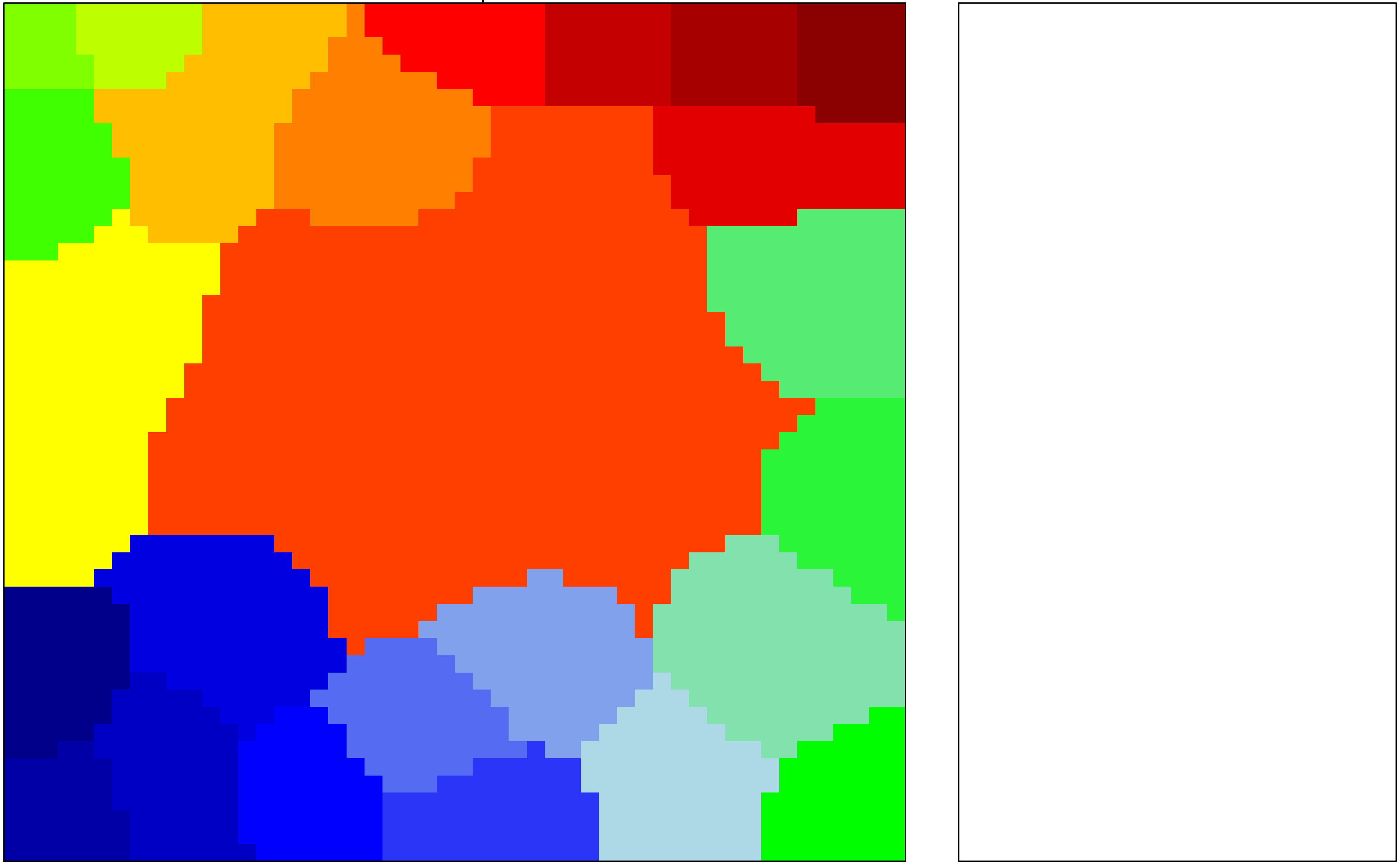
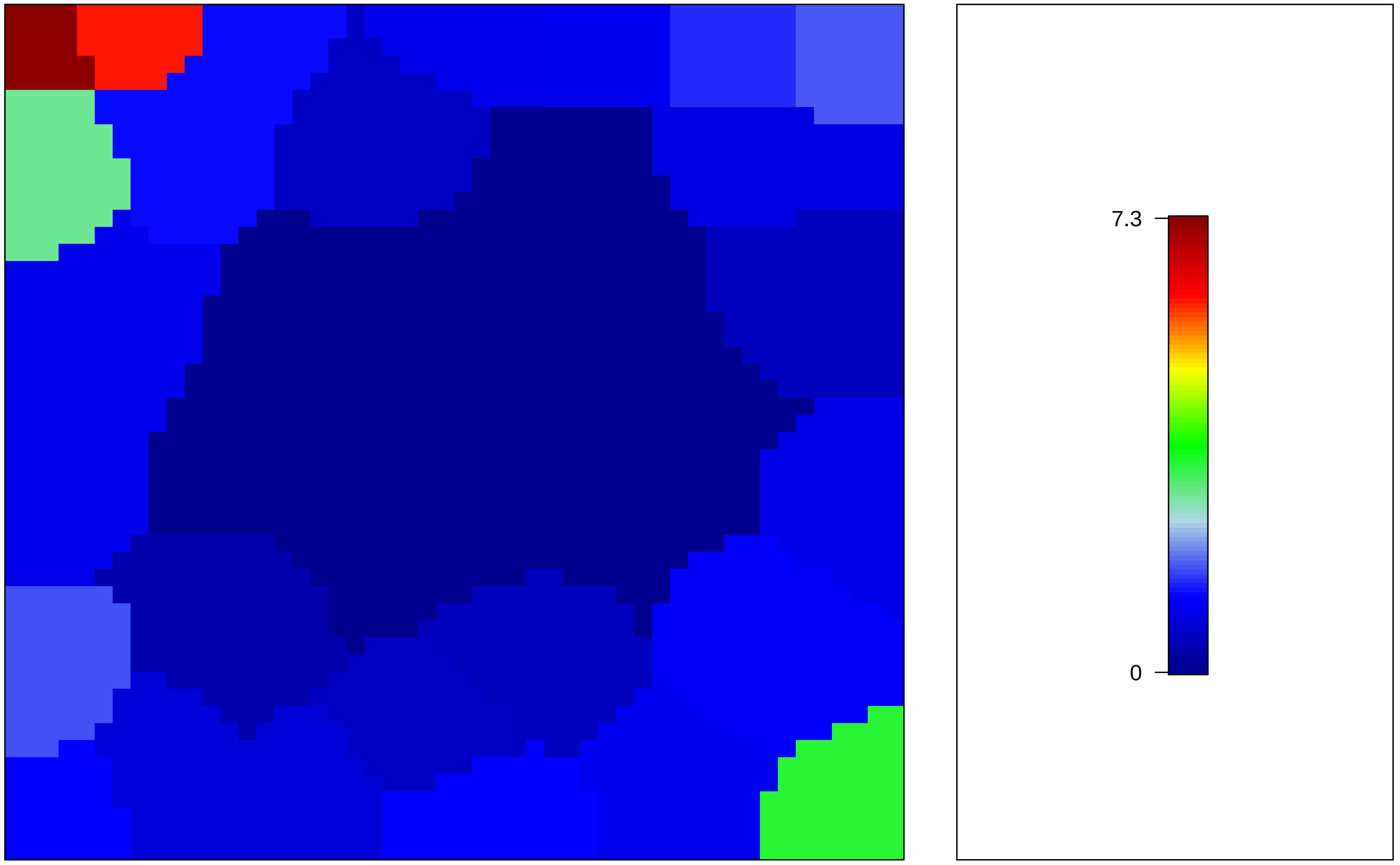
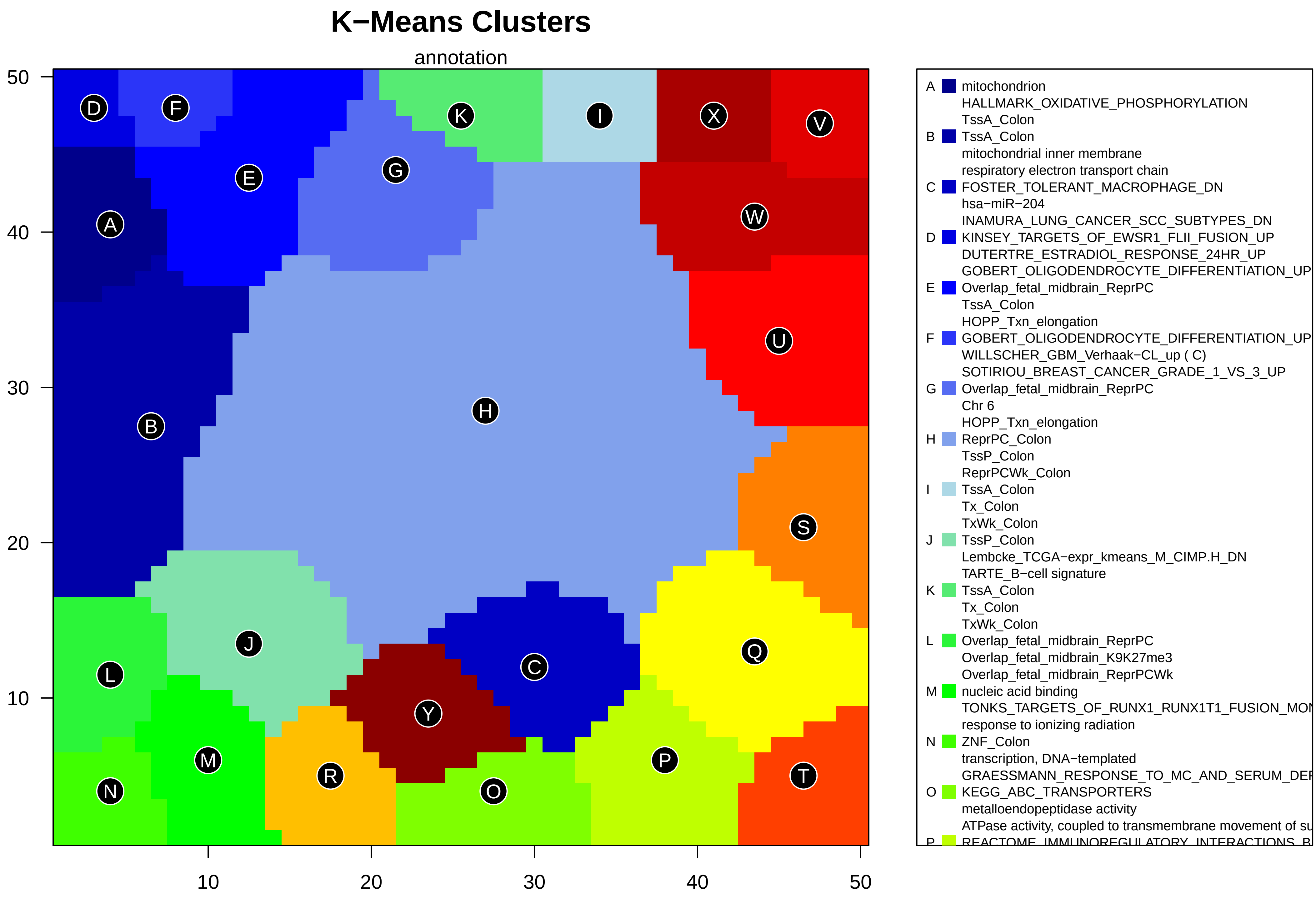
K−Means Clusters

landscape



K−Means Clusters




K−Means Clusters
annotation
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E
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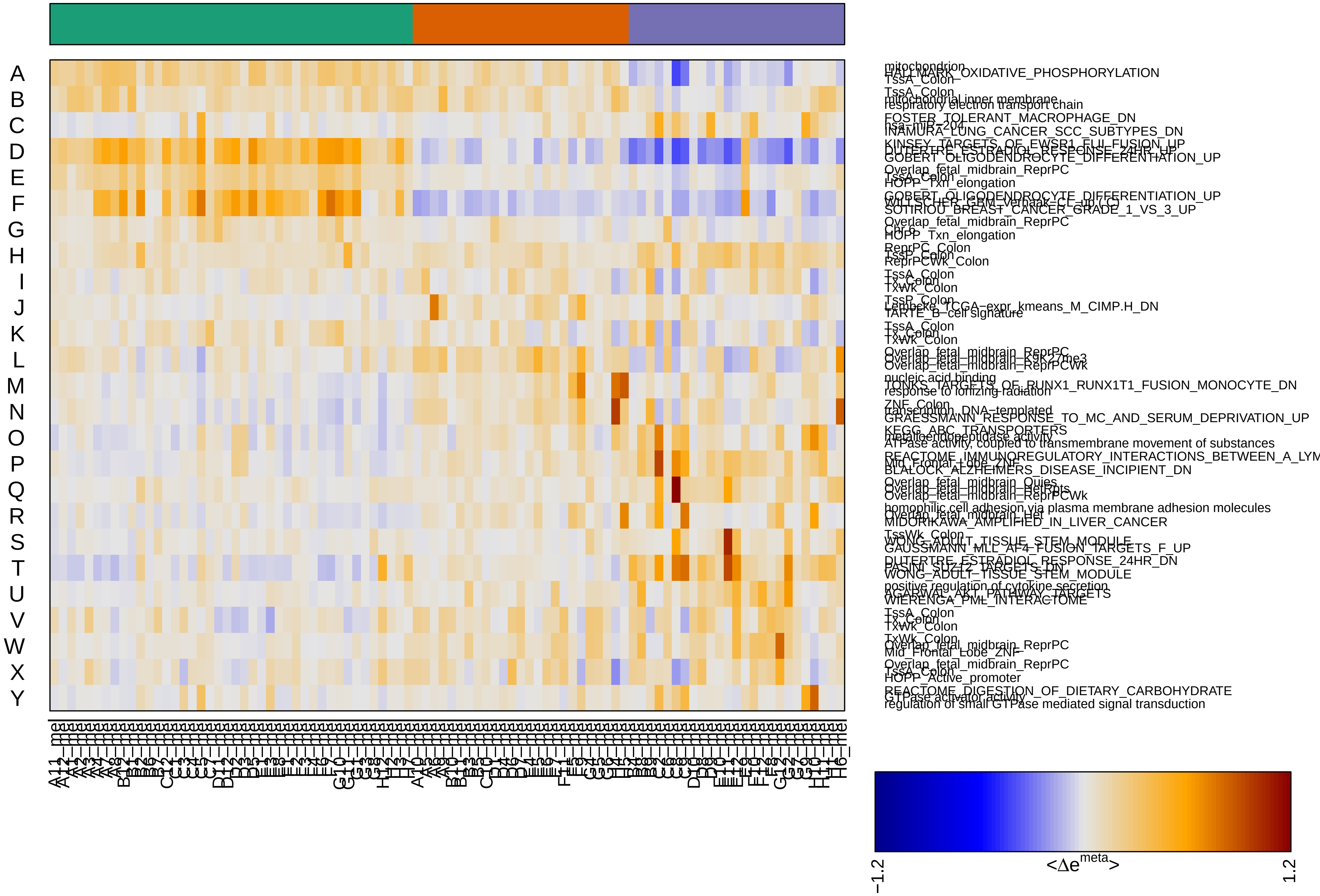
T
A
mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
TssA_Colon
B
TssA_Colon
mitochondrial inner membrane
respiratory electron transport chain
C
FOSTER_TOLERANT_MACROPHAGE_DN
hsa−miR−204
INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN
D
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
E
Overlap_fetal_midbrain_ReprPC
TssA_Colon
HOPP_Txn_elongation
F
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
WILLSCHER_GBM_Verhaak−CL_up (C)
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
G
Overlap_fetal_midbrain_ReprPC
Chr 6
HOPP_Txn_elongation
H
ReprPC_Colon
TssP_Colon
ReprPCWk_Colon
I
TssA_Colon
Tx_Colon
TxWk_Colon
J
TssP_Colon
Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
TARTE_B−cell signature
K
TssA_Colon
Tx_Colon
TxWk_Colon
L
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_ReprPCWk
M
nucleic acid binding
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MON
response to ionizing radiation
N
ZNF_Colon
transcription, DNA−templated
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEF
O
KEGG_ABC_TRANSPORTERS
metalloendopeptidase activity
ATPase activity, coupled to transmembrane movement of su
P
REACTOME_IMMUNOREGULATORY_INTERACTIONS_B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mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
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hsa-miR-204
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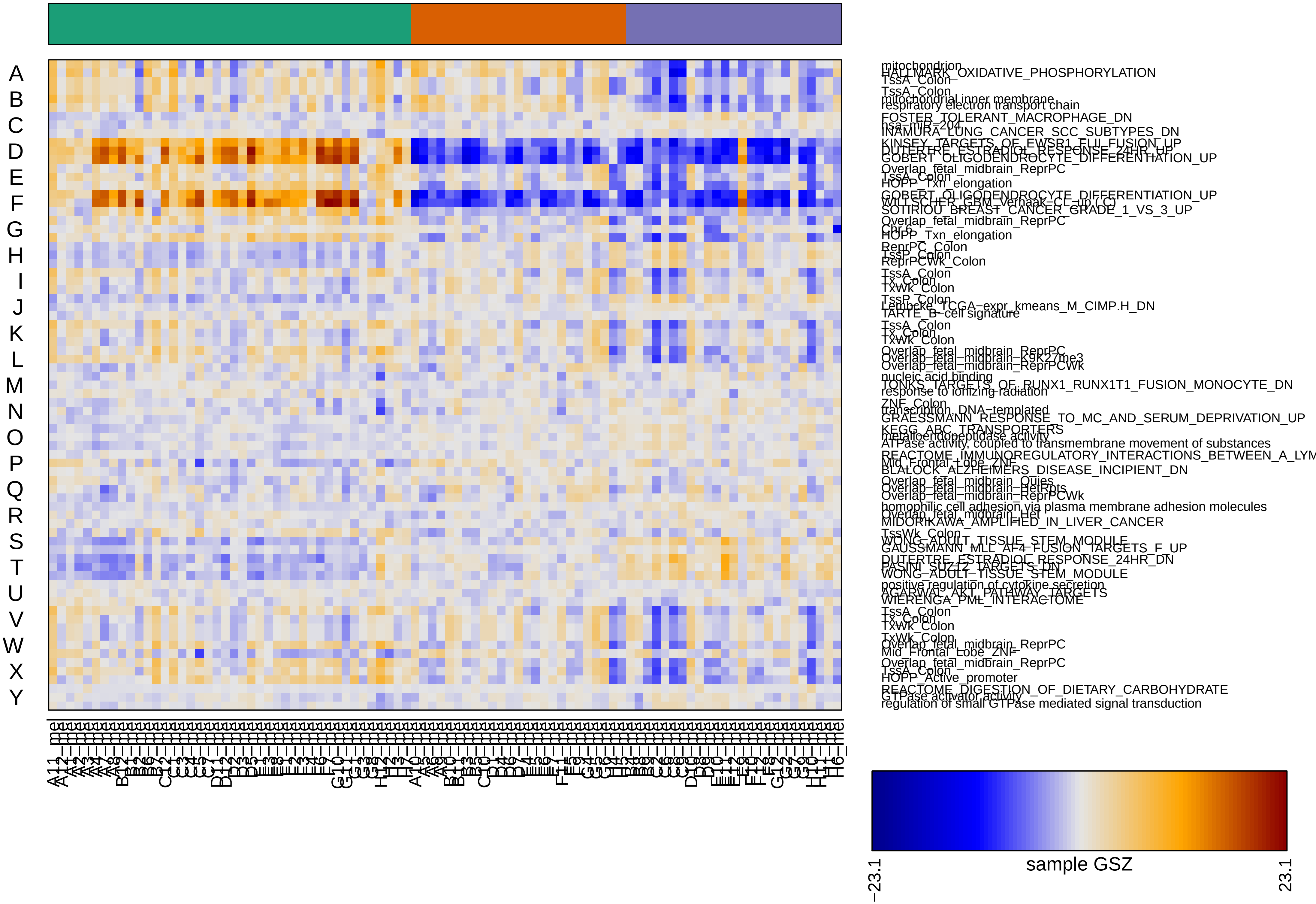
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
Overlap_fetal_midbrain_ReprPC
TssA_Colon
HOPP_Txn_elongation
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
WILLSCHER_GBM_Verhaak-CL-up (C)
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
Overlap_fetal_midbrain_ReprPC
Chr 6
HOPP_Txn_elongation
ReprPC_Colon
TssP_Colon
ReprPCWk_Colon
TssA_Colon
Tx_Colon
TxWk_Colon
TssP_Colon
Lembcke_TCGA-expr_kmeans_M_CIMP.H_DN
TARTE_B-cell signature
TssA_Colon
Tx_Colon
TxWk_Colon
Overlap_fetal_midbrain_ReprPC
Overlap-fetal-midbrain-K9K27me3
Overlap-fetal-midbrain-ReprPCWk
nucleic acid binding
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
response to ionizing radiation
ZNF_Colon
transcription, DNA-templated
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP
KEGG_ABC_TRANSPORTERS
metalloendopeptidase activity
ATPase activity, coupled to transmembrane movement of substances
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
Mid_Frontal_Lobe_ZNF
BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN
Overlap_fetal_midbrain_Quies
Overlap-fetal-midbrain-HetRpts
Overlap-fetal-midbrain-ReprPCWk
homophilic cell adhesion via plasma membrane adhesion molecules
Overlap_fetal_midbrain_Het
MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
TssWk_Colon
WONG_ADULT_TISSUE_STEM_MODULE
GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
PASINI_SUZ12_TARGETS_DN
WONG-ADULT-TISSUE-STEM_MODULE
positive regulation of cytokine secretion
AGARWAL_AKT_PATHWAY_TARGETS
WIERENGA_PML_INTERACTOME
TssA_Colon
Tx_Colon
TxWk_Colon
TxWk_Colon
Overlap_fetal_midbrain_ReprPC
Mid_Frontal_Lobe_ZNF
Overlap_fetal_midbrain_ReprPC
TssA_Colon
HOPP_Active_promoter
REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
GTPase activator activity
regulation of small GTPase mediated signal transduction
-1.2
<Δe^meta>
1.2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TssP_Colon
ReprPCWk_Colon
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Tx_Colon
TxWk_Colon
Overlap_fetal_midbrain_ReprPC
Overlap-fetal-midbrain-K9K27me3
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Overlap-fetal-midbrain-ReprPCWk
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TssWk_Colon
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GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
PASINI_SUZ12_TARGETS_DN
WONG-ADULT-TISSUE-STEM_MODULE
positive regulation of cytokine secretion
AGARWAL_AKT_PATHWAY_TARGETS
WIERENGA_PML_INTERACTOME
TssA_Colon
Tx_Colon
TxWk_Colon
TxWk_Colon
Overlap_fetal_midbrain_ReprPC
Mid_Frontal_Lobe_ZNF
Overlap_fetal_midbrain_ReprPC
TssA_Colon
HOPP_Active_promoter
REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
GTPase activator activity
regulation of small GTPase mediated signal transduction
−23.1
sample GSZ
23.1

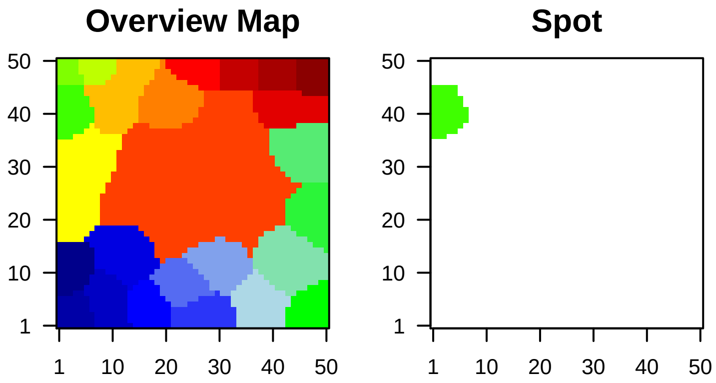
K−Means Clusters

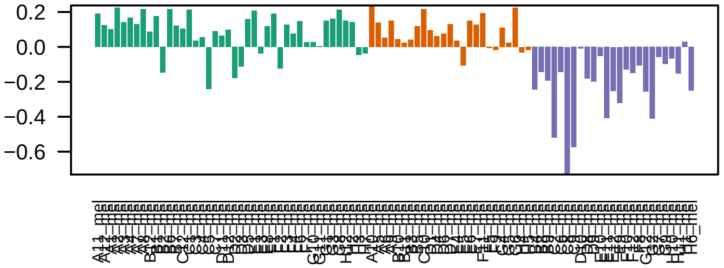
Spot Summary: A

metagenes = 57
genes = 593

<r> metagenes = 0.89
<r> genes = 0.12
beta: r2= 2.86 / log p= −Inf

samples with spot = 21 (22.8 %)
MSC1 : 15 (35.7 %)
MSC2 : 6 (24 %)



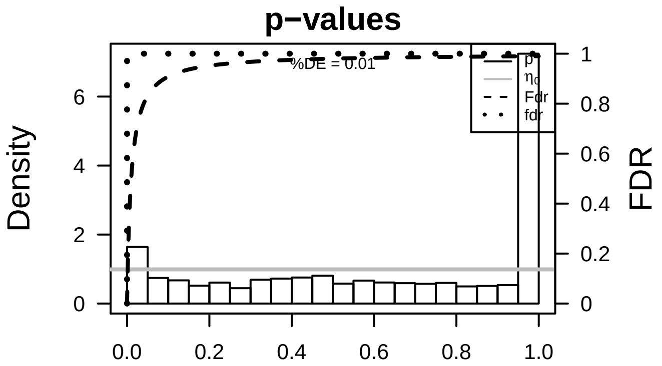


Spot Genelist

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	SLC25A27	1.92	−0.36	0.24	SLC25A27	solute carrier family 25, member 27 [Source:HGNC Symbol;A
3	IGFLR1	1.76	−0.35	0.32	IGFLR1	IGF−like family receptor 1 [Source:HGNC Symbol;Acc:HGNC
4	MARCH3	1.72	−0.43	0.33	MARCH3	membrane−associated ring finger (C3HC4) 3, E3 ubiquitin pr
5	BCS1L	1.71	−0.91	0.27	BCS1L	BC1 (ubiquinol−cytochrome c reductase) synthesis−like [Sou
6	THUMPD2	1.71	−1.04	0.28	THUMPD2	THUMP domain containing 2 [Source:HGNC Symbol;Acc:HG
7	ZNF30	1.71	−0.15	0.26	ZNF30	zinc finger protein 30 [Source:HGNC Symbol;Acc:HGNC:130
8	GAPDHS	1.71	−1.17	0.59	GAPDHS	glyceraldehyde−3−phosphate dehydrogenase, spermatogeni
9	ST6GALNAC	1.69	−0.39	0.32	ST6GALNAC3	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
10	PLA2G15	1.68	−0.42	0.23	PLA2G15	phospholipase A2, group XV [Source:HGNC Symbol;Acc:HG
11	TRMT1	1.65	−0.71	0.36	TRMT1	tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:H
12	MCCC1	1.64	−0.58	0.24	MCCC1	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
13	ZNF141	1.64	−0.32	0.26	ZNF141	zinc finger protein 141 [Source:HGNC Symbol;Acc:HGNC:12
14	NMRK2	1.63	−1.2	0.71	NMRK2	nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:H
15	NT5DC1	1.63	−0.93	0.28	NT5DC1	5'−nucleotidase domain containing 1 [Source:HGNC Symbol;
16	SEPSECS	1.63	−0.31	0.32	SEPSECS	Sep (O−phosphoserine) tRNA:Sec (selenocysteine) tRNA sy
17	FAM81A	1.62	−0.21	0.22	FAM81A	family with sequence similarity 81, member A [Source:HGNC
18	WIPF3	1.62	−0.29	0.33	WIPF3	WAS/WASL interacting protein family, member 3 [Source:HG
19	MED24	1.62	−0.74	0.24	MED24	mediator complex subunit 24 [Source:HGNC Symbol;Acc:HG
20	ANO2	1.61	−0.48	0.34	ANO2	anoctamin 2, calcium activated chloride channel [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−28	149 / 1468	CC	mitochondrion
2	8e−24	47 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	2e−23	485 / 9482	Colon	TssA_Colon
4	2e−22	65 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
5	8e−22	61 / 368	GSEA	STEIN_ESRRA_TARGETS_UP
6	2e−20	62 / 401	CC	mitochondrial inner membrane
7	1e−19	87 / 756	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
8	3e−19	392 / 7203	Colon	TssF_Colon
9	4e−19	458 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
10	4e−18	66 / 500	GSEA	STEIN_ESRRA_TARGETS
11	6e−17	105 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
12	7e−17	58 / 421	GSEA	MOOTHA_MITOCHONDRIA
13	2e−15	54 / 398	GSEA	MOOTHA_PGC
14	8e−15	367 / 6929	Lympl	HOPP_Txn_elongation
15	2e−14	58 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
16	3e−14	455 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
17	3e−14	414 / 8205	CC	cytoplasm
18	5e−14	46 / 325	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
19	5e−13	440 / 9027	Colon	Tx_Colon
20	6e−13	84 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
21	6e−13	386 / 7592	Lympl	HOPP_Active_promoter
22	1e−12	106 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	1e−12	40 / 278	GSEA	MANALO_HYPOXIA_DN
24	2e−12	19 / 63	Glio	Stuehler_Proteins_up_in_STS
25	2e−12	127 / 1730	BP	small molecule metabolic process
26	7e−12	59 / 562	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
27	1e−11	57 / 536	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_UP
28	1e−11	41 / 312	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
29	6e−11	281 / 5184	Lympl	HOPP_Txn_transition
30	8e−11	32 / 213	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
31	1e−10	40 / 322	BP	mitochondrion organization
32	2e−10	41 / 338	GSEA	DAIRKEE_TERT_TARGETS_UP
33	2e−10	465 / 9988	CC	organelle
34	2e−10	33 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
35	2e−10	486 / 10605	CC	intracellular
36	3e−10	72 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
37	4e−10	14 / 42	Lympl	CARO_OxPhos_in_DLBCL_UP
38	8e−10	71 / 834	GSEA	LEE_BMP2_TARGETS_DN
39	9e−10	105 / 1460	GSEA	PUJANA_BRCA1_PCC_NETWORK
40	9e−10	9 / 15	GSEA	MOOTHA_TCA



Aging

Rank	p−value	#in/all	Geneset
1	0.2	5 / 44	HORVATH_aging_genes meth UP
2	0.8	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−12	127 / 1730	small molecule metabolic process
2	1e−10	40 / 322	mitochondrion organization
3	4e−09	11 / 28	tricarboxylic acid cycle
4	3e−08	35 / 311	generation of precursor metabolites and energy
5	2e−07	48 / 541	oxidation−reduction process
6	4e−07	20 / 135	cellular metabolic process
7	1e−06	10 / 37	gluconeogenesis
8	9e−06	80 / 1237	metabolic process
9	1e−05	10 / 47	protein targeting to mitochondrion
10	3e−05	25 / 255	cellular amino acid metabolic process
11	3e−05	6 / 17	mitochondrial respiratory chain complex I assembly
12	4e−05	26 / 277	translation
13	6e−05	14 / 104	glucose metabolic process
14	8e−05	17 / 147	tRNA metabolic process
15	1e−04	5 / 13	melanin biosynthetic process
16	1e−04	24 / 259	protein targeting
17	4e−04	7 / 35	glycolytic process
18	5e−04	5 / 18	melanocyte differentiation
19	7e−04	76 / 1325	catabolic process
20	7e−04	16 / 162	ribosome biogenesis

Brain

Rank	p−value	#in/all	Geneset
1	4e−19	458 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−14	455 / 9330	Overlap_fetal_midbrain_ReprPC
3	1e−08	441 / 9528	Overlap_fetal_midbrain_Quies
4	7e−05	161 / 3081	Mid_Frontal_Lobe_ZNF
5	1e−04	52 / 765	Mid_Frontal_Lobe_Het
6	2e−04	278 / 5940	Overlap_fetal_midbrain_HetRpts
7	3e−03	73 / 1333	Fetal_ReprPCWk
8	4e−02	21 / 349	Fetal_ZNF
9	4e−02	114 / 2462	Mid_Frontal_Lobe_HetRpts
10	2e−01	39 / 831	Fetal_HetRpts
11	3e−01	366 / 9020	Overlap_fetal_midbrain_ReprPCWk
12	5e−01	74 / 1845	Fetal_Quies
13	6e−01	6 / 156	Mid_Frontal_Lobe_TssA
14	7e−01	21 / 564	Mid_Frontal_Lobe_EnhP
15	7e−01	29 / 786	Fetal_EnhG
16	8e−01	5 / 158	Overlap_fetal_midbrain_Het
17	8e−01	2 / 69	Overlap_fetal_midbrain_Tx
18	8e−01	10 / 304	Fetal_Het
19	8e−01	27 / 769	Overlap_fetal_midbrain_ZNF
20	8e−01	5 / 163	Fetal_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 16	GENTLES_modul2
2	3e−03	2 / 15	RHODES_CANCER_META_SIGNATURE
3	4e−02	5 / 47	PanCan_DNARepair_geneset_nanostring
4	5e−02	2 / 14	LIU_COMMON_CANCER_GENES
5	6e−02	12 / 180	SPANG_LPS−index2
6	6e−02	2 / 10	GENTLES_modul5
7	7e−02	4 / 40	ZHANG_MM_up
8	8e−02	2 / 12	LIU_BREAST_CANCER
9	1e−01	8 / 120	PanCan_CC+Apop_geneset_nanostring
10	1e−01	2 / 15	GENTLES_modul1
11	1e−01	2 / 15	GENTLES_modul10
12	1e−01	2 / 16	GENTLES_modul7
13	2e−01	3 / 40	PanCan_HK_geneset_nanostring
14	2e−01	23 / 489	Lembcke_Normal vs Adenoma
15	2e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	3e−01	8 / 156	PanCan_PI3K_geneset_nanostring
17	3e−01	4 / 70	SHAUGHNESSY_MM high risk
18	3e−01	0 / 14	LIU_LIVER_CANCER
19	4e−01	13 / 298	SPANG_BCL6−index2
20	4e−01	1 / 13	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	3e−28	149 / 1468	mitochondrion
2	2e−20	62 / 401	mitochondrial inner membrane
3	3e−14	414 / 8205	cytoplasm
4	2e−10	465 / 9988	organelle
5	2e−10	486 / 10605	intracellular
6	3e−09	32 / 246	mitochondrial matrix
7	2e−08	137 / 2193	extracellular exosome
8	3e−07	147 / 2507	cytosol
9	6e−06	509 / 11774	cell
10	7e−06	18 / 135	myelin sheath
11	8e−05	15 / 120	mitochondrial outer membrane
12	2e−04	10 / 63	mitochondrial intermembrane space
13	2e−04	164 / 3214	protein complex
14	3e−04	12 / 92	spliceosomal complex
15	3e−04	6 / 24	mitochondrial ribosome
16	3e−04	11 / 80	mitochondrial membrane
17	3e−04	12 / 94	melanosome
18	4e−04	4 / 10	methylosome
19	5e−04	31 / 412	lysosome
20	1e−03	4 / 13	sperm principal piece

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	62 / 993	Chr 2
2	3e−02	42 / 775	Chr 12
3	5e−02	31 / 576	Chr 9
4	1e−01	13 / 221	Chr 18
5	1e−01	28 / 552	Chr 10
6	1e−01	24 / 469	Chr 8
7	2e−01	32 / 687	Chr 6
8	4e−01	7 / 151	Chr 21
9	4e−01	43 / 1037	Chr 19
10	5e−01	34 / 840	Chr 17
11	5e−01	19 / 465	Chr 15
12	5e−01	22 / 551	Chr X
13	6e−01	13 / 335	Chr 22
14	6e−01	27 / 696	Chr 5
15	6e−01	25 / 649	Chr 16
16	7e−01	14 / 398	Chr 20
17	8e−01	27 / 801	Chr 11
18	9e−01	7 / 262	Chr 13
19	9e−01	21 / 689	Chr 7
20	9e−01	26 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−23	485 / 9482	TssA_Colon
2	3e−19	392 / 7203	TssF_Colon
3	5e−13	440 / 9027	Tx_Colon
4	2e−09	410 / 8580	TxWk_Colon
5	8e−07	58 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
6	2e−05	48 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	1e−04	378 / 8415	Quies3_Colon
8	1e−04	277 / 5880	TssD2_Colon
9	5e−04	421 / 9653	Enh_Colon
10	1e−03	442 / 10290	TssWk_Colon
11	3e−03	138 / 2798	TxEnhG1_Colon
12	8e−03	43 / 739	TxEnhG2_Colon
13	2e−02	230 / 5155	EnhWk1_Colon
14	1e−01	2 / 16	Juehling−MSI−enriched−in−6
15	2e−01	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
16	2e−01	28 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
17	2e−01	115 / 2698	EnhA_Colon
18	3e−01	4 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
19	3e−01	1 / 8	Boland_CRC−MSI−TGC
20	3e−01	1 / 8	Marisa_CRC−C6

Disease

Rank	p−value	#in/all	Geneset
1	0.07	24 / 435	GUDJ_psoriasis up
2	0.56	1 / 20	BCHETNIA_EBM−DM up
3	0.90	8 / 294	GUDJ_psoriasis down
4	1.00	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−12	19 / 63	Stuehler_Proteins_up_in_STS
2	4e−03	14 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
3	6e−03	25 / 365	Down_b
4	8e−03	48 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	1e−02	6 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	4e−02	2 / 8	Colman_survival_robust
7	7e−02	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
8	7e−02	19 / 332	Up
9	1e−01	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	1e−01	3 / 32	Donson−innate immunity−associated with LTS in HGA
11	1e−01	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
12	2e−01	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
13	2e−01	16 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	2e−01	3 / 38	OL vs. OPC
15	2e−01	4 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
16	2e−01	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
17	3e−01	2 / 26	Christensen_hypomethylated_in_ependymoma
18	3e−01	1 / 9	VERHAAK_Brain
19	3e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma
20	3e−01	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−22	65 / 405	MOOTHA_HUMAN_MITODB_6_2002
2	8e−22	61 / 368	STEIN_ESRRA_TARGETS_UP
3	1e−19	87 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
4	4e−18	66 / 500	STEIN_ESRRA_TARGETS
5	6e−17	105 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
6	7e−17	58 / 421	MOOTHA_MITOCHONDRIA
7	2e−15	54 / 398	MOOTHA_PGC
8	2e−14	58 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
9	5e−14	46 / 325	PENG_GLUTAMINE_DEPRIVATION_DN
10	6e−13	84 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
11	1e−12	106 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
12	1e−12	40 / 278	MANALO_HYPOXIA_DN
13	7e−12	59 / 562	CAIRO_HEPATOBLASTOMA_CLASSES_UP
14	1e−11	57 / 536	TIEN_INTESTINE_PROBIOTICS_24HR_UP
15	1e−11	41 / 312	WONG_EMBRYONIC_STEM_CELL_CORE
16	8e−11	32 / 213	WONG_MITOCHONDRIA_GENE_MODULE
17	2e−10	41 / 338	DAIRKEE_TERT_TARGETS_UP
18	2e−10	33 / 233	PENG_RAPAMYCIN_RESPONSE_DN
19	3e−10	72 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
20	8e−10	71 / 834	LEE_BMP2_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	8e−24	47 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	8e−09	23 / 141	HALLMARK_FATTY_ACID_METABOLISM
3	4e−07	24 / 188	HALLMARK_ADIPOGENESIS
4	2e−06	12 / 57	HALLMARK_MYC_TARGETS_V2
5	3e−06	23 / 196	HALLMARK_MTORC1_SIGNALING
6	2e−05	21 / 188	HALLMARK_MYC_TARGETS_V1
7	6e−03	15 / 183	HALLMARK_GLYCOLYSIS
8	8e−03	14 / 169	HALLMARK_XENOBIOTIC_METABOLISM
9	1e−02	9 / 93	HALLMARK_PEROXISOME
10	3e−02	8 / 91	HALLMARK_PROTEIN_SECRETION
11	3e−02	12 / 162	HALLMARK_COMPLEMENT
12	5e−02	13 / 197	HALLMARK_E2F_TARGETS
13	7e−02	10 / 146	HALLMARK_DNA_REPAIR
14	7e−02	6 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	9e−02	7 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
16	1e−01	4 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
17	1e−01	9 / 146	HALLMARK_UV_RESPONSE_UP
18	2e−01	10 / 174	HALLMARK_HEME_METABOLISM
19	2e−01	6 / 94	HALLMARK_ANDROGEN_RESPONSE
20	2e−01	9 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
2	0.3	1 / 10	DUMEAUX_Smoking literature genes up
3	0.4	3 / 62	DUMEAUX_Smoking enriched genes
4	0.5	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.5	1 / 18	DUMEAUX_High bmi enriched genes
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	

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−15	367 / 6929	HOPP_Txn_elongation
2	6e−13	386 / 7592	HOPP_Active_promoter
3	6e−11	281 / 5184	HOPP_Txn_transition
4	4e−10	14 / 42	CARO_OxPhos_in_DLBCL_UP
5	3e−09	356 / 7209	HOPP_Weak_promoter
6	2e−05	28 / 294	TARTE_Plasmablast signature
7	6e−05	307 / 6564	HOPP_Strong_enhancer
8	1e−03	10 / 82	ROSOLOWSKI_green UP
9	4e−03	11 / 109	ROSOLOWSKI_green total
10	4e−02	7 / 80	Aukema_BCL2 DN_BCL6 UP
11	6e−02	239 / 5538	HOPP_Weak_txn
12	8e−02	16 / 275	TARTE_Mature plasma cell signature
13	1e−01	1 / 3	WRIGHT_custom GCB−DLBCL UP
14	1e−01	6 / 86	ROSOLOWSKI_red total
15	1e−01	21 / 410	SPANG_CD40 6hrs DN
16	2e−01	236 / 5693	HOPP_Weak_enhancer
17	2e−01	4 / 61	SPANG_LPS 6hrs DN
18	2e−01	50 / 1128	SPANG_BCR DN
19	3e−01	7 / 129	DAVE_BL−vs−DLBCL
20	3e−01	1 / 8	MASCQUE_GCB UP

MF

Rank	p−value	#in/all	Geneset
1	3e−07	92 / 1365	RNA binding
2	1e−06	11 / 45	NAD binding
3	2e−05	34 / 394	catalytic activity
4	2e−05	67 / 1007	poly(A) RNA binding
5	2e−05	45 / 592	oxidoreductase activity
6	4e−04	8 / 46	transferase activity, transferring alkyl or aryl (other than methyl) groups
7	6e−04	7 / 37	coenzyme binding
8	2e−03	14 / 142	isomerase activity
9	4e−03	4 / 17	fatty−acyl−CoA binding
10	4e−03	4 / 17	sialyltransferase activity
11	4e−03	6 / 39	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
12	4e−03	6 / 39	SNARE binding
13	4e−03	5 / 28	hydrogen ion transmembrane transporter activity
14	8e−03	3 / 11	protein deacetylase activity
15	1e−02	3 / 12	NAD−dependent histone deacetylase activity (H4−K16 specific)
16	1e−02	3 / 12	oxidoreductase activity, acting on NAD(P)H
17	1e−02	5 / 35	aminoacyl−tRNA ligase activity
18	1e−02	4 / 23	protein disulfide oxidoreductase activity
19	1e−02	4 / 23	proton−transporting ATPase activity, rotational mechanism
20	1e−02	9 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	11 / 96	hsa−miR−513b
2	0.006	14 / 164	hsa−miR−323b−5p
3	0.009	7 / 60	hsa−miR−126*
4	0.029	2 / 7	hsa−miR−339−3p
5	0.030	5 / 44	hsa−miR−640
6	0.035	8 / 95	hsa−miR−125a−3p
7	0.038	3 / 19	hsa−miR−645
8	0.053	6 / 68	hsa−miR−361−3p
9	0.061	11 / 163	hsa−miR−495
10	0.063	6 / 71	hsa−miR−578
11	0.068	2 / 11	hsa−miR−604
12	0.071	5 / 56	hsa−miR−892a
13	0.071	14 / 228	hsa−miR−124
14	0.078	8 / 112	hsa−miR−297
15	0.080	5 / 58	hsa−miR−409−5p
16	0.081	6 / 76	hsa−miR−620
17	0.083	3 / 26	hsa−miR−337−5p
18	0.084	4 / 42	hsa−miR−769−3p
19	0.086	9 / 134	hsa−miR−488
20	0.096	4 / 44	hsa−miR−658

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	BENTINK_myc.1
2	0.4	1 / 13	BENTINK_src.10
3	0.4	1 / 14	BENTINK_e2f3.1
4	0.4	1 / 14	BENTINK_src.2
5	1.0	0 / 12	GUSTAFSON_PI3K_UP
6	1.0	0 / 13	GUSTAFSON_PI3K_DN
7	1.0	0 / 12	BENTINK_e2f3.2
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	7e−08	111 / 1701	HEBENSTREIT_high expression TF
2	7e−08	84 / 1171	KIM_MYC targets
3	2e−07	94 / 1400	ICGC_Myc_targets
4	2e−06	239 / 4689	ICGC_Taf1_targets
5	2e−05	11 / 59	MYC_Targets UP
6	5e−05	240 / 4909	ICGC_Stat5_targets
7	5e−05	198 / 3924	ICGC_Zeb1_targets
8	1e−04	202 / 4054	ICGC_Egr1_targets
9	1e−04	217 / 4414	ICGC_Bclaf101388_targets
10	2e−04	228 / 4706	ICGC_Sp1_targets
11	2e−04	234 / 4879	ICGC_Pmlsc71910_targets
12	3e−04	82 / 1418	ICGC_Ets1_targets
13	3e−04	115 / 2137	ICGC_SrfV0416101_targets
14	3e−04	77 / 1314	ICGC_Usf1_targets
15	3e−04	222 / 4617	ICGC_Tcf12_targets
16	4e−04	228 / 4774	ICGC_Foxm1_targets
17	5e−04	257 / 5495	ICGC_Yy1_targets
18	5e−04	251 / 5355	ICGC_Pol2_targets
19	6e−04	245 / 5219	ICGC_Tcf3_targets
20	7e−04	272 / 5890	ICGC_Elf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	3 / 23	VAQUERIZAS_Adrenal cortex
2	0.13	2 / 16	VAQUERIZAS_Pancreas
3	0.13	2 / 16	VAQUERIZAS_Adrenal gland
4	0.13	2 / 16	VAQUERIZAS_Salivary gland
5	0.19	3 / 38	VAQUERIZAS_Whole brain
6	0.23	2 / 23	VAQUERIZAS_Spinal cord
7	0.23	2 / 23	VAQUERIZAS_Trachea
8	0.25	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
9	0.31	1 / 9	VAQUERIZAS_Kidney
10	0.36	1 / 11	VAQUERIZAS_Fetal liver
11	0.42	2 / 36	VAQUERIZAS_Fetal brain
12	0.44	2 / 37	VAQUERIZAS_Thymus
13	0.46	1 / 15	VAQUERIZAS_Fetal thyroid
14	0.50	1 / 17	VAQUERIZAS_Pituitary
15	0.65	1 / 26	VAQUERIZAS_Liver
16	0.67	1 / 27	VAQUERIZAS_Lymph node
17	0.69	1 / 29	VAQUERIZAS_Smooth muscle
18	0.69	1 / 29	VAQUERIZAS_Fetal lung
19	0.80	1 / 40	VAQUERIZAS_Thyroid
20	0.81	1 / 41	VAQUERIZAS_Placenta

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 16	PALMER_Lymphocytes signature up
2	0.09	2 / 13	WIRTH_B−cells
3	0.18	6 / 95	WIRTH_Muscle
4	0.24	10 / 194	PALMER_B−Cell signature up
5	0.31	1 / 9	PALMER_CD8+ T−Cell signature up
6	0.36	1 / 11	WIRTH_Cortex cerebri
7	0.37	2 / 32	WIRTH_Pancreas
8	0.41	1 / 13	WIRTH_Thyroid gland
9	0.54	9 / 225	PALMER_Granulocytes signature up
10	0.62	4 / 107	WIRTH_Testis
11	0.67	4 / 114	PALMER_T−Cell signature up
12	0.83	11 / 350	WIRTH_Nervous System
13	0.94	9 / 350	WIRTH_Immune system
14	1.00	0 / 11	WIRTH_Sec. lymphoid organs
15	1.00	0 / 11	WIRTH_Prim. lymphoid organs
16	1.00	0 / 8	WIRTH_Tonsil
17	1.00	0 / 12	WIRTH_Thymus
18	1.00	0 / 12	WIRTH_Lymphocytes
19	1.00	0 / 5	WIRTH_Bone marrow
20	1.00	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	55 / 1115	LU_BPDE 1h DN
2	0.91	133 / 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	

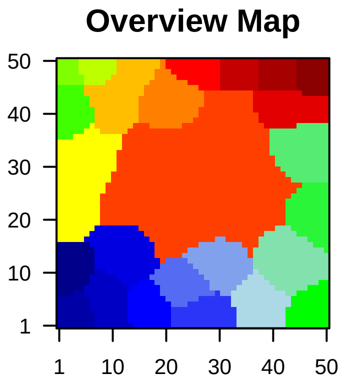
K−Means Clusters

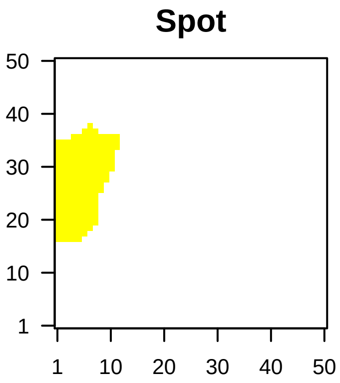
Spot Summary: B

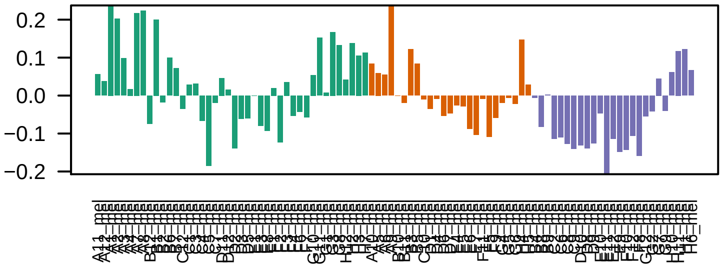
metagenes = 185
genes = 787

<r> metagenes = 0.65
<r> genes = 0.05
beta: r2= 1.03 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 7 (16.7 %)
MSC2 : 2 (8 %)





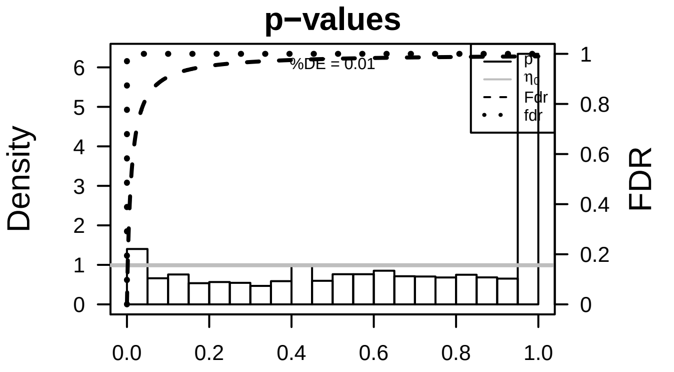


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	EFTUD1	2.12	−0.77	0.34	EFTUD1	elongation factor Tu GTP binding domain containing 1 [Sourc
2	RARRES1	2.09	−0.09	0.29	RARRES1	retinoic acid receptor responder (tazarotene induced) 1 [Sour
3	SIPA1L3	2.07	−0.3	0.26	SIPA1L3	signal−induced proliferation−associated 1 like 3 [Source:HGN
4	PEX16	1.94	−0.14	0.3	PEX16	peroxisomal biogenesis factor 16 [Source:HGNC Symbol;Acc
5	RAB40B	1.91	−0.31	0.29	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
6	RNF157	1.89	−0.33	0.26	RNF157	ring finger protein 157 [Source:HGNC Symbol;Acc:HGNC:29
7	OMG	1.88	−0.22	0.3	OMG	oligodendrocyte myelin glycoprotein [Source:HGNC Symbol;
8	ZBTB48	1.88	−0.26	0.27	ZBTB48	zinc finger and BTB domain containing 48 [Source:HGNC Sy
9	SETD9	1.88	−0.63	0.37	SETD9	SET domain containing 9 [Source:HGNC Symbol;Acc:HGNC:
10	MAP4K3	1.86	−0.43	0.25	MAP4K3	mitogen−activated protein kinase kinase kinase kinase 3 [Sou
11	ARRDC1	1.83	−0.36	0.26	ARRDC1	arrestin domain containing 1 [Source:HGNC Symbol;Acc:HG
12	NSMCE4A	1.83	−0.38	0.29	NSMCE4A	non−SMC element 4 homolog A (S. cerevisiae) [Source:HGN
13	PPP1R13L	1.82	−0.03	0.32	PPP1R13L	protein phosphatase 1, regulatory subunit 13 like [Source:HG
14	KCNU1	1.78	−0.02	0.4	KCNU1	potassium channel, subfamily U, member 1 [Source:HGNC S
15	TAZ	1.78	−0.27	0.28	TAZ	tafazzin [Source:HGNC Symbol;Acc:HGNC:11577]
16	SERPINF1	1.78	−0.45	0.32	SERPINF1	serpin peptidase inhibitor, clade F (alpha−2 antiplasmin, pigm
17	FAM131A	1.78	−0.18	0.29	FAM131A	family with sequence similarity 131, member A [Source:HGN
18	CHN1	1.77	−0.26	0.26	CHN1	chimerin 1 [Source:HGNC Symbol;Acc:HGNC:1943]
19	DBNDD2	1.77	−0.24	0.33	DBNDD2	dysbindin (dystrobrevin binding protein 1) domain containing
20	SLC25A15	1.76	−0.29	0.25	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transp

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−26	631 / 9482	Colon	TssA_Colon
2	4e−23	76 / 401	CC	mitochondrial inner membrane
3	3e−21	35 / 94	BP	respiratory electron transport chain
4	5e−21	37 / 107	GSEA	KEGG_OXIDATIVE_PHOSPHORYLATION
5	5e−21	32 / 78	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
6	8e−21	162 / 1468	CC	mitochondrion
7	9e−21	41 / 135	BP	cellular metabolic process
8	9e−21	594 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
9	2e−20	504 / 7203	Colon	TssF_Colon
10	3e−20	49 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	5e−19	36 / 114	GSEA	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPO
12	9e−19	27 / 62	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
13	1e−18	31 / 85	GSEA	MOOTHA_VOXPHOS
14	1e−18	588 / 9027	Colon	Tx_Colon
15	4e−18	114 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
16	6e−17	32 / 102	GSEA	KEGG_PARKINSONS_DISEASE
17	1e−16	103 / 831	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
18	2e−16	67 / 421	GSEA	MOOTHA_MITOCHONDRIA
19	6e−16	84 / 619	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
20	2e−14	62 / 405	GSEA	MOOTHA_HUMAN_MITODB_6_2002
21	3e−14	86 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
22	1e−13	530 / 8205	CC	cytoplasm
23	2e−13	35 / 157	GSEA	KEGG_HUNTINGTONS_DISEASE
24	3e−13	33 / 142	GSEA	KEGG_ALZHEIMERS_DISEASE
25	3e−13	51 / 311	BP	generation of precursor metabolites and energy
26	3e−13	41 / 213	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
27	6e−13	51 / 316	GSEA	HSIAO_HOUSEKEEPING_GENES
28	2e−12	640 / 10605	CC	intracellular
29	4e−12	64 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
30	2e−11	576 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
31	2e−11	539 / 8580	Colon	TxWk_Colon
32	3e−11	59 / 440	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
33	3e−11	585 / 9528	Brain	Overlap_fetal_midbrain_Quies
34	5e−10	354 / 5184	Lymph	HOPP_Txn_transition
35	5e−10	326 / 4689	TF	ICGC_Taf1_targets
36	7e−10	601 / 9988	CC	organelle
37	1e−09	16 / 48	BP	hydrogen ion transmembrane transport
38	2e−09	389 / 5880	Colon	TssD2_Colon
39	3e−09	146 / 1730	BP	small molecule metabolic process
40	3e−09	30 / 167	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13



Aging

Rank	p−value	#in/all	Geneset
1	0.08	9 / 100	HORVATH_aging_genes meth DOWN
2	0.60	2 / 38	TESCHENDORFF_age_hypermethylated
3	0.94	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	3e−21	35 / 94	respiratory electron transport chain
2	9e−21	41 / 135	cellular metabolic process
3	3e−13	51 / 311	generation of precursor metabolites and energy
4	1e−09	16 / 48	hydrogen ion transmembrane transport
5	3e−09	146 / 1730	small molecule metabolic process
6	2e−08	8 / 12	oxidative phosphorylation
7	3e−06	38 / 322	mitochondrion organization
8	4e−06	34 / 277	translation
9	5e−06	11 / 40	mitochondrial electron transport, NADH to ubiquinone
10	6e−06	16 / 83	mitochondrial translational elongation
11	9e−06	17 / 96	mitochondrial translation
12	2e−05	15 / 83	mitochondrial translational initiation
13	2e−05	15 / 83	mitochondrial translational termination
14	4e−04	182 / 2755	transport
15	1e−03	24 / 229	RNA splicing
16	1e−03	21 / 193	protein folding
17	1e−03	5 / 17	mitochondrial ATP synthesis coupled proton transport
18	2e−03	5 / 19	negative regulation of proteolysis
19	3e−03	4 / 12	carboxylic acid metabolic process
20	3e−03	53 / 687	gene expression

Brain

Rank	p−value	#in/all	Geneset
1	9e−21	594 / 9013	Overlap_fetal_midbrain_K9K27me3
2	2e−11	576 / 9330	Overlap_fetal_midbrain_ReprPC
3	3e−11	585 / 9528	Overlap_fetal_midbrain_Quies
4	3e−08	225 / 3081	Mid_Frontal_Lobe_ZNF
5	1e−03	60 / 765	Mid_Frontal_Lobe_Het
6	4e−03	92 / 1333	Fetal_ReprPCWk
7	6e−03	347 / 5940	Overlap_fetal_midbrain_HetRpts
8	5e−02	51 / 769	Overlap_fetal_midbrain_ZNF
9	8e−02	53 / 831	Fetal_HetRpts
10	1e−01	142 / 2462	Mid_Frontal_Lobe_HetRpts
11	2e−01	485 / 9020	Overlap_fetal_midbrain_ReprPCWk
12	3e−01	19 / 304	Fetal_Het
13	3e−01	21 / 349	Fetal_ZNF
14	3e−01	102 / 1845	Fetal_Quies
15	3e−01	10 / 158	Overlap_fetal_midbrain_Het
16	5e−01	56 / 1050	Fetal_EnhP
17	8e−01	7 / 163	Fetal_ReprPC
18	8e−01	26 / 564	Mid_Frontal_Lobe_EnhP
19	8e−01	30 / 656	Overlap_fetal_midbrain_EnhP
20	8e−01	147 / 2972	Mid_Frontal_Lobe_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.008	4 / 16	GENTLES_modul2
2	0.008	4 / 16	GENTLES_modul16
3	0.013	3 / 10	GENTLES_modul5
4	0.085	3 / 20	PanCan_ChromMod_geneset_nanostring
5	0.102	1 / 2	GENTLES_modul8
6	0.129	2 / 12	LIU_PROSTATE_CANCER_UP
7	0.150	1 / 3	ZHANG_MGUS up
8	0.154	13 / 180	SPANG_LPS−index2
9	0.166	2 / 14	LIU_LIVER_CANCER
10	0.185	2 / 15	GENTLES_modul1
11	0.185	2 / 15	GENTLES_modul10
12	0.205	2 / 16	GENTLES_modul6
13	0.205	2 / 16	GENTLES_modul7
14	0.245	4 / 48	KUIPER_MM poor survival
15	0.277	29 / 489	Lembcke_Normal vs Adenoma
16	0.308	5 / 70	SHAUGHNESSY_MM high risk
17	0.315	1 / 7	GENTLES_modul18
18	0.352	3 / 40	ZHANG_MM up
19	0.352	3 / 40	PanCan_HK_geneset_nanostring
20	0.505	1 / 13	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	4e−23	76 / 401	mitochondrial inner membrane
2	8e−21	162 / 1468	mitochondrion
3	1e−13	530 / 8205	cytoplasm
4	2e−12	640 / 10605	intracellular
5	7e−10	601 / 9988	organelle
6	1e−08	14 / 41	mitochondrial respiratory chain complex I
7	2e−08	8 / 12	mitochondrial respiratory chain
8	4e−06	99 / 1201	endoplasmic reticulum
9	7e−06	666 / 11774	cell
10	1e−04	15 / 94	melanosome
11	1e−04	18 / 128	ribosome
12	1e−04	152 / 2193	extracellular exosome
13	2e−04	210 / 3214	protein complex
14	4e−04	722 / 13191	cellular_component
15	9e−04	12 / 80	mitochondrial membrane
16	1e−03	4 / 10	endoplasmic reticulum chaperone complex
17	2e−03	10 / 63	mitochondrial intermembrane space
18	2e−03	52 / 649	endoplasmic reticulum membrane
19	2e−03	166 / 2576	membrane
20	2e−03	5 / 19	mitochondrial proton−transporting ATP synthase complex

Chr

Rank	p−value	#in/all	Geneset
1	8e−05	70 / 840	Chr 17
2	9e−03	72 / 1037	Chr 19
3	3e−02	41 / 576	Chr 9
4	1e−01	12 / 151	Chr 21
5	2e−01	15 / 221	Chr 18
6	2e−01	47 / 801	Chr 11
7	2e−01	49 / 838	Chr 3
8	3e−01	38 / 649	Chr 16
9	3e−01	24 / 398	Chr 20
10	5e−01	25 / 469	Chr 8
11	6e−01	24 / 465	Chr 15
12	6e−01	28 / 552	Chr 10
13	6e−01	35 / 689	Chr 7
14	6e−01	35 / 696	Chr 5
15	7e−01	34 / 687	Chr 6
16	7e−01	16 / 335	Chr 22
17	7e−01	26 / 551	Chr X
18	9e−01	24 / 558	Chr 4
19	9e−01	45 / 993	Chr 2
20	9e−01	10 / 262	Chr 13

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−26	631 / 9482	TssA_Colon
2	2e−20	504 / 7203	TssF_Colon
3	1e−18	588 / 9027	Tx_Colon
4	2e−11	539 / 8580	TxWk_Colon
5	2e−09	389 / 5880	TssD2_Colon
6	3e−07	203 / 2798	TxEnhG1_Colon
7	4e−07	571 / 9653	Enh_Colon
8	1e−04	320 / 5155	EnhWk1_Colon
9	5e−04	54 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	9e−04	485 / 8415	Quies3_Colon
11	3e−03	57 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
12	4e−03	56 / 739	TxEnhG2_Colon
13	5e−03	170 / 2698	EnhA_Colon
14	3e−02	8 / 71	Marisa_CRC−cluster−g
15	9e−02	39 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
16	1e−01	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
17	2e−01	2 / 15	TCGA_Mutated−in−CRC_hypermutated
18	2e−01	552 / 10290	TssWk_Colon
19	2e−01	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
20	3e−01	54 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.3	2 / 20	BCHETNIA_EBM−DM up
2	0.4	1 / 11	BCHETNIA_EBM up
3	1.0	15 / 435	GUDJ_psoriasis up
4	1.0	8 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	9e−05	12 / 63	Stuehler_Proteins_up_in_STS
2	2e−03	18 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
3	6e−03	31 / 365	Down_b
4	9e−03	28 / 332	Up
5	5e−02	6 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	9e−02	8 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	1e−01	6 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	1e−01	2 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
9	2e−01	2 / 15	VERHAAK_CL subtype
10	2e−01	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
11	2e−01	2 / 16	VERHAAK_NL subtype
12	2e−01	4 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
13	2e−01	3 / 32	Colman_survival_associated
14	2e−01	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
15	2e−01	2 / 18	Barbus_GBM_STS_vs._LTS
16	3e−01	1 / 6	neurons_glio
17	3e−01	48 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
18	4e−01	6 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
19	4e−01	1 / 9	Phillips PN up vs MES & Prolif
20	4e−01	2 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−21	37 / 107	KEGG_OXIDATIVE_PHOSPHORYLATION
2	5e−21	32 / 78	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
3	5e−19	36 / 114	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
4	9e−19	27 / 62	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
5	1e−18	31 / 85	MOOTHA_VOXPHOS
6	4e−18	114 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	6e−17	32 / 102	KEGG_PARKINSONS_DISEASE
8	1e−16	103 / 831	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
9	2e−16	67 / 421	MOOTHA_MITOCHONDRIA
10	6e−16	84 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
11	2e−14	62 / 405	MOOTHA_HUMAN_MITODB_6_2002
12	3e−14	86 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
13	2e−13	35 / 157	KEGG_HUNTINGTONS_DISEASE
14	3e−13	33 / 142	KEGG_ALZHEIMERS_DISEASE
15	3e−13	41 / 213	WONG_MITOCHONDRIA_GENE_MODULE
16	6e−13	51 / 316	HSIAO_HOUSEKEEPING_GENES
17	4e−12	64 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
18	3e−11	59 / 440	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
19	3e−09	30 / 167	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
20	3e−09	119 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−20	49 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	2e−07	29 / 188	HALLMARK_MYC_TARGETS_V1
3	5e−05	24 / 188	HALLMARK_ADIPOGENESIS
4	2e−04	19 / 146	HALLMARK_UV_RESPONSE_UP
5	4e−03	16 / 146	HALLMARK_DNA_REPAIR
6	1e−02	11 / 94	HALLMARK_ANDROGEN_RESPONSE
7	3e−02	11 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	3e−02	10 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	8e−02	14 / 174	HALLMARK_HEME_METABOLISM
10	1e−01	5 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	1e−01	5 / 53	HALLMARK_TGF_BETA_SIGNALING
12	2e−01	14 / 196	HALLMARK_MTORC1_SIGNALING
13	2e−01	5 / 57	HALLMARK_MYC_TARGETS_V2
14	2e−01	3 / 29	HALLMARK_NOTCH_SIGNALING
15	2e−01	7 / 93	HALLMARK_PEROXISOME
16	3e−01	12 / 183	HALLMARK_GLYCOLYSIS
17	3e−01	6 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
18	3e−01	8 / 126	HALLMARK_ALLOGRAFT_REJECTION
19	3e−01	6 / 91	HALLMARK_PROTEIN_SECRETION
20	3e−01	5 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.2	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
3	0.6	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.8	2 / 62	DUMEAUX_Smoking enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
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 / 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	5e−10	354 / 5184	HOPP_Txn_transition
2	7e−09	442 / 6929	HOPP_Txn_elongation
3	8e−07	465 / 7592	HOPP_Active_promoter
4	1e−04	6 / 16	ROSOLOWSKI_red UP
5	6e−04	424 / 7209	HOPP_Weak_promoter
6	5e−03	11 / 86	ROSOLOWSKI_red total
7	6e−03	34 / 410	SPANG_CD40 6hrs DN
8	7e−03	9 / 66	TARTE_Plasma cell signature
9	9e−03	378 / 6564	HOPP_Strong_enhancer
10	2e−02	6 / 42	CARO_OxPhos_in_DLBCL_UP
11	2e−02	24 / 294	TARTE_Plasmablast signature
12	5e−02	2 / 7	CARO_OxPhos_vs_BCR_UP
13	5e−02	3 / 16	DAVE_BL Inter
14	8e−02	3 / 19	DAVE_c−myc BL UP
15	8e−02	70 / 1128	SPANG_BCR DN
16	1e−01	9 / 109	ROSOLOWSKI_green total
17	1e−01	7 / 80	Aukema_BCL2 DN_BCL6 UP
18	3e−01	6 / 82	ROSOLOWSKI_green UP
19	3e−01	4 / 50	SPANG_BAFF 9hrs DN
20	3e−01	69 / 1218	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	2e−08	11 / 25	cytochrome−c oxidase activity
2	3e−08	64 / 592	oxidoreductase activity
3	6e−07	12 / 40	NADH dehydrogenase (ubiquinone) activity
4	9e−06	108 / 1365	RNA binding
5	3e−05	83 / 1007	poly(A) RNA binding
6	7e−05	13 / 71	structural constituent of ribosome
7	6e−04	13 / 87	unfolded protein binding
8	1e−03	7 / 33	peptide binding
9	1e−03	5 / 17	glycosaminoglycan binding
10	2e−03	4 / 11	proton−transporting ATP synthase activity, rotational mechanism
11	3e−03	6 / 28	hydrogen ion transmembrane transporter activity
12	3e−03	5 / 20	translation elongation factor activity
13	4e−03	11 / 83	translation factor activity, RNA binding
14	1e−02	4 / 18	glutathione transferase activity
15	1e−02	3 / 10	ubiquitin−ubiquitin ligase activity
16	2e−02	4 / 19	3'−5'−exoribonuclease activity
17	2e−02	7 / 51	ubiquitin binding
18	2e−02	9 / 77	electron carrier activity
19	2e−02	11 / 104	iron ion binding
20	2e−02	6 / 42	protein kinase C binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	16 / 141	hsa−miR−138
2	0.003	7 / 38	hsa−miR−490−5p
3	0.005	12 / 97	hsa−miR−624
4	0.006	26 / 291	hsa−miR−34c−5p
5	0.006	11 / 88	hsa−miR−505
6	0.007	5 / 24	hsa−miR−1225−5p
7	0.009	10 / 80	hsa−miR−942
8	0.010	5 / 26	hsa−miR−337−5p
9	0.012	11 / 96	hsa−miR−133a
10	0.013	11 / 97	hsa−miR−133b
11	0.017	9 / 75	hsa−miR−513c
12	0.018	23 / 274	hsa−miR−548h
13	0.019	5 / 30	hsa−miR−371−3p
14	0.019	6 / 41	hsa−miR−1308
15	0.022	5 / 31	hsa−miR−558
16	0.024	17 / 191	hsa−miR−520d−5p
17	0.024	27 / 343	hsa−miR−548b−5p
18	0.026	8 / 68	hsa−miR−606
19	0.026	4 / 22	hsa−miR−516a−5p
20	0.027	22 / 269	hsa−miR−449a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 12	GUSTAFSON_PI3K_UP
2	0.6	1 / 15	BENTINK_ras.6
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	5e−10	326 / 4689	ICGC_Taf1_targets
2	4e−07	323 / 4909	ICGC_Stat5_targets
3	7e−07	161 / 2136	ICGC_GabpPcr2_targets
4	1e−06	319 / 4879	ICGC_Pmlsc71910_targets
5	1e−06	293 / 4414	ICGC_Bclaf101388_targets
6	2e−06	303 / 4617	ICGC_Tcf12_targets
7	2e−06	264 / 3924	ICGC_Zeb1_targets
8	2e−06	270 / 4032	ICGC_Creb1_targets
9	2e−06	351 / 5495	ICGC_Yy1_targets
10	2e−06	271 / 4054	ICGC_Egr1_targets
11	3e−06	371 / 5890	ICGC_Elf1_targets
12	6e−06	343 / 5408	ICGC_Pou2_targets
13	6e−06	111 / 1400	ICGC_Myc_targets
14	6e−06	308 / 4774	ICGC_Foxm1_targets
15	7e−06	96 / 1171	KIM_MYC targets
16	7e−06	332 / 5219	ICGC_Tcf3_targets
17	2e−05	378 / 6114	ICGC_Runx3_targets
18	5e−05	325 / 5200	ICGC_Mta3_targets
19	5e−05	280 / 4385	ICGC_Atf2_targets
20	6e−05	304 / 4829	ICGC_Nficsc81335_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.06	3 / 17	VAQUERIZAS_Heart
2	0.06	5 / 40	VAQUERIZAS_Thyroid
3	0.20	2 / 16	VAQUERIZAS_Pancreas
4	0.22	10 / 143	VAQUERIZAS_General
5	0.38	4 / 59	VAQUERIZAS_Whole blood
6	0.42	3 / 45	VAQUERIZAS_Uterus
7	0.52	2 / 33	VAQUERIZAS_Prostate
8	0.58	1 / 16	VAQUERIZAS_Adrenal gland
9	0.58	1 / 16	VAQUERIZAS_Salivary gland
10	0.59	3 / 58	VAQUERIZAS_Lung
11	0.60	1 / 17	VAQUERIZAS_Pituitary
12	0.75	1 / 26	VAQUERIZAS_Liver
13	0.77	1 / 27	VAQUERIZAS_Lymph node
14	0.79	1 / 29	VAQUERIZAS_Fetal lung
15	0.86	1 / 37	VAQUERIZAS_Thymus
16	0.87	1 / 38	VAQUERIZAS_Testis
17	1.00	0 / 36	VAQUERIZAS_Fetal brain
18	1.00	0 / 41	VAQUERIZAS_Placenta
19	1.00	0 / 29	VAQUERIZAS_Smooth muscle
20	1.00	0 / 9	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	19 / 225	PALMER_Granulocytes signature up
2	0.05	3 / 16	PALMER_Lymphocytes signature up
3	0.15	9 / 114	PALMER_T−Cell signature up
4	0.42	1 / 10	WIRTH_Thalamus
5	0.48	1 / 12	WIRTH_Lymphocytes
6	0.48	1 / 12	WIRTH_Cerebellum
7	0.50	1 / 13	WIRTH_B−cells
8	0.50	1 / 13	WIRTH_Thyroid gland
9	0.53	1 / 14	WIRTH_Telencephalon
10	0.67	17 / 350	WIRTH_Immune system
11	0.82	1 / 32	WIRTH_Pancreas
12	0.83	15 / 350	WIRTH_Nervous System
13	0.89	7 / 194	PALMER_B−Cell signature up
14	0.92	1 / 46	WIRTH_Liver
15	0.98	2 / 107	WIRTH_Testis
16	0.99	1 / 95	WIRTH_Muscle
17	1.00	0 / 11	WIRTH_Sec. lymphoid organs
18	1.00	0 / 11	WIRTH_Prim. lymphoid organs
19	1.00	0 / 8	WIRTH_Tonsil
20	1.00	0 / 12	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	63 / 1115	LU_BPDE 1h DN
2	1.0	169 / 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	

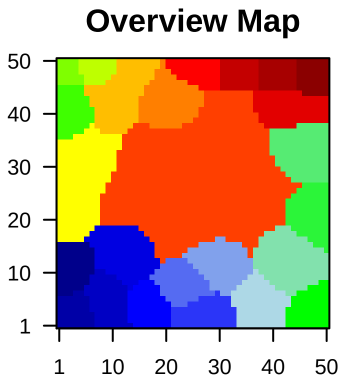
K−Means Clusters

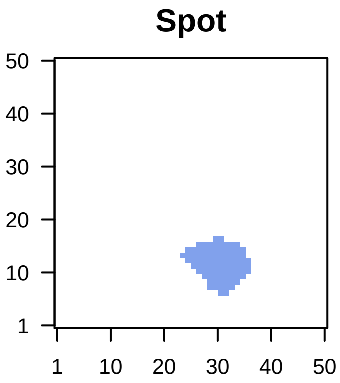
Spot Summary: C

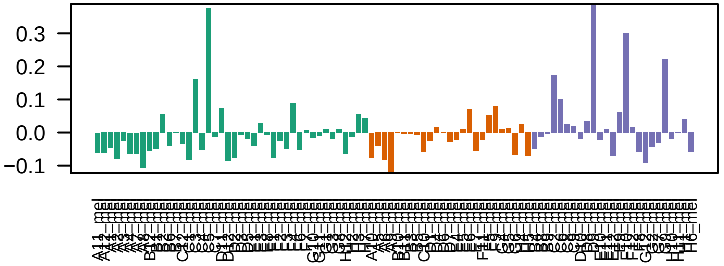
metagenes = 87
genes = 462

<r> metagenes = 0.7
<r> genes = 0.07
beta: r2= 0.55 / log p= −Inf

samples with spot = 6 (6.5 %)
MSC1 : 2 (4.8 %)
MSC3 : 4 (16 %)


Overview Map


Spot

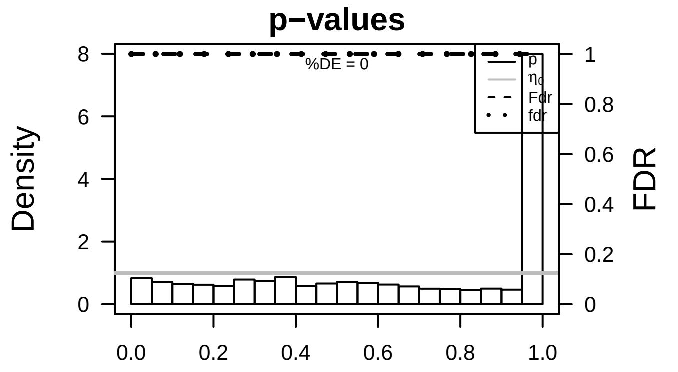


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	IGF2BP2	2.5	−0.05	0.75	IGF2BP2	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
2	ACSF2	2.1	−0.18	0.48	ACSF2	acyl−CoA synthetase family member 2 [Source:HGNC Symbo
3	CFAP44	2.06	−0.34	0.27	CFAP44	cilia and flagella associated protein 44 [Source:HGNC Symbo
4	TMEM135	2.05	−0.37	0.32	TMEM135	transmembrane protein 135 [Source:HGNC Symbol;Acc:HGN
5	ASTE1	2.04	−0.51	0.41	ASTE1	asteroid homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:
6	CEBPZOS	2.03	−0.32	0.44	CEBPZOS	CEBPZ opposite strand [Source:HGNC Symbol;Acc:HGNC:4
7	GDA	1.99	−0.03	0.68	GDA	guanine deaminase [Source:HGNC Symbol;Acc:HGNC:4212
8	KLF4	1.99	−0.11	0.44	KLF4	Kruppel−like factor 4 (gut) [Source:HGNC Symbol;Acc:HGNC
9	SHISA2	1.94	−0.19	0.38	SHISA2	shisa family member 2 [Source:HGNC Symbol;Acc:HGNC:20
10	DOCK10	1.91	−0.27	0.36	DOCK10	dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:HGN
11	PLXDC1	1.9	−0.05	0.51	PLXDC1	plexin domain containing 1 [Source:HGNC Symbol;Acc:HGN
12	ASB9	1.89	−0.09	0.51	ASB9	ankyrin repeat and SOCS box containing 9 [Source:HGNC Sy
13	PIK3R1	1.88	−0.62	0.26	PIK3R1	phosphoinositide−3−kinase, regulatory subunit 1 (alpha) [Sou
14	OR52H1	1.86	−0.02	0.69	OR52H1	olfactory receptor, family 52, subfamily H, member 1 [Source:
15	MEIS1	1.84	−0.61	0.39	MEIS1	Meis homeobox 1 [Source:HGNC Symbol;Acc:HGNC:7000]
16	SLC9B1	1.83	−0.14	0.37	SLC9B1	solute carrier family 9, subfamily B (NHA1, cation proton antip
17	ANKMY1	1.82	−0.19	0.47	ANKMY1	ankyrin repeat and MYND domain containing 1 [Source:HGN
18	FGF13	1.8	−0.12	0.37	FGF13	fibroblast growth factor 13 [Source:HGNC Symbol;Acc:HGNC
19	LRIG2	1.79	−0.37	0.36	LRIG2	leucine−rich repeats and immunoglobulin−like domains 2 [Sou
20	DZIP1L	1.79	−0.21	0.45	DZIP1L	DAZ interacting zinc finger protein 1−like [Source:HGNC Sym

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	28 / 372	GSEA	FOSTER_TOLERANT_MACROPHAGE_DN
2	1e−04	13 / 123	miRN	hsa−miR−204
3	3e−04	3 / 5	GSEA	INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN
4	3e−04	7 / 43	Colon	Marisa_CRC−cluster−f
5	3e−04	12 / 119	miRN	hsa−miR−380
6	4e−04	7 / 44	GSEA	DAWSON_METHYLATED_IN_LYMPHOMA_TCL1
7	5e−04	11 / 108	miRN	hsa−miR−211
8	6e−04	5 / 23	GSEA	CHIBA_RESPONSE_TO_TSA_DN
9	8e−04	29 / 493	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
10	8e−04	11 / 113	Canc	PanCan_Driver_Gene_geneset_nanostring
11	1e−03	6 / 39	BP	synapse assembly
12	1e−03	7 / 54	BP	cellular response to heat
13	1e−03	3 / 8	GSEA	TCGA_GLIOBLASTOMA_MUTATED
14	2e−03	4 / 17	MF	TBP−class protein binding
15	2e−03	4 / 17	GSEA	BIOCARTA_PTEN_PATHWAY
16	2e−03	149 / 3897	Colon	Quies1_Colon
17	2e−03	5 / 30	GSEA	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS
18	2e−03	3 / 9	GSEA	ST_STAT3_PATHWAY
19	2e−03	23 / 386	MF	nucleotide binding
20	2e−03	347 / 10290	Colon	TssWk_Colon
21	2e−03	5 / 31	GSEA	PID_AR_NONGENOMIC_PATHWAY
22	3e−03	9 / 94	GSEA	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN
23	3e−03	18 / 278	GSEA	GABRIELY_MIR21_TARGETS
24	3e−03	7 / 61	GSEA	COATES_MACROPHAGE_M1_VS_M2_DN
25	3e−03	12 / 153	GSEA	DOANE_RESPONSE_TO_ANDROGEN_UP
26	3e−03	31 / 590	BP	cell morphogenesis
27	3e−03	48 / 1033	MF	nucleic acid binding
28	3e−03	7 / 63	GSEA	LINDVALL_IMMORTALIZED_BY_TERT_UP
29	3e−03	26 / 471	GSEA	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
30	3e−03	12 / 156	BP	cell migration
31	4e−03	28 / 523	miRN	hsa−miR−106a
32	4e−03	308 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
33	4e−03	102 / 2563	Lympl	HOPP_Heterochrom
34	4e−03	6 / 49	GSEA	LEE_LIVER_CANCER_MYC_E2F1_UP
35	4e−03	3 / 11	MF	nucleosome binding
36	4e−03	3 / 11	BP	regulation of cell−cell adhesion
37	4e−03	3 / 11	BP	regulation of focal adhesion assembly
38	4e−03	4 / 22	GSEA	BIOCARTA_ECM_PATHWAY
39	4e−03	4 / 22	GSEA	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY
40	4e−03	20 / 337	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.4	4 / 100	HORVATH_aging_genes meth DOWN
3	0.9	2 / 111	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	6 / 39	synapse assembly
2	0.001	7 / 54	cellular response to heat
3	0.003	31 / 590	cell morphogenesis
4	0.003	12 / 156	cell migration
5	0.004	3 / 11	regulation of cell−cell adhesion
6	0.004	3 / 11	regulation of focal adhesion assembly
7	0.005	4 / 23	intrinsic apoptotic signaling pathway by p53 class mediator
8	0.005	3 / 12	negative regulation of focal adhesion assembly
9	0.005	15 / 229	RNA splicing
10	0.007	7 / 72	T cell receptor signaling pathway
11	0.007	88 / 2210	anatomical structure development
12	0.008	3 / 14	positive regulation of excitatory postsynaptic membrane potential
13	0.009	7 / 76	protein glycosylation
14	0.011	6 / 61	palate development
15	0.012	6 / 62	canonical Wnt signaling pathway
16	0.012	3 / 16	heterotypic cell−cell adhesion
17	0.012	3 / 16	negative regulation of anoikis
18	0.012	3 / 16	response to ATP
19	0.012	33 / 705	locomotion
20	0.013	4 / 30	long−term synaptic potentiation

Brain

Rank	p−value	#in/all	Geneset
1	0.004	308 / 9020	Overlap_fetal_midbrain_ReprPCWk
2	0.016	318 / 9528	Overlap_fetal_midbrain_Quies
3	0.021	45 / 1065	Overlap_fetal_midbrain_Enh
4	0.058	36 / 884	Overlap_fetal_midbrain_EnhG
5	0.063	35 / 862	Overlap_fetal_midbrain_TxTrans
6	0.074	200 / 5940	Overlap_fetal_midbrain_HetRpts
7	0.085	28 / 686	Overlap_fetal_midbrain_TssA
8	0.089	17 / 383	Fetal_Tx
9	0.130	292 / 9013	Overlap_fetal_midbrain_K9K27me3
10	0.154	76 / 2185	Fetal_TssA
11	0.161	22 / 564	Mid_Frontal_Lobe_EnhP
12	0.185	30 / 812	Mid_Frontal_Lobe_TssP
13	0.240	66 / 1949	Fetal_TssF
14	0.249	21 / 574	Overlap_fetal_midbrain_TssP
15	0.251	28 / 786	Fetal_EnhG
16	0.269	64 / 1907	Fetal_TxTrans
17	0.278	35 / 1013	Fetal_TssP
18	0.281	27 / 769	Overlap_fetal_midbrain_ZNF
19	0.287	296 / 9330	Overlap_fetal_midbrain_ReprPC
20	0.354	28 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	8e−04	11 / 113	PanCan_Driver_Gene_geneset_nanostring
2	9e−02	4 / 55	PanCan_JAK−ST_geneset_nanostring
3	1e−01	2 / 18	PanCan_Notch_geneset_nanostring
4	1e−01	5 / 82	PanCan_TXmisReg_geneset_nanostring
5	1e−01	1 / 5	WANG_ER_DN
6	2e−01	6 / 121	PanCan_MAPK_geneset_nanostring
7	2e−01	7 / 156	PanCan_PI3K_geneset_nanostring
8	3e−01	5 / 111	PanCan_RAS_geneset_nanostring
9	3e−01	1 / 10	GENTLES_modul3
10	3e−01	3 / 61	PanCan_Wnt_geneset_nanostring
11	3e−01	1 / 12	LIU_PROSTATE_CANCER_UP
12	3e−01	1 / 12	BEN−PORATH_DN
13	4e−01	1 / 14	LIU_LIVER_CANCER
14	4e−01	1 / 14	LIU_PROSTATE_CANCER_DN
15	4e−01	1 / 15	GENTLES_modul10
16	4e−01	2 / 48	KUIPER_MM poor survival
17	5e−01	0 / 12	LIU_BREAST_CANCER
18	6e−01	0 / 15	RHODES_CANCER_META_SIGNATURE
19	6e−01	12 / 401	Lembcke_Colonic Inflammation
20	6e−01	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	0.005	3 / 12	PRC1 complex
2	0.009	6 / 58	neuronal postsynaptic density
3	0.010	4 / 28	cytoplasmic stress granule
4	0.013	7 / 81	centriole
5	0.034	7 / 99	cell cortex
6	0.036	112 / 3088	plasma membrane
7	0.040	10 / 170	nuclear speck
8	0.041	3 / 25	PcG protein complex
9	0.044	2 / 11	nuclear periphery
10	0.052	2 / 12	STAGA complex
11	0.068	2 / 14	exocyst
12	0.076	5 / 73	basement membrane
13	0.083	12 / 246	dendrite
14	0.084	5 / 75	blood microparticle
15	0.087	2 / 16	excitatory synapse
16	0.087	5 / 76	cell projection
17	0.088	3 / 34	rough endoplasmic reticulum
18	0.093	191 / 5696	nucleus
19	0.094	3 / 35	integral component of Golgi membrane
20	0.094	3 / 35	mitotic spindle

Chr

Rank	p−value	#in/all	Geneset
1	0.01	62 / 1500	Chr 1
2	0.07	34 / 838	Chr 3
3	0.07	18 / 398	Chr 20
4	0.14	37 / 993	Chr 2
5	0.17	29 / 775	Chr 12
6	0.19	22 / 576	Chr 9
7	0.27	20 / 552	Chr 10
8	0.37	19 / 558	Chr 4
9	0.39	16 / 469	Chr 8
10	0.47	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
11	0.52	25 / 801	Chr 11
12	0.57	8 / 262	Chr 13
13	0.59	21 / 696	Chr 5
14	0.68	13 / 462	Chr 14
15	0.69	6 / 221	Chr 18
16	0.74	15 / 551	Chr X
17	0.78	12 / 465	Chr 15
18	0.83	22 / 840	Chr 17
19	0.85	3 / 151	Chr 21
20	0.86	16 / 649	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	7 / 43	Marisa_CRC−cluster−f
2	2e−03	149 / 3897	Quies1_Colon
3	2e−03	347 / 10290	TssWk_Colon
4	6e−03	288 / 8415	Quies3_Colon
5	1e−02	20 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
6	2e−02	2 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
7	4e−02	5 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
8	5e−02	71 / 1889	ReprPCWk_Colon
9	6e−02	18 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
10	1e−01	6 / 102	Marisa_CRC−cluster−d
11	1e−01	117 / 3383	EnhWk2_Colon
12	1e−01	2 / 18	Boland_CRC−MSI−A6−A10
13	1e−01	76 / 2142	ReprPC_Colon
14	1e−01	18 / 427	Quies2_Colon
15	1e−01	1 / 5	Juehling−MSI−enriched−in−8−to−9
16	1e−01	1 / 5	Budinska_A_Surface crypt−like_UP
17	1e−01	3 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
18	2e−01	16 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
19	2e−01	277 / 8580	TxWk_Colon
20	2e−01	11 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.01	17 / 294	GUDJ_psoriasis down
2	0.29	1 / 11	BCHETNIA_EBM up
3	0.47	1 / 20	BCHETNIA_EBM−DM up
4	0.93	9 / 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	0.005	7 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	0.005	4 / 23	WIRTH_PN subtype
3	0.017	4 / 32	Donson−innate immunity−associated with LTS in HGA
4	0.033	3 / 23	Donson−Misc immune function−associated with LTS in HGA
5	0.060	2 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
6	0.060	3 / 29	shaw_responders_down_in_oligo_glioma
7	0.069	5 / 71	Weller_LGG_A_vs_O_UP
8	0.084	5 / 75	GIEZELT_GBM_STS_down_VS_LTS
9	0.106	2 / 18	Barbus_GBM_STS_vs._LTS
10	0.113	3 / 38	OL vs. OPC
11	0.126	4 / 62	cultured astroglia vs. in vivo astrocytes
12	0.143	4 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
13	0.146	1 / 5	oligodendrocytes_glio
14	0.148	2 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
15	0.166	4 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
16	0.172	1 / 6	shaw_responders_up_in_oligo_glioma
17	0.179	3 / 47	mature astrocytes
18	0.193	6 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
19	0.198	1 / 7	Shaw_up_in_1p19qdel
20	0.204	4 / 75	Weller_LGG_A_vs_O_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−05	28 / 372	FOSTER_TOLERANT_MACROPHAGE_DN
2	3e−04	3 / 5	INAMURA_LUNG_CANCER_SCC_SUBTYPES_DN
3	4e−04	7 / 44	DAWSON_METHYLATED_IN_LYMPHOMA_TCL1
4	6e−04	5 / 23	CHIBA_RESPONSE_TO_TSA_DN
5	8e−04	29 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
6	1e−03	3 / 8	TCGA_GLIOBLASTOMA_MUTATED
7	2e−03	4 / 17	BIOCARTA_PTEN_PATHWAY
8	2e−03	5 / 30	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS
9	2e−03	3 / 9	ST_STAT3_PATHWAY
10	2e−03	5 / 31	PID_AR_NONGENOMIC_PATHWAY
11	3e−03	9 / 94	PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN
12	3e−03	18 / 278	GABRIELY_MIR21_TARGETS
13	3e−03	7 / 61	COATES_MACROPHAGE_M1_VS_M2_DN
14	3e−03	12 / 153	DOANE_RESPONSE_TO_ANDROGEN_UP
15	3e−03	7 / 63	LINDVALL_IMMORTALIZED_BY_TERT_UP
16	3e−03	26 / 471	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
17	4e−03	6 / 49	LEE_LIVER_CANCER_MYC_E2F1_UP
18	4e−03	4 / 22	BIOCARTA_ECM_PATHWAY
19	4e−03	4 / 22	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY
20	4e−03	20 / 337	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP

HM

Rank	p−value	#in/all	Geneset
1	0.02	10 / 148	HALLMARK_KRAS_SIGNALING_UP
2	0.05	3 / 26	HALLMARK_ANGIOGENESIS
3	0.07	3 / 31	HALLMARK_HEDGEHOG_SIGNALING
4	0.15	8 / 167	HALLMARK_APICAL_JUNCTION
5	0.16	8 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.24	7 / 162	HALLMARK_COMPLEMENT
7	0.31	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.32	2 / 37	HALLMARK_APICAL_SURFACE
9	0.34	4 / 95	HALLMARK_SPERMATOGENESIS
10	0.36	5 / 127	HALLMARK_KRAS_SIGNALING_DN
11	0.44	5 / 140	HALLMARK_APOPTOSIS
12	0.46	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	0.47	6 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	0.49	6 / 181	HALLMARK_P53_PATHWAY
15	0.53	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
16	0.53	2 / 57	HALLMARK_MYC_TARGETS_V2
17	0.54	3 / 91	HALLMARK_PROTEIN_SECRETION
18	0.54	3 / 91	HALLMARK_BILE_ACID_METABOLISM
19	0.58	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
20	0.60	5 / 167	HALLMARK_IL2_STAT5_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 7	DUMEAUX_Women normal BMI literature genes up
2	0.27	1 / 10	DUMEAUX_Smoking literature genes up
3	0.58	2 / 62	DUMEAUX_Smoking enriched genes
4	0.64	1 / 32	DUMEAUX_Fasting enriched genes
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers 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	0.004	102 / 2563	HOPP_Heterochrom
2	0.007	198 / 5538	HOPP_Weak_txn
3	0.013	248 / 7209	HOPP_Weak_promoter
4	0.028	197 / 5693	HOPP_Weak_enhancer
5	0.033	3 / 23	DAVE_Immune response 1
6	0.046	222 / 6564	HOPP_Strong_enhancer
7	0.072	119 / 3396	HOPP_Repressed
8	0.078	6 / 96	Subero_DLBCL_hyper_meth
9	0.098	13 / 280	SPANG_CD40 6hrs UP
10	0.103	229 / 6929	HOPP_Txn_elongation
11	0.107	5 / 81	Subero_INT_hyper_meth
12	0.111	5 / 82	ROSOLOWSKI_green UP
13	0.116	4 / 60	Subero_T−ALL_hyper_meth
14	0.133	248 / 7592	HOPP_Active_promoter
15	0.181	76 / 2211	HOPP_Repetitive
16	0.181	2 / 25	Subero_T−PLL_hypo_meth
17	0.223	1 / 8	YAMANE_AICDA_targets_nonrecruited
18	0.239	5 / 107	SPANG_LPS 6hrs UP
19	0.247	1 / 9	Subero_B−ALL_hypo_meth
20	0.251	5 / 109	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	0.002	4 / 17	TBP−class protein binding
2	0.002	23 / 386	nucleotide binding
3	0.003	48 / 1033	nucleic acid binding
4	0.004	3 / 11	nucleosome binding
5	0.004	9 / 102	mRNA binding
6	0.005	4 / 23	virus receptor activity
7	0.007	5 / 39	cell adhesion molecule binding
8	0.007	4 / 25	aminopeptidase activity
9	0.008	5 / 40	heat shock protein binding
10	0.008	4 / 26	SH2 domain binding
11	0.008	3 / 14	DNA binding, bending
12	0.008	3 / 14	HMG box domain binding
13	0.009	16 / 265	hydrolase activity
14	0.012	3 / 16	acetylglucosaminyltransferase activity
15	0.012	3 / 16	phosphatidylinositol−3,4−bisphosphate binding
16	0.014	23 / 450	sequence−specific DNA binding
17	0.014	20 / 376	chromatin binding
18	0.014	13 / 210	transferase activity, transferring glycosyl groups
19	0.015	3 / 17	histone methyltransferase activity (H3−K4 specific)
20	0.015	3 / 17	mitogen−activated protein kinase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	13 / 123	hsa−miR−204
2	3e−04	12 / 119	hsa−miR−380
3	5e−04	11 / 108	hsa−miR−211
4	4e−03	28 / 523	hsa−miR−106a
5	5e−03	17 / 269	hsa−miR−101
6	6e−03	21 / 370	hsa−miR−144
7	9e−03	6 / 58	hsa−miR−187
8	9e−03	2 / 5	hsa−miR−585
9	1e−02	27 / 541	hsa−miR−17
10	1e−02	28 / 569	hsa−miR−20b
11	1e−02	7 / 80	hsa−miR−876−5p
12	1e−02	27 / 552	hsa−miR−93
13	1e−02	7 / 82	hsa−miR−188−5p
14	1e−02	17 / 303	hsa−miR−18b
15	2e−02	17 / 314	hsa−miR−520c−3p
16	2e−02	7 / 88	hsa−miR−10a
17	2e−02	12 / 196	hsa−miR−9
18	2e−02	7 / 89	hsa−miR−10b
19	2e−02	4 / 35	hsa−miR−1287
20	2e−02	28 / 607	hsa−miR−20a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 14	BENTINK_src.2
2	0.32	1 / 12	BENTINK_e2f3.2
3	0.34	1 / 13	GUSTAFSON_PI3K_DN
4	0.34	1 / 13	BENTINK_myc.1
5	1.00	0 / 12	GUSTAFSON_PI3K_UP
6	1.00	0 / 14	BENTINK_e2f3.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 9	BENTINK_ras.4
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.08	137 / 3966	ICGC_Pu1_targets
2	0.08	148 / 4314	ICGC_Ebfsc137065_targets
3	0.09	1 / 3	MYC_Signal transduction UP
4	0.10	43 / 1139	HEBENSTREIT_low expression TF
5	0.12	52 / 1418	ICGC_Ets1_targets
6	0.12	67 / 1872	ICGC_Mef2_targets
7	0.16	46 / 1273	ICGC_P300_targets
8	0.24	44 / 1266	ICGC_NrsfPcr1_targets
9	0.30	89 / 2714	ICGC_Irf4_targets
10	0.31	157 / 4879	ICGC_Pmlsc71910_targets
11	0.31	131 / 4054	ICGC_Egr1_targets
12	0.33	95 / 2927	ICGC_Rad21_targets
13	0.37	147 / 4617	ICGC_Tcf12_targets
14	0.38	43 / 1314	ICGC_Usf1_targets
15	0.39	20 / 595	ICGC_NrsfPcr2_targets
16	0.39	23 / 690	ICGC_Atf3_targets
17	0.42	164 / 5200	ICGC_Mta3_targets
18	0.43	117 / 3700	ICGC_Nfatc1_targets
19	0.43	68 / 2137	ICGC_SrfV0416101_targets
20	0.46	172 / 5495	ICGC_Yy1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 7	VAQUERIZAS_Appendix
2	0.02	3 / 19	VAQUERIZAS_Tonsil
3	0.03	3 / 23	VAQUERIZAS_Trachea
4	0.03	3 / 23	VAQUERIZAS_Adrenal cortex
5	0.05	2 / 12	VAQUERIZAS_Skin
6	0.08	2 / 15	VAQUERIZAS_Fetal thyroid
7	0.08	3 / 33	VAQUERIZAS_Prostate
8	0.09	2 / 16	VAQUERIZAS_Salivary gland
9	0.11	3 / 38	VAQUERIZAS_Testis
10	0.13	3 / 41	VAQUERIZAS_Placenta
11	0.19	2 / 26	VAQUERIZAS_Liver
12	0.20	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
13	0.20	2 / 27	VAQUERIZAS_Lymph node
14	0.23	2 / 29	VAQUERIZAS_Smooth muscle
15	0.23	2 / 29	VAQUERIZAS_Fetal lung
16	0.25	1 / 9	VAQUERIZAS_Kidney
17	0.27	3 / 58	VAQUERIZAS_Lung
18	0.28	3 / 59	VAQUERIZAS_Whole blood
19	0.29	1 / 11	VAQUERIZAS_Fetal liver
20	0.32	2 / 37	VAQUERIZAS_Thymus

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 10	WIRTH_Thalamus
2	0.05	17 / 350	WIRTH_Immune system
3	0.14	6 / 114	PALMER_T−Cell signature up
4	0.20	14 / 350	WIRTH_Nervous System
5	0.24	5 / 107	WIRTH_Testis
6	0.25	1 / 9	PALMER_CD8+ T−Cell signature up
7	0.34	1 / 13	WIRTH_B−cells
8	0.34	1 / 13	WIRTH_Thyroid gland
9	0.34	4 / 95	WIRTH_Muscle
10	0.40	1 / 16	PALMER_Lymphocytes signature up
11	0.40	8 / 225	PALMER_Granulocytes signature up
12	0.42	2 / 46	WIRTH_Liver
13	0.56	6 / 194	PALMER_B−Cell signature up
14	0.64	1 / 32	WIRTH_Pancreas
15	0.67	2 / 74	WIRTH_Mucosa
16	0.73	1 / 41	WIRTH_Homeostasis
17	1.00	0 / 11	WIRTH_Sec. lymphoid organs
18	1.00	0 / 11	WIRTH_Prim. lymphoid organs
19	1.00	0 / 8	WIRTH_Tonsil
20	1.00	0 / 12	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	115 / 3682	LU_BPDE 0.005 DN
2	0.6	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	

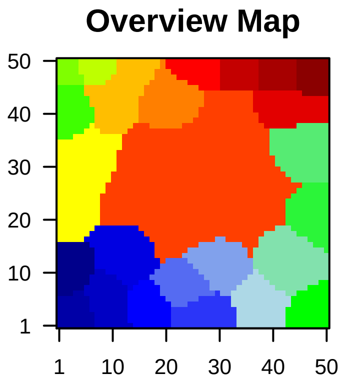
K−Means Clusters

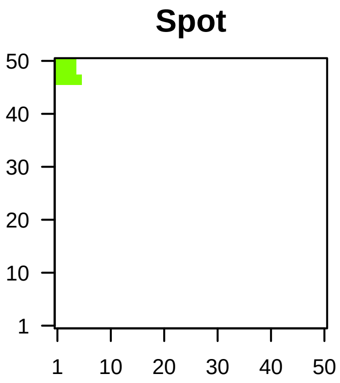
Spot Summary: D

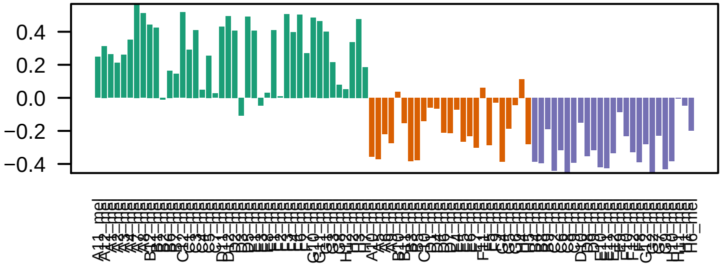
metagenes = 22
genes = 310

<r> metagenes = 0.95
<r> genes = 0.23
beta: r2= 7.27 / log p= −Inf

samples with spot = 32 (34.8 %)
MSC1 : 32 (76.2 %)





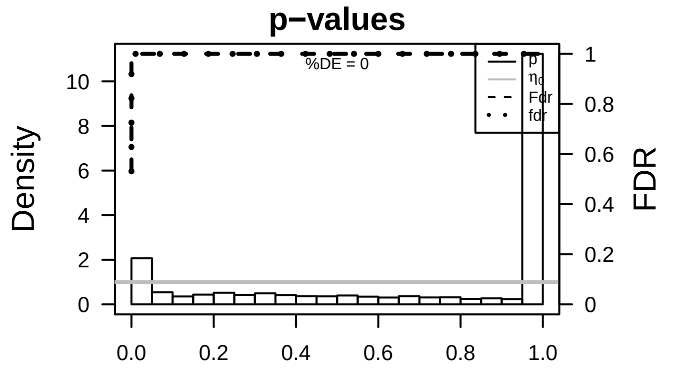


Spot Genelist

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	C4orf33	1.97	−0.26	0.29	C4orf33	chromosome 4 open reading frame 33 [Source:HGNC Symb
4	RNASEH2B	1.84	−0.73	0.47	RNASEH2B	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
5	RAD51	1.81	−0.59	0.62	RAD51	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
6	GINS4	1.81	−0.28	0.4	GINS4	GINS complex subunit 4 (Sld5 homolog) [Source:HGNC Sym
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	ESCO2	1.68	−0.56	0.74	ESCO2	establishment of sister chromatid cohesion N−acetyltransfera
11	NCAPH2	1.68	−0.47	0.42	NCAPH2	non−SMC condensin II complex, subunit H2 [Source:HGNC
12	CDCA5	1.68	−0.6	0.79	CDCA5	cell division cycle associated 5 [Source:HGNC Symbol;Acc:H
13	ORC1	1.67	−0.3	0.59	ORC1	origin recognition complex, subunit 1 [Source:HGNC Symbol;
14	ERI1	1.67	−0.32	0.35	ERI1	exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:23994]
15	FBXO5	1.66	−0.48	0.68	FBXO5	F−box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
16	TIFA	1.66	−0.19	0.52	TIFA	TRAF−interacting protein with forkhead−associated domain [
17	DTL	1.66	−0.94	0.84	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
18	POC1A	1.66	−0.34	0.45	POC1A	POC1 centriolar protein A [Source:HGNC Symbol;Acc:HGNC
19	CCNE2	1.65	−0.54	0.71	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
20	MTBP	1.64	−0.38	0.33	MTBP	MDM2 binding protein [Source:HGNC Symbol;Acc:HGNC:74

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	171 / 1192	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	1e−99	114 / 305	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	1e−99	126 / 550	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	3e−80	83 / 242	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	4e−76	83 / 267	GSE	ZHANG_TLX_TARGETS_60HR_DN
6	4e−70	112 / 700	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	5e−67	138 / 1251	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	2e−65	68 / 197	HM	HALLMARK_E2F_TARGETS
9	1e−64	111 / 768	BP	DNA metabolic process
10	4e−61	83 / 390	GSE	PUJANA_BRCA2_PCC_NETWORK
11	4e−61	90 / 485	GSE	CHICAS_RB1_TARGETS_SENESCENT
12	9e−60	124 / 1110	BP	cell cycle
13	1e−56	75 / 335	GSE	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
14	6e−55	86 / 505	GSE	BERENJENO_TRANSFORMED_BY_RHOA_UP
15	1e−53	104 / 834	GSE	LEE_BMP2_TARGETS_DN
16	3e−53	78 / 412	BP	mitotic cell cycle
17	1e−52	71 / 327	GSE	BLUM_RESPONSE_TO_SALIRASIB_DN
18	3e−52	41 / 68	GSE	VERNELL_RETINOBLASTOMA_PATHWAY_UP
19	2e−50	51 / 139	BP	DNA replication
20	2e−48	104 / 944	GSE	NUYTTEN_EZH2_TARGETS_DN
21	4e−47	71 / 388	GSE	REACTOME_CELL_CYCLE
22	8e−47	55 / 198	GSE	FUJII_YBX1_TARGETS_DN
23	1e−46	64 / 301	GSE	REACTOME_CELL_CYCLE_MITOTIC
24	1e−45	90 / 724	GSE	PUJANA_CHEK2_PCC_NETWORK
25	2e−44	77 / 517	GSE	FEVR_CTNNB1_TARGETS_DN
26	7e−44	121 / 1460	GSE	PUJANA_BRCA1_PCC_NETWORK
27	1e−43	39 / 84	GSE	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
28	8e−43	39 / 87	GSE	ZHANG_TLX_TARGETS_UP
29	1e−42	46 / 142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
30	2e−42	70 / 436	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
31	2e−40	57 / 278	GSE	MANALO_HYPOXIA_DN
32	6e−40	46 / 160	GSE	PUJANA_XPRSS_INT_NETWORK
33	8e−40	78 / 616	GSE	BENPORATH_CYCLING_GENES
34	9e−40	47 / 171	GSE	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
35	3e−39	77 / 609	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
36	7e−39	40 / 113	GSE	PUJANA_BRCA_CENTERED_NETWORK
37	9e−38	35 / 81	GSE	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
38	3e−37	46 / 181	GSE	REACTOME_DNA_REPLICATION
39	1e−36	45 / 175	GSE	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
40	1e−36	42 / 145	GSE	CHANG_CYCLING_GENES



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 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−64	111 / 768	DNA metabolic process
2	9e−60	124 / 1110	cell cycle
3	3e−53	78 / 412	mitotic cell cycle
4	2e−50	51 / 139	DNA replication
5	4e−34	23 / 29	DNA strand elongation involved in DNA replication
6	4e−30	177 / 3980	cellular nitrogen compound metabolic process
7	5e−28	47 / 298	DNA repair
8	4e−22	62 / 721	chromosome organization
9	6e−22	15 / 20	telomere maintenance via semi−conservative replication
10	5e−20	15 / 24	telomere maintenance via recombination
11	5e−20	28 / 139	G1/S transition of mitotic cell cycle
12	1e−18	14 / 23	DNA replication initiation
13	7e−17	29 / 195	cellular response to DNA damage stimulus
14	7e−16	18 / 65	telomere maintenance
15	9e−14	10 / 16	nucleotide−excision repair, DNA gap filling
16	1e−13	16 / 63	double−strand break repair
17	3e−11	128 / 3644	biosynthetic process
18	3e−10	9 / 22	regulation of transcription involved in G1/S transition of mitotic cell cycle
19	3e−10	10 / 30	DNA damage checkpoint
20	4e−10	27 / 312	mitotic nuclear division

Brain

Rank	p−value	#in/all	Geneset
1	7e−12	249 / 9330	Overlap_fetal_midbrain_ReprPC
2	7e−07	69 / 1845	Fetal_Quies
3	8e−06	224 / 9013	Overlap_fetal_midbrain_K9K27me3
4	1e−03	39 / 1122	Fetal_K9K27me3
5	8e−03	28 / 831	Fetal_HetRpts
6	2e−02	206 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	3e−02	140 / 5940	Overlap_fetal_midbrain_HetRpts
8	2e−01	33 / 1333	Fetal_ReprPCWk
9	2e−01	30 / 1236	Mid_Frontal_Lobe_ReprPCWk
10	3e−01	8 / 304	Fetal_Het
11	3e−01	13 / 534	Mid_Frontal_Lobe_EnhG
12	3e−01	22 / 953	Fetal_Enh
13	4e−01	201 / 9528	Overlap_fetal_midbrain_Quies
14	6e−01	21 / 1050	Fetal_EnhP
15	7e−01	3 / 163	Fetal_ReprPC
16	8e−01	18 / 989	Mid_Frontal_Lobe_Quies
17	8e−01	9 / 564	Mid_Frontal_Lobe_EnhP
18	9e−01	2 / 166	Mid_Frontal_Lobe_Tx
19	9e−01	10 / 656	Overlap_fetal_midbrain_EnhP
20	9e−01	17 / 1065	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	2e−30	61 / 489	Lembcke_Normal vs Adenoma
2	1e−24	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	7e−16	16 / 47	PanCan_DNARepair_geneset_nanostring
4	5e−11	18 / 120	PanCan_CC+Apop_geneset_nanostring
5	5e−07	6 / 16	WOLFER_overlap genes
6	1e−06	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
7	3e−04	5 / 29	KUIPER_MM good survival
8	1e−03	3 / 10	GENTLES_modul3
9	2e−03	0 / 15	RHODES_CANCER_META_SIGNATURE
10	4e−03	3 / 16	GENTLES_modul2
11	3e−02	2 / 13	BEN−PORATH_UP
12	3e−02	6 / 113	PanCan_Driver_Gene_geneset_nanostring
13	4e−02	2 / 15	GENTLES_modul1
14	4e−02	2 / 16	GENTLES_modul6
15	6e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
16	8e−02	3 / 48	KUIPER_MM poor survival
17	2e−01	3 / 70	SHAUGHNESSY_MM high risk
18	3e−01	1 / 14	LIU_COMMON_CANCER_GENES
19	3e−01	1 / 16	GENTLES_modul7
20	5e−01	0 / 12	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	1e−36	77 / 663	chromosome
2	3e−35	147 / 2577	nucleoplasm
3	4e−28	213 / 5696	nucleus
4	7e−18	38 / 331	nuclear chromosome
5	2e−15	268 / 9988	organelle
6	1e−13	274 / 10605	intracellular
7	1e−09	113 / 3214	protein complex
8	6e−09	28 / 377	centrosome
9	6e−08	280 / 11774	cell
10	1e−07	39 / 747	nucleolus
11	3e−07	30 / 512	microtubule organizing center
12	3e−07	10 / 59	chromosome, centromeric region
13	8e−07	12 / 97	chromatin
14	3e−06	10 / 75	condensed chromosome kinetochore
15	2e−05	5 / 17	replication fork
16	2e−05	10 / 93	spindle pole
17	3e−05	12 / 135	nuclear chromatin
18	7e−05	19 / 332	nuclear envelope
19	8e−05	6 / 35	condensed nuclear chromosome
20	1e−04	4 / 13	Fanconi anaemia nuclear complex

Chr

Rank	p−value	#in/all	Geneset
1	0.007	21 / 558	Chr 4
2	0.009	12 / 262	Chr 13
3	0.018	10 / 221	Chr 18
4	0.074	23 / 801	Chr 11
5	0.092	11 / 335	Chr 22
6	0.197	17 / 649	Chr 16
7	0.207	5 / 151	Chr 21
8	0.263	12 / 465	Chr 15
9	0.368	11 / 462	Chr 14
10	0.423	13 / 576	Chr 9
11	0.448	9 / 398	Chr 20
12	0.478	12 / 551	Chr X
13	0.480	18 / 838	Chr 3
14	0.515	10 / 469	Chr 8
15	0.572	14 / 687	Chr 6
16	0.576	14 / 689	Chr 7
17	0.602	11 / 552	Chr 10
18	0.863	11 / 696	Chr 5
19	0.888	12 / 775	Chr 12
20	0.897	13 / 840	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−10	247 / 9482	TssA_Colon
2	5e−07	217 / 8415	Quies3_Colon
3	7e−07	34 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	2e−06	250 / 10290	TssWk_Colon
5	2e−05	34 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
6	2e−04	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
7	8e−04	178 / 7203	TssF_Colon
8	8e−03	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
9	1e−02	2 / 8	Boland_CRC−MMR−system
10	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
11	5e−02	2 / 18	Boland_CRC−MSI−A6−A10
12	2e−01	1 / 8	Marisa_CRC−C3
13	2e−01	16 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	2e−01	1 / 9	KIM_MSI−in−EC
15	2e−01	187 / 8580	TxWk_Colon
16	2e−01	1 / 13	TCGA−CRC_less−agressive−disease−markers
17	2e−01	85 / 3812	TssD1_Colon
18	3e−01	1 / 15	Juehling_HNPCC−mutated−in−4
19	3e−01	193 / 9027	Tx_Colon
20	4e−01	2 / 71	Marisa_CRC−cluster−g

Disease

Rank	p−value	#in/all	Geneset
1	4e−05	23 / 435	GUDJ_psoriasis up
2	9e−01	4 / 294	GUDJ_psoriasis down
3	1e+00	0 / 11	BCHETNIA_EBM up
4	1e+00	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1e−42	46 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	2e−06	10 / 71	Weller_LGG_gradeII−vs−III_DOWN
3	7e−04	32 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
4	4e−03	2 / 5	Phillips Prolif up vs PN & MES
5	4e−03	15 / 332	Up
6	5e−02	2 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
7	2e−01	1 / 9	Mukasa_UP_in_GBM
8	3e−01	2 / 49	developing astrocytes
9	3e−01	1 / 16	KIM deleted & downregulated in LTS
10	4e−01	3 / 103	GIEZELT_GBM_WT_up_VS_mut
11	4e−01	1 / 22	KIM prognostic signature LTS vs. STS
12	4e−01	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
13	4e−01	2 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	4e−01	2 / 70	Weller_LGG_1p19qDel−vs−intact_UP
15	5e−01	1 / 29	shaw_responders_down_in_oligo_glioma
16	5e−01	1 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
17	5e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
18	6e−01	1 / 47	Vishal_subnetwork signature of survival in GBM
19	6e−01	6 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
20	6e−01	3 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	171 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	1e−99	114 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	1e−99	126 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	3e−80	83 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	4e−76	83 / 267	ZHANG_TLX_TARGETS_60HR_DN
6	4e−70	112 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	5e−67	138 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	4e−61	83 / 390	PUJANA_BRCA2_PCC_NETWORK
9	4e−61	90 / 485	CHICAS_RB1_TARGETS_SENESCENT
10	1e−56	75 / 335	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
11	6e−55	86 / 505	BERENJENO_TRANSFORMED_BY_RHOA_UP
12	1e−53	104 / 834	LEE_BMP2_TARGETS_DN
13	1e−52	71 / 327	BLUM_RESPONSE_TO_SALIRASIB_DN
14	3e−52	41 / 68	VERNELL_RETINOBLASTOMA_PATHWAY_UP
15	2e−48	104 / 944	NUYTTEN_EZH2_TARGETS_DN
16	4e−47	71 / 388	REACTOME_CELL_CYCLE
17	8e−47	55 / 198	FUJII_YBX1_TARGETS_DN
18	1e−46	64 / 301	REACTOME_CELL_CYCLE_MITOTIC
19	1e−45	90 / 724	PUJANA_CHEK2_PCC_NETWORK
20	2e−44	77 / 517	FEVR_CTNNB1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−65	68 / 197	HALLMARK_E2F_TARGETS
2	9e−20	32 / 196	HALLMARK_G2M_CHECKPOINT
3	1e−08	17 / 146	HALLMARK_DNA_REPAIR
4	8e−08	18 / 188	HALLMARK_MYC_TARGETS_V1
5	6e−05	14 / 195	HALLMARK_MITOTIC_SPINDLE
6	2e−04	12 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
7	8e−04	12 / 196	HALLMARK_MTORC1_SIGNALING
8	4e−03	9 / 146	HALLMARK_UV_RESPONSE_UP
9	3e−02	4 / 57	HALLMARK_MYC_TARGETS_V2
10	7e−02	6 / 140	HALLMARK_APOPTOSIS
11	1e−01	6 / 162	HALLMARK_COMPLEMENT
12	2e−01	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	3e−01	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
14	3e−01	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	3e−01	5 / 174	HALLMARK_HEME_METABOLISM
16	3e−01	3 / 93	HALLMARK_PEROXISOME
17	3e−01	3 / 94	HALLMARK_ANDROGEN_RESPONSE
18	3e−01	3 / 95	HALLMARK_SPERMATOGENESIS
19	3e−01	5 / 181	HALLMARK_P53_PATHWAY
20	3e−01	4 / 141	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−22	227 / 6929	HOPP_Txn_elongation
2	2e−15	33 / 294	TARTE_Plasmablast signature
3	1e−13	221 / 7592	HOPP_Active_promoter
4	2e−13	170 / 5184	HOPP_Txn_transition
5	5e−07	14 / 129	DAVE_BL−vs−DLBCL
6	1e−06	178 / 6564	HOPP_Strong_enhancer
7	8e−04	178 / 7209	HOPP_Weak_promoter
8	3e−03	13 / 256	SPANG_IL21 DN
9	6e−03	2 / 6	MASCQUE_mBL UP
10	6e−03	6 / 80	Aukema_BCL2 DN_BCL6 UP
11	8e−03	38 / 1218	SPANG_BCR UP
12	2e−02	3 / 30	TARTE_B−cell signature
13	3e−02	2 / 13	YAMANE_AICDA_targets_recruited
14	1e−01	4 / 89	ROSOLOWSKI_blue total
15	1e−01	2 / 29	Subero_DLBCL_hypo_meth
16	1e−01	2 / 30	Subero_INT_hypo_meth
17	1e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
18	2e−01	1 / 8	MASCQUE_GCB UP
19	2e−01	28 / 1128	SPANG_BCR DN
20	2e−01	1 / 13	WRIGHT_GCB UP

MF

Rank	p−value	#in/all	Geneset
1	2e−10	10 / 29	DNA−directed DNA polymerase activity
2	3e−10	30 / 376	chromatin binding
3	3e−09	81 / 2037	DNA binding
4	1e−08	18 / 167	helicase activity
5	2e−08	12 / 71	single−stranded DNA binding
6	7e−08	231 / 8984	protein binding
7	1e−06	6 / 18	3'−5' exonuclease activity
8	2e−06	13 / 123	nucleotidyltransferase activity
9	4e−06	24 / 405	ligase activity
10	6e−06	6 / 23	DNA helicase activity
11	6e−06	7 / 35	4 iron, 4 sulfur cluster binding
12	9e−06	14 / 164	nuclease activity
13	1e−05	8 / 54	damaged DNA binding
14	2e−05	50 / 1309	ATP binding
15	2e−05	6 / 29	ATP−dependent DNA helicase activity
16	3e−05	21 / 364	ATPase activity
17	8e−05	12 / 152	histone binding
18	1e−04	4 / 13	nucleocytoplasmic transporter activity
19	7e−04	4 / 20	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anhyd
20	8e−04	4 / 21	exonuclease activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	19 / 344	hsa−miR−548d−5p
2	2e−04	18 / 328	hsa−miR−520d−3p
3	4e−04	17 / 318	hsa−miR−302a
4	5e−04	17 / 328	hsa−miR−548a−5p
5	7e−04	9 / 115	hsa−miR−154
6	7e−04	10 / 140	hsa−miR−522
7	9e−04	17 / 343	hsa−miR−548b−5p
8	9e−04	18 / 376	hsa−miR−373
9	2e−03	16 / 329	hsa−miR−302d
10	2e−03	11 / 182	hsa−miR−374a
11	2e−03	10 / 157	hsa−miR−548o
12	2e−03	15 / 307	hsa−miR−302b
13	2e−03	15 / 310	hsa−miR−548i
14	2e−03	15 / 314	hsa−miR−548c−5p
15	3e−03	6 / 69	hsa−miR−499−3p
16	3e−03	8 / 119	hsa−miR−380
17	4e−03	4 / 31	hsa−miR−626
18	4e−03	15 / 328	hsa−miR−18a
19	4e−03	18 / 433	hsa−miR−548n
20	5e−03	4 / 33	hsa−miR−615−5p

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	2e−05	46 / 1171	KIM_MYC targets
2	3e−05	131 / 4689	ICGC_Taf1_targets
3	1e−04	114 / 4032	ICGC_Creb1_targets
4	2e−04	130 / 4829	ICGC_Nficsc81335_targets
5	7e−04	3 / 9	MYC_DNA repair UP
6	1e−03	6 / 59	MYC_Targets UP
7	3e−03	119 / 4617	ICGC_Tcf12_targets
8	4e−03	98 / 3700	ICGC_Nfatc1_targets
9	4e−03	124 / 4879	ICGC_Pmlsc71910_targets
10	4e−03	120 / 4706	ICGC_Sp1_targets
11	5e−03	135 / 5408	ICGC_Pou2_targets
12	5e−03	119 / 4682	ICGC_Pol24_targets
13	5e−03	113 / 4414	ICGC_Bclaf101388_targets
14	5e−03	105 / 4054	ICGC_Egr1_targets
15	6e−03	21 / 553	ICGC_RxraPcr1_targets
16	7e−03	123 / 4909	ICGC_Stat5_targets
17	7e−03	144 / 5890	ICGC_Elf1_targets
18	8e−03	111 / 4385	ICGC_Atf2_targets
19	9e−03	148 / 6114	ICGC_Runx3_targets
20	1e−02	134 / 5495	ICGC_Yy1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	VAQUERIZAS_Fetal liver
2	0.04	3 / 38	VAQUERIZAS_Testis
3	0.10	2 / 26	VAQUERIZAS_Liver
4	0.18	2 / 37	VAQUERIZAS_Thymus
5	0.27	1 / 15	VAQUERIZAS_Bone marrow
6	0.61	1 / 45	VAQUERIZAS_Uterus
7	0.71	1 / 58	VAQUERIZAS_Lung
8	0.95	1 / 143	VAQUERIZAS_General
9	1.00	0 / 36	VAQUERIZAS_Fetal brain
10	1.00	0 / 41	VAQUERIZAS_Placenta
11	1.00	0 / 33	VAQUERIZAS_Prostate
12	1.00	0 / 29	VAQUERIZAS_Smooth muscle
13	1.00	0 / 9	VAQUERIZAS_Kidney
14	1.00	0 / 23	VAQUERIZAS_Spinal cord
15	1.00	0 / 38	VAQUERIZAS_Whole brain
16	1.00	0 / 40	VAQUERIZAS_Thyroid
17	1.00	0 / 59	VAQUERIZAS_Whole blood
18	1.00	0 / 7	VAQUERIZAS_Appendix
19	1.00	0 / 29	VAQUERIZAS_Fetal lung
20	1.00	0 / 16	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.002	3 / 12	WIRTH_Thymus
2	0.195	10 / 350	WIRTH_Immune system
3	0.207	1 / 11	WIRTH_Prim. lymphoid organs
4	0.223	1 / 12	WIRTH_Cerebellum
5	0.379	5 / 194	PALMER_B−Cell signature up
6	0.992	1 / 225	PALMER_Granulocytes signature up
7	0.995	2 / 350	WIRTH_Nervous System
8	1.000	0 / 32	WIRTH_Pancreas
9	1.000	0 / 11	WIRTH_Sec. lymphoid organs
10	1.000	0 / 13	WIRTH_B−cells
11	1.000	0 / 8	WIRTH_Tonsil
12	1.000	0 / 12	WIRTH_Lymphocytes
13	1.000	0 / 5	WIRTH_Bone marrow
14	1.000	0 / 11	WIRTH_Globus pallidus
15	1.000	0 / 14	WIRTH_Telencephalon
16	1.000	0 / 11	WIRTH_Cortex cerebri
17	1.000	0 / 10	WIRTH_Hippocampus
18	1.000	0 / 10	WIRTH_Thalamus
19	1.000	0 / 107	WIRTH_Testis
20	1.000	0 / 41	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.09	30 / 1115	LU_BPDE 1h DN
2	1.00	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	

K−Means Clusters

Spot Summary: E

metagenes = 115
genes = 566

<r> metagenes = 0.78
<r> genes = 0.05
beta: r2= 1.27 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 9 (21.4 %)

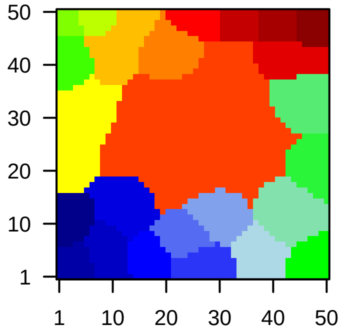
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	JMJD7	2.04	−0.18	0.24	JMJD7	jumonji domain containing 7 [Source:HGNC Symbol;Acc:HGN
2	TMEM71	2.04	−0.12	0.25	TMEM71	transmembrane protein 71 [Source:HGNC Symbol;Acc:HGN
3	PHYHIPL	1.94	−0.16	0.35	PHYHIPL	phytanoyl−CoA 2−hydroxylase interacting protein−like [Sourc
4	ISG20	1.9	−0.29	0.24	ISG20	interferon stimulated exonuclease gene 20kDa [Source:HGN
5	EME1	1.85	−0.41	0.26	EME1	essential meiotic structure−specific endonuclease 1 [Source:
6	HSD17B6	1.83	−0.06	0.33	HSD17B6	hydroxysteroid (17−beta) dehydrogenase 6 [Source:HGNC S
7	CHTF18	1.83	−0.47	0.32	CHTF18	CTF18, chromosome transmission fidelity factor 18 homolog
8	DHTKD1	1.81	−0.39	0.39	DHTKD1	dehydrogenase E1 and transketolase domain containing 1 [S
9	RHBDD1	1.8	−0.31	0.24	RHBDD1	rhomboid domain containing 1 [Source:HGNC Symbol;Acc:H
10	ASH2L	1.79	−0.43	0.38	ASH2L	ash2 (absent, small, or homeotic)−like (Drosophila) [Source:
11	DDHD2	1.79	−0.25	0.25	DDHD2	DDHD domain containing 2 [Source:HGNC Symbol;Acc:HGN
12	INPP1	1.75	−0.34	0.29	INPP1	inositol polyphosphate−1−phosphatase [Source:HGNC Symb
13	MYD88	1.72	−0.18	0.22	MYD88	myeloid differentiation primary response 88 [Source:HGNC S
14	CEP44	1.72	−0.41	0.36	CEP44	centrosomal protein 44kDa [Source:HGNC Symbol;Acc:HGN
15	C19orf47	1.71	−0.25	0.36	C19orf47	chromosome 19 open reading frame 47 [Source:HGNC Symb
16	ZNF101	1.71	−0.32	0.24	ZNF101	zinc finger protein 101 [Source:HGNC Symbol;Acc:HGNC:12
17	C15orf41	1.7	−0.3	0.25	C15orf41	chromosome 15 open reading frame 41 [Source:HGNC Symb
18	STRA6	1.68	−0.03	0.39	STRA6	stimulated by retinoic acid 6 [Source:HGNC Symbol;Acc:HGN
19	S100B	1.66	−0.6	0.29	S100B	S100 calcium binding protein B [Source:HGNC Symbol;Acc:
20	ITGB4	1.66	−0.12	0.31	ITGB4	integrin, beta 4 [Source:HGNC Symbol;Acc:HGNC:6158]

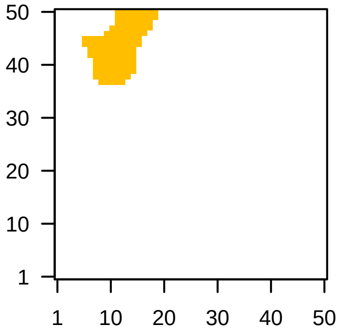
Geneset Overrepresentation

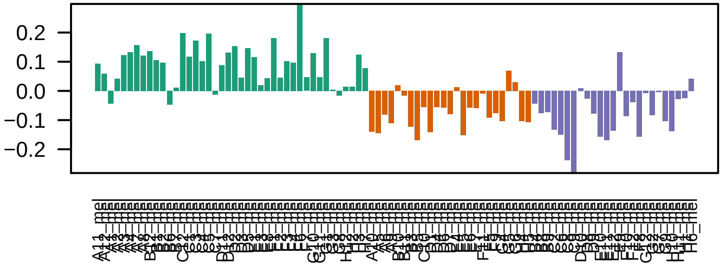
Rank	p−value	#in/all	Geneset	
1	2e−27	469 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	4e−27	473 / 9482	Colon	TssA_Colon
3	1e−26	386 / 6929	Lympl	HOPP_Txn_elongation
4	4e−22	132 / 1460	GSEA	PUJANA_BRCA1_PCC_NETWORK
5	1e−20	323 / 5696	CC	nucleus
6	8e−20	300 / 5184	Lympl	HOPP_Txn_transition
7	3e−19	425 / 8580	Colon	TxWk_Colon
8	5e−19	439 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
9	8e−19	439 / 9027	Colon	Tx_Colon
10	1e−18	389 / 7592	Lympl	HOPP_Active_promoter
11	2e−18	109 / 1192	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	5e−18	180 / 2577	CC	nucleoplasm
13	2e−16	483 / 10605	CC	intracellular
14	2e−16	411 / 8415	Colon	Quies3_Colon
15	4e−16	463 / 9988	CC	organelle
16	4e−16	76 / 724	GSEA	PUJANA_CHEK2_PCC_NETWORK
17	4e−16	31 / 136	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
18	7e−16	318 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
19	2e−15	32 / 154	GSEA	REACTOME_MRNA_PROCESSING
20	4e−15	34 / 177	BP	mRNA splicing, via spliceosome
21	1e−14	51 / 393	BP	mRNA processing
22	6e−13	86 / 1007	MF	poly(A) RNA binding
23	8e−13	26 / 124	GSEA	KEGG_SPLICEOSOME
24	1e−12	24 / 107	GSEA	REACTOME_MRNA_SPLICING
25	2e−12	98 / 1251	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
26	5e−12	101 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
27	6e−12	224 / 3980	BP	cellular nitrogen compound metabolic process
28	1e−11	102 / 1365	MF	RNA binding
29	2e−11	21 / 92	CC	spliceosomal complex
30	5e−11	125 / 1858	GSEA	PILON_KLF1_TARGETS_DN
31	2e−10	32 / 229	BP	RNA splicing
32	2e−10	62 / 687	BP	gene expression
33	3e−10	65 / 747	CC	nucleolus
34	4e−10	62 / 700	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
35	5e−10	28 / 188	HM	HALLMARK_MYC_TARGETS_V1
36	8e−10	453 / 10290	Colon	TssWk_Colon
37	1e−09	42 / 390	GSEA	PUJANA_BRCA2_PCC_NETWORK
38	2e−09	499 / 11774	CC	cell
39	3e−09	38 / 344	miRN	hsa−miR−548d−5p
40	5e−09	17 / 79	CC	catalytic step 2 spliceosome

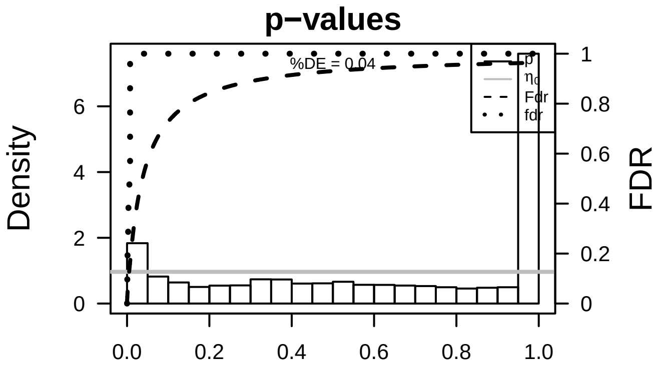
Overview Map



Spot







Aging

Rank	p−value	#in/all	Geneset
1	0.4	5 / 111	HORVATH_aging_genes meth UP
2	0.7	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	

BP

Rank	p−value	#in/all	Geneset
1	4e−15	34 / 177	mRNA splicing, via spliceosome
2	1e−14	51 / 393	mRNA processing
3	6e−12	224 / 3980	cellular nitrogen compound metabolic process
4	2e−10	32 / 229	RNA splicing
5	2e−10	62 / 687	gene expression
6	2e−07	9 / 25	RNA splicing, via transesterification reactions
7	2e−07	191 / 3644	biosynthetic process
8	2e−06	73 / 1110	cell cycle
9	2e−05	11 / 61	mRNA export from nucleus
10	3e−05	52 / 768	DNA metabolic process
11	9e−05	23 / 251	nucleocytoplasmic transport
12	1e−04	8 / 41	mRNA 3'−end processing
13	2e−04	10 / 65	double−strand break repair via homologous recombination
14	3e−04	8 / 46	termination of RNA polymerase II transcription
15	4e−04	24 / 298	DNA repair
16	4e−04	5 / 18	double−strand break repair via nonhomologous end joining
17	5e−04	30 / 412	mitotic cell cycle
18	5e−04	9 / 62	viral life cycle
19	7e−04	6 / 29	regulation of glucose transport
20	7e−04	6 / 29	viral transcription

Brain

Rank	p−value	#in/all	Geneset
1	2e−27	469 / 9330	Overlap_fetal_midbrain_ReprPC
2	5e−19	439 / 9013	Overlap_fetal_midbrain_K9K27me3
3	7e−16	318 / 5940	Overlap_fetal_midbrain_HetRpts
4	3e−08	421 / 9528	Overlap_fetal_midbrain_Quies
5	8e−08	401 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	7e−03	43 / 769	Overlap_fetal_midbrain_ZNF
7	3e−02	52 / 1050	Fetal_EnhP
8	4e−02	47 / 953	Fetal_Enh
9	2e−01	78 / 1845	Fetal_Quies
10	2e−01	35 / 786	Fetal_EnhG
11	2e−01	48 / 1122	Fetal_K9K27me3
12	2e−01	36 / 831	Fetal_HetRpts
13	2e−01	124 / 3081	Mid_Frontal_Lobe_ZNF
14	3e−01	14 / 304	Fetal_Het
15	3e−01	15 / 349	Fetal_ZNF
16	4e−01	7 / 158	Overlap_fetal_midbrain_Het
17	5e−01	29 / 765	Mid_Frontal_Lobe_Het
18	6e−01	24 / 656	Overlap_fetal_midbrain_EnhP
19	6e−01	49 / 1333	Fetal_ReprPCWk
20	7e−01	5 / 156	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 15	RHODES_CANCER_META_SIGNATURE
2	2e−02	3 / 15	GENTLES_modul1
3	2e−02	3 / 15	GENTLES_modul4
4	2e−02	3 / 15	GENTLES_modul10
5	3e−02	5 / 48	KUIPER_MM poor survival
6	5e−02	6 / 70	SHAUGHNESSY_MM high risk
7	7e−02	2 / 12	LIU_BREAST_CANCER
8	1e−01	2 / 14	LIU_COMMON_CANCER_GENES
9	1e−01	1 / 14	LIU_LIVER_CANCER
10	1e−01	2 / 15	WANG_ER_UP
11	1e−01	2 / 16	GENTLES_modul6
12	1e−01	2 / 16	GENTLES_modul14
13	2e−01	23 / 489	Lembcke_Normal vs Adenoma
14	2e−01	7 / 120	PanCan_CC+Apop_geneset_nanostring
15	2e−01	3 / 40	ZHANG_MM up
16	2e−01	3 / 40	PanCan_HK_geneset_nanostring
17	3e−01	3 / 47	PanCan_DNARepair_geneset_nanostring
18	3e−01	1 / 10	GENTLES_modul3
19	3e−01	1 / 10	GENTLES_modul5
20	3e−01	1 / 10	GENTLES_modul13

CC

Rank	p−value	#in/all	Geneset
1	1e−20	323 / 5696	nucleus
2	5e−18	180 / 2577	nucleoplasm
3	2e−16	483 / 10605	intracellular
4	4e−16	463 / 9988	organelle
5	2e−11	21 / 92	spliceosomal complex
6	3e−10	65 / 747	nucleolus
7	2e−09	499 / 11774	cell
8	5e−09	17 / 79	catalytic step 2 spliceosome
9	3e−06	50 / 663	chromosome
10	6e−06	362 / 8205	cytoplasm
11	2e−05	19 / 170	nuclear speck
12	2e−04	157 / 3214	protein complex
13	3e−04	8 / 47	Cajal body
14	3e−04	13 / 113	spindle
15	4e−04	9 / 60	nuclear pore
16	6e−04	12 / 105	ribonucleoprotein complex
17	9e−04	25 / 331	nuclear chromosome
18	1e−03	11 / 97	chromatin
19	2e−03	8 / 59	chromosome, centromeric region
20	2e−03	5 / 24	U12−type spliceosomal complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	27 / 469	Chr 8
2	0.04	42 / 840	Chr 17
3	0.11	31 / 649	Chr 16
4	0.16	22 / 462	Chr 14
5	0.22	25 / 558	Chr 4
6	0.24	30 / 687	Chr 6
7	0.25	42 / 993	Chr 2
8	0.33	29 / 696	Chr 5
9	0.40	19 / 465	Chr 15
10	0.46	9 / 221	Chr 18
11	0.51	32 / 838	Chr 3
12	0.51	6 / 151	Chr 21
13	0.52	57 / 1500	Chr 1
14	0.52	21 / 551	Chr X
15	0.54	10 / 262	Chr 13
16	0.55	15 / 398	Chr 20
17	0.63	29 / 801	Chr 11
18	0.77	23 / 689	Chr 7
19	0.82	10 / 335	Chr 22
20	0.84	34 / 1037	Chr 19

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−27	473 / 9482	TssA_Colon
2	3e−19	425 / 8580	TxWk_Colon
3	8e−19	439 / 9027	Tx_Colon
4	2e−16	411 / 8415	Quies3_Colon
5	8e−10	453 / 10290	TssWk_Colon
6	3e−05	320 / 7203	TssF_Colon
7	1e−04	44 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	3e−04	48 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	2e−02	3 / 16	Juehling−MSI−enriched−in−6
10	3e−02	12 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	7e−02	16 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	1e−01	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
13	1e−01	3 / 33	Marisa_CRC−cluster−e
14	2e−01	235 / 5880	TssD2_Colon
15	2e−01	1 / 5	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
16	2e−01	376 / 9653	Enh_Colon
17	3e−01	1 / 8	Boland_CRC−MMR−system
18	3e−01	1 / 8	Marisa_CRC−C3
19	3e−01	1 / 8	Juehling−MSI−enriched−in−7
20	3e−01	1 / 9	KIM_MSI−in−EC

Disease

Rank	p−value	#in/all	Geneset
1	0.5	1 / 20	BCHETNIA_EBM−DM up
2	0.8	13 / 435	GUDJ_psoriasis up
3	1.0	4 / 294	GUDJ_psoriasis down
4	1.0	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	4e−06	30 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	2e−04	27 / 332	Up
3	4e−04	4 / 10	WILLSCHER_GBM_LTSmut_proteomics−A_UP
4	2e−03	49 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	5e−02	4 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	7e−02	1 / 2	WILLSCHER_GBM_LTSmut_proteomics−E_UP
7	8e−02	3 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
8	1e−01	1 / 3	Sturm_GBM_Meth_overexpression_K_mesenchymal_UP
9	1e−01	5 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	1e−01	6 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	2e−01	3 / 40	in vivo astrocytes vs. cultured astroglia
12	2e−01	7 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	2e−01	1 / 6	shaw_responders_up_in_oligo_glioma
14	2e−01	1 / 7	KIM amplified & overexpressed in LTS
15	3e−01	3 / 47	mature astrocytes
16	3e−01	1 / 9	Mukasa_UP_in_GBM
17	3e−01	4 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
18	3e−01	5 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
19	3e−01	1 / 11	Martinez_Glio_hypermeth
20	3e−01	1 / 11	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−22	132 / 1460	PUJANA_BRCA1_PCC_NETWORK
2	2e−18	109 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	4e−16	76 / 724	PUJANA_CHEK2_PCC_NETWORK
4	4e−16	31 / 136	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
5	2e−15	32 / 154	REACTOME_MRNA_PROCESSING
6	8e−13	26 / 124	KEGG_SPLICEOSOME
7	1e−12	24 / 107	REACTOME_MRNA_SPLICING
8	2e−12	98 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	5e−12	101 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	5e−11	125 / 1858	PILON_KLF1_TARGETS_DN
11	4e−10	62 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	1e−09	42 / 390	PUJANA_BRCA2_PCC_NETWORK
13	5e−09	86 / 1199	PUJANA_ATM_PCC_NETWORK
14	3e−08	66 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
15	4e−08	23 / 160	PUJANA_XPRSS_INT_NETWORK
16	6e−08	13 / 53	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM
17	7e−08	58 / 729	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
18	1e−07	106 / 1693	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
19	2e−07	20 / 135	WHITFIELD_CELL_CYCLE_G1_S
20	2e−07	50 / 609	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP

HM

Rank	p−value	#in/all	Geneset
1	5e−10	28 / 188	HALLMARK_MYC_TARGETS_V1
2	1e−07	25 / 197	HALLMARK_E2F_TARGETS
3	1e−03	17 / 196	HALLMARK_G2M_CHECKPOINT
4	2e−02	13 / 183	HALLMARK_GLYCOLYSIS
5	2e−02	9 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	9e−02	9 / 140	HALLMARK_APOPTOSIS
7	1e−01	9 / 146	HALLMARK_DNA_REPAIR
8	1e−01	6 / 93	HALLMARK_PEROXISOME
9	2e−01	6 / 95	HALLMARK_SPERMATOGENESIS
10	2e−01	6 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	2e−01	8 / 141	HALLMARK_FATTY_ACID_METABOLISM
12	2e−01	4 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	2e−01	9 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	2e−01	10 / 196	HALLMARK_MTORC1_SIGNALING
15	3e−01	7 / 140	HALLMARK_INFLAMMATORY_RESPONSE
16	3e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
17	3e−01	7 / 146	HALLMARK_UV_RESPONSE_UP
18	3e−01	9 / 195	HALLMARK_MITOTIC_SPINDLE
19	4e−01	8 / 176	HALLMARK_HYPOXIA
20	4e−01	3 / 57	HALLMARK_MYC_TARGETS_V2

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	3 / 32	DUMEAUX_Fasting enriched genes
2	0.1	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
3	0.5	1 / 18	DUMEAUX_High bmi enriched genes
4	0.7	2 / 62	DUMEAUX_Smoking 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 / 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	1e−26	386 / 6929	HOPP_Txn_elongation
2	8e−20	300 / 5184	HOPP_Txn_transition
3	1e−18	389 / 7592	HOPP_Active_promoter
4	4e−07	331 / 7209	HOPP_Weak_promoter
5	1e−06	304 / 6564	HOPP_Strong_enhancer
6	4e−03	247 / 5693	HOPP_Weak_enhancer
7	5e−03	240 / 5538	HOPP_Weak_txn
8	7e−03	59 / 1128	SPANG_BCR DN
9	9e−03	20 / 294	TARTE_Plasmablast signature
10	1e−02	25 / 410	SPANG_CD40 6hrs DN
11	2e−02	61 / 1218	SPANG_BCR UP
12	5e−02	7 / 89	ROSOLOWSKI_blue total
13	1e−01	5 / 66	TARTE_Plasma cell signature
14	1e−01	4 / 50	SPANG_BAFF 9hrs DN
15	2e−01	13 / 256	SPANG_IL21 DN
16	2e−01	3 / 43	LENZ_Stromal signature 2
17	2e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
18	3e−01	1 / 8	YAMANE_AICDA_targets_nonrecruited
19	3e−01	1 / 10	DAVE_BL_DN
20	3e−01	1 / 10	Shaknovich_ABC_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	6e−13	86 / 1007	poly(A) RNA binding
2	1e−11	102 / 1365	RNA binding
3	6e−05	17 / 152	histone binding
4	7e−05	384 / 8984	protein binding
5	5e−04	16 / 164	nuclease activity
6	2e−03	4 / 15	lysine−acetylated histone binding
7	3e−03	7 / 52	double−stranded RNA binding
8	4e−03	7 / 53	transferase activity
9	5e−03	3 / 10	histone methyltransferase activity
10	6e−03	24 / 361	binding
11	7e−03	55 / 1033	nucleic acid binding
12	7e−03	98 / 2037	DNA binding
13	1e−02	4 / 23	DNA helicase activity
14	1e−02	8 / 81	double−stranded DNA binding
15	1e−02	24 / 386	nucleotide binding
16	2e−02	27 / 456	protein binding transcription factor activity
17	2e−02	3 / 15	hydrolase activity, acting on acid anhydrides
18	2e−02	7 / 71	cysteine−type endopeptidase activity
19	2e−02	515 / 13179	molecular_function
20	2e−02	4 / 28	Ran GTPase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−09	38 / 344	hsa−miR−548d−5p
2	1e−08	26 / 190	hsa−miR−548d−3p
3	4e−08	34 / 314	hsa−miR−548c−5p
4	6e−07	29 / 274	hsa−miR−548h
5	9e−07	33 / 343	hsa−miR−548b−5p
6	2e−06	29 / 293	hsa−miR−548j
7	6e−06	15 / 101	hsa−miR−516b
8	6e−06	25 / 243	hsa−miR−122
9	6e−06	24 / 228	hsa−miR−124
10	2e−05	28 / 310	hsa−miR−548i
11	2e−05	29 / 328	hsa−miR−548a−5p
12	4e−05	15 / 118	hsa−miR−625
13	5e−05	20 / 195	hsa−miR−206
14	6e−05	28 / 328	hsa−miR−520d−3p
15	6e−05	19 / 181	hsa−miR−1
16	8e−05	29 / 353	hsa−let−7i
17	1e−04	11 / 75	hsa−miR−592
18	1e−04	10 / 63	hsa−miR−1285
19	2e−04	14 / 118	hsa−miR−509−3p
20	2e−04	13 / 105	hsa−miR−376b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 12	GUSTAFSON_PI3K_UP
2	0.08	2 / 13	BENTINK_myc.1
3	0.10	2 / 14	BENTINK_e2f3.1
4	0.10	2 / 14	BENTINK_src.2
5	0.29	1 / 9	BENTINK_ras.4
6	0.37	1 / 12	BENTINK_ras.1
7	0.44	1 / 15	BENTINK_ras.6
8	1.00	0 / 13	GUSTAFSON_PI3K_DN
9	1.00	0 / 12	BENTINK_e2f3.2
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−06	227 / 4689	ICGC_Taf1_targets
2	3e−05	72 / 1171	KIM_MYC targets
3	4e−04	9 / 59	MYC_Targets UP
4	4e−04	223 / 4879	ICGC_Pmlsc71910_targets
5	5e−04	184 / 3924	ICGC_Zeb1_targets
6	6e−04	202 / 4385	ICGC_Atf2_targets
7	6e−04	76 / 1383	ICGC_Six5_targets
8	6e−04	109 / 2137	ICGC_SrfV0416101_targets
9	6e−04	211 / 4617	ICGC_Tcf12_targets
10	1e−03	201 / 4414	ICGC_Bclaf101388_targets
11	1e−03	2 / 2	MYC_Chromatin_modification UP
12	2e−03	87 / 1701	HEBENSTREIT_high expression TF
13	2e−03	210 / 4706	ICGC_Sp1_targets
14	3e−03	229 / 5200	ICGC_Mta3_targets
15	3e−03	214 / 4829	ICGC_Nficsc81335_targets
16	3e−03	217 / 4909	ICGC_Stat5_targets
17	3e−03	182 / 4032	ICGC_Creb1_targets
18	4e−03	239 / 5495	ICGC_Yy1_targets
19	4e−03	182 / 4054	ICGC_Egr1_targets
20	5e−03	233 / 5355	ICGC_Pol2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	5 / 59	VAQUERIZAS_Whole blood
2	0.08	3 / 27	VAQUERIZAS_Lymph node
3	0.16	2 / 19	VAQUERIZAS_Tonsil
4	0.30	2 / 29	VAQUERIZAS_Fetal lung
5	0.41	2 / 37	VAQUERIZAS_Thymus
6	0.43	2 / 38	VAQUERIZAS_Whole brain
7	0.46	1 / 16	VAQUERIZAS_Salivary gland
8	0.48	1 / 17	VAQUERIZAS_Pituitary
9	0.59	1 / 23	VAQUERIZAS_Spinal cord
10	0.65	2 / 58	VAQUERIZAS_Lung
11	0.67	1 / 29	VAQUERIZAS_Smooth muscle
12	0.75	1 / 36	VAQUERIZAS_Fetal brain
13	0.79	1 / 40	VAQUERIZAS_Thyroid
14	0.80	1 / 41	VAQUERIZAS_Placenta
15	0.80	4 / 143	VAQUERIZAS_General
16	1.00	0 / 26	VAQUERIZAS_Liver
17	1.00	0 / 33	VAQUERIZAS_Prostate
18	1.00	0 / 45	VAQUERIZAS_Uterus
19	1.00	0 / 9	VAQUERIZAS_Kidney
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 12	WIRTH_Lymphocytes
2	3e−02	21 / 350	WIRTH_Immune system
3	6e−02	2 / 11	WIRTH_Globus pallidus
4	3e−01	1 / 8	WIRTH_Tonsil
5	3e−01	1 / 9	PALMER_CD8+ T−Cell signature up
6	3e−01	1 / 10	WIRTH_Thalamus
7	4e−01	1 / 12	WIRTH_Cerebellum
8	4e−01	1 / 13	WIRTH_Thyroid gland
9	5e−01	3 / 74	WIRTH_Mucosa
10	6e−01	8 / 225	PALMER_Granulocytes signature up
11	7e−01	6 / 194	PALMER_B−Cell signature up
12	9e−01	10 / 350	WIRTH_Nervous System
13	9e−01	2 / 114	PALMER_T−Cell signature up
14	1e+00	1 / 107	WIRTH_Testis
15	1e+00	0 / 32	WIRTH_Pancreas
16	1e+00	0 / 11	WIRTH_Sec. lymphoid organs
17	1e+00	0 / 11	WIRTH_Prim. lymphoid organs
18	1e+00	0 / 13	WIRTH_B−cells
19	1e+00	0 / 12	WIRTH_Thymus
20	1e+00	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	37 / 1115	LU_BPDE 1h DN
2	1.0	96 / 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	

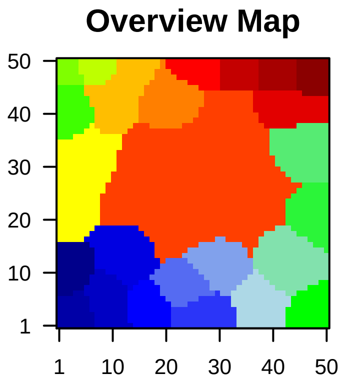
K−Means Clusters

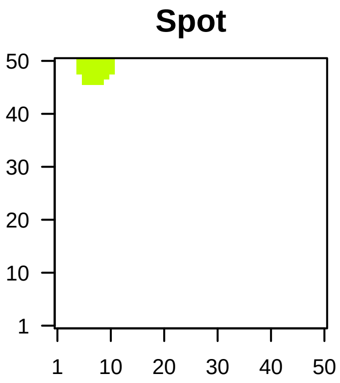
Spot Summary: F

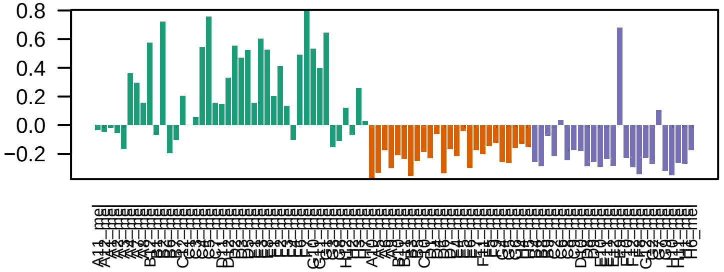
metagenes = 30
genes = 332

<r> metagenes = 0.96
<r> genes = 0.25
beta: r2= 5.95 / log p= −Inf

samples with spot = 25 (27.2 %)
MSC1 : 24 (57.1 %)
MSC3 : 1 (4 %)





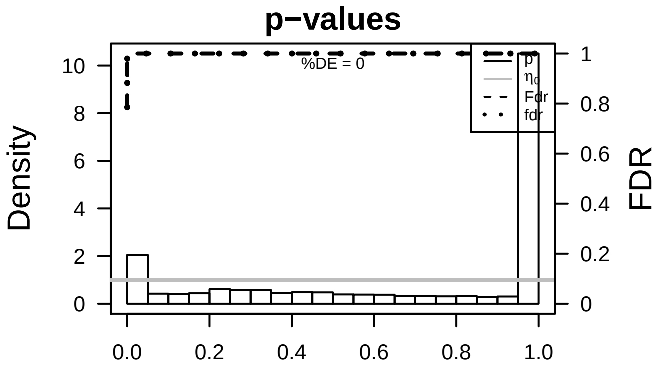


Spot Genelist

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	AURKB	2.03	−0.61	0.79	AURKB	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
9	CKAP2L	2.01	−0.57	0.84	CKAP2L	cytoskeleton associated protein 2−like [Source:HGNC Symb
10	CDC20	2	−0.67	0.71	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
11	KIF20A	1.98	−0.39	0.74	KIF20A	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
12	NDC80	1.96	−0.62	0.87	NDC80	NDC80 kinetochore complex component [Source:HGNC Sym
13	DLGAP5	1.93	−0.47	0.78	DLGAP5	discs, large (Drosophila) homolog−associated protein 5 [Sour
14	PRR11	1.93	−0.5	0.75	PRR11	proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
15	RRM2	1.92	−0.76	0.86	RRM2	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
16	ITGA6	1.91	−0.26	0.33	ITGA6	integrin, alpha 6 [Source:HGNC Symbol;Acc:HGNC:6142]
17	SGOL1	1.91	−0.72	0.75	SGOL1	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
18	HIST1H4E	1.9	−0.46	0.45	HIST1H4E	histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
19	FCGR2A	1.9	−0.23	0.29	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32) [Source:
20	CDCA3	1.88	−0.49	0.83	CDCA3	cell division cycle associated 3 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	136 / 550	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	2e−98	81 / 142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
3	3e−83	10 / 16	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	4e−83	121 / 616	GSE	BENPORATH_CYCLING_GENES
5	6e−83	72 / 139	GSE	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	7e−81	125 / 700	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	3e−75	87 / 291	GSE	HORIUCHI_WTAP_TARGETS_DN
8	5e−75	89 / 312	BP	mitotic nuclear division
9	6e−75	98 / 409	BP	cell division
10	3e−73	99 / 436	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	6e−70	139 / 1110	BP	cell cycle
12	7e−69	129 / 944	GSE	NUYTTEN_EZH2_TARGETS_DN
13	6e−67	65 / 155	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
14	8e−67	140 / 1192	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
15	4e−66	63 / 145	GSE	CHANG_CYCLING_GENES
16	8e−66	75 / 242	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
17	4e−63	139 / 1251	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
18	1e−62	79 / 305	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
19	2e−60	66 / 196	HM	HALLMARK_G2M_CHECKPOINT
20	1e−58	85 / 412	BP	mitotic cell cycle
21	3e−58	65 / 201	GSE	WHITFIELD_CELL_CYCLE_G2_M
22	9e−58	61 / 170	GSE	WHITFIELD_CELL_CYCLE_G2
23	5e−56	81 / 390	GSE	PUJANA_BRCA2_PCC_NETWORK
24	3e−55	70 / 270	GSE	BASAKI_YBX1_TARGETS_UP
25	5e−55	53 / 124	GSE	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
26	3e−53	48 / 99	GSE	LEE_EARLY_T_LYMPHOCYTE_UP
27	8e−53	57 / 165	GSE	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
28	2e−52	47 / 96	GSE	CROONQUIST_IL6_DEPRIVATION_DN
29	2e−50	76 / 388	GSE	REACTOME_CELL_CYCLE
30	2e−50	48 / 110	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
31	4e−49	58 / 197	HM	HALLMARK_E2F_TARGETS
32	5e−49	54 / 162	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
33	6e−48	53 / 160	BP	chromosome segregation
34	7e−48	59 / 216	GSE	MARKEY_RB1_ACUTE_LOF_DN
35	3e−47	42 / 84	GSE	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
36	5e−47	47 / 118	GSE	ODONNELL_TFRC_TARGETS_DN
37	6e−47	66 / 301	GSE	REACTOME_CELL_CYCLE_MITOTIC
38	6e−47	80 / 489	Canc	Lembcke_Normal vs Adenoma
39	3e−45	100 / 862	GSE	JOHNSTONE_PARVB_TARGETS_3_DN
40	5e−45	70 / 373	GSE	VECCHI_GASTRIC_CANCER_EARLY_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.04	6 / 111	HORVATH_aging_genes meth UP
2	0.90	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	5e−75	89 / 312	mitotic nuclear division
2	6e−75	98 / 409	cell division
3	6e−70	139 / 1110	cell cycle
4	1e−58	85 / 412	mitotic cell cycle
5	6e−48	53 / 160	chromosome segregation
6	6e−27	71 / 721	chromosome organization
7	2e−21	57 / 581	cytoskeleton organization
8	1e−19	28 / 133	G2/M transition of mitotic cell cycle
9	2e−19	14 / 20	mitotic sister chromatid segregation
10	1e−17	60 / 768	DNA metabolic process
11	5e−14	51 / 694	protein complex assembly
12	1e−13	14 / 41	CENP−A containing nucleosome assembly
13	3e−13	20 / 108	nucleosome assembly
14	1e−12	16 / 68	microtubule−based movement
15	4e−11	10 / 24	mitotic cytokinesis
16	7e−11	51 / 843	macromolecular complex assembly
17	6e−10	10 / 30	mitotic metaphase plate congression
18	7e−10	63 / 1255	cellular component assembly
19	1e−09	10 / 32	mitotic spindle assembly checkpoint
20	2e−09	14 / 78	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent

Brain

Rank	p−value	#in/all	Geneset
1	6e−16	275 / 9330	Overlap_fetal_midbrain_ReprPC
2	4e−06	40 / 831	Fetal_HetRpts
3	2e−05	238 / 9013	Overlap_fetal_midbrain_K9K27me3
4	6e−05	66 / 1845	Fetal_Quies
5	4e−03	39 / 1122	Fetal_K9K27me3
6	3e−02	8 / 163	Fetal_ReprPC
7	3e−02	40 / 1333	Fetal_ReprPCWk
8	1e−01	6 / 158	Overlap_fetal_midbrain_Het
9	3e−01	7 / 229	Mid_Frontal_Lobe_TxTrans
10	3e−01	26 / 1050	Fetal_EnhP
11	4e−01	9 / 349	Fetal_ZNF
12	5e−01	23 / 989	Mid_Frontal_Lobe_Quies
13	5e−01	134 / 5940	Overlap_fetal_midbrain_HetRpts
14	6e−01	27 / 1236	Mid_Frontal_Lobe_ReprPCWk
15	6e−01	10 / 468	Mid_Frontal_Lobe_TssF
16	7e−01	16 / 769	Overlap_fetal_midbrain_ZNF
17	7e−01	6 / 304	Fetal_Het
18	7e−01	16 / 786	Fetal_EnhG
19	8e−01	1 / 69	Overlap_fetal_midbrain_Tx
20	8e−01	18 / 953	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	3e−83	10 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	6e−47	80 / 489	Lembcke_Normal vs Adenoma
3	1e−30	8 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	9e−06	2 / 15	RHODES_CANCER_META_SIGNATURE
5	2e−05	5 / 16	WOLFER_overlap genes
6	2e−05	9 / 70	SHAUGHNESSY_MM high risk
7	9e−05	7 / 48	KUIPER_MM poor survival
8	1e−04	4 / 13	BEN−PORATH_UP
9	4e−04	10 / 120	PanCan_CC+Apop_geneset_nanostring
10	4e−04	5 / 29	KUIPER_MM good survival
11	1e−03	3 / 10	GENTLES_modul3
12	4e−03	1 / 14	LIU_COMMON_CANCER_GENES
13	5e−03	3 / 16	GENTLES_modul16
14	2e−01	2 / 40	PanCan_HK_geneset_nanostring
15	2e−01	1 / 12	LIU_BREAST_CANCER
16	2e−01	1 / 12	LIU_PROSTATE_CANCER_UP
17	3e−01	3 / 82	PanCan_TXmisReg_geneset_nanostring
18	3e−01	1 / 15	WANG_ER_UP
19	3e−01	1 / 15	GENTLES_modul4
20	3e−01	1 / 16	GENTLES_modul7

CC

Rank	p−value	#in/all	Geneset
1	2e−39	83 / 663	chromosome
2	1e−30	108 / 1465	cytoskeleton
3	6e−25	25 / 65	kinetochore
4	4e−23	25 / 75	condensed chromosome kinetochore
5	8e−23	215 / 5696	nucleus
6	1e−22	55 / 512	microtubule organizing center
7	9e−22	26 / 93	spindle pole
8	1e−21	22 / 59	chromosome, centromeric region
9	2e−19	26 / 113	spindle
10	8e−19	43 / 377	centrosome
11	1e−18	17 / 38	spindle microtubule
12	6e−18	141 / 3214	protein complex
13	1e−15	32 / 250	microtubule
14	3e−14	112 / 2507	cytosol
15	7e−14	15 / 48	kinesin complex
16	8e−14	293 / 10605	intracellular
17	9e−14	21 / 115	midbody
18	6e−13	111 / 2577	nucleoplasm
19	1e−11	277 / 9988	organelle
20	2e−10	239 / 8205	cytoplasm

Chr

Rank	p−value	#in/all	Geneset
1	0.005	29 / 775	Chr 12
2	0.033	17 / 465	Chr 15
3	0.077	18 / 558	Chr 4
4	0.137	40 / 1500	Chr 1
5	0.151	20 / 696	Chr 5
6	0.155	14 / 462	Chr 14
7	0.175	16 / 552	Chr 10
8	0.200	19 / 687	Chr 6
9	0.253	13 / 469	Chr 8
10	0.297	25 / 993	Chr 2
11	0.364	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
12	0.534	6 / 262	Chr 13
13	0.553	5 / 221	Chr 18
14	0.641	12 / 576	Chr 9
15	0.660	3 / 151	Chr 21
16	0.670	8 / 398	Chr 20
17	0.764	6 / 335	Chr 22
18	0.903	14 / 840	Chr 17
19	0.914	13 / 801	Chr 11
20	0.940	13 / 838	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−14	49 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	1e−09	45 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
3	4e−08	273 / 10290	TssWk_Colon
4	1e−06	252 / 9482	TssA_Colon
5	6e−03	106 / 3812	TssD1_Colon
6	1e−02	2 / 8	Marisa_CRC−C6
7	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
8	7e−02	175 / 7203	TssF_Colon
9	8e−02	5 / 102	Marisa_CRC−cluster−d
10	9e−02	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
11	1e−01	143 / 5880	TssD2_Colon
12	1e−01	1 / 5	Budinska_C_CIMP−H−like_UP
13	1e−01	2 / 29	Marisa_CRC−cluster−c
14	1e−01	198 / 8415	Quies3_Colon
15	2e−01	1 / 8	Marisa_CRC−C1
16	2e−01	1 / 9	KIM_MSI−in−EC
17	3e−01	1 / 15	TCGA_Mutated−in−CRC_hypermutated
18	3e−01	1 / 15	Budinska_B_Lower crypt−like_UP
19	3e−01	1 / 16	Juehling−MSI−enriched−in−6
20	3e−01	1 / 17	Vilar_hypermutated−in−CRC

Disease

Rank	p−value	#in/all	Geneset
1	3e−25	54 / 435	GUDJ_psoriasis up
2	2e−01	1 / 11	BCHETNIA_EBM up
3	4e−01	1 / 20	BCHETNIA_EBM−DM up
4	1e+00	2 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	2e−98	81 / 142	WILLSCHER_GBM_Verhaak−CL_up (C)
2	5e−34	28 / 49	developing astrocytes
3	4e−17	20 / 71	Weller_LGG_gradeII−vs−III_DOWN
4	1e−07	11 / 62	cultured astroglia vs. in vivo astrocytes
5	2e−03	5 / 39	OPC
6	2e−03	32 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
7	5e−03	2 / 5	Phillips Prolif up vs PN & MES
8	7e−03	6 / 75	Weller_LGG_A_vs_O_DOWN
9	2e−02	2 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
10	9e−02	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
11	1e−01	2 / 25	Shaw_down_in_1p19q
12	1e−01	2 / 29	shaw_responders_down_in_oligo_glioma
13	2e−01	3 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	2e−01	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	3e−01	1 / 14	VERHAAK_PN subtype
16	3e−01	1 / 15	VERHAAK_MES subtype
17	3e−01	2 / 49	OL vs. MOG− OL
18	4e−01	1 / 23	WIRTH_PN subtype
19	4e−01	3 / 103	GIEZELT_GBM_WT_up_VS_mut
20	4e−01	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	136 / 550	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	3e−83	10 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	4e−83	121 / 616	BENPORATH_CYCLING_GENES
4	6e−83	72 / 139	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	7e−81	125 / 700	MARSON_BOUND_BY_E2F4_UNSTIMULATED
6	3e−75	87 / 291	HORIUCHI_WTAP_TARGETS_DN
7	3e−73	99 / 436	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	7e−69	129 / 944	NUYTTEN_EZH2_TARGETS_DN
9	6e−67	65 / 155	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
10	8e−67	140 / 1192	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
11	4e−66	63 / 145	CHANG_CYCLING_GENES
12	8e−66	75 / 242	KOBAYASHI_EGFR_SIGNALING_24HR_DN
13	4e−63	139 / 1251	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	1e−62	79 / 305	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
15	3e−58	65 / 201	WHITFIELD_CELL_CYCLE_G2_M
16	9e−58	61 / 170	WHITFIELD_CELL_CYCLE_G2
17	5e−56	81 / 390	PUJANA_BRCA2_PCC_NETWORK
18	3e−55	70 / 270	BASAKI_YBX1_TARGETS_UP
19	5e−55	53 / 124	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
20	3e−53	48 / 99	LEE_EARLY_T_LYMPHOCYTE_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−60	66 / 196	HALLMARK_G2M_CHECKPOINT
2	4e−49	58 / 197	HALLMARK_E2F_TARGETS
3	4e−26	39 / 195	HALLMARK_MITOTIC_SPINDLE
4	1e−06	12 / 95	HALLMARK_SPERMATOGENESIS
5	8e−03	10 / 183	HALLMARK_GLYCOLYSIS
6	2e−02	6 / 93	HALLMARK_PEROXISOME
7	6e−02	8 / 188	HALLMARK_MYC_TARGETS_V1
8	1e−01	7 / 174	HALLMARK_HEME_METABOLISM
9	1e−01	6 / 141	HALLMARK_FATTY_ACID_METABOLISM
10	1e−01	4 / 91	HALLMARK_BILE_ACID_METABOLISM
11	2e−01	6 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	2e−01	6 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
13	2e−01	5 / 146	HALLMARK_DNA_REPAIR
14	3e−01	6 / 196	HALLMARK_MTORC1_SIGNALING
15	3e−01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
16	4e−01	2 / 57	HALLMARK_MYC_TARGETS_V2
17	4e−01	4 / 140	HALLMARK_APOPTOSIS
18	4e−01	5 / 188	HALLMARK_ADIPOGENESIS
19	4e−01	3 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
20	5e−01	1 / 29	HALLMARK_NOTCH_SIGNALING

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	1e−25	261 / 7592	HOPP_Active_promoter
2	5e−24	44 / 294	TARTE_Plasmablast signature
3	9e−21	238 / 6929	HOPP_Txn_elongation
4	7e−11	173 / 5184	HOPP_Txn_transition
5	5e−09	213 / 7209	HOPP_Weak_promoter
6	3e−08	16 / 129	DAVE_BL−vs−DLBCL
7	7e−08	57 / 1218	SPANG_BCR UP
8	5e−06	11 / 89	ROSOLOWSKI_blue total
9	7e−04	4 / 19	DAVE_c−myc BL UP
10	3e−03	152 / 5693	HOPP_Weak_enhancer
11	5e−03	147 / 5538	HOPP_Weak_txn
12	2e−02	166 / 6564	HOPP_Strong_enhancer
13	5e−02	2 / 16	DAVE_BL Inter
14	7e−02	1 / 3	WRIGHT_custom GCB−DLBCL UP
15	1e−01	4 / 82	ROSOLOWSKI_green UP
16	2e−01	1 / 8	MASCQUE_GCB UP
17	2e−01	1 / 8	YAMANE_AICDA_targets_nonrecruited
18	2e−01	4 / 109	ROSOLOWSKI_green total
19	3e−01	1 / 13	BENTINK_mBL UP
20	3e−01	1 / 13	WRIGHT_GCB UP

MF

Rank	p−value	#in/all	Geneset
1	7e−21	31 / 156	microtubule binding
2	2e−12	16 / 69	microtubule motor activity
3	7e−10	253 / 8984	protein binding
4	9e−10	40 / 609	cytoskeletal protein binding
5	8e−07	6 / 16	ATP−dependent microtubule motor activity, plus−end−directed
6	3e−06	22 / 316	protein kinase binding
7	2e−04	12 / 152	histone binding
8	2e−04	4 / 14	DNA binding, bending
9	2e−04	20 / 364	ATPase activity
10	4e−04	5 / 29	nucleosomal DNA binding
11	8e−04	19 / 373	protein heterodimerization activity
12	2e−03	41 / 1149	enzyme binding
13	2e−03	3 / 12	cyclin−dependent protein serine/threonine kinase inhibitor activity
14	4e−03	44 / 1309	ATP binding
15	5e−03	6 / 71	single−stranded DNA binding
16	5e−03	6 / 72	structural constituent of cytoskeleton
17	8e−03	4 / 36	tubulin binding
18	9e−03	308 / 13179	molecular_function
19	1e−02	60 / 2037	DNA binding
20	2e−02	3 / 25	protein serine/threonine/tyrosine kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−06	14 / 135	hsa−miR−28−5p
2	5e−04	8 / 83	hsa−miR−582−3p
3	1e−03	11 / 166	hsa−miR−548g
4	1e−03	9 / 119	hsa−miR−217
5	2e−03	11 / 176	hsa−miR−23b
6	2e−03	11 / 179	hsa−miR−582−5p
7	3e−03	5 / 43	hsa−miR−661
8	4e−03	10 / 164	hsa−miR−323b−5p
9	5e−03	10 / 170	hsa−miR−7
10	5e−03	10 / 170	hsa−miR−452
11	5e−03	5 / 50	hsa−miR−610
12	6e−03	6 / 74	hsa−miR−708
13	7e−03	14 / 296	hsa−miR−25
14	7e−03	15 / 327	hsa−miR−590−3p
15	7e−03	6 / 76	hsa−miR−509−3−5p
16	7e−03	11 / 208	hsa−miR−432
17	8e−03	7 / 101	hsa−miR−325
18	8e−03	10 / 182	hsa−miR−23a
19	8e−03	5 / 56	hsa−miR−384
20	8e−03	8 / 129	hsa−miR−576−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 15	BENTINK_ras.6
2	0.24	1 / 12	BENTINK_e2f3.2
3	0.24	1 / 12	BENTINK_ras.1
4	0.25	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	

TF

Rank	p−value	#in/all	Geneset
1	2e−05	56 / 1418	ICGC_Ets1_targets
2	6e−05	47 / 1171	KIM_MYC targets
3	1e−03	115 / 4032	ICGC_Creb1_targets
4	5e−03	54 / 1701	HEBENSTREIT_high expression TF
5	7e−03	45 / 1383	ICGC_Six5_targets
6	7e−03	126 / 4689	ICGC_Taf1_targets
7	1e−02	126 / 4774	ICGC_Foxm1_targets
8	2e−02	126 / 4829	ICGC_Nficsc81335_targets
9	2e−02	122 / 4682	ICGC_Pol24_targets
10	3e−02	126 / 4879	ICGC_Pmlsc71910_targets
11	3e−02	54 / 1878	ICGC_Cebpbsc150_targets
12	4e−02	121 / 4706	ICGC_Sp1_targets
13	6e−02	135 / 5408	ICGC_Pou2_targets
14	1e−01	1 / 5	MYC_Apoptosis UP
15	1e−01	1 / 5	MYC_Cell growth and proliferation UP
16	1e−01	1 / 5	MYC_TF and cofactors
17	1e−01	142 / 5890	ICGC_Elf1_targets
18	1e−01	133 / 5495	ICGC_Yy1_targets
19	1e−01	3 / 59	MYC_Targets UP
20	2e−01	1 / 8	MYC_Cell cycle UP

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	VAQUERIZAS_Skin
2	0.3	1 / 17	VAQUERIZAS_Heart
3	0.3	1 / 19	VAQUERIZAS_Tonsil
4	0.4	2 / 59	VAQUERIZAS_Whole blood
5	0.5	1 / 29	VAQUERIZAS_Smooth muscle
6	0.5	1 / 33	VAQUERIZAS_Prostate
7	0.6	1 / 37	VAQUERIZAS_Thymus
8	0.6	1 / 38	VAQUERIZAS_Testis
9	0.6	1 / 40	VAQUERIZAS_Thyroid
10	0.7	1 / 58	VAQUERIZAS_Lung
11	0.8	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 / 45	VAQUERIZAS_Uterus
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 / 7	VAQUERIZAS_Appendix
20	1.0	0 / 29	VAQUERIZAS_Fetal lung

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	6 / 114	PALMER_T−Cell signature up
2	0.20	1 / 10	WIRTH_Thalamus
3	0.24	1 / 12	WIRTH_Cerebellum
4	0.24	7 / 225	PALMER_Granulocytes signature up
5	0.53	8 / 350	WIRTH_Immune system
6	0.81	3 / 194	PALMER_B−Cell signature up
7	0.90	5 / 350	WIRTH_Nervous System
8	1.00	0 / 32	WIRTH_Pancreas
9	1.00	0 / 11	WIRTH_Sec. lymphoid organs
10	1.00	0 / 11	WIRTH_Prim. lymphoid organs
11	1.00	0 / 13	WIRTH_B−cells
12	1.00	0 / 8	WIRTH_Tonsil
13	1.00	0 / 12	WIRTH_Thymus
14	1.00	0 / 12	WIRTH_Lymphocytes
15	1.00	0 / 5	WIRTH_Bone marrow
16	1.00	0 / 11	WIRTH_Globus pallidus
17	1.00	0 / 14	WIRTH_Telencephalon
18	1.00	0 / 11	WIRTH_Cortex cerebri
19	1.00	0 / 10	WIRTH_Hippocampus
20	1.00	0 / 107	WIRTH_Testis

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	29 / 1115	LU_BPDE 1h DN
2	1.0	68 / 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	

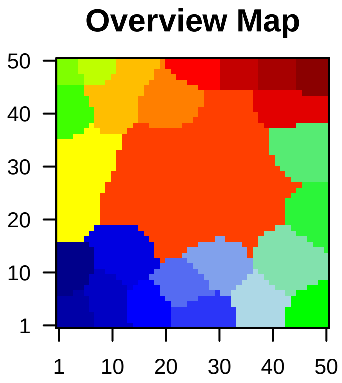
K−Means Clusters

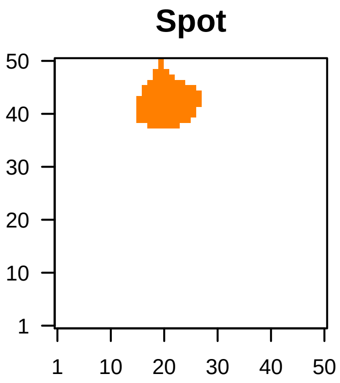
Spot Summary: G

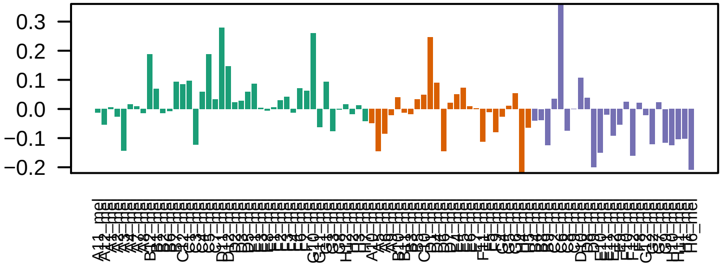
metagenes = 99
genes = 321

<r> metagenes = 0.81
<r> genes = 0.06
beta: r2= 0.61 / log p= −Inf

samples with spot = 7 (7.6 %)
MSC1 : 5 (11.9 %)
MSC2 : 1 (4 %)
MSC3 : 1 (4 %)





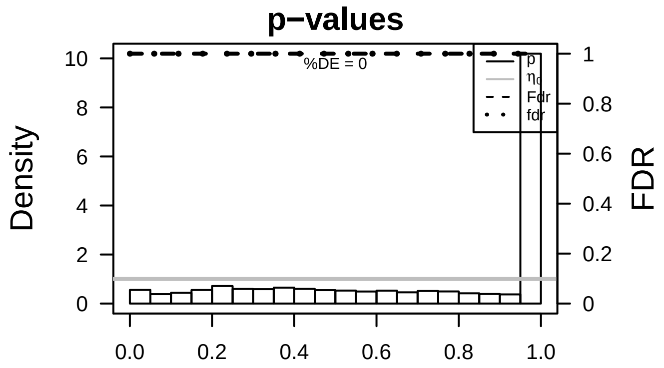


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	SLC25A21	1.95	−0.08	0.49	SLC25A21	solute carrier family 25 (mitochondrial oxoadipate carrier), me
2	KLHL32	1.89	−0.06	0.37	KLHL32	kelch−like family member 32 [Source:HGNC Symbol;Acc:HGI
3	ERI2	1.89	−0.37	0.35	ERI2	ERI1 exoribonuclease family member 2 [Source:HGNC Symb
4	SHQ1	1.79	−0.67	0.29	SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor [Source:HG
5	MPP3	1.79	−0.19	0.22	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily m
6	CRISPLD1	1.78	−0.25	0.28	CRISPLD1	cysteine−rich secretory protein LCCL domain containing 1 [S
7	USP41	1.78	−0.26	0.29	USP41	ubiquitin specific peptidase 41 [Source:HGNC Symbol;Acc:H
8	RFX2	1.78	−0.41	0.34	RFX2	regulatory factor X, 2 (influences HLA class II expression) [Sc
9	AURKC	1.77	−0.17	0.31	AURKC	aurora kinase C [Source:HGNC Symbol;Acc:HGNC:11391]
10	FAXC	1.75	−0.16	0.43	FAXC	failed axon connections homolog (Drosophila) [Source:HGNC
11	DISP2	1.71	−0.05	0.31	DISP2	dispatched homolog 2 (Drosophila) [Source:HGNC Symbol;A
12	GPRC5D	1.69	−0.02	0.4	GPRC5D	G protein−coupled receptor, class C, group 5, member D [Sou
13	AP3M2	1.69	−0.65	0.34	AP3M2	adaptor−related protein complex 3, mu 2 subunit [Source:HGI
14	LPAR2	1.66	−0.05	0.33	LPAR2	lysophosphatidic acid receptor 2 [Source:HGNC Symbol;Acc:
15	ZNF438	1.65	−0.08	0.38	ZNF438	zinc finger protein 438 [Source:HGNC Symbol;Acc:HGNC:21
16	UCN2	1.65	−0.02	0.37	UCN2	urocortin 2 [Source:HGNC Symbol;Acc:HGNC:18414]
17	DISP1	1.64	−0.17	0.29	DISP1	dispatched homolog 1 (Drosophila) [Source:HGNC Symbol;A
18	ZNF823	1.63	−0.26	0.26	ZNF823	zinc finger protein 823 [Source:HGNC Symbol;Acc:HGNC:30
19	TXNRD3	1.63	−0.07	0.27	TXNRD3	thioredoxin reductase 3 [Source:HGNC Symbol;Acc:HGNC:2
20	LRRC6	1.62	−0.12	0.25	LRRC6	leucine rich repeat containing 6 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−07	243 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	2e−06	35 / 687	Chr	Chr 6
3	3e−05	186 / 6929	Lymp	HOPP_Txn_elongation
4	3e−05	200 / 7592	Lymp	HOPP_Active_promoter
5	3e−05	164 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	5e−05	238 / 9482	Colon	TssA_Colon
7	8e−05	145 / 5184	Lymp	HOPP_Txn_transition
8	7e−04	17 / 322	BP	mitochondrion organization
9	7e−04	12 / 184	GSE	REACTOME_HIV_INFECTION
10	7e−04	223 / 9027	Colon	Tx_Colon
11	9e−04	222 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
12	9e−04	213 / 8580	Colon	TxWk_Colon
13	1e−03	29 / 724	GSE	PUJANA_CHEK2_PCC_NETWORK
14	1e−03	32 / 840	GSE	GEORGES_TARGETS_OF_MIR192_AND_MIR215
15	1e−03	247 / 10290	Colon	TssWk_Colon
16	1e−03	3 / 11	BP	motile cilium assembly
17	2e−03	11 / 177	GSE	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA
18	2e−03	5 / 41	GSE	KEGG_PROTEASOME
19	2e−03	4 / 25	MF	ATP−dependent helicase activity
20	2e−03	3 / 12	CC	transcription export complex
21	2e−03	37 / 1050	Brain	Fetal_EnhP
22	3e−03	7 / 87	miRN	hsa−miR−595
23	3e−03	4 / 28	BP	vesicle organization
24	3e−03	3 / 14	MF	phospholipase A2 activity
25	3e−03	219 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
26	3e−03	4 / 29	BP	sphingolipid biosynthetic process
27	3e−03	5 / 47	GSE	REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G
28	3e−03	17 / 376	GSE	OSMAN_BLADDER_CANCER_UP
29	4e−03	3 / 15	BP	Golgi to plasma membrane transport
30	4e−03	4 / 30	GSE	YANG_BREAST_CANCER_ESR1_LASER_UP
31	4e−03	20 / 478	GSE	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
32	4e−03	24 / 619	GSE	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
33	4e−03	2 / 5	miRN	hsa−miR−1268
34	5e−03	12 / 233	GSE	PENG_RAPAMYCIN_RESPONSE_DN
35	5e−03	18 / 422	BP	viral process
36	5e−03	146 / 5693	Lymp	HOPP_Weak_enhancer
37	5e−03	35 / 1033	MF	nucleic acid binding
38	6e−03	19 / 462	Chr	Chr 14
39	6e−03	11 / 209	GSE	BROWNE_HCMV_INFECTION_16HR_UP
40	6e−03	10 / 181	GSE	PENG_LEUCINE_DEPRIVATION_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.6	2 / 100	HORVATH_aging_genes meth DOWN
3	0.7	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	7e−04	17 / 322	mitochondrion organization
2	1e−03	3 / 11	motile cilium assembly
3	3e−03	4 / 28	vesicle organization
4	3e−03	4 / 29	sphingolipid biosynthetic process
5	4e−03	3 / 15	Golgi to plasma membrane transport
6	5e−03	18 / 422	viral process
7	6e−03	22 / 570	symbiosis, encompassing mutualism through parasitism
8	7e−03	5 / 55	regulation of cell migration
9	7e−03	9 / 155	ubiquitin−dependent protein catabolic process
10	8e−03	8 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
11	9e−03	3 / 20	triglyceride metabolic process
12	1e−02	50 / 1664	transcription, DNA−templated
13	1e−02	5 / 62	DNA damage response, signal transduction by p53 class mediator resulting in
14	1e−02	11 / 229	RNA splicing
15	1e−02	41 / 1325	catabolic process
16	1e−02	5 / 64	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
17	1e−02	3 / 23	spliceosomal complex assembly
18	1e−02	4 / 44	DNA duplex unwinding
19	2e−02	5 / 68	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
20	2e−02	5 / 69	transcription elongation from RNA polymerase II promoter

Brain

Rank	p−value	#in/all	Geneset
1	5e−07	243 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−05	164 / 5940	Overlap_fetal_midbrain_HetRpts
3	9e−04	222 / 9013	Overlap_fetal_midbrain_K9K27me3
4	2e−03	37 / 1050	Fetal_EnhP
5	3e−03	219 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	7e−03	227 / 9528	Overlap_fetal_midbrain_Quies
7	7e−03	9 / 158	Overlap_fetal_midbrain_Het
8	1e−01	10 / 304	Fetal_Het
9	2e−01	15 / 564	Mid_Frontal_Lobe_EnhP
10	2e−01	72 / 3081	Mid_Frontal_Lobe_ZNF
11	3e−01	27 / 1122	Fetal_K9K27me3
12	3e−01	20 / 831	Fetal_HetRpts
13	3e−01	9 / 349	Fetal_ZNF
14	4e−01	42 / 1845	Fetal_Quies
15	4e−01	18 / 769	Overlap_fetal_midbrain_ZNF
16	5e−01	22 / 989	Mid_Frontal_Lobe_Quies
17	5e−01	19 / 884	Overlap_fetal_midbrain_EnhG
18	6e−01	52 / 2462	Mid_Frontal_Lobe_HetRpts
19	6e−01	22 / 1065	Overlap_fetal_midbrain_Enh
20	7e−01	13 / 656	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 7	GENTLES_modul18
2	0.2	1 / 12	LIU_PROSTATE_CANCER_UP
3	0.3	4 / 121	PanCan_MAPK_geneset_nanostring
4	0.3	1 / 15	GENTLES_modul10
5	0.3	1 / 15	GENTLES_modul11
6	0.3	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.4	2 / 61	PanCan_Wnt_geneset_nanostring
8	0.4	1 / 22	PanCan_HH_geneset_nanostring
9	0.4	0 / 14	LIU_COMMON_CANCER_GENES
10	0.4	3 / 111	PanCan_RAS_geneset_nanostring
11	0.5	1 / 29	KUIPER_MM good survival
12	0.5	4 / 180	SPANG_LPS−index2
13	0.6	1 / 40	PanCan_HK_geneset_nanostring
14	0.6	10 / 489	Lembcke_Normal vs Adenoma
15	0.6	1 / 44	PanCan_TGF−B_geneset_nanostring
16	0.6	1 / 47	PanCan_DNARepair_geneset_nanostring
17	0.7	1 / 48	KUIPER_MM poor survival
18	0.7	2 / 113	PanCan_Driver_Gene_geneset_nanostring
19	0.7	2 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.7	0 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	0.002	3 / 12	transcription export complex
2	0.006	237 / 9988	organelle
3	0.008	73 / 2577	nucleoplasm
4	0.008	5 / 57	proteasome complex
5	0.010	248 / 10605	intracellular
6	0.013	143 / 5696	nucleus
7	0.027	6 / 106	trans−Golgi network
8	0.031	2 / 13	pseudopodium
9	0.036	2 / 14	trans−Golgi network transport vesicle
10	0.041	2 / 15	BAF−type complex
11	0.046	2 / 16	vacuolar membrane
12	0.046	6 / 120	mitochondrial outer membrane
13	0.051	2 / 17	integral component of mitochondrial outer membrane
14	0.051	2 / 17	proteasome accessory complex
15	0.057	2 / 18	proteasome core complex
16	0.058	3 / 41	mitochondrial respiratory chain complex I
17	0.069	2 / 20	retromer complex
18	0.075	2 / 21	transcription factor TFIID complex
19	0.076	7 / 170	nuclear speck
20	0.081	2 / 22	mitochondrial large ribosomal subunit

Chr

Rank	p−value	#in/all	Geneset
1	2e−06	35 / 687	Chr 6
2	6e−03	19 / 462	Chr 14
3	3e−02	13 / 335	Chr 22
4	4e−02	26 / 838	Chr 3
5	9e−02	28 / 993	Chr 2
6	2e−01	13 / 469	Chr 8
7	3e−01	17 / 689	Chr 7
8	3e−01	6 / 221	Chr 18
9	4e−01	24 / 1037	Chr 19
10	4e−01	18 / 775	Chr 12
11	4e−01	13 / 558	Chr 4
12	6e−01	3 / 151	Chr 21
13	7e−01	11 / 552	Chr 10
14	8e−01	8 / 465	Chr 15
15	8e−01	4 / 262	Chr 13
16	8e−01	12 / 696	Chr 5
17	9e−01	8 / 576	Chr 9
18	9e−01	5 / 398	Chr 20
19	9e−01	9 / 649	Chr 16
20	1e+00	12 / 840	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−05	238 / 9482	TssA_Colon
2	7e−04	223 / 9027	Tx_Colon
3	9e−04	213 / 8580	TxWk_Colon
4	1e−03	247 / 10290	TssWk_Colon
5	1e−02	100 / 3812	TssD1_Colon
6	3e−02	100 / 3897	Quies1_Colon
7	4e−02	198 / 8415	Quies3_Colon
8	6e−02	23 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	1e−01	28 / 1038	HetRpts_Colon
10	1e−01	166 / 7203	TssF_Colon
11	2e−01	2 / 33	Marisa_CRC−cluster−e
12	2e−01	1 / 9	TCGA−CRC_agressive−disease−markers
13	2e−01	35 / 1386	Het_Colon
14	2e−01	12 / 427	Quies2_Colon
15	3e−01	1 / 15	Budinska_B_Lower crypt−like_UP
16	3e−01	15 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
17	3e−01	1 / 17	Vilar_mutated−in−CRC−CamP
18	3e−01	5 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
19	3e−01	64 / 2798	TxEnhG1_Colon
20	3e−01	10 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.3	11 / 435	GUDJ_psoriasis up
2	0.4	1 / 20	BCHETNIA_EBM−DM up
3	0.8	5 / 294	GUDJ_psoriasis down
4	1.0	0 / 11	BCHETNIA_EBM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.06	2 / 18	Barbus_GBM_STS_vs._LTS
2	0.08	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
3	0.09	2 / 23	WIRTH_PN subtype
4	0.09	3 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
5	0.11	2 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
6	0.14	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
7	0.15	23 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.16	3 / 63	Stuehler_Proteins_up_in_STS
9	0.17	3 / 65	GIEZELT_GBM_STS_up_VS_LTS
10	0.18	3 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
11	0.19	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
12	0.21	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
13	0.22	3 / 75	Weller_LGG_A_vs_O_DOWN
14	0.23	1 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
15	0.27	2 / 47	Weller_LGG_gradeII−vs−III_UP
16	0.27	2 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
17	0.29	9 / 332	Up
18	0.30	1 / 16	KIM deleted & downregulated in LTS
19	0.33	1 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
20	0.37	3 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	12 / 184	REACTOME_HIV_INFECTION
2	1e−03	29 / 724	PUJANA_CHEK2_PCC_NETWORK
3	1e−03	32 / 840	GEORGES_TARGETS_OF_MIR192_AND_MIR215
4	2e−03	11 / 177	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA
5	2e−03	5 / 41	KEGG_PROTEASOME
6	3e−03	5 / 47	REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G
7	3e−03	17 / 376	OSMAN_BLADDER_CANCER_UP
8	4e−03	4 / 30	YANG_BREAST_CANCER_ESR1_LASER_UP
9	4e−03	20 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
10	4e−03	24 / 619	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
11	5e−03	12 / 233	PENG_RAPAMYCIN_RESPONSE_DN
12	6e−03	11 / 209	BROWNE_HCMV_INFECTION_16HR_UP
13	6e−03	10 / 181	PENG_LEUCINE_DEPRIVATION_DN
14	7e−03	5 / 55	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C
15	7e−03	2 / 6	HE_PTEN_TARGETS_DN
16	7e−03	15 / 337	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
17	7e−03	13 / 275	GRADE_COLON_AND_RECTAL_CANCER_UP
18	7e−03	16 / 373	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
19	8e−03	25 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
20	8e−03	5 / 58	REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS

HM

Rank	p−value	#in/all	Geneset
1	0.008	10 / 188	HALLMARK_MYC_TARGETS_V1
2	0.066	8 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	0.088	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.094	2 / 24	HALLMARK_PANCREAS_BETA_CELLS
5	0.114	7 / 188	HALLMARK_ADIPOGENESIS
6	0.187	5 / 140	HALLMARK_INFLAMMATORY_RESPONSE
7	0.190	5 / 141	HALLMARK_FATTY_ACID_METABOLISM
8	0.270	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.291	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.388	4 / 146	HALLMARK_UV_RESPONSE_UP
11	0.434	1 / 26	HALLMARK_ANGIOGENESIS
12	0.470	1 / 29	HALLMARK_NOTCH_SIGNALING
13	0.499	4 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.515	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
15	0.520	3 / 127	HALLMARK_KRAS_SIGNALING_DN
16	0.521	4 / 174	HALLMARK_HEME_METABOLISM
17	0.545	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
18	0.589	2 / 91	HALLMARK_PROTEIN_SECRETION
19	0.589	2 / 91	HALLMARK_BILE_ACID_METABOLISM
20	0.601	2 / 93	HALLMARK_PEROXISOME

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	3e−05	186 / 6929	HOPP_Txn_elongation
2	3e−05	200 / 7592	HOPP_Active_promoter
3	8e−05	145 / 5184	HOPP_Txn_transition
4	5e−03	146 / 5693	HOPP_Weak_enhancer
5	7e−03	178 / 7209	HOPP_Weak_promoter
6	1e−02	162 / 6564	HOPP_Strong_enhancer
7	4e−02	2 / 14	Subero_MCL_hyper_meth
8	8e−02	5 / 107	SPANG_LPS 6hrs UP
9	1e−01	9 / 268	SPANG_IL21 UP
10	1e−01	30 / 1128	SPANG_BCR DN
11	1e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
12	1e−01	32 / 1218	SPANG_BCR UP
13	2e−01	129 / 5538	HOPP_Weak_txn
14	2e−01	1 / 8	Subero_B−CLL_hypo_meth
15	2e−01	4 / 109	ROSOLOWSKI_green total
16	2e−01	2 / 40	Subero_mBL_hyper_meth
17	2e−01	1 / 13	WRIGHT_GCB UP
18	2e−01	1 / 13	Subero_MCL_hypo_meth
19	2e−01	3 / 80	Aukema_BCL2 DN_BCL6 UP
20	3e−01	8 / 280	SPANG_CD40 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	4 / 25	ATP−dependent helicase activity
2	0.003	3 / 14	phospholipase A2 activity
3	0.005	35 / 1033	nucleic acid binding
4	0.011	9 / 167	helicase activity
5	0.016	58 / 2037	DNA binding
6	0.019	5 / 71	ubiquitin−specific protease activity
7	0.019	2 / 10	type I transforming growth factor beta receptor binding
8	0.024	3 / 29	ATP−dependent DNA helicase activity
9	0.027	2 / 12	poly(A) binding
10	0.031	2 / 13	protein kinase C activity
11	0.036	2 / 14	apolipoprotein binding
12	0.041	2 / 15	ARF guanyl−nucleotide exchange factor activity
13	0.045	3 / 37	DNA−directed RNA polymerase activity
14	0.046	2 / 16	phosphatidylinositol−3,4−bisphosphate binding
15	0.046	30 / 1007	poly(A) RNA binding
16	0.051	6 / 123	nucleotidyltransferase activity
17	0.052	3 / 39	RNA polymerase II transcription regulatory region sequence−specific DNA bir
18	0.055	3 / 40	NADH dehydrogenase (ubiquinone) activity
19	0.057	2 / 18	threonine−type endopeptidase activity
20	0.063	208 / 8984	protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	7 / 87	hsa−miR−595
2	0.004	2 / 5	hsa−miR−1268
3	0.007	2 / 6	hsa−miR−523
4	0.007	12 / 243	hsa−miR−122
5	0.007	6 / 79	hsa−miR−542−3p
6	0.012	13 / 294	hsa−miR−561
7	0.013	3 / 23	hsa−miR−24−1*
8	0.017	6 / 95	hsa−miR−888
9	0.018	9 / 182	hsa−miR−374a
10	0.019	8 / 154	hsa−miR−139−5p
11	0.020	9 / 186	hsa−miR−586
12	0.021	8 / 157	hsa−miR−512−3p
13	0.032	6 / 110	hsa−miR−491−3p
14	0.035	10 / 239	hsa−miR−152
15	0.037	4 / 58	hsa−miR−219−1−3p
16	0.041	4 / 60	hsa−miR−1200
17	0.048	3 / 38	hsa−miR−1258
18	0.057	4 / 67	hsa−miR−1246
19	0.065	4 / 70	hsa−miR−502−5p
20	0.068	5 / 101	hsa−miR−325

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 / 13	BENTINK_src.10
4	1.0	0 / 12	GUSTAFSON_PI3K_UP
5	1.0	0 / 13	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.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	0.05	21 / 653	ICGC_SrfPcr2_targets
2	0.05	34 / 1171	KIM_MYC targets
3	0.16	43 / 1701	HEBENSTREIT_high expression TF
4	0.18	1 / 9	MYC_RNA processing binding UP
5	0.20	52 / 2136	ICGC_GabpPcr2_targets
6	0.20	52 / 2137	ICGC_SrfV0416101_targets
7	0.33	55 / 2391	ICGC_Pbx3_targets
8	0.37	32 / 1383	ICGC_Six5_targets
9	0.40	32 / 1400	ICGC_Myc_targets
10	0.41	14 / 595	ICGC_NrsfPcr2_targets
11	0.43	89 / 4032	ICGC_Creb1_targets
12	0.48	107 / 4909	ICGC_Stat5_targets
13	0.50	25 / 1139	HEBENSTREIT_low expression TF
14	0.50	59 / 2714	ICGC_Irf4_targets
15	0.53	15 / 690	ICGC_Atf3_targets
16	0.54	127 / 5890	ICGC_Elf1_targets
17	0.56	85 / 3966	ICGC_Pu1_targets
18	0.56	112 / 5219	ICGC_Tcf3_targets
19	0.56	28 / 1314	ICGC_Usf1_targets
20	0.57	40 / 1878	ICGC_Cebpbsc150_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.009	4 / 38	VAQUERIZAS_Testis
2	0.039	4 / 59	VAQUERIZAS_Whole blood
3	0.055	3 / 40	VAQUERIZAS_Thyroid
4	0.108	2 / 26	VAQUERIZAS_Liver
5	0.115	2 / 27	VAQUERIZAS_Lymph node
6	0.159	2 / 33	VAQUERIZAS_Prostate
7	0.190	2 / 37	VAQUERIZAS_Thymus
8	0.214	1 / 11	VAQUERIZAS_Fetal liver
9	0.222	2 / 41	VAQUERIZAS_Placenta
10	0.280	1 / 15	VAQUERIZAS_Bone marrow
11	0.280	1 / 15	VAQUERIZAS_Fetal thyroid
12	0.358	2 / 58	VAQUERIZAS_Lung
13	0.395	1 / 23	VAQUERIZAS_Spinal cord
14	0.470	1 / 29	VAQUERIZAS_Smooth muscle
15	0.470	1 / 29	VAQUERIZAS_Fetal lung
16	0.545	1 / 36	VAQUERIZAS_Fetal brain
17	0.819	2 / 143	VAQUERIZAS_General
18	1.000	0 / 45	VAQUERIZAS_Uterus
19	1.000	0 / 9	VAQUERIZAS_Kidney
20	1.000	0 / 38	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	5 / 114	PALMER_T−Cell signature up
2	0.2	4 / 95	WIRTH_Muscle
3	0.2	4 / 107	WIRTH_Testis
4	0.2	1 / 11	WIRTH_Cortex cerebri
5	0.2	1 / 12	WIRTH_Cerebellum
6	0.5	1 / 32	WIRTH_Pancreas
7	0.6	1 / 46	WIRTH_Liver
8	0.7	4 / 225	PALMER_Granulocytes signature up
9	0.8	6 / 350	WIRTH_Nervous System
10	0.8	3 / 194	PALMER_B−Cell signature up
11	0.8	1 / 74	WIRTH_Mucosa
12	1.0	3 / 350	WIRTH_Immune system
13	1.0	0 / 11	WIRTH_Sec. lymphoid organs
14	1.0	0 / 11	WIRTH_Prim. lymphoid organs
15	1.0	0 / 13	WIRTH_B−cells
16	1.0	0 / 8	WIRTH_Tonsil
17	1.0	0 / 12	WIRTH_Thymus
18	1.0	0 / 12	WIRTH_Lymphocytes
19	1.0	0 / 5	WIRTH_Bone marrow
20	1.0	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	82 / 3682	LU_BPDE 0.005 DN
2	0.9	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	

K−Means Clusters

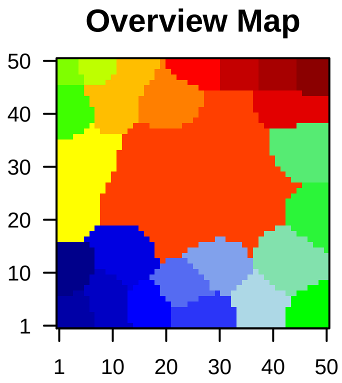
Spot Summary: H

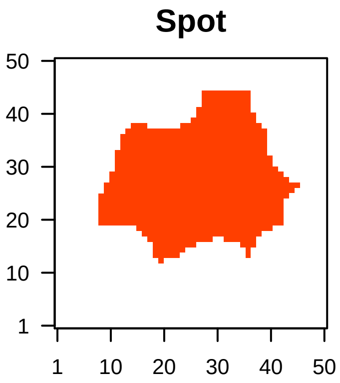
metagenes = 732
genes = 2434

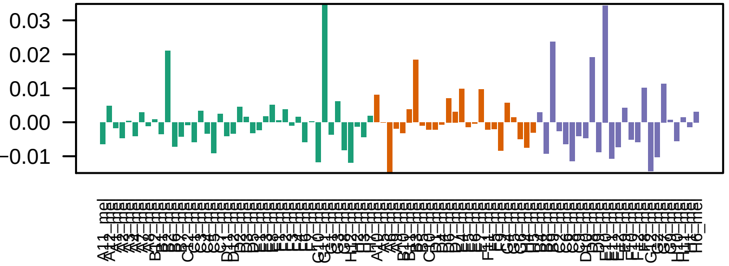
<r> metagenes = 0.04

beta: r2= 0.04 / log p= −1.18

samples with spot = 0 (0 %)





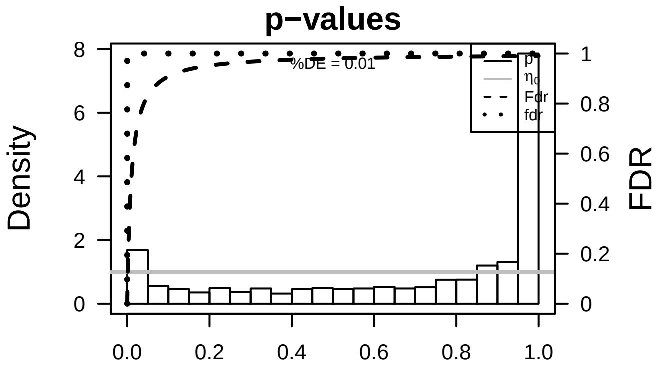


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TTR	2.58	−0.06	0.41	TTR	transthyretin [Source:HGNC Symbol;Acc:HGNC:12405]
2	OPHN1	2.4	−0.43	0.41	OPHN1	oligophrenin 1 [Source:HGNC Symbol;Acc:HGNC:8148]
3	CACNA2D1	2.14	−0.28	0.44	CACNA2D1	calcium channel, voltage−dependent, alpha 2/delta subunit 1
4	MGP	2.08	−0.05	0.39	MGP	matrix Gla protein [Source:HGNC Symbol;Acc:HGNC:7060]
5	RDH12	2.07	−0.08	0.56	RDH12	retinol dehydrogenase 12 (all−trans/9−cis/11−cis) [Source:HG
6	RORA	2.04	−0.07	0.7	RORA	RAR−related orphan receptor A [Source:HGNC Symbol;Acc:
7	CADPS	2.03	−0.06	0.23	CADPS	Ca++−dependent secretion activator [Source:HGNC Symbol;
8	FBLN5	2.02	−0.06	0.46	FBLN5	fibulin 5 [Source:HGNC Symbol;Acc:HGNC:3602]
9	LRRIQ1	1.99	−0.05	0.56	LRRIQ1	leucine−rich repeats and IQ motif containing 1 [Source:HGN
10	UBB	1.97	−0.09	0.41	UBB	ubiquitin B [Source:HGNC Symbol;Acc:HGNC:12463]
11	RIBC1	1.95	−0.05	0.53	RIBC1	RIB43A domain with coiled−coils 1 [Source:HGNC Symbol;A
12	ZFR2	1.92	−0.07	0.47	ZFR2	zinc finger RNA binding protein 2 [Source:HGNC Symbol;Acc
13	TGFB3	1.9	−0.05	0.32	TGFB3	transforming growth factor, beta 3 [Source:HGNC Symbol;Ac
14	S100A6	1.89	−0.08	0.64	S100A6	S100 calcium binding protein A6 [Source:HGNC Symbol;Acc:
15	ZNF583	1.87	−0.02	0.65	ZNF583	zinc finger protein 583 [Source:HGNC Symbol;Acc:HGNC:26
16	TRPV2	1.85	−0.03	0.21	TRPV2	transient receptor potential cation channel, subfamily V, mem
17	ZCCHC18	1.85	−0.02	0.6	ZCCHC18	zinc finger, CCHC domain containing 18 [Source:HGNC Sym
18	IKZF4	1.85	−0.22	0.34	IKZF4	IKAROS family zinc finger 4 (Eos) [Source:HGNC Symbol;Ac
19	KMO	1.85	−0.03	0.45	KMO	kynurenine 3−monooxygenase (kynurenine 3−hydroxylase) [S
20	PLAC1	1.84	−0.03	0.44	PLAC1	placenta−specific 1 [Source:HGNC Symbol;Acc:HGNC:9044]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	716 / 2142	Colon	ReprPC_Colon
2	3e−86	682 / 2159	Colon	TssP_Colon
3	8e−85	620 / 1889	Colon	ReprPCWk_Colon
4	6e−83	926 / 3396	Lymp	HOPP_Repressed
5	7e−76	471 / 1317	Colon	EnhP_Colon
6	2e−60	415 / 1207	Brain	Overlap_fetal_midbrain_TssF
7	8e−54	319 / 862	Brain	Overlap_fetal_midbrain_TxTrans
8	4e−53	273 / 686	Brain	Overlap_fetal_midbrain_TssA
9	8e−40	279 / 812	Brain	Mid_Frontal_Lobe_TssP
10	5e−39	352 / 1139	TF	HEBENSTREIT_low expression TF
11	3e−35	142 / 312	GSE	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
12	1e−33	244 / 720	GSE	BENPORATH_ES_WITH_H3K27ME3
13	3e−33	105 / 199	GSE	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
14	4e−33	700 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
15	3e−32	548 / 2188	Lymp	HOPP_Poised_promoter
16	5e−32	547 / 2185	Brain	Fetal_TssA
17	2e−28	172 / 468	Brain	Mid_Frontal_Lobe_TssF
18	6e−26	693 / 3088	CC	plasma membrane
19	2e−25	162 / 452	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	2e−25	113 / 264	GSE	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
21	2e−24	146 / 396	GSE	BENPORATH_PRC2_TARGETS
22	1e−23	97 / 217	GSE	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
23	5e−23	96 / 217	MF	G−protein coupled receptor activity
24	8e−23	208 / 674	GSE	BENPORATH_SUZ12_TARGETS
25	3e−22	458 / 1907	Brain	Fetal_TxTrans
26	5e−22	217 / 724	GSE	BENPORATH_EED_TARGETS
27	4e−21	139 / 395	GSE	MARTENS_TRETINOIN_RESPONSE_UP
28	4e−21	260 / 936	GSE	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
29	3e−20	137 / 394	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
30	1e−19	646 / 2984	CC	integral component of membrane
31	2e−19	186 / 616	GSE	NABA_MATRISOME
32	7e−19	98 / 250	Colon	K9K27me3_Colon
33	4e−18	212 / 751	CC	integral component of plasma membrane
34	6e−17	158 / 519	BP	cell−cell signaling
35	7e−17	116 / 338	BP	G−protein coupled receptor signaling pathway
36	1e−16	115 / 336	BP	neurological system process
37	3e−16	110 / 319	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
38	4e−16	168 / 574	Brain	Overlap_fetal_midbrain_TssP
39	2e−15	78 / 198	GSE	REACTOME_GPCR_LIGAND_BINDING
40	5e−15	226 / 866	MF	signal transducer activity



Aging

Rank	p−value	#in/all	Geneset
1	0.01	12 / 38	TESCHENDORFF_age_hypermethylated
2	0.24	21 / 111	HORVATH_aging_genes meth UP
3	0.55	16 / 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	6e−17	158 / 519	cell−cell signaling
2	7e−17	116 / 338	G−protein coupled receptor signaling pathway
3	1e−16	115 / 336	neurological system process
4	2e−13	81 / 225	ion transport
5	2e−11	38 / 78	regulation of ion transmembrane transport
6	5e−11	163 / 626	cell adhesion
7	5e−10	49 / 126	homophilic cell adhesion via plasma membrane adhesion molecules
8	8e−09	15 / 20	calcium ion−dependent exocytosis of neurotransmitter
9	1e−08	68 / 216	immune response
10	2e−08	13 / 16	regulation of calcium ion−dependent exocytosis
11	3e−08	80 / 275	synaptic transmission
12	5e−08	29 / 65	potassium ion transmembrane transport
13	8e−07	60 / 202	inflammatory response
14	1e−06	432 / 2210	anatomical structure development
15	2e−06	15 / 26	detection of chemical stimulus involved in sensory perception of smell
16	1e−05	18 / 39	neuropeptide signaling pathway
17	1e−05	12 / 20	detection of chemical stimulus involved in sensory perception of bitter taste
18	1e−05	17 / 36	synaptic vesicle exocytosis
19	2e−05	25 / 67	positive regulation of cytosolic calcium ion concentration
20	3e−05	52 / 186	ion transmembrane transport

Brain

Rank	p−value	#in/all	Geneset
1	2e−60	415 / 1207	Overlap_fetal_midbrain_TssF
2	8e−54	319 / 862	Overlap_fetal_midbrain_TxTrans
3	4e−53	273 / 686	Overlap_fetal_midbrain_TssA
4	8e−40	279 / 812	Mid_Frontal_Lobe_TssP
5	4e−33	700 / 2972	Mid_Frontal_Lobe_ReprPC
6	5e−32	547 / 2185	Fetal_TssA
7	2e−28	172 / 468	Mid_Frontal_Lobe_TssF
8	3e−22	458 / 1907	Fetal_TxTrans
9	4e−16	168 / 574	Overlap_fetal_midbrain_TssP
10	1e−14	358 / 1548	Mid_Frontal_Lobe_K9K27me3
11	2e−13	82 / 229	Mid_Frontal_Lobe_TxTrans
12	6e−13	65 / 166	Mid_Frontal_Lobe_Tx
13	2e−11	145 / 534	Mid_Frontal_Lobe_EnhG
14	2e−10	411 / 1949	Fetal_TssF
15	4e−10	109 / 383	Fetal_Tx
16	7e−10	277 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	3e−08	53 / 156	Mid_Frontal_Lobe_TssA
18	9e−07	28 / 69	Overlap_fetal_midbrain_Tx
19	8e−05	144 / 668	Mid_Frontal_Lobe_Enh
20	7e−04	196 / 989	Mid_Frontal_Lobe_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	3e−08	107 / 401	Lembcke_Colonic Inflammation
2	5e−02	7 / 22	PanCan_HH_geneset_nanostring
3	7e−02	24 / 111	PanCan_RAS_geneset_nanostring
4	9e−02	3 / 7	GENTLES_modul18
5	1e−01	14 / 61	PanCan_Wnt_geneset_nanostring
6	1e−01	25 / 121	PanCan_MAPK_geneset_nanostring
7	1e−01	4 / 12	LIU_BREAST_CANCER
8	2e−01	17 / 82	PanCan_TXmisReg_geneset_nanostring
9	2e−01	30 / 156	PanCan_PI3K_geneset_nanostring
10	2e−01	2 / 5	WANG_ER_DN
11	2e−01	3 / 10	GENTLES_modul13
12	2e−01	4 / 15	WANG_ER_UP
13	2e−01	4 / 15	GENTLES_modul11
14	3e−01	11 / 55	PanCan_JAK−ST_geneset_nanostring
15	3e−01	4 / 18	PanCan_Notch_geneset_nanostring
16	5e−01	2 / 14	LIU_LIVER_CANCER
17	5e−01	2 / 11	GENTLES_modul17
18	6e−01	1 / 14	LIU_PROSTATE_CANCER_DN
19	8e−01	2 / 16	GENTLES_modul7
20	8e−01	6 / 48	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	6e−26	693 / 3088	plasma membrane
2	1e−19	646 / 2984	integral component of membrane
3	4e−18	212 / 751	integral component of plasma membrane
4	3e−09	186 / 775	extracellular space
5	3e−09	17 / 24	keratin filament
6	2e−07	24 / 51	voltage−gated potassium channel complex
7	7e−07	88 / 332	cell junction
8	2e−06	46 / 144	postsynaptic membrane
9	3e−06	588 / 3132	extracellular region
10	7e−06	65 / 239	proteinaceous extracellular matrix
11	3e−05	9 / 13	MHC class II protein complex
12	1e−04	10 / 18	voltage−gated calcium channel complex
13	2e−04	7 / 10	connexon complex
14	7e−04	21 / 64	anchored component of membrane
15	2e−03	32 / 119	external side of plasma membrane
16	2e−03	17 / 51	collagen trimer
17	2e−03	14 / 39	endocytic vesicle membrane
18	3e−03	27 / 99	receptor complex
19	3e−03	7 / 14	anchored component of external side of plasma membrane
20	4e−03	56 / 246	dendrite

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	220 / 1037	Chr 19
2	9e−05	122 / 551	Chr X
3	1e−01	147 / 840	Chr 17
4	1e−01	72 / 398	Chr 20
5	2e−01	113 / 649	Chr 16
6	3e−01	45 / 262	Chr 13
7	3e−01	38 / 221	Chr 18
8	4e−01	4 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
9	5e−01	55 / 335	Chr 22
10	5e−01	91 / 558	Chr 4
11	5e−01	25 / 151	Chr 21
12	6e−01	132 / 838	Chr 3
13	6e−01	126 / 801	Chr 11
14	7e−01	70 / 465	Chr 15
15	7e−01	106 / 696	Chr 5
16	8e−01	104 / 687	Chr 6
17	8e−01	104 / 689	Chr 7
18	8e−01	151 / 993	Chr 2
19	9e−01	65 / 469	Chr 8
20	9e−01	111 / 775	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	716 / 2142	ReprPC_Colon
2	3e−86	682 / 2159	TssP_Colon
3	8e−85	620 / 1889	ReprPCWk_Colon
4	7e−76	471 / 1317	EnhP_Colon
5	2e−25	162 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	3e−20	137 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
7	7e−19	98 / 250	K9K27me3_Colon
8	3e−16	110 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	3e−14	162 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
10	2e−13	85 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
11	1e−11	117 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
12	4e−09	91 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
13	1e−08	77 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	1e−06	59 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
15	1e−05	279 / 1386	Het_Colon
16	2e−05	90 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
17	2e−04	45 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
18	5e−04	606 / 3383	EnhWk2_Colon
19	1e−03	203 / 1038	HetRpts_Colon
20	2e−03	11 / 27	Pentrack_CRC_TCGA_corr_S_normal_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.03	7 / 20	BCHETNIA_EBM−DM up
2	0.41	49 / 294	GUDJ_psoriasis down
3	0.55	2 / 11	BCHETNIA_EBM up
4	0.76	65 / 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	4e−10	28 / 52	Sturm_GBM_Meth_overexpression_B_adult_UP
2	2e−05	27 / 74	WIRTH_Normal Brain
3	6e−05	17 / 40	in vivo astrocytes vs. cultured astroglia
4	1e−04	31 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	6e−04	17 / 47	Weller_LGG_gradeII−vs−III_UP
6	2e−03	14 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	2e−03	45 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
8	2e−03	20 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
9	7e−03	20 / 71	Weller_LGG_A_vs_O_UP
10	7e−03	75 / 356	Down_a
11	9e−03	11 / 32	Donson−innate immunity−associated with LTS in HGA
12	9e−03	14 / 45	Christensen_hypermethylated_in_primary_glioblastoma
13	1e−02	19 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	1e−02	11 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
15	2e−02	12 / 39	OPC
16	2e−02	28 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	3e−02	18 / 70	Weller_LGG_1p19qDel−vs−intact_UP
18	3e−02	19 / 75	GIEZELT_GBM_STS_down_VS_LTS
19	3e−02	10 / 33	Christensen_hypomethylated_in_primary_glioblastoma
20	5e−02	16 / 65	GIEZELT_GBM_STS_up_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−35	142 / 312	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
2	1e−33	244 / 720	BENPORATH_ES_WITH_H3K27ME3
3	3e−33	105 / 199	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
4	2e−25	113 / 264	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
5	2e−24	146 / 396	BENPORATH_PRC2_TARGETS
6	1e−23	97 / 217	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
7	8e−23	208 / 674	BENPORATH_SUZ12_TARGETS
8	5e−22	217 / 724	BENPORATH_EED_TARGETS
9	4e−21	139 / 395	MARTENS_TRETINOIN_RESPONSE_UP
10	4e−21	260 / 936	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
11	2e−19	186 / 616	NABA_MATRISOME
12	2e−15	78 / 198	REACTOME_GPCR_LIGAND_BINDING
13	1e−14	59 / 134	MEISSNER_BRAIN_HCP_WITH_H3K27ME3
14	3e−14	61 / 143	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
15	5e−13	56 / 132	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
16	5e−13	127 / 427	NABA_MATRISOME_ASSOCIATED
17	4e−11	203 / 823	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
18	1e−10	110 / 379	REACTOME_SIGNALING_BY_GPCR
19	2e−10	112 / 391	MEISSNER_NPC_HCP_WITH_H3K4ME2
20	2e−10	214 / 892	YOSHIMURA_MAPK8_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	7e−08	45 / 127	HALLMARK_KRAS_SIGNALING_DN
2	5e−05	38 / 126	HALLMARK_ALLOGRAFT_REJECTION
3	1e−04	12 / 24	HALLMARK_PANCREAS_BETA_CELLS
4	1e−03	37 / 140	HALLMARK_INFLAMMATORY_RESPONSE
5	1e−02	27 / 107	HALLMARK_COAGULATION
6	8e−02	34 / 167	HALLMARK_APICAL_JUNCTION
7	9e−02	14 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
8	1e−01	29 / 148	HALLMARK_KRAS_SIGNALING_UP
9	2e−01	7 / 31	HALLMARK_HEDGEHOG_SIGNALING
10	3e−01	30 / 165	HALLMARK_MYOGENESIS
11	3e−01	30 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
12	3e−01	6 / 29	HALLMARK_NOTCH_SIGNALING
13	4e−01	17 / 95	HALLMARK_SPERMATOGENESIS
14	4e−01	28 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	5e−01	28 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
16	5e−01	28 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
17	7e−01	25 / 169	HALLMARK_XENOBIOTIC_METABOLISM
18	8e−01	23 / 167	HALLMARK_IL2_STAT5_SIGNALING
19	8e−01	22 / 162	HALLMARK_COMPLEMENT
20	9e−01	4 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−04	21 / 62	DUMEAUX_Smoking enriched genes
2	3e−02	4 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
3	2e−01	5 / 18	DUMEAUX_High bmi enriched genes
4	2e−01	4 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	5e−01	2 / 10	DUMEAUX_Smoking literature genes up
6	6e−01	1 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
7	6e−01	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1e+00	1 / 32	DUMEAUX_Fasting enriched genes
9	1e+00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	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	6e−83	926 / 3396	HOPP_Repressed
2	3e−32	548 / 2188	HOPP_Poised_promoter
3	3e−06	17 / 33	LEE_Developmental_regulators
4	5e−05	479 / 2563	HOPP_Heterochrom
5	5e−03	61 / 275	TARTE_Mature plasma cell signature
6	8e−03	22 / 81	Subero_INT_hyper_meth
7	8e−03	13 / 40	Subero_mBL_hyper_meth
8	2e−02	12 / 39	ROSOLOWSKI_blue DOWN
9	2e−02	7 / 19	Subero_MM_hyper_meth
10	3e−02	23 / 96	Subero_DLBCL_hyper_meth
11	3e−02	13 / 47	Subero_FL_hyper_meth
12	4e−02	10 / 34	Subero_B−ALL_hyper_meth
13	5e−02	15 / 60	Subero_T−ALL_hyper_meth
14	5e−02	20 / 86	ROSOLOWSKI_red total
15	6e−02	7 / 23	DAVE_Immune response 1
16	8e−02	5 / 15	WRIGHT_ABC UP
17	1e−01	4 / 13	YAMANE_AICDA_targets_recruited
18	2e−01	3 / 10	DAVE_BL UP
19	2e−01	3 / 10	Shaknovich_ABC_hypo_meth
20	2e−01	9 / 43	LENZ_Stromal signature 2

MF

Rank	p−value	#in/all	Geneset
1	5e−23	96 / 217	G−protein coupled receptor activity
2	5e−15	226 / 866	signal transducer activity
3	6e−11	43 / 98	ion channel activity
4	2e−08	134 / 530	calcium ion binding
5	1e−07	34 / 85	transmembrane signaling receptor activity
6	2e−07	18 / 32	voltage−gated potassium channel activity
7	1e−06	31 / 81	serine−type endopeptidase activity
8	2e−06	15 / 26	olfactory receptor activity
9	4e−06	29 / 77	cytokine activity
10	6e−06	108 / 450	sequence−specific DNA binding
11	7e−06	155 / 695	transmembrane transporter activity
12	2e−05	14 / 27	chemokine activity
13	2e−05	21 / 52	hormone activity
14	4e−05	29 / 86	heme binding
15	1e−04	15 / 34	scavenger receptor activity
16	2e−04	15 / 35	clathrin binding
17	2e−04	11 / 22	delayed rectifier potassium channel activity
18	3e−04	8 / 13	taste receptor activity
19	3e−04	8 / 13	voltage−gated sodium channel activity
20	4e−04	10 / 20	potassium channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.3	3 / 11	hsa−miR−1180
2	0.3	6 / 30	hsa−miR−1293
3	0.4	4 / 19	hsa−miR−645
4	0.4	5 / 25	hsa−miR−100
5	0.4	2 / 8	hsa−miR−886−3p
6	0.5	2 / 10	hsa−miR−933
7	0.5	7 / 42	hsa−miR−642
8	0.5	6 / 36	hsa−miR−769−5p
9	0.6	3 / 18	hsa−miR−564
10	0.6	1 / 5	hsa−miR−1281
11	0.6	4 / 25	hsa−miR−663b
12	0.6	4 / 25	hsa−miR−99a
13	0.6	4 / 25	hsa−miR−99b
14	0.7	2 / 14	hsa−miR−891a
15	0.7	6 / 44	hsa−miR−658
16	0.8	1 / 8	hsa−miR−566
17	0.8	3 / 24	hsa−miR−220b
18	0.8	1 / 9	hsa−miR−373*
19	0.8	6 / 49	hsa−miR−208b
20	0.8	2 / 19	hsa−miR−563

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	4 / 14	BENTINK_e2f3.1
2	0.6	2 / 13	GUSTAFSON_PI3K_DN
3	0.9	1 / 12	GUSTAFSON_PI3K_UP
4	0.9	1 / 12	BENTINK_e2f3.2
5	0.9	1 / 12	BENTINK_ras.1
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	5e−39	352 / 1139	HEBENSTREIT_low expression TF
2	1e−02	117 / 595	ICGC_NrsfPcr2_targets
3	3e−01	1 / 2	MYC_Cell cycle DOWN
4	8e−01	1 / 8	MYC_Cell cycle UP
5	8e−01	1 / 9	MYC_Targets DOWN
6	8e−01	1 / 9	MYC_RNA processing binding UP
7	8e−01	2 / 19	MYC_Metabolism UP
8	9e−01	1 / 11	MYC_Protein synthesis degradation UP
9	9e−01	444 / 2927	ICGC_Rad21_targets
10	1e+00	5 / 59	MYC_Targets UP
11	1e+00	179 / 1273	ICGC_P300_targets
12	1e+00	324 / 2416	ICGC_Bcl3_targets
13	1e+00	70 / 653	ICGC_SrfPcr2_targets
14	1e+00	153 / 1266	ICGC_NrsfPcr1_targets
15	1e+00	259 / 2013	ICGC_Bcl11_targets
16	1e+00	51 / 553	ICGC_RxraPcr1_targets
17	1e+00	222 / 1872	ICGC_Mef2_targets
18	1e+00	62 / 690	ICGC_Atf3_targets
19	1e+00	565 / 4314	ICGC_Ebfsc137065_targets
20	1e+00	343 / 2836	ICGC_BatfPcr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	6 / 15	VAQUERIZAS_Bone marrow
2	0.16	3 / 9	VAQUERIZAS_Kidney
3	0.21	8 / 36	VAQUERIZAS_Fetal brain
4	0.25	4 / 16	VAQUERIZAS_Adrenal gland
5	0.31	5 / 23	VAQUERIZAS_Spinal cord
6	0.31	5 / 23	VAQUERIZAS_Adrenal cortex
7	0.41	5 / 26	VAQUERIZAS_Liver
8	0.49	3 / 16	VAQUERIZAS_Pancreas
9	0.59	6 / 38	VAQUERIZAS_Whole brain
10	0.60	2 / 12	VAQUERIZAS_Skin
11	0.61	3 / 19	VAQUERIZAS_Tonsil
12	0.71	1 / 7	VAQUERIZAS_Tongue
13	0.73	5 / 37	VAQUERIZAS_Thymus
14	0.74	3 / 23	VAQUERIZAS_Trachea
15	0.75	2 / 16	VAQUERIZAS_Salivary gland
16	0.78	2 / 17	VAQUERIZAS_Pituitary
17	0.84	7 / 58	VAQUERIZAS_Lung
18	0.85	19 / 143	VAQUERIZAS_General
19	0.85	1 / 11	VAQUERIZAS_Fetal liver
20	0.87	3 / 29	VAQUERIZAS_Fetal lung

Tissue

Rank	p−value	#in/all	Geneset
1	4e−09	99 / 350	WIRTH_Nervous System
2	4e−07	30 / 74	WIRTH_Mucosa
3	1e−06	17 / 32	WIRTH_Placenta
4	4e−05	19 / 46	WIRTH_Liver
5	4e−05	34 / 107	WIRTH_Testis
6	5e−05	31 / 95	WIRTH_Muscle
7	3e−04	16 / 41	WIRTH_Homeostasis
8	8e−04	13 / 32	WIRTH_Pancreas
9	3e−03	4 / 5	WIRTH_Bone marrow
10	1e−02	5 / 10	WIRTH_Hippocampus
11	1e−01	38 / 194	PALMER_B−Cell signature up
12	2e−01	3 / 9	PALMER_CD8+ T−Cell signature up
13	2e−01	3 / 10	WIRTH_Thalamus
14	3e−01	21 / 114	PALMER_T−Cell signature up
15	3e−01	3 / 12	WIRTH_Thymus
16	3e−01	39 / 225	PALMER_Granulocytes signature up
17	4e−01	59 / 350	WIRTH_Immune system
18	4e−01	2 / 8	WIRTH_Tonsil
19	5e−01	2 / 11	WIRTH_Sec. lymphoid organs
20	5e−01	2 / 11	WIRTH_Prim. lymphoid organs

Toxic

Rank	p−value	#in/all	Geneset
1	4e−07	689 / 3682	LU_BPDE 0.005 DN
2	1e+00	137 / 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	

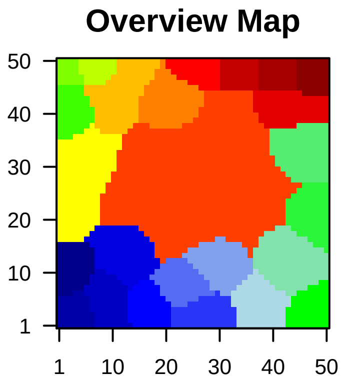
K−Means Clusters

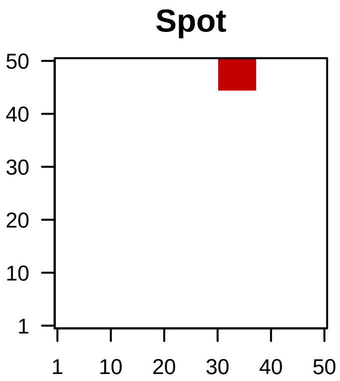
Spot Summary: I

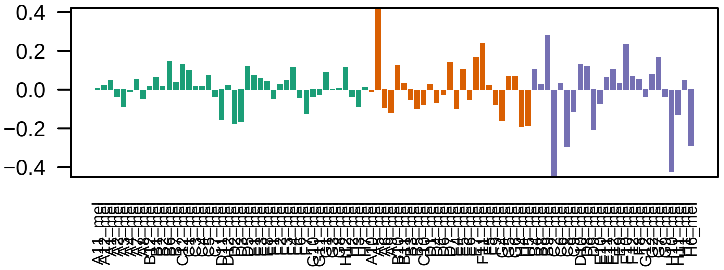
metagenes = 42
genes = 282

<r> metagenes = 0.86
<r> genes = 0.07
beta: r2= 1.06 / log p= −Inf

samples with spot = 7 (7.6 %)
MSC1 : 1 (2.4 %)
MSC2 : 3 (12 %)
MSC3 : 3 (12 %)


Overview Map


Spot

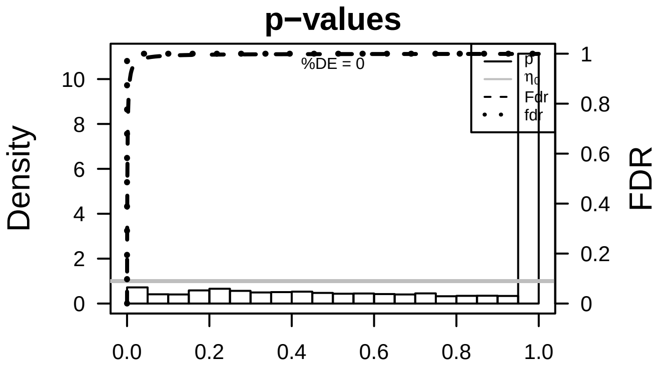


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	TYK2	2.19	−0.38	0.23	TYK2	tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:12440]
2	PTPN21	2	−0.19	0.26	PTPN21	protein tyrosine phosphatase, non−receptor type 21 [Source:I
3	BAAT	1.99	−0.45	0.28	BAAT	bile acid CoA:amino acid N−acyltransferase [Source:HGNC S
4	SLC44A2	1.9	−0.2	0.28	SLC44A2	solute carrier family 44 (choline transporter), member 2 [Sour
5	FAM179B	1.85	−0.27	0.24	FAM179B	family with sequence similarity 179, member B [Source:HGN
6	PLCG1	1.83	−0.72	0.36	PLCG1	phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
7	SLC25A35	1.83	−0.09	0.35	SLC25A35	solute carrier family 25, member 35 [Source:HGNC Symbol;A
8	FBXW4	1.8	−0.4	0.22	FBXW4	F−box and WD repeat domain containing 4 [Source:HGNC S
9	RAD51B	1.8	−0.76	0.28	RAD51B	RAD51 paralog B [Source:HGNC Symbol;Acc:HGNC:9822]
10	C8orf46	1.75	−0.18	0.27	C8orf46	chromosome 8 open reading frame 46 [Source:HGNC Symbo
11	PLD6	1.73	−0.29	0.35	PLD6	phospholipase D family, member 6 [Source:HGNC Symbol;Ac
12	DMWD	1.7	−0.24	0.22	DMWD	dystrophia myotonica, WD repeat containing [Source:HGNC
13	ENPP5	1.7	−0.2	0.33	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putati
14	DAK	1.69	−0.31	0.33	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae) [Source:H
15	PABPC1L	1.68	−0.4	0.26	PABPC1L	poly(A) binding protein, cytoplasmic 1−like [Source:HGNC Sy
16	POLR3F	1.67	−0.67	0.28	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa [S
17	GLYCTK	1.67	−0.22	0.29	GLYCTK	glycerate kinase [Source:HGNC Symbol;Acc:HGNC:24247]
18	MTRF1	1.66	−0.48	0.25	MTRF1	mitochondrial translational release factor 1 [Source:HGNC Sy
19	IL7	1.65	−0.24	0.26	IL7	interleukin 7 [Source:HGNC Symbol;Acc:HGNC:6023]
20	RALGDS	1.64	−0.14	0.29	RALGDS	ral guanine nucleotide dissociation stimulator [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−12	233 / 9482	Colon	TssA_Colon
2	2e−12	225 / 9027	Colon	Tx_Colon
3	4e−12	217 / 8580	Colon	TxWk_Colon
4	3e−11	222 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
5	3e−09	161 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	1e−07	187 / 7592	Lympl	HOPP_Active_promoter
7	1e−07	217 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
8	2e−07	140 / 5184	Lympl	HOPP_Txn_transition
9	7e−07	15 / 167	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
10	1e−06	171 / 6929	Lympl	HOPP_Txn_elongation
11	4e−06	50 / 1365	MF	RNA binding
12	8e−05	37 / 1007	MF	poly(A) RNA binding
13	2e−04	30 / 775	Chr	Chr 12
14	2e−04	63 / 2136	TF	ICGC_GabpPcr2_targets
15	2e−04	59 / 1975	BP	cellular protein modification process
16	2e−04	4 / 17	MF	RNA polymerase II core binding
17	3e−04	165 / 7203	Colon	TssF_Colon
18	4e−04	27 / 706	GSEA	BENPORATH_MYC_MAX_TARGETS
19	4e−04	46 / 1468	CC	mitochondrion
20	4e−04	183 / 8205	CC	cytoplasm
21	5e−04	7 / 74	GSEA	SWEET_KRAS_ONCOGENIC_SIGNATURE
22	5e−04	225 / 10605	CC	intracellular
23	6e−04	206 / 9528	Brain	Overlap_fetal_midbrain_Quies
24	7e−04	38 / 1171	TF	KIM_MYC targets
25	8e−04	12 / 213	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
26	8e−04	4 / 23	BP	ncRNA metabolic process
27	8e−04	163 / 7209	Lympl	HOPP_Weak_promoter
28	9e−04	22 / 553	TF	ICGC_RxraPcr1_targets
29	9e−04	5 / 40	GSEA	KEGG_NUCLEOTIDE_EXCISION_REPAIR
30	1e−03	7 / 83	BP	mitochondrial translational elongation
31	1e−03	15 / 316	GSEA	HSIAO_HOUSEKEEPING_GENES
32	1e−03	213 / 9988	CC	organelle
33	1e−03	92 / 3644	BP	biosynthetic process
34	1e−03	18 / 421	GSEA	MOOTHA_MITOCHONDRIA
35	1e−03	80 / 3081	Brain	Mid_Frontal_Lobe_ZNF
36	1e−03	9 / 137	GSEA	JISON_SICKLE_CELL_DISEASE_DN
37	1e−03	3 / 12	BP	histone H2A monoubiquitination
38	1e−03	4 / 26	BP	mRNA polyadenylation
39	1e−03	4 / 26	GSEA	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS
40	1e−03	17 / 393	BP	mRNA processing


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	2e−04	59 / 1975	cellular protein modification process
2	8e−04	4 / 23	ncRNA metabolic process
3	1e−03	7 / 83	mitochondrial translational elongation
4	1e−03	92 / 3644	biosynthetic process
5	1e−03	3 / 12	histone H2A monoubiquitination
6	1e−03	4 / 26	mRNA polyadenylation
7	1e−03	17 / 393	mRNA processing
8	2e−03	6 / 69	transcription elongation from RNA polymerase II promoter
9	2e−03	7 / 94	respiratory electron transport chain
10	2e−03	4 / 29	spliceosomal snRNP assembly
11	2e−03	7 / 96	mitochondrial translation
12	2e−03	13 / 277	translation
13	3e−03	3 / 15	regulation of DNA−templated transcription, elongation
14	3e−03	8 / 131	ribonucleoprotein complex assembly
15	4e−03	8 / 132	proteasome−mediated ubiquitin−dependent protein catabolic process
16	4e−03	8 / 135	cellular metabolic process
17	5e−03	4 / 37	transcription from RNA polymerase III promoter
18	6e−03	7 / 115	protein N−linked glycosylation via asparagine
19	6e−03	26 / 815	lipid metabolic process
20	7e−03	16 / 422	viral process

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	222 / 9013	Overlap_fetal_midbrain_K9K27me3
2	3e−09	161 / 5940	Overlap_fetal_midbrain_HetRpts
3	1e−07	217 / 9330	Overlap_fetal_midbrain_ReprPC
4	6e−04	206 / 9528	Overlap_fetal_midbrain_Quies
5	1e−03	80 / 3081	Mid_Frontal_Lobe_ZNF
6	2e−02	188 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	7e−02	33 / 1333	Fetal_ReprPCWk
8	9e−02	6 / 163	Fetal_ReprPC
9	1e−01	9 / 304	Fetal_Het
10	1e−01	19 / 769	Overlap_fetal_midbrain_ZNF
11	2e−01	20 / 831	Fetal_HetRpts
12	2e−01	13 / 534	Mid_Frontal_Lobe_EnhG
13	3e−01	13 / 564	Mid_Frontal_Lobe_EnhP
14	3e−01	17 / 765	Mid_Frontal_Lobe_Het
15	6e−01	3 / 166	Mid_Frontal_Lobe_Tx
16	7e−01	6 / 349	Fetal_ZNF
17	7e−01	17 / 989	Mid_Frontal_Lobe_Quies
18	7e−01	32 / 1845	Fetal_Quies
19	7e−01	6 / 383	Fetal_Tx
20	8e−01	17 / 1050	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	12 / 298	SPANG_BCL6−index2
2	0.01	2 / 10	GENTLES_modul5
3	0.02	2 / 14	LIU_LIVER_CANCER
4	0.04	0 / 14	LIU_COMMON_CANCER_GENES
5	0.17	2 / 40	PanCan_HK_geneset_nanostring
6	0.25	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.25	1 / 15	GENTLES_modul4
8	0.26	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	0.26	1 / 16	GENTLES_modul14
10	0.33	0 / 12	LIU_BREAST_CANCER
11	0.43	1 / 29	KUIPER_MM good survival
12	0.59	1 / 47	PanCan_DNARepair_geneset_nanostring
13	0.60	1 / 48	KUIPER_MM poor survival
14	0.65	1 / 55	PanCan_JAK−ST_geneset_nanostring
15	0.69	0 / 15	RHODES_CANCER_META_SIGNATURE
16	0.74	1 / 70	SHAUGHNESSY_MM high risk
17	0.79	0 / 12	LIU_PROSTATE_CANCER_UP
18	0.79	1 / 82	PanCan_TXmisReg_geneset_nanostring
19	0.86	2 / 180	SPANG_LPS−index2
20	0.89	1 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	4e−04	46 / 1468	mitochondrion
2	4e−04	183 / 8205	cytoplasm
3	5e−04	225 / 10605	intracellular
4	1e−03	213 / 9988	organelle
5	4e−03	16 / 401	mitochondrial inner membrane
6	7e−03	3 / 21	transcription elongation factor complex
7	1e−02	3 / 24	Cul3−RING ubiquitin ligase complex
8	1e−02	3 / 24	mitochondrial ribosome
9	1e−02	64 / 2577	nucleoplasm
10	2e−02	6 / 109	peroxisome
11	2e−02	3 / 30	peroxisomal matrix
12	2e−02	3 / 33	Golgi stack
13	2e−02	2 / 13	transcription factor TFTC complex
14	3e−02	236 / 11774	cell
15	3e−02	2 / 14	Cul4−RING E3 ubiquitin ligase complex
16	3e−02	32 / 1201	endoplasmic reticulum
17	3e−02	2 / 15	integral component of mitochondrial inner membrane
18	3e−02	6 / 128	ribosome
19	4e−02	2 / 17	multivesicular body
20	4e−02	2 / 17	replication fork

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	30 / 775	Chr 12
2	2e−02	16 / 462	Chr 14
3	2e−01	9 / 335	Chr 22
4	2e−01	10 / 398	Chr 20
5	3e−01	11 / 469	Chr 8
6	3e−01	15 / 687	Chr 6
7	3e−01	31 / 1500	Chr 1
8	4e−01	12 / 558	Chr 4
9	4e−01	5 / 221	Chr 18
10	5e−01	20 / 1037	Chr 19
11	5e−01	11 / 576	Chr 9
12	6e−01	5 / 262	Chr 13
13	6e−01	10 / 552	Chr 10
14	6e−01	18 / 993	Chr 2
15	8e−01	13 / 801	Chr 11
16	8e−01	2 / 151	Chr 21
17	9e−01	9 / 649	Chr 16
18	9e−01	6 / 465	Chr 15
19	9e−01	7 / 551	Chr X
20	9e−01	9 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−12	233 / 9482	TssA_Colon
2	2e−12	225 / 9027	Tx_Colon
3	4e−12	217 / 8580	TxWk_Colon
4	3e−04	165 / 7203	TssF_Colon
5	6e−03	214 / 10290	TssWk_Colon
6	3e−02	175 / 8415	Quies3_Colon
7	5e−02	64 / 2798	TxEnhG1_Colon
8	9e−02	194 / 9653	Enh_Colon
9	1e−01	1 / 8	KIM_CRC−MSI−regulated_DN
10	2e−01	119 / 5880	TssD2_Colon
11	3e−01	102 / 5155	EnhWk1_Colon
12	3e−01	20 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	3e−01	9 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	4e−01	15 / 739	TxEnhG2_Colon
15	4e−01	15 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	5e−01	51 / 2698	EnhA_Colon
17	6e−01	1 / 43	Marisa_CRC−cluster−f
18	6e−01	20 / 1079	ZNF_Colon
19	6e−01	3 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	7e−01	11 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.9	5 / 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	0.01	8 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
2	0.01	4 / 47	Vishal_subnetwork signature of survival in GBM
3	0.03	4 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
4	0.05	23 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.07	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	0.07	2 / 23	Donson−Misc immune function−associated with LTS in HGA
7	0.07	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
8	0.12	3 / 63	Stuehler_Proteins_up_in_STS
9	0.13	1 / 7	KIM amplified & overexpressed in LTS
10	0.13	4 / 103	GIEZELT_GBM_WT_up_VS_mut
11	0.19	1 / 11	Mukasa_UP_in_Astroglioma
12	0.19	1 / 11	astrocytes_glio
13	0.25	1 / 15	VERHAAK_CL subtype
14	0.25	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
15	0.29	8 / 332	Up
16	0.34	1 / 22	KIM prognostic signature LTS vs. STS
17	0.37	2 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
18	0.39	1 / 26	Christensen_hypomethylated_in_ependymoma
19	0.40	1 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
20	0.42	3 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−07	15 / 167	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
2	4e−04	27 / 706	BENPORATH_MYC_MAX_TARGETS
3	5e−04	7 / 74	SWEET_KRAS_ONCOGENIC_SIGNATURE
4	8e−04	12 / 213	WONG_MITOCHONDRIA_GENE_MODULE
5	9e−04	5 / 40	KEGG_NUCLEOTIDE_EXCISION_REPAIR
6	1e−03	15 / 316	HSIAO_HOUSEKEEPING_GENES
7	1e−03	18 / 421	MOOTHA_MITOCHONDRIA
8	1e−03	9 / 137	JISON_SICKLE_CELL_DISEASE_DN
9	1e−03	4 / 26	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_
10	2e−03	30 / 890	ACEVEDO_LIVER_CANCER_UP
11	2e−03	3 / 13	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_UP
12	2e−03	14 / 309	REACTOME_METABOLISM_OF_PROTEINS
13	2e−03	17 / 414	ROME_INSULIN_TARGETS_IN_MUSCLE_UP
14	2e−03	17 / 416	SHEN_SMARCA2_TARGETS_UP
15	3e−03	3 / 15	BIOCARTA_TNFR2_PATHWAY
16	3e−03	19 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
17	3e−03	9 / 157	KEGG_HUNTINGTONS_DISEASE
18	3e−03	6 / 76	JIANG_HYPOXIA_CANCER
19	3e−03	11 / 221	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_DN
20	4e−03	6 / 78	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS

HM

Rank	p−value	#in/all	Geneset
1	0.03	8 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.06	6 / 146	HALLMARK_DNA_REPAIR
3	0.07	7 / 188	HALLMARK_ADIPOGENESIS
4	0.07	7 / 188	HALLMARK_MYC_TARGETS_V1
5	0.22	5 / 169	HALLMARK_XENOBIOTIC_METABOLISM
6	0.26	3 / 93	HALLMARK_PEROXISOME
7	0.26	3 / 94	HALLMARK_ANDROGEN_RESPONSE
8	0.31	5 / 196	HALLMARK_MTORC1_SIGNALING
9	0.31	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	0.33	3 / 107	HALLMARK_COAGULATION
11	0.37	4 / 162	HALLMARK_COMPLEMENT
12	0.40	4 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.43	4 / 176	HALLMARK_HYPOXIA
14	0.48	3 / 137	HALLMARK_UV_RESPONSE_DN
15	0.50	3 / 141	HALLMARK_FATTY_ACID_METABOLISM
16	0.51	4 / 196	HALLMARK_G2M_CHECKPOINT
17	0.52	2 / 91	HALLMARK_PROTEIN_SECRETION
18	0.53	3 / 148	HALLMARK_KRAS_SIGNALING_UP
19	0.55	2 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
20	0.66	1 / 57	HALLMARK_MYC_TARGETS_V2

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−07	187 / 7592	HOPP_Active_promoter
2	2e−07	140 / 5184	HOPP_Txn_transition
3	1e−06	171 / 6929	HOPP_Txn_elongation
4	8e−04	163 / 7209	HOPP_Weak_promoter
5	1e−01	1 / 8	MASCQUE_ABC UP
6	2e−01	2 / 42	CARO_OxPhos_in_DLBCL_UP
7	2e−01	7 / 247	ZHANG_DLBCL_mutated
8	2e−01	7 / 256	SPANG_IL21 DN
9	2e−01	4 / 129	DAVE_BL−vs−DLBCL
10	2e−01	2 / 50	SPANG_BAFF 9hrs DN
11	3e−01	1 / 17	DAVE_NFkB BL DN
12	3e−01	129 / 6564	HOPP_Strong_enhancer
13	3e−01	1 / 19	DAVE_c−myc BL UP
14	4e−01	1 / 23	DAVE_Immune response 1
15	4e−01	25 / 1218	SPANG_BCR UP
16	5e−01	2 / 82	ROSOLOWSKI_green UP
17	5e−01	6 / 294	TARTE_Plasmablast signature
18	5e−01	2 / 86	ROSOLOWSKI_red total
19	5e−01	2 / 89	ROSOLOWSKI_blue total
20	6e−01	21 / 1128	SPANG_BCR DN

MF

Rank	p−value	#in/all	Geneset
1	4e−06	50 / 1365	RNA binding
2	8e−05	37 / 1007	poly(A) RNA binding
3	2e−04	4 / 17	RNA polymerase II core binding
4	4e−03	3 / 17	sulfuric ester hydrolase activity
5	7e−03	31 / 1033	nucleic acid binding
6	8e−03	15 / 394	catalytic activity
7	1e−02	5 / 71	structural constituent of ribosome
8	1e−02	2 / 10	protein phosphatase type 1 regulator activity
9	2e−02	14 / 386	nucleotide binding
10	2e−02	2 / 11	cAMP response element binding
11	2e−02	2 / 11	phospholipase C activity
12	2e−02	5 / 83	translation factor activity, RNA binding
13	2e−02	5 / 86	ubiquitin−like protein binding
14	2e−02	2 / 13	mannosyltransferase activity
15	2e−02	2 / 13	myosin V binding
16	3e−02	3 / 34	DNA−dependent ATPase activity
17	3e−02	8 / 189	methyltransferase activity
18	3e−02	3 / 36	protein self−association
19	3e−02	3 / 36	tRNA binding
20	3e−02	2 / 15	amino acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	8 / 134	hsa−miR−488
2	0.005	4 / 37	hsa−miR−1274a
3	0.007	6 / 90	hsa−miR−216a
4	0.014	6 / 104	hsa−miR−210
5	0.014	6 / 104	hsa−miR−525−5p
6	0.015	2 / 10	hsa−miR−887
7	0.020	5 / 82	hsa−miR−767−5p
8	0.022	3 / 32	hsa−miR−631
9	0.024	3 / 33	hsa−miR−1296
10	0.031	4 / 63	hsa−miR−455−3p
11	0.040	4 / 68	hsa−miR−193b
12	0.040	2 / 17	hsa−miR−1298
13	0.044	5 / 102	hsa−miR−377
14	0.059	3 / 47	hsa−miR−518e*
15	0.069	3 / 50	hsa−miR−487a
16	0.075	2 / 24	hsa−miR−632
17	0.078	5 / 120	hsa−miR−105
18	0.078	5 / 120	hsa−miR−579
19	0.080	5 / 121	hsa−miR−543
20	0.081	2 / 25	hsa−miR−597

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_e2f3.2
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 / 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	2e−04	63 / 2136	ICGC_GabpPcr2_targets
2	7e−04	38 / 1171	KIM_MYC targets
3	9e−04	22 / 553	ICGC_RxraPcr1_targets
4	2e−03	42 / 1400	ICGC_Myc_targets
5	6e−03	109 / 4689	ICGC_Taf1_targets
6	3e−02	91 / 4032	ICGC_Creb1_targets
7	3e−02	98 / 4385	ICGC_Atf2_targets
8	3e−02	118 / 5408	ICGC_Pou2_targets
9	3e−02	52 / 2137	ICGC_SrfV0416101_targets
10	3e−02	108 / 4909	ICGC_Stat5_targets
11	4e−02	107 / 4879	ICGC_Pmlsc71910_targets
12	5e−02	35 / 1383	ICGC_Six5_targets
13	6e−02	102 / 4706	ICGC_Sp1_targets
14	6e−02	125 / 5890	ICGC_Elf1_targets
15	6e−02	104 / 4829	ICGC_Nficsc81335_targets
16	9e−02	34 / 1418	ICGC_Ets1_targets
17	1e−01	60 / 2714	ICGC_Irf4_targets
18	1e−01	18 / 690	ICGC_Atf3_targets
19	1e−01	39 / 1701	HEBENSTREIT_high expression TF
20	1e−01	53 / 2391	ICGC_Pbx3_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 32	WIRTH_Placenta
2	0.2	1 / 11	WIRTH_Cortex cerebri
3	0.2	1 / 13	WIRTH_Thyroid gland
4	0.2	1 / 14	WIRTH_Telencephalon
5	0.3	1 / 16	PALMER_Lymphocytes signature up
6	0.5	7 / 350	WIRTH_Immune system
7	0.5	1 / 41	WIRTH_Homeostasis
8	0.6	2 / 107	WIRTH_Testis
9	0.7	3 / 194	PALMER_B−Cell signature up
10	0.8	1 / 74	WIRTH_Mucosa
11	0.8	3 / 225	PALMER_Granulocytes signature up
12	0.9	1 / 114	PALMER_T−Cell signature up
13	1.0	2 / 350	WIRTH_Nervous System
14	1.0	0 / 32	WIRTH_Pancreas
15	1.0	0 / 11	WIRTH_Sec. lymphoid organs
16	1.0	0 / 11	WIRTH_Prim. lymphoid organs
17	1.0	0 / 13	WIRTH_B−cells
18	1.0	0 / 8	WIRTH_Tonsil
19	1.0	0 / 12	WIRTH_Thymus
20	1.0	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	21 / 1115	LU_BPDE 1h DN
2	0.7	66 / 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	

K−Means Clusters

Spot Summary: J

metagenes = 107
genes = 356

<r> metagenes = 0.66
<r> genes = 0.13
beta: r2= 0.36 / log p= −9.6

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

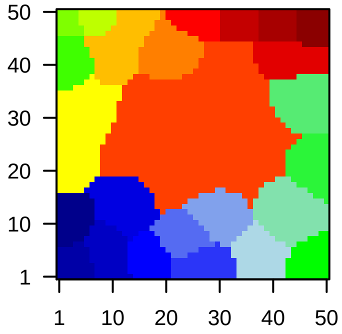
Spot Genelist

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 Symb
3	MDK	2.02	−0.1	0.54	MDK	midkine (neurite growth−promoting factor 2) [Source:HGNC
4	C10orf107	1.93	−0.08	0.67	C10orf107	chromosome 10 open reading frame 107 [Source:HGNC Sy
5	ZNF302	1.89	−0.05	0.25	ZNF302	zinc finger protein 302 [Source:HGNC Symbol;Acc:HGNC:13
6	ANKS1B	1.88	−0.13	0.64	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B [
7	MEGF10	1.88	−0.23	0.44	MEGF10	multiple EGF−like−domains 10 [Source:HGNC Symbol;Acc:H
8	ZNF442	1.86	−0.19	0.45	ZNF442	zinc finger protein 442 [Source:HGNC Symbol;Acc:HGNC:20
9	GANC	1.84	−0.25	0.37	GANC	glucosidase, alpha; neutral C [Source:HGNC Symbol;Acc:HG
10	NEK3	1.8	−0.27	0.32	NEK3	NIMA−related kinase 3 [Source:HGNC Symbol;Acc:HGNC:7
11	C9orf92	1.79	−0.1	0.62	C9orf92	chromosome 9 open reading frame 92 [Source:HGNC Symb
12	MDGA2	1.77	−0.23	0.41	MDGA2	MAM domain containing glycosylphosphatidylinositol anchor
13	THAP9	1.76	−0.33	0.34	THAP9	THAP domain containing 9 [Source:HGNC Symbol;Acc:HGN
14	IL33	1.75	−0.05	0.64	IL33	interleukin 33 [Source:HGNC Symbol;Acc:HGNC:16028]
15	MCU	1.74	−0.18	0.47	MCU	mitochondrial calcium uniporter [Source:HGNC Symbol;Acc:
16	CD53	1.74	−0.03	0.31	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
17	NFKBIE	1.74	−0.22	0.3	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B−
18	SNAP25	1.72	−0.13	0.43	SNAP25	synaptosomal−associated protein, 25kDa [Source:HGNC Sy
19	ZSCAN26	1.72	−0.31	0.26	ZSCAN26	zinc finger and SCAN domain containing 26 [Source:HGNC
20	GIT2	1.69	−0.46	0.25	GIT2	G protein−coupled receptor kinase interacting ArfGAP 2 [Sou

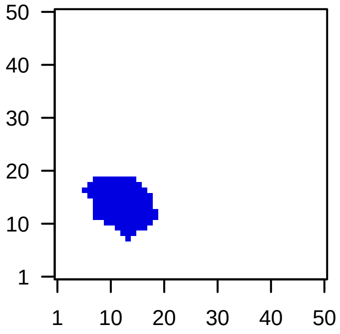
Geneset Overrepresentation

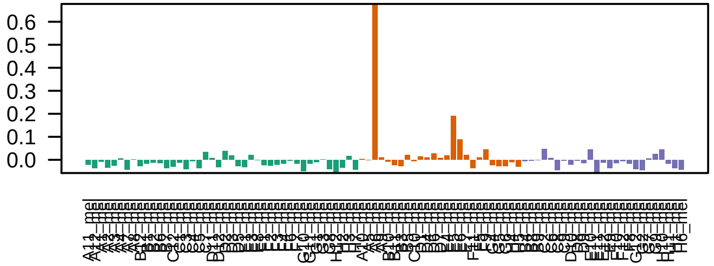
Rank	p−value	#in/all	Geneset	
1	6e−07	86 / 2159	Colon	TssP_Colon
2	3e−05	21 / 319	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	6e−05	6 / 30	Lymp	TARTE_B−cell signature
4	8e−05	6 / 31	GSE	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
5	2e−04	52 / 1317	Colon	EnhP_Colon
6	3e−04	4 / 14	BP	negative regulation of interferon−gamma production
7	3e−04	46 / 1139	TF	HEBENSTREIT_low expression TF
8	3e−04	75 / 2142	Colon	ReprPC_Colon
9	4e−04	34 / 775	CC	extracellular space
10	4e−04	3 / 7	Lifest	DUMEAUX_Women normal BMI literature genes up
11	4e−04	108 / 3396	Lymp	HOPP_Repressed
12	5e−04	67 / 1889	Colon	ReprPCWk_Colon
13	8e−04	28 / 616	GSE	NABA_MATRISOME
14	9e−04	4 / 19	TF Ti	VAQUERIZAS_Tonsil
15	1e−03	46 / 1207	Brain	Overlap_fetal_midbrain_TssF
16	1e−03	12 / 179	GSE	NABA_SECRETED_FACTORS
17	1e−03	73 / 2188	Lymp	HOPP_Poised_promoter
18	1e−03	17 / 314	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	2e−03	55 / 1548	Brain	Mid_Frontal_Lobe_K9K27me3
20	2e−03	2 / 3	GSE	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
21	2e−03	4 / 23	BP	hyaluronan metabolic process
22	2e−03	4 / 23	GSE	REACTOME_OLFACTORY_SIGNALING_PATHWAY
23	2e−03	5 / 38	GSE	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
24	2e−03	72 / 2185	Brain	Fetal_TssA
25	2e−03	96 / 3088	CC	plasma membrane
26	3e−03	7 / 78	GSE	ROVERSI_GLIOMA_COPY_NUMBER_UP
27	3e−03	5 / 41	MF	phosphatase binding
28	3e−03	4 / 26	BP	detection of chemical stimulus involved in sensory perception of smell
29	3e−03	4 / 26	MF	olfactory receptor activity
30	3e−03	20 / 427	GSE	NABA_MATRISOME_ASSOCIATED
31	3e−03	92 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
32	3e−03	3 / 13	BP	behavioral response to pain
33	3e−03	3 / 13	BP	response to vitamin D
34	3e−03	3 / 13	GSE	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
35	3e−03	18 / 370	GSE	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
36	4e−03	4 / 27	GSE	HAHTOLA_SEZARY_SYNDROM_DN
37	4e−03	7 / 85	BP	response to virus
38	4e−03	18 / 379	GSE	REACTOME_SIGNALING_BY_GPCR
39	5e−03	46 / 1308	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_UP
40	5e−03	9 / 134	GSE	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED

Overview Map

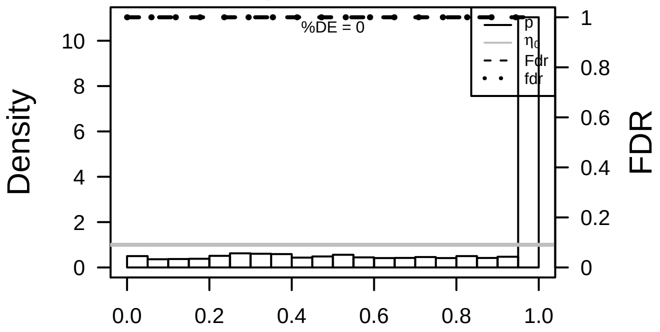


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.5	3 / 111	HORVATH_aging_genes meth UP
3	0.7	2 / 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	8e−04	4 / 14	negative regulation of interferon−gamma production
2	2e−03	4 / 23	hyaluronan metabolic process
3	3e−03	4 / 26	detection of chemical stimulus involved in sensory perception of smell
4	3e−03	3 / 13	behavioral response to pain
5	3e−03	3 / 13	response to vitamin D
6	4e−03	7 / 85	response to virus
7	6e−03	3 / 16	calcium ion−dependent exocytosis
8	7e−03	5 / 50	steroid hormone mediated signaling pathway
9	8e−03	5 / 52	protein localization to plasma membrane
10	8e−03	12 / 225	ion transport
11	8e−03	5 / 53	response to cytokine
12	8e−03	32 / 863	transmembrane transport
13	1e−02	3 / 20	response to zinc ion
14	1e−02	3 / 21	positive regulation of peptidyl−threonine phosphorylation
15	2e−02	4 / 41	pattern specification process
16	2e−02	3 / 25	cell aging
17	2e−02	12 / 260	nervous system development
18	2e−02	2 / 10	DNA integration
19	2e−02	2 / 10	positive regulation of interleukin−4 production
20	2e−02	2 / 10	regulation of sodium ion transmembrane transporter activity

Brain

Rank	p−value	#in/all	Geneset
1	0.001	46 / 1207	Overlap_fetal_midbrain_TssF
2	0.002	55 / 1548	Mid_Frontal_Lobe_K9K27me3
3	0.002	72 / 2185	Fetal_TssA
4	0.003	92 / 2972	Mid_Frontal_Lobe_ReprPC
5	0.007	33 / 884	Overlap_fetal_midbrain_EnhG
6	0.012	9 / 156	Mid_Frontal_Lobe_TssA
7	0.014	60 / 1907	Fetal_TxTrans
8	0.021	11 / 229	Mid_Frontal_Lobe_TxTrans
9	0.024	5 / 69	Overlap_fetal_midbrain_Tx
10	0.031	28 / 812	Mid_Frontal_Lobe_TssP
11	0.032	35 / 1065	Overlap_fetal_midbrain_Enh
12	0.034	21 / 574	Overlap_fetal_midbrain_TssP
13	0.049	23 / 668	Mid_Frontal_Lobe_Enh
14	0.053	19 / 534	Mid_Frontal_Lobe_EnhG
15	0.086	37 / 1236	Mid_Frontal_Lobe_ReprPCWk
16	0.099	55 / 1949	Fetal_TssF
17	0.127	18 / 564	Mid_Frontal_Lobe_EnhP
18	0.142	21 / 686	Overlap_fetal_midbrain_TssA
19	0.206	22 / 765	Mid_Frontal_Lobe_Het
20	0.222	49 / 1845	Fetal_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.1	0 / 14	LIU_PROSTATE_CANCER_DN
3	0.2	3 / 61	PanCan_Wnt_geneset_nanostring
4	0.3	2 / 44	PanCan_TGF−B_geneset_nanostring
5	0.3	1 / 14	LIU_COMMON_CANCER_GENES
6	0.3	1 / 15	WANG_ER_UP
7	0.3	1 / 15	GENTLES_modul10
8	0.3	1 / 16	WOLFER_overlap genes
9	0.3	1 / 16	GENTLES_modul14
10	0.4	2 / 55	PanCan_JAK−ST_geneset_nanostring
11	0.4	0 / 12	LIU_BREAST_CANCER
12	0.4	1 / 22	PanCan_HH_geneset_nanostring
13	0.5	2 / 70	SHAUGHNESSY_MM high risk
14	0.5	0 / 14	LIU_LIVER_CANCER
15	0.6	2 / 82	PanCan_TXmisReg_geneset_nanostring
16	0.7	1 / 47	PanCan_DNARepair_geneset_nanostring
17	0.7	8 / 401	Lembcke_Colonic Inflammation
18	0.8	2 / 113	PanCan_Driver_Gene_geneset_nanostring
19	0.8	2 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.8	2 / 121	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	4e−04	34 / 775	extracellular space
2	2e−03	96 / 3088	plasma membrane
3	8e−03	6 / 73	basement membrane
4	9e−03	4 / 35	cell periphery
5	1e−02	8 / 132	basolateral plasma membrane
6	2e−02	4 / 41	cleavage furrow
7	3e−02	14 / 332	cell junction
8	3e−02	5 / 75	blood microparticle
9	4e−02	3 / 31	brush border membrane
10	4e−02	3 / 32	chloride channel complex
11	5e−02	7 / 138	cell−cell junction
12	6e−02	7 / 144	postsynaptic membrane
13	6e−02	10 / 239	proteinaceous extracellular matrix
14	6e−02	2 / 17	membrane−bounded vesicle
15	7e−02	2 / 19	calcium channel complex
16	7e−02	2 / 19	mitochondrial proton−transporting ATP synthase complex
17	7e−02	2 / 19	stereocilium
18	8e−02	3 / 42	synaptic vesicle membrane
19	9e−02	24 / 751	integral component of plasma membrane
20	9e−02	5 / 99	receptor complex

Chr

Rank	p−value	#in/all	Geneset
1	0.1	25 / 801	Chr 11
2	0.1	31 / 1037	Chr 19
3	0.1	43 / 1500	Chr 1
4	0.1	20 / 649	Chr 16
5	0.1	18 / 576	Chr 9
6	0.2	12 / 398	Chr 20
7	0.2	16 / 551	Chr X
8	0.3	10 / 335	Chr 22
9	0.3	19 / 696	Chr 5
10	0.4	20 / 775	Chr 12
11	0.4	14 / 552	Chr 10
12	0.6	16 / 687	Chr 6
13	0.7	10 / 462	Chr 14
14	0.7	3 / 151	Chr 21
15	0.8	4 / 221	Chr 18
16	0.8	9 / 465	Chr 15
17	0.9	4 / 262	Chr 13
18	0.9	15 / 838	Chr 3
19	0.9	18 / 993	Chr 2
20	0.9	9 / 558	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−07	86 / 2159	TssP_Colon
2	3e−05	21 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	2e−04	52 / 1317	EnhP_Colon
4	3e−04	75 / 2142	ReprPC_Colon
5	5e−04	67 / 1889	ReprPCWk_Colon
6	1e−03	17 / 314	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	3e−02	15 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
8	4e−02	43 / 1386	Het_Colon
9	5e−02	1 / 2	Hewish_dMMR−secondary−mutations_Immune_surveillance
10	5e−02	33 / 1038	HetRpts_Colon
11	6e−02	30 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
12	7e−02	4 / 66	Marisa_CRC−cluster−h
13	7e−02	16 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
14	9e−02	14 / 394	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	1e−01	91 / 3383	EnhWk2_Colon
16	1e−01	14 / 427	Quies2_Colon
17	1e−01	9 / 250	K9K27me3_Colon
18	2e−01	13 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
19	2e−01	1 / 8	Marisa_CRC−C6
20	2e−01	2 / 33	Marisa_CRC−cluster−e

Disease

Rank	p−value	#in/all	Geneset
1	0.2	10 / 294	GUDJ_psoriasis down
2	0.8	8 / 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 / 8	Donson−chemokines/cytokines−associated with LTS in HGA
2	0.03	2 / 11	Donson−immune cell intra signaling−associated with LTS in HGA
3	0.03	5 / 74	WIRTH_Normal Brain
4	0.03	6 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	0.05	3 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
6	0.06	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.06	3 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
8	0.07	2 / 18	Shinawi_with_increased_methylation_in_STS
9	0.07	4 / 65	GIEZELT_GBM_STS_up_VS_LTS
10	0.09	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
11	0.10	3 / 47	Weller_LGG_gradeII−vs−III_UP
12	0.11	3 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
13	0.11	1 / 5	oligodendrocytes_glio
14	0.11	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
15	0.19	1 / 9	Mukasa_UP_in_GBM
16	0.23	3 / 70	Weller_LGG_1p19qDel−vs−intact_UP
17	0.24	2 / 39	OPC
18	0.25	2 / 40	in vivo astrocytes vs. cultured astroglia
19	0.27	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
20	0.30	1 / 15	VERHAAK_MES subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−05	6 / 31	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
2	8e−04	28 / 616	NABA_MATRISOME
3	1e−03	12 / 179	NABA_SECRETED_FACTORS
4	2e−03	2 / 3	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
5	2e−03	4 / 23	REACTOME_OLFACTORY_SIGNALING_PATHWAY
6	2e−03	5 / 38	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
7	3e−03	7 / 78	ROVERSI_GLIOMA_COPY_NUMBER_UP
8	3e−03	20 / 427	NABA_MATRISOME_ASSOCIATED
9	3e−03	3 / 13	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
10	3e−03	18 / 370	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
11	4e−03	4 / 27	HAHTOLA_SEZARY_SYNDROM_DN
12	4e−03	18 / 379	REACTOME_SIGNALING_BY_GPCR
13	5e−03	46 / 1308	DODD_NASOPHARYNGEAL_CARCINOMA_UP
14	5e−03	9 / 134	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
15	6e−03	9 / 139	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION
16	7e−03	3 / 17	BIOCARTA_NDKDYNAMIN_PATHWAY
17	7e−03	6 / 72	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
18	8e−03	28 / 724	BENPORATH_EED_TARGETS
19	9e−03	6 / 75	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AM
20	9e−03	5 / 54	BROWNE_INTERFERON_RESPONSIVE_GENES

HM

Rank	p−value	#in/all	Geneset
1	0.03	9 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	0.05	8 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.17	4 / 91	HALLMARK_BILE_ACID_METABOLISM
4	0.18	5 / 126	HALLMARK_ALLOGRAFT_REJECTION
5	0.22	6 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.22	2 / 37	HALLMARK_APICAL_SURFACE
7	0.34	3 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.40	5 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.42	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	0.44	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
11	0.47	4 / 148	HALLMARK_KRAS_SIGNALING_UP
12	0.53	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
13	0.54	4 / 162	HALLMARK_COMPLEMENT
14	0.56	4 / 167	HALLMARK_APICAL_JUNCTION
15	0.57	4 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	0.58	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	0.64	3 / 137	HALLMARK_UV_RESPONSE_DN
18	0.65	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
19	0.65	2 / 93	HALLMARK_PEROXISOME
20	0.66	3 / 141	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 7	DUMEAUX_Women normal BMI literature genes up
2	4e−01	1 / 18	DUMEAUX_High bmi enriched genes
3	5e−01	1 / 32	DUMEAUX_Fasting enriched genes
4	8e−01	1 / 62	DUMEAUX_Smoking enriched genes
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers 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	6e−05	6 / 30	TARTE_B−cell signature
2	4e−04	108 / 3396	HOPP_Repressed
3	1e−03	73 / 2188	HOPP_Poised_promoter
4	2e−02	2 / 10	DAVE_BL UP
5	1e−01	60 / 2211	HOPP_Repetitive
6	2e−01	2 / 29	Subero_DLBCL_hypo_meth
7	2e−01	1 / 8	Subero_MM_hypo_meth
8	2e−01	2 / 33	LEE_Developmental_regulators
9	3e−01	8 / 256	SPANG_IL21 DN
10	3e−01	1 / 15	DAVE_Immune response 2
11	4e−01	1 / 20	SPANG_BAFF 9hrs UP
12	4e−01	6 / 212	LENZ_Stromal signature 1
13	4e−01	3 / 96	Subero_DLBCL_hyper_meth
14	4e−01	63 / 2563	HOPP_Heterochrom
15	4e−01	2 / 61	SPANG_LPS 6hrs DN
16	5e−01	1 / 25	Subero_T−PLL_hypo_meth
17	5e−01	3 / 107	SPANG_LPS 6hrs UP
18	5e−01	7 / 275	TARTE_Mature plasma cell signature
19	5e−01	7 / 280	SPANG_CD40 6hrs UP
20	5e−01	10 / 410	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	0.003	5 / 41	phosphatase binding
2	0.003	4 / 26	olfactory receptor activity
3	0.007	3 / 17	receptor signaling complex scaffold activity
4	0.010	6 / 77	cytokine activity
5	0.018	5 / 64	beta−catenin binding
6	0.022	2 / 10	ephrin receptor activity
7	0.022	2 / 10	guanylate kinase activity
8	0.022	2 / 10	proteoglycan binding
9	0.023	3 / 26	chloride channel activity
10	0.023	3 / 26	endopeptidase inhibitor activity
11	0.023	4 / 46	steroid hormone receptor activity
12	0.026	3 / 27	chemokine activity
13	0.034	3 / 30	hydrolase activity, hydrolyzing O−glycosyl compounds
14	0.037	2 / 13	neuropeptide hormone activity
15	0.037	2 / 13	taste receptor activity
16	0.038	6 / 104	growth factor activity
17	0.042	2 / 14	regulatory region DNA binding
18	0.042	2 / 14	RNA polymerase II transcription factor binding transcription factor activity invo
19	0.044	4 / 56	phosphoprotein phosphatase activity
20	0.048	2 / 15	fibroblast growth factor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	2 / 12	hsa−miR−652
2	0.06	5 / 90	hsa−miR−216b
3	0.14	3 / 54	hsa−miR−518d−5p
4	0.14	3 / 54	hsa−miR−520c−5p
5	0.16	1 / 7	hsa−miR−339−3p
6	0.16	3 / 58	hsa−miR−328
7	0.17	2 / 31	hsa−miR−892b
8	0.18	2 / 33	hsa−miR−615−5p
9	0.21	5 / 133	hsa−miR−198
10	0.22	2 / 37	hsa−miR−635
11	0.25	2 / 40	hsa−miR−647
12	0.26	3 / 75	hsa−miR−592
13	0.27	4 / 110	hsa−miR−22
14	0.27	1 / 13	hsa−miR−638
15	0.30	2 / 46	hsa−miR−346
16	0.30	1 / 15	hsa−miR−191*
17	0.31	2 / 47	hsa−miR−1291
18	0.33	2 / 49	hsa−miR−519b−5p
19	0.33	2 / 49	hsa−miR−519c−5p
20	0.34	1 / 17	hsa−miR−1298

Pathw ACT

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	BENTINK_myc.1
2	0.3	1 / 13	BENTINK_src.10
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	GUSTAFSON_PI3K_DN
5	1.0	0 / 14	BENTINK_e2f3.1
6	1.0	0 / 12	BENTINK_e2f3.2
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 9	BENTINK_ras.4
9	1.0	0 / 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	3e−04	46 / 1139	HEBENSTREIT_low expression TF
2	3e−02	84 / 2927	ICGC_Rad21_targets
3	2e−01	74 / 2836	ICGC_BatfPcr1_targets
4	2e−01	53 / 2013	ICGC_Bcl11_targets
5	3e−01	15 / 553	ICGC_RxraPcr1_targets
6	4e−01	1 / 19	MYC_Metabolism UP
7	4e−01	32 / 1273	ICGC_P300_targets
8	5e−01	129 / 5374	ICGC_Pax5_targets
9	5e−01	102 / 4314	ICGC_Ebfsc137065_targets
10	6e−01	144 / 6114	ICGC_Runx3_targets
11	6e−01	126 / 5408	ICGC_Pou2_targets
12	7e−01	13 / 595	ICGC_NrsfPcr2_targets
13	7e−01	42 / 1872	ICGC_Mef2_targets
14	7e−01	61 / 2714	ICGC_Irf4_targets
15	7e−01	54 / 2416	ICGC_Bcl3_targets
16	8e−01	1 / 59	MYC_Targets UP
17	8e−01	124 / 5495	ICGC_Yy1_targets
18	8e−01	26 / 1266	ICGC_NrsfPcr1_targets
19	8e−01	132 / 5890	ICGC_Elf1_targets
20	8e−01	13 / 690	ICGC_Atf3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 19	VAQUERIZAS_Tonsil
2	1e−02	4 / 37	VAQUERIZAS_Thymus
3	2e−02	3 / 26	VAQUERIZAS_Liver
4	3e−02	3 / 27	VAQUERIZAS_Lymph node
5	5e−02	4 / 58	VAQUERIZAS_Lung
6	2e−01	1 / 7	VAQUERIZAS_Tongue
7	2e−01	3 / 59	VAQUERIZAS_Whole blood
8	3e−01	1 / 15	VAQUERIZAS_Bone marrow
9	3e−01	1 / 16	VAQUERIZAS_Pancreas
10	3e−01	1 / 16	VAQUERIZAS_Salivary gland
11	3e−01	1 / 17	VAQUERIZAS_Pituitary
12	3e−01	1 / 17	VAQUERIZAS_Heart
13	4e−01	1 / 23	VAQUERIZAS_Trachea
14	5e−01	1 / 29	VAQUERIZAS_Smooth muscle
15	5e−01	1 / 29	VAQUERIZAS_Fetal lung
16	7e−01	1 / 45	VAQUERIZAS_Uterus
17	7e−01	3 / 143	VAQUERIZAS_General
18	1e+00	0 / 36	VAQUERIZAS_Fetal brain
19	1e+00	0 / 41	VAQUERIZAS_Placenta
20	1e+00	0 / 33	VAQUERIZAS_Prostate

Tissue

Rank	p−value	#in/all	Geneset
1	0.01	2 / 8	WIRTH_Tonsil
2	0.04	2 / 14	WIRTH_Telencephalon
3	0.07	3 / 41	WIRTH_Homeostasis
4	0.13	12 / 350	WIRTH_Nervous System
5	0.18	7 / 194	PALMER_B−Cell signature up
6	0.23	1 / 11	WIRTH_Prim. lymphoid organs
7	0.25	1 / 12	WIRTH_Cerebellum
8	0.26	3 / 74	WIRTH_Mucosa
9	0.30	2 / 46	WIRTH_Liver
10	0.54	1 / 32	WIRTH_Pancreas
11	0.62	5 / 225	PALMER_Granulocytes signature up
12	0.66	2 / 95	WIRTH_Muscle
13	0.73	2 / 107	WIRTH_Testis
14	0.73	7 / 350	WIRTH_Immune system
15	1.00	0 / 11	WIRTH_Sec. lymphoid organs
16	1.00	0 / 13	WIRTH_B−cells
17	1.00	0 / 12	WIRTH_Thymus
18	1.00	0 / 12	WIRTH_Lymphocytes
19	1.00	0 / 5	WIRTH_Bone marrow
20	1.00	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	31 / 1115	LU_BPDE 1n DN
2	0.3	93 / 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	

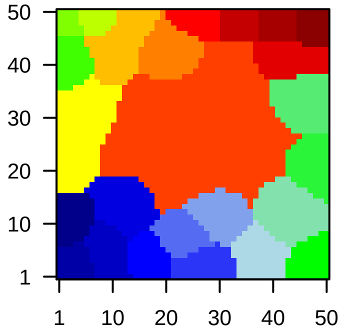
K−Means Clusters

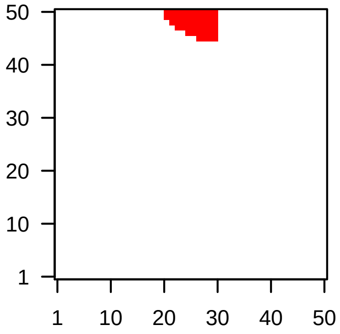
Spot Summary: K

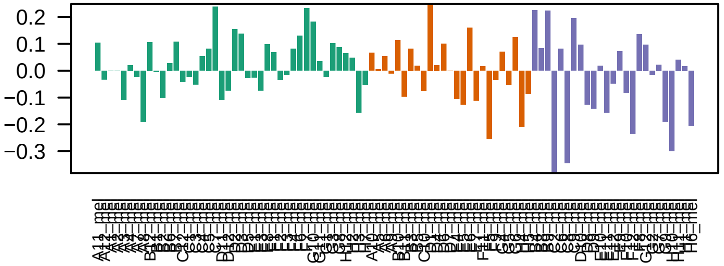
metagenes = 47
genes = 316

<r> metagenes = 0.83
<r> genes = 0.06
beta: r2= 1.01 / log p= −Inf

samples with spot = 9 (9.8 %)
MSC1 : 4 (9.5 %)
MSC2 : 2 (8 %)
MSC3 : 3 (12 %)


Overview Map


Spot

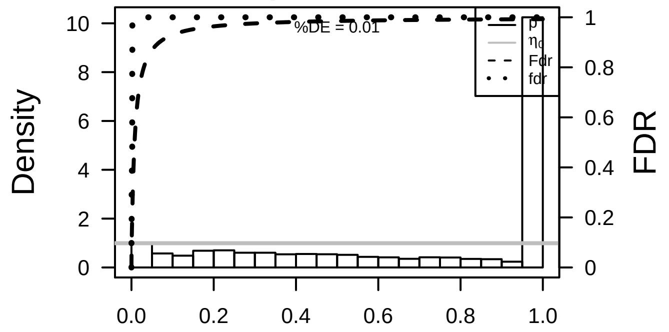


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	HIST1H2BB	2.23	−0.03	0.27	HIST1H2BB	histone cluster 1, H2bb [Source:HGNC Symbol;Acc:HGNC:47
2	MAP2K6	1.94	−0.24	0.3	MAP2K6	mitogen−activated protein kinase kinase 6 [Source:HGNC Sy
3	ZNF443	1.89	−0.18	0.28	ZNF443	zinc finger protein 443 [Source:HGNC Symbol;Acc:HGNC:20
4	PLCD1	1.88	−0.23	0.34	PLCD1	phospholipase C, delta 1 [Source:HGNC Symbol;Acc:HGNC:
5	FUT10	1.85	−0.25	0.35	FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase) [Source
6	ZNF571	1.81	−0.1	0.33	ZNF571	zinc finger protein 571 [Source:HGNC Symbol;Acc:HGNC:25
7	EDC3	1.8	−0.56	0.34	EDC3	enhancer of mRNA decapping 3 [Source:HGNC Symbol;Acc:
8	PCK2	1.77	−0.36	0.39	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial) [Sourc
9	NLE1	1.76	−0.27	0.26	NLE1	notchless homolog 1 (Drosophila) [Source:HGNC Symbol;Ac
10	ZNF57	1.75	−0.34	0.27	ZNF57	zinc finger protein 57 [Source:HGNC Symbol;Acc:HGNC:131
11	RCOR1	1.74	−0.27	0.23	RCOR1	REST corepressor 1 [Source:HGNC Symbol;Acc:HGNC:174
12	DUS2	1.74	−0.32	0.32	DUS2	dihydrouridine synthase 2 [Source:HGNC Symbol;Acc:HGNC
13	POMT2	1.72	−0.24	0.26	POMT2	protein−O−mannosyltransferase 2 [Source:HGNC Symbol;Ac
14	TRIM68	1.72	−0.24	0.3	TRIM68	tripartite motif containing 68 [Source:HGNC Symbol;Acc:HGN
15	PROSER3	1.71	−0.29	0.25	PROSER3	proline and serine rich 3 [Source:HGNC Symbol;Acc:HGNC:
16	IFT172	1.7	−0.2	0.23	IFT172	intraflagellar transport 172 [Source:HGNC Symbol;Acc:HGNC
17	CHUK	1.69	−0.53	0.27	CHUK	conserved helix−loop−helix ubiquitous kinase [Source:HGNC
18	FAM188A	1.68	−0.51	0.24	FAM188A	family with sequence similarity 188, member A [Source:HGN
19	POLI	1.67	−0.5	0.34	POLI	polymerase (DNA directed) iota [Source:HGNC Symbol;Acc:
20	LRRC8B	1.66	−0.26	0.34	LRRC8B	leucine rich repeat containing 8 family, member B [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−18	271 / 9482	Colon	TssA_Colon
2	2e−17	261 / 9027	Colon	Tx_Colon
3	4e−15	248 / 8580	Colon	TxWk_Colon
4	8e−15	215 / 6929	Lymph	HOPP_Txn_elongation
5	2e−14	260 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
6	3e−12	249 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
7	3e−11	184 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
8	6e−10	163 / 5184	Lymph	HOPP_Txn_transition
9	4e−08	261 / 10290	Colon	TssWk_Colon
10	1e−07	207 / 7592	Lymph	HOPP_Active_promoter
11	2e−06	28 / 494	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
12	3e−06	25 / 414	GSEA	ROME_INSULIN_TARGETS_IN_MUSCLE_UP
13	1e−05	35 / 756	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
14	2e−05	47 / 1171	TF	KIM_MYC targets
15	3e−05	8 / 57	CC	proteasome complex
16	3e−05	137 / 4829	TF	ICGC_Nficsc81335_targets
17	3e−05	214 / 8415	Colon	Quies3_Colon
18	4e−05	72 / 2136	TF	ICGC_GabpPcr2_targets
19	6e−05	11 / 122	BP	protein polyubiquitination
20	6e−05	235 / 9528	Brain	Overlap_fetal_midbrain_Quies
21	7e−05	117 / 4032	TF	ICGC_Creb1_targets
22	7e−05	132 / 4689	TF	ICGC_Taf1_targets
23	9e−05	255 / 10605	CC	intracellular
24	2e−04	7 / 55	GSEA	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C
25	2e−04	48 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
26	2e−04	6 / 41	GSEA	KEGG_PROTEASOME
27	2e−04	7 / 58	GSEA	REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS
28	2e−04	8 / 77	GSEA	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THA
29	2e−04	6 / 42	miRN	hsa−miR−769−3p
30	3e−04	12 / 168	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
31	3e−04	11 / 147	BP	tRNA metabolic process
32	3e−04	184 / 7209	Lymph	HOPP_Weak_promoter
33	3e−04	6 / 44	GSEA	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_A
34	3e−04	6 / 44	GSEA	REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_
35	3e−04	57 / 1701	TF	HEBENSTREIT_high expression TF
36	3e−04	7 / 62	BP	DNA damage response, signal transduction by p53 class mediator resulting
37	3e−04	7 / 62	GSEA	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_A
38	3e−04	29 / 685	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
39	4e−04	6 / 45	GSEA	REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_
40	4e−04	7 / 63	GSEA	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	6e−05	11 / 122	protein polyubiquitination
2	3e−04	11 / 147	tRNA metabolic process
3	3e−04	7 / 62	DNA damage response, signal transduction by p53 class mediator resulting in
4	4e−04	7 / 64	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
5	5e−04	6 / 48	regulation of cellular amino acid metabolic process
6	6e−04	7 / 68	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
7	6e−04	7 / 69	antigen processing and presentation of exogenous peptide antigen via MHC c
8	8e−04	7 / 72	regulation of ubiquitin−protein ligase activity involved in mitotic cell cycle
9	9e−04	7 / 73	antigen processing and presentation of exogenous peptide antigen via MHC c
10	1e−03	7 / 78	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent p
11	2e−03	4 / 25	protein tetramerization
12	2e−03	3 / 13	snRNA processing
13	4e−03	3 / 15	anterograde synaptic vesicle transport
14	4e−03	3 / 15	positive regulation of protein autophosphorylation
15	4e−03	3 / 15	protein localization to organelle
16	4e−03	3 / 16	mammary gland alveolus development
17	4e−03	3 / 16	positive regulation of receptor internalization
18	4e−03	3 / 16	RNA modification
19	4e−03	7 / 96	antigen processing and presentation of peptide antigen via MHC class I
20	5e−03	3 / 17	pseudouridine synthesis

Brain

Rank	p−value	#in/all	Geneset
1	2e−14	260 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−12	249 / 9013	Overlap_fetal_midbrain_K9K27me3
3	3e−11	184 / 5940	Overlap_fetal_midbrain_HetRpts
4	6e−05	235 / 9528	Overlap_fetal_midbrain_Quies
5	2e−03	87 / 3081	Mid_Frontal_Lobe_ZNF
6	6e−03	214 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	7e−03	27 / 769	Overlap_fetal_midbrain_ZNF
8	1e−01	21 / 765	Mid_Frontal_Lobe_Het
9	3e−01	31 / 1333	Fetal_ReprPCWk
10	4e−01	13 / 564	Mid_Frontal_Lobe_EnhP
11	4e−01	4 / 158	Overlap_fetal_midbrain_Het
12	5e−01	4 / 163	Fetal_ReprPC
13	5e−01	7 / 304	Fetal_Het
14	5e−01	39 / 1845	Fetal_Quies
15	6e−01	7 / 349	Fetal_ZNF
16	6e−01	25 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	6e−01	13 / 656	Overlap_fetal_midbrain_EnhP
18	7e−01	13 / 668	Mid_Frontal_Lobe_Enh
19	7e−01	22 / 1122	Fetal_K9K27me3
20	7e−01	16 / 831	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	4 / 40	PanCan_HK_geneset_nanostring
2	0.04	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
3	0.04	2 / 15	GENTLES_modul1
4	0.04	2 / 16	GENTLES_modul6
5	0.05	3 / 40	ZHANG_MM up
6	0.09	7 / 180	SPANG_LPS−index2
7	0.10	1 / 5	WANG_ER_DN
8	0.25	0 / 12	LIU_PROSTATE_CANCER_UP
9	0.30	8 / 298	SPANG_BCL6−index2
10	0.36	0 / 12	LIU_BREAST_CANCER
11	0.46	1 / 29	KUIPER_MM good survival
12	0.48	0 / 14	LIU_LIVER_CANCER
13	0.48	3 / 121	PanCan_MAPK_geneset_nanostring
14	0.59	0 / 14	LIU_PROSTATE_CANCER_DN
15	0.69	2 / 111	PanCan_RAS_geneset_nanostring
16	0.72	9 / 489	Lembcke_Normal vs Adenoma
17	0.73	1 / 61	PanCan_Wnt_geneset_nanostring
18	0.78	1 / 70	SHAUGHNESSY_MM high risk
19	0.83	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	0.85	2 / 156	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−05	8 / 57	proteasome complex
2	9e−05	255 / 10605	intracellular
3	1e−03	238 / 9988	organelle
4	2e−03	3 / 13	integrator complex
5	5e−03	3 / 17	proteasome accessory complex
6	6e−03	37 / 1132	Golgi apparatus
7	6e−03	3 / 18	proteasome core complex
8	1e−02	5 / 63	mitochondrial intermembrane space
9	1e−02	267 / 11774	cell
10	1e−02	71 / 2577	nucleoplasm
11	2e−02	11 / 246	mitochondrial matrix
12	2e−02	43 / 1468	mitochondrion
13	3e−02	2 / 12	Golgi transport complex
14	3e−02	2 / 12	SMN complex
15	3e−02	192 / 8205	cytoplasm
16	3e−02	2 / 13	proteasome regulatory particle
17	3e−02	2 / 13	TCTN−B9D complex
18	3e−02	17 / 487	intracellular membrane−bounded organelle
19	3e−02	2 / 14	Cul4−RING E3 ubiquitin ligase complex
20	4e−02	82 / 3214	protein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.01	26 / 775	Chr 12
2	0.08	15 / 469	Chr 8
3	0.15	19 / 687	Chr 6
4	0.15	18 / 649	Chr 16
5	0.19	13 / 462	Chr 14
6	0.22	5 / 151	Chr 21
7	0.29	25 / 1037	Chr 19
8	0.39	13 / 551	Chr X
9	0.41	16 / 696	Chr 5
10	0.42	8 / 335	Chr 22
11	0.47	9 / 398	Chr 20
12	0.50	15 / 689	Chr 7
13	0.53	12 / 558	Chr 4
14	0.62	17 / 838	Chr 3
15	0.62	17 / 840	Chr 17
16	0.70	4 / 221	Chr 18
17	0.78	8 / 465	Chr 15
18	0.84	9 / 552	Chr 10
19	0.86	17 / 993	Chr 2
20	0.87	9 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−18	271 / 9482	TssA_Colon
2	2e−17	261 / 9027	Tx_Colon
3	4e−15	248 / 8580	TxWk_Colon
4	4e−08	261 / 10290	TssWk_Colon
5	3e−05	214 / 8415	Quies3_Colon
6	2e−03	80 / 2798	TxEnhG1_Colon
7	8e−03	175 / 7203	TssF_Colon
8	2e−02	25 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	5e−02	124 / 5155	EnhWk1_Colon
10	9e−02	92 / 3812	TssD1_Colon
11	1e−01	19 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	1e−01	2 / 29	Marisa_CRC−cluster−c
13	1e−01	135 / 5880	TssD2_Colon
14	1e−01	215 / 9653	Enh_Colon
15	2e−01	20 / 739	TxEnhG2_Colon
16	2e−01	64 / 2698	EnhA_Colon
17	3e−01	2 / 50	Ang_CRC_Hypermethylated
18	3e−01	1 / 18	Ang_CRC=CIMPH−vs−L_hypo
19	3e−01	10 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
20	4e−01	25 / 1079	ZNF_Colon

Disease

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

Glio

Rank	p−value	#in/all	Geneset
1	0.009	2 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
2	0.026	13 / 332	Up
3	0.033	4 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
4	0.050	4 / 65	GIEZELT_GBM_STS_up_VS_LTS
5	0.059	25 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.082	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
7	0.090	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
8	0.136	10 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	0.148	2 / 32	Donson−innate immunity−associated with LTS in HGA
10	0.157	11 / 365	Down_b
11	0.176	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
12	0.211	1 / 11	Mukasa_UP_in_Astroglioma
13	0.211	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
14	0.264	2 / 47	Vishal_subnetwork signature of survival in GBM
15	0.276	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
16	0.283	3 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
17	0.324	3 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
18	0.377	1 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
19	0.389	2 / 63	Stuehler_Proteins_up_in_STS
20	0.404	2 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	28 / 494	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
2	3e−06	25 / 414	ROME_INSULIN_TARGETS_IN_MUSCLE_UP
3	1e−05	35 / 756	WEI_MYCN_TARGETS_WITH_E_BOX
4	2e−04	7 / 55	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C
5	2e−04	48 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	2e−04	6 / 41	KEGG_PROTEASOME
7	2e−04	7 / 58	REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS
8	2e−04	8 / 77	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_
9	3e−04	12 / 168	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
10	3e−04	6 / 44	REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANT
11	3e−04	6 / 44	REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF
12	3e−04	7 / 62	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND
13	3e−04	29 / 685	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
14	4e−04	6 / 45	REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_CO
15	4e−04	7 / 63	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_P
16	4e−04	6 / 46	REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT
17	4e−04	33 / 834	LEE_BMP2_TARGETS_DN
18	4e−04	7 / 65	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION
19	5e−04	6 / 47	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC
20	5e−04	6 / 47	REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1

HM

Rank	p−value	#in/all	Geneset
1	0.003	11 / 196	HALLMARK_MTORC1_SIGNALING
2	0.019	9 / 188	HALLMARK_MYC_TARGETS_V1
3	0.048	8 / 188	HALLMARK_ADIPOGENESIS
4	0.070	7 / 169	HALLMARK_XENOBIOTIC_METABOLISM
5	0.081	6 / 141	HALLMARK_FATTY_ACID_METABOLISM
6	0.141	2 / 31	HALLMARK_HEDGEHOG_SIGNALING
7	0.201	5 / 146	HALLMARK_UV_RESPONSE_UP
8	0.203	4 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	0.247	6 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.324	3 / 94	HALLMARK_ANDROGEN_RESPONSE
11	0.348	4 / 140	HALLMARK_APOPTOSIS
12	0.350	5 / 183	HALLMARK_GLYCOLYSIS
13	0.366	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	0.429	1 / 26	HALLMARK_ANGIOGENESIS
15	0.469	2 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
16	0.504	3 / 126	HALLMARK_ALLOGRAFT_REJECTION
17	0.540	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
18	0.549	1 / 37	HALLMARK_APICAL_SURFACE
19	0.576	3 / 140	HALLMARK_INFLAMMATORY_RESPONSE
20	0.580	2 / 91	HALLMARK_PROTEIN_SECRETION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 10	DUMEAUX_Smoking literature genes up
2	0.3	1 / 18	DUMEAUX_High bmi enriched genes
3	0.5	1 / 32	DUMEAUX_Fasting enriched genes
4	0.7	1 / 62	DUMEAUX_Smoking enriched genes
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	8e−15	215 / 6929	HOPP_Txn_elongation
2	6e−10	163 / 5184	HOPP_Txn_transition
3	1e−07	207 / 7592	HOPP_Active_promoter
4	3e−04	184 / 7209	HOPP_Weak_promoter
5	4e−03	14 / 294	TARTE_Plasmablast signature
6	3e−02	2 / 13	WRIGHT_GCB UP
7	4e−02	33 / 1128	SPANG_BCR DN
8	4e−02	2 / 16	ROSOLOWSKI_red UP
9	6e−02	154 / 6564	HOPP_Strong_enhancer
10	6e−02	10 / 268	SPANG_IL21 UP
11	2e−01	1 / 8	MASCQUE_GCB UP
12	2e−01	1 / 10	DAVE_BL UP
13	2e−01	2 / 42	CARO_OxPhos_in_DLBCL_UP
14	2e−01	2 / 43	LENZ_Stromal signature 2
15	3e−01	124 / 5538	HOPP_Weak_txn
16	3e−01	11 / 410	SPANG_CD40 6hrs DN
17	3e−01	1 / 14	Subero_MCL_hyper_meth
18	3e−01	3 / 86	ROSOLOWSKI_red total
19	3e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
20	3e−01	125 / 5693	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	0.002	3 / 13	pseudouridine synthase activity
2	0.004	4 / 30	iron−sulfur cluster binding
3	0.006	43 / 1365	RNA binding
4	0.006	3 / 18	threonine−type endopeptidase activity
5	0.007	4 / 36	tRNA binding
6	0.010	6 / 85	histone deacetylase binding
7	0.018	2 / 10	proteasome binding
8	0.022	2 / 11	metal ion transmembrane transporter activity
9	0.023	4 / 51	translation initiation factor activity
10	0.026	7 / 136	lyase activity
11	0.030	2 / 13	NAD+ binding
12	0.030	2 / 13	platelet−derived growth factor receptor binding
13	0.030	2 / 13	zinc ion transmembrane transporter activity
14	0.032	5 / 83	translation factor activity, RNA binding
15	0.032	7 / 142	isomerase activity
16	0.038	3 / 35	4 iron, 4 sulfur cluster binding
17	0.038	3 / 35	aminoacyl−tRNA ligase activity
18	0.048	6 / 123	nucleotidyltransferase activity
19	0.052	14 / 405	ligase activity
20	0.055	2 / 18	2 iron, 2 sulfur cluster binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 42	hsa−miR−769−3p
2	5e−04	10 / 130	hsa−miR−383
3	8e−04	15 / 274	hsa−miR−1244
4	1e−03	10 / 143	hsa−miR−338−5p
5	1e−03	8 / 102	hsa−miR−1301
6	2e−03	18 / 386	hsa−let−7c
7	2e−03	5 / 43	hsa−miR−423−3p
8	2e−03	7 / 85	hsa−miR−423−5p
9	2e−03	3 / 13	hsa−miR−638
10	2e−03	14 / 275	hsa−miR−577
11	2e−03	8 / 110	hsa−miR−22
12	3e−03	16 / 347	hsa−let−7a
13	4e−03	9 / 143	hsa−miR−24
14	4e−03	11 / 203	hsa−miR−545
15	6e−03	9 / 155	hsa−miR−429
16	7e−03	15 / 343	hsa−let−7e
17	7e−03	6 / 80	hsa−miR−942
18	7e−03	7 / 105	hsa−miR−1271
19	8e−03	9 / 161	hsa−miR−802
20	9e−03	8 / 136	hsa−miR−155

PathwAct

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	BENTINK_ras.4
2	0.2	1 / 13	BENTINK_myc.1
3	0.3	1 / 14	BENTINK_e2f3.1
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 / 12	BENTINK_ras.1
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−05	47 / 1171	KIM_MYC targets
2	3e−05	137 / 4829	ICGC_Nficsc81335_targets
3	4e−05	72 / 2136	ICGC_GabpPcr2_targets
4	7e−05	117 / 4032	ICGC_Creb1_targets
5	7e−05	132 / 4689	ICGC_Taf1_targets
6	3e−04	57 / 1701	HEBENSTREIT_high expression TF
7	5e−04	121 / 4385	ICGC_Atf2_targets
8	1e−03	131 / 4909	ICGC_Stat5_targets
9	1e−03	103 / 3700	ICGC_Nfatc1_targets
10	5e−03	148 / 5890	ICGC_Elf1_targets
11	7e−03	125 / 4879	ICGC_Pmlsc71910_targets
12	7e−03	44 / 1418	ICGC_Ets1_targets
13	7e−03	132 / 5200	ICGC_Mta3_targets
14	1e−02	135 / 5408	ICGC_Pou2_targets
15	1e−02	150 / 6114	ICGC_Runx3_targets
16	1e−02	42 / 1400	ICGC_Myc_targets
17	2e−02	136 / 5495	ICGC_Yy1_targets
18	2e−02	112 / 4414	ICGC_Bclaf101388_targets
19	2e−02	118 / 4706	ICGC_Sp1_targets
20	2e−02	41 / 1383	ICGC_Six5_targets

TF Tissue

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

Tissue

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

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	26 / 1115	LU_BPDE 1h DN
2	0.8	72 / 3682	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

K−Means Clusters

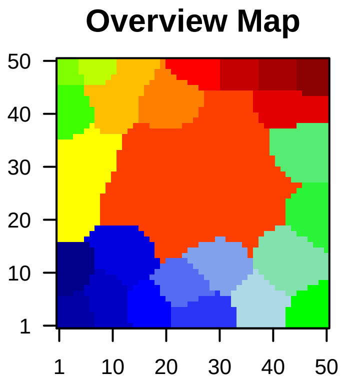
Spot Summary: L

metagenes = 61
genes = 596

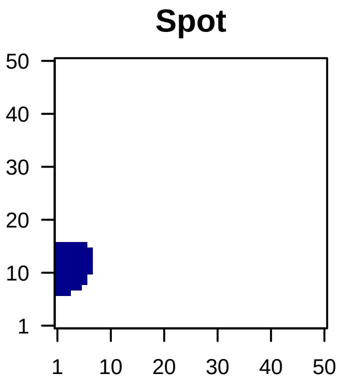
<r> metagenes = 0.81
<r> genes = 0.08
beta: r2= 1.67 / log p= −Inf

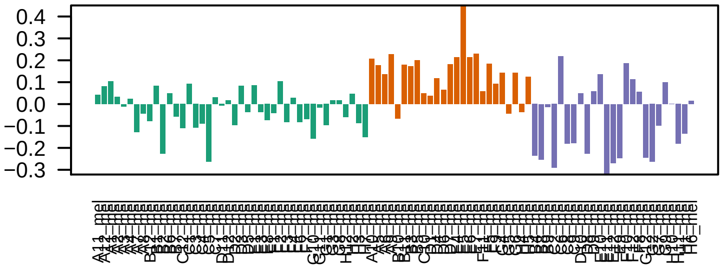
samples with spot = 14 (15.2 %)
MSC2 : 12 (48 %)
MSC3 : 2 (8 %)

Overview Map



Spot





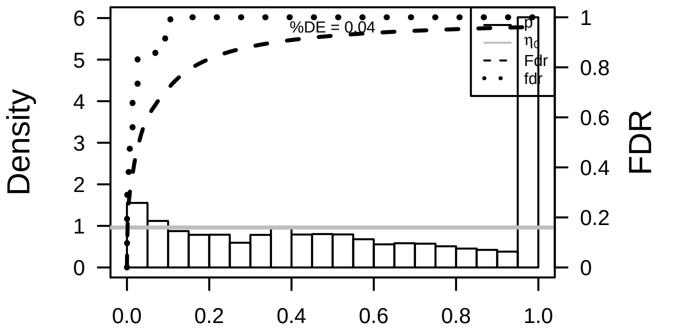
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	FZD3	2.09	−0.27	0.28	FZD3	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4
2	SLC25A14	2.08	−0.21	0.26	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member
3	POPDC2	2.06	−0.33	0.46	POPDC2	popeye domain containing 2 [Source:HGNC Symbol;Acc:HGI
4	RNF40	1.97	−0.54	0.27	RNF40	ring finger protein 40, E3 ubiquitin protein ligase [Source:HGI
5	EGLN3	1.89	−0.41	0.36	EGLN3	egl−9 family hypoxia−inducible factor 3 [Source:HGNC Symb
6	KCNQ5	1.87	−0.46	0.35	KCNQ5	potassium channel, voltage gated KQT−like subfamily Q, mer
7	TKTL1	1.87	−0.19	0.27	TKTL1	transketolase−like 1 [Source:HGNC Symbol;Acc:HGNC:1183
8	CFAP61	1.86	−0.52	0.45	CFAP61	cilia and flagella associated protein 61 [Source:HGNC Symb
9	LYRM9	1.85	−0.31	0.28	LYRM9	LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
10	CC2D1B	1.84	−0.41	0.22	CC2D1B	coiled−coil and C2 domain containing 1B [Source:HGNC Sym
11	TAPBPL	1.83	−0.08	0.34	TAPBPL	TAP binding protein−like [Source:HGNC Symbol;Acc:HGNC:
12	PLA2G4B	1.82	−0.16	0.33	PLA2G4B	phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym
13	SLC26A4	1.8	−0.16	0.43	SLC26A4	solute carrier family 26 (anion exchanger), member 4 [Source
14	KRTAP19−1	1.78	−0.78	0.4	KRTAP19−1	keratin associated protein 19−1 [Source:HGNC Symbol;Acc:
15	LCMT2	1.75	−0.37	0.3	LCMT2	leucine carboxyl methyltransferase 2 [Source:HGNC Symbol;
16	TMEM150A	1.75	−0.24	0.35	TMEM150A	transmembrane protein 150A [Source:HGNC Symbol;Acc:HG
17	RDH14	1.75	−0.43	0.31	RDH14	retinol dehydrogenase 14 (all−trans/9−cis/11−cis) [Source:HG
18	GAS8	1.75	−0.56	0.29	GAS8	growth arrest−specific 8 [Source:HGNC Symbol;Acc:HGNC:4
19	BBS5	1.74	−0.64	0.36	BBS5	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
20	TTC7B	1.74	−0.65	0.19	TTC7B	tetratricopeptide repeat domain 7B [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−21	476 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	9e−14	444 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
3	3e−12	439 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
4	1e−11	455 / 9528	Brain	Overlap_fetal_midbrain_Quies
5	6e−11	314 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
6	8e−10	407 / 8415	Colon	Quies3_Colon
7	9e−09	9 / 18	BP	melanocyte differentiation
8	1e−08	442 / 9482	Colon	TssA_Colon
9	4e−08	341 / 6929	Lympl	HOPP_Txn_elongation
10	8e−08	421 / 9027	Colon	Tx_Colon
11	2e−07	266 / 5184	Lympl	HOPP_Txn_transition
12	5e−07	8 / 20	BP	semaphorin−plexin signaling pathway
13	5e−07	400 / 8580	Colon	TxWk_Colon
14	2e−06	13 / 67	BP	pigmentation
15	3e−06	358 / 7592	Lympl	HOPP_Active_promoter
16	8e−06	314 / 6564	Lympl	HOPP_Strong_enhancer
17	1e−05	143 / 2576	CC	membrane
18	1e−05	6 / 15	BP	developmental pigmentation
19	2e−05	5 / 10	MF	semaphorin receptor binding
20	3e−05	275 / 5693	Lympl	HOPP_Weak_enhancer
21	3e−05	29 / 317	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38
22	3e−05	9 / 42	GSEA	PID_RHOA_REG_PATHWAY
23	4e−05	195 / 3812	Colon	TssD1_Colon
24	4e−05	19 / 167	GSEA	KIM_MYC_AMPLIFICATION_TARGETS_UP
25	5e−05	251 / 5155	Colon	EnhWk1_Colon
26	6e−05	88 / 1468	CC	mitochondrion
27	7e−05	61 / 925	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
28	9e−05	452 / 10290	Colon	TssWk_Colon
29	1e−04	5 / 13	GSEA	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
30	1e−04	372 / 8205	CC	cytoplasm
31	1e−04	6 / 21	BP	melanosome transport
32	1e−04	70 / 1128	Lympl	SPANG_BCR DN
33	1e−04	278 / 5880	Colon	TssD2_Colon
34	2e−04	44 / 620	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
35	2e−04	331 / 7209	Lympl	HOPP_Weak_promoter
36	2e−04	172 / 3383	Colon	EnhWk2_Colon
37	2e−04	42 / 590	BP	cell morphogenesis
38	2e−04	18 / 174	HM	HALLMARK_ESTROGEN_RESPONSE_EARLY
39	2e−04	48 / 705	BP	locomotion
40	2e−04	5 / 15	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	6 / 100	HORVATH_aging_genes meth DOWN
2	0.8	3 / 111	HORVATH_aging_genes meth UP
3	1.0	0 / 38	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−09	9 / 18	melanocyte differentiation
2	5e−07	8 / 20	semaphorin−plexin signaling pathway
3	2e−06	13 / 67	pigmentation
4	1e−05	6 / 15	developmental pigmentation
5	1e−04	6 / 21	melanosome transport
6	2e−04	42 / 590	cell morphogenesis
7	2e−04	48 / 705	locomotion
8	5e−04	8 / 47	positive regulation of osteoblast differentiation
9	8e−04	25 / 312	axon guidance
10	9e−04	5 / 20	cellular response to fibroblast growth factor stimulus
11	1e−03	9 / 65	regulation of Rho protein signal transduction
12	1e−03	4 / 13	melanin biosynthetic process
13	1e−03	4 / 13	positive regulation of smooth muscle cell migration
14	3e−03	9 / 75	regulation of catalytic activity
15	3e−03	4 / 16	chondrocyte development
16	3e−03	4 / 16	mitochondrial transport
17	4e−03	23 / 316	small GTPase mediated signal transduction
18	5e−03	16 / 195	cellular response to DNA damage stimulus
19	6e−03	12 / 129	insulin receptor signaling pathway
20	6e−03	4 / 19	positive regulation of erythrocyte differentiation

Brain

Rank	p−value	#in/all	Geneset
1	5e−21	476 / 9330	Overlap_fetal_midbrain_ReprPC
2	9e−14	444 / 9013	Overlap_fetal_midbrain_K9K27me3
3	3e−12	439 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	1e−11	455 / 9528	Overlap_fetal_midbrain_Quies
5	6e−11	314 / 5940	Overlap_fetal_midbrain_HetRpts
6	8e−04	155 / 3081	Mid_Frontal_Lobe_ZNF
7	1e−02	52 / 953	Fetal_Enh
8	4e−02	54 / 1065	Overlap_fetal_midbrain_Enh
9	5e−02	41 / 786	Fetal_EnhG
10	8e−02	44 / 884	Overlap_fetal_midbrain_EnhG
11	9e−02	49 / 1013	Fetal_TssP
12	1e−01	33 / 656	Overlap_fetal_midbrain_EnhP
13	1e−01	38 / 769	Overlap_fetal_midbrain_ZNF
14	1e−01	40 / 831	Fetal_HetRpts
15	1e−01	49 / 1050	Fetal_EnhP
16	3e−01	26 / 574	Overlap_fetal_midbrain_TssP
17	3e−01	14 / 304	Fetal_Het
18	3e−01	29 / 668	Mid_Frontal_Lobe_Enh
19	4e−01	90 / 2185	Fetal_TssA
20	4e−01	15 / 349	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	6 / 55	PanCan_JAK−ST_geneset_nanostring
2	0.03	5 / 44	PanCan_TGF−B_geneset_nanostring
3	0.03	9 / 111	PanCan_RAS_geneset_nanostring
4	0.04	0 / 14	LIU_PROSTATE_CANCER_DN
5	0.06	12 / 180	SPANG_LPS−index2
6	0.08	1 / 2	GENTLES_modul8
7	0.09	2 / 13	GENTLES_modul12
8	0.12	2 / 15	GENTLES_modul4
9	0.13	2 / 16	GENTLES_modul7
10	0.13	2 / 16	GENTLES_modul16
11	0.14	16 / 298	SPANG_BCL6−index2
12	0.17	9 / 156	PanCan_PI3K_geneset_nanostring
13	0.20	7 / 120	PanCan_CC+Apop_geneset_nanostring
14	0.21	3 / 40	PanCan_HK_geneset_nanostring
15	0.22	1 / 12	LIU_PROSTATE_CANCER_UP
16	0.25	19 / 401	Lembcke_Colonic Inflammation
17	0.30	6 / 113	PanCan_Driver_Gene_geneset_nanostring
18	0.30	3 / 48	KUIPER_MM poor survival
19	0.31	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	0.33	1 / 10	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	1e−05	143 / 2576	membrane
2	6e−05	88 / 1468	mitochondrion
3	1e−04	372 / 8205	cytoplasm
4	4e−04	12 / 94	melanosome
5	1e−03	41 / 616	endosome
6	2e−03	20 / 246	mitochondrial matrix
7	3e−03	151 / 3088	plasma membrane
8	5e−03	495 / 11774	cell
9	5e−03	124 / 2507	cytosol
10	8e−03	3 / 11	filopodium tip
11	9e−03	4 / 21	immunological synapse
12	1e−02	14 / 175	early endosome
13	1e−02	6 / 47	endocytic vesicle
14	1e−02	8 / 76	extrinsic component of membrane
15	1e−02	10 / 108	late endosome
16	1e−02	6 / 48	peroxisomal membrane
17	1e−02	10 / 109	peroxisome
18	2e−02	447 / 10605	intracellular
19	2e−02	25 / 401	mitochondrial inner membrane
20	2e−02	5 / 41	mitochondrial nucleoid

Chr

Rank	p−value	#in/all	Geneset
1	0.01	34 / 576	Chr 9
2	0.02	46 / 838	Chr 3
3	0.03	32 / 558	Chr 4
4	0.03	27 / 465	Chr 15
5	0.06	26 / 469	Chr 8
6	0.17	14 / 262	Chr 13
7	0.17	12 / 221	Chr 18
8	0.26	8 / 151	Chr 21
9	0.31	34 / 775	Chr 12
10	0.37	42 / 993	Chr 2
11	0.42	35 / 840	Chr 17
12	0.45	23 / 552	Chr 10
13	0.48	19 / 462	Chr 14
14	0.58	13 / 335	Chr 22
15	0.59	27 / 696	Chr 5
16	0.79	24 / 689	Chr 7
17	0.81	13 / 398	Chr 20
18	0.85	53 / 1500	Chr 1
19	0.87	21 / 649	Chr 16
20	0.89	26 / 801	Chr 11

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−10	407 / 8415	Quies3_Colon
2	1e−08	442 / 9482	TssA_Colon
3	8e−08	421 / 9027	Tx_Colon
4	5e−07	400 / 8580	TxWk_Colon
5	4e−05	195 / 3812	TssD1_Colon
6	5e−05	251 / 5155	EnhWk1_Colon
7	9e−05	452 / 10290	TssWk_Colon
8	1e−04	278 / 5880	TssD2_Colon
9	2e−04	172 / 3383	EnhWk2_Colon
10	6e−04	191 / 3897	Quies1_Colon
11	7e−04	32 / 436	K9acLow_Colon
12	9e−04	421 / 9653	Enh_Colon
13	1e−03	324 / 7203	TssF_Colon
14	2e−02	3 / 15	Budinska_B_Lower crypt−like_UP
15	3e−02	2 / 7	Juehling_HNPCC−mutated−in−5
16	4e−02	10 / 131	Marisa_CRC−cluster−a
17	4e−02	48 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	5e−02	2 / 9	KIM_MSI−in−EC
19	5e−02	8 / 102	Marisa_CRC−cluster−d
20	7e−02	22 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.007	21 / 294	GUDJ_psoriasis down
2	0.757	15 / 435	GUDJ_psoriasis up
3	1.000	0 / 11	BCHETNIA_EBM up
4	1.000	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.03	12 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
2	0.03	4 / 29	shaw_responders_down_in_oligo_glioma
3	0.04	5 / 47	Vishat_subnetwork signature of survival in GBM
4	0.04	6 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
5	0.05	19 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	0.07	2 / 11	Christensen_hypermethylated_in_ependymoma
7	0.07	2 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
8	0.07	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
9	0.12	18 / 332	Up
10	0.14	5 / 68	GIEZELT_GBM_WT_down_VS_mut
11	0.15	40 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.17	5 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	0.18	1 / 5	oligodendrocytes_glio
14	0.18	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
15	0.24	4 / 63	Stuehler_Proteins_up_in_STS
16	0.25	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
17	0.26	2 / 25	Shaw_down_in_1p19q
18	0.29	3 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
19	0.31	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
20	0.31	3 / 49	OL vs. MOG−OL

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	29 / 317	PHONG_TNF_RESPONSE_NOT_VIA_P38
2	3e−05	9 / 42	PID_RHOA_REG_PATHWAY
3	4e−05	19 / 167	KIM_MYC_AMPLIFICATION_TARGETS_UP
4	7e−05	61 / 925	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
5	1e−04	5 / 13	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
6	2e−04	44 / 620	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
7	2e−04	5 / 15	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
8	2e−04	7 / 32	SIMBULAN_UV_RESPONSE_NORMAL_DN
9	2e−04	3 / 4	KERLEY_RESPONSE_TO_CISPLATIN_DN
10	3e−04	7 / 34	PID_RAC1_REG_PATHWAY
11	4e−04	29 / 367	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
12	4e−04	29 / 368	STEIN_ESRRA_TARGETS_UP
13	4e−04	4 / 10	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX5_UP
14	5e−04	35 / 482	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
15	7e−04	9 / 61	REACTOME_SEMAPHORIN_INTERACTIONS
16	7e−04	6 / 28	PID_IL2_PI3K_PATHWAY
17	9e−04	19 / 212	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
18	1e−03	21 / 249	BHAT_ESR1_TARGETS_VIA_AKT1_UP
19	1e−03	30 / 410	LIM_MAMMARY_STEM_CELL_UP
20	1e−03	8 / 53	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE

HM

Rank	p−value	#in/all	Geneset
1	2e−04	18 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	1e−03	11 / 94	HALLMARK_ANDROGEN_RESPONSE
3	2e−03	16 / 174	HALLMARK_HEME_METABOLISM
4	2e−03	8 / 57	HALLMARK_MYC_TARGETS_V2
5	2e−02	13 / 165	HALLMARK_MYOGENESIS
6	2e−02	11 / 137	HALLMARK_UV_RESPONSE_DN
7	2e−02	11 / 140	HALLMARK_APOPTOSIS
8	3e−02	14 / 196	HALLMARK_MTORC1_SIGNALING
9	4e−02	13 / 188	HALLMARK_ADIPOGENESIS
10	4e−02	12 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
11	5e−02	12 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	7e−02	8 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	7e−02	7 / 91	HALLMARK_PROTEIN_SECRETION
14	7e−02	11 / 167	HALLMARK_IL2_STAT5_SIGNALING
15	7e−02	6 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
16	9e−02	7 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
17	1e−01	12 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
18	1e−01	3 / 29	HALLMARK_NOTCH_SIGNALING
19	1e−01	9 / 141	HALLMARK_FATTY_ACID_METABOLISM
20	2e−01	10 / 181	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.5	1 / 18	DUMEAUX_High bmi 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 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−08	341 / 6929	HOPP_Txn_elongation
2	2e−07	266 / 5184	HOPP_Txn_transition
3	3e−06	358 / 7592	HOPP_Active_promoter
4	8e−06	314 / 6564	HOPP_Strong_enhancer
5	3e−05	275 / 5693	HOPP_Weak_enhancer
6	1e−04	70 / 1128	SPANG_BCR DN
7	2e−04	331 / 7209	HOPP_Weak_promoter
8	5e−04	260 / 5538	HOPP_Weak_txn
9	7e−04	117 / 2211	HOPP_Repetitive
10	4e−03	4 / 17	DAVE_NFkB BL DN
11	5e−03	9 / 80	Aukema_BCL2 DN_BCL6 UP
12	5e−03	19 / 247	ZHANG_DLBCL mutated
13	4e−02	3 / 19	DAVE_c−myc BL UP
14	4e−02	24 / 410	SPANG_CD40 6hrs DN
15	5e−02	14 / 212	LENZ_Stromal signature 1
16	9e−02	2 / 13	BENTINK_mBL UP
17	1e−01	2 / 15	DAVE_Immune response 2
18	1e−01	2 / 15	WRIGHT_ABC UP
19	1e−01	5 / 66	TARTE_Plasma cell signature
20	1e−01	113 / 2563	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	2e−05	5 / 10	semaphorin receptor binding
2	4e−04	4 / 10	Rac guanyl−nucleotide exchange factor activity
3	7e−04	5 / 19	cAMP binding
4	1e−03	9 / 66	Rho guanyl−nucleotide exchange factor activity
5	3e−03	5 / 26	growth factor binding
6	4e−03	4 / 17	Ras GTPase binding
7	5e−03	25 / 361	binding
8	6e−03	4 / 19	1−phosphatidylinositol binding
9	6e−03	3 / 10	cytoskeletal adaptor activity
10	6e−03	3 / 10	semaphorin receptor activity
11	6e−03	9 / 84	guanyl−nucleotide exchange factor activity
12	1e−02	3 / 12	Ras guanyl−nucleotide exchange factor activity
13	1e−02	386 / 8984	protein binding
14	2e−02	30 / 501	identical protein binding
15	2e−02	4 / 26	protein kinase inhibitor activity
16	2e−02	3 / 15	spectrin binding
17	2e−02	5 / 41	ATPase binding
18	2e−02	26 / 430	lipid binding
19	2e−02	3 / 16	death receptor binding
20	3e−02	9 / 111	protein binding, bridging

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−04	24 / 294	hsa−miR−561
2	9e−04	18 / 196	hsa−miR−9
3	2e−03	22 / 274	hsa−miR−1244
4	2e−03	15 / 162	hsa−miR−96
5	2e−03	18 / 214	hsa−miR−182
6	3e−03	21 / 270	hsa−miR−30b
7	3e−03	12 / 119	hsa−miR−519e
8	3e−03	9 / 77	hsa−miR−1261
9	4e−03	11 / 107	hsa−miR−190b
10	5e−03	27 / 395	hsa−miR−301b
11	5e−03	25 / 358	hsa−let−7d
12	5e−03	21 / 284	hsa−miR−503
13	6e−03	20 / 269	hsa−miR−30d
14	6e−03	12 / 130	hsa−miR−383
15	6e−03	14 / 164	hsa−miR−323b−5p
16	6e−03	25 / 366	hsa−miR−519b−3p
17	7e−03	10 / 100	hsa−miR−574−5p
18	7e−03	30 / 467	hsa−miR−301a
19	9e−03	17 / 224	hsa−miR−181b
20	9e−03	20 / 280	hsa−miR−30c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	2 / 9	BENTINK_ras.4
2	0.08	2 / 12	BENTINK_ras.1
3	0.39	1 / 12	GUSTAFSON_PI3K_UP
4	0.39	1 / 12	BENTINK_e2f3.2
5	0.41	1 / 13	GUSTAFSON_PI3K_DN
6	0.41	1 / 13	BENTINK_myc.1
7	0.46	1 / 15	BENTINK_ras.6
8	1.00	0 / 14	BENTINK_e2f3.1
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	8e−04	139 / 2714	ICGC_Irf4_targets
2	4e−03	202 / 4314	ICGC_Ebfsc137065_targets
3	4e−03	191 / 4054	ICGC_Egr1_targets
4	4e−03	97 / 1878	ICGC_Cebpbsc150_targets
5	6e−03	216 / 4682	ICGC_Pol24_targets
6	6e−03	96 / 1872	ICGC_Mef2_targets
7	9e−03	63 / 1171	KIM_MYC_targets
8	1e−02	223 / 4909	ICGC_Stat5_targets
9	1e−02	136 / 2836	ICGC_BatfPcr1_targets
10	1e−02	202 / 4414	ICGC_Bclaf101388_targets
11	1e−02	213 / 4689	ICGC_Taf1_targets
12	2e−02	99 / 2013	ICGC_Bcl11_targets
13	2e−02	244 / 5495	ICGC_Yy1_targets
14	3e−02	71 / 1418	ICGC_Ets1_targets
15	3e−02	215 / 4829	ICGC_Nficsc81335_targets
16	3e−02	36 / 653	ICGC_SrfPcr2_targets
17	3e−02	212 / 4774	ICGC_Foxm1_targets
18	4e−02	112 / 2391	ICGC_Pbx3_targets
19	4e−02	178 / 3966	ICGC_Pu1_targets
20	4e−02	82 / 1701	HEBENSTREIT_high expression TF

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	3 / 19	VAQUERIZAS_Tonsil
2	0.09	3 / 27	VAQUERIZAS_Lymph node
3	0.19	3 / 38	VAQUERIZAS_Whole brain
4	0.21	8 / 143	VAQUERIZAS_General
5	0.21	3 / 40	VAQUERIZAS_Thyroid
6	0.31	1 / 9	VAQUERIZAS_Kidney
7	0.32	2 / 29	VAQUERIZAS_Smooth muscle
8	0.41	3 / 58	VAQUERIZAS_Lung
9	0.42	3 / 59	VAQUERIZAS_Whole blood
10	0.50	1 / 17	VAQUERIZAS_Pituitary
11	0.61	1 / 23	VAQUERIZAS_Spinal cord
12	0.61	1 / 23	VAQUERIZAS_Trachea
13	0.65	1 / 26	VAQUERIZAS_Liver
14	0.69	1 / 29	VAQUERIZAS_Fetal lung
15	0.74	1 / 33	VAQUERIZAS_Prostate
16	0.77	1 / 36	VAQUERIZAS_Fetal brain
17	0.78	1 / 37	VAQUERIZAS_Thymus
18	0.79	1 / 38	VAQUERIZAS_Testis
19	0.81	1 / 41	VAQUERIZAS_Placenta
20	0.84	1 / 45	VAQUERIZAS_Uterus

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	14 / 194	PALMER_B−Cell signature up
2	0.24	17 / 350	WIRTH_Immune system
3	0.30	6 / 114	PALMER_T−Cell signature up
4	0.36	1 / 11	WIRTH_Prim. lymphoid organs
5	0.36	1 / 11	WIRTH_Cortex cerebri
6	0.39	1 / 12	WIRTH_Thymus
7	0.39	1 / 12	WIRTH_Lymphocytes
8	0.39	1 / 12	WIRTH_Cerebellum
9	0.41	1 / 13	WIRTH_Thyroid gland
10	0.43	5 / 107	WIRTH_Testis
11	0.49	2 / 41	WIRTH_Homeostasis
12	0.55	9 / 225	PALMER_Granulocytes signature up
13	0.85	1 / 46	WIRTH_Liver
14	0.90	10 / 350	WIRTH_Nervous System
15	0.90	2 / 95	WIRTH_Muscle
16	0.95	1 / 74	WIRTH_Mucosa
17	1.00	0 / 32	WIRTH_Pancreas
18	1.00	0 / 11	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_B−cells
20	1.00	0 / 8	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	46 / 1115	LU_BPDE 1h DN
2	0.7	143 / 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	

K−Means Clusters

Spot Summary: M

metagenes = 69
genes = 637

<r> metagenes = 0.71
<r> genes = 0.08
beta: r2= 0.81 / log p= −Inf

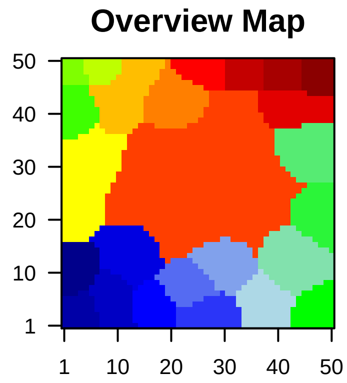
samples with spot = 4 (4.3 %)
MSC2 : 4 (16 %)

Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PDCD11	2.19	−0.54	0.24	PDCD11	programmed cell death 11 [Source:HGNC Symbol;Acc:HGNC
2	ZNF483	2.09	−0.13	0.46	ZNF483	zinc finger protein 483 [Source:HGNC Symbol;Acc:HGNC:23
3	METAP1D	2.04	−0.33	0.31	METAP1D	methionyl aminopeptidase type 1D (mitochondrial) [Source:H
4	ADARB1	2.04	−0.86	0.37	ADARB1	adenosine deaminase, RNA−specific, B1 [Source:HGNC Sym
5	C1orf111	2.02	−0.07	0.66	C1orf111	chromosome 1 open reading frame 111 [Source:HGNC Symb
6	SLC24A1	1.94	−0.09	0.54	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchange
7	GPR183	1.92	−0.15	0.49	GPR183	G protein−coupled receptor 183 [Source:HGNC Symbol;Acc:
8	SEPP1	1.92	−0.03	0.77	SEPP1	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGNC
9	C11orf71	1.91	−0.28	0.42	C11orf71	chromosome 11 open reading frame 71 [Source:HGNC Symb
10	HDAC11	1.91	−0.17	0.36	HDAC11	histone deacetylase 11 [Source:HGNC Symbol;Acc:HGNC:1
11	FCGRT	1.9	−0.05	0.36	FCGRT	Fc fragment of IgG, receptor, transporter, alpha [Source:HGN
12	RHPN2	1.85	−0.17	0.36	RHPN2	rhophilin, Rho GTPase binding protein 2 [Source:HGNC Sym
13	EPB41L4A	1.84	−0.28	0.28	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A [Source:HGN
14	PIGL	1.84	−0.33	0.26	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L [Sou
15	KCNIP4	1.84	−0.07	0.63	KCNIP4	Kv channel interacting protein 4 [Source:HGNC Symbol;Acc:
16	FGFBP2	1.83	−0.07	0.48	FGFBP2	fibroblast growth factor binding protein 2 [Source:HGNC Sym
17	RENBP	1.83	−0.24	0.45	RENBP	renin binding protein [Source:HGNC Symbol;Acc:HGNC:995
18	ZNF77	1.83	−0.17	0.42	ZNF77	zinc finger protein 77 [Source:HGNC Symbol;Acc:HGNC:131
19	STKLD1	1.82	−0.11	0.34	STKLD1	serine/threonine kinase−like domain containing 1 [Source:HG
20	TRAF2	1.82	−0.16	0.33	TRAF2	TNF receptor−associated factor 2 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−04	67 / 1033	MF	nucleic acid binding
2	6e−04	8 / 45	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
3	6e−04	8 / 46	BP	response to ionizing radiation
4	1e−03	45 / 656	Brain	Overlap_fetal_midbrain_EnhP
5	2e−03	4 / 13	MF	antigen binding
6	2e−03	4 / 13	GSEA	TSAI_DNAJB4_TARGETS_UP
7	2e−03	37 / 527	GSEA	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
8	3e−03	20 / 237	GSEA	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN
9	3e−03	116 / 2136	TF	ICGC_GabpPcr2_targets
10	3e−03	110 / 2013	TF	ICGC_Bcl11_targets
11	3e−03	6 / 35	GSEA	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
12	3e−03	103 / 1872	TF	ICGC_Mef2_targets
13	4e−03	7 / 47	GSEA	LEE_EARLY_T_LYMPHOCYTE_DN
14	4e−03	152 / 2927	TF	ICGC_Rad21_targets
15	4e−03	3 / 8	GSEA	BIOCARTA_SODD_PATHWAY
16	5e−03	15 / 167	GSEA	BROWNE_HCMV_INFECTION_18HR_UP
17	6e−03	284 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
18	6e−03	5 / 28	GSEA	BIOCARTA_TNFR1_PATHWAY
19	6e−03	63 / 1079	Colon	ZNF_Colon
20	6e−03	6 / 40	GSEA	MIKKELSEN_NPC_LCP_WITH_H3K4ME3
21	7e−03	7 / 53	BP	phosphatidylinositol biosynthetic process
22	7e−03	62 / 1065	Brain	Overlap_fetal_midbrain_Enh
23	7e−03	3 / 10	BP	cardiac muscle cell proliferation
24	7e−03	3 / 10	BP	production of miRNAs involved in gene silencing by miRNA
25	8e−03	26 / 367	GSEA	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
26	8e−03	24 / 331	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
27	8e−03	194 / 3924	TF	ICGC_Zeb1_targets
28	8e−03	7 / 55	GSEA	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
29	9e−03	13 / 145	miRN	hsa−miR−922
30	9e−03	4 / 20	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_D
31	9e−03	9 / 84	miRN	hsa−miR−339−5p
32	9e−03	5 / 31	GSEA	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_DN
33	9e−03	228 / 4706	TF	ICGC_Sp1_targets
34	1e−02	71 / 1266	TF	ICGC_NrsfPcr1_targets
35	1e−02	125 / 2416	TF	ICGC_Bcl3_targets
36	1e−02	6 / 44	GSEA	REACTOME_PI_METABOLISM
37	1e−02	17 / 215	miRN	hsa−miR−199a−3p
38	1e−02	4 / 21	GSEA	LA_MEN1_TARGETS
39	1e−02	8 / 72	GSEA	JAIN_NFKB_SIGNALING
40	1e−02	23 / 325	GSEA	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY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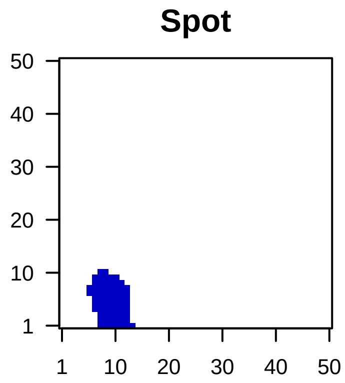
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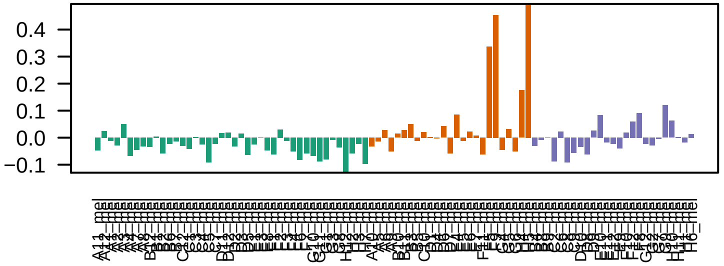
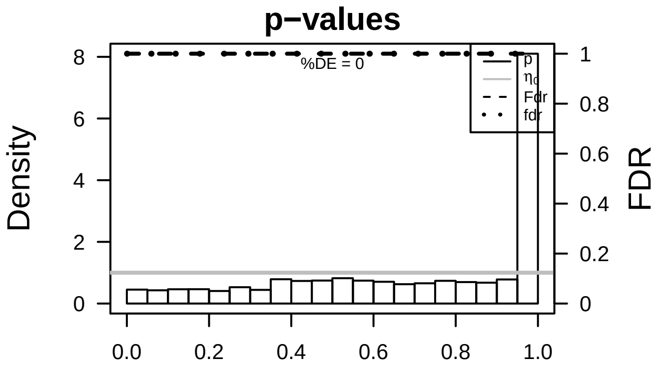



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 111	HORVATH_aging_genes meth UP
2	0.4	5 / 100	HORVATH_aging_genes meth DOWN
3	0.8	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	6e−04	8 / 46	response to ionizing radiation
2	7e−03	7 / 53	phosphatidylinositol biosynthetic process
3	7e−03	3 / 10	cardiac muscle cell proliferation
4	7e−03	3 / 10	production of miRNAs involved in gene silencing by miRNA
5	1e−02	3 / 12	cardiac epithelial to mesenchymal transition
6	1e−02	3 / 12	cerebellar Purkinje cell layer development
7	1e−02	4 / 22	one−carbon metabolic process
8	1e−02	12 / 136	phospholipid metabolic process
9	2e−02	3 / 14	positive regulation of chemokine production
10	2e−02	3 / 14	positive regulation of JAK−STAT cascade
11	2e−02	7 / 65	potassium ion transmembrane transport
12	2e−02	11 / 130	protein dephosphorylation
13	2e−02	4 / 26	positive regulation of extrinsic apoptotic signaling pathway
14	2e−02	3 / 15	negative regulation of cell cycle arrest
15	2e−02	3 / 15	peptide hormone processing
16	2e−02	3 / 15	regulation of JNK cascade
17	3e−02	4 / 28	response to gamma radiation
18	3e−02	3 / 17	pseudouridine synthesis
19	3e−02	8 / 88	peptidyl−tyrosine dephosphorylation
20	4e−02	81 / 1565	regulation of transcription, DNA−templated

Brain

Rank	p−value	#in/all	Geneset
1	0.001	45 / 656	Overlap_fetal_midbrain_EnhP
2	0.006	284 / 5940	Overlap_fetal_midbrain_HetRpts
3	0.007	62 / 1065	Overlap_fetal_midbrain_Enh
4	0.024	50 / 884	Overlap_fetal_midbrain_EnhG
5	0.025	408 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	0.026	45 / 786	Fetal_EnhG
7	0.102	76 / 1548	Mid_Frontal_Lobe_K9K27me3
8	0.119	51 / 1013	Fetal_TssP
9	0.146	39 / 769	Overlap_fetal_midbrain_ZNF
10	0.149	49 / 989	Mid_Frontal_Lobe_Quies
11	0.169	29 / 564	Mid_Frontal_Lobe_EnhP
12	0.208	135 / 2972	Mid_Frontal_Lobe_ReprPC
13	0.251	89 / 1949	Fetal_TssF
14	0.253	414 / 9528	Overlap_fetal_midbrain_Quies
15	0.253	45 / 953	Fetal_Enh
16	0.289	36 / 765	Mid_Frontal_Lobe_Het
17	0.347	8 / 156	Mid_Frontal_Lobe_TssA
18	0.381	47 / 1050	Fetal_EnhP
19	0.388	50 / 1122	Fetal_K9K27me3
20	0.422	24 / 534	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	3 / 20	PanCan_ChromMod_geneset_nanostring
2	0.13	2 / 15	GENTLES_modul11
3	0.18	2 / 18	PanCan_Notch_geneset_nanostring
4	0.35	1 / 10	GENTLES_modul13
5	0.36	9 / 180	SPANG_LPS−index2
6	0.38	1 / 11	GENTLES_modul17
7	0.42	3 / 55	PanCan_JAK−ST_geneset_nanostring
8	0.46	1 / 14	LIU_LIVER_CANCER
9	0.48	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	0.48	1 / 15	GENTLES_modul1
11	0.48	1 / 15	GENTLES_modul4
12	0.50	1 / 16	WOLFER_overlap genes
13	0.50	1 / 16	GENTLES_modul2
14	0.50	1 / 16	GENTLES_modul14
15	0.51	2 / 40	PanCan_HK_geneset_nanostring
16	0.53	5 / 113	PanCan_Driver_Gene_geneset_nanostring
17	0.58	3 / 70	SHAUGHNESSY_MM high risk
18	0.76	4 / 121	PanCan_MAPK_geneset_nanostring
19	0.82	1 / 40	ZHANG_MM up
20	0.86	3 / 111	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.01	3 / 12	XY body
2	0.03	4 / 27	condensed chromosome
3	0.04	4 / 31	brush border membrane
4	0.06	5 / 51	voltage−gated potassium channel complex
5	0.06	2 / 10	MHC class I protein complex
6	0.06	2 / 10	pericentric heterochromatin
7	0.07	12 / 175	early endosome
8	0.08	2 / 11	RISC complex
9	0.09	2 / 12	npBAF complex
10	0.10	2 / 13	DNA−directed RNA polymerase I complex
11	0.10	2 / 13	nBAF complex
12	0.10	2 / 13	SWI/SNF complex
13	0.11	3 / 27	photoreceptor connecting cilium
14	0.11	5 / 60	nuclear pore
15	0.12	5 / 61	cytoplasmic mRNA processing body
16	0.13	2 / 15	BAF−type complex
17	0.13	2 / 15	dendrite cytoplasm
18	0.13	2 / 15	extrinsic component of plasma membrane
19	0.13	3 / 30	sarcomere
20	0.14	6 / 83	endomembrane system

Chr

Rank	p−value	#in/all	Geneset
1	0.01	36 / 576	Chr 9
2	0.05	32 / 552	Chr 10
3	0.10	26 / 465	Chr 15
4	0.19	9 / 151	Chr 21
5	0.34	19 / 398	Chr 20
6	0.35	26 / 558	Chr 4
7	0.53	20 / 469	Chr 8
8	0.54	42 / 993	Chr 2
9	0.56	11 / 262	Chr 13
10	0.57	63 / 1500	Chr 1
11	0.58	29 / 696	Chr 5
12	0.58	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
13	0.60	43 / 1037	Chr 19
14	0.65	34 / 840	Chr 17
15	0.73	25 / 649	Chr 16
16	0.73	30 / 775	Chr 12
17	0.77	26 / 689	Chr 7
18	0.79	30 / 801	Chr 11
19	0.84	7 / 221	Chr 18
20	0.85	11 / 335	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.006	63 / 1079	ZNF_Colon
2	0.024	74 / 1386	Het_Colon
3	0.028	57 / 1038	HetRpts_Colon
4	0.043	2 / 8	KIM_CRC−MSI−regulated_DN
5	0.055	20 / 319	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	0.069	8 / 102	Marisa_CRC−cluster−d
7	0.077	129 / 2698	EnhA_Colon
8	0.126	8 / 117	Marisa_CRC−cluster−b
9	0.129	15 / 255	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	0.132	22 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	0.137	264 / 5880	TssD2_Colon
12	0.149	5 / 66	Marisa_CRC−cluster−h
13	0.155	155 / 3383	EnhWk2_Colon
14	0.157	378 / 8580	TxWk_Colon
15	0.158	371 / 8415	Quies3_Colon
16	0.160	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
17	0.160	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
18	0.164	3 / 33	Marisa_CRC−cluster−e
19	0.173	231 / 5155	EnhWk1_Colon
20	0.182	30 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 11	BCHETNIA_EBM up
2	0.4	20 / 435	GUDJ_psoriasis up
3	0.9	8 / 294	GUDJ_psoriasis down
4	1.0	0 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	2 / 9	Phillips PN up vs MES & Prolif
2	0.06	5 / 49	OL vs. MOG− OL
3	0.08	1 / 2	laffaire_hypometh_LGG_vs_control
4	0.08	1 / 2	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
5	0.09	2 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
6	0.13	18 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.13	2 / 15	VERHAAK_MES subtype
8	0.16	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
9	0.16	2 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
10	0.16	5 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
11	0.16	5 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	0.17	3 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
13	0.20	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
14	0.23	1 / 6	shaw_responders_up_in_oligo_glioma
15	0.23	1 / 6	neurons_glio
16	0.26	10 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
17	0.26	18 / 356	Down_a
18	0.26	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
19	0.26	1 / 7	KIM_amplified & overexpressed in LTS
20	0.29	2 / 25	Shaw_down_in_1p19q

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	8 / 45	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN
2	2e−03	4 / 13	TSAI_DNAJB4_TARGETS_UP
3	2e−03	37 / 527	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
4	3e−03	20 / 237	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN
5	3e−03	6 / 35	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
6	4e−03	7 / 47	LEE_EARLY_T_LYMPHOCYTE_DN
7	4e−03	3 / 8	BIOCARTA_SODD_PATHWAY
8	5e−03	15 / 167	BROWNE_HCMV_INFECTION_18HR_UP
9	6e−03	5 / 28	BIOCARTA_TNFR1_PATHWAY
10	6e−03	6 / 40	MIKKELSEN_NPC_LCP_WITH_H3K4ME3
11	8e−03	26 / 367	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
12	8e−03	24 / 331	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
13	8e−03	7 / 55	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
14	9e−03	4 / 20	RICKMAN_HEAD_AND_NECK_CANCER_D
15	9e−03	5 / 31	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_DN
16	1e−02	6 / 44	REACTOME_PI_METABOLISM
17	1e−02	4 / 21	LA_MEN1_TARGETS
18	1e−02	8 / 72	JAIN_NFKB_SIGNALING
19	1e−02	23 / 325	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
20	1e−02	5 / 33	SIG_CD40PATHWAYMAP

HM

Rank	p−value	#in/all	Geneset
1	0.02	11 / 127	HALLMARK_KRAS_SIGNALING_DN
2	0.07	4 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.18	9 / 148	HALLMARK_KRAS_SIGNALING_UP
4	0.30	9 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.35	2 / 29	HALLMARK_NOTCH_SIGNALING
6	0.43	8 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.45	6 / 126	HALLMARK_ALLOGRAFT_REJECTION
8	0.47	2 / 37	HALLMARK_APICAL_SURFACE
9	0.54	7 / 162	HALLMARK_COMPLEMENT
10	0.55	6 / 140	HALLMARK_APOPTOSIS
11	0.57	7 / 167	HALLMARK_IL2_STAT5_SIGNALING
12	0.58	4 / 95	HALLMARK_SPERMATOGENESIS
13	0.59	4 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.69	4 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	0.69	7 / 188	HALLMARK_ADIPOGENESIS
16	0.71	6 / 165	HALLMARK_MYOGENESIS
17	0.73	2 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
18	0.75	5 / 146	HALLMARK_UV_RESPONSE_UP
19	0.76	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	0.77	3 / 94	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	3 / 32	DUMEAUX_Fasting enriched genes
2	0.2	1 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.3	4 / 62	DUMEAUX_Smoking enriched genes
4	0.4	1 / 10	DUMEAUX_Smoking literature genes up
5	0.5	1 / 18	DUMEAUX_High bmi enriched genes
6	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 4	DUMEAUX_Estrogen related in 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	0.04	60 / 1128	SPANG_BCR DN
2	0.08	253 / 5538	HOPP_Weak_txn
3	0.08	16 / 256	SPANG_IL21 DN
4	0.10	9 / 129	DAVE_BL−vs−DLBCL
5	0.10	2 / 13	YAMANE_AICDA_targets_recruited
6	0.11	23 / 410	SPANG_CD40 6hrs DN
7	0.12	1 / 3	WRIGHT_custom GCB−DLBCL UP
8	0.14	104 / 2211	HOPP_Repetitive
9	0.23	1 / 6	DAVE_MHCCII BL DN
10	0.29	1 / 8	MASCQUE_GCB UP
11	0.29	1 / 8	MASCQUE_ABC UP
12	0.29	1 / 8	Subero_MM_hypo_meth
13	0.31	4 / 66	TARTE_Plasma cell signature
14	0.35	2 / 29	Subero_DLBCL_hypo_meth
15	0.36	3 / 50	SPANG_BAFF 9hrs DN
16	0.36	12 / 247	ZHANG_DLBCL mutated
17	0.36	247 / 5693	HOPP_Weak_enhancer
18	0.37	2 / 30	Subero_INT_hypo_meth
19	0.38	1 / 11	Subero_T−ALL_hypo_meth
20	0.43	1 / 13	WRIGHT_GCB UP

MF

Rank	p−value	#in/all	Geneset
1	3e−04	67 / 1033	nucleic acid binding
2	2e−03	4 / 13	antigen binding
3	2e−02	4 / 23	hydrolase activity, acting on ester bonds
4	2e−02	97 / 1859	metal ion binding
5	2e−02	5 / 38	protein serine/threonine phosphatase activity
6	2e−02	6 / 52	double−stranded RNA binding
7	2e−02	4 / 26	endopeptidase inhibitor activity
8	2e−02	3 / 15	ARF guanyl−nucleotide exchange factor activity
9	3e−02	57 / 1040	zinc ion binding
10	3e−02	9 / 102	mRNA binding
11	4e−02	8 / 89	protein tyrosine phosphatase activity
12	4e−02	10 / 123	nucleotidyltransferase activity
13	4e−02	3 / 19	acyl−CoA dehydrogenase activity
14	5e−02	32 / 550	protein homodimerization activity
15	5e−02	232 / 4992	ion binding
16	6e−02	3 / 21	histone deacetylase activity
17	6e−02	3 / 22	calmodulin−dependent protein kinase activity
18	6e−02	3 / 22	delayed rectifier potassium channel activity
19	6e−02	3 / 22	oxidoreductase activity, acting on the CH−CH group of donors
20	7e−02	7 / 85	metalloendopeptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.009	13 / 145	hsa−miR−922
2	0.009	9 / 84	hsa−miR−339−5p
3	0.011	17 / 215	hsa−miR−199a−3p
4	0.015	14 / 171	hsa−miR−607
5	0.016	6 / 48	hsa−miR−524−3p
6	0.017	7 / 63	hsa−miR−1285
7	0.019	13 / 160	hsa−miR−1297
8	0.019	5 / 37	hsa−miR−1274a
9	0.022	17 / 233	hsa−miR−26a
10	0.023	8 / 82	hsa−miR−767−5p
11	0.028	9 / 101	hsa−miR−325
12	0.029	5 / 41	hsa−miR−532−3p
13	0.030	17 / 242	hsa−miR−26b
14	0.035	5 / 43	hsa−miR−661
15	0.040	17 / 251	hsa−miR−548l
16	0.041	5 / 45	hsa−miR−660
17	0.041	5 / 45	hsa−miR−411
18	0.045	6 / 61	hsa−miR−612
19	0.050	4 / 33	hsa−miR−589
20	0.053	2 / 9	hsa−miR−720

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 14	BENTINK_src.2
2	0.4	1 / 13	BENTINK_myc.1
3	0.5	1 / 15	BENTINK_ras.6
4	1.0	0 / 12	GUSTAFSON_PI3K_UP
5	1.0	0 / 13	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 12	BENTINK_e2f3.2
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 9	BENTINK_ras.4
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	0.003	116 / 2136	ICGC_GabpPcr2_targets
2	0.003	110 / 2013	ICGC_Bcl11_targets
3	0.003	103 / 1872	ICGC_Mef2_targets
4	0.004	152 / 2927	ICGC_Rad21_targets
5	0.008	194 / 3924	ICGC_Zeb1_targets
6	0.009	228 / 4706	ICGC_Sp1_targets
7	0.010	71 / 1266	ICGC_NrsfPcr1_targets
8	0.010	125 / 2416	ICGC_Bcl3_targets
9	0.013	234 / 4879	ICGC_Pmlsc71910_targets
10	0.015	197 / 4054	ICGC_Egr1_targets
11	0.016	248 / 5219	ICGC_Tcf3_targets
12	0.016	260 / 5495	ICGC_Yy1_targets
13	0.018	211 / 4385	ICGC_Atf2_targets
14	0.018	224 / 4682	ICGC_Pol24_targets
15	0.019	195 / 4032	ICGC_Creb1_targets
16	0.019	253 / 5355	ICGC_Pol2_targets
17	0.020	192 / 3966	ICGC_Pu1_targets
18	0.023	109 / 2137	ICGC_SrfV0416101_targets
19	0.023	211 / 4414	ICGC_Bclaf101388_targets
20	0.023	223 / 4689	ICGC_Taf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	11 / 143	VAQUERIZAS_General
2	0.25	3 / 41	VAQUERIZAS_Placenta
3	0.26	1 / 7	VAQUERIZAS_Tongue
4	0.41	1 / 12	VAQUERIZAS_Skin
5	0.46	2 / 36	VAQUERIZAS_Fetal brain
6	0.48	1 / 15	VAQUERIZAS_Fetal thyroid
7	0.49	2 / 38	VAQUERIZAS_Whole brain
8	0.49	2 / 38	VAQUERIZAS_Testis
9	0.51	2 / 40	VAQUERIZAS_Thyroid
10	0.52	1 / 17	VAQUERIZAS_Heart
11	0.63	1 / 23	VAQUERIZAS_Spinal cord
12	0.76	1 / 33	VAQUERIZAS_Prostate
13	0.86	1 / 45	VAQUERIZAS_Uterus
14	0.92	1 / 58	VAQUERIZAS_Lung
15	1.00	0 / 26	VAQUERIZAS_Liver
16	1.00	0 / 29	VAQUERIZAS_Smooth muscle
17	1.00	0 / 9	VAQUERIZAS_Kidney
18	1.00	0 / 37	VAQUERIZAS_Thymus
19	1.00	0 / 59	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	22 / 350	WIRTH_Immune system
2	0.08	2 / 11	WIRTH_Prim. lymphoid organs
3	0.29	1 / 8	WIRTH_Tonsil
4	0.40	2 / 32	WIRTH_Pancreas
5	0.40	2 / 32	WIRTH_Placenta
6	0.53	2 / 41	WIRTH_Homeostasis
7	0.54	5 / 114	PALMER_T−Cell signature up
8	0.59	8 / 194	PALMER_B−Cell signature up
9	0.59	2 / 46	WIRTH_Liver
10	0.62	3 / 74	WIRTH_Mucosa
11	0.67	4 / 107	WIRTH_Testis
12	0.75	8 / 225	PALMER_Granulocytes signature up
13	0.78	3 / 95	WIRTH_Muscle
14	0.88	11 / 350	WIRTH_Nervous System
15	1.00	0 / 11	WIRTH_Sec. lymphoid organs
16	1.00	0 / 13	WIRTH_B−cells
17	1.00	0 / 12	WIRTH_Thymus
18	1.00	0 / 12	WIRTH_Lymphocytes
19	1.00	0 / 5	WIRTH_Bone marrow
20	1.00	0 / 11	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	56 / 1115	LU_BPDE 1h DN
2	0.4	161 / 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	

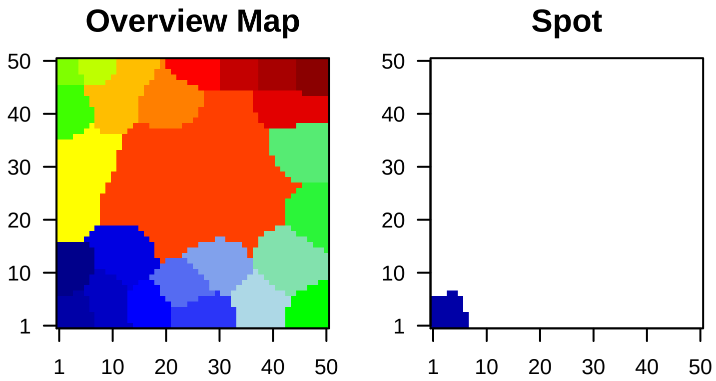
K−Means Clusters

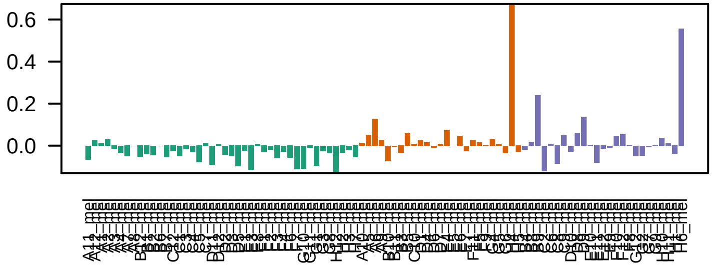
Spot Summary: N

metagenes = 41
genes = 641

<r> metagenes = 0.78
<r> genes = 0.09
beta: r2= 1.21 / log p= −Inf

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



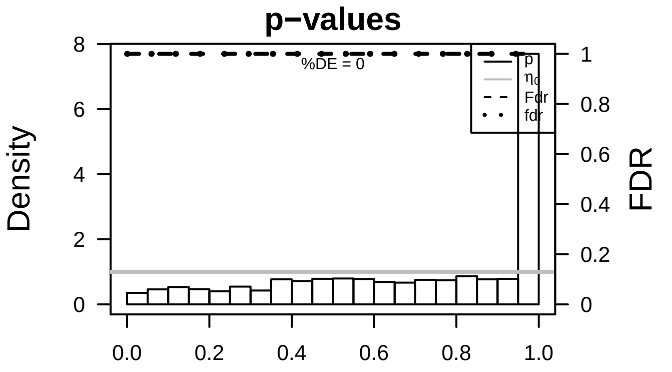


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	HORMAD1	2.38	−0.23	0.34	HORMAD1	HORMA domain containing 1 [Source:HGNC Symbol;Acc:HG
2	SCHIP1	2.29	−0.1	0.48	SCHIP1	schwannomin interacting protein 1 [Source:HGNC Symbol;Ac
3	NINL	2.26	−0.04	0.79	NINL	ninein−like [Source:HGNC Symbol;Acc:HGNC:29163]
4	PAN2	2.19	−0.24	0.32	PAN2	PAN2 poly(A) specific ribonuclease subunit [Source:HGNC Sy
5	GPR107	2.16	−0.36	0.34	GPR107	G protein−coupled receptor 107 [Source:HGNC Symbol;Acc:
6	MAGEA1	2.11	−0.1	0.48	MAGEA1	melanoma antigen family A1 [Source:HGNC Symbol;Acc:HG
7	C14orf93	2.1	−0.34	0.43	C14orf93	chromosome 14 open reading frame 93 [Source:HGNC Symb
8	NPL	2.03	−0.15	0.37	NPL	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
9	GARNL3	2.01	−0.2	0.26	GARNL3	GTPase activating Rap/RanGAP domain−like 3 [Source:HGN
10	COL4A5	2.01	−0.07	0.46	COL4A5	collagen, type IV, alpha 5 [Source:HGNC Symbol;Acc:HGNC:
11	FAM154B	1.99	−0.18	0.3		
12	THNSL2	1.98	−0.03	0.7	THNSL2	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
13	TMEM164	1.95	−0.23	0.42	TMEM164	transmembrane protein 164 [Source:HGNC Symbol;Acc:HGN
14	IFI44	1.95	−0.25	0.34	IFI44	interferon−induced protein 44 [Source:HGNC Symbol;Acc:HG
15	CFP	1.94	−0.03	0.87	CFP	complement factor properdin [Source:HGNC Symbol;Acc:HG
16	RANBP3L	1.9	−0.03	0.86	RANBP3L	RAN binding protein 3−like [Source:HGNC Symbol;Acc:HGN
17	LPHN1	1.9	−0.17	0.32		
18	PORCN	1.88	−0.18	0.38	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
19	PCDHGC3	1.86	−0.36	0.29	PCDHGC3	protocadherin gamma subfamily C, 3 [Source:HGNC Symbol;
20	WWC1	1.86	−0.12	0.48	WWC1	WW and C2 domain containing 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−05	72 / 1079	Colon	ZNF_Colon
2	2e−04	100 / 1664	BP	transcription, DNA−templated
3	4e−04	18 / 172	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP
4	6e−04	6 / 26	GSEA	EINAV_INTERFERON_SIGNATURE_IN_CANCER
5	7e−04	7 / 36	BP	erythrocyte differentiation
6	8e−04	346 / 7203	Colon	TssF_Colon
7	8e−04	4 / 11	BP	tRNA modification
8	9e−04	106 / 1859	MF	metal ion binding
9	1e−03	13 / 115	GSEA	TSENG_IRS1_TARGETS_DN
10	1e−03	441 / 9528	Brain	Overlap_fetal_midbrain_Quies
11	2e−03	64 / 1037	Chr	Chr 19
12	2e−03	4 / 13	Lymph	BENTINK_mBL UP
13	2e−03	8 / 54	GSEA	DASU_IL6_SIGNALING_UP
14	2e−03	3 / 7	GSEA	JIANG_CORE_DUPLICON_GENES
15	3e−03	4 / 15	BP	keratinization
16	3e−03	131 / 2462	Brain	Mid_Frontal_Lobe_HetRpts
17	4e−03	146 / 2798	Colon	TxEnhG1_Colon
18	4e−03	4 / 16	BP	calcium ion import
19	4e−03	7 / 49	GSEA	LEE_LIVER_CANCER_MYC_E2F1_UP
20	6e−03	32 / 469	GSEA	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP
21	6e−03	4 / 18	GSEA	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP
22	7e−03	8 / 67	GSEA	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
23	7e−03	3 / 10	BP	regulation of cytokine production
24	8e−03	41 / 649	Chr	Chr 16
25	8e−03	4 / 19	GSEA	FARMER_BREAST_CANCER_CLUSTER_7
26	8e−03	79 / 1418	TF	ICGC_Ets1_targets
27	8e−03	45 / 730	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
28	8e−03	5 / 30	GSEA	REACTOME_NCAM1_INTERACTIONS
29	9e−03	8 / 69	GSEA	DER_IFN_ALPHA_RESPONSE_UP
30	9e−03	15 / 178	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
31	9e−03	4 / 20	BP	behavioral fear response
32	9e−03	4 / 20	CC	dynein complex
33	9e−03	4 / 20	MF	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anh
34	9e−03	4 / 20	GSEA	ZHANG_INTERFERON_RESPONSE
35	9e−03	5 / 31	GSEA	KAAB_FAILED_HEART_ATRIUM_UP
36	1e−02	8 / 70	GSEA	VANLOO_SP3_TARGETS_DN
37	1e−02	3 / 11	GSEA	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
38	1e−02	279 / 5880	Colon	TssD2_Colon
39	1e−02	7 / 57	GSEA	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP
40	1e−02	2 / 4	GSEA	HAEGERSTRAND_RESPONSE_TO_IMATINIB



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	2e−04	100 / 1664	transcription, DNA−templated
2	7e−04	7 / 36	erythrocyte differentiation
3	8e−04	4 / 11	tRNA modification
4	3e−03	4 / 15	keratinization
5	4e−03	4 / 16	calcium ion import
6	7e−03	3 / 10	regulation of cytokine production
7	9e−03	4 / 20	behavioral fear response
8	1e−02	10 / 101	RNA processing
9	2e−02	5 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
10	2e−02	3 / 14	response to morphine
11	3e−02	3 / 16	positive regulation of sodium ion transport
12	3e−02	3 / 16	regulation of protein catabolic process
13	3e−02	3 / 16	tRNA methylation
14	3e−02	6 / 56	protein O−linked glycosylation
15	3e−02	190 / 3980	cellular nitrogen compound metabolic process
16	4e−02	3 / 18	2−oxoglutarate metabolic process
17	4e−02	174 / 3644	biosynthetic process
18	4e−02	3 / 19	cochlea morphogenesis
19	5e−02	80 / 1565	regulation of transcription, DNA−templated
20	5e−02	4 / 33	face morphogenesis

Brain

Rank	p−value	#in/all	Geneset
1	0.001	441 / 9528	Overlap_fetal_midbrain_Quies
2	0.003	131 / 2462	Mid_Frontal_Lobe_HetRpts
3	0.014	40 / 656	Overlap_fetal_midbrain_EnhP
4	0.017	153 / 3081	Mid_Frontal_Lobe_ZNF
5	0.028	407 / 9013	Overlap_fetal_midbrain_K9K27me3
6	0.095	140 / 2972	Mid_Frontal_Lobe_ReprPC
7	0.108	66 / 1333	Fetal_ReprPCWk
8	0.114	412 / 9330	Overlap_fetal_midbrain_ReprPC
9	0.148	266 / 5940	Overlap_fetal_midbrain_HetRpts
10	0.153	92 / 1949	Fetal_TssF
11	0.231	37 / 765	Mid_Frontal_Lobe_Het
12	0.241	37 / 769	Overlap_fetal_midbrain_ZNF
13	0.267	392 / 9020	Overlap_fetal_midbrain_ReprPCWk
14	0.269	49 / 1050	Fetal_EnhP
15	0.271	12 / 229	Mid_Frontal_Lobe_TxTrans
16	0.294	38 / 812	Mid_Frontal_Lobe_TssP
17	0.297	86 / 1907	Fetal_TxTrans
18	0.340	25 / 534	Mid_Frontal_Lobe_EnhG
19	0.347	8 / 156	Mid_Frontal_Lobe_TssA
20	0.512	7 / 158	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	3 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.08	12 / 180	SPANG_LPS−index2
3	0.14	17 / 298	SPANG_BCL6−index2
4	0.15	2 / 16	GENTLES_modul2
5	0.26	7 / 121	PanCan_MAPK_geneset_nanostring
6	0.33	6 / 111	PanCan_RAS_geneset_nanostring
7	0.35	8 / 156	PanCan_PI3K_geneset_nanostring
8	0.37	1 / 14	LIU_LIVER_CANCER
9	0.41	1 / 12	BEN−PORATH_DN
10	0.44	18 / 401	Lembcke_Colonic Inflammation
11	0.45	0 / 12	LIU_PROSTATE_CANCER_UP
12	0.46	1 / 14	LIU_PROSTATE_CANCER_DN
13	0.48	1 / 15	WANG_ER_UP
14	0.50	1 / 16	GENTLES_modul7
15	0.50	1 / 16	GENTLES_modul16
16	0.54	0 / 14	LIU_COMMON_CANCER_GENES
17	0.54	1 / 18	PanCan_Notch_geneset_nanostring
18	0.58	3 / 70	SHAUGHNESSY_MM high risk
19	0.58	5 / 120	PanCan_CC+Apop_geneset_nanostring
20	0.61	20 / 489	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	0.009	4 / 20	dynein complex
2	0.016	6 / 48	clathrin−coated vesicle
3	0.037	4 / 30	small−subunit processome
4	0.039	3 / 18	intraciliary transport particle B
5	0.049	5 / 47	actin filament
6	0.057	7 / 81	late endosome membrane
7	0.065	5 / 51	axoneme
8	0.065	5 / 51	collagen trimer
9	0.077	2 / 11	acetylcholine−gated channel complex
10	0.077	2 / 11	CD40 receptor complex
11	0.080	3 / 24	cortical actin cytoskeleton
12	0.090	2 / 12	HOPS complex
13	0.090	2 / 12	npBAF complex
14	0.092	9 / 127	cytoplasmic vesicle
15	0.096	4 / 41	ciliary tip
16	0.104	57 / 1132	Golgi apparatus
17	0.104	2 / 13	integrator complex
18	0.104	2 / 13	nBAF complex
19	0.104	2 / 13	Sin3 complex
20	0.104	2 / 13	SWI/SNF complex

Chr

Rank	p−value	#in/all	Geneset
1	0.002	64 / 1037	Chr 19
2	0.008	41 / 649	Chr 16
3	0.024	46 / 801	Chr 11
4	0.075	32 / 576	Chr 9
5	0.125	19 / 335	Chr 22
6	0.251	27 / 551	Chr X
7	0.251	40 / 840	Chr 17
8	0.325	26 / 552	Chr 10
9	0.325	13 / 262	Chr 13
10	0.341	11 / 221	Chr 18
11	0.422	21 / 465	Chr 15
12	0.438	21 / 469	Chr 8
13	0.502	20 / 462	Chr 14
14	0.566	63 / 1500	Chr 1
15	0.576	29 / 696	Chr 5
16	0.626	6 / 151	Chr 21
17	0.863	30 / 838	Chr 3
18	0.900	35 / 993	Chr 2
19	0.914	18 / 558	Chr 4
20	0.992	18 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−05	72 / 1079	ZNF_Colon
2	8e−04	346 / 7203	TssF_Colon
3	4e−03	146 / 2798	TxEnhG1_Colon
4	1e−02	279 / 5880	TssD2_Colon
5	2e−02	136 / 2698	EnhA_Colon
6	2e−02	245 / 5155	EnhWk1_Colon
7	3e−02	388 / 8580	TxWk_Colon
8	4e−02	2 / 8	Marisa_CRC−C1
9	5e−02	404 / 9027	Tx_Colon
10	7e−02	455 / 10290	TssWk_Colon
11	1e−01	2 / 15	Juehling_HNPCC−mutated−in−4
12	1e−01	2 / 15	Budinska_B_Lower crypt−like_UP
13	1e−01	2 / 16	Juehling−MSI−enriched−in−6
14	2e−01	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
15	2e−01	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
16	2e−01	3 / 33	Marisa_CRC−cluster−e
17	2e−01	414 / 9482	TssA_Colon
18	2e−01	421 / 9653	Enh_Colon
19	2e−01	65 / 1386	Het_Colon
20	2e−01	1 / 6	Budinska_E_Mixed_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.4	20 / 435	GUDJ_psoriasis up
2	1.0	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	0.08	4 / 38	OL vs. OPC
2	0.08	7 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.08	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
4	0.10	2 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
5	0.14	4 / 47	mature astrocytes
6	0.14	4 / 47	Weller_LGG_gradeII−vs−III_UP
7	0.16	5 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	0.18	2 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
9	0.19	17 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	0.26	2 / 23	Donson−Misc immune function−associated with LTS in HGA
11	0.26	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
12	0.29	1 / 8	VERHAAK_PN_Brain
13	0.30	4 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
14	0.32	2 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
15	0.32	3 / 47	Vishal_subnetwork signature of survival in GBM
16	0.32	3 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
17	0.32	1 / 9	VERHAAK_Brain
18	0.32	1 / 9	Phillips PN up vs MES & Prolif
19	0.32	1 / 9	WILLSCHER_GBM_Verhaak−PNmut_up (M)
20	0.35	3 / 49	OL vs. MOG−OL

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	18 / 172	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP
2	6e−04	6 / 26	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	1e−03	13 / 115	TSENG_IRS1_TARGETS_DN
4	2e−03	8 / 54	DASU_IL6_SIGNALING_UP
5	2e−03	3 / 7	JIANG_CORE_DUPLICON_GENES
6	4e−03	7 / 49	LEE_LIVER_CANCER_MYC_E2F1_UP
7	6e−03	32 / 469	GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP
8	6e−03	4 / 18	HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP
9	7e−03	8 / 67	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
10	8e−03	4 / 19	FARMER_BREAST_CANCER_CLUSTER_7
11	8e−03	45 / 730	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
12	8e−03	5 / 30	REACTOME_NCAM1_INTERACTIONS
13	9e−03	8 / 69	DER_IFN_ALPHA_RESPONSE_UP
14	9e−03	15 / 178	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
15	9e−03	4 / 20	ZHANG_INTERFERON_RESPONSE
16	9e−03	5 / 31	KAAB_FAILED_HEART_ATRIUM_UP
17	1e−02	8 / 70	VANLOO_SP3_TARGETS_DN
18	1e−02	3 / 11	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
19	1e−02	7 / 57	HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP
20	1e−02	2 / 4	HAEGERSTRAND_RESPONSE_TO_IMATINIB

HM

Rank	p−value	#in/all	Geneset
1	0.01	9 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	0.06	12 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.17	8 / 126	HALLMARK_ALLOGRAFT_REJECTION
4	0.21	10 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.24	10 / 181	HALLMARK_P53_PATHWAY
6	0.28	8 / 146	HALLMARK_UV_RESPONSE_UP
7	0.37	7 / 137	HALLMARK_UV_RESPONSE_DN
8	0.39	7 / 140	HALLMARK_INFLAMMATORY_RESPONSE
9	0.42	8 / 167	HALLMARK_APICAL_JUNCTION
10	0.43	8 / 169	HALLMARK_XENOBIOTIC_METABOLISM
11	0.56	7 / 165	HALLMARK_MYOGENESIS
12	0.69	4 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	0.72	1 / 29	HALLMARK_NOTCH_SIGNALING
14	0.73	6 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	0.74	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
16	0.75	3 / 91	HALLMARK_PROTEIN_SECRETION
17	0.75	3 / 91	HALLMARK_BILE_ACID_METABOLISM
18	0.76	6 / 174	HALLMARK_HEME_METABOLISM
19	0.76	5 / 148	HALLMARK_KRAS_SIGNALING_UP
20	0.78	3 / 95	HALLMARK_SPERMATOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
2	0.3	4 / 62	DUMEAUX_Smoking enriched genes
3	0.5	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.5	1 / 18	DUMEAUX_High bmi enriched genes
5	0.8	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 / 4	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Hormon therapy 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	0.002	4 / 13	BENTINK_mBL UP
2	0.024	2 / 6	MASCQUE_mBL UP
3	0.072	24 / 410	SPANG_CD40 6hrs DN
4	0.079	62 / 1218	SPANG_BCR UP
5	0.081	16 / 256	SPANG_IL21 DN
6	0.162	2 / 17	Aukema_BCL2 UP_BCL6 DN
7	0.164	3 / 33	LEE_Developmental_regulators
8	0.230	3 / 39	ROSOLOWSKI_blue DOWN
9	0.267	100 / 2211	HOPP_Repetitive
10	0.324	1 / 9	Subero_B−ALL_hypo_meth
11	0.353	1 / 10	DAVE_BL_DN
12	0.359	3 / 50	SPANG_BAFF 9hrs DN
13	0.361	12 / 247	ZHANG_DLBCL mutated
14	0.428	2 / 34	Subero_B−ALL_hyper_meth
15	0.432	1 / 13	YAMANE_AICDA_targets_recruited
16	0.432	1 / 13	Subero_MCL_hypo_meth
17	0.484	3 / 61	SPANG_LPS 6hrs DN
18	0.497	5 / 109	ROSOLOWSKI_green total
19	0.502	1 / 16	DAVE_BL Inter
20	0.537	3 / 66	TARTE_Plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	9e−04	106 / 1859	metal ion binding
2	9e−03	4 / 20	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anhyd
3	1e−02	59 / 1033	nucleic acid binding
4	1e−02	3 / 12	poly(U) RNA binding
5	2e−02	14 / 174	transcription corepressor activity
6	2e−02	16 / 210	transferase activity, transferring glycosyl groups
7	2e−02	9 / 94	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
8	2e−02	105 / 2037	DNA binding
9	3e−02	5 / 40	extracellular matrix structural constituent
10	4e−02	3 / 18	proline−rich region binding
11	4e−02	233 / 4992	ion binding
12	6e−02	5 / 49	pyridoxal phosphate binding
13	6e−02	3 / 21	R−SMAD binding
14	6e−02	22 / 364	ATPase activity
15	6e−02	3 / 22	RNA polymerase II transcription coactivator activity
16	6e−02	5 / 51	ubiquitinyl hydrolase activity
17	6e−02	2 / 10	acetylcholine−activated cation−selective channel activity
18	6e−02	2 / 10	semaphorin receptor activity
19	7e−02	6 / 67	phosphotransferase activity, alcohol group as acceptor
20	7e−02	54 / 1040	zinc ion binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	10 / 102	hsa−miR−224
2	0.02	8 / 79	hsa−miR−569
3	0.03	3 / 16	hsa−miR−220a
4	0.04	4 / 31	hsa−miR−296−5p
5	0.04	5 / 46	hsa−miR−874
6	0.05	7 / 77	hsa−miR−1305
7	0.05	10 / 130	hsa−miR−145
8	0.05	8 / 96	hsa−miR−125a−5p
9	0.06	6 / 65	hsa−miR−326
10	0.07	6 / 68	hsa−miR−606
11	0.07	3 / 23	hsa−miR−1250
12	0.07	3 / 23	hsa−miR−1228
13	0.09	9 / 127	hsa−miR−520a−5p
14	0.11	9 / 133	hsa−miR−198
15	0.11	7 / 96	hsa−miR−125b
16	0.13	4 / 46	hsa−miR−346
17	0.13	2 / 15	hsa−miR−744
18	0.14	6 / 82	hsa−miR−365
19	0.14	7 / 101	hsa−miR−603
20	0.14	10 / 159	hsa−miR−298

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	2 / 12	BENTINK_e2f3.2
2	0.10	2 / 13	BENTINK_myc.1
3	0.10	2 / 13	BENTINK_src.10
4	0.41	1 / 12	BENTINK_ras.1
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 / 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	0.008	79 / 1418	ICGC_Ets1_targets
2	0.010	250 / 5219	ICGC_Tcf3_targets
3	0.012	76 / 1383	ICGC_Six5_targets
4	0.013	194 / 3966	ICGC_Pu1_targets
5	0.015	287 / 6114	ICGC_Runx3_targets
6	0.019	136 / 2714	ICGC_Irf4_targets
7	0.025	275 / 5890	ICGC_Elf1_targets
8	0.025	189 / 3924	ICGC_Zeb1_targets
9	0.028	210 / 4414	ICGC_Bclaf101388_targets
10	0.059	247 / 5355	ICGC_Pol2_targets
11	0.091	225 / 4909	ICGC_Stat5_targets
12	0.092	103 / 2136	ICGC_GabpPcr2_targets
13	0.093	216 / 4706	ICGC_Sp1_targets
14	0.095	91 / 1872	ICGC_Mef2_targets
15	0.104	186 / 4032	ICGC_Creb1_targets
16	0.107	244 / 5374	ICGC_Pax5_targets
17	0.108	198 / 4314	ICGC_Ebfsc137065_targets
18	0.114	220 / 4829	ICGC_Nficsc81335_targets
19	0.114	245 / 5408	ICGC_Pou2_targets
20	0.128	210 / 4617	ICGC_Tcf12_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	12 / 143	VAQUERIZAS_General
2	0.32	2 / 27	VAQUERIZAS_Lymph node
3	0.46	2 / 36	VAQUERIZAS_Fetal brain
4	0.48	1 / 15	VAQUERIZAS_Bone marrow
5	0.49	2 / 38	VAQUERIZAS_Whole brain
6	0.49	2 / 38	VAQUERIZAS_Testis
7	0.50	1 / 16	VAQUERIZAS_Adrenal gland
8	0.52	1 / 17	VAQUERIZAS_Pituitary
9	0.52	1 / 17	VAQUERIZAS_Heart
10	0.56	1 / 19	VAQUERIZAS_Tonsil
11	0.63	1 / 23	VAQUERIZAS_Trachea
12	0.63	1 / 23	VAQUERIZAS_Adrenal cortex
13	0.68	1 / 26	VAQUERIZAS_Liver
14	0.71	2 / 58	VAQUERIZAS_Lung
15	0.72	1 / 29	VAQUERIZAS_Fetal lung
16	0.76	1 / 33	VAQUERIZAS_Prostate
17	0.82	1 / 40	VAQUERIZAS_Thyroid
18	0.83	1 / 41	VAQUERIZAS_Placenta
19	0.86	1 / 45	VAQUERIZAS_Uterus
20	1.00	0 / 29	VAQUERIZAS_Smooth muscle

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	6 / 95	WIRTH_Muscle
2	0.3	17 / 350	WIRTH_Nervous System
3	0.4	1 / 10	WIRTH_Thalamus
4	0.4	1 / 11	WIRTH_Prim. lymphoid organs
5	0.4	1 / 11	WIRTH_Globus pallidus
6	0.4	1 / 12	WIRTH_Thymus
7	0.6	3 / 74	WIRTH_Mucosa
8	0.6	14 / 350	WIRTH_Immune system
9	0.7	4 / 107	WIRTH_Testis
10	0.7	4 / 114	PALMER_T−Cell signature up
11	0.8	1 / 32	WIRTH_Pancreas
12	0.8	1 / 32	WIRTH_Placenta
13	0.8	6 / 194	PALMER_B−Cell signature up
14	0.8	7 / 225	PALMER_Granulocytes signature up
15	0.9	1 / 46	WIRTH_Liver
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 / 12	WIRTH_Lymphocytes
20	1.0	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.08	57 / 1115	LU_BPDE 1n DN
2	0.58	155 / 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	

K−Means Clusters

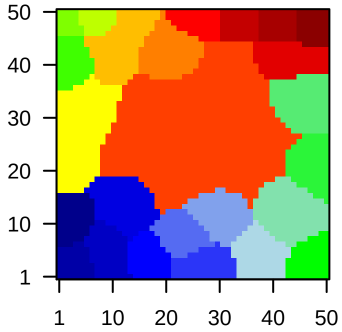
Spot Summary: O

metagenes = 63
genes = 670

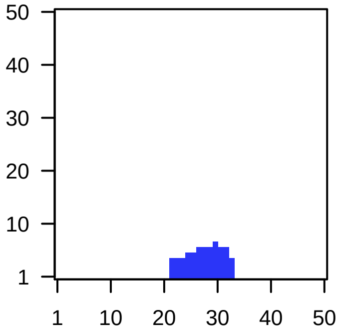
<r> metagenes = 0.86
<r> genes = 0.24
beta: r2= 1.22 / log p= −Inf

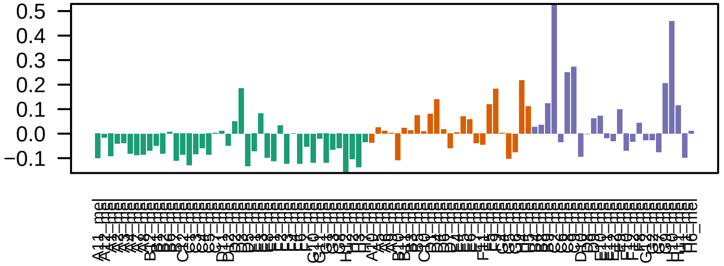
samples with spot = 8 (8.7 %)
MSC1 : 1 (2.4 %)
MSC2 : 2 (8 %)
MSC3 : 5 (20 %)

Overview Map



Spot





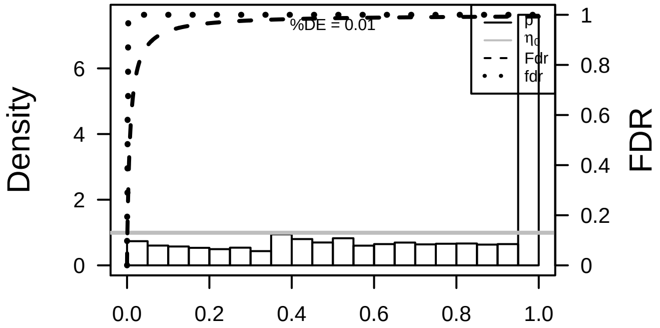
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PIGB	1.97	−0.55	0.32	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B [Sou
2	AKAP7	1.92	−0.37	0.36	AKAP7	A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Ac
3	TRIM52	1.9	−0.29	0.38	TRIM52	tripartite motif containing 52 [Source:HGNC Symbol;Acc:HGN
4	PELP1	1.9	−0.32	0.55	PELP1	proline, glutamate and leucine rich protein 1 [Source:HGNC S
5	STAT5B	1.88	−0.43	0.48	STAT5B	signal transducer and activator of transcription 5B [Source:HC
6	RCBTB2	1.87	−0.27	0.37	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (PC
7	CAPNS2	1.85	−0.05	0.5	CAPNS2	calpain, small subunit 2 [Source:HGNC Symbol;Acc:HGNC:1
8	BMP4	1.84	−0.21	0.45	BMP4	bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:H
9	AKR1C2	1.81	−0.32	0.34	AKR1C2	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
10	ATRNL1	1.8	−0.3	0.22	ATRNL1	attractin−like 1 [Source:HGNC Symbol;Acc:HGNC:29063]
11	BBS10	1.74	−0.2	0.49	BBS10	Bardet−Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGN
12	ITPR1	1.7	−0.28	0.26	ITPR1	inositol 1,4,5−trisphosphate receptor, type 1 [Source:HGNC S
13	ATG2B	1.7	−0.32	0.46	ATG2B	autophagy related 2B [Source:HGNC Symbol;Acc:HGNC:201
14	ADAMTS16	1.7	−0.24	0.34	ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif, 16
15	C11orf57	1.7	−0.44	0.31	C11orf57	chromosome 11 open reading frame 57 [Source:HGNC Symb
16	ZNF701	1.68	−0.41	0.35	ZNF701	zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25
17	HMOX1	1.67	−0.13	0.36	HMOX1	heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:H
18	ZNF264	1.67	−0.28	0.42	ZNF264	zinc finger protein 264 [Source:HGNC Symbol;Acc:HGNC:13
19	SSX5	1.66	−0.14	0.38	SSX5	synovial sarcoma, X breakpoint 5 [Source:HGNC Symbol;Acc
20	ZNF550	1.66	−0.21	0.31	ZNF550	zinc finger protein 550 [Source:HGNC Symbol;Acc:HGNC:28

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−13	16 / 37	GSEA	KEGG_ABC_TRANSPORTERS
2	5e−11	21 / 85	MF	metalloendopeptidase activity
3	6e−11	15 / 41	MF	ATPase activity, coupled to transmembrane movement of substances
4	9e−11	9 / 12	Cance	BEN−PORATH_DN
5	3e−10	12 / 27	GSEA	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
6	3e−08	8 / 14	BP	cAMP biosynthetic process
7	4e−07	7 / 13	MF	transmembrane receptor protein serine/threonine kinase activity
8	4e−07	7 / 13	GSEA	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS
9	5e−07	9 / 25	BP	adenylate cyclase−activating G−protein coupled receptor signaling pathway
10	7e−07	7 / 14	MF	aldehyde dehydrogenase (NAD) activity
11	1e−06	6 / 10	MF	adenylate cyclase activity
12	2e−06	21 / 149	GSEA	NABA_ECM_REGULATORS
13	2e−06	7 / 16	MF	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD
14	5e−06	6 / 12	BP	cyclic nucleotide biosynthetic process
15	5e−06	6 / 12	MF	phosphorus−oxygen lyase activity
16	5e−06	6 / 12	GSEA	PID_LPA4_PATHWAY
17	5e−06	6 / 12	GSEA	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
18	1e−05	14 / 83	GSEA	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION
19	2e−05	5 / 9	GSEA	REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY
20	2e−05	20 / 159	CC	extracellular matrix
21	2e−05	8 / 28	BP	intracellular transport
22	2e−05	13 / 75	MF	metallopeptidase activity
23	2e−05	12 / 67	GSEA	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
24	3e−05	14 / 91	HM	HALLMARK_BILE_ACID_METABOLISM
25	4e−05	25 / 239	CC	proteinaceous extracellular matrix
26	5e−05	4 / 6	GSEA	REACTOME_ETHANOL_OXIDATION
27	5e−05	6 / 17	BP	long−chain fatty acid metabolic process
28	5e−05	5 / 11	MF	aldo−keto reductase (NADP) activity
29	6e−05	71 / 1040	MF	zinc ion binding
30	1e−04	6 / 19	BP	protein targeting to Golgi
31	2e−04	33 / 388	BP	proteolysis
32	2e−04	83 / 1309	MF	ATP binding
33	2e−04	5 / 14	MF	transforming growth factor beta−activated receptor activity
34	2e−04	5 / 14	Cance	LIU_PROSTATE_CANCER_DN
35	2e−04	7 / 30	GSEA	PID_ARF6_PATHWAY
36	3e−04	8 / 41	GSEA	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
37	3e−04	5 / 15	BP	activation of protein kinase A activity
38	3e−04	5 / 15	TF	NOWICK_TF
39	3e−04	5 / 15	GSEA	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
40	3e−04	13 / 99	GSEA	REACTOME_SIGNALING_BY_EGFR_IN_CANCER

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	5 / 111	HORVATH_aging_genes meth UP
2	0.6	4 / 100	HORVATH_aging_genes meth DOWN
3	0.8	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	3e−08	8 / 14	cAMP biosynthetic process
2	5e−07	9 / 25	adenylate cyclase−activating G−protein coupled receptor signaling pathway
3	5e−06	6 / 12	cyclic nucleotide biosynthetic process
4	2e−05	8 / 28	intracellular transport
5	5e−05	6 / 17	long−chain fatty acid metabolic process
6	1e−04	6 / 19	protein targeting to Golgi
7	2e−04	33 / 388	proteolysis
8	3e−04	5 / 15	activation of protein kinase A activity
9	3e−04	6 / 23	secondary metabolic process
10	3e−04	7 / 32	adenylate cyclase−inhibiting G−protein coupled receptor signaling pathway
11	8e−04	6 / 27	adenylate cyclase−modulating G−protein coupled receptor signaling pathway
12	8e−04	6 / 27	retina homeostasis
13	8e−04	6 / 27	water transport
14	9e−04	4 / 11	activin receptor signaling pathway
15	9e−04	4 / 11	cellular aldehyde metabolic process
16	9e−04	8 / 48	activation of phospholipase C activity
17	1e−03	4 / 12	positive regulation of synaptic transmission, GABAergic
18	2e−03	10 / 79	positive regulation of angiogenesis
19	2e−03	8 / 54	response to wounding
20	2e−03	5 / 22	renal water homeostasis

Brain

Rank	p−value	#in/all	Geneset
1	0.03	13 / 166	Mid_Frontal_Lobe_Tx
2	0.05	45 / 812	Mid_Frontal_Lobe_TssP
3	0.12	14 / 229	Mid_Frontal_Lobe_TxTrans
4	0.17	5 / 69	Overlap_fetal_midbrain_Tx
5	0.19	102 / 2185	Fetal_TssA
6	0.23	63 / 1333	Fetal_ReprPCWk
7	0.26	37 / 769	Overlap_fetal_midbrain_ZNF
8	0.30	138 / 3081	Mid_Frontal_Lobe_ZNF
9	0.35	132 / 2972	Mid_Frontal_Lobe_ReprPC
10	0.36	8 / 156	Mid_Frontal_Lobe_TssA
11	0.37	87 / 1949	Fetal_TssF
12	0.37	8 / 158	Overlap_fetal_midbrain_Het
13	0.45	47 / 1065	Overlap_fetal_midbrain_Enh
14	0.45	21 / 468	Mid_Frontal_Lobe_TssF
15	0.48	49 / 1122	Fetal_K9K27me3
16	0.51	29 / 668	Mid_Frontal_Lobe_Enh
17	0.51	52 / 1207	Overlap_fetal_midbrain_TssF
18	0.52	38 / 884	Overlap_fetal_midbrain_EnhG
19	0.53	23 / 534	Mid_Frontal_Lobe_EnhG
20	0.56	81 / 1907	Fetal_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	9e−11	9 / 12	BEN−PORATH_DN
2	2e−04	5 / 14	LIU_PROSTATE_CANCER_DN
3	2e−03	4 / 13	BEN−PORATH_UP
4	9e−03	11 / 113	PanCan_Driver_Gene_geneset_nanostring
5	4e−02	3 / 18	PanCan_Notch_geneset_nanostring
6	9e−02	2 / 12	LIU_PROSTATE_CANCER_UP
7	1e−01	4 / 44	PanCan_TGF−B_geneset_nanostring
8	1e−01	2 / 15	GENTLES_modul4
9	2e−01	11 / 180	SPANG_LPS−index2
10	4e−01	14 / 298	SPANG_BCL6−index2
11	4e−01	3 / 55	PanCan_JAK−ST_geneset_nanostring
12	4e−01	1 / 13	GENTLES_modul12
13	5e−01	1 / 14	LIU_COMMON_CANCER_GENES
14	5e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	5e−01	1 / 15	WANG_ER_UP
16	5e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	5e−01	1 / 16	GENTLES_modul6
18	5e−01	1 / 16	GENTLES_modul16
19	6e−01	1 / 20	PanCan_ChromMod_geneset_nanostring
20	6e−01	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−05	20 / 159	extracellular matrix
2	4e−05	25 / 239	proteinaceous extracellular matrix
3	2e−03	12 / 109	peroxisome
4	4e−03	10 / 87	recycling endosome
5	1e−02	3 / 11	Gemini of coiled bodies
6	1e−02	3 / 12	SMN complex
7	2e−02	6 / 48	clathrin−coated vesicle
8	2e−02	6 / 52	coated pit
9	3e−02	3 / 17	SMN−Sm protein complex
10	4e−02	4 / 30	peroxisomal matrix
11	4e−02	4 / 30	sarcomere
12	5e−02	7 / 78	ubiquitin ligase complex
13	5e−02	5 / 48	stress fiber
14	7e−02	4 / 37	lateral plasma membrane
15	8e−02	3 / 24	Cul3−RING ubiquitin ligase complex
16	9e−02	4 / 39	autophagic vacuole
17	9e−02	4 / 40	recycling endosome membrane
18	9e−02	2 / 12	U4/U6 x U5 tri−snRNP complex
19	1e−01	6 / 75	blood microparticle
20	1e−01	2 / 13	axolemma

Chr

Rank	p−value	#in/all	Geneset
1	0.003	38 / 552	Chr 10
2	0.135	50 / 993	Chr 2
3	0.194	21 / 398	Chr 20
4	0.224	34 / 689	Chr 7
5	0.290	69 / 1500	Chr 1
6	0.372	47 / 1037	Chr 19
7	0.439	21 / 465	Chr 15
8	0.441	29 / 649	Chr 16
9	0.520	20 / 462	Chr 14
10	0.585	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
11	0.593	24 / 576	Chr 9
12	0.602	35 / 840	Chr 17
13	0.635	6 / 151	Chr 21
14	0.663	34 / 838	Chr 3
15	0.670	28 / 696	Chr 5
16	0.687	13 / 335	Chr 22
17	0.747	21 / 551	Chr X
18	0.752	30 / 775	Chr 12
19	0.799	9 / 262	Chr 13
20	0.843	7 / 221	Chr 18

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.03	3 / 16	TCGA_Mutated−in−CRC_non−hypermutated
2	0.04	17 / 250	K9K27me3_Colon
3	0.06	17 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	0.11	4 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	0.13	4 / 45	Ang_CRC−CIMPH−vs=L_hyper
6	0.13	2 / 15	Juehling_HNPCC−mutated−in−4
7	0.15	47 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
8	0.15	2 / 16	Vilar_non−hypermutated−in−CRC
9	0.16	64 / 1317	EnhP_Colon
10	0.17	4 / 50	Ang_CRC_Hypermethylated
11	0.17	51 / 1038	HetRpts_Colon
12	0.18	2 / 18	Ang_CRC−CIMPH−vs−L_hypo
13	0.20	1 / 5	Budinska_A_Surface crypt−like_UP
14	0.20	21 / 400	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
15	0.25	19 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
16	0.26	4 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
17	0.26	28 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
18	0.26	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
19	0.29	2 / 25	Ang_CRC_Hypomethylated
20	0.30	1 / 8	KIM_CRC=MSI−regulated_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.05	19 / 294	GUDJ_psoriasis down
2	0.08	2 / 11	BCHETNIA_EBM up
3	0.21	2 / 20	BCHETNIA_EBM−DM up
4	0.94	13 / 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	0.03	2 / 7	Phillips MES up vs Prolif & PN
2	0.07	3 / 22	KIM prognostic signature LTS vs. STS
3	0.08	1 / 2	laffaire_hypometh_LGG_vs_control
4	0.10	3 / 26	Christensen_hypomethylated_in_ependymoma
5	0.11	21 / 365	Down_b
6	0.15	2 / 16	KIM deleted & downregulated in LTS
7	0.16	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
8	0.21	3 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
9	0.21	3 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
10	0.21	5 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
11	0.24	4 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
12	0.24	6 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
13	0.25	3 / 40	in vivo astrocytes vs. cultured astroglia
14	0.26	6 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	0.26	1 / 7	KIM amplified & overexpressed in LTS
16	0.26	1 / 7	Shaw_up_in_1p19qdel
17	0.29	4 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
18	0.30	3 / 45	Christensen_hypermethylated_in_primary_glioblastoma
19	0.32	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
20	0.33	1 / 9	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−13	16 / 37	KEGG_ABC_TRANSPORTERS
2	3e−10	12 / 27	REACTOME_ABC_FAMILY_PROTEINS_MEDIATED_TRANSPORT
3	4e−07	7 / 13	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS
4	2e−06	21 / 149	NABA_ECM_REGULATORS
5	5e−06	6 / 12	PID_LPA4_PATHWAY
6	5e−06	6 / 12	REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY
7	1e−05	14 / 83	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION
8	2e−05	5 / 9	REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY
9	2e−05	12 / 67	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
10	5e−05	4 / 6	REACTOME_ETHANOL_OXIDATION
11	2e−04	5 / 14	LIU_PROSTATE_CANCER_DN
12	2e−04	7 / 30	PID_ARF6_PATHWAY
13	3e−04	8 / 41	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
14	3e−04	5 / 15	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
15	3e−04	13 / 99	REACTOME_SIGNALING_BY_EGFR_IN_CANCER
16	4e−04	9 / 54	PID_ENDOTHELIN_PATHWAY
17	6e−04	12 / 93	REACTOME_SIGNALING_BY_FGFR
18	7e−04	13 / 107	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
19	7e−04	7 / 36	KEGG_FATTY_ACID_METABOLISM
20	7e−04	3 / 5	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1

HM

Rank	p−value	#in/all	Geneset
1	3e−05	14 / 91	HALLMARK_BILE_ACID_METABOLISM
2	4e−02	6 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	5e−02	8 / 94	HALLMARK_ANDROGEN_RESPONSE
4	5e−02	8 / 95	HALLMARK_SPERMATOGENESIS
5	1e−01	3 / 29	HALLMARK_NOTCH_SIGNALING
6	1e−01	11 / 176	HALLMARK_HYPOXIA
7	1e−01	11 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	1e−01	3 / 31	HALLMARK_HEDGEHOG_SIGNALING
9	2e−01	10 / 169	HALLMARK_XENOBIOTIC_METABOLISM
10	2e−01	3 / 37	HALLMARK_APICAL_SURFACE
11	3e−01	10 / 181	HALLMARK_P53_PATHWAY
12	3e−01	8 / 140	HALLMARK_INFLAMMATORY_RESPONSE
13	3e−01	9 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	4e−01	5 / 91	HALLMARK_PROTEIN_SECRETION
15	4e−01	5 / 93	HALLMARK_PEROXISOME
16	4e−01	7 / 137	HALLMARK_UV_RESPONSE_DN
17	4e−01	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
18	4e−01	7 / 141	HALLMARK_FATTY_ACID_METABOLISM
19	4e−01	3 / 57	HALLMARK_MYC_TARGETS_V2
20	5e−01	7 / 148	HALLMARK_KRAS_SIGNALING_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
2	0.3	4 / 62	DUMEAUX_Smoking enriched genes
3	0.4	2 / 32	DUMEAUX_Fasting enriched genes
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
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	0.03	166 / 3396	HOPP_Repressed
2	0.10	107 / 2211	HOPP_Repetitive
3	0.11	15 / 247	ZHANG_DLBCL mutated
4	0.12	2 / 14	Subero_mBL_hypo_meth
5	0.13	3 / 29	Subero_DLBCL_hypo_meth
6	0.14	3 / 30	Subero_INT_hypo_meth
7	0.16	1 / 4	MASCQUE_mBL DOWN
8	0.16	2 / 17	Aukema_BCL2 UP_BCL6 DN
9	0.22	54 / 1128	SPANG_BCR DN
10	0.23	1 / 6	DAVE_MHCCII BL DN
11	0.28	3 / 43	LENZ_Stromal signature 2
12	0.32	115 / 2563	HOPP_Heterochrom
13	0.33	1 / 9	Subero_B−ALL_hypo_meth
14	0.33	3 / 47	Subero_FL_hyper_meth
15	0.37	13 / 268	SPANG_IL21 UP
16	0.40	5 / 96	Subero_DLBCL_hyper_meth
17	0.41	1 / 12	BENTINK_mBL DOWN
18	0.42	2 / 33	LEE_Developmental_regulators
19	0.44	1 / 13	BENTINK_mBL UP
20	0.46	1 / 14	Subero_MCL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	5e−11	21 / 85	metalloendopeptidase activity
2	6e−11	15 / 41	ATPase activity, coupled to transmembrane movement of substances
3	4e−07	7 / 13	transmembrane receptor protein serine/threonine kinase activity
4	7e−07	7 / 14	aldehyde dehydrogenase (NAD) activity
5	1e−06	6 / 10	adenylate cyclase activity
6	2e−06	7 / 16	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD o
7	5e−06	6 / 12	phosphorus−oxygen lyase activity
8	2e−05	13 / 75	metallopeptidase activity
9	5e−05	5 / 11	aldo−keto reductase (NADP) activity
10	6e−05	71 / 1040	zinc ion binding
11	2e−04	83 / 1309	ATP binding
12	2e−04	5 / 14	transforming growth factor beta−activated receptor activity
13	6e−04	4 / 10	cholesterol transporter activity
14	6e−04	4 / 10	glucocorticoid receptor binding
15	6e−04	7 / 35	receptor signaling protein serine/threonine kinase activity
16	1e−03	251 / 4992	ion binding
17	1e−03	4 / 12	activin binding
18	2e−03	4 / 13	long−chain fatty acid−CoA ligase activity
19	2e−03	4 / 13	protein kinase A binding
20	4e−03	31 / 433	peptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	12 / 100	hsa−miR−1299
2	0.005	7 / 49	hsa−miR−1224−3p
3	0.007	8 / 66	hsa−miR−140−3p
4	0.010	5 / 31	hsa−miR−617
5	0.010	8 / 70	hsa−miR−876−3p
6	0.010	13 / 146	hsa−miR−655
7	0.011	11 / 116	hsa−miR−498
8	0.019	8 / 78	hsa−miR−890
9	0.020	5 / 37	hsa−miR−197
10	0.020	3 / 14	hsa−miR−891a
11	0.021	4 / 25	hsa−miR−517c
12	0.024	14 / 181	hsa−miR−1
13	0.025	6 / 53	hsa−miR−337−3p
14	0.028	6 / 54	hsa−miR−513a−5p
15	0.033	5 / 42	hsa−miR−483−5p
16	0.036	10 / 121	hsa−miR−543
17	0.038	4 / 30	hsa−miR−654−5p
18	0.039	5 / 44	hsa−miR−640
19	0.042	14 / 195	hsa−miR−206
20	0.042	4 / 31	hsa−miR−17*

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	GUSTAFSON_PI3K_DN
2	0.5	1 / 14	BENTINK_e2f3.1
3	0.5	1 / 14	BENTINK_src.2
4	0.5	1 / 15	BENTINK_ras.6
5	1.0	0 / 12	GUSTAFSON_PI3K_UP
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 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 15	NOWICK_TF
2	3e−01	27 / 553	ICGC_RxraPcr1_targets
3	4e−01	125 / 2836	ICGC_BatfPcr1_targets
4	5e−01	55 / 1273	ICGC_P300_targets
5	6e−01	115 / 2714	ICGC_Irf4_targets
6	6e−01	84 / 2013	ICGC_Bcl11_targets
7	6e−01	167 / 3966	ICGC_Pu1_targets
8	7e−01	24 / 595	ICGC_NrsfPcr2_targets
9	7e−01	45 / 1139	HEBENSTREIT_low expression TF
10	9e−01	116 / 2927	ICGC_Rad21_targets
11	9e−01	92 / 2391	ICGC_Pbx3_targets
12	9e−01	46 / 1266	ICGC_NrsfPcr1_targets
13	9e−01	22 / 653	ICGC_SrfPcr2_targets
14	9e−01	92 / 2416	ICGC_Bcl3_targets
15	9e−01	69 / 1872	ICGC_Mef2_targets
16	9e−01	206 / 5219	ICGC_Tcf3_targets
17	9e−01	68 / 1878	ICGC_Cebpbsc150_targets
18	1e+00	210 / 5374	ICGC_Pax5_targets
19	1e+00	59 / 1701	HEBENSTREIT_high expression TF
20	1e+00	180 / 4682	ICGC_Pol24_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 15	VAQUERIZAS_Bone marrow
2	0.1	2 / 16	VAQUERIZAS_Pancreas
3	0.3	2 / 27	VAQUERIZAS_Lymph node
4	0.3	1 / 9	VAQUERIZAS_Kidney
5	0.4	1 / 12	VAQUERIZAS_Skin
6	0.5	3 / 58	VAQUERIZAS_Lung
7	0.5	3 / 59	VAQUERIZAS_Whole blood
8	0.5	2 / 38	VAQUERIZAS_Testis
9	0.7	1 / 26	VAQUERIZAS_Liver
10	0.7	1 / 29	VAQUERIZAS_Fetal lung
11	0.8	1 / 33	VAQUERIZAS_Prostate
12	0.8	1 / 36	VAQUERIZAS_Fetal brain
13	0.8	1 / 38	VAQUERIZAS_Whole brain
14	0.8	1 / 41	VAQUERIZAS_Placenta
15	0.9	1 / 45	VAQUERIZAS_Uterus
16	1.0	2 / 143	VAQUERIZAS_General
17	1.0	0 / 29	VAQUERIZAS_Smooth muscle
18	1.0	0 / 23	VAQUERIZAS_Spinal cord
19	1.0	0 / 37	VAQUERIZAS_Thymus
20	1.0	0 / 40	VAQUERIZAS_Thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	0.09	8 / 107	WIRTH_Testis
2	0.09	2 / 12	WIRTH_Cerebellum
3	0.10	4 / 41	WIRTH_Homeostasis
4	0.10	6 / 74	WIRTH_Mucosa
5	0.13	4 / 46	WIRTH_Liver
6	0.25	18 / 350	WIRTH_Immune system
7	0.33	1 / 9	PALMER_CD8+ T−Cell signature up
8	0.36	1 / 10	WIRTH_Hippocampus
9	0.39	5 / 95	WIRTH_Muscle
10	0.40	2 / 32	WIRTH_Placenta
11	0.44	1 / 13	WIRTH_Thyroid gland
12	0.46	1 / 14	WIRTH_Telencephalon
13	0.51	1 / 16	PALMER_Lymphocytes signature up
14	0.60	8 / 194	PALMER_B−Cell signature up
15	0.63	9 / 225	PALMER_Granulocytes signature up
16	0.73	4 / 114	PALMER_T−Cell signature up
17	0.83	12 / 350	WIRTH_Nervous System
18	1.00	0 / 32	WIRTH_Pancreas
19	1.00	0 / 11	WIRTH_Sec. lymphoid organs
20	1.00	0 / 11	WIRTH_Prim. lymphoid organs

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	47 / 1115	LU_BPDE 1n DN
2	0.8	149 / 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	

K−Means Clusters

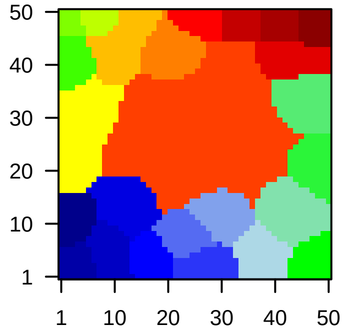
Spot Summary: P

metagenes = 84
genes = 667

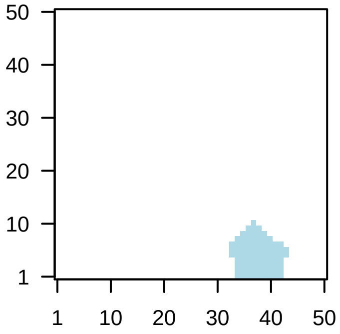
<r> metagenes = 0.8
<r> genes = 0.13
beta: r2= 1.07 / log p= −Inf

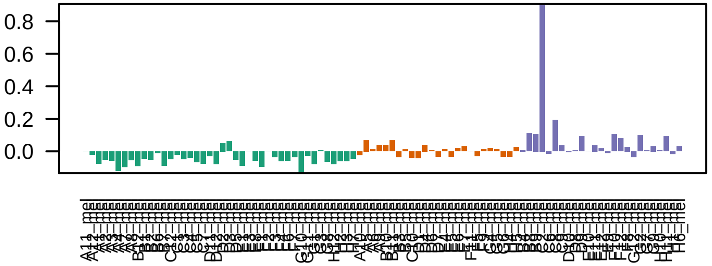
samples with spot = 2 (2.2 %)
MSC3 : 2 (8 %)

Overview Map



Spot





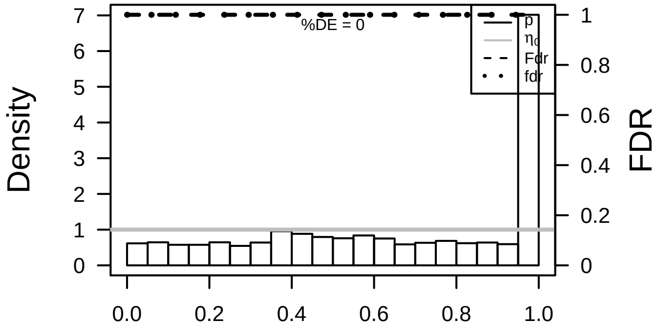
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	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	MYO5B	2.19	−0.18	0.41	MYO5B	myosin VB [Source:HGNC Symbol;Acc:HGNC:7603]
4	DOCK9	2.15	−0.22	0.37	DOCK9	dedicator of cytokinesis 9 [Source:HGNC Symbol;Acc:HGNC
5	CPNE7	2.15	−0.03	0.94	CPNE7	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
6	KLHDC8B	2.08	−0.34	0.35	KLHDC8B	kelch domain containing 8B [Source:HGNC Symbol;Acc:HGN
7	WDR90	2.04	−0.35	0.29	WDR90	WD repeat domain 90 [Source:HGNC Symbol;Acc:HGNC:26
8	C2orf42	2.03	−0.28	0.43	C2orf42	chromosome 2 open reading frame 42 [Source:HGNC Symbo
9	HSF4	1.98	−0.15	0.42	HSF4	heat shock transcription factor 4 [Source:HGNC Symbol;Acc:
10	CLDN15	1.9	−0.12	0.65	CLDN15	claudin 15 [Source:HGNC Symbol;Acc:HGNC:2036]
11	SLC10A7	1.89	−0.17	0.4	SLC10A7	solute carrier family 10, member 7 [Source:HGNC Symbol;Ac
12	SNX16	1.89	−0.17	0.26	SNX16	sorting nexin 16 [Source:HGNC Symbol;Acc:HGNC:14980]
13	STAMBPL1	1.85	−0.35	0.41	STAMBPL1	STAM binding protein−like 1 [Source:HGNC Symbol;Acc:HGN
14	BBS1	1.84	−0.26	0.32	BBS1	Bardet−Biedl syndrome 1 [Source:HGNC Symbol;Acc:HGNC
15	FHL3	1.83	−0.11	0.6	FHL3	four and a half LIM domains 3 [Source:HGNC Symbol;Acc:H
16	PPP1R12B	1.81	−0.43	0.28	PPP1R12B	protein phosphatase 1, regulatory subunit 12B [Source:HGN
17	ZNF280D	1.8	−0.69	0.33	ZNF280D	zinc finger protein 280D [Source:HGNC Symbol;Acc:HGNC:2
18	RFX3	1.8	−0.12	0.34	RFX3	regulatory factor X, 3 (influences HLA class II expression) [Sc
19	ARL6	1.79	−0.24	0.4	ARL6	ADP−ribosylation factor−like 6 [Source:HGNC Symbol;Acc:H
20	C15orf65	1.79	−0.07	0.65	C15orf65	chromosome 15 open reading frame 65 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	9 / 36	GSE	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LY
2	7e−04	171 / 3081	Brain	Mid_Frontal_Lobe_ZNF
3	9e−04	16 / 148	GSE	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN
4	1e−03	20 / 209	GSE	IVANOVA_HEMATOPOIESIS_STEM_CELL
5	1e−03	7 / 38	BP	cellular response to amino acid stimulus
6	2e−03	6 / 29	miRN	hsa−miR−1225−3p
7	2e−03	5 / 20	BP	negative regulation of T cell proliferation
8	2e−03	14 / 127	miRN	hsa−miR−323−3p
9	2e−03	5 / 21	GSE	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	2e−03	71 / 1132	CC	Golgi apparatus
11	2e−03	8 / 53	BP	regulation of immune response
12	2e−03	7 / 42	GSE	IKEDA_MIR133_TARGETS_UP
13	2e−03	34 / 457	GSE	SENESE_HDAC3_TARGETS_UP
14	2e−03	9 / 66	GSE	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCY
15	3e−03	8 / 54	GSE	REACTOME_RNA_POL_I_PROMOTER_OPENING
16	3e−03	7 / 43	miRN	hsa−miR−766
17	3e−03	3 / 7	GSE	MIKKELSEN_DEDIFFERENTIATED_STATE_DN
18	3e−03	4 / 14	GSE	BIOCARTA_PITX2_PATHWAY
19	3e−03	8 / 55	miRN	hsa−miR−191
20	3e−03	17 / 180	GSE	GAL_LEUKEMIC_STEM_CELL_DN
21	3e−03	5 / 23	BP	gene silencing by RNA
22	3e−03	299 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
23	3e−03	6 / 33	GSE	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
24	3e−03	9 / 68	miRN	hsa−miR−361−3p
25	4e−03	11 / 96	miRN	hsa−miR−133a
26	4e−03	8 / 57	miRN	hsa−miR−889
27	4e−03	8 / 57	Glio	GIEZELT_GBM_STSwt_down_VS_LTSwt
28	4e−03	33 / 451	GSE	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
29	4e−03	4 / 15	GSE	GALE_APL_WITH_FLT3_MUTATED_DN
30	4e−03	45 / 668	Brain	Mid_Frontal_Lobe_Enh
31	4e−03	18 / 201	GSE	RAO_BOUND_BY_SALL4
32	4e−03	8 / 58	MF	cysteine−type peptidase activity
33	4e−03	22 / 268	miRN	hsa−miR−363
34	5e−03	9 / 72	GSE	REACTOME_MEIOTIC_RECOMBINATION
35	5e−03	17 / 189	GSE	MULLIGHAN_MLL_SIGNATURE_1_DN
36	5e−03	11 / 100	GSE	REACTOME_MEIOSIS
37	5e−03	22 / 271	miRN	hsa−miR−92a
38	6e−03	3 / 9	GSE	REACTOME_ROLE_OF_DCC_IN_REGULATING_APOPTOSIS
39	6e−03	10 / 89	miRN	hsa−miR−608
40	6e−03	5 / 27	miRN	hsa−miR−521

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	6 / 111	HORVATH_aging_genes meth UP
2	0.5	5 / 100	HORVATH_aging_genes meth DOWN
3	0.8	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	0.001	7 / 38	cellular response to amino acid stimulus
2	0.002	5 / 20	negative regulation of T cell proliferation
3	0.002	8 / 53	regulation of immune response
4	0.003	5 / 23	gene silencing by RNA
5	0.008	3 / 10	activation of transmembrane receptor protein tyrosine kinase activity
6	0.008	3 / 10	cell−cell junction assembly
7	0.008	3 / 10	proteoglycan biosynthetic process
8	0.014	6 / 45	defense response
9	0.014	3 / 12	positive regulation of protein export from nucleus
10	0.018	4 / 23	limb development
11	0.018	4 / 23	negative regulation of fibroblast proliferation
12	0.018	3 / 13	actin filament−based movement
13	0.018	3 / 13	megakaryocyte development
14	0.022	3 / 14	acyl−CoA metabolic process
15	0.026	10 / 111	Notch signaling pathway
16	0.027	4 / 26	cellular response to organic substance
17	0.027	3 / 15	regulation of cytoskeleton organization
18	0.027	6 / 52	fat cell differentiation
19	0.027	23 / 336	protein ubiquitination
20	0.028	5 / 39	positive regulation of neuron apoptotic process

Brain

Rank	p−value	#in/all	Geneset
1	7e−04	171 / 3081	Mid_Frontal_Lobe_ZNF
2	3e−03	299 / 5940	Overlap_fetal_midbrain_HetRpts
3	4e−03	45 / 668	Mid_Frontal_Lobe_Enh
4	4e−02	424 / 9020	Overlap_fetal_midbrain_ReprPCWk
5	5e−02	444 / 9528	Overlap_fetal_midbrain_Quies
6	5e−02	53 / 953	Fetal_Enh
7	7e−02	43 / 765	Mid_Frontal_Lobe_Het
8	9e−02	43 / 786	Fetal_EnhG
9	1e−01	108 / 2185	Fetal_TssA
10	1e−01	31 / 564	Mid_Frontal_Lobe_EnhP
11	2e−01	50 / 989	Mid_Frontal_Lobe_Quies
12	2e−01	28 / 534	Mid_Frontal_Lobe_EnhG
13	2e−01	52 / 1050	Fetal_EnhP
14	2e−01	43 / 862	Overlap_fetal_midbrain_TxTrans
15	2e−01	50 / 1013	Fetal_TssP
16	3e−01	33 / 656	Overlap_fetal_midbrain_EnhP
17	3e−01	9 / 163	Fetal_ReprPC
18	3e−01	408 / 9013	Overlap_fetal_midbrain_K9K27me3
19	3e−01	91 / 1949	Fetal_TssF
20	4e−01	27 / 574	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	0 / 14	LIU_PROSTATE_CANCER_DN
2	0.11	12 / 180	SPANG_LPS−index2
3	0.12	18 / 298	SPANG_BCL6−index2
4	0.13	23 / 401	Lembcke_Colonic Inflammation
5	0.16	4 / 48	KUIPER_MM poor survival
6	0.20	1 / 5	WANG_ER_DN
7	0.26	3 / 40	ZHANG_MM up
8	0.29	4 / 61	PanCan_Wnt_geneset_nanostring
9	0.29	1 / 12	LIU_PROSTATE_CANCER_UP
10	0.39	1 / 11	GENTLES_modul17
11	0.42	1 / 12	BEN−PORATH_DN
12	0.45	1 / 13	GENTLES_modul12
13	0.50	1 / 15	RHODES_CANCER_META_SIGNATURE
14	0.50	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	0.50	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	0.50	1 / 15	WANG_ER_UP
17	0.60	1 / 20	PanCan_ChromMod_geneset_nanostring
18	0.61	3 / 70	SHAUGHNESSY_MM high risk
19	0.63	1 / 22	PanCan_HH_geneset_nanostring
20	0.79	4 / 120	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.002	71 / 1132	Golgi apparatus
2	0.014	6 / 45	SNARE complex
3	0.019	5 / 35	mediator complex
4	0.019	6 / 48	stress fiber
5	0.021	9 / 92	early endosome membrane
6	0.023	4 / 25	PcG protein complex
7	0.024	8 / 79	nucleosome
8	0.029	12 / 145	endoplasmic reticulum lumen
9	0.032	3 / 16	vacuolar membrane
10	0.038	9 / 102	cytoplasmic vesicle membrane
11	0.050	8 / 91	nuclear matrix
12	0.052	4 / 32	nuclear nucleosome
13	0.053	6 / 61	cytoplasmic mRNA processing body
14	0.055	27 / 438	Golgi membrane
15	0.055	7 / 77	ciliary basal body
16	0.064	3 / 21	clathrin adaptor complex
17	0.064	3 / 21	secretory granule membrane
18	0.070	2 / 10	apical dendrite
19	0.070	2 / 10	beta−catenin destruction complex
20	0.070	2 / 10	cell−cell contact zone

Chr

Rank	p−value	#in/all	Geneset
1	0.02	27 / 398	Chr 20
2	0.04	41 / 689	Chr 7
3	0.15	30 / 552	Chr 10
4	0.19	15 / 262	Chr 13
5	0.22	2 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
6	0.29	41 / 840	Chr 17
7	0.35	33 / 687	Chr 6
8	0.41	39 / 838	Chr 3
9	0.43	37 / 801	Chr 11
10	0.47	45 / 993	Chr 2
11	0.49	21 / 462	Chr 14
12	0.52	29 / 649	Chr 16
13	0.64	14 / 335	Chr 22
14	0.66	23 / 551	Chr X
15	0.66	64 / 1500	Chr 1
16	0.68	19 / 465	Chr 15
17	0.74	23 / 576	Chr 9
18	0.77	8 / 221	Chr 18
19	0.82	21 / 558	Chr 4
20	0.84	17 / 469	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	22 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
2	0.010	15 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
3	0.015	10 / 102	Marisa_CRC−cluster−d
4	0.016	256 / 5155	EnhWk1_Colon
5	0.016	63 / 1079	ZNF_Colon
6	0.021	29 / 436	K9acLow_Colon
7	0.026	19 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	0.037	3 / 17	Vilar_mutated−in−CRC−CamP
9	0.038	7 / 71	Marisa_CRC−cluster−g
10	0.044	142 / 2798	TxEnhG1_Colon
11	0.047	396 / 8415	Quies3_Colon
12	0.062	42 / 739	TxEnhG2_Colon
13	0.075	190 / 3897	Quies1_Colon
14	0.087	1 / 2	Budinska_A_Surface crypt−like_DOWN
15	0.087	1 / 2	Budinska_C_CIMP−H−like_DOWN
16	0.116	277 / 5880	TssD2_Colon
17	0.134	416 / 9027	Tx_Colon
18	0.142	2 / 15	Juehling_HNPCC−mutated−in−4
19	0.158	2 / 16	TCGA_Mutated−in−CRC_non−hypermutated
20	0.158	2 / 16	Vilar_non−hypermutated−in−CRC

Disease

Rank	p−value	#in/all	Geneset
1	0.2	16 / 294	GUDJ_psoriasis down
2	1.0	12 / 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	8 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
2	0.007	4 / 18	Barbus_GBM_STS_vs_LTS
3	0.007	4 / 18	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
4	0.011	3 / 11	Mukasa_UP_in_Astroglioma
5	0.016	8 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
6	0.027	3 / 15	VERHAAK_MES subtype
7	0.076	22 / 356	Down_a
8	0.082	6 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	0.083	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
10	0.083	2 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
11	0.091	6 / 70	Weller_LGG_1p19qDel−vs−intact_UP
12	0.137	3 / 29	shaw_responders_down_in_oligo_glioma
13	0.163	5 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
14	0.167	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
15	0.190	2 / 18	Shinawi_with_increased_methylation_in_STS
16	0.204	1 / 5	WILLSCHER_GBM_STSwt_proteomics−N_UP
17	0.217	5 / 72	laffaire_hypermeth_LGG_vs_control
18	0.233	5 / 74	WIRTH_Normal Brain
19	0.273	1 / 7	Phillips MES up vs Prolif & PN
20	0.273	2 / 23	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 36	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
2	9e−04	16 / 148	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_DN
3	1e−03	20 / 209	IVANOVA_HEMATOPOIESIS_STEM_CELL
4	2e−03	5 / 21	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
5	2e−03	7 / 42	IKEDA_MIR133_TARGETS_UP
6	2e−03	34 / 457	SENESE_HDAC3_TARGETS_UP
7	2e−03	9 / 66	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE
8	3e−03	8 / 54	REACTOME_RNA_POL_I_PROMOTER_OPENING
9	3e−03	3 / 7	MIKKELSEN_DEDIFFERENTIATED_STATE_DN
10	3e−03	4 / 14	BIOCARTA_PITX2_PATHWAY
11	3e−03	17 / 180	GAL_LEUKEMIC_STEM_CELL_DN
12	3e−03	6 / 33	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
13	4e−03	33 / 451	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
14	4e−03	4 / 15	GALE_APL_WITH_FLT3_MUTATED_DN
15	4e−03	18 / 201	RAO_BOUND_BY_SALL4
16	5e−03	9 / 72	REACTOME_MEIOTIC_RECOMBINATION
17	5e−03	17 / 189	MULLIGHAN_MLL_SIGNATURE_1_DN
18	5e−03	11 / 100	REACTOME_MEIOSIS
19	6e−03	3 / 9	REACTOME_ROLE_OF_DCC_IN_REGULATING_APOPTOSIS
20	7e−03	5 / 28	PATTERSON_DOCETAXEL_RESISTANCE

HM

Rank	p−value	#in/all	Geneset
1	0.07	4 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
2	0.11	9 / 126	HALLMARK_ALLOGRAFT_REJECTION
3	0.12	7 / 93	HALLMARK_PEROXISOME
4	0.19	6 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	0.21	4 / 53	HALLMARK_TGF_BETA_SIGNALING
6	0.21	10 / 167	HALLMARK_IL2_STAT5_SIGNALING
7	0.23	5 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	0.30	9 / 162	HALLMARK_COMPLEMENT
9	0.33	9 / 167	HALLMARK_APICAL_JUNCTION
10	0.34	8 / 148	HALLMARK_KRAS_SIGNALING_UP
11	0.39	9 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.42	9 / 181	HALLMARK_P53_PATHWAY
13	0.43	5 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.45	8 / 165	HALLMARK_MYOGENESIS
15	0.50	2 / 37	HALLMARK_APICAL_SURFACE
16	0.50	9 / 195	HALLMARK_MITOTIC_SPINDLE
17	0.51	8 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	0.52	5 / 107	HALLMARK_COAGULATION
19	0.58	4 / 91	HALLMARK_BILE_ACID_METABOLISM
20	0.60	6 / 140	HALLMARK_INFLAMMATORY_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	3 / 32	DUMEAUX_Fasting enriched genes
2	0.6	1 / 18	DUMEAUX_High bmi enriched genes
3	0.9	1 / 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	0.03	2 / 6	DAVE_MHCCII BL DN
2	0.05	18 / 268	SPANG_IL21 UP
3	0.07	18 / 275	TARTE_Mature plasma cell signature
4	0.07	311 / 6564	HOPP_Strong_enhancer
5	0.09	111 / 2211	HOPP_Repetitive
6	0.09	4 / 39	ROSOLOWSKI_blue DOWN
7	0.10	3 / 25	Subero_T−PLL_hypo_meth
8	0.11	2 / 13	Subero_MCL_hypo_meth
9	0.14	352 / 7592	HOPP_Active_promoter
10	0.15	3 / 30	TARTE_B−cell signature
11	0.17	1 / 4	MASCQUE_mBL DOWN
12	0.22	8 / 129	DAVE_BL−vs−DLBCL
13	0.24	12 / 212	LENZ_Stromal signature 1
14	0.26	3 / 40	Subero_mBL_hyper_meth
15	0.31	1 / 8	YAMANE_AICDA_targets_nonrecruited
16	0.31	1 / 8	Subero_B−CLL_hypo_meth
17	0.31	54 / 1128	SPANG_BCR DN
18	0.31	58 / 1218	SPANG_BCR UP
19	0.32	315 / 6929	HOPP_Txn_elongation
20	0.34	1 / 9	Subero_B−ALL_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	0.004	8 / 58	cysteine−type peptidase activity
2	0.015	5 / 33	RNA polymerase II transcription cofactor activity
3	0.015	4 / 22	calmodulin−dependent protein kinase activity
4	0.021	5 / 36	G−protein beta/gamma−subunit complex binding
5	0.021	5 / 36	SNAP receptor activity
6	0.025	12 / 142	calmodulin binding
7	0.025	7 / 65	protease binding
8	0.027	3 / 15	phosphatidylinositol−4−phosphate binding
9	0.027	3 / 15	phospholipid−translocating ATPase activity
10	0.028	25 / 373	protein heterodimerization activity
11	0.032	3 / 16	ATP−dependent microtubule motor activity, plus−end−directed
12	0.038	5 / 42	RNA polymerase II core promoter sequence−specific DNA binding
13	0.053	47 / 830	nucleic acid binding transcription factor activity
14	0.057	4 / 33	guanyl nucleotide binding
15	0.070	2 / 10	gamma−catenin binding
16	0.070	2 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
17	0.071	26 / 430	lipid binding
18	0.071	27 / 450	sequence−specific DNA binding
19	0.072	3 / 22	RNA polymerase II transcription coactivator activity
20	0.075	4 / 36	enzyme activator activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	6 / 29	hsa−miR−1225−3p
2	0.002	14 / 127	hsa−miR−323−3p
3	0.003	7 / 43	hsa−miR−766
4	0.003	8 / 55	hsa−miR−191
5	0.003	9 / 68	hsa−miR−361−3p
6	0.004	11 / 96	hsa−miR−133a
7	0.004	8 / 57	hsa−miR−889
8	0.004	22 / 268	hsa−miR−363
9	0.005	22 / 271	hsa−miR−92a
10	0.006	10 / 89	hsa−miR−608
11	0.006	5 / 27	hsa−miR−521
12	0.009	7 / 53	hsa−miR−1279
13	0.009	4 / 19	hsa−miR−542−5p
14	0.009	24 / 321	hsa−miR−32
15	0.011	10 / 97	hsa−miR−133b
16	0.011	24 / 327	hsa−miR−367
17	0.013	15 / 177	hsa−miR−548e
18	0.014	3 / 12	hsa−miR−652
19	0.016	6 / 46	hsa−miR−146b−3p
20	0.016	6 / 46	hsa−miR−1256

PathwAct

Rank	p−value	#in/all	Geneset
1	0.1	2 / 13	BENTINK_src.10
2	0.4	1 / 12	GUSTAFSON_PI3K_UP
3	0.4	1 / 13	GUSTAFSON_PI3K_DN
4	0.5	1 / 14	BENTINK_src.2
5	0.5	1 / 15	BENTINK_ras.6
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 12	BENTINK_e2f3.2
8	1.0	0 / 13	BENTINK_myc.1
9	1.0	0 / 12	BENTINK_ras.1
10	1.0	0 / 9	BENTINK_ras.4
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	143 / 2836	ICGC_BatfPcr1_targets
2	0.05	195 / 3966	ICGC_Pu1_targets
3	0.12	119 / 2416	ICGC_Bcl3_targets
4	0.13	1 / 3	MYC_Tumor supressor genes UP
5	0.13	65 / 1273	ICGC_P300_targets
6	0.19	34 / 653	ICGC_SrfPcr2_targets
7	0.20	83 / 1701	HEBENSTREIT_high expression TF
8	0.20	1 / 5	MYC_Apoptosis UP
9	0.20	1 / 5	MYC_TF and cofactors
10	0.22	249 / 5374	ICGC_Pax5_targets
11	0.22	222 / 4774	ICGC_Foxm1_targets
12	0.22	242 / 5219	ICGC_Tcf3_targets
13	0.23	241 / 5200	ICGC_Mta3_targets
14	0.24	138 / 2927	ICGC_Rad21_targets
15	0.24	173 / 3700	ICGC_Nfatc1_targets
16	0.25	214 / 4617	ICGC_Tcf12_targets
17	0.25	113 / 2391	ICGC_Pbx3_targets
18	0.27	30 / 595	ICGC_NrsfPcr2_targets
19	0.27	225 / 4879	ICGC_Pmlsc71910_targets
20	0.29	34 / 690	ICGC_Atf3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.008	5 / 29	VAQUERIZAS_Smooth muscle
2	0.049	5 / 45	VAQUERIZAS_Uterus
3	0.087	4 / 38	VAQUERIZAS_Whole brain
4	0.106	10 / 143	VAQUERIZAS_General
5	0.108	4 / 41	VAQUERIZAS_Placenta
6	0.174	2 / 17	VAQUERIZAS_Pituitary
7	0.215	3 / 36	VAQUERIZAS_Fetal brain
8	0.263	3 / 40	VAQUERIZAS_Thyroid
9	0.273	2 / 23	VAQUERIZAS_Trachea
10	0.373	2 / 29	VAQUERIZAS_Fetal lung
11	0.394	1 / 11	VAQUERIZAS_Fetal liver
12	0.436	2 / 33	VAQUERIZAS_Prostate
13	0.495	1 / 15	VAQUERIZAS_Fetal thyroid
14	0.495	2 / 37	VAQUERIZAS_Thymus
15	0.518	1 / 16	VAQUERIZAS_Adrenal gland
16	0.518	1 / 16	VAQUERIZAS_Salivary gland
17	0.650	1 / 23	VAQUERIZAS_Spinal cord
18	0.650	1 / 23	VAQUERIZAS_Adrenal cortex
19	0.694	1 / 26	VAQUERIZAS_Liver
20	0.737	2 / 58	VAQUERIZAS_Lung

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 14	WIRTH_Telencephalon
2	0.3	6 / 107	WIRTH_Testis
3	0.4	1 / 10	WIRTH_Thalamus
4	0.4	1 / 11	WIRTH_Cortex cerebri
5	0.4	1 / 13	WIRTH_B−cells
6	0.4	1 / 13	WIRTH_Thyroid gland
7	0.6	5 / 114	PALMER_T−Cell signature up
8	0.6	4 / 95	WIRTH_Muscle
9	0.6	3 / 74	WIRTH_Mucosa
10	0.8	1 / 32	WIRTH_Pancreas
11	0.8	1 / 32	WIRTH_Placenta
12	0.9	6 / 194	PALMER_B−Cell signature up
13	0.9	11 / 350	WIRTH_Immune system
14	0.9	11 / 350	WIRTH_Nervous System
15	1.0	5 / 225	PALMER_Granulocytes signature up
16	1.0	0 / 11	WIRTH_Sec. lymphoid organs
17	1.0	0 / 11	WIRTH_Prim. lymphoid organs
18	1.0	0 / 8	WIRTH_Tonsil
19	1.0	0 / 12	WIRTH_Thymus
20	1.0	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	55 / 1115	LU_BPDE 1n DN
2	0.3	169 / 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	

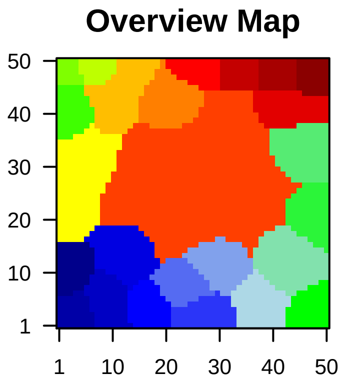
K−Means Clusters

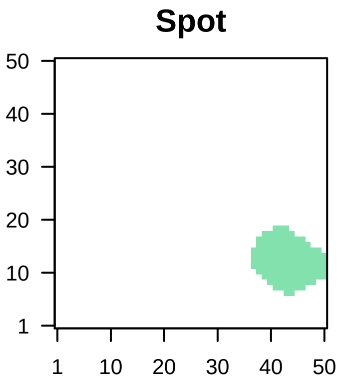
Spot Summary: Q

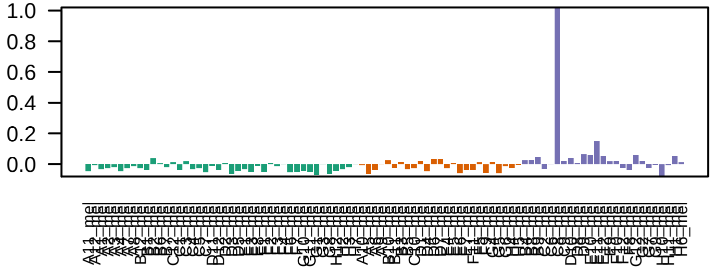
metagenes = 125
genes = 831

<r> metagenes = 0.8
<r> genes = 0.12
beta: r2= 1.14 / log p= −Inf

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





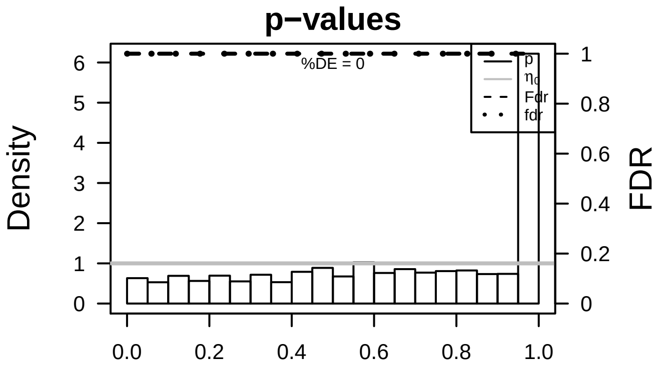


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	PLA2G4C	2.46	−0.18	0.51	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium−independen
2	FOLR3	2.37	−0.05	0.84	FOLR3	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:HGNC
3	KRTAP21−2	2.37	−0.09	0.56	KRTAP21−2	keratin associated protein 21−2 [Source:HGNC Symbol;Acc:
4	GPR133	2.19	−0.03	0.96		
5	HIST1H4H	2.16	−0.25	0.44	HIST1H4H	histone cluster 1, H4h [Source:HGNC Symbol;Acc:HGNC:47
6	FBXL2	2.11	−0.4	0.39	FBXL2	F−box and leucine−rich repeat protein 2 [Source:HGNC Sym
7	MNDA	2.08	−0.03	0.96	MNDA	myeloid cell nuclear differentiation antigen [Source:HGNC Sy
8	NREP	2.03	−0.33	0.4	NREP	neuronal regeneration related protein [Source:HGNC Symbol
9	CADM1	2.03	−0.14	0.49	CADM1	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:
10	TUBA4A	2.01	−0.13	0.45	TUBA4A	tubulin, alpha 4a [Source:HGNC Symbol;Acc:HGNC:12407]
11	PHKA2	2.01	−0.19	0.51	PHKA2	phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
12	RTN1	2	−0.05	0.87	RTN1	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]
13	NCAM2	2	−0.23	0.4	NCAM2	neural cell adhesion molecule 2 [Source:HGNC Symbol;Acc:
14	DCN	1.98	−0.06	0.65	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
15	SLC14A1	1.98	−0.03	0.93	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd bl
16	KIAA1324L	1.97	−0.39	0.3	KIAA1324L	KIAA1324−like [Source:HGNC Symbol;Acc:HGNC:21945]
17	DGKA	1.96	−0.05	0.41	DGKA	diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;A
18	EXOC6	1.92	−0.58	0.2	EXOC6	exocyst complex component 6 [Source:HGNC Symbol;Acc:H
19	PRKAG2	1.92	−0.36	0.32	PRKAG2	protein kinase, AMP−activated, gamma 2 non−catalytic subu
20	WFDC3	1.92	−0.04	0.65	WFDC3	WAP four−disulfide core domain 3 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−05	582 / 9528	Brain	Overlap_fetal_midbrain_Quies
2	5e−05	383 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
3	2e−04	548 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
4	5e−04	44 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
5	6e−04	545 / 9027	Colon	Tx_Colon
6	9e−04	519 / 8580	Colon	TxWk_Colon
7	9e−04	63 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
8	1e−03	8 / 39	GSEA	LIAO_HAVE_SOX4_BINDING_SITES
9	1e−03	262 / 4032	TF	ICGC_Creb1_targets
10	1e−03	6 / 23	BP	sensory perception of taste
11	1e−03	5 / 16	BP	positive regulation of branching involved in ureteric bud morphogenesis
12	1e−03	5 / 16	GSEA	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3
13	2e−03	4 / 10	MF	hedgehog receptor activity
14	2e−03	4 / 10	BP	necroptotic process
15	2e−03	77 / 995	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
16	2e−03	6 / 25	BP	bone mineralization
17	2e−03	44 / 506	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
18	2e−03	12 / 84	CC	PML body
19	2e−03	4 / 11	MF	C2H2 zinc finger domain binding
20	3e−03	108 / 1500	Chr	Chr 1
21	3e−03	97 / 1325	BP	catabolic process
22	3e−03	21 / 196	GSEA	CHANG_CORE_SERUM_RESPONSE_DN
23	3e−03	3 / 6	GSEA	REACTOME_ELEVATION_OF_CYTOSOLIC_CA2_LEVELS
24	3e−03	296 / 4682	TF	ICGC_Pol24_targets
25	3e−03	5 / 19	BP	olfactory bulb development
26	3e−03	5 / 19	GSEA	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS
27	3e−03	4 / 12	GSEA	KEGG_SULFUR_METABOLISM
28	3e−03	4 / 12	GSEA	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
29	3e−03	27 / 278	GSEA	GABRIELY_MIR21_TARGETS
30	3e−03	17 / 148	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
31	4e−03	6 / 28	MF	ADP binding
32	4e−03	9 / 57	GSEA	ROSS_AML_WITH_PML_RARA_FUSION
33	4e−03	437 / 7209	Lymph	HOPP_Weak_promoter
34	4e−03	35 / 396	GSEA	JOHNSTONE_PARVB_TARGETS_3_UP
35	4e−03	4 / 13	GSEA	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS
36	5e−03	277 / 4385	TF	ICGC_Atf2_targets
37	5e−03	16 / 140	BP	cellular lipid metabolic process
38	5e−03	9 / 59	GSEA	REACTOME_PLATELET_HOMEOSTASIS
39	5e−03	10 / 70	GSEA	PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2
40	5e−03	3 / 7	Colon	Marisa_CRC−C5



Aging

Rank	p−value	#in/all	Geneset
1	0.2	9 / 111	HORVATH_aging_genes meth UP
2	0.5	6 / 100	HORVATH_aging_genes meth DOWN
3	0.6	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	0.001	6 / 23	sensory perception of taste
2	0.001	5 / 16	positive regulation of branching involved in ureteric bud morphogenesis
3	0.002	4 / 10	necroptotic process
4	0.002	6 / 25	bone mineralization
5	0.003	97 / 1325	catabolic process
6	0.003	5 / 19	olfactory bulb development
7	0.005	16 / 140	cellular lipid metabolic process
8	0.006	10 / 71	multicellular organism growth
9	0.006	6 / 31	cellular defense response
10	0.010	4 / 16	3'−phosphoadenosine 5'−phosphosulfate metabolic process
11	0.011	5 / 25	endochondral ossification
12	0.013	6 / 36	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
13	0.015	11 / 94	sensory perception of sound
14	0.015	5 / 27	positive regulation of epithelial to mesenchymal transition
15	0.015	3 / 10	neuron cell−cell adhesion
16	0.015	3 / 10	positive regulation of p38MAPK cascade
17	0.015	3 / 10	response to UV−C
18	0.020	3 / 11	hematopoietic stem cell proliferation
19	0.020	3 / 11	relaxation of cardiac muscle
20	0.022	10 / 87	calcium ion transmembrane transport

Brain

Rank	p−value	#in/all	Geneset
1	3e−05	582 / 9528	Overlap_fetal_midbrain_Quies
2	5e−05	383 / 5940	Overlap_fetal_midbrain_HetRpts
3	2e−04	548 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	5e−02	522 / 9013	Overlap_fetal_midbrain_K9K27me3
5	7e−02	40 / 564	Mid_Frontal_Lobe_EnhP
6	7e−02	538 / 9330	Overlap_fetal_midbrain_ReprPC
7	7e−02	188 / 3081	Mid_Frontal_Lobe_ZNF
8	8e−02	59 / 884	Overlap_fetal_midbrain_EnhG
9	1e−01	62 / 953	Fetal_Enh
10	1e−01	67 / 1050	Fetal_EnhP
11	2e−01	21 / 304	Fetal_Het
12	2e−01	61 / 989	Mid_Frontal_Lobe_Quies
13	2e−01	23 / 349	Fetal_ZNF
14	2e−01	47 / 765	Mid_Frontal_Lobe_Het
15	3e−01	48 / 786	Fetal_EnhG
16	3e−01	51 / 862	Overlap_fetal_midbrain_TxTrans
17	3e−01	170 / 2972	Mid_Frontal_Lobe_ReprPC
18	3e−01	141 / 2462	Mid_Frontal_Lobe_HetRpts
19	4e−01	62 / 1065	Overlap_fetal_midbrain_Enh
20	4e−01	65 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	0 / 14	LIU_PROSTATE_CANCER_DN
2	0.05	3 / 15	WANG_ER_UP
3	0.12	28 / 401	Lembcke_Colonic Inflammation
4	0.18	4 / 40	ZHANG_MM up
5	0.18	4 / 40	PanCan_HK_geneset_nanostring
6	0.18	2 / 14	LIU_LIVER_CANCER
7	0.22	2 / 16	GENTLES_modul14
8	0.23	4 / 44	PanCan_TGF−B_geneset_nanostring
9	0.25	5 / 61	PanCan_Wnt_geneset_nanostring
10	0.29	1 / 12	LIU_PROSTATE_CANCER_UP
11	0.33	1 / 7	GENTLES_modul18
12	0.35	2 / 22	PanCan_HH_geneset_nanostring
13	0.43	1 / 10	GENTLES_modul3
14	0.48	2 / 29	KUIPER_MM good survival
15	0.51	7 / 121	PanCan_MAPK_geneset_nanostring
16	0.52	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	0.58	1 / 15	GENTLES_modul4
18	0.58	1 / 15	GENTLES_modul10
19	0.59	16 / 298	SPANG_BCL6−index2
20	0.60	1 / 16	GENTLES_modul6

CC

Rank	p−value	#in/all	Geneset
1	0.002	12 / 84	PML body
2	0.005	7 / 39	intercalated disc
3	0.010	6 / 34	ciliary membrane
4	0.011	5 / 25	clathrin−coated endocytic vesicle membrane
5	0.011	5 / 25	MLL1 complex
6	0.019	6 / 39	autophagic vacuole
7	0.025	188 / 2984	integral component of membrane
8	0.029	8 / 66	integral component of endoplasmic reticulum membrane
9	0.041	53 / 751	integral component of plasma membrane
10	0.045	12 / 125	lamellipodium
11	0.047	4 / 25	heterochromatin
12	0.047	3 / 15	autophagic vacuole membrane
13	0.048	34 / 456	vacuole
14	0.057	5 / 38	cis−Golgi network
15	0.067	8 / 78	ubiquitin ligase complex
16	0.070	159 / 2576	membrane
17	0.073	19 / 239	proteinaceous extracellular matrix
18	0.074	3 / 18	podosome
19	0.074	3 / 18	protein phosphatase type 2A complex
20	0.075	5 / 41	mitochondrial nucleoid

Chr

Rank	p−value	#in/all	Geneset
1	0.003	108 / 1500	Chr 1
2	0.031	57 / 801	Chr 11
3	0.114	51 / 775	Chr 12
4	0.285	34 / 552	Chr 10
5	0.305	2 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
6	0.307	34 / 558	Chr 4
7	0.339	28 / 462	Chr 14
8	0.340	41 / 689	Chr 7
9	0.365	41 / 696	Chr 5
10	0.386	38 / 649	Chr 16
11	0.418	32 / 551	Chr X
12	0.487	15 / 262	Chr 13
13	0.511	26 / 465	Chr 15
14	0.604	56 / 1037	Chr 19
15	0.677	44 / 840	Chr 17
16	0.682	17 / 335	Chr 22
17	0.781	34 / 687	Chr 6
18	0.793	28 / 576	Chr 9
19	0.845	18 / 398	Chr 20
20	0.918	46 / 993	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−04	545 / 9027	Tx_Colon
2	9e−04	519 / 8580	TxWk_Colon
3	5e−03	3 / 7	Marisa_CRC−C5
4	7e−03	501 / 8415	Quies3_Colon
5	7e−03	242 / 3812	TssD1_Colon
6	1e−02	317 / 5155	EnhWk1_Colon
7	1e−02	245 / 3897	Quies1_Colon
8	1e−02	357 / 5880	TssD2_Colon
9	2e−02	598 / 10290	TssWk_Colon
10	4e−02	22 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
11	5e−02	137 / 2159	TssP_Colon
12	5e−02	2 / 7	Juehling_HNPCC−mutated−in−5
13	5e−02	557 / 9653	Enh_Colon
14	6e−02	3 / 16	Juehling−MSI−enriched−in−6
15	7e−02	2 / 8	Boland_CRC−MSI−TGC
16	7e−02	2 / 8	Marisa_CRC−C3
17	9e−02	170 / 2798	TxEnhG1_Colon
18	1e−01	2 / 10	KIM_MSI−in−CRC
19	1e−01	69 / 1079	ZNF_Colon
20	1e−01	116 / 1889	ReprPCWk_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.02	25 / 294	GUDJ_psoriasis down
2	0.31	2 / 20	BCHETNIA_EBM−DM up
3	0.47	1 / 11	BCHETNIA_EBM up
4	1.00	12 / 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	0.01	4 / 16	VERHAAK_NL subtype
2	0.03	8 / 68	GIEZELT_GBM_WT_down_VS_mut
3	0.04	28 / 356	Down_a
4	0.05	58 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
5	0.05	4 / 26	Christensen_hypomethylated_in_ependymoma
6	0.05	2 / 7	Shaw_up_in_1p19qdel
7	0.06	5 / 39	OPC
8	0.08	7 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	0.09	7 / 70	Weller_LGG_1p19qDel−vs−intact_UP
10	0.10	2 / 10	Christensen_hypomethylated_in_grade2_astrocytoma
11	0.11	4 / 33	Christensen_hypomethylated_in_primary_glioblastoma
12	0.12	5 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
13	0.12	2 / 11	astrocytes_glio
14	0.12	7 / 75	Weller_LGG_A_vs_O_DOWN
15	0.15	6 / 65	Weller_LGG_1p19qDel−vs−intact_DOWN
16	0.16	1 / 3	Martinez_Glio_hypometh
17	0.16	2 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
18	0.26	3 / 32	Donson−innate immunity−associated with LTS in HGA
19	0.26	2 / 18	Barbus_GBM_STS_vs._LTS
20	0.29	4 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	44 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	9e−04	63 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
3	1e−03	8 / 39	LIAO_HAVE_SOX4_BINDING_SITES
4	1e−03	5 / 16	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3
5	2e−03	77 / 995	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
6	2e−03	44 / 506	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
7	3e−03	21 / 196	CHANG_CORE_SERUM_RESPONSE_DN
8	3e−03	3 / 6	REACTOME_ELEVATION_OF_CYTOSOLIC_CA2_LEVELS
9	3e−03	5 / 19	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS
10	3e−03	4 / 12	KEGG_SULFUR_METABOLISM
11	3e−03	4 / 12	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
12	3e−03	27 / 278	GABRIELY_MIR21_TARGETS
13	3e−03	17 / 148	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
14	4e−03	9 / 57	ROSS_AML_WITH_PML_RARA_FUSION
15	4e−03	35 / 396	JOHNSTONE_PARVB_TARGETS_3_UP
16	4e−03	4 / 13	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS
17	5e−03	9 / 59	REACTOME_PLATELET_HOMEOSTASIS
18	5e−03	10 / 70	PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2
19	5e−03	20 / 193	KARLSSON_TGFB1_TARGETS_DN
20	6e−03	20 / 195	SENESE_HDAC1_AND_HDAC2_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	18 / 183	HALLMARK_GLYCOLYSIS
2	0.02	16 / 165	HALLMARK_MYOGENESIS
3	0.06	9 / 91	HALLMARK_BILE_ACID_METABOLISM
4	0.12	7 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	0.18	13 / 176	HALLMARK_HYPOXIA
6	0.18	13 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.22	12 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	0.29	13 / 196	HALLMARK_MTORC1_SIGNALING
9	0.34	4 / 53	HALLMARK_TGF_BETA_SIGNALING
10	0.35	9 / 137	HALLMARK_UV_RESPONSE_DN
11	0.41	10 / 162	HALLMARK_COMPLEMENT
12	0.46	10 / 169	HALLMARK_XENOBIOTIC_METABOLISM
13	0.49	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.50	10 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.52	11 / 195	HALLMARK_MITOTIC_SPINDLE
16	0.60	2 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
17	0.60	5 / 94	HALLMARK_ANDROGEN_RESPONSE
18	0.62	5 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
19	0.63	9 / 174	HALLMARK_HEME_METABOLISM
20	0.67	7 / 141	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.16	1 / 3	DUMEAUX_Exercising non smoker literature enriched genes
3	0.20	2 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.43	1 / 10	DUMEAUX_Smoking literature genes up
5	0.54	2 / 32	DUMEAUX_Fasting enriched genes
6	0.68	3 / 62	DUMEAUX_Smoking enriched genes
7	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 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	0.004	437 / 7209	HOPP_Weak_promoter
2	0.008	87 / 1218	SPANG_BCR UP
3	0.014	452 / 7592	HOPP_Active_promoter
4	0.017	414 / 6929	HOPP_Txn_elongation
5	0.035	11 / 107	SPANG_LPS 6hrs UP
6	0.039	23 / 280	SPANG_CD40 6hrs UP
7	0.047	4 / 25	Subero_T−PLL_hypo_meth
8	0.048	330 / 5538	HOPP_Weak_txn
9	0.051	7 / 61	SPANG_LPS 6hrs DN
10	0.069	385 / 6564	HOPP_Strong_enhancer
11	0.098	136 / 2211	HOPP_Repetitive
12	0.109	20 / 268	SPANG_IL21 UP
13	0.180	2 / 14	Subero_mBL_hypo_meth
14	0.185	152 / 2563	HOPP_Heterochrom
15	0.190	328 / 5693	HOPP_Weak_enhancer
16	0.201	2 / 15	DAVE_Immune response 2
17	0.232	129 / 2188	HOPP_Poised_promoter
18	0.284	2 / 19	Subero_MM_hyper_meth
19	0.300	4 / 50	SPANG_BAFF 9hrs DN
20	0.366	1 / 8	MASCQUE_ABC UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	4 / 10	hedgehog receptor activity
2	0.002	4 / 11	C2H2 zinc finger domain binding
3	0.004	6 / 28	ADP binding
4	0.006	4 / 14	bitter taste receptor activity
5	0.011	18 / 180	protein domain specific binding
6	0.013	4 / 17	sulfuric ester hydrolase activity
7	0.013	6 / 36	calcium channel activity
8	0.015	3 / 10	glutathione binding
9	0.015	3 / 10	voltage−gated ion channel activity
10	0.019	4 / 19	acyl−CoA dehydrogenase activity
11	0.020	3 / 11	substrate−specific transmembrane transporter activity
12	0.022	4 / 20	WW domain binding
13	0.024	8 / 64	flavin adenine dinucleotide binding
14	0.031	4 / 22	oxidoreductase activity, acting on the CH−CH group of donors
15	0.032	3 / 13	nucleocytoplasmic transporter activity
16	0.034	7 / 56	transcription cofactor activity
17	0.036	4 / 23	MAP kinase kinase kinase activity
18	0.039	3 / 14	diacylglycerol kinase activity
19	0.042	8 / 71	ubiquitin−specific protease activity
20	0.046	28 / 361	binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.009	6 / 33	hsa−miR−1274b
2	0.012	20 / 208	hsa−miR−432
3	0.012	24 / 264	hsa−miR−30a
4	0.016	44 / 569	hsa−miR−20b
5	0.025	26 / 312	hsa−miR−30e
6	0.026	23 / 269	hsa−miR−30d
7	0.029	7 / 54	hsa−miR−513a−5p
8	0.036	4 / 23	hsa−miR−1227
9	0.037	11 / 108	hsa−miR−211
10	0.040	6 / 46	hsa−miR−581
11	0.042	5 / 35	hsa−miR−770−5p
12	0.043	9 / 84	hsa−miR−220c
13	0.049	20 / 242	hsa−miR−26b
14	0.053	10 / 101	hsa−miR−516b
15	0.056	39 / 541	hsa−miR−17
16	0.063	12 / 132	hsa−miR−199b−5p
17	0.064	14 / 161	hsa−miR−802
18	0.067	6 / 52	hsa−miR−370
19	0.067	7 / 65	hsa−miR−550
20	0.074	31 / 426	hsa−miR−519d

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 12	BENTINK_e2f3.2
2	0.2	2 / 13	GUSTAFSON_PI3K_DN
3	0.2	2 / 14	BENTINK_src.2
4	0.4	1 / 9	BENTINK_ras.4
5	0.5	1 / 12	BENTINK_ras.1
6	0.6	1 / 14	BENTINK_e2f3.1
7	1.0	0 / 12	GUSTAFSON_PI3K_UP
8	1.0	0 / 13	BENTINK_myc.1
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	0.001	262 / 4032	ICGC_Creb1_targets
2	0.003	296 / 4682	ICGC_Pol24_targets
3	0.005	277 / 4385	ICGC_Atf2_targets
4	0.005	294 / 4689	ICGC_Taf1_targets
5	0.008	303 / 4879	ICGC_Pmlsc71910_targets
6	0.008	276 / 4414	ICGC_Bclaf101388_targets
7	0.009	97 / 1383	ICGC_Six5_targets
8	0.012	319 / 5200	ICGC_Mta3_targets
9	0.012	98 / 1418	ICGC_Ets1_targets
10	0.014	297 / 4829	ICGC_Nficsc81335_targets
11	0.021	288 / 4706	ICGC_Sp1_targets
12	0.024	324 / 5355	ICGC_Pol2_targets
13	0.024	325 / 5374	ICGC_Pax5_targets
14	0.028	264 / 4314	ICGC_Ebfsc137065_targets
15	0.030	154 / 2416	ICGC_Bcl3_targets
16	0.034	152 / 2391	ICGC_Pbx3_targets
17	0.034	289 / 4774	ICGC_Foxm1_targets
18	0.036	85 / 1266	ICGC_NrsfPcr1_targets
19	0.041	247 / 4054	ICGC_Egr1_targets
20	0.046	323 / 5408	ICGC_Pou2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	4 / 33	VAQUERIZAS_Prostate
2	0.1	2 / 12	VAQUERIZAS_Skin
3	0.2	4 / 40	VAQUERIZAS_Thyroid
4	0.2	4 / 45	VAQUERIZAS_Uterus
5	0.2	2 / 17	VAQUERIZAS_Pituitary
6	0.2	2 / 17	VAQUERIZAS_Heart
7	0.4	2 / 23	VAQUERIZAS_Spinal cord
8	0.4	3 / 41	VAQUERIZAS_Placenta
9	0.4	4 / 58	VAQUERIZAS_Lung
10	0.4	4 / 59	VAQUERIZAS_Whole blood
11	0.5	1 / 11	VAQUERIZAS_Fetal liver
12	0.5	2 / 29	VAQUERIZAS_Fetal lung
13	0.5	8 / 143	VAQUERIZAS_General
14	0.6	1 / 14	VAQUERIZAS_Ovary
15	0.6	1 / 15	VAQUERIZAS_Fetal thyroid
16	0.6	1 / 16	VAQUERIZAS_Salivary gland
17	0.6	2 / 36	VAQUERIZAS_Fetal brain
18	0.6	2 / 37	VAQUERIZAS_Thymus
19	0.7	1 / 23	VAQUERIZAS_Adrenal cortex
20	0.8	1 / 26	VAQUERIZAS_Liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	4 / 41	WIRTH_Homeostasis
2	0.4	5 / 74	WIRTH_Mucosa
3	0.4	6 / 95	WIRTH_Muscle
4	0.4	1 / 10	WIRTH_Hippocampus
5	0.5	1 / 11	WIRTH_Prim. lymphoid organs
6	0.5	1 / 11	WIRTH_Globus pallidus
7	0.5	1 / 11	WIRTH_Cortex cerebri
8	0.5	1 / 12	WIRTH_Thymus
9	0.5	2 / 32	WIRTH_Pancreas
10	0.6	1 / 16	PALMER_Lymphocytes signature up
11	0.6	6 / 114	PALMER_T−Cell signature up
12	0.7	18 / 350	WIRTH_Immune system
13	0.7	5 / 107	WIRTH_Testis
14	0.8	1 / 32	WIRTH_Placenta
15	0.8	8 / 194	PALMER_B−Cell signature up
16	0.9	1 / 46	WIRTH_Liver
17	1.0	13 / 350	WIRTH_Nervous System
18	1.0	7 / 225	PALMER_Granulocytes signature up
19	1.0	0 / 11	WIRTH_Sec. lymphoid organs
20	1.0	0 / 13	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	72 / 1115	LU_BPDE 1h DN
2	0.2	217 / 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	

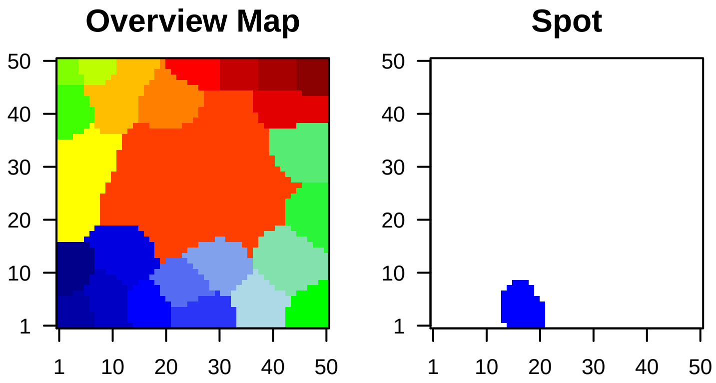
K−Means Clusters

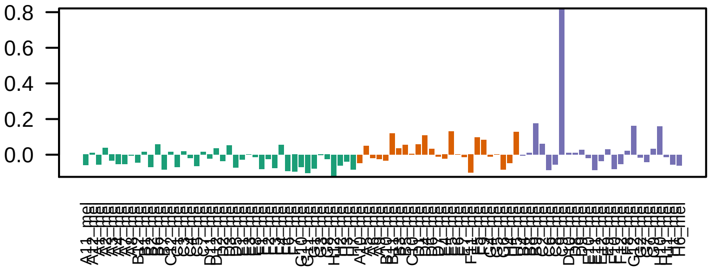
Spot Summary: R

metagenes = 60
genes = 505

<r> metagenes = 0.82
<r> genes = 0.13
beta: r2= 0.8 / log p= −Inf

samples with spot = 4 (4.3 %)
MSC3 : 4 (16 %)



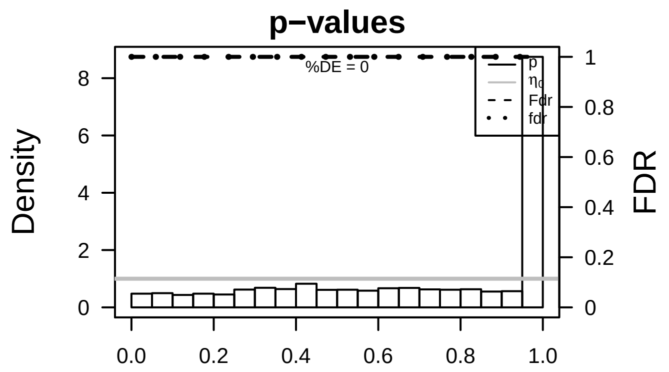


Spot Genelist

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	MUTYH	1.96	−0.34	0.3	MUTYH	mutY homolog [Source:HGNC Symbol;Acc:HGNC:7527]
5	SLC25A53	1.94	−0.16	0.42	SLC25A53	solute carrier family 25, member 53 [Source:HGNC Symbol;A
6	STAC	1.9	−0.21	0.35	STAC	SH3 and cysteine rich domain [Source:HGNC Symbol;Acc:H
7	ZNF558	1.9	−0.12	0.53	ZNF558	zinc finger protein 558 [Source:HGNC Symbol;Acc:HGNC:26
8	E2F5	1.86	−0.2	0.38	E2F5	E2F transcription factor 5, p130−binding [Source:HGNC Sym
9	OSR2	1.84	−0.06	0.67	OSR2	odd−skipped related transciption factor 2 [Source:HGNC Sym
10	ULK2	1.8	−0.23	0.27	ULK2	unc−51 like autophagy activating kinase 2 [Source:HGNC Sy
11	WDR54	1.78	−0.34	0.3	WDR54	WD repeat domain 54 [Source:HGNC Symbol;Acc:HGNC:25
12	MBD5	1.78	−0.22	0.32	MBD5	methyl−CpG binding domain protein 5 [Source:HGNC Symbo
13	HDGFRP2	1.77	−0.28	0.34		
14	SPATA25	1.76	−0.03	0.77	SPATA25	spermatogenesis associated 25 [Source:HGNC Symbol;Acc:
15	ADSSL1	1.73	−0.2	0.23	ADSSL1	adenylosuccinate synthase like 1 [Source:HGNC Symbol;Acc
16	NUDT13	1.7	−0.15	0.46	NUDT13	nudix (nucleoside diphosphate linked moiety X)−type motif 13
17	RELL1	1.69	−0.22	0.43	RELL1	RELT−like 1 [Source:HGNC Symbol;Acc:HGNC:27379]
18	EML1	1.69	−0.35	0.39	EML1	echinoderm microtubule associated protein like 1 [Source:HG
19	DNAJB2	1.67	−0.1	0.61	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2 [Source:HGN
20	RORB	1.67	−0.16	0.4	RORB	RAR−related orphan receptor B [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−06	17 / 126	BP	homophilic cell adhesion via plasma membrane adhesion molecules
2	1e−06	19 / 158	Brain	Overlap_fetal_midbrain_Het
3	2e−05	9 / 45	GSEA	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
4	2e−04	45 / 769	Brain	Overlap_fetal_midbrain_ZNF
5	3e−04	6 / 29	GSEA	DANG_MYC_TARGETS_DN
6	5e−04	6 / 31	CC	membrane coat
7	8e−04	14 / 156	Brain	Mid_Frontal_Lobe_TssA
8	1e−03	7 / 50	GSEA	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
9	2e−03	12 / 132	miRN	hsa−miR−320d
10	2e−03	4 / 16	BP	regulation of centrosome duplication
11	2e−03	31 / 530	MF	calcium ion binding
12	2e−03	4 / 17	BP	zinc II ion transport
13	2e−03	4 / 17	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_DN
14	2e−03	52 / 1033	MF	nucleic acid binding
15	2e−03	13 / 156	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
16	2e−03	273 / 7203	Colon	TssF_Colon
17	3e−03	228 / 5880	Colon	TssD2_Colon
18	3e−03	3 / 9	miRN	hsa−miR−202*
19	3e−03	3 / 9	GSEA	PETRETTO_BLOOD_PRESSURE_UP
20	3e−03	6 / 43	BP	rhythmic process
21	3e−03	5 / 30	GSEA	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP
22	3e−03	7 / 58	BP	protein ubiquitination involved in ubiquitin−dependent protein catabolic proc
23	3e−03	20 / 304	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
24	3e−03	6 / 44	BP	signal transduction by phosphorylation
25	4e−03	12 / 146	miRN	hsa−miR−320c
26	4e−03	6 / 46	GSEA	BROWNE_HCMV_INFECTION_1HR_UP
27	5e−03	17 / 250	miRN	hsa−miR−520a−3p
28	5e−03	13 / 170	miRN	hsa−miR−320b
29	5e−03	3 / 11	BP	phosphorelay signal transduction system
30	5e−03	24 / 405	MF	ligase activity
31	5e−03	18 / 275	Lymp	TARTE_Mature plasma cell signature
32	6e−03	8 / 82	GSEA	WINZEN_DEGRADED_VIA_KHSRP
33	6e−03	194 / 4992	MF	ion binding
34	7e−03	3 / 12	GSEA	IVANOV_MUTATED_IN_COLON_CANCER
35	7e−03	5 / 36	BP	myelination
36	7e−03	4 / 23	BP	intrinsic apoptotic signaling pathway by p53 class mediator
37	7e−03	38 / 747	CC	nucleolus
38	8e−03	199 / 5155	Colon	EnhWk1_Colon
39	8e−03	9 / 104	miRN	hsa−miR−525−5p
40	8e−03	7 / 69	miRN	hsa−miR−499−3p



Aging

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

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	3 / 22	PanCan_HH_geneset_nanostring
2	0.08	2 / 14	LIU_COMMON_CANCER_GENES
3	0.09	2 / 15	GENTLES_modul11
4	0.10	2 / 16	GENTLES_modul16
5	0.18	3 / 44	PanCan_TGF−B_geneset_nanostring
6	0.23	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.26	8 / 180	SPANG_LPS−index2
8	0.29	0 / 12	LIU_PROSTATE_CANCER_UP
9	0.33	5 / 113	PanCan_Driver_Gene_geneset_nanostring
10	0.34	3 / 61	PanCan_Wnt_geneset_nanostring
11	0.38	18 / 489	Lembcke_Normal vs Adenoma
12	0.39	2 / 40	PanCan_HK_geneset_nanostring
13	0.40	1 / 15	RHODES_CANCER_META_SIGNATURE
14	0.51	0 / 12	LIU_BREAST_CANCER
15	0.51	4 / 111	PanCan_RAS_geneset_nanostring
16	0.60	5 / 156	PanCan_PI3K_geneset_nanostring
17	0.63	1 / 29	KUIPER_MM good survival
18	0.67	9 / 298	SPANG_BCL6−index2
19	0.77	2 / 82	PanCan_TXmisReg_geneset_nanostring
20	0.77	3 / 120	PanCan_CC+Apop_geneset_nanostring

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	273 / 7203	TssF_Colon
2	0.003	228 / 5880	TssD2_Colon
3	0.008	199 / 5155	EnhWk1_Colon
4	0.010	111 / 2698	EnhA_Colon
5	0.018	311 / 8580	TxWk_Colon
6	0.022	112 / 2798	TxEnhG1_Colon
7	0.025	35 / 739	TxEnhG2_Colon
8	0.049	321 / 9027	Tx_Colon
9	0.059	335 / 9482	TssA_Colon
10	0.070	5 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
11	0.104	9 / 165	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	0.128	9 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
13	0.157	1 / 5	Juehling−MSI−enriched−in−8−to−9
14	0.178	334 / 9653	Enh_Colon
15	0.178	30 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
16	0.210	23 / 571	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
17	0.225	291 / 8415	Quies3_Colon
18	0.236	12 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
19	0.239	1 / 8	KIM_CRC−MSI−regulated_DN
20	0.258	5 / 102	Marisa_CRC−cluster−d

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 45	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
2	3e−04	6 / 29	DANG_MYC_TARGETS_DN
3	1e−03	7 / 50	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
4	2e−03	4 / 17	KIM_ALL_DISORDERS_CALB1_CORR_DN
5	2e−03	13 / 156	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
6	3e−03	3 / 9	PETRETTO_BLOOD_PRESSURE_UP
7	3e−03	5 / 30	SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP
8	3e−03	20 / 304	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
9	4e−03	6 / 46	BROWNE_HCMV_INFECTION_1HR_UP
10	6e−03	8 / 82	WINZEN_DEGRADED_VIA_KHSRP
11	7e−03	3 / 12	IVANOV_MUTATED_IN_COLON_CANCER
12	9e−03	10 / 124	MCBRYAN_PUBERTAL_BREAST_5_6WK_DN
13	9e−03	24 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
14	1e−02	5 / 41	GYORFFY_DOXORUBICIN_RESISTANCE
15	1e−02	34 / 674	BENPORATH_SUZ12_TARGETS
16	1e−02	8 / 92	JAZAG_TGFB1_SIGNALING_UP
17	1e−02	6 / 59	BYSTROEM_CORRELATED_WITH_IL5_DN
18	2e−02	4 / 29	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_UP
19	2e−02	2 / 6	FARMER_BREAST_CANCER_CLUSTER_8
20	2e−02	11 / 155	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.005	18 / 275	TARTE_Mature plasma cell signature
2	0.080	236 / 6564	HOPP_Strong_enhancer
3	0.098	200 / 5538	HOPP_Weak_txn
4	0.144	2 / 20	SPANG_BAFF 9hrs UP
5	0.157	1 / 5	WRIGHT_custom ABC−DLBCL UP
6	0.174	47 / 1218	SPANG_BCR UP
7	0.185	1 / 6	DAVE_MHCCII BL DN
8	0.212	200 / 5693	HOPP_Weak_enhancer
9	0.220	5 / 96	Subero_DLBCL_hyper_meth
10	0.239	1 / 8	MASCQUE_ABC UP
11	0.239	1 / 8	Subero_MM_hypo_meth
12	0.264	1 / 9	Subero_B−ALL_hypo_meth
13	0.289	1 / 10	Shaknovich_ABC_hypo_meth
14	0.290	5 / 107	SPANG_LPS 6hrs UP
15	0.317	2 / 34	Subero_B−ALL_hyper_meth
16	0.317	10 / 247	ZHANG_DLBCL mutated
17	0.317	41 / 1128	SPANG_BCR DN
18	0.327	3 / 60	Subero_T−ALL_hyper_meth
19	0.335	247 / 7209	HOPP_Weak_promoter
20	0.421	1 / 16	ROSOLOWSKI_red UP

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	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	

Tissue

Rank	p−value	#in/all	Geneset
1	0.3	2 / 32	WIRTH_Pancreas
2	0.3	1 / 11	WIRTH_Globus pallidus
3	0.3	1 / 12	WIRTH_Lymphocytes
4	0.4	1 / 13	WIRTH_B−cells
5	0.4	1 / 13	WIRTH_Thyroid gland
6	0.4	4 / 95	WIRTH_Muscle
7	0.4	1 / 16	PALMER_Lymphocytes signature up
8	0.7	1 / 32	WIRTH_Placenta
9	0.7	2 / 74	WIRTH_Mucosa
10	0.8	1 / 41	WIRTH_Homeostasis
11	0.9	2 / 114	PALMER_T−Cell signature up
12	0.9	4 / 225	PALMER_Granulocytes signature up
13	1.0	3 / 194	PALMER_B−Cell signature up
14	1.0	1 / 107	WIRTH_Testis
15	1.0	6 / 350	WIRTH_Immune system
16	1.0	2 / 350	WIRTH_Nervous System
17	1.0	0 / 11	WIRTH_Sec. lymphoid organs
18	1.0	0 / 11	WIRTH_Prim. lymphoid organs
19	1.0	0 / 8	WIRTH_Tonsil
20	1.0	0 / 12	WIRTH_Thymus

BP

Rank	p−value	#in/all	Geneset
1	1e−06	17 / 126	homophilic cell adhesion via plasma membrane adhesion molecules
2	2e−03	4 / 16	regulation of centrosome duplication
3	2e−03	4 / 17	zinc II ion transport
4	3e−03	6 / 43	rhythmic process
5	3e−03	7 / 58	protein ubiquitination involved in ubiquitin−dependent protein catabolic process
6	3e−03	6 / 44	signal transduction by phosphorylation
7	5e−03	3 / 11	phosphorelay signal transduction system
8	7e−03	5 / 36	myelination
9	7e−03	4 / 23	intrinsic apoptotic signaling pathway by p53 class mediator
10	1e−02	5 / 40	viral entry into host cell
11	1e−02	4 / 27	positive regulation of protein serine/threonine kinase activity
12	1e−02	7 / 75	nucleotide−excision repair
13	1e−02	10 / 132	regulation of gene expression
14	1e−02	6 / 59	smoothened signaling pathway
15	2e−02	3 / 16	cell−substrate adhesion
16	2e−02	3 / 17	endocytic recycling
17	2e−02	5 / 46	heart morphogenesis
18	2e−02	6 / 63	response to endoplasmic reticulum stress
19	2e−02	3 / 18	heparan sulfate proteoglycan biosynthetic process
20	2e−02	4 / 32	chondrocyte differentiation

CC

Rank	p−value	#in/all	Geneset
1	5e−04	6 / 31	membrane coat
2	7e−03	38 / 747	nucleolus
3	1e−02	216 / 5696	nucleus
4	2e−02	3 / 16	anchored component of plasma membrane
5	2e−02	3 / 18	intraciliary transport particle B
6	4e−02	102 / 2577	nucleoplasm
7	4e−02	8 / 115	midbody
8	4e−02	2 / 10	viral nucleocapsid
9	5e−02	2 / 11	Gemini of coiled bodies
10	6e−02	2 / 12	node of Ranvier
11	6e−02	2 / 12	SMN complex
12	7e−02	2 / 13	chromocenter
13	7e−02	2 / 13	COPI vesicle coat
14	7e−02	2 / 13	transcription factor TFTC complex
15	7e−02	6 / 87	recycling endosome
16	7e−02	3 / 29	cell−cell adherens junction
17	7e−02	4 / 47	Cajal body
18	7e−02	99 / 2576	membrane
19	9e−02	2 / 15	CCR4−NOT complex
20	9e−02	2 / 15	mitochondrial envelope

Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 11	BCHETNIA_EBM up
2	0.5	1 / 20	BCHETNIA_EBM−DM up
3	0.7	9 / 294	GUDJ_psoriasis down
4	0.8	12 / 435	GUDJ_psoriasis up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

HM

Rank	p−value	#in/all	Geneset
1	0.05	9 / 140	HALLMARK_APOPTOSIS
2	0.07	4 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	0.09	8 / 137	HALLMARK_UV_RESPONSE_DN
4	0.16	9 / 181	HALLMARK_P53_PATHWAY
5	0.19	5 / 91	HALLMARK_PROTEIN_SECRETION
6	0.22	2 / 26	HALLMARK_ANGIOGENESIS
7	0.30	8 / 188	HALLMARK_ADIPOGENESIS
8	0.33	3 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	0.35	2 / 37	HALLMARK_APICAL_SURFACE
10	0.37	6 / 146	HALLMARK_DNA_REPAIR
11	0.40	4 / 95	HALLMARK_SPERMATOGENESIS
12	0.45	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	0.48	7 / 195	HALLMARK_MITOTIC_SPINDLE
14	0.53	6 / 174	HALLMARK_HEME_METABOLISM
15	0.53	2 / 53	HALLMARK_TGF_BETA_SIGNALING
16	0.55	6 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
17	0.63	3 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	0.64	5 / 162	HALLMARK_COMPLEMENT
19	0.65	1 / 31	HALLMARK_HEDGEHOG_SIGNALING
20	0.66	5 / 167	HALLMARK_APICAL_JUNCTION

MF

Rank	p−value	#in/all	Geneset
1	0.002	31 / 530	calcium ion binding
2	0.002	52 / 1033	nucleic acid binding
3	0.005	24 / 405	ligase activity
4	0.006	194 / 4992	ion binding
5	0.013	3 / 15	protein serine/threonine kinase activator activity
6	0.015	3 / 16	RNA polymerase II carboxy−terminal domain kinase activity
7	0.018	5 / 46	steroid hormone receptor activity
8	0.019	4 / 31	beta−tubulin binding
9	0.021	78 / 1859	metal ion binding
10	0.025	7 / 86	ubiquitin−like protein binding
11	0.029	4 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
12	0.032	4 / 36	phosphatidylinositol−4,5−bisphosphate binding
13	0.032	4 / 36	tubulin binding
14	0.036	3 / 22	Wnt−protein binding
15	0.036	14 / 244	ubiquitin−protein transferase activity
16	0.037	20 / 386	nucleotide binding
17	0.042	2 / 10	cAMP response element binding protein binding
18	0.042	2 / 10	receptor signaling protein tyrosine kinase activity
19	0.048	4 / 41	peptidyl−prolyl cis−trans isomerase activity
20	0.051	2 / 11	cAMP response element binding

TF

Rank	p−value	#in/all	Geneset
1	0.02	156 / 4054	ICGC_Egr1_targets
2	0.03	115 / 2927	ICGC_Rad21_targets
3	0.04	173 / 4617	ICGC_Tcf12_targets
4	0.04	81 / 2013	ICGC_Bcl11_targets
5	0.05	28 / 595	ICGC_NrsfPcr2_targets
6	0.06	75 / 1878	ICGC_Cebpbsc150_targets
7	0.07	54 / 1314	ICGC_Usf1_targets
8	0.09	30 / 690	ICGC_Atf3_targets
9	0.10	137 / 3700	ICGC_Nfatc1_targets
10	0.10	92 / 2416	ICGC_Bcl3_targets
11	0.11	144 / 3924	ICGC_Zeb1_targets
12	0.12	170 / 4689	ICGC_Taf1_targets
13	0.14	187 / 5219	ICGC_Tcf3_targets
14	0.15	54 / 1400	ICGC_Myc_targets
15	0.18	64 / 1701	HEBENSTREIT_high expression TF
16	0.18	70 / 1872	ICGC_Mef2_targets
17	0.19	99 / 2714	ICGC_Irf4_targets
18	0.19	142 / 3966	ICGC_Pu1_targets
19	0.19	184 / 5200	ICGC_Mta3_targets
20	0.20	48 / 1266	ICGC_NrsfPcr1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	37 / 1115	LU_BPDE 1h DN
2	0.8	115 / 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	1e−06	19 / 158	Overlap_fetal_midbrain_Het
2	2e−04	45 / 769	Overlap_fetal_midbrain_ZNF
3	8e−04	14 / 156	Mid_Frontal_Lobe_TssA
4	7e−02	43 / 1013	Fetal_TssP
5	7e−02	38 / 884	Overlap_fetal_midbrain_EnhG
6	7e−02	117 / 3081	Mid_Frontal_Lobe_ZNF
7	9e−02	317 / 9013	Overlap_fetal_midbrain_K9K27me3
8	1e−01	35 / 831	Fetal_HetRpts
9	1e−01	28 / 656	Overlap_fetal_midbrain_EnhP
10	1e−01	33 / 812	Mid_Frontal_Lobe_TssP
11	2e−01	210 / 5940	Overlap_fetal_midbrain_HetRpts
12	2e−01	51 / 1333	Fetal_ReprPCWk
13	2e−01	329 / 9528	Overlap_fetal_midbrain_Quies
14	2e−01	40 / 1050	Fetal_EnhP
15	3e−01	7 / 163	Fetal_ReprPC
16	4e−01	307 / 9020	Overlap_fetal_midbrain_ReprPCWk
17	4e−01	9 / 229	Mid_Frontal_Lobe_TxTrans
18	5e−01	84 / 2462	Mid_Frontal_Lobe_HetRpts
19	5e−01	18 / 534	Mid_Frontal_Lobe_EnhG
20	6e−01	25 / 765	Mid_Frontal_Lobe_Het

Chr

Rank	p−value	#in/all	Geneset
1	0.03	3 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
2	0.04	32 / 696	Chr 5
3	0.23	19 / 469	Chr 8
4	0.29	26 / 689	Chr 7
5	0.36	15 / 398	Chr 20
6	0.38	21 / 576	Chr 9
7	0.44	36 / 1037	Chr 19
8	0.46	8 / 221	Chr 18
9	0.48	16 / 462	Chr 14
10	0.50	16 / 465	Chr 15
11	0.58	5 / 151	Chr 21
12	0.60	49 / 1500	Chr 1
13	0.62	27 / 840	Chr 17
14	0.62	32 / 993	Chr 2
15	0.67	17 / 551	Chr X
16	0.68	17 / 552	Chr 10
17	0.69	20 / 649	Chr 16
18	0.69	26 / 838	Chr 3
19	0.69	10 / 335	Chr 22
20	0.69	17 / 558	Chr 4

Glio

Rank	p−value	#in/all	Geneset
1	0.01	6 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
2	0.02	8 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
3	0.03	6 / 72	laffaire_hypermeth_LGG_vs_control
4	0.05	2 / 11	WILLSCHER_GBM_LTSwt_proteomics−C_UP
5	0.07	4 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
6	0.08	2 / 14	VERHAAK_PN subtype
7	0.10	7 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	0.11	5 / 75	GIEZELT_GBM_STS_down_VS_LTS
9	0.12	6 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
10	0.13	7 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	0.13	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
12	0.20	4 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
13	0.21	5 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	0.23	4 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
15	0.24	4 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
16	0.26	13 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	0.26	1 / 9	Phillips PN up vs MES & Prolif
18	0.29	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−A_UP
19	0.31	1 / 11	Christensen_hypermethylated_in_ependymoma
20	0.31	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.88	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 / 5	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 18	DUMEAUX_High bmi enriched genes
11	1.00	0 / 32	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	12 / 132	hsa−miR−320d
2	0.003	3 / 9	hsa−miR−202*
3	0.004	12 / 146	hsa−miR−320c
4	0.005	17 / 250	hsa−miR−520a−3p
5	0.005	13 / 170	hsa−miR−320b
6	0.008	9 / 104	hsa−miR−525−5p
7	0.008	7 / 69	hsa−miR−499−3p
8	0.009	7 / 70	hsa−miR−935
9	0.009	4 / 25	hsa−miR−941
10	0.011	7 / 73	hsa−miR−184
11	0.013	22 / 391	hsa−miR−519a
12	0.015	6 / 60	hsa−miR−296−3p
13	0.015	6 / 60	hsa−miR−1200
14	0.015	4 / 29	hsa−miR−1225−3p
15	0.016	17 / 284	hsa−miR−320a
16	0.016	7 / 78	hsa−miR−1321
17	0.018	12 / 179	hsa−miR−582−5p
18	0.019	11 / 160	hsa−miR−1297
19	0.020	10 / 141	hsa−miR−138
20	0.021	7 / 83	hsa−miR−576−5p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 11	VAQUERIZAS_Fetal liver
2	0.06	4 / 45	VAQUERIZAS_Uterus
3	0.07	3 / 29	VAQUERIZAS_Smooth muscle
4	0.07	3 / 29	VAQUERIZAS_Fetal lung
5	0.08	2 / 14	VAQUERIZAS_Ovary
6	0.09	2 / 15	VAQUERIZAS_Fetal thyroid
7	0.10	2 / 16	VAQUERIZAS_Adrenal gland
8	0.11	2 / 17	VAQUERIZAS_Pituitary
9	0.12	3 / 36	VAQUERIZAS_Fetal brain
10	0.13	4 / 58	VAQUERIZAS_Lung
11	0.15	3 / 40	VAQUERIZAS_Thyroid
12	0.18	2 / 23	VAQUERIZAS_Spinal cord
13	0.18	2 / 23	VAQUERIZAS_Adrenal cortex
14	0.21	1 / 7	VAQUERIZAS_Appendix
15	0.21	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
16	0.21	1 / 7	VAQUERIZAS_Tongue
17	0.22	2 / 26	VAQUERIZAS_Liver
18	0.26	1 / 9	VAQUERIZAS_Kidney
19	0.30	2 / 33	VAQUERIZAS_Prostate
20	0.37	2 / 38	VAQUERIZAS_Testis

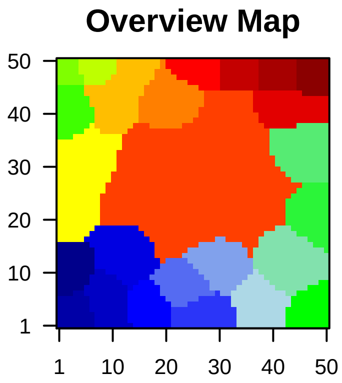
K−Means Clusters

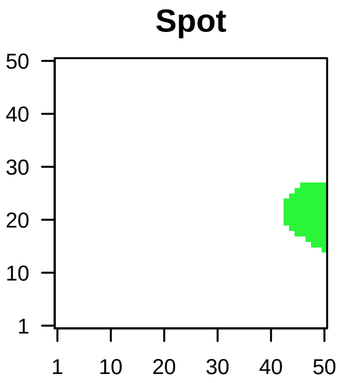
Spot Summary: S

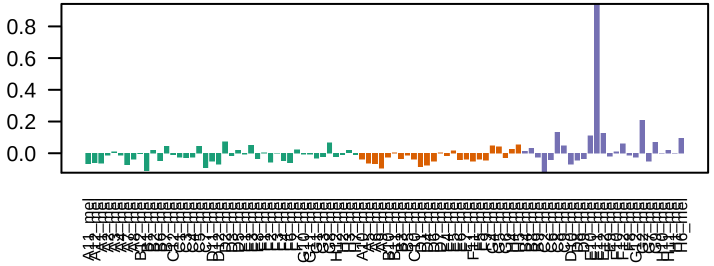
metagenes = 79
genes = 526

<r> metagenes = 0.83
<r> genes = 0.13
beta: r2= 0.98 / log p= −Inf

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


Overview Map


Spot

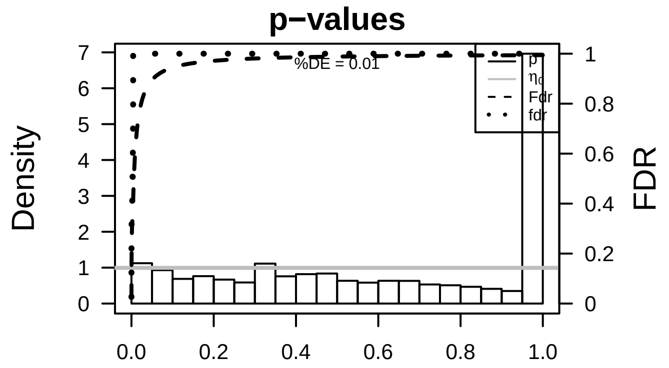


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	VCAN	2.39	−0.1	0.64	VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]
2	SLCO3A1	2.13	−0.27	0.43	SLCO3A1	solute carrier organic anion transporter family, member 3A1 [S
3	SIDT2	1.98	−0.08	0.21	SIDT2	SID1 transmembrane family, member 2 [Source:HGNC Symb
4	SCN2A	1.98	−0.06	0.67	SCN2A	sodium channel, voltage gated, type II alpha subunit [Source:
5	CLHC1	1.96	−0.28	0.35	CLHC1	clathrin heavy chain linker domain containing 1 [Source:HGN
6	CEMIP	1.96	−0.23	0.46	CEMIP	cell migration inducing protein, hyaluronan binding [Source:H
7	OXTR	1.94	−0.06	0.76	OXTR	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]
8	MYL4	1.93	−0.04	0.81	MYL4	myosin, light chain 4, alkali; atrial, embryonic [Source:HGNC
9	PHLDB2	1.91	−0.23	0.46	PHLDB2	pleckstrin homology−like domain, family B, member 2 [Source
10	CHL1	1.89	−0.05	0.73	CHL1	cell adhesion molecule L1−like [Source:HGNC Symbol;Acc:H
11	CCDC81	1.88	−0.05	0.77	CCDC81	coiled−coil domain containing 81 [Source:HGNC Symbol;Acc
12	SDC2	1.85	−0.15	0.51	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
13	GAD1	1.84	−0.07	0.72	GAD1	glutamate decarboxylase 1 (brain, 67kDa) [Source:HGNC Sy
14	SAMD9L	1.83	−0.22	0.3	SAMD9L	sterile alpha motif domain containing 9−like [Source:HGNC S
15	TAB1	1.82	−0.27	0.31	TAB1	TGF−beta activated kinase 1/MAP3K7 binding protein 1 [Sou
16	DDX25	1.82	−0.16	0.41	DDX25	DEAD (Asp−Glu−Ala−Asp) box helicase 25 [Source:HGNC S
17	FBXO3	1.81	−0.52	0.27	FBXO3	F−box protein 3 [Source:HGNC Symbol;Acc:HGNC:13582]
18	HIST1H2BH	1.8	−0.08	0.54	HIST1H2BH	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:HGNC:47
19	NEGR1	1.79	−0.04	0.78	NEGR1	neuronal growth regulator 1 [Source:HGNC Symbol;Acc:HGN
20	PTPRO	1.79	−0.04	0.3	PTPRO	protein tyrosine phosphatase, receptor type, O [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−06	407 / 10290	Colon	TssWk_Colon
2	6e−06	43 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
3	1e−05	18 / 160	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
4	1e−05	17 / 146	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
5	2e−05	25 / 283	GSEA	PEREZ_TP63_TARGETS
6	6e−05	22 / 245	GSEA	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
7	6e−05	6 / 21	GSEA	REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATIO
8	8e−05	14 / 120	BP	transforming growth factor beta receptor signaling pathway
9	2e−04	10 / 71	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
10	2e−04	18 / 195	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
11	2e−04	9 / 59	GSEA	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX
12	3e−04	4 / 10	GSEA	REACTOME_THE_ACTIVATION_OF_ARYLSULFATASES
13	3e−04	8 / 49	CC	Golgi lumen
14	3e−04	9 / 62	GSEA	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP
15	3e−04	32 / 472	GSEA	SENESE_HDAC3_TARGETS_DN
16	4e−04	10 / 77	GSEA	SWEET_KRAS_TARGETS_UP
17	4e−04	16 / 173	GSEA	PEREZ_TP53_AND_TP63_TARGETS
18	5e−04	8 / 53	HM	HALLMARK_TGF_BETA_SIGNALING
19	5e−04	11 / 95	GSEA	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
20	5e−04	95 / 1949	Brain	Fetal_TssF
21	5e−04	10 / 81	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
22	6e−04	29 / 427	Colon	Quies2_Colon
23	6e−04	38 / 618	GSEA	GOZGIT_ESR1_TARGETS_DN
24	6e−04	43 / 730	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
25	8e−04	16 / 184	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
26	8e−04	3 / 6	GSEA	MAINA_HYPOXIA_VHL_TARGETS_UP
27	9e−04	47 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
28	9e−04	27 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
29	1e−03	35 / 569	miRN	hsa−miR−20b
30	1e−03	8 / 59	GSEA	ZHAN_MULTIPLE_MYELOMA_UP
31	1e−03	7 / 46	GSEA	CROMER_TUMORIGENESIS_UP
32	1e−03	52 / 953	Brain	Fetal_Enh
33	1e−03	351 / 9020	Brain	Overlap_fetal_midbrain_ReprPCWk
34	1e−03	9 / 74	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
35	1e−03	26 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
36	1e−03	37 / 620	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
37	1e−03	46 / 823	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
38	1e−03	349 / 8984	MF	protein binding
39	1e−03	3 / 7	Glio	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
40	1e−03	103 / 2211	Lympl	HOPP_Repetitive


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 100	HORVATH_aging_genes meth DOWN
2	0.6	4 / 111	HORVATH_aging_genes meth UP
3	0.7	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	8e−05	14 / 120	transforming growth factor beta receptor signaling pathway
2	2e−03	7 / 49	response to mechanical stimulus
3	2e−03	6 / 38	negative regulation of ERK1 and ERK2 cascade
4	2e−03	4 / 16	tRNA methylation
5	2e−03	5 / 27	negative regulation of MAP kinase activity
6	3e−03	6 / 41	positive regulation of synapse assembly
7	4e−03	4 / 19	membrane depolarization during action potential
8	4e−03	4 / 19	neuronal action potential
9	4e−03	3 / 10	signal transduction in response to DNA damage
10	5e−03	9 / 92	extracellular matrix disassembly
11	6e−03	120 / 2755	transport
12	7e−03	18 / 269	extracellular matrix organization
13	7e−03	6 / 49	negative regulation of translation
14	8e−03	3 / 12	positive regulation of urine volume
15	8e−03	4 / 23	positive regulation of ATPase activity
16	9e−03	10 / 119	skeletal system development
17	9e−03	8 / 84	endoplasmic reticulum unfolded protein response
18	1e−02	32 / 590	cell morphogenesis
19	1e−02	25 / 435	cellular protein metabolic process
20	1e−02	3 / 15	regulation of cytoskeleton organization

Brain

Rank	p−value	#in/all	Geneset
1	5e−04	95 / 1949	Fetal_TssF
2	1e−03	52 / 953	Fetal_Enh
3	1e−03	351 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	3e−03	33 / 564	Mid_Frontal_Lobe_EnhP
5	7e−03	41 / 786	Fetal_EnhG
6	8e−03	86 / 1907	Fetal_TxTrans
7	1e−02	129 / 3081	Mid_Frontal_Lobe_ZNF
8	2e−02	233 / 5940	Overlap_fetal_midbrain_HetRpts
9	3e−02	349 / 9330	Overlap_fetal_midbrain_ReprPC
10	3e−02	29 / 574	Overlap_fetal_midbrain_TssP
11	3e−02	51 / 1122	Fetal_K9K27me3
12	5e−02	20 / 383	Fetal_Tx
13	6e−02	31 / 656	Overlap_fetal_midbrain_EnhP
14	8e−02	44 / 1013	Fetal_TssP
15	1e−01	75 / 1845	Fetal_Quies
16	1e−01	45 / 1065	Overlap_fetal_midbrain_Enh
17	1e−01	347 / 9528	Overlap_fetal_midbrain_Quies
18	2e−01	85 / 2185	Fetal_TssA
19	2e−01	328 / 9013	Overlap_fetal_midbrain_K9K27me3
20	2e−01	32 / 765	Mid_Frontal_Lobe_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	7 / 82	PanCan_TxmisReg_geneset_nanostring
2	0.04	1 / 12	LIU_BREAST_CANCER
3	0.09	0 / 14	LIU_PROSTATE_CANCER_DN
4	0.10	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.10	7 / 113	PanCan_Driver_Gene_geneset_nanostring
6	0.11	2 / 16	GENTLES_modul14
7	0.15	2 / 20	PanCan_ChromMod_geneset_nanostring
8	0.17	18 / 401	Lembcke_Colonic Inflammation
9	0.31	3 / 55	PanCan_JAK−ST_geneset_nanostring
10	0.33	1 / 11	GENTLES_modul17
11	0.39	1 / 14	LIU_LIVER_CANCER
12	0.42	1 / 15	RHODES_CANCER_META_SIGNATURE
13	0.42	1 / 15	GENTLES_modul4
14	0.44	1 / 16	GENTLES_modul16
15	0.48	1 / 18	PanCan_Notch_geneset_nanostring
16	0.55	1 / 22	PanCan_HH_geneset_nanostring
17	0.55	0 / 12	LIU_PROSTATE_CANCER_UP
18	0.61	4 / 120	PanCan_CC+Apop_geneset_nanostring
19	0.62	4 / 121	PanCan_MAPK_geneset_nanostring
20	0.64	2 / 61	PanCan_Wnt_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−04	8 / 49	Golgi lumen
2	2e−03	13 / 145	endoplasmic reticulum lumen
3	4e−03	9 / 89	tight junction
4	4e−03	13 / 159	extracellular matrix
5	6e−03	4 / 21	clathrin adaptor complex
6	6e−03	8 / 79	nucleosome
7	8e−03	3 / 12	axonal growth cone
8	1e−02	9 / 102	cytoplasmic vesicle membrane
9	1e−02	3 / 15	eukaryotic 43S preinitiation complex
10	1e−02	3 / 15	eukaryotic 48S preinitiation complex
11	1e−02	110 / 2576	membrane
12	2e−02	3 / 16	eukaryotic translation initiation factor 3 complex
13	2e−02	10 / 138	cell−cell junction
14	2e−02	4 / 32	nuclear nucleosome
15	4e−02	5 / 54	intermediate filament cytoskeleton
16	4e−02	14 / 239	proteinaceous extracellular matrix
17	4e−02	4 / 38	cis−Golgi network
18	5e−02	4 / 39	autophagic vacuole
19	5e−02	91 / 2193	extracellular exosome
20	5e−02	35 / 745	cytoplasmic membrane−bounded vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.03	19 / 335	Chr 22
2	0.04	37 / 775	Chr 12
3	0.16	11 / 221	Chr 18
4	0.20	59 / 1500	Chr 1
5	0.25	32 / 801	Chr 11
6	0.27	33 / 838	Chr 3
7	0.28	7 / 151	Chr 21
8	0.29	40 / 1037	Chr 19
9	0.34	32 / 840	Chr 17
10	0.38	26 / 689	Chr 7
11	0.39	18 / 469	Chr 8
12	0.46	17 / 462	Chr 14
13	0.49	25 / 696	Chr 5
14	0.51	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
15	0.56	20 / 576	Chr 9
16	0.58	9 / 262	Chr 13
17	0.66	33 / 993	Chr 2
18	0.75	17 / 552	Chr 10
19	0.83	16 / 558	Chr 4
20	0.84	20 / 687	Chr 6

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−06	407 / 10290	TssWk_Colon
2	6e−04	29 / 427	Quies2_Colon
3	3e−03	165 / 3897	Quies1_Colon
4	9e−03	158 / 3812	TssD1_Colon
5	1e−02	327 / 8580	TxWk_Colon
6	2e−02	22 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
7	2e−02	319 / 8415	Quies3_Colon
8	2e−02	340 / 9027	Tx_Colon
9	4e−02	49 / 1079	ZNF_Colon
10	4e−02	114 / 2798	TxEnhG1_Colon
11	4e−02	200 / 5155	EnhWk1_Colon
12	5e−02	135 / 3383	EnhWk2_Colon
13	8e−02	355 / 9653	Enh_Colon
14	9e−02	8 / 131	Marisa_CRC−cluster−a
15	1e−01	2 / 17	Vilar_hypermutated−in−CRC
16	1e−01	1 / 4	Hewish_dMMR−secondary−mutations_Apoptosis
17	1e−01	85 / 2159	TssP_Colon
18	2e−01	4 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
19	2e−01	17 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
20	2e−01	10 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.06	16 / 294	GUDJ_psoriasis down
2	0.20	19 / 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	8e−04	16 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
2	1e−03	3 / 7	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
3	3e−03	22 / 332	Up
4	6e−03	3 / 11	Christensen_hypermethylated_in_ependymoma
5	9e−03	9 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
6	2e−02	6 / 62	cultured astroglia vs. in vivo astrocytes
7	6e−02	2 / 11	Martinez_Glio_hypermeth
8	6e−02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
9	7e−02	5 / 63	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
10	7e−02	4 / 45	Christensen_hypermethylated_in_primary_glioblastoma
11	9e−02	4 / 49	OL vs. MOG− OL
12	1e−01	5 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
13	1e−01	3 / 32	Colman_survival_associated
14	1e−01	3 / 33	Christensen_hypomethylated_in_primary_glioblastoma
15	1e−01	2 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
16	1e−01	4 / 57	GIEZELT_GBM_STSwt_down_VS_LTSwt
17	1e−01	3 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
18	2e−01	35 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
19	2e−01	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
20	2e−01	8 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−06	43 / 594	WONG_ADULT_TISSUE_STEM_MODULE
2	1e−05	18 / 160	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
3	1e−05	17 / 146	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
4	2e−05	25 / 283	PEREZ_TP63_TARGETS
5	6e−05	22 / 245	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
6	6e−05	6 / 21	REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_
7	2e−04	10 / 71	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_
8	2e−04	18 / 195	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
9	2e−04	9 / 59	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX
10	3e−04	4 / 10	REACTOME_THE_ACTIVATION_OF_ARYLSULFATASES
11	3e−04	9 / 62	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP
12	3e−04	32 / 472	SENESE_HDAC3_TARGETS_DN
13	4e−04	10 / 77	SWEET_KRAS_TARGETS_UP
14	4e−04	16 / 173	PEREZ_TP53_AND_TP63_TARGETS
15	5e−04	11 / 95	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
16	5e−04	10 / 81	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL
17	6e−04	38 / 618	GOZGIT_ESR1_TARGETS_DN
18	6e−04	43 / 730	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
19	8e−04	3 / 6	MAINA_HYPOXIA_VHL_TARGETS_UP
20	9e−04	47 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN

HM

Rank	p−value	#in/all	Geneset
1	5e−04	8 / 53	HALLMARK_TGF_BETA_SIGNALING
2	4e−03	10 / 107	HALLMARK_COAGULATION
3	6e−03	13 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	1e−02	8 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	2e−02	12 / 176	HALLMARK_HYPOXIA
6	3e−02	11 / 167	HALLMARK_APICAL_JUNCTION
7	4e−02	11 / 174	HALLMARK_HEME_METABOLISM
8	5e−02	11 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	1e−01	3 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
10	1e−01	9 / 167	HALLMARK_IL2_STAT5_SIGNALING
11	1e−01	9 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	2e−01	7 / 127	HALLMARK_KRAS_SIGNALING_DN
13	2e−01	7 / 137	HALLMARK_UV_RESPONSE_DN
14	2e−01	2 / 26	HALLMARK_ANGIOGENESIS
15	2e−01	8 / 169	HALLMARK_XENOBIOTIC_METABOLISM
16	3e−01	8 / 183	HALLMARK_GLYCOLYSIS
17	3e−01	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
18	4e−01	6 / 140	HALLMARK_INFLAMMATORY_RESPONSE
19	4e−01	6 / 146	HALLMARK_UV_RESPONSE_UP
20	4e−01	6 / 148	HALLMARK_KRAS_SIGNALING_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 7	DUMEAUX_Women normal BMI literature genes up
2	0.05	2 / 10	DUMEAUX_Smoking literature genes up
3	0.10	3 / 32	DUMEAUX_Fasting enriched genes
4	0.13	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	1.00	0 / 62	DUMEAUX_Smoking enriched genes
6	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers 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	0.001	103 / 2211	HOPP_Repetitive
2	0.004	18 / 256	SPANG_IL21 DN
3	0.005	19 / 280	SPANG_CD40 6hrs UP
4	0.027	52 / 1128	SPANG_BCR DN
5	0.063	5 / 61	SPANG_LPS 6hrs DN
6	0.090	269 / 7209	HOPP_Weak_promoter
7	0.094	246 / 6564	HOPP_Strong_enhancer
8	0.095	215 / 5693	HOPP_Weak_enhancer
9	0.128	11 / 212	LENZ_Stromal signature 1
10	0.133	1 / 4	Shaknovich_ABC_hyper_meth
11	0.164	1 / 5	WRIGHT_custom ABC−DLBCL UP
12	0.173	13 / 275	TARTE_Mature plasma cell signature
13	0.174	278 / 7592	HOPP_Active_promoter
14	0.225	97 / 2563	HOPP_Heterochrom
15	0.249	1 / 8	Subero_B−CLL_hypo_meth
16	0.266	202 / 5538	HOPP_Weak_txn
17	0.323	81 / 2188	HOPP_Poised_promoter
18	0.324	5 / 107	SPANG_LPS 6hrs UP
19	0.337	2 / 34	Subero_B−ALL_hyper_meth
20	0.338	5 / 109	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	0.001	349 / 8984	protein binding
2	0.003	4 / 18	actin monomer binding
3	0.004	5 / 31	transcription regulatory region sequence−specific DNA binding
4	0.009	4 / 24	antioxidant activity
5	0.009	4 / 24	N−acetyltransferase activity
6	0.010	3 / 13	voltage−gated sodium channel activity
7	0.014	3 / 15	hyaluronic acid binding
8	0.017	3 / 16	cysteine−type endopeptidase activator activity involved in apoptotic process
9	0.018	4 / 29	nucleosomal DNA binding
10	0.020	7 / 78	Rab GTPase binding
11	0.020	3 / 17	sulfuric ester hydrolase activity
12	0.024	7 / 81	serine−type endopeptidase activity
13	0.029	87 / 2037	DNA binding
14	0.031	26 / 501	identical protein binding
15	0.032	41 / 866	signal transducer activity
16	0.040	12 / 193	transferase activity, transferring acyl groups
17	0.041	6 / 72	structural constituent of cytoskeleton
18	0.045	3 / 23	hydrolase activity, acting on ester bonds
19	0.046	2 / 10	FAD binding
20	0.046	2 / 10	hedgehog receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	35 / 569	hsa−miR−20b
2	0.002	33 / 541	hsa−miR−17
3	0.002	36 / 607	hsa−miR−20a
4	0.003	8 / 69	hsa−miR−499−3p
5	0.003	19 / 269	hsa−miR−101
6	0.003	6 / 42	hsa−miR−192
7	0.004	14 / 179	hsa−miR−582−5p
8	0.005	9 / 92	hsa−miR−425
9	0.008	14 / 191	hsa−miR−641
10	0.009	5 / 37	hsa−miR−215
11	0.009	11 / 138	hsa−miR−136
12	0.011	29 / 523	hsa−miR−106a
13	0.012	15 / 222	hsa−miR−185
14	0.015	13 / 187	hsa−miR−382
15	0.016	12 / 168	hsa−miR−520h
16	0.017	3 / 16	hsa−miR−220a
17	0.018	4 / 29	hsa−miR−1237
18	0.019	14 / 214	hsa−miR−548m
19	0.020	8 / 96	hsa−miR−125a−5p
20	0.021	9 / 116	hsa−miR−376c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 13	BENTINK_src.10
2	0.28	1 / 9	BENTINK_ras.4
3	0.35	1 / 12	BENTINK_e2f3.2
4	0.35	1 / 12	BENTINK_ras.1
5	0.37	1 / 13	GUSTAFSON_PI3K_DN
6	0.42	1 / 15	BENTINK_ras.6
7	1.00	0 / 12	GUSTAFSON_PI3K_UP
8	1.00	0 / 14	BENTINK_e2f3.1
9	1.00	0 / 13	BENTINK_myc.1
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	0.02	118 / 2836	ICGC_Batf-cr1_targets
2	0.03	159 / 3966	ICGC_Pu1_targets
3	0.05	79 / 1872	ICGC_Mef2_targets
4	0.05	84 / 2013	ICGC_Bcl11_targets
5	0.06	233 / 6114	ICGC_Runx3_targets
6	0.08	116 / 2927	ICGC_Rad21_targets
7	0.08	223 / 5890	ICGC_Elf1_targets
8	0.08	49 / 1139	HEBENSTREIT_low expression TF
9	0.08	54 / 1273	ICGC_P300_targets
10	0.10	179 / 4689	ICGC_Taf1_targets
11	0.12	164 / 4314	ICGC_Ebfsc137065_targets
12	0.13	94 / 2391	ICGC_Pbx3_targets
13	0.15	200 / 5355	ICGC_Pol2_targets
14	0.15	184 / 4909	ICGC_Stat5_targets
15	0.16	74 / 1878	ICGC_Cebpbsc150_targets
16	0.17	204 / 5495	ICGC_Yy1_targets
17	0.17	67 / 1701	HEBENSTREIT_high expression TF
18	0.17	83 / 2137	ICGC_SrfV0416101_targets
19	0.18	29 / 690	ICGC_Atf3_targets
20	0.18	193 / 5200	ICGC_Mta3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.07	4 / 45	VAQUERIZAS_Uterus
2	0.08	2 / 14	VAQUERIZAS_Ovary
3	0.19	2 / 23	VAQUERIZAS_Trachea
4	0.19	2 / 23	VAQUERIZAS_Adrenal cortex
5	0.25	2 / 27	VAQUERIZAS_Lymph node
6	0.27	2 / 29	VAQUERIZAS_Smooth muscle
7	0.28	1 / 9	VAQUERIZAS_Kidney
8	0.39	2 / 38	VAQUERIZAS_Testis
9	0.39	6 / 143	VAQUERIZAS_General
10	0.41	2 / 40	VAQUERIZAS_Thyroid
11	0.44	1 / 16	VAQUERIZAS_Adrenal gland
12	0.46	1 / 17	VAQUERIZAS_Heart
13	0.56	1 / 23	VAQUERIZAS_Spinal cord
14	0.62	2 / 59	VAQUERIZAS_Whole blood
15	0.65	1 / 29	VAQUERIZAS_Fetal lung
16	0.69	1 / 33	VAQUERIZAS_Prostate
17	0.72	1 / 36	VAQUERIZAS_Fetal brain
18	0.73	1 / 37	VAQUERIZAS_Thymus
19	0.74	1 / 38	VAQUERIZAS_Whole brain
20	0.88	1 / 58	VAQUERIZAS_Lung

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 5	WIRTH_Bone marrow
2	0.2	16 / 350	WIRTH_Nervous System
3	0.3	15 / 350	WIRTH_Immune system
4	0.3	2 / 32	WIRTH_Pancreas
5	0.3	5 / 107	WIRTH_Testis
6	0.3	1 / 11	WIRTH_Sec. lymphoid organs
7	0.3	1 / 12	WIRTH_Lymphocytes
8	0.4	5 / 114	PALMER_T−Cell signature up
9	0.4	1 / 14	WIRTH_Telencephalon
10	0.5	2 / 46	WIRTH_Liver
11	0.5	7 / 194	PALMER_B−Cell signature up
12	0.7	7 / 225	PALMER_Granulocytes signature up
13	0.7	2 / 74	WIRTH_Mucosa
14	0.8	1 / 41	WIRTH_Homeostasis
15	1.0	0 / 11	WIRTH_Prim. lymphoid organs
16	1.0	0 / 13	WIRTH_B−cells
17	1.0	0 / 8	WIRTH_Tonsil
18	1.0	0 / 12	WIRTH_Thymus
19	1.0	0 / 11	WIRTH_Globus pallidus
20	1.0	0 / 11	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	130 / 3682	LU_BPDE 0.005 DN
2	0.9	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	

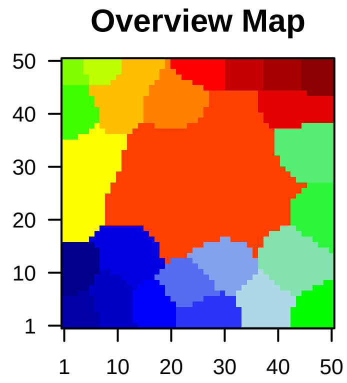
K−Means Clusters

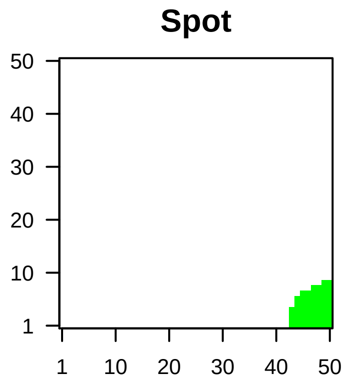
Spot Summary: T

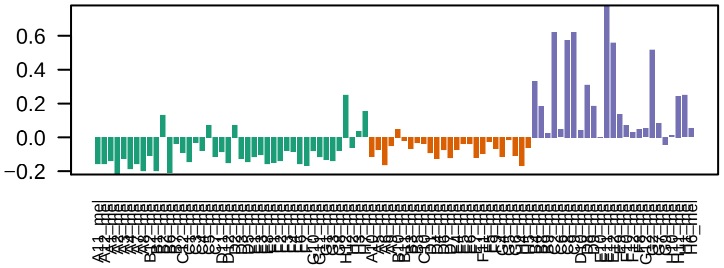
metagenes = 58
genes = 638

<r> metagenes = 0.89
<r> genes = 0.14
beta: r2= 3.35 / log p= −Inf

samples with spot = 14 (15.2 %)
MSC1 : 2 (4.8 %)
MSC3 : 12 (48 %)


Overview Map


Spot

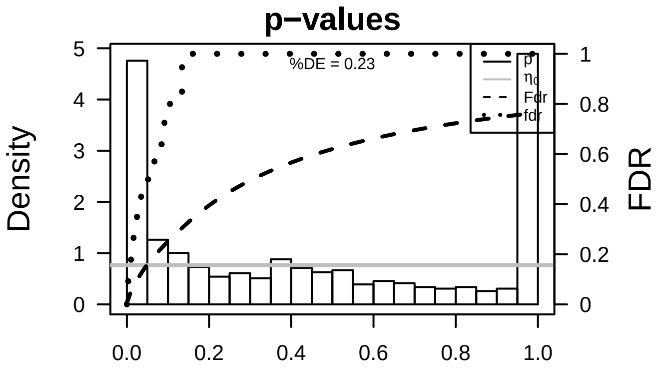


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	LUM	3.07	−0.63	0.39	LUM	lumican [Source:HGNC Symbol;Acc:HGNC:6724]
2	DKK1	2.85	−0.31	0.63	DKK1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Sy
3	IL24	2.78	−0.11	0.59	IL24	interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
4	HBEGF	2.46	−0.25	0.53	HBEGF	heparin−binding EGF−like growth factor [Source:HGNC Symb
5	ANXA1	2.44	−0.5	0.78	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
6	FADS3	2.35	−0.24	0.56	FADS3	fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35
7	PTPRZ1	2.31	−0.37	0.7	PTPRZ1	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
8	NAV3	2.3	−0.23	0.73	NAV3	neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998
9	RGS4	2.3	−0.3	0.4	RGS4	regulator of G−protein signaling 4 [Source:HGNC Symbol;Acc
10	A2M	2.29	−0.9	0.52	A2M	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
11	RGS2	2.26	−0.52	0.33	RGS2	regulator of G−protein signaling 2 [Source:HGNC Symbol;Acc
12	KCNJ2	2.26	−0.25	0.68	KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2
13	HIST1H3D	2.25	−0.35	0.37	HIST1H3D	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
14	FN1	2.23	−1.04	0.4	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
15	SERPINI1	2.21	−0.56	0.39	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
16	LMCD1	2.2	−0.68	0.32	LMCD1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
17	VTN	2.14	−0.36	0.67	VTN	vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
18	SLC40A1	2.11	−0.56	0.38	SLC40A1	solute carrier family 40 (iron−regulated transporter), member
19	ARRDC3	2.09	−0.76	0.5	ARRDC3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:HG
20	CAV1	2.08	−0.76	0.44	CAV1	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−34	90 / 472	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	6e−33	69 / 286	GSEA	PASINI_SUZ12_TARGETS_DN
3	4e−29	94 / 594	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
4	2e−27	104 / 749	GSEA	CUI_TCF21_TARGETS_2_DN
5	7e−25	73 / 425	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	1e−23	50 / 212	Lymph	LENZ_Stromal signature 1
7	7e−21	56 / 302	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
8	2e−20	93 / 761	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
9	2e−20	63 / 385	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
10	2e−20	98 / 833	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
11	6e−20	104 / 930	GSEA	NUYTTEN_EZH2_TARGETS_UP
12	2e−18	39 / 168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	1e−17	60 / 401	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
14	6e−17	51 / 308	CC	focal adhesion
15	1e−16	66 / 494	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
16	6e−16	42 / 227	GSEA	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
17	3e−15	57 / 410	GSEA	LIM_MAMMARY_STEM_CELL_UP
18	4e−15	31 / 131	Colon	Marisa_CRC−cluster−a
19	7e−15	56 / 406	GSEA	BAELDE_DIABETIC_NEPHROPATHY_DN
20	1e−14	42 / 245	GSEA	WANG_SMARCE1_TARGETS_UP
21	1e−14	34 / 164	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
22	2e−14	45 / 283	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
23	3e−14	43 / 263	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
24	4e−14	82 / 784	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
25	6e−14	3 / 14	Canc	LIU_PROSTATE_CANCER_DN
26	6e−14	33 / 163	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
27	2e−13	31 / 149	GSEA	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
28	2e−13	39 / 234	GSEA	LU_AGING_BRAIN_UP
29	4e−13	58 / 473	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
30	6e−13	29 / 137	HM	HALLMARK_UV_RESPONSE_DN
31	7e−13	54 / 426	GSEA	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
32	1e−12	37 / 222	GSEA	UDAYAKUMAR_MED1_TARGETS_DN
33	2e−12	36 / 215	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
34	2e−12	30 / 153	GSEA	WU_CELL_MIGRATION
35	3e−12	23 / 91	GSEA	BROWNE_HCMV_INFECTION_20HR_DN
36	4e−12	30 / 157	GSEA	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
37	5e−12	34 / 200	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
38	6e−12	25 / 111	GSEA	ZHU_CMV_ALL_DN
39	8e−12	70 / 683	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
40	9e−12	50 / 400	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.002	12 / 111	HORVATH_aging_genes meth UP
2	0.138	17 / 100	HORVATH_aging_genes meth DOWN
3	0.490	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	2e−09	194 / 3068	signal transduction
2	4e−09	60 / 626	cell adhesion
3	1e−08	23 / 134	cell junction organization
4	8e−08	144 / 2210	anatomical structure development
5	9e−07	51 / 581	cytoskeleton organization
6	1e−06	19 / 122	plasma membrane organization
7	1e−06	58 / 705	locomotion
8	1e−06	105 / 1556	cell differentiation
9	2e−06	30 / 269	extracellular matrix organization
10	2e−06	18 / 115	cell cycle arrest
11	2e−06	30 / 271	positive regulation of apoptotic process
12	5e−06	32 / 312	axon guidance
13	9e−06	8 / 26	hippo signaling
14	9e−06	9 / 34	dendrite morphogenesis
15	1e−05	48 / 581	negative regulation of transcription from RNA polymerase II promoter
16	2e−05	48 / 590	cell morphogenesis
17	3e−05	7 / 22	actin filament bundle assembly
18	3e−05	5 / 10	cell−cell junction assembly
19	4e−05	38 / 443	anatomical structure formation involved in morphogenesis
20	4e−05	19 / 156	cell migration

Brain

Rank	p−value	#in/all	Geneset
1	2e−11	478 / 9330	Overlap_fetal_midbrain_ReprPC
2	1e−10	88 / 1013	Fetal_TssP
3	1e−08	454 / 9020	Overlap_fetal_midbrain_ReprPCWk
4	1e−08	324 / 5940	Overlap_fetal_midbrain_HetRpts
5	3e−06	49 / 574	Overlap_fetal_midbrain_TssP
6	4e−06	461 / 9528	Overlap_fetal_midbrain_Quies
7	1e−05	74 / 1050	Fetal_EnhP
8	2e−05	132 / 2185	Fetal_TssA
9	2e−04	30 / 349	Fetal_ZNF
10	3e−04	112 / 1907	Fetal_TxTrans
11	4e−04	113 / 1949	Fetal_TssF
12	1e−03	46 / 668	Mid_Frontal_Lobe_Enh
13	3e−03	24 / 304	Fetal_Het
14	5e−03	418 / 9013	Overlap_fetal_midbrain_K9K27me3
15	8e−03	27 / 383	Fetal_Tx
16	1e−02	47 / 786	Fetal_EnhG
17	2e−02	45 / 769	Overlap_fetal_midbrain_ZNF
18	3e−02	53 / 953	Fetal_Enh
19	4e−02	12 / 158	Overlap_fetal_midbrain_Het
20	8e−02	58 / 1122	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	6e−14	3 / 14	LIU_PROSTATE_CANCER_DN
2	1e−05	20 / 156	PanCan_PI3K_geneset_nanostring
3	6e−05	35 / 401	Lembcke_Colonic Inflammation
4	9e−05	28 / 298	SPANG_BCL6−index2
5	7e−04	11 / 82	PanCan_TXmisReg_geneset_nanostring
6	9e−04	13 / 111	PanCan_RAS_geneset_nanostring
7	2e−03	7 / 44	PanCan_TGF−B_geneset_nanostring
8	5e−03	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	5e−03	2 / 3	ZHANG_MGUS up
10	1e−02	3 / 11	GENTLES_modul17
11	2e−02	7 / 61	PanCan_Wnt_geneset_nanostring
12	3e−02	6 / 55	PanCan_JAK−ST_geneset_nanostring
13	3e−02	10 / 120	PanCan_CC+Apop_geneset_nanostring
14	7e−02	2 / 10	GENTLES_modul13
15	8e−02	9 / 121	PanCan_MAPK_geneset_nanostring
16	8e−02	6 / 70	SHAUGHNESSY_MM high risk
17	9e−02	4 / 40	ZHANG_MM up
18	1e−01	2 / 13	GENTLES_modul12
19	1e−01	1 / 12	LIU_PROSTATE_CANCER_UP
20	2e−01	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	6e−17	51 / 308	focal adhesion
2	3e−11	33 / 202	actin cytoskeleton
3	2e−08	40 / 352	cell surface
4	1e−07	22 / 138	cell−cell junction
5	1e−07	104 / 1465	cytoskeleton
6	3e−07	141 / 2193	extracellular exosome
7	4e−07	29 / 239	proteinaceous extracellular matrix
8	5e−07	184 / 3088	plasma membrane
9	1e−06	16 / 89	Z disc
10	7e−06	180 / 3132	extracellular region
11	1e−05	13 / 73	basement membrane
12	2e−05	20 / 159	extracellular matrix
13	3e−05	10 / 48	stress fiber
14	9e−05	16 / 125	lamellipodium
15	1e−04	15 / 113	postsynaptic density
16	3e−04	12 / 85	ruffle
17	3e−04	13 / 99	cell cortex
18	3e−04	9 / 52	caveola
19	3e−04	6 / 23	integrin complex
20	4e−04	7 / 33	cell leading edge

Chr

Rank	p−value	#in/all	Geneset
1	0.001	88 / 1500	Chr 1
2	0.005	52 / 838	Chr 3
3	0.025	41 / 696	Chr 5
4	0.025	34 / 558	Chr 4
5	0.031	40 / 687	Chr 6
6	0.322	8 / 151	Chr 21
7	0.335	13 / 262	Chr 13
8	0.372	45 / 993	Chr 2
9	0.411	36 / 801	Chr 11
10	0.419	25 / 552	Chr 10
11	0.437	21 / 465	Chr 15
12	0.472	34 / 775	Chr 12
13	0.478	10 / 221	Chr 18
14	0.517	20 / 462	Chr 14
15	0.584	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
16	0.642	16 / 398	Chr 20
17	0.780	26 / 689	Chr 7
18	0.968	13 / 469	Chr 8
19	0.973	19 / 649	Chr 16
20	0.979	16 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−15	31 / 131	Marisa_CRC−cluster−a
2	3e−14	43 / 263	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	2e−11	25 / 117	Marisa_CRC−cluster−b
4	8e−11	39 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	1e−10	235 / 3812	TssD1_Colon
6	2e−10	511 / 10290	TssWk_Colon
7	1e−09	235 / 3897	Quies1_Colon
8	2e−07	200 / 3383	EnhWk2_Colon
9	1e−06	462 / 9482	TssA_Colon
10	6e−06	440 / 9027	Tx_Colon
11	7e−06	421 / 8580	TxWk_Colon
12	2e−05	412 / 8415	Quies3_Colon
13	6e−05	154 / 2698	EnhA_Colon
14	7e−05	267 / 5155	EnhWk1_Colon
15	3e−04	455 / 9653	Enh_Colon
16	3e−04	32 / 390	Pentrack_CRC_TCGA_corr_C_normal_UP
17	6e−04	34 / 436	K9acLow_Colon
18	1e−03	151 / 2798	TxEnhG1_Colon
19	2e−03	7 / 43	Marisa_CRC−cluster−f
20	3e−03	48 / 739	TxEnhG2_Colon

Disease

Rank	p−value	#in/all	Geneset
1	4e−04	26 / 294	GUDJ_psoriasis down
2	8e−01	16 / 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	7e−08	19 / 103	GIEZELT_GBM_WT_up_VS_mut
2	1e−05	12 / 62	cultured astroglia vs. in vivo astrocytes
3	5e−05	8 / 32	Colman_survival_associated
4	1e−03	18 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
5	1e−03	8 / 49	OL vs. MOG−OL
6	2e−03	11 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	1e−02	7 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
8	1e−02	4 / 22	KIM prognostic signature LTS vs. STS
9	2e−02	22 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	2e−02	5 / 39	OPC
11	3e−02	9 / 100	Christensen_hypermethylated_in_grade2_oligoastrocytoma
12	3e−02	3 / 16	KIM deleted & downregulated in LTS
13	3e−02	22 / 332	Up
14	4e−02	10 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
15	5e−02	5 / 47	Vishal_subnetwork signature of survival in GBM
16	5e−02	2 / 9	Christensen_hypomethylated_in_grade3_oligoastrocytoma
17	5e−02	2 / 9	Mukasa_UP_in_GBM
18	6e−02	8 / 97	Christensen_hypermethylated_in_grade3_astrocytoma
19	6e−02	5 / 49	Sturm_GBM_Meth_overexpression_D_G34_UP
20	7e−02	9 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−34	90 / 472	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	6e−33	69 / 286	PASINI_SUZ12_TARGETS_DN
3	4e−29	94 / 594	WONG_ADULT_TISSUE_STEM_MODULE
4	2e−27	104 / 749	CUI_TCF21_TARGETS_2_DN
5	7e−25	73 / 425	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	7e−21	56 / 302	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
7	2e−20	93 / 761	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
8	2e−20	63 / 385	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
9	2e−20	98 / 833	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	6e−20	104 / 930	NUYTTEN_EZH2_TARGETS_UP
11	1e−17	60 / 401	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
12	1e−16	66 / 494	CHICAS_RB1_TARGETS_CONFLUENT
13	6e−16	42 / 227	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
14	3e−15	57 / 410	LIM_MAMMARY_STEM_CELL_UP
15	7e−15	56 / 406	BAELDE_DIABETIC_NEPHROPATHY_DN
16	1e−14	42 / 245	WANG_SMARCE1_TARGETS_UP
17	1e−14	34 / 164	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
18	2e−14	45 / 283	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
19	4e−14	82 / 784	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
20	6e−14	3 / 14	LIU_PROSTATE_CANCER_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−18	39 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	6e−13	29 / 137	HALLMARK_UV_RESPONSE_DN
3	9e−09	27 / 177	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	1e−08	27 / 181	HALLMARK_P53_PATHWAY
5	3e−08	26 / 176	HALLMARK_HYPOXIA
6	8e−06	19 / 140	HALLMARK_APOPTOSIS
7	8e−05	7 / 26	HALLMARK_ANGIOGENESIS
8	9e−05	19 / 165	HALLMARK_MYOGENESIS
9	1e−04	19 / 167	HALLMARK_APICAL_JUNCTION
10	3e−04	18 / 167	HALLMARK_IL2_STAT5_SIGNALING
11	7e−04	12 / 94	HALLMARK_ANDROGEN_RESPONSE
12	7e−04	19 / 195	HALLMARK_MITOTIC_SPINDLE
13	2e−03	15 / 148	HALLMARK_KRAS_SIGNALING_UP
14	2e−03	8 / 53	HALLMARK_TGF_BETA_SIGNALING
15	3e−03	16 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
16	4e−03	7 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
17	6e−03	11 / 107	HALLMARK_COAGULATION
18	1e−02	5 / 31	HALLMARK_HEDGEHOG_SIGNALING
19	5e−02	13 / 183	HALLMARK_GLYCOLYSIS
20	7e−02	4 / 37	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	3 / 18	DUMEAUX_High bmi enriched genes
2	0.13	2 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.16	3 / 32	DUMEAUX_Fasting enriched genes
4	0.16	1 / 4	DUMEAUX_Estrogen related in smokers literature genes up
5	0.50	3 / 62	DUMEAUX_Smoking enriched genes
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	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	1e−23	50 / 212	LENZ_Stromal signature 1
2	9e−11	154 / 2188	HOPP_Poised_promoter
3	5e−07	304 / 5693	HOPP_Weak_enhancer
4	7e−07	198 / 3396	HOPP_Repressed
5	1e−06	156 / 2563	HOPP_Heterochrom
6	4e−06	17 / 109	ROSOLOWSKI_green total
7	3e−05	132 / 2211	HOPP_Repetitive
8	4e−05	13 / 82	ROSOLOWSKI_green UP
9	4e−04	8 / 43	LENZ_Stromal signature 2
10	4e−04	25 / 280	SPANG_CD40 6hrs UP
11	5e−04	323 / 6564	HOPP_Strong_enhancer
12	1e−03	23 / 268	SPANG_IL21 UP
13	1e−03	347 / 7209	HOPP_Weak_promoter
14	4e−03	67 / 1128	SPANG_BCR DN
15	5e−03	269 / 5538	HOPP_Weak_txn
16	8e−03	4 / 19	Subero_MM_hyper_meth
17	8e−03	10 / 96	Subero_DLBCL_hyper_meth
18	9e−03	4 / 20	SPANG_BAFF 9hrs UP
19	1e−02	6 / 47	Subero_FL_hyper_meth
20	2e−02	20 / 275	TARTE_Mature plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	7e−11	63 / 609	cytoskeletal protein binding
2	3e−09	19 / 86	integrin binding
3	8e−09	453 / 8984	protein binding
4	6e−07	31 / 271	actin binding
5	1e−06	17 / 102	actin filament binding
6	1e−05	45 / 530	calcium ion binding
7	5e−05	6 / 17	insulin−like growth factor binding
8	5e−05	14 / 95	heparin binding
9	2e−04	19 / 174	transcription corepressor activity
10	2e−04	9 / 49	collagen binding
11	2e−04	5 / 14	G−protein alpha−subunit binding
12	3e−04	14 / 111	protein binding, bridging
13	4e−04	56 / 820	sequence−specific DNA binding transcription factor activity
14	4e−04	5 / 16	extracellular matrix binding
15	7e−04	30 / 373	protein heterodimerization activity
16	8e−04	5 / 18	laminin binding
17	9e−04	55 / 830	nucleic acid binding transcription factor activity
18	9e−04	11 / 84	RNA polymerase II core promoter proximal region sequence−specific DNA bir
19	1e−03	21 / 233	RNA polymerase II core promoter proximal region sequence−specific DNA bir
20	1e−03	250 / 4992	ion binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−09	36 / 268	hsa−miR−363
2	1e−09	60 / 607	hsa−miR−20a
3	2e−09	40 / 327	hsa−miR−367
4	4e−09	39 / 321	hsa−miR−32
5	2e−08	30 / 222	hsa−miR−520g
6	1e−07	32 / 263	hsa−miR−92b
7	1e−07	51 / 541	hsa−miR−17
8	2e−07	37 / 340	hsa−miR−142−5p
9	2e−07	32 / 271	hsa−miR−92a
10	2e−07	24 / 168	hsa−miR−520h
11	3e−07	24 / 170	hsa−miR−183
12	4e−07	48 / 517	hsa−miR−106b
13	6e−07	20 / 129	hsa−miR−576−3p
14	6e−07	43 / 447	hsa−miR−130b
15	1e−06	32 / 296	hsa−miR−25
16	2e−06	31 / 282	hsa−miR−570
17	2e−06	24 / 187	hsa−miR−944
18	2e−06	37 / 376	hsa−miR−373
19	2e−06	19 / 129	hsa−miR−1272
20	3e−06	33 / 318	hsa−miR−302a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 13	BENTINK_src.10
2	0.4	1 / 12	GUSTAFSON_PI3K_UP
3	0.4	1 / 12	BENTINK_ras.1
4	0.4	1 / 13	GUSTAFSON_PI3K_DN
5	0.5	1 / 14	BENTINK_e2f3.1
6	1.0	0 / 12	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.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	0.005	3 / 9	MYC_Targets DOWN
2	0.008	150 / 2927	ICGC_Rad21_targets
3	0.012	71 / 1266	ICGC_NrsfPcr1_targets
4	0.042	61 / 1139	HEBENSTREIT_low expression TF
5	0.071	93 / 1872	ICGC_Mef2_targets
6	0.084	1 / 2	MYC_Cell cycle DOWN
7	0.084	1 / 2	MYC_ECM cell adhesion DOWN
8	0.128	63 / 1273	ICGC_P300_targets
9	0.156	132 / 2836	ICGC_BatfPcr1_targets
10	0.168	95 / 2013	ICGC_Bcl11_targets
11	0.172	181 / 3966	ICGC_Pu1_targets
12	0.197	1 / 5	MYC_TF and cofactors
13	0.330	107 / 2391	ICGC_Pbx3_targets
14	0.385	172 / 3924	ICGC_Zeb1_targets
15	0.410	27 / 595	ICGC_NrsfPcr2_targets
16	0.423	25 / 553	ICGC_RxraPcr1_targets
17	0.450	82 / 1878	ICGC_Cebpbsc150_targets
18	0.468	74 / 1701	HEBENSTREIT_high expression TF
19	0.482	1 / 15	NOWICK_TF
20	0.530	28 / 653	ICGC_SrfPcr2_targets

TF Tissue

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

Tissue

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 11	WIRTH_Sec. lymphoid organs
2	4e−03	17 / 194	PALMER_B−Cell signature up
3	1e−02	3 / 11	WIRTH_Cortex cerebri
4	2e−02	10 / 114	PALMER_T−Cell signature up
5	9e−02	2 / 12	WIRTH_Thymus
6	1e−01	2 / 14	WIRTH_Telencephalon
7	3e−01	12 / 225	PALMER_Granulocytes signature up
8	3e−01	1 / 9	PALMER_CD8+ T−Cell signature up
9	4e−01	5 / 95	WIRTH_Muscle
10	4e−01	1 / 13	WIRTH_B−cells
11	6e−01	2 / 46	WIRTH_Liver
12	6e−01	3 / 74	WIRTH_Mucosa
13	6e−01	14 / 350	WIRTH_Nervous System
14	8e−01	1 / 32	WIRTH_Placenta
15	8e−01	12 / 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	0.3	163 / 3682	LU_BPDE 0.005 DN
2	0.9	40 / 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	

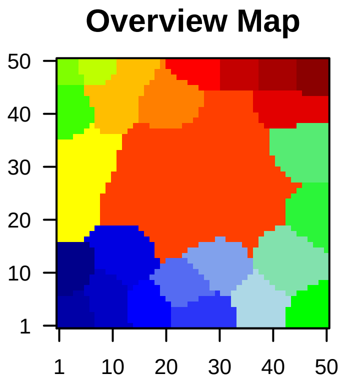
K−Means Clusters

Spot Summary: U

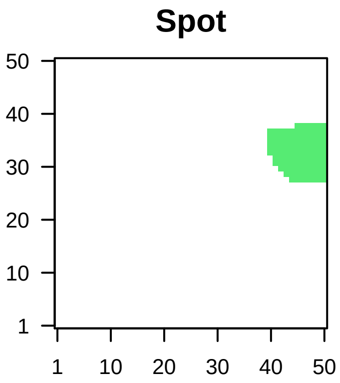
metagenes = 105
genes = 642

<r> metagenes = 0.67
<r> genes = 0.06
beta: r2= 0.56 / log p= −Inf

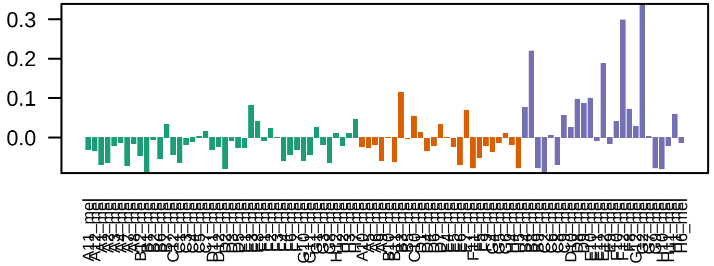
samples with spot = 4 (4.3 %)
MSC3 : 4 (16 %)



Overview Map



Spot

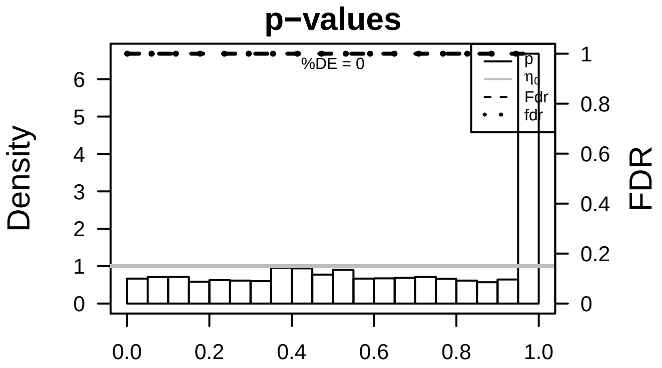


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	GPX3	2.45	−0.18	0.52	GPX3	glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:
2	P2RX7	2.1	−0.56	0.41	P2RX7	purinergic receptor P2X, ligand gated ion channel, 7 [Source:
3	CXCL1	2.09	−0.14	0.29	CXCL1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
4	CFAP69	2.05	−0.11	0.47	CFAP69	cilia and flagella associated protein 69 [Source:HGNC Symbo
5	NR2E3	2	−0.07	0.47	NR2E3	nuclear receptor subfamily 2, group E, member 3 [Source:HG
6	GSG1L	1.94	−0.03	0.75	GSG1L	GSG1−like [Source:HGNC Symbol;Acc:HGNC:28283]
7	CD33	1.91	−0.17	0.46	CD33	CD33 molecule [Source:HGNC Symbol;Acc:HGNC:1659]
8	F13A1	1.88	−0.1	0.59	F13A1	coagulation factor XIII, A1 polypeptide [Source:HGNC Symbo
9	GALNT14	1.86	−0.24	0.42	GALNT14	polypeptide N−acetylgalactosaminyltransferase 14 [Source:H
10	OR10A2	1.85	−0.02	0.78	OR10A2	olfactory receptor, family 10, subfamily A, member 2 [Source:
11	ALOX12B	1.84	−0.08	0.66	ALOX12B	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
12	KLRG1	1.83	−0.25	0.3	KLRG1	killer cell lectin−like receptor subfamily G, member 1 [Source:
13	RASL11A	1.83	−0.04	0.7	RASL11A	RAS−like, family 11, member A [Source:HGNC Symbol;Acc:H
14	DES	1.82	−0.02	0.76	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
15	CLTCL1	1.81	−0.09	0.59	CLTCL1	clathrin, heavy chain−like 1 [Source:HGNC Symbol;Acc:HGN
16	STXBP2	1.81	−0.17	0.35	STXBP2	syntaxin binding protein 2 [Source:HGNC Symbol;Acc:HGNC
17	THSD7A	1.8	−0.15	0.46	THSD7A	thrombospondin, type I, domain containing 7A [Source:HGNC
18	PHF11	1.78	−0.21	0.47	PHF11	PHD finger protein 11 [Source:HGNC Symbol;Acc:HGNC:17
19	N4BP2L1	1.77	−0.12	0.33	N4BP2L1	NEDD4 binding protein 2−like 1 [Source:HGNC Symbol;Acc:H
20	SLC7A7	1.77	−0.16	0.32	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−04	5 / 13	BP	positive regulation of cytokine secretion
2	4e−04	4 / 9	GSE	AGARWAL_AKT_PATHWAY_TARGETS
3	5e−04	7 / 34	GSE	WIERENGA_PML_INTERACTOME
4	5e−04	15 / 132	CC	basolateral plasma membrane
5	6e−04	4 / 10	GSE	REACTOME_COPI_MEDIATED_TRANSPORT
6	6e−04	5 / 17	GSE	STEGER_ADIPOGENESIS_DN
7	6e−04	8 / 45	Colon	Ang_CRC−CIMPH−vs−L_hyper
8	1e−03	28 / 350	Tissu	WIRTH_Nervous System
9	1e−03	8 / 50	Colon	Ang_CRC_Hypermethylated
10	1e−03	5 / 20	GSE	PID_GLYPICAN_1PATHWAY
11	2e−03	121 / 2185	Brain	Fetal_TssA
12	2e−03	31 / 409	BP	cell motility
13	2e−03	158 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
14	2e−03	7 / 41	BP	positive regulation of MAP kinase activity
15	2e−03	9 / 65	GSE	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA
16	2e−03	11 / 91	HM	HALLMARK_PROTEIN_SECRETION
17	2e−03	4 / 13	BP	COPI coating of Golgi vesicle
18	2e−03	6 / 31	GSE	KEGG_ARACHIDONIC_ACID_METABOLISM
19	2e−03	6 / 31	GSE	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN
20	2e−03	9 / 66	BP	platelet degranulation
21	2e−03	16 / 166	MF	receptor activity
22	2e−03	4 / 14	GSE	KANG_AR_TARGETS_UP
23	2e−03	10 / 81	Lymp	Subero_INT_hyper_meth
24	2e−03	3 / 7	Glio	KIM_epithelial−mesenchymal−transition related genes_decreased expressi
25	2e−03	3 / 7	GSE	MIKI_COEXPRESSED_WITH_CYP19A1
26	3e−03	5 / 23	GSE	REACTOME_LYSOSOME_VESICLE_BIOGENESIS
27	3e−03	9 / 70	GSE	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
28	3e−03	6 / 35	GSE	LIU_TARGETS_OF_VMYB_VS_CMYB_DN
29	4e−03	41 / 616	GSE	NABA_MATRISOME
30	4e−03	5 / 25	MF	aminopeptidase activity
31	4e−03	5 / 25	miRN	hsa−miR−663b
32	4e−03	5 / 25	GSE	BIOCARTA_IL1R_PATHWAY
33	4e−03	4 / 16	BP	ERK1 and ERK2 cascade
34	4e−03	7 / 48	GSE	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
35	4e−03	12 / 117	GSE	REACTOME_MEMBRANE_TRAFFICKING
36	5e−03	16 / 179	GSE	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
37	5e−03	11 / 103	Glio	GIEZELT_GBM_WT_up_VS_mut
38	5e−03	117 / 2172	BP	response to stress
39	5e−03	15 / 165	GSE	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
40	5e−03	4 / 17	MF	RNA polymerase II core binding



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.08	4 / 38	TESCHENDORFF_age_hypermethylated
2	0.71	4 / 111	HORVATH_aging_genes meth UP
3	0.93	2 / 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−04	5 / 13	positive regulation of cytokine secretion
2	2e−03	31 / 409	cell motility
3	2e−03	7 / 41	positive regulation of MAP kinase activity
4	2e−03	4 / 13	COPI coating of Golgi vesicle
5	2e−03	9 / 66	platelet degranulation
6	4e−03	4 / 16	ERK1 and ERK2 cascade
7	5e−03	117 / 2172	response to stress
8	6e−03	4 / 18	activation of NF−kappaB−inducing kinase activity
9	7e−03	14 / 156	cell migration
10	8e−03	3 / 10	negative regulation of cardiac muscle cell apoptotic process
11	8e−03	6 / 41	negative regulation of phosphatase activity
12	8e−03	5 / 30	positive regulation of cell division
13	9e−03	12 / 128	visual perception
14	9e−03	4 / 20	glutamine metabolic process
15	1e−02	6 / 44	post−Golgi vesicle−mediated transport
16	1e−02	5 / 32	fertilization
17	1e−02	4 / 21	regulation of reactive oxygen species metabolic process
18	1e−02	11 / 117	regulation of mitochondrion degradation
19	1e−02	3 / 12	protein O−linked mannosylation
20	1e−02	43 / 705	locomotion

Brain

Rank	p−value	#in/all	Geneset
1	0.002	121 / 2185	Fetal_TssA
2	0.002	158 / 2972	Mid_Frontal_Lobe_ReprPC
3	0.008	129 / 2462	Mid_Frontal_Lobe_HetRpts
4	0.019	50 / 862	Overlap_fetal_midbrain_TxTrans
5	0.020	56 / 989	Mid_Frontal_Lobe_Quies
6	0.036	32 / 534	Mid_Frontal_Lobe_EnhG
7	0.051	65 / 1236	Mid_Frontal_Lobe_ReprPCWk
8	0.052	98 / 1949	Fetal_TssF
9	0.058	54 / 1013	Fetal_TssP
10	0.061	51 / 953	Fetal_Enh
11	0.079	36 / 656	Overlap_fetal_midbrain_EnhP
12	0.130	89 / 1845	Fetal_Quies
13	0.155	25 / 468	Mid_Frontal_Lobe_TssF
14	0.155	30 / 574	Overlap_fetal_midbrain_TssP
15	0.175	5 / 69	Overlap_fetal_midbrain_Tx
16	0.213	89 / 1907	Fetal_TxTrans
17	0.226	33 / 668	Mid_Frontal_Lobe_Enh
18	0.240	9 / 158	Overlap_fetal_midbrain_Het
19	0.244	57 / 1207	Overlap_fetal_midbrain_TssF
20	0.245	18 / 349	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	14 / 156	PanCan_PI3K_geneset_nanostring
2	0.008	11 / 111	PanCan_RAS_geneset_nanostring
3	0.036	10 / 121	PanCan_MAPK_geneset_nanostring
4	0.064	24 / 401	Lembcke_Colonic Inflammation
5	0.134	2 / 15	RHODES_CANCER_META_SIGNATURE
6	0.246	3 / 40	PanCan_HK_geneset_nanostring
7	0.277	5 / 82	PanCan_TXmisReg_geneset_nanostring
8	0.356	1 / 10	GENTLES_modul13
9	0.383	1 / 11	GENTLES_modul17
10	0.423	3 / 55	PanCan_JAK−ST_geneset_nanostring
11	0.503	0 / 14	LIU_PROSTATE_CANCER_DN
12	0.505	1 / 16	GENTLES_modul16
13	0.518	2 / 40	ZHANG_MM_up
14	0.570	2 / 44	PanCan_TGF−B_geneset_nanostring
15	0.585	1 / 20	PanCan_ChromMod_geneset_nanostring
16	0.592	5 / 120	PanCan_CC+Apop_geneset_nanostring
17	0.629	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
18	0.633	12 / 298	SPANG_BCL6−index2
19	0.721	1 / 29	KUIPER_MM good survival
20	0.721	4 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	5e−04	15 / 132	basolateral plasma membrane
2	9e−03	6 / 42	neuromuscular junction
3	9e−03	15 / 177	synapse
4	1e−02	8 / 70	sarcolemma
5	1e−02	6 / 45	SNARE complex
6	2e−02	5 / 37	platelet alpha granule lumen
7	2e−02	156 / 3132	extracellular region
8	2e−02	6 / 51	axoneme
9	2e−02	14 / 178	apical plasma membrane
10	3e−02	4 / 27	photoreceptor inner segment
11	3e−02	3 / 16	M band
12	4e−02	4 / 30	sarcomere
13	5e−02	4 / 32	chloride channel complex
14	5e−02	18 / 276	cilium
15	6e−02	3 / 21	anaphase−promoting complex
16	6e−02	3 / 21	transcription elongation factor complex
17	7e−02	7 / 83	endomembrane system
18	7e−02	2 / 10	ionotropic glutamate receptor complex
19	7e−02	5 / 51	collagen trimer
20	7e−02	5 / 51	endoplasmic reticulum−Golgi intermediate compartment

Chr

Rank	p−value	#in/all	Geneset
1	0.03	29 / 462	Chr 14
2	0.05	28 / 469	Chr 8
3	0.06	32 / 558	Chr 4
4	0.13	34 / 649	Chr 16
5	0.14	41 / 801	Chr 11
6	0.20	18 / 335	Chr 22
7	0.21	28 / 552	Chr 10
8	0.28	33 / 687	Chr 6
9	0.35	19 / 398	Chr 20
10	0.47	7 / 151	Chr 21
11	0.49	65 / 1500	Chr 1
12	0.50	24 / 551	Chr X
13	0.53	20 / 465	Chr 15
14	0.53	36 / 840	Chr 17
15	0.58	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
16	0.67	28 / 696	Chr 5
17	0.69	40 / 993	Chr 2
18	0.69	10 / 262	Chr 13
19	0.75	22 / 576	Chr 9
20	0.88	24 / 689	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−04	8 / 45	Ang_CRC−CIMPH−vs−L_hyper
2	1e−03	8 / 50	Ang_CRC_Hypermethylated
3	1e−02	101 / 1889	ReprPCWk_Colon
4	1e−02	11 / 117	Marisa_CRC−cluster−b
5	1e−02	112 / 2142	ReprPC_Colon
6	5e−02	163 / 3383	EnhWk2_Colon
7	7e−02	71 / 1386	Het_Colon
8	8e−02	6 / 71	Marisa_CRC−cluster−g
9	1e−01	32 / 591	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
10	1e−01	53 / 1038	HetRpts_Colon
11	1e−01	5 / 60	Pentrack_CRC_TCGA_group.over_A_normal_UP
12	1e−01	12 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	2e−01	1 / 4	Kaneda_CIMP−group1
14	2e−01	24 / 452	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
15	2e−01	45 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
16	3e−01	175 / 3897	Quies1_Colon
17	3e−01	1 / 8	Marisa_CRC−C2
18	3e−01	1 / 8	Juehling−MSI−enriched−in−7
19	3e−01	4 / 66	Marisa_CRC−cluster−h
20	3e−01	4 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.08	18 / 294	GUDJ_psoriasis down
2	0.38	1 / 11	BCHETNIA_EBM up
3	0.41	20 / 435	GUDJ_psoriasis up
4	0.58	1 / 20	BCHETNIA_EBM−DM up
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	3 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
2	0.005	11 / 103	GIEZELT_GBM_WT_up_VS_mut
3	0.016	4 / 23	Donson−Misc immune function−associated with LTS in HGA
4	0.034	2 / 7	Phillips MES up vs Prolif & PN
5	0.034	23 / 356	Down_a
6	0.049	8 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	0.054	13 / 184	WILLSCHER_GBM_Verhaak−CL & MES_up
8	0.057	4 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
9	0.078	2 / 11	Mukasa_UP_in_Astroglioma
10	0.078	2 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
11	0.090	9 / 125	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	0.103	5 / 58	Christensen_hypermethylated_in_grade2_astrocytoma
13	0.123	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
14	0.127	5 / 62	cultured astroglia vs. in vivo astrocytes
15	0.134	2 / 15	VERHAAK_MES subtype
16	0.135	8 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	0.161	1 / 4	Donson−adaptive−immunity−associated with LTS in HGA
18	0.164	2 / 17	Christensen_hypomethylated_in_grade3_astrocytoma
19	0.168	5 / 68	GIEZELT_GBM_WT_down_VS_mut
20	0.220	5 / 75	GIEZELT_GBM_STS_down_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 9	AGARWAL_AKT_PATHWAY_TARGETS
2	5e−04	7 / 34	WIERENGA_PML_INTERACTOME
3	6e−04	4 / 10	REACTOME_COPI_MEDIATED_TRANSPORT
4	6e−04	5 / 17	STEGER_ADIPOGENESIS_DN
5	1e−03	5 / 20	PID_GLYPICAN_1PATHWAY
6	2e−03	9 / 65	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
7	2e−03	6 / 31	KEGG_ARACHIDONIC_ACID_METABOLISM
8	2e−03	6 / 31	CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN
9	2e−03	4 / 14	KANG_AR_TARGETS_UP
10	2e−03	3 / 7	MIKI_COEXPRESSED_WITH_CYP19A1
11	3e−03	5 / 23	REACTOME_LYSOSOME_VESICLE_BIOGENESIS
12	3e−03	9 / 70	TANAKA_METHYLATED_IN_ESOPHAGEAL_CARCINOMA
13	3e−03	6 / 35	LIU_TARGETS_OF_VMYB_VS_CMYB_DN
14	4e−03	41 / 616	NABA_MATRISOME
15	4e−03	5 / 25	BIOCARTA_IL1R_PATHWAY
16	4e−03	7 / 48	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
17	4e−03	12 / 117	REACTOME_MEMBRANE_TRAFFICKING
18	5e−03	16 / 179	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
19	5e−03	15 / 165	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
20	5e−03	4 / 17	KEGG_NITROGEN_METABOLISM

HM

Rank	p−value	#in/all	Geneset
1	0.002	11 / 91	HALLMARK_PROTEIN_SECRETION
2	0.047	12 / 162	HALLMARK_COMPLEMENT
3	0.080	10 / 140	HALLMARK_INFLAMMATORY_RESPONSE
4	0.090	8 / 107	HALLMARK_COAGULATION
5	0.109	11 / 168	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	0.180	8 / 127	HALLMARK_KRAS_SIGNALING_DN
7	0.216	10 / 174	HALLMARK_HEME_METABOLISM
8	0.231	6 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.255	8 / 140	HALLMARK_APOPTOSIS
10	0.303	9 / 169	HALLMARK_XENOBIOTIC_METABOLISM
11	0.308	2 / 26	HALLMARK_ANGIOGENESIS
12	0.319	5 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	0.329	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.329	10 / 195	HALLMARK_MITOTIC_SPINDLE
15	0.335	10 / 196	HALLMARK_MTORC1_SIGNALING
16	0.394	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	0.400	3 / 53	HALLMARK_TGF_BETA_SIGNALING
18	0.441	8 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
19	0.453	7 / 148	HALLMARK_KRAS_SIGNALING_UP
20	0.476	2 / 37	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	5 / 62	DUMEAUX_Smoking enriched genes
2	0.2	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
3	0.3	1 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
4	0.4	1 / 10	DUMEAUX_Smoking literature genes up
5	0.4	2 / 32	DUMEAUX_Fasting enriched genes
6	0.5	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
7	0.5	1 / 18	DUMEAUX_High bmi enriched genes
8	1.0	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
9	1.0	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
10	1.0	0 / 5	DUMEAUX_Estrogen related 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	0.002	10 / 81	Subero_INT_hyper_meth
2	0.008	10 / 96	Subero_DLBCL_hyper_meth
3	0.014	7 / 60	Subero_T−ALL_hyper_meth
4	0.020	168 / 3396	HOPP_Repressed
5	0.020	3 / 14	Subero_MCL_hyper_meth
6	0.040	15 / 212	LENZ_Stromal signature 1
7	0.041	110 / 2188	HOPP_Poised_promoter
8	0.066	2 / 10	DAVE_BL_DN
9	0.091	4 / 40	Subero_mBL_hyper_meth
10	0.105	2 / 13	WRIGHT_GCB UP
11	0.142	4 / 47	Subero_FL_hyper_meth
12	0.178	3 / 34	Subero_B−ALL_hyper_meth
13	0.281	3 / 43	LENZ_Stromal signature 2
14	0.296	1 / 8	MASCQUE_GCB UP
15	0.296	1 / 8	Subero_MM_hypo_meth
16	0.308	13 / 256	SPANG_IL21 DN
17	0.315	4 / 66	TARTE_Plasma cell signature
18	0.327	6 / 109	ROSOLOWSKI_green total
19	0.356	1 / 10	DAVE_BL UP
20	0.356	114 / 2563	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	0.002	16 / 166	receptor activity
2	0.004	5 / 25	aminopeptidase activity
3	0.005	4 / 17	RNA polymerase II core binding
4	0.006	4 / 18	mitogen−activated protein kinase kinase kinase binding
5	0.008	3 / 10	aromatase activity
6	0.008	3 / 10	oxidoreductase activity, acting on paired donors, with incorporation or reductic
7	0.013	65 / 1149	enzyme binding
8	0.013	6 / 46	steroid hormone receptor activity
9	0.016	5 / 35	ligand−activated sequence−specific DNA binding RNA polymerase II transcrip
10	0.016	3 / 13	NAD+ binding
11	0.027	4 / 27	potassium channel regulator activity
12	0.029	3 / 16	acetylglucosaminyltransferase activity
13	0.029	49 / 866	signal transducer activity
14	0.030	5 / 41	phosphatase binding
15	0.039	5 / 44	oxidoreductase activity, acting on paired donors, with incorporation or reductic
16	0.043	5 / 45	calcium−dependent protein binding
17	0.066	2 / 10	deoxyribonuclease activity
18	0.066	3 / 22	delayed rectifier potassium channel activity
19	0.066	3 / 22	epidermal growth factor receptor binding
20	0.066	3 / 22	oxygen binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	5 / 25	hsa−miR−663b
2	0.015	6 / 47	hsa−miR−575
3	0.018	24 / 353	hsa−let−7i
4	0.046	5 / 46	hsa−miR−1322
5	0.053	6 / 63	hsa−miR−455−3p
6	0.054	2 / 9	hsa−miR−373*
7	0.059	11 / 150	hsa−miR−338−3p
8	0.071	6 / 68	hsa−miR−649
9	0.071	6 / 68	hsa−miR−342−3p
10	0.073	7 / 85	hsa−miR−510
11	0.079	4 / 38	hsa−miR−490−5p
12	0.080	7 / 87	hsa−miR−188−3p
13	0.082	18 / 293	hsa−miR−202
14	0.105	2 / 13	hsa−miR−574−3p
15	0.119	2 / 14	hsa−miR−671−3p
16	0.119	2 / 14	hsa−miR−452*
17	0.123	19 / 331	hsa−let−7g
18	0.123	10 / 153	hsa−miR−583
19	0.124	6 / 79	hsa−miR−569
20	0.124	17 / 291	hsa−miR−34c−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 9	BENTINK_ras.4
2	0.4	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 / 12	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.1	65 / 1314	ICGC_Usf1_targets
2	0.2	55 / 1139	HEBENSTREIT_low expression TF
3	0.2	66 / 1383	ICGC_Six5_targets
4	0.2	61 / 1273	ICGC_P300_targets
5	0.4	1 / 11	MYC_Protein synthesis degradation UP
6	0.5	30 / 690	ICGC_Atf3_targets
7	0.6	101 / 2391	ICGC_Pbx3_targets
8	0.6	23 / 553	ICGC_RxraPcr1_targets
9	0.6	89 / 2137	ICGC_SrfV0416101_targets
10	0.7	83 / 2013	ICGC_Bcl11_targets
11	0.7	195 / 4682	ICGC_Pol24_targets
12	0.7	23 / 595	ICGC_NrsfPcr2_targets
13	0.7	225 / 5408	ICGC_Pou2_targets
14	0.8	86 / 2136	ICGC_GabpPcr2_targets
15	0.8	56 / 1418	ICGC_Ets1_targets
16	0.8	75 / 1878	ICGC_Cebpbsc150_targets
17	0.8	222 / 5374	ICGC_Pax5_targets
18	0.8	221 / 5355	ICGC_Pol2_targets
19	0.8	162 / 3966	ICGC_Pu1_targets
20	0.8	193 / 4706	ICGC_Sp1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 7	VAQUERIZAS_Skeletal.muscle.psoas
2	0.12	2 / 14	VAQUERIZAS_Ovary
3	0.22	3 / 38	VAQUERIZAS_Testis
4	0.26	3 / 41	VAQUERIZAS_Placenta
5	0.26	1 / 7	VAQUERIZAS_Tongue
6	0.30	3 / 45	VAQUERIZAS_Uterus
7	0.53	1 / 17	VAQUERIZAS_Pituitary
8	0.53	1 / 17	VAQUERIZAS_Heart
9	0.64	1 / 23	VAQUERIZAS_Spinal cord
10	0.69	1 / 27	VAQUERIZAS_Lymph node
11	0.72	2 / 58	VAQUERIZAS_Lung
12	0.77	1 / 33	VAQUERIZAS_Prostate
13	0.80	1 / 37	VAQUERIZAS_Thymus
14	0.81	1 / 38	VAQUERIZAS_Whole brain
15	0.87	4 / 143	VAQUERIZAS_General
16	0.93	1 / 59	VAQUERIZAS_Whole blood
17	1.00	0 / 36	VAQUERIZAS_Fetal brain
18	1.00	0 / 26	VAQUERIZAS_Liver
19	1.00	0 / 29	VAQUERIZAS_Smooth muscle
20	1.00	0 / 9	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.001	28 / 350	WIRTH_Nervous System
2	0.010	3 / 11	WIRTH_Sec. lymphoid organs
3	0.043	2 / 8	WIRTH_Tonsil
4	0.258	3 / 41	WIRTH_Homeostasis
5	0.317	3 / 46	WIRTH_Liver
6	0.327	1 / 9	PALMER_CD8+ T−Cell signature up
7	0.356	1 / 10	WIRTH_Hippocampus
8	0.403	2 / 32	WIRTH_Placenta
9	0.410	1 / 12	WIRTH_Thymus
10	0.410	1 / 12	WIRTH_Lymphocytes
11	0.460	1 / 14	WIRTH_Telencephalon
12	0.503	10 / 225	PALMER_Granulocytes signature up
13	0.588	4 / 95	WIRTH_Muscle
14	0.681	4 / 107	WIRTH_Testis
15	0.833	2 / 74	WIRTH_Mucosa
16	0.845	6 / 194	PALMER_B−Cell signature up
17	0.892	11 / 350	WIRTH_Immune system
18	0.993	1 / 114	PALMER_T−Cell signature up
19	1.000	0 / 32	WIRTH_Pancreas
20	1.000	0 / 11	WIRTH_Prim. lymphoid organs

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	172 / 3682	LU_BPDE 0.005 DN
2	0.6	47 / 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	

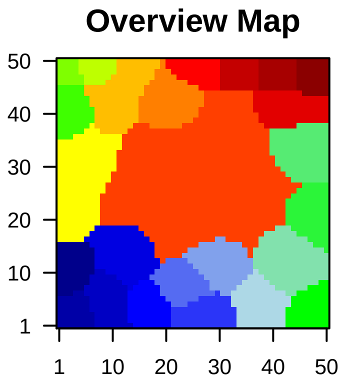
K−Means Clusters

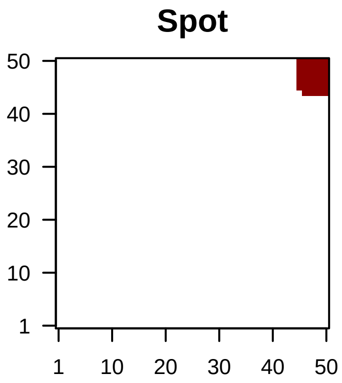
Spot Summary: V

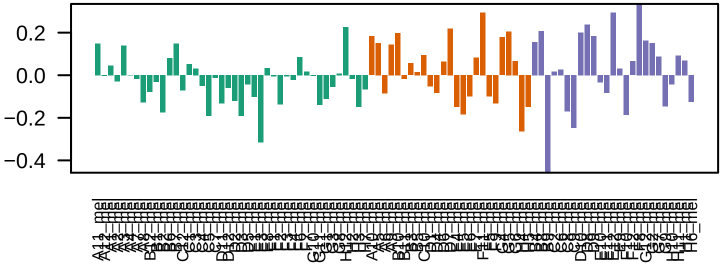
metagenes = 41
genes = 488

<r> metagenes = 0.85
<r> genes = 0.07
beta: r2= 1.71 / log p= −Inf

samples with spot = 19 (20.7 %)
MSC1 : 3 (7.1 %)
MSC2 : 7 (28 %)
MSC3 : 9 (36 %)


Overview Map


Spot

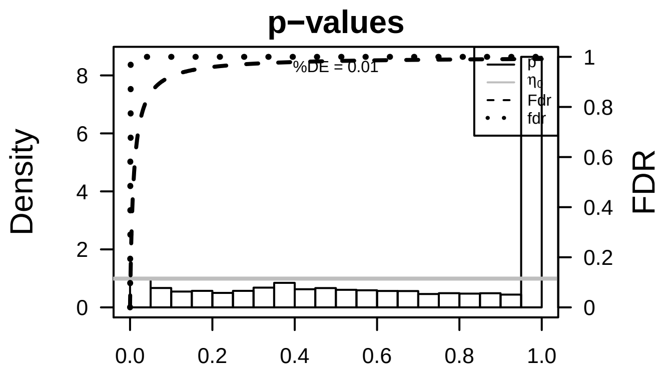


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ITIH3	2.03	−0.28	0.21	ITIH3	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
2	PIBF1	1.97	−0.47	0.28	PIBF1	progesterone immunomodulatory binding factor 1 [Source:HG
3	NECAB2	1.9	−0.43	0.35	NECAB2	N−terminal EF−hand calcium binding protein 2 [Source:HGN
4	LUZP6	1.88	−1.03	0.3	LUZP6	leucine zipper protein 6 [Source:HGNC Symbol;Acc:HGNC:3
5	OAS1	1.86	−0.2	0.37	OAS1	2'−5'−oligoadenylate synthetase 1, 40/46kDa [Source:HGNC
6	CC2D2A	1.84	−0.51	0.36	CC2D2A	coiled−coil and C2 domain containing 2A [Source:HGNC Syn
7	ZFP62	1.82	−0.44	0.25	ZFP62	ZFP62 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:
8	GSDMB	1.8	−0.19	0.37	GSDMB	gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]
9	GORAB	1.77	−0.45	0.34	GORAB	golgin, RAB6−interacting [Source:HGNC Symbol;Acc:HGNC:
10	C1orf109	1.77	−0.59	0.29	C1orf109	chromosome 1 open reading frame 109 [Source:HGNC Symb
11	GDF15	1.77	−1.15	0.38	GDF15	growth differentiation factor 15 [Source:HGNC Symbol;Acc:H
12	PACRGL	1.76	−0.36	0.23	PACRGL	PARK2 co−regulated−like [Source:HGNC Symbol;Acc:HGNC
13	C1S	1.74	−0.17	0.44	C1S	complement component 1, s subcomponent [Source:HGNC S
14	PPCDC	1.72	−0.42	0.2	PPCDC	phosphopantothenoylcysteine decarboxylase [Source:HGNC
15	TMEM53	1.71	−0.39	0.29	TMEM53	transmembrane protein 53 [Source:HGNC Symbol;Acc:HGN
16	BBS4	1.71	−0.53	0.31	BBS4	Bardet−Biedl syndrome 4 [Source:HGNC Symbol;Acc:HGNC
17	CYP19A1	1.7	−0.37	0.31	CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1 [Sour
18	UGP2	1.7	−1.72	0.24	UGP2	UDP−glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
19	NLRC5	1.7	−0.18	0.25	NLRC5	NLR family, CARD domain containing 5 [Source:HGNC Symb
20	VASP	1.69	−0.36	0.28	VASP	vasodilator−stimulated phosphoprotein [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−28	417 / 9482	Colon	TssA_Colon
2	5e−24	397 / 9027	Colon	Tx_Colon
3	2e−22	381 / 8580	Colon	TxWk_Colon
4	1e−21	400 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
5	1e−20	327 / 6929	Lympl	HOPP_Txn_elongation
6	1e−16	337 / 7592	Lympl	HOPP_Active_promoter
7	8e−16	377 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
8	1e−15	254 / 5184	Lympl	HOPP_Txn_transition
9	2e−11	339 / 8205	CC	cytoplasm
10	1e−09	91 / 1468	CC	mitochondrion
11	3e−09	299 / 7203	Colon	TssF_Colon
12	7e−09	256 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
13	7e−08	22 / 176	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
14	5e−07	328 / 8415	Colon	Quies3_Colon
15	8e−07	365 / 9653	Colon	Enh_Colon
16	2e−06	108 / 2136	TF	ICGC_GabpPcr2_targets
17	2e−06	265 / 6564	Lympl	HOPP_Strong_enhancer
18	2e−06	359 / 9528	Brain	Overlap_fetal_midbrain_Quies
19	3e−06	36 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
20	5e−06	67 / 1171	TF	KIM_MYC targets
21	6e−06	18 / 162	BP	ribosome biogenesis
22	7e−06	389 / 10605	CC	intracellular
23	9e−06	283 / 7209	Lympl	HOPP_Weak_promoter
24	1e−05	22 / 235	GSEA	BLUM_RESPONSE_TO_SALIRASIB_UP
25	1e−05	32 / 424	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
26	1e−05	24 / 277	BP	translation
27	2e−05	213 / 5155	Colon	EnhWk1_Colon
28	2e−05	30 / 393	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_UP
29	2e−05	377 / 10290	Colon	TssWk_Colon
30	3e−05	44 / 706	GSEA	BENPORATH_MYC_MAX_TARGETS
31	3e−05	37 / 555	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
32	4e−05	9 / 51	GSEA	JIANG_AGING_CEREBRAL_CORTEX_DN
33	4e−05	127 / 2798	Colon	TxEnhG1_Colon
34	7e−05	13 / 111	GSEA	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
35	7e−05	193 / 4689	TF	ICGC_Taf1_targets
36	7e−05	85 / 1730	BP	small molecule metabolic process
37	9e−05	40 / 649	CC	endoplasmic reticulum membrane
38	1e−04	6 / 24	GSEA	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
39	1e−04	32 / 476	GSEA	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
40	1e−04	7 / 35	MF	aminoacyl−tRNA ligase activity


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.9	2 / 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	

BP

Rank	p−value	#in/all	Geneset
1	6e−06	18 / 162	ribosome biogenesis
2	1e−05	24 / 277	translation
3	7e−05	85 / 1730	small molecule metabolic process
4	2e−04	64 / 1237	metabolic process
5	2e−04	31 / 478	protein transport
6	3e−04	14 / 147	tRNA metabolic process
7	5e−04	7 / 44	tRNA aminoacylation for protein translation
8	6e−04	119 / 2755	transport
9	1e−03	4 / 15	ferrous iron transport
10	2e−03	4 / 17	cellular respiration
11	2e−03	37 / 687	gene expression
12	4e−03	3 / 10	tRNA splicing, via endonucleolytic cleavage and ligation
13	4e−03	7 / 62	negative regulation of catalytic activity
14	4e−03	7 / 63	cellular response to insulin stimulus
15	4e−03	18 / 276	nucleobase−containing compound catabolic process
16	6e−03	3 / 12	ubiquinone biosynthetic process
17	9e−03	59 / 1325	catabolic process
18	1e−02	3 / 14	nucleotide metabolic process
19	1e−02	4 / 27	intra−Golgi vesicle−mediated transport
20	1e−02	3 / 15	lipid particle organization

Brain

Rank	p−value	#in/all	Geneset
1	1e−21	400 / 9330	Overlap_fetal_midbrain_ReprPC
2	8e−16	377 / 9013	Overlap_fetal_midbrain_K9K27me3
3	7e−09	256 / 5940	Overlap_fetal_midbrain_HetRpts
4	2e−06	359 / 9528	Overlap_fetal_midbrain_Quies
5	2e−03	326 / 9020	Overlap_fetal_midbrain_ReprPCWk
6	4e−02	117 / 3081	Mid_Frontal_Lobe_ZNF
7	4e−02	16 / 304	Fetal_Het
8	4e−02	55 / 1333	Fetal_ReprPCWk
9	7e−02	17 / 349	Fetal_ZNF
10	7e−02	33 / 769	Overlap_fetal_midbrain_ZNF
11	1e−01	42 / 1050	Fetal_EnhP
12	2e−01	30 / 765	Mid_Frontal_Lobe_Het
13	2e−01	32 / 831	Fetal_HetRpts
14	3e−01	36 / 989	Mid_Frontal_Lobe_Quies
15	4e−01	33 / 953	Fetal_Enh
16	4e−01	23 / 656	Overlap_fetal_midbrain_EnhP
17	4e−01	6 / 158	Overlap_fetal_midbrain_Het
18	4e−01	27 / 786	Fetal_EnhG
19	5e−01	81 / 2462	Mid_Frontal_Lobe_HetRpts
20	6e−01	40 / 1236	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	1 / 12	LIU_PROSTATE_CANCER_UP
2	0.037	16 / 298	SPANG_BCL6−index2
3	0.065	1 / 14	LIU_COMMON_CANCER_GENES
4	0.066	2 / 13	GENTLES_modul12
5	0.068	3 / 29	KUIPER_MM good survival
6	0.072	10 / 180	SPANG_LPS−index2
7	0.095	2 / 16	GENTLES_modul6
8	0.095	2 / 16	GENTLES_modul14
9	0.283	1 / 10	GENTLES_modul3
10	0.329	1 / 12	LIU_BREAST_CANCER
11	0.331	0 / 15	RHODES_CANCER_META_SIGNATURE
12	0.378	2 / 40	ZHANG_MM up
13	0.378	2 / 40	PanCan_HK_geneset_nanostring
14	0.393	1 / 15	WANG_ER_UP
15	0.393	1 / 15	GENTLES_modul1
16	0.393	1 / 15	GENTLES_modul10
17	0.413	1 / 16	GENTLES_modul7
18	0.506	3 / 82	PanCan_TXmisReg_geneset_nanostring
19	0.649	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
20	0.673	2 / 70	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	2e−11	339 / 8205	cytoplasm
2	1e−09	91 / 1468	mitochondrion
3	7e−06	389 / 10605	intracellular
4	9e−05	40 / 649	endoplasmic reticulum membrane
5	1e−04	19 / 223	lysosomal membrane
6	1e−04	28 / 401	mitochondrial inner membrane
7	2e−04	363 / 9988	organelle
8	2e−04	4 / 10	WASH complex
9	2e−04	43 / 747	nucleolus
10	3e−04	8 / 54	transport vesicle
11	1e−03	4 / 15	BLOC−1 complex
12	2e−03	95 / 2193	extracellular exosome
13	2e−03	27 / 456	vacuole
14	3e−03	106 / 2507	cytosol
15	3e−03	57 / 1201	endoplasmic reticulum
16	3e−03	11 / 128	ribosome
17	5e−03	24 / 412	lysosome
18	5e−03	8 / 81	late endosome membrane
19	5e−03	4 / 22	pre−autophagosomal structure
20	5e−03	27 / 487	intracellular membrane−bounded organelle

Chr

Rank	p−value	#in/all	Geneset
1	0.05	34 / 775	Chr 12
2	0.08	28 / 649	Chr 16
3	0.14	28 / 687	Chr 6
4	0.19	19 / 465	Chr 15
5	0.19	27 / 689	Chr 7
6	0.26	18 / 462	Chr 14
7	0.28	18 / 469	Chr 8
8	0.31	29 / 801	Chr 11
9	0.37	6 / 151	Chr 21
10	0.44	19 / 552	Chr 10
11	0.49	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
12	0.49	9 / 262	Chr 13
13	0.54	18 / 551	Chr X
14	0.54	13 / 398	Chr 20
15	0.57	27 / 840	Chr 17
16	0.59	33 / 1037	Chr 19
17	0.71	17 / 576	Chr 9
18	0.72	25 / 838	Chr 3
19	0.73	6 / 221	Chr 18
20	0.82	15 / 558	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−28	417 / 9482	TssA_Colon
2	5e−24	397 / 9027	Tx_Colon
3	2e−22	381 / 8580	TxWk_Colon
4	3e−09	299 / 7203	TssF_Colon
5	5e−07	328 / 8415	Quies3_Colon
6	8e−07	365 / 9653	Enh_Colon
7	2e−05	213 / 5155	EnhWk1_Colon
8	2e−05	377 / 10290	TssWk_Colon
9	4e−05	127 / 2798	TxEnhG1_Colon
10	2e−03	223 / 5880	TssD2_Colon
11	7e−03	110 / 2698	EnhA_Colon
12	1e−02	36 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
13	6e−02	5 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
14	1e−01	27 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	1e−01	30 / 739	TxEnhG2_Colon
16	2e−01	35 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
17	2e−01	1 / 8	KIM_CRC−MSI−regulated_DN
18	2e−01	1 / 8	Marisa_CRC−C2
19	3e−01	7 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
20	4e−01	1 / 13	TCGA−CRC_less−agressive−disease−markers

Disease

Rank	p−value	#in/all	Geneset
1	1	9 / 435	GUDJ_psoriasis up
2	1	2 / 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	0.003	43 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.057	2 / 12	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
3	0.095	2 / 16	VERHAAK_NL subtype
4	0.116	2 / 18	Shinawi_with_increased_methylation_in_STS
5	0.125	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
6	0.153	1 / 5	Phillips Prolif up vs PN & MES
7	0.161	2 / 22	WILLSCHER_GBM_proteomics_wtOnly_SpotC
8	0.183	4 / 68	GIEZELT_GBM_WT_down_VS_mut
9	0.195	5 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
10	0.199	3 / 47	WILLSCHER_GBM_Verhaak−PNwt_up
11	0.221	2 / 27	Sturm_GBM_Meth_overexpression_H_K27_UP
12	0.234	13 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
13	0.279	14 / 356	Down_a
14	0.294	13 / 332	Up
15	0.307	1 / 11	astrocytes_glio
16	0.307	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
17	0.307	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
18	0.318	4 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
19	0.341	3 / 63	Stuehler_Proteins_up_in_STS
20	0.351	1 / 13	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−08	22 / 176	TIEN_INTESTINE_PROBIOTICS_24HR_DN
2	3e−06	36 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
3	1e−05	22 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
4	1e−05	32 / 424	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
5	2e−05	30 / 393	MITSIADES_RESPONSE_TO_APLIDIN_UP
6	3e−05	44 / 706	BENPORATH_MYC_MAX_TARGETS
7	3e−05	37 / 555	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
8	4e−05	9 / 51	JIANG_AGING_CEREBRAL_CORTEX_DN
9	7e−05	13 / 111	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
10	1e−04	6 / 24	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
11	1e−04	32 / 476	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
12	1e−04	60 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
13	1e−04	14 / 135	KAAB_FAILED_HEART_ATRIUM_DN
14	1e−04	19 / 223	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP
15	2e−04	41 / 696	NUYTTEN_NIPP1_TARGETS_UP
16	2e−04	67 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
17	2e−04	24 / 329	WANG_LMO4_TARGETS_DN
18	3e−04	32 / 502	KIM_ALL_DISORDERS_CALB1_CORR_UP
19	3e−04	22 / 293	DOUGLAS_BMI1_TARGETS_DN
20	3e−04	10 / 80	SASSON_RESPONSE_TO_FORSKOLIN_UP

HM

Rank	p−value	#in/all	Geneset
1	0.02	10 / 146	HALLMARK_DNA_REPAIR
2	0.03	8 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	0.03	11 / 174	HALLMARK_HEME_METABOLISM
4	0.04	7 / 96	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	0.05	10 / 169	HALLMARK_XENOBIOTIC_METABOLISM
6	0.06	11 / 196	HALLMARK_MTORC1_SIGNALING
7	0.09	10 / 188	HALLMARK_ADIPOGENESIS
8	0.09	5 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.12	4 / 57	HALLMARK_MYC_TARGETS_V2
10	0.12	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	0.14	6 / 107	HALLMARK_COAGULATION
12	0.16	5 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	0.20	3 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.22	8 / 176	HALLMARK_HYPOXIA
15	0.23	6 / 126	HALLMARK_ALLOGRAFT_REJECTION
16	0.25	8 / 183	HALLMARK_GLYCOLYSIS
17	0.28	7 / 162	HALLMARK_COMPLEMENT
18	0.31	6 / 140	HALLMARK_APOPTOSIS
19	0.31	3 / 60	HALLMARK_IL6_JAK_STAT3_SIGNALING
20	0.48	6 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	2 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.66	1 / 32	DUMEAUX_Fasting enriched genes
3	0.87	1 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 3	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 4	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 5	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 5	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 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	1e−20	327 / 6929	HOPP_Txn_elongation
2	1e−16	337 / 7592	HOPP_Active_promoter
3	1e−15	254 / 5184	HOPP_Txn_transition
4	2e−06	265 / 6564	HOPP_Strong_enhancer
5	9e−06	283 / 7209	HOPP_Weak_promoter
6	6e−03	56 / 1218	SPANG_BCR UP
7	3e−02	21 / 410	SPANG_CD40 6hrs DN
8	3e−02	15 / 268	SPANG_IL21 UP
9	5e−02	5 / 61	SPANG_LPS 6hrs DN
10	5e−02	47 / 1128	SPANG_BCR DN
11	8e−02	2 / 15	DAVE_Immune response 2
12	1e−01	194 / 5538	HOPP_Weak_txn
13	1e−01	2 / 20	SPANG_BAFF 9hrs UP
14	2e−01	1 / 5	WRIGHT_custom ABC−DLBCL UP
15	2e−01	5 / 89	ROSOLOWSKI_blue total
16	2e−01	13 / 294	TARTE_Plasmablast signature
17	2e−01	4 / 66	TARTE_Plasma cell signature
18	2e−01	12 / 280	SPANG_CD40 6hrs UP
19	2e−01	1 / 8	YAMANE_AICDA_targets_nonrecruited
20	3e−01	2 / 30	TARTE_B−cell signature

MF

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 35	aminoacyl−tRNA ligase activity
2	1e−03	5 / 26	protein kinase inhibitor activity
3	2e−03	4 / 16	ferrous iron transmembrane transporter activity
4	4e−03	3 / 10	ribosomal small subunit binding
5	8e−03	61 / 1365	RNA binding
6	8e−03	4 / 25	transferase activity, transferring acyl groups other than amino−acyl groups
7	1e−02	8 / 95	hydrolase activity, acting on glycosyl bonds
8	3e−02	3 / 20	NAD+ ADP−ribosyltransferase activity
9	3e−02	6 / 71	structural constituent of ribosome
10	3e−02	4 / 36	tRNA binding
11	3e−02	9 / 136	lyase activity
12	4e−02	17 / 322	GTP binding
13	4e−02	3 / 23	proton−transporting ATPase activity, rotational mechanism
14	4e−02	2 / 10	cAMP response element binding protein binding
15	4e−02	2 / 10	deoxyribonuclease activity
16	4e−02	2 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
17	4e−02	3 / 24	snoRNA binding
18	4e−02	12 / 210	transferase activity, transferring glycosyl groups
19	4e−02	4 / 41	ATPase binding
20	5e−02	2 / 11	acetyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	14 / 179	hsa−miR−520f
2	0.003	5 / 31	hsa−miR−296−5p
3	0.005	9 / 100	hsa−miR−574−5p
4	0.016	13 / 203	hsa−miR−545
5	0.017	5 / 46	hsa−miR−874
6	0.019	6 / 65	hsa−miR−326
7	0.020	13 / 208	hsa−miR−432
8	0.022	24 / 471	hsa−miR−15b
9	0.022	12 / 189	hsa−miR−513a−3p
10	0.022	11 / 168	hsa−miR−520h
11	0.025	5 / 51	hsa−miR−508−5p
12	0.027	5 / 52	hsa−miR−345
13	0.028	25 / 507	hsa−miR−15a
14	0.029	23 / 459	hsa−miR−195
15	0.030	17 / 314	hsa−miR−520c−3p
16	0.031	13 / 222	hsa−miR−520g
17	0.032	4 / 37	hsa−miR−760
18	0.033	2 / 9	hsa−miR−720
19	0.035	15 / 272	hsa−miR−520b
20	0.035	4 / 38	hsa−miR−1277

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 13	BENTINK_myc.1
2	0.26	1 / 9	BENTINK_ras.4
3	0.35	1 / 13	BENTINK_src.10
4	0.39	1 / 15	BENTINK_ras.6
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 / 12	BENTINK_e2f3.2
9	1.00	0 / 12	BENTINK_ras.1
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	2e−06	108 / 2136	ICGC_Gabpbcr2_targets
2	5e−06	67 / 1171	KIM_MYC targets
3	7e−05	193 / 4689	ICGC_Taf1_targets
4	1e−04	181 / 4385	ICGC_Atf2_targets
5	3e−04	180 / 4414	ICGC_Bclaf101388_targets
6	4e−04	196 / 4909	ICGC_Stat5_targets
7	4e−04	68 / 1383	ICGC_Six5_targets
8	1e−03	162 / 4032	ICGC_Creb1_targets
9	1e−03	191 / 4879	ICGC_Pmlsc71910_targets
10	2e−03	157 / 3924	ICGC_Zeb1_targets
11	2e−03	65 / 1400	ICGC_Myc_targets
12	3e−03	183 / 4706	ICGC_Sp1_targets
13	3e−03	187 / 4829	ICGC_Nficsc81335_targets
14	6e−03	207 / 5495	ICGC_Yy1_targets
15	7e−03	145 / 3700	ICGC_Nfatc1_targets
16	8e−03	59 / 1314	ICGC_Usf1_targets
17	1e−02	202 / 5408	ICGC_Pou2_targets
18	1e−02	88 / 2137	ICGC_SrfV0416101_targets
19	1e−02	179 / 4774	ICGC_Foxm1_targets
20	2e−02	78 / 1878	ICGC_Cebpbsc150_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.4	1 / 15	VAQUERIZAS_Bone marrow
2	0.4	1 / 16	VAQUERIZAS_Adrenal gland
3	0.5	1 / 23	VAQUERIZAS_Adrenal cortex
4	0.6	1 / 26	VAQUERIZAS_Liver
5	0.6	2 / 59	VAQUERIZAS_Whole blood
6	0.6	1 / 29	VAQUERIZAS_Fetal lung
7	0.7	1 / 38	VAQUERIZAS_Testis
8	0.8	1 / 45	VAQUERIZAS_Uterus
9	0.9	1 / 58	VAQUERIZAS_Lung
10	1.0	2 / 143	VAQUERIZAS_General
11	1.0	0 / 36	VAQUERIZAS_Fetal brain
12	1.0	0 / 41	VAQUERIZAS_Placenta
13	1.0	0 / 33	VAQUERIZAS_Prostate
14	1.0	0 / 29	VAQUERIZAS_Smooth muscle
15	1.0	0 / 9	VAQUERIZAS_Kidney
16	1.0	0 / 23	VAQUERIZAS_Spinal cord
17	1.0	0 / 38	VAQUERIZAS_Whole brain
18	1.0	0 / 37	VAQUERIZAS_Thymus
19	1.0	0 / 40	VAQUERIZAS_Thyroid
20	1.0	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.07	2 / 13	WIRTH_B−cells
2	0.07	12 / 225	PALMER_Granulocytes signature up
3	0.30	8 / 194	PALMER_B−Cell signature up
4	0.31	1 / 11	WIRTH_Sec. lymphoid organs
5	0.31	1 / 11	WIRTH_Globus pallidus
6	0.31	1 / 11	WIRTH_Cortex cerebri
7	0.33	1 / 12	WIRTH_Lymphocytes
8	0.33	1 / 12	WIRTH_Cerebellum
9	0.37	1 / 14	WIRTH_Telencephalon
10	0.41	1 / 16	PALMER_Lymphocytes signature up
11	0.52	4 / 114	PALMER_T−Cell signature up
12	0.66	1 / 32	WIRTH_Placenta
13	0.81	9 / 350	WIRTH_Immune system
14	0.82	2 / 95	WIRTH_Muscle
15	0.87	2 / 107	WIRTH_Testis
16	1.00	3 / 350	WIRTH_Nervous System
17	1.00	0 / 32	WIRTH_Pancreas
18	1.00	0 / 11	WIRTH_Prim. lymphoid organs
19	1.00	0 / 8	WIRTH_Tonsil
20	1.00	0 / 12	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	44 / 1115	LU_BPDE 1n DN
2	0.7	115 / 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	

K−Means Clusters

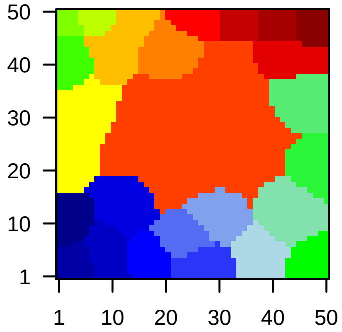
Spot Summary: W

metagenes = 83
genes = 537

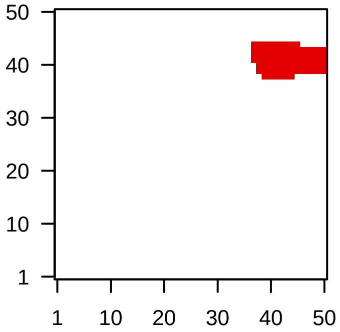
<r> metagenes = 0.73
<r> genes = 0.09
beta: r2= 0.92 / log p= −Inf

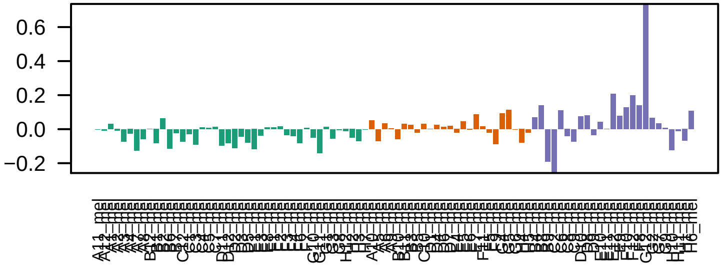
samples with spot = 3 (3.3 %)
MSC3 : 3 (12 %)

Overview Map



Spot





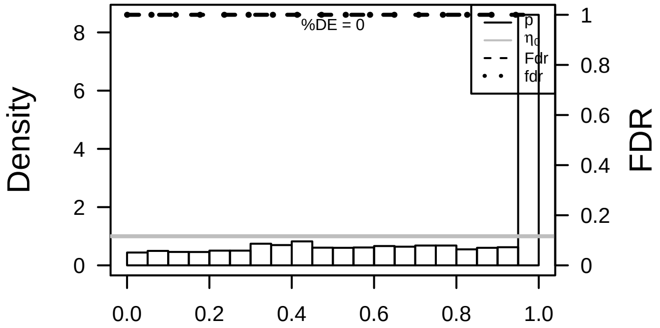
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	CCL18	2.45	−0.48	0.42	CCL18	chemokine (C−C motif) ligand 18 (pulmonary and activation−
2	CDKL1	2.2	−0.24	0.39	CDKL1	cyclin−dependent kinase−like 1 (CDC2−related kinase) [Sour
3	PRDM6	2.01	−0.06	0.5	PRDM6	PR domain containing 6 [Source:HGNC Symbol;Acc:HGNC:
4	MLLT10	1.93	−0.65	0.3	MLLT10	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
5	POT1	1.93	−0.64	0.29	POT1	protection of telomeres 1 [Source:HGNC Symbol;Acc:HGNC:
6	PAFAH2	1.89	−0.22	0.4	PAFAH2	platelet−activating factor acetylhydrolase 2, 40kDa [Source:H
7	ZNF287	1.87	−0.07	0.57	ZNF287	zinc finger protein 287 [Source:HGNC Symbol;Acc:HGNC:13
8	NEK11	1.84	−0.18	0.3	NEK11	NIMA−related kinase 11 [Source:HGNC Symbol;Acc:HGNC:1
9	FBXO16	1.84	−0.09	0.39	FBXO16	F−box protein 16 [Source:HGNC Symbol;Acc:HGNC:13618]
10	LIN37	1.83	−0.13	0.35	LIN37	lin−37 DREAM MuvB core complex component [Source:HGN
11	ZNF221	1.83	−0.1	0.43	ZNF221	zinc finger protein 221 [Source:HGNC Symbol;Acc:HGNC:13
12	TMEM55B	1.81	−0.24	0.38	TMEM55B	transmembrane protein 55B [Source:HGNC Symbol;Acc:HGN
13	SLC22A1	1.81	−0.09	0.66	SLC22A1	solute carrier family 22 (organic cation transporter), member
14	THBS3	1.78	−0.1	0.52	THBS3	thrombospondin 3 [Source:HGNC Symbol;Acc:HGNC:11787]
15	TBC1D19	1.77	−0.25	0.44	TBC1D19	TBC1 domain family, member 19 [Source:HGNC Symbol;Acc
16	PLN	1.77	−0.35	0.37	PLN	phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
17	SPTLC3	1.76	−0.07	0.57	SPTLC3	serine palmitoyltransferase, long chain base subunit 3 [Sourc
18	SLC25A42	1.76	−0.06	0.63	SLC25A42	solute carrier family 25, member 42 [Source:HGNC Symbol;A
19	WDR83	1.74	−0.16	0.27	WDR83	WD repeat domain 83 [Source:HGNC Symbol;Acc:HGNC:32
20	PFKFB4	1.74	−0.13	0.5	PFKFB4	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 4 [S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−06	359 / 8580	Colon	TxWk_Colon
2	9e−06	383 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
3	2e−05	151 / 3081	Brain	Mid_Frontal_Lobe_ZNF
4	4e−05	369 / 9027	Colon	Tx_Colon
5	9e−05	5 / 14	BP	negative regulation of proteasomal ubiquitin−dependent protein catabolic p
6	1e−04	76 / 1383	TF	ICGC_Six5_targets
7	2e−04	29 / 385	GSEA	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
8	6e−04	242 / 5693	Lymph	HOPP_Weak_enhancer
9	6e−04	377 / 9482	Colon	TssA_Colon
10	1e−03	359 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−03	10 / 89	GSEA	ZHU_CMV_24_HR_UP
12	1e−03	35 / 568	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3
13	2e−03	15 / 177	GSEA	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA
14	2e−03	232 / 5538	Lymph	HOPP_Weak_txn
15	3e−03	6 / 40	miRN	hsa−miR−518d−3p
16	3e−03	100 / 2136	TF	ICGC_GabpPcr2_targets
17	3e−03	39 / 683	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
18	3e−03	305 / 7592	Lymph	HOPP_Active_promoter
19	3e−03	334 / 8415	Colon	Quies3_Colon
20	4e−03	39 / 689	Chr	Chr 7
21	4e−03	8 / 70	miRN	hsa−miR−375
22	4e−03	8 / 71	GSEA	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
23	4e−03	5 / 30	GSEA	YANG_BREAST_CANCER_ESR1_LASER_UP
24	4e−03	4 / 19	GSEA	REACTOME_SHC_MEDIATED_CASCADE
25	4e−03	4 / 19	GSEA	TOMLINS_METASTASIS_DN
26	4e−03	290 / 7209	Lymph	HOPP_Weak_promoter
27	5e−03	6 / 44	BP	DNA duplex unwinding
28	5e−03	37 / 656	Brain	Overlap_fetal_midbrain_EnhP
29	6e−03	10 / 108	GSEA	ZHU_CMV_ALL_UP
30	6e−03	7 / 60	GSEA	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
31	6e−03	7 / 61	GSEA	REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRAN
32	7e−03	6 / 47	GSEA	REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1
33	7e−03	9 / 94	BP	DNA recombination
34	7e−03	10 / 112	miRN	hsa−miR−875−3p
35	7e−03	4 / 22	BP	negative regulation of TOR signaling
36	7e−03	4 / 22	GSEA	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_UP
37	7e−03	2 / 4	GSEA	PARK_TRETINOIN_RESPONSE
38	8e−03	9 / 96	GSEA	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP
39	8e−03	3 / 12	GSEA	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_DN
40	9e−03	4 / 23	miRN	hsa−miR−24−1*

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	7 / 111	HORVATH_aging_genes meth UP
2	0.4	2 / 38	TESCHENDORFF_age_hypermethylated
3	0.7	3 / 100	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−05	5 / 14	negative regulation of proteasomal ubiquitin−dependent protein catabolic proc
2	5e−03	6 / 44	DNA duplex unwinding
3	7e−03	9 / 94	DNA recombination
4	7e−03	4 / 22	negative regulation of TOR signaling
5	1e−02	4 / 24	regulation of lipid metabolic process
6	1e−02	4 / 24	response to starvation
7	1e−02	3 / 14	nucleotide metabolic process
8	2e−02	5 / 41	positive regulation of MAP kinase activity
9	2e−02	10 / 129	autophagy
10	2e−02	3 / 16	negative regulation of autophagy
11	2e−02	4 / 29	brown fat cell differentiation
12	2e−02	4 / 29	glycogen metabolic process
13	2e−02	4 / 30	regulation of cell differentiation
14	3e−02	3 / 18	regulation of sensory perception of pain
15	3e−02	61 / 1325	catabolic process
16	3e−02	5 / 48	regulation of cellular amino acid metabolic process
17	3e−02	4 / 34	retrograde vesicle−mediated transport, Golgi to ER
18	3e−02	3 / 20	carbohydrate phosphorylation
19	4e−02	6 / 68	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
20	4e−02	6 / 70	activation of cysteine−type endopeptidase activity involved in apoptotic proces

Brain

Rank	p−value	#in/all	Geneset
1	9e−06	383 / 9330	Overlap_fetal_midbrain_ReprPC
2	2e−05	151 / 3081	Mid_Frontal_Lobe_ZNF
3	1e−03	359 / 9013	Overlap_fetal_midbrain_K9K27me3
4	5e−03	37 / 656	Overlap_fetal_midbrain_EnhP
5	2e−02	107 / 2462	Mid_Frontal_Lobe_HetRpts
6	4e−02	345 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	4e−02	234 / 5940	Overlap_fetal_midbrain_HetRpts
8	6e−02	59 / 1333	Fetal_ReprPCWk
9	6e−02	361 / 9528	Overlap_fetal_midbrain_Quies
10	1e−01	30 / 668	Mid_Frontal_Lobe_Enh
11	1e−01	36 / 831	Fetal_HetRpts
12	2e−01	73 / 1845	Fetal_Quies
13	2e−01	32 / 765	Mid_Frontal_Lobe_Het
14	2e−01	17 / 383	Fetal_Tx
15	3e−01	74 / 1907	Fetal_TxTrans
16	3e−01	41 / 1050	Fetal_EnhP
17	3e−01	31 / 786	Fetal_EnhG
18	4e−01	26 / 686	Overlap_fetal_midbrain_TssA
19	4e−01	72 / 1949	Fetal_TssF
20	4e−01	33 / 884	Overlap_fetal_midbrain_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	2 / 15	RHODES_CANCER_META_SIGNATURE
2	0.1	2 / 15	GENTLES_modul11
3	0.1	2 / 16	GENTLES_modul14
4	0.2	2 / 20	PanCan_ChromMod_geneset_nanostring
5	0.2	8 / 156	PanCan_PI3K_geneset_nanostring
6	0.2	4 / 70	SHAUGHNESSY_MM high risk
7	0.3	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.3	0 / 14	LIU_LIVER_CANCER
9	0.3	1 / 11	GENTLES_modul17
10	0.3	0 / 12	LIU_PROSTATE_CANCER_UP
11	0.4	1 / 13	GENTLES_modul12
12	0.4	12 / 298	SPANG_BCL6−index2
13	0.4	1 / 14	LIU_COMMON_CANCER_GENES
14	0.4	2 / 40	PanCan_HK_geneset_nanostring
15	0.4	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
16	0.4	1 / 16	GENTLES_modul7
17	0.5	1 / 18	PanCan_Notch_geneset_nanostring
18	0.6	1 / 22	PanCan_HH_geneset_nanostring
19	0.6	4 / 111	PanCan_RAS_geneset_nanostring
20	0.6	3 / 82	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.01	3 / 13	proteasome regulatory particle
2	0.02	6 / 57	proteasome complex
3	0.02	4 / 28	SCF ubiquitin ligase complex
4	0.02	3 / 17	proteasome accessory complex
5	0.03	3 / 19	ciliary base
6	0.03	3 / 19	nuclear chromosome, telomeric region
7	0.04	400 / 10605	intracellular
8	0.05	315 / 8205	cytoplasm
9	0.05	11 / 175	early endosome
10	0.07	2 / 12	basal part of cell
11	0.07	12 / 205	neuron projection
12	0.07	4 / 43	cytoplasmic microtubule
13	0.07	4 / 44	motile cilium
14	0.08	2 / 13	COPI vesicle coat
15	0.08	24 / 491	perinuclear region of cytoplasm
16	0.09	2 / 14	ER to Golgi transport vesicle
17	0.09	2 / 14	NuA4 histone acetyltransferase complex
18	0.10	102 / 2507	cytosol
19	0.10	3 / 31	membrane coat
20	0.10	3 / 31	microtubule associated complex

Chr

Rank	p−value	#in/all	Geneset
1	0.004	39 / 689	Chr 7
2	0.016	36 / 687	Chr 6
3	0.066	27 / 551	Chr X
4	0.110	63 / 1500	Chr 1
5	0.207	35 / 840	Chr 17
6	0.234	42 / 1037	Chr 19
7	0.323	33 / 838	Chr 3
8	0.346	11 / 262	Chr 13
9	0.374	27 / 696	Chr 5
10	0.394	25 / 649	Chr 16
11	0.426	18 / 469	Chr 8
12	0.500	17 / 462	Chr 14
13	0.634	19 / 558	Chr 4
14	0.747	25 / 775	Chr 12
15	0.776	12 / 398	Chr 20
16	0.896	23 / 801	Chr 11
17	0.904	29 / 993	Chr 2
18	0.913	3 / 151	Chr 21
19	0.951	11 / 465	Chr 15
20	0.958	14 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−06	359 / 8580	TxWk_Colon
2	4e−05	369 / 9027	Tx_Colon
3	6e−04	377 / 9482	TssA_Colon
4	3e−03	334 / 8415	Quies3_Colon
5	3e−02	51 / 1079	ZNF_Colon
6	4e−02	390 / 10290	TssWk_Colon
7	4e−02	15 / 250	K9K27me3_Colon
8	5e−02	11 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	7e−02	277 / 7203	TssF_Colon
10	7e−02	4 / 43	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
11	8e−02	152 / 3812	TssD1_Colon
12	9e−02	3 / 29	Marisa_CRC−cluster−c
13	1e−01	109 / 2698	EnhA_Colon
14	1e−01	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
15	2e−01	1 / 5	Budinska_C_CIMP−H−like_UP
16	2e−01	1 / 6	Budinska_E_Mixed_UP
17	2e−01	56 / 1386	Het_Colon
18	2e−01	1 / 7	Kaneda_CIMP−group2
19	2e−01	42 / 1038	HetRpts_Colon
20	3e−01	1 / 8	Juehling−MSI−enriched−in−7

Disease

Rank	p−value	#in/all	Geneset
1	0.7	14 / 435	GUDJ_psoriasis up
2	0.9	7 / 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	0.1	5 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
2	0.1	1 / 3	Donson−migration tethering and rolling−associated with LTS in HGA
3	0.1	6 / 94	WILLSCHER_GBM_proteomics_wtOnly_SpotB
4	0.1	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
5	0.2	36 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.2	2 / 23	WIRTH_PN subtype
7	0.2	5 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	0.2	16 / 356	Down_a
9	0.2	4 / 68	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.2	14 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	0.3	1 / 8	Colman_survival_robust
12	0.3	4 / 73	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	0.3	1 / 9	VERHAAK_Brain
14	0.3	4 / 75	GIEZELT_GBM_STS_down_VS_LTS
15	0.3	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
16	0.3	15 / 365	Down_b
17	0.3	2 / 34	WILLSCHER_GBM_Verhaak−PNmut_down (G)
18	0.4	1 / 13	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
19	0.4	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
20	0.4	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	29 / 385	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
2	1e−03	10 / 89	ZHU_CMV_24_HR_UP
3	1e−03	35 / 568	MIKKELSEN_ES_ICP_WITH_H3K4ME3
4	2e−03	15 / 177	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA
5	3e−03	39 / 683	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
6	4e−03	8 / 71	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
7	4e−03	5 / 30	YANG_BREAST_CANCER_ESR1_LASER_UP
8	4e−03	4 / 19	REACTOME_SHC_MEDIATED_CASCADE
9	4e−03	4 / 19	TOMLINS_METASTASIS_DN
10	6e−03	10 / 108	ZHU_CMV_ALL_UP
11	6e−03	7 / 60	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
12	6e−03	7 / 61	REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSI
13	7e−03	6 / 47	REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1
14	7e−03	4 / 22	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_UP
15	7e−03	2 / 4	PARK_TRETINOIN_RESPONSE
16	8e−03	9 / 96	LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP
17	8e−03	3 / 12	MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_DN
18	9e−03	5 / 36	REACTOME_SIGNALING_BY_FGFR_MUTANTS
19	1e−02	18 / 271	ZHANG_TLX_TARGETS_60HR_UP
20	1e−02	3 / 13	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION

HM

Rank	p−value	#in/all	Geneset
1	0.1	10 / 183	HALLMARK_GLYCOLYSIS
2	0.2	6 / 107	HALLMARK_COAGULATION
3	0.2	5 / 91	HALLMARK_PROTEIN_SECRETION
4	0.2	7 / 141	HALLMARK_FATTY_ACID_METABOLISM
5	0.3	7 / 146	HALLMARK_DNA_REPAIR
6	0.4	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.4	4 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.4	4 / 93	HALLMARK_PEROXISOME
9	0.5	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	0.6	6 / 167	HALLMARK_APICAL_JUNCTION
11	0.6	6 / 169	HALLMARK_XENOBIOTIC_METABOLISM
12	0.6	1 / 24	HALLMARK_PANCREAS_BETA_CELLS
13	0.6	6 / 176	HALLMARK_HYPOXIA
14	0.6	1 / 26	HALLMARK_ANGIOGENESIS
15	0.6	6 / 181	HALLMARK_P53_PATHWAY
16	0.6	3 / 91	HALLMARK_BILE_ACID_METABOLISM
17	0.7	1 / 29	HALLMARK_NOTCH_SIGNALING
18	0.7	3 / 95	HALLMARK_SPERMATOGENESIS
19	0.7	5 / 165	HALLMARK_MYOGENESIS
20	0.7	5 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.5	1 / 18	DUMEAUX_High bmi enriched genes
3	0.7	1 / 32	DUMEAUX_Fasting enriched genes
4	1.0	0 / 62	DUMEAUX_Smoking 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 / 4	DUMEAUX_Estrogen related in smokers literature genes up
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	6e−04	242 / 5693	HOPP_Weak_enhancer
2	2e−03	232 / 5538	HOPP_Weak_txn
3	3e−03	305 / 7592	HOPP_Active_promoter
4	4e−03	290 / 7209	HOPP_Weak_promoter
5	4e−02	8 / 107	SPANG_LPS 6hrs UP
6	4e−02	270 / 6929	HOPP_Txn_elongation
7	5e−02	2 / 10	DAVE_BL_DN
8	1e−01	1 / 4	Shaknovich_ABC_hyper_meth
9	1e−01	2 / 19	DAVE_c−myc BL UP
10	2e−01	13 / 268	SPANG_IL21 UP
11	2e−01	13 / 280	SPANG_CD40 6hrs UP
12	2e−01	246 / 6564	HOPP_Strong_enhancer
13	2e−01	5 / 89	ROSOLOWSKI_blue total
14	3e−01	1 / 8	MASCQUE_ABC UP
15	3e−01	2 / 30	Subero_INT_hypo_meth
16	3e−01	2 / 33	LEE_Developmental_regulators
17	4e−01	1 / 12	BENTINK_mBL DOWN
18	4e−01	83 / 2211	HOPP_Repetitive
19	4e−01	1 / 13	YAMANE_AICDA_targets_recruited
20	4e−01	190 / 5184	HOPP_Txn_transition

MF

Rank	p−value	#in/all	Geneset
1	0.02	3 / 15	fibroblast growth factor binding
2	0.02	42 / 830	nucleic acid binding transcription factor activity
3	0.02	3 / 17	fatty−acyl−CoA binding
4	0.02	5 / 46	manganese ion binding
5	0.03	40 / 820	sequence−specific DNA binding transcription factor activity
6	0.03	7 / 84	guanyl−nucleotide exchange factor activity
7	0.03	200 / 4992	ion binding
8	0.04	11 / 167	helicase activity
9	0.04	4 / 36	chromatin DNA binding
10	0.04	6 / 71	cysteine−type endopeptidase activity
11	0.05	4 / 38	protein complex scaffold
12	0.05	2 / 10	ribosomal small subunit binding
13	0.05	3 / 23	DNA helicase activity
14	0.05	487 / 13179	molecular_function
15	0.05	21 / 398	protein tyrosine kinase activity
16	0.05	3 / 24	snoRNA binding
17	0.06	7 / 95	heparin binding
18	0.06	5 / 58	cysteine−type peptidase activity
19	0.06	2 / 11	nucleosome binding
20	0.06	2 / 11	poly(A)−specific ribonuclease activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	6 / 40	hsa−miR−518d−3p
2	0.004	8 / 70	hsa−miR−375
3	0.007	10 / 112	hsa−miR−875−3p
4	0.009	4 / 23	hsa−miR−24−1*
5	0.009	9 / 98	hsa−miR−147
6	0.009	12 / 153	hsa−miR−200c
7	0.012	7 / 69	hsa−miR−518c
8	0.013	6 / 54	hsa−miR−518d−5p
9	0.013	6 / 54	hsa−miR−520c−5p
10	0.013	7 / 70	hsa−miR−628−3p
11	0.015	5 / 41	hsa−miR−518b
12	0.016	19 / 307	hsa−miR−302b
13	0.020	8 / 94	hsa−miR−526a
14	0.020	19 / 315	hsa−miR−302c
15	0.021	7 / 77	hsa−miR−205
16	0.027	13 / 198	hsa−miR−181c
17	0.030	19 / 329	hsa−miR−302d
18	0.030	4 / 33	hsa−miR−1274b
19	0.030	10 / 140	hsa−miR−522
20	0.031	9 / 121	hsa−miR−212

PathwAct

Rank	p−value	#in/all	Geneset
1	0.4	1 / 12	GUSTAFSON_PI3K_UP
2	0.4	1 / 13	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	BENTINK_e2f3.1
4	1.0	0 / 12	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 9	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−04	76 / 1383	ICGC_Six5_targets
2	3e−03	100 / 2136	ICGC_GabpPcr2_targets
3	1e−02	201 / 4879	ICGC_Pmlsc71910_targets
4	2e−02	181 / 4385	ICGC_Atf2_targets
5	2e−02	195 / 4774	ICGC_Foxm1_targets
6	2e−02	167 / 4032	ICGC_Creb1_targets
7	2e−02	162 / 3924	ICGC_Zeb1_targets
8	2e−02	191 / 4706	ICGC_Sp1_targets
9	3e−02	55 / 1171	KIM_MYC targets
10	3e−02	180 / 4414	ICGC_Bclaf101388_targets
11	3e−02	166 / 4054	ICGC_Egr1_targets
12	3e−02	189 / 4689	ICGC_Taf1_targets
13	3e−02	152 / 3700	ICGC_Nfatc1_targets
14	4e−02	241 / 6114	ICGC_Runx3_targets
15	4e−02	82 / 1878	ICGC_Cebpbsc150_targets
16	4e−02	218 / 5495	ICGC_Yy1_targets
17	4e−02	196 / 4909	ICGC_Stat5_targets
18	5e−02	214 / 5408	ICGC_Pou2_targets
19	5e−02	206 / 5200	ICGC_Mta3_targets
20	5e−02	32 / 653	ICGC_SrfPcr2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	3 / 38	VAQUERIZAS_Whole brain
2	0.2	2 / 23	VAQUERIZAS_Spinal cord
3	0.3	7 / 143	VAQUERIZAS_General
4	0.4	1 / 12	VAQUERIZAS_Skin
5	0.4	2 / 38	VAQUERIZAS_Testis
6	0.4	1 / 15	VAQUERIZAS_Bone marrow
7	0.4	1 / 15	VAQUERIZAS_Fetal thyroid
8	0.4	1 / 16	VAQUERIZAS_Salivary gland
9	0.5	1 / 17	VAQUERIZAS_Pituitary
10	0.5	1 / 17	VAQUERIZAS_Heart
11	0.7	1 / 29	VAQUERIZAS_Smooth muscle
12	0.7	1 / 36	VAQUERIZAS_Fetal brain
13	0.8	1 / 40	VAQUERIZAS_Thyroid
14	0.8	1 / 41	VAQUERIZAS_Placenta
15	0.8	1 / 45	VAQUERIZAS_Uterus
16	0.9	1 / 58	VAQUERIZAS_Lung
17	0.9	1 / 59	VAQUERIZAS_Whole blood
18	1.0	0 / 26	VAQUERIZAS_Liver
19	1.0	0 / 33	VAQUERIZAS_Prostate
20	1.0	0 / 9	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	2 / 11	WIRTH_Globus pallidus
2	0.31	1 / 10	WIRTH_Hippocampus
3	0.33	1 / 11	WIRTH_Prim. lymphoid organs
4	0.36	1 / 12	WIRTH_Cerebellum
5	0.38	1 / 13	WIRTH_Thyroid gland
6	0.42	9 / 225	PALMER_Granulocytes signature up
7	0.44	1 / 16	PALMER_Lymphocytes signature up
8	0.50	2 / 46	WIRTH_Liver
9	0.50	3 / 74	WIRTH_Mucosa
10	0.61	12 / 350	WIRTH_Nervous System
11	0.67	3 / 95	WIRTH_Muscle
12	0.69	1 / 32	WIRTH_Pancreas
13	0.69	1 / 32	WIRTH_Placenta
14	0.72	11 / 350	WIRTH_Immune system
15	0.75	3 / 107	WIRTH_Testis
16	0.78	3 / 114	PALMER_T−Cell signature up
17	0.92	4 / 194	PALMER_B−Cell signature up
18	1.00	0 / 11	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_B−cells
20	1.00	0 / 8	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	141 / 3682	LU_BPDE 0.005 DN
2	0.6	39 / 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	

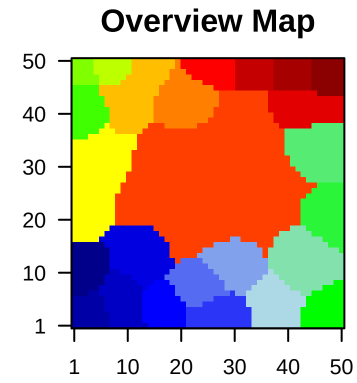
K−Means Clusters

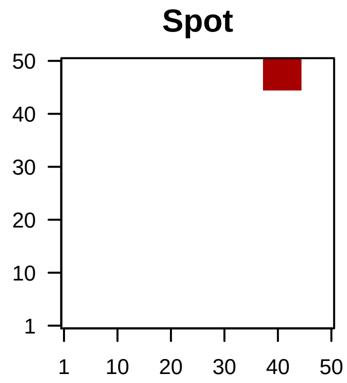
Spot Summary: X

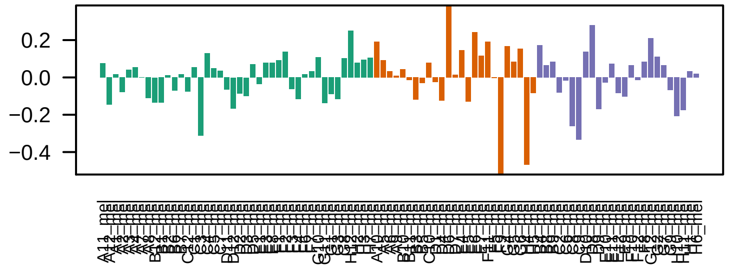
metagenes = 42
genes = 328

<r> metagenes = 0.85
<r> genes = 0.07
beta: r2= 1.45 / log p= −Inf

samples with spot = 11 (12 %)
MSC1 : 1 (2.4 %)
MSC2 : 7 (28 %)
MSC3 : 3 (12 %)





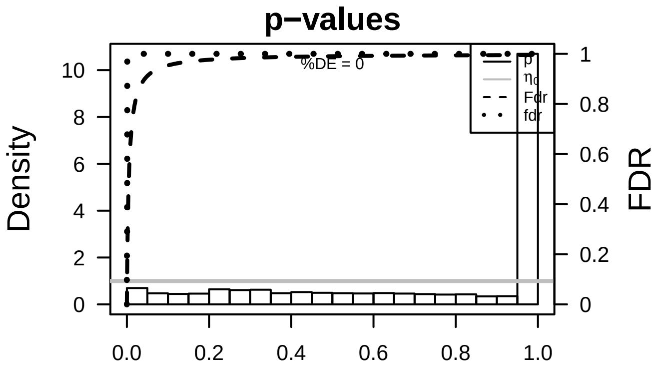


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENO3	2.58	−1.04	0.3	ENO3	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:HGNC:
2	EML6	1.97	−0.15	0.34	EML6	echinoderm microtubule associated protein like 6 [Source:HG
3	MYO1E	1.87	−0.47	0.35	MYO1E	myosin IE [Source:HGNC Symbol;Acc:HGNC:7599]
4	ITLN2	1.83	−0.1	0.24	ITLN2	intelectin 2 [Source:HGNC Symbol;Acc:HGNC:20599]
5	EMC1	1.82	−0.59	0.33	EMC1	ER membrane protein complex subunit 1 [Source:HGNC Sym
6	WDR89	1.82	−0.36	0.26	WDR89	WD repeat domain 89 [Source:HGNC Symbol;Acc:HGNC:20
7	SRD5A3	1.79	−0.45	0.24	SRD5A3	steroid 5 alpha−reductase 3 [Source:HGNC Symbol;Acc:HGN
8	EARS2	1.77	−0.56	0.34	EARS2	glutamyl−tRNA synthetase 2, mitochondrial [Source:HGNC S
9	AP4M1	1.75	−0.28	0.24	AP4M1	adaptor−related protein complex 4, mu 1 subunit [Source:HG
10	LIPG	1.72	−0.32	0.27	LIPG	lipase, endothelial [Source:HGNC Symbol;Acc:HGNC:6623]
11	SELL	1.69	−0.16	0.33	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
12	ZMYM6NB	1.68	−0.38	0.19	ZMYM6NB	ZMYM6 neighbor [Source:HGNC Symbol;Acc:HGNC:40021]
13	GABRA5	1.67	−0.18	0.24	GABRA5	gamma−aminobutyric acid (GABA) A receptor, alpha 5 [Sourc
14	GULP1	1.65	−0.53	0.26	GULP1	GULP, engulfment adaptor PTB domain containing 1 [Source:
15	PGBD2	1.63	−0.39	0.31	PGBD2	piggyBac transposable element derived 2 [Source:HGNC Syr
16	STK11IP	1.61	−0.17	0.35	STK11IP	serine/threonine kinase 11 interacting protein [Source:HGNC
17	SEC24D	1.59	−0.54	0.31	SEC24D	SEC24 family member D [Source:HGNC Symbol;Acc:HGNC:
18	LIPT1	1.57	−0.38	0.29	LIPT1	lipoyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:29569]
19	FUCA1	1.57	−0.24	0.34	FUCA1	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:H
20	GPX8	1.56	−0.72	0.32	GPX8	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−22	284 / 9330	Brain	Overlap_fetal_midbrain_ReprPC
2	3e−21	285 / 9482	Colon	TssA_Colon
3	3e−20	248 / 7592	Lympl	HOPP_Active_promoter
4	1e−18	231 / 6929	Lympl	HOPP_Txn_elongation
5	3e−11	255 / 9013	Brain	Overlap_fetal_midbrain_K9K27me3
6	3e−10	215 / 7209	Lympl	HOPP_Weak_promoter
7	2e−09	250 / 9027	Colon	Tx_Colon
8	4e−09	183 / 5940	Brain	Overlap_fetal_midbrain_HetRpts
9	5e−09	232 / 8205	CC	cytoplasm
10	2e−08	163 / 5184	Lympl	HOPP_Txn_transition
11	3e−08	237 / 8580	Colon	TxWk_Colon
12	4e−08	233 / 8415	Colon	Quies3_Colon
13	3e−07	30 / 478	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	7e−07	169 / 5693	Lympl	HOPP_Weak_enhancer
15	3e−06	42 / 890	GSEA	ACEVEDO_LIVER_CANCER_UP
16	3e−06	16 / 182	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
17	4e−06	20 / 277	BP	translation
18	4e−06	162 / 5538	Lympl	HOPP_Weak_txn
19	2e−05	17 / 235	GSEA	BLUM_RESPONSE_TO_SALIRASIB_UP
20	4e−05	244 / 9528	Brain	Overlap_fetal_midbrain_Quies
21	6e−05	8 / 61	GSEA	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS
22	7e−05	53 / 1400	TF	ICGC_Myc_targets
23	8e−05	258 / 10290	Colon	TssWk_Colon
24	9e−05	9 / 83	BP	mitochondrial translational termination
25	9e−05	35 / 800	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
26	1e−04	30 / 659	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
27	2e−04	44 / 1126	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
28	2e−04	60 / 1701	TF	HEBENSTREIT_high expression TF
29	2e−04	16 / 255	BP	cellular amino acid metabolic process
30	2e−04	18 / 309	BP	intracellular protein transport
31	3e−04	9 / 96	BP	mitochondrial translation
32	3e−04	6 / 42	GSEA	REACTOME_TRNA_AMINOACYLATION
33	3e−04	5 / 28	GSEA	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
34	3e−04	39 / 993	Chr	Chr 2
35	4e−04	6 / 44	BP	tRNA aminoacylation for protein translation
36	4e−04	21 / 416	GSEA	SHEN_SMARCA2_TARGETS_UP
37	4e−04	11 / 147	BP	tRNA metabolic process
38	4e−04	261 / 10605	CC	intracellular
39	4e−04	59 / 1730	BP	small molecule metabolic process
40	4e−04	48 / 1326	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	4e−06	20 / 277	translation
2	9e−05	9 / 83	mitochondrial translational termination
3	2e−04	16 / 255	cellular amino acid metabolic process
4	2e−04	18 / 309	intracellular protein transport
5	3e−04	9 / 96	mitochondrial translation
6	4e−04	6 / 44	tRNA aminoacylation for protein translation
7	4e−04	11 / 147	tRNA metabolic process
8	4e−04	59 / 1730	small molecule metabolic process
9	5e−04	8 / 83	mitochondrial translational elongation
10	5e−04	8 / 83	mitochondrial translational initiation
11	6e−04	16 / 285	organelle organization
12	2e−03	16 / 322	mitochondrion organization
13	2e−03	21 / 478	protein transport
14	3e−03	7 / 84	antigen processing and presentation of exogenous peptide antigen via MHC c
15	3e−03	3 / 14	COPII vesicle coating
16	3e−03	3 / 14	tRNA aminoacylation
17	6e−03	3 / 17	associative learning
18	8e−03	3 / 19	positive regulation of TOR signaling
19	1e−02	3 / 21	adipose tissue development
20	1e−02	4 / 40	mitochondrial electron transport, NADH to ubiquinone

Brain

Rank	p−value	#in/all	Geneset
1	3e−22	284 / 9330	Overlap_fetal_midbrain_ReprPC
2	3e−11	255 / 9013	Overlap_fetal_midbrain_K9K27me3
3	4e−09	183 / 5940	Overlap_fetal_midbrain_HetRpts
4	4e−05	244 / 9528	Overlap_fetal_midbrain_Quies
5	8e−04	33 / 831	Fetal_HetRpts
6	7e−03	221 / 9020	Overlap_fetal_midbrain_ReprPCWk
7	6e−02	33 / 1122	Fetal_K9K27me3
8	9e−02	12 / 349	Fetal_ZNF
9	2e−01	74 / 3081	Mid_Frontal_Lobe_ZNF
10	2e−01	9 / 304	Fetal_Het
11	3e−01	45 / 1845	Fetal_Quies
12	3e−01	32 / 1333	Fetal_ReprPCWk
13	4e−01	23 / 953	Fetal_Enh
14	5e−01	4 / 158	Overlap_fetal_midbrain_Het
15	5e−01	4 / 163	Fetal_ReprPC
16	6e−01	27 / 1236	Mid_Frontal_Lobe_ReprPCWk
17	6e−01	12 / 564	Mid_Frontal_Lobe_EnhP
18	6e−01	22 / 1050	Fetal_EnhP
19	6e−01	16 / 769	Overlap_fetal_midbrain_ZNF
20	7e−01	16 / 786	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	3 / 29	KUIPER_MM good survival
2	0.05	2 / 16	GENTLES_modul7
3	0.07	4 / 70	SHAUGHNESSY_MM high risk
4	0.20	1 / 10	GENTLES_modul5
5	0.21	9 / 298	SPANG_BCL6−index2
6	0.28	1 / 15	GENTLES_modul10
7	0.30	1 / 16	GENTLES_modul6
8	0.43	0 / 14	LIU_COMMON_CANCER_GENES
9	0.59	1 / 40	ZHANG_MM up
10	0.65	1 / 47	PanCan_DNARepair_geneset_nanostring
11	0.67	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.75	0 / 15	RHODES_CANCER_META_SIGNATURE
13	0.84	0 / 12	LIU_PROSTATE_CANCER_UP
14	0.86	0 / 14	LIU_PROSTATE_CANCER_DN
15	0.91	2 / 180	SPANG_LPS−index2
16	0.92	1 / 111	PanCan_RAS_geneset_nanostring
17	0.92	7 / 489	Lembcke_Normal vs Adenoma
18	0.93	1 / 121	PanCan_MAPK_geneset_nanostring
19	0.97	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	0.97	1 / 156	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	5e−09	232 / 8205	cytoplasm
2	4e−04	261 / 10605	intracellular
3	6e−04	20 / 401	mitochondrial inner membrane
4	1e−03	246 / 9988	organelle
5	2e−03	9 / 128	ribosome
6	6e−03	47 / 1468	mitochondrion
7	6e−03	4 / 34	ER to Golgi transport vesicle membrane
8	1e−02	89 / 3214	protein complex
9	1e−02	64 / 2193	extracellular exosome
10	1e−02	4 / 41	mitochondrial respiratory chain complex I
11	2e−02	38 / 1201	endoplasmic reticulum
12	2e−02	2 / 10	ER membrane protein complex
13	2e−02	2 / 11	Gemini of coiled bodies
14	3e−02	2 / 12	dendrite membrane
15	3e−02	2 / 12	SMN complex
16	3e−02	2 / 13	integrator complex
17	3e−02	2 / 13	sperm principal piece
18	4e−02	4 / 57	proteasome complex
19	4e−02	2 / 14	cytoplasmic dynein complex
20	4e−02	2 / 14	ER to Golgi transport vesicle

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	39 / 993	Chr 2
2	2e−03	28 / 696	Chr 5
3	1e−02	25 / 689	Chr 7
4	1e−02	18 / 462	Chr 14
5	2e−01	14 / 469	Chr 8
6	2e−01	22 / 801	Chr 11
7	2e−01	7 / 221	Chr 18
8	3e−01	36 / 1500	Chr 1
9	4e−01	4 / 151	Chr 21
10	4e−01	13 / 551	Chr X
11	5e−01	8 / 335	Chr 22
12	5e−01	19 / 838	Chr 3
13	7e−01	14 / 687	Chr 6
14	7e−01	9 / 465	Chr 15
15	8e−01	12 / 649	Chr 16
16	9e−01	6 / 398	Chr 20
17	9e−01	8 / 558	Chr 4
18	9e−01	3 / 262	Chr 13
19	1e+00	11 / 775	Chr 12
20	1e+00	7 / 576	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−21	285 / 9482	TssA_Colon
2	2e−09	250 / 9027	Tx_Colon
3	3e−08	237 / 8580	TxWk_Colon
4	4e−08	233 / 8415	Quies3_Colon
5	8e−05	258 / 10290	TssWk_Colon
6	1e−03	187 / 7203	TssF_Colon
7	1e−03	3 / 10	KIM_MSI−in−CRC
8	8e−03	27 / 748	Pentrack_CRC_TCGA_corr_R_normal_DN
9	1e−02	2 / 8	Juehling−MSI−enriched−in−7
10	1e−02	9 / 173	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	2e−02	5 / 66	Pentrack_CRC_TCGA_corr_N_msi−h_DN
12	3e−02	22 / 648	Pentrack_CRC_TCGA_group.over_C_normal_DN
13	1e−01	1 / 7	Marisa_CRC−C5
14	2e−01	1 / 8	KIM_CRC−MSI−regulated_DN
15	2e−01	1 / 8	Marisa_CRC−C1
16	2e−01	1 / 9	TCGA−CRC_agressive−disease−markers
17	2e−01	25 / 934	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	2e−01	1 / 11	Budinska_B_Lower crypt−like_DOWN
19	3e−01	8 / 281	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
20	3e−01	1 / 18	Ang_CRC−CIMPH−vs−L_hypo

Disease

Rank	p−value	#in/all	Geneset
1	0.7	8 / 435	GUDJ_psoriasis up
2	1.0	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	0.005	5 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
2	0.023	13 / 315	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.023	2 / 11	WILLSCHER_GBM_LTSmut_proteomics−B_UP
4	0.042	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
5	0.044	1 / 2	WILLSCHER_GBM_LTSmut_proteomics−E_UP
6	0.048	4 / 62	cultured astroglia vs. in vivo astrocytes
7	0.050	4 / 63	Stuehler_Proteins_up_in_STS
8	0.086	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
9	0.125	1 / 6	neurons_glio
10	0.141	6 / 159	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	0.173	3 / 65	GIEZELT_GBM_STS_up_VS_LTS
12	0.174	23 / 843	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.182	1 / 9	Christensen_hypomethylated_in_grade2_oligodendroglioma
14	0.197	2 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
15	0.197	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
16	0.205	2 / 38	Sturm_GBM_Meth_overexpression_F_IDH_UP
17	0.218	1 / 11	Christensen_hypermethylated_in_ependymoma
18	0.218	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
19	0.285	1 / 15	VERHAAK_MES subtype
20	0.313	9 / 332	Up

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−07	30 / 478	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	3e−06	42 / 890	ACEVEDO_LIVER_CANCER_UP
3	3e−06	16 / 182	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
4	2e−05	17 / 235	BLUM_RESPONSE_TO_SALIRASIB_UP
5	6e−05	8 / 61	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS
6	9e−05	35 / 800	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
7	1e−04	30 / 659	SCHLOSSER_SERUM_RESPONSE_DN
8	2e−04	44 / 1126	BLALOCK_ALZHEIMERS_DISEASE_DN
9	3e−04	6 / 42	REACTOME_TRNA_AMINOACYLATION
10	3e−04	5 / 28	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
11	4e−04	21 / 416	SHEN_SMARCA2_TARGETS_UP
12	4e−04	48 / 1326	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	6e−04	23 / 493	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
14	8e−04	12 / 183	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP
15	8e−04	12 / 184	HOLLMANN_APOPTOSIS_VIA_CD40_UP
16	1e−03	8 / 92	BRUINS_UVC_RESPONSE_MIDDLE
17	1e−03	8 / 93	HELLER_SILENCED_BY_METHYLATION_DN
18	1e−03	26 / 609	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
19	1e−03	20 / 421	MOOTHA_MITOCHONDRIA
20	1e−03	9 / 117	REACTOME_MEMBRANE_TRAFFICKING

HM

Rank	p−value	#in/all	Geneset
1	5e−04	13 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	4e−03	10 / 167	HALLMARK_IL2_STAT5_SIGNALING
3	7e−02	8 / 196	HALLMARK_MTORC1_SIGNALING
4	8e−02	4 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	9e−02	5 / 109	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	1e−01	6 / 146	HALLMARK_DNA_REPAIR
7	1e−01	4 / 91	HALLMARK_PROTEIN_SECRETION
8	2e−01	4 / 94	HALLMARK_ANDROGEN_RESPONSE
9	2e−01	6 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	2e−01	6 / 169	HALLMARK_XENOBIOTIC_METABOLISM
11	2e−01	5 / 148	HALLMARK_KRAS_SIGNALING_UP
12	2e−01	6 / 188	HALLMARK_ADIPOGENESIS
13	3e−01	2 / 47	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	3e−01	5 / 162	HALLMARK_COMPLEMENT
15	3e−01	3 / 93	HALLMARK_PEROXISOME
16	4e−01	4 / 146	HALLMARK_UV_RESPONSE_UP
17	4e−01	1 / 26	HALLMARK_ANGIOGENESIS
18	6e−01	1 / 37	HALLMARK_APICAL_SURFACE
19	6e−01	2 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
20	6e−01	2 / 91	HALLMARK_BILE_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 5	DUMEAUX_Monocytes in smokers literature genes up
2	0.5	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 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 18	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−20	248 / 7592	HOPP_Active_promoter
2	1e−18	231 / 6929	HOPP_Txn_elongation
3	3e−10	215 / 7209	HOPP_Weak_promoter
4	2e−08	163 / 5184	HOPP_Txn_transition
5	7e−07	169 / 5693	HOPP_Weak_enhancer
6	4e−06	162 / 5538	HOPP_Weak_txn
7	8e−04	44 / 1218	SPANG_BCR UP
8	9e−03	2 / 7	CARO_OxPhos_vs_BCR_UP
9	7e−02	3 / 42	CARO_OxPhos_in_DLBCL_UP
10	9e−02	1 / 4	Shaknovich_ABC_hyper_meth
11	2e−01	1 / 8	MASCQUE_GCB UP
12	2e−01	154 / 6564	HOPP_Strong_enhancer
13	2e−01	2 / 43	LENZ_Stromal signature 2
14	3e−01	28 / 1128	SPANG_BCR DN
15	3e−01	3 / 86	ROSOLOWSKI_red total
16	3e−01	3 / 89	ROSOLOWSKI_blue total
17	3e−01	1 / 19	Subero_MM_hyper_meth
18	4e−01	2 / 61	SPANG_LPS 6hrs DN
19	5e−01	1 / 30	TARTE_B−cell signature
20	5e−01	2 / 82	ROSOLOWSKI_green UP

MF

Rank	p−value	#in/all	Geneset
1	0.001	7 / 71	structural constituent of ribosome
2	0.001	3 / 10	glutathione binding
3	0.001	3 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
4	0.002	3 / 12	low−density lipoprotein particle receptor binding
5	0.006	3 / 17	aspartic−type endopeptidase activity
6	0.007	4 / 35	aminoacyl−tRNA ligase activity
7	0.008	4 / 36	tRNA binding
8	0.011	4 / 40	NADH dehydrogenase (ubiquinone) activity
9	0.021	3 / 27	thyroid hormone receptor binding
10	0.023	2 / 11	ATPase activity, coupled
11	0.023	2 / 11	quinone binding
12	0.024	32 / 1007	poly(A) RNA binding
13	0.027	41 / 1365	RNA binding
14	0.028	2 / 12	enhancer sequence−specific DNA binding
15	0.028	2 / 12	misfolded protein binding
16	0.028	2 / 12	phospholipase activity
17	0.028	2 / 12	RNA polymerase II transcription factor binding transcription factor activity
18	0.028	3 / 30	cyclin−dependent protein serine/threonine kinase activity
19	0.029	15 / 394	catalytic activity
20	0.040	20 / 592	oxidoreductase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	11 / 175	hsa−miR−548k
2	0.009	4 / 37	hsa−miR−215
3	0.009	10 / 189	hsa−miR−513a−3p
4	0.011	8 / 137	hsa−miR−656
5	0.013	8 / 140	hsa−miR−409−3p
6	0.016	8 / 147	hsa−miR−143
7	0.019	5 / 70	hsa−miR−935
8	0.019	5 / 70	hsa−miR−628−3p
9	0.024	18 / 488	hsa−miR−103
10	0.027	7 / 132	hsa−miR−320d
11	0.028	4 / 52	hsa−miR−431
12	0.029	4 / 53	hsa−miR−552
13	0.030	15 / 395	hsa−miR−301b
14	0.030	3 / 31	hsa−miR−17*
15	0.036	8 / 171	hsa−miR−607
16	0.037	4 / 57	hsa−miR−193a−3p
17	0.039	3 / 34	hsa−miR−34c−3p
18	0.039	4 / 58	hsa−miR−627
19	0.040	5 / 85	hsa−miR−567
20	0.043	7 / 146	hsa−miR−320c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 14	BENTINK_e2f3.1
2	0.3	1 / 14	BENTINK_src.2
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 / 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	7e−05	53 / 1400	ICGC_Myc_targets
2	2e−04	60 / 1701	HEBENSTREIT_high expression TF
3	2e−03	67 / 2136	ICGC_GabpPcr2_targets
4	4e−03	40 / 1171	KIM_MYC targets
5	8e−03	57 / 1878	ICGC_Cebpbsc150_targets
6	1e−02	43 / 1383	ICGC_Six5_targets
7	2e−02	122 / 4689	ICGC_Taf1_targets
8	2e−02	114 / 4385	ICGC_Atf2_targets
9	3e−02	124 / 4879	ICGC_Pmlsc71910_targets
10	4e−02	119 / 4682	ICGC_Pol24_targets
11	4e−02	122 / 4829	ICGC_Nficsc81335_targets
12	4e−02	1 / 2	MYC_ECM cell adhesion DOWN
13	5e−02	112 / 4414	ICGC_Bclaf101388_targets
14	5e−02	134 / 5408	ICGC_Pou2_targets
15	9e−02	21 / 690	ICGC_Atf3_targets
16	9e−02	39 / 1418	ICGC_Ets1_targets
17	1e−01	100 / 4032	ICGC_Creb1_targets
18	1e−01	1 / 5	MYC_TF and cofactors
19	1e−01	119 / 4909	ICGC_Stat5_targets
20	1e−01	61 / 2391	ICGC_Pbx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	2 / 17	VAQUERIZAS_Heart
2	0.14	1 / 7	VAQUERIZAS_Skeletal.muscle.psoas
3	0.30	1 / 16	VAQUERIZAS_Salivary gland
4	0.40	1 / 23	VAQUERIZAS_Trachea
5	0.44	1 / 26	VAQUERIZAS_Liver
6	0.52	1 / 33	VAQUERIZAS_Prostate
7	0.55	1 / 36	VAQUERIZAS_Fetal brain
8	0.56	1 / 37	VAQUERIZAS_Thymus
9	0.59	1 / 40	VAQUERIZAS_Thyroid
10	0.62	3 / 143	VAQUERIZAS_General
11	1.00	0 / 41	VAQUERIZAS_Placenta
12	1.00	0 / 29	VAQUERIZAS_Smooth muscle
13	1.00	0 / 45	VAQUERIZAS_Uterus
14	1.00	0 / 9	VAQUERIZAS_Kidney
15	1.00	0 / 23	VAQUERIZAS_Spinal cord
16	1.00	0 / 38	VAQUERIZAS_Whole brain
17	1.00	0 / 59	VAQUERIZAS_Whole blood
18	1.00	0 / 7	VAQUERIZAS_Appendix
19	1.00	0 / 29	VAQUERIZAS_Fetal lung
20	1.00	0 / 58	VAQUERIZAS_Lung

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 13	WIRTH_B−cells
2	0.06	9 / 225	PALMER_Granulocytes signature up
3	0.20	1 / 10	WIRTH_Hippocampus
4	0.25	1 / 13	WIRTH_Thyroid gland
5	0.30	1 / 16	PALMER_Lymphocytes signature up
6	0.79	6 / 350	WIRTH_Immune system
7	0.81	3 / 194	PALMER_B−Cell signature up
8	0.88	1 / 95	WIRTH_Muscle
9	1.00	2 / 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 / 8	WIRTH_Tonsil
14	1.00	0 / 12	WIRTH_Thymus
15	1.00	0 / 12	WIRTH_Lymphocytes
16	1.00	0 / 5	WIRTH_Bone marrow
17	1.00	0 / 11	WIRTH_Globus pallidus
18	1.00	0 / 14	WIRTH_Telencephalon
19	1.00	0 / 11	WIRTH_Cortex cerebri
20	1.00	0 / 10	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	22 / 1115	LU_BPDE 1n DN
2	1.0	64 / 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	

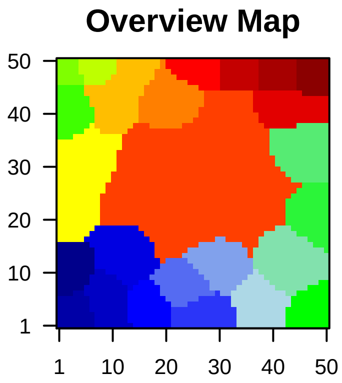
K−Means Clusters

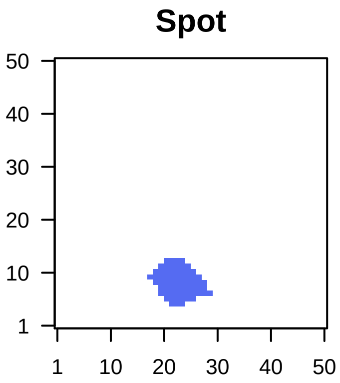
Spot Summary: Y

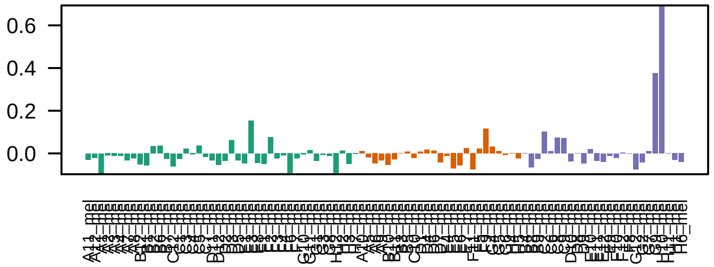
metagenes = 66
genes = 539

<r> metagenes = 0.84
<r> genes = 0.16
beta: r2= 0.61 / log p= −Inf

samples with spot = 3 (3.3 %)
MSC1 : 1 (2.4 %)
MSC3 : 2 (8 %)





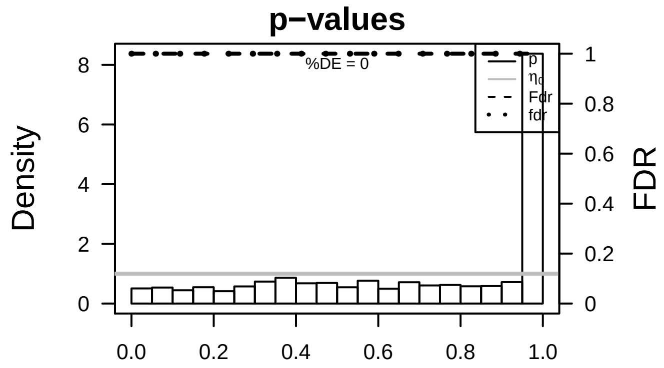


Spot Genelist

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	ZNF625−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	STAB2	1.84	−0.04	0.28	STAB2	stabilin 2 [Source:HGNC Symbol;Acc:HGNC:18629]
16	PTPLA	1.83	−0.81	0.36		
17	AGO2	1.83	−0.49	0.27	AGO2	argonaute RISC catalytic component 2 [Source:HGNC Symb
18	HIST1H4A	1.82	−0.02	0.32	HIST1H4A	histone cluster 1, H4a [Source:HGNC Symbol;Acc:HGNC:47
19	LRP5L	1.81	−0.12	0.47	LRP5L	low density lipoprotein receptor−related protein 5−like [Source
20	SOX9	1.79	−0.07	0.66	SOX9	SRY (sex determining region Y)−box 9 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−06	4 / 5	GSE	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
2	3e−05	21 / 217	MF	GTPase activator activity
3	4e−05	15 / 124	BP	regulation of small GTPase mediated signal transduction
4	5e−05	4 / 7	GSE	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
5	1e−04	29 / 382	BP	positive regulation of GTPase activity
6	4e−04	12 / 105	GSE	REACTOME_SIGNALING_BY_RHO_GTPASES
7	4e−04	18 / 203	miRN	hsa−miR−33a
8	4e−04	138 / 2972	Brain	Mid_Frontal_Lobe_ReprPC
9	5e−04	6 / 29	GSE	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES
10	7e−04	6 / 31	BP	cell maturation
11	9e−04	4 / 13	GSE	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
12	1e−03	9 / 74	Glio	WIRTH_Normal Brain
13	2e−03	15 / 176	miRN	hsa−miR−199b−3p
14	2e−03	5 / 26	GSE	RIZ_ERYTHROID_DIFFERENTIATION_HEMGN
15	2e−03	5 / 27	BP	water transport
16	2e−03	23 / 338	BP	G−protein coupled receptor signaling pathway
17	3e−03	7 / 53	BP	positive regulation of protein ubiquitination
18	3e−03	12 / 132	miRN	hsa−miR−199b−5p
19	3e−03	9 / 83	GSE	LEIN_CHOROID_PLEXUS_MARKERS
20	3e−03	19 / 264	GSE	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
21	3e−03	4 / 18	MF	galactosyltransferase activity
22	4e−03	6 / 42	GSE	REACTOME_ION_CHANNEL_TRANSPORT
23	4e−03	7 / 56	BP	cellular iron ion homeostasis
24	4e−03	5 / 30	Lymp	Subero_INT_hypo_meth
25	4e−03	6 / 43	miRN	hsa−miR−412
26	4e−03	6 / 43	GSE	KEGG_BASAL_CELL_CARCINOMA
27	4e−03	5 / 31	GSE	KEGG_STARCH_AND_SUCROSE_METABOLISM
28	5e−03	3 / 10	CC	high−density lipoprotein particle
29	5e−03	3 / 10	MF	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane m
30	5e−03	3 / 10	MF	lipid transporter activity
31	5e−03	3 / 10	CC	vacuolar proton−transporting V−type ATPase complex
32	5e−03	4 / 20	GSE	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
33	5e−03	14 / 179	GSE	NABA_SECRETED_FACTORS
34	5e−03	5 / 32	BP	O−glycan processing
35	6e−03	3 / 11	MF	structural constituent of eye lens
36	6e−03	3 / 11	Lymp	Subero_T−ALL_hypo_meth
37	6e−03	15 / 203	miRN	hsa−miR−545
38	6e−03	10 / 111	GSE	LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q
39	7e−03	5 / 34	BP	positive regulation of interleukin−6 production
40	7e−03	64 / 1317	Colon	EnhP_Colon



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 38	TESCHENDORFF_age_hypermethylated
2	0.8	3 / 111	HORVATH_aging_genes meth UP
3	1.0	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	4e−05	15 / 124	regulation of small GTPase mediated signal transduction
2	1e−04	29 / 382	positive regulation of GTPase activity
3	7e−04	6 / 31	cell maturation
4	2e−03	5 / 27	water transport
5	2e−03	23 / 338	G−protein coupled receptor signaling pathway
6	3e−03	7 / 53	positive regulation of protein ubiquitination
7	4e−03	7 / 56	cellular iron ion homeostasis
8	5e−03	5 / 32	O−glycan processing
9	7e−03	5 / 34	positive regulation of interleukin−6 production
10	7e−03	4 / 22	odontogenesis
11	7e−03	4 / 22	vasculature development
12	8e−03	3 / 12	mammary gland epithelial cell differentiation
13	8e−03	4 / 23	keratan sulfate biosynthetic process
14	1e−02	20 / 316	small GTPase mediated signal transduction
15	1e−02	3 / 13	embryonic camera−type eye morphogenesis
16	1e−02	3 / 13	glial cell differentiation
17	1e−02	3 / 13	negative regulation of translational initiation
18	1e−02	5 / 38	cellular response to cAMP
19	1e−02	4 / 25	positive regulation of BMP signaling pathway
20	1e−02	3 / 14	negative regulation of protein complex assembly

Brain

Rank	p−value	#in/all	Geneset
1	4e−04	138 / 2972	Mid_Frontal_Lobe_ReprPC
2	1e−02	108 / 2462	Mid_Frontal_Lobe_HetRpts
3	1e−02	72 / 1548	Mid_Frontal_Lobe_K9K27me3
4	3e−02	42 / 862	Overlap_fetal_midbrain_TxTrans
5	3e−02	47 / 989	Mid_Frontal_Lobe_Quies
6	3e−02	11 / 163	Fetal_ReprPC
7	3e−02	34 / 686	Overlap_fetal_midbrain_TssA
8	4e−02	55 / 1207	Overlap_fetal_midbrain_TssF
9	5e−02	38 / 812	Mid_Frontal_Lobe_TssP
10	1e−01	88 / 2185	Fetal_TssA
11	2e−01	51 / 1236	Mid_Frontal_Lobe_ReprPCWk
12	2e−01	21 / 468	Mid_Frontal_Lobe_TssF
13	2e−01	75 / 1907	Fetal_TxTrans
14	3e−01	10 / 229	Mid_Frontal_Lobe_TxTrans
15	3e−01	23 / 574	Overlap_fetal_midbrain_TssP
16	3e−01	43 / 1122	Fetal_K9K27me3
17	4e−01	26 / 668	Mid_Frontal_Lobe_Enh
18	4e−01	40 / 1050	Fetal_EnhP
19	4e−01	30 / 786	Fetal_EnhG
20	4e−01	3 / 69	Overlap_fetal_midbrain_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	2 / 22	PanCan_HH_geneset_nanostring
2	0.2	3 / 44	PanCan_TGF−B_geneset_nanostring
3	0.2	1 / 7	GENTLES_modul18
4	0.3	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.3	17 / 401	Lembcke_Colonic Inflammation
6	0.3	1 / 10	GENTLES_modul13
7	0.3	1 / 11	GENTLES_modul17
8	0.4	3 / 61	PanCan_Wnt_geneset_nanostring
9	0.4	1 / 13	BEN−PORATH_UP
10	0.4	1 / 13	GENTLES_modul12
11	0.4	5 / 113	PanCan_Driver_Gene_geneset_nanostring
12	0.4	1 / 15	GENTLES_modul1
13	0.4	2 / 40	ZHANG_MM up
14	0.4	5 / 120	PanCan_CC+Apop_geneset_nanostring
15	0.4	1 / 16	GENTLES_modul14
16	0.5	7 / 180	SPANG_LPS−index2
17	0.5	1 / 20	PanCan_ChromMod_geneset_nanostring
18	0.6	4 / 111	PanCan_RAS_geneset_nanostring
19	0.6	3 / 82	PanCan_TXmisReg_geneset_nanostring
20	0.6	2 / 55	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.005	3 / 10	high−density lipoprotein particle
2	0.005	3 / 10	vacuolar proton−transporting V−type ATPase complex
3	0.008	13 / 169	transcription factor complex
4	0.021	7 / 78	dendritic spine
5	0.021	3 / 17	membrane−bounded vesicle
6	0.037	5 / 52	perikaryon
7	0.047	2 / 10	DNA replication factor A complex
8	0.047	2 / 10	low−density lipoprotein particle
9	0.047	2 / 10	very−low−density lipoprotein particle
10	0.057	2 / 11	Golgi−associated vesicle membrane
11	0.064	3 / 26	basal plasma membrane
12	0.078	5 / 64	Golgi cisterna membrane
13	0.083	3 / 29	heterotrimeric G−protein complex
14	0.087	2 / 14	male germ cell nucleus
15	0.090	35 / 775	extracellular space
16	0.108	4 / 51	collagen trimer
17	0.108	4 / 51	filopodium
18	0.110	2 / 16	anchored component of plasma membrane
19	0.122	2 / 17	cytoplasmic ribonucleoprotein granule
20	0.127	33 / 751	integral component of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.009	37 / 689	Chr 7
2	0.012	40 / 775	Chr 12
3	0.093	17 / 335	Chr 22
4	0.131	26 / 576	Chr 9
5	0.146	13 / 262	Chr 13
6	0.183	24 / 551	Chr X
7	0.188	35 / 838	Chr 3
8	0.327	40 / 1037	Chr 19
9	0.417	37 / 993	Chr 2
10	0.517	1 / 20	Chr CHR_HSCHR6_MHC_QBL_CTG1
11	0.574	24 / 687	Chr 6
12	0.599	19 / 552	Chr 10
13	0.668	51 / 1500	Chr 1
14	0.743	27 / 840	Chr 17
15	0.841	24 / 801	Chr 11
16	0.852	13 / 465	Chr 15
17	0.900	5 / 221	Chr 18
18	0.907	10 / 398	Chr 20
19	0.912	19 / 696	Chr 5
20	0.950	11 / 469	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	64 / 1317	EnhP_Colon
2	0.018	94 / 2142	ReprPC_Colon
3	0.024	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
4	0.031	2 / 8	Boland_CRC−MMR−system
5	0.044	81 / 1889	ReprPCWk_Colon
6	0.048	91 / 2159	TssP_Colon
7	0.062	136 / 3383	EnhWk2_Colon
8	0.070	1 / 2	Budinska_D_Mesenchymal_DOWN
9	0.090	153 / 3897	Quies1_Colon
10	0.094	13 / 242	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
11	0.110	2 / 16	TCGA_Mutated−in−CRC_non−hypermutated
12	0.110	2 / 16	Vilar_non−hypermutated−in−CRC
13	0.134	2 / 18	Ang_CRC−CIMPH−vs−L_hypo
14	0.166	1 / 5	Juehling−MSI−enriched−in−8−to−9
15	0.166	1 / 5	Budinska_A_Surface crypt−like_UP
16	0.175	10 / 199	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
17	0.176	17 / 371	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
18	0.224	2 / 25	Ang_CRC_Hypomethylated
19	0.252	1 / 8	Marisa_CRC−C3
20	0.252	1 / 8	Marisa_CRC−C6

Disease

Rank	p−value	#in/all	Geneset
1	0.4	12 / 294	GUDJ_psoriasis down
2	0.9	11 / 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	0.001	9 / 74	WIRTH_Normal Brain
2	0.010	5 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
3	0.024	2 / 7	WILLSCHER_GBM_LTSwt_proteomics=G_UP
4	0.036	6 / 69	GIEZELT_GBM_STSwt_up_VS_LTSwt
5	0.042	4 / 37	Christensen_hypomethylated_in_secondary_glioblastoma
6	0.051	6 / 75	GIEZELT_GBM_STS_down_VS_LTS
7	0.067	7 / 100	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
8	0.091	6 / 87	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	0.095	5 / 68	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	0.112	3 / 33	Christensen_hypomethylated_in_primary_glioblastoma
11	0.134	2 / 18	Barbus_GBM_STS_vs._LTS
12	0.145	3 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
13	0.198	2 / 23	Donson−Misc immune function−associated with LTS in HGA
14	0.225	4 / 68	GIEZELT_GBM_WT_down_VS_mut
15	0.225	1 / 7	Shaw_up_in_1p19qdel
16	0.246	6 / 118	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	0.252	1 / 8	VERHAAK_PN_Brain
18	0.252	1 / 8	Colman_survival_robust
19	0.271	4 / 74	Christensen_hypermethylated_in_secondary_glioblastoma
20	0.279	1 / 9	Christensen_hypomethylated_in_grade2_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−06	4 / 5	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
2	5e−05	4 / 7	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
3	4e−04	12 / 105	REACTOME_SIGNALING_BY_RHO_GTPASES
4	5e−04	6 / 29	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES
5	9e−04	4 / 13	REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
6	2e−03	5 / 26	RIZ_ERYTHROID_DIFFERENTIATION_HEMGN
7	3e−03	9 / 83	LEIN_CHOROID_PLEXUS_MARKERS
8	3e−03	19 / 264	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
9	4e−03	6 / 42	REACTOME_ION_CHANNEL_TRANSPORT
10	4e−03	6 / 43	KEGG_BASAL_CELL_CARCINOMA
11	4e−03	5 / 31	KEGG_STARCH_AND_SUCROSE_METABOLISM
12	5e−03	4 / 20	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
13	5e−03	14 / 179	NABA_SECRETED_FACTORS
14	6e−03	10 / 111	LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q
15	7e−03	4 / 22	REACTOME_KERATAN_SULFATE_BIOSYNTHESIS
16	7e−03	2 / 4	SHARMA_ASTROCYTOMA_WITH_NF1_SYNDROM
17	8e−03	4 / 23	ABBUD_LIF_SIGNALING_1_DN
18	9e−03	14 / 192	KIM_WT1_TARGETS_12HR_DN
19	1e−02	14 / 195	SHEN_SMARCA2_TARGETS_DN
20	1e−02	4 / 25	MA_PITUITARY_FETAL_VS_ADULT_UP

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 37	HALLMARK_APICAL_SURFACE
2	0.1	4 / 57	HALLMARK_MYC_TARGETS_V2
3	0.2	9 / 170	HALLMARK_ESTROGEN_RESPONSE_LATE
4	0.2	5 / 87	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	0.3	8 / 169	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	0.4	6 / 146	HALLMARK_UV_RESPONSE_UP
7	0.4	6 / 148	HALLMARK_KRAS_SIGNALING_UP
8	0.5	3 / 74	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.5	5 / 137	HALLMARK_UV_RESPONSE_DN
10	0.6	5 / 140	HALLMARK_APOPTOSIS
11	0.6	2 / 53	HALLMARK_TGF_BETA_SIGNALING
12	0.6	6 / 174	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	0.6	6 / 176	HALLMARK_HYPOXIA
14	0.6	1 / 26	HALLMARK_ANGIOGENESIS
15	0.6	6 / 183	HALLMARK_GLYCOLYSIS
16	0.7	1 / 29	HALLMARK_NOTCH_SIGNALING
17	0.7	5 / 167	HALLMARK_APICAL_JUNCTION
18	0.7	5 / 167	HALLMARK_IL2_STAT5_SIGNALING
19	0.7	1 / 36	HALLMARK_WNT_BETA_CATENIN_SIGNALING
20	0.7	3 / 107	HALLMARK_COAGULATION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	4 / 62	DUMEAUX_Smoking enriched genes
2	0.3	1 / 8	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.7	1 / 32	DUMEAUX_Fasting 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 / 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	0.004	5 / 30	Subero_INT_hypo_meth
2	0.006	3 / 11	Subero_T−ALL_hypo_meth
3	0.011	17 / 256	SPANG_IL21 DN
4	0.018	142 / 3396	HOPP_Repressed
5	0.019	4 / 29	Subero_DLBCL_hypo_meth
6	0.047	2 / 10	Shaknovich_ABC_hypo_meth
7	0.058	3 / 25	Subero_T−PLL_hypo_meth
8	0.066	2 / 12	BENTINK_mBL DOWN
9	0.098	2 / 15	WRIGHT_ABC UP
10	0.122	88 / 2188	HOPP_Poised_promoter
11	0.135	1 / 4	Shaknovich_ABC_hyper_meth
12	0.157	5 / 80	Aukema_BCL2 DN_BCL6 UP
13	0.173	4 / 61	SPANG_LPS 6hrs DN
14	0.205	99 / 2563	HOPP_Heterochrom
15	0.252	1 / 8	MASCQUE_ABC UP
16	0.252	1 / 8	YAMANE_AICDA_targets_nonrecruited
17	0.252	1 / 8	Subero_B−CLL_hypo_meth
18	0.267	205 / 5538	HOPP_Weak_txn
19	0.279	12 / 275	TARTE_Mature plasma cell signature
20	0.305	1 / 10	DAVE_BL_DN

MF

Rank	p−value	#in/all	Geneset
1	3e−05	21 / 217	GTPase activator activity
2	3e−03	4 / 18	galactosyltransferase activity
3	5e−03	3 / 10	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane move
4	5e−03	3 / 10	lipid transporter activity
5	6e−03	3 / 11	structural constituent of eye lens
6	1e−02	3 / 14	diacylglycerol kinase activity
7	1e−02	3 / 14	phosphatidylserine binding
8	1e−02	84 / 1859	metal ion binding
9	1e−02	4 / 26	transforming growth factor beta receptor binding
10	1e−02	5 / 41	G−protein coupled receptor binding
11	2e−02	3 / 16	NAD+ kinase activity
12	2e−02	14 / 217	G−protein coupled receptor activity
13	3e−02	4 / 33	estrogen receptor binding
14	3e−02	6 / 66	Rho guanyl−nucleotide exchange factor activity
15	3e−02	4 / 34	calcium−dependent phospholipid binding
16	4e−02	5 / 52	hormone activity
17	4e−02	4 / 37	endonuclease activity
18	5e−02	2 / 10	acetylgalactosaminyltransferase activity
19	5e−02	2 / 10	sodium channel activity
20	5e−02	3 / 24	cation channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	18 / 203	hsa−miR−33a
2	2e−03	15 / 176	hsa−miR−199b−3p
3	3e−03	12 / 132	hsa−miR−199b−5p
4	4e−03	6 / 43	hsa−miR−412
5	6e−03	15 / 203	hsa−miR−545
6	7e−03	21 / 327	hsa−miR−590−3p
7	1e−02	11 / 139	hsa−miR−132
8	1e−02	3 / 14	hsa−miR−147b
9	1e−02	13 / 180	hsa−miR−302e
10	2e−02	10 / 130	hsa−miR−145
11	2e−02	17 / 272	hsa−miR−520b
12	2e−02	13 / 191	hsa−miR−641
13	2e−02	17 / 280	hsa−miR−30c
14	3e−02	7 / 82	hsa−miR−1179
15	3e−02	4 / 33	hsa−miR−934
16	3e−02	12 / 182	hsa−miR−573
17	3e−02	8 / 103	hsa−miR−1284
18	3e−02	16 / 268	hsa−miR−363
19	3e−02	5 / 50	hsa−miR−1201
20	3e−02	16 / 269	hsa−miR−30d

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	GUSTAFSON_PI3K_DN
2	0.4	1 / 15	BENTINK_ras.6
3	1.0	0 / 12	GUSTAFSON_PI3K_UP
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	0.1	2 / 15	NOWICK_TF
2	0.1	48 / 1139	HEBENSTREIT_low expression TF
3	0.2	78 / 2013	ICGC_Bcl11_targets
4	0.3	53 / 1400	ICGC_Myc_targets
5	0.4	25 / 653	ICGC_SrfPcr2_targets
6	0.4	51 / 1383	ICGC_Six5_targets
7	0.5	46 / 1273	ICGC_P300_targets
8	0.5	1 / 19	MYC_Metabolism UP
9	0.7	18 / 553	ICGC_RxraPcr1_targets
10	0.8	43 / 1314	ICGC_Usf1_targets
11	0.8	18 / 595	ICGC_NrsfPcr2_targets
12	0.8	70 / 2136	ICGC_GabpPcr2_targets
13	0.9	134 / 4032	ICGC_Creb1_targets
14	0.9	88 / 2714	ICGC_Irf4_targets
15	0.9	175 / 5219	ICGC_Tcf3_targets
16	0.9	53 / 1701	HEBENSTREIT_high expression TF
17	0.9	1 / 59	MYC_Targets UP
18	0.9	179 / 5374	ICGC_Pax5_targets
19	0.9	58 / 1878	ICGC_Cebpbsc150_targets
20	0.9	19 / 690	ICGC_Atf3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 16	VAQUERIZAS_Pancreas
2	0.1	3 / 36	VAQUERIZAS_Fetal brain
3	0.1	3 / 37	VAQUERIZAS_Thymus
4	0.2	3 / 38	VAQUERIZAS_Whole brain
5	0.2	2 / 23	VAQUERIZAS_Spinal cord
6	0.3	2 / 33	VAQUERIZAS_Prostate
7	0.4	3 / 59	VAQUERIZAS_Whole blood
8	0.4	2 / 38	VAQUERIZAS_Testis
9	0.4	1 / 14	VAQUERIZAS_Ovary
10	0.4	1 / 15	VAQUERIZAS_Fetal thyroid
11	0.4	2 / 41	VAQUERIZAS_Placenta
12	0.4	1 / 16	VAQUERIZAS_Adrenal gland
13	0.4	1 / 16	VAQUERIZAS_Salivary gland
14	0.5	1 / 17	VAQUERIZAS_Pituitary
15	0.6	1 / 23	VAQUERIZAS_Trachea
16	0.6	1 / 23	VAQUERIZAS_Adrenal cortex
17	0.6	1 / 27	VAQUERIZAS_Lymph node
18	0.7	1 / 29	VAQUERIZAS_Fetal lung
19	0.8	4 / 143	VAQUERIZAS_General
20	0.8	1 / 40	VAQUERIZAS_Thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	0.01	21 / 350	WIRTH_Nervous System
2	0.18	3 / 41	WIRTH_Homeostasis
3	0.23	3 / 46	WIRTH_Liver
4	0.32	2 / 32	WIRTH_Pancreas
5	0.33	1 / 11	WIRTH_Prim. lymphoid organs
6	0.33	1 / 11	WIRTH_Globus pallidus
7	0.34	5 / 107	WIRTH_Testis
8	0.39	5 / 114	PALMER_T−Cell signature up
9	0.40	1 / 14	WIRTH_Telencephalon
10	0.60	12 / 350	WIRTH_Immune system
11	0.82	6 / 225	PALMER_Granulocytes signature up
12	0.83	5 / 194	PALMER_B−Cell signature up
13	0.86	2 / 95	WIRTH_Muscle
14	0.93	1 / 74	WIRTH_Mucosa
15	1.00	0 / 11	WIRTH_Sec. lymphoid organs
16	1.00	0 / 13	WIRTH_B−cells
17	1.00	0 / 8	WIRTH_Tonsil
18	1.00	0 / 12	WIRTH_Thymus
19	1.00	0 / 12	WIRTH_Lymphocytes
20	1.00	0 / 5	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	147 / 3682	LU_BPDE 0.005 DN
2	0.58	39 / 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	