / 15	L−ascorbic acid binding
3	0.037	2 / 15	phosphatidylinositol−4−phosphate binding
4	0.037	3 / 36	SNAP receptor activity
5	0.040	3 / 37	sulfotransferase activity
6	0.042	2 / 16	ATP−dependent microtubule motor activity, plus−end−directed
7	0.044	4 / 65	protease binding
8	0.045	3 / 39	SNARE binding
9	0.055	4 / 70	phospholipid binding
10	0.072	6 / 142	calmodulin binding
11	0.087	23 / 830	nucleic acid binding transcription factor activity
12	0.097	4 / 85	transmembrane signaling receptor activity
13	0.099	46 / 1859	metal ion binding
14	0.102	6 / 156	protein C−terminus binding
15	0.105	2 / 27	voltage−gated calcium channel activity
16	0.107	3 / 56	phosphoprotein phosphatase activity
17	0.110	277 / 13179	molecular_function
18	0.139	2 / 32	Rac GTPase binding
19	0.146	2 / 33	receptor tyrosine kinase binding
20	0.153	2 / 34	scavenger receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 29	hsa−miR−1225−3p
2	0.03	2 / 14	hsa−miR−452*
3	0.04	5 / 89	hsa−miR−608
4	0.04	4 / 64	hsa−miR−371−5p
5	0.05	3 / 41	hsa−miR−601
6	0.06	2 / 19	hsa−miR−542−5p
7	0.07	3 / 46	hsa−miR−1322
8	0.09	2 / 25	hsa−miR−432*
9	0.10	3 / 54	hsa−miR−940
10	0.11	2 / 27	hsa−miR−521
11	0.11	5 / 124	hsa−miR−493
12	0.13	1 / 7	hsa−miR−339−3p
13	0.14	2 / 32	hsa−miR−631
14	0.14	5 / 134	hsa−miR−488
15	0.15	1 / 8	hsa−miR−566
16	0.15	3 / 66	hsa−miR−648
17	0.16	4 / 104	hsa−miR−210
18	0.17	2 / 36	hsa−miR−127−3p
19	0.17	5 / 144	hsa−miR−548f
20	0.18	4 / 107	hsa−miR−146b−5p

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	0.006	36 / 1139	HEBENSTREIT_low expression TF
2	0.084	70 / 2927	ICGC_Rad21_targets
3	0.117	19 / 690	ICGC_Atf3_targets
4	0.136	57 / 2416	ICGC_Bcl3_targets
5	0.186	17 / 653	ICGC_SrfPcr2_targets
6	0.270	112 / 5200	ICGC_Mta3_targets
7	0.292	30 / 1314	ICGC_Usf1_targets
8	0.300	29 / 1273	ICGC_P300_targets
9	0.306	80 / 3700	ICGC_Nfatc1_targets
10	0.382	113 / 5374	ICGC_Pax5_targets
11	0.420	109 / 5219	ICGC_Tcf3_targets
12	0.436	82 / 3924	ICGC_Zeb1_targets
13	0.446	13 / 595	ICGC_NrsfPcr2_targets
14	0.452	114 / 5495	ICGC_Yy1_targets
15	0.458	111 / 5355	ICGC_Pol2_targets
16	0.469	59 / 2836	ICGC_BatfPcr1_targets
17	0.518	100 / 4879	ICGC_Pmlsc71910_targets
18	0.534	81 / 3966	ICGC_Pu1_targets
19	0.539	88 / 4314	ICGC_Ebfsc137065_targets
20	0.541	41 / 2013	ICGC_Bcl11_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	3 / 38	VAQUERIZAS_Whole brain
2	0.05	3 / 41	VAQUERIZAS_Placenta
3	0.17	5 / 143	VAQUERIZAS_General
4	0.20	2 / 40	VAQUERIZAS_Thyroid
5	0.24	2 / 45	VAQUERIZAS_Uterus
6	0.28	1 / 16	VAQUERIZAS_Adrenal gland
7	0.30	1 / 17	VAQUERIZAS_Pituitary
8	0.38	1 / 23	VAQUERIZAS_Adrenal cortex
9	0.45	1 / 29	VAQUERIZAS_Fetal lung
10	0.50	1 / 33	VAQUERIZAS_Prostate
11	0.53	1 / 36	VAQUERIZAS_Fetal brain
12	0.70	1 / 58	VAQUERIZAS_Lung
13	1.00	0 / 26	VAQUERIZAS_Liver
14	1.00	0 / 29	VAQUERIZAS_Smooth muscle
15	1.00	0 / 9	VAQUERIZAS_Kidney
16	1.00	0 / 23	VAQUERIZAS_Spinal cord
17	1.00	0 / 37	VAQUERIZAS_Thymus
18	1.00	0 / 59	VAQUERIZAS_Whole blood
19	1.00	0 / 7	VAQUERIZAS_Appendix
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	4 / 107	WIRTH_Testis
2	0.2	1 / 10	WIRTH_Thalamus
3	0.3	9 / 350	WIRTH_Nervous System
4	0.3	3 / 95	WIRTH_Muscle
5	0.4	3 / 114	PALMER_T−Cell signature up
6	0.5	1 / 32	WIRTH_Pancreas
7	0.5	1 / 32	WIRTH_Placenta
8	0.8	3 / 194	PALMER_B−Cell signature up
9	0.8	1 / 74	WIRTH_Mucosa
10	0.8	5 / 350	WIRTH_Immune system
11	1.0	1 / 225	PALMER_Granulocytes signature up
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	0.2	82 / 3682	LU_BPDE 0.005 DN
2	0.4	24 / 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	

Correlation Clusters

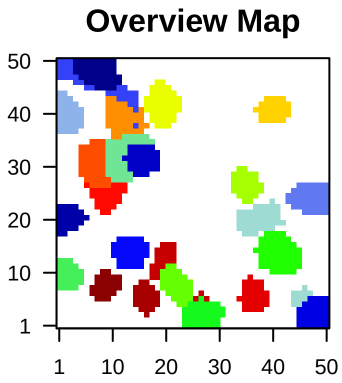
Spot Summary: Q

metagenes = 51
genes = 67

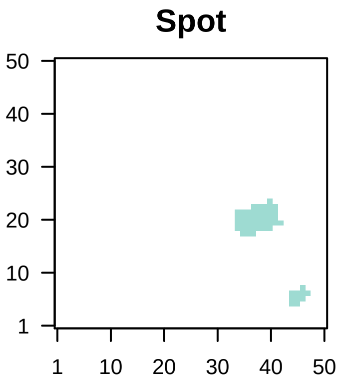
<r> metagenes = 0.91
<r> genes = 0.16
beta: r2= 1.62 / log p= −Inf

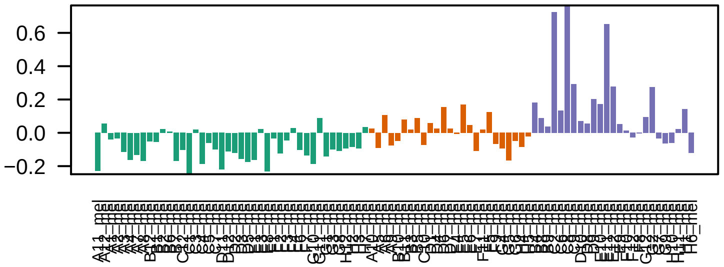
samples with spot = 10 (10.9 %)
MSC2 : 1 (4 %)
MSC3 : 9 (36 %)

Overview Map



Spot





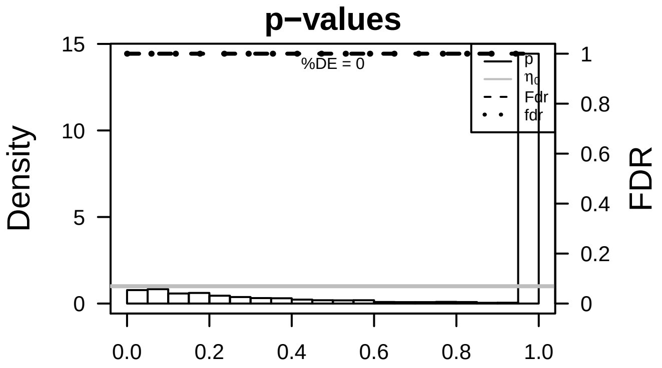
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ZNF383	1.77	−0.16	0.55	ZNF383	zinc finger protein 383 [Source:HGNC Symbol;Acc:HGNC:18
2	FAM65B	1.73	−0.09	0.75	FAM65B	family with sequence similarity 65, member B [Source:HGNC
3	HSPG2	1.69	−0.27	0.33	HSPG2	heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:H
4	EXOC6B	1.66	−0.54	0.38	EXOC6B	exocyst complex component 6B [Source:HGNC Symbol;Acc:
5	FNBP1L	1.58	−0.56	0.33	FNBP1L	formin binding protein 1−like [Source:HGNC Symbol;Acc:HG
6	DUSP10	1.52	−0.84	0.4	DUSP10	dual specificity phosphatase 10 [Source:HGNC Symbol;Acc:
7	PIAS3	1.51	−0.37	0.3	PIAS3	protein inhibitor of activated STAT, 3 [Source:HGNC Symbol;
8	EHD2	1.48	−0.17	0.56	EHD2	EH−domain containing 2 [Source:HGNC Symbol;Acc:HGNC:
9	RUNX1	1.45	−0.83	0.41	RUNX1	runt−related transcription factor 1 [Source:HGNC Symbol;Acc
10	HEG1	1.41	−0.34	0.44	HEG1	heart development protein with EGF−like domains 1 [Source:
11	RASA1	1.41	−0.47	0.32	RASA1	RAS p21 protein activator (GTPase activating protein) 1 [Sou
12	FAT4	1.4	−0.06	0.76	FAT4	FAT atypical cadherin 4 [Source:HGNC Symbol;Acc:HGNC:2
13	BDNF	1.4	−0.09	0.74	BDNF	brain−derived neurotrophic factor [Source:HGNC Symbol;Acc
14	HIST2H2AA4	1.39	−0.5	0.47	HIST2H2AA4	histone cluster 2, H2aa4 [Source:HGNC Symbol;Acc:HGNC:
15	RTN2	1.37	−0.21	0.42	RTN2	reticulon 2 [Source:HGNC Symbol;Acc:HGNC:10468]
16	INTS6	1.35	−0.71	0.24	INTS6	integrator complex subunit 6 [Source:HGNC Symbol;Acc:HG
17	MED13L	1.31	−0.91	0.27	MED13L	mediator complex subunit 13−like [Source:HGNC Symbol;Acc
18	BAZ2A	1.3	−0.95	0.24	BAZ2A	bromodomain adjacent to zinc finger domain, 2A [Source:HG
19	RAD50	1.29	−1.07	0.31	RAD50	RAD50 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:
20	MYH9	1.29	−1.04	0.45	MYH9	myosin, heavy chain 9, non−muscle [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	58 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	5e−05	10 / 473	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
3	9e−05	6 / 164	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
4	1e−04	3 / 21	BP	glutamate secretion
5	3e−04	6 / 200	GSEA	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
6	4e−04	6 / 217	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
7	5e−04	3 / 35	GSEA	CHUNG_BLISTER_CYTOTOXICITY_DN
8	6e−04	5 / 149	GSEA	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
9	9e−04	6 / 247	Lymph	ZHANG_DLBCL mutated
10	9e−04	4 / 95	miRN	hsa−miR−125a−3p
11	1e−03	2 / 11	BP	antibacterial humoral response
12	1e−03	4 / 102	MF	actin filament binding
13	1e−03	4 / 102	miRN	hsa−miR−410
14	1e−03	9 / 590	BP	cell morphogenesis
15	1e−03	2 / 12	BP	innate immune response in mucosa
16	1e−03	1 / 15	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1e−03	3 / 50	GSEA	ZHU_CMV_8_HR_DN
18	2e−03	2 / 13	BP	actin filament−based movement
19	2e−03	2 / 15	BP	embryonic hemopoiesis
20	2e−03	6 / 294	miRN	hsa−miR−561
21	2e−03	4 / 122	BP	plasma membrane organization
22	3e−03	3 / 61	GSEA	BEIER_GLIOMA_STEM_CELL_DN
23	3e−03	4 / 128	BP	endocytosis
24	3e−03	6 / 309	GSEA	YAGI_AML_WITH_11Q23_REARRANGED
25	3e−03	3 / 64	GSEA	REACTOME_AMYLOIDS
26	3e−03	7 / 435	GSEA	GARY_CD5_TARGETS_UP
27	4e−03	2 / 20	MF	activating transcription factor binding
28	4e−03	13 / 1266	TF	ICGC_NrsfPcr1_targets
29	4e−03	6 / 335	GSEA	YAGI_AML_WITH_INV_16_TRANSLOCATION
30	4e−03	10 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
31	4e−03	3 / 71	miRN	hsa−miR−331−3p
32	4e−03	3 / 72	GSEA	PID_SMAD2_3NUCLEAR_PATHWAY
33	4e−03	3 / 72	GSEA	REACTOME_MEIOTIC_RECOMBINATION
34	4e−03	2 / 22	MF	RNA polymerase II transcription coactivator activity
35	4e−03	7 / 456	miRN	hsa−miR−130a
36	4e−03	4 / 148	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
37	5e−03	2 / 23	GSEA	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_
38	5e−03	2 / 23	GSEA	VALK_AML_CLUSTER_8
39	5e−03	7 / 471	GSEA	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
40	5e−03	22 / 2836	TF	ICGC_BatfPcr1_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	3 / 111	HORVATH_aging_genes meth UP
2	0.36	1 / 100	HORVATH_aging_genes meth DOWN
3	1.00	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 21	glutamate secretion
2	1e−03	2 / 11	antibacterial humoral response
3	1e−03	9 / 590	cell morphogenesis
4	1e−03	2 / 12	innate immune response in mucosa
5	2e−03	2 / 13	actin filament−based movement
6	2e−03	2 / 15	embryonic hemopoiesis
7	2e−03	4 / 122	plasma membrane organization
8	3e−03	4 / 128	endocytosis
9	6e−03	2 / 25	embryonic organ development
10	6e−03	3 / 81	ephrin receptor signaling pathway
11	7e−03	10 / 897	vesicle−mediated transport
12	8e−03	18 / 2210	anatomical structure development
13	8e−03	2 / 30	dendrite development
14	9e−03	2 / 31	inner ear development
15	9e−03	2 / 32	regulation of synaptic plasticity
16	1e−02	2 / 33	defense response to Gram−positive bacterium
17	1e−02	2 / 35	branching involved in ureteric bud morphogenesis
18	1e−02	2 / 37	termination of G−protein coupled receptor signaling pathway
19	1e−02	2 / 38	actin cytoskeleton reorganization
20	1e−02	5 / 312	axon guidance

Brain

Rank	p−value	#in/all	Geneset
1	1e−05	58 / 9330	Overlap_fetal_midbrain_ReprPC
2	8e−03	37 / 5940	Overlap_fetal_midbrain_HetRpts
3	1e−02	50 / 9013	Overlap_fetal_midbrain_K9K27me3
4	5e−02	9 / 1050	Fetal_EnhP
5	5e−02	4 / 304	Fetal_Het
6	7e−02	4 / 349	Fetal_ZNF
7	8e−02	49 / 9528	Overlap_fetal_midbrain_Quies
8	1e−01	46 / 9020	Overlap_fetal_midbrain_ReprPCWk
9	3e−01	5 / 769	Overlap_fetal_midbrain_ZNF
10	3e−01	1 / 69	Overlap_fetal_midbrain_Tx
11	3e−01	5 / 786	Fetal_EnhG
12	3e−01	6 / 1013	Fetal_TssP
13	3e−01	5 / 831	Fetal_HetRpts
14	3e−01	4 / 656	Overlap_fetal_midbrain_EnhP
15	4e−01	5 / 953	Fetal_Enh
16	4e−01	3 / 534	Mid_Frontal_Lobe_EnhG
17	5e−01	9 / 1845	Fetal_Quies
18	5e−01	3 / 574	Overlap_fetal_midbrain_TssP
19	5e−01	2 / 383	Fetal_Tx
20	5e−01	5 / 1065	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.046	4 / 298	SPANG_BCL6−index2
3	0.049	1 / 11	GENTLES_modul17
4	0.052	0 / 12	LIU_PROSTATE_CANCER_UP
5	0.053	2 / 82	PanCan_TXmisReg_geneset_nanostring
6	0.057	1 / 13	GENTLES_modul12
7	0.078	1 / 18	PanCan_Notch_geneset_nanostring
8	0.087	1 / 20	PanCan_ChromMod_geneset_nanostring
9	0.092	2 / 113	PanCan_Driver_Gene_geneset_nanostring
10	0.104	2 / 121	PanCan_MAPK_geneset_nanostring
11	0.107	4 / 401	Lembcke_Colonic Inflammation
12	0.166	1 / 40	ZHANG_MM up
13	0.166	1 / 40	PanCan_HK_geneset_nanostring
14	0.181	1 / 44	PanCan_TGF−B_geneset_nanostring
15	0.192	1 / 47	PanCan_DNARepair_geneset_nanostring
16	0.195	2 / 180	SPANG_LPS−index2
17	0.195	1 / 48	KUIPER_MM poor survival
18	0.221	1 / 55	PanCan_JAK−ST_geneset_nanostring
19	0.242	1 / 61	PanCan_Wnt_geneset_nanostring
20	0.420	1 / 120	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.005	3 / 79	nucleosome
2	0.007	3 / 85	ruffle
3	0.010	2 / 33	Golgi stack
4	0.010	3 / 99	cell cortex
5	0.011	2 / 35	myosin complex
6	0.012	3 / 105	ribonucleoprotein complex
7	0.013	4 / 202	actin cytoskeleton
8	0.029	7 / 663	chromosome
9	0.038	3 / 164	endosome membrane
10	0.041	3 / 169	transcription factor complex
11	0.043	2 / 73	basement membrane
12	0.044	1 / 10	MHC class I protein complex
13	0.044	1 / 10	pronucleus
14	0.049	1 / 11	Arp2/3 protein complex
15	0.049	1 / 11	intrinsic component of the cytoplasmic side of the plasma membrane
16	0.052	2 / 81	apical part of cell
17	0.053	1 / 12	actomyosin
18	0.053	1 / 12	AMP−activated protein kinase complex
19	0.054	2 / 83	synaptic vesicle
20	0.057	1 / 13	filopodium membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.03	3 / 151	Chr 21
2	0.09	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
3	0.11	3 / 262	Chr 13
4	0.14	10 / 1500	Chr 1
5	0.20	5 / 687	Chr 6
6	0.29	6 / 993	Chr 2
7	0.29	5 / 801	Chr 11
8	0.33	6 / 1037	Chr 19
9	0.45	2 / 335	Chr 22
10	0.54	2 / 398	Chr 20
11	0.57	3 / 649	Chr 16
12	0.61	3 / 696	Chr 5
13	0.63	2 / 465	Chr 15
14	0.74	3 / 838	Chr 3
15	0.74	2 / 576	Chr 9
16	0.87	2 / 775	Chr 12
17	0.90	2 / 840	Chr 17
18	0.92	1 / 552	Chr 10
19	0.92	1 / 558	Chr 4
20	0.96	1 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	50 / 9027	Tx_Colon
2	0.02	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
3	0.02	35 / 5880	TssD2_Colon
4	0.03	47 / 8580	TxWk_Colon
5	0.03	4 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
6	0.04	4 / 281	Pentrack_CRC_TCGA_group.over_B_msi=h_UP
7	0.05	5 / 436	K9acLow_Colon
8	0.05	18 / 2698	EnhA_Colon
9	0.06	8 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	0.06	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	0.07	49 / 9482	TssA_Colon
12	0.08	1 / 18	Boland_CRC−MSI−A6−A10
13	0.09	23 / 3897	Quies1_Colon
14	0.11	38 / 7203	TssF_Colon
15	0.11	17 / 2798	TxEnhG1_Colon
16	0.12	6 / 739	TxEnhG2_Colon
17	0.12	22 / 3812	TssD1_Colon
18	0.12	2 / 131	Marisa_CRC−cluster−a
19	0.13	43 / 8415	Quies3_Colon
20	0.14	51 / 10290	TssWk_Colon

Disease

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

Glio

Rank	p−value	#in/all	Geneset
1	0.1	1 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
2	0.2	3 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.2	3 / 332	Up
4	0.2	1 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
5	0.2	2 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
6	0.2	1 / 63	Stuehler_Proteins_up_in_STS
7	0.3	1 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
8	0.3	1 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
9	0.3	1 / 75	GIEZELT_GBM_STS_down_VS_LTS
10	0.5	2 / 356	Down_a
11	0.7	3 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.8	1 / 365	Down_b
13	1.0	0 / 15	VERHAAK_CL subtype
14	1.0	0 / 15	VERHAAK_MES subtype
15	1.0	0 / 16	VERHAAK_NL subtype
16	1.0	0 / 14	VERHAAK_PN subtype
17	1.0	0 / 23	WIRTH_PN subtype
18	1.0	0 / 74	WIRTH_Normal Brain
19	1.0	0 / 9	VERHAAK_Brain
20	1.0	0 / 8	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−05	10 / 473	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
2	9e−05	6 / 164	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
3	3e−04	6 / 200	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
4	4e−04	6 / 217	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
5	5e−04	3 / 35	CHUNG_BLISTER_CYTOTOXICITY_DN
6	6e−04	5 / 149	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
7	1e−03	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	1e−03	3 / 50	ZHU_CMV_8_HR_DN
9	3e−03	3 / 61	BEIER_GLIOMA_STEM_CELL_DN
10	3e−03	6 / 309	YAGI_AML_WITH_11Q23_REARRANGED
11	3e−03	3 / 64	REACTOME_AMYLOIDS
12	3e−03	7 / 435	GARY_CD5_TARGETS_UP
13	4e−03	6 / 335	YAGI_AML_WITH_INV_16_TRANSLOCATION
14	4e−03	10 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	4e−03	3 / 72	PID_SMAD2_3NUCLEAR_PATHWAY
16	4e−03	3 / 72	REACTOME_MEIOTIC_RECOMBINATION
17	4e−03	4 / 148	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
18	5e−03	2 / 23	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_CO
19	5e−03	2 / 23	VALK_AML_CLUSTER_8
20	5e−03	7 / 471	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN

HM

Rank	p−value	#in/all	Geneset
1	0.009	2 / 31	HALLMARK_HEDGEHOG_SIGNALING
2	0.012	4 / 195	HALLMARK_MITOTIC_SPINDLE
3	0.024	3 / 137	HALLMARK_UV_RESPONSE_DN
4	0.039	3 / 165	HALLMARK_MYOGENESIS
5	0.150	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.174	2 / 167	HALLMARK_APICAL_JUNCTION
7	0.185	2 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	0.192	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.208	2 / 188	HALLMARK_ADIPOGENESIS
10	0.353	1 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.471	1 / 140	HALLMARK_APOPTOSIS
12	0.485	1 / 146	HALLMARK_UV_RESPONSE_UP
13	0.534	1 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.536	1 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	0.536	1 / 169	HALLMARK_XENOBIOTIC_METABOLISM
16	0.547	1 / 174	HALLMARK_HEME_METABOLISM
17	0.551	1 / 176	HALLMARK_HYPOXIA
18	0.561	1 / 181	HALLMARK_P53_PATHWAY
19	0.565	1 / 183	HALLMARK_GLYCOLYSIS
20	0.590	1 / 196	HALLMARK_G2M_CHECKPOINT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.009	2 / 32	DUMEAUX_Fasting enriched genes
2	0.078	1 / 18	DUMEAUX_High bmi enriched genes
3	1.000	0 / 62	DUMEAUX_Smoking enriched genes
4	1.000	0 / 10	DUMEAUX_Smoking literature genes up
5	1.000	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.000	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.000	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.000	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.000	0 / 7	DUMEAUX_Women normal BMI literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−04	6 / 247	ZHANG_DLBCL_mutated
2	3e−02	1 / 6	DAVE_MHCCII BL DN
3	5e−02	2 / 82	ROSOLOWSKI_green UP
4	7e−02	1 / 15	WRIGHT_ABC UP
5	7e−02	9 / 1128	SPANG_BCR DN
6	7e−02	3 / 212	LENZ_Stromal signature 1
7	8e−02	1 / 19	DAVE_c−myc BL UP
8	9e−02	2 / 109	ROSOLOWSKI_green total
9	1e−01	2 / 129	DAVE_BL−vs−DLBCL
10	1e−01	28 / 5184	HOPP_Txn_transition
11	2e−01	1 / 43	LENZ_Stromal signature 2
12	2e−01	13 / 2188	HOPP_Poised_promoter
13	3e−01	1 / 81	Subero_INT_hyper_meth
14	3e−01	2 / 256	SPANG_IL21 DN
15	4e−01	1 / 96	Subero_DLBCL_hyper_meth
16	4e−01	2 / 294	TARTE_Plasmablast signature
17	5e−01	32 / 6929	HOPP_Txn_elongation
18	5e−01	12 / 2563	HOPP_Heterochrom
19	7e−01	14 / 3396	HOPP_Repressed
20	7e−01	28 / 6564	HOPP_Strong_enhancer

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 102	actin filament binding
2	0.004	2 / 20	activating transcription factor binding
3	0.004	2 / 22	RNA polymerase II transcription coactivator activity
4	0.007	6 / 373	protein heterodimerization activity
5	0.007	2 / 28	ADP binding
6	0.008	2 / 30	RNA polymerase II transcription factor binding
7	0.013	3 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
8	0.016	2 / 43	SMAD binding
9	0.021	2 / 50	motor activity
10	0.026	3 / 142	calmodulin binding
11	0.032	6 / 530	calcium ion binding
12	0.033	2 / 63	RNA polymerase II transcription regulatory region sequence−specific DNA bir
13	0.042	2 / 72	structural constituent of cytoskeleton
14	0.044	1 / 10	acetylgalactosaminyltransferase activity
15	0.044	1 / 10	actin−dependent ATPase activity
16	0.048	3 / 180	protein domain specific binding
17	0.049	1 / 11	acetyltransferase activity
18	0.049	1 / 11	SUMO transferase activity
19	0.052	5 / 450	sequence−specific DNA binding
20	0.053	1 / 12	core promoter proximal region sequence−specific DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 95	hsa−miR−125a−3p
2	1e−03	4 / 102	hsa−miR−410
3	2e−03	6 / 294	hsa−miR−561
4	4e−03	3 / 71	hsa−miR−331−3p
5	4e−03	7 / 456	hsa−miR−130a
6	5e−03	6 / 358	hsa−let−7d
7	6e−03	2 / 25	hsa−miR−1273
8	7e−03	4 / 170	hsa−miR−7
9	9e−03	6 / 395	hsa−miR−301b
10	1e−02	3 / 100	hsa−miR−574−5p
11	1e−02	3 / 102	hsa−miR−224
12	1e−02	3 / 102	hsa−miR−377
13	1e−02	3 / 112	hsa−miR−297
14	1e−02	2 / 41	hsa−miR−601
15	2e−02	6 / 447	hsa−miR−130b
16	2e−02	4 / 214	hsa−miR−182
17	2e−02	3 / 119	hsa−miR−1248
18	2e−02	3 / 120	hsa−miR−421
19	2e−02	3 / 123	hsa−miR−204
20	2e−02	2 / 46	hsa−miR−346

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	1 / 12	GUSTAFSON_PI3K_UP
2	0.06	1 / 13	GUSTAFSON_PI3K_DN
3	0.06	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	0.004	13 / 1266	ICGC_NrsfPcr1_targets
2	0.005	22 / 2836	ICGC_BatfPcr1_targets
3	0.007	17 / 2013	ICGC_Bcl11_targets
4	0.010	13 / 1418	ICGC_Ets1_targets
5	0.012	17 / 2137	ICGC_SrfV0416101_targets
6	0.016	21 / 2927	ICGC_Rad21_targets
7	0.020	26 / 3966	ICGC_Pu1_targets
8	0.039	13 / 1701	HEBENSTREIT_high expression TF
9	0.039	31 / 5219	ICGC_Tcf3_targets
10	0.053	18 / 2714	ICGC_Irf4_targets
11	0.058	10 / 1273	ICGC_P300_targets
12	0.064	16 / 2391	ICGC_Pbx3_targets
13	0.070	28 / 4829	ICGC_Nficsc81335_targets
14	0.075	13 / 1878	ICGC_Cebpbsc150_targets
15	0.075	24 / 4032	ICGC_Creb1_targets
16	0.130	5 / 595	ICGC_NrsfPcr2_targets
17	0.132	26 / 4706	ICGC_Sp1_targets
18	0.147	22 / 3924	ICGC_Zeb1_targets
19	0.163	31 / 5890	ICGC_Elf1_targets
20	0.166	25 / 4617	ICGC_Tcf12_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	1 / 16	VAQUERIZAS_Pancreas
2	0.15	1 / 36	VAQUERIZAS_Fetal brain
3	0.15	1 / 37	VAQUERIZAS_Thymus
4	0.16	1 / 38	VAQUERIZAS_Whole brain
5	0.48	1 / 143	VAQUERIZAS_General
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 / 40	VAQUERIZAS_Thyroid
14	1.00	0 / 59	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 29	VAQUERIZAS_Fetal lung
17	1.00	0 / 58	VAQUERIZAS_Lung
18	1.00	0 / 23	VAQUERIZAS_Trachea
19	1.00	0 / 11	VAQUERIZAS_Fetal liver
20	1.00	0 / 19	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 11	WIRTH_Cortex cerebri
2	0.35	1 / 95	WIRTH_Muscle
3	0.47	2 / 350	WIRTH_Nervous System
4	0.59	1 / 194	PALMER_B−Cell signature up
5	0.80	1 / 350	WIRTH_Immune system
6	1.00	0 / 32	WIRTH_Pancreas
7	1.00	0 / 11	WIRTH_Sec. lymphoid organs
8	1.00	0 / 11	WIRTH_Prim. lymphoid organs
9	1.00	0 / 13	WIRTH_B−cells
10	1.00	0 / 8	WIRTH_Tonsil
11	1.00	0 / 12	WIRTH_Thymus
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 5	WIRTH_Bone marrow
14	1.00	0 / 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 / 107	WIRTH_Testis
20	1.00	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	13 / 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	

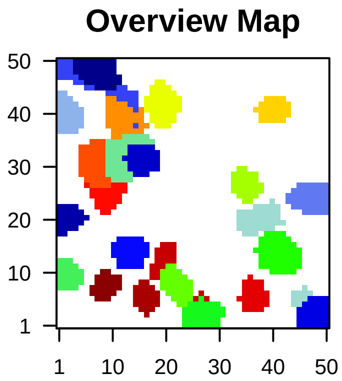
Correlation Clusters

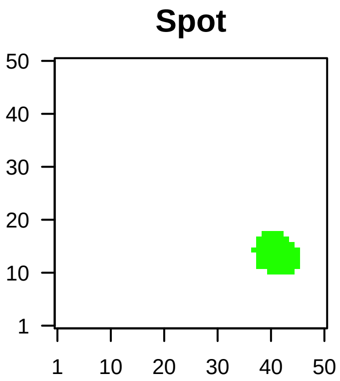
Spot Summary: R

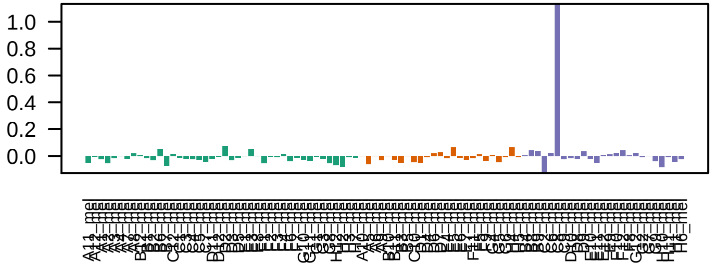
metagenes = 55
genes = 437

<r> metagenes = 0.95
<r> genes = 0.21
beta: r2= 1.05 / log p= −Inf

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





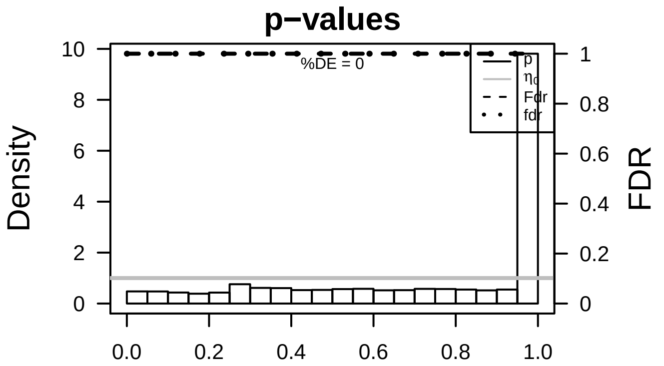


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	KRTAP21−2	2.37	−0.09	0.56	KRTAP21−2	keratin associated protein 21−2 [Source:HGNC Symbol;Acc:H
2	GPR133	2.19	−0.03	0.96		
3	FBXL2	2.11	−0.4	0.39	FBXL2	F−box and leucine−rich repeat protein 2 [Source:HGNC Symb
4	MNDA	2.08	−0.03	0.96	MNDA	myeloid cell nuclear differentiation antigen [Source:HGNC Sy
5	NREP	2.03	−0.33	0.4	NREP	neuronal regeneration related protein [Source:HGNC Symbol
6	TUBA4A	2.01	−0.13	0.45	TUBA4A	tubulin, alpha 4a [Source:HGNC Symbol;Acc:HGNC:12407]
7	PHKA2	2.01	−0.19	0.51	PHKA2	phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
8	NCAM2	2	−0.23	0.4	NCAM2	neural cell adhesion molecule 2 [Source:HGNC Symbol;Acc:H
9	DCN	1.98	−0.06	0.65	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
10	SLC14A1	1.98	−0.03	0.93	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd bl
11	KIAA1324L	1.97	−0.39	0.3	KIAA1324L	KIAA1324−like [Source:HGNC Symbol;Acc:HGNC:21945]
12	DGKA	1.96	−0.05	0.41	DGKA	diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Ac
13	PRKAG2	1.92	−0.36	0.32	PRKAG2	protein kinase, AMP−activated, gamma 2 non−catalytic subur
14	WFDC3	1.92	−0.04	0.65	WFDC3	WAP four−disulfide core domain 3 [Source:HGNC Symbol;Ac
15	GAB1	1.9	−0.32	0.44	GAB1	GRB2−associated binding protein 1 [Source:HGNC Symbol;A
16	MAP3K4	1.9	−0.43	0.26	MAP3K4	mitogen−activated protein kinase kinase kinase 4 [Source:HG
17	CCDC149	1.89	−0.13	0.59	CCDC149	coiled−coil domain containing 149 [Source:HGNC Symbol;Ac
18	MMAA	1.89	−0.07	0.49	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type [Sou
19	PCOLCE2	1.88	−0.07	0.31	PCOLCE2	procollagen C−endopeptidase enhancer 2 [Source:HGNC Sy
20	FHIT	1.87	−0.64	0.28	FHIT	fragile histidine triad [Source:HGNC Symbol;Acc:HGNC:3701

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−05	6 / 23	BP	sensory perception of taste
2	2e−04	90 / 2159	Colon	TssP_Colon
3	3e−04	4 / 12	GSEA	KEGG_SULFUR_METABOLISM
4	3e−04	4 / 12	GSEA	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
5	6e−04	4 / 14	MF	bitter taste receptor activity
6	8e−04	6 / 39	GSEA	LIAO_HAVE_SOX4_BINDING_SITES
7	8e−04	21 / 336	BP	neurological system process
8	9e−04	86 / 2142	Colon	ReprPC_Colon
9	2e−03	4 / 18	GSEA	MCCABE_HOXC6_TARGETS_DN
10	2e−03	5 / 30	GSEA	KEGG_TASTE_TRANSDUCTION
11	2e−03	9 / 94	BP	sensory perception of sound
12	2e−03	115 / 3088	CC	plasma membrane
13	2e−03	76 / 1889	Colon	ReprPCWk_Colon
14	2e−03	4 / 19	GSEA	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS
15	2e−03	4 / 20	BP	detection of chemical stimulus involved in sensory perception of bitter taste
16	3e−03	3 / 10	BP	positive regulation of p38MAPK cascade
17	3e−03	5 / 34	CC	ciliary membrane
18	3e−03	110 / 2984	CC	integral component of membrane
19	3e−03	4 / 22	BP	positive regulation of phosphorylation
20	4e−03	49 / 1139	TF	HEBENSTREIT_low expression TF
21	4e−03	5 / 36	MF	calcium channel activity
22	4e−03	5 / 36	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
23	4e−03	8 / 87	BP	calcium ion transmembrane transport
24	4e−03	198 / 5880	Colon	TssD2_Colon
25	4e−03	35 / 751	CC	integral component of plasma membrane
26	4e−03	5 / 37	MF	sulfotransferase activity
27	4e−03	15 / 239	CC	proteinaceous extracellular matrix
28	4e−03	3 / 12	GSEA	REACTOME_NFKB_ACTIVATION_THROUGH_FADD_RIP1_PATHWAY_M
29	4e−03	3 / 12	GSEA	HUMMERICH_BENIGN_SKIN_TUMOR_DN
30	4e−03	3 / 12	GSEA	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
31	4e−03	14 / 217	MF	G−protein coupled receptor activity
32	5e−03	122 / 3396	Lymph	HOPP_Repressed
33	5e−03	6 / 54	miRN	hsa−miR−513a−5p
34	5e−03	23 / 443	BP	anatomical structure formation involved in morphogenesis
35	5e−03	9 / 112	GSEA	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS
36	5e−03	4 / 25	CC	clathrin−coated endocytic vesicle membrane
37	5e−03	4 / 25	CC	MLL1 complex
38	6e−03	11 / 156	GSEA	RIGGI_EWING_SARCOMA_PROGENITOR_DN
39	6e−03	4 / 26	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
40	6e−03	4 / 26	GSEA	AIGNER_ZEB1_TARGETS



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.3	4 / 100	HORVATH_aging_genes meth DOWN
3	0.6	3 / 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	4e−05	6 / 23	sensory perception of taste
2	8e−04	21 / 336	neurological system process
3	2e−03	9 / 94	sensory perception of sound
4	2e−03	4 / 20	detection of chemical stimulus involved in sensory perception of bitter taste
5	3e−03	3 / 10	positive regulation of p38MAPK cascade
6	3e−03	4 / 22	positive regulation of phosphorylation
7	4e−03	5 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
8	4e−03	8 / 87	calcium ion transmembrane transport
9	5e−03	23 / 443	anatomical structure formation involved in morphogenesis
10	8e−03	28 / 590	cell morphogenesis
11	8e−03	5 / 43	skin development
12	9e−03	7 / 81	vitamin metabolic process
13	1e−02	3 / 16	3'−phosphoadenosine 5'−phosphosulfate metabolic process
14	1e−02	4 / 31	cellular defense response
15	1e−02	4 / 31	muscle cell differentiation
16	1e−02	4 / 32	placenta development
17	1e−02	3 / 18	regulation of heart rate by cardiac conduction
18	2e−02	5 / 53	blood vessel development
19	2e−02	3 / 20	adult behavior
20	2e−02	6 / 75	water−soluble vitamin metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.008	107 / 2972	Mid_Frontal_Lobe_ReprPC
2	0.011	37 / 862	Overlap_fetal_midbrain_TxTrans
3	0.016	48 / 1207	Overlap_fetal_midbrain_TssF
4	0.025	58 / 1548	Mid_Frontal_Lobe_K9K27me3
5	0.033	21 / 468	Mid_Frontal_Lobe_TssF
6	0.038	77 / 2185	Fetal_TssA
7	0.083	33 / 884	Overlap_fetal_midbrain_EnhG
8	0.099	22 / 564	Mid_Frontal_Lobe_EnhP
9	0.113	22 / 574	Overlap_fetal_midbrain_TssP
10	0.131	10 / 229	Mid_Frontal_Lobe_TxTrans
11	0.173	34 / 989	Mid_Frontal_Lobe_Quies
12	0.197	28 / 812	Mid_Frontal_Lobe_TssP
13	0.199	24 / 686	Overlap_fetal_midbrain_TssA
14	0.229	26 / 765	Mid_Frontal_Lobe_Het
15	0.269	60 / 1907	Fetal_TxTrans
16	0.272	22 / 656	Overlap_fetal_midbrain_EnhP
17	0.306	34 / 1065	Overlap_fetal_midbrain_Enh
18	0.311	282 / 9528	Overlap_fetal_midbrain_Quies
19	0.322	13 / 383	Fetal_Tx
20	0.341	75 / 2462	Mid_Frontal_Lobe_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	2 / 15	WANG_ER_UP
2	0.08	17 / 401	Lembcke_Colonic Inflammation
3	0.10	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.28	5 / 121	PanCan_MAPK_geneset_nanostring
5	0.32	2 / 40	PanCan_HK_geneset_nanostring
6	0.34	1 / 14	LIU_LIVER_CANCER
7	0.37	2 / 44	PanCan_TGF−B_geneset_nanostring
8	0.38	1 / 16	GENTLES_modul14
9	0.42	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	0.48	1 / 22	PanCan_HH_geneset_nanostring
11	0.53	2 / 61	PanCan_Wnt_geneset_nanostring
12	0.57	1 / 29	KUIPER_MM good survival
13	0.58	0 / 14	LIU_COMMON_CANCER_GENES
14	0.63	3 / 111	PanCan_RAS_geneset_nanostring
15	0.64	3 / 113	PanCan_Driver_Gene_geneset_nanostring
16	0.67	4 / 156	PanCan_PI3K_geneset_nanostring
17	0.68	3 / 120	PanCan_CC+Apop_geneset_nanostring
18	0.69	0 / 12	LIU_PROSTATE_CANCER_UP
19	0.69	1 / 40	ZHANG_MM up
20	0.80	1 / 55	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.002	115 / 3088	plasma membrane
2	0.003	5 / 34	ciliary membrane
3	0.003	110 / 2984	integral component of membrane
4	0.004	35 / 751	integral component of plasma membrane
5	0.004	15 / 239	proteinaceous extracellular matrix
6	0.005	4 / 25	clathrin−coated endocytic vesicle membrane
7	0.005	4 / 25	MLL1 complex
8	0.009	3 / 15	autophagic vacuole membrane
9	0.013	5 / 49	Golgi lumen
10	0.014	3 / 18	podosome
11	0.015	9 / 132	basolateral plasma membrane
12	0.018	4 / 35	adherens junction
13	0.026	4 / 39	autophagic vacuole
14	0.026	4 / 39	intercalated disc
15	0.031	14 / 276	cilium
16	0.032	2 / 10	fascia adherens
17	0.038	4 / 44	motile cilium
18	0.046	2 / 12	cullin−RING ubiquitin ligase complex
19	0.046	2 / 12	Golgi−associated vesicle
20	0.059	8 / 144	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	0.08	38 / 1037	Chr 19
2	0.13	51 / 1500	Chr 1
3	0.13	24 / 649	Chr 16
4	0.19	27 / 775	Chr 12
5	0.27	16 / 462	Chr 14
6	0.29	23 / 696	Chr 5
7	0.31	26 / 801	Chr 11
8	0.34	18 / 552	Chr 10
9	0.35	22 / 689	Chr 7
10	0.45	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
11	0.49	8 / 262	Chr 13
12	0.51	10 / 335	Chr 22
13	0.56	16 / 558	Chr 4
14	0.64	15 / 551	Chr X
15	0.70	15 / 576	Chr 9
16	0.71	18 / 687	Chr 6
17	0.77	5 / 221	Chr 18
18	0.80	11 / 465	Chr 15
19	0.82	9 / 398	Chr 20
20	0.85	24 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	90 / 2159	TssP_Colon
2	9e−04	86 / 2142	ReprPC_Colon
3	2e−03	76 / 1889	ReprPCWk_Colon
4	4e−03	198 / 5880	TssD2_Colon
5	2e−02	26 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
6	3e−02	50 / 1317	EnhP_Colon
7	3e−02	2 / 10	KIM_MSI−in−CRC
8	5e−02	15 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	5e−02	36 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	7e−02	2 / 15	TCGA_Mutated−in−CRC_hypermutated
11	7e−02	127 / 3897	Quies1_Colon
12	8e−02	2 / 16	Juehling−MSI−enriched−in−6
13	8e−02	12 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
14	9e−02	163 / 5155	EnhWk1_Colon
15	9e−02	2 / 18	Boland_CRC−MSI−A6−A10
16	1e−01	15 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
17	1e−01	1 / 5	Juehling−MSI−enriched−in−8−to−9
18	2e−01	21 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
19	2e−01	17 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	2e−01	290 / 9653	Enh_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.09	13 / 294	GUDJ_psoriasis down
2	0.94	8 / 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	0.02	18 / 356	Down_a
2	0.04	3 / 26	Christensen_hypomethylated_in_ependymoma
3	0.04	2 / 11	astrocytes_glio
4	0.05	2 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
5	0.08	2 / 16	VERHAAK_NL subtype
6	0.08	1 / 3	Martinez_Glio_hypometh
7	0.09	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
8	0.15	4 / 70	Weller_LGG_1p19qDel−vs−intact_UP
9	0.16	1 / 6	neurons_glio
10	0.17	8 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
11	0.17	3 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
12	0.17	4 / 75	Weller_LGG_A_vs_O_DOWN
13	0.19	3 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
14	0.21	1 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
15	0.23	1 / 9	Phillips PN up vs MES & Prolif
16	0.23	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
17	0.25	2 / 33	Christensen_hypomethylated_in_primary_glioblastoma
18	0.26	1 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
19	0.28	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
20	0.29	3 / 65	GIEZELT_GBM_STS_up_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 12	KEGG_SULFUR_METABOLISM
2	3e−04	4 / 12	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
3	8e−04	6 / 39	LIAO_HAVE_SOX4_BINDING_SITES
4	2e−03	4 / 18	MCCABE_HOXC6_TARGETS_DN
5	2e−03	5 / 30	KEGG_TASTE_TRANSDUCTION
6	2e−03	4 / 19	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS
7	4e−03	3 / 12	REACTOME_NFKB_ACTIVATION_THROUGH_FADD_RIP1_PATHWAY_MEI
8	4e−03	3 / 12	HUMMERICH_BENIGN_SKIN_TUMOR_DN
9	4e−03	3 / 12	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
10	5e−03	9 / 112	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS
11	6e−03	11 / 156	RIGGI_EWING_SARCOMA_PROGENITOR_DN
12	6e−03	4 / 26	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
13	6e−03	4 / 26	AIGNER_ZEB1_TARGETS
14	6e−03	5 / 41	HEIDENBLAD_AMPLICON_8Q24_DN
15	8e−03	18 / 328	MCCABE_BOUND_BY_HOXC6
16	8e−03	13 / 209	IVANOVA_HEMATOPOIESIS_STEM_CELL
17	9e−03	3 / 15	BIOCARTA_TNFR2_PATHWAY
18	9e−03	3 / 15	RODRIGUES_NTN1_TARGETS_UP
19	9e−03	18 / 333	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
20	9e−03	13 / 212	ZWANG_DOWN_BY_2ND_EGF_PULSE

HM

Rank	p−value	#in/all	Geneset
1	0.02	11 / 183	HALLMARK_GLYCOLYSIS
2	0.11	8 / 165	HALLMARK_MYOGENESIS
3	0.14	8 / 176	HALLMARK_HYPOXIA
4	0.22	7 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	0.41	6 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	0.51	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
7	0.52	3 / 95	HALLMARK_SPERMATOGENESIS
8	0.53	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.55	5 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	0.55	5 / 169	HALLMARK_XENOBIOTIC_METABOLISM
11	0.57	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.60	3 / 107	HALLMARK_COAGULATION
13	0.64	5 / 188	HALLMARK_ADIPOGENESIS
14	0.70	4 / 162	HALLMARK_COMPLEMENT
15	0.72	3 / 127	HALLMARK_KRAS_SIGNALING_DN
16	0.72	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
17	0.75	2 / 91	HALLMARK_BILE_ACID_METABOLISM
18	0.75	4 / 174	HALLMARK_HEME_METABOLISM
19	0.76	2 / 94	HALLMARK_ANDROGEN_RESPONSE
20	0.78	3 / 141	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.008	2 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.085	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
3	0.255	1 / 10	DUMEAUX_Smoking literature genes up
4	0.357	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.541	2 / 62	DUMEAUX_Smoking enriched genes
6	1.000	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.000	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.000	0 / 18	DUMEAUX_High bmi enriched genes
11	1.000	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.005	122 / 3396	HOPP_Repressed
2	0.029	78 / 2188	HOPP_Poised_promoter
3	0.065	13 / 280	SPANG_CD40 6hrs UP
4	0.069	2 / 15	DAVE_Immune response 2
5	0.091	6 / 107	SPANG_LPS 6hrs UP
6	0.104	2 / 19	Subero_MM_hyper_meth
7	0.143	2 / 23	DAVE_Immune response 1
8	0.163	2 / 25	Subero_T−PLL_hypo_meth
9	0.177	3 / 50	SPANG_BAFF 9hrs DN
10	0.210	1 / 8	MASCQUE_ABC UP
11	0.210	1 / 8	Subero_MM_hypo_meth
12	0.253	80 / 2563	HOPP_Heterochrom
13	0.314	2 / 39	ROSOLOWSKI_blue DOWN
14	0.318	1 / 13	BENTINK_mBL_UP
15	0.338	1 / 14	Subero_mBL_hypo_meth
16	0.356	2 / 43	LENZ_Stromal signature 2
17	0.445	1 / 20	SPANG_BAFF 9hrs UP
18	0.477	65 / 2211	HOPP_Repetitive
19	0.519	8 / 268	SPANG_IL21 UP
20	0.530	12 / 410	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	6e−04	4 / 14	bitter taste receptor activity
2	4e−03	5 / 36	calcium channel activity
3	4e−03	5 / 37	sulfotransferase activity
4	4e−03	14 / 217	G−protein coupled receptor activity
5	6e−03	5 / 41	copper ion binding
6	7e−03	32 / 695	transmembrane transporter activity
7	8e−03	8 / 98	ion channel activity
8	2e−02	3 / 19	MAP kinase kinase activity
9	2e−02	3 / 20	WW domain binding
10	3e−02	3 / 23	MAP kinase kinase kinase activity
11	3e−02	35 / 866	signal transducer activity
12	3e−02	2 / 10	calcium−activated potassium channel activity
13	3e−02	2 / 10	ephrin receptor activity
14	3e−02	2 / 10	hedgehog receptor activity
15	4e−02	2 / 11	mismatched DNA binding
16	4e−02	2 / 11	substrate−specific transmembrane transporter activity
17	4e−02	3 / 27	voltage−gated calcium channel activity
18	6e−02	5 / 71	PDZ domain binding
19	6e−02	2 / 14	diacylglycerol kinase activity
20	7e−02	2 / 15	spectrin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	6 / 54	hsa−miR−513a−5p
2	0.011	7 / 84	hsa−miR−220c
3	0.060	4 / 51	hsa−miR−508−5p
4	0.064	4 / 52	hsa−miR−370
5	0.070	3 / 33	hsa−miR−615−5p
6	0.080	5 / 79	hsa−miR−542−3p
7	0.080	3 / 35	hsa−miR−770−5p
8	0.101	6 / 110	hsa−miR−199a−5p
9	0.111	6 / 113	hsa−miR−507
10	0.122	3 / 42	hsa−miR−192
11	0.135	4 / 68	hsa−miR−193b
12	0.153	2 / 24	hsa−miR−220b
13	0.186	6 / 132	hsa−miR−199b−5p
14	0.190	6 / 133	hsa−miR−485−5p
15	0.191	4 / 78	hsa−miR−1321
16	0.226	5 / 112	hsa−miR−297
17	0.227	2 / 31	hsa−miR−617
18	0.229	3 / 57	hsa−miR−193a−3p
19	0.248	5 / 116	hsa−miR−376c
20	0.249	2 / 33	hsa−miR−1274b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 12	BENTINK_e2f3.2
2	0.3	1 / 13	GUSTAFSON_PI3K_DN
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.004	49 / 1139	HEBENSTREIT_low expression TF
2	0.043	134 / 4054	ICGC_Egr1_targets
3	0.078	150 / 4682	ICGC_Pol24_targets
4	0.113	137 / 4314	ICGC_Ebfsc137065_targets
5	0.122	95 / 2927	ICGC_Rad21_targets
6	0.126	128 / 4032	ICGC_Creb1_targets
7	0.135	79 / 2416	ICGC_Bcl3_targets
8	0.142	78 / 2391	ICGC_Pbx3_targets
9	0.143	167 / 5374	ICGC_Pax5_targets
10	0.154	166 / 5355	ICGC_Pol2_targets
11	0.178	124 / 3966	ICGC_Pu1_targets
12	0.194	166 / 5408	ICGC_Pou2_targets
13	0.207	24 / 690	ICGC_Atf3_targets
14	0.219	144 / 4689	ICGC_Taf1_targets
15	0.234	144 / 4706	ICGC_Sp1_targets
16	0.248	135 / 4414	ICGC_Bclaf101388_targets
17	0.252	41 / 1266	ICGC_NrsfPcr1_targets
18	0.264	67 / 2137	ICGC_SrfV0416101_targets
19	0.269	158 / 5219	ICGC_Tcf3_targets
20	0.282	44 / 1383	ICGC_Six5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.09	2 / 17	VAQUERIZAS_Heart
2	0.11	3 / 40	VAQUERIZAS_Thyroid
3	0.14	2 / 23	VAQUERIZAS_Spinal cord
4	0.25	2 / 33	VAQUERIZAS_Prostate
5	0.28	1 / 11	VAQUERIZAS_Fetal liver
6	0.28	2 / 36	VAQUERIZAS_Fetal brain
7	0.29	2 / 37	VAQUERIZAS_Thymus
8	0.30	1 / 12	VAQUERIZAS_Skin
9	0.36	1 / 15	VAQUERIZAS_Fetal thyroid
10	0.38	1 / 16	VAQUERIZAS_Salivary gland
11	0.39	1 / 17	VAQUERIZAS_Pituitary
12	0.51	2 / 59	VAQUERIZAS_Whole blood
13	0.54	1 / 26	VAQUERIZAS_Liver
14	0.60	4 / 143	VAQUERIZAS_General
15	0.67	1 / 38	VAQUERIZAS_Whole brain
16	0.67	1 / 38	VAQUERIZAS_Testis
17	0.70	1 / 41	VAQUERIZAS_Placenta
18	0.73	1 / 45	VAQUERIZAS_Uterus
19	0.82	1 / 58	VAQUERIZAS_Lung
20	1.00	0 / 29	VAQUERIZAS_Smooth muscle

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	5 / 74	WIRTH_Mucosa
2	0.12	3 / 41	WIRTH_Homeostasis
3	0.24	2 / 32	WIRTH_Pancreas
4	0.26	1 / 10	WIRTH_Hippocampus
5	0.28	1 / 11	WIRTH_Globus pallidus
6	0.28	1 / 11	WIRTH_Cortex cerebri
7	0.30	4 / 95	WIRTH_Muscle
8	0.30	1 / 12	WIRTH_Thymus
9	0.38	1 / 16	PALMER_Lymphocytes signature up
10	0.38	4 / 107	WIRTH_Testis
11	0.65	3 / 114	PALMER_T−Cell signature up
12	0.67	5 / 194	PALMER_B−Cell signature up
13	0.80	8 / 350	WIRTH_Immune system
14	0.89	7 / 350	WIRTH_Nervous System
15	0.90	4 / 225	PALMER_Granulocytes signature up
16	1.00	0 / 11	WIRTH_Sec. lymphoid organs
17	1.00	0 / 11	WIRTH_Prim. lymphoid organs
18	1.00	0 / 13	WIRTH_B−cells
19	1.00	0 / 8	WIRTH_Tonsil
20	1.00	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	111 / 3682	LU_BPDE 0.005 DN
2	0.4	34 / 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	

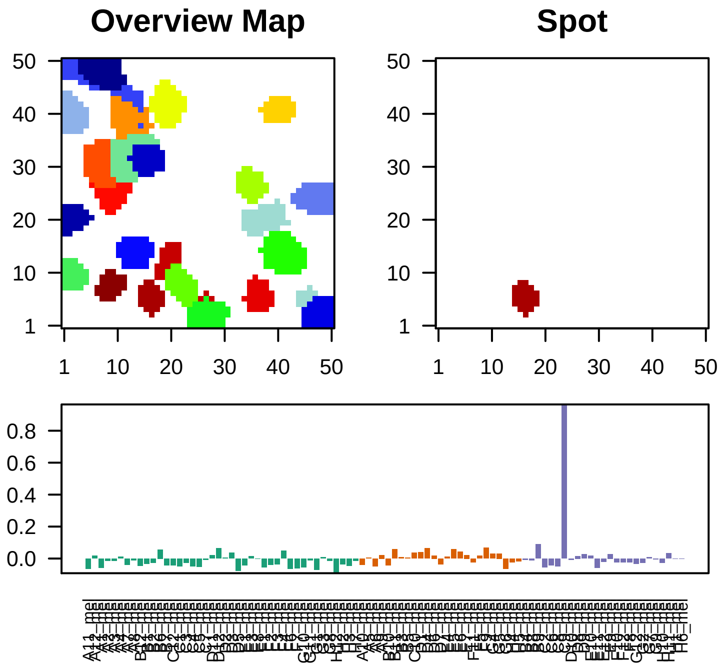
Correlation Clusters

Spot Summary: S

metagenes = 25
genes = 232

<r> metagenes = 0.93
<r> genes = 0.24
beta: r2= 0.62 / log p= −Inf

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

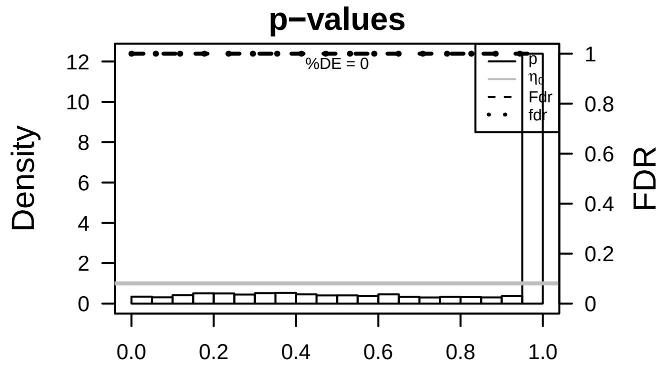


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LRRC27	2.04	−0.16	0.57	LRRC27	leucine rich repeat containing 27 [Source:HGNC Symbol;Acc:
2	IFT46	1.98	−0.27	0.26	IFT46	intraflagellar transport 46 [Source:HGNC Symbol;Acc:HGNC:
3	CLCN5	1.98	−0.19	0.6	CLCN5	chloride channel, voltage−sensitive 5 [Source:HGNC Symbol;
4	SLC25A53	1.94	−0.16	0.42	SLC25A53	solute carrier family 25, member 53 [Source:HGNC Symbol;A
5	E2F5	1.86	−0.2	0.38	E2F5	E2F transcription factor 5, p130−binding [Source:HGNC Sym
6	OSR2	1.84	−0.06	0.67	OSR2	odd−skipped related transciption factor 2 [Source:HGNC Sym
7	ULK2	1.8	−0.23	0.27	ULK2	unc−51 like autophagy activating kinase 2 [Source:HGNC Sy
8	WDR54	1.78	−0.34	0.3	WDR54	WD repeat domain 54 [Source:HGNC Symbol;Acc:HGNC:25
9	MBD5	1.78	−0.22	0.32	MBD5	methyl−CpG binding domain protein 5 [Source:HGNC Symbo
10	HDGFRP2	1.77	−0.28	0.34		
11	SPATA25	1.76	−0.03	0.77	SPATA25	spermatogenesis associated 25 [Source:HGNC Symbol;Acc:
12	RELL1	1.69	−0.22	0.43	RELL1	RELT−like 1 [Source:HGNC Symbol;Acc:HGNC:27379]
13	DNAJB2	1.67	−0.1	0.61	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:HGN
14	CDC34	1.67	−0.3	0.35	CDC34	cell division cycle 34 [Source:HGNC Symbol;Acc:HGNC:173
15	BMF	1.66	−0.16	0.54	BMF	Bcl2 modifying factor [Source:HGNC Symbol;Acc:HGNC:241
16	PCDH18	1.66	−0.21	0.29	PCDH18	protocadherin 18 [Source:HGNC Symbol;Acc:HGNC:14268]
17	ZNF487	1.65	−0.19	0.41	ZNF487	zinc finger protein 487 [Source:HGNC Symbol;Acc:HGNC:23
18	YPEL3	1.65	−0.12	0.53	YPEL3	yippee−like 3 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
19	CTTNBP2	1.65	−0.09	0.5	CTTNBP2	cortactin binding protein 2 [Source:HGNC Symbol;Acc:HGNC
20	CCDC121	1.64	−0.15	0.27	CCDC121	coiled−coil domain containing 121 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−11	17 / 126	BP	homophilic cell adhesion via plasma membrane adhesion molecules
2	3e−09	16 / 158	Brain	Overlap_fetal_midbrain_Het
3	9e−07	13 / 156	Brain	Mid_Frontal_Lobe_TssA
4	3e−06	24 / 530	MF	calcium ion binding
5	6e−06	12 / 156	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
6	2e−05	29 / 812	Brain	Mid_Frontal_Lobe_TssP
7	4e−05	24 / 626	BP	cell adhesion
8	5e−05	23 / 595	TF	ICGC_NrsfPcr2_targets
9	1e−04	14 / 275	Lymp	TARTE_Mature plasma cell signature
10	3e−04	6 / 58	Glio	Christensen_hypermethylated_in_grade2_astrocytoma
11	6e−04	5 / 45	GSEA	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
12	8e−04	7 / 97	Glio	Christensen_hypermethylated_in_grade3_astrocytoma
13	8e−04	22 / 674	GSEA	BENPORATH_SUZ12_TARGETS
14	1e−03	23 / 739	Colon	TxEnhG2_Colon
15	2e−03	6 / 82	GSEA	WINZEN_DEGRADED_VIA_KHSRP
16	2e−03	3 / 16	BP	regulation of centrosome duplication
17	2e−03	22 / 724	GSEA	BENPORATH_EED_TARGETS
18	2e−03	3 / 17	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_DN
19	3e−03	9 / 188	GSEA	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN
20	3e−03	4 / 40	GSEA	HALMOS_CEBPA_TARGETS_DN
21	5e−03	3 / 22	Canc	PanCan_HH_geneset_nanostring
22	5e−03	5 / 72	Glio	laffaire_hypermeth_LGG_vs_control
23	5e−03	3 / 23	BP	intrinsic apoptotic signaling pathway by p53 class mediator
24	5e−03	24 / 884	Brain	Overlap_fetal_midbrain_EnhG
25	6e−03	4 / 46	GSEA	BROWNE_HCMV_INFECTION_1HR_UP
26	6e−03	20 / 696	Chr	Chr 5
27	6e−03	2 / 8	Lifest	DUMEAUX_Hormon therapy in non smokers literature genes up
28	7e−03	4 / 50	GSEA	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
29	8e−03	2 / 9	GSEA	PETRETTO_BLOOD_PRESSURE_UP
30	8e−03	2 / 9	GSEA	LY_AGING_MIDDLE_UP
31	8e−03	3 / 27	BP	oligodendrocyte differentiation
32	8e−03	20 / 720	GSEA	BENPORATH_ES_WITH_H3K27ME3
33	1e−02	4 / 54	BP	positive regulation of epithelial cell proliferation
34	1e−02	2 / 10	BP	eyelid development in camera−type eye
35	1e−02	2 / 10	BP	outflow tract septum morphogenesis
36	1e−02	2 / 10	GSEA	GHANDHI_BYSTANDER_IRRADIATION_DN
37	1e−02	3 / 29	GSEA	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP
38	1e−02	10 / 272	BP	embryo development
39	1e−02	36 / 1565	BP	regulation of transcription, DNA−templated
40	1e−02	6 / 118	Glio	Christensen_hypermethylated_in_grade3_oligoastrocytoma



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 109	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	1e−11	17 / 126	homophilic cell adhesion via plasma membrane adhesion molecules
2	4e−05	24 / 626	cell adhesion
3	2e−03	3 / 16	regulation of centrosome duplication
4	5e−03	3 / 23	intrinsic apoptotic signaling pathway by p53 class mediator
5	8e−03	3 / 27	oligodendrocyte differentiation
6	1e−02	4 / 54	positive regulation of epithelial cell proliferation
7	1e−02	2 / 10	eyelid development in camera−type eye
8	1e−02	2 / 10	outflow tract septum morphogenesis
9	1e−02	10 / 272	embryo development
10	1e−02	36 / 1565	regulation of transcription, DNA−templated
11	1e−02	2 / 11	phosphorelay signal transduction system
12	1e−02	3 / 32	chondrocyte differentiation
13	2e−02	2 / 13	thyroid gland development
14	2e−02	3 / 38	DNA−templated transcription, initiation
15	2e−02	3 / 38	negative regulation of cell cycle
16	2e−02	2 / 15	middle ear morphogenesis
17	2e−02	2 / 16	cell−substrate adhesion
18	2e−02	2 / 16	retinoic acid receptor signaling pathway
19	3e−02	3 / 41	DNA catabolic process, endonucleolytic
20	3e−02	3 / 42	cell fate commitment

Brain

Rank	p−value	#in/all	Geneset
1	3e−09	16 / 158	Overlap_fetal_midbrain_Het
2	9e−07	13 / 156	Mid_Frontal_Lobe_TssA
3	2e−05	29 / 812	Mid_Frontal_Lobe_TssP
4	5e−03	24 / 884	Overlap_fetal_midbrain_EnhG
5	2e−02	20 / 769	Overlap_fetal_midbrain_ZNF
6	2e−02	30 / 1333	Fetal_ReprPCWk
7	4e−02	6 / 163	Fetal_ReprPC
8	5e−02	16 / 656	Overlap_fetal_midbrain_EnhP
9	7e−02	23 / 1065	Overlap_fetal_midbrain_Enh
10	7e−02	16 / 686	Overlap_fetal_midbrain_TssA
11	1e−01	21 / 1013	Fetal_TssP
12	2e−01	17 / 862	Overlap_fetal_midbrain_TxTrans
13	2e−01	33 / 1845	Fetal_Quies
14	3e−01	2 / 69	Overlap_fetal_midbrain_Tx
15	3e−01	15 / 831	Fetal_HetRpts
16	3e−01	51 / 3081	Mid_Frontal_Lobe_ZNF
17	3e−01	49 / 2972	Mid_Frontal_Lobe_ReprPC
18	4e−01	35 / 2185	Fetal_TssA
19	4e−01	9 / 534	Mid_Frontal_Lobe_EnhG
20	5e−01	19 / 1207	Overlap_fetal_midbrain_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	3 / 22	PanCan_HH_geneset_nanostring
2	0.031	3 / 44	PanCan_TGF−B_geneset_nanostring
3	0.176	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.196	1 / 14	LIU_COMMON_CANCER_GENES
5	0.209	1 / 15	RHODES_CANCER_META_SIGNATURE
6	0.209	1 / 15	GENTLES_modul11
7	0.221	1 / 16	GENTLES_modul16
8	0.244	2 / 61	PanCan_Wnt_geneset_nanostring
9	0.358	0 / 12	LIU_PROSTATE_CANCER_UP
10	0.489	8 / 489	Lembcke_Normal vs Adenoma
11	0.515	2 / 111	PanCan_RAS_geneset_nanostring
12	0.557	2 / 120	PanCan_CC+Apop_geneset_nanostring
13	0.562	2 / 121	PanCan_MAPK_geneset_nanostring
14	0.577	1 / 55	PanCan_JAK−ST_geneset_nanostring
15	0.682	4 / 298	SPANG_BCL6−index2
16	0.699	2 / 156	PanCan_PI3K_geneset_nanostring
17	0.723	1 / 82	PanCan_TXmisReg_geneset_nanostring
18	0.748	5 / 401	Lembcke_Colonic Inflammation
19	0.771	2 / 180	SPANG_LPS−index2
20	0.830	1 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	anchored component of plasma membrane
2	0.03	60 / 3088	plasma membrane
3	0.03	2 / 18	intraciliary transport particle B
4	0.03	4 / 77	ciliary basal body
5	0.05	2 / 24	Cul3−RING ubiquitin ligase complex
6	0.06	7 / 223	lysosomal membrane
7	0.07	2 / 27	photoreceptor inner segment
8	0.08	2 / 31	membrane coat
9	0.08	6 / 196	nuclear membrane
10	0.09	55 / 2984	integral component of membrane
11	0.09	2 / 32	nuclear nucleosome
12	0.09	48 / 2576	membrane
13	0.10	2 / 34	rough endoplasmic reticulum
14	0.12	3 / 78	dendritic spine
15	0.13	3 / 81	late endosome membrane
16	0.13	2 / 41	ciliary tip
17	0.14	5 / 178	apical plasma membrane
18	0.14	1 / 10	IkappaB kinase complex
19	0.14	1 / 10	neuron projection terminus
20	0.14	1 / 10	viral nucleocapsid

Chr

Rank	p−value	#in/all	Geneset
1	0.006	20 / 696	Chr 5
2	0.109	11 / 465	Chr 15
3	0.183	14 / 689	Chr 7
4	0.256	19 / 1037	Chr 19
5	0.277	8 / 398	Chr 20
6	0.281	11 / 576	Chr 9
7	0.322	15 / 840	Chr 17
8	0.350	10 / 551	Chr X
9	0.418	6 / 335	Chr 22
10	0.424	11 / 649	Chr 16
11	0.442	8 / 469	Chr 8
12	0.448	4 / 221	Chr 18
13	0.486	9 / 552	Chr 10
14	0.499	9 / 558	Chr 4
15	0.756	11 / 838	Chr 3
16	0.774	13 / 993	Chr 2
17	0.793	20 / 1500	Chr 1
18	0.907	1 / 151	Chr 21
19	0.958	6 / 687	Chr 6
20	0.976	3 / 462	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	23 / 739	TxEnhG2_Colon
2	0.019	4 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
3	0.047	104 / 5880	TssD2_Colon
4	0.050	52 / 2698	EnhA_Colon
5	0.055	21 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	0.057	124 / 7203	TssF_Colon
7	0.059	29 / 1386	Het_Colon
8	0.066	3 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
9	0.127	21 / 1038	HetRpts_Colon
10	0.131	1 / 9	TCGA−CRC_agressive−disease−markers
11	0.143	2 / 43	Marisa_CRC−cluster−f
12	0.177	12 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	0.177	87 / 5155	EnhWk1_Colon
14	0.204	156 / 9653	Enh_Colon
15	0.209	1 / 15	Juehling_HNPCC−mutated−in−4
16	0.221	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
17	0.221	1 / 16	Vilar_non−hypermutated−in−CRC
18	0.253	4 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
19	0.259	8 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
20	0.268	8 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 20	BCHETNIA_EBM−DM up
2	0.7	4 / 294	GUDJ_psoriasis down
3	0.8	5 / 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	3e−04	6 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
2	8e−04	7 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
3	5e−03	5 / 72	laffaire_hypermeth_LGG_vs_control
4	1e−02	6 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
5	1e−02	6 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	2e−02	2 / 14	VERHAAK_PN subtype
7	2e−02	5 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
8	3e−02	4 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
9	4e−02	3 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
10	6e−02	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
11	1e−01	3 / 75	GIEZELT_GBM_STS_down_VS_LTS
12	2e−01	2 / 45	Christensen_hypermethylated_in_primary_glioblastoma
13	2e−01	1 / 11	Christensen_hypermethylated_in_ependymoma
14	2e−01	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
15	2e−01	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
16	2e−01	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
17	2e−01	1 / 15	VERHAAK_CL subtype
18	3e−01	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
19	3e−01	1 / 23	WIRTH_PN subtype
20	3e−01	1 / 26	Christensen_hypomethylated_in_ependymoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−06	12 / 156	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
2	6e−04	5 / 45	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
3	8e−04	22 / 674	BENPORATH_SUZ12_TARGETS
4	2e−03	6 / 82	WINZEN_DEGRADED_VIA_KHSRP
5	2e−03	22 / 724	BENPORATH_EED_TARGETS
6	2e−03	3 / 17	KIM_ALL_DISORDERS_CALB1_CORR_DN
7	3e−03	9 / 188	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN
8	3e−03	4 / 40	HALMOS_CEBPA_TARGETS_DN
9	6e−03	4 / 46	BROWNE_HCMV_INFECTION_1HR_UP
10	7e−03	4 / 50	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
11	8e−03	2 / 9	PETRETTO_BLOOD_PRESSURE_UP
12	8e−03	2 / 9	LY_AGING_MIDDLE_UP
13	8e−03	20 / 720	BENPORATH_ES_WITH_H3K27ME3
14	1e−02	2 / 10	GHANDHI_BYSTANDER_IRRADIATION_DN
15	1e−02	3 / 29	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP
16	1e−02	5 / 85	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP
17	1e−02	2 / 11	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
18	1e−02	2 / 12	SU_THYMUS
19	2e−02	5 / 95	NIKOLSKY_BREAST_CANCER_17Q11_Q21_AMPLICON
20	2e−02	3 / 36	HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_UP

HM

Rank	p−value	#in/all	Geneset
1	0.2	4 / 140	HALLMARK_APOPTOSIS
2	0.2	5 / 195	HALLMARK_MITOTIC_SPINDLE
3	0.2	4 / 146	HALLMARK_UV_RESPONSE_UP
4	0.2	2 / 53	HALLMARK_TGF_BETA_SIGNALING
5	0.3	4 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	0.3	4 / 181	HALLMARK_P53_PATHWAY
7	0.4	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
8	0.4	3 / 146	HALLMARK_DNA_REPAIR
9	0.4	3 / 148	HALLMARK_KRAS_SIGNALING_UP
10	0.4	2 / 91	HALLMARK_PROTEIN_SECRETION
11	0.4	2 / 95	HALLMARK_SPERMATOGENESIS
12	0.4	1 / 37	HALLMARK_APICAL_SURFACE
13	0.5	3 / 162	HALLMARK_COMPLEMENT
14	0.5	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.5	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
16	0.6	2 / 137	HALLMARK_UV_RESPONSE_DN
17	0.7	2 / 167	HALLMARK_APICAL_JUNCTION
18	0.7	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
19	0.7	2 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
20	0.7	2 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	2 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.621	1 / 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 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.000	0 / 18	DUMEAUX_High bmi enriched genes
11	1.000	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−04	14 / 275	TARTE_Mature plasma cell signature
2	6e−02	4 / 96	Subero_DLBCL_hyper_meth
3	7e−02	3 / 60	Subero_T−ALL_hyper_meth
4	8e−02	1 / 5	WRIGHT_custom ABC−DLBCL UP
5	1e−01	2 / 34	Subero_B−ALL_hyper_meth
6	1e−01	1 / 8	MASCQUE_ABC UP
7	1e−01	1 / 8	Subero_MM_hypo_meth
8	1e−01	3 / 81	Subero_INT_hyper_meth
9	1e−01	1 / 9	Subero_B−ALL_hypo_meth
10	2e−01	6 / 247	ZHANG_DLBCL mutated
11	2e−01	108 / 6564	HOPP_Strong_enhancer
12	3e−01	1 / 19	Subero_MM_hyper_meth
13	3e−01	1 / 20	SPANG_BAFF 9hrs UP
14	3e−01	1 / 25	Subero_T−PLL_hypo_meth
15	3e−01	21 / 1218	SPANG_BCR UP
16	4e−01	1 / 29	Subero_DLBCL_hypo_meth
17	4e−01	1 / 30	Subero_INT_hypo_meth
18	4e−01	36 / 2188	HOPP_Poised_promoter
19	4e−01	5 / 268	SPANG_IL21 UP
20	4e−01	1 / 33	LEE_Developmental_regulators

MF

Rank	p−value	#in/all	Geneset
1	3e−06	24 / 530	calcium ion binding
2	1e−02	2 / 11	retinol dehydrogenase activity
3	2e−02	2 / 13	solute:proton antiporter activity
4	3e−02	6 / 149	protein dimerization activity
5	3e−02	91 / 4992	ion binding
6	4e−02	2 / 21	exonuclease activity
7	4e−02	4 / 85	metalloendopeptidase activity
8	5e−02	2 / 22	oxygen binding
9	6e−02	2 / 26	chloride channel activity
10	6e−02	2 / 26	transforming growth factor beta receptor binding
11	6e−02	37 / 1859	metal ion binding
12	7e−02	40 / 2037	DNA binding
13	7e−02	2 / 29	insulin receptor binding
14	7e−02	3 / 63	RNA polymerase II transcription regulatory region sequence−specific DNA bir
15	8e−02	2 / 30	transmembrane receptor protein tyrosine kinase activity
16	8e−02	2 / 31	beta−tubulin binding
17	9e−02	7 / 244	ubiquitin−protein transferase activity
18	9e−02	4 / 109	RNA polymerase II regulatory region sequence−specific DNA binding
19	1e−01	3 / 71	PDZ domain binding
20	1e−01	5 / 164	nuclease activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	6 / 118	hsa−miR−625
2	0.02	5 / 105	hsa−miR−376b
3	0.02	3 / 40	hsa−miR−647
4	0.03	4 / 73	hsa−miR−184
5	0.03	2 / 18	hsa−miR−380*
6	0.03	4 / 77	hsa−miR−205
7	0.04	3 / 48	hsa−miR−628−5p
8	0.04	6 / 161	hsa−miR−511
9	0.04	12 / 437	hsa−miR−19b
10	0.04	2 / 21	hsa−miR−1282
11	0.04	12 / 443	hsa−miR−19a
12	0.05	3 / 54	hsa−miR−330−5p
13	0.06	2 / 25	hsa−miR−941
14	0.07	4 / 98	hsa−miR−21
15	0.07	3 / 60	hsa−miR−671−5p
16	0.07	4 / 99	hsa−miR−376a
17	0.07	2 / 28	hsa−miR−591
18	0.08	4 / 103	hsa−miR−1284
19	0.08	5 / 149	hsa−miR−518a−5p
20	0.08	2 / 31	hsa−miR−17*

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 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	5e−05	23 / 595	ICGC_NrsfPcr2_targets
2	2e−02	59 / 2927	ICGC_Rad21_targets
3	2e−02	30 / 1314	ICGC_Usf1_targets
4	3e−02	49 / 2416	ICGC_Bcl3_targets
5	3e−02	75 / 3966	ICGC_Pu1_targets
6	4e−02	41 / 2013	ICGC_Bcl11_targets
7	4e−02	75 / 4054	ICGC_Egr1_targets
8	7e−02	37 / 1872	ICGC_Mef2_targets
9	8e−02	82 / 4617	ICGC_Tcf12_targets
10	8e−02	67 / 3700	ICGC_Nfatc1_targets
11	9e−02	91 / 5219	ICGC_Tcf3_targets
12	1e−01	70 / 3924	ICGC_Zeb1_targets
13	1e−01	82 / 4689	ICGC_Taf1_targets
14	1e−01	25 / 1266	ICGC_NrsfPcr1_targets
15	1e−01	27 / 1400	ICGC_Myc_targets
16	1e−01	35 / 1878	ICGC_Cebpbsc150_targets
17	2e−01	91 / 5374	ICGC_Pax5_targets
18	2e−01	43 / 2391	ICGC_Pbx3_targets
19	2e−01	74 / 4314	ICGC_Ebfsc137065_targets
20	2e−01	48 / 2714	ICGC_Irf4_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 36	VAQUERIZAS_Fetal brain
2	0.02	2 / 15	VAQUERIZAS_Fetal thyroid
3	0.03	3 / 45	VAQUERIZAS_Uterus
4	0.05	2 / 23	VAQUERIZAS_Spinal cord
5	0.07	2 / 29	VAQUERIZAS_Smooth muscle
6	0.07	2 / 29	VAQUERIZAS_Fetal lung
7	0.12	2 / 38	VAQUERIZAS_Testis
8	0.13	2 / 40	VAQUERIZAS_Thyroid
9	0.13	1 / 9	VAQUERIZAS_Kidney
10	0.20	1 / 14	VAQUERIZAS_Ovary
11	0.22	1 / 16	VAQUERIZAS_Adrenal gland
12	0.23	2 / 58	VAQUERIZAS_Lung
13	0.23	1 / 17	VAQUERIZAS_Pituitary
14	0.23	1 / 17	VAQUERIZAS_Heart
15	0.38	3 / 143	VAQUERIZAS_General
16	0.40	1 / 33	VAQUERIZAS_Prostate
17	0.44	1 / 37	VAQUERIZAS_Thymus
18	0.45	1 / 38	VAQUERIZAS_Whole brain
19	0.47	1 / 41	VAQUERIZAS_Placenta
20	0.60	1 / 59	VAQUERIZAS_Whole blood

Tissue

Rank	p−value	#in/all	Geneset
1	0.3	2 / 74	WIRTH_Mucosa
2	0.4	1 / 32	WIRTH_Pancreas
3	0.4	1 / 32	WIRTH_Placenta
4	0.4	2 / 95	WIRTH_Muscle
5	0.5	1 / 41	WIRTH_Homeostasis
6	0.6	3 / 194	PALMER_B−Cell signature up
7	0.8	1 / 107	WIRTH_Testis
8	0.9	2 / 225	PALMER_Granulocytes signature up
9	1.0	2 / 350	WIRTH_Nervous System
10	1.0	1 / 350	WIRTH_Immune system
11	1.0	0 / 11	WIRTH_Sec. lymphoid organs
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 13	WIRTH_B−cells
14	1.0	0 / 8	WIRTH_Tonsil
15	1.0	0 / 12	WIRTH_Thymus
16	1.0	0 / 12	WIRTH_Lymphocytes
17	1.0	0 / 5	WIRTH_Bone marrow
18	1.0	0 / 11	WIRTH_Globus pallidus
19	1.0	0 / 14	WIRTH_Telencephalon
20	1.0	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	18 / 1115	LU_BPDE 1h DN
2	0.5	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	

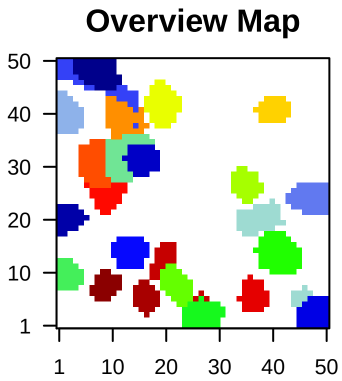
Correlation Clusters

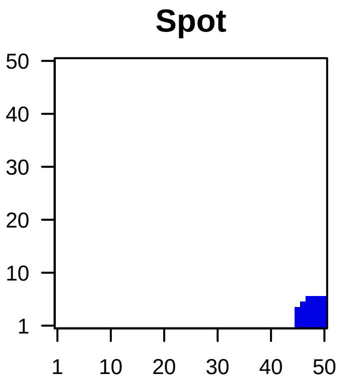
Spot Summary: T

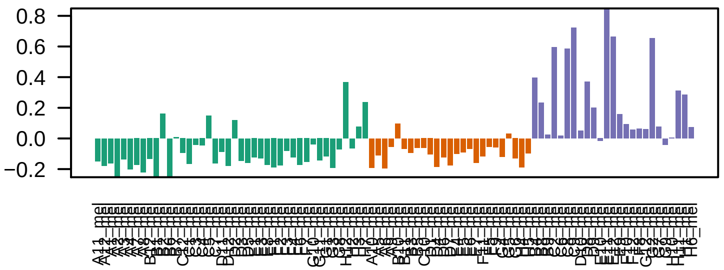
metagenes = 33
genes = 438

<r> metagenes = 0.95
<r> genes = 0.17
beta: r2= 4.02 / log p= −Inf

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


Overview Map


Spot

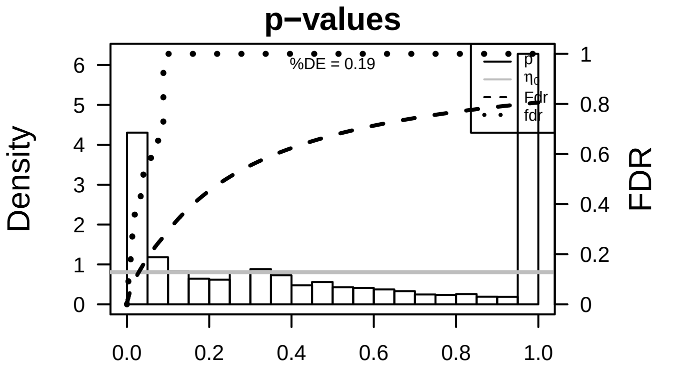


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	DKK1	2.85	−0.31	0.63	DKK1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Sy
2	IL24	2.78	−0.11	0.59	IL24	interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
3	HBEGF	2.46	−0.25	0.53	HBEGF	heparin−binding EGF−like growth factor [Source:HGNC Symb
4	ANXA1	2.44	−0.5	0.78	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
5	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;Acc
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;Acc
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;A
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	2e−32	73 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	2e−30	56 / 286	GSEA	PASINI_SUZ12_TARGETS_DN
3	3e−25	72 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
4	2e−24	80 / 749	GSEA	CUI_TCF21_TARGETS_2_DN
5	7e−23	49 / 302	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	2e−21	85 / 930	GSEA	NUYTTEN_EZH2_TARGETS_UP
7	3e−21	40 / 212	Lymp	LENZ_Stromal signature 1
8	1e−20	55 / 425	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
9	3e−20	35 / 168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	6e−19	51 / 401	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
11	2e−18	71 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
12	1e−16	40 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
13	2e−16	37 / 245	GSEA	WANG_SMARCE1_TARGETS_UP
14	2e−16	48 / 410	GSEA	LIM_MAMMARY_STEM_CELL_UP
15	2e−16	53 / 494	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
16	4e−16	46 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
17	1e−15	70 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
18	1e−14	34 / 234	GSEA	LU_AGING_BRAIN_UP
19	1e−14	45 / 406	GSEA	BAELDE_DIABETIC_NEPHROPATHY_DN
20	3e−14	33 / 227	GSEA	ONDER_CDH1_TARGETS_2_UP
21	6e−14	38 / 308	CC	focal adhesion
22	6e−14	48 / 475	GSEA	ONKEN_UVEAL_MELANOMA_DN
23	1e−13	21 / 91	GSEA	BROWNE_HCMV_INFECTION_20HR_DN
24	2e−13	31 / 215	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
25	3e−13	2 / 14	Canc	LIU_PROSTATE_CANCER_DN
26	3e−13	27 / 163	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
27	6e−13	73 / 1013	Brain	Fetal_TssP
28	1e−12	43 / 426	GSEA	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
29	3e−12	41 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
30	4e−12	24 / 143	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
31	5e−12	23 / 131	Colon	Marisa_CRC−cluster−a
32	6e−12	26 / 171	GSEA	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
33	8e−12	39 / 377	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
34	8e−12	60 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
35	1e−11	24 / 149	GSEA	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_
36	1e−11	51 / 609	MF	cytoskeletal protein binding
37	2e−11	27 / 195	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
38	2e−11	26 / 181	HM	HALLMARK_P53_PATHWAY
39	2e−11	117 / 2188	Lymp	HOPP_Poised_promoter
40	3e−11	29 / 227	GSEA	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.02	8 / 111	HORVATH_aging_genes meth UP
2	0.17	5 / 100	HORVATH_aging_genes meth DOWN
3	0.31	2 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−10	49 / 626	cell adhesion
2	1e−09	113 / 2210	anatomical structure development
3	7e−08	42 / 581	cytoskeleton organization
4	3e−07	46 / 705	locomotion
5	4e−07	25 / 269	extracellular matrix organization
6	1e−06	15 / 115	cell cycle arrest
7	2e−06	12 / 74	wound healing
8	2e−06	78 / 1556	cell differentiation
9	2e−06	131 / 3068	signal transduction
10	2e−06	16 / 134	cell junction organization
11	3e−06	32 / 443	anatomical structure formation involved in morphogenesis
12	7e−06	26 / 336	negative regulation of cell proliferation
13	1e−05	29 / 409	cell motility
14	1e−05	14 / 122	plasma membrane organization
15	2e−05	22 / 271	positive regulation of apoptotic process
16	3e−05	7 / 31	visual learning
17	3e−05	36 / 590	cell morphogenesis
18	3e−05	11 / 83	muscle contraction
19	3e−05	6 / 22	actin filament bundle assembly
20	3e−05	5 / 14	negative regulation of Rho protein signal transduction

Brain

Rank	p−value	#in/all	Geneset
1	6e−13	73 / 1013	Fetal_TssP
2	8e−07	92 / 1907	Fetal_TxTrans
3	1e−06	101 / 2185	Fetal_TssA
4	2e−06	312 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	3e−06	38 / 574	Overlap_fetal_midbrain_TssP
6	3e−06	319 / 9330	Overlap_fetal_midbrain_ReprPC
7	2e−05	88 / 1949	Fetal_TssF
8	5e−05	215 / 5940	Overlap_fetal_midbrain_HetRpts
9	3e−04	51 / 1050	Fetal_EnhP
10	2e−03	309 / 9528	Overlap_fetal_midbrain_Quies
11	3e−03	33 / 668	Mid_Frontal_Lobe_Enh
12	4e−03	20 / 349	Fetal_ZNF
13	2e−02	16 / 304	Fetal_Het
14	2e−02	10 / 158	Overlap_fetal_midbrain_Het
15	2e−02	45 / 1122	Fetal_K9K27me3
16	2e−02	39 / 953	Fetal_Enh
17	3e−02	33 / 786	Fetal_EnhG
18	3e−02	18 / 383	Fetal_Tx
19	6e−02	20 / 468	Mid_Frontal_Lobe_TssF
20	1e−01	54 / 1548	Mid_Frontal_Lobe_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	3e−13	2 / 14	LIU_PROSTATE_CANCER_DN
2	6e−05	15 / 156	PanCan_PI3K_geneset_nanostring
3	4e−04	25 / 401	Lembcke_Colonic Inflammation
4	2e−03	6 / 44	PanCan_TGF−B_geneset_nanostring
5	3e−03	2 / 3	ZHANG_MGUS up
6	9e−03	6 / 61	PanCan_Wnt_geneset_nanostring
7	2e−02	8 / 111	PanCan_RAS_geneset_nanostring
8	3e−02	2 / 10	GENTLES_modul13
9	4e−02	2 / 11	GENTLES_modul17
10	6e−02	14 / 298	SPANG_BCL6−index2
11	6e−02	7 / 120	PanCan_CC+Apop_geneset_nanostring
12	9e−02	5 / 82	PanCan_TXmisReg_geneset_nanostring
13	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	2e−01	1 / 14	LIU_LIVER_CANCER
15	3e−01	5 / 121	PanCan_MAPK_geneset_nanostring
16	3e−01	1 / 12	LIU_BREAST_CANCER
17	3e−01	0 / 14	LIU_COMMON_CANCER_GENES
18	3e−01	1 / 13	GENTLES_modul12
19	3e−01	2 / 40	ZHANG_MM up
20	3e−01	3 / 70	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	6e−14	38 / 308	focal adhesion
2	1e−09	25 / 202	actin cytoskeleton
3	2e−08	32 / 352	cell surface
4	3e−08	139 / 3088	plasma membrane
5	4e−08	107 / 2193	extracellular exosome
6	7e−08	139 / 3132	extracellular region
7	2e−07	24 / 239	proteinaceous extracellular matrix
8	3e−07	77 / 1465	cytoskeleton
9	3e−06	16 / 138	cell−cell junction
10	5e−06	17 / 159	extracellular matrix
11	9e−06	9 / 48	stress fiber
12	1e−05	12 / 89	Z disc
13	2e−05	14 / 125	lamellipodium
14	2e−04	41 / 775	extracellular space
15	3e−04	9 / 73	basement membrane
16	4e−04	6 / 33	cell leading edge
17	5e−04	5 / 23	integrin complex
18	5e−04	11 / 113	postsynaptic density
19	7e−04	10 / 99	cell cortex
20	7e−04	6 / 37	platelet alpha granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.002	40 / 838	Chr 3
2	0.002	29 / 558	Chr 4
3	0.003	34 / 696	Chr 5
4	0.051	28 / 687	Chr 6
5	0.092	53 / 1500	Chr 1
6	0.139	21 / 552	Chr 10
7	0.326	8 / 221	Chr 18
8	0.378	22 / 689	Chr 7
9	0.429	24 / 775	Chr 12
10	0.504	14 / 465	Chr 15
11	0.509	8 / 262	Chr 13
12	0.546	29 / 993	Chr 2
13	0.606	13 / 462	Chr 14
14	0.653	4 / 151	Chr 21
15	0.731	12 / 469	Chr 8
16	0.739	10 / 398	Chr 20
17	0.808	20 / 801	Chr 11
18	0.955	11 / 576	Chr 9
19	0.966	10 / 551	Chr X
20	0.986	11 / 649	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−12	23 / 131	Marisa_CRC−cluster−a
2	2e−10	20 / 117	Marisa_CRC−cluster−b
3	2e−10	360 / 10290	TssWk_Colon
4	2e−10	30 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	3e−09	167 / 3812	TssD1_Colon
6	2e−08	167 / 3897	Quies1_Colon
7	7e−08	27 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
8	4e−06	140 / 3383	EnhWk2_Colon
9	3e−04	283 / 8415	Quies3_Colon
10	6e−04	24 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
11	1e−03	105 / 2698	EnhA_Colon
12	1e−03	4 / 17	Vilar_mutated−in−CRC−CamP
13	2e−03	6 / 43	Marisa_CRC−cluster−f
14	2e−03	3 / 9	Budinska_D_Mesenchymal_UP
15	3e−03	180 / 5155	EnhWk1_Colon
16	3e−03	281 / 8580	TxWk_Colon
17	3e−03	306 / 9482	TssA_Colon
18	4e−03	293 / 9027	Tx_Colon
19	5e−03	23 / 436	K9acLow_Colon
20	5e−03	12 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	7e−06	24 / 294	GUDJ_psoriasis down
2	6e−01	12 / 435	GUDJ_psoriasis up
3	1e+00	0 / 11	BCHETNIA_EBM up
4	1e+00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−06	11 / 62	cultured astroglia vs. in vivo astrocytes
2	2e−06	14 / 103	GIEZELT_GBM_WT_up_VS_mut
3	3e−05	7 / 32	Colman_survival_associated
4	1e−04	11 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
5	5e−04	7 / 49	OL vs. MOG−OL
6	3e−03	13 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
7	4e−03	4 / 22	KIM prognostic signature LTS vs. STS
8	7e−03	6 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
9	8e−03	9 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
10	9e−03	8 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	1e−02	3 / 16	KIM deleted & downregulated in LTS
12	1e−02	9 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	2e−02	17 / 332	Up
14	2e−02	7 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
15	3e−02	4 / 39	OPC
16	4e−02	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
17	4e−02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
18	5e−02	4 / 47	Vishal_subnetwork signature of survival in GBM
19	5e−02	5 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
20	6e−02	4 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−32	73 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	2e−30	56 / 286	PASINI_SUZ12_TARGETS_DN
3	3e−25	72 / 594	WONG_ADULT_TISSUE_STEM_MODULE
4	2e−24	80 / 749	CUI_TCF21_TARGETS_2_DN
5	7e−23	49 / 302	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	2e−21	85 / 930	NUYTTEN_EZH2_TARGETS_UP
7	1e−20	55 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
8	6e−19	51 / 401	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
9	2e−18	71 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
10	1e−16	40 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
11	2e−16	37 / 245	WANG_SMARCE1_TARGETS_UP
12	2e−16	48 / 410	LIM_MAMMARY_STEM_CELL_UP
13	2e−16	53 / 494	CHICAS_RB1_TARGETS_CONFLUENT
14	4e−16	46 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
15	1e−15	70 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
16	1e−14	34 / 234	LU_AGING_BRAIN_UP
17	1e−14	45 / 406	BAELDE_DIABETIC_NEPHROPATHY_DN
18	3e−14	33 / 227	ONDER_CDH1_TARGETS_2_UP
19	6e−14	48 / 475	ONKEN_UVEAL_MELANOMA_DN
20	1e−13	21 / 91	BROWNE_HCMV_INFECTION_20HR_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−20	35 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	2e−11	26 / 181	HALLMARK_P53_PATHWAY
3	8e−11	22 / 137	HALLMARK_UV_RESPONSE_DN
4	2e−09	23 / 176	HALLMARK_HYPOXIA
5	2e−09	23 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	9e−05	6 / 26	HALLMARK_ANGIOGENESIS
7	1e−04	15 / 165	HALLMARK_MYOGENESIS
8	1e−04	15 / 167	HALLMARK_APICAL_JUNCTION
9	4e−04	7 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	9e−04	7 / 53	HALLMARK_TGF_BETA_SIGNALING
11	9e−04	12 / 140	HALLMARK_APOPTOSIS
12	4e−03	11 / 148	HALLMARK_KRAS_SIGNALING_UP
13	6e−03	8 / 94	HALLMARK_ANDROGEN_RESPONSE
14	1e−02	11 / 167	HALLMARK_IL2_STAT5_SIGNALING
15	2e−02	4 / 37	HALLMARK_APICAL_SURFACE
16	3e−02	11 / 195	HALLMARK_MITOTIC_SPINDLE
17	3e−02	10 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	4e−02	7 / 107	HALLMARK_COAGULATION
19	6e−02	8 / 140	HALLMARK_INFLAMMATORY_RESPONSE
20	6e−02	3 / 31	HALLMARK_HEDGEHOG_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 18	DUMEAUX_High bmi enriched genes
2	0.1	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
3	0.4	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.5	2 / 62	DUMEAUX_Smoking enriched genes
5	0.6	1 / 32	DUMEAUX_Fasting enriched genes
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−21	40 / 212	LENZ_Stromal signature 1
2	2e−11	117 / 2188	HOPP_Poised_promoter
3	1e−07	147 / 3396	HOPP_Repressed
4	2e−07	220 / 5693	HOPP_Weak_enhancer
5	3e−06	113 / 2563	HOPP_Heterochrom
6	8e−06	99 / 2211	HOPP_Repetitive
7	9e−05	12 / 109	ROSOLOWSKI_green total
8	2e−04	7 / 43	LENZ_Stromal signature 2
9	2e−04	20 / 280	SPANG_CD40 6hrs UP
10	7e−04	9 / 82	ROSOLOWSKI_green UP
11	9e−04	245 / 7209	HOPP_Weak_promoter
12	9e−04	195 / 5538	HOPP_Weak_txn
13	1e−03	18 / 268	SPANG_IL21 UP
14	1e−03	225 / 6564	HOPP_Strong_enhancer
15	2e−03	4 / 19	Subero_MM_hyper_meth
16	2e−03	4 / 20	SPANG_BAFF 9hrs UP
17	7e−03	8 / 96	Subero_DLBCL_hyper_meth
18	8e−03	16 / 275	TARTE_Mature plasma cell signature
19	1e−02	7 / 81	Subero_INT_hyper_meth
20	1e−02	5 / 47	Subero_FL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	1e−11	51 / 609	cytoskeletal protein binding
2	9e−10	324 / 8984	protein binding
3	4e−09	16 / 86	integrin binding
4	2e−06	24 / 271	actin binding
5	4e−06	13 / 95	heparin binding
6	7e−06	35 / 530	calcium ion binding
7	7e−05	5 / 16	extracellular matrix binding
8	1e−04	5 / 17	insulin−like growth factor binding
9	1e−04	5 / 18	laminin binding
10	2e−04	11 / 102	actin filament binding
11	5e−04	7 / 49	collagen binding
12	6e−04	17 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
13	6e−04	4 / 14	G−protein alpha−subunit binding
14	6e−04	14 / 174	transcription corepressor activity
15	1e−03	5 / 29	structural constituent of muscle
16	2e−03	10 / 111	protein binding, bridging
17	2e−03	27 / 501	identical protein binding
18	2e−03	22 / 378	structural molecule activity
19	2e−03	24 / 430	lipid binding
20	2e−03	406 / 13179	molecular_function

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−07	19 / 170	hsa−miR−183
2	1e−06	16 / 129	hsa−miR−576−3p
3	2e−06	19 / 183	hsa−miR−1283
4	3e−06	32 / 447	hsa−miR−130b
5	4e−06	39 / 607	hsa−miR−20a
6	1e−05	18 / 187	hsa−miR−944
7	1e−05	25 / 327	hsa−miR−367
8	2e−05	16 / 157	hsa−miR−512−3p
9	3e−05	34 / 541	hsa−miR−17
10	3e−05	24 / 321	hsa−miR−32
11	3e−05	35 / 569	hsa−miR−20b
12	3e−05	22 / 282	hsa−miR−570
13	4e−05	27 / 391	hsa−miR−519a
14	5e−05	20 / 250	hsa−miR−524−5p
15	6e−05	32 / 517	hsa−miR−106b
16	9e−05	16 / 181	hsa−miR−29c
17	9e−05	12 / 110	hsa−miR−491−3p
18	1e−04	13 / 129	hsa−miR−1272
19	1e−04	10 / 80	hsa−miR−562
20	1e−04	29 / 467	hsa−miR−301a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	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	

TF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 9	MYC_Targets DOWN
2	0.012	47 / 1139	HEBENSTREIT_low expression TF
3	0.025	103 / 2927	ICGC_Rad21_targets
4	0.058	1 / 2	MYC_Cell cycle DOWN
5	0.058	1 / 2	MYC_ECM cell adhesion DOWN
6	0.085	46 / 1273	ICGC_P300_targets
7	0.087	65 / 1872	ICGC_Mef2_targets
8	0.106	45 / 1266	ICGC_NrsfPcr1_targets
9	0.139	1 / 5	MYC_TF and cofactors
10	0.318	63 / 2013	ICGC_Bcl11_targets
11	0.350	37 / 1171	KIM_MYC targets
12	0.361	1 / 15	NOWICK_TF
13	0.464	118 / 3966	ICGC_Pu1_targets
14	0.467	51 / 1701	HEBENSTREIT_high expression TF
15	0.494	84 / 2836	ICGC_BatfPcr1_targets
16	0.527	71 / 2416	ICGC_Bcl3_targets
17	0.586	17 / 595	ICGC_NrsfPcr2_targets
18	0.623	155 / 5355	ICGC_Pol2_targets
19	0.643	124 / 4314	ICGC_Ebfsc137065_targets
20	0.665	15 / 553	ICGC_RxraPcr1_targets

TF_Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 11	WIRTH_Sec. lymphoid organs
2	5e−03	13 / 194	PALMER_B−Cell signature up
3	2e−02	8 / 114	PALMER_T−Cell signature up
4	5e−02	2 / 12	WIRTH_Thymus
5	6e−02	2 / 14	WIRTH_Telencephalon
6	2e−01	9 / 225	PALMER_Granulocytes signature up
7	2e−01	1 / 9	PALMER_CD8+ T−Cell signature up
8	3e−01	1 / 11	WIRTH_Cortex cerebri
9	3e−01	4 / 95	WIRTH_Muscle
10	3e−01	1 / 13	WIRTH_B−cells
11	3e−01	12 / 350	WIRTH_Nervous System
12	4e−01	2 / 46	WIRTH_Liver
13	6e−01	1 / 32	WIRTH_Placenta
14	6e−01	2 / 74	WIRTH_Mucosa
15	8e−01	8 / 350	WIRTH_Immune system
16	1e+00	0 / 32	WIRTH_Pancreas
17	1e+00	0 / 11	WIRTH_Prim. lymphoid organs
18	1e+00	0 / 8	WIRTH_Tonsil
19	1e+00	0 / 12	WIRTH_Lymphocytes
20	1e+00	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.05	124 / 3682	LU_BPDE 0.005 DN
2	0.51	33 / 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	

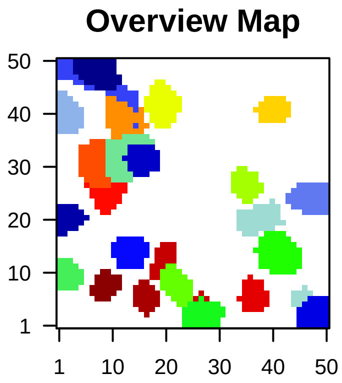
Correlation Clusters

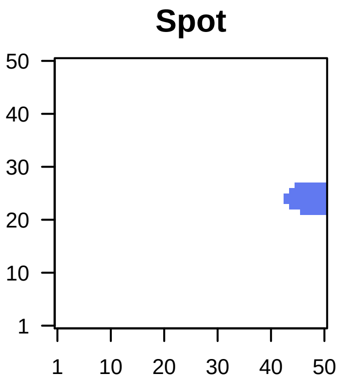
Spot Summary: U

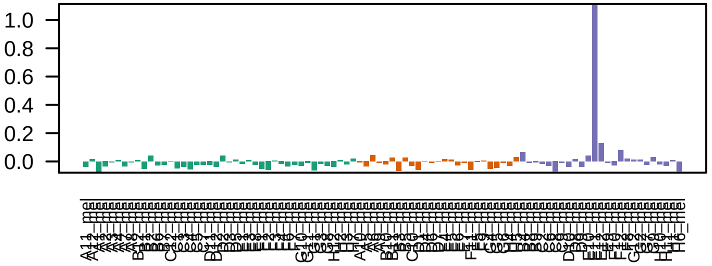
metagenes = 41
genes = 293

<r> metagenes = 0.93
<r> genes = 0.24
beta: r2= 0.88 / log p= −Inf

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





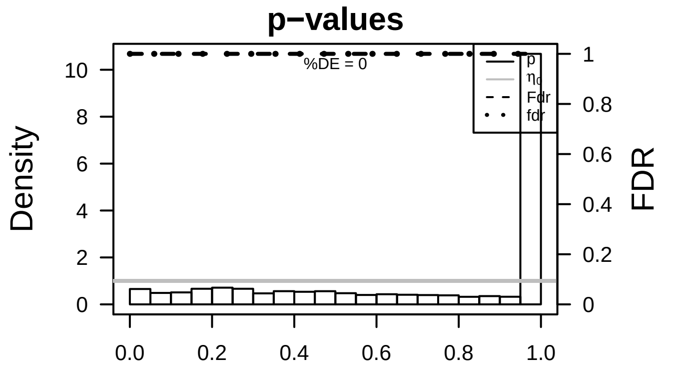


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	VCAN	2.39	−0.1	0.64	VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]
2	SIDT2	1.98	−0.08	0.21	SIDT2	SID1 transmembrane family, member 2 [Source:HGNC Symb
3	SCN2A	1.98	−0.06	0.67	SCN2A	sodium channel, voltage gated, type II alpha subunit [Source:
4	CLHC1	1.96	−0.28	0.35	CLHC1	clathrin heavy chain linker domain containing 1 [Source:HGN
5	CEMIP	1.96	−0.23	0.46	CEMIP	cell migration inducing protein, hyaluronan binding [Source:H
6	OXTR	1.94	−0.06	0.76	OXTR	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]
7	MYL4	1.93	−0.04	0.81	MYL4	myosin, light chain 4, alkali; atrial, embryonic [Source:HGNC
8	PHLDB2	1.91	−0.23	0.46	PHLDB2	pleckstrin homology−like domain, family B, member 2 [Source
9	CHL1	1.89	−0.05	0.73	CHL1	cell adhesion molecule L1−like [Source:HGNC Symbol;Acc:H
10	CCDC81	1.88	−0.05	0.77	CCDC81	coiled−coil domain containing 81 [Source:HGNC Symbol;Acc
11	SDC2	1.85	−0.15	0.51	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
12	GAD1	1.84	−0.07	0.72	GAD1	glutamate decarboxylase 1 (brain, 67kDa) [Source:HGNC Sy
13	SAMD9L	1.83	−0.22	0.3	SAMD9L	sterile alpha motif domain containing 9−like [Source:HGNC S
14	TAB1	1.82	−0.27	0.31	TAB1	TGF−beta activated kinase 1/MAP3K7 binding protein 1 [Sou
15	DDX25	1.82	−0.16	0.41	DDX25	DEAD (Asp−Glu−Ala−Asp) box helicase 25 [Source:HGNC S
16	FBXO3	1.81	−0.52	0.27	FBXO3	F−box protein 3 [Source:HGNC Symbol;Acc:HGNC:13582]
17	HIST1H2BH	1.8	−0.08	0.54	HIST1H2BH	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:HGNC:47
18	NEGR1	1.79	−0.04	0.78	NEGR1	neuronal growth regulator 1 [Source:HGNC Symbol;Acc:HGN
19	PTPRO	1.79	−0.04	0.3	PTPRO	protein tyrosine phosphatase, receptor type, O [Source:HGN
20	TPCN1	1.78	−0.2	0.31	TPCN1	two pore segment channel 1 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−07	70 / 1949	Brain	Fetal_TssF
2	4e−06	24 / 427	Colon	Quies2_Colon
3	4e−06	30 / 618	GSEA	GOZGIT_ESR1_TARGETS_DN
4	1e−05	18 / 283	GSEA	PEREZ_TP63_TARGETS
5	6e−05	67 / 2159	Colon	TssP_Colon
6	1e−04	60 / 1907	Brain	Fetal_TxTrans
7	1e−04	11 / 146	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
8	2e−04	3 / 7	Glio	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
9	3e−04	19 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
10	4e−04	31 / 823	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
11	5e−04	8 / 93	GSEA	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4
12	5e−04	7 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
13	5e−04	4 / 20	GSEA	MARKS_HDAC_TARGETS_UP
14	6e−04	11 / 173	GSEA	PEREZ_TP53_AND_TP63_TARGETS
15	8e−04	10 / 152	GSEA	PEDRIOLI_MIR31_TARGETS_UP
16	8e−04	5 / 38	GSEA	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_
17	9e−04	8 / 102	GSEA	CHEBOTAEV_GR_TARGETS_DN
18	9e−04	23 / 574	Brain	Overlap_fetal_midbrain_TssP
19	1e−03	3 / 11	GSEA	SA_PROGRAMMED_CELL_DEATH
20	1e−03	10 / 160	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
21	1e−03	6 / 62	Glio	cultured astroglia vs. in vivo astrocytes
22	1e−03	14 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
23	1e−03	3 / 12	CC	axonal growth cone
24	2e−03	41 / 1308	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
25	2e−03	10 / 168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
26	2e−03	5 / 46	GSEA	CROMER_TUMORIGENESIS_UP
27	2e−03	8 / 119	BP	skeletal system development
28	2e−03	7 / 94	GSEA	WANG_HCP_PROSTATE_CANCER
29	3e−03	7 / 95	GSEA	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
30	3e−03	5 / 49	CC	Golgi lumen
31	3e−03	6 / 72	GSEA	REACTOME_MEIOTIC_RECOMBINATION
32	3e−03	4 / 31	GSEA	FRASOR_RESPONSE_TO_ESTRADIOL_UP
33	3e−03	4 / 31	GSEA	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN
34	3e−03	34 / 1065	Brain	Overlap_fetal_midbrain_Enh
35	3e−03	12 / 245	GSEA	WANG_SMARCE1_TARGETS_UP
36	3e−03	11 / 214	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
37	3e−03	3 / 16	MF	cysteine−type endopeptidase activator activity involved in apoptotic process
38	3e−03	7 / 100	GSEA	REACTOME_MEIOSIS
39	4e−03	9 / 156	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
40	4e−03	5 / 53	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 38	TESCHENDORFF_age_hypermethylated
2	0.6	2 / 111	HORVATH_aging_genes meth UP
3	0.9	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	0.002	8 / 119	skeletal system development
2	0.005	3 / 18	smooth muscle cell differentiation
3	0.006	3 / 19	membrane depolarization during action potential
4	0.007	4 / 39	synapse assembly
5	0.008	4 / 40	adult locomotory behavior
6	0.010	3 / 23	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion m
7	0.010	3 / 23	positive regulation of ATPase activity
8	0.010	3 / 23	reciprocal meiotic recombination
9	0.012	5 / 70	activation of cysteine−type endopeptidase activity involved in apoptotic proces
10	0.014	4 / 48	JNK cascade
11	0.015	4 / 49	response to mechanical stimulus
12	0.015	3 / 27	negative regulation of MAP kinase activity
13	0.015	2 / 10	dermatan sulfate biosynthetic process
14	0.015	2 / 10	maternal behavior
15	0.015	2 / 10	microvillus assembly
16	0.015	2 / 10	outflow tract septum morphogenesis
17	0.019	2 / 11	response to corticosterone
18	0.019	2 / 11	retrograde transport, endosome to plasma membrane
19	0.020	3 / 30	response to progesterone
20	0.021	20 / 626	cell adhesion

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	70 / 1949	Fetal_TssF
2	1e−04	60 / 1907	Fetal_TxTrans
3	9e−04	23 / 574	Overlap_fetal_midbrain_TssP
4	3e−03	34 / 1065	Overlap_fetal_midbrain_Enh
5	5e−03	59 / 2185	Fetal_TssA
6	2e−02	19 / 564	Mid_Frontal_Lobe_EnhP
7	2e−02	26 / 884	Overlap_fetal_midbrain_EnhG
8	2e−02	29 / 1013	Fetal_TssP
9	3e−02	21 / 686	Overlap_fetal_midbrain_TssA
10	3e−02	27 / 953	Fetal_Enh
11	4e−02	13 / 383	Fetal_Tx
12	5e−02	24 / 862	Overlap_fetal_midbrain_TxTrans
13	6e−02	22 / 786	Fetal_EnhG
14	8e−02	68 / 2972	Mid_Frontal_Lobe_ReprPC
15	9e−02	44 / 1845	Fetal_Quies
16	1e−01	18 / 668	Mid_Frontal_Lobe_Enh
17	1e−01	21 / 812	Mid_Frontal_Lobe_TssP
18	1e−01	29 / 1207	Overlap_fetal_midbrain_TssF
19	2e−01	27 / 1122	Fetal_K9K27me3
20	2e−01	5 / 166	Mid_Frontal_Lobe_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	4 / 82	PanCan_TXmisReg_geneset_nanostring
2	0.16	11 / 401	Lembcke_Colonic Inflammation
3	0.20	1 / 11	GENTLES_modul17
4	0.21	1 / 12	LIU_BREAST_CANCER
5	0.26	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.26	1 / 15	GENTLES_modul4
7	0.33	1 / 20	PanCan_ChromMod_geneset_nanostring
8	0.34	2 / 61	PanCan_Wnt_geneset_nanostring
9	0.35	1 / 22	PanCan_HH_geneset_nanostring
10	0.61	1 / 48	KUIPER_MM poor survival
11	0.65	2 / 113	PanCan_Driver_Gene_geneset_nanostring
12	0.66	1 / 55	PanCan_JAK−ST_geneset_nanostring
13	0.69	3 / 180	SPANG_LPS−index2
14	0.69	2 / 121	PanCan_MAPK_geneset_nanostring
15	0.73	0 / 14	LIU_COMMON_CANCER_GENES
16	0.77	0 / 14	LIU_PROSTATE_CANCER_DN
17	0.81	2 / 156	PanCan_PI3K_geneset_nanostring
18	0.85	7 / 489	Lembcke_Normal vs Adenoma
19	0.91	1 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.98	2 / 298	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	0.001	3 / 12	axonal growth cone
2	0.003	5 / 49	Golgi lumen
3	0.008	6 / 89	tight junction
4	0.013	8 / 159	extracellular matrix
5	0.015	6 / 102	cytoplasmic vesicle membrane
6	0.019	5 / 79	nucleosome
7	0.020	9 / 205	neuron projection
8	0.021	75 / 3088	plasma membrane
9	0.022	2 / 12	node of Ranvier
10	0.024	3 / 32	nuclear nucleosome
11	0.026	2 / 13	TCTN−B9D complex
12	0.030	2 / 14	clathrin−coated vesicle membrane
13	0.036	4 / 64	anchored component of membrane
14	0.045	9 / 239	proteinaceous extracellular matrix
15	0.046	3 / 41	presynaptic membrane
16	0.054	6 / 138	cell−cell junction
17	0.057	2 / 20	ciliary transition zone
18	0.061	4 / 76	extrinsic component of membrane
19	0.079	2 / 24	keratin filament
20	0.081	3 / 52	coated pit

Chr

Rank	p−value	#in/all	Geneset
1	0.005	26 / 775	Chr 12
2	0.122	10 / 335	Chr 22
3	0.222	19 / 801	Chr 11
4	0.293	23 / 1037	Chr 19
5	0.311	11 / 469	Chr 8
6	0.326	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
7	0.341	4 / 151	Chr 21
8	0.370	15 / 689	Chr 7
9	0.385	15 / 696	Chr 5
10	0.475	14 / 687	Chr 6
11	0.476	17 / 840	Chr 17
12	0.531	11 / 558	Chr 4
13	0.574	11 / 576	Chr 9
14	0.575	16 / 838	Chr 3
15	0.584	5 / 262	Chr 13
16	0.630	4 / 221	Chr 18
17	0.685	8 / 462	Chr 14
18	0.692	8 / 465	Chr 15
19	0.703	27 / 1500	Chr 1
20	0.754	9 / 551	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−06	24 / 427	Quies2_Colon
2	6e−05	67 / 2159	TssP_Colon
3	5e−03	96 / 3897	Quies1_Colon
4	6e−03	10 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
5	8e−03	40 / 1386	Het_Colon
6	8e−03	57 / 2142	ReprPC_Colon
7	1e−02	15 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
8	2e−02	50 / 1889	ReprPCWk_Colon
9	6e−02	78 / 3383	EnhWk2_Colon
10	7e−02	213 / 10290	TssWk_Colon
11	7e−02	86 / 3812	TssD1_Colon
12	8e−02	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
13	8e−02	27 / 1038	HetRpts_Colon
14	1e−01	6 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	1e−01	27 / 1079	ZNF_Colon
16	1e−01	1 / 7	Kaneda_CIMP−group2
17	2e−01	11 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
18	2e−01	1 / 9	Budinska_D_Mesenchymal_UP
19	2e−01	12 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	2e−01	10 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	0.03	11 / 294	GUDJ_psoriasis down
2	0.23	11 / 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	2e−04	3 / 7	WILLSCHER_GBM_LTSwt_proteomics−G_UP
2	1e−03	6 / 62	cultured astroglia vs. in vivo astrocytes
3	1e−02	9 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
4	1e−02	5 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
5	1e−02	6 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
6	2e−02	2 / 11	Christensen_hypermethylated_in_ependymoma
7	3e−02	4 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
8	6e−02	4 / 75	GIEZELT_GBM_STS_down_VS_LTS
9	7e−02	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	1e−01	2 / 32	Colman_survival_associated
11	1e−01	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
12	1e−01	1 / 8	VERHAAK_PN_Brain
13	2e−01	10 / 356	Down_a
14	2e−01	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
15	2e−01	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
16	2e−01	3 / 74	WIRTH_Normal Brain
17	2e−01	1 / 11	Martinez_Glio_hypermeth
18	2e−01	1 / 11	astrocytes_glio
19	2e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
20	2e−01	2 / 45	Christensen_hypermethylated_in_primary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−06	30 / 618	GOZGIT_ESR1_TARGETS_DN
2	1e−05	18 / 283	PEREZ_TP63_TARGETS
3	1e−04	11 / 146	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
4	3e−04	19 / 400	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
5	4e−04	31 / 823	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
6	5e−04	8 / 93	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4
7	5e−04	7 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
8	5e−04	4 / 20	MARKS_HDAC_TARGETS_UP
9	6e−04	11 / 173	PEREZ_TP53_AND_TP63_TARGETS
10	8e−04	10 / 152	PEDRIOLI_MIR31_TARGETS_UP
11	8e−04	5 / 38	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_UP
12	9e−04	8 / 102	CHEBOTAEV_GR_TARGETS_DN
13	1e−03	3 / 11	SA_PROGRAMMED_CELL_DEATH
14	1e−03	10 / 160	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
15	1e−03	14 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
16	2e−03	41 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
17	2e−03	5 / 46	CROMER_TUMORIGENESIS_UP
18	2e−03	7 / 94	WANG_HCP_PROSTATE_CANCER
19	3e−03	7 / 95	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
20	3e−03	6 / 72	REACTOME_MEIOTIC_RECOMBINATION

HM

Rank	p−value	#in/all	Geneset
1	0.002	10 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	0.005	7 / 107	HALLMARK_COAGULATION
3	0.091	4 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	0.091	2 / 26	HALLMARK_ANGIOGENESIS
5	0.109	6 / 167	HALLMARK_APICAL_JUNCTION
6	0.126	6 / 174	HALLMARK_HEME_METABOLISM
7	0.156	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.265	5 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	0.277	2 / 53	HALLMARK_TGF_BETA_SIGNALING
10	0.284	3 / 95	HALLMARK_SPERMATOGENESIS
11	0.412	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.421	4 / 169	HALLMARK_XENOBIOTIC_METABOLISM
13	0.425	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
14	0.451	4 / 176	HALLMARK_HYPOXIA
15	0.453	3 / 127	HALLMARK_KRAS_SIGNALING_DN
16	0.458	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
17	0.473	4 / 181	HALLMARK_P53_PATHWAY
18	0.481	4 / 183	HALLMARK_GLYCOLYSIS
19	0.503	3 / 137	HALLMARK_UV_RESPONSE_DN
20	0.546	3 / 146	HALLMARK_UV_RESPONSE_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 32	DUMEAUX_Fasting enriched genes
2	0.2	1 / 10	DUMEAUX_Smoking literature genes up
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	58 / 2211	HOPP_Repetitive
2	0.02	82 / 3396	HOPP_Repressed
3	0.03	55 / 2188	HOPP_Poised_promoter
4	0.08	1 / 4	Shaknovich_ABC_hyper_meth
5	0.11	3 / 60	Subero_T−ALL_hyper_meth
6	0.12	3 / 61	SPANG_LPS 6hrs DN
7	0.12	7 / 212	LENZ_Stromal signature 1
8	0.13	8 / 256	SPANG_IL21 DN
9	0.17	8 / 275	TARTE_Mature plasma cell signature
10	0.18	8 / 280	SPANG_CD40 6hrs UP
11	0.18	2 / 40	Subero_mBL_hyper_meth
12	0.20	56 / 2563	HOPP_Heterochrom
13	0.21	3 / 81	Subero_INT_hyper_meth
14	0.23	2 / 47	Subero_FL_hyper_meth
15	0.29	1 / 17	Aukema_BCL2 UP_BCL6 DN
16	0.29	3 / 96	Subero_DLBCL_hyper_meth
17	0.35	3 / 107	SPANG_LPS 6hrs UP
18	0.35	6 / 247	ZHANG_DLBCL mutated
19	0.36	24 / 1128	SPANG_BCR DN
20	0.48	1 / 33	LEE_Developmental_regulators

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 16	cysteine−type endopeptidase activator activity involved in apoptotic process
2	0.005	3 / 18	actin monomer binding
3	0.013	4 / 47	GDP binding
4	0.015	2 / 10	hedgehog receptor activity
5	0.018	25 / 820	sequence−specific DNA binding transcription factor activity
6	0.022	3 / 31	transcription regulatory region sequence−specific DNA binding
7	0.026	2 / 13	voltage−gated sodium channel activity
8	0.031	17 / 530	calcium ion binding
9	0.034	2 / 15	hyaluronic acid binding
10	0.038	2 / 16	K63−linked polyubiquitin binding
11	0.043	3 / 40	extracellular matrix structural constituent
12	0.043	5 / 98	ion channel activity
13	0.053	24 / 866	signal transducer activity
14	0.057	2 / 20	peptide hormone binding
15	0.057	3 / 45	calcium−dependent protein binding
16	0.058	23 / 830	nucleic acid binding transcription factor activity
17	0.059	14 / 450	sequence−specific DNA binding
18	0.066	4 / 78	Rab GTPase binding
19	0.068	2 / 22	Wnt−protein binding
20	0.074	2 / 23	phosphoric diester hydrolase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	8 / 180	hsa−miR−302e
2	0.03	9 / 222	hsa−miR−185
3	0.04	5 / 97	hsa−miR−624
4	0.04	11 / 314	hsa−miR−520c−3p
5	0.05	4 / 70	hsa−miR−628−3p
6	0.05	8 / 209	hsa−miR−196a
7	0.06	9 / 250	hsa−miR−520a−3p
8	0.07	16 / 541	hsa−miR−17
9	0.07	7 / 182	hsa−miR−573
10	0.07	4 / 80	hsa−miR−942
11	0.09	9 / 272	hsa−miR−520b
12	0.09	16 / 569	hsa−miR−20b
13	0.11	2 / 29	hsa−miR−1237
14	0.11	3 / 60	hsa−miR−296−3p
15	0.11	9 / 288	hsa−miR−34a
16	0.12	3 / 61	hsa−miR−514
17	0.12	11 / 376	hsa−miR−373
18	0.13	7 / 214	hsa−miR−548m
19	0.13	12 / 426	hsa−miR−519d
20	0.13	8 / 258	hsa−miR−520e

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	BENTINK_ras.4
2	0.2	1 / 12	BENTINK_e2f3.2
3	0.2	1 / 12	BENTINK_ras.1
4	0.2	1 / 13	GUSTAFSON_PI3K_DN
5	0.2	1 / 13	BENTINK_src.10
6	1.0	0 / 12	GUSTAFSON_PI3K_UP
7	1.0	0 / 14	BENTINK_e2f3.1
8	1.0	0 / 13	BENTINK_myc.1
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	0.01	33 / 1139	HEBENSTREIT_low expression TF
2	0.21	63 / 2927	ICGC_Rad21_targets
3	0.31	1 / 19	MYC_Metabolism UP
4	0.49	78 / 3966	ICGC_Pu1_targets
5	0.59	13 / 690	ICGC_Atf3_targets
6	0.62	38 / 2013	ICGC_Bcl11_targets
7	0.63	12 / 653	ICGC_SrfPcr2_targets
8	0.67	24 / 1314	ICGC_Usf1_targets
9	0.68	116 / 6114	ICGC_Runx3_targets
10	0.69	1 / 59	MYC_Targets UP
11	0.70	34 / 1872	ICGC_Mef2_targets
12	0.70	39 / 2137	ICGC_SrfV0416101_targets
13	0.72	52 / 2836	ICGC_BatfPcr1_targets
14	0.75	43 / 2391	ICGC_Pbx3_targets
15	0.77	33 / 1878	ICGC_Cebpbsc150_targets
16	0.77	79 / 4314	ICGC_Ebfsc137065_targets
17	0.81	21 / 1266	ICGC_NrsfPcr1_targets
18	0.82	42 / 2416	ICGC_Bcl3_targets
19	0.82	108 / 5890	ICGC_Elf1_targets
20	0.82	21 / 1273	ICGC_P300_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 14	VAQUERIZAS_Ovary
2	0.07	2 / 23	VAQUERIZAS_Trachea
3	0.07	2 / 23	VAQUERIZAS_Adrenal cortex
4	0.16	1 / 9	VAQUERIZAS_Kidney
5	0.17	2 / 38	VAQUERIZAS_Testis
6	0.22	2 / 45	VAQUERIZAS_Uterus
7	0.27	1 / 16	VAQUERIZAS_Adrenal gland
8	0.29	1 / 17	VAQUERIZAS_Heart
9	0.36	1 / 23	VAQUERIZAS_Spinal cord
10	0.44	1 / 29	VAQUERIZAS_Smooth muscle
11	0.44	1 / 29	VAQUERIZAS_Fetal lung
12	0.51	1 / 36	VAQUERIZAS_Fetal brain
13	0.53	1 / 38	VAQUERIZAS_Whole brain
14	0.53	3 / 143	VAQUERIZAS_General
15	0.55	1 / 40	VAQUERIZAS_Thyroid
16	0.68	1 / 58	VAQUERIZAS_Lung
17	0.69	1 / 59	VAQUERIZAS_Whole blood
18	1.00	0 / 41	VAQUERIZAS_Placenta
19	1.00	0 / 26	VAQUERIZAS_Liver
20	1.00	0 / 33	VAQUERIZAS_Prostate

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	12 / 350	WIRTH_Nervous System
2	0.09	1 / 5	WIRTH_Bone marrow
3	0.16	4 / 107	WIRTH_Testis
4	0.18	4 / 114	PALMER_T−Cell signature up
5	0.21	1 / 12	WIRTH_Lymphocytes
6	0.23	2 / 46	WIRTH_Liver
7	0.47	1 / 32	WIRTH_Pancreas
8	0.53	4 / 194	PALMER_B−Cell signature up
9	0.56	1 / 41	WIRTH_Homeostasis
10	0.68	6 / 350	WIRTH_Immune system
11	0.77	1 / 74	WIRTH_Mucosa
12	0.82	3 / 225	PALMER_Granulocytes signature up
13	1.00	0 / 11	WIRTH_Sec. lymphoid organs
14	1.00	0 / 11	WIRTH_Prim. lymphoid organs
15	1.00	0 / 13	WIRTH_B−cells
16	1.00	0 / 8	WIRTH_Tonsil
17	1.00	0 / 12	WIRTH_Thymus
18	1.00	0 / 11	WIRTH_Globus pallidus
19	1.00	0 / 14	WIRTH_Telencephalon
20	1.00	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.07	83 / 3682	LU_BPDE 0.005 DN
2	0.93	16 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

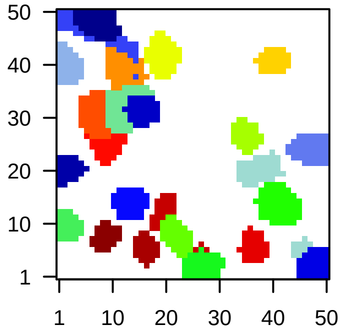
Spot Summary: V

metagenes = 28
genes = 236

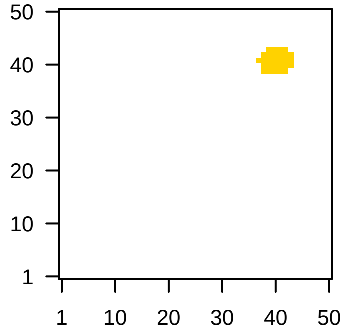
<r> metagenes = 0.95
<r> genes = 0.24
beta: r2= 0.67 / log p= −Inf

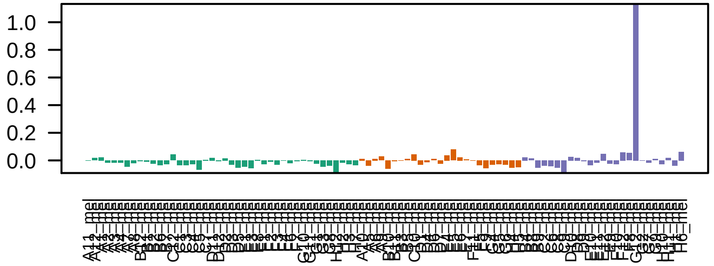
samples with spot = 1 (1.1 %)
MSC3 : 1 (4 %)

Overview Map



Spot





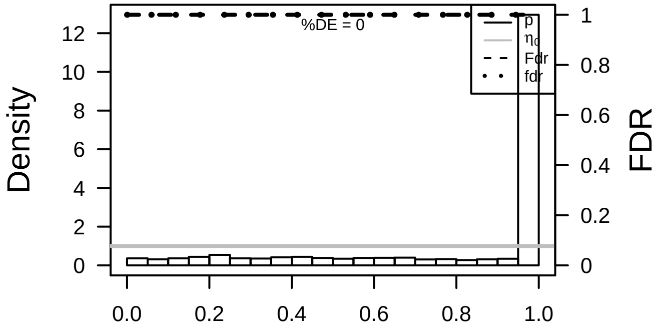
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CDKL1	2.2	−0.24	0.39	CDKL1	cyclin−dependent kinase−like 1 (CDC2−related kinase) [Sour
2	PRDM6	2.01	−0.06	0.5	PRDM6	PR domain containing 6 [Source:HGNC Symbol;Acc:HGNC:
3	MLLT10	1.93	−0.65	0.3	MLLT10	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
4	PAFAH2	1.89	−0.22	0.4	PAFAH2	platelet−activating factor acetylhydrolase 2, 40kDa [Source:H
5	ZNF287	1.87	−0.07	0.57	ZNF287	zinc finger protein 287 [Source:HGNC Symbol;Acc:HGNC:13
6	FBXO16	1.84	−0.09	0.39	FBXO16	F−box protein 16 [Source:HGNC Symbol;Acc:HGNC:13618]
7	ZNF221	1.83	−0.1	0.43	ZNF221	zinc finger protein 221 [Source:HGNC Symbol;Acc:HGNC:13
8	TMEM55B	1.81	−0.24	0.38	TMEM55B	transmembrane protein 55B [Source:HGNC Symbol;Acc:HGN
9	SLC22A1	1.81	−0.09	0.66	SLC22A1	solute carrier family 22 (organic cation transporter), member
10	THBS3	1.78	−0.1	0.52	THBS3	thrombospondin 3 [Source:HGNC Symbol;Acc:HGNC:11787]
11	TBC1D19	1.77	−0.25	0.44	TBC1D19	TBC1 domain family, member 19 [Source:HGNC Symbol;Acc
12	SPTLC3	1.76	−0.07	0.57	SPTLC3	serine palmitoyltransferase, long chain base subunit 3 [Sourc
13	SLC25A42	1.76	−0.06	0.63	SLC25A42	solute carrier family 25, member 42 [Source:HGNC Symbol;A
14	WDR83	1.74	−0.16	0.27	WDR83	WD repeat domain 83 [Source:HGNC Symbol;Acc:HGNC:32
15	PFKFB4	1.74	−0.13	0.5	PFKFB4	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 4 [S
16	PFKP	1.73	−0.4	0.4	PFKP	phosphofructokinase, platelet [Source:HGNC Symbol;Acc:HG
17	RNASET2	1.72	−0.12	0.51	RNASET2	ribonuclease T2 [Source:HGNC Symbol;Acc:HGNC:21686]
18	ZNF34	1.71	−0.21	0.29	ZNF34	zinc finger protein 34 [Source:HGNC Symbol;Acc:HGNC:130
19	HIP1	1.71	−0.31	0.32	HIP1	huntingtin interacting protein 1 [Source:HGNC Symbol;Acc:H
20	PPARG	1.7	−0.14	0.29	PPARG	peroxisome proliferator−activated receptor gamma [Source:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−05	57 / 2188	Lymp	HOPP_Poised_promoter
2	1e−04	79 / 3396	Lymp	HOPP_Repressed
3	1e−04	71 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
4	4e−04	37 / 1308	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_UP
5	5e−04	59 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
6	6e−04	12 / 250	Colon	K9K27me3_Colon
7	7e−04	48 / 1907	Brain	Fetal_TxTrans
8	1e−03	3 / 13	GSE	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION
9	1e−03	3 / 13	GSE	VALK_AML_WITH_11Q23_REARRANGED
10	2e−03	3 / 15	MF	fibroblast growth factor binding
11	2e−03	19 / 568	GSE	MIKKELSEN_ES_ICP_WITH_H3K4ME3
12	2e−03	51 / 2159	Colon	TssP_Colon
13	2e−03	4 / 36	GSE	REACTOME_SIGNALING_BY_FGFR_MUTANTS
14	3e−03	21 / 686	Brain	Overlap_fetal_midbrain_TssA
15	3e−03	45 / 1889	Colon	ReprPCWk_Colon
16	3e−03	3 / 19	GSE	REACTOME_SHC_MEDIATED_CASCADE
17	3e−03	3 / 19	GSE	VALK_AML_CLUSTER_16
18	3e−03	21 / 689	Chr	Chr 7
19	4e−03	6 / 94	GSE	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
20	4e−03	4 / 41	BP	positive regulation of MAP kinase activity
21	4e−03	49 / 2142	Colon	ReprPC_Colon
22	5e−03	2 / 7	GSE	REACTOME_FGFR4_LIGAND_BINDING_AND_ACTIVATION
23	6e−03	4 / 46	MF	manganese ion binding
24	6e−03	6 / 104	GSE	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
25	6e−03	3 / 24	BP	regulation of lipid metabolic process
26	6e−03	3 / 24	GSE	ROZANOV_MMP14_TARGETS_DN
27	6e−03	4 / 47	GSE	PID_FGF_PATHWAY
28	6e−03	4 / 47	GSE	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_D
29	6e−03	6 / 105	GSE	REACTOME_SIGNALING_BY_RHO_GTPASES
30	7e−03	8 / 175	CC	early endosome
31	7e−03	4 / 49	GSE	NAGASHIMA_NRG1_SIGNALING_DN
32	8e−03	3 / 26	GSE	REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING
33	8e−03	8 / 180	GSE	COLDREN_GEFITINIB_RESISTANCE_DN
34	8e−03	13 / 383	Brain	Fetal_Tx
35	8e−03	97 / 4992	MF	ion binding
36	8e−03	2 / 9	GSE	HASEGAWA_TUMORIGENESIS_BY_RET_C634R
37	8e−03	13 / 385	GSE	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
38	9e−03	3 / 27	GSE	REACTOME_FRS2_MEDIATED_CASCADE
39	9e−03	3 / 27	GSE	MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN
40	1e−02	3 / 28	miRN	hsa−miR−1292

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.03	5 / 111	HORVATH_aging_genes meth UP
2	0.12	2 / 38	TESCHENDORFF_age_hypermethylated
3	1.00	0 / 100	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	6 / 156	PanCan_PI3K_geneset_nanostring
2	0.09	1 / 14	LIU_COMMON_CANCER_GENES
3	0.14	3 / 82	PanCan_TXmisReg_geneset_nanostring
4	0.16	1 / 11	GENTLES_modul17
5	0.18	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.19	1 / 13	GENTLES_modul12
7	0.21	1 / 15	RHODES_CANCER_META_SIGNATURE
8	0.21	1 / 15	GENTLES_modul11
9	0.25	1 / 18	PanCan_Notch_geneset_nanostring
10	0.26	3 / 111	PanCan_RAS_geneset_nanostring
11	0.30	1 / 22	PanCan_HH_geneset_nanostring
12	0.30	3 / 121	PanCan_MAPK_geneset_nanostring
13	0.32	4 / 180	SPANG_LPS−index2
14	0.37	0 / 12	LIU_PROSTATE_CANCER_UP
15	0.42	0 / 14	LIU_PROSTATE_CANCER_DN
16	0.45	7 / 401	Lembcke_Colonic Inflammation
17	0.51	8 / 489	Lembcke_Normal vs Adenoma
18	0.54	1 / 48	KUIPER_MM poor survival
19	0.58	1 / 55	PanCan_JAK−ST_geneset_nanostring
20	0.70	4 / 298	SPANG_BCL6−index2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−04	12 / 250	K9K27me3_Colon
2	2e−03	51 / 2159	TssP_Colon
3	3e−03	45 / 1889	ReprPCWk_Colon
4	4e−03	49 / 2142	ReprPC_Colon
5	2e−02	16 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
6	3e−02	3 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
7	3e−02	10 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
8	3e−02	31 / 1386	Het_Colon
9	4e−02	29 / 1317	EnhP_Colon
10	5e−02	11 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	6e−02	9 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
12	9e−02	70 / 3812	TssD1_Colon
13	1e−01	1 / 7	Kaneda_CIMP−group2
14	1e−01	70 / 3897	Quies1_Colon
15	1e−01	21 / 1038	HetRpts_Colon
16	2e−01	2 / 45	Ang_CRC−CIMPH−vs−L_hyper
17	2e−01	1 / 11	Budinska_B_Lower crypt−like_DOWN
18	2e−01	49 / 2698	EnhA_Colon
19	2e−01	9 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
20	2e−01	1 / 13	TCGA−CRC_less−agressive−disease−markers

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	37 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
2	1e−03	3 / 13	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION
3	1e−03	3 / 13	VALK_AML_WITH_11Q23_REARRANGED
4	2e−03	19 / 568	MIKKELSEN_ES_ICP_WITH_H3K4ME3
5	2e−03	4 / 36	REACTOME_SIGNALING_BY_FGFR_MUTANTS
6	3e−03	3 / 19	REACTOME_SHC_MEDIATED_CASCADE
7	3e−03	3 / 19	VALK_AML_CLUSTER_16
8	4e−03	6 / 94	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
9	5e−03	2 / 7	REACTOME_FGFR4_LIGAND_BINDING_AND_ACTIVATION
10	6e−03	6 / 104	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
11	6e−03	3 / 24	ROZANOV_MMP14_TARGETS_DN
12	6e−03	4 / 47	PID_FGF_PATHWAY
13	6e−03	4 / 47	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN
14	6e−03	6 / 105	REACTOME_SIGNALING_BY_RHO_GTPASES
15	7e−03	4 / 49	NAGASHIMA_NRG1_SIGNALING_DN
16	8e−03	3 / 26	REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING
17	8e−03	8 / 180	COLDREN_GEFITINIB_RESISTANCE_DN
18	8e−03	2 / 9	HASEGAWA_TUMORIGENESIS_BY_RET_C634R
19	8e−03	13 / 385	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
20	9e−03	3 / 27	REACTOME_FRS2_MEDIATED_CASCADE

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−05	57 / 2188	HOPP_Poised_promoter
2	1e−04	79 / 3396	HOPP_Repressed
3	4e−02	104 / 5693	HOPP_Weak_enhancer
4	6e−02	1 / 4	Shaknovich_ABC_hyper_meth
5	7e−02	99 / 5538	HOPP_Weak_txn
6	8e−02	2 / 30	Subero_INT_hypo_meth
7	9e−02	4 / 107	SPANG_LPS 6hrs UP
8	1e−01	48 / 2563	HOPP_Heterochrom
9	1e−01	1 / 8	MASCQUE_ABC UP
10	1e−01	7 / 268	SPANG_IL21 UP
11	1e−01	1 / 10	DAVE_BL_DN
12	2e−01	1 / 13	YAMANE_AICDA_targets_recruited
13	2e−01	6 / 247	ZHANG_DLBCL mutated
14	2e−01	1 / 14	Subero_mBL_hypo_meth
15	2e−01	1 / 15	WRIGHT_ABC UP
16	2e−01	1 / 17	DAVE_NFkB BL DN
17	4e−01	1 / 29	Subero_DLBCL_hypo_meth
18	4e−01	1 / 33	LEE_Developmental_regulators
19	4e−01	1 / 34	Subero_B−ALL_hyper_meth
20	4e−01	4 / 212	LENZ_Stromal signature 1

Pathw Act

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	9 / 350	WIRTH_Nervous System
2	0.1	1 / 10	WIRTH_Hippocampus
3	0.2	1 / 11	WIRTH_Prim. lymphoid organs
4	0.2	2 / 46	WIRTH_Liver
5	0.2	3 / 95	WIRTH_Muscle
6	0.3	2 / 74	WIRTH_Mucosa
7	0.4	1 / 32	WIRTH_Pancreas
8	0.4	1 / 32	WIRTH_Placenta
9	0.5	2 / 107	WIRTH_Testis
10	0.5	2 / 114	PALMER_T−Cell signature up
11	0.7	5 / 350	WIRTH_Immune system
12	0.7	3 / 225	PALMER_Granulocytes signature up
13	1.0	0 / 11	WIRTH_Sec. 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

BP

Rank	p−value	#in/all	Geneset
1	0.004	4 / 41	positive regulation of MAP kinase activity
2	0.006	3 / 24	regulation of lipid metabolic process
3	0.011	3 / 29	glycogen metabolic process
4	0.012	3 / 30	regulation of cell differentiation
5	0.012	11 / 316	small GTPase mediated signal transduction
6	0.014	6 / 124	regulation of small GTPase mediated signal transduction
7	0.015	2 / 12	embryonic digestive tract morphogenesis
8	0.015	2 / 12	white fat cell differentiation
9	0.016	18 / 653	homeostatic process
10	0.016	3 / 34	cellular response to glucose stimulus
11	0.017	2 / 13	embryonic morphogenesis
12	0.017	2 / 13	positive regulation of chondrocyte differentiation
13	0.020	2 / 14	drug transmembrane transport
14	0.020	3 / 37	termination of G−protein coupled receptor signaling pathway
15	0.023	2 / 15	histone H4−K20 demethylation
16	0.023	2 / 15	positive regulation of cardiac muscle cell proliferation
17	0.023	2 / 15	response to vitamin A
18	0.025	5 / 104	glucose metabolic process
19	0.026	2 / 16	calcium ion−dependent exocytosis
20	0.026	2 / 16	negative regulation of megakaryocyte differentiation

CC

Rank	p−value	#in/all	Geneset
1	0.007	8 / 175	early endosome
2	0.015	2 / 12	basal part of cell
3	0.023	2 / 15	acrosomal membrane
4	0.023	2 / 15	RNA polymerase II transcription factor complex
5	0.036	2 / 19	ciliary base
6	0.049	3 / 52	secretory granule
7	0.054	3 / 54	transport vesicle
8	0.063	2 / 26	basal plasma membrane
9	0.072	2 / 28	SCF ubiquitin ligase complex
10	0.092	4 / 108	late endosome
11	0.106	2 / 35	integral component of Golgi membrane
12	0.108	6 / 205	neuron projection
13	0.112	14 / 616	endosome
14	0.130	3 / 79	nucleosome
15	0.137	3 / 81	late endosome membrane
16	0.143	4 / 127	cytoplasmic vesicle
17	0.143	2 / 42	photoreceptor outer segment
18	0.148	1 / 10	cell−cell contact zone
19	0.148	1 / 10	MHC class I protein complex
20	0.148	1 / 10	myosin filament

Disease

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

HM

Rank	p−value	#in/all	Geneset
1	0.1	5 / 176	HALLMARK_HYPOXIA
2	0.2	5 / 183	HALLMARK_GLYCOLYSIS
3	0.2	3 / 107	HALLMARK_COAGULATION
4	0.3	4 / 165	HALLMARK_MYOGENESIS
5	0.3	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	0.3	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	0.3	1 / 26	HALLMARK_ANGIOGENESIS
8	0.4	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
9	0.5	3 / 167	HALLMARK_APICAL_JUNCTION
10	0.5	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.5	1 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
12	0.5	3 / 181	HALLMARK_P53_PATHWAY
13	0.6	3 / 188	HALLMARK_ADIPOGENESIS
14	0.6	1 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	0.6	2 / 137	HALLMARK_UV_RESPONSE_DN
16	0.7	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
17	0.7	2 / 148	HALLMARK_KRAS_SIGNALING_UP
18	0.7	2 / 162	HALLMARK_COMPLEMENT
19	0.7	2 / 167	HALLMARK_IL2_STAT5_SIGNALING
20	0.8	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 15	fibroblast growth factor binding
2	0.006	4 / 46	manganese ion binding
3	0.008	97 / 4992	ion binding
4	0.011	5 / 84	guanyl−nucleotide exchange factor activity
5	0.015	2 / 12	enhancer sequence−specific DNA binding
6	0.017	5 / 95	heparin binding
7	0.023	2 / 15	histone demethylase activity (H4−K20 specific)
8	0.023	21 / 830	nucleic acid binding transcription factor activity
9	0.025	4 / 70	phospholipid binding
10	0.025	12 / 398	protein tyrosine kinase activity
11	0.026	8 / 223	phosphatase activity
12	0.026	18 / 691	kinase activity
13	0.036	2 / 19	cAMP binding
14	0.036	2 / 19	ion transmembrane transporter activity
15	0.036	20 / 820	sequence−specific DNA binding transcription factor activity
16	0.039	2 / 20	activating transcription factor binding
17	0.042	5 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activity
18	0.042	3 / 49	pyridoxal phosphate binding
19	0.051	2 / 23	DNA helicase activity
20	0.055	2 / 24	snoRNA binding

TF

Rank	p−value	#in/all	Geneset
1	0.06	25 / 1139	HEBENSTREIT_low expression TF
2	0.15	13 / 595	ICGC_NrsfPcr2_targets
3	0.30	50 / 2927	ICGC_Rad21_targets
4	0.65	66 / 4314	ICGC_Ebfsc137065_targets
5	0.70	19 / 1314	ICGC_Usf1_targets
6	0.79	26 / 1872	ICGC_Mef2_targets
7	0.80	28 / 2013	ICGC_Bcl11_targets
8	0.82	8 / 653	ICGC_SrfPcr2_targets
9	0.86	8 / 690	ICGC_Atf3_targets
10	0.87	89 / 6114	ICGC_Runx3_targets
11	0.88	6 / 553	ICGC_RxraPcr1_targets
12	0.90	54 / 3924	ICGC_Zeb1_targets
13	0.90	17 / 1400	ICGC_Myc_targets
14	0.92	77 / 5495	ICGC_Yy1_targets
15	0.94	74 / 5355	ICGC_Pol2_targets
16	0.94	14 / 1266	ICGC_NrsfPcr1_targets
17	0.94	74 / 5374	ICGC_Pax5_targets
18	0.95	34 / 2714	ICGC_Irf4_targets
19	0.96	29 / 2391	ICGC_Pbx3_targets
20	0.96	64 / 4774	ICGC_Foxm1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	71 / 3682	LU_BPDE 0.005 DN
2	0.94	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	

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	71 / 2972	Mid_Frontal_Lobe_ReprPC
2	5e−04	59 / 2462	Mid_Frontal_Lobe_HetRpts
3	7e−04	48 / 1907	Fetal_TxTrans
4	3e−03	21 / 686	Overlap_fetal_midbrain_TssA
5	8e−03	13 / 383	Fetal_Tx
6	1e−02	23 / 862	Overlap_fetal_midbrain_TxTrans
7	1e−02	19 / 668	Mid_Frontal_Lobe_Enh
8	1e−02	43 / 1949	Fetal_TssF
9	2e−02	29 / 1207	Overlap_fetal_midbrain_TssF
10	2e−02	35 / 1548	Mid_Frontal_Lobe_K9K27me3
11	2e−02	40 / 1845	Fetal_Quies
12	3e−02	17 / 656	Overlap_fetal_midbrain_EnhP
13	4e−02	21 / 884	Overlap_fetal_midbrain_EnhG
14	5e−02	24 / 1065	Overlap_fetal_midbrain_Enh
15	5e−02	44 / 2185	Fetal_TssA
16	8e−02	22 / 1013	Fetal_TssP
17	2e−01	24 / 1236	Mid_Frontal_Lobe_ReprPCWk
18	2e−01	12 / 564	Mid_Frontal_Lobe_EnhP
19	2e−01	12 / 574	Overlap_fetal_midbrain_TssP
20	2e−01	11 / 534	Mid_Frontal_Lobe_EnhG

Chr

Rank	p−value	#in/all	Geneset
1	0.003	21 / 689	Chr 7
2	0.025	18 / 687	Chr 6
3	0.063	23 / 1037	Chr 19
4	0.198	10 / 462	Chr 14
5	0.310	13 / 696	Chr 5
6	0.375	10 / 551	Chr X
7	0.390	10 / 558	Chr 4
8	0.390	14 / 801	Chr 11
9	0.400	5 / 262	Chr 13
10	0.424	25 / 1500	Chr 1
11	0.461	14 / 840	Chr 17
12	0.466	8 / 469	Chr 8
13	0.571	13 / 838	Chr 3
14	0.606	6 / 398	Chr 20
15	0.704	9 / 649	Chr 16
16	0.868	2 / 221	Chr 18
17	0.898	6 / 576	Chr 9
18	0.957	10 / 993	Chr 2
19	0.965	7 / 775	Chr 12
20	0.977	4 / 552	Chr 10

Glio

Rank	p−value	#in/all	Geneset
1	0.02	4 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
2	0.05	1 / 3	Donson−migration tethering and rolling−associated with LTS in HGA
3	0.06	10 / 356	Down_a
4	0.06	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
5	0.09	3 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	0.10	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	0.12	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
8	0.13	1 / 9	VERHAAK_Brain
9	0.16	3 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	0.19	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
11	0.21	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
12	0.25	1 / 18	Barbus_GBM_STS_vs._LTS
13	0.30	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
14	0.31	1 / 23	WIRTH_PN subtype
15	0.32	2 / 72	laffaire_hypermeth_LGG_vs_control
16	0.32	2 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
17	0.33	2 / 74	WIRTH_Normal Brain
18	0.33	2 / 75	GIEZELT_GBM_STS_down_VS_LTS
19	0.37	1 / 29	shaw_responders_down_in_oligo_glioma
20	0.45	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	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	

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.01	3 / 28	hsa−miR−1292
2	0.08	1 / 5	hsa−miR−585
3	0.08	3 / 63	hsa−miR−455−3p
4	0.09	1 / 6	hsa−miR−937
5	0.12	2 / 38	hsa−miR−517*
6	0.13	2 / 40	hsa−miR−518d−3p
7	0.14	2 / 41	hsa−miR−532−3p
8	0.15	3 / 85	hsa−miR−423−5p
9	0.15	3 / 85	hsa−miR−567
10	0.20	2 / 52	hsa−miR−370
11	0.20	4 / 146	hsa−miR−655
12	0.20	4 / 147	hsa−miR−506
13	0.21	1 / 15	hsa−miR−551a
14	0.21	1 / 15	hsa−miR−744
15	0.22	2 / 56	hsa−miR−384
16	0.22	4 / 153	hsa−miR−200c
17	0.23	1 / 16	hsa−miR−302a*
18	0.23	2 / 57	hsa−miR−1260
19	0.23	7 / 315	hsa−miR−302c
20	0.23	2 / 58	hsa−miR−324−3p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 38	VAQUERIZAS_Testis
2	0.2	1 / 17	VAQUERIZAS_Pituitary
3	0.2	1 / 17	VAQUERIZAS_Heart
4	0.3	1 / 23	VAQUERIZAS_Spinal cord
5	0.4	3 / 143	VAQUERIZAS_General
6	0.5	1 / 38	VAQUERIZAS_Whole brain
7	0.5	1 / 45	VAQUERIZAS_Uterus
8	1.0	0 / 36	VAQUERIZAS_Fetal brain
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 / 9	VAQUERIZAS_Kidney
14	1.0	0 / 37	VAQUERIZAS_Thymus
15	1.0	0 / 40	VAQUERIZAS_Thyroid
16	1.0	0 / 59	VAQUERIZAS_Whole blood
17	1.0	0 / 7	VAQUERIZAS_Appendix
18	1.0	0 / 29	VAQUERIZAS_Fetal lung
19	1.0	0 / 58	VAQUERIZAS_Lung
20	1.0	0 / 16	VAQUERIZAS_Pancreas

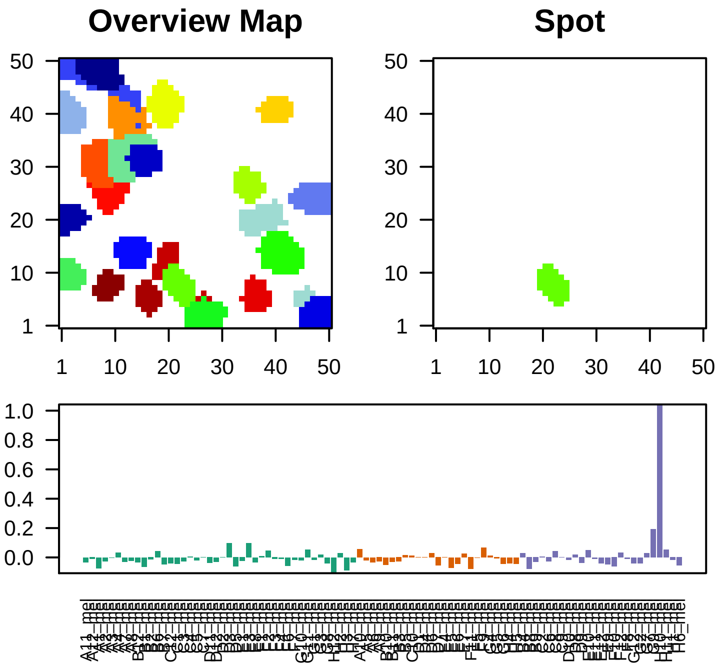
Correlation Clusters

Spot Summary: W

metagenes = 34
genes = 258

<r> metagenes = 0.93
<r> genes = 0.22
beta: r2= 0.75 / log p= −Inf

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

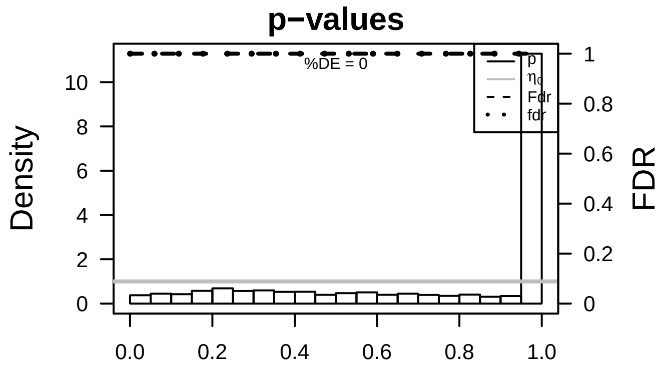


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	MDGA1	2.66	−0.09	0.7	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor
2	UCN	2.09	−0.09	0.57	UCN	urocortin [Source:HGNC Symbol;Acc:HGNC:12516]
3	FAM214A	2.08	−0.56	0.27	FAM214A	family with sequence similarity 214, member A [Source:HGN
4	DGKD	1.97	−0.29	0.3	DGKD	diacylglycerol kinase, delta 130kDa [Source:HGNC Symbol;A
5	GPR82	1.95	−0.17	0.4	GPR82	G protein−coupled receptor 82 [Source:HGNC Symbol;Acc:H
6	LACE1	1.9	−0.39	0.28	LACE1	lactation elevated 1 [Source:HGNC Symbol;Acc:HGNC:1641
7	CPM	1.9	−0.35	0.37	CPM	carboxypeptidase M [Source:HGNC Symbol;Acc:HGNC:2311
8	BEND7	1.89	−0.18	0.51	BEND7	BEN domain containing 7 [Source:HGNC Symbol;Acc:HGNC
9	MFSD9	1.89	−0.22	0.46	MFSD9	major facilitator superfamily domain containing 9 [Source:HG
10	PCOLCE	1.89	−0.09	0.58	PCOLCE	procollagen C−endopeptidase enhancer [Source:HGNC Sym
11	PPP1R3E	1.88	−0.08	0.55	PPP1R3E	protein phosphatase 1, regulatory subunit 3E [Source:HGNC
12	ZNF625−ZNF	1.87	−0.15	0.35	ZNF625−ZNF20	25−ZNF20 readthrough (NMD candidate) [Source:HGN
13	GAB3	1.85	−0.1	0.46	GAB3	GRB2−associated binding protein 3 [Source:HGNC Symbol;
14	LAT	1.85	−0.11	0.49	LAT	linker for activation of T cells [Source:HGNC Symbol;Acc:HG
15	AGO2	1.83	−0.49	0.27	AGO2	argonaute RISC catalytic component 2 [Source:HGNC Symb
16	LRP5L	1.81	−0.12	0.47	LRP5L	low density lipoprotein receptor−related protein 5−like [Sourc
17	SOX9	1.79	−0.07	0.66	SOX9	SRY (sex determining region Y)−box 9 [Source:HGNC Symb
18	ENGASE	1.77	−0.15	0.45	ENGASE	endo−beta−N−acetylglucosaminidase [Source:HGNC Symbo
19	CHAC1	1.75	−0.08	0.65	CHAC1	ChaC glutathione−specific gamma−glutamylcyclotransferase
20	FAM227B	1.72	−0.12	0.52	FAM227B	family with sequence similarity 227, member B [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−07	4 / 5	GSE	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
2	2e−04	5 / 31	GSE	KEGG_STARCH_AND_SUCROSE_METABOLISM
3	5e−04	28 / 823	GSE	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
4	6e−04	7 / 83	GSE	LEIN_CHOROID_PLEXUS_MARKERS
5	7e−04	73 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
6	8e−04	15 / 335	Chr	Chr 22
7	1e−03	13 / 280	miRN	hsa−miR−30c
8	2e−03	42 / 1548	Brain	Mid_Frontal_Lobe_K9K27me3
9	2e−03	3 / 16	GSE	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
10	3e−03	13 / 304	GSE	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
11	3e−03	12 / 270	miRN	hsa−miR−30b
12	4e−03	9 / 178	GSE	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
13	4e−03	5 / 61	GSE	HUANG_GATA2_TARGETS_DN
14	4e−03	3 / 19	BP	cAMP−mediated signaling
15	4e−03	4 / 38	GSE	SAGIV_CD24_TARGETS_DN
16	4e−03	14 / 361	GSE	LU_EZH2_TARGETS_DN
17	4e−03	5 / 62	BP	canonical Wnt signaling pathway
18	5e−03	47 / 1859	MF	metal ion binding
19	5e−03	59 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
20	5e−03	6 / 91	GSE	MARZEC_IL2_SIGNALING_UP
21	6e−03	4 / 42	GSE	PID_PTP1B_PATHWAY
22	6e−03	6 / 95	MF	hydrolase activity, acting on glycosyl bonds
23	6e−03	11 / 264	miRN	hsa−miR−30a
24	6e−03	11 / 264	GSE	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
25	7e−03	6 / 98	GSE	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
26	7e−03	11 / 269	miRN	hsa−miR−30d
27	8e−03	3 / 24	BP	digestion
28	8e−03	7 / 132	miRN	hsa−miR−199b−5p
29	9e−03	8 / 167	GSE	BROWNE_HCMV_INFECTION_18HR_UP
30	9e−03	4 / 47	GSE	MCCLUNG_CREB1_TARGETS_DN
31	9e−03	3 / 25	BP	positive regulation of BMP signaling pathway
32	9e−03	3 / 25	GSE	MA_PITUITARY_FETAL_VS_ADULT_UP
33	9e−03	12 / 315	miRN	hsa−miR−559
34	1e−02	3 / 27	BP	positive regulation of DNA replication
35	1e−02	3 / 27	GSE	ZHAN_MULTIPLE_MYELOMA_DN
36	1e−02	4 / 51	miRN	hsa−miR−556−3p
37	1e−02	12 / 327	GSE	DELACROIX_RARG_BOUND_MEF
38	1e−02	3 / 28	BP	tricarboxylic acid cycle
39	1e−02	3 / 28	GSE	KEGG_CITRATE_CYCLE_TCA_CYCLE
40	1e−02	3 / 28	GSE	HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 111	HORVATH_aging_genes meth UP
2	0.8	1 / 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	0.004	3 / 19	cAMP−mediated signaling
2	0.004	5 / 62	canonical Wnt signaling pathway
3	0.008	3 / 24	digestion
4	0.009	3 / 25	positive regulation of BMP signaling pathway
5	0.011	3 / 27	positive regulation of DNA replication
6	0.012	3 / 28	tricarboxylic acid cycle
7	0.015	3 / 30	epithelial to mesenchymal transition
8	0.015	2 / 11	actin polymerization or depolymerization
9	0.015	2 / 11	axoneme assembly
10	0.018	2 / 12	endothelial cell differentiation
11	0.018	2 / 12	mammary gland epithelial cell differentiation
12	0.018	2 / 12	positive regulation of calcium ion import
13	0.021	2 / 13	embryonic camera−type eye morphogenesis
14	0.021	2 / 13	glial cell differentiation
15	0.021	2 / 13	macrophage differentiation
16	0.021	2 / 13	negative regulation of translational initiation
17	0.021	2 / 13	positive regulation of chondrocyte differentiation
18	0.021	2 / 13	signal transduction involved in regulation of gene expression
19	0.021	3 / 34	lactation
20	0.021	3 / 34	positive regulation of interleukin−6 production

Brain

Rank	p−value	#in/all	Geneset
1	7e−04	73 / 2972	Mid_Frontal_Lobe_ReprPC
2	2e−03	42 / 1548	Mid_Frontal_Lobe_K9K27me3
3	5e−03	59 / 2462	Mid_Frontal_Lobe_HetRpts
4	9e−02	17 / 686	Overlap_fetal_midbrain_TssA
5	9e−02	23 / 989	Mid_Frontal_Lobe_Quies
6	1e−01	27 / 1207	Overlap_fetal_midbrain_TssF
7	2e−01	44 / 2185	Fetal_TssA
8	2e−01	8 / 304	Fetal_Het
9	2e−01	19 / 862	Overlap_fetal_midbrain_TxTrans
10	2e−01	11 / 468	Mid_Frontal_Lobe_TssF
11	3e−01	37 / 1907	Fetal_TxTrans
12	3e−01	12 / 574	Overlap_fetal_midbrain_TssP
13	3e−01	22 / 1122	Fetal_K9K27me3
14	3e−01	4 / 163	Fetal_ReprPC
15	3e−01	16 / 812	Mid_Frontal_Lobe_TssP
16	3e−01	2 / 69	Overlap_fetal_midbrain_Tx
17	4e−01	13 / 668	Mid_Frontal_Lobe_Enh
18	5e−01	19 / 1050	Fetal_EnhP
19	5e−01	18 / 1013	Fetal_TssP
20	5e−01	7 / 383	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	2 / 22	PanCan_HH_geneset_nanostring
2	0.12	1 / 7	GENTLES_modul18
3	0.20	1 / 13	GENTLES_modul12
4	0.23	1 / 15	GENTLES_modul1
5	0.24	1 / 16	GENTLES_modul14
6	0.29	2 / 61	PanCan_Wnt_geneset_nanostring
7	0.29	1 / 20	PanCan_ChromMod_geneset_nanostring
8	0.30	3 / 111	PanCan_RAS_geneset_nanostring
9	0.34	3 / 120	PanCan_CC+Apop_geneset_nanostring
10	0.35	3 / 121	PanCan_MAPK_geneset_nanostring
11	0.41	0 / 12	LIU_PROSTATE_CANCER_UP
12	0.42	2 / 82	PanCan_TXmisReg_geneset_nanostring
13	0.51	3 / 156	PanCan_PI3K_geneset_nanostring
14	0.54	7 / 401	Lembcke_Colonic Inflammation
15	0.56	1 / 47	PanCan_DNARepair_geneset_nanostring
16	0.58	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	0.59	5 / 298	SPANG_BCL6−index2
18	0.61	3 / 180	SPANG_LPS−index2
19	0.62	1 / 55	PanCan_JAK−ST_geneset_nanostring
20	0.86	1 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.03	2 / 17	cytoplasmic ribonucleoprotein granule
2	0.06	3 / 52	perikaryon
3	0.07	6 / 169	transcription factor complex
4	0.08	19 / 775	extracellular space
5	0.12	2 / 35	mitotic spindle
6	0.14	11 / 438	Golgi membrane
7	0.16	1 / 10	DNA replication factor A complex
8	0.16	1 / 10	mRNA cap binding complex
9	0.16	1 / 10	vacuolar proton−transporting V−type ATPase complex
10	0.16	2 / 42	intercellular bridge
11	0.17	1 / 11	Golgi−associated vesicle membrane
12	0.17	1 / 11	photoreceptor outer segment membrane
13	0.17	1 / 11	RISC complex
14	0.19	1 / 12	AMP−activated protein kinase complex
15	0.20	3 / 89	tight junction
16	0.20	1 / 13	transcription factor TFTC complex
17	0.22	1 / 14	cytoplasmic dynein complex
18	0.22	1 / 14	male germ cell nucleus
19	0.22	1 / 14	trans−Golgi network transport vesicle
20	0.22	2 / 51	filopodium

Chr

Rank	p−value	#in/all	Geneset
1	8e−04	15 / 335	Chr 22
2	3e−02	19 / 689	Chr 7
3	5e−02	20 / 775	Chr 12
4	1e−01	14 / 576	Chr 9
5	1e−01	19 / 838	Chr 3
6	3e−01	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
7	4e−01	11 / 551	Chr X
8	5e−01	5 / 262	Chr 13
9	5e−01	18 / 1037	Chr 19
10	5e−01	4 / 221	Chr 18
11	6e−01	25 / 1500	Chr 1
12	6e−01	9 / 552	Chr 10
13	7e−01	16 / 993	Chr 2
14	8e−01	10 / 687	Chr 6
15	8e−01	10 / 696	Chr 5
16	8e−01	6 / 465	Chr 15
17	8e−01	11 / 801	Chr 11
18	9e−01	5 / 469	Chr 8
19	9e−01	6 / 558	Chr 4
20	1e+00	9 / 840	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 2	Budinska_D_Mesenchymal_DOWN
2	0.06	11 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
3	0.08	1 / 5	Budinska_A_Surface crypt−like_UP
4	0.11	29 / 1317	EnhP_Colon
5	0.12	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
6	0.13	1 / 8	Boland_CRC−MMR−system
7	0.13	1 / 8	Marisa_CRC−C3
8	0.14	44 / 2159	TssP_Colon
9	0.14	10 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
10	0.14	7 / 250	K9K27me3_Colon
11	0.17	2 / 43	Marisa_CRC−cluster−f
12	0.19	20 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	0.20	1 / 13	TCGA−CRC_less−agressive−disease−markers
14	0.23	1 / 15	TCGA_Mutated−in−CRC_hypermutated
15	0.24	6 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
16	0.24	1 / 16	TCGA_Mutated−in−CRC_non−hypermutated
17	0.24	1 / 16	Vilar_non−hypermutated−in−CRC
18	0.24	9 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
19	0.26	1 / 17	Vilar_hypermutated−in−CRC
20	0.26	3 / 102	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.2	7 / 294	GUDJ_psoriasis down
2	0.8	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	0.03	4 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
2	0.04	4 / 74	WIRTH_Normal Brain
3	0.04	4 / 75	GIEZELT_GBM_STS_down_VS_LTS
4	0.06	2 / 23	Donson−Misc immune function−associated with LTS in HGA
5	0.12	1 / 7	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
6	0.12	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	0.13	3 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	0.13	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
9	0.14	2 / 38	OL vs. OPC
10	0.15	4 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
11	0.19	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
12	0.19	3 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
13	0.23	1 / 15	VERHAAK_CL subtype
14	0.27	1 / 18	Barbus_GBM_STS_vs._LTS
15	0.29	17 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
16	0.33	2 / 68	GIEZELT_GBM_WT_down_VS_mut
17	0.35	2 / 71	Weller_LGG_A_vs_O_UP
18	0.35	2 / 71	Weller_LGG_gradeII−vs−III_DOWN
19	0.36	2 / 72	laffaire_hypermeth_LGG_vs_control
20	0.37	2 / 74	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−07	4 / 5	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
2	2e−04	5 / 31	KEGG_STARCH_AND_SUCROSE_METABOLISM
3	5e−04	28 / 823	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
4	6e−04	7 / 83	LEIN_CHOROID_PLEXUS_MARKERS
5	2e−03	3 / 16	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
6	3e−03	13 / 304	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
7	4e−03	9 / 178	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
8	4e−03	5 / 61	HUANG_GATA2_TARGETS_DN
9	4e−03	4 / 38	SAGIV_CD24_TARGETS_DN
10	4e−03	14 / 361	LU_EZH2_TARGETS_DN
11	5e−03	6 / 91	MARZEC_IL2_SIGNALING_UP
12	6e−03	4 / 42	PID_PTP1B_PATHWAY
13	6e−03	11 / 264	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
14	7e−03	6 / 98	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
15	9e−03	8 / 167	BROWNE_HCMV_INFECTION_18HR_UP
16	9e−03	4 / 47	MCCLUNG_CREB1_TARGETS_DN
17	9e−03	3 / 25	MA_PITUITARY_FETAL_VS_ADULT_UP
18	1e−02	3 / 27	ZHAN_MULTIPLE_MYELOMA_DN
19	1e−02	12 / 327	DELACROIX_RARG_BOUND_MEF
20	1e−02	3 / 28	KEGG_CITRATE_CYCLE_TCA_CYCLE

HM

Rank	p−value	#in/all	Geneset
1	0.03	3 / 37	HALLMARK_APICAL_SURFACE
2	0.06	4 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.25	4 / 148	HALLMARK_KRAS_SIGNALING_UP
4	0.26	2 / 57	HALLMARK_MYC_TARGETS_V2
5	0.33	4 / 167	HALLMARK_IL2_STAT5_SIGNALING
6	0.34	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
7	0.37	1 / 26	HALLMARK_ANGIOGENESIS
8	0.39	4 / 183	HALLMARK_GLYCOLYSIS
9	0.40	1 / 29	HALLMARK_NOTCH_SIGNALING
10	0.42	3 / 137	HALLMARK_UV_RESPONSE_DN
11	0.44	3 / 140	HALLMARK_APOPTOSIS
12	0.47	3 / 146	HALLMARK_UV_RESPONSE_UP
13	0.53	3 / 162	HALLMARK_COMPLEMENT
14	0.56	2 / 107	HALLMARK_COAGULATION
15	0.56	3 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	0.56	3 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
17	0.57	2 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
18	0.58	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	0.58	3 / 174	HALLMARK_HEME_METABOLISM
20	0.59	3 / 176	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 32	DUMEAUX_Fasting enriched genes
2	0.7	1 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	2 / 10	Shaknovich_ABC_hypo_meth
2	0.01	10 / 256	SPANG_IL21 DN
3	0.07	1 / 4	Shaknovich_ABC_hyper_meth
4	0.07	2 / 25	Subero_T−PLL_hypo_meth
5	0.09	2 / 30	Subero_INT_hypo_meth
6	0.13	1 / 8	YAMANE_AICDA_targets_nonrecruited
7	0.13	1 / 8	Subero_B−CLL_hypo_meth
8	0.16	1 / 10	DAVE_BL_DN
9	0.16	104 / 5538	HOPP_Weak_txn
10	0.16	3 / 80	Aukema_BCL2 DN_BCL6 UP
11	0.17	1 / 11	Subero_T−ALL_hypo_meth
12	0.23	1 / 15	WRIGHT_ABC UP
13	0.26	1 / 17	DAVE_NFkB BL DN
14	0.29	2 / 61	SPANG_LPS 6hrs DN
15	0.31	22 / 1128	SPANG_BCR DN
16	0.34	6 / 275	TARTE_Mature plasma cell signature
17	0.40	1 / 29	Subero_DLBCL_hypo_meth
18	0.42	2 / 82	ROSOLOWSKI_green UP
19	0.45	1 / 34	Subero_B−ALL_hyper_meth
20	0.45	39 / 2188	HOPP_Poised_promoter

MF

Rank	p−value	#in/all	Geneset
1	0.005	47 / 1859	metal ion binding
2	0.006	6 / 95	hydrolase activity, acting on glycosyl bonds
3	0.015	2 / 11	RNA polymerase binding
4	0.018	2 / 12	enhancer sequence−specific DNA binding
5	0.018	2 / 12	Notch binding
6	0.018	2 / 12	Wnt−activated receptor activity
7	0.024	2 / 14	diacylglycerol kinase activity
8	0.027	2 / 15	dioxygenase activity
9	0.031	2 / 16	NAD+ kinase activity
10	0.034	3 / 41	G−protein coupled receptor binding
11	0.038	2 / 18	cytokine receptor activity
12	0.038	2 / 18	galactosyltransferase activity
13	0.055	2 / 22	Wnt−protein binding
14	0.058	5 / 120	sequence−specific DNA binding RNA polymerase II transcription factor activity
15	0.061	3 / 52	hormone activity
16	0.064	2 / 24	N−acetyltransferase activity
17	0.073	3 / 56	phosphoprotein phosphatase activity
18	0.077	20 / 820	sequence−specific DNA binding transcription factor activity
19	0.079	2 / 27	frizzled binding
20	0.079	2 / 27	voltage−gated calcium channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	13 / 280	hsa−miR−30c
2	0.003	12 / 270	hsa−miR−30b
3	0.006	11 / 264	hsa−miR−30a
4	0.007	11 / 269	hsa−miR−30d
5	0.008	7 / 132	hsa−miR−199b−5p
6	0.009	12 / 315	hsa−miR−559
7	0.012	4 / 51	hsa−miR−556−3p
8	0.014	8 / 182	hsa−miR−573
9	0.015	9 / 222	hsa−miR−520g
10	0.017	4 / 57	hsa−miR−1302
11	0.018	8 / 191	hsa−miR−641
12	0.020	11 / 312	hsa−miR−30e
13	0.021	2 / 13	hsa−miR−574−3p
14	0.022	10 / 275	hsa−miR−577
15	0.022	3 / 35	hsa−miR−1287
16	0.024	2 / 14	hsa−miR−147b
17	0.025	7 / 165	hsa−miR−153
18	0.026	6 / 130	hsa−miR−145
19	0.026	4 / 65	hsa−miR−30e*
20	0.027	4 / 66	hsa−miR−140−3p

PathwAct

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

TF

Rank	p−value	#in/all	Geneset
1	0.1	41 / 2013	ICGC_Bcl11_targets
2	0.3	26 / 1314	ICGC_Usf1_targets
3	0.3	1 / 19	MYC_Metabolism UP
4	0.3	87 / 4829	ICGC_Nficsc81335_targets
5	0.3	35 / 1878	ICGC_Cebpbsc150_targets
6	0.3	73 / 4032	ICGC_Creb1_targets
7	0.4	108 / 6114	ICGC_Runx3_targets
8	0.4	13 / 690	ICGC_Atf3_targets
9	0.4	104 / 5890	ICGC_Elf1_targets
10	0.4	92 / 5219	ICGC_Tcf3_targets
11	0.4	43 / 2416	ICGC_Bcl3_targets
12	0.6	24 / 1400	ICGC_Myc_targets
13	0.6	84 / 4909	ICGC_Stat5_targets
14	0.6	11 / 653	ICGC_SrfPcr2_targets
15	0.6	91 / 5355	ICGC_Pol2_targets
16	0.6	23 / 1383	ICGC_Six5_targets
17	0.6	62 / 3700	ICGC_Nfatc1_targets
18	0.6	28 / 1701	HEBENSTREIT_high expression TF
19	0.6	1 / 59	MYC_Targets UP
20	0.6	68 / 4054	ICGC_Egr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 16	VAQUERIZAS_Pancreas
2	0.08	3 / 59	VAQUERIZAS_Whole blood
3	0.11	2 / 33	VAQUERIZAS_Prostate
4	0.13	2 / 36	VAQUERIZAS_Fetal brain
5	0.14	2 / 38	VAQUERIZAS_Whole brain
6	0.22	1 / 14	VAQUERIZAS_Ovary
7	0.23	1 / 15	VAQUERIZAS_Fetal thyroid
8	0.24	1 / 16	VAQUERIZAS_Adrenal gland
9	0.24	1 / 16	VAQUERIZAS_Salivary gland
10	0.26	1 / 17	VAQUERIZAS_Pituitary
11	0.33	1 / 23	VAQUERIZAS_Spinal cord
12	0.33	1 / 23	VAQUERIZAS_Trachea
13	0.33	1 / 23	VAQUERIZAS_Adrenal cortex
14	0.38	1 / 27	VAQUERIZAS_Lymph node
15	0.40	1 / 29	VAQUERIZAS_Fetal lung
16	0.48	1 / 37	VAQUERIZAS_Thymus
17	0.49	1 / 38	VAQUERIZAS_Testis
18	0.50	1 / 40	VAQUERIZAS_Thyroid
19	0.51	1 / 41	VAQUERIZAS_Placenta
20	0.54	1 / 45	VAQUERIZAS_Uterus

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 11	WIRTH_Globus pallidus
2	0.3	3 / 107	WIRTH_Testis
3	0.3	3 / 114	PALMER_T−Cell signature up
4	0.4	7 / 350	WIRTH_Nervous System
5	0.4	1 / 32	WIRTH_Pancreas
6	0.5	1 / 41	WIRTH_Homeostasis
7	0.7	3 / 194	PALMER_B−Cell signature up
8	0.8	3 / 225	PALMER_Granulocytes signature up
9	0.8	1 / 95	WIRTH_Muscle
10	0.9	4 / 350	WIRTH_Immune system
11	1.0	0 / 11	WIRTH_Sec. lymphoid organs
12	1.0	0 / 11	WIRTH_Prim. lymphoid organs
13	1.0	0 / 13	WIRTH_B−cells
14	1.0	0 / 8	WIRTH_Tonsil
15	1.0	0 / 12	WIRTH_Thymus
16	1.0	0 / 12	WIRTH_Lymphocytes
17	1.0	0 / 5	WIRTH_Bone marrow
18	1.0	0 / 14	WIRTH_Telencephalon
19	1.0	0 / 11	WIRTH_Cortex cerebri
20	1.0	0 / 10	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	66 / 3682	LU_BPDE 0.005 DN
2	0.6	19 / 1115	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

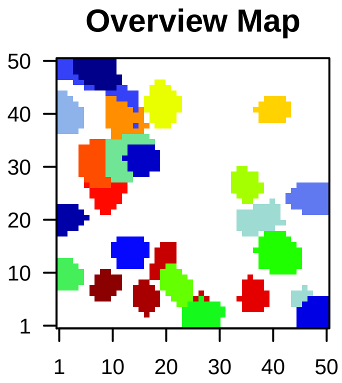
Correlation Clusters

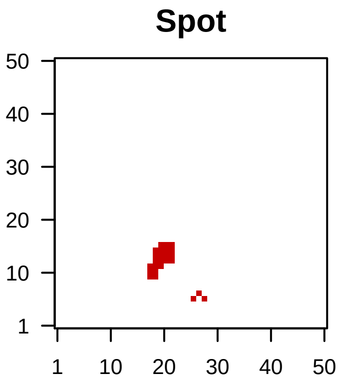
Spot Summary: X

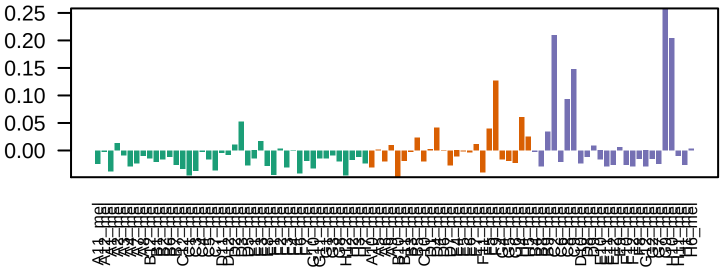
metagenes = 25
genes = 261

<r> metagenes = 0.92
<r> genes = 0.41
beta: r2= 0.18 / log p= −4.68

samples with spot = 3 (3.3 %)
MSC3 : 3 (12 %)


Overview Map


Spot

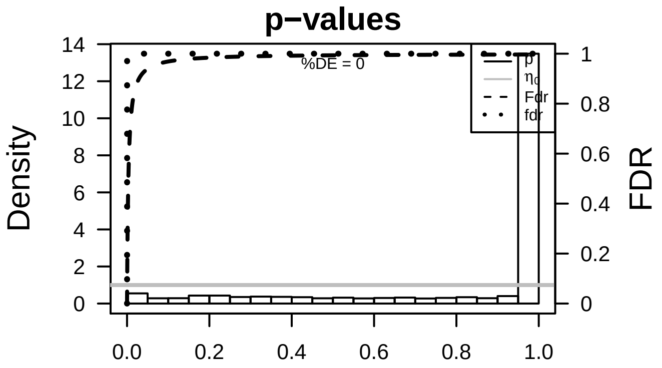


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TRIM52	1.9	−0.29	0.38	TRIM52	tripartite motif containing 52 [Source:HGNC Symbol;Acc:HGN
2	RGS5	1.66	−0.3	0.4	RGS5	regulator of G−protein signaling 5 [Source:HGNC Symbol;Acc
3	B4GALNT4	1.55	−0.05	0.33	B4GALNT4	beta−1,4−N−acetyl−galactosaminyl transferase 4 [Source:HG
4	ARHGAP24	1.54	−0.11	0.21	ARHGAP24	Rho GTPase activating protein 24 [Source:HGNC Symbol;Acc
5	BMX	1.5	−0.05	0.38	BMX	BMX non−receptor tyrosine kinase [Source:HGNC Symbol;Ac
6	MRI1	1.48	−0.15	0.21	MRI1	methylthioribose−1−phosphate isomerase 1 [Source:HGNC S
7	ADAMTS17	1.47	−0.1	0.45	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif, 17
8	ASIC4	1.44	−0.07	0.32	ASIC4	acid sensing (proton gated) ion channel family member 4 [Sou
9	AQP4	1.42	−0.06	0.42	AQP4	aquaporin 4 [Source:HGNC Symbol;Acc:HGNC:637]
10	APOC1	1.42	−0.07	0.42	APOC1	apolipoprotein C−I [Source:HGNC Symbol;Acc:HGNC:607]
11	PERP	1.39	−0.37	0.33	PERP	PERP, TP53 apoptosis effector [Source:HGNC Symbol;Acc:H
12	AC003006.7	1.36	−0.13	0.46		
13	CCR9	1.32	−0.04	0.36	CCR9	chemokine (C−C motif) receptor 9 [Source:HGNC Symbol;Ac
14	AMIGO1	1.29	−0.1	0.27	AMIGO1	adhesion molecule with Ig−like domain 1 [Source:HGNC Sym
15	CAGE1	1.28	−0.03	0.18	CAGE1	cancer antigen 1 [Source:HGNC Symbol;Acc:HGNC:21622]
16	BFSP1	1.28	−0.04	0.31	BFSP1	beaded filament structural protein 1, filensin [Source:HGNC S
17	ANGPTL6	1.27	−0.1	0.33	ANGPTL6	angiopoietin−like 6 [Source:HGNC Symbol;Acc:HGNC:23140
18	SAMD11	1.24	−0.06	0.73	SAMD11	sterile alpha motif domain containing 11 [Source:HGNC Symb
19	ZC3H12C	1.22	−0.32	0.5	ZC3H12C	zinc finger CCCH−type containing 12C [Source:HGNC Symb
20	AKR1E2	1.22	−0.1	0.36	AKR1E2	aldo−keto reductase family 1, member E2 [Source:HGNC Syr

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−16	116 / 3396	Lympl	HOPP_Repressed
2	1e−12	81 / 2142	Colon	ReprPC_Colon
3	3e−12	74 / 1889	Colon	ReprPCWk_Colon
4	5e−08	10 / 58	GSEA	KEGG_CARDIAC_MUSCLE_CONTRACTION
5	5e−08	70 / 2159	Colon	TssP_Colon
6	9e−08	70 / 2188	Lympl	HOPP_Poised_promoter
7	3e−07	7 / 27	MF	chemokine activity
8	4e−07	6 / 18	CC	voltage−gated calcium channel complex
9	1e−06	12 / 124	BP	regulation of small GTPase mediated signal transduction
10	3e−06	4 / 7	GSEA	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
11	6e−06	37 / 989	Brain	Mid_Frontal_Lobe_Quies
12	1e−05	10 / 105	GSEA	REACTOME_SIGNALING_BY_RHO_GTPASES
13	1e−05	13 / 179	GSEA	NABA_SECRETED_FACTORS
14	2e−05	6 / 32	BP	cell chemotaxis
15	2e−05	41 / 1207	Brain	Overlap_fetal_midbrain_TssF
16	2e−05	79 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
17	2e−05	22 / 468	Brain	Mid_Frontal_Lobe_TssF
18	3e−05	43 / 1317	Colon	EnhP_Colon
19	3e−05	32 / 862	Brain	Overlap_fetal_midbrain_TxTrans
20	5e−05	27 / 686	Brain	Overlap_fetal_midbrain_TssA
21	5e−05	19 / 395	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
22	7e−05	5 / 26	MF	transforming growth factor beta receptor binding
23	7e−05	5 / 26	GSEA	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
24	9e−05	5 / 27	MF	voltage−gated calcium channel activity
25	9e−05	5 / 27	BP	water transport
26	9e−05	13 / 216	BP	immune response
27	1e−04	8 / 84	GSEA	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
28	1e−04	13 / 217	MF	GTPase activator activity
29	1e−04	5 / 29	GSEA	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES
30	2e−04	32 / 936	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
31	2e−04	10 / 143	GSEA	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
32	2e−04	59 / 2185	Brain	Fetal_TssA
33	2e−04	7 / 72	GSEA	KEGG_DILATED_CARDIOMYOPATHY
34	3e−04	7 / 73	BP	chemotaxis
35	3e−04	3 / 8	GSEA	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_FGF3
36	3e−04	19 / 452	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
37	3e−04	38 / 1236	Brain	Mid_Frontal_Lobe_ReprPCWk
38	3e−04	10 / 153	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
39	3e−04	4 / 20	GSEA	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
40	4e−04	28 / 812	Brain	Mid_Frontal_Lobe_TssP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 111	HORVATH_aging_genes meth UP
2	0.1	2 / 38	TESCHENDORFF_age_hypermethylated
3	0.8	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	1e−06	12 / 124	regulation of small GTPase mediated signal transduction
2	2e−05	6 / 32	cell chemotaxis
3	9e−05	5 / 27	water transport
4	9e−05	13 / 216	immune response
5	3e−04	7 / 73	chemotaxis
6	5e−04	5 / 39	SMAD protein signal transduction
7	7e−04	20 / 519	cell−cell signaling
8	7e−04	7 / 87	calcium ion transmembrane transport
9	2e−03	4 / 31	cell maturation
10	2e−03	6 / 78	regulation of ion transmembrane transport
11	2e−03	4 / 33	positive regulation of pathway−restricted SMAD protein phosphorylation
12	2e−03	5 / 55	BMP signaling pathway
13	3e−03	15 / 382	positive regulation of GTPase activity
14	3e−03	10 / 202	inflammatory response
15	3e−03	3 / 17	acute−phase response
16	3e−03	3 / 17	regulation of vasoconstriction
17	3e−03	13 / 316	small GTPase mediated signal transduction
18	3e−03	3 / 18	camera−type eye morphogenesis
19	3e−03	3 / 18	phototransduction
20	4e−03	5 / 60	response to glucocorticoid

Brain

Rank	p−value	#in/all	Geneset
1	6e−06	37 / 989	Mid_Frontal_Lobe_Quies
2	2e−05	41 / 1207	Overlap_fetal_midbrain_TssF
3	2e−05	79 / 2972	Mid_Frontal_Lobe_ReprPC
4	2e−05	22 / 468	Mid_Frontal_Lobe_TssF
5	3e−05	32 / 862	Overlap_fetal_midbrain_TxTrans
6	5e−05	27 / 686	Overlap_fetal_midbrain_TssA
7	2e−04	59 / 2185	Fetal_TssA
8	3e−04	38 / 1236	Mid_Frontal_Lobe_ReprPCWk
9	4e−04	28 / 812	Mid_Frontal_Lobe_TssP
10	3e−03	41 / 1548	Mid_Frontal_Lobe_K9K27me3
11	1e−02	46 / 1907	Fetal_TxTrans
12	3e−02	4 / 69	Overlap_fetal_midbrain_Tx
13	4e−02	8 / 229	Mid_Frontal_Lobe_TxTrans
14	5e−02	43 / 1949	Fetal_TssF
15	7e−02	6 / 166	Mid_Frontal_Lobe_Tx
16	7e−02	17 / 668	Mid_Frontal_Lobe_Enh
17	7e−02	15 / 574	Overlap_fetal_midbrain_TssP
18	8e−02	14 / 534	Mid_Frontal_Lobe_EnhG
19	8e−02	21 / 884	Overlap_fetal_midbrain_EnhG
20	1e−01	5 / 156	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	4 / 44	PanCan_TGF−B_geneset_nanostring
2	0.045	12 / 401	Lembcke_Colonic Inflammation
3	0.155	4 / 121	PanCan_MAPK_geneset_nanostring
4	0.159	1 / 10	GENTLES_modul13
5	0.174	1 / 11	GENTLES_modul17
6	0.202	1 / 13	BEN−PORATH_UP
7	0.229	1 / 15	WANG_ER_UP
8	0.229	1 / 15	GENTLES_modul11
9	0.374	4 / 180	SPANG_LPS−index2
10	0.413	2 / 82	PanCan_TXmisReg_geneset_nanostring
11	0.500	1 / 40	ZHANG_MM up
12	0.653	1 / 61	PanCan_Wnt_geneset_nanostring
13	0.682	0 / 14	LIU_COMMON_CANCER_GENES
14	0.860	1 / 113	PanCan_Driver_Gene_geneset_nanostring
15	0.876	1 / 120	PanCan_CC+Apop_geneset_nanostring
16	0.965	0 / 14	LIU_PROSTATE_CANCER_DN
17	0.966	2 / 298	SPANG_BCL6−index2
18	0.991	3 / 489	Lembcke_Normal vs Adenoma
19	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
20	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	4e−07	6 / 18	voltage−gated calcium channel complex
2	5e−04	3 / 10	high−density lipoprotein particle
3	8e−03	23 / 775	extracellular space
4	1e−02	5 / 78	dendritic spine
5	1e−02	4 / 51	collagen trimer
6	1e−02	8 / 177	synapse
7	1e−02	2 / 10	low−density lipoprotein particle
8	1e−02	2 / 10	vacuolar proton−transporting V−type ATPase complex
9	1e−02	2 / 10	very−low−density lipoprotein particle
10	2e−02	2 / 12	PRC1 complex
11	2e−02	3 / 33	sarcoplasmic reticulum
12	2e−02	21 / 751	integral component of plasma membrane
13	2e−02	3 / 36	T−tubule
14	3e−02	3 / 39	endocytic vesicle membrane
15	3e−02	2 / 17	membrane−bounded vesicle
16	6e−02	3 / 52	perikaryon
17	7e−02	2 / 25	heterochromatin
18	7e−02	2 / 25	PcG protein complex
19	7e−02	2 / 26	basal plasma membrane
20	1e−01	3 / 70	sarcolemma

Chr

Rank	p−value	#in/all	Geneset
1	0.01	28 / 1037	Chr 19
2	0.03	21 / 775	Chr 12
3	0.08	8 / 262	Chr 13
4	0.13	19 / 840	Chr 17
5	0.24	12 / 551	Chr X
6	0.26	4 / 151	Chr 21
7	0.35	19 / 993	Chr 2
8	0.51	26 / 1500	Chr 1
9	0.51	14 / 801	Chr 11
10	0.52	12 / 687	Chr 6
11	0.53	4 / 221	Chr 18
12	0.55	8 / 465	Chr 15
13	0.69	5 / 335	Chr 22
14	0.81	6 / 462	Chr 14
15	0.82	5 / 398	Chr 20
16	0.84	7 / 552	Chr 10
17	0.87	7 / 576	Chr 9
18	0.87	8 / 649	Chr 16
19	0.92	8 / 696	Chr 5
20	0.92	10 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−12	81 / 2142	ReprPC_Colon
2	3e−12	74 / 1889	ReprPCWk_Colon
3	5e−08	70 / 2159	TssP_Colon
4	3e−05	43 / 1317	EnhP_Colon
5	3e−04	19 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	1e−02	10 / 250	K9K27me3_Colon
7	2e−02	13 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
8	2e−02	11 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	3e−02	9 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	7e−02	78 / 3897	Quies1_Colon
11	8e−02	11 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
12	8e−02	68 / 3383	EnhWk2_Colon
13	1e−01	1 / 6	Budinska_E_Mixed_UP
14	1e−01	10 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
15	1e−01	6 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
16	1e−01	1 / 8	Marisa_CRC−C6
17	2e−01	9 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
18	2e−01	6 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
19	3e−01	19 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	3e−01	1 / 18	Ang_CRC−CIMPH−vs−L_hypo

Disease

Rank	p−value	#in/all	Geneset
1	0.2	10 / 435	GUDJ_psoriasis up
2	0.9	3 / 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 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
2	0.007	5 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
3	0.009	5 / 74	WIRTH_Normal Brain
4	0.009	5 / 75	GIEZELT_GBM_STS_down_VS_LTS
5	0.025	3 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
6	0.040	7 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
7	0.051	1 / 3	Donson−migration tethering and rolling−associated with LTS in HGA
8	0.110	2 / 33	Christensen_hypomethylated_in_primary_glioblastoma
9	0.112	3 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	0.114	1 / 7	Shaw_up_in_1p19qdel
11	0.114	1 / 7	WILLSCHER_GBM_LTSwt_proteomics−G_UP
12	0.115	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
13	0.129	1 / 8	Colman_survival_robust
14	0.133	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
15	0.138	3 / 75	Weller_LGG_A_vs_O_DOWN
16	0.144	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
17	0.144	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
18	0.144	1 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
19	0.144	1 / 9	Mukasa_UP_in_GBM
20	0.144	1 / 9	Phillips PN up vs MES & Prolif

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−08	10 / 58	KEGG_CARDIAC_MUSCLE_CONTRACTION
2	3e−06	4 / 7	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
3	1e−05	10 / 105	REACTOME_SIGNALING_BY_RHO_GTPASES
4	1e−05	13 / 179	NABA_SECRETED_FACTORS
5	5e−05	19 / 395	MARTENS_TRETINOIN_RESPONSE_UP
6	7e−05	5 / 26	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
7	1e−04	8 / 84	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
8	1e−04	5 / 29	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES
9	2e−04	32 / 936	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
10	2e−04	10 / 143	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
11	2e−04	7 / 72	KEGG_DILATED_CARDIOMYOPATHY
12	3e−04	3 / 8	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_FGF3
13	3e−04	10 / 153	LEE_DIFFERENTIATING_T_LYMPHOCYTE
14	3e−04	4 / 20	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
15	4e−04	18 / 427	NABA_MATRISOME_ASSOCIATED
16	5e−04	5 / 38	MIKKELSEN_MCV6_ICP_WITH_H3K27ME3
17	5e−04	6 / 58	ENGELMANN_CANCER_PROGENITORS_DN
18	5e−04	5 / 39	REACTOME_AQUAPORIN_MEDIATED_TRANSPORT
19	6e−04	4 / 23	KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS
20	6e−04	11 / 198	REACTOME_GPCR_LIGAND_BINDING

HM

Rank	p−value	#in/all	Geneset
1	0.2	5 / 167	HALLMARK_APICAL_JUNCTION
2	0.2	4 / 126	HALLMARK_ALLOGRAFT_REJECTION
3	0.2	4 / 140	HALLMARK_INFLAMMATORY_RESPONSE
4	0.4	3 / 127	HALLMARK_KRAS_SIGNALING_DN
5	0.5	3 / 146	HALLMARK_UV_RESPONSE_UP
6	0.5	3 / 162	HALLMARK_COMPLEMENT
7	0.5	3 / 165	HALLMARK_MYOGENESIS
8	0.6	2 / 107	HALLMARK_COAGULATION
9	0.6	3 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.6	3 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.7	2 / 141	HALLMARK_FATTY_ACID_METABOLISM
12	0.7	1 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	0.8	2 / 169	HALLMARK_XENOBIOTIC_METABOLISM
14	0.8	2 / 174	HALLMARK_HEME_METABOLISM
15	0.8	2 / 176	HALLMARK_HYPOXIA
16	0.8	2 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
17	0.8	2 / 181	HALLMARK_P53_PATHWAY
18	0.8	2 / 183	HALLMARK_GLYCOLYSIS
19	0.8	1 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
20	0.9	1 / 140	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.7	1 / 62	DUMEAUX_Smoking enriched genes
2	1.0	0 / 10	DUMEAUX_Smoking literature genes up
3	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
4	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.0	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 18	DUMEAUX_High bmi enriched genes
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−16	116 / 3396	HOPP_Repressed
2	9e−08	70 / 2188	HOPP_Poised_promoter
3	2e−02	2 / 12	BENTINK_mBL DOWN
4	2e−02	57 / 2563	HOPP_Heterochrom
5	2e−01	1 / 10	DAVE_BL UP
6	2e−01	1 / 11	Subero_T−ALL_hypo_meth
7	2e−01	2 / 47	Subero_FL_hyper_meth
8	2e−01	3 / 96	Subero_DLBCL_hyper_meth
9	3e−01	1 / 17	DAVE_NFkB BL DN
10	3e−01	1 / 19	Subero_MM_hyper_meth
11	3e−01	2 / 61	SPANG_LPS 6hrs DN
12	3e−01	2 / 66	TARTE_Plasma cell signature
13	3e−01	1 / 23	DAVE_Immune response 1
14	4e−01	1 / 29	Subero_DLBCL_hypo_meth
15	4e−01	2 / 81	Subero_INT_hyper_meth
16	4e−01	1 / 34	Subero_B−ALL_hyper_meth
17	5e−01	1 / 40	Subero_mBL_hyper_meth
18	5e−01	1 / 43	LENZ_Stromal signature 2
19	6e−01	1 / 60	Subero_T−ALL_hyper_meth
20	7e−01	2 / 129	DAVE_BL−vs−DLBCL

MF

Rank	p−value	#in/all	Geneset
1	3e−07	7 / 27	chemokine activity
2	7e−05	5 / 26	transforming growth factor beta receptor binding
3	9e−05	5 / 27	voltage−gated calcium channel activity
4	1e−04	13 / 217	GTPase activator activity
5	2e−03	23 / 695	transmembrane transporter activity
6	2e−03	6 / 77	cytokine activity
7	1e−02	2 / 10	acetylgalactosaminyltransferase activity
8	1e−02	2 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
9	1e−02	2 / 10	lipid transporter activity
10	1e−02	2 / 10	sodium channel activity
11	1e−02	2 / 11	structural constituent of eye lens
12	2e−02	13 / 386	nucleotide binding
13	2e−02	2 / 14	phosphatidylserine binding
14	2e−02	4 / 64	beta−catenin binding
15	3e−02	2 / 15	phospholipid−translocating ATPase activity
16	3e−02	2 / 16	cofactor binding
17	3e−02	5 / 104	growth factor activity
18	4e−02	13 / 430	lipid binding
19	4e−02	2 / 18	galactosyltransferase activity
20	4e−02	2 / 19	calcium channel regulator activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.09	2 / 30	hsa−miR−1293
2	0.11	1 / 7	hsa−miR−611
3	0.13	2 / 36	hsa−miR−644
4	0.15	2 / 40	hsa−miR−647
5	0.21	2 / 49	hsa−miR−519b−5p
6	0.21	2 / 49	hsa−miR−519c−5p
7	0.24	2 / 54	hsa−miR−518d−5p
8	0.24	2 / 54	hsa−miR−520c−5p
9	0.28	1 / 19	hsa−miR−563
10	0.31	1 / 21	hsa−miR−662
11	0.32	1 / 22	hsa−miR−668
12	0.33	1 / 23	hsa−miR−323−5p
13	0.33	1 / 23	hsa−miR−1250
14	0.34	1 / 24	hsa−miR−483−3p
15	0.35	2 / 71	hsa−miR−578
16	0.35	1 / 25	hsa−miR−517c
17	0.35	1 / 25	hsa−miR−941
18	0.36	2 / 73	hsa−miR−184
19	0.38	1 / 28	hsa−miR−591
20	0.40	1 / 29	hsa−miR−1225−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_src.10
2	0.2	1 / 14	BENTINK_e2f3.1
3	0.2	1 / 14	BENTINK_src.2
4	1.0	0 / 12	GUSTAFSON_PI3K_UP
5	1.0	0 / 13	GUSTAFSON_PI3K_DN
6	1.0	0 / 12	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 9	BENTINK_ras.4
10	1.0	0 / 15	BENTINK_ras.6
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	0.001	34 / 1139	HEBENSTREIT_low expression TF
2	0.027	2 / 15	NOWICK_TF
3	0.347	24 / 1273	ICGC_P300_targets
4	0.771	31 / 2013	ICGC_Bcl11_targets
5	0.774	46 / 2927	ICGC_Rad21_targets
6	0.807	8 / 595	ICGC_NrsfPcr2_targets
7	0.955	24 / 1872	ICGC_Mef2_targets
8	0.967	38 / 2836	ICGC_BatfPcr1_targets
9	0.973	16 / 1400	ICGC_Myc_targets
10	0.981	60 / 4314	ICGC_Ebfsc137065_targets
11	0.987	13 / 1266	ICGC_NrsfPcr1_targets
12	0.989	5 / 653	ICGC_SrfPcr2_targets
13	0.990	29 / 2416	ICGC_Bcl3_targets
14	0.994	14 / 1418	ICGC_Ets1_targets
15	0.994	74 / 5374	ICGC_Pax5_targets
16	0.997	50 / 3966	ICGC_Pu1_targets
17	0.998	4 / 690	ICGC_Atf3_targets
18	0.999	68 / 5219	ICGC_Tcf3_targets
19	0.999	29 / 2714	ICGC_Irf4_targets
20	0.999	58 / 4682	ICGC_Pol24_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.5	1 / 37	VAQUERIZAS_Thymus
2	0.5	1 / 41	VAQUERIZAS_Placenta
3	1.0	0 / 36	VAQUERIZAS_Fetal brain
4	1.0	0 / 26	VAQUERIZAS_Liver
5	1.0	0 / 33	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 45	VAQUERIZAS_Uterus
8	1.0	0 / 143	VAQUERIZAS_General
9	1.0	0 / 9	VAQUERIZAS_Kidney
10	1.0	0 / 23	VAQUERIZAS_Spinal cord
11	1.0	0 / 38	VAQUERIZAS_Whole brain
12	1.0	0 / 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	0.001	15 / 350	WIRTH_Nervous System
2	0.005	4 / 41	WIRTH_Homeostasis
3	0.010	6 / 107	WIRTH_Testis
4	0.083	1 / 5	WIRTH_Bone marrow
5	0.104	2 / 32	WIRTH_Pancreas
6	0.134	3 / 74	WIRTH_Mucosa
7	0.174	1 / 11	WIRTH_Prim. lymphoid organs
8	0.188	1 / 12	WIRTH_Thymus
9	0.224	3 / 95	WIRTH_Muscle
10	0.550	1 / 46	WIRTH_Liver
11	0.560	6 / 350	WIRTH_Immune system
12	0.586	2 / 114	PALMER_T−Cell signature up
13	0.651	3 / 194	PALMER_B−Cell signature up
14	0.746	3 / 225	PALMER_Granulocytes signature up
15	1.000	0 / 11	WIRTH_Sec. lymphoid organs
16	1.000	0 / 13	WIRTH_B−cells
17	1.000	0 / 8	WIRTH_Tonsil
18	1.000	0 / 12	WIRTH_Lymphocytes
19	1.000	0 / 11	WIRTH_Globus pallidus
20	1.000	0 / 14	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	72 / 3682	LU_BPDE 0.005 DN
2	0.6	18 / 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	