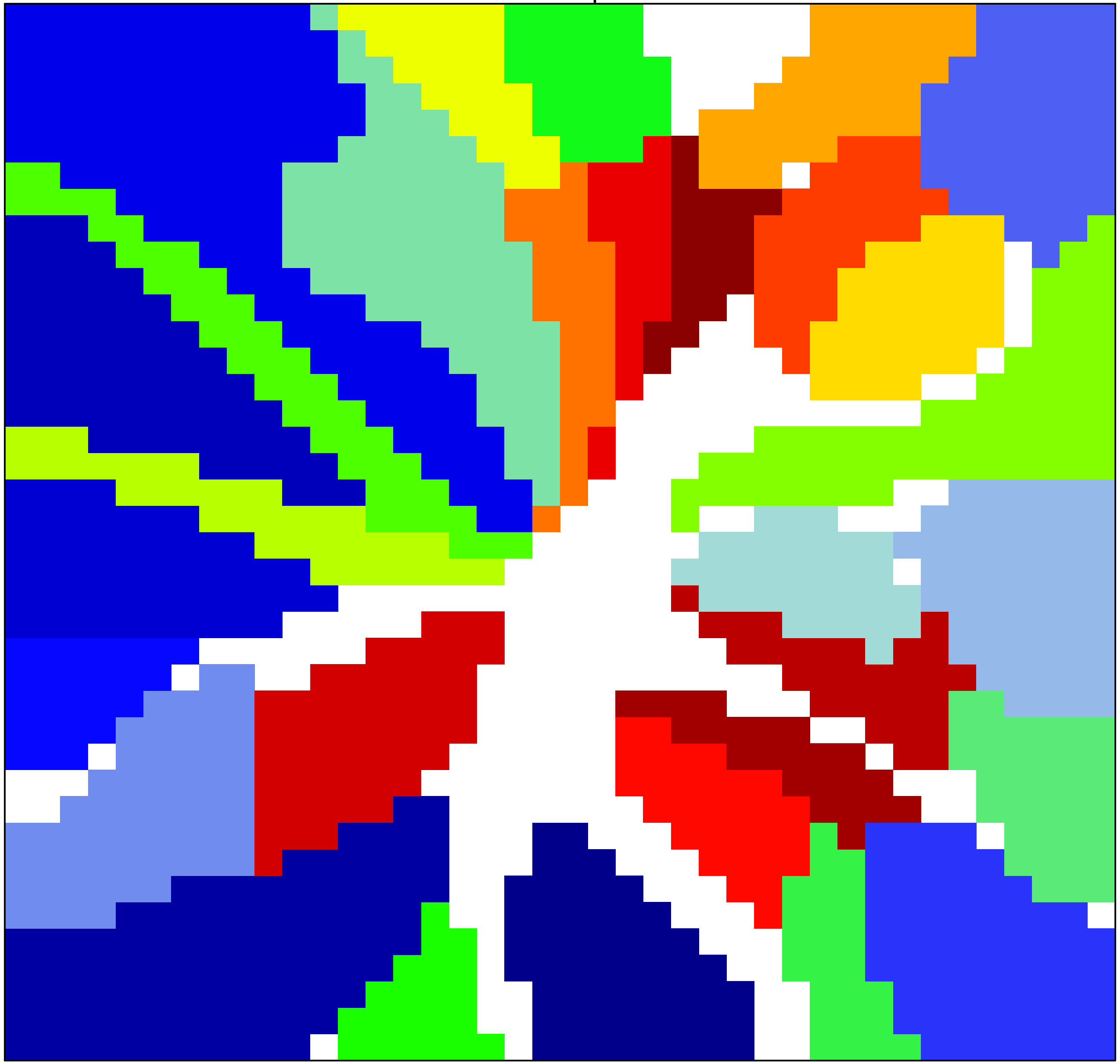
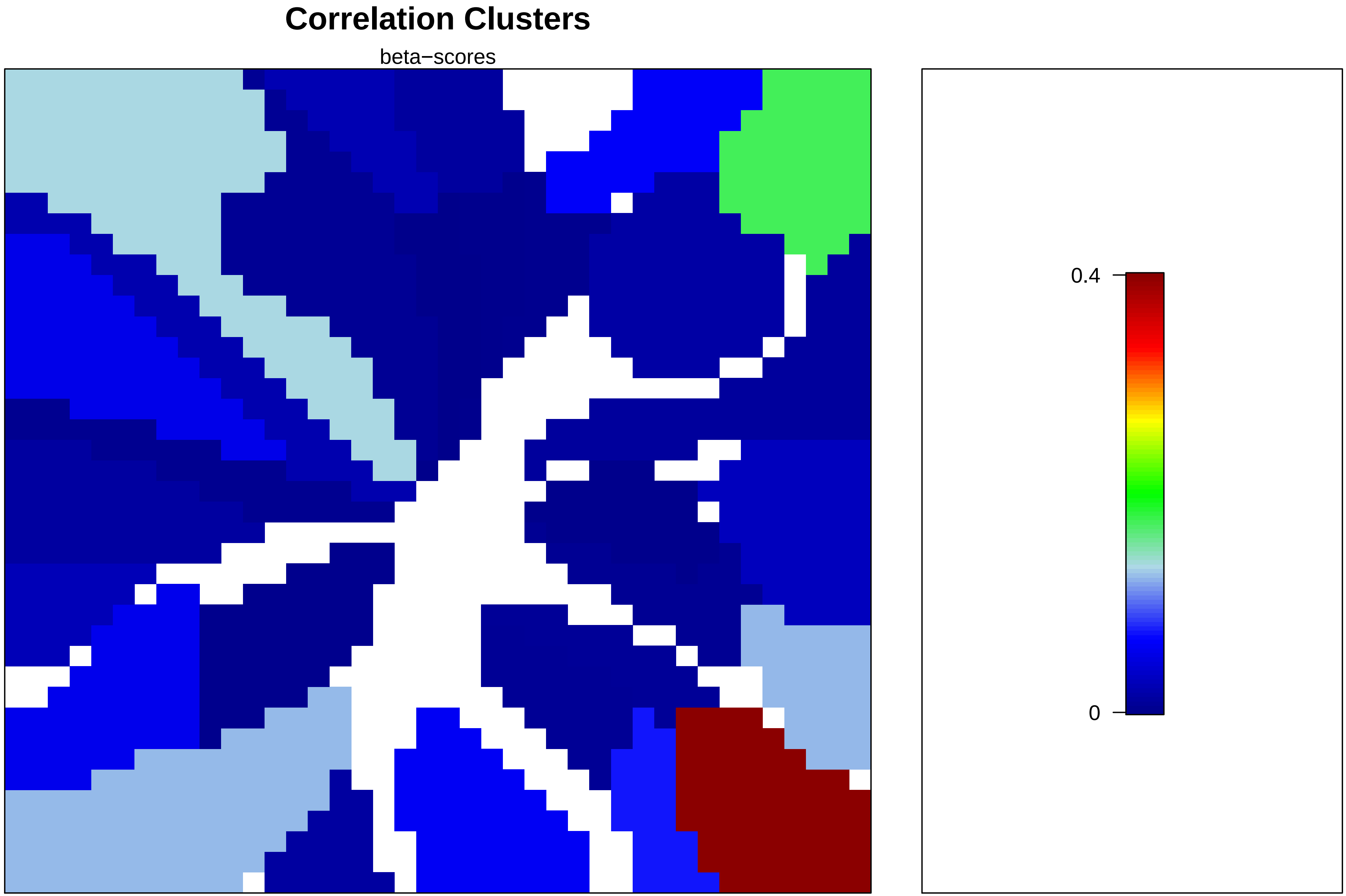
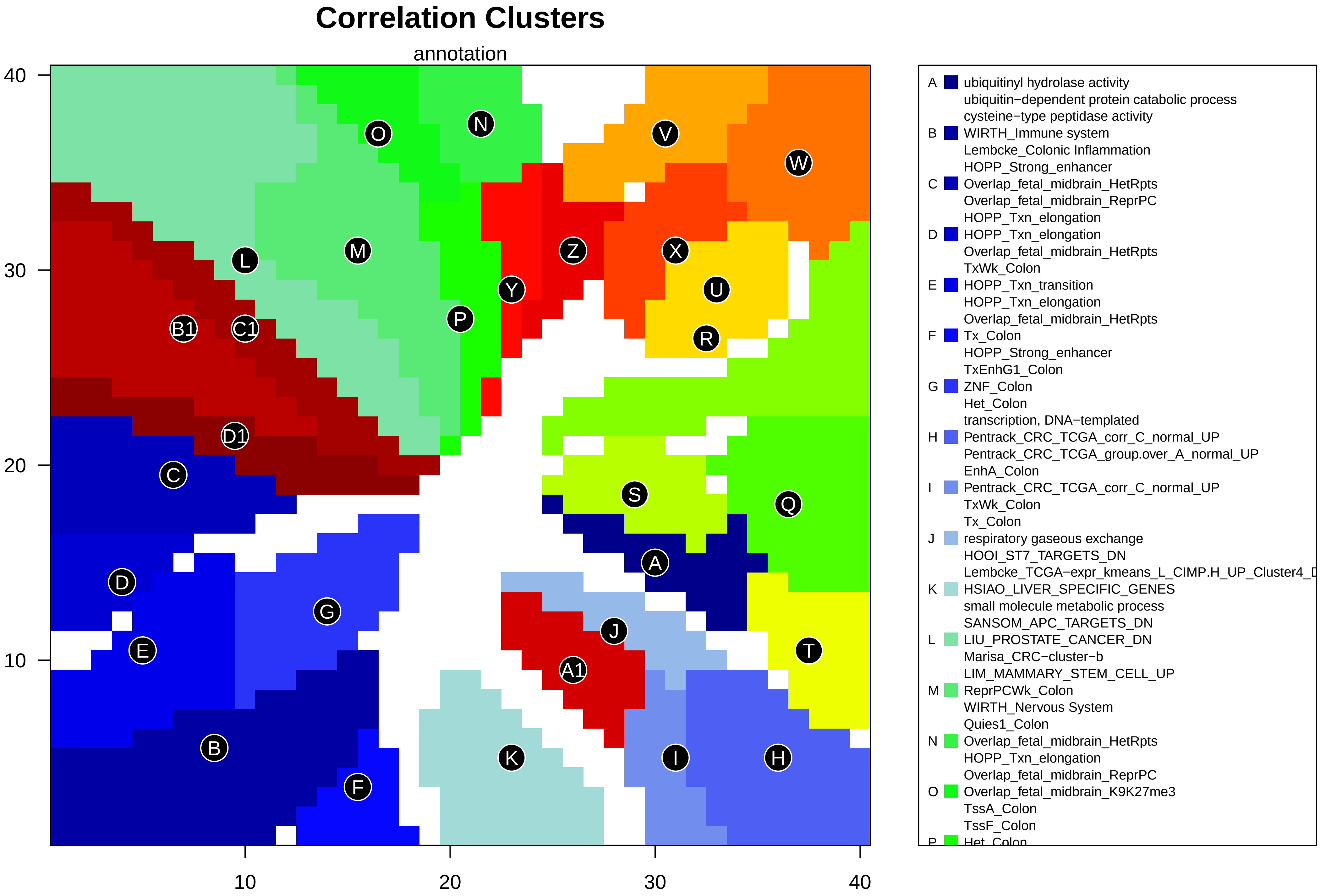
Correlation Clusters

landscape

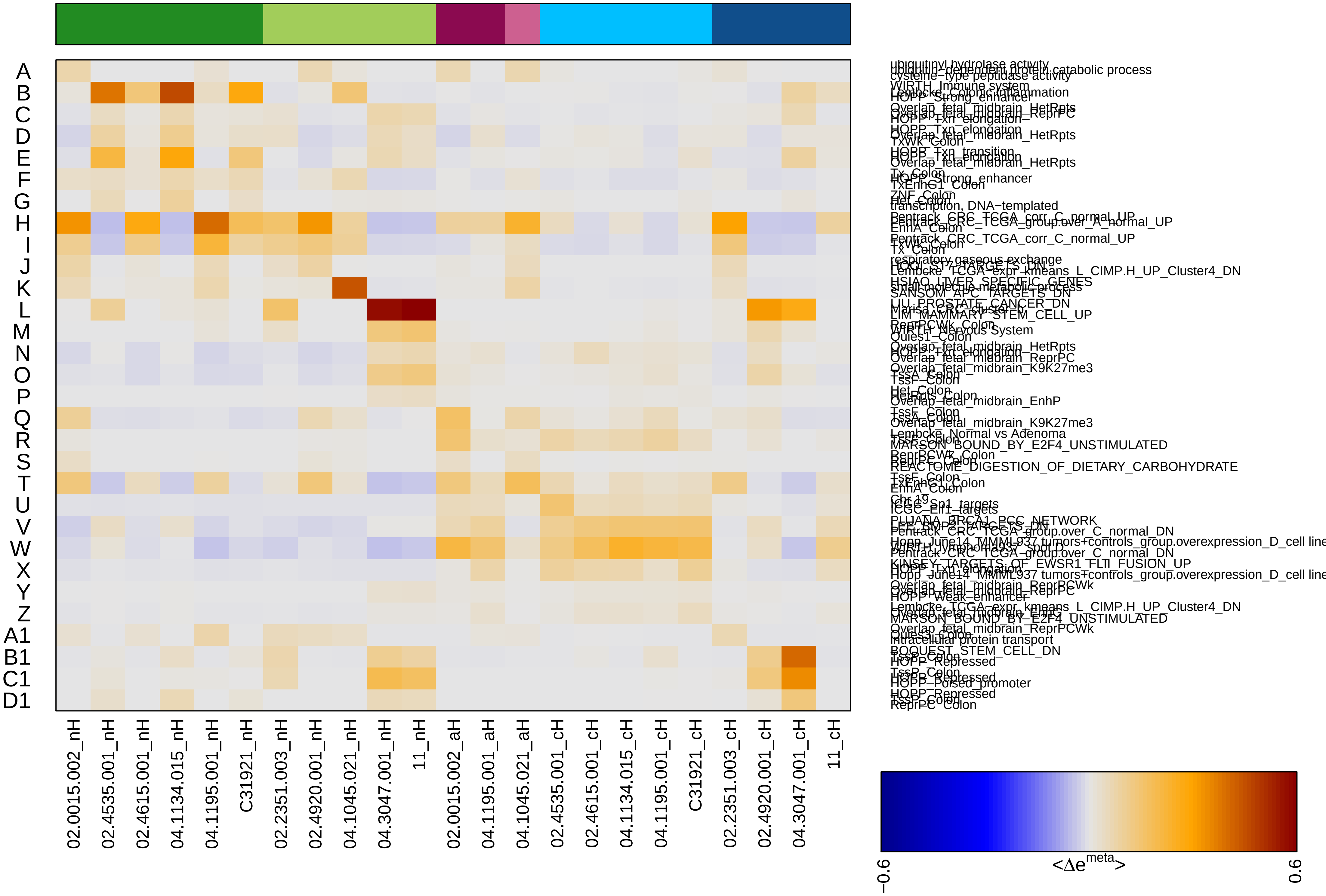



Correlation Clusters
beta−scores
0.4
0



Correlation Clusters

annotation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Z
A1
B1
C1
D1
ubiquitinyl hydrolase activity
ubiquitin−dependent protein catabolic process
cysteine−type peptidase activity
WIRTH_Immune system
Lembcke_Colonic inflammation
HOPP_Strong_enhancer
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
HOPP_Txn_elongation
HOPP_Txn_elongation
Overlap_fetal_midbrain_HetRpts
TxWk_Colon
HOPP_Txn_transition
HOPP_Txn_elongation
Overlap_fetal_midbrain_HetRpts
Tx_Colon
HOPP_Strong_enhancer
TxEnhG1_Colon
ZNF_Colon
Het_Colon
transcription, DNA−templated
Pentrack_CRC_TCGA_corr_C_normal_UP
Pentrack_CRC_TCGA_group.over_A_normal_UP
EnhA_Colon
Pentrack_CRC_TCGA_corr_C_normal_UP
TxWk_Colon
Tx_Colon
respiratory gaseous exchange
HOOI_ST7_TARGETS_DN
Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
HSIAO_LIVER_SPECIFIC_GENES
small molecule metabolic process
SANSOM_APC_TARGETS_DN
LIU_PROSTATE_CANCER_DN
Marisa_CRC_cluster_b
LIM_MAMMARY_STEM_CELL_UP
ReprPCWk_Colon
WIRTH_Nervous System
Quies1_Colon
Overlap_fetal_midbrain_HetRpts
HOPP_Txn_elongation
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
TssA_Colon
TssF_Colon
Het_Colon
HetRpts_Colon
Overlap_fetal_midbrain_EnhP
TssF_Colon
TssA_Colon
Overlap_fetal_midbrain_K9K27me3
Lembcke_Normal vs Adenoma
TssF_Colon
MARSON_BOUND_BY_E2F4_UNSTIMULATED
ReprPCWk_Colon
ReprPC_Colon
REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
TssF_Colon
TxEnhG1_Colon
EnhA_Colon
Chr 19
ICGC−Sp1_targets
ICGC−Elf1−targets
PUJANA_BRCA1_PCC_NETWORK
LEE_BMP2_TARGETS_DN
Pentrack_CRC_TCGA_group.over_C_normal_DN
Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
WIRTH_lymphoma937_spot D
Pentrack_CRC_TCGA_group.over_C_normal_DN
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
HOPP_Txn_elongation
Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
Overlap_fetal_midbrain_ReprPCWk
Overlap_fetal_midbrain_ReprPC
HOPP_Weak_enhancer
Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
Overlap_fetal_midbrain_EnhG
MARSON_BOUND_BY_E2F4_UNSTIMULATED
Overlap_fetal_midbrain_ReprPCWk
Quies3_Colon
intracellular protein transport
BOQUEST_STEM_CELL_DN
TssP_Colon
HOPP_Repressed
TssP_Colon
HOPP_Repressed
HOPP_Poised_promoter
HOPP_Repressed
TssP_Colon
ReprPC_Colon
02.0015.002_nH
02.4535.001_nH
02.4615.001_nH
04.1134.015_nH
04.1195.001_nH
C31921_nH
02.2351.003_nH
02.4920.001_nH
04.1045.021_nH
04.3047.001_nH
11_nH
02.0015.002_aH
04.1195.001_aH
04.1045.021_aH
02.4535.001_cH
02.4615.001_cH
04.1134.015_cH
04.1195.001_cH
C31921_cH
02.2351.003_cH
02.4920.001_cH
04.3047.001_cH
11_cH
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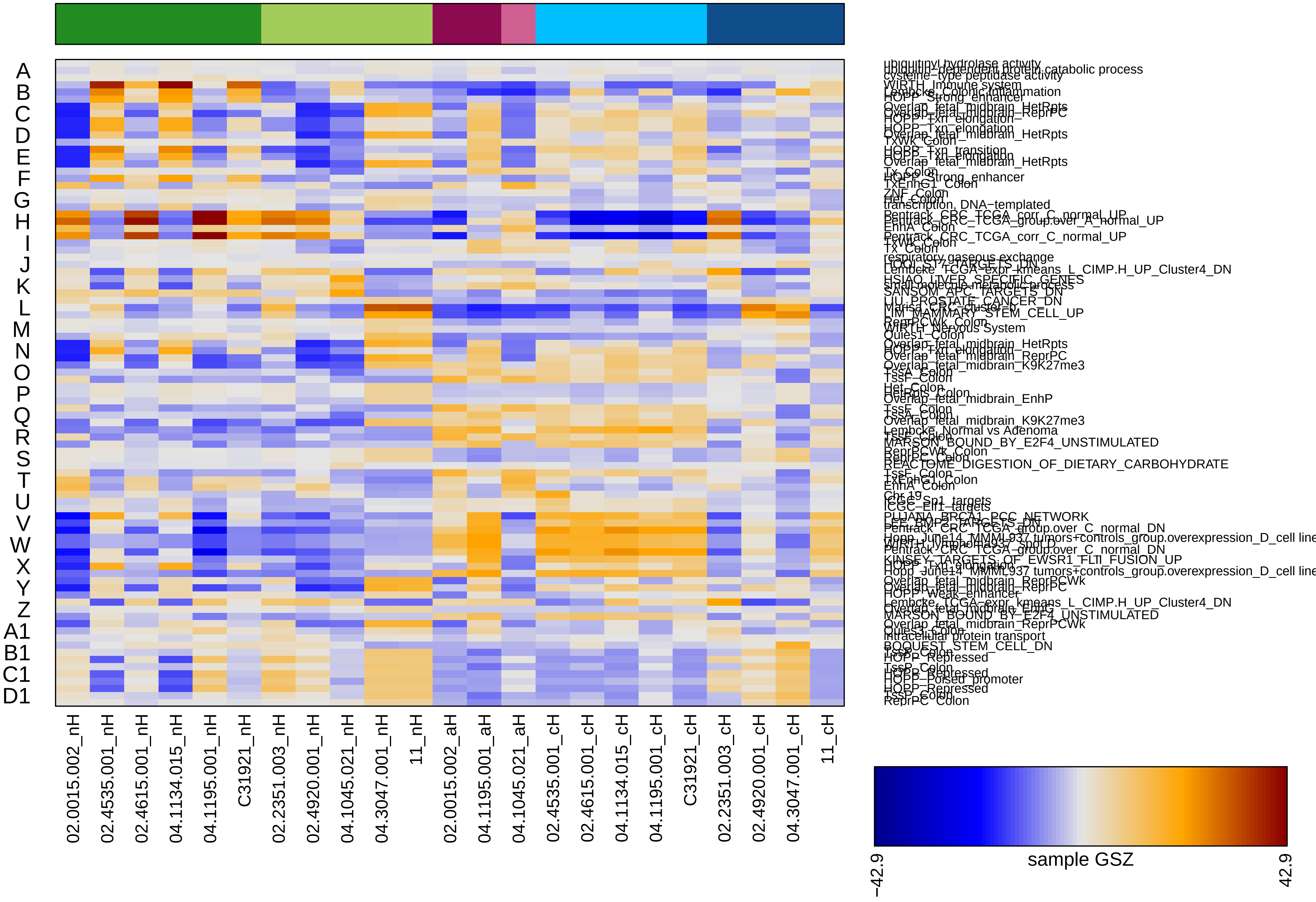
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X
Y
Z
A1
B1
C1
D1
02.0015.002_nH
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02.4615.001_nH
04.1134.015_nH
04.1195.001_nH
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04.1045.021_aH
02.4535.001_cH
02.4615.001_cH
04.1134.015_cH
04.1195.001_cH
C31921_cH
02.2351.003_cH
02.4920.001_cH
04.3047.001_cH
11_cH
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TssF_Colon
Het_Colon
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TssP_Colon
HOPP_Repressed
TssP_Colon
HOPP_Repressed
HOPP_Poised_promoter
HOPP_Repressed
TssP_Colon
ReprPC_Colon
−42.9
sample GSZ
42.9

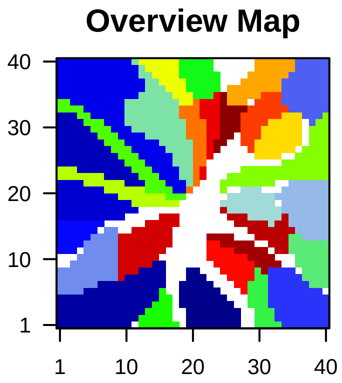
Correlation Clusters

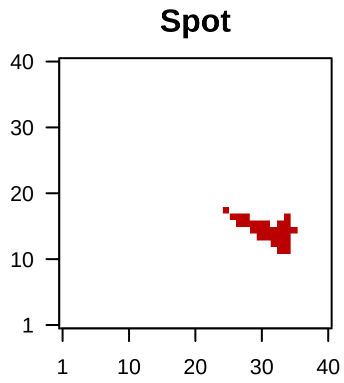
Spot Summary: A

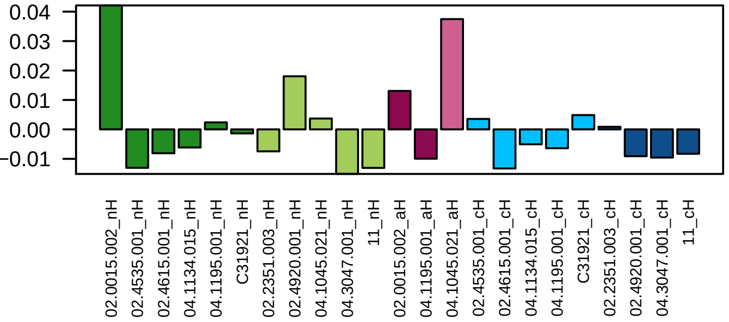
metagenes = 29
genes = 297

<r> metagenes = 0.94
<r> genes = 0.46
beta: r2= 0 / log p= −0.12

samples with spot = 0 (0 %)


Overview Map


Spot

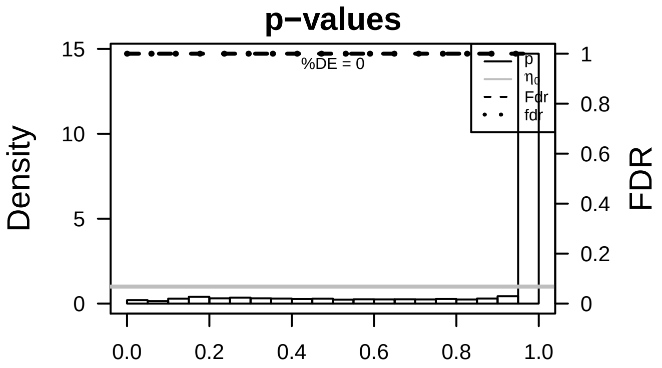


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.34	−0.02	0.56		
2	ENSG000001	0.34	−0.02	0.56	CTAG1B	cancer/testis antigen 1B [Source:HGNC Symbol;Acc:HGNC:2
3	ENSG000002	0.3	−0.02	0.61		long intergenic non−protein coding RNA 955 [Source:HGNC S
4	ENSG000001	0.23	−0.04	0.24	TNNC1	troponin C type 1 (slow) [Source:HGNC Symbol;Acc:HGNC:1
5	ENSG000001	0.23	−0.12	0.57	ME3	malic enzyme 3, NADP(+)−dependent, mitochondrial [Source
6	ENSG000001	0.23	−0.03	0.75	KRT12	keratin 12, type I [Source:HGNC Symbol;Acc:HGNC:6414]
7	ENSG000001	0.18	−0.09	0.63	U2AF1L4	U2 small nuclear RNA auxiliary factor 1−like 4 [Source:HGNC
8	ENSG000002	0.18	−0.15	0.73		WAS protein family homolog 4 pseudogene [Source:HGNC S
9	ENSG000001	0.17	−0.07	0.62	FBXO46	F−box protein 46 [Source:HGNC Symbol;Acc:HGNC:25069]
10	ENSG000001	0.16	−0.05	0.46	OPLAH	5−oxoprolinase (ATP−hydrolysing) [Source:HGNC Symbol;Ac
11	ENSG000001	0.16	−0.08	0.32	ZNF165	zinc finger protein 165 [Source:HGNC Symbol;Acc:HGNC:12
12	ENSG000001	0.16	−0.09	0.52	BMP1	bone morphogenetic protein 1 [Source:HGNC Symbol;Acc:H
13	ENSG000000	0.15	−0.07	0.86	VPS9D1	VPS9 domain containing 1 [Source:HGNC Symbol;Acc:HGN
14	ENSG000001	0.15	−0.05	0.91	ATG4B	autophagy related 4B, cysteine peptidase [Source:HGNC Syr
15	ENSG000001	0.15	−0.05	0.64	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae) [Source:HGNC Sy
16	ENSG000002	0.15	−0.02	0.77	CRYBB2	crystallin, beta B2 [Source:HGNC Symbol;Acc:HGNC:2398]
17	ENSG000002	0.14	−0.08	0.81	CDK11B	cyclin−dependent kinase 11B [Source:HGNC Symbol;Acc:HG
18	ENSG000002	0.14	−0.07	0.75		
19	ENSG000001	0.13	−0.07	0.63	TOE1	target of EGR1, member 1 (nuclear) [Source:HGNC Symbol;A
20	ENSG000002	0.13	−0.03	0.78	GLI4	GLI family zinc finger 4 [Source:HGNC Symbol;Acc:HGNC:43

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−15	16 / 73	MF	ubiquitinyl hydrolase activity
2	1e−08	16 / 185	BP	ubiquitin−dependent protein catabolic process
3	3e−07	9 / 64	MF	cysteine−type peptidase activity
4	3e−06	28 / 735	Chr	Chr 4
5	7e−06	8 / 69	BP	regulation of proteasomal protein catabolic process
6	9e−06	8 / 71	BP	protein deubiquitination
7	1e−05	9 / 97	MF	cysteine−type endopeptidase activity
8	5e−05	8 / 90	MF	ubiquitin−specific protease activity
9	8e−04	3 / 13	GSEA	KRISHNAN_FURIN_TARGETS_DN
10	8e−04	7 / 104	BP	potassium ion transmembrane transport
11	8e−04	36 / 1425	Chr	Chr 19
12	1e−03	6 / 82	GSEA	ZWANG_EGF_INTERVAL_UP
13	2e−03	6 / 91	GSEA	REACTOME_POTASSIUM_CHANNELS
14	3e−03	23 / 842	CC	endoplasmic reticulum
15	3e−03	4 / 41	MF	4 iron, 4 sulfur cluster binding
16	3e−03	5 / 68	BP	protein localization
17	3e−03	8 / 170	BP	proteasome−mediated ubiquitin−dependent protein catabolic process
18	6e−03	22 / 847	Chr	Chr 16
19	7e−03	6 / 115	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
20	7e−03	13 / 407	GSEA	RATTENBACHER_BOUND_BY_CELF1
21	7e−03	32 / 1394	Brain	Mid_Frontal_Lobe_Quies
22	7e−03	44 / 2084	Brain	Mid_Frontal_Lobe_K9K27me3
23	8e−03	6 / 118	GSEA	KEGG_LYSOSOME
24	8e−03	3 / 28	GSEA	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY
25	8e−03	4 / 54	CC	synaptic vesicle membrane
26	9e−03	2 / 10	BP	negative regulation of transcription elongation from RNA polymerase II pror
27	9e−03	2 / 10	BP	regulation of synaptic transmission, GABAergic
28	1e−02	3 / 31	MF	iron−sulfur cluster binding
29	1e−02	3 / 31	GSEA	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
30	1e−02	3 / 32	BP	DNA metabolic process
31	1e−02	3 / 32	GSEA	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM
32	1e−02	5 / 95	BP	potassium ion transport
33	1e−02	2 / 12	BP	embryonic skeletal joint morphogenesis
34	1e−02	2 / 12	MF	MAP kinase tyrosine/serine/threonine phosphatase activity
35	1e−02	6 / 132	MF	ion channel activity
36	1e−02	3 / 35	MF	carboxylic ester hydrolase activity
37	1e−02	9 / 261	GSEA	REACTOME_NEURONAL_SYSTEM
38	1e−02	2 / 13	MF	endodeoxyribonuclease activity
39	1e−02	22 / 917	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
40	2e−02	8 / 219	GSEA	ZWANG_DOWN_BY_2ND_EGF_PULSE


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	2 / 123	HORVATH_aging_genes meth DOWN
2	1.0	0 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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−08	16 / 185	ubiquitin−dependent protein catabolic process
2	7e−06	8 / 69	regulation of proteasomal protein catabolic process
3	9e−06	8 / 71	protein deubiquitination
4	8e−04	7 / 104	potassium ion transmembrane transport
5	3e−03	5 / 68	protein localization
6	3e−03	8 / 170	proteasome−mediated ubiquitin−dependent protein catabolic process
7	9e−03	2 / 10	negative regulation of transcription elongation from RNA polymerase II promo
8	9e−03	2 / 10	regulation of synaptic transmission, GABAergic
9	1e−02	3 / 32	DNA metabolic process
10	1e−02	5 / 95	potassium ion transport
11	1e−02	2 / 12	embryonic skeletal joint morphogenesis
12	2e−02	2 / 14	inner ear receptor stereocilium organization
13	2e−02	7 / 186	visual perception
14	2e−02	2 / 15	DNA methylation involved in gamete generation
15	2e−02	2 / 15	high−density lipoprotein particle remodeling
16	2e−02	2 / 16	positive regulation of mRNA splicing, via spliceosome
17	3e−02	2 / 18	cellular response to nitrogen starvation
18	3e−02	2 / 18	mitochondrial respiratory chain complex I assembly
19	3e−02	2 / 18	reverse cholesterol transport
20	3e−02	2 / 18	tissue homeostasis

Brain

Rank	p−value	#in/all	Geneset
1	0.007	32 / 1394	Mid_Frontal_Lobe_Quies
2	0.007	44 / 2084	Mid_Frontal_Lobe_K9K27me3
3	0.019	54 / 2820	Mid_Frontal_Lobe_HetRpts
4	0.025	35 / 1713	Mid_Frontal_Lobe_ReprPCWk
5	0.068	59 / 3370	Mid_Frontal_Lobe_ZNF
6	0.127	44 / 2549	Fetal_TssF
7	0.278	15 / 865	Mid_Frontal_Lobe_Het
8	0.392	45 / 2956	Fetal_TssA
9	0.395	60 / 3977	Mid_Frontal_Lobe_ReprPC
10	0.548	4 / 268	Mid_Frontal_Lobe_TssA
11	0.585	37 / 2603	Fetal_TxTrans
12	0.650	23 / 1680	Fetal_ReprPCWk
13	0.664	20 / 1478	Overlap_fetal_midbrain_TxTrans
14	0.688	15 / 1137	Fetal_Enh
15	0.789	1 / 106	Overlap_fetal_midbrain_Tx
16	0.808	11 / 939	Fetal_HetRpts
17	0.827	7 / 641	Mid_Frontal_Lobe_EnhP
18	0.845	14 / 1210	Fetal_TssP
19	0.854	2 / 232	Fetal_ReprPC
20	0.857	10 / 910	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	3 / 50	PanCan_DNARepair_geneset_nanostring
2	0.11	2 / 40	PanCan_HK_geneset_nanostring
3	0.12	1 / 9	WANG_ER_DN
4	0.16	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.20	1 / 15	BEN−PORATH_UP
6	0.28	1 / 22	PanCan_ChromMod_geneset_nanostring
7	0.30	1 / 24	PanCan_Notch_geneset_nanostring
8	0.31	2 / 78	PanCan_Wnt_geneset_nanostring
9	0.42	1 / 37	KUIPER_MM good survival
10	0.53	1 / 51	PanCan_TGF−B_geneset_nanostring
11	0.54	2 / 123	PanCan_Driver_Gene_geneset_nanostring
12	0.65	2 / 152	PanCan_MAPK_geneset_nanostring
13	0.76	1 / 97	PanCan_TXmisReg_geneset_nanostring
14	0.79	2 / 198	PanCan_PI3K_geneset_nanostring
15	0.87	1 / 140	PanCan_RAS_geneset_nanostring
16	1.00	1 / 550	Lembcke_Normal vs Adenoma
17	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
18	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
19	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.00	0 / 15	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.003	23 / 842	endoplasmic reticulum
2	0.008	4 / 54	synaptic vesicle membrane
3	0.015	3 / 36	photoreceptor connecting cilium
4	0.022	2 / 16	synaptic membrane
5	0.028	2 / 18	exocyst
6	0.034	2 / 20	high−density lipoprotein particle
7	0.034	4 / 84	voltage−gated potassium channel complex
8	0.037	2 / 21	M band
9	0.044	2 / 23	membrane−bounded vesicle
10	0.074	3 / 67	acrosomal vesicle
11	0.076	17 / 799	nucleolus
12	0.101	2 / 37	microtubule associated complex
13	0.105	2 / 38	photoreceptor inner segment
14	0.115	2 / 40	myofibril
15	0.130	3 / 86	extrinsic component of membrane
16	0.136	1 / 10	beta−catenin destruction complex
17	0.136	1 / 10	striated muscle thin filament
18	0.149	1 / 11	P granule
19	0.149	2 / 47	axon terminus
20	0.154	2 / 48	lateral plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	3e−06	28 / 735	Chr 4
2	8e−04	36 / 1425	Chr 19
3	6e−03	22 / 847	Chr 16
4	4e−02	9 / 318	Chr 13
5	1e−01	21 / 1083	Chr 17
6	3e−01	20 / 1172	Chr 11
7	3e−01	11 / 613	Chr 14
8	3e−01	8 / 436	Chr 22
9	3e−01	11 / 651	Chr 8
10	5e−01	11 / 746	Chr X
11	5e−01	3 / 191	Chr 21
12	7e−01	26 / 1920	Chr 1
13	9e−01	8 / 745	Chr 9
14	9e−01	5 / 522	Chr 20
15	9e−01	5 / 582	Chr 15
16	9e−01	10 / 1017	Chr 12
17	9e−01	8 / 862	Chr 5
18	9e−01	10 / 1043	Chr 3
19	1e+00	6 / 715	Chr 10
20	1e+00	11 / 1228	Chr 2

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.08	16 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
2	0.10	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
3	0.14	1 / 10	Juehling_HNPCC−mutated−in−5
4	0.16	52 / 3122	TxEnhG1_Colon
5	0.16	1 / 12	KIM_MSI−in−CRC
6	0.20	1 / 15	TCGA_Mutated−in−CRC_hypermutated
7	0.27	8 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	0.30	2 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
9	0.33	11 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	0.41	10 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	0.45	18 / 1178	ZNF_Colon
12	0.50	86 / 5889	EnhWk1_Colon
13	0.54	45 / 3112	EnhA_Colon
14	0.57	117 / 8123	TssF_Colon
15	0.58	29 / 2041	EnhP_Colon
16	0.59	1 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
17	0.63	12 / 877	TxEnhG2_Colon
18	0.63	96 / 6761	TssD2_Colon
19	0.66	3 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
20	0.67	1 / 76	Marisa_CRC−cluster−g

Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 37	BCHETNIA_EBM−DM up
2	0.8	4 / 399	GUDJ_psoriasis down
3	1.0	1 / 608	GUDJ_psoriasis up
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	22 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
2	0.02	2 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
3	0.20	2 / 56	mature astrocytes
4	0.21	3 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
5	0.21	1 / 16	VERHAAK_CL subtype
6	0.27	2 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	0.33	2 / 81	Weller_LGG_gradeII−vs−III_UP
8	0.37	47 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
9	0.46	23 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	0.52	1 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
11	0.53	1 / 52	OL vs. OPC
12	0.55	1 / 55	Gorovets_LGG_PG_subclass
13	0.56	5 / 344	Up
14	0.57	1 / 58	OL vs. MOG− OL
15	0.58	1 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
16	0.59	1 / 61	in vivo astrocytes vs. cultured astroglia
17	0.60	1 / 63	OPC
18	0.62	12 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
19	0.64	1 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
20	0.67	6 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−04	3 / 13	KRISHNAN_FURIN_TARGETS_DN
2	1e−03	6 / 82	ZWANG_EGF_INTERVAL_UP
3	2e−03	6 / 91	REACTOME_POTASSIUM_CHANNELS
4	7e−03	6 / 115	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
5	7e−03	13 / 407	RATTENBACHER_BOUND_BY_CELF1
6	8e−03	6 / 118	KEGG_LYSOSOME
7	8e−03	3 / 28	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY
8	1e−02	3 / 31	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
9	1e−02	3 / 32	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM
10	1e−02	9 / 261	REACTOME_NEURONAL_SYSTEM
11	2e−02	8 / 219	ZWANG_DOWN_BY_2ND_EGF_PULSE
12	2e−02	10 / 322	PURBEY_TARGETS_OF_CTBP1_NOT_SATB1_UP
13	2e−02	2 / 17	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1
14	2e−02	2 / 17	GRATIAS_RETINOBLASTOMA_16Q24
15	2e−02	2 / 17	KANG_AR_TARGETS_UP
16	3e−02	3 / 46	PID_LKB1_PATHWAY
17	3e−02	2 / 19	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP
18	3e−02	9 / 301	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
19	3e−02	3 / 48	KEGG_MTOR_SIGNALING_PATHWAY
20	4e−02	3 / 50	SU_LIVER

HM

Rank	p−value	#in/all	Geneset
1	0.4	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
2	0.5	3 / 193	HALLMARK_KRAS_SIGNALING_DN
3	0.5	3 / 195	HALLMARK_MYOGENESIS
4	0.6	2 / 128	HALLMARK_SPERMATOGENESIS
5	0.6	2 / 146	HALLMARK_DNA_REPAIR
6	0.6	1 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	0.7	2 / 181	HALLMARK_ALLOGRAFT_REJECTION
8	0.8	2 / 190	HALLMARK_APICAL_JUNCTION
9	0.8	2 / 193	HALLMARK_XENOBIOTIC_METABOLISM
10	0.8	2 / 194	HALLMARK_INFLAMMATORY_RESPONSE
11	0.8	1 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.8	2 / 196	HALLMARK_MITOTIC_SPINDLE
13	0.8	2 / 196	HALLMARK_P53_PATHWAY
14	0.8	2 / 198	HALLMARK_HYPOXIA
15	0.8	2 / 198	HALLMARK_GLYCOLYSIS
16	0.8	2 / 199	HALLMARK_MTORC1_SIGNALING
17	0.8	1 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
18	0.8	1 / 112	HALLMARK_BILE_ACID_METABOLISM
19	0.9	1 / 132	HALLMARK_COAGULATION
20	0.9	1 / 140	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	2 / 91	DUMEAUX_Smoking enriched genes
2	1.0	0 / 11	DUMEAUX_Smoking literature genes up
3	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	Shaknovich_ABC_hypo_meth
2	0.4	1 / 35	Subero_T−PLL_hypo_meth
3	0.4	1 / 38	TARTE_B−cell signature
4	0.4	3 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
5	0.5	3 / 171	WIRTH_lymphoma937_spot C
6	0.5	7 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC−
7	0.5	7 / 458	WIRTH_lymphoma937_spot I
8	0.5	39 / 2658	HOPP_Repetitive
9	0.6	1 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
10	0.7	1 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_G
11	0.7	1 / 75	WIRTH_lymphoma937_spot IM
12	0.7	6 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
13	0.7	4 / 347	WIRTH_lymphoma937_spot H
14	0.7	17 / 1333	SPANG_BCR UP
15	0.8	1 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
16	0.9	1 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
17	0.9	3 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
18	0.9	4 / 500	WIRTH_lymphoma937_spot J
19	0.9	2 / 304	ZHANG_DLBCL mutated
20	0.9	3 / 414	TARTE_Mature plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	6e−15	16 / 73	ubiquitinyl hydrolase activity
2	3e−07	9 / 64	cysteine−type peptidase activity
3	1e−05	9 / 97	cysteine−type endopeptidase activity
4	5e−05	8 / 90	ubiquitin−specific protease activity
5	3e−03	4 / 41	4 iron, 4 sulfur cluster binding
6	1e−02	3 / 31	iron−sulfur cluster binding
7	1e−02	2 / 12	MAP kinase tyrosine/serine/threonine phosphatase activity
8	1e−02	6 / 132	ion channel activity
9	1e−02	3 / 35	carboxylic ester hydrolase activity
10	1e−02	2 / 13	endodeoxyribonuclease activity
11	2e−02	4 / 69	beta−catenin binding
12	2e−02	3 / 39	phosphoprotein binding
13	2e−02	3 / 40	potassium channel activity
14	2e−02	3 / 41	protein self−association
15	2e−02	3 / 43	oxygen binding
16	3e−02	2 / 19	structural constituent of eye lens
17	4e−02	2 / 21	oxidoreductase activity, acting on paired donors, with incorporation or reductio
18	4e−02	3 / 51	pyridoxal phosphate binding
19	4e−02	2 / 22	ribonucleoprotein complex binding
20	4e−02	2 / 22	steroid hydroxylase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	2 / 59	hsa−miR−665
2	0.2	1 / 17	hsa−miR−1298
3	0.2	4 / 170	hsa−miR−137
4	0.3	2 / 68	hsa−miR−637
5	0.3	1 / 22	hsa−miR−1288
6	0.3	1 / 23	hsa−miR−596
7	0.3	2 / 73	hsa−miR−361−3p
8	0.3	1 / 26	hsa−miR−943
9	0.3	1 / 27	hsa−miR−483−3p
10	0.3	1 / 27	hsa−miR−337−5p
11	0.4	1 / 30	hsa−miR−486−5p
12	0.4	2 / 86	hsa−miR−567
13	0.4	3 / 148	hsa−miR−24
14	0.4	3 / 150	hsa−miR−491−5p
15	0.4	1 / 32	hsa−miR−1237
16	0.4	2 / 91	hsa−miR−10a
17	0.4	1 / 34	hsa−miR−555
18	0.4	2 / 93	hsa−miR−10b
19	0.4	1 / 38	hsa−miR−1269
20	0.5	2 / 106	hsa−miR−210

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.1	41 / 2342	ICGC_GabpPcr2_targets
2	0.5	32 / 2149	ICGC_Mef2_targets
3	0.5	66 / 4566	ICGC_Egr1_targets
4	0.6	11 / 766	ICGC_Atf3_targets
5	0.6	40 / 2827	ICGC_Bcl3_targets
6	0.6	33 / 2354	ICGC_SrfV0416101_targets
7	0.6	10 / 731	ICGC_SrfPcr2_targets
8	0.7	24 / 1798	HEBENSTREIT_low expression TF
9	0.8	9 / 745	ICGC_NrsfPcr2_targets
10	0.8	82 / 6005	ICGC_Mta3_targets
11	0.8	42 / 3177	ICGC_Irf4_targets
12	0.8	7 / 619	ICGC_RxraPcr1_targets
13	0.8	19 / 1547	ICGC_Ets1_targets
14	0.8	58 / 4436	ICGC_Zeb1_targets
15	0.8	55 / 4230	ICGC_Nfatc1_targets
16	0.8	45 / 3511	ICGC_Rad21_targets
17	0.9	73 / 5526	ICGC_Pmlsc71910_targets
18	0.9	68 / 5173	ICGC_Taf1_targets
19	0.9	73 / 5578	ICGC_Stat5_targets
20	0.9	91 / 6862	ICGC_Elf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.4	1 / 33	VAQUERIZAS_Liver
2	0.6	1 / 67	VAQUERIZAS_Whole blood
3	0.7	2 / 155	VAQUERIZAS_General
4	1.0	0 / 41	VAQUERIZAS_Fetal brain
5	1.0	0 / 45	VAQUERIZAS_Placenta
6	1.0	0 / 37	VAQUERIZAS_Prostate
7	1.0	0 / 30	VAQUERIZAS_Smooth muscle
8	1.0	0 / 49	VAQUERIZAS_Uterus
9	1.0	0 / 12	VAQUERIZAS_Kidney
10	1.0	0 / 25	VAQUERIZAS_Spinal cord
11	1.0	0 / 46	VAQUERIZAS_Whole brain
12	1.0	0 / 42	VAQUERIZAS_Thymus
13	1.0	0 / 42	VAQUERIZAS_Thyroid
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 31	VAQUERIZAS_Fetal lung
16	1.0	0 / 64	VAQUERIZAS_Lung
17	1.0	0 / 18	VAQUERIZAS_Pancreas
18	1.0	0 / 24	VAQUERIZAS_Trachea
19	1.0	0 / 16	VAQUERIZAS_Fetal liver
20	1.0	0 / 22	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 47	WIRTH_Placenta
2	0.1	4 / 141	WIRTH_Muscle
3	0.3	2 / 82	WIRTH_Homeostasis
4	0.3	4 / 202	WIRTH_Testis
5	0.4	1 / 30	PALMER_Lymphocytes signature up
6	0.5	2 / 115	WIRTH_Liver
7	0.5	1 / 54	WIRTH_Pancreas
8	0.9	1 / 137	WIRTH_Mucosa
9	0.9	2 / 259	PALMER_Granulocytes signature up
10	0.9	4 / 476	WIRTH_Nervous System
11	1.0	1 / 208	PALMER_B−Cell signature up
12	1.0	2 / 427	WIRTH_Immune system
13	1.0	0 / 6	WIRTH_Pituitary gland
14	1.0	0 / 13	WIRTH_Sec. lymphoid organs
15	1.0	0 / 13	WIRTH_Prim. lymphoid organs
16	1.0	0 / 14	WIRTH_B−cells
17	1.0	0 / 12	WIRTH_Tonsil
18	1.0	0 / 14	WIRTH_Thymus
19	1.0	0 / 12	WIRTH_Lymphocytes
20	1.0	0 / 14	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	15 / 1343	LU_BPDE 1h DN
2	1.0	57 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

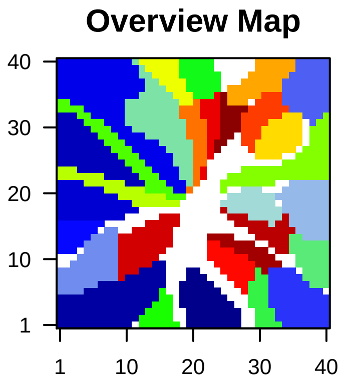
Spot Summary: B

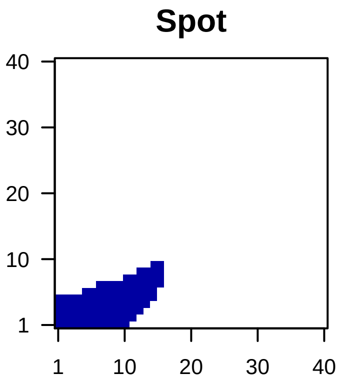
metagenes = 98
genes = 1094

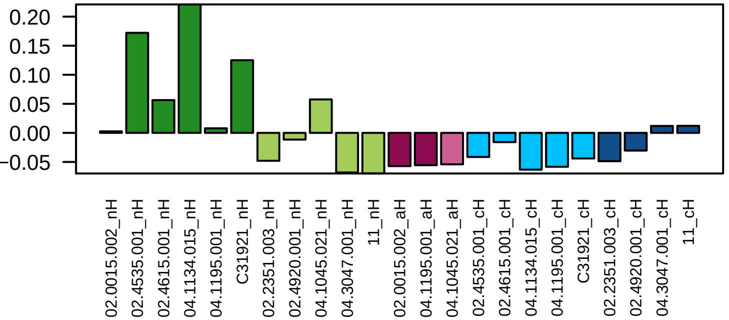
<r> metagenes = 0.95

beta: r2= 0.11 / log p= −0.91

samples with spot = 5 (21.7 %)
MLH1_normHNPCC : 4 (66.7 %)
other_normHNPCC : 1 (20 %)





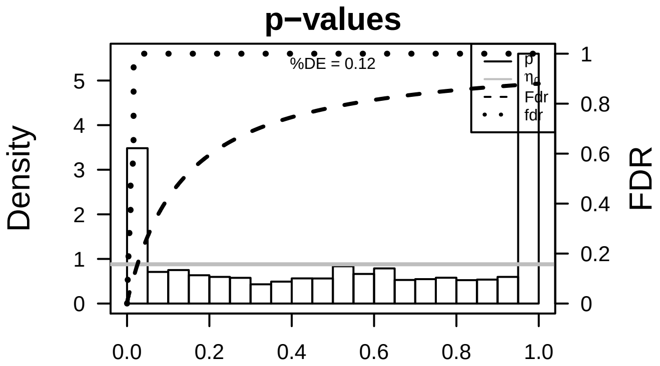


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.4	−0.53	0.81	FDCSP	follicular dendritic cell secreted protein [Source:HGNC Symb
2	ENSG000001	1.34	−0.7	0.88	CCL21	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
3	ENSG000001	1.14	−0.59	0.92	CCL19	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
4	ENSG000001	1.14	−0.52	0.91	CXCL13	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
5	ENSG000002	1.11	−0.68	0.47	UBD	ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
6	ENSG000001	1.01	−0.54	0.93	CD52	CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
7	ENSG000001	0.95	−0.25	0.92	CR2	complement component (3d/Epstein Barr virus) receptor 2 [S
8	ENSG000002	0.95	−0.72	0.5		MT−RNR2−like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
9	ENSG000001	0.93	−0.22	0.99	CCR7	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
10	ENSG000001	0.89	−0.51	0.93	CXCR4	chemokine (C−X−C motif) receptor 4 [Source:HGNC Symbol;
11	ENSG000001	0.85	−0.35	0.96	LCP1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
12	ENSG000002	0.85	−0.8	0.45		MT−RNR2−like 9 [Source:HGNC Symbol;Acc:HGNC:37166]
13	ENSG000001	0.85	−0.2	0.93	IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
14	ENSG000001	0.84	−0.29	0.96	MS4A1	membrane−spanning 4−domains, subfamily A, member 1 [So
15	ENSG000001	0.83	−0.25	0.95	GIMAP7	GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:
16	ENSG000001	0.82	−0.25	0.94	ETS1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
17	ENSG000001	0.82	−0.39	0.91	CD79A	CD79a molecule, immunoglobulin−associated alpha [Source:
18	ENSG000001	0.81	−0.24	0.98	FCMR	Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HG
19	ENSG000000	0.8	−0.2	0.98	PTPRC	protein tyrosine phosphatase, receptor type, C [Source:HGN
20	ENSG000001	0.79	−0.35	0.97	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	237 / 427	Tissu	WIRTH_Immune system
2	1e−99	226 / 574	Canc	Lembcke_Colonic Inflammation
3	1e−99	781 / 7592	Lymp	HOPP_Strong_enhancer
4	1e−99	393 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
5	1e−99	182 / 436	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	6e−84	124 / 263	GSE	WALLACE_PROSTATE_CANCER_RACE_UP
7	4e−77	99 / 175	GSE	LEE_DIFFERENTIATING_T_LYMPHOCYTE
8	5e−61	101 / 246	GSE	QI_PLASMACYTOMA_UP
9	3e−59	116 / 343	BP	immune response
10	3e−53	552 / 5643	Lymp	HOPP_Txn_transition
11	3e−52	122 / 435	GSE	RODWELL_AGING_KIDNEY_UP
12	4e−52	95 / 259	GSE	POOLA_INVASIVE_BREAST_CANCER_UP
13	3e−51	222 / 1340	GSE	PUJANA_ATM_PCC_NETWORK
14	6e−51	87 / 220	GSE	MCLACHLAN_DENTAL_CARIES_UP
15	4e−50	203 / 1165	GSE	CHEN_METABOLIC_SYNDROM_NETWORK
16	1e−48	123 / 473	GSE	ZHENG_BOUND_BY_FOXP3
17	9e−46	75 / 181	HM	HALLMARK_ALLOGRAFT_REJECTION
18	1e−44	159 / 823	GSE	REACTOME_IMMUNE_SYSTEM
19	4e−43	89 / 279	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
20	1e−42	77 / 208	Tissu	PALMER_B−Cell signature up
21	2e−41	77 / 215	GSE	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
22	2e−40	75 / 210	GSE	MCLACHLAN_DENTAL_CARIES_DN
23	9e−40	50 / 87	GSE	BASSO_CD40_SIGNALING_UP
24	1e−39	95 / 347	Lymp	WIRTH_lymphoma937_spot H
25	1e−39	291 / 2401	TF	ICGC_Bcl11_targets
26	2e−39	117 / 522	GSE	SMID_BREAST_CANCER_LUMINAL_B_DN
27	2e−38	92 / 336	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−
28	1e−37	186 / 1215	Lymp	SPANG_BCR DN
29	2e−37	56 / 122	BP	adaptive immune response
30	2e−36	89 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
31	2e−35	83 / 297	GSE	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
32	2e−34	57 / 140	Tissu	PALMER_T−Cell signature up
33	4e−34	130 / 707	BP	innate immune response
34	2e−33	57 / 145	Lymp	WIRTH_lymphoma937_spot F
35	2e−33	57 / 145	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_t
36	4e−32	65 / 201	CC	external side of plasma membrane
37	9e−32	45 / 92	BP	T cell receptor signaling pathway
38	1e−30	34 / 51	GSE	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
39	7e−30	37 / 64	BP	T cell costimulation
40	1e−29	85 / 368	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_2B



Aging

Rank	p−value	#in/all	Geneset
1	0.6	3 / 57	TESCHENDORFF_age_hypermethylated
2	0.7	6 / 123	HORVATH_aging_genes meth DOWN
3	0.7	7 / 144	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−59	116 / 343	immune response
2	2e−37	56 / 122	adaptive immune response
3	4e−34	130 / 707	innate immune response
4	9e−32	45 / 92	T cell receptor signaling pathway
5	7e−30	37 / 64	T cell costimulation
6	1e−27	77 / 326	inflammatory response
7	1e−25	37 / 78	regulation of immune response
8	1e−23	29 / 50	T cell activation
9	8e−23	23 / 31	B cell receptor signaling pathway
10	3e−22	33 / 73	interferon−gamma−mediated signaling pathway
11	7e−22	159 / 1279	signal transduction
12	5e−21	61 / 270	cytokine−mediated signaling pathway
13	3e−19	28 / 61	antigen processing and presentation
14	2e−17	25 / 54	positive regulation of T cell proliferation
15	4e−16	51 / 246	cell surface receptor signaling pathway
16	3e−15	19 / 35	T cell differentiation
17	2e−14	11 / 11	antigen processing and presentation of peptide or polysaccharide antigen via
18	5e−14	32 / 118	transmembrane receptor protein tyrosine kinase signaling pathway
19	3e−13	16 / 29	B cell activation
20	1e−12	66 / 451	positive regulation of GTPase activity

Brain

Rank	p−value	#in/all	Geneset
1	8e−11	311 / 3977	Mid_Frontal_Lobe_ReprPC
2	6e−10	169 / 1890	Overlap_fetal_midbrain_TssF
3	2e−07	206 / 2603	Fetal_TxTrans
4	2e−07	171 / 2084	Mid_Frontal_Lobe_K9K27me3
5	3e−06	141 / 1713	Mid_Frontal_Lobe_ReprPCWk
6	9e−06	117 / 1394	Mid_Frontal_Lobe_Quies
7	1e−04	117 / 1478	Overlap_fetal_midbrain_TxTrans
8	4e−04	182 / 2549	Fetal_TssF
9	3e−03	84 / 1108	Overlap_fetal_midbrain_TssA
10	5e−03	198 / 2956	Fetal_TssA
11	7e−03	13 / 106	Overlap_fetal_midbrain_Tx
12	7e−03	29 / 317	Mid_Frontal_Lobe_Tx
13	8e−03	88 / 1210	Fetal_TssP
14	1e−02	95 / 1327	Mid_Frontal_Lobe_TssP
15	1e−02	44 / 552	Fetal_Tx
16	2e−02	60 / 805	Mid_Frontal_Lobe_EnhG
17	3e−02	67 / 940	Mid_Frontal_Lobe_Enh
18	4e−02	60 / 840	Mid_Frontal_Lobe_TssF
19	2e−01	19 / 268	Mid_Frontal_Lobe_TssA
20	2e−01	71 / 1137	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	226 / 574	Lembcke_Colonic Inflammation
2	8e−28	77 / 324	SPANG_BCL6−index2
3	6e−11	11 / 16	GENTLES_modul18
4	8e−09	33 / 191	SPANG_LPS−index2
5	9e−07	8 / 16	GENTLES_modul11
6	4e−06	7 / 14	GENTLES_modul12
7	2e−05	16 / 86	PanCan_JAK−ST_geneset_nanostring
8	2e−04	18 / 123	PanCan_Driver_Gene_geneset_nanostring
9	1e−03	5 / 16	GENTLES_modul14
10	3e−03	3 / 6	ZHANG_MGUS up
11	4e−03	16 / 136	PanCan_CC+Apop_geneset_nanostring
12	8e−03	12 / 97	PanCan_TXmisReg_geneset_nanostring
13	9e−03	20 / 198	PanCan_PI3K_geneset_nanostring
14	1e−02	16 / 152	PanCan_MAPK_geneset_nanostring
15	1e−02	15 / 140	PanCan_RAS_geneset_nanostring
16	7e−02	8 / 78	PanCan_Wnt_geneset_nanostring
17	2e−01	3 / 24	PanCan_Notch_geneset_nanostring
18	2e−01	2 / 16	WANG_ER_UP
19	4e−01	1 / 15	LIU_BREAST_CANCER
20	5e−01	2 / 28	PanCan_HH_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	4e−32	65 / 201	external side of plasma membrane
2	1e−25	336 / 3507	plasma membrane
3	1e−20	16 / 16	MHC class II protein complex
4	5e−15	13 / 15	T cell receptor complex
5	5e−14	136 / 1250	integral component of plasma membrane
6	8e−13	22 / 61	extrinsic component of cytoplasmic side of plasma membrane
7	1e−11	70 / 523	cell surface
8	1e−10	251 / 3059	membrane
9	4e−10	12 / 22	integral component of lumenal side of endoplasmic reticulum membrane
10	6e−10	14 / 32	immunological synapse
11	3e−09	239 / 2974	cytosol
12	3e−08	13 / 35	ER to Golgi transport vesicle membrane
13	6e−08	10 / 21	mast cell granule
14	4e−06	26 / 171	cell−cell junction
15	8e−06	12 / 47	trans−Golgi network membrane
16	1e−05	12 / 49	phagocytic vesicle membrane
17	2e−05	7 / 17	phagocytic cup
18	4e−05	10 / 39	clathrin−coated endocytic vesicle membrane
19	5e−05	9 / 32	transport vesicle membrane
20	7e−05	25 / 190	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	4e−05	85 / 976	Chr 6
2	2e−02	35 / 436	Chr 22
3	1e−01	91 / 1425	Chr 19
4	1e−01	119 / 1920	Chr 1
5	2e−01	63 / 1017	Chr 12
6	4e−01	50 / 847	Chr 16
7	4e−01	12 / 191	Chr 21
8	4e−01	44 / 746	Chr X
9	5e−01	49 / 859	Chr 7
10	5e−01	59 / 1043	Chr 3
11	5e−01	61 / 1083	Chr 17
12	5e−01	18 / 318	Chr 13
13	6e−01	48 / 862	Chr 5
14	6e−01	64 / 1172	Chr 11
15	7e−01	32 / 613	Chr 14
16	8e−01	35 / 715	Chr 10
17	8e−01	12 / 272	Chr 18
18	9e−01	61 / 1228	Chr 2
19	9e−01	34 / 735	Chr 4
20	9e−01	25 / 582	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	393 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−36	89 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	1e−19	76 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	2e−19	87 / 532	K9acLow_Colon
5	2e−15	97 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
6	8e−11	773 / 11968	TssWk_Colon
7	4e−10	50 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
8	7e−10	251 / 3112	EnhA_Colon
9	2e−08	416 / 5889	EnhWk1_Colon
10	1e−07	316 / 4327	EnhWk2_Colon
11	9e−07	17 / 76	Marisa_CRC−cluster−g
12	2e−06	737 / 11791	Enh_Colon
13	3e−06	232 / 3122	TxEnhG1_Colon
14	2e−05	601 / 9470	Quies3_Colon
15	2e−05	7 / 17	TCGA−CRC_less−agressive−disease−markers
16	5e−04	7 / 26	Ang_CRC−CIMPH−vs−L_hypo
17	7e−04	19 / 148	Marisa_CRC−cluster−a
18	7e−04	8 / 36	Ang_CRC_Hypomethylated
19	3e−03	285 / 4379	TssD1_Colon
20	8e−03	4 / 15	Budinska_B_Lower crypt−like_DOWN

Disease

Rank	p−value	#in/all	Geneset
1	3e−10	74 / 608	GUDJ_psoriasis up
2	1e+00	9 / 399	GUDJ_psoriasis down
3	1e+00	0 / 22	BCHETNIA_EBM up
4	1e+00	0 / 2	BCHETNIA_EBM down
5	1e+00	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−43	89 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	1e−16	24 / 53	Donson−innate immunity−associated with LTS in HGA
3	4e−16	31 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
4	6e−16	19 / 33	Donson−Misc immune function−associated with LTS in HGA
5	2e−15	41 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
6	3e−13	28 / 96	Weller_LGG_A_vs_O_UP
7	7e−09	63 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
8	1e−08	7 / 8	Donson−adaptive−immunity−associated with LTS in HGA
9	9e−08	9 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
10	8e−07	6 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
11	1e−06	231 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
12	4e−06	7 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
13	3e−05	14 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
14	6e−04	8 / 35	shaw_responders_down_in_oligo_glioma
15	7e−04	8 / 36	Shaw_down_in_1p19q
16	1e−03	5 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
17	2e−03	10 / 59	Christensen_hypomethylated_in_primary_glioblastoma
18	5e−03	12 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
19	5e−03	3 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
20	1e−02	10 / 77	Weller_LGG_gradeII−vs−III_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	182 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	6e−84	124 / 263	WALLACE_PROSTATE_CANCER_RACE_UP
3	4e−77	99 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE
4	5e−61	101 / 246	QI_PLASMACYTOMA_UP
5	3e−52	122 / 435	RODWELL_AGING_KIDNEY_UP
6	4e−52	95 / 259	POOLA_INVASIVE_BREAST_CANCER_UP
7	3e−51	222 / 1340	PUJANA_ATM_PCC_NETWORK
8	6e−51	87 / 220	MCLACHLAN_DENTAL_CARIES_UP
9	4e−50	203 / 1165	CHEN_METABOLIC_SYNDROM_NETWORK
10	1e−48	123 / 473	ZHENG_BOUND_BY_FOXP3
11	1e−44	159 / 823	REACTOME_IMMUNE_SYSTEM
12	2e−41	77 / 215	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
13	2e−40	75 / 210	MCLACHLAN_DENTAL_CARIES_DN
14	9e−40	50 / 87	BASSO_CD40_SIGNALING_UP
15	2e−39	117 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
16	2e−35	83 / 297	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
17	1e−30	34 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
18	1e−29	85 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
19	6e−28	225 / 1914	PILON_KLF1_TARGETS_DN
20	8e−27	32 / 53	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN

HM

Rank	p−value	#in/all	Geneset
1	9e−46	75 / 181	HALLMARK_ALLOGRAFT_REJECTION
2	6e−27	57 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	3e−17	46 / 192	HALLMARK_COMPLEMENT
4	5e−16	45 / 197	HALLMARK_IL2_STAT5_SIGNALING
5	6e−15	43 / 194	HALLMARK_INFLAMMATORY_RESPONSE
6	7e−14	27 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	2e−08	32 / 189	HALLMARK_KRAS_SIGNALING_UP
8	3e−08	32 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	9e−06	17 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	2e−03	14 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	1e−02	7 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
12	2e−02	16 / 157	HALLMARK_APOPTOSIS
13	2e−02	18 / 190	HALLMARK_APICAL_JUNCTION
14	5e−02	17 / 196	HALLMARK_MITOTIC_SPINDLE
15	5e−02	17 / 196	HALLMARK_P53_PATHWAY
16	1e−01	5 / 44	HALLMARK_APICAL_SURFACE
17	2e−01	14 / 198	HALLMARK_HYPOXIA
18	2e−01	3 / 30	HALLMARK_NOTCH_SIGNALING
19	3e−01	11 / 155	HALLMARK_UV_RESPONSE_UP
20	3e−01	13 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 17	DUMEAUX_High bmi enriched genes
2	2e−03	4 / 11	DUMEAUX_Women normal BMI literature genes up
3	1e−02	3 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	1e−01	8 / 91	DUMEAUX_Smoking enriched genes
5	5e−01	1 / 11	DUMEAUX_Smoking literature genes up
6	6e−01	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 33	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−99	781 / 7592	HOPP_Strong_enhancer
2	3e−53	552 / 5643	HOPP_Txn_transition
3	1e−39	95 / 347	WIRTH_lymphoma937_spot H
4	2e−38	92 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
5	1e−37	186 / 1215	SPANG_BCR DN
6	2e−33	57 / 145	WIRTH_lymphoma937_spot F
7	2e−33	57 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
8	1e−28	77 / 315	WIRTH_lymphoma937_spot E
9	5e−28	76 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
10	6e−28	94 / 466	SPANG_CD40 6hrs DN
11	2e−26	76 / 332	SPANG_CD40 6hrs UP
12	7e−24	66 / 279	SPANG_IL21 DN
13	2e−22	576 / 7491	HOPP_Txn_elongation
14	2e−19	43 / 150	DAVE_BL−vs−DLBCL
15	6e−17	21 / 38	TARTE_B−cell signature
16	3e−16	601 / 8358	HOPP_Active_promoter
17	2e−15	76 / 500	WIRTH_lymphoma937_spot J
18	1e−14	73 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
19	2e−14	15 / 22	DAVE_NFkB BL DN
20	6e−12	30 / 123	SPANG_LPS 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	1e−21	752 / 10693	protein binding
2	1e−11	41 / 219	receptor activity
3	1e−11	18 / 45	non−membrane spanning protein tyrosine kinase activity
4	4e−09	34 / 196	transmembrane signaling receptor activity
5	1e−08	11 / 23	peptide antigen binding
6	1e−07	15 / 52	SH3/SH2 adaptor activity
7	1e−07	12 / 33	tumor necrosis factor receptor binding
8	2e−07	13 / 40	cytokine receptor activity
9	8e−07	34 / 241	GTPase activator activity
10	9e−07	8 / 16	MHC class II protein complex binding
11	2e−06	20 / 108	guanyl−nucleotide exchange factor activity
12	3e−06	14 / 58	cell adhesion molecule binding
13	7e−06	9 / 26	coreceptor activity
14	8e−06	7 / 15	regulatory region DNA binding
15	8e−06	20 / 117	protein tyrosine kinase activity
16	1e−05	42 / 370	receptor binding
17	2e−05	27 / 198	signal transducer activity
18	2e−05	19 / 114	SH3 domain binding
19	2e−05	6 / 12	C−C chemokine receptor activity
20	4e−05	6 / 13	G−protein coupled purinergic nucleotide receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	16 / 126	hsa−miR−421
2	0.004	9 / 57	hsa−miR−1302
3	0.007	7 / 41	hsa−miR−601
4	0.014	5 / 26	hsa−miR−99a
5	0.014	5 / 26	hsa−miR−100
6	0.015	25 / 278	hsa−miR−101
7	0.019	18 / 187	hsa−miR−34b
8	0.024	11 / 99	hsa−miR−133a
9	0.025	10 / 87	hsa−miR−767−5p
10	0.027	6 / 41	hsa−miR−758
11	0.028	24 / 280	hsa−miR−30d
12	0.028	10 / 89	hsa−miR−423−5p
13	0.030	10 / 90	hsa−miR−587
14	0.031	11 / 103	hsa−miR−624
15	0.037	10 / 93	hsa−miR−608
16	0.037	8 / 68	hsa−miR−499−3p
17	0.040	8 / 69	hsa−miR−648
18	0.041	7 / 57	hsa−miR−891b
19	0.043	14 / 149	hsa−miR−135a
20	0.046	25 / 309	hsa−miR−18b

PathwAct

Rank	p−value	#in/all	Geneset
1	0.2	2 / 14	BENTINK_src.10
2	0.2	2 / 15	GUSTAFSON_PI3K_DN
3	0.4	1 / 10	BENTINK_ras.4
4	0.5	1 / 12	BENTINK_ras.1
5	0.5	1 / 13	BENTINK_e2f3.2
6	0.6	1 / 15	BENTINK_ras.6
7	1.0	0 / 14	GUSTAFSON_PI3K_UP
8	1.0	0 / 14	BENTINK_e2f3.1
9	1.0	0 / 14	BENTINK_myc.1
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−39	291 / 2401	ICGC_Bcl11_targets
2	9e−28	328 / 3305	ICGC_BatfPcr1_targets
3	1e−27	423 / 4714	ICGC_Pu1_targets
4	2e−27	242 / 2149	ICGC_Mef2_targets
5	6e−22	179 / 1523	ICGC_P300_targets
6	8e−21	223 / 2133	ICGC_Cebpbsc150_targets
7	2e−19	293 / 3177	ICGC_Irf4_targets
8	2e−17	437 / 5512	ICGC_Nficsc81335_targets
9	6e−15	253 / 2827	ICGC_Bcl3_targets
10	9e−15	392 / 4969	ICGC_Atf2_targets
11	1e−12	336 / 4230	ICGC_Nfatc1_targets
12	4e−12	452 / 6157	ICGC_Tcf3_targets
13	1e−11	459 / 6313	ICGC_Pou2_targets
14	3e−11	386 / 5135	ICGC_Ebfsc137065_targets
15	3e−10	371 / 4987	ICGC_Bclaf101388_targets
16	8e−10	405 / 5578	ICGC_Stat5_targets
17	3e−09	394 / 5453	ICGC_Foxm1_targets
18	2e−08	394 / 5526	ICGC_Pmlsc71910_targets
19	5e−08	420 / 6005	ICGC_Mta3_targets
20	6e−08	490 / 7202	ICGC_Runx3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	3e−15	18 / 31	VAQUERIZAS_Lymph node
2	2e−11	13 / 22	VAQUERIZAS_Tonsil
3	6e−11	21 / 67	VAQUERIZAS_Whole blood
4	4e−08	14 / 42	VAQUERIZAS_Thymus
5	7e−05	7 / 20	VAQUERIZAS_Bone marrow
6	8e−04	11 / 64	VAQUERIZAS_Lung
7	1e−01	5 / 46	VAQUERIZAS_Whole brain
8	2e−01	4 / 37	VAQUERIZAS_Prostate
9	2e−01	2 / 13	VAQUERIZAS_Skin
10	2e−01	4 / 41	VAQUERIZAS_Fetal brain
11	2e−01	4 / 42	VAQUERIZAS_Thyroid
12	2e−01	2 / 16	VAQUERIZAS_Fetal liver
13	2e−01	2 / 16	VAQUERIZAS_Fetal thyroid
14	2e−01	2 / 17	VAQUERIZAS_Salivary gland
15	3e−01	3 / 31	VAQUERIZAS_Fetal lung
16	3e−01	3 / 33	VAQUERIZAS_Liver
17	4e−01	10 / 155	VAQUERIZAS_General
18	4e−01	3 / 41	VAQUERIZAS_Testis
19	5e−01	3 / 45	VAQUERIZAS_Placenta
20	5e−01	1 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	1e−99	237 / 427	WIRTH_Immune system
2	1e−42	77 / 208	PALMER_B−Cell signature up
3	2e−34	57 / 140	PALMER_T−Cell signature up
4	2e−04	30 / 259	PALMER_Granulocytes signature up
5	5e−04	5 / 13	PALMER_CD8+ T−Cell signature up
6	2e−01	2 / 14	WIRTH_Thalamus
7	5e−01	1 / 13	WIRTH_Globus pallidus
8	5e−01	1 / 13	WIRTH_Cortex cerebri
9	6e−01	1 / 14	WIRTH_B−cells
10	6e−01	1 / 15	WIRTH_Cerebellum
11	6e−01	1 / 16	WIRTH_Hippocampus
12	9e−01	5 / 141	WIRTH_Muscle
13	1e+00	1 / 82	WIRTH_Homeostasis
14	1e+00	9 / 476	WIRTH_Nervous System
15	1e+00	0 / 6	WIRTH_Pituitary gland
16	1e+00	0 / 54	WIRTH_Pancreas
17	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
18	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
19	1e+00	0 / 12	WIRTH_Tonsil
20	1e+00	0 / 14	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	87 / 1343	LU_BPDE 1h DN
2	1.0	212 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

Spot Summary: C

metagenes = 53
genes = 580

<r> metagenes = 0.94
<r> genes = 0.6
beta: r2= 0.01 / log p= −0.2

samples with spot = 3 (13 %)
MLH1_normHNPCC : 1 (16.7 %)
other_normHNPCC : 2 (40 %)

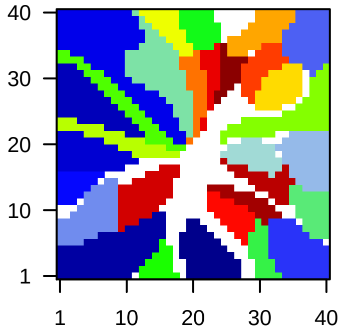
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.25	−0.13	0.64	TRAFD1	TRAF−type zinc finger domain containing 1 [Source:HGNC S
2	ENSG000001	0.23	−0.09	0.87	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2 [Sourc
3	ENSG000002	0.21	−0.05	0.71		
4	ENSG000002	0.2	−0.12	0.81		Iduronate 2−sulfatase (Hunter syndrome), isoform CRA_e; U
5	ENSG000001	0.19	−0.1	0.76	KAT2B	K(lysine) acetyltransferase 2B [Source:HGNC Symbol;Acc:H
6	ENSG000001	0.18	−0.09	0.93	IL11RA	interleukin 11 receptor, alpha [Source:HGNC Symbol;Acc:HG
7	ENSG000000	0.18	−0.07	0.94	RNF216	ring finger protein 216 [Source:HGNC Symbol;Acc:HGNC:21
8	ENSG000001	0.18	−0.1	0.88	NDNL2	necdin−like 2 [Source:HGNC Symbol;Acc:HGNC:7677]
9	ENSG000001	0.18	−0.03	0.85	TMEM71	transmembrane protein 71 [Source:HGNC Symbol;Acc:HGN
10	ENSG000002	0.17	−0.12	0.9		SNRPN upstream reading frame [Source:HGNC Symbol;Acc:
11	ENSG000001	0.17	−0.1	0.89		
12	ENSG000001	0.17	−0.06	0.97	SATB1	SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541
13	ENSG000001	0.17	−0.08	0.86	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit [
14	ENSG000001	0.16	−0.08	0.83	KIAA0430	KIAA0430 [Source:HGNC Symbol;Acc:HGNC:29562]
15	ENSG000001	0.16	−0.05	0.93	NBPF20	neuroblastoma breakpoint family, member 20 [Source:HGNC
16	ENSG000001	0.16	−0.11	0.87	NUMA1	nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;A
17	ENSG000001	0.15	−0.06	0.85	P2RY14	purinergic receptor P2Y, G−protein coupled, 14 [Source:HGN
18	ENSG000001	0.15	−0.1	0.84	PKN1	protein kinase N1 [Source:HGNC Symbol;Acc:HGNC:9405]
19	ENSG000001	0.15	−0.11	0.71	THAP11	THAP domain containing 11 [Source:HGNC Symbol;Acc:HG
20	ENSG000001	0.15	−0.12	0.78	ZMAT2	zinc finger, matrin−type 2 [Source:HGNC Symbol;Acc:HGNC:

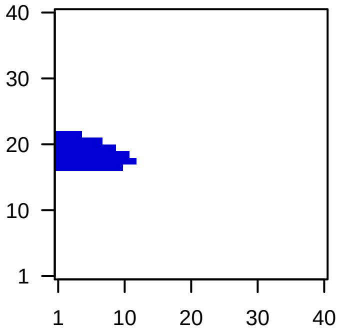
Geneset Overrepresentation

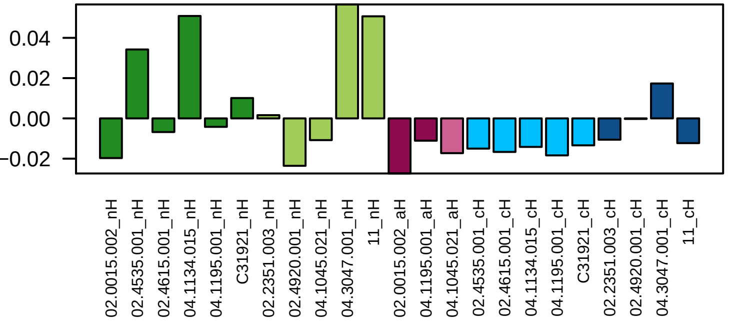
Rank	p−value	#in/all	Geneset	
1	2e−79	408 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
2	6e−57	485 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
3	1e−56	410 / 7491	Lymph	HOPP_Txn_elongation
4	1e−50	456 / 9470	Colon	Quies3_Colon
5	6e−49	451 / 9390	Colon	TxWk_Colon
6	3e−45	416 / 8358	Lymph	HOPP_Active_promoter
7	4e−44	466 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
8	1e−43	456 / 9930	Colon	Tx_Colon
9	3e−40	450 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
10	2e−35	455 / 10475	Colon	TssA_Colon
11	2e−34	308 / 5643	Lymph	HOPP_Txn_transition
12	4e−34	461 / 10800	Brain	Overlap_fetal_midbrain_Quies
13	1e−29	481 / 11968	Colon	TssWk_Colon
14	1e−24	87 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	2e−23	362 / 8147	Lymph	HOPP_Weak_promoter
16	3e−20	127 / 1807	BP	transcription, DNA−templated
17	2e−19	59 / 500	Lymph	WIRTH_lymphoma937_spot J
18	2e−18	94 / 1178	Colon	ZNF_Colon
19	4e−18	56 / 484	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−
20	2e−17	289 / 6389	Lymph	HOPP_Weak_txn
21	3e−17	248 / 5173	TF	ICGC_Taf1_targets
22	6e−17	326 / 7592	Lymph	HOPP_Strong_enhancer
23	1e−16	53 / 471	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
24	2e−15	116 / 1803	MF	DNA binding
25	5e−15	85 / 1134	MF	nucleic acid binding
26	5e−15	115 / 1808	BP	regulation of transcription, DNA−templated
27	8e−15	145 / 2554	CC	nucleoplasm
28	3e−14	109 / 1713	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
29	2e−13	45 / 420	GSEA	SHEN_SMARCA2_TARGETS_UP
30	2e−13	61 / 712	Brain	Overlap_fetal_midbrain_EnhP
31	2e−13	233 / 5101	CC	nucleus
32	9e−13	209 / 4470	TF	ICGC_Creb1_targets
33	1e−12	37 / 311	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
34	2e−11	266 / 6324	TF	ICGC_Yy1_targets
35	4e−11	114 / 2040	MF	metal ion binding
36	8e−11	219 / 4969	TF	ICGC_Atf2_targets
37	1e−10	278 / 6784	Lymph	HOPP_Weak_enhancer
38	1e−10	55 / 705	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
39	1e−10	237 / 5526	TF	ICGC_Pmlsc71910_targets
40	1e−10	58 / 773	GSEA	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN

Overview Map

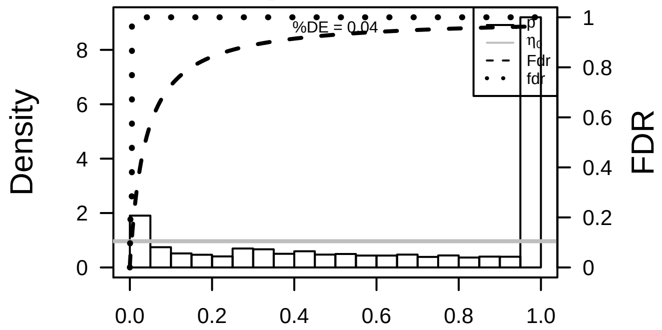


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	4 / 123	HORVATH_aging_genes meth DOWN
2	0.6	4 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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−20	127 / 1807	transcription, DNA−templated
2	5e−15	115 / 1808	regulation of transcription, DNA−templated
3	5e−07	13 / 78	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
4	5e−06	7 / 24	nonmotile primary cilium assembly
5	7e−06	8 / 35	histone acetylation
6	1e−05	18 / 185	ubiquitin−dependent protein catabolic process
7	2e−05	24 / 304	DNA repair
8	2e−05	19 / 208	chromatin organization
9	2e−05	27 / 366	protein ubiquitination
10	3e−05	9 / 54	phosphatidylinositol biosynthetic process
11	1e−04	4 / 10	regulation of transcription from RNA polymerase III promoter
12	3e−04	8 / 56	regulation of growth
13	3e−04	5 / 21	phosphatidylinositol dephosphorylation
14	4e−04	5 / 22	B cell homeostasis
15	1e−03	6 / 39	transcription from RNA polymerase III promoter
16	1e−03	6 / 41	histone H3 acetylation
17	1e−03	5 / 28	regulation of transcription from RNA polymerase II promoter in response to hy
18	2e−03	12 / 147	insulin receptor signaling pathway
19	2e−03	4 / 18	Golgi to endosome transport
20	2e−03	8 / 75	positive regulation of peptidyl−serine phosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	2e−79	408 / 6320	Overlap_fetal_midbrain_HetRpts
2	6e−57	485 / 10239	Overlap_fetal_midbrain_ReprPC
3	4e−44	466 / 10278	Overlap_fetal_midbrain_ReprPCWk
4	3e−40	450 / 9923	Overlap_fetal_midbrain_K9K27me3
5	4e−34	461 / 10800	Overlap_fetal_midbrain_Quies
6	2e−13	61 / 712	Overlap_fetal_midbrain_EnhP
7	1e−08	60 / 910	Fetal_EnhG
8	2e−06	65 / 1182	Fetal_EnhP
9	2e−06	63 / 1137	Fetal_Enh
10	6e−06	143 / 3370	Mid_Frontal_Lobe_ZNF
11	1e−04	37 / 641	Mid_Frontal_Lobe_EnhP
12	4e−03	40 / 855	Overlap_fetal_midbrain_ZNF
13	8e−03	19 / 342	Fetal_Het
14	2e−02	52 / 1279	Overlap_fetal_midbrain_Enh
15	6e−02	51 / 1356	Fetal_K9K27me3
16	8e−02	41 / 1084	Overlap_fetal_midbrain_EnhG
17	1e−01	17 / 400	Fetal_ZNF
18	1e−01	9 / 191	Overlap_fetal_midbrain_Het
19	2e−01	33 / 940	Mid_Frontal_Lobe_Enh
20	4e−01	4 / 106	Overlap_fetal_midbrain_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	11 / 123	PanCan_Driver_Gene_geneset_nanostring
2	0.005	4 / 24	PanCan_Notch_geneset_nanostring
3	0.007	5 / 40	PanCan_HK_geneset_nanostring
4	0.009	7 / 78	PanCan_Wnt_geneset_nanostring
5	0.015	7 / 86	PanCan_JAK−ST_geneset_nanostring
6	0.054	8 / 136	PanCan_CC+Apop_geneset_nanostring
7	0.067	4 / 51	PanCan_TGF−B_geneset_nanostring
8	0.113	14 / 324	SPANG_BCL6−index2
9	0.166	4 / 71	SHAUGHNESSY_MM high risk
10	0.206	2 / 28	PanCan_HH_geneset_nanostring
11	0.241	1 / 9	WANG_ER_DN
12	0.248	8 / 198	PanCan_PI3K_geneset_nanostring
13	0.309	6 / 152	PanCan_MAPK_geneset_nanostring
14	0.348	1 / 14	LIU_PROSTATE_CANCER_UP
15	0.348	1 / 14	BEN−PORATH_DN
16	0.387	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	0.387	1 / 16	GENTLES_modul11
18	0.387	1 / 16	GENTLES_modul14
19	0.387	1 / 16	GENTLES_modul18
20	0.414	5 / 140	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	8e−15	145 / 2554	nucleoplasm
2	2e−13	233 / 5101	nucleus
3	1e−06	208 / 5185	cytoplasm
4	3e−05	77 / 1604	intracellular
5	5e−04	5 / 23	histone acetyltransferase complex
6	1e−03	9 / 88	PML body
7	3e−03	4 / 21	ciliary transition zone
8	3e−03	114 / 2974	cytosol
9	4e−03	3 / 11	cullin−RING ubiquitin ligase complex
10	5e−03	4 / 23	nuclear heterochromatin
11	5e−03	7 / 69	cytoplasmic mRNA processing body
12	5e−03	9 / 107	growth cone
13	5e−03	7 / 70	axoneme
14	7e−03	5 / 40	spindle microtubule
15	7e−03	5 / 41	chromosome, telomeric region
16	8e−03	15 / 246	endosome
17	8e−03	8 / 95	centriole
18	8e−03	39 / 864	Golgi apparatus
19	9e−03	3 / 15	Ada2/Gcn5/Ada3 transcription activator complex
20	1e−02	4 / 29	RNA polymerase II transcription factor complex

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	51 / 1043	Chr 3
2	1e−02	28 / 582	Chr 15
3	6e−02	15 / 318	Chr 13
4	7e−02	69 / 1920	Chr 1
5	2e−01	8 / 191	Chr 21
6	2e−01	30 / 862	Chr 5
7	3e−01	25 / 746	Chr X
8	4e−01	39 / 1228	Chr 2
9	5e−01	30 / 976	Chr 6
10	5e−01	22 / 715	Chr 10
11	6e−01	21 / 735	Chr 4
12	7e−01	17 / 613	Chr 14
13	7e−01	24 / 859	Chr 7
14	7e−01	7 / 272	Chr 18
15	7e−01	28 / 1017	Chr 12
16	8e−01	22 / 847	Chr 16
17	9e−01	12 / 522	Chr 20
18	9e−01	36 / 1425	Chr 19
19	9e−01	15 / 651	Chr 8
20	9e−01	25 / 1083	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−50	456 / 9470	Quies3_Colon
2	6e−49	451 / 9390	TxWk_Colon
3	1e−43	456 / 9930	Tx_Colon
4	2e−35	455 / 10475	TssA_Colon
5	1e−29	481 / 11968	TssWk_Colon
6	2e−18	94 / 1178	ZNF_Colon
7	2e−08	189 / 4379	TssD1_Colon
8	9e−08	203 / 4879	Quies1_Colon
9	7e−05	81 / 1753	Het_Colon
10	2e−04	5 / 19	Vilar_hypermutated−in−CRC
11	3e−04	285 / 8123	TssF_Colon
12	1e−03	58 / 1281	HetRpts_Colon
13	1e−03	10 / 105	Marisa_CRC−cluster−d
14	8e−03	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
15	9e−03	3 / 15	TCGA_Mutated−in−CRC_hypermutated
16	1e−02	2 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
17	1e−02	3 / 17	TCGA_Mutated−in−CRC_non−hypermutated
18	2e−02	2 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
19	2e−02	152 / 4327	EnhWk2_Colon
20	2e−02	3 / 19	Vilar_non−hypermutated−in−CRC

Disease

Rank	p−value	#in/all	Geneset
1	0.5	1 / 22	BCHETNIA_EBM up
2	0.7	1 / 37	BCHETNIA_EBM−DM up
3	1.0	7 / 399	GUDJ_psoriasis down
4	1.0	4 / 608	GUDJ_psoriasis up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	5e−09	59 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
2	7e−08	101 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	9e−08	111 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	2e−07	29 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	7e−04	9 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	4e−03	3 / 11	KIM amplified & overexpressed in LTS
7	5e−03	7 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	5e−02	6 / 90	Weller_LGG_A_vs_O_DOWN
9	6e−02	16 / 344	Up
10	7e−02	3 / 31	KIM prognostic signature LTS vs. STS
11	9e−02	4 / 56	mature astrocytes
12	1e−01	5 / 81	GIEZELT_GBM_STS_up_VS_LTS
13	1e−01	1 / 5	Phillips Prolif up vs PN & MES
14	2e−01	16 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
15	2e−01	4 / 83	GIEZELT_GBM_WT_down_VS_mut
16	3e−01	2 / 34	WIRTH_PN subtype
17	3e−01	2 / 35	shaw_responders_down_in_oligo_glioma
18	3e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
19	4e−01	1 / 15	Mukasa_UP_in_GBM
20	4e−01	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−24	87 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	1e−16	53 / 471	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
3	3e−14	109 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
4	2e−13	45 / 420	SHEN_SMARCA2_TARGETS_UP
5	1e−12	37 / 311	DAZARD_RESPONSE_TO_UV_NHEK_DN
6	1e−10	55 / 705	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
7	1e−10	58 / 773	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
8	2e−10	56 / 736	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
9	1e−09	57 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
10	1e−09	46 / 568	HAMAI_APOPTOSIS_VIA_TRAIL_UP
11	3e−09	30 / 286	GABRIELY_MIR21_TARGETS
12	4e−09	59 / 866	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
13	2e−08	31 / 329	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
14	1e−07	19 / 149	DAZARD_UV_RESPONSE_CLUSTER_G6
15	2e−07	32 / 383	OSMAN_BLADDER_CANCER_UP
16	7e−07	95 / 1914	PILON_KLF1_TARGETS_DN
17	1e−06	24 / 261	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN
18	2e−06	21 / 215	CHEN_HOXA5_TARGETS_9HR_UP
19	3e−06	81 / 1612	BLALOCK_ALZHEIMERS_DISEASE_UP
20	4e−06	9 / 43	SIG_BCR_SIGNALING_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.003	14 / 196	HALLMARK_MITOTIC_SPINDLE
2	0.061	3 / 30	HALLMARK_NOTCH_SIGNALING
3	0.071	4 / 52	HALLMARK_TGF_BETA_SIGNALING
4	0.131	7 / 140	HALLMARK_UV_RESPONSE_DN
5	0.152	7 / 146	HALLMARK_DNA_REPAIR
6	0.154	5 / 94	HALLMARK_PROTEIN_SECRETION
7	0.189	6 / 128	HALLMARK_SPERMATOGENESIS
8	0.199	5 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.342	4 / 98	HALLMARK_ANDROGEN_RESPONSE
10	0.378	7 / 196	HALLMARK_G2M_CHECKPOINT
11	0.505	3 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	0.511	6 / 190	HALLMARK_APICAL_JUNCTION
13	0.513	5 / 157	HALLMARK_APOPTOSIS
14	0.668	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
15	0.690	4 / 155	HALLMARK_UV_RESPONSE_UP
16	0.694	5 / 193	HALLMARK_HEME_METABOLISM
17	0.706	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
18	0.840	4 / 194	HALLMARK_INFLAMMATORY_RESPONSE
19	0.843	4 / 195	HALLMARK_MYOGENESIS
20	0.851	4 / 198	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−04	6 / 33	DUMEAUX_Fasting enriched genes
2	3e−01	1 / 11	DUMEAUX_Smoking literature genes up
3	5e−01	3 / 91	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1e+00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1e+00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1e+00	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1e+00	0 / 17	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−56	410 / 7491	HOPP_Txn_elongation
2	3e−45	416 / 8358	HOPP_Active_promoter
3	2e−34	308 / 5643	HOPP_Txn_transition
4	2e−23	362 / 8147	HOPP_Weak_promoter
5	2e−19	59 / 500	WIRTH_lymphoma937_spot J
6	4e−18	56 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
7	2e−17	289 / 6389	HOPP_Weak_txn
8	6e−17	326 / 7592	HOPP_Strong_enhancer
9	1e−10	278 / 6784	HOPP_Weak_enhancer
10	5e−08	76 / 1333	SPANG_BCR_UP
11	2e−06	28 / 347	WIRTH_lymphoma937_spot H
12	4e−06	27 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
13	7e−06	118 / 2658	HOPP_Repetitive
14	2e−03	19 / 302	SPANG_IL21_UP
15	4e−03	53 / 1215	SPANG_BCR_DN
16	1e−02	23 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC−
17	1e−02	23 / 458	WIRTH_lymphoma937_spot I
18	3e−02	4 / 38	TARTE_B−cell signature
19	1e−01	6 / 105	ROSOLOWSKI_blue total
20	2e−01	18 / 466	SPANG_CD40_6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	2e−15	116 / 1803	DNA binding
2	5e−15	85 / 1134	nucleic acid binding
3	4e−11	114 / 2040	metal ion binding
4	1e−08	32 / 341	binding
5	1e−07	26 / 262	ubiquitin−protein transferase activity
6	2e−07	59 / 962	transcription factor activity, sequence−specific DNA binding
7	2e−07	27 / 286	ligase activity
8	2e−07	67 / 1164	zinc ion binding
9	3e−06	375 / 10693	protein binding
10	1e−05	8 / 38	histone acetyltransferase activity
11	1e−04	4 / 10	microtubule plus−end binding
12	2e−04	17 / 207	RNA polymerase II regulatory region sequence−specific DNA binding
13	4e−04	10 / 90	histone binding
14	5e−04	8 / 61	damaged DNA binding
15	5e−04	4 / 13	acetyltransferase activity
16	2e−03	8 / 76	helicase activity
17	3e−03	8 / 79	phosphatidylinositol binding
18	3e−03	6 / 49	SNARE binding
19	4e−03	12 / 161	ubiquitin protein ligase activity
20	5e−03	4 / 23	bHLH transcription factor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−10	46 / 536	hsa−miR−106b
2	2e−09	46 / 573	hsa−miR−93
3	3e−09	45 / 562	hsa−miR−17
4	1e−08	47 / 631	hsa−miR−20a
5	1e−08	45 / 591	hsa−miR−20b
6	7e−08	41 / 542	hsa−miR−106a
7	7e−08	34 / 403	hsa−miR−519a
8	2e−07	37 / 480	hsa−miR−301a
9	3e−07	35 / 447	hsa−miR−519d
10	3e−07	30 / 352	hsa−miR−142−5p
11	5e−07	31 / 378	hsa−miR−519b−3p
12	1e−06	27 / 312	hsa−miR−548i
13	1e−06	33 / 435	hsa−miR−372
14	1e−06	26 / 297	hsa−miR−548j
15	2e−06	30 / 381	hsa−miR−144
16	2e−06	27 / 324	hsa−miR−559
17	2e−06	31 / 407	hsa−miR−301b
18	3e−06	28 / 348	hsa−miR−548d−5p
19	4e−06	14 / 106	hsa−miR−1284
20	5e−06	24 / 280	hsa−miR−548h

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 15	GUSTAFSON_PI3K_DN
2	0.31	1 / 12	BENTINK_ras.1
3	0.35	1 / 14	GUSTAFSON_PI3K_UP
4	0.35	1 / 14	BENTINK_myc.1
5	0.37	1 / 15	BENTINK_ras.6
6	1.00	0 / 14	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 10	BENTINK_ras.4
9	1.00	0 / 14	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−17	248 / 5173	ICGC_Taf1_targets
2	9e−13	209 / 4470	ICGC_Creb1_targets
3	2e−11	266 / 6324	ICGC_Yy1_targets
4	8e−11	219 / 4969	ICGC_Atf2_targets
5	1e−10	237 / 5526	ICGC_Pmlsc71910_targets
6	5e−10	236 / 5578	ICGC_Stat5_targets
7	8e−10	233 / 5512	ICGC_Nficsc81335_targets
8	2e−09	214 / 4987	ICGC_Bclaf101388_targets
9	2e−09	227 / 5393	ICGC_Sp1_targets
10	7e−09	245 / 6005	ICGC_Mta3_targets
11	1e−08	254 / 6313	ICGC_Pou2_targets
12	2e−08	117 / 2342	ICGC_GabpPcr2_targets
13	5e−08	83 / 1503	ICGC_Six5_targets
14	6e−08	268 / 6862	ICGC_Elf1_targets
15	1e−07	217 / 5308	ICGC_Tcf12_targets
16	1e−07	277 / 7202	ICGC_Runx3_targets
17	2e−07	191 / 4566	ICGC_Egr1_targets
18	2e−07	220 / 5453	ICGC_Foxm1_targets
19	2e−07	105 / 2133	ICGC_Cebpbsc150_targets
20	2e−07	248 / 6322	ICGC_Pol2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.003	12 / 155	VAQUERIZAS_General
2	0.013	4 / 31	VAQUERIZAS_Lymph node
3	0.060	4 / 49	VAQUERIZAS_Uterus
4	0.061	3 / 30	VAQUERIZAS_Smooth muscle
5	0.132	3 / 42	VAQUERIZAS_Thymus
6	0.161	3 / 46	VAQUERIZAS_Whole brain
7	0.262	2 / 33	VAQUERIZAS_Liver
8	0.264	1 / 10	VAQUERIZAS_Skeletal.muscle.psoas
9	0.307	2 / 37	VAQUERIZAS_Prostate
10	0.328	3 / 67	VAQUERIZAS_Whole blood
11	0.351	2 / 41	VAQUERIZAS_Fetal brain
12	0.362	2 / 42	VAQUERIZAS_Thyroid
13	0.387	1 / 16	VAQUERIZAS_Fetal liver
14	0.387	1 / 16	VAQUERIZAS_Fetal thyroid
15	0.535	1 / 25	VAQUERIZAS_Spinal cord
16	0.578	2 / 64	VAQUERIZAS_Lung
17	0.613	1 / 31	VAQUERIZAS_Fetal lung
18	0.715	1 / 41	VAQUERIZAS_Testis
19	1.000	0 / 45	VAQUERIZAS_Placenta
20	1.000	0 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	9 / 208	PALMER_B−Cell signature up
2	0.3	1 / 13	WIRTH_Globus pallidus
3	0.3	1 / 14	WIRTH_Thymus
4	0.3	1 / 14	WIRTH_Thalamus
5	0.3	1 / 14	WIRTH_Thyroid gland
6	0.8	1 / 47	WIRTH_Placenta
7	0.8	6 / 259	PALMER_Granulocytes signature up
8	0.8	3 / 140	PALMER_T−Cell signature up
9	1.0	9 / 476	WIRTH_Nervous System
10	1.0	1 / 202	WIRTH_Testis
11	1.0	4 / 427	WIRTH_Immune system
12	1.0	0 / 6	WIRTH_Pituitary gland
13	1.0	0 / 54	WIRTH_Pancreas
14	1.0	0 / 13	WIRTH_Sec. lymphoid organs
15	1.0	0 / 13	WIRTH_Prim. lymphoid organs
16	1.0	0 / 14	WIRTH_B−cells
17	1.0	0 / 12	WIRTH_Tonsil
18	1.0	0 / 12	WIRTH_Lymphocytes
19	1.0	0 / 14	WIRTH_Bone marrow
20	1.0	0 / 15	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.05	51 / 1343	LU_BPDE 1h DN
2	1.00	132 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

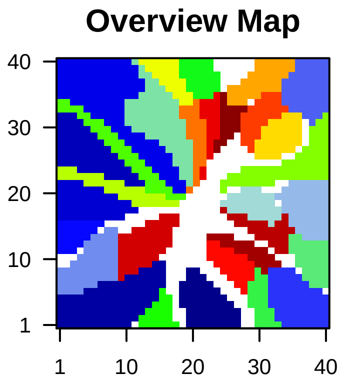
Correlation Clusters

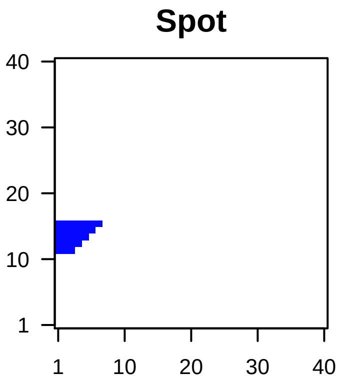
Spot Summary: D

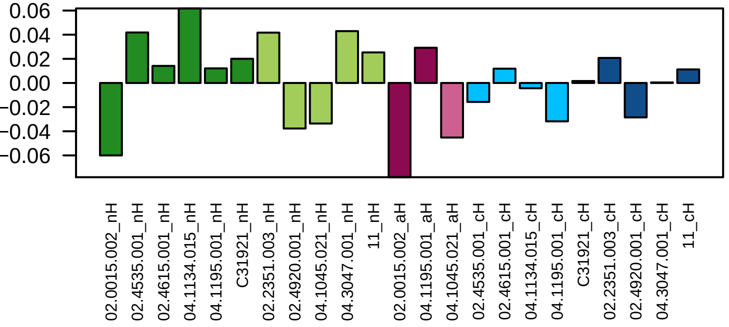
metagenes = 25
genes = 314

<r> metagenes = 0.97
<r> genes = 0.53
beta: r2= 0.02 / log p= −0.31

samples with spot = 1 (4.3 %)
MLH1_normHNPCC : 1 (16.7 %)





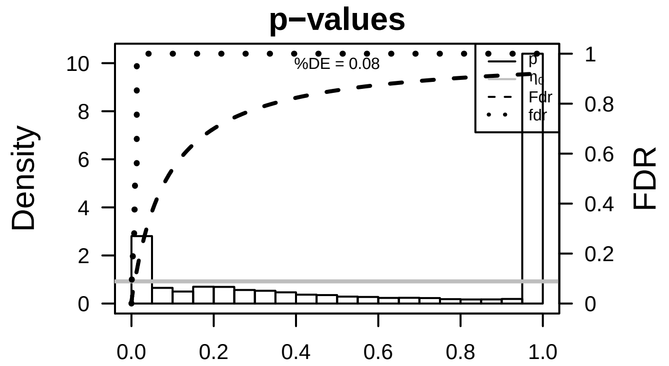


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	0.5	−0.11	0.52	RAB27A	RAB27A, member RAS oncogene family [Source:HGNC Sym
2	ENSG000001	0.37	−0.23	0.53	CCNG1	cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
3	ENSG000001	0.33	−0.34	0.63		
4	ENSG000001	0.27	−0.1	0.32	PARP9	poly (ADP−ribose) polymerase family, member 9 [Source:HGI
5	ENSG000002	0.25	−0.18	0.54		
6	ENSG000001	0.23	−0.1	0.63	SH3D19	SH3 domain containing 19 [Source:HGNC Symbol;Acc:HGNC
7	ENSG000001	0.23	−0.07	0.73	PRRC2C	proline−rich coiled−coil 2C [Source:HGNC Symbol;Acc:HGNC
8	ENSG000002	0.22	−0.16	0.69		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F5I
9	ENSG000000	0.22	−0.16	0.85	MAT2B	methionine adenosyltransferase II, beta [Source:HGNC Symb
10	ENSG000001	0.21	−0.24	0.57	CALM3	calmodulin 3 (phosphorylase kinase, delta) [Source:HGNC Sy
11	ENSG000001	0.2	−0.14	0.59	ZNF664	zinc finger protein 664 [Source:HGNC Symbol;Acc:HGNC:25
12	ENSG000001	0.2	−0.21	0.68	YWHAZ	tyrosine 3−monooxygenase/tryptophan 5−monooxygenase ac
13	ENSG000001	0.2	−0.27	0.66	H3F3A	H3 histone, family 3A [Source:HGNC Symbol;Acc:HGNC:476
14	ENSG000001	0.2	−0.24	0.61	PRDX3	peroxiredoxin 3 [Source:HGNC Symbol;Acc:HGNC:9354]
15	ENSG000002	0.19	−0.28	0.86		
16	ENSG000000	0.19	−0.23	0.65	BZW1	basic leucine zipper and W2 domains 1 [Source:HGNC Symb
17	ENSG000001	0.19	−0.13	0.78	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3 [Source:H
18	ENSG000001	0.19	−0.2	0.66	TMED7	transmembrane emp24 protein transport domain containing 7
19	ENSG000001	0.18	−0.07	0.73	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast) [Sou
20	ENSG000001	0.17	−0.13	0.66	ACBD3	acyl−CoA binding domain containing 3 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−58	257 / 7491	Lympl	HOPP_Txn_elongation
2	2e−54	234 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
3	2e−51	275 / 9390	Colon	TxWk_Colon
4	2e−49	216 / 5643	Lympl	HOPP_Txn_transition
5	8e−49	282 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
6	2e−48	278 / 9930	Colon	Tx_Colon
7	5e−39	246 / 8358	Lympl	HOPP_Active_promoter
8	7e−36	270 / 10475	Colon	TssA_Colon
9	9e−36	257 / 9470	Colon	Quies3_Colon
10	1e−27	251 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−27	66 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
12	2e−26	254 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
13	1e−20	251 / 10800	Brain	Overlap_fetal_midbrain_Quies
14	2e−20	47 / 568	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
15	3e−20	104 / 2554	CC	nucleoplasm
16	3e−19	209 / 8147	Lympl	HOPP_Weak_promoter
17	8e−19	70 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
18	7e−18	48 / 685	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
19	1e−17	41 / 503	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
20	2e−17	83 / 1914	GSEA	PILON_KLF1_TARGETS_DN
21	4e−17	37 / 420	GSEA	SHEN_SMARCA2_TARGETS_UP
22	5e−17	39 / 471	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
23	2e−16	72 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
24	6e−16	34 / 381	miRN	hsa−miR−144
25	7e−16	257 / 11968	Colon	TssWk_Colon
26	1e−15	65 / 1352	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
27	5e−15	146 / 5101	CC	nucleus
28	8e−15	33 / 391	miRN	hsa−miR−454
29	8e−15	35 / 442	miRN	hsa−miR−548n
30	2e−14	43 / 683	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
31	2e−14	38 / 539	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
32	3e−14	32 / 383	GSEA	OSMAN_BLADDER_CANCER_UP
33	3e−14	188 / 7592	Lympl	HOPP_Strong_enhancer
34	1e−13	35 / 480	miRN	hsa−miR−301a
35	1e−13	26 / 260	miRN	hsa−miR−548l
36	2e−13	27 / 286	GSEA	GABRIELY_MIR21_TARGETS
37	5e−13	22 / 189	miRN	hsa−miR−1283
38	6e−13	27 / 300	GSEA	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
39	7e−13	27 / 303	miRN	hsa−miR−561
40	1e−12	28 / 334	miRN	hsa−miR−590−3p



Aging

Rank	p−value	#in/all	Geneset
1	[illegible]	1 / 63	HORVATH_aging_genes meth UP
2	0.9	1 / 123	HORVATH_aging_genes meth DOWN
3	1.0	0 / 57	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−12	69 / 1807	transcription, DNA−templated
2	1e−09	17 / 162	membrane organization
3	9e−08	38 / 913	positive regulation of transcription from RNA polymerase II promoter
4	8e−07	26 / 539	small GTPase mediated signal transduction
5	7e−06	8 / 62	ER to Golgi vesicle−mediated transport
6	7e−06	18 / 329	intracellular protein transport
7	1e−05	31 / 820	gene expression
8	1e−05	13 / 191	vesicle−mediated transport
9	2e−05	22 / 488	regulation of transcription from RNA polymerase II promoter
10	2e−05	27 / 680	negative regulation of transcription from RNA polymerase II promoter
11	3e−05	52 / 1808	regulation of transcription, DNA−templated
12	3e−05	8 / 76	transcription elongation from RNA polymerase II promoter
13	3e−05	22 / 512	transcription from RNA polymerase II promoter
14	4e−05	13 / 208	chromatin organization
15	1e−04	21 / 512	protein transport
16	1e−04	17 / 366	protein ubiquitination
17	1e−04	4 / 17	positive regulation of histone H3−K4 methylation
18	1e−04	13 / 239	transcription initiation from RNA polymerase II promoter
19	1e−04	7 / 71	Rab protein signal transduction
20	2e−04	7 / 75	TRIF−dependent toll−like receptor signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	2e−54	234 / 6320	Overlap_fetal_midbrain_HetRpts
2	8e−49	282 / 10239	Overlap_fetal_midbrain_ReprPC
3	1e−27	251 / 9923	Overlap_fetal_midbrain_K9K27me3
4	2e−26	254 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	1e−20	251 / 10800	Overlap_fetal_midbrain_Quies
6	8e−06	40 / 1182	Fetal_EnhP
7	2e−05	38 / 1137	Fetal_Enh
8	7e−04	27 / 855	Overlap_fetal_midbrain_ZNF
9	1e−03	14 / 342	Fetal_Het
10	1e−02	24 / 910	Fetal_EnhG
11	1e−02	13 / 400	Fetal_ZNF
12	3e−02	68 / 3370	Mid_Frontal_Lobe_ZNF
13	2e−01	15 / 712	Overlap_fetal_midbrain_EnhP
14	4e−01	4 / 191	Overlap_fetal_midbrain_Het
15	5e−01	11 / 641	Mid_Frontal_Lobe_EnhP
16	6e−01	21 / 1356	Fetal_K9K27me3
17	8e−01	13 / 939	Fetal_HetRpts
18	9e−01	9 / 865	Mid_Frontal_Lobe_Het
19	1e+00	19 / 1680	Fetal_ReprPCWk
20	1e+00	4 / 552	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 123	PanCan_Driver_Gene_geneset_nanostring
2	2e−03	3 / 16	GENTLES_modul14
3	5e−02	3 / 51	PanCan_TGF−B_geneset_nanostring
4	9e−02	6 / 191	SPANG_LPS−index2
5	1e−01	3 / 78	PanCan_Wnt_geneset_nanostring
6	2e−01	3 / 97	PanCan_TXmisReg_geneset_nanostring
7	2e−01	1 / 15	GENTLES_modul4
8	2e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
9	2e−01	1 / 16	GENTLES_modul6
10	3e−01	0 / 16	RHODES_CANCER_META_SIGNATURE
11	3e−01	2 / 71	SHAUGHNESSY_MM high risk
12	4e−01	6 / 324	SPANG_BCL6−index2
13	4e−01	0 / 14	LIU_PROSTATE_CANCER_UP
14	5e−01	1 / 37	KUIPER_MM good survival
15	5e−01	1 / 40	PanCan_HK_geneset_nanostring
16	5e−01	1 / 41	ZHANG_MM up
17	6e−01	1 / 50	PanCan_DNARepair_geneset_nanostring
18	6e−01	2 / 136	PanCan_CC+Apop_geneset_nanostring
19	7e−01	2 / 140	PanCan_RAS_geneset_nanostring
20	7e−01	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	3e−20	104 / 2554	nucleoplasm
2	5e−15	146 / 5101	nucleus
3	5e−06	10 / 100	chromatin
4	6e−06	78 / 2974	cytosol
5	2e−05	7 / 51	transcriptional repressor complex
6	3e−05	31 / 864	Golgi apparatus
7	4e−05	116 / 5185	cytoplasm
8	4e−05	12 / 180	nuclear speck
9	4e−05	4 / 13	COPI vesicle coat
10	3e−04	21 / 558	intracellular membrane−bounded organelle
11	6e−04	7 / 88	PML body
12	6e−04	4 / 25	PcG protein complex
13	8e−04	7 / 94	nuclear matrix
14	1e−03	3 / 14	apical junction complex
15	2e−03	3 / 15	trans−Golgi network transport vesicle
16	2e−03	10 / 204	early endosome
17	2e−03	11 / 245	lysosomal membrane
18	3e−03	24 / 799	nucleolus
19	3e−03	7 / 116	late endosome
20	3e−03	3 / 18	transcriptionally active chromatin

Chr

Rank	p−value	#in/all	Geneset
1	0.006	12 / 318	Chr 13
2	0.010	19 / 651	Chr 8
3	0.024	22 / 862	Chr 5
4	0.042	16 / 613	Chr 14
5	0.080	39 / 1920	Chr 1
6	0.141	16 / 735	Chr 4
7	0.198	5 / 191	Chr 21
8	0.246	20 / 1043	Chr 3
9	0.261	23 / 1228	Chr 2
10	0.269	14 / 715	Chr 10
11	0.278	6 / 272	Chr 18
12	0.337	10 / 522	Chr 20
13	0.467	10 / 582	Chr 15
14	0.581	16 / 1017	Chr 12
15	0.617	15 / 976	Chr 6
16	0.769	10 / 745	Chr 9
17	0.770	10 / 746	Chr X
18	0.837	5 / 436	Chr 22
19	0.967	8 / 847	Chr 16
20	0.970	8 / 859	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−51	275 / 9390	TxWk_Colon
2	2e−48	278 / 9930	Tx_Colon
3	7e−36	270 / 10475	TssA_Colon
4	9e−36	257 / 9470	Quies3_Colon
5	7e−16	257 / 11968	TssWk_Colon
6	1e−04	126 / 5889	EnhWk1_Colon
7	1e−04	99 / 4379	TssD1_Colon
8	6e−04	160 / 8123	TssF_Colon
9	1e−02	3 / 30	Marisa_CRC−cluster−c
10	2e−02	8 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	2e−02	208 / 11791	Enh_Colon
12	4e−02	2 / 21	Juehling−MSI−enriched−in−6
13	1e−01	25 / 1178	ZNF_Colon
14	1e−01	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
15	1e−01	1 / 7	Juehling−MSI−enriched−in−8−to−9
16	1e−01	3 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
17	1e−01	1 / 9	Boland_CRC−MSI−TGC
18	2e−01	1 / 10	KIM_MSI−in−EC
19	2e−01	3 / 105	Marisa_CRC−cluster−d
20	2e−01	1 / 17	TCGA_Mutated−in−CRC_non−hypermutated

Disease

Rank	p−value	#in/all	Geneset
1	0.8	8 / 608	GUDJ_psoriasis up
2	1.0	2 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−11	26 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	3e−11	78 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	7e−07	35 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	1e−06	60 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	1e−05	18 / 344	Up
6	5e−03	5 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	5e−03	5 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	9e−03	4 / 50	Vishal_subnetwork signature of survival in GBM
9	2e−02	7 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	7e−02	2 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP
11	1e−01	3 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	2e−01	3 / 83	GIEZELT_GBM_WT_down_VS_mut
13	2e−01	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
14	2e−01	2 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	3e−01	2 / 63	Stuehler_Proteins_up_in_STS
16	4e−01	2 / 81	GIEZELT_GBM_STS_up_VS_LTS
17	4e−01	2 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
18	4e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
19	5e−01	3 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
20	5e−01	1 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−27	66 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	2e−20	47 / 568	HAMAI_APOPTOSIS_VIA_TRAIL_UP
3	8e−19	70 / 1340	PUJANA_ATM_PCC_NETWORK
4	7e−18	48 / 685	SCHLOSSER_SERUM_RESPONSE_DN
5	1e−17	41 / 503	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
6	2e−17	83 / 1914	PILON_KLF1_TARGETS_DN
7	4e−17	37 / 420	SHEN_SMARCA2_TARGETS_UP
8	5e−17	39 / 471	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
9	2e−16	72 / 1563	PUJANA_BRCA1_PCC_NETWORK
10	1e−15	65 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	2e−14	43 / 683	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
12	2e−14	38 / 539	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
13	3e−14	32 / 383	OSMAN_BLADDER_CANCER_UP
14	2e−13	27 / 286	GABRIELY_MIR21_TARGETS
15	6e−13	27 / 300	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
16	5e−12	31 / 434	SENESE_HDAC1_TARGETS_UP
17	2e−10	33 / 568	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
18	4e−10	38 / 747	PUJANA_CHEK2_PCC_NETWORK
19	2e−09	38 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
20	4e−09	28 / 475	ENK_UV_RESPONSE_KERATINOCYTE_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−08	12 / 94	HALLMARK_PROTEIN_SECRETION
2	1e−02	8 / 196	HALLMARK_MITOTIC_SPINDLE
3	3e−02	5 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
4	4e−02	7 / 196	HALLMARK_P53_PATHWAY
5	5e−02	3 / 52	HALLMARK_TGF_BETA_SIGNALING
6	1e−01	6 / 199	HALLMARK_ADIPOGENESIS
7	1e−01	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	2e−01	5 / 192	HALLMARK_COMPLEMENT
9	2e−01	5 / 195	HALLMARK_MYC_TARGETS_V1
10	2e−01	3 / 98	HALLMARK_ANDROGEN_RESPONSE
11	2e−01	5 / 197	HALLMARK_E2F_TARGETS
12	2e−01	5 / 199	HALLMARK_MTORC1_SIGNALING
13	2e−01	4 / 154	HALLMARK_FATTY_ACID_METABOLISM
14	3e−01	3 / 112	HALLMARK_BILE_ACID_METABOLISM
15	4e−01	4 / 193	HALLMARK_HEME_METABOLISM
16	4e−01	3 / 140	HALLMARK_UV_RESPONSE_DN
17	4e−01	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
18	4e−01	3 / 146	HALLMARK_DNA_REPAIR
19	4e−01	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
20	5e−01	2 / 102	HALLMARK_PEROXISOME

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 33	DUMEAUX_Fasting enriched genes
2	1.0	0 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	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−58	257 / 7491	HOPP_Txn_elongation
2	2e−49	216 / 5643	HOPP_Txn_transition
3	5e−39	246 / 8358	HOPP_Active_promoter
4	3e−19	209 / 8147	HOPP_Weak_promoter
5	3e−14	188 / 7592	HOPP_Strong_enhancer
6	7e−12	161 / 6389	HOPP_Weak_txn
7	5e−09	159 / 6784	HOPP_Weak_enhancer
8	6e−06	41 / 1215	SPANG_BCR DN
9	5e−05	9 / 105	ROSOLOWSKI_blue total
10	1e−03	63 / 2658	HOPP_Repetitive
11	3e−02	14 / 500	WIRTH_lymphoma937_spot J
12	4e−02	9 / 279	SPANG_IL21 DN
13	5e−02	13 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
14	5e−02	4 / 87	ROSOLOWSKI_red total
15	1e−01	18 / 811	WIRTH_lymphoma937_spot D
16	1e−01	4 / 115	ROSOLOWSKI_green total
17	1e−01	8 / 304	ZHANG_DLBCL mutated
18	1e−01	1 / 8	MASCQUE_GCB UP
19	1e−01	27 / 1333	SPANG_BCR UP
20	1e−01	1 / 9	MASCQUE_ABC UP

MF

Rank	p−value	#in/all	Geneset
1	2e−08	220 / 10693	protein binding
2	2e−07	21 / 341	binding
3	3e−06	39 / 1091	poly(A) RNA binding
4	3e−06	55 / 1803	DNA binding
5	1e−05	9 / 89	histone deacetylase binding
6	2e−05	7 / 53	GDP binding
7	4e−05	14 / 243	transcription coactivator activity
8	8e−05	18 / 394	chromatin binding
9	8e−05	15 / 291	transcription factor binding
10	1e−04	14 / 262	ubiquitin−protein transferase activity
11	2e−04	13 / 250	GTPase activity
12	3e−04	5 / 36	RNA polymerase II activating transcription factor binding
13	3e−04	4 / 21	nuclear hormone receptor binding
14	6e−04	7 / 90	histone binding
15	7e−04	10 / 178	protein C−terminus binding
16	8e−04	13 / 286	ligase activity
17	1e−03	10 / 189	transcription corepressor activity
18	1e−03	15 / 371	GTP binding
19	1e−03	10 / 191	transcription regulatory region DNA binding
20	2e−03	3 / 16	protein kinase A regulatory subunit binding

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−16	34 / 381	hsa−miR−144
2	8e−15	33 / 391	hsa−miR−454
3	8e−15	35 / 442	hsa−miR−548n
4	1e−13	35 / 480	hsa−miR−301a
5	1e−13	26 / 260	hsa−miR−548l
6	5e−13	22 / 189	hsa−miR−1283
7	7e−13	27 / 303	hsa−miR−561
8	1e−12	28 / 334	hsa−miR−590−3p
9	5e−12	32 / 462	hsa−miR−130b
10	1e−11	33 / 509	hsa−miR−107
11	1e−11	19 / 160	hsa−miR−139−5p
12	1e−10	24 / 300	hsa−miR−186
13	2e−10	25 / 329	hsa−miR−520c−3p
14	2e−10	15 / 106	hsa−miR−1284
15	2e−10	19 / 187	hsa−miR−381
16	2e−10	21 / 233	hsa−miR−520g
17	3e−10	31 / 509	hsa−miR−103
18	4e−10	19 / 195	hsa−miR−641
19	5e−10	19 / 196	hsa−miR−520d−5p
20	5e−10	17 / 153	hsa−miR−518a−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 15	BENTINK_ras.6
2	0.18	1 / 12	BENTINK_ras.1
3	0.19	1 / 13	BENTINK_e2f3.2
4	0.20	1 / 14	BENTINK_myc.1
5	0.22	1 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 14	GUSTAFSON_PI3K_UP
7	1.00	0 / 14	BENTINK_e2f3.1
8	1.00	0 / 10	BENTINK_ras.4
9	1.00	0 / 14	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	4e−11	137 / 5173	ICGC_Taf1_targets
2	5e−11	61 / 1547	ICGC_Ets1_targets
3	9e−08	71 / 2342	ICGC_GabpPcr2_targets
4	1e−07	113 / 4470	ICGC_Creb1_targets
5	2e−07	114 / 4566	ICGC_Egr1_targets
6	4e−07	130 / 5512	ICGC_Nficsc81335_targets
7	4e−07	120 / 4969	ICGC_Atf2_targets
8	7e−07	130 / 5578	ICGC_Stat5_targets
9	9e−07	119 / 4987	ICGC_Bclaf101388_targets
10	2e−06	127 / 5526	ICGC_Pmlsc71910_targets
11	8e−06	121 / 5308	ICGC_Tcf12_targets
12	9e−06	65 / 2354	ICGC_SrfV0416101_targets
13	9e−06	47 / 1503	ICGC_Six5_targets
14	1e−05	123 / 5453	ICGC_Foxm1_targets
15	2e−05	137 / 6313	ICGC_Pou2_targets
16	6e−05	135 / 6324	ICGC_Yy1_targets
17	8e−05	118 / 5393	ICGC_Sp1_targets
18	1e−04	128 / 6005	ICGC_Mta3_targets
19	2e−04	119 / 5552	ICGC_Pol24_targets
20	3e−04	55 / 2133	ICGC_Cebpbsc150_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.005	5 / 67	VAQUERIZAS_Whole blood
2	0.013	7 / 155	VAQUERIZAS_General
3	0.108	1 / 7	VAQUERIZAS_Appendix
4	0.142	2 / 41	VAQUERIZAS_Testis
5	0.147	2 / 42	VAQUERIZAS_Thyroid
6	0.254	1 / 18	VAQUERIZAS_Pancreas
7	0.387	1 / 30	VAQUERIZAS_Smooth muscle
8	0.488	1 / 41	VAQUERIZAS_Fetal brain
9	0.520	1 / 45	VAQUERIZAS_Placenta
10	0.550	1 / 49	VAQUERIZAS_Uterus
11	1.000	0 / 33	VAQUERIZAS_Liver
12	1.000	0 / 37	VAQUERIZAS_Prostate
13	1.000	0 / 12	VAQUERIZAS_Kidney
14	1.000	0 / 25	VAQUERIZAS_Spinal cord
15	1.000	0 / 46	VAQUERIZAS_Whole brain
16	1.000	0 / 42	VAQUERIZAS_Thymus
17	1.000	0 / 31	VAQUERIZAS_Fetal lung
18	1.000	0 / 64	VAQUERIZAS_Lung
19	1.000	0 / 24	VAQUERIZAS_Trachea
20	1.000	0 / 16	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	7e−06	21 / 427	WIRTH_Immune system
2	2e−02	2 / 13	WIRTH_Cortex cerebri
3	2e−01	1 / 14	WIRTH_Thalamus
4	6e−01	4 / 259	PALMER_Granulocytes signature up
5	7e−01	2 / 140	PALMER_T−Cell signature up
6	1e+00	1 / 202	WIRTH_Testis
7	1e+00	1 / 208	PALMER_B−Cell signature up
8	1e+00	1 / 476	WIRTH_Nervous System
9	1e+00	0 / 6	WIRTH_Pituitary gland
10	1e+00	0 / 54	WIRTH_Pancreas
11	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
12	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
13	1e+00	0 / 14	WIRTH_B−cells
14	1e+00	0 / 12	WIRTH_Tonsil
15	1e+00	0 / 14	WIRTH_Thymus
16	1e+00	0 / 12	WIRTH_Lymphocytes
17	1e+00	0 / 14	WIRTH_Bone marrow
18	1e+00	0 / 13	WIRTH_Globus pallidus
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	25 / 1343	LU_BPDE 1h DN
2	1.0	68 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

Spot Summary: E

metagenes = 57
genes = 617

<r> metagenes = 0.94
<r> genes = 0.58
beta: r2= 0.05 / log p= −0.51

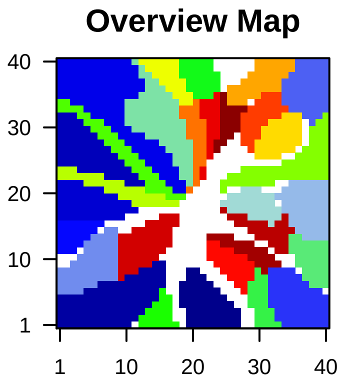
samples with spot = 4 (17.4 %)
MLH1_normHNPCC : 3 (50 %)
other_cancerHNPCC : 1 (25 %)

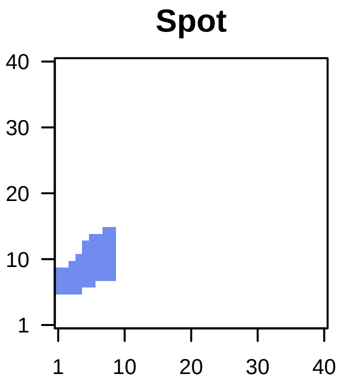
Spot Genelist

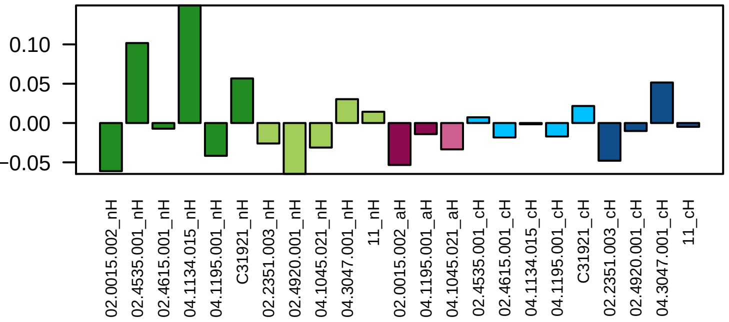
Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.54	−0.37	0.7	BHLHE40	basic helix−loop−helix family, member e40 [Source:HGNC Sy
2	ENSG000002	0.52	−0.34	0.61		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:M0
3	ENSG000002	0.51	−0.35	0.9		
4	ENSG000001	0.49	−0.2	0.78	ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HG
5	ENSG000001	0.48	−0.24	0.85	GOLGA8A	golgin A8 family, member A [Source:HGNC Symbol;Acc:HGN
6	ENSG000001	0.46	−0.28	0.9		
7	ENSG000002	0.46	−0.19	0.92	GOLGA8B	golgin A8 family, member B [Source:HGNC Symbol;Acc:HGN
8	ENSG000001	0.44	−0.23	0.44	STAT1	signal transducer and activator of transcription 1, 91kDa [Sou
9	ENSG000002	0.42	−0.33	0.91		
10	ENSG000001	0.4	−0.43	0.74	PABPC3	poly(A) binding protein, cytoplasmic 3 [Source:HGNC Symbol
11	ENSG000002	0.4	−0.28	0.92		
12	ENSG000001	0.39	−0.24	0.74	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix−loop−he
13	ENSG000001	0.39	−0.34	0.74	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
14	ENSG000001	0.39	−0.21	0.92	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
15	ENSG000002	0.38	−0.2	0.77		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3I
16	ENSG000001	0.37	−0.22	0.56	RPS15A	ribosomal protein S15a [Source:HGNC Symbol;Acc:HGNC:1
17	ENSG000001	0.37	−0.08	0.91	SLFN5	schlafen family member 5 [Source:HGNC Symbol;Acc:HGNC
18	ENSG000000	0.36	−0.15	0.46	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3
19	ENSG000001	0.36	−0.09	0.78	LPAR6	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:
20	ENSG000001	0.36	−0.26	0.88	HNRNPDL	heterogeneous nuclear ribonucleoprotein D−like [Source:HGI

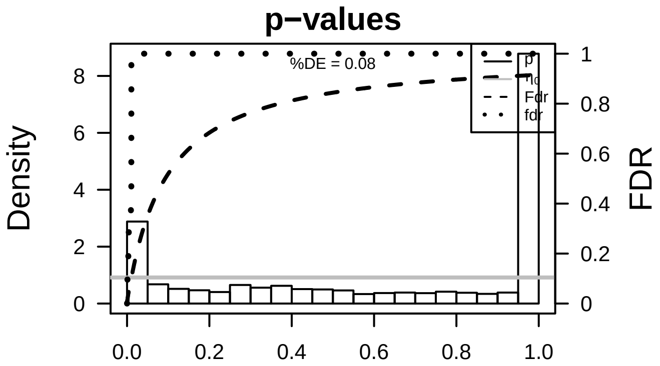
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−86	406 / 5643	Lympl	HOPP_Txn_transition
2	3e−74	450 / 7491	Lympl	HOPP_Txn_elongation
3	1e−72	410 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
4	5e−68	509 / 9930	Colon	Tx_Colon
5	3e−60	484 / 9390	Colon	TxWk_Colon
6	6e−59	510 / 10475	Colon	TssA_Colon
7	4e−55	148 / 1091	MF	poly(A) RNA binding
8	8e−55	498 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
9	2e−48	435 / 8358	Lympl	HOPP_Active_promoter
10	8e−48	218 / 2554	CC	nucleoplasm
11	8e−47	93 / 484	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
12	2e−46	94 / 500	Lympl	WIRTH_lymphoma937_spot J
13	2e−46	476 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
14	3e−45	320 / 5101	CC	nucleus
15	2e−38	140 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
16	6e−32	118 / 1134	MF	nucleic acid binding
17	2e−27	367 / 7592	Lympl	HOPP_Strong_enhancer
18	1e−26	132 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
19	7e−25	378 / 8147	Lympl	HOPP_Weak_promoter
20	1e−24	42 / 182	BP	mRNA splicing, via spliceosome
21	1e−24	90 / 855	Brain	Overlap_fetal_midbrain_ZNF
22	2e−24	47 / 237	BP	RNA splicing
23	8e−23	413 / 9470	Colon	Quies3_Colon
24	3e−22	135 / 1807	BP	transcription, DNA−templated
25	3e−22	450 / 10800	Brain	Overlap_fetal_midbrain_Quies
26	5e−22	56 / 385	MF	nucleotide binding
27	5e−21	38 / 180	CC	nuclear speck
28	5e−21	132 / 1803	MF	DNA binding
29	7e−21	35 / 151	GSEA	REACTOME_MRNA_PROCESSING
30	1e−20	63 / 513	MF	RNA binding
31	1e−20	478 / 11968	Colon	TssWk_Colon
32	1e−20	33 / 134	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
33	9e−20	80 / 820	BP	gene expression
34	9e−20	29 / 105	GSEA	REACTOME_MRNA_SPLICING
35	3e−19	148 / 2253	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
36	6e−19	36 / 183	BP	mRNA processing
37	4e−18	34 / 170	GSEA	JISON_SICKLE_CELL_DISEASE_DN
38	2e−17	35 / 191	Brain	Overlap_fetal_midbrain_Het
39	1e−16	118 / 1713	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
40	7e−16	36 / 225	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP


Overview Map


Spot




p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	1 / 123	HORVATH_aging_genes meth DOWN
2	1	1 / 144	HORVATH_aging_genes meth UP
3	1	0 / 57	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−24	42 / 182	mRNA splicing, via spliceosome
2	2e−24	47 / 237	RNA splicing
3	3e−22	135 / 1807	transcription, DNA−templated
4	9e−20	80 / 820	gene expression
5	6e−19	36 / 183	mRNA processing
6	2e−14	117 / 1808	regulation of transcription, DNA−templated
7	3e−14	24 / 109	RNA processing
8	2e−12	11 / 19	mRNA splice site selection
9	5e−10	13 / 44	termination of RNA polymerase II transcription
10	3e−09	12 / 41	mRNA 3'−end processing
11	6e−09	9 / 21	negative regulation of mRNA splicing, via spliceosome
12	4e−08	41 / 512	transcription from RNA polymerase II promoter
13	5e−08	9 / 26	regulation of RNA splicing
14	7e−08	13 / 64	mRNA export from nucleus
15	1e−07	19 / 142	translational initiation
16	3e−07	41 / 549	viral process
17	6e−07	8 / 25	RNA splicing, via transesterification reactions
18	2e−06	24 / 259	translation
19	3e−06	21 / 208	chromatin organization
20	6e−06	54 / 913	positive regulation of transcription from RNA polymerase II promoter

Brain

Rank	p−value	#in/all	Geneset
1	1e−72	410 / 6320	Overlap_fetal_midbrain_HetRpts
2	8e−55	498 / 10239	Overlap_fetal_midbrain_ReprPC
3	2e−46	476 / 9923	Overlap_fetal_midbrain_K9K27me3
4	1e−24	90 / 855	Overlap_fetal_midbrain_ZNF
5	3e−22	450 / 10800	Overlap_fetal_midbrain_Quies
6	2e−17	35 / 191	Overlap_fetal_midbrain_Het
7	1e−14	412 / 10278	Overlap_fetal_midbrain_ReprPCWk
8	2e−09	163 / 3370	Mid_Frontal_Lobe_ZNF
9	3e−03	42 / 865	Mid_Frontal_Lobe_Het
10	3e−03	36 / 712	Overlap_fetal_midbrain_EnhP
11	1e−02	51 / 1182	Fetal_EnhP
12	3e−02	66 / 1680	Fetal_ReprPCWk
13	5e−02	19 / 400	Fetal_ZNF
14	2e−01	14 / 342	Fetal_Het
15	2e−01	34 / 939	Fetal_HetRpts
16	3e−01	32 / 910	Fetal_EnhG
17	4e−01	38 / 1137	Fetal_Enh
18	5e−01	20 / 641	Mid_Frontal_Lobe_EnhP
19	7e−01	6 / 232	Fetal_ReprPC
20	9e−01	34 / 1356	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	5e−04	12 / 123	PanCan_Driver_Gene_geneset_nanostring
2	1e−03	4 / 16	GENTLES_modul14
3	1e−03	1 / 16	LIU_COMMON_CANCER_GENES
4	1e−02	18 / 324	SPANG_BCL6−index2
5	2e−02	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	3e−02	3 / 22	PanCan_ChromMod_geneset_nanostring
7	4e−02	4 / 41	ZHANG_MM up
8	8e−02	4 / 52	KUIPER_MM poor survival
9	1e−01	3 / 40	PanCan_HK_geneset_nanostring
10	1e−01	9 / 191	SPANG_LPS−index2
11	2e−01	1 / 9	WANG_ER_DN
12	3e−01	6 / 136	PanCan_CC+Apop_geneset_nanostring
13	3e−01	1 / 10	GENTLES_modul3
14	3e−01	2 / 37	KUIPER_MM good survival
15	4e−01	1 / 14	LIU_PROSTATE_CANCER_UP
16	4e−01	1 / 14	GENTLES_modul12
17	4e−01	4 / 97	PanCan_TXmisReg_geneset_nanostring
18	4e−01	1 / 15	LIU_BREAST_CANCER
19	4e−01	1 / 15	BEN−PORATH_UP
20	4e−01	1 / 16	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	8e−48	218 / 2554	nucleoplasm
2	3e−45	320 / 5101	nucleus
3	5e−21	38 / 180	nuclear speck
4	2e−13	67 / 799	nucleolus
5	6e−12	19 / 82	catalytic step 2 spliceosome
6	1e−09	20 / 121	ribonucleoprotein complex
7	2e−08	16 / 92	spliceosomal complex
8	3e−07	9 / 31	cytoplasmic stress granule
9	4e−06	212 / 5185	cytoplasm
10	8e−05	8 / 46	Cajal body
11	9e−05	11 / 88	chromosome
12	2e−04	4 / 10	viral nucleocapsid
13	2e−04	76 / 1604	intracellular
14	5e−04	5 / 22	histone methyltransferase complex
15	1e−03	4 / 15	U1 snRNP
16	1e−03	5 / 26	MLL1 complex
17	1e−03	10 / 100	chromatin
18	1e−03	4 / 16	eukaryotic translation initiation factor 3 complex
19	2e−03	6 / 41	chromosome, telomeric region
20	2e−03	7 / 59	cytosolic large ribosomal subunit

Chr

Rank	p−value	#in/all	Geneset
1	0.06	41 / 1017	Chr 12
2	0.08	41 / 1043	Chr 3
3	0.13	33 / 859	Chr 7
4	0.15	21 / 522	Chr 20
5	0.15	23 / 582	Chr 15
6	0.16	68 / 1920	Chr 1
7	0.20	13 / 318	Chr 13
8	0.23	35 / 976	Chr 6
9	0.39	7 / 191	Chr 21
10	0.53	27 / 862	Chr 5
11	0.57	22 / 715	Chr 10
12	0.64	35 / 1172	Chr 11
13	0.65	25 / 847	Chr 16
14	0.72	21 / 746	Chr X
15	0.73	31 / 1083	Chr 17
16	0.73	17 / 613	Chr 14
17	0.74	18 / 651	Chr 8
18	0.75	7 / 272	Chr 18
19	0.84	19 / 735	Chr 4
20	0.88	10 / 436	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−68	509 / 9930	Tx_Colon
2	3e−60	484 / 9390	TxWk_Colon
3	6e−59	510 / 10475	TssA_Colon
4	8e−23	413 / 9470	Quies3_Colon
5	1e−20	478 / 11968	TssWk_Colon
6	9e−14	343 / 8123	TssF_Colon
7	1e−11	59 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	3e−10	157 / 3122	TxEnhG1_Colon
9	9e−09	58 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
10	2e−05	417 / 11791	Enh_Colon
11	3e−05	259 / 6761	TssD2_Colon
12	3e−05	7 / 30	Marisa_CRC−cluster−c
13	4e−05	62 / 1178	ZNF_Colon
14	5e−05	229 / 5889	EnhWk1_Colon
15	5e−05	178 / 4379	TssD1_Colon
16	7e−05	49 / 877	TxEnhG2_Colon
17	6e−04	9 / 76	Marisa_CRC−cluster−g
18	2e−02	8 / 105	Marisa_CRC−cluster−d
19	2e−02	18 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
20	4e−02	2 / 10	KIM_CRC−MSI−regulated_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.7	1 / 37	BCHETNIA_EBM−DM up
2	1.0	11 / 608	GUDJ_psoriasis up
3	1.0	5 / 399	GUDJ_psoriasis down
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−19	148 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−13	122 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−08	31 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	4e−07	6 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
5	7e−07	55 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
6	2e−05	5 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
7	2e−04	24 / 344	Up
8	3e−04	9 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	6e−03	2 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
10	6e−03	7 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	2e−02	5 / 50	Vishal_subnetwork signature of survival in GBM
12	5e−02	3 / 27	Barbus_GBM_STS_vs._LTS
13	7e−02	2 / 14	Christensen_hypermethylated_in_ependymoma
14	9e−02	2 / 16	VERHAAK_CL subtype
15	9e−02	2 / 16	VERHAAK_PN subtype
16	1e−01	2 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
17	1e−01	6 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
18	2e−01	5 / 90	Weller_LGG_A_vs_O_DOWN
19	2e−01	6 / 119	GIEZELT_GBM_WT_up_VS_mut
20	2e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−38	140 / 1340	PUJANA_ATM_PCC_NETWORK
2	1e−26	132 / 1563	PUJANA_BRCA1_PCC_NETWORK
3	7e−21	35 / 151	REACTOME_MRNA_PROCESSING
4	1e−20	33 / 134	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
5	9e−20	29 / 105	REACTOME_MRNA_SPLICING
6	4e−18	34 / 170	JISON_SICKLE_CELL_DISEASE_DN
7	1e−16	118 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
8	7e−16	36 / 225	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
9	2e−15	68 / 747	PUJANA_CHEK2_PCC_NETWORK
10	3e−15	29 / 150	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
11	4e−15	123 / 1914	PILON_KLF1_TARGETS_DN
12	5e−15	45 / 368	OSMAN_BLADDER_CANCER_DN
13	2e−13	28 / 162	PUJANA_XPRSS_INT_NETWORK
14	3e−13	24 / 120	KEGG_SPLICEOSOME
15	9e−13	44 / 408	PUJANA_BRCA2_PCC_NETWORK
16	8e−12	13 / 33	REACTOME_MRNA_3_END_PROCESSING
17	2e−11	42 / 414	ZHANG_BREAST_CANCER_PROGENITORS_UP
18	2e−11	35 / 301	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
19	4e−11	19 / 90	HOEBEKE_LYMPHOID_STEM_CELL_UP
20	7e−11	79 / 1168	MARSON_BOUND_BY_FOXP3_UNSTIMULATED

HM

Rank	p−value	#in/all	Geneset
1	4e−06	20 / 197	HALLMARK_E2F_TARGETS
2	5e−05	18 / 196	HALLMARK_G2M_CHECKPOINT
3	1e−04	17 / 195	HALLMARK_MYC_TARGETS_V1
4	7e−02	8 / 140	HALLMARK_UV_RESPONSE_DN
5	9e−02	8 / 146	HALLMARK_DNA_REPAIR
6	1e−01	6 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e−01	5 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	2e−01	9 / 198	HALLMARK_HYPOXIA
9	2e−01	5 / 94	HALLMARK_PROTEIN_SECRETION
10	2e−01	5 / 98	HALLMARK_ANDROGEN_RESPONSE
11	3e−01	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	3e−01	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
13	4e−01	7 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	4e−01	4 / 102	HALLMARK_PEROXISOME
15	4e−01	4 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
16	5e−01	6 / 181	HALLMARK_ALLOGRAFT_REJECTION
17	5e−01	5 / 155	HALLMARK_UV_RESPONSE_UP
18	6e−01	6 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	6e−01	6 / 196	HALLMARK_MITOTIC_SPINDLE
20	6e−01	6 / 197	HALLMARK_IL2_STAT5_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	6e−06	8 / 33	DUMEAUX_Fasting enriched genes
2	3e−01	1 / 11	DUMEAUX_Women normal BMI literature genes up
3	9e−01	1 / 91	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 11	DUMEAUX_Smoking literature genes up
5	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1e+00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−86	406 / 5643	HOPP_Txn_transition
2	3e−74	450 / 7491	HOPP_Txn_elongation
3	2e−48	435 / 8358	HOPP_Active_promoter
4	8e−47	93 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
5	2e−46	94 / 500	WIRTH_lymphoma937_spot J
6	2e−27	367 / 7592	HOPP_Strong_enhancer
7	7e−25	378 / 8147	HOPP_Weak_promoter
8	8e−13	86 / 1215	SPANG_BCR DN
9	3e−08	32 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	5e−08	32 / 347	WIRTH_lymphoma937_spot H
11	2e−04	255 / 6784	HOPP_Weak_enhancer
12	8e−04	28 / 466	SPANG_CD40 6hrs DN
13	6e−03	9 / 105	ROSOLOWSKI_blue total
14	8e−03	228 / 6389	HOPP_Weak_txn
15	1e−02	6 / 63	SPANG_BAFF 9hrs DN
16	3e−02	8 / 115	ROSOLOWSKI_green total
17	3e−02	15 / 279	SPANG_IL21 DN
18	1e−01	3 / 38	TARTE_B−cell signature
19	1e−01	2 / 20	DAVE_BL Inter
20	2e−01	2 / 22	DAVE_NFkB BL DN

MF

Rank	p−value	#in/all	Geneset
1	4e−55	148 / 1091	poly(A) RNA binding
2	6e−32	118 / 1134	nucleic acid binding
3	5e−22	56 / 385	nucleotide binding
4	5e−21	132 / 1803	DNA binding
5	1e−20	63 / 513	RNA binding
6	1e−10	410 / 10693	protein binding
7	1e−08	36 / 394	chromatin binding
8	2e−07	25 / 243	transcription coactivator activity
9	3e−07	60 / 962	transcription factor activity, sequence−specific DNA binding
10	1e−06	6 / 13	poly(A) binding
11	4e−06	12 / 76	helicase activity
12	8e−06	64 / 1164	zinc ion binding
13	2e−05	24 / 291	transcription factor binding
14	2e−05	7 / 29	ATP−dependent DNA helicase activity
15	3e−05	12 / 93	mRNA binding
16	1e−04	5 / 17	histone methyltransferase activity (H3−K4 specific)
17	1e−04	5 / 17	lysine−acetylated histone binding
18	1e−04	9 / 63	ATP−dependent RNA helicase activity
19	2e−04	6 / 27	thyroid hormone receptor binding
20	4e−04	16 / 191	transcription regulatory region DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−12	47 / 482	hsa−miR−195
2	4e−11	35 / 307	hsa−miR−548c−3p
3	1e−10	31 / 257	hsa−miR−524−5p
4	4e−10	33 / 300	hsa−miR−186
5	6e−10	26 / 197	hsa−miR−330−3p
6	6e−10	26 / 197	hsa−miR−548d−3p
7	8e−10	31 / 276	hsa−miR−30a
8	1e−09	31 / 279	hsa−miR−577
9	1e−09	29 / 248	hsa−miR−122
10	1e−09	31 / 280	hsa−miR−30d
11	2e−09	43 / 493	hsa−miR−15b
12	2e−09	31 / 283	hsa−miR−1244
13	2e−09	34 / 334	hsa−miR−590−3p
14	2e−09	24 / 179	hsa−miR−607
15	3e−09	25 / 196	hsa−miR−513a−3p
16	3e−09	25 / 196	hsa−miR−520d−5p
17	3e−09	43 / 504	hsa−miR−16
18	7e−09	26 / 220	hsa−miR−199a−3p
19	1e−08	30 / 289	hsa−miR−320a
20	1e−08	22 / 165	hsa−miR−512−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 14	BENTINK_src.2
2	8e−02	2 / 15	BENTINK_ras.6
3	3e−01	1 / 13	BENTINK_e2f3.2
4	4e−01	1 / 14	GUSTAFSON_PI3K_UP
5	4e−01	1 / 14	BENTINK_myc.1
6	4e−01	1 / 14	BENTINK_src.10
7	4e−01	1 / 15	GUSTAFSON_PI3K_DN
8	1e+00	0 / 14	BENTINK_e2f3.1
9	1e+00	0 / 12	BENTINK_ras.1
10	1e+00	0 / 10	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	5e−12	238 / 5173	ICGC_Taf1_targets
2	3e−11	97 / 1547	ICGC_Ets1_targets
3	5e−11	85 / 1294	KIM_MYC targets
4	3e−10	243 / 5512	ICGC_Nficsc81335_targets
5	5e−10	126 / 2342	ICGC_GabpPcr2_targets
6	1e−09	204 / 4470	ICGC_Creb1_targets
7	4e−09	240 / 5578	ICGC_Stat5_targets
8	6e−09	114 / 2133	ICGC_Cebpbsc150_targets
9	7e−09	90 / 1549	ICGC_Myc_targets
10	1e−08	217 / 4969	ICGC_Atf2_targets
11	2e−08	190 / 4230	ICGC_Nfatc1_targets
12	2e−07	228 / 5453	ICGC_Foxm1_targets
13	2e−07	197 / 4566	ICGC_Egr1_targets
14	4e−07	255 / 6313	ICGC_Pou2_targets
15	5e−07	82 / 1503	ICGC_Six5_targets
16	8e−07	209 / 4987	ICGC_Bclaf101388_targets
17	1e−06	226 / 5526	ICGC_Pmlsc71910_targets
18	7e−06	103 / 2149	ICGC_Mef2_targets
19	1e−05	213 / 5308	ICGC_Tcf12_targets
20	2e−05	109 / 2354	ICGC_SrfV0416101_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	4e−04	14 / 155	VAQUERIZAS_General
2	3e−03	5 / 31	VAQUERIZAS_Lymph node
3	4e−03	4 / 22	VAQUERIZAS_Tonsil
4	5e−03	7 / 67	VAQUERIZAS_Whole blood
5	1e−02	5 / 42	VAQUERIZAS_Thymus
6	1e−02	4 / 30	VAQUERIZAS_Smooth muscle
7	1e−01	2 / 17	VAQUERIZAS_Salivary gland
8	1e−01	3 / 41	VAQUERIZAS_Fetal brain
9	1e−01	3 / 42	VAQUERIZAS_Thyroid
10	2e−01	2 / 23	VAQUERIZAS_Pituitary
11	3e−01	1 / 12	VAQUERIZAS_Kidney
12	3e−01	3 / 64	VAQUERIZAS_Lung
13	4e−01	1 / 16	VAQUERIZAS_Fetal liver
14	4e−01	1 / 16	VAQUERIZAS_Fetal thyroid
15	4e−01	2 / 45	VAQUERIZAS_Placenta
16	4e−01	1 / 17	VAQUERIZAS_Adrenal gland
17	4e−01	1 / 18	VAQUERIZAS_Pancreas
18	5e−01	1 / 20	VAQUERIZAS_Bone marrow
19	5e−01	1 / 24	VAQUERIZAS_Trachea
20	6e−01	1 / 31	VAQUERIZAS_Fetal lung

Tissue

Rank	p−value	#in/all	Geneset
1	7e−14	47 / 427	WIRTH_Immune system
2	6e−03	14 / 208	PALMER_B−Cell signature up
3	2e−01	2 / 30	PALMER_Lymphocytes signature up
4	3e−01	1 / 12	WIRTH_Lymphocytes
5	3e−01	1 / 13	WIRTH_Globus pallidus
6	4e−01	1 / 15	WIRTH_Cerebellum
7	9e−01	5 / 259	PALMER_Granulocytes signature up
8	9e−01	2 / 140	PALMER_T−Cell signature up
9	1e+00	2 / 202	WIRTH_Testis
10	1e+00	2 / 476	WIRTH_Nervous System
11	1e+00	0 / 6	WIRTH_Pituitary gland
12	1e+00	0 / 54	WIRTH_Pancreas
13	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
14	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
15	1e+00	0 / 14	WIRTH_B−cells
16	1e+00	0 / 12	WIRTH_Tonsil
17	1e+00	0 / 14	WIRTH_Thymus
18	1e+00	0 / 14	WIRTH_Bone marrow
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 13	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	48 / 1343	LU_BPDE 1h DN
2	1.0	102 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

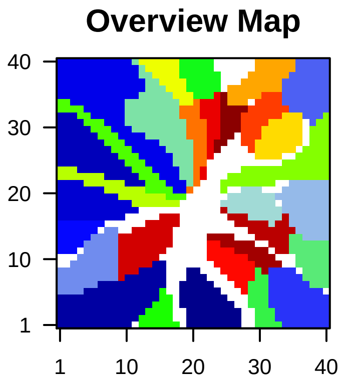
Correlation Clusters

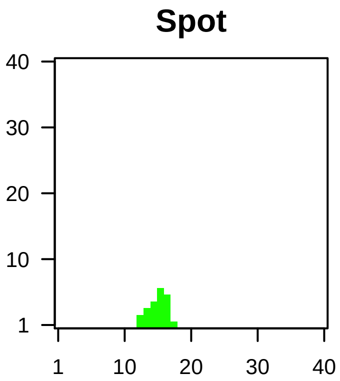
Spot Summary: F

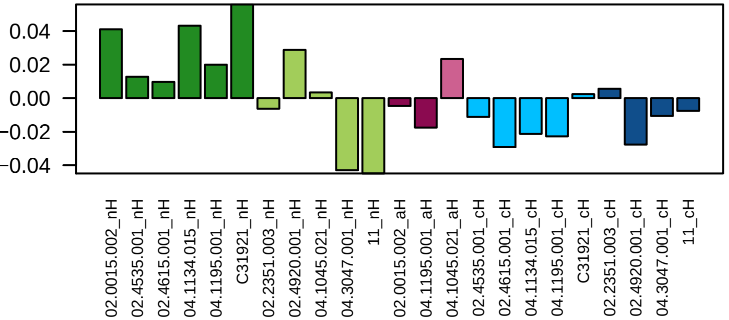
metagenes = 21
genes = 186

<r> metagenes = 0.94
<r> genes = 0.4
beta: r2= 0.01 / log p= −0.2

samples with spot = 1 (4.3 %)
MLH1_normHNPCC : 1 (16.7 %)


Overview Map


Spot

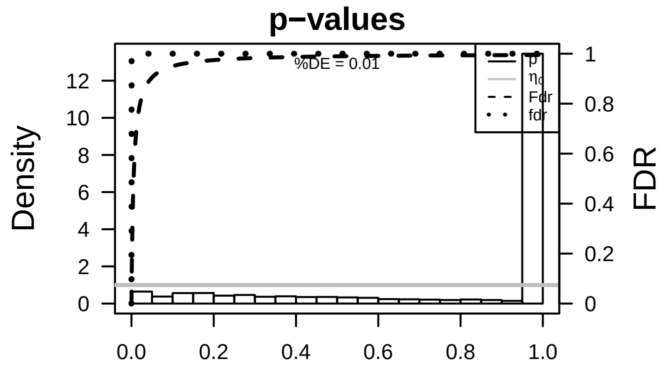


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.46	−0.14	0.64	CENPT	centromere protein T [Source:HGNC Symbol;Acc:HGNC:257
2	ENSG000001	0.37	−0.11	0.41		
3	ENSG000001	0.35	−0.07	0.5	ABCC5	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
4	ENSG000001	0.31	−0.14	0.43	LDLR	low density lipoprotein receptor [Source:HGNC Symbol;Acc:
5	ENSG000000	0.27	−0.02	0.38	DDX3Y	DEAD (Asp−Glu−Ala−Asp) box helicase 3, Y−linked [Source:
6	ENSG000000	0.27	−0.02	0.44	KDM5D	lysine (K)−specific demethylase 5D [Source:HGNC Symbol;A
7	ENSG000001	0.26	−0.1	0.57	PLEC	plectin [Source:HGNC Symbol;Acc:HGNC:9069]
8	ENSG000002	0.22	−0.09	0.71	SAP25	Sin3A−associated protein, 25kDa [Source:HGNC Symbol;Ac
9	ENSG000001	0.21	−0.19	0.74	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 [Sour
10	ENSG000002	0.21	−0.11	0.46	PPP1R10	protein phosphatase 1, regulatory subunit 10 [Source:HGNC
11	ENSG000001	0.2	−0.08	0.51	FAM43A	family with sequence similarity 43, member A [Source:HGNC
12	ENSG000001	0.19	−0.08	0.53	NPIPB6	nuclear pore complex interacting protein family, member B6 [
13	ENSG000002	0.19	−0.23	0.73	AP1G2	adaptor−related protein complex 1, gamma 2 subunit [Source
14	ENSG000000	0.19	−0.07	0.6	UNC13D	unc−13 homolog D (C. elegans) [Source:HGNC Symbol;Acc:
15	ENSG000001	0.19	−0.13	0.7	TRIM25	tripartite motif containing 25 [Source:HGNC Symbol;Acc:HG
16	ENSG000001	0.18	−0.12	0.47	FOXO3	forkhead box O3 [Source:HGNC Symbol;Acc:HGNC:3821]
17	ENSG000001	0.18	−0.14	0.68	RSRP1	arginine/serine−rich protein 1 [Source:HGNC Symbol;Acc:HG
18	ENSG000001	0.18	−0.16	0.62	TCIRG1	T−cell, immune regulator 1, ATPase, H+ transporting, lysoso
19	ENSGR00001	0.18	−0.05	0.64		
20	ENSG000001	0.18	−0.14	0.45	STK38	serine/threonine kinase 38 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−13	143 / 9930	Colon	Tx_Colon
2	4e−13	121 / 7592	Lymph	HOPP_Strong_enhancer
3	7e−13	70 / 3122	Colon	TxEnhG1_Colon
4	1e−11	144 / 10475	Colon	TssA_Colon
5	2e−11	97 / 5643	Lymph	HOPP_Txn_transition
6	6e−11	133 / 9390	Colon	TxWk_Colon
7	8e−11	121 / 8123	Colon	TssF_Colon
8	1e−08	61 / 3112	Colon	EnhA_Colon
9	2e−07	77 / 4714	TF	ICGC_Pu1_targets
10	2e−07	145 / 11791	Colon	Enh_Colon
11	4e−07	19 / 500	Lymph	WIRTH_lymphoma937_spot J
12	5e−07	128 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
13	7e−07	84 / 5512	TF	ICGC_Nficsc81335_targets
14	8e−07	80 / 5173	TF	ICGC_Taf1_targets
15	9e−07	135 / 10800	Brain	Overlap_fetal_midbrain_Quies
16	9e−07	104 / 7491	Lymph	HOPP_Txn_elongation
17	1e−06	59 / 3370	Brain	Mid_Frontal_Lobe_ZNF
18	1e−06	87 / 5889	Colon	EnhWk1_Colon
19	2e−06	43 / 2149	TF	ICGC_Mef2_targets
20	2e−06	71 / 4470	TF	ICGC_Creb1_targets
21	4e−06	17 / 484	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
22	8e−06	80 / 5453	TF	ICGC_Foxm1_targets
23	9e−06	89 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
24	1e−05	81 / 5578	TF	ICGC_Stat5_targets
25	1e−05	93 / 6761	Colon	TssD2_Colon
26	1e−05	94 / 6862	TF	ICGC_Elf1_targets
27	1e−05	80 / 5526	TF	ICGC_Pmlsc71910_targets
28	1e−05	48 / 2719	TF	ICGC_Pbx3_targets
29	1e−05	55 / 3305	TF	ICGC_BatfPcr1_targets
30	2e−05	88 / 6313	TF	ICGC_Pou2_targets
31	2e−05	97 / 7202	TF	ICGC_Runx3_targets
32	2e−05	53 / 3177	TF	ICGC_Irf4_targets
33	3e−05	37 / 1914	GSEA	PILON_KLF1_TARGETS_DN
34	3e−05	13 / 347	Lymph	WIRTH_lymphoma937_spot H
35	4e−05	68 / 4566	TF	ICGC_Egr1_targets
36	4e−05	76 / 5308	TF	ICGC_Tcf12_targets
37	5e−05	72 / 4969	TF	ICGC_Atf2_targets
38	5e−05	83 / 6005	TF	ICGC_Mta3_targets
39	6e−05	78 / 5552	TF	ICGC_Pol24_targets
40	9e−05	63 / 4230	TF	ICGC_Nfatc1_targets


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 123	HORVATH_aging_genes meth DOWN
2	0.4	1 / 57	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 144	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	6e−04	3 / 18	negative regulation of MAPK cascade
2	3e−03	6 / 150	endocytosis
3	4e−03	3 / 32	mitotic cell cycle checkpoint
4	4e−03	3 / 33	negative regulation of protein kinase B signaling
5	4e−03	2 / 10	protein deglycosylation
6	4e−03	2 / 10	Rap protein signal transduction
7	4e−03	3 / 34	negative regulation of MAP kinase activity
8	4e−03	5 / 111	dephosphorylation
9	7e−03	13 / 617	protein phosphorylation
10	8e−03	7 / 237	in utero embryonic development
11	8e−03	4 / 83	positive regulation of peptidyl−tyrosine phosphorylation
12	9e−03	5 / 132	protein polyubiquitination
13	9e−03	8 / 304	DNA repair
14	1e−02	7 / 246	cell surface receptor signaling pathway
15	1e−02	6 / 191	lipid metabolic process
16	1e−02	2 / 17	oocyte maturation
17	1e−02	3 / 52	positive regulation of proteasomal ubiquitin−dependent protein catabolic proce
18	1e−02	4 / 97	peptidyl−tyrosine dephosphorylation
19	2e−02	2 / 20	melanosome organization
20	2e−02	3 / 55	post−Golgi vesicle−mediated transport

Brain

Rank	p−value	#in/all	Geneset
1	5e−07	128 / 9923	Overlap_fetal_midbrain_K9K27me3
2	9e−07	135 / 10800	Overlap_fetal_midbrain_Quies
3	1e−06	59 / 3370	Mid_Frontal_Lobe_ZNF
4	9e−06	89 / 6320	Overlap_fetal_midbrain_HetRpts
5	4e−03	116 / 10239	Overlap_fetal_midbrain_ReprPC
6	2e−02	15 / 865	Mid_Frontal_Lobe_Het
7	3e−02	18 / 1182	Fetal_EnhP
8	4e−02	14 / 855	Overlap_fetal_midbrain_ZNF
9	5e−02	110 / 10278	Overlap_fetal_midbrain_ReprPCWk
10	6e−02	35 / 2820	Mid_Frontal_Lobe_HetRpts
11	2e−01	20 / 1680	Fetal_ReprPCWk
12	2e−01	29 / 2603	Fetal_TxTrans
13	2e−01	5 / 342	Fetal_Het
14	2e−01	9 / 712	Overlap_fetal_midbrain_EnhP
15	3e−01	3 / 191	Overlap_fetal_midbrain_Het
16	3e−01	27 / 2549	Fetal_TssF
17	3e−01	5 / 400	Fetal_ZNF
18	5e−01	39 / 3977	Mid_Frontal_Lobe_ReprPC
19	5e−01	11 / 1084	Overlap_fetal_midbrain_EnhG
20	6e−01	28 / 2956	Fetal_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	2 / 40	PanCan_HK_geneset_nanostring
2	0.09	6 / 324	SPANG_BCL6−index2
3	0.13	1 / 15	LIU_BREAST_CANCER
4	0.30	0 / 16	LIU_LIVER_CANCER
5	0.55	2 / 191	SPANG_LPS−index2
6	0.73	1 / 136	PanCan_CC+Apop_geneset_nanostring
7	0.99	0 / 16	LIU_PROSTATE_CANCER_DN
8	1.00	1 / 574	Lembcke_Colonic Inflammation
9	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
10	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
11	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.00	0 / 16	LIU_COMMON_CANCER_GENES
14	1.00	0 / 14	LIU_PROSTATE_CANCER_UP
15	1.00	0 / 16	WANG_ER_UP
16	1.00	0 / 9	WANG_ER_DN
17	1.00	0 / 16	WOLFER_overlap genes
18	1.00	0 / 14	BEN−PORATH_DN
19	1.00	0 / 15	BEN−PORATH_UP
20	1.00	0 / 16	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 14	Golgi−associated vesicle
2	2e−03	6 / 135	cytoplasmic membrane−bounded vesicle
3	3e−03	8 / 245	lysosomal membrane
4	5e−03	2 / 11	CD40 receptor complex
5	5e−03	2 / 11	clathrin−coated vesicle membrane
6	6e−03	3 / 39	recycling endosome membrane
7	9e−03	3 / 45	cleavage furrow
8	1e−02	3 / 53	clathrin−coated vesicle
9	1e−02	4 / 98	recycling endosome
10	2e−02	3 / 55	coated pit
11	2e−02	2 / 22	clathrin adaptor complex
12	2e−02	3 / 61	intermediate filament cytoskeleton
13	3e−02	4 / 121	trans−Golgi network
14	4e−02	2 / 32	membrane coat
15	4e−02	3 / 77	ruffle membrane
16	5e−02	9 / 497	Golgi membrane
17	5e−02	38 / 3059	membrane
18	5e−02	2 / 39	clathrin−coated endocytic vesicle membrane
19	6e−02	2 / 43	cytoplasmic side of plasma membrane
20	7e−02	3 / 100	chromatin

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	19 / 847	Chr 16
2	2e−03	21 / 1083	Chr 17
3	1e−02	10 / 436	Chr 22
4	3e−02	2 / 30	Chr Y
5	3e−01	7 / 582	Chr 15
6	4e−01	13 / 1228	Chr 2
7	4e−01	11 / 1043	Chr 3
8	4e−01	8 / 745	Chr 9
9	5e−01	10 / 976	Chr 6
10	5e−01	3 / 272	Chr 18
11	6e−01	5 / 522	Chr 20
12	7e−01	10 / 1172	Chr 11
13	7e−01	5 / 613	Chr 14
14	7e−01	7 / 859	Chr 7
15	7e−01	7 / 862	Chr 5
16	8e−01	8 / 1017	Chr 12
17	8e−01	15 / 1920	Chr 1
18	8e−01	5 / 735	Chr 4
19	9e−01	10 / 1425	Chr 19
20	9e−01	4 / 746	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−13	143 / 9930	Tx_Colon
2	7e−13	70 / 3122	TxEnhG1_Colon
3	1e−11	144 / 10475	TssA_Colon
4	6e−11	133 / 9390	TxWk_Colon
5	8e−11	121 / 8123	TssF_Colon
6	1e−08	61 / 3112	EnhA_Colon
7	2e−07	145 / 11791	Enh_Colon
8	1e−06	87 / 5889	EnhWk1_Colon
9	1e−05	93 / 6761	TssD2_Colon
10	3e−04	137 / 11968	TssWk_Colon
11	3e−03	110 / 9470	Quies3_Colon
12	4e−03	2 / 10	Juehling−MSI−enriched−in−7
13	4e−02	14 / 877	TxEnhG2_Colon
14	8e−02	3 / 105	Marisa_CRC−cluster−d
15	8e−02	2 / 49	Marisa_CRC−cluster−f
16	8e−02	1 / 9	Marisa_CRC−C2
17	9e−02	1 / 10	TCGA−CRC_agressive−disease−markers
18	2e−01	2 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
19	2e−01	1 / 20	Juehling_HNPCC−mutated−in−4
20	2e−01	7 / 532	K9acLow_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.4	7 / 608	GUDJ_psoriasis up
2	1.0	0 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
2	0.054	2 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
3	0.083	2 / 50	Vishal_subnetwork signature of survival in GBM
4	0.091	3 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
5	0.092	2 / 53	Donson−innate immunity−associated with LTS in HGA
6	0.101	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
7	0.109	1 / 12	Phillips PN up vs MES & Prolif
8	0.134	12 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
9	0.143	1 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
10	0.145	2 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	0.151	1 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
12	0.182	2 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	0.235	5 / 344	Up
14	0.293	1 / 36	Shaw_down_in_1p19q
15	0.343	21 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
16	0.372	4 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
17	0.394	1 / 52	OL vs. OPC
18	0.412	2 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
19	0.434	1 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
20	0.455	1 / 63	Stuehler_Proteins_up_in_STS

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	37 / 1914	PILON_KLF1_TARGETS_DN
2	1e−04	8 / 149	SENGUPTA_EBNA1_ANTICORRELATED
3	3e−04	11 / 321	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
4	4e−04	23 / 1103	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
5	7e−04	12 / 413	MITSIADES_RESPONSE_TO_APLIDIN_UP
6	7e−04	10 / 301	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
7	8e−04	10 / 307	DOUGLAS_BMI1_TARGETS_DN
8	2e−03	11 / 397	FOSTER_TOLERANT_MACROPHAGE_DN
9	2e−03	2 / 7	RUNNE_GENDER_EFFECT_UP
10	2e−03	17 / 804	CUI_TCF21_TARGETS_2_DN
11	2e−03	6 / 138	HUANG_GATA2_TARGETS_UP
12	3e−03	3 / 30	REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBA
13	3e−03	6 / 150	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
14	4e−03	3 / 33	HAN_JNK_SINGALING_UP
15	4e−03	2 / 10	RADAEVA_RESPONSE_TO_IFNA1_DN
16	6e−03	3 / 38	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
17	6e−03	3 / 39	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP
18	7e−03	3 / 40	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_UP
19	7e−03	3 / 41	XU_CREBBP_TARGETS_DN
20	8e−03	8 / 297	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN

HM

Rank	p−value	#in/all	Geneset
1	0.09	3 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	0.10	4 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.11	4 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	0.11	4 / 193	HALLMARK_KRAS_SIGNALING_DN
5	0.12	4 / 196	HALLMARK_P53_PATHWAY
6	0.17	3 / 146	HALLMARK_DNA_REPAIR
7	0.19	3 / 157	HALLMARK_APOPTOSIS
8	0.21	2 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
9	0.23	2 / 94	HALLMARK_PROTEIN_SECRETION
10	0.28	3 / 194	HALLMARK_INFLAMMATORY_RESPONSE
11	0.35	1 / 44	HALLMARK_APICAL_SURFACE
12	0.35	2 / 128	HALLMARK_SPERMATOGENESIS
13	0.44	2 / 155	HALLMARK_UV_RESPONSE_UP
14	0.50	1 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	0.52	2 / 181	HALLMARK_ALLOGRAFT_REJECTION
16	0.56	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
17	0.56	2 / 195	HALLMARK_MYOGENESIS
18	0.56	2 / 196	HALLMARK_MITOTIC_SPINDLE
19	0.57	2 / 199	HALLMARK_MTORC1_SIGNALING
20	0.61	1 / 98	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 91	DUMEAUX_Smoking enriched genes
2	1	0 / 11	DUMEAUX_Smoking literature genes up
3	1	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 17	DUMEAUX_High bmi enriched genes
11	1	0 / 33	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−13	121 / 7592	HOPP_Strong_enhancer
2	2e−11	97 / 5643	HOPP_Txn_transition
3	4e−07	19 / 500	WIRTH_lymphoma937_spot J
4	9e−07	104 / 7491	HOPP_Txn_elongation
5	4e−06	17 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
6	3e−05	13 / 347	WIRTH_lymphoma937_spot H
7	1e−04	12 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
8	4e−04	103 / 8358	HOPP_Active_promoter
9	6e−04	24 / 1215	SPANG_BCR DN
10	1e−03	3 / 21	ROSOLOWSKI_red UP
11	2e−03	5 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
12	1e−02	4 / 92	WIRTH_lymphoma937_spot A
13	2e−02	7 / 279	SPANG_IL21 DN
14	3e−02	4 / 123	SPANG_LPS 6hrs UP
15	5e−02	3 / 87	ROSOLOWSKI_red total
16	5e−02	19 / 1333	SPANG_BCR UP
17	6e−02	4 / 150	DAVE_BL−vs−DLBCL
18	8e−02	88 / 8147	HOPP_Weak_promoter
19	9e−02	1 / 10	Shaknovich_ABC_hypo_meth
20	1e−01	2 / 63	SPANG_BAFF 9hrs DN

MF

Rank	p−value	#in/all	Geneset
1	1e−04	12 / 350	protein serine/threonine kinase activity
2	4e−03	21 / 1164	zinc ion binding
3	5e−03	12 / 527	protein kinase activity
4	6e−03	2 / 12	RNA helicase activity
5	6e−03	8 / 286	ligase activity
6	9e−03	4 / 84	Rab GTPase binding
7	1e−02	4 / 89	protease binding
8	1e−02	2 / 17	GTP−dependent protein binding
9	1e−02	23 / 1448	ATP binding
10	1e−02	3 / 52	RNA polymerase II core promoter sequence−specific DNA binding
11	1e−02	4 / 97	protein tyrosine phosphatase activity
12	2e−02	3 / 56	transcriptional repressor activity, RNA polymerase II transcription regulatory re
13	2e−02	2 / 22	proton−transporting ATPase activity, rotational mechanism
14	2e−02	5 / 161	ubiquitin protein ligase activity
15	2e−02	3 / 63	ATP−dependent RNA helicase activity
16	2e−02	2 / 25	substrate−specific transmembrane transporter activity
17	3e−02	4 / 118	phosphatase activity
18	3e−02	6 / 241	GTPase activator activity
19	3e−02	2 / 29	protein serine/threonine/tyrosine kinase activity
20	3e−02	2 / 29	Rab guanyl−nucleotide exchange factor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	8 / 240	hsa−miR−27a
2	0.002	4 / 59	hsa−miR−187
3	0.005	13 / 591	hsa−miR−20b
4	0.009	7 / 245	hsa−miR−214
5	0.011	4 / 89	hsa−miR−188−3p
6	0.012	3 / 49	hsa−miR−346
7	0.012	7 / 255	hsa−miR−27b
8	0.013	4 / 95	hsa−miR−299−3p
9	0.014	3 / 53	hsa−miR−508−5p
10	0.014	11 / 536	hsa−miR−106b
11	0.015	6 / 208	hsa−miR−545
12	0.016	9 / 403	hsa−miR−519a
13	0.017	3 / 56	hsa−miR−513a−5p
14	0.017	4 / 102	hsa−miR−150
15	0.017	5 / 156	hsa−miR−338−3p
16	0.020	2 / 23	hsa−miR−1227
17	0.022	11 / 573	hsa−miR−93
18	0.024	2 / 25	hsa−miR−602
19	0.024	2 / 25	hsa−miR−663
20	0.024	6 / 231	hsa−miR−181b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	BENTINK_e2f3.1
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 14	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 10	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 14	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−07	77 / 4714	ICGC_Pu1_targets
2	7e−07	84 / 5512	ICGC_Nficsc81335_targets
3	8e−07	80 / 5173	ICGC_Taf1_targets
4	2e−06	43 / 2149	ICGC_Mef2_targets
5	2e−06	71 / 4470	ICGC_Creb1_targets
6	8e−06	80 / 5453	ICGC_Foxm1_targets
7	1e−05	81 / 5578	ICGC_Stat5_targets
8	1e−05	94 / 6862	ICGC_Elf1_targets
9	1e−05	80 / 5526	ICGC_Pmlsc71910_targets
10	1e−05	48 / 2719	ICGC_Pbx3_targets
11	1e−05	55 / 3305	ICGC_BatfPcr1_targets
12	2e−05	88 / 6313	ICGC_Pou2_targets
13	2e−05	97 / 7202	ICGC_Runx3_targets
14	2e−05	53 / 3177	ICGC_Irf4_targets
15	4e−05	68 / 4566	ICGC_Egr1_targets
16	4e−05	76 / 5308	ICGC_Tcf12_targets
17	5e−05	72 / 4969	ICGC_Atf2_targets
18	5e−05	83 / 6005	ICGC_Mta3_targets
19	6e−05	78 / 5552	ICGC_Pol24_targets
20	9e−05	63 / 4230	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.01	2 / 19	VAQUERIZAS_Heart
2	0.13	2 / 64	VAQUERIZAS_Lung
3	0.14	2 / 67	VAQUERIZAS_Whole blood
4	0.18	1 / 20	VAQUERIZAS_Bone marrow
5	0.21	1 / 25	VAQUERIZAS_Spinal cord
6	0.33	1 / 42	VAQUERIZAS_Thymus
7	0.33	1 / 42	VAQUERIZAS_Thyroid
8	0.44	2 / 155	VAQUERIZAS_General
9	1.00	0 / 41	VAQUERIZAS_Fetal brain
10	1.00	0 / 45	VAQUERIZAS_Placenta
11	1.00	0 / 33	VAQUERIZAS_Liver
12	1.00	0 / 37	VAQUERIZAS_Prostate
13	1.00	0 / 30	VAQUERIZAS_Smooth muscle
14	1.00	0 / 49	VAQUERIZAS_Uterus
15	1.00	0 / 12	VAQUERIZAS_Kidney
16	1.00	0 / 46	VAQUERIZAS_Whole brain
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 31	VAQUERIZAS_Fetal lung
19	1.00	0 / 18	VAQUERIZAS_Pancreas
20	1.00	0 / 24	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.003	11 / 427	WIRTH_Immune system
2	0.389	2 / 140	PALMER_T−Cell signature up
3	0.406	1 / 54	WIRTH_Pancreas
4	0.595	2 / 208	PALMER_B−Cell signature up
5	0.713	2 / 259	PALMER_Granulocytes signature up
6	0.744	1 / 141	WIRTH_Muscle
7	0.838	3 / 476	WIRTH_Nervous System
8	0.859	1 / 202	WIRTH_Testis
9	1.000	0 / 6	WIRTH_Pituitary gland
10	1.000	0 / 13	WIRTH_Sec. lymphoid organs
11	1.000	0 / 13	WIRTH_Prim. lymphoid organs
12	1.000	0 / 14	WIRTH_B−cells
13	1.000	0 / 12	WIRTH_Tonsil
14	1.000	0 / 14	WIRTH_Thymus
15	1.000	0 / 12	WIRTH_Lymphocytes
16	1.000	0 / 14	WIRTH_Bone marrow
17	1.000	0 / 13	WIRTH_Globus pallidus
18	1.000	0 / 15	WIRTH_Telencephalon
19	1.000	0 / 13	WIRTH_Cortex cerebri
20	1.000	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	8 / 1343	LU_BPDE 1h DN
2	1.0	20 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

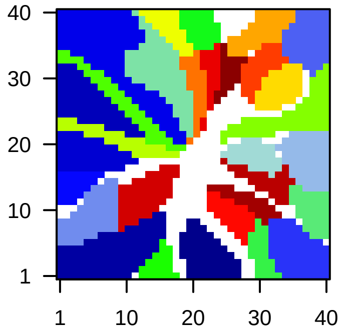
Spot Summary: G

metagenes = 52
genes = 532

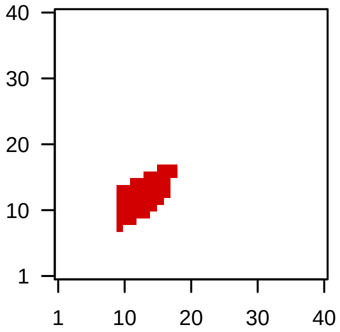
<r> metagenes = 0.95
<r> genes = 0.43
beta: r2= 0 / log p= −0.06

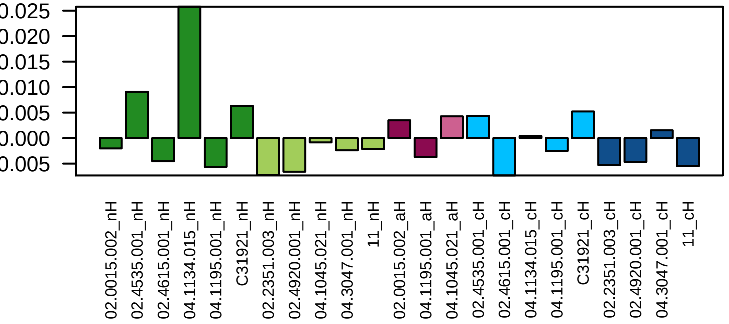
samples with spot = 0 (0 %)

Overview Map



Spot





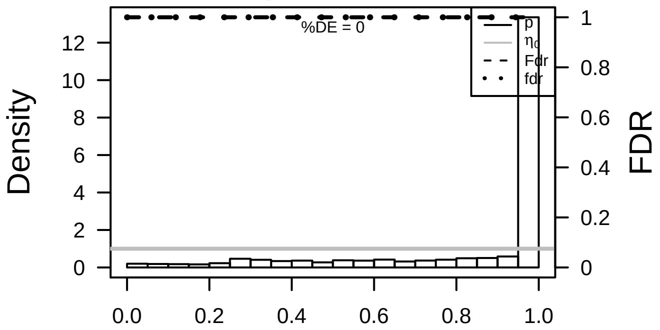
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.16	−0.06	0.55	TAZ	tafazzin [Source:HGNC Symbol;Acc:HGNC:11577]
2	ENSG000000	0.11	−0.07	0.62	DHPS	deoxyhypusine synthase [Source:HGNC Symbol;Acc:HGNC:
3	ENSG000002	0.11	−0.04	0.64	KMT2B	lysine (K)−specific methyltransferase 2B [Source:HGNC Sym
4	ENSG000001	0.11	−0.05	0.34	TBC1D17	TBC1 domain family, member 17 [Source:HGNC Symbol;Acc
5	ENSG000001	0.11	−0.04	0.82	ZBTB24	zinc finger and BTB domain containing 24 [Source:HGNC Sy
6	ENSG000000	0.1	−0.04	0.58	GRIPAP1	GRIP1 associated protein 1 [Source:HGNC Symbol;Acc:HGN
7	ENSG000001	0.1	−0.05	0.63	AKAP8	A kinase (PRKA) anchor protein 8 [Source:HGNC Symbol;Ac
8	ENSG000001	0.1	−0.07	0.39	GGT7	gamma−glutamyltransferase 7 [Source:HGNC Symbol;Acc:H
9	ENSG000002	0.09	−0.01	0.76		
10	ENSG000001	0.09	−0.06	0.6	CCAR2	cell cycle and apoptosis regulator 2 [Source:HGNC Symbol;A
11	ENSG000002	0.09	−0.05	0.6	VPS52	vacuolar protein sorting 52 homolog (S. cerevisiae) [Source:H
12	ENSG000001	0.09	−0.05	0.75	FAM104A	family with sequence similarity 104, member A [Source:HGN
13	ENSG000001	0.09	−0.06	0.76	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 8
14	ENSG000002	0.09	−0.04	0.66		
15	ENSG000001	0.09	−0.05	0.73	THEM4	thioesterase superfamily member 4 [Source:HGNC Symbol;A
16	ENSG000001	0.09	−0.04	0.58	CBLB	Cbl proto−oncogene B, E3 ubiquitin protein ligase [Source:H
17	ENSG000001	0.09	−0.14	0.41	CD2BP2	CD2 (cytoplasmic tail) binding protein 2 [Source:HGNC Symb
18	ENSG000001	0.08	−0.01	0.24	USP9Y	ubiquitin specific peptidase 9, Y−linked [Source:HGNC Symb
19	ENSG000001	0.08	−0.05	0.71	PPP6R2	protein phosphatase 6, regulatory subunit 2 [Source:HGNC S
20	ENSG000001	0.08	−0.04	0.82	ANKRD13D	ankyrin repeat domain 13 family, member D [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−11	72 / 1178	Colon	ZNF_Colon
2	1e−10	92 / 1753	Colon	Het_Colon
3	5e−10	92 / 1807	BP	transcription, DNA−templated
4	3e−09	90 / 1808	BP	regulation of transcription, DNA−templated
5	5e−09	70 / 1281	Colon	HetRpts_Colon
6	7e−09	64 / 1134	MF	nucleic acid binding
7	2e−08	46 / 712	Brain	Overlap_fetal_midbrain_EnhP
8	6e−08	36 / 500	Lymp	WIRTH_lymphoma937_spot J
9	2e−07	34 / 484	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
10	2e−06	88 / 2040	MF	metal ion binding
11	2e−06	25 / 329	GSEA	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
12	3e−06	55 / 1084	Brain	Overlap_fetal_midbrain_EnhG
13	4e−05	47 / 962	MF	transcription factor activity, sequence−specific DNA binding
14	9e−05	74 / 1803	MF	DNA binding
15	2e−04	55 / 1279	Brain	Overlap_fetal_midbrain_Enh
16	3e−04	13 / 159	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_3_UP
17	4e−04	4 / 14	MF	bitter taste receptor activity
18	6e−04	64 / 1604	CC	intracellular
19	6e−04	3 / 7	GSEA	RUNNE_GENDER_EFFECT_UP
20	6e−04	5 / 27	BP	detection of chemical stimulus involved in sensory perception of bitter taste
21	7e−04	58 / 1425	Chr	Chr 19
22	2e−03	6 / 51	MF	voltage−gated potassium channel activity
23	3e−03	3 / 11	BP	histone H3−K4 trimethylation
24	3e−03	3 / 11	BP	phosphorelay signal transduction system
25	3e−03	13 / 202	Tissu	WIRTH_Testis
26	3e−03	9 / 114	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_1_UP
27	3e−03	5 / 39	GSEA	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS
28	5e−03	3 / 14	BP	regulation of DNA−templated transcription, elongation
29	6e−03	7 / 81	Glio	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
30	6e−03	13 / 219	GSEA	ZWANG_DOWN_BY_2ND_EGF_PULSE
31	6e−03	8 / 104	BP	potassium ion transmembrane transport
32	7e−03	3 / 15	GSEA	REACTOME_AMINE_DERIVED_HORMONES
33	7e−03	8 / 106	Brain	Overlap_fetal_midbrain_Tx
34	1e−02	4 / 32	BP	sensory perception of taste
35	1e−02	8 / 112	BP	methylation
36	1e−02	23 / 517	Glio	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
37	1e−02	3 / 18	MF	G−protein coupled peptide receptor activity
38	1e−02	3 / 19	MF	cyclin binding
39	1e−02	3 / 19	CC	nonmotile primary cilium
40	1e−02	10 / 166	MF	RNA polymerase II transcription factor activity, sequence−specific DNA bin

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	4 / 123	HORVATH_aging_genes meth DOWN
2	0.4	2 / 57	TESCHENDORFF_age_hypermethylated
3	0.9	2 / 144	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−10	92 / 1807	transcription, DNA−templated
2	3e−09	90 / 1808	regulation of transcription, DNA−templated
3	6e−04	5 / 27	detection of chemical stimulus involved in sensory perception of bitter taste
4	3e−03	3 / 11	histone H3−K4 trimethylation
5	3e−03	3 / 11	phosphorelay signal transduction system
6	5e−03	3 / 14	regulation of DNA−templated transcription, elongation
7	6e−03	8 / 104	potassium ion transmembrane transport
8	1e−02	4 / 32	sensory perception of taste
9	1e−02	8 / 112	methylation
10	2e−02	5 / 58	response to calcium ion
11	2e−02	8 / 126	anatomical structure morphogenesis
12	2e−02	3 / 22	blastocyst development
13	2e−02	3 / 24	sensory perception of chemical stimulus
14	3e−02	6 / 88	sodium ion transmembrane transport
15	3e−02	3 / 26	gene silencing by RNA
16	3e−02	3 / 26	positive regulation of TOR signaling
17	3e−02	4 / 45	anion transmembrane transport
18	3e−02	2 / 11	cilium organization
19	3e−02	2 / 11	lens fiber cell development
20	3e−02	2 / 11	striatum development

Brain

Rank	p−value	#in/all	Geneset
1	2e−08	46 / 712	Overlap_fetal_midbrain_EnhP
2	3e−06	55 / 1084	Overlap_fetal_midbrain_EnhG
3	2e−04	55 / 1279	Overlap_fetal_midbrain_Enh
4	7e−03	8 / 106	Overlap_fetal_midbrain_Tx
5	9e−02	44 / 1356	Fetal_K9K27me3
6	1e−01	27 / 805	Mid_Frontal_Lobe_EnhG
7	1e−01	36 / 1137	Fetal_Enh
8	2e−01	72 / 2443	Fetal_Quies
9	2e−01	27 / 855	Overlap_fetal_midbrain_ZNF
10	2e−01	12 / 342	Fetal_Het
11	2e−01	74 / 2549	Fetal_TssF
12	2e−01	36 / 1182	Fetal_EnhP
13	4e−01	18 / 641	Mid_Frontal_Lobe_EnhP
14	5e−01	23 / 840	Mid_Frontal_Lobe_TssF
15	5e−01	168 / 6320	Overlap_fetal_midbrain_HetRpts
16	5e−01	55 / 2084	Mid_Frontal_Lobe_K9K27me3
17	5e−01	24 / 910	Fetal_EnhG
18	5e−01	270 / 10239	Overlap_fetal_midbrain_ReprPC
19	6e−01	8 / 317	Mid_Frontal_Lobe_Tx
20	6e−01	43 / 1680	Fetal_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	3 / 40	PanCan_HK_geneset_nanostring
2	0.11	6 / 123	PanCan_Driver_Gene_geneset_nanostring
3	0.17	2 / 28	PanCan_HH_geneset_nanostring
4	0.28	1 / 16	LIU_COMMON_CANCER_GENES
5	0.31	1 / 14	BEN−PORATH_DN
6	0.35	1 / 16	LIU_LIVER_CANCER
7	0.35	1 / 16	GENTLES_modul14
8	0.37	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	0.40	3 / 86	PanCan_JAK−ST_geneset_nanostring
10	0.63	1 / 37	KUIPER_MM good survival
11	0.67	1 / 41	ZHANG_MM up
12	0.74	1 / 50	PanCan_DNARepair_geneset_nanostring
13	0.75	1 / 52	KUIPER_MM poor survival
14	0.88	1 / 78	PanCan_Wnt_geneset_nanostring
15	0.91	0 / 14	LIU_PROSTATE_CANCER_UP
16	0.93	1 / 97	PanCan_TXmisReg_geneset_nanostring
17	0.96	2 / 191	SPANG_LPS−index2
18	1.00	1 / 198	PanCan_PI3K_geneset_nanostring
19	1.00	2 / 324	SPANG_BCL6−index2
20	1.00	0 / 16	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−04	64 / 1604	intracellular
2	1e−02	3 / 19	nonmotile primary cilium
3	2e−02	4 / 42	ciliary membrane
4	4e−02	2 / 13	integrator complex
5	8e−02	2 / 18	transcriptionally active chromatin
6	9e−02	3 / 40	condensed nuclear chromosome
7	1e−01	2 / 20	connexon complex
8	1e−01	2 / 20	gap junction
9	1e−01	2 / 21	M band
10	1e−01	2 / 21	transcription elongation factor complex
11	1e−01	2 / 21	transcription factor TFIID complex
12	1e−01	5 / 95	centriole
13	1e−01	2 / 22	anaphase−promoting complex
14	1e−01	2 / 22	I band
15	1e−01	147 / 5101	nucleus
16	1e−01	2 / 26	synaptonemal complex
17	2e−01	2 / 29	aggresome
18	2e−01	4 / 84	Golgi lumen
19	2e−01	4 / 84	voltage−gated potassium channel complex
20	2e−01	2 / 32	polysome

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	58 / 1425	Chr 19
2	4e−02	3 / 30	Chr Y
3	1e−01	16 / 436	Chr 22
4	2e−01	24 / 745	Chr 9
5	2e−01	31 / 1017	Chr 12
6	3e−01	22 / 715	Chr 10
7	3e−01	31 / 1043	Chr 3
8	3e−01	31 / 1083	Chr 17
9	5e−01	18 / 651	Chr 8
10	6e−01	16 / 613	Chr 14
11	6e−01	19 / 735	Chr 4
12	6e−01	22 / 859	Chr 7
13	6e−01	31 / 1228	Chr 2
14	7e−01	21 / 847	Chr 16
15	7e−01	14 / 582	Chr 15
16	7e−01	21 / 862	Chr 5
17	7e−01	6 / 272	Chr 18
18	7e−01	23 / 976	Chr 6
19	8e−01	6 / 318	Chr 13
20	9e−01	10 / 522	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−11	72 / 1178	ZNF_Colon
2	1e−10	92 / 1753	Het_Colon
3	5e−09	70 / 1281	HetRpts_Colon
4	2e−02	5 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	3e−02	17 / 389	K9K27me3_Colon
6	7e−02	20 / 525	Quies2_Colon
7	7e−02	2 / 17	TCGA_Mutated−in−CRC_non−hypermutated
8	8e−02	143 / 4879	Quies1_Colon
9	9e−02	2 / 19	Vilar_non−hypermutated−in−CRC
10	1e−01	2 / 20	Vilar_mutated−in−CRC−CamP
11	1e−01	2 / 20	Juehling_HNPCC−mutated−in−4
12	2e−01	9 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
13	2e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
14	2e−01	1 / 8	Boland_CRC−MMR−system
15	2e−01	1 / 10	KIM_CRC−MSI−regulated_DN
16	3e−01	83 / 2947	ReprPCWk_Colon
17	3e−01	12 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
18	3e−01	94 / 3406	ReprPC_Colon
19	3e−01	22 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
20	4e−01	24 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.6	1 / 37	BCHETNIA_EBM−DM up
2	1.0	6 / 399	GUDJ_psoriasis down
3	1.0	8 / 608	GUDJ_psoriasis up
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.006	7 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
2	0.011	23 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
3	0.020	5 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
4	0.028	7 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
5	0.030	34 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
6	0.045	10 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
7	0.064	4 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
8	0.080	93 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
9	0.090	5 / 90	Weller_LGG_A_vs_O_DOWN
10	0.103	7 / 150	Sturm_GBM_Meth_overexpression_B_adult_UP
11	0.135	7 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
12	0.165	3 / 53	Gorovets_LGG_EPL_subclass
13	0.255	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
14	0.275	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
15	0.294	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
16	0.311	13 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
17	0.331	1 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
18	0.362	3 / 81	GIEZELT_GBM_STS_up_VS_LTS
19	0.376	3 / 83	GIEZELT_GBM_WT_down_VS_mut
20	0.410	22 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	25 / 329	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
2	3e−04	13 / 159	FIGUEROA_AML_METHYLATION_CLUSTER_3_UP
3	6e−04	3 / 7	RUNNE_GENDER_EFFECT_UP
4	3e−03	9 / 114	FIGUEROA_AML_METHYLATION_CLUSTER_1_UP
5	3e−03	5 / 39	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS
6	6e−03	13 / 219	ZWANG_DOWN_BY_2ND_EGF_PULSE
7	7e−03	3 / 15	REACTOME_AMINE_DERIVED_HORMONES
8	2e−02	3 / 22	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON
9	2e−02	7 / 104	FIGUEROA_AML_METHYLATION_CLUSTER_4_UP
10	2e−02	2 / 9	REACTOME_HORMONE_LIGAND_BINDING_RECEPTORS
11	3e−02	2 / 10	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
12	3e−02	10 / 187	MIKKELSEN_MEF_ICP_WITH_H3K27ME3
13	3e−02	6 / 87	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AM
14	3e−02	11 / 215	CHEN_HOXA5_TARGETS_9HR_UP
15	3e−02	14 / 301	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
16	3e−02	7 / 114	FIGUEROA_AML_METHYLATION_CLUSTER_7_UP
17	3e−02	6 / 91	REACTOME_POTASSIUM_CHANNELS
18	3e−02	3 / 27	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	3e−02	9 / 167	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
20	4e−02	2 / 12	MIKKELSEN_NPC_ICP_WITH_H3K27ME3

HM

Rank	p−value	#in/all	Geneset
1	0.07	9 / 193	HALLMARK_KRAS_SIGNALING_DN
2	0.25	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
3	0.42	6 / 197	HALLMARK_IL2_STAT5_SIGNALING
4	0.51	3 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	0.66	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.66	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	0.69	1 / 44	HALLMARK_APICAL_SURFACE
8	0.76	2 / 102	HALLMARK_PEROXISOME
9	0.86	2 / 128	HALLMARK_SPERMATOGENESIS
10	0.89	3 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.91	1 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	0.95	1 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	0.95	1 / 112	HALLMARK_BILE_ACID_METABOLISM
14	0.96	2 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	0.96	2 / 189	HALLMARK_KRAS_SIGNALING_UP
16	0.96	2 / 192	HALLMARK_COMPLEMENT
17	0.97	2 / 193	HALLMARK_XENOBIOTIC_METABOLISM
18	0.97	2 / 196	HALLMARK_P53_PATHWAY
19	0.97	2 / 197	HALLMARK_E2F_TARGETS
20	0.98	1 / 154	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.22	4 / 91	DUMEAUX_Smoking enriched genes
3	1.00	0 / 11	DUMEAUX_Smoking literature genes up
4	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 17	DUMEAUX_High bmi enriched genes
11	1.00	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−08	36 / 500	WIRTH_lymphoma937_spot J
2	2e−07	34 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
3	8e−02	184 / 6389	HOPP_Weak_txn
4	1e−01	4 / 67	LEE_Developmental_regulators
5	1e−01	80 / 2658	HOPP_Repetitive
6	2e−01	207 / 7491	HOPP_Txn_elongation
7	3e−01	1 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
8	3e−01	10 / 304	ZHANG_DLBCL mutated
9	3e−01	1 / 15	BENTINK_mBL UP
10	4e−01	1 / 21	ROSOLOWSKI_red UP
11	4e−01	3 / 92	WIRTH_lymphoma937_spot A
12	5e−01	3 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
13	5e−01	1 / 24	Subero_mBL_hypo_meth
14	5e−01	179 / 6784	HOPP_Weak_enhancer
15	6e−01	148 / 5643	HOPP_Txn_transition
16	7e−01	1 / 48	Subero_INT_hypo_meth
17	7e−01	1 / 49	Subero_DLBCL_hypo_meth
18	8e−01	86 / 3457	HOPP_Heterochrom
19	8e−01	2 / 105	ROSOLOWSKI_blue total
20	8e−01	193 / 7592	HOPP_Strong_enhancer

MF

Rank	p−value	#in/all	Geneset
1	7e−09	64 / 1134	nucleic acid binding
2	2e−06	88 / 2040	metal ion binding
3	4e−05	47 / 962	transcription factor activity, sequence−specific DNA binding
4	9e−05	74 / 1803	DNA binding
5	4e−04	4 / 14	bitter taste receptor activity
6	2e−03	6 / 51	voltage−gated potassium channel activity
7	1e−02	3 / 18	G−protein coupled peptide receptor activity
8	1e−02	3 / 19	cyclin binding
9	1e−02	10 / 166	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
10	3e−02	2 / 10	palmitoyl−CoA hydrolase activity
11	3e−02	15 / 333	RNA polymerase II core promoter proximal region sequence−specific DNA bir
12	4e−02	2 / 12	C−C chemokine receptor activity
13	4e−02	2 / 12	folic acid binding
14	4e−02	2 / 13	taste receptor activity
15	5e−02	2 / 14	solute:proton antiporter activity
16	6e−02	2 / 15	hydrolase activity, acting on acid anhydrides
17	6e−02	2 / 15	neuropeptide receptor activity
18	6e−02	2 / 15	phospholipase activity
19	6e−02	2 / 15	protein phosphatase 1 binding
20	6e−02	7 / 132	ion channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	5 / 75	hsa−miR−876−3p
2	0.09	4 / 63	hsa−miR−671−5p
3	0.12	3 / 45	hsa−miR−885−3p
4	0.14	2 / 25	hsa−miR−220b
5	0.14	2 / 25	hsa−miR−609
6	0.14	5 / 104	hsa−miR−516b
7	0.16	3 / 53	hsa−miR−337−3p
8	0.17	2 / 28	hsa−miR−675
9	0.18	3 / 56	hsa−miR−513a−5p
10	0.19	3 / 57	hsa−miR−1302
11	0.20	4 / 87	hsa−miR−220c
12	0.21	1 / 9	hsa−miR−202*
13	0.22	2 / 33	hsa−miR−342−5p
14	0.22	3 / 61	hsa−miR−126*
15	0.23	3 / 62	hsa−miR−1200
16	0.24	1 / 10	hsa−miR−933
17	0.24	4 / 94	hsa−miR−378
18	0.24	3 / 64	hsa−miR−1243
19	0.26	2 / 37	hsa−miR−588
20	0.26	3 / 67	hsa−miR−643

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.03	29 / 766	ICGC_Atf3_targets
2	0.04	75 / 2342	ICGC_GabpPcr2_targets
3	0.08	1 / 3	MYC_Signal transduction UP
4	0.13	158 / 5526	ICGC_Pmlsc71910_targets
5	0.15	135 / 4714	ICGC_Pu1_targets
6	0.19	145 / 5135	ICGC_Ebfsc137065_targets
7	0.20	168 / 6005	ICGC_Mta3_targets
8	0.20	70 / 2401	ICGC_Bcl11_targets
9	0.21	176 / 6322	ICGC_Pol2_targets
10	0.21	151 / 5393	ICGC_Sp1_targets
11	0.23	175 / 6313	ICGC_Pou2_targets
12	0.25	23 / 745	ICGC_NrsfPcr2_targets
13	0.28	176 / 6406	ICGC_Pax5_targets
14	0.28	138 / 4987	ICGC_Bclaf101388_targets
15	0.29	123 / 4436	ICGC_Zeb1_targets
16	0.31	142 / 5173	ICGC_Taf1_targets
17	0.32	43 / 1506	ICGC_Usf1_targets
18	0.33	88 / 3177	ICGC_Irf4_targets
19	0.35	186 / 6862	ICGC_Elf1_targets
20	0.35	1 / 16	NOWICK_TF

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 8	VAQUERIZAS_Tongue
2	0.2	6 / 155	VAQUERIZAS_General
3	0.2	1 / 10	VAQUERIZAS_Skeletal.muscle.psoas
4	0.3	2 / 45	VAQUERIZAS_Placenta
5	0.7	1 / 41	VAQUERIZAS_Testis
6	0.8	1 / 67	VAQUERIZAS_Whole blood
7	1.0	0 / 41	VAQUERIZAS_Fetal brain
8	1.0	0 / 33	VAQUERIZAS_Liver
9	1.0	0 / 37	VAQUERIZAS_Prostate
10	1.0	0 / 30	VAQUERIZAS_Smooth muscle
11	1.0	0 / 49	VAQUERIZAS_Uterus
12	1.0	0 / 12	VAQUERIZAS_Kidney
13	1.0	0 / 25	VAQUERIZAS_Spinal cord
14	1.0	0 / 46	VAQUERIZAS_Whole brain
15	1.0	0 / 42	VAQUERIZAS_Thymus
16	1.0	0 / 42	VAQUERIZAS_Thyroid
17	1.0	0 / 7	VAQUERIZAS_Appendix
18	1.0	0 / 31	VAQUERIZAS_Fetal lung
19	1.0	0 / 64	VAQUERIZAS_Lung
20	1.0	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.003	13 / 202	WIRTH_Testis
2	0.171	6 / 141	WIRTH_Muscle
3	0.294	1 / 13	WIRTH_Cortex cerebri
4	0.331	1 / 15	WIRTH_Cerebellum
5	0.369	3 / 82	WIRTH_Homeostasis
6	0.589	3 / 115	WIRTH_Liver
7	0.717	1 / 47	WIRTH_Placenta
8	0.765	1 / 54	WIRTH_Pancreas
9	0.799	9 / 427	WIRTH_Immune system
10	0.881	2 / 137	WIRTH_Mucosa
11	0.888	2 / 140	PALMER_T−Cell signature up
12	0.916	3 / 208	PALMER_B−Cell signature up
13	0.988	6 / 476	WIRTH_Nervous System
14	0.999	1 / 259	PALMER_Granulocytes signature up
15	1.000	0 / 6	WIRTH_Pituitary gland
16	1.000	0 / 13	WIRTH_Sec. lymphoid organs
17	1.000	0 / 13	WIRTH_Prim. lymphoid organs
18	1.000	0 / 14	WIRTH_B−cells
19	1.000	0 / 12	WIRTH_Tonsil
20	1.000	0 / 14	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	35 / 1343	LU_BPDE 1n DN
2	0.7	135 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

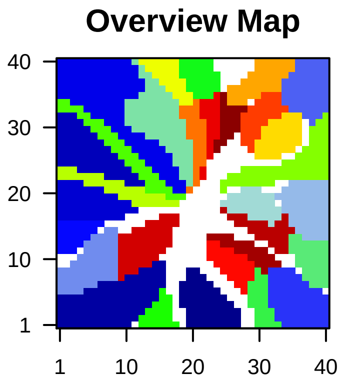
Correlation Clusters

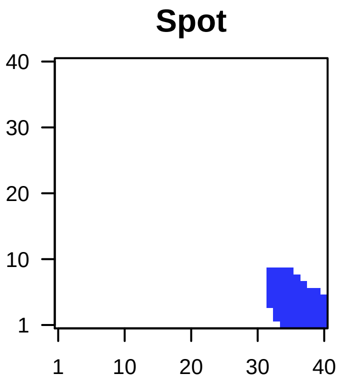
Spot Summary: H

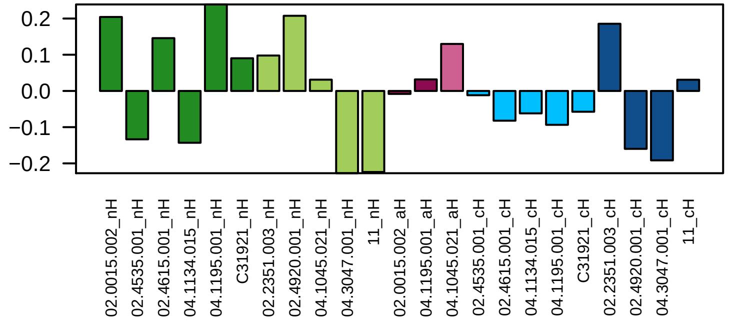
metagenes = 64
genes = 802

<r> metagenes = 0.94
<r> genes = 0.58
beta: r2= 0.35 / log p= −2.56

samples with spot = 8 (34.8 %)
MLH1_normHNPCC : 4 (66.7 %)
other_normHNPCC : 2 (40 %)
other_adenomaHNPCC : 1 (100 %)
other_cancerHNPCC : 1 (25 %)





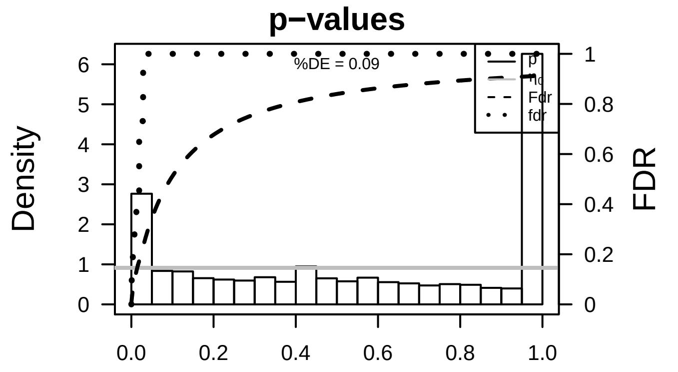


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	1.55	−0.86	0.88	PHGR1	proline/histidine/glycine−rich 1 [Source:HGNC Symbol;Acc:H
2	ENSG000001	1.42	−0.99	0.88	GUCA2A	guanylate cyclase activator 2A (guanylin) [Source:HGNC Sym
3	ENSG000001	1.33	−0.38	0.47	PP7080	uncharacterized LOC25845 [Source:EntrezGene;Acc:25845]
4	ENSG000001	1.3	−0.63	0.75	AQP8	aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG000001	1.28	−0.52	0.63	ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;A
6	ENSG000000	1.26	−0.59	0.72	CLCA4	chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
7	ENSG000000	1.24	−0.81	0.85	SLC26A3	solute carrier family 26 (anion exchanger), member 3 [Source
8	ENSG000000	1.24	−0.99	0.8	CEACAM7	carcinoembryonic antigen−related cell adhesion molecule 7 [
9	ENSG000001	1.24	−0.49	0.77	ZG16	zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGN
10	ENSG000000	1.22	−0.52	0.82	GUCA2B	guanylate cyclase activator 2B (uroguanylin) [Source:HGNC
11	ENSG000001	1.21	−0.51	0.67	TFF1	trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	−0.44	0.7	PRAP1	proline−rich acidic protein 1 [Source:HGNC Symbol;Acc:HGN
13	ENSG000002	1.15	−0.61	0.85		
14	ENSG000001	1.13	−1.09	0.89	FABP1	fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:
15	ENSG000001	1.12	−0.37	0.74	AKR1B10	aldo−keto reductase family 1, member B10 (aldose reductase
16	ENSG000001	1.1	−0.7	0.56	PI3	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
17	ENSG000001	1.06	−1.31	0.63	PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	ENSG000001	1.02	−1.15	0.69	CEACAM5	carcinoembryonic antigen−related cell adhesion molecule 5 [
19	ENSG000001	1	−0.96	0.9	KRT20	keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
20	ENSG000001	1	−0.35	0.8	C11orf86	chromosome 11 open reading frame 86 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	174 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
2	7e−77	73 / 104	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
3	6e−54	307 / 3112	Colon	EnhA_Colon
4	1e−53	307 / 3122	Colon	TxEnhG1_Colon
5	2e−53	60 / 110	Colon	Marisa_CRC−cluster−h
6	3e−48	440 / 5889	Colon	EnhWk1_Colon
7	2e−46	606 / 9930	Colon	Tx_Colon
8	8e−42	663 / 11791	Colon	Enh_Colon
9	4e−39	67 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
10	2e−38	70 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
11	2e−35	85 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
12	1e−34	241 / 2638	CC	extracellular exosome
13	2e−34	178 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
14	2e−31	84 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
15	5e−31	81 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
16	1e−29	98 / 643	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
17	5e−29	95 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
18	3e−28	542 / 9390	Colon	TxWk_Colon
19	1e−27	95 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
20	7e−27	112 / 877	Colon	TxEnhG2_Colon
21	1e−25	95 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
22	7e−25	41 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
23	1e−23	39 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
24	3e−23	41 / 144	Lymph	WIRTH_lymphoma937_spot G
25	3e−23	475 / 8123	Colon	TssF_Colon
26	4e−23	570 / 10475	Colon	TssA_Colon
27	2e−22	40 / 142	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsi
28	5e−22	412 / 6761	Colon	TssD2_Colon
29	1e−20	87 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
30	1e−19	50 / 262	GSEA	SABATES_COLORECTAL_ADENOMA_DN
31	3e−19	23 / 49	Colon	Marisa_CRC−cluster−f
32	3e−19	48 / 248	GSEA	JAEGER_METASTASIS_DN
33	6e−18	513 / 9470	Colon	Quies3_Colon
34	1e−17	609 / 11968	Colon	TssWk_Colon
35	3e−17	64 / 465	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
36	4e−17	31 / 115	GSEA	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
37	1e−16	33 / 137	Tissu	WIRTH_Mucosa
38	2e−16	107 / 1103	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
39	2e−15	52 / 351	GSEA	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
40	7e−15	27 / 102	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT



Aging

Rank	p−value	#in/all	Geneset
1	0.4	6 / 123	HORVATH_aging_genes meth DOWN
2	0.6	6 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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−14	121 / 1418	small molecule metabolic process
2	1e−12	12 / 19	cellular glucuronidation
3	1e−09	90 / 1118	metabolic process
4	5e−09	25 / 154	xenobiotic metabolic process
5	1e−08	10 / 23	flavonoid biosynthetic process
6	1e−08	10 / 23	flavonoid glucuronidation
7	1e−06	12 / 52	O−glycan processing
8	1e−06	13 / 62	steroid metabolic process
9	2e−06	9 / 29	actin filament bundle assembly
10	2e−06	7 / 16	cellular sodium ion homeostasis
11	4e−06	10 / 40	excretion
12	5e−06	7 / 18	3'−phosphoadenosine 5'−phosphosulfate metabolic process
13	3e−05	12 / 71	cellular response to hormone stimulus
14	7e−05	18 / 152	cellular lipid metabolic process
15	9e−05	6 / 19	epithelial cell morphogenesis
16	9e−05	12 / 78	protein O−linked glycosylation
17	9e−05	7 / 27	keratan sulfate biosynthetic process
18	1e−04	11 / 67	cell−cell junction organization
19	1e−04	13 / 91	ephrin receptor signaling pathway
20	2e−04	13 / 97	protein glycosylation

Brain

Rank	p−value	#in/all	Geneset
1	4e−12	247 / 3977	Mid_Frontal_Lobe_ReprPC
2	5e−09	121 / 1713	Mid_Frontal_Lobe_ReprPCWk
3	6e−09	184 / 2956	Fetal_TssA
4	2e−07	124 / 1890	Overlap_fetal_midbrain_TssF
5	3e−07	159 / 2603	Fetal_TxTrans
6	4e−07	97 / 1394	Mid_Frontal_Lobe_Quies
7	9e−07	131 / 2084	Mid_Frontal_Lobe_K9K27me3
8	2e−06	152 / 2549	Fetal_TssF
9	2e−05	95 / 1478	Overlap_fetal_midbrain_TxTrans
10	2e−04	154 / 2820	Mid_Frontal_Lobe_HetRpts
11	4e−04	81 / 1327	Mid_Frontal_Lobe_TssP
12	6e−04	74 / 1210	Fetal_TssP
13	9e−04	68 / 1108	Overlap_fetal_midbrain_TssA
14	7e−03	28 / 408	Mid_Frontal_Lobe_TxTrans
15	8e−03	50 / 840	Mid_Frontal_Lobe_TssF
16	1e−01	29 / 552	Fetal_Tx
17	1e−01	40 / 805	Mid_Frontal_Lobe_EnhG
18	2e−01	17 / 317	Mid_Frontal_Lobe_Tx
19	2e−01	44 / 940	Mid_Frontal_Lobe_Enh
20	4e−01	73 / 1680	Fetal_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	19 / 191	SPANG_LPS−index2
2	4e−03	1 / 14	LIU_PROSTATE_CANCER_UP
3	1e−02	23 / 324	SPANG_BCL6−index2
4	3e−02	3 / 16	LIU_PROSTATE_CANCER_DN
5	3e−02	3 / 16	WANG_ER_UP
6	5e−02	8 / 97	PanCan_TXmisReg_geneset_nanostring
7	5e−02	2 / 9	WANG_ER_DN
8	7e−02	13 / 198	PanCan_PI3K_geneset_nanostring
9	1e−01	2 / 15	GENTLES_modul4
10	1e−01	2 / 15	GENTLES_modul13
11	1e−01	2 / 16	GENTLES_modul18
12	2e−01	1 / 16	LIU_COMMON_CANCER_GENES
13	2e−01	4 / 51	PanCan_TGF−B_geneset_nanostring
14	2e−01	8 / 136	PanCan_CC+Apop_geneset_nanostring
15	2e−01	1 / 6	ZHANG_MGUS up
16	2e−01	8 / 140	PanCan_RAS_geneset_nanostring
17	2e−01	3 / 41	ZHANG_MM up
18	4e−01	1 / 14	GENTLES_modul12
19	5e−01	0 / 16	LIU_LIVER_CANCER
20	5e−01	1 / 16	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	1e−34	241 / 2638	extracellular exosome
2	2e−13	20 / 60	brush border
3	2e−10	37 / 268	apical plasma membrane
4	1e−09	214 / 3507	plasma membrane
5	2e−07	229 / 4052	integral component of membrane
6	2e−07	25 / 185	basolateral plasma membrane
7	3e−06	17 / 110	bicellular tight junction
8	2e−05	25 / 235	lysosome
9	2e−05	14 / 91	apical part of cell
10	5e−05	46 / 596	perinuclear region of cytoplasm
11	5e−05	169 / 3059	membrane
12	6e−05	40 / 497	Golgi membrane
13	6e−05	8 / 34	cortical actin cytoskeleton
14	8e−05	12 / 77	ruffle membrane
15	4e−04	8 / 43	intercalated disc
16	4e−04	19 / 190	membrane raft
17	7e−04	6 / 27	stereocilium
18	8e−04	20 / 216	actin cytoskeleton
19	9e−04	8 / 49	microvillus
20	9e−04	8 / 49	myosin complex

Chr

Rank	p−value	#in/all	Geneset
1	0.009	50 / 847	Chr 16
2	0.021	98 / 1920	Chr 1
3	0.047	33 / 582	Chr 15
4	0.077	59 / 1172	Chr 11
5	0.104	49 / 976	Chr 6
6	0.176	11 / 191	Chr 21
7	0.263	56 / 1228	Chr 2
8	0.413	47 / 1083	Chr 17
9	0.447	37 / 859	Chr 7
10	0.460	32 / 745	Chr 9
11	0.465	12 / 272	Chr 18
12	0.553	42 / 1017	Chr 12
13	0.602	58 / 1425	Chr 19
14	0.621	42 / 1043	Chr 3
15	0.661	34 / 862	Chr 5
16	0.686	20 / 522	Chr 20
17	0.737	16 / 436	Chr 22
18	0.847	25 / 715	Chr 10
19	0.880	25 / 735	Chr 4
20	0.988	17 / 651	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	174 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
2	7e−77	73 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
3	6e−54	307 / 3112	EnhA_Colon
4	1e−53	307 / 3122	TxEnhG1_Colon
5	2e−53	60 / 110	Marisa_CRC−cluster−h
6	3e−48	440 / 5889	EnhWk1_Colon
7	2e−46	606 / 9930	Tx_Colon
8	8e−42	663 / 11791	Enh_Colon
9	1e−29	98 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	5e−29	95 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	3e−28	542 / 9390	TxWk_Colon
12	7e−27	112 / 877	TxEnhG2_Colon
13	3e−23	475 / 8123	TssF_Colon
14	4e−23	570 / 10475	TssA_Colon
15	5e−22	412 / 6761	TssD2_Colon
16	1e−20	87 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
17	3e−19	23 / 49	Marisa_CRC−cluster−f
18	6e−18	513 / 9470	Quies3_Colon
19	1e−17	609 / 11968	TssWk_Colon
20	5e−14	105 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	1e−12	66 / 608	GUDJ_psoriasis up
2	2e−01	21 / 399	GUDJ_psoriasis down
3	8e−01	1 / 37	BCHETNIA_EBM−DM up
4	1e+00	0 / 22	BCHETNIA_EBM up
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−08	184 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	1e−07	106 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	6e−04	9 / 58	OL vs. MOG− OL
4	2e−03	36 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	1e−02	14 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
6	2e−02	5 / 36	Shaw_down_in_1p19q
7	3e−02	19 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
8	3e−02	3 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
9	3e−02	44 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
10	3e−02	9 / 103	GIEZELT_GBM_STS_down_VS. LTS
11	4e−02	6 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
12	4e−02	20 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP
13	5e−02	27 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
14	5e−02	2 / 9	oligodendrocytes_glio
15	5e−02	21 / 344	Up
16	5e−02	6 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
17	7e−02	6 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
18	9e−02	7 / 92	laffaire_hypermeth_LGG_vs_control
19	1e−01	5 / 59	Christensen_hypomethylated_in_primary_glioblastoma
20	1e−01	2 / 14	Christensen_hypermethylated_in_ependymoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−39	67 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
2	2e−38	70 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
3	2e−35	85 / 412	LIM_MAMMARY_STEM_CELL_DN
4	2e−34	178 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
5	2e−31	84 / 455	ONDER_CDH1_TARGETS_2_DN
6	5e−31	81 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
7	1e−27	95 / 641	FEVR_CTNNB1_TARGETS_UP
8	1e−25	95 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
9	7e−25	41 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
10	1e−23	39 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
11	1e−19	50 / 262	SABATES_COLORECTAL_ADENOMA_DN
12	3e−19	48 / 248	JAEGER_METASTASIS_DN
13	3e−17	64 / 465	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
14	4e−17	31 / 115	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
15	2e−16	107 / 1103	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
16	2e−15	52 / 351	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
17	7e−15	27 / 102	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
18	1e−14	43 / 261	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
19	3e−14	61 / 495	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
20	4e−14	81 / 786	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3

HM

Rank	p−value	#in/all	Geneset
1	6e−10	30 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
2	3e−09	29 / 196	HALLMARK_P53_PATHWAY
3	1e−08	28 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	5e−07	22 / 154	HALLMARK_FATTY_ACID_METABOLISM
5	5e−07	22 / 155	HALLMARK_UV_RESPONSE_UP
6	5e−07	25 / 193	HALLMARK_XENOBIOTIC_METABOLISM
7	1e−05	22 / 189	HALLMARK_KRAS_SIGNALING_UP
8	6e−05	21 / 192	HALLMARK_COMPLEMENT
9	9e−05	14 / 102	HALLMARK_PEROXISOME
10	1e−04	18 / 157	HALLMARK_APOPTOSIS
11	1e−04	20 / 190	HALLMARK_APICAL_JUNCTION
12	5e−04	19 / 193	HALLMARK_HEME_METABOLISM
13	5e−04	19 / 194	HALLMARK_INFLAMMATORY_RESPONSE
14	6e−04	19 / 197	HALLMARK_IL2_STAT5_SIGNALING
15	7e−04	19 / 199	HALLMARK_ADIPOGENESIS
16	7e−04	10 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	8e−04	18 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	3e−03	11 / 98	HALLMARK_ANDROGEN_RESPONSE
19	7e−03	16 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	7e−03	11 / 112	HALLMARK_BILE_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	3 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.142	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.180	6 / 91	DUMEAUX_Smoking enriched genes
4	0.319	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
5	0.516	1 / 17	DUMEAUX_High bmi enriched genes
6	1.000	0 / 11	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.000	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−23	41 / 144	WIRTH_lymphoma937_spot G
2	2e−22	40 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
3	4e−05	159 / 2838	HOPP_Poised_promoter
4	5e−05	259 / 5039	HOPP_Repressed
5	1e−03	3 / 6	DAVE_MHCCII BL DN
6	3e−03	24 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
7	3e−03	24 / 315	WIRTH_lymphoma937_spot E
8	1e−02	9 / 87	Aukema_BCL2 DN_BCL6 UP
9	1e−02	18 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
10	1e−02	4 / 23	SPANG_BAFF 9hrs UP
11	2e−02	10 / 115	ROSOLOWSKI_green total
12	3e−02	6 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
13	3e−02	7 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
14	4e−02	7 / 75	WIRTH_lymphoma937_spot IM
15	4e−02	164 / 3457	HOPP_Heterochrom
16	5e−02	3 / 20	Subero_MCL_hypo_meth
17	5e−02	5 / 48	Subero_INT_hypo_meth
18	6e−02	339 / 7592	HOPP_Strong_enhancer
19	6e−02	7 / 83	ROSOLOWSKI_green UP
20	6e−02	10 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP

MF

Rank	p−value	#in/all	Geneset
1	2e−07	11 / 37	transferase activity, transferring hexosyl groups
2	2e−07	10 / 30	glucuronosyltransferase activity
3	1e−06	18 / 113	actin filament binding
4	3e−05	7 / 23	galactosyltransferase activity
5	1e−04	5 / 13	carbonate dehydratase activity
6	2e−04	6 / 21	calcium−dependent cysteine−type endopeptidase activity
7	4e−04	10 / 67	flavin adenine dinucleotide binding
8	8e−04	21 / 232	hydrolase activity
9	9e−04	6 / 28	cadherin binding
10	1e−03	45 / 672	calcium ion binding
11	2e−03	18 / 198	signal transducer activity
12	2e−03	5 / 22	transferase activity, transferring acyl groups other than amino−acyl groups
13	2e−03	10 / 81	drug binding
14	2e−03	9 / 69	beta−catenin binding
15	2e−03	5 / 23	WW domain binding
16	3e−03	10 / 85	PDZ domain binding
17	3e−03	4 / 15	retinoic acid binding
18	3e−03	5 / 25	steroid binding
19	4e−03	7 / 48	sulfotransferase activity
20	4e−03	4 / 16	fatty acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	10 / 84	hsa−miR−365
2	0.015	9 / 92	hsa−miR−362−5p
3	0.015	11 / 124	hsa−miR−579
4	0.015	8 / 77	hsa−miR−651
5	0.018	5 / 37	hsa−miR−588
6	0.027	11 / 136	hsa−miR−485−5p
7	0.032	9 / 105	hsa−miR−590−5p
8	0.036	5 / 44	hsa−miR−483−5p
9	0.037	7 / 75	hsa−miR−184
10	0.037	14 / 197	hsa−miR−548d−3p
11	0.040	22 / 352	hsa−miR−142−5p
12	0.044	11 / 147	hsa−miR−138
13	0.045	13 / 184	hsa−miR−374a
14	0.054	11 / 152	hsa−miR−633
15	0.056	33 / 591	hsa−miR−20b
16	0.056	26 / 447	hsa−miR−519d
17	0.061	8 / 101	hsa−miR−603
18	0.063	8 / 102	hsa−miR−500
19	0.064	26 / 453	hsa−miR−424
20	0.069	5 / 53	hsa−miR−337−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 14	BENTINK_src.10
2	0.3	1 / 10	BENTINK_ras.4
3	0.4	1 / 14	GUSTAFSON_PI3K_UP
4	0.4	1 / 14	BENTINK_e2f3.1
5	0.5	1 / 15	GUSTAFSON_PI3K_DN
6	0.5	1 / 15	BENTINK_ras.6
7	1.0	0 / 13	BENTINK_e2f3.2
8	1.0	0 / 14	BENTINK_myc.1
9	1.0	0 / 12	BENTINK_ras.1
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.003	99 / 1798	HEBENSTREIT_low expression TF
2	0.008	245 / 5135	ICGC_Ebfsc137065_targets
3	0.017	170 / 3511	ICGC_Rad21_targets
4	0.020	139 / 2827	ICGC_Bcl3_targets
5	0.082	1 / 2	MYC_Cell cycle DOWN
6	0.123	88 / 1867	HEBENSTREIT_high expression TF
7	0.128	199 / 4436	ICGC_Zeb1_targets
8	0.319	1 / 9	MYC_Targets DOWN
9	0.441	102 / 2401	ICGC_Bcl11_targets
10	0.452	266 / 6322	ICGC_Pol2_targets
11	0.468	269 / 6406	ICGC_Pax5_targets
12	0.477	233 / 5552	ICGC_Pol24_targets
13	0.560	285 / 6862	ICGC_Elf1_targets
14	0.574	1 / 20	MYC_Metabolism UP
15	0.608	254 / 6157	ICGC_Tcf3_targets
16	0.636	260 / 6324	ICGC_Yy1_targets
17	0.640	29 / 731	ICGC_SrfPcr2_targets
18	0.669	30 / 766	ICGC_Atf3_targets
19	0.675	220 / 5393	ICGC_Sp1_targets
20	0.701	191 / 4714	ICGC_Pu1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	7e−04	5 / 18	VAQUERIZAS_Pancreas
2	2e−02	4 / 24	VAQUERIZAS_Trachea
3	2e−02	7 / 64	VAQUERIZAS_Lung
4	4e−02	3 / 19	VAQUERIZAS_Heart
5	7e−02	4 / 37	VAQUERIZAS_Prostate
6	1e−01	2 / 13	VAQUERIZAS_Skin
7	1e−01	4 / 45	VAQUERIZAS_Placenta
8	1e−01	3 / 31	VAQUERIZAS_Fetal lung
9	2e−01	3 / 33	VAQUERIZAS_Liver
10	2e−01	2 / 22	VAQUERIZAS_Tonsil
11	3e−01	3 / 42	VAQUERIZAS_Thyroid
12	3e−01	1 / 7	VAQUERIZAS_Appendix
13	3e−01	1 / 8	VAQUERIZAS_Tongue
14	4e−01	1 / 12	VAQUERIZAS_Kidney
15	5e−01	1 / 16	VAQUERIZAS_Fetal liver
16	5e−01	1 / 16	VAQUERIZAS_Ovary
17	5e−01	1 / 17	VAQUERIZAS_Salivary gland
18	6e−01	2 / 46	VAQUERIZAS_Whole brain
19	7e−01	1 / 25	VAQUERIZAS_Adrenal cortex
20	7e−01	1 / 31	VAQUERIZAS_Lymph node

Tissue

Rank	p−value	#in/all	Geneset
1	1e−16	33 / 137	WIRTH_Mucosa
2	4e−06	6 / 12	WIRTH_Tonsil
3	3e−05	26 / 259	PALMER_Granulocytes signature up
4	7e−03	9 / 82	WIRTH_Homeostasis
5	5e−02	14 / 208	PALMER_B−Cell signature up
6	1e−01	2 / 13	WIRTH_Prim. lymphoid organs
7	1e−01	2 / 14	WIRTH_Thalamus
8	1e−01	2 / 15	WIRTH_Telencephalon
9	2e−01	4 / 54	WIRTH_Pancreas
10	4e−01	1 / 13	WIRTH_Sec. lymphoid organs
11	4e−01	1 / 14	WIRTH_B−cells
12	4e−01	1 / 14	WIRTH_Bone marrow
13	4e−01	1 / 14	WIRTH_Thyroid gland
14	5e−01	1 / 15	WIRTH_Cerebellum
15	5e−01	6 / 140	PALMER_T−Cell signature up
16	7e−01	4 / 115	WIRTH_Liver
17	1e+00	2 / 141	WIRTH_Muscle
18	1e+00	10 / 427	WIRTH_Immune system
19	1e+00	7 / 476	WIRTH_Nervous System
20	1e+00	0 / 6	WIRTH_Pituitary gland

Toxic

Rank	p−value	#in/all	Geneset
1	0.7	53 / 1343	LU_BPDE 1h DN
2	0.8	212 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

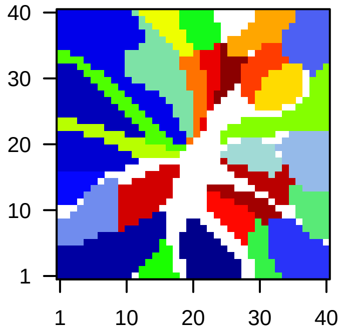
Spot Summary: I

\# metagenes = 25
\# genes = 314

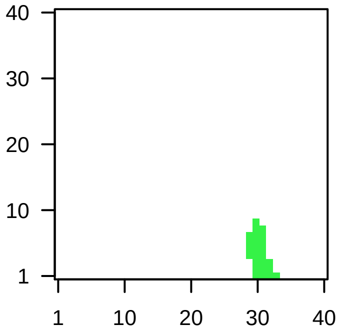
<r> metagenes = 0.95
<r> genes = 0.48
beta: r2= 0.07 / log p= −0.62

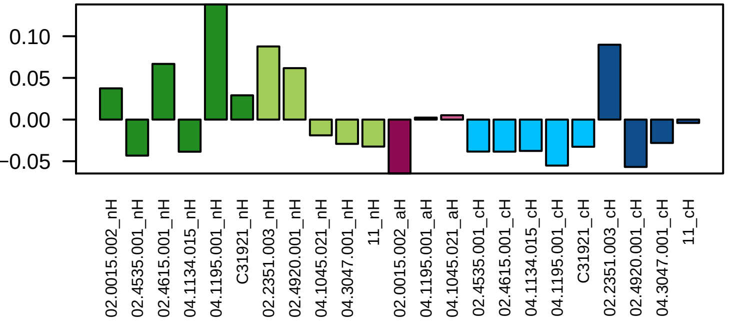
\# samples with spot = 5 (21.7 %)
MLH1_normHNPCC : 2 (33.3 %)
other_normHNPCC : 2 (40 %)
other_cancerHNPCC : 1 (25 %)

Overview Map



Spot





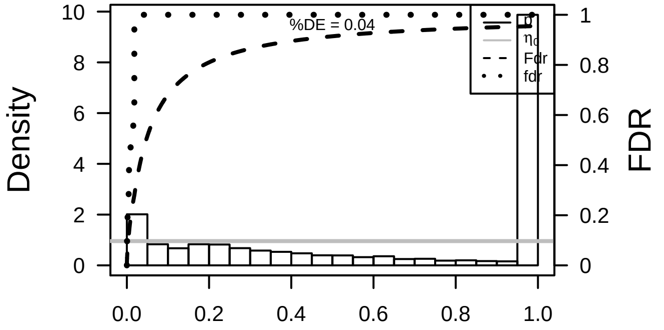
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.6	−0.11	0.39	RETNLB	resistin like beta [Source:HGNC Symbol;Acc:HGNC:20388]
2	ENSG000001	0.58	−0.49	0.53	MT1E	metallothionein 1E [Source:HGNC Symbol;Acc:HGNC:7397]
3	ENSG000001	0.49	−0.1	0.79	DDX60	DEAD (Asp−Glu−Ala−Asp) box polypeptide 60 [Source:HGN
4	ENSG000001	0.48	−0.09	0.38	ATOH1	atonal bHLH transcription factor 1 [Source:HGNC Symbol;Ac
5	ENSG000002	0.44	−0.12	0.75	SAMD9	sterile alpha motif domain containing 9 [Source:HGNC Symb
6	ENSG000001	0.43	−0.1	0.88	CLIC5	chloride intracellular channel 5 [Source:HGNC Symbol;Acc:H
7	ENSG000001	0.42	−0.2	0.83	MXI1	MAX interactor 1, dimerization protein [Source:HGNC Symbo
8	ENSG000001	0.4	−0.07	0.18	CHGA	chromogranin A [Source:HGNC Symbol;Acc:HGNC:1929]
9	ENSG000001	0.4	−0.08	0.56	CAPN9	calpain 9 [Source:HGNC Symbol;Acc:HGNC:1486]
10	ENSG000001	0.4	−0.18	0.26	RASL11A	RAS−like, family 11, member A [Source:HGNC Symbol;Acc:H
11	ENSG000001	0.39	−0.33	0.46	ID3	inhibitor of DNA binding 3, dominant negative helix−loop−heli
12	ENSG000001	0.39	−0.05	0.58	CMPK2	cytidine monophosphate (UMP−CMP) kinase 2, mitochondria
13	ENSG000002	0.38	−0.17	0.5		
14	ENSG000001	0.38	−0.07	0.67	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:I
15	ENSG000002	0.36	−0.18	0.63		
16	ENSG000002	0.36	−0.19	0.68	MT1M	metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296
17	ENSG000000	0.36	−0.34	0.61	KLF6	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:HGNC:2235
18	ENSG000001	0.35	−0.21	0.44	ECH1	enoyl CoA hydratase 1, peroxisomal [Source:HGNC Symbol;A
19	ENSG000002	0.34	−0.12	0.34		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:U3I
20	ENSG000001	0.34	−0.18	0.6	CPT1A	carnitine palmitoyltransferase 1A (liver) [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−32	58 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
2	6e−30	248 / 9390	Colon	TxWk_Colon
3	9e−28	252 / 9930	Colon	Tx_Colon
4	2e−27	245 / 9470	Colon	Quies3_Colon
5	2e−23	252 / 10475	Colon	TssA_Colon
6	4e−22	177 / 5889	Colon	EnhWk1_Colon
7	2e−19	50 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
8	6e−17	260 / 11968	Colon	TssWk_Colon
9	3e−15	233 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
10	2e−14	35 / 453	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
11	9e−14	237 / 10800	Brain	Overlap_fetal_midbrain_Quies
12	2e−11	245 / 11791	Colon	Enh_Colon
13	8e−10	218 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
14	2e−09	153 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
15	2e−09	44 / 1005	GSEA	NUYTTEN_EZH2_TARGETS_UP
16	4e−09	186 / 8358	Lympl	HOPP_Active_promoter
17	6e−09	37 / 786	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
18	7e−09	30 / 549	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
19	2e−08	29 / 541	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
20	2e−08	169 / 7491	Lympl	HOPP_Txn_elongation
21	4e−08	27 / 495	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
22	6e−08	207 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
23	8e−08	25 / 446	miRN	hsa−miR−19b
24	1e−07	19 / 277	miRN	hsa−miR−363
25	2e−07	6 / 17	BP	cell separation after cytokinesis
26	2e−07	6 / 17	BP	regulation of centrosome duplication
27	2e−07	19 / 283	miRN	hsa−miR−1244
28	2e−07	48 / 1352	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
29	2e−07	34 / 791	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
30	3e−07	5 / 10	BP	regulation of mitotic spindle assembly
31	3e−07	5 / 10	BP	viral budding via host ESCRT complex
32	3e−07	24 / 444	miRN	hsa−let−7b
33	3e−07	34 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
34	5e−07	85 / 3122	Colon	TxEnhG1_Colon
35	7e−07	27 / 568	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
36	7e−07	22 / 401	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
37	7e−07	24 / 468	GSEA	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
38	8e−07	9 / 63	GSEA	AMIT_SERUM_RESPONSE_120_MCF10A
39	9e−07	174 / 8147	Lympl	HOPP_Weak_promoter
40	1e−06	25 / 509	miRN	hsa−miR−107

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.09	5 / 144	HORVATH_aging_genes meth UP
2	0.60	2 / 123	HORVATH_aging_genes meth DOWN
3	1.00	0 / 57	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−07	6 / 17	cell separation after cytokinesis
2	2e−07	6 / 17	regulation of centrosome duplication
3	3e−07	5 / 10	regulation of mitotic spindle assembly
4	3e−07	5 / 10	viral budding via host ESCRT complex
5	8e−06	5 / 18	nucleus organization
6	9e−06	6 / 31	mitotic metaphase plate congression
7	1e−05	23 / 512	protein transport
8	1e−05	4 / 10	positive regulation of viral release from host cell
9	4e−05	15 / 272	neurotrophin TRK receptor signaling pathway
10	6e−05	6 / 42	fatty acid beta−oxidation
11	6e−05	4 / 14	vacuolar transport
12	8e−05	12 / 194	epidermal growth factor receptor signaling pathway
13	1e−04	7 / 68	endosomal transport
14	2e−04	7 / 75	positive regulation of peptidyl−serine phosphorylation
15	4e−04	5 / 38	endosome to lysosome transport
16	6e−04	9 / 144	viral life cycle
17	9e−04	9 / 152	actin cytoskeleton organization
18	9e−04	9 / 152	cellular lipid metabolic process
19	1e−03	3 / 13	negative regulation of peptidyl−threonine phosphorylation
20	1e−03	3 / 13	positive regulation of exosomal secretion

Brain

Rank	p−value	#in/all	Geneset
1	3e−15	233 / 10278	Overlap_fetal_midbrain_ReprPCWk
2	9e−14	237 / 10800	Overlap_fetal_midbrain_Quies
3	8e−10	218 / 10239	Overlap_fetal_midbrain_ReprPC
4	2e−09	153 / 6320	Overlap_fetal_midbrain_HetRpts
5	6e−08	207 / 9923	Overlap_fetal_midbrain_K9K27me3
6	3e−03	74 / 3370	Mid_Frontal_Lobe_ZNF
7	6e−03	30 / 1137	Fetal_Enh
8	2e−02	29 / 1210	Fetal_TssP
9	4e−02	15 / 552	Fetal_Tx
10	4e−02	20 / 805	Mid_Frontal_Lobe_EnhG
11	5e−02	30 / 1356	Fetal_K9K27me3
12	6e−02	56 / 2820	Mid_Frontal_Lobe_HetRpts
13	6e−02	51 / 2549	Fetal_TssF
14	1e−01	15 / 641	Mid_Frontal_Lobe_EnhP
15	1e−01	9 / 342	Fetal_Het
16	1e−01	56 / 2956	Fetal_TssA
17	2e−01	19 / 940	Mid_Frontal_Lobe_Enh
18	2e−01	9 / 400	Fetal_ZNF
19	2e−01	23 / 1182	Fetal_EnhP
20	2e−01	18 / 910	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	17 / 324	SPANG_BCL6−index2
2	3e−04	11 / 191	SPANG_LPS−index2
3	3e−03	8 / 152	PanCan_MAPK_geneset_nanostring
4	2e−02	1 / 14	LIU_PROSTATE_CANCER_UP
5	2e−02	6 / 136	PanCan_CC+Apop_geneset_nanostring
6	2e−01	4 / 140	PanCan_RAS_geneset_nanostring
7	2e−01	1 / 14	BEN−PORATH_DN
8	2e−01	2 / 52	KUIPER_MM poor survival
9	2e−01	1 / 15	BEN−PORATH_UP
10	2e−01	5 / 198	PanCan_PI3K_geneset_nanostring
11	2e−01	1 / 16	LIU_LIVER_CANCER
12	2e−01	1 / 16	GENTLES_modul6
13	2e−01	1 / 16	GENTLES_modul18
14	3e−01	3 / 123	PanCan_Driver_Gene_geneset_nanostring
15	3e−01	0 / 15	LIU_BREAST_CANCER
16	4e−01	1 / 28	PanCan_HH_geneset_nanostring
17	4e−01	2 / 86	PanCan_JAK−ST_geneset_nanostring
18	6e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
19	6e−01	1 / 51	PanCan_TGF−B_geneset_nanostring
20	7e−01	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	1e−06	8 / 49	autophagosome
2	4e−06	72 / 2638	extracellular exosome
3	1e−05	15 / 246	endosome
4	2e−05	76 / 2974	cytosol
5	3e−04	22 / 596	perinuclear region of cytoplasm
6	4e−04	111 / 5185	cytoplasm
7	5e−04	16 / 378	focal adhesion
8	5e−04	7 / 86	extrinsic component of membrane
9	5e−04	7 / 87	late endosome membrane
10	9e−04	10 / 185	endosome membrane
11	1e−03	18 / 497	Golgi membrane
12	2e−03	4 / 34	peroxisomal matrix
13	3e−03	7 / 116	late endosome
14	3e−03	10 / 216	actin cytoskeleton
15	3e−03	8 / 152	microtubule cytoskeleton
16	6e−03	9 / 204	early endosome
17	8e−03	6 / 106	peroxisome
18	8e−03	3 / 26	pre−autophagosomal structure
19	1e−02	6 / 122	cell cortex
20	1e−02	3 / 32	membrane coat

Chr

Rank	p−value	#in/all	Geneset
1	0.005	11 / 272	Chr 18
2	0.015	11 / 318	Chr 13
3	0.028	42 / 1920	Chr 1
4	0.055	18 / 735	Chr 4
5	0.075	15 / 613	Chr 14
6	0.099	26 / 1228	Chr 2
7	0.238	12 / 582	Chr 15
8	0.375	4 / 191	Chr 21
9	0.377	13 / 715	Chr 10
10	0.386	18 / 1017	Chr 12
11	0.519	16 / 976	Chr 6
12	0.629	18 / 1172	Chr 11
13	0.667	11 / 745	Chr 9
14	0.713	6 / 436	Chr 22
15	0.746	7 / 522	Chr 20
16	0.772	15 / 1083	Chr 17
17	0.831	11 / 862	Chr 5
18	0.833	8 / 651	Chr 8
19	0.859	9 / 746	Chr X
20	0.870	13 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−32	58 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
2	6e−30	248 / 9390	TxWk_Colon
3	9e−28	252 / 9930	Tx_Colon
4	2e−27	245 / 9470	Quies3_Colon
5	2e−23	252 / 10475	TssA_Colon
6	4e−22	177 / 5889	EnhWk1_Colon
7	6e−17	260 / 11968	TssWk_Colon
8	2e−11	245 / 11791	Enh_Colon
9	5e−07	85 / 3122	TxEnhG1_Colon
10	1e−06	173 / 8123	TssF_Colon
11	3e−05	144 / 6761	TssD2_Colon
12	2e−04	75 / 3112	EnhA_Colon
13	4e−04	8 / 110	Marisa_CRC−cluster−h
14	6e−04	96 / 4379	TssD1_Colon
15	1e−03	5 / 49	Marisa_CRC−cluster−f
16	4e−03	21 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
17	5e−03	90 / 4327	EnhWk2_Colon
18	1e−02	4 / 55	Marisa_CRC−cluster−e
19	2e−02	29 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	3e−02	2 / 17	TCGA_Mutated−in−CRC_non−hypermutated

Disease

Rank	p−value	#in/all	Geneset
1	0.002	15 / 399	GUDJ_psoriasis down
2	0.021	17 / 608	GUDJ_psoriasis up
3	0.121	2 / 37	BCHETNIA_EBM−DM up
4	0.302	1 / 22	BCHETNIA_EBM up
5	1.000	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	19 / 344	Up
2	4e−03	25 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
3	1e−02	2 / 11	KIM amplified & overexpressed in LTS
4	1e−02	3 / 31	KIM prognostic signature LTS vs. STS
5	2e−02	11 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	2e−02	7 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	2e−02	35 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
8	4e−02	5 / 119	GIEZELT_GBM_WT_up_VS_mut
9	1e−01	4 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	1e−01	3 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
11	2e−01	38 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
12	2e−01	10 / 434	Down_a
13	2e−01	3 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
14	2e−01	10 / 436	Down_b
15	2e−01	1 / 15	WILLSCHER_GBM_STSwt_proteomics−Q_UP
16	2e−01	2 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
17	2e−01	2 / 56	mature astrocytes
18	2e−01	1 / 16	VERHAAK_CL subtype
19	2e−01	1 / 16	VERHAAK_MES subtype
20	2e−01	2 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−19	50 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
2	2e−14	35 / 453	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
3	2e−09	44 / 1005	NUYTTEN_EZH2_TARGETS_UP
4	6e−09	37 / 786	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
5	7e−09	30 / 549	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
6	2e−08	29 / 541	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
7	4e−08	27 / 495	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
8	2e−07	48 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
9	2e−07	34 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
10	3e−07	34 / 804	CUI_TCF21_TARGETS_2_DN
11	7e−07	27 / 568	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
12	7e−07	22 / 401	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
13	7e−07	24 / 468	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
14	8e−07	9 / 63	AMIT_SERUM_RESPONSE_120_MCF10A
15	1e−06	30 / 699	KRIEG_HYPOXIA_NOT_VIA_KDM3A
16	1e−06	17 / 261	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
17	1e−06	22 / 419	BAELDE_DIABETIC_NEPHROPATHY_DN
18	2e−06	15 / 211	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
19	3e−06	15 / 217	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
20	3e−06	6 / 26	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRA

HM

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 52	HALLMARK_TGF_BETA_SIGNALING
2	4e−04	11 / 198	HALLMARK_HYPOXIA
3	6e−04	7 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	9e−04	10 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	1e−03	7 / 98	HALLMARK_ANDROGEN_RESPONSE
6	4e−03	9 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	4e−03	9 / 193	HALLMARK_HEME_METABOLISM
8	5e−03	9 / 198	HALLMARK_GLYCOLYSIS
9	5e−03	9 / 199	HALLMARK_ADIPOGENESIS
10	1e−02	6 / 112	HALLMARK_BILE_ACID_METABOLISM
11	2e−02	8 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	3e−02	5 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	4e−02	6 / 157	HALLMARK_APOPTOSIS
14	7e−02	4 / 94	HALLMARK_PROTEIN_SECRETION
15	8e−02	4 / 102	HALLMARK_PEROXISOME
16	9e−02	6 / 192	HALLMARK_COMPLEMENT
17	1e−01	5 / 154	HALLMARK_FATTY_ACID_METABOLISM
18	2e−01	4 / 140	HALLMARK_UV_RESPONSE_DN
19	2e−01	5 / 189	HALLMARK_KRAS_SIGNALING_UP
20	2e−01	5 / 196	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	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−09	186 / 8358	HOPP_Active_promoter
2	2e−08	169 / 7491	HOPP_Txn_elongation
3	9e−07	174 / 8147	HOPP_Weak_promoter
4	1e−06	43 / 1215	SPANG_BCR DN
5	3e−04	153 / 7592	HOPP_Strong_enhancer
6	5e−04	4 / 23	SPANG_BAFF 9hrs UP
7	6e−04	138 / 6784	HOPP_Weak_enhancer
8	7e−04	64 / 2658	HOPP_Repetitive
9	9e−04	8 / 123	SPANG_LPS 6hrs UP
10	2e−03	14 / 347	WIRTH_lymphoma937_spot H
11	2e−03	128 / 6389	HOPP_Weak_txn
12	2e−03	115 / 5643	HOPP_Txn_transition
13	3e−03	13 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
14	2e−02	9 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	2e−02	60 / 2838	HOPP_Poised_promoter
16	2e−02	71 / 3457	HOPP_Heterochrom
17	2e−02	11 / 332	SPANG_CD40 6hrs UP
18	3e−02	3 / 42	CARO_OxPhos_in_DLBCL_UP
19	3e−02	4 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
20	3e−02	4 / 75	WIRTH_lymphoma937_spot IM

MF

Rank	p−value	#in/all	Geneset
1	8e−04	201 / 10693	protein binding
2	1e−03	10 / 191	magnesium ion binding
3	2e−03	11 / 245	ubiquitin protein ligase binding
4	2e−03	3 / 17	death receptor binding
5	4e−03	4 / 39	cholesterol binding
6	4e−03	12 / 301	actin binding
7	1e−02	6 / 113	actin filament binding
8	1e−02	2 / 10	1−acylglycerol−3−phosphate O−acyltransferase activity
9	1e−02	5 / 84	Rab GTPase binding
10	1e−02	12 / 350	protein serine/threonine kinase activity
11	1e−02	4 / 57	ubiquitin binding
12	1e−02	4 / 58	phosphoprotein phosphatase activity
13	1e−02	5 / 89	protease binding
14	2e−02	2 / 12	ATPase activity, coupled
15	2e−02	12 / 371	GTP binding
16	2e−02	9 / 250	GTPase activity
17	2e−02	4 / 66	ATPase binding
18	2e−02	2 / 15	cation transmembrane transporter activity
19	2e−02	2 / 15	small GTPase binding
20	3e−02	3 / 39	RNA polymerase II transcription factor activity, ligand−activated sequence−sp

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−08	25 / 446	hsa−miR−19b
2	1e−07	19 / 277	hsa−miR−363
3	2e−07	19 / 283	hsa−miR−1244
4	3e−07	24 / 444	hsa−let−7b
5	1e−06	25 / 509	hsa−miR−107
6	2e−06	14 / 181	hsa−miR−199b−3p
7	2e−06	11 / 112	hsa−miR−1271
8	2e−06	17 / 270	hsa−miR−92b
9	3e−06	21 / 400	hsa−let−7c
10	3e−06	24 / 509	hsa−miR−103
11	5e−06	22 / 452	hsa−miR−19a
12	1e−05	17 / 304	hsa−miR−25
13	1e−05	16 / 279	hsa−miR−92a
14	1e−05	16 / 279	hsa−miR−577
15	3e−05	17 / 333	hsa−miR−32
16	6e−05	10 / 132	hsa−miR−1272
17	9e−05	17 / 360	hsa−let−7a
18	1e−04	11 / 168	hsa−miR−96
19	1e−04	11 / 170	hsa−miR−495
20	1e−04	16 / 334	hsa−miR−18a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 12	BENTINK_ras.1
2	0.20	1 / 14	BENTINK_src.10
3	1.00	0 / 14	GUSTAFSON_PI3K_UP
4	1.00	0 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 14	BENTINK_e2f3.1
6	1.00	0 / 13	BENTINK_e2f3.2
7	1.00	0 / 14	BENTINK_myc.1
8	1.00	0 / 10	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	5e−04	49 / 1867	HEBENSTREIT_high expression TF
2	8e−02	1 / 5	MYC_TF and cofactors
3	1e−01	52 / 2719	ICGC_Pbx3_targets
4	1e−01	62 / 3305	ICGC_BatfPcr1_targets
5	1e−01	1 / 9	MYC_Targets DOWN
6	1e−01	99 / 5552	ICGC_Pol24_targets
7	2e−01	25 / 1294	KIM_MYC targets
8	2e−01	44 / 2401	ICGC_Bcl11_targets
9	3e−01	56 / 3177	ICGC_Irf4_targets
10	3e−01	101 / 6005	ICGC_Mta3_targets
11	3e−01	106 / 6313	ICGC_Pou2_targets
12	4e−01	106 / 6324	ICGC_Yy1_targets
13	4e−01	120 / 7202	ICGC_Runx3_targets
14	4e−01	79 / 4714	ICGC_Pu1_targets
15	4e−01	83 / 4969	ICGC_Atf2_targets
16	4e−01	106 / 6406	ICGC_Pax5_targets
17	4e−01	11 / 619	ICGC_RxraPcr1_targets
18	4e−01	85 / 5135	ICGC_Ebfsc137065_targets
19	4e−01	91 / 5512	ICGC_Nficsc81335_targets
20	5e−01	91 / 5526	ICGC_Pmlsc71910_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	4 / 64	VAQUERIZAS_Lung
2	0.03	2 / 18	VAQUERIZAS_Pancreas
3	0.04	2 / 19	VAQUERIZAS_Heart
4	0.04	2 / 20	VAQUERIZAS_Bone marrow
5	0.15	2 / 42	VAQUERIZAS_Thyroid
6	0.17	2 / 45	VAQUERIZAS_Placenta
7	0.19	1 / 13	VAQUERIZAS_Skin
8	0.30	2 / 67	VAQUERIZAS_Whole blood
9	0.31	1 / 23	VAQUERIZAS_Pituitary
10	0.34	1 / 25	VAQUERIZAS_Spinal cord
11	0.39	1 / 30	VAQUERIZAS_Smooth muscle
12	0.45	1 / 37	VAQUERIZAS_Prostate
13	0.50	1 / 42	VAQUERIZAS_Thymus
14	0.53	1 / 46	VAQUERIZAS_Whole brain
15	1.00	0 / 41	VAQUERIZAS_Fetal brain
16	1.00	0 / 33	VAQUERIZAS_Liver
17	1.00	0 / 49	VAQUERIZAS_Uterus
18	1.00	0 / 155	VAQUERIZAS_General
19	1.00	0 / 12	VAQUERIZAS_Kidney
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.01	10 / 259	PALMER_Granulocytes signature up
2	0.19	1 / 13	PALMER_CD8+ T−Cell signature up
3	0.20	1 / 14	WIRTH_Thymus
4	0.22	1 / 15	WIRTH_Cerebellum
5	0.38	2 / 82	WIRTH_Homeostasis
6	0.59	1 / 54	WIRTH_Pancreas
7	0.85	2 / 208	PALMER_B−Cell signature up
8	0.90	1 / 140	PALMER_T−Cell signature up
9	0.90	1 / 141	WIRTH_Muscle
10	0.92	4 / 427	WIRTH_Immune system
11	0.98	3 / 476	WIRTH_Nervous System
12	1.00	0 / 6	WIRTH_Pituitary gland
13	1.00	0 / 13	WIRTH_Sec. lymphoid organs
14	1.00	0 / 13	WIRTH_Prim. lymphoid organs
15	1.00	0 / 14	WIRTH_B−cells
16	1.00	0 / 12	WIRTH_Tonsil
17	1.00	0 / 12	WIRTH_Lymphocytes
18	1.00	0 / 14	WIRTH_Bone marrow
19	1.00	0 / 13	WIRTH_Globus pallidus
20	1.00	0 / 15	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	22 / 1343	LU_BPDE 1h DN
2	0.8	80 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

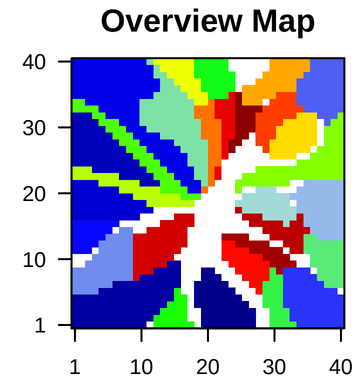
Correlation Clusters

Spot Summary: J

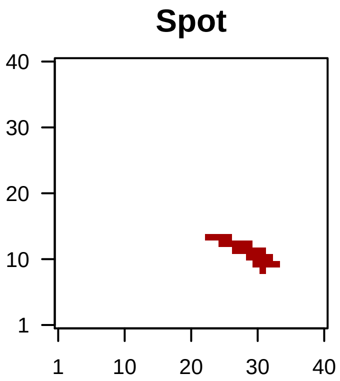
metagenes = 23
genes = 227

<r> metagenes = 0.95
<r> genes = 0.41
beta: r2= 0.01 / log p= −0.15

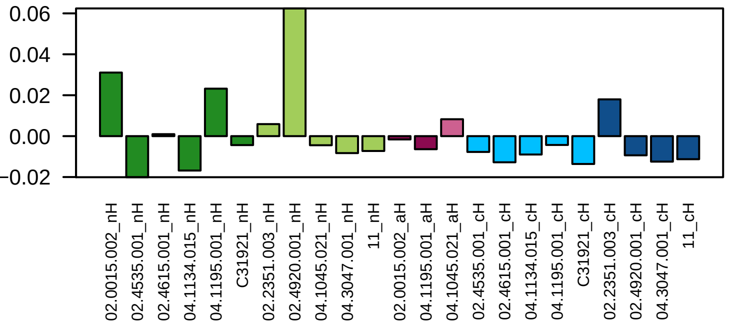
samples with spot = 1 (4.3 %)
other_normHNPCC : 1 (20 %)



Overview Map



Spot

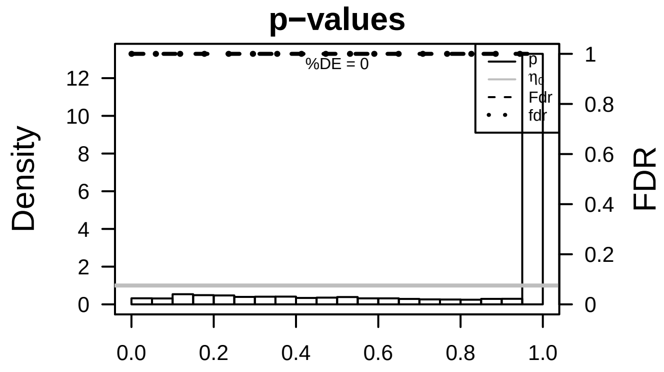


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.28	−0.01	0.73	SFTPC	surfactant protein C [Source:HGNC Symbol;Acc:HGNC:1080
2	ENSG000002	0.26	−0.03	0.84		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H0
3	ENSG000001	0.24	−0.03	0.91	KRT15	keratin 15, type I [Source:HGNC Symbol;Acc:HGNC:6421]
4	ENSG000001	0.23	−0.06	0.73		
5	ENSG000001	0.22	−0.03	0.82	HIST1H3D	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
6	ENSG000001	0.22	−0.06	0.69	ANKRD37	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:HGNC
7	ENSG000001	0.22	−0.09	0.61	SELK	selenoprotein K [Source:EntrezGene;Acc:58515]
8	ENSG000002	0.21	−0.02	0.83		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3
9	ENSG000002	0.21	−0.05	0.78		
10	ENSG000001	0.21	−0.03	0.84	WFDC3	WAP four−disulfide core domain 3 [Source:HGNC Symbol;Ac
11	ENSG000000	0.2	−0.04	0.77	GIPR	gastric inhibitory polypeptide receptor [Source:HGNC Symbo
12	ENSG000002	0.19	−0.02	0.78	C11orf91	chromosome 11 open reading frame 91 [Source:HGNC Sym
13	ENSG000000	0.19	−0.05	0.65	BAMBI	BMP and activin membrane−bound inhibitor [Source:HGNC
14	ENSG000001	0.18	−0.12	0.72	RNF7	ring finger protein 7 [Source:HGNC Symbol;Acc:HGNC:1007
15	ENSG000001	0.18	−0.02	0.73		
16	ENSG000001	0.18	−0.02	0.72	FAM25G	family with sequence similarity 25, member G [Source:HGNC
17	ENSG000001	0.18	−0.02	0.72		
18	ENSG000001	0.17	−0.04	0.42	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis) [Sour
19	ENSG000000	0.17	−0.06	0.55	USP2	ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG
20	ENSG000001	0.17	−0.14	0.4	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−05	5 / 35	BP	respiratory gaseous exchange
2	3e−04	7 / 114	GSEA	HOOI_ST7_TARGETS_DN
3	4e−04	19 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
4	4e−04	8 / 152	GSEA	NABA_ECM_AFFILIATED
5	4e−04	3 / 13	GSEA	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
6	1e−03	69 / 4327	Colon	EnhWk2_Colon
7	2e−03	5 / 75	Colon	Pentrack_CRC_TCGA_corr_N_msi−h_DN
8	3e−03	4 / 53	CC	nucleosome
9	3e−03	2 / 8	GSEA	LIU_CDX2_TARGETS_DN
10	4e−03	3 / 28	GSEA	REACTOME_RNA_POL_I_PROMOTER_OPENING
11	4e−03	128 / 9470	Colon	Quies3_Colon
12	4e−03	3 / 29	GSEA	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_M
13	4e−03	3 / 29	GSEA	TAKADA_GASTRIC_CANCER_COPY_NUMBER_DN
14	5e−03	55 / 3457	Lymp	HOPP_Heterochrom
15	6e−03	3 / 33	GSEA	PID_SYNDECAN_2_PATHWAY
16	7e−03	2 / 11	CC	Cul2−RING ubiquitin ligase complex
17	7e−03	3 / 34	BP	negative regulation of cell adhesion
18	8e−03	7 / 197	GSEA	PEDRIOLI_MIR31_TARGETS_UP
19	8e−03	20 / 967	GSEA	MARSON_BOUND_BY_FOXP3_STIMULATED
20	8e−03	11 / 410	GSEA	RIGGI_EWING_SARCOMA_PROGENITOR_UP
21	8e−03	2 / 12	GSEA	REACTOME_ERKS_ARE_INACTIVATED
22	8e−03	4 / 70	GSEA	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
23	9e−03	5 / 110	Colon	Marisa_CRC−cluster−h
24	9e−03	28 / 1527	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
25	9e−03	42 / 2549	Brain	Fetal_TssF
26	9e−03	7 / 204	GSEA	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP
27	9e−03	2 / 13	BP	regulation of embryonic development
28	1e−02	4 / 73	GSEA	REACTOME_PLATELET_HOMEOSTASIS
29	1e−02	10 / 370	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
30	1e−02	3 / 40	CC	cell leading edge
31	1e−02	2 / 14	BP	cellular response to nitric oxide
32	1e−02	2 / 14	MF	glycine binding
33	1e−02	2 / 14	MF	MAP kinase activity
34	1e−02	4 / 76	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQU
35	1e−02	3 / 41	TF Ti	VAQUERIZAS_Testis
36	1e−02	4 / 77	GSEA	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
37	1e−02	5 / 119	BP	positive regulation of cytosolic calcium ion concentration
38	1e−02	3 / 42	BP	lung alveolus development
39	1e−02	151 / 11791	Colon	Enh_Colon
40	1e−02	2 / 15	GSEA	REACTOME_PLATELET_SENSITIZATION_BY_LDL



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.8	1 / 123	HORVATH_aging_genes meth DOWN
2	1.0	0 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 35	respiratory gaseous exchange
2	7e−03	3 / 34	negative regulation of cell adhesion
3	9e−03	2 / 13	regulation of embryonic development
4	1e−02	2 / 14	cellular response to nitric oxide
5	1e−02	5 / 119	positive regulation of cytosolic calcium ion concentration
6	1e−02	3 / 42	lung alveolus development
7	1e−02	2 / 16	response to growth factor
8	2e−02	2 / 17	blood coagulation, intrinsic pathway
9	2e−02	2 / 17	intracellular transport of virus
10	2e−02	3 / 48	response to retinoic acid
11	2e−02	2 / 18	intraciliary transport
12	2e−02	2 / 19	negative regulation of ossification
13	2e−02	2 / 21	phosphatidylinositol dephosphorylation
14	3e−02	2 / 22	negative regulation of smoothened signaling pathway
15	3e−02	2 / 22	regulation of protein phosphatase type 2A activity
16	3e−02	8 / 316	nervous system development
17	3e−02	3 / 59	sensory perception of pain
18	3e−02	2 / 24	regulation of neuron projection development
19	3e−02	4 / 106	cellular response to lipopolysaccharide
20	3e−02	3 / 62	single fertilization

Brain

Rank	p−value	#in/all	Geneset
1	0.009	42 / 2549	Fetal_TssF
2	0.016	14 / 641	Mid_Frontal_Lobe_EnhP
3	0.037	21 / 1210	Fetal_TssP
4	0.045	39 / 2603	Fetal_TxTrans
5	0.069	26 / 1680	Fetal_ReprPCWk
6	0.119	53 / 3977	Mid_Frontal_Lobe_ReprPC
7	0.141	40 / 2956	Fetal_TssA
8	0.238	23 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	0.244	19 / 1394	Mid_Frontal_Lobe_Quies
10	0.258	18 / 1327	Mid_Frontal_Lobe_TssP
11	0.274	4 / 232	Fetal_ReprPC
12	0.347	26 / 2084	Mid_Frontal_Lobe_K9K27me3
13	0.365	30 / 2443	Fetal_Quies
14	0.391	16 / 1279	Overlap_fetal_midbrain_Enh
15	0.395	34 / 2820	Mid_Frontal_Lobe_HetRpts
16	0.412	10 / 787	Overlap_fetal_midbrain_TssP
17	0.497	22 / 1890	Overlap_fetal_midbrain_TssF
18	0.510	11 / 939	Fetal_HetRpts
19	0.516	10 / 855	Overlap_fetal_midbrain_ZNF
20	0.574	9 / 805	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	4 / 140	PanCan_RAS_geneset_nanostring
2	0.19	0 / 16	LIU_COMMON_CANCER_GENES
3	0.22	2 / 78	PanCan_Wnt_geneset_nanostring
4	0.39	3 / 198	PanCan_PI3K_geneset_nanostring
5	0.44	1 / 51	PanCan_TGF−B_geneset_nanostring
6	0.45	1 / 52	KUIPER_MM poor survival
7	0.52	2 / 152	PanCan_MAPK_geneset_nanostring
8	0.63	1 / 86	PanCan_JAK−ST_geneset_nanostring
9	0.67	1 / 97	PanCan_TXmisReg_geneset_nanostring
10	0.72	3 / 324	SPANG_BCL6−index2
11	0.89	1 / 191	SPANG_LPS−index2
12	0.89	0 / 16	LIU_PROSTATE_CANCER_DN
13	1.00	1 / 574	Lembcke_Colonic Inflammation
14	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
15	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
16	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.00	0 / 15	LIU_BREAST_CANCER
19	1.00	0 / 16	LIU_LIVER_CANCER
20	1.00	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	0.003	4 / 53	nucleosome
2	0.007	2 / 11	Cul2−RING ubiquitin ligase complex
3	0.011	3 / 40	cell leading edge
4	0.018	2 / 18	extrinsic component of plasma membrane
5	0.020	2 / 19	nuclear nucleosome
6	0.022	2 / 20	connexon complex
7	0.049	20 / 1176	extracellular space
8	0.057	2 / 34	peroxisomal matrix
9	0.058	3 / 77	primary cilium
10	0.060	9 / 431	cellular_component
11	0.062	3 / 79	collagen trimer
12	0.063	6 / 245	lysosomal membrane
13	0.067	2 / 37	microtubule associated complex
14	0.067	2 / 37	nuclear body
15	0.076	3 / 86	extrinsic component of membrane
16	0.080	4 / 142	cilium
17	0.087	2 / 43	ciliary tip
18	0.101	2 / 47	chloride channel complex
19	0.102	5 / 216	actin cytoskeleton
20	0.104	2 / 48	platelet alpha granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.02	15 / 715	Chr 10
2	0.04	21 / 1228	Chr 2
3	0.14	12 / 735	Chr 4
4	0.18	16 / 1083	Chr 17
5	0.20	5 / 272	Chr 18
6	0.23	14 / 976	Chr 6
7	0.47	14 / 1172	Chr 11
8	0.52	10 / 859	Chr 7
9	0.53	10 / 862	Chr 5
10	0.53	22 / 1920	Chr 1
11	0.53	12 / 1043	Chr 3
12	0.62	8 / 746	Chr X
13	0.66	6 / 582	Chr 15
14	0.67	15 / 1425	Chr 19
15	0.71	6 / 613	Chr 14
16	0.72	5 / 522	Chr 20
17	0.76	6 / 651	Chr 8
18	0.93	6 / 847	Chr 16
19	0.93	5 / 745	Chr 9
20	0.95	7 / 1017	Chr 12

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	19 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
2	1e−03	69 / 4327	EnhWk2_Colon
3	2e−03	5 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
4	4e−03	128 / 9470	Quies3_Colon
5	9e−03	5 / 110	Marisa_CRC−cluster−h
6	1e−02	151 / 11791	Enh_Colon
7	2e−02	48 / 3112	EnhA_Colon
8	2e−02	82 / 5889	EnhWk1_Colon
9	5e−02	12 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
10	8e−02	19 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
11	8e−02	1 / 7	Juehling−MSI−enriched−in−8−to−9
12	1e−01	1 / 9	Marisa_CRC−C2
13	1e−01	2 / 49	Marisa_CRC−cluster−f
14	1e−01	1 / 12	KIM_MSI−in−CRC
15	2e−01	1 / 20	Vilar_mutated−in−CRC−CamP
16	2e−01	55 / 4379	TssD1_Colon
17	3e−01	17 / 1281	HetRpts_Colon
18	3e−01	59 / 4879	Quies1_Colon
19	3e−01	2 / 105	Marisa_CRC−cluster−d
20	4e−01	7 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.03	2 / 22	BCHETNIA_EBM up
2	0.35	1 / 37	BCHETNIA_EBM−DM up
3	0.92	4 / 608	GUDJ_psoriasis up
4	0.94	2 / 399	GUDJ_psoriasis down
5	1.00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	28 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
2	0.014	2 / 16	VERHAAK_NL subtype
3	0.088	4 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
4	0.106	8 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
5	0.119	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
6	0.121	3 / 106	WIRTH_Normal Brain
7	0.125	8 / 434	Down_a
8	0.127	2 / 54	Hopp_Sturm_GBM_Epi3_B1_G34_DN
9	0.129	1 / 12	WILLSCHER_GBM_LTSwt_proteomics−C_UP
10	0.129	3 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	0.138	2 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
12	0.139	1 / 13	VERHAAK_Brain
13	0.139	9 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
14	0.142	2 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
15	0.158	1 / 15	neurons_glio
16	0.168	1 / 16	astrocytes_glio
17	0.205	4 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
18	0.237	2 / 81	Weller_LGG_gradeII−vs−III_UP
19	0.279	2 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
20	0.295	5 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	7 / 114	HOOI_ST7_TARGETS_DN
2	4e−04	8 / 152	NABA_ECM_AFFILIATED
3	4e−04	3 / 13	NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
4	3e−03	2 / 8	LIU_CDX2_TARGETS_DN
5	4e−03	3 / 28	REACTOME_RNA_POL_I_PROMOTER_OPENING
6	4e−03	3 / 29	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP
7	4e−03	3 / 29	TAKADA_GASTRIC_CANCER_COPY_NUMBER_DN
8	6e−03	3 / 33	PID_SYNDECAN_2_PATHWAY
9	8e−03	7 / 197	PEDRIOLI_MIR31_TARGETS_UP
10	8e−03	20 / 967	MARSON_BOUND_BY_FOXP3_STIMULATED
11	8e−03	11 / 410	RIGGI_EWING_SARCOMA_PROGENITOR_UP
12	8e−03	2 / 12	REACTOME_ERKS_ARE_INACTIVATED
13	8e−03	4 / 70	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
14	9e−03	7 / 204	BHAT_ESR1_TARGETS_NOT_VIA_AKT1_UP
15	1e−02	4 / 73	REACTOME_PLATELET_HOMEOSTASIS
16	1e−02	10 / 370	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
17	1e−02	4 / 76	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_TURQUOIS
18	1e−02	4 / 77	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
19	1e−02	2 / 15	REACTOME_PLATELET_SENSITIZATION_BY_LDL
20	1e−02	10 / 381	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP

HM

Rank	p−value	#in/all	Geneset
1	0.2	4 / 192	HALLMARK_COMPLEMENT
2	0.2	4 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.2	3 / 140	HALLMARK_UV_RESPONSE_DN
4	0.3	2 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	0.3	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
6	0.3	1 / 36	HALLMARK_ANGIOGENESIS
7	0.3	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
8	0.4	3 / 196	HALLMARK_P53_PATHWAY
9	0.4	2 / 132	HALLMARK_COAGULATION
10	0.5	2 / 157	HALLMARK_APOPTOSIS
11	0.6	2 / 193	HALLMARK_XENOBIOTIC_METABOLISM
12	0.7	2 / 194	HALLMARK_INFLAMMATORY_RESPONSE
13	0.7	2 / 196	HALLMARK_MITOTIC_SPINDLE
14	0.7	2 / 198	HALLMARK_HYPOXIA
15	0.7	2 / 199	HALLMARK_ADIPOGENESIS
16	0.7	1 / 112	HALLMARK_BILE_ACID_METABOLISM
17	0.8	1 / 154	HALLMARK_FATTY_ACID_METABOLISM
18	0.9	1 / 181	HALLMARK_ALLOGRAFT_REJECTION
19	0.9	1 / 189	HALLMARK_KRAS_SIGNALING_UP
20	0.9	1 / 193	HALLMARK_HEME_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
2	1.0	0 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.005	55 / 3457	HOPP_Heterochrom
2	0.027	4 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
3	0.038	10 / 458	WIRTH_lymphoma937_spot I
4	0.064	2 / 36	Subero_MM_hyper_meth
5	0.073	9 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
6	0.074	4 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
7	0.085	67 / 5039	HOPP_Repressed
8	0.104	2 / 48	Subero_INT_hypo_meth
9	0.134	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
10	0.141	5 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
11	0.158	1 / 15	Subero_B−ALL_hypo_meth
12	0.167	3 / 123	SPANG_LPS 6hrs UP
13	0.181	6 / 332	SPANG_CD40 6hrs UP
14	0.205	1 / 20	Subero_MCL_hypo_meth
15	0.207	2 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
16	0.211	2 / 75	WIRTH_lymphoma937_spot IM
17	0.238	83 / 6784	HOPP_Weak_enhancer
18	0.241	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
19	0.283	2 / 92	WIRTH_lymphoma937_spot A
20	0.287	2 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

MF

Rank	p−value	#in/all	Geneset
1	0.01	2 / 14	glycine binding
2	0.01	2 / 14	MAP kinase activity
3	0.02	3 / 49	phosphoric diester hydrolase activity
4	0.02	2 / 21	protein phosphatase type 2A regulator activity
5	0.03	3 / 60	peptide binding
6	0.04	2 / 29	Rab guanyl−nucleotide exchange factor activity
7	0.05	2 / 30	cysteine−type endopeptidase inhibitor activity
8	0.05	2 / 31	repressing transcription factor binding
9	0.05	3 / 73	ubiquitinyl hydrolase activity
10	0.07	5 / 192	carbohydrate binding
11	0.08	3 / 90	ubiquitin−specific protease activity
12	0.09	2 / 44	extracellular ligand−gated ion channel activity
13	0.09	2 / 45	scavenger receptor activity
14	0.10	3 / 97	cysteine−type endopeptidase activity
15	0.11	1 / 10	low−density lipoprotein receptor activity
16	0.11	1 / 10	microtubule plus−end binding
17	0.11	1 / 10	protein kinase B binding
18	0.11	8 / 420	protein heterodimerization activity
19	0.12	1 / 11	hydrolase activity, acting on glycosyl bonds
20	0.12	1 / 11	NAD−dependent histone deacetylase activity (H3−K14 specific)

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	11 / 447	hsa−miR−519d
2	0.03	3 / 56	hsa−miR−208a
3	0.03	10 / 435	hsa−miR−372
4	0.03	8 / 321	hsa−miR−302b
5	0.04	5 / 160	hsa−miR−139−5p
6	0.04	8 / 333	hsa−miR−302a
7	0.05	11 / 542	hsa−miR−106a
8	0.06	11 / 562	hsa−miR−17
9	0.06	5 / 184	hsa−miR−582−5p
10	0.07	5 / 191	hsa−miR−302e
11	0.08	2 / 41	hsa−miR−758
12	0.08	8 / 393	hsa−miR−373
13	0.08	2 / 42	hsa−miR−525−3p
14	0.09	7 / 330	hsa−miR−302c
15	0.09	6 / 266	hsa−miR−520a−3p
16	0.09	10 / 536	hsa−miR−106b
17	0.09	3 / 94	hsa−miR−216b
18	0.10	7 / 344	hsa−miR−302d
19	0.10	2 / 48	hsa−miR−524−3p
20	0.11	6 / 283	hsa−miR−1244

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.04	25 / 1523	ICGC_P300_targets
2	0.31	34 / 2719	ICGC_Pbx3_targets
3	0.32	67 / 5552	ICGC_Pol24_targets
4	0.33	30 / 2401	ICGC_Bcl11_targets
5	0.33	72 / 6005	ICGC_Mta3_targets
6	0.40	22 / 1798	HEBENSTREIT_low expression TF
7	0.41	38 / 3177	ICGC_Irf4_targets
8	0.41	26 / 2149	ICGC_Mef2_targets
9	0.44	62 / 5308	ICGC_Tcf12_targets
10	0.45	58 / 4969	ICGC_Atf2_targets
11	0.46	18 / 1506	ICGC_Usf1_targets
12	0.46	9 / 731	ICGC_SrfPcr2_targets
13	0.48	9 / 745	ICGC_NrsfPcr2_targets
14	0.51	59 / 5135	ICGC_Ebfsc137065_targets
15	0.52	54 / 4714	ICGC_Pu1_targets
16	0.52	17 / 1472	ICGC_NrsfPcr1_targets
17	0.54	73 / 6406	ICGC_Pax5_targets
18	0.55	32 / 2827	ICGC_Bcl3_targets
19	0.59	26 / 2342	ICGC_GabpPcr2_targets
20	0.60	61 / 5453	ICGC_Foxm1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.01	3 / 41	VAQUERIZAS_Testis
2	0.09	2 / 45	VAQUERIZAS_Placenta
3	0.17	1 / 16	VAQUERIZAS_Fetal liver
4	0.20	1 / 19	VAQUERIZAS_Heart
5	0.25	1 / 25	VAQUERIZAS_Spinal cord
6	0.32	1 / 33	VAQUERIZAS_Liver
7	0.41	1 / 46	VAQUERIZAS_Whole brain
8	0.43	1 / 49	VAQUERIZAS_Uterus
9	0.54	1 / 67	VAQUERIZAS_Whole blood
10	0.83	1 / 155	VAQUERIZAS_General
11	1.00	0 / 41	VAQUERIZAS_Fetal brain
12	1.00	0 / 37	VAQUERIZAS_Prostate
13	1.00	0 / 30	VAQUERIZAS_Smooth muscle
14	1.00	0 / 12	VAQUERIZAS_Kidney
15	1.00	0 / 42	VAQUERIZAS_Thymus
16	1.00	0 / 42	VAQUERIZAS_Thyroid
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 31	VAQUERIZAS_Fetal lung
19	1.00	0 / 64	VAQUERIZAS_Lung
20	1.00	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 54	WIRTH_Pancreas
2	0.14	1 / 13	PALMER_CD8+ T−Cell signature up
3	0.16	1 / 15	WIRTH_Cerebellum
4	0.42	1 / 47	WIRTH_Placenta
5	0.48	2 / 141	WIRTH_Muscle
6	0.61	1 / 82	WIRTH_Homeostasis
7	0.64	5 / 476	WIRTH_Nervous System
8	0.73	1 / 115	WIRTH_Liver
9	0.79	1 / 137	WIRTH_Mucosa
10	0.80	1 / 140	PALMER_T−Cell signature up
11	0.90	1 / 202	WIRTH_Testis
12	0.91	1 / 208	PALMER_B−Cell signature up
13	0.99	1 / 427	WIRTH_Immune system
14	1.00	0 / 6	WIRTH_Pituitary gland
15	1.00	0 / 13	WIRTH_Sec. lymphoid organs
16	1.00	0 / 13	WIRTH_Prim. lymphoid organs
17	1.00	0 / 14	WIRTH_B−cells
18	1.00	0 / 12	WIRTH_Tonsil
19	1.00	0 / 14	WIRTH_Thymus
20	1.00	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	67 / 5285	LU_BPDE 0.005 DN
2	0.2	19 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

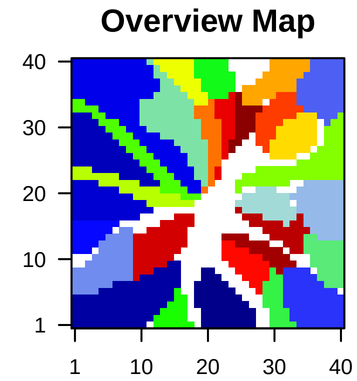
Correlation Clusters

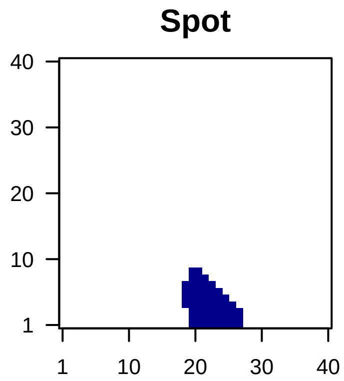
Spot Summary: K

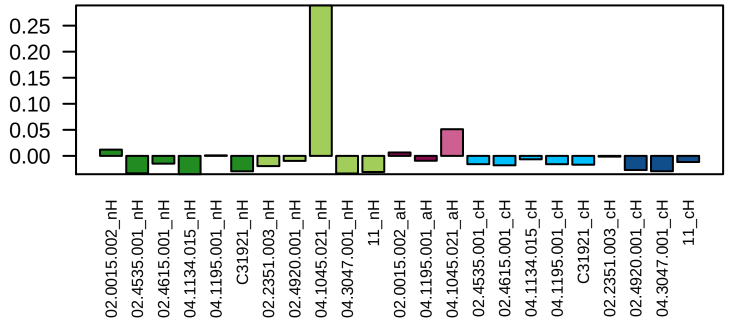
metagenes = 55
genes = 500

<r> metagenes = 0.96
<r> genes = 0.61
beta: r2= 0.05 / log p= −0.55

samples with spot = 2 (8.7 %)
other_normHNPCC : 1 (20 %)
other_adenomaHNPCC : 1 (100 %)


Overview Map


Spot

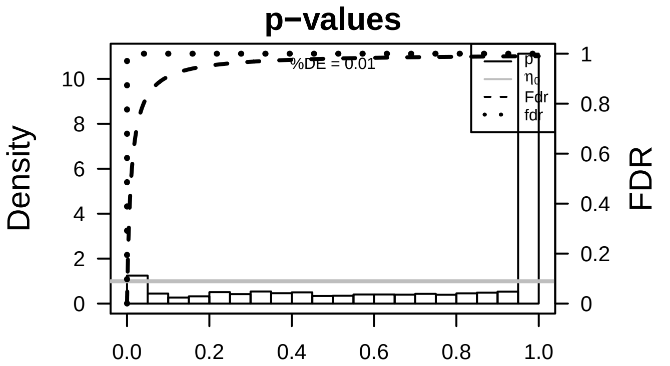


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	2.14	−0.26	0.98	ALDOB	aldolase B, fructose−bisphosphate [Source:HGNC Symbol;Ac
2	ENSG000001	2	−0.1	0.96	APOA4	apolipoprotein A−IV [Source:HGNC Symbol;Acc:HGNC:602]
3	ENSG000001	1.85	−0.15	0.98	RBP2	retinol binding protein 2, cellular [Source:HGNC Symbol;Acc:
4	ENSG000001	1.46	−0.07	0.96	APOC3	apolipoprotein C−III [Source:HGNC Symbol;Acc:HGNC:610]
5	ENSG000001	1.38	−0.08	0.97	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4 [Sourc
6	ENSG000001	1.36	−0.06	0.96	S100G	S100 calcium binding protein G [Source:HGNC Symbol;Acc:
7	ENSG000000	1.3	−0.29	0.88	SMIM24	small integral membrane protein 24 [Source:HGNC Symbol;A
8	ENSG000001	1.24	−0.06	0.96	APOA1	apolipoprotein A−I [Source:HGNC Symbol;Acc:HGNC:600]
9	ENSG000000	1.18	−0.06	0.96	APOB	apolipoprotein B [Source:HGNC Symbol;Acc:HGNC:603]
10	ENSG000001	1.13	−0.18	0.96	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), memb
11	ENSG000002	1.12	−0.08	0.96	GSTA1	glutathione S−transferase alpha 1 [Source:HGNC Symbol;Ac
12	ENSG000001	1.11	−0.06	0.96	CCL25	chemokine (C−C motif) ligand 25 [Source:HGNC Symbol;Acc
13	ENSG000001	1.09	−0.34	0.69	SERPINA1	serpin peptidase inhibitor, clade A (alpha−1 antiproteinase, ar
14	ENSG000001	1.07	−0.23	0.95	FBP1	fructose−1,6−bisphosphatase 1 [Source:HGNC Symbol;Acc:
15	ENSG000000	1.06	−0.08	0.96	CREB3L3	cAMP responsive element binding protein 3−like 3 [Source:H
16	ENSG000001	1.04	−0.09	0.86	DEFA5	defensin, alpha 5, Paneth cell−specific [Source:HGNC Symbo
17	ENSG000000	0.98	−0.05	0.96	FOLH1B	folate hydrolase (prostate−specific membrane antigen) 1 [Sou
18	ENSG000000	0.98	−0.1	0.95	SI	sucrase−isomaltase (alpha−glucosidase) [Source:HGNC Sym
19	ENSG000001	0.97	−0.21	0.94	CBR1	carbonyl reductase 1 [Source:HGNC Symbol;Acc:HGNC:154
20	ENSG000001	0.95	−0.22	0.76	FABP2	fatty acid binding protein 2, intestinal [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−28	46 / 229	GSEA	HSIAO_LIVER_SPECIFIC_GENES
2	3e−27	111 / 1418	BP	small molecule metabolic process
3	4e−26	53 / 346	GSEA	SANSOM_APC_TARGETS_DN
4	1e−20	46 / 336	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
5	3e−19	31 / 154	BP	xenobiotic metabolic process
6	4e−19	34 / 193	HM	HALLMARK_XENOBIOTIC_METABOLISM
7	2e−18	29 / 141	GSEA	OHGUCHI_LIVER_HNF4A_TARGETS_DN
8	1e−17	21 / 67	GSEA	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
9	2e−17	30 / 164	GSEA	LEE_LIVER_CANCER_SURVIVAL_UP
10	9e−17	151 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
11	9e−17	36 / 257	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
12	1e−16	25 / 115	Tissu	WIRTH_Liver
13	6e−16	21 / 80	GSEA	WOO_LIVER_CANCER_RECURRENCE_DN
14	4e−15	25 / 132	GSEA	REACTOME_BIOLOGICAL_OXIDATIONS
15	4e−15	57 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
16	1e−14	131 / 2638	CC	extracellular exosome
17	2e−14	18 / 64	BP	cholesterol homeostasis
18	5e−14	53 / 640	BP	oxidation−reduction process
19	6e−14	48 / 541	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
20	2e−13	26 / 170	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
21	4e−13	46 / 526	GSEA	ACEVEDO_LIVER_CANCER_DN
22	4e−13	30 / 235	MF	transporter activity
23	4e−13	32 / 268	CC	apical plasma membrane
24	2e−12	31 / 268	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
25	7e−12	48 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
26	8e−12	54 / 753	BP	transmembrane transport
27	8e−12	49 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
28	1e−11	37 / 396	GSEA	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECUL
29	1e−11	167 / 4052	CC	integral component of membrane
30	7e−11	15 / 65	GSEA	REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS
31	7e−11	18 / 100	GSEA	SERVITJA_ISLET_HNF1A_TARGETS_DN
32	9e−11	33 / 346	GSEA	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
33	1e−10	15 / 68	GSEA	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
34	2e−10	10 / 24	BP	triglyceride homeostasis
35	3e−10	13 / 51	MF	monooxygenase activity
36	4e−10	14 / 62	GSEA	KEGG_RETINOL_METABOLISM
37	6e−10	10 / 27	BP	cholesterol efflux
38	1e−09	13 / 56	BP	digestion
39	1e−09	25 / 231	GSEA	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
40	1e−09	28 / 287	MF	oxidoreductase activity


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.01	8 / 123	HORVATH_aging_genes meth DOWN
2	0.18	3 / 57	TESCHENDORFF_age_hypermethylated
3	0.31	5 / 144	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−27	111 / 1418	small molecule metabolic process
2	3e−19	31 / 154	xenobiotic metabolic process
3	2e−14	18 / 64	cholesterol homeostasis
4	5e−14	53 / 640	oxidation−reduction process
5	8e−12	54 / 753	transmembrane transport
6	2e−10	10 / 24	triglyceride homeostasis
7	6e−10	10 / 27	cholesterol efflux
8	1e−09	13 / 56	digestion
9	9e−09	12 / 54	arachidonic acid metabolic process
10	1e−08	11 / 44	glutathione metabolic process
11	1e−08	7 / 13	fructose metabolic process
12	1e−08	12 / 56	retinoid metabolic process
13	2e−08	36 / 491	transport
14	3e−08	10 / 38	lipoprotein metabolic process
15	5e−08	12 / 62	steroid metabolic process
16	9e−08	27 / 325	response to drug
17	1e−07	29 / 375	carbohydrate metabolic process
18	4e−07	13 / 88	response to nutrient
19	5e−07	8 / 29	drug metabolic process
20	2e−06	18 / 191	lipid metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.001	64 / 1713	Mid_Frontal_Lobe_ReprPCWk
2	0.011	70 / 2084	Mid_Frontal_Lobe_K9K27me3
3	0.024	120 / 3977	Mid_Frontal_Lobe_ReprPC
4	0.042	30 / 840	Mid_Frontal_Lobe_TssF
5	0.063	59 / 1890	Overlap_fetal_midbrain_TssF
6	0.064	45 / 1394	Mid_Frontal_Lobe_Quies
7	0.090	31 / 940	Mid_Frontal_Lobe_Enh
8	0.142	9 / 232	Fetal_ReprPC
9	0.163	73 / 2549	Fetal_TssF
10	0.178	74 / 2603	Fetal_TxTrans
11	0.185	25 / 805	Mid_Frontal_Lobe_EnhG
12	0.191	11 / 317	Mid_Frontal_Lobe_Tx
13	0.209	43 / 1478	Overlap_fetal_midbrain_TxTrans
14	0.288	4 / 106	Overlap_fetal_midbrain_Tx
15	0.288	19 / 641	Mid_Frontal_Lobe_EnhP
16	0.454	21 / 787	Overlap_fetal_midbrain_TssP
17	0.473	11 / 408	Mid_Frontal_Lobe_TxTrans
18	0.588	42 / 1680	Fetal_ReprPCWk
19	0.602	74 / 2956	Fetal_TssA
20	0.660	13 / 552	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	1 / 16	LIU_LIVER_CANCER
2	0.12	1 / 15	LIU_BREAST_CANCER
3	0.32	1 / 15	GENTLES_modul10
4	0.34	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	0.34	1 / 16	LIU_PROSTATE_CANCER_DN
6	0.34	1 / 16	GENTLES_modul7
7	0.34	1 / 16	GENTLES_modul16
8	0.41	0 / 14	LIU_PROSTATE_CANCER_UP
9	0.45	9 / 324	SPANG_BCL6−index2
10	0.62	1 / 37	KUIPER_MM good survival
11	0.65	1 / 40	PanCan_HK_geneset_nanostring
12	0.71	13 / 574	Lembcke_Colonic Inflammation
13	0.74	1 / 52	KUIPER_MM poor survival
14	0.87	3 / 191	SPANG_LPS−index2
15	0.90	10 / 550	Lembcke_Normal vs Adenoma
16	0.92	1 / 97	PanCan_TXmisReg_geneset_nanostring
17	0.96	2 / 198	PanCan_PI3K_geneset_nanostring
18	0.97	1 / 136	PanCan_CC+Apop_geneset_nanostring
19	0.97	1 / 140	PanCan_RAS_geneset_nanostring
20	0.98	1 / 152	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−14	131 / 2638	extracellular exosome
2	4e−13	32 / 268	apical plasma membrane
3	1e−11	167 / 4052	integral component of membrane
4	2e−08	11 / 46	brush border membrane
5	3e−08	12 / 60	brush border
6	7e−07	6 / 14	chylomicron
7	2e−06	60 / 1250	integral component of plasma membrane
8	7e−06	41 / 767	endoplasmic reticulum membrane
9	8e−06	6 / 20	very−low−density lipoprotein particle
10	1e−05	114 / 3059	membrane
11	7e−05	5 / 18	microvillus membrane
12	3e−04	29 / 558	intracellular membrane−bounded organelle
13	3e−04	120 / 3507	plasma membrane
14	8e−04	4 / 17	anchored component of external side of plasma membrane
15	1e−03	4 / 20	high−density lipoprotein particle
16	2e−03	9 / 106	peroxisome
17	2e−03	5 / 34	peroxisomal matrix
18	2e−03	53 / 1374	extracellular region
19	2e−03	3 / 11	secretory granule lumen
20	3e−03	12 / 185	basolateral plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	4e−04	34 / 715	Chr 10
2	2e−02	39 / 1083	Chr 17
3	3e−02	18 / 436	Chr 22
4	3e−01	22 / 735	Chr 4
5	3e−01	33 / 1172	Chr 11
6	3e−01	17 / 582	Chr 15
7	3e−01	24 / 847	Chr 16
8	4e−01	24 / 859	Chr 7
9	4e−01	27 / 976	Chr 6
10	4e−01	8 / 272	Chr 18
11	4e−01	17 / 613	Chr 14
12	4e−01	18 / 651	Chr 8
13	5e−01	27 / 1043	Chr 3
14	5e−01	5 / 191	Chr 21
15	6e−01	30 / 1228	Chr 2
16	7e−01	7 / 318	Chr 13
17	8e−01	16 / 745	Chr 9
18	8e−01	43 / 1920	Chr 1
19	9e−01	30 / 1425	Chr 19
20	9e−01	16 / 862	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−15	57 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
2	7e−12	48 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	3e−09	44 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
4	5e−05	148 / 4327	EnhWk2_Colon
5	7e−05	52 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	6e−02	19 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
7	6e−02	6 / 110	Marisa_CRC−cluster−h
8	1e−01	5 / 105	Marisa_CRC−cluster−d
9	2e−01	24 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
10	2e−01	3 / 55	Marisa_CRC−cluster−e
11	2e−01	183 / 6761	TssD2_Colon
12	2e−01	83 / 2947	ReprPCWk_Colon
13	2e−01	1 / 9	Boland_CRC−MSI−TGC
14	2e−01	1 / 10	Marisa_CRC−C1
15	2e−01	310 / 11791	Enh_Colon
16	2e−01	7 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
17	3e−01	93 / 3406	ReprPC_Colon
18	3e−01	131 / 4879	Quies1_Colon
19	3e−01	13 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
20	3e−01	3 / 76	Marisa_CRC−cluster−g

Disease

Rank	p−value	#in/all	Geneset
1	0.8	8 / 399	GUDJ_psoriasis down
2	0.9	11 / 608	GUDJ_psoriasis up
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−17	151 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	3e−05	40 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	9e−04	26 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	1e−02	35 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
5	1e−02	2 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
6	6e−02	2 / 16	astrocytes_glio
7	7e−02	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
8	8e−02	4 / 63	Stuehler_Proteins_up_in_STS
9	1e−01	2 / 21	KIM deleted & downregulated in LTS
10	1e−01	1 / 5	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
11	1e−01	3 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
12	1e−01	1 / 6	laffaire_hypometh_LGG_vs_control
13	2e−01	3 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
14	2e−01	2 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP
15	2e−01	2 / 31	KIM prognostic signature LTS vs. STS
16	2e−01	4 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
17	2e−01	3 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
18	2e−01	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
19	2e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
20	3e−01	2 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−28	46 / 229	HSIAO_LIVER_SPECIFIC_GENES
2	4e−26	53 / 346	SANSOM_APC_TARGETS_DN
3	1e−20	46 / 336	VECCHI_GASTRIC_CANCER_EARLY_DN
4	2e−18	29 / 141	OHGUCHI_LIVER_HNF4A_TARGETS_DN
5	1e−17	21 / 67	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
6	2e−17	30 / 164	LEE_LIVER_CANCER_SURVIVAL_UP
7	9e−17	36 / 257	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
8	6e−16	21 / 80	WOO_LIVER_CANCER_RECURRENCE_DN
9	4e−15	25 / 132	REACTOME_BIOLOGICAL_OXIDATIONS
10	6e−14	48 / 541	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
11	2e−13	26 / 170	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
12	4e−13	46 / 526	ACEVEDO_LIVER_CANCER_DN
13	2e−12	31 / 268	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
14	8e−12	49 / 641	FEVR_CTNNB1_TARGETS_UP
15	1e−11	37 / 396	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES
16	7e−11	15 / 65	REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS
17	7e−11	18 / 100	SERVITJA_ISLET_HNF1A_TARGETS_DN
18	9e−11	33 / 346	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
19	1e−10	15 / 68	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
20	4e−10	14 / 62	KEGG_RETINOL_METABOLISM

HM

Rank	p−value	#in/all	Geneset
1	4e−19	34 / 193	HALLMARK_XENOBIOTIC_METABOLISM
2	1e−06	14 / 112	HALLMARK_BILE_ACID_METABOLISM
3	3e−05	13 / 132	HALLMARK_COAGULATION
4	2e−03	11 / 154	HALLMARK_FATTY_ACID_METABOLISM
5	2e−03	5 / 37	HALLMARK_PANCREAS_BETA_CELLS
6	5e−03	12 / 199	HALLMARK_ADIPOGENESIS
7	3e−02	10 / 193	HALLMARK_HEME_METABOLISM
8	3e−02	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	3e−02	10 / 198	HALLMARK_HYPOXIA
10	3e−02	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	3e−02	10 / 198	HALLMARK_GLYCOLYSIS
12	6e−02	9 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	1e−01	8 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
14	2e−01	7 / 192	HALLMARK_COMPLEMENT
15	2e−01	5 / 128	HALLMARK_SPERMATOGENESIS
16	3e−01	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	3e−01	2 / 44	HALLMARK_APICAL_SURFACE
18	3e−01	5 / 146	HALLMARK_DNA_REPAIR
19	4e−01	6 / 189	HALLMARK_KRAS_SIGNALING_UP
20	6e−01	5 / 193	HALLMARK_KRAS_SIGNALING_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.2	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.2	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.2	1 / 11	DUMEAUX_Smoking literature genes up
5	0.2	1 / 11	DUMEAUX_Women normal BMI literature genes up
6	0.4	1 / 17	DUMEAUX_High bmi enriched genes
7	0.9	1 / 91	DUMEAUX_Smoking enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−04	8 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_C
2	3e−03	7 / 75	WIRTH_lymphoma937_spot IM
3	2e−02	2 / 8	MASCQUE_GCB UP
4	2e−02	4 / 42	CARO_OxPhos_in_DLBCL_UP
5	3e−02	6 / 92	WIRTH_lymphoma937_spot A
6	3e−02	6 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
7	4e−02	147 / 5039	HOPP_Repressed
8	4e−02	2 / 12	DAVE_BL UP
9	6e−02	2 / 16	WRIGHT_GCB UP
10	8e−02	4 / 63	SPANG_BAFF 9hrs DN
11	9e−02	2 / 20	DAVE_BL Inter
12	1e−01	15 / 414	TARTE_Mature plasma cell signature
13	1e−01	99 / 3457	HOPP_Heterochrom
14	2e−01	3 / 59	LENZ_Stromal signature 2
15	3e−01	1 / 12	Subero_MM_hypo_meth
16	3e−01	2 / 40	ROSOLOWSKI_blue DOWN
17	3e−01	1 / 14	DAVE_BL_DN
18	3e−01	2 / 48	Subero_INT_hypo_meth
19	4e−01	3 / 83	ROSOLOWSKI_green UP
20	4e−01	2 / 49	Subero_DLBCL_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	4e−13	30 / 235	transporter activity
2	3e−10	13 / 51	monooxygenase activity
3	1e−09	28 / 287	oxidoreductase activity
4	2e−08	17 / 124	heme binding
5	3e−08	13 / 72	oxidoreductase activity, acting on paired donors, with incorporation or reductic
6	8e−07	16 / 143	iron ion binding
7	8e−07	7 / 22	steroid hydroxylase activity
8	4e−06	6 / 18	cholesterol transporter activity
9	4e−06	5 / 11	aldo−keto reductase (NADP) activity
10	7e−06	27 / 407	catalytic activity
11	7e−06	5 / 12	dipeptidase activity
12	1e−05	6 / 21	lipid transporter activity
13	1e−05	6 / 21	oxidoreductase activity, acting on paired donors, with incorporation or reductic
14	1e−05	8 / 43	oxygen binding
15	2e−05	6 / 23	carboxypeptidase activity
16	3e−05	6 / 25	steroid binding
17	4e−05	5 / 16	arachidonic acid epoxygenase activity
18	7e−05	5 / 18	glucose transmembrane transporter activity
19	7e−05	5 / 18	neurotransmitter:sodium symporter activity
20	1e−04	5 / 20	aromatase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	4 / 83	hsa−miR−562
2	0.2	2 / 34	hsa−miR−555
3	0.2	3 / 66	hsa−miR−618
4	0.2	1 / 11	hsa−miR−487b
5	0.3	2 / 39	hsa−miR−501−3p
6	0.3	2 / 40	hsa−miR−502−3p
7	0.3	3 / 73	hsa−miR−548b−3p
8	0.3	1 / 15	hsa−miR−452*
9	0.3	2 / 46	hsa−miR−660
10	0.3	1 / 16	hsa−miR−551b
11	0.4	1 / 17	hsa−miR−551a
12	0.4	1 / 17	hsa−miR−1298
13	0.4	2 / 49	hsa−miR−518e*
14	0.4	2 / 50	hsa−miR−302b*
15	0.4	3 / 87	hsa−miR−339−5p
16	0.4	2 / 54	hsa−miR−1279
17	0.4	4 / 127	hsa−miR−625
18	0.4	3 / 92	hsa−miR−362−5p
19	0.4	4 / 131	hsa−miR−145
20	0.4	2 / 59	hsa−miR−665

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	3e−04	70 / 1798	HEBENSTREIT_low expression TF
2	2e−01	22 / 731	ICGC_SrfPcr2_targets
3	4e−01	1 / 20	MYC_Metabolism UP
4	6e−01	89 / 3511	ICGC_Rad21_targets
5	7e−01	36 / 1506	ICGC_Usf1_targets
6	7e−01	14 / 619	ICGC_RxraPcr1_targets
7	7e−01	17 / 745	ICGC_NrsfPcr2_targets
8	8e−01	35 / 1523	ICGC_P300_targets
9	8e−01	135 / 5552	ICGC_Pol24_targets
10	8e−01	33 / 1472	ICGC_NrsfPcr1_targets
11	8e−01	1 / 66	MYC_Targets UP
12	8e−01	123 / 5135	ICGC_Ebfsc137065_targets
13	8e−01	129 / 5393	ICGC_Sp1_targets
14	9e−01	111 / 4714	ICGC_Pu1_targets
15	9e−01	76 / 3305	ICGC_BatfPcr1_targets
16	9e−01	61 / 2719	ICGC_Pbx3_targets
17	9e−01	172 / 7202	ICGC_Runx3_targets
18	9e−01	53 / 2401	ICGC_Bcl11_targets
19	9e−01	145 / 6157	ICGC_Tcf3_targets
20	9e−01	140 / 6005	ICGC_Mta3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 37	VAQUERIZAS_Prostate
2	0.3	1 / 12	VAQUERIZAS_Kidney
3	0.4	1 / 17	VAQUERIZAS_Adrenal gland
4	0.4	5 / 155	VAQUERIZAS_General
5	0.4	1 / 19	VAQUERIZAS_Heart
6	0.5	1 / 25	VAQUERIZAS_Adrenal cortex
7	0.6	1 / 31	VAQUERIZAS_Lymph node
8	0.6	1 / 33	VAQUERIZAS_Liver
9	0.7	1 / 41	VAQUERIZAS_Testis
10	0.7	1 / 42	VAQUERIZAS_Thyroid
11	0.7	1 / 45	VAQUERIZAS_Placenta
12	0.7	1 / 49	VAQUERIZAS_Uterus
13	1.0	0 / 41	VAQUERIZAS_Fetal brain
14	1.0	0 / 30	VAQUERIZAS_Smooth muscle
15	1.0	0 / 25	VAQUERIZAS_Spinal cord
16	1.0	0 / 46	VAQUERIZAS_Whole brain
17	1.0	0 / 42	VAQUERIZAS_Thymus
18	1.0	0 / 67	VAQUERIZAS_Whole blood
19	1.0	0 / 7	VAQUERIZAS_Appendix
20	1.0	0 / 31	VAQUERIZAS_Fetal lung

Tissue

Rank	p−value	#in/all	Geneset
1	1e−16	25 / 115	WIRTH_Liver
2	2e−09	15 / 82	WIRTH_Homeostasis
3	4e−02	10 / 208	PALMER_B−Cell signature up
4	5e−02	2 / 14	WIRTH_Bone marrow
5	7e−02	11 / 259	PALMER_Granulocytes signature up
6	3e−01	1 / 14	WIRTH_Thymus
7	3e−01	1 / 16	WIRTH_Hippocampus
8	4e−01	2 / 54	WIRTH_Pancreas
9	5e−01	4 / 140	PALMER_T−Cell signature up
10	7e−01	1 / 47	WIRTH_Placenta
11	8e−01	10 / 476	WIRTH_Nervous System
12	9e−01	2 / 141	WIRTH_Muscle
13	1e+00	1 / 137	WIRTH_Mucosa
14	1e+00	1 / 202	WIRTH_Testis
15	1e+00	2 / 427	WIRTH_Immune system
16	1e+00	0 / 6	WIRTH_Pituitary gland
17	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
18	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
19	1e+00	0 / 14	WIRTH_B−cells
20	1e+00	0 / 12	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	154 / 5285	LU_BPDE 0.005 DN
2	0.85	29 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

Spot Summary: L

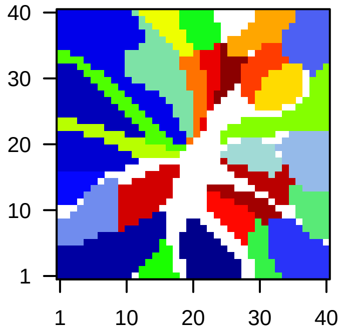
metagenes = 133
genes = 1666

<r> metagenes = 0.94

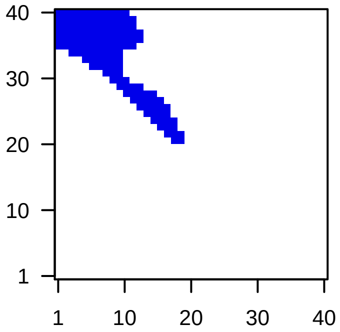
beta: r2= 0.12 / log p= −0.97

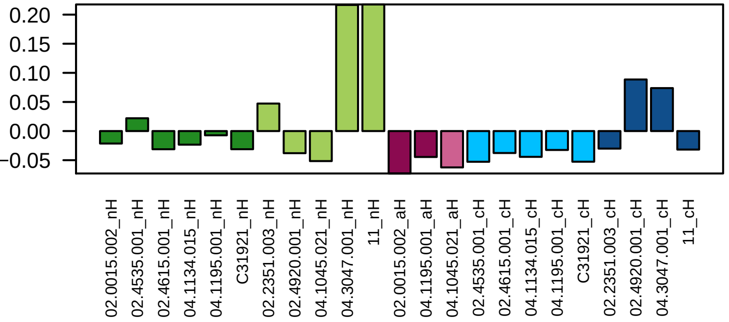
samples with spot = 4 (17.4 %)
other_normHNPCC : 2 (40 %)
other_cancerHNPCC : 2 (50 %)

Overview Map



Spot





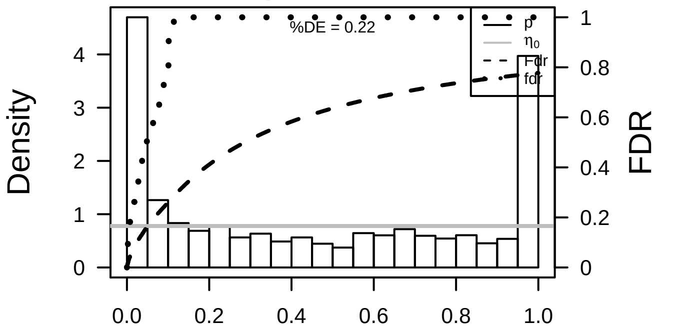
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.59	−0.8	0.83	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	ENSG000001	1.46	−0.53	0.93	MYH11	myosin, heavy chain 11, smooth muscle [Source:HGNC Syml
3	ENSG000001	1.44	−0.52	0.91	CNN1	calponin 1, basic, smooth muscle [Source:HGNC Symbol;Acc
4	ENSG000001	1.42	−0.68	0.88	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
5	ENSG000002	1.37	−0.24	0.43	MTRNR2L1	MT−RNR2−like 1 [Source:HGNC Symbol;Acc:HGNC:37155]
6	ENSG000001	1.35	−0.91	0.87	MYL9	myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:I
7	ENSG000001	1.32	−0.37	0.95	SYNM	synemin, intermediate filament protein [Source:HGNC Symbo
8	ENSG000001	1.3	−0.58	0.95	FLNA	filamin A, alpha [Source:HGNC Symbol;Acc:HGNC:3754]
9	ENSG000001	1.29	−0.49	0.92	TPM2	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
10	ENSG000001	1.24	−0.52	0.7	IGFBP7	insulin−like growth factor binding protein 7 [Source:HGNC Sy
11	ENSG000001	1.21	−0.38	0.96	CSRP1	cysteine and glycine−rich protein 1 [Source:HGNC Symbol;A
12	ENSG000001	1.2	−0.74	0.89	TAGLN	transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
13	ENSG000000	1.17	−0.45	0.93	HSPB6	heat shock protein, alpha−crystallin−related, B6 [Source:HGN
14	ENSG000000	1.17	−0.25	0.96	NDE1	nudE neurodevelopment protein 1 [Source:HGNC Symbol;Ac
15	ENSG000001	1.17	−0.39	0.98	CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
16	ENSG000000	1.17	−0.4	0.96	FHL1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:HC
17	ENSG000001	1.17	−0.36	0.97	LMOD1	leiomodin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
18	ENSG000001	1.14	−0.57	0.92	ACTA2	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
19	ENSG000000	1.14	−0.3	0.98	MYLK	myosin light chain kinase [Source:HGNC Symbol;Acc:HGNC:
20	ENSG000001	1.12	−0.31	0.96	PLN	phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−75	5 / 16	Cance	LIU_PROSTATE_CANCER_DN
2	3e−74	97 / 132	Colon	Marisa_CRC−cluster−b
3	2e−51	156 / 478	GSEA	LIM_MAMMARY_STEM_CELL_UP
4	1e−48	696 / 5039	Lympl	HOPP_Repressed
5	3e−42	448 / 2838	Lympl	HOPP_Poised_promoter
6	4e−37	645 / 4879	Colon	Quies1_Colon
7	5e−36	460 / 3109	Colon	TssP_Colon
8	4e−35	132 / 476	Tissu	WIRTH_Nervous System
9	3e−34	164 / 692	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
10	6e−33	99 / 303	GSEA	PASINI_SUZ12_TARGETS_DN
11	1e−30	120 / 445	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
12	4e−30	133 / 535	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
13	6e−30	1103 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
14	9e−30	111 / 399	Disea	GUDJ_psoriasis down
15	6e−29	72 / 189	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
16	1e−28	1141 / 10800	Brain	Overlap_fetal_midbrain_Quies
17	6e−27	81 / 249	GSEA	BOQUEST_STEM_CELL_UP
18	2e−26	88 / 292	GSEA	CHANDRAN_METASTASIS_DN
19	1e−25	150 / 711	GSEA	LEE_BMP2_TARGETS_UP
20	1e−25	62 / 160	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
21	2e−25	107 / 418	GSEA	SWEET_LUNG_CANCER_KRAS_DN
22	2e−25	69 / 196	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
23	3e−24	85 / 294	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
24	3e−24	30 / 40	GSEA	TOMLINS_PROSTATE_CANCER_DN
25	1e−23	96 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
26	2e−23	78 / 261	Lympl	LENZ_Stromal signature 1
27	7e−23	75 / 248	GSEA	ONDER_CDH1_TARGETS_2_UP
28	9e−23	113 / 490	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
29	2e−22	118 / 530	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
30	1e−21	539 / 4379	Colon	TssD1_Colon
31	4e−21	63 / 195	HM	HALLMARK_MYOGENESIS
32	6e−21	152 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
33	2e−20	1201 / 11968	Colon	TssWk_Colon
34	3e−20	1059 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
35	4e−20	85 / 336	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
36	9e−20	112 / 525	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
37	2e−19	52 / 148	Colon	Marisa_CRC−cluster−a
38	2e−19	91 / 384	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_DN
39	9e−19	95 / 419	GSEA	BAELDE_DIABETIC_NEPHROPATHY_DN
40	1e−18	521 / 4327	Colon	EnhWk2_Colon

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.003	23 / 144	HORVATH_aging_genes meth UP
2	0.035	17 / 123	HORVATH_aging_genes meth DOWN
3	0.553	5 / 57	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−17	106 / 523	cell adhesion
2	3e−14	37 / 105	muscle contraction
3	4e−13	43 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
4	2e−11	73 / 373	axon guidance
5	2e−10	13 / 19	regulation of cardiac muscle contraction by regulation of the release of seques
6	1e−08	168 / 1279	signal transduction
7	5e−08	56 / 306	extracellular matrix organization
8	2e−07	74 / 466	blood coagulation
9	2e−07	25 / 94	muscle organ development
10	3e−07	14 / 34	regulation of heart rate
11	4e−07	40 / 200	heart development
12	1e−06	22 / 82	positive regulation of neuron projection development
13	1e−06	14 / 37	digestive tract development
14	2e−06	53 / 316	nervous system development
15	2e−06	13 / 34	substrate adhesion−dependent cell spreading
16	7e−06	41 / 231	brain development
17	1e−05	9 / 19	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic
18	1e−05	13 / 39	platelet aggregation
19	1e−05	22 / 95	axonogenesis
20	2e−05	7 / 12	relaxation of cardiac muscle

Brain

Rank	p−value	#in/all	Geneset
1	6e−30	1103 / 10278	Overlap_fetal_midbrain_ReprPCWk
2	1e−28	1141 / 10800	Overlap_fetal_midbrain_Quies
3	3e−20	1059 / 10239	Overlap_fetal_midbrain_ReprPC
4	4e−17	191 / 1210	Fetal_TssP
5	1e−15	693 / 6320	Overlap_fetal_midbrain_HetRpts
6	5e−13	360 / 2956	Fetal_TssA
7	3e−10	175 / 1279	Overlap_fetal_midbrain_Enh
8	4e−10	120 / 787	Overlap_fetal_midbrain_TssP
9	4e−09	305 / 2603	Fetal_TxTrans
10	9e−09	177 / 1356	Fetal_K9K27me3
11	1e−08	965 / 9923	Overlap_fetal_midbrain_K9K27me3
12	1e−08	158 / 1182	Fetal_EnhP
13	4e−08	41 / 191	Overlap_fetal_midbrain_Het
14	1e−07	125 / 910	Fetal_EnhG
15	2e−06	47 / 268	Mid_Frontal_Lobe_TssA
16	6e−06	141 / 1137	Fetal_Enh
17	7e−06	135 / 1084	Overlap_fetal_midbrain_EnhG
18	1e−05	54 / 342	Fetal_Het
19	3e−05	76 / 552	Fetal_Tx
20	3e−05	93 / 712	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	3e−75	5 / 16	LIU_PROSTATE_CANCER_DN
2	8e−07	9 / 15	GENTLES_modul17
3	4e−05	29 / 152	PanCan_MAPK_geneset_nanostring
4	2e−04	7 / 16	GENTLES_modul16
5	7e−04	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	9e−04	24 / 140	PanCan_RAS_geneset_nanostring
7	2e−03	6 / 16	GENTLES_modul11
8	2e−03	30 / 198	PanCan_PI3K_geneset_nanostring
9	9e−03	41 / 324	SPANG_BCL6−index2
10	3e−02	4 / 15	BEN−PORATH_UP
11	4e−02	24 / 191	SPANG_LPS−index2
12	7e−02	13 / 97	PanCan_TXmisReg_geneset_nanostring
13	1e−01	2 / 16	LIU_LIVER_CANCER
14	1e−01	6 / 37	KUIPER_MM good survival
15	1e−01	3 / 15	GENTLES_modul13
16	1e−01	7 / 51	PanCan_TGF−B_geneset_nanostring
17	2e−01	14 / 123	PanCan_Driver_Gene_geneset_nanostring
18	2e−01	9 / 78	PanCan_Wnt_geneset_nanostring
19	3e−01	2 / 15	LIU_BREAST_CANCER
20	4e−01	3 / 28	PanCan_HH_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−16	37 / 91	sarcolemma
2	3e−15	39 / 109	Z disc
3	3e−14	80 / 378	focal adhesion
4	5e−12	409 / 3507	plasma membrane
5	2e−10	49 / 216	actin cytoskeleton
6	1e−09	13 / 21	costamere
7	2e−09	552 / 5185	cytoplasm
8	7e−09	307 / 2638	extracellular exosome
9	1e−08	67 / 381	cytoskeleton
10	6e−08	25 / 88	basement membrane
11	2e−07	69 / 422	cell junction
12	2e−07	41 / 202	extracellular matrix
13	2e−06	14 / 39	T−tubule
14	3e−06	52 / 312	dendrite
15	9e−06	14 / 43	sarcomere
16	1e−05	44 / 259	synapse
17	1e−05	30 / 151	lamellipodium
18	1e−05	45 / 270	proteinaceous extracellular matrix
19	2e−05	317 / 2974	cytosol
20	2e−05	8 / 16	dystrophin−associated glycoprotein complex

Chr

Rank	p−value	#in/all	Geneset
1	7e−06	112 / 862	Chr 5
2	2e−04	92 / 735	Chr 4
3	2e−03	84 / 715	Chr 10
4	1e−02	129 / 1228	Chr 2
5	4e−02	78 / 746	Chr X
6	1e−01	65 / 651	Chr 8
7	1e−01	84 / 859	Chr 7
8	2e−01	71 / 745	Chr 9
9	3e−01	26 / 272	Chr 18
10	3e−01	56 / 613	Chr 14
11	4e−01	29 / 318	Chr 13
12	4e−01	92 / 1043	Chr 3
13	5e−01	166 / 1920	Chr 1
14	6e−01	92 / 1083	Chr 17
15	9e−01	43 / 582	Chr 15
16	9e−01	74 / 976	Chr 6
17	9e−01	89 / 1172	Chr 11
18	9e−01	76 / 1017	Chr 12
19	9e−01	29 / 436	Chr 22
20	1e+00	31 / 522	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−74	97 / 132	Marisa_CRC−cluster−b
2	4e−37	645 / 4879	Quies1_Colon
3	5e−36	460 / 3109	TssP_Colon
4	1e−21	539 / 4379	TssD1_Colon
5	2e−20	1201 / 11968	TssWk_Colon
6	2e−19	52 / 148	Marisa_CRC−cluster−a
7	1e−18	521 / 4327	EnhWk2_Colon
8	1e−17	96 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
9	4e−14	410 / 3406	ReprPC_Colon
10	1e−13	362 / 2947	ReprPCWk_Colon
11	2e−13	98 / 525	Quies2_Colon
12	2e−12	70 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
13	2e−09	70 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
14	2e−09	1127 / 11791	Enh_Colon
15	9e−09	83 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
16	3e−08	8 / 9	Budinska_D_Mesenchymal_UP
17	3e−07	210 / 1753	Het_Colon
18	5e−07	161 / 1281	HetRpts_Colon
19	5e−07	21 / 73	Ang_CRC−CIMPH−vs−L_hyper
20	2e−06	21 / 78	Ang_CRC_Hypermethylated

Disease

Rank	p−value	#in/all	Geneset
1	9e−30	111 / 399	GUDJ_psoriasis down
2	1e+00	22 / 608	GUDJ_psoriasis up
3	1e+00	0 / 22	BCHETNIA_EBM up
4	1e+00	0 / 2	BCHETNIA_EBM down
5	1e+00	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−08	73 / 434	Down_a
2	8e−08	34 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
3	7e−07	25 / 99	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
4	1e−05	12 / 34	WIRTH_PN subtype
5	2e−05	51 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	3e−05	63 / 436	Down_b
7	6e−05	15 / 56	mature astrocytes
8	6e−05	16 / 63	OPC
9	2e−04	6 / 12	Phillips MES up vs Prolif & PN
10	4e−04	21 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	5e−04	22 / 119	GIEZELT_GBM_WT_up_VS_mut
12	7e−04	20 / 106	WIRTH_Normal Brain
13	7e−04	10 / 36	Colman_survival_associated
14	1e−03	6 / 15	VERHAAK_PN_Brain
15	1e−03	6 / 15	Mukasa_UP_in_GBM
16	1e−03	165 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
17	2e−03	58 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
18	3e−03	9 / 36	Shaw_down_in_1p19q
19	3e−03	4 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
20	4e−03	17 / 97	Weller_LGG_1p19qDel−vs−intact_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−75	5 / 16	LIU_PROSTATE_CANCER_DN
2	2e−51	156 / 478	LIM_MAMMARY_STEM_CELL_UP
3	3e−34	164 / 692	WONG_ADULT_TISSUE_STEM_MODULE
4	6e−33	99 / 303	PASINI_SUZ12_TARGETS_DN
5	1e−30	120 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	4e−30	133 / 535	CHICAS_RB1_TARGETS_CONFLUENT
7	6e−29	72 / 189	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
8	6e−27	81 / 249	BOQUEST_STEM_CELL_UP
9	2e−26	88 / 292	CHANDRAN_METASTASIS_DN
10	1e−25	150 / 711	LEE_BMP2_TARGETS_UP
11	1e−25	62 / 160	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
12	2e−25	107 / 418	SWEET_LUNG_CANCER_KRAS_DN
13	2e−25	69 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	3e−24	85 / 294	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
15	3e−24	30 / 40	TOMLINS_PROSTATE_CANCER_DN
16	1e−23	96 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
17	7e−23	75 / 248	ONDER_CDH1_TARGETS_2_UP
18	9e−23	113 / 490	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
19	2e−22	118 / 530	KIM_ALL_DISORDERS_CALB1_CORR_UP
20	6e−21	152 / 804	CUI_TCF21_TARGETS_2_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−21	63 / 195	HALLMARK_MYOGENESIS
2	1e−16	57 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	2e−08	34 / 140	HALLMARK_UV_RESPONSE_DN
4	3e−05	34 / 190	HALLMARK_APICAL_JUNCTION
5	6e−03	28 / 196	HALLMARK_MITOTIC_SPINDLE
6	1e−02	27 / 199	HALLMARK_ADIPOGENESIS
7	3e−02	25 / 193	HALLMARK_HEME_METABOLISM
8	3e−02	21 / 157	HALLMARK_APOPTOSIS
9	3e−02	25 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	3e−02	7 / 36	HALLMARK_HEDGEHOG_SIGNALING
11	3e−02	8 / 44	HALLMARK_APICAL_SURFACE
12	5e−02	24 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
13	6e−02	24 / 198	HALLMARK_HYPOXIA
14	6e−02	23 / 189	HALLMARK_KRAS_SIGNALING_UP
15	6e−02	17 / 132	HALLMARK_COAGULATION
16	8e−02	8 / 52	HALLMARK_TGF_BETA_SIGNALING
17	1e−01	5 / 30	HALLMARK_NOTCH_SIGNALING
18	1e−01	22 / 197	HALLMARK_IL2_STAT5_SIGNALING
19	1e−01	12 / 98	HALLMARK_ANDROGEN_RESPONSE
20	2e−01	11 / 94	HALLMARK_PROTEIN_SECRETION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	4 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.06	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.30	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	0.39	9 / 91	DUMEAUX_Smoking enriched genes
5	0.56	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
6	0.63	1 / 11	DUMEAUX_Smoking literature genes up
7	0.78	1 / 17	DUMEAUX_High bmi enriched genes
8	0.79	2 / 33	DUMEAUX_Fasting enriched genes
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 11	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−48	696 / 5039	HOPP_Repressed
2	3e−42	448 / 2838	HOPP_Poised_promoter
3	2e−23	78 / 261	LENZ_Stromal signature 1
4	2e−13	332 / 2658	HOPP_Repetitive
5	3e−11	78 / 414	TARTE_Mature plasma cell signature
6	4e−10	701 / 6784	HOPP_Weak_enhancer
7	5e−10	62 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
8	6e−10	62 / 315	WIRTH_lymphoma937_spot E
9	3e−08	382 / 3457	HOPP_Heterochrom
10	1e−07	647 / 6389	HOPP_Weak_txn
11	2e−06	30 / 138	Subero_DLBCL_hyper_meth
12	3e−05	16 / 59	LENZ_Stromal signature 2
13	1e−04	24 / 122	Subero_INT_hyper_meth
14	1e−04	20 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
15	2e−04	17 / 75	Subero_FL_hyper_meth
16	2e−04	8 / 21	DAVE_Immune response 2
17	4e−04	19 / 94	Subero_T−ALL_hyper_meth
18	5e−04	9 / 29	DAVE_Immune response 1
19	6e−04	25 / 145	WIRTH_lymphoma937_spot F
20	6e−04	25 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons

MF

Rank	p−value	#in/all	Geneset
1	8e−18	1085 / 10693	protein binding
2	4e−14	118 / 672	calcium ion binding
3	5e−09	58 / 301	actin binding
4	3e−07	47 / 250	GTPase activity
5	2e−06	60 / 371	GTP binding
6	2e−06	24 / 98	ion channel binding
7	2e−06	14 / 39	structural constituent of muscle
8	3e−06	36 / 186	microtubule binding
9	2e−05	16 / 58	cytoskeletal protein binding
10	3e−05	32 / 172	calmodulin binding
11	3e−05	15 / 53	GDP binding
12	7e−05	13 / 45	SMAD binding
13	1e−04	88 / 693	protein homodimerization activity
14	2e−04	35 / 217	protein domain specific binding
15	3e−04	12 / 45	tubulin binding
16	5e−04	25 / 142	heparin binding
17	5e−04	7 / 18	guanyl nucleotide binding
18	7e−04	6 / 14	transcription factor activity, RNA polymerase II transcription factor binding
19	1e−03	6 / 15	nitric−oxide synthase binding
20	1e−03	19 / 102	integrin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−12	96 / 536	hsa−miR−106b
2	3e−11	83 / 452	hsa−miR−19a
3	4e−11	82 / 446	hsa−miR−19b
4	8e−11	104 / 631	hsa−miR−20a
5	1e−10	95 / 562	hsa−miR−17
6	2e−10	98 / 591	hsa−miR−20b
7	1e−09	90 / 542	hsa−miR−106a
8	5e−09	75 / 435	hsa−miR−372
9	8e−09	71 / 407	hsa−miR−301b
10	8e−09	91 / 573	hsa−miR−93
11	8e−09	72 / 416	hsa−miR−519c−3p
12	9e−09	56 / 291	hsa−miR−570
13	1e−08	61 / 333	hsa−miR−32
14	2e−08	79 / 480	hsa−miR−301a
15	2e−08	74 / 442	hsa−miR−548n
16	3e−08	76 / 462	hsa−miR−130b
17	5e−08	61 / 344	hsa−miR−302d
18	5e−08	36 / 158	hsa−miR−200c
19	6e−08	38 / 173	hsa−miR−183
20	7e−08	76 / 471	hsa−miR−130a

PathwAct

Rank	p−value	#in/all	Geneset
1	0.03	4 / 14	BENTINK_e2f3.1
2	0.05	3 / 10	BENTINK_ras.4
3	0.28	2 / 12	BENTINK_ras.1
4	0.38	2 / 15	BENTINK_ras.6
5	0.69	1 / 13	BENTINK_e2f3.2
6	0.72	1 / 14	GUSTAFSON_PI3K_UP
7	0.72	1 / 14	BENTINK_myc.1
8	1.00	0 / 15	GUSTAFSON_PI3K_DN
9	1.00	0 / 14	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	2e−09	113 / 745	ICGC_NrsfPcr2_targets
2	2e−08	221 / 1798	HEBENSTREIT_low expression TF
3	3e−05	171 / 1472	ICGC_NrsfPcr1_targets
4	6e−04	353 / 3511	ICGC_Rad21_targets
5	4e−03	219 / 2149	ICGC_Mef2_targets
6	5e−03	4 / 9	MYC_Targets DOWN
7	5e−03	241 / 2401	ICGC_Bcl11_targets
8	7e−03	2 / 2	MYC_ECM cell adhesion DOWN
9	3e−02	151 / 1506	ICGC_Usf1_targets
10	5e−02	268 / 2827	ICGC_Bcl3_targets
11	6e−02	2 / 5	MYC_TF and cofactors
12	1e−01	466 / 5135	ICGC_Ebfsc137065_targets
13	1e−01	143 / 1523	ICGC_P300_targets
14	3e−01	244 / 2719	ICGC_Pbx3_targets
15	3e−01	491 / 5552	ICGC_Pol24_targets
16	3e−01	68 / 731	ICGC_SrfPcr2_targets
17	3e−01	293 / 3305	ICGC_BatfPcr1_targets
18	4e−01	279 / 3177	ICGC_Irf4_targets
19	5e−01	393 / 4566	ICGC_Egr1_targets
20	6e−01	587 / 6862	ICGC_Elf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	5e−05	14 / 49	VAQUERIZAS_Uterus
2	2e−03	11 / 46	VAQUERIZAS_Whole brain
3	2e−03	6 / 16	VAQUERIZAS_Ovary
4	1e−02	6 / 23	VAQUERIZAS_Pituitary
5	1e−02	5 / 17	VAQUERIZAS_Adrenal gland
6	2e−02	6 / 25	VAQUERIZAS_Spinal cord
7	2e−02	6 / 25	VAQUERIZAS_Adrenal cortex
8	2e−02	11 / 64	VAQUERIZAS_Lung
9	1e−01	5 / 31	VAQUERIZAS_Fetal lung
10	1e−01	4 / 24	VAQUERIZAS_Trachea
11	2e−01	3 / 17	VAQUERIZAS_Salivary gland
12	2e−01	17 / 155	VAQUERIZAS_General
13	2e−01	2 / 10	VAQUERIZAS_Skeletal.muscle.psoas
14	3e−01	5 / 41	VAQUERIZAS_Fetal brain
15	3e−01	5 / 45	VAQUERIZAS_Placenta
16	4e−01	4 / 37	VAQUERIZAS_Prostate
17	5e−01	2 / 18	VAQUERIZAS_Pancreas
18	5e−01	1 / 7	VAQUERIZAS_Appendix
19	5e−01	3 / 30	VAQUERIZAS_Smooth muscle
20	5e−01	4 / 42	VAQUERIZAS_Thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	4e−35	132 / 476	WIRTH_Nervous System
2	3e−03	5 / 13	WIRTH_Sec. lymphoid organs
3	1e−02	21 / 141	WIRTH_Muscle
4	6e−02	18 / 140	PALMER_T−Cell signature up
5	1e−01	3 / 14	WIRTH_Thymus
6	1e−01	28 / 259	PALMER_Granulocytes signature up
7	3e−01	2 / 13	WIRTH_Globus pallidus
8	3e−01	2 / 13	WIRTH_Cortex cerebri
9	3e−01	2 / 14	WIRTH_B−cells
10	3e−01	2 / 14	WIRTH_Thyroid gland
11	4e−01	2 / 16	WIRTH_Hippocampus
12	6e−01	17 / 208	PALMER_B−Cell signature up
13	7e−01	1 / 12	WIRTH_Tonsil
14	7e−01	1 / 12	WIRTH_Lymphocytes
15	7e−01	1 / 13	WIRTH_Prim. lymphoid organs
16	7e−01	1 / 13	PALMER_CD8+ T−Cell signature up
17	7e−01	1 / 15	WIRTH_Telencephalon
18	7e−01	2 / 30	PALMER_Lymphocytes signature up
19	9e−01	3 / 54	WIRTH_Pancreas
20	9e−01	2 / 47	WIRTH_Placenta

Toxic

Rank	p−value	#in/all	Geneset
1	2e−09	561 / 5285	LU_BPDE 0.005 DN
2	1e−02	139 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

Spot Summary: M

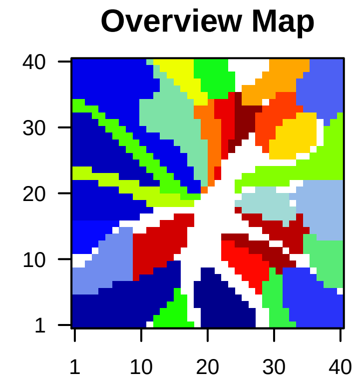
metagenes = 81
genes = 1034

<r> metagenes = 0.95

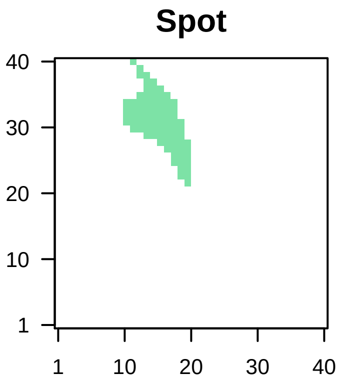
beta: r2= 0.01 / log p= −0.13

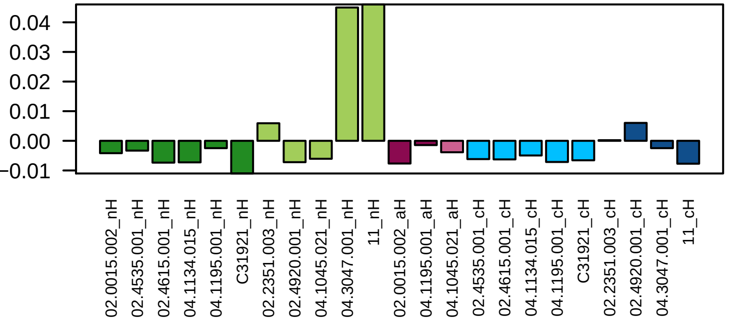
samples with spot = 0 (0 %)

Overview Map



Spot





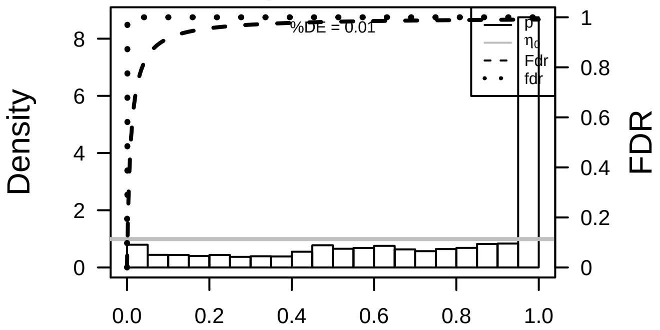
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.28	−0.36	0.33		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:V9(
2	ENSG000001	0.25	−0.19	0.55	CDK2AP1	cyclin−dependent kinase 2 associated protein 1 [Source:HGN
3	ENSG000002	0.24	−0.03	0.26	LY6G6F	lymphocyte antigen 6 complex, locus G6F [Source:HGNC Sy
4	ENSG000001	0.23	−0.13	0.47	ADAM9	ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Ac
5	ENSG000000	0.2	−0.14	0.49	COQ9	coenzyme Q9 [Source:HGNC Symbol;Acc:HGNC:25302]
6	ENSG000001	0.19	−0.05	0.77	TPD52L1	tumor protein D52−like 1 [Source:HGNC Symbol;Acc:HGNC:
7	ENSG000001	0.19	−0.07	0.49	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1 [S
8	ENSG000001	0.19	−0.03	0.68	KRT17	keratin 17, type I [Source:HGNC Symbol;Acc:HGNC:6427]
9	ENSG000002	0.18	−0.07	0.64	TRNP1	TMF1−regulated nuclear protein 1 [Source:HGNC Symbol;Ac
10	ENSG000001	0.18	−0.09	0.78	PCMT1	protein−L−isoaspartate (D−aspartate) O−methyltransferase [S
11	ENSG000001	0.17	−0.02	0.75	TAGLN3	transgelin 3 [Source:HGNC Symbol;Acc:HGNC:29868]
12	ENSG000001	0.17	−0.06	0.86	C11orf74	chromosome 11 open reading frame 74 [Source:HGNC Symb
13	ENSG000000	0.17	−0.1	0.52	DLD	dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
14	ENSG000002	0.17	−0.05	0.69	LOC105379861	neuropeptide Y receptor Y4 [Source:HGNC Symbol;Acc:HGN
15	ENSG000001	0.17	−0.06	0.79	ZNF503	zinc finger protein 503 [Source:HGNC Symbol;Acc:HGNC:23
16	ENSG000002	0.17	−0.15	0.55		Uncharacterized protein; cDNA FLJ60496 [Source:UniProtKB
17	ENSG000000	0.17	−0.15	0.58	DDX1	DEAD (Asp−Glu−Ala−Asp) box helicase 1 [Source:HGNC Sy
18	ENSG000001	0.17	−0.07	0.8	ZADH2	zinc binding alcohol dehydrogenase domain containing 2 [Sou
19	ENSG000000	0.17	−0.12	0.6	TMEM14A	transmembrane protein 14A [Source:HGNC Symbol;Acc:HGN
20	ENSG000001	0.16	−0.15	0.59	CTDSPL	CTD (carboxy−terminal domain, RNA polymerase II, polypept

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−26	285 / 2947	Colon	ReprPCWk_Colon
2	1e−24	87 / 476	Tissu	WIRTH_Nervous System
3	1e−23	400 / 4879	Colon	Quies1_Colon
4	1e−23	288 / 3109	Colon	TssP_Colon
5	3e−23	306 / 3406	Colon	ReprPC_Colon
6	2e−21	136 / 1084	Brain	Overlap_fetal_midbrain_EnhG
7	8e−21	687 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
8	1e−19	147 / 1279	Brain	Overlap_fetal_midbrain_Enh
9	4e−19	181 / 1753	Colon	Het_Colon
10	6e−17	385 / 5039	Lymph	HOPP_Repressed
11	4e−16	77 / 525	Colon	Quies2_Colon
12	6e−15	135 / 1281	Colon	HetRpts_Colon
13	2e−11	177 / 2041	Colon	EnhP_Colon
14	2e−11	217 / 2658	Lymph	HOPP_Repetitive
15	3e−11	160 / 1798	TF	HEBENSTREIT_low expression TF
16	3e−11	227 / 2838	Lymph	HOPP_Poised_promoter
17	8e−11	57 / 422	CC	cell junction
18	9e−11	33 / 171	GSEA	VERHAAK_GLIOBLASTOMA_PRONEURAL
19	1e−09	45 / 312	CC	dendrite
20	2e−09	64 / 546	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
21	5e−09	50 / 386	Colon	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
22	6e−09	23 / 106	Glio	WIRTH_Normal Brain
23	1e−08	52 / 419	BP	synaptic transmission
24	2e−08	74 / 712	Brain	Overlap_fetal_midbrain_EnhP
25	4e−08	37 / 258	CC	axon
26	5e−08	14 / 45	BP	synapse assembly
27	5e−08	118 / 1356	Brain	Fetal_K9K27me3
28	7e−08	41 / 310	Colon	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
29	1e−07	95 / 1041	GSEA	BENPORATH_ES_WITH_H3K27ME3
30	2e−07	51 / 442	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
31	2e−07	48 / 410	GSEA	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
32	3e−07	8 / 15	BP	neuron cell−cell adhesion
33	5e−07	648 / 10800	Brain	Overlap_fetal_midbrain_Quies
34	5e−07	88 / 971	GSEA	BENPORATH_SUZ12_TARGETS
35	7e−07	29 / 198	CC	postsynaptic membrane
36	7e−07	618 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
37	2e−06	12 / 43	CC	ciliary tip
38	2e−06	38 / 316	BP	nervous system development
39	2e−06	73 / 787	Brain	Overlap_fetal_midbrain_TssP
40	3e−06	10 / 31	BP	neuronal action potential

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.03	7 / 57	TESCHENDORFF_age_hypermethylated
2	0.36	9 / 144	HORVATH_aging_genes meth UP
3	0.90	4 / 123	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−08	52 / 419	synaptic transmission
2	5e−08	14 / 45	synapse assembly
3	3e−07	8 / 15	neuron cell−cell adhesion
4	2e−06	38 / 316	nervous system development
5	3e−06	10 / 31	neuronal action potential
6	4e−06	6 / 10	presynaptic membrane assembly
7	2e−05	6 / 12	vocalization behavior
8	3e−05	16 / 93	neuropeptide signaling pathway
9	4e−05	12 / 57	positive regulation of synapse assembly
10	7e−05	7 / 21	modulation of synaptic transmission
11	1e−04	15 / 95	axonogenesis
12	1e−04	15 / 95	locomotory behavior
13	2e−04	7 / 25	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion m
14	3e−04	11 / 60	learning
15	3e−04	16 / 114	regulation of membrane potential
16	4e−04	6 / 20	action potential
17	5e−04	16 / 118	cilium assembly
18	6e−04	5 / 14	glutamate receptor signaling pathway
19	6e−04	7 / 29	adult behavior
20	7e−04	9 / 47	heterophilic cell−cell adhesion via plasma membrane cell adhesion molecules

Brain

Rank	p−value	#in/all	Geneset
1	2e−21	136 / 1084	Overlap_fetal_midbrain_EnhG
2	8e−21	687 / 10278	Overlap_fetal_midbrain_ReprPCWk
3	1e−19	147 / 1279	Overlap_fetal_midbrain_Enh
4	2e−08	74 / 712	Overlap_fetal_midbrain_EnhP
5	5e−08	118 / 1356	Fetal_K9K27me3
6	5e−07	648 / 10800	Overlap_fetal_midbrain_Quies
7	7e−07	618 / 10239	Overlap_fetal_midbrain_ReprPC
8	2e−06	73 / 787	Overlap_fetal_midbrain_TssP
9	1e−04	200 / 2956	Fetal_TssA
10	5e−04	86 / 1137	Fetal_Enh
11	7e−04	73 / 940	Mid_Frontal_Lobe_Enh
12	2e−03	95 / 1327	Mid_Frontal_Lobe_TssP
13	2e−03	128 / 1890	Overlap_fetal_midbrain_TssF
14	3e−03	45 / 552	Fetal_Tx
15	4e−03	67 / 910	Fetal_EnhG
16	8e−03	242 / 3977	Mid_Frontal_Lobe_ReprPC
17	2e−02	47 / 641	Mid_Frontal_Lobe_EnhP
18	2e−02	96 / 1478	Overlap_fetal_midbrain_TxTrans
19	2e−02	56 / 805	Mid_Frontal_Lobe_EnhG
20	4e−02	555 / 9923	Overlap_fetal_midbrain_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	4 / 28	PanCan_HH_geneset_nanostring
2	0.12	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.16	1 / 16	LIU_COMMON_CANCER_GENES
4	0.23	6 / 78	PanCan_Wnt_geneset_nanostring
5	0.33	2 / 22	PanCan_ChromMod_geneset_nanostring
6	0.39	1 / 9	WANG_ER_DN
7	0.45	1 / 11	GENTLES_modul5
8	0.53	1 / 14	LIU_PROSTATE_CANCER_UP
9	0.53	1 / 14	BEN−PORATH_DN
10	0.56	1 / 15	GENTLES_modul4
11	0.56	1 / 15	GENTLES_modul10
12	0.58	1 / 16	GENTLES_modul16
13	0.59	0 / 16	LIU_LIVER_CANCER
14	0.63	2 / 40	PanCan_HK_geneset_nanostring
15	0.70	7 / 152	PanCan_MAPK_geneset_nanostring
16	0.73	0 / 15	LIU_BREAST_CANCER
17	0.76	2 / 51	PanCan_TGF−B_geneset_nanostring
18	0.76	4 / 97	PanCan_TXmisReg_geneset_nanostring
19	0.77	0 / 16	LIU_PROSTATE_CANCER_DN
20	0.87	1 / 37	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	8e−11	57 / 422	cell junction
2	1e−09	45 / 312	dendrite
3	4e−08	37 / 258	axon
4	7e−07	29 / 198	postsynaptic membrane
5	2e−06	12 / 43	ciliary tip
6	8e−06	32 / 259	synapse
7	1e−05	15 / 77	primary cilium
8	1e−05	37 / 329	neuronal cell body
9	2e−05	21 / 142	cilium
10	4e−05	12 / 58	presynaptic membrane
11	7e−05	7 / 21	excitatory synapse
12	8e−05	5 / 10	juxtaparanode region of axon
13	4e−04	5 / 13	ionotropic glutamate receptor complex
14	6e−04	14 / 97	synaptic vesicle
15	7e−04	11 / 67	neuronal postsynaptic density
16	1e−03	11 / 70	axoneme
17	2e−03	12 / 84	voltage−gated potassium channel complex
18	2e−03	6 / 25	ciliary base
19	2e−03	13 / 99	dendritic spine
20	2e−03	16 / 136	postsynaptic density

Chr

Rank	p−value	#in/all	Geneset
1	0.001	27 / 272	Chr 18
2	0.019	53 / 746	Chr X
3	0.021	52 / 735	Chr 4
4	0.095	48 / 745	Chr 9
5	0.124	22 / 318	Chr 13
6	0.155	63 / 1043	Chr 3
7	0.244	35 / 582	Chr 15
8	0.281	70 / 1228	Chr 2
9	0.352	57 / 1017	Chr 12
10	0.420	34 / 613	Chr 14
11	0.507	46 / 862	Chr 5
12	0.510	52 / 976	Chr 6
13	0.584	27 / 522	Chr 20
14	0.621	44 / 859	Chr 7
15	0.645	73 / 1425	Chr 19
16	0.772	34 / 715	Chr 10
17	0.801	8 / 191	Chr 21
18	0.806	1 / 30	Chr Y
19	0.815	30 / 651	Chr 8
20	0.881	38 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−26	285 / 2947	ReprPCWk_Colon
2	1e−23	400 / 4879	Quies1_Colon
3	1e−23	288 / 3109	TssP_Colon
4	3e−23	306 / 3406	ReprPC_Colon
5	4e−19	181 / 1753	Het_Colon
6	4e−16	77 / 525	Quies2_Colon
7	6e−15	135 / 1281	HetRpts_Colon
8	2e−11	177 / 2041	EnhP_Colon
9	5e−09	50 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
10	7e−08	41 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
11	2e−07	51 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
12	2e−05	284 / 4327	EnhWk2_Colon
13	1e−04	91 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	4e−04	37 / 389	K9K27me3_Colon
15	6e−04	25 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
16	2e−03	85 / 1178	ZNF_Colon
17	6e−03	40 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
18	1e−02	668 / 11968	TssWk_Colon
19	8e−02	3 / 19	Vilar_non−hypermutated−in−CRC
20	1e−01	2 / 10	TCGA−CRC_agressive−disease−markers

Disease

Rank	p−value	#in/all	Geneset
1	0.7	19 / 399	GUDJ_psoriasis down
2	0.9	1 / 37	BCHETNIA_EBM−DM up
3	1.0	7 / 608	GUDJ_psoriasis up
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	6e−09	23 / 106	WIRTH_Normal Brain
2	3e−06	14 / 61	in vivo astrocytes vs. cultured astroglia
3	3e−06	47 / 434	Down_a
4	1e−05	17 / 97	Weller_LGG_1p19qDel−vs−intact_UP
5	3e−05	21 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
6	4e−05	12 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	1e−03	12 / 81	Weller_LGG_gradeII−vs−III_UP
8	3e−03	16 / 137	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
9	3e−03	12 / 90	Weller_LGG_A_vs_O_DOWN
10	3e−03	6 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP
11	4e−03	4 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
12	2e−02	34 / 436	Down_b
13	2e−02	8 / 63	OPC
14	2e−02	10 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
15	2e−02	11 / 103	GIEZELT_GBM_STS_down_VS_LTS
16	3e−02	139 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
17	3e−02	9 / 83	GIEZELT_GBM_WT_down_VS_mut
18	4e−02	3 / 15	VERHAAK_PN_Brain
19	6e−02	7 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
20	8e−02	6 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−11	33 / 171	VERHAAK_GLIOBLASTOMA_PRONEURAL
2	2e−09	64 / 546	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
3	1e−07	95 / 1041	BENPORATH_ES_WITH_H3K27ME3
4	2e−07	48 / 410	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
5	5e−07	88 / 971	BENPORATH_SUZ12_TARGETS
6	5e−06	46 / 431	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
7	9e−06	58 / 604	BENPORATH_PRC2_TARGETS
8	2e−05	27 / 210	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
9	2e−05	86 / 1036	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
10	3e−05	96 / 1197	BLALOCK_ALZHEIMERS_DISEASE_DN
11	4e−05	5 / 9	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
12	8e−05	79 / 966	BENPORATH_EED_TARGETS
13	2e−04	59 / 686	MIKKELSEN_ES_ICP_WITH_H3K4ME3
14	2e−04	41 / 429	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
15	6e−04	14 / 97	MIKKELSEN_IPS_WITH_HCP_H3K27ME3
16	6e−04	45 / 511	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
17	7e−04	9 / 47	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
18	7e−04	8 / 38	MIKKELSEN_ES_HCP_WITH_H3K27ME3
19	2e−03	8 / 45	MCCLUNG_DELTA_FOSB_TARGETS_8WK
20	3e−03	25 / 261	REACTOME_NEURONAL_SYSTEM

HM

Rank	p−value	#in/all	Geneset
1	0.001	21 / 193	HALLMARK_KRAS_SIGNALING_DN
2	0.040	12 / 128	HALLMARK_SPERMATOGENESIS
3	0.082	5 / 44	HALLMARK_APICAL_SURFACE
4	0.244	8 / 112	HALLMARK_BILE_ACID_METABOLISM
5	0.306	7 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	0.428	11 / 190	HALLMARK_APICAL_JUNCTION
7	0.462	11 / 195	HALLMARK_MYOGENESIS
8	0.563	5 / 94	HALLMARK_PROTEIN_SECRETION
9	0.577	10 / 193	HALLMARK_HEME_METABOLISM
10	0.590	10 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.634	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	0.636	5 / 102	HALLMARK_PEROXISOME
13	0.709	2 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.759	6 / 140	HALLMARK_UV_RESPONSE_DN
15	0.771	4 / 98	HALLMARK_ANDROGEN_RESPONSE
16	0.831	8 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
17	0.860	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
18	0.867	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
19	0.898	7 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
20	0.952	6 / 196	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.7	4 / 91	DUMEAUX_Smoking enriched genes
3	0.8	1 / 33	DUMEAUX_Fasting enriched genes
4	1.0	0 / 11	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−17	385 / 5039	HOPP_Repressed
2	2e−11	217 / 2658	HOPP_Repetitive
3	3e−11	227 / 2838	HOPP_Poised_promoter
4	3e−05	233 / 3457	HOPP_Heterochrom
5	4e−02	33 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
6	7e−02	32 / 458	WIRTH_lymphoma937_spot I
7	9e−02	22 / 304	ZHANG_DLBCL mutated
8	1e−01	378 / 6784	HOPP_Weak_enhancer
9	1e−01	355 / 6389	HOPP_Weak_txn
10	2e−01	6 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
11	2e−01	16 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
12	2e−01	2 / 15	BENTINK_mBL UP
13	2e−01	10 / 138	Subero_DLBCL_hyper_meth
14	2e−01	6 / 75	Subero_FL_hyper_meth
15	3e−01	15 / 240	WIRTH_lymphoma937_spot B
16	3e−01	3 / 36	Subero_MM_hyper_meth
17	3e−01	8 / 122	Subero_INT_hyper_meth
18	3e−01	2 / 23	SPANG_BAFF 9hrs UP
19	4e−01	6 / 92	WIRTH_lymphoma937_spot A
20	4e−01	6 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

MF

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 14	ligand−gated ion channel activity
2	9e−04	10 / 58	cell adhesion molecule binding
3	3e−03	43 / 527	protein kinase activity
4	4e−03	4 / 13	neurexin family protein binding
5	5e−03	29 / 328	enzyme binding
6	8e−03	5 / 24	neuropeptide hormone activity
7	9e−03	29 / 341	binding
8	9e−03	7 / 45	phosphatidylinositol−4,5−bisphosphate binding
9	1e−02	7 / 46	scaffold protein binding
10	1e−02	4 / 18	extracellular−glutamate−gated ion channel activity
11	1e−02	4 / 18	ionotropic glutamate receptor activity
12	1e−02	4 / 18	ionotropic glutamate receptor binding
13	1e−02	3 / 10	cAMP response element binding protein binding
14	1e−02	3 / 10	hedgehog receptor activity
15	2e−02	77 / 1134	nucleic acid binding
16	2e−02	4 / 19	G−protein alpha−subunit binding
17	2e−02	4 / 20	sialyltransferase activity
18	2e−02	5 / 31	cyclin−dependent protein serine/threonine kinase activity
19	2e−02	5 / 31	delayed rectifier potassium channel activity
20	3e−02	4 / 22	acetylcholine−activated cation−selective channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	7 / 62	hsa−miR−514
2	0.05	5 / 39	hsa−miR−501−3p
3	0.06	5 / 40	hsa−miR−502−3p
4	0.06	10 / 108	hsa−miR−605
5	0.06	8 / 80	hsa−miR−1321
6	0.10	11 / 134	hsa−miR−335
7	0.10	7 / 75	hsa−miR−657
8	0.12	5 / 49	hsa−miR−654−3p
9	0.12	7 / 78	hsa−miR−1827
10	0.13	33 / 504	hsa−miR−16
11	0.13	7 / 79	hsa−miR−509−3−5p
12	0.14	5 / 52	hsa−miR−1224−3p
13	0.14	9 / 112	hsa−miR−1271
14	0.14	4 / 38	hsa−miR−215
15	0.14	3 / 25	hsa−miR−1228
16	0.16	6 / 69	hsa−miR−1184
17	0.17	3 / 27	hsa−miR−337−5p
18	0.17	4 / 41	hsa−miR−601
19	0.17	8 / 102	hsa−miR−150
20	0.19	4 / 43	hsa−miR−192

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.4	1 / 10	BENTINK_ras.4
2	0.5	1 / 13	BENTINK_e2f3.2
3	0.6	1 / 15	BENTINK_ras.6
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 14	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 14	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−11	160 / 1798	HEBENSTREIT_low expression TF
2	6e−05	65 / 745	ICGC_NrsfPcr2_targets
3	3e−02	95 / 1472	ICGC_NrsfPcr1_targets
4	4e−02	208 / 3511	ICGC_Rad21_targets
5	5e−02	94 / 1503	ICGC_Six5_targets
6	5e−02	49 / 731	ICGC_SrfPcr2_targets
7	1e−01	354 / 6324	ICGC_Yy1_targets
8	2e−01	396 / 7202	ICGC_Runx3_targets
9	3e−01	372 / 6862	ICGC_Elf1_targets
10	3e−01	342 / 6322	ICGC_Pol2_targets
11	4e−01	118 / 2149	ICGC_Mef2_targets
12	4e−01	83 / 1506	ICGC_Usf1_targets
13	5e−01	342 / 6406	ICGC_Pax5_targets
14	5e−01	274 / 5135	ICGC_Ebfsc137065_targets
15	5e−01	320 / 6005	ICGC_Mta3_targets
16	5e−01	150 / 2827	ICGC_Bcl3_targets
17	6e−01	126 / 2401	ICGC_Bcl11_targets
18	6e−01	287 / 5453	ICGC_Foxm1_targets
19	6e−01	1 / 16	NOWICK_TF
20	6e−01	166 / 3177	ICGC_Irf4_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	4 / 25	VAQUERIZAS_Spinal cord
2	0.05	2 / 7	VAQUERIZAS_Appendix
3	0.17	4 / 41	VAQUERIZAS_Testis
4	0.27	2 / 19	VAQUERIZAS_Heart
5	0.31	10 / 155	VAQUERIZAS_General
6	0.31	3 / 37	VAQUERIZAS_Prostate
7	0.44	3 / 46	VAQUERIZAS_Whole brain
8	0.48	1 / 12	VAQUERIZAS_Kidney
9	0.58	1 / 16	VAQUERIZAS_Fetal thyroid
10	0.65	2 / 41	VAQUERIZAS_Fetal brain
11	0.66	2 / 42	VAQUERIZAS_Thyroid
12	0.70	2 / 45	VAQUERIZAS_Placenta
13	0.71	1 / 23	VAQUERIZAS_Pituitary
14	0.81	1 / 30	VAQUERIZAS_Smooth muscle
15	0.82	1 / 31	VAQUERIZAS_Fetal lung
16	0.83	1 / 33	VAQUERIZAS_Liver
17	0.97	1 / 64	VAQUERIZAS_Lung
18	0.97	1 / 67	VAQUERIZAS_Whole blood
19	1.00	0 / 49	VAQUERIZAS_Uterus
20	1.00	0 / 42	VAQUERIZAS_Thymus

Tissue

Rank	p−value	#in/all	Geneset
1	1e−24	87 / 476	WIRTH_Nervous System
2	7e−02	12 / 141	WIRTH_Muscle
3	1e−01	2 / 13	WIRTH_Prim. lymphoid organs
4	2e−01	2 / 14	WIRTH_Thalamus
5	2e−01	2 / 14	WIRTH_Thyroid gland
6	3e−01	4 / 54	WIRTH_Pancreas
7	4e−01	12 / 202	WIRTH_Testis
8	5e−01	1 / 14	WIRTH_Thymus
9	6e−01	1 / 15	WIRTH_Cerebellum
10	6e−01	1 / 16	WIRTH_Hippocampus
11	7e−01	2 / 47	WIRTH_Placenta
12	8e−01	3 / 82	WIRTH_Homeostasis
13	1e+00	2 / 137	WIRTH_Mucosa
14	1e+00	5 / 259	PALMER_Granulocytes signature up
15	1e+00	3 / 208	PALMER_B−Cell signature up
16	1e+00	1 / 140	PALMER_T−Cell signature up
17	1e+00	1 / 427	WIRTH_Immune system
18	1e+00	0 / 6	WIRTH_Pituitary gland
19	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
20	1e+00	0 / 14	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	3e−05	337 / 5285	LU_BPDE 0.005 DN
2	3e−01	75 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

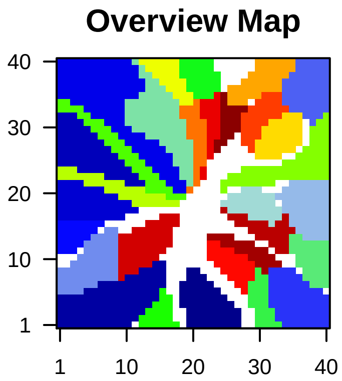
Correlation Clusters

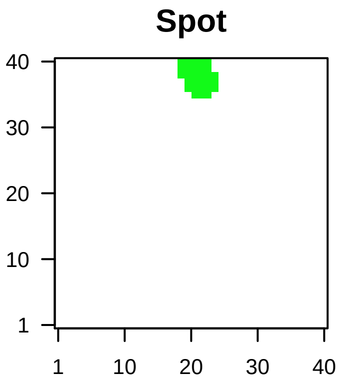
Spot Summary: N

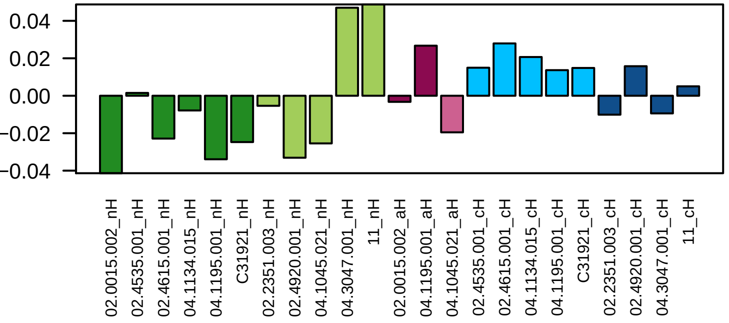
metagenes = 29
genes = 301

<r> metagenes = 0.93
<r> genes = 0.5
beta: r2= 0.01 / log p= −0.19

samples with spot = 0 (0 %)





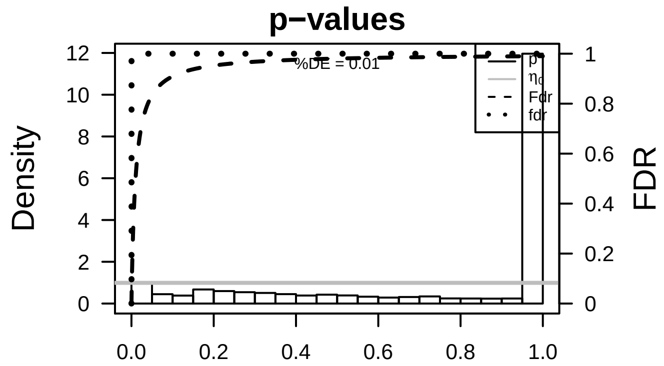


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.29	−0.03	0.32		
2	ENSG000001	0.22	−0.04	0.45	APCDD1	adenomatosis polyposis coli down−regulated 1 [Source:HGN
3	ENSG000002	0.2	−0.15	0.61	PGAM4	phosphoglycerate mutase family member 4 [Source:HGNC S
4	ENSG000001	0.2	−0.06	0.47	FADS2	fatty acid desaturase 2 [Source:HGNC Symbol;Acc:HGNC:35
5	ENSG000001	0.18	−0.08	0.69	PM20D2	peptidase M20 domain containing 2 [Source:HGNC Symbol;A
6	ENSG000001	0.17	−0.07	0.77	GPSM2	G−protein signaling modulator 2 [Source:HGNC Symbol;Acc:
7	ENSG000001	0.16	−0.1	0.87	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (
8	ENSG000002	0.16	−0.17	0.68	TIMM23B	translocase of inner mitochondrial membrane 23 homolog B (
9	ENSG000001	0.15	−0.1	0.59	BCAS2	breast carcinoma amplified sequence 2 [Source:HGNC Symb
10	ENSG000001	0.14	−0.17	0.65	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, al
11	ENSG000001	0.14	−0.11	0.65	HSPA4	heat shock 70kDa protein 4 [Source:HGNC Symbol;Acc:HGN
12	ENSG000001	0.14	−0.07	0.58	RARG	retinoic acid receptor, gamma [Source:HGNC Symbol;Acc:HC
13	ENSG000001	0.14	−0.1	0.67	RBBP4	retinoblastoma binding protein 4 [Source:HGNC Symbol;Acc:
14	ENSG000000	0.13	−0.1	0.8	TXLNA	taxilin alpha [Source:HGNC Symbol;Acc:HGNC:30685]
15	ENSG000001	0.13	−0.11	0.44	TMCO3	transmembrane and coiled−coil domains 3 [Source:HGNC Sy
16	ENSG000001	0.13	−0.09	0.82	SLC39A6	solute carrier family 39 (zinc transporter), member 6 [Source:
17	ENSG000001	0.12	−0.06	0.84	CLCC1	chloride channel CLIC−like 1 [Source:HGNC Symbol;Acc:HG
18	ENSG000001	0.12	−0.1	0.66	SLC4A2	solute carrier family 4 (anion exchanger), member 2 [Source:
19	ENSG000001	0.12	−0.07	0.72	IMPACT	impact RWD domain protein [Source:HGNC Symbol;Acc:HGN
20	ENSG000001	0.12	−0.13	0.79	ETF1	eukaryotic translation termination factor 1 [Source:HGNC Syr

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−39	209 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
2	3e−37	225 / 7491	Lympl	HOPP_Txn_elongation
3	4e−33	257 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
4	2e−32	259 / 10475	Colon	TssA_Colon
5	5e−29	240 / 9390	Colon	TxWk_Colon
6	1e−27	245 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
7	2e−26	243 / 9930	Colon	Tx_Colon
8	7e−26	220 / 8358	Lympl	HOPP_Active_promoter
9	2e−19	224 / 9470	Colon	Quies3_Colon
10	2e−17	158 / 5643	Lympl	HOPP_Txn_transition
11	5e−16	63 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
12	2e−15	227 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
13	2e−14	232 / 10800	Brain	Overlap_fetal_midbrain_Quies
14	6e−13	244 / 11968	Colon	TssWk_Colon
15	8e−12	42 / 807	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
16	2e−11	42 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
17	4e−11	41 / 811	Lympl	WIRTH_lymphoma937_spot D
18	7e−11	183 / 8147	Lympl	HOPP_Weak_promoter
19	7e−10	40 / 859	GSEA	LEE_BMP2_TARGETS_DN
20	4e−09	48 / 1228	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
21	9e−09	38 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
22	1e−08	25 / 415	GSEA	GARY_CD5_TARGETS_DN
23	2e−08	53 / 1503	TF	ICGC_Six5_targets
24	2e−08	125 / 5173	TF	ICGC_Taf1_targets
25	1e−07	38 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
26	1e−07	60 / 1914	GSEA	PILON_KLF1_TARGETS_DN
27	2e−07	20 / 326	GSEA	RICKMAN_METASTASIS_UP
28	5e−07	9 / 62	GSEA	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
29	7e−07	126 / 5526	TF	ICGC_Pmlsc71910_targets
30	1e−06	125 / 5512	TF	ICGC_Nficsc81335_targets
31	1e−06	27 / 610	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
32	1e−06	35 / 925	GSEA	ACEVEDO_LIVER_CANCER_UP
33	1e−06	16 / 242	GSEA	REACTOME_METABOLISM_OF_RNA
34	2e−06	33 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
35	2e−06	49 / 1549	TF	ICGC_Myc_targets
36	2e−06	31 / 775	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
37	2e−06	167 / 8123	Colon	TssF_Colon
38	2e−06	8 / 56	CC	proteasome complex
39	3e−06	30 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
40	3e−06	52 / 1713	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 123	HORVATH_aging_genes meth DOWN
2	0.9	1 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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	31 / 820	gene expression
2	9e−06	7 / 48	protein targeting to mitochondrion
3	7e−05	7 / 65	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
4	9e−05	18 / 410	mitotic cell cycle
5	1e−04	7 / 70	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
6	2e−04	7 / 74	regulation of ubiquitin−protein ligase activity involved in mitotic cell cycle
7	3e−04	7 / 80	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent p
8	3e−04	4 / 21	nucleotide−excision repair, DNA damage removal
9	6e−04	9 / 151	G1/S transition of mitotic cell cycle
10	1e−03	5 / 49	regulation of cellular amino acid metabolic process
11	1e−03	8 / 132	protein polyubiquitination
12	1e−03	6 / 75	negative regulation of gene expression, epigenetic
13	2e−03	7 / 109	RNA processing
14	2e−03	10 / 208	chromatin organization
15	2e−03	8 / 148	negative regulation of canonical Wnt signaling pathway
16	3e−03	6 / 88	regulation of gene expression, epigenetic
17	4e−03	5 / 65	DNA damage response, signal transduction by p53 class mediator resulting in
18	4e−03	8 / 161	programmed cell death
19	4e−03	3 / 21	regulation of cell morphogenesis
20	4e−03	7 / 129	positive regulation of canonical Wnt signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	4e−39	209 / 6320	Overlap_fetal_midbrain_HetRpts
2	4e−33	257 / 10239	Overlap_fetal_midbrain_ReprPC
3	1e−27	245 / 9923	Overlap_fetal_midbrain_K9K27me3
4	2e−15	227 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	2e−14	232 / 10800	Overlap_fetal_midbrain_Quies
6	6e−03	30 / 1182	Fetal_EnhP
7	1e−02	13 / 400	Fetal_ZNF
8	3e−02	66 / 3370	Mid_Frontal_Lobe_ZNF
9	1e−01	18 / 855	Overlap_fetal_midbrain_ZNF
10	2e−01	31 / 1680	Fetal_ReprPCWk
11	3e−01	21 / 1137	Fetal_Enh
12	3e−01	17 / 939	Fetal_HetRpts
13	3e−01	13 / 712	Overlap_fetal_midbrain_EnhP
14	4e−01	11 / 641	Mid_Frontal_Lobe_EnhP
15	4e−01	6 / 342	Fetal_Het
16	5e−01	4 / 232	Fetal_ReprPC
17	5e−01	38 / 2443	Fetal_Quies
18	7e−01	13 / 910	Fetal_EnhG
19	7e−01	18 / 1279	Overlap_fetal_midbrain_Enh
20	7e−01	19 / 1356	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	14 / 550	Lembcke_Normal vs Adenoma
2	0.07	0 / 16	RHODES_CANCER_META_SIGNATURE
3	0.14	2 / 41	ZHANG_MM up
4	0.18	2 / 50	PanCan_DNARepair_geneset_nanostring
5	0.20	2 / 52	KUIPER_MM poor survival
6	0.22	1 / 16	LIU_COMMON_CANCER_GENES
7	0.29	1 / 22	PanCan_ChromMod_geneset_nanostring
8	0.31	2 / 71	SHAUGHNESSY_MM high risk
9	0.32	1 / 24	PanCan_Notch_geneset_nanostring
10	0.35	2 / 78	PanCan_Wnt_geneset_nanostring
11	0.47	1 / 40	PanCan_HK_geneset_nanostring
12	0.54	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	0.58	2 / 123	PanCan_Driver_Gene_geneset_nanostring
14	0.64	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	0.67	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	0.74	1 / 86	PanCan_JAK−ST_geneset_nanostring
17	0.82	2 / 198	PanCan_PI3K_geneset_nanostring
18	0.84	0 / 16	LIU_PROSTATE_CANCER_DN
19	0.88	1 / 136	PanCan_CC+Apop_geneset_nanostring
20	0.89	1 / 140	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−06	8 / 56	proteasome complex
2	7e−06	45 / 1441	mitochondrion
3	2e−05	5 / 23	histone acetyltransferase complex
4	5e−05	7 / 61	nuclear pore
5	2e−04	63 / 2554	nucleoplasm
6	3e−04	4 / 21	transcription elongation factor complex
7	4e−04	26 / 799	nucleolus
8	7e−04	4 / 26	MLL1 complex
9	1e−03	3 / 13	proteasome regulatory particle, base subcomplex
10	2e−03	3 / 16	ESC/E(Z) complex
11	2e−03	103 / 5101	nucleus
12	2e−03	3 / 17	proteasome accessory complex
13	4e−03	3 / 21	ciliary transition zone
14	5e−03	102 / 5185	cytoplasm
15	1e−02	2 / 12	holo TFIIH complex
16	1e−02	3 / 33	COP9 signalosome
17	2e−02	6 / 130	mitochondrial outer membrane
18	2e−02	2 / 13	proteasome regulatory particle
19	2e−02	13 / 431	cellular_component
20	2e−02	2 / 15	Ada2/Gcn5/Ada3 transcription activator complex

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	14 / 318	Chr 13
2	2e−02	25 / 1043	Chr 3
3	3e−02	19 / 746	Chr X
4	7e−02	8 / 272	Chr 18
5	7e−02	26 / 1228	Chr 2
6	2e−01	21 / 1083	Chr 17
7	2e−01	15 / 745	Chr 9
8	2e−01	9 / 436	Chr 22
9	4e−01	15 / 862	Chr 5
10	4e−01	10 / 582	Chr 15
11	4e−01	12 / 715	Chr 10
12	5e−01	10 / 613	Chr 14
13	6e−01	8 / 522	Chr 20
14	7e−01	12 / 859	Chr 7
15	7e−01	10 / 735	Chr 4
16	8e−01	27 / 1920	Chr 1
17	9e−01	12 / 1017	Chr 12
18	9e−01	14 / 1172	Chr 11
19	9e−01	11 / 976	Chr 6
20	9e−01	9 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−32	259 / 10475	TssA_Colon
2	5e−29	240 / 9390	TxWk_Colon
3	2e−26	243 / 9930	Tx_Colon
4	2e−19	224 / 9470	Quies3_Colon
5	6e−13	244 / 11968	TssWk_Colon
6	2e−11	42 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
7	2e−06	167 / 8123	TssF_Colon
8	3e−06	29 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	6e−03	113 / 5889	EnhWk1_Colon
10	2e−02	85 / 4379	TssD1_Colon
11	2e−02	124 / 6761	TssD2_Colon
12	2e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
13	3e−02	4 / 76	Marisa_CRC−cluster−g
14	1e−01	1 / 7	Juehling−MSI−enriched−in−8−to−9
15	1e−01	1 / 10	Budinska_E_Mixed_UP
16	3e−01	1 / 19	Boland_CRC−MSI−A6−A10
17	3e−01	1 / 20	Budinska_B_Lower crypt−like_UP
18	3e−01	1 / 21	Juehling−MSI−enriched−in−6
19	4e−01	1 / 30	Marisa_CRC−cluster−c
20	5e−01	2 / 105	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	0.1	2 / 37	BCHETNIA_EBM−DM up
2	0.3	1 / 22	BCHETNIA_EBM up
3	0.9	6 / 608	GUDJ_psoriasis up
4	1.0	3 / 399	GUDJ_psoriasis down
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−05	17 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−03	54 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−03	48 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−02	11 / 344	Up
5	2e−02	3 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	4e−02	21 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
7	1e−01	3 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	1e−01	3 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	2e−01	3 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	2e−01	1 / 12	WILLSCHER_GBM_LTSwt_proteomics−C_UP
11	2e−01	2 / 50	Vishal_subnetwork signature of survival in GBM
12	2e−01	3 / 96	Weller_LGG_A_vs_O_UP
13	2e−01	2 / 53	Gorovets_LGG_EPL_subclass
14	2e−01	3 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	4e−01	1 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP
16	4e−01	2 / 83	GIEZELT_GBM_WT_down_VS_mut
17	4e−01	1 / 30	Gorovets_LGG_NB_subclass
18	4e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
19	5e−01	2 / 103	GIEZELT_GBM_STS_down_VS_LTS
20	5e−01	1 / 49	Noushmehr_Pron_GCIMP_hypermeth_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−16	63 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
2	7e−10	40 / 859	LEE_BMP2_TARGETS_DN
3	4e−09	48 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	9e−09	38 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
5	1e−08	25 / 415	GARY_CD5_TARGETS_DN
6	1e−07	38 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	1e−07	60 / 1914	PILON_KLF1_TARGETS_DN
8	2e−07	20 / 326	RICKMAN_METASTASIS_UP
9	5e−07	9 / 62	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
10	1e−06	27 / 610	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
11	1e−06	35 / 925	ACEVEDO_LIVER_CANCER_UP
12	1e−06	16 / 242	REACTOME_METABOLISM_OF_RNA
13	2e−06	33 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
14	2e−06	31 / 775	WEI_MYCN_TARGETS_WITH_E_BOX
15	3e−06	30 / 747	PUJANA_CHEK2_PCC_NETWORK
16	3e−06	52 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
17	1e−05	7 / 49	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
18	1e−05	27 / 683	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
19	1e−05	47 / 1563	PUJANA_BRCA1_PCC_NETWORK
20	2e−05	7 / 52	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C

HM

Rank	p−value	#in/all	Geneset
1	0.004	9 / 199	HALLMARK_MTORC1_SIGNALING
2	0.130	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.199	3 / 98	HALLMARK_ANDROGEN_RESPONSE
4	0.201	5 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	0.223	4 / 154	HALLMARK_FATTY_ACID_METABOLISM
6	0.231	2 / 58	HALLMARK_MYC_TARGETS_V2
7	0.253	3 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.326	3 / 128	HALLMARK_SPERMATOGENESIS
9	0.366	4 / 195	HALLMARK_MYC_TARGETS_V1
10	0.370	4 / 196	HALLMARK_P53_PATHWAY
11	0.378	1 / 30	HALLMARK_NOTCH_SIGNALING
12	0.402	3 / 146	HALLMARK_DNA_REPAIR
13	0.434	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
14	0.435	2 / 94	HALLMARK_PROTEIN_SECRETION
15	0.440	3 / 155	HALLMARK_UV_RESPONSE_UP
16	0.443	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
17	0.477	2 / 102	HALLMARK_PEROXISOME
18	0.482	2 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
19	0.527	2 / 112	HALLMARK_BILE_ACID_METABOLISM
20	0.597	3 / 196	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.22	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	1.00	0 / 91	DUMEAUX_Smoking enriched genes
4	1.00	0 / 11	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 17	DUMEAUX_High bmi enriched genes
11	1.00	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−37	225 / 7491	HOPP_Txn_elongation
2	7e−26	220 / 8358	HOPP_Active_promoter
3	2e−17	158 / 5643	HOPP_Txn_transition
4	8e−12	42 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
5	4e−11	41 / 811	WIRTH_lymphoma937_spot D
6	7e−11	183 / 8147	HOPP_Weak_promoter
7	3e−06	138 / 6389	HOPP_Weak_txn
8	3e−05	41 / 1333	SPANG_BCR UP
9	1e−03	145 / 7592	HOPP_Strong_enhancer
10	4e−03	129 / 6784	HOPP_Weak_enhancer
11	1e−02	9 / 240	WIRTH_lymphoma937_spot B
12	2e−02	14 / 466	SPANG_CD40 6hrs DN
13	3e−02	8 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
14	5e−02	6 / 171	WIRTH_lymphoma937_spot C
15	1e−01	5 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
16	1e−01	3 / 79	SPANG_LPS 6hrs DN
17	2e−01	1 / 12	Subero_MM_hypo_meth
18	2e−01	7 / 317	TARTE_Plasmablast signature
19	3e−01	3 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
20	3e−01	3 / 116	WIRTH_lymphoma937_spot MM

MF

Rank	p−value	#in/all	Geneset
1	1e−04	34 / 1091	poly(A) RNA binding
2	1e−04	199 / 10693	protein binding
3	3e−04	5 / 38	histone acetyltransferase activity
4	5e−04	19 / 513	RNA binding
5	2e−03	15 / 407	catalytic activity
6	3e−03	4 / 37	DNA−dependent ATPase activity
7	4e−03	3 / 20	3'−5' exonuclease activity
8	4e−03	3 / 20	RNA polymerase II core binding
9	5e−03	3 / 22	translation elongation factor activity
10	5e−03	4 / 45	methylated histone binding
11	8e−03	12 / 341	binding
12	1e−02	3 / 30	Wnt−protein binding
13	1e−02	5 / 90	histone binding
14	1e−02	2 / 12	proteasome binding
15	2e−02	2 / 13	nucleocytoplasmic transporter activity
16	2e−02	4 / 63	ATP−dependent RNA helicase activity
17	2e−02	33 / 1448	ATP binding
18	2e−02	2 / 14	magnesium ion transmembrane transporter activity
19	2e−02	3 / 37	aminoacyl−tRNA ligase activity
20	3e−02	2 / 16	RNA polymerase II carboxy−terminal domain kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	8 / 104	hsa−miR−21
2	1e−03	7 / 105	hsa−miR−590−5p
3	2e−03	6 / 87	hsa−miR−220c
4	3e−03	4 / 37	hsa−miR−518e
5	4e−03	10 / 237	hsa−miR−124
6	4e−03	8 / 164	hsa−miR−298
7	5e−03	6 / 102	hsa−miR−150
8	6e−03	4 / 47	hsa−miR−1256
9	6e−03	6 / 105	hsa−miR−224
10	7e−03	6 / 106	hsa−miR−1284
11	7e−03	6 / 107	hsa−miR−377
12	8e−03	8 / 181	hsa−miR−199b−3p
13	8e−03	14 / 431	hsa−miR−497
14	8e−03	3 / 27	hsa−miR−1273
15	8e−03	6 / 112	hsa−miR−146a
16	9e−03	11 / 307	hsa−miR−34c−5p
17	1e−02	13 / 393	hsa−miR−373
18	1e−02	10 / 266	hsa−miR−520a−3p
19	1e−02	4 / 54	hsa−miR−518f
20	1e−02	5 / 85	hsa−miR−630

PathwAct

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.2
2	0.2	1 / 15	BENTINK_ras.6
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 14	BENTINK_e2f3.1
6	1.0	0 / 14	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 10	BENTINK_ras.4
9	1.0	0 / 14	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−08	53 / 1503	ICGC_Six5_targets
2	2e−08	125 / 5173	ICGC_Taf1_targets
3	7e−07	126 / 5526	ICGC_Pmlsc71910_targets
4	1e−06	125 / 5512	ICGC_Nficsc81335_targets
5	2e−06	49 / 1549	ICGC_Myc_targets
6	3e−06	124 / 5552	ICGC_Pol24_targets
7	3e−06	105 / 4470	ICGC_Creb1_targets
8	3e−06	114 / 4987	ICGC_Bclaf101388_targets
9	5e−06	106 / 4566	ICGC_Egr1_targets
10	5e−06	119 / 5308	ICGC_Tcf12_targets
11	6e−06	136 / 6324	ICGC_Yy1_targets
12	6e−06	120 / 5393	ICGC_Sp1_targets
13	7e−06	123 / 5578	ICGC_Stat5_targets
14	9e−06	135 / 6313	ICGC_Pou2_targets
15	9e−06	144 / 6862	ICGC_Elf1_targets
16	2e−05	25 / 619	ICGC_RxraPcr1_targets
17	2e−05	119 / 5453	ICGC_Foxm1_targets
18	2e−05	148 / 7202	ICGC_Runx3_targets
19	2e−05	128 / 6005	ICGC_Mta3_targets
20	4e−05	61 / 2342	ICGC_GabpPcr2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	VAQUERIZAS_Fetal thyroid
2	0.3	1 / 23	VAQUERIZAS_Pituitary
3	0.4	1 / 30	VAQUERIZAS_Smooth muscle
4	0.5	1 / 41	VAQUERIZAS_Fetal brain
5	0.5	1 / 41	VAQUERIZAS_Testis
6	0.5	1 / 42	VAQUERIZAS_Thyroid
7	0.5	1 / 45	VAQUERIZAS_Placenta
8	0.9	1 / 155	VAQUERIZAS_General
9	1.0	0 / 33	VAQUERIZAS_Liver
10	1.0	0 / 37	VAQUERIZAS_Prostate
11	1.0	0 / 49	VAQUERIZAS_Uterus
12	1.0	0 / 12	VAQUERIZAS_Kidney
13	1.0	0 / 25	VAQUERIZAS_Spinal cord
14	1.0	0 / 46	VAQUERIZAS_Whole brain
15	1.0	0 / 42	VAQUERIZAS_Thymus
16	1.0	0 / 67	VAQUERIZAS_Whole blood
17	1.0	0 / 7	VAQUERIZAS_Appendix
18	1.0	0 / 31	VAQUERIZAS_Fetal lung
19	1.0	0 / 64	VAQUERIZAS_Lung
20	1.0	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	WIRTH_Thymus
2	0.2	1 / 15	WIRTH_Telencephalon
3	0.7	2 / 141	WIRTH_Muscle
4	0.8	2 / 202	WIRTH_Testis
5	1.0	1 / 427	WIRTH_Immune system
6	1.0	0 / 6	WIRTH_Pituitary gland
7	1.0	0 / 54	WIRTH_Pancreas
8	1.0	0 / 13	WIRTH_Sec. lymphoid organs
9	1.0	0 / 13	WIRTH_Prim. lymphoid organs
10	1.0	0 / 14	WIRTH_B−cells
11	1.0	0 / 12	WIRTH_Tonsil
12	1.0	0 / 12	WIRTH_Lymphocytes
13	1.0	0 / 14	WIRTH_Bone marrow
14	1.0	0 / 476	WIRTH_Nervous System
15	1.0	0 / 13	WIRTH_Globus pallidus
16	1.0	0 / 13	WIRTH_Cortex cerebri
17	1.0	0 / 16	WIRTH_Hippocampus
18	1.0	0 / 14	WIRTH_Thalamus
19	1.0	0 / 15	WIRTH_Cerebellum
20	1.0	0 / 82	WIRTH_Homeostasis

Toxic

Rank	p−value	#in/all	Geneset
1	0.001	36 / 1343	LU_BPDE 1h DN
2	0.979	68 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

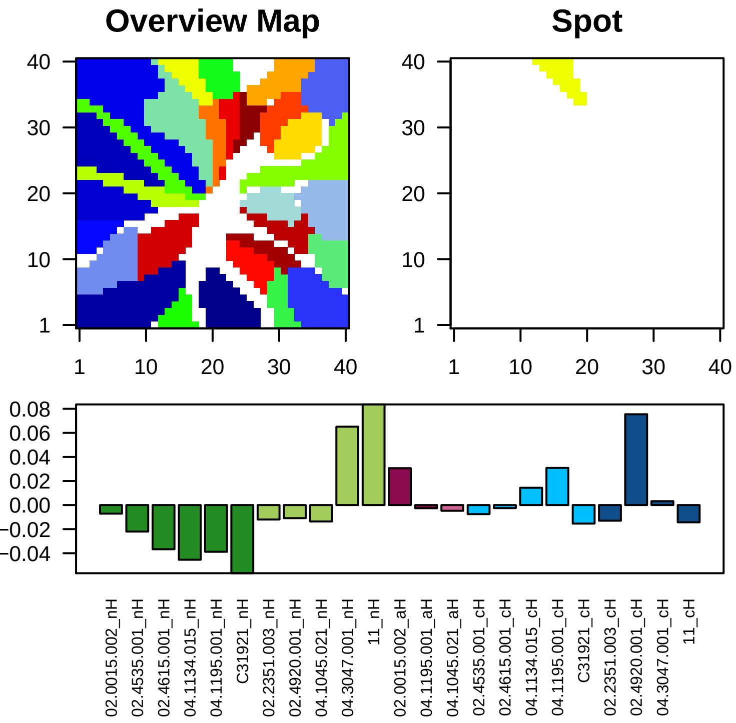
Correlation Clusters

Spot Summary: O

metagenes = 27
genes = 294

<r> metagenes = 0.97
<r> genes = 0.5
beta: r2= 0.02 / log p= −0.28

samples with spot = 3 (13 %)
other_normHNPCC : 2 (40 %)
other_cancerHNPCC : 1 (25 %)

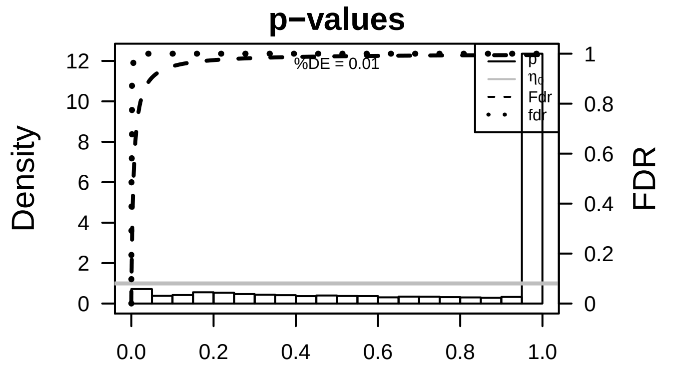


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.6	−0.03	0.46	SPINK13	serine peptidase inhibitor, Kazal type 13 (putative) [Source:H
2	ENSG000001	0.53	−0.03	0.47	SPINK6	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
3	ENSG000001	0.43	−0.24	0.9	COPRS	coordinator of PRMT5, differentiation stimulator [Source:HGN
4	ENSG000000	0.42	−0.05	0.68	HSD17B6	hydroxysteroid (17−beta) dehydrogenase 6 [Source:HGNC S
5	ENSG000001	0.37	−0.08	0.58	PLEKHA4	pleckstrin homology domain containing, family A (phosphoino
6	ENSG000001	0.36	−0.36	0.52	SDC4	syndecan 4 [Source:HGNC Symbol;Acc:HGNC:10661]
7	ENSG000001	0.34	−0.02	0.59	ASB5	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
8	ENSG000001	0.34	−0.11	0.56	IGFBP6	insulin−like growth factor binding protein 6 [Source:HGNC Sy
9	ENSG000001	0.32	−0.14	0.56	PKDCC	protein kinase domain containing, cytoplasmic [Source:HGN
10	ENSG000001	0.31	−0.13	0.73	SYNC	syncoilin, intermediate filament protein [Source:HGNC Symb
11	ENSG000000	0.28	−0.07	0.56	PHGDH	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
12	ENSG000002	0.26	−0.3	0.36	RNASE4	ribonuclease, RNase A family, 4 [Source:HGNC Symbol;Acc:
13	ENSG000001	0.26	−0.11	0.7	CTNNAL1	catenin (cadherin−associated protein), alpha−like 1 [Source:
14	ENSG000001	0.26	−0.08	0.67	LOXL2	lysyl oxidase−like 2 [Source:HGNC Symbol;Acc:HGNC:6666]
15	ENSG000001	0.25	−0.16	0.63	S100A13	S100 calcium binding protein A13 [Source:HGNC Symbol;Ac
16	ENSG000000	0.24	−0.21	0.66	CD99	CD99 molecule [Source:HGNC Symbol;Acc:HGNC:7082]
17	ENSG000001	0.24	−0.21	0.87	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 1
18	ENSG000001	0.23	−0.08	0.76	UFSP2	UFM1−specific peptidase 2 [Source:HGNC Symbol;Acc:HGN
19	ENSG000001	0.23	−0.46	0.72	CD151	CD151 molecule (Raph blood group) [Source:HGNC Symbol;
20	ENSG000001	0.23	−0.11	0.65	CENPB	centromere protein B, 80kDa [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−23	233 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
2	3e−23	240 / 10475	Colon	TssA_Colon
3	1e−17	196 / 8123	Colon	TssF_Colon
4	4e−15	221 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
5	3e−11	207 / 9930	Colon	Tx_Colon
6	5e−11	183 / 8358	Lympl	HOPP_Active_promoter
7	8e−11	198 / 9390	Colon	TxWk_Colon
8	1e−10	179 / 8147	Lympl	HOPP_Weak_promoter
9	2e−09	38 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
10	1e−08	91 / 3370	Brain	Mid_Frontal_Lobe_ZNF
11	5e−08	160 / 7491	Lympl	HOPP_Txn_elongation
12	6e−07	206 / 10800	Brain	Overlap_fetal_midbrain_Quies
13	8e−07	24 / 499	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
14	1e−06	33 / 865	Brain	Mid_Frontal_Lobe_Het
15	2e−06	10 / 96	BP	respiratory electron transport chain
16	2e−06	142 / 6761	Colon	TssD2_Colon
17	3e−06	7 / 41	BP	mitochondrial electron transport, NADH to ubiquinone
18	3e−06	7 / 41	MF	NADH dehydrogenase (ubiquinone) activity
19	4e−06	8 / 60	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
20	4e−06	13 / 177	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
21	4e−06	7 / 44	CC	mitochondrial respiratory chain complex I
22	4e−06	183 / 9470	Colon	Quies3_Colon
23	6e−06	133 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
24	8e−06	10 / 111	GSEA	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSP
25	8e−06	11 / 136	BP	cellular metabolic process
26	1e−05	12 / 167	GSEA	KEGG_HUNTINGTONS_DISEASE
27	1e−05	15 / 263	GSEA	LU_EZH2_TARGETS_UP
28	2e−05	8 / 76	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
29	3e−05	40 / 1333	Lympl	SPANG_BCR UP
30	3e−05	4 / 13	CC	proteasome regulatory particle, base subcomplex
31	5e−05	9 / 109	GSEA	KEGG_PARKINSONS_DISEASE
32	1e−04	10 / 148	GSEA	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_DN
33	1e−04	211 / 11791	Colon	Enh_Colon
34	1e−04	4 / 17	CC	proteasome accessory complex
35	1e−04	25 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
36	1e−04	16 / 356	GSEA	DAIRKEE_TERT_TARGETS_UP
37	1e−04	128 / 6389	Lympl	HOPP_Weak_txn
38	2e−04	27 / 830	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
39	3e−04	7 / 83	GSEA	MOOTHA_VOXPHOS
40	3e−04	10 / 169	Glio	WILLSCHER_GBM_proteomics_wtOnly_Differencelist



Aging

Rank	p−value	#in/all	Geneset
1	0.9	1 / 123	HORVATH_aging_genes meth DOWN
2	0.9	1 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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−06	10 / 96	respiratory electron transport chain
2	3e−06	7 / 41	mitochondrial electron transport, NADH to ubiquinone
3	8e−06	11 / 136	cellular metabolic process
4	6e−04	13 / 291	organelle organization
5	9e−04	4 / 29	centrosome organization
6	1e−03	3 / 15	regulation of protein catabolic process
7	2e−03	24 / 820	gene expression
8	2e−03	3 / 18	positive regulation of chondrocyte differentiation
9	4e−03	4 / 41	glycosaminoglycan biosynthetic process
10	4e−03	4 / 41	protein peptidyl−prolyl isomerization
11	4e−03	7 / 132	protein polyubiquitination
12	4e−03	3 / 22	microtubule bundle formation
13	5e−03	6 / 101	anterior/posterior pattern specification
14	5e−03	3 / 23	melanosome transport
15	5e−03	5 / 73	antigen processing and presentation of exogenous peptide antigen via MHC c
16	6e−03	5 / 74	microtubule cytoskeleton organization
17	6e−03	34 / 1418	small molecule metabolic process
18	7e−03	5 / 77	antigen processing and presentation of exogenous peptide antigen via MHC c
19	7e−03	4 / 49	regulation of cellular amino acid metabolic process
20	7e−03	4 / 50	embryonic skeletal system morphogenesis

Brain

Rank	p−value	#in/all	Geneset
1	3e−23	233 / 9923	Overlap_fetal_midbrain_K9K27me3
2	4e−15	221 / 10239	Overlap_fetal_midbrain_ReprPC
3	1e−08	91 / 3370	Mid_Frontal_Lobe_ZNF
4	6e−07	206 / 10800	Overlap_fetal_midbrain_Quies
5	1e−06	33 / 865	Mid_Frontal_Lobe_Het
6	6e−06	133 / 6320	Overlap_fetal_midbrain_HetRpts
7	1e−03	15 / 400	Fetal_ZNF
8	3e−03	26 / 939	Fetal_HetRpts
9	2e−02	50 / 2443	Fetal_Quies
10	4e−02	173 / 10278	Overlap_fetal_midbrain_ReprPCWk
11	1e−01	51 / 2820	Mid_Frontal_Lobe_HetRpts
12	1e−01	32 / 1680	Fetal_ReprPCWk
13	2e−01	17 / 855	Overlap_fetal_midbrain_ZNF
14	2e−01	13 / 641	Mid_Frontal_Lobe_EnhP
15	4e−01	6 / 342	Fetal_Het
16	5e−01	19 / 1210	Fetal_TssP
17	6e−01	17 / 1137	Fetal_Enh
18	6e−01	25 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	7e−01	16 / 1182	Fetal_EnhP
20	7e−01	19 / 1394	Mid_Frontal_Lobe_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.024	2 / 16	GENTLES_modul1
3	0.089	0 / 16	LIU_COMMON_CANCER_GENES
4	0.189	2 / 52	KUIPER_MM poor survival
5	0.219	1 / 16	WANG_ER_UP
6	0.219	1 / 16	GENTLES_modul2
7	0.219	1 / 16	GENTLES_modul6
8	0.225	11 / 550	Lembcke_Normal vs Adenoma
9	0.263	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
10	0.310	1 / 24	PanCan_Notch_geneset_nanostring
11	0.390	0 / 16	LIU_PROSTATE_CANCER_DN
12	0.461	1 / 40	PanCan_HK_geneset_nanostring
13	0.469	1 / 41	ZHANG_MM up
14	0.661	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	0.667	1 / 71	SHAUGHNESSY_MM high risk
16	0.777	1 / 97	PanCan_TXmisReg_geneset_nanostring
17	0.876	3 / 324	SPANG_BCL6−index2
18	0.886	1 / 140	PanCan_RAS_geneset_nanostring
19	0.948	1 / 191	SPANG_LPS−index2
20	0.999	2 / 574	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	4e−06	7 / 44	mitochondrial respiratory chain complex I
2	3e−05	4 / 13	proteasome regulatory particle, base subcomplex
3	1e−04	4 / 17	proteasome accessory complex
4	7e−04	38 / 1441	mitochondrion
5	9e−04	3 / 13	proteasome regulatory particle
6	9e−04	16 / 425	mitochondrial inner membrane
7	3e−03	6 / 90	ciliary basal body
8	5e−03	100 / 5185	cytoplasm
9	5e−03	55 / 2554	nucleoplasm
10	8e−03	5 / 81	ubiquitin ligase complex
11	1e−02	2 / 10	BBSome
12	1e−02	4 / 56	proteasome complex
13	1e−02	13 / 411	centrosome
14	1e−02	6 / 124	midbody
15	1e−02	2 / 12	transcription export complex
16	2e−02	2 / 13	transcription factor TFTC complex
17	2e−02	3 / 36	mediator complex
18	2e−02	3 / 36	photoreceptor connecting cilium
19	2e−02	3 / 37	nuclear body
20	3e−02	2 / 17	pericentriolar material

Chr

Rank	p−value	#in/all	Geneset
1	0.02	15 / 522	Chr 20
2	0.03	7 / 191	Chr 21
3	0.09	37 / 1920	Chr 1
4	0.13	24 / 1228	Chr 2
5	0.17	17 / 859	Chr 7
6	0.17	15 / 745	Chr 9
7	0.19	22 / 1172	Chr 11
8	0.34	15 / 862	Chr 5
9	0.49	17 / 1083	Chr 17
10	0.54	13 / 847	Chr 16
11	0.54	10 / 651	Chr 8
12	0.59	11 / 746	Chr X
13	0.60	15 / 1017	Chr 12
14	0.60	9 / 613	Chr 14
15	0.66	10 / 715	Chr 10
16	0.72	4 / 318	Chr 13
17	0.79	7 / 582	Chr 15
18	0.82	12 / 976	Chr 6
19	0.93	11 / 1043	Chr 3
20	0.96	3 / 436	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−23	240 / 10475	TssA_Colon
2	1e−17	196 / 8123	TssF_Colon
3	3e−11	207 / 9930	Tx_Colon
4	8e−11	198 / 9390	TxWk_Colon
5	2e−09	38 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
6	2e−06	142 / 6761	TssD2_Colon
7	4e−06	183 / 9470	Quies3_Colon
8	1e−04	211 / 11791	Enh_Colon
9	1e−04	25 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	1e−03	208 / 11968	TssWk_Colon
11	5e−03	65 / 3112	EnhA_Colon
12	1e−02	63 / 3122	TxEnhG1_Colon
13	2e−02	19 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	3e−02	106 / 5889	EnhWk1_Colon
15	1e−01	1 / 10	TCGA−CRC_agressive−disease−markers
16	1e−01	1 / 10	Marisa_CRC−C1
17	2e−01	5 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
18	3e−01	1 / 19	Boland_CRC−MSI−A6−A10
19	3e−01	21 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	3e−01	7 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.7	5 / 399	GUDJ_psoriasis down
2	1.0	4 / 608	GUDJ_psoriasis up
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−04	10 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
2	1e−03	5 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
3	7e−03	44 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	1e−02	48 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	2e−02	4 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	6e−02	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
7	7e−02	3 / 63	Stuehler_Proteins_up_in_STS
8	7e−02	11 / 436	Down_b
9	9e−02	1 / 6	Sturm_GBM_Meth_overexpression_K_mesenchymal_UP
10	2e−01	1 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
11	2e−01	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
12	2e−01	1 / 13	Mukasa_UP_in_Astroglioma
13	2e−01	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
14	2e−01	2 / 53	Gorovets_LGG_EPL_subclass
15	2e−01	2 / 55	Gorovets_LGG_PG_subclass
16	2e−01	3 / 103	GIEZELT_GBM_STS_down_VS_LTS
17	2e−01	2 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
18	2e−01	1 / 16	VERHAAK_MES subtype
19	2e−01	1 / 16	VERHAAK_NL subtype
20	2e−01	1 / 16	Donson−chemokines/cytokines−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−07	24 / 499	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	4e−06	8 / 60	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
3	4e−06	13 / 177	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
4	8e−06	10 / 111	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
5	1e−05	12 / 167	KEGG_HUNTINGTONS_DISEASE
6	1e−05	15 / 263	LU_EZH2_TARGETS_UP
7	2e−05	8 / 76	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
8	5e−05	9 / 109	KEGG_PARKINSONS_DISEASE
9	1e−04	10 / 148	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_DN
10	1e−04	16 / 356	DAIRKEE_TERT_TARGETS_UP
11	2e−04	27 / 830	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
12	3e−04	7 / 83	MOOTHA_VOXPHOS
13	3e−04	8 / 111	KEGG_OXIDATIVE_PHOSPHORYLATION
14	4e−04	25 / 773	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
15	5e−04	16 / 404	MOOTHA_PGC
16	7e−04	10 / 190	KRIEG_KDM3A_TARGETS_NOT_HYPOXIA
17	8e−04	36 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
18	9e−04	23 / 727	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
19	1e−03	10 / 207	WONG_MITOCHONDRIA_GENE_MODULE
20	1e−03	7 / 109	BOUDOUKHA_BOUND_BY_IGF2BP2

HM

Rank	p−value	#in/all	Geneset
1	0.001	10 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.032	6 / 155	HALLMARK_UV_RESPONSE_UP
3	0.125	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
4	0.188	5 / 198	HALLMARK_GLYCOLYSIS
5	0.206	3 / 102	HALLMARK_PEROXISOME
6	0.211	4 / 154	HALLMARK_FATTY_ACID_METABOLISM
7	0.242	3 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.350	4 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.353	4 / 196	HALLMARK_MITOTIC_SPINDLE
10	0.360	4 / 198	HALLMARK_HYPOXIA
11	0.360	4 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	0.371	1 / 30	HALLMARK_NOTCH_SIGNALING
13	0.388	3 / 146	HALLMARK_DNA_REPAIR
14	0.397	2 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	0.427	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
16	0.509	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
17	0.514	2 / 112	HALLMARK_BILE_ACID_METABOLISM
18	0.552	1 / 52	HALLMARK_TGF_BETA_SIGNALING
19	0.559	3 / 190	HALLMARK_APICAL_JUNCTION
20	0.566	3 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	1.0	0 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	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−11	183 / 8358	HOPP_Active_promoter
2	1e−10	179 / 8147	HOPP_Weak_promoter
3	5e−08	160 / 7491	HOPP_Txn_elongation
4	3e−05	40 / 1333	SPANG_BCR UP
5	1e−04	128 / 6389	HOPP_Weak_txn
6	8e−04	25 / 811	WIRTH_lymphoma937_spot D
7	2e−03	24 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
8	4e−03	4 / 42	CARO_OxPhos_in_DLBCL_UP
9	9e−03	124 / 6784	HOPP_Weak_enhancer
10	1e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
11	1e−01	5 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
12	1e−01	5 / 171	WIRTH_lymphoma937_spot C
13	1e−01	3 / 83	ROSOLOWSKI_green UP
14	2e−01	1 / 14	DAVE_BL_DN
15	2e−01	1 / 18	Aukema_BCL2 UP_BCL6 DN
16	3e−01	3 / 115	ROSOLOWSKI_green total
17	3e−01	2 / 67	LEE_Developmental_regulators
18	3e−01	1 / 21	DAVE_Immune response 2
19	3e−01	1 / 21	Subero_MCL_hyper_meth
20	3e−01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN

MF

Rank	p−value	#in/all	Geneset
1	3e−06	7 / 41	NADH dehydrogenase (ubiquinone) activity
2	4e−03	4 / 41	peptidyl−prolyl cis−trans isomerase activity
3	1e−02	2 / 10	thiolester hydrolase activity
4	1e−02	3 / 31	iron−sulfur cluster binding
5	1e−02	3 / 33	beta−tubulin binding
6	2e−02	3 / 39	DNA−directed RNA polymerase activity
7	2e−02	2 / 16	dynein binding
8	2e−02	3 / 41	4 iron, 4 sulfur cluster binding
9	3e−02	12 / 420	protein heterodimerization activity
10	3e−02	5 / 113	methyltransferase activity
11	3e−02	2 / 19	alpha−tubulin binding
12	3e−02	2 / 19	TBP−class protein binding
13	4e−02	2 / 20	enzyme regulator activity
14	4e−02	2 / 20	RNA polymerase II core binding
15	4e−02	3 / 49	SNARE binding
16	4e−02	2 / 21	acetylglucosaminyltransferase activity
17	4e−02	2 / 21	fibroblast growth factor binding
18	4e−02	2 / 21	protein phosphatase type 2A regulator activity
19	5e−02	3 / 53	copper ion binding
20	5e−02	3 / 53	transferase activity, transferring glycosyl groups

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	4 / 79	hsa−miR−205
2	0.05	8 / 257	hsa−miR−524−5p
3	0.05	2 / 23	hsa−miR−668
4	0.05	2 / 24	hsa−miR−1250
5	0.06	2 / 26	hsa−miR−941
6	0.07	4 / 101	hsa−miR−603
7	0.07	5 / 144	hsa−miR−338−5p
8	0.07	1 / 5	hsa−miR−1268
9	0.08	6 / 196	hsa−miR−520d−5p
10	0.09	2 / 32	hsa−miR−631
11	0.09	3 / 70	hsa−miR−873
12	0.10	3 / 72	hsa−miR−935
13	0.10	2 / 36	hsa−miR−34c−3p
14	0.11	3 / 77	hsa−miR−422a
15	0.11	3 / 77	hsa−miR−513c
16	0.14	3 / 84	hsa−miR−486−3p
17	0.14	3 / 84	hsa−miR−188−5p
18	0.15	2 / 44	hsa−miR−661
19	0.15	4 / 133	hsa−miR−383
20	0.16	1 / 11	hsa−miR−604

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 14	BENTINK_e2f3.1
2	0.19	1 / 14	BENTINK_src.2
3	1.00	0 / 14	GUSTAFSON_PI3K_UP
4	1.00	0 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 14	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 10	BENTINK_ras.4
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 14	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	4e−04	36 / 1294	KIM_MYC targets
2	1e−03	45 / 1867	HEBENSTREIT_high expression TF
3	1e−02	34 / 1503	ICGC_Six5_targets
4	2e−02	95 / 5173	ICGC_Taf1_targets
5	8e−02	31 / 1547	ICGC_Ets1_targets
6	1e−01	96 / 5578	ICGC_Stat5_targets
7	1e−01	1 / 9	MYC_Targets DOWN
8	1e−01	78 / 4566	ICGC_Egr1_targets
9	2e−01	42 / 2354	ICGC_SrfV0416101_targets
10	2e−01	105 / 6324	ICGC_Yy1_targets
11	2e−01	113 / 6862	ICGC_Elf1_targets
12	2e−01	75 / 4470	ICGC_Creb1_targets
13	2e−01	41 / 2342	ICGC_GabpPcr2_targets
14	2e−01	91 / 5512	ICGC_Nficsc81335_targets
15	2e−01	91 / 5526	ICGC_Pmlsc71910_targets
16	2e−01	27 / 1523	ICGC_P300_targets
17	3e−01	70 / 4230	ICGC_Nfatc1_targets
18	3e−01	99 / 6157	ICGC_Tcf3_targets
19	3e−01	80 / 4969	ICGC_Atf2_targets
20	4e−01	71 / 4436	ICGC_Zeb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.08	2 / 30	VAQUERIZAS_Smooth muscle
2	0.23	1 / 17	VAQUERIZAS_Adrenal gland
3	0.32	1 / 25	VAQUERIZAS_Adrenal cortex
4	0.38	1 / 31	VAQUERIZAS_Fetal lung
5	0.42	3 / 155	VAQUERIZAS_General
6	0.47	1 / 41	VAQUERIZAS_Testis
7	0.48	1 / 42	VAQUERIZAS_Thyroid
8	0.51	1 / 46	VAQUERIZAS_Whole brain
9	0.53	1 / 49	VAQUERIZAS_Uterus
10	0.63	1 / 64	VAQUERIZAS_Lung
11	1.00	0 / 41	VAQUERIZAS_Fetal brain
12	1.00	0 / 45	VAQUERIZAS_Placenta
13	1.00	0 / 33	VAQUERIZAS_Liver
14	1.00	0 / 37	VAQUERIZAS_Prostate
15	1.00	0 / 12	VAQUERIZAS_Kidney
16	1.00	0 / 25	VAQUERIZAS_Spinal cord
17	1.00	0 / 42	VAQUERIZAS_Thymus
18	1.00	0 / 67	VAQUERIZAS_Whole blood
19	1.00	0 / 7	VAQUERIZAS_Appendix
20	1.00	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 13	WIRTH_Globus pallidus
2	0.18	1 / 13	WIRTH_Sec. lymphoid organs
3	0.21	1 / 15	WIRTH_Telencephalon
4	0.37	1 / 30	PALMER_Lymphocytes signature up
5	0.57	1 / 54	WIRTH_Pancreas
6	0.76	3 / 259	PALMER_Granulocytes signature up
7	0.89	1 / 140	PALMER_T−Cell signature up
8	0.89	1 / 141	WIRTH_Muscle
9	0.96	1 / 202	WIRTH_Testis
10	0.98	3 / 476	WIRTH_Nervous System
11	1.00	0 / 6	WIRTH_Pituitary gland
12	1.00	0 / 427	WIRTH_Immune system
13	1.00	0 / 13	WIRTH_Prim. lymphoid organs
14	1.00	0 / 14	WIRTH_B−cells
15	1.00	0 / 12	WIRTH_Tonsil
16	1.00	0 / 14	WIRTH_Thymus
17	1.00	0 / 12	WIRTH_Lymphocytes
18	1.00	0 / 14	WIRTH_Bone marrow
19	1.00	0 / 13	WIRTH_Cortex cerebri
20	1.00	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	28 / 1343	LU_BPDE 1h DN
2	0.76	76 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

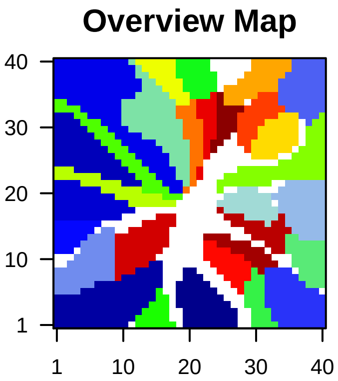
Correlation Clusters

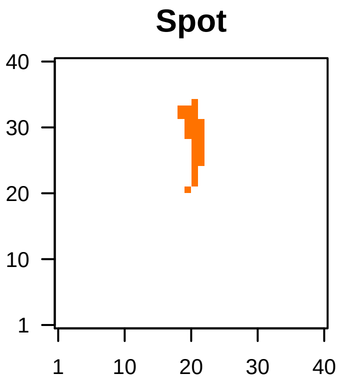
Spot Summary: P

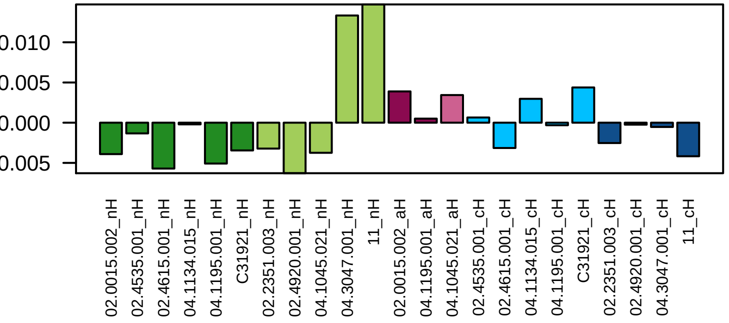
metagenes = 28
genes = 340

<r> metagenes = 0.95
<r> genes = 0.41
beta: r2= 0 / log p= −0.04

samples with spot = 0 (0 %)





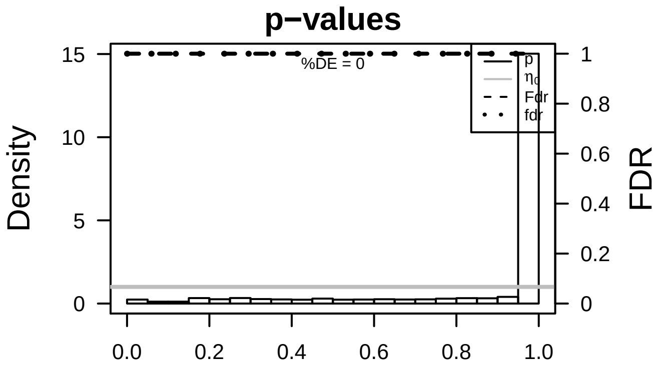


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.08	−0.04	0.66	CCDC146	coiled−coil domain containing 146 [Source:HGNC Symbol;Ac
2	ENSG000001	0.07	−0.04	0.62	DNMT3A	DNA (cytosine−5−)−methyltransferase 3 alpha [Source:HGNC
3	ENSG000001	0.07	−0.06	0.41	CAMKK2	calcium/calmodulin−dependent protein kinase kinase 2, beta
4	ENSG000001	0.07	−0.05	0.74		
5	ENSG000001	0.06	−0.04	0.62	UQCC1	ubiquinol−cytochrome c reductase complex assembly factor 1
6	ENSG000001	0.06	−0.06	0.39	GOLGB1	golgin B1 [Source:HGNC Symbol;Acc:HGNC:4429]
7	ENSG000001	0.06	−0.01	0.51	ASTN2	astrotactin 2 [Source:HGNC Symbol;Acc:HGNC:17021]
8	ENSG000001	0.06	−0.03	0.68	MPV17L	MPV17 mitochondrial membrane protein−like [Source:HGNC
9	ENSG000001	0.05	−0.01	0.79	ZDHHC11	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
10	ENSG000001	0.05	−0.03	0.64	TPCN2	two pore segment channel 2 [Source:HGNC Symbol;Acc:HGI
11	ENSG000002	0.05	−0.02	0.57		
12	ENSG000000	0.05	−0.03	0.49	SETD1A	SET domain containing 1A [Source:HGNC Symbol;Acc:HGNC
13	ENSG000001	0.05	−0.03	0.78	DZIP3	DAZ interacting zinc finger protein 3 [Source:HGNC Symbol;A
14	ENSG000001	0.05	−0.03	0.6	AHI1	Abelson helper integration site 1 [Source:HGNC Symbol;Acc:
15	ENSG000001	0.05	−0.01	0.68	EFHC2	EF−hand domain (C−terminal) containing 2 [Source:HGNC S
16	ENSG000001	0.05	−0.01	0.78	BHMT	betaine−−homocysteine S−methyltransferase [Source:HGNC
17	ENSG000001	0.05	−0.02	0.76	RAB33B	RAB33B, member RAS oncogene family [Source:HGNC Sym
18	ENSG000001	0.05	−0.02	0.78	PAIP2B	poly(A) binding protein interacting protein 2B [Source:HGNC
19	ENSG000001	0.05	−0.02	0.64	NHS	Nance−Horan syndrome (congenital cataracts and dental anc
20	ENSG000001	0.05	−0.02	0.55	FLRT3	fibronectin leucine rich transmembrane protein 3 [Source:HGI

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−10	67 / 1753	Colon	Het_Colon
2	4e−09	52 / 1281	Colon	HetRpts_Colon
3	6e−09	36 / 712	Brain	Overlap_fetal_midbrain_EnhP
4	1e−08	51 / 1279	Brain	Overlap_fetal_midbrain_Enh
5	2e−08	48 / 1178	Colon	ZNF_Colon
6	7e−08	44 / 1084	Brain	Overlap_fetal_midbrain_EnhG
7	4e−07	24 / 431	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
8	8e−06	61 / 2040	MF	metal ion binding
9	3e−05	116 / 4879	Colon	Quies1_Colon
10	1e−04	22 / 525	Colon	Quies2_Colon
11	2e−04	9 / 118	BP	cilium assembly
12	2e−04	5 / 33	BP	protein polymerization
13	2e−04	36 / 1134	MF	nucleic acid binding
14	6e−04	45 / 1604	CC	intracellular
15	7e−04	5 / 42	CC	ciliary membrane
16	7e−04	49 / 1807	BP	transcription, DNA−templated
17	7e−04	3 / 11	BP	inner dynein arm assembly
18	9e−04	7 / 90	CC	ciliary basal body
19	1e−03	29 / 917	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
20	1e−03	7 / 95	CC	centriole
21	1e−03	6 / 70	CC	axoneme
22	1e−03	3 / 13	CC	TCTN−B9D complex
23	1e−03	48 / 1808	BP	regulation of transcription, DNA−templated
24	2e−03	3 / 14	BP	motile cilium assembly
25	2e−03	4 / 31	MF	delayed rectifier potassium channel activity
26	2e−03	80 / 3457	Lymph	HOPP_Heterochrom
27	2e−03	28 / 910	Brain	Fetal_EnhG
28	2e−03	33 / 1137	Brain	Fetal_Enh
29	2e−03	5 / 53	Glio	Gorovets_LGG_EPL_subclass
30	3e−03	2 / 5	GSEA	TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP
31	3e−03	3 / 18	GSEA	REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY
32	4e−03	4 / 38	BP	microtubule−based process
33	4e−03	2 / 6	GSEA	PALOMERO_GSI_SENSITIVITY_UP
34	4e−03	42 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
35	4e−03	4 / 39	GSEA	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS
36	4e−03	13 / 329	GSEA	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
37	5e−03	3 / 21	GSEA	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_
38	5e−03	3 / 21	GSEA	FINETTI_BREAST_CANCERS_KINOME_BLUE
39	6e−03	2 / 7	GSEA	TESAR_ALK_TARGETS_EPISC_4D_UP
40	6e−03	3 / 22	BP	cilium movement



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 144	HORVATH_aging_genes meth UP
2	0.9	1 / 123	HORVATH_aging_genes meth DOWN
3	1.0	0 / 57	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	9 / 118	cilium assembly
2	2e−04	5 / 33	protein polymerization
3	7e−04	49 / 1807	transcription, DNA−templated
4	7e−04	3 / 11	inner dynein arm assembly
5	1e−03	48 / 1808	regulation of transcription, DNA−templated
6	2e−03	3 / 14	motile cilium assembly
7	4e−03	4 / 38	microtubule−based process
8	6e−03	3 / 22	cilium movement
9	6e−03	5 / 68	smoothened signaling pathway
10	9e−03	6 / 104	potassium ion transmembrane transport
11	1e−02	4 / 52	response to stimulus
12	1e−02	4 / 52	sperm motility
13	1e−02	4 / 53	heart looping
14	1e−02	6 / 114	regulation of membrane potential
15	1e−02	6 / 115	regulation of ion transmembrane transport
16	1e−02	2 / 11	cilium organization
17	1e−02	2 / 11	phosphorelay signal transduction system
18	2e−02	3 / 32	sensory perception of taste
19	2e−02	11 / 308	ion transport
20	2e−02	3 / 33	neurotransmitter transport

Brain

Rank	p−value	#in/all	Geneset
1	6e−09	36 / 712	Overlap_fetal_midbrain_EnhP
2	1e−08	51 / 1279	Overlap_fetal_midbrain_Enh
3	7e−08	44 / 1084	Overlap_fetal_midbrain_EnhG
4	2e−03	28 / 910	Fetal_EnhG
5	2e−03	33 / 1137	Fetal_Enh
6	1e−02	196 / 10278	Overlap_fetal_midbrain_ReprPCWk
7	3e−02	29 / 1182	Fetal_EnhP
8	6e−02	20 / 805	Mid_Frontal_Lobe_EnhG
9	1e−01	13 / 552	Fetal_Tx
10	2e−01	48 / 2443	Fetal_Quies
11	2e−01	10 / 408	Mid_Frontal_Lobe_TxTrans
12	2e−01	8 / 317	Mid_Frontal_Lobe_Tx
13	2e−01	37 / 1890	Overlap_fetal_midbrain_TssF
14	2e−01	27 / 1356	Fetal_K9K27me3
15	3e−01	48 / 2603	Fetal_TxTrans
16	3e−01	112 / 6320	Overlap_fetal_midbrain_HetRpts
17	3e−01	18 / 940	Mid_Frontal_Lobe_Enh
18	4e−01	5 / 232	Fetal_ReprPC
19	4e−01	177 / 10239	Overlap_fetal_midbrain_ReprPC
20	4e−01	12 / 641	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	2 / 40	PanCan_HK_geneset_nanostring
2	0.2	1 / 14	LIU_PROSTATE_CANCER_UP
3	0.2	1 / 16	LIU_COMMON_CANCER_GENES
4	0.3	0 / 15	LIU_BREAST_CANCER
5	0.3	3 / 123	PanCan_Driver_Gene_geneset_nanostring
6	0.4	2 / 86	PanCan_JAK−ST_geneset_nanostring
7	0.6	1 / 51	PanCan_TGF−B_geneset_nanostring
8	0.6	1 / 52	KUIPER_MM poor survival
9	0.7	1 / 78	PanCan_Wnt_geneset_nanostring
10	1.0	0 / 16	LIU_PROSTATE_CANCER_DN
11	1.0	3 / 550	Lembcke_Normal vs Adenoma
12	1.0	1 / 324	SPANG_BCL6−index2
13	1.0	1 / 574	Lembcke_Colonic Inflammation
14	1.0	0 / 16	RHODES_CANCER_META_SIGNATURE
15	1.0	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
16	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.0	0 / 16	LIU_LIVER_CANCER
19	1.0	0 / 16	WANG_ER_UP
20	1.0	0 / 9	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−04	45 / 1604	intracellular
2	7e−04	5 / 42	ciliary membrane
3	9e−04	7 / 90	ciliary basal body
4	1e−03	7 / 95	centriole
5	1e−03	6 / 70	axoneme
6	1e−03	3 / 13	TCTN−B9D complex
7	1e−02	7 / 142	cilium
8	1e−02	2 / 10	BBSome
9	1e−02	5 / 84	voltage−gated potassium channel complex
10	2e−02	10 / 282	microtubule
11	2e−02	5 / 96	intermediate filament
12	4e−02	4 / 77	primary cilium
13	4e−02	2 / 20	nuclear chromosome, telomeric region
14	7e−02	2 / 26	presynaptic active zone
15	9e−02	3 / 61	motile cilium
16	1e−01	2 / 36	photoreceptor connecting cilium
17	2e−01	2 / 42	cis−Golgi network
18	2e−01	1 / 11	asymmetric synapse
19	2e−01	1 / 11	axonemal dynein complex
20	2e−01	1 / 11	sodium:potassium−exchanging ATPase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.05	19 / 746	Chr X
2	0.11	6 / 191	Chr 21
3	0.16	14 / 613	Chr 14
4	0.18	7 / 272	Chr 18
5	0.22	14 / 651	Chr 8
6	0.27	24 / 1228	Chr 2
7	0.32	20 / 1043	Chr 3
8	0.37	19 / 1017	Chr 12
9	0.38	20 / 1083	Chr 17
10	0.43	34 / 1920	Chr 1
11	0.53	20 / 1172	Chr 11
12	0.61	14 / 862	Chr 5
13	0.62	12 / 745	Chr 9
14	0.63	23 / 1425	Chr 19
15	0.69	15 / 976	Chr 6
16	0.78	8 / 582	Chr 15
17	0.78	10 / 715	Chr 10
18	0.78	12 / 847	Chr 16
19	0.81	10 / 735	Chr 4
20	0.88	6 / 522	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−10	67 / 1753	Het_Colon
2	4e−09	52 / 1281	HetRpts_Colon
3	2e−08	48 / 1178	ZNF_Colon
4	3e−05	116 / 4879	Quies1_Colon
5	1e−04	22 / 525	Quies2_Colon
6	2e−02	73 / 3406	ReprPC_Colon
7	2e−02	64 / 2947	ReprPCWk_Colon
8	3e−02	29 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
9	4e−02	2 / 19	Boland_CRC−MSI−A6−A10
10	6e−02	3 / 52	Pentrack_CRC_TCGA_corr_S_normal_DN
11	1e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
12	1e−01	1 / 8	Boland_CRC−MMR−system
13	1e−01	41 / 2041	EnhP_Colon
14	2e−01	1 / 10	Budinska_E_Mixed_UP
15	2e−01	8 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
16	2e−01	81 / 4379	TssD1_Colon
17	2e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
18	3e−01	1 / 17	TCGA_Mutated−in−CRC_non−hypermutated
19	3e−01	2 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
20	3e−01	57 / 3109	TssP_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.7	6 / 399	GUDJ_psoriasis down
2	1.0	4 / 608	GUDJ_psoriasis up
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	29 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
2	0.002	5 / 53	Gorovets_LGG_EPL_subclass
3	0.017	4 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
4	0.024	8 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
5	0.027	45 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	0.042	49 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	0.101	11 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
8	0.106	5 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
9	0.128	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
10	0.148	2 / 40	Christensen_hypomethylated_in_ependymoma
11	0.168	3 / 83	GIEZELT_GBM_WT_down_VS_mut
12	0.172	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
13	0.193	3 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	0.200	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
15	0.220	3 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
16	0.227	1 / 15	VERHAAK_PN_Brain
17	0.238	3 / 99	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
18	0.240	1 / 16	VERHAAK_NL subtype
19	0.240	1 / 16	astrocytes_glio
20	0.253	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−07	24 / 431	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
2	3e−03	2 / 5	TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP
3	3e−03	3 / 18	REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY
4	4e−03	2 / 6	PALOMERO_GSI_SENSITIVITY_UP
5	4e−03	42 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
6	4e−03	4 / 39	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS
7	4e−03	13 / 329	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
8	5e−03	3 / 21	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY
9	5e−03	3 / 21	FINETTI_BREAST_CANCERS_KINOME_BLUE
10	6e−03	2 / 7	TESAR_ALK_TARGETS_EPISC_4D_UP
11	8e−03	4 / 46	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN
12	9e−03	3 / 26	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_
13	1e−02	2 / 9	MCCABE_HOXC6_TARGETS_UP
14	1e−02	12 / 326	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	1e−02	2 / 10	KORKOLA_CHORIOCARCINOMA_DN
16	1e−02	2 / 10	KORKOLA_SEMINOMA_DN
17	1e−02	3 / 30	KEGG_BASAL_TRANSCRIPTION_FACTORS
18	1e−02	2 / 11	KORKOLA_EMBRYONAL_CARCINOMA_DN
19	2e−02	3 / 32	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM
20	2e−02	4 / 59	KORKOLA_YOLK_SAC_TUMOR

HM

Rank	p−value	#in/all	Geneset
1	0.1	6 / 193	HALLMARK_KRAS_SIGNALING_DN
2	0.1	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
3	0.5	2 / 98	HALLMARK_ANDROGEN_RESPONSE
4	0.6	2 / 128	HALLMARK_SPERMATOGENESIS
5	0.7	1 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.8	2 / 195	HALLMARK_MYOGENESIS
7	0.8	2 / 196	HALLMARK_MITOTIC_SPINDLE
8	0.9	1 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	0.9	2 / 198	HALLMARK_GLYCOLYSIS
10	0.9	1 / 140	HALLMARK_UV_RESPONSE_DN
11	0.9	1 / 146	HALLMARK_DNA_REPAIR
12	0.9	1 / 154	HALLMARK_FATTY_ACID_METABOLISM
13	1.0	1 / 181	HALLMARK_ALLOGRAFT_REJECTION
14	1.0	1 / 193	HALLMARK_XENOBIOTIC_METABOLISM
15	1.0	1 / 193	HALLMARK_HEME_METABOLISM
16	1.0	1 / 198	HALLMARK_HYPOXIA
17	1.0	1 / 199	HALLMARK_MTORC1_SIGNALING
18	1.0	0 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	1.0	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
20	1.0	0 / 52	HALLMARK_TGF_BETA_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 33	DUMEAUX_Fasting enriched genes
2	0.5	2 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	80 / 3457	HOPP_Heterochrom
2	0.024	102 / 5039	HOPP_Repressed
3	0.093	12 / 458	WIRTH_lymphoma937_spot I
4	0.120	53 / 2658	HOPP_Repetitive
5	0.145	11 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
6	0.158	1 / 10	Shaknovich_ABC_hypo_meth
7	0.186	1 / 12	Subero_MM_hypo_meth
8	0.261	26 / 1333	SPANG_BCR UP
9	0.303	1 / 21	Subero_MCL_hyper_meth
10	0.390	2 / 79	SPANG_LPS 6hrs DN
11	0.411	111 / 6389	HOPP_Weak_txn
12	0.417	50 / 2838	HOPP_Poised_promoter
13	0.452	1 / 35	Subero_T−PLL_hypo_meth
14	0.466	2 / 92	WIRTH_lymphoma937_spot A
15	0.477	2 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
16	0.562	1 / 48	Subero_INT_hypo_meth
17	0.586	5 / 302	SPANG_IL21 UP
18	0.618	1 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
19	0.655	1 / 62	Subero_mBL_hyper_meth
20	0.674	112 / 6784	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	8e−06	61 / 2040	metal ion binding
2	2e−04	36 / 1134	nucleic acid binding
3	2e−03	4 / 31	delayed rectifier potassium channel activity
4	6e−03	6 / 96	structural constituent of cytoskeleton
5	9e−03	44 / 1803	DNA binding
6	9e−03	3 / 26	histone acetyltransferase binding
7	1e−02	4 / 51	voltage−gated potassium channel activity
8	2e−02	2 / 13	taste receptor activity
9	2e−02	2 / 14	bitter taste receptor activity
10	3e−02	6 / 132	ion channel activity
11	4e−02	18 / 667	molecular_function
12	4e−02	5 / 113	methyltransferase activity
13	4e−02	2 / 20	phosphatidylinositol−3,5−bisphosphate binding
14	6e−02	2 / 23	cAMP binding
15	6e−02	7 / 204	structural molecule activity
16	6e−02	23 / 962	transcription factor activity, sequence−specific DNA binding
17	7e−02	2 / 26	calmodulin−dependent protein kinase activity
18	7e−02	6 / 172	calmodulin binding
19	8e−02	2 / 28	phosphatidylinositol−3−phosphate binding
20	1e−01	2 / 31	repressing transcription factor binding

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.03	3 / 41	hsa−miR−532−3p
2	0.13	1 / 8	hsa−miR−886−3p
3	0.16	1 / 10	hsa−miR−720
4	0.18	2 / 46	hsa−miR−660
5	0.22	5 / 188	hsa−miR−520f
6	0.22	2 / 52	hsa−miR−628−5p
7	0.25	2 / 57	hsa−miR−151−3p
8	0.29	2 / 63	hsa−miR−526b*
9	0.29	3 / 111	hsa−miR−361−5p
10	0.30	2 / 65	hsa−miR−612
11	0.31	1 / 22	hsa−miR−1288
12	0.32	2 / 67	hsa−miR−1285
13	0.33	2 / 70	hsa−miR−342−3p
14	0.34	1 / 24	hsa−miR−1225−5p
15	0.34	5 / 226	hsa−miR−185
16	0.35	1 / 25	hsa−miR−602
17	0.35	1 / 25	hsa−miR−432*
18	0.36	1 / 26	hsa−miR−943
19	0.38	2 / 77	hsa−miR−509−5p
20	0.40	2 / 81	hsa−miR−584

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.05	40 / 1798	HEBENSTREIT_low expression TF
2	0.24	1 / 16	NOWICK_TF
3	0.59	12 / 731	ICGC_SrfPcr2_targets
4	0.66	12 / 766	ICGC_Atf3_targets
5	0.66	44 / 2719	ICGC_Pbx3_targets
6	0.67	57 / 3511	ICGC_Rad21_targets
7	0.73	9 / 619	ICGC_RxraPcr1_targets
8	0.77	36 / 2342	ICGC_GabpPcr2_targets
9	0.80	101 / 6322	ICGC_Pol2_targets
10	0.80	22 / 1503	ICGC_Six5_targets
11	0.80	22 / 1506	ICGC_Usf1_targets
12	0.84	48 / 3177	ICGC_Irf4_targets
13	0.89	41 / 2827	ICGC_Bcl3_targets
14	0.89	69 / 4566	ICGC_Egr1_targets
15	0.89	21 / 1549	ICGC_Myc_targets
16	0.89	9 / 745	ICGC_NrsfPcr2_targets
17	0.91	78 / 5173	ICGC_Taf1_targets
18	0.91	84 / 5552	ICGC_Pol24_targets
19	0.92	62 / 4230	ICGC_Nfatc1_targets
20	0.93	97 / 6406	ICGC_Pax5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	VAQUERIZAS_Skin
2	0.3	1 / 23	VAQUERIZAS_Pituitary
3	0.5	1 / 37	VAQUERIZAS_Prostate
4	0.5	1 / 41	VAQUERIZAS_Fetal brain
5	0.5	1 / 46	VAQUERIZAS_Whole brain
6	0.6	1 / 49	VAQUERIZAS_Uterus
7	0.7	2 / 155	VAQUERIZAS_General
8	1.0	0 / 45	VAQUERIZAS_Placenta
9	1.0	0 / 33	VAQUERIZAS_Liver
10	1.0	0 / 30	VAQUERIZAS_Smooth muscle
11	1.0	0 / 12	VAQUERIZAS_Kidney
12	1.0	0 / 25	VAQUERIZAS_Spinal cord
13	1.0	0 / 42	VAQUERIZAS_Thymus
14	1.0	0 / 42	VAQUERIZAS_Thyroid
15	1.0	0 / 67	VAQUERIZAS_Whole blood
16	1.0	0 / 7	VAQUERIZAS_Appendix
17	1.0	0 / 31	VAQUERIZAS_Fetal lung
18	1.0	0 / 64	VAQUERIZAS_Lung
19	1.0	0 / 18	VAQUERIZAS_Pancreas
20	1.0	0 / 24	VAQUERIZAS_Trachea

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	6 / 202	WIRTH_Testis
2	0.2	1 / 14	WIRTH_B−cells
3	0.2	2 / 54	WIRTH_Pancreas
4	0.3	10 / 476	WIRTH_Nervous System
5	0.6	2 / 115	WIRTH_Liver
6	0.7	2 / 137	WIRTH_Mucosa
7	0.7	2 / 141	WIRTH_Muscle
8	0.8	1 / 82	WIRTH_Homeostasis
9	1.0	0 / 6	WIRTH_Pituitary gland
10	1.0	0 / 427	WIRTH_Immune system
11	1.0	0 / 13	WIRTH_Sec. lymphoid organs
12	1.0	0 / 13	WIRTH_Prim. lymphoid organs
13	1.0	0 / 12	WIRTH_Tonsil
14	1.0	0 / 14	WIRTH_Thymus
15	1.0	0 / 12	WIRTH_Lymphocytes
16	1.0	0 / 14	WIRTH_Bone marrow
17	1.0	0 / 13	WIRTH_Globus pallidus
18	1.0	0 / 15	WIRTH_Telencephalon
19	1.0	0 / 13	WIRTH_Cortex cerebri
20	1.0	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	99 / 5285	LU_BPDE 0.005 DN
2	1.0	16 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

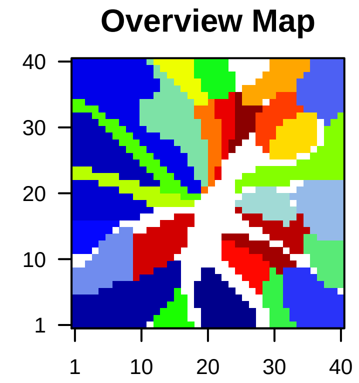
Correlation Clusters

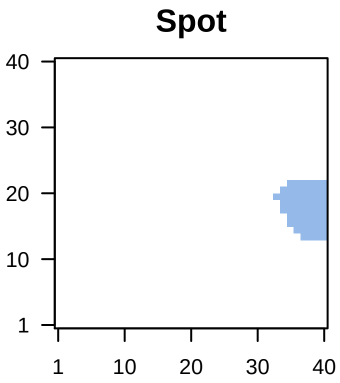
Spot Summary: Q

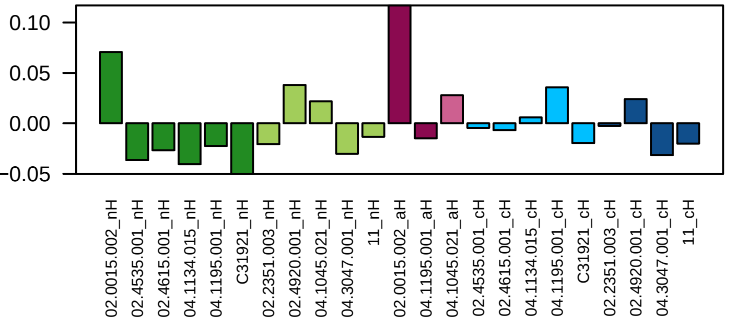
metagenes = 56
genes = 700

<r> metagenes = 0.94
<r> genes = 0.5
beta: r2= 0.03 / log p= −0.33

samples with spot = 2 (8.7 %)
MLH1_normHNPCC : 1 (16.7 %)
MLH1_adenomaHNPCC : 1 (50 %)





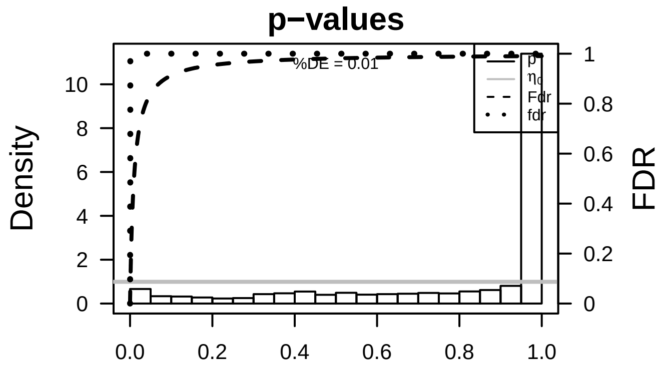


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.86	−0.35	0.69		cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
2	ENSG000002	0.8	−0.27	0.72	CRIP1	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
3	ENSG000001	0.56	−0.1	0.73	TNNC2	troponin C type 2 (fast) [Source:HGNC Symbol;Acc:HGNC:11
4	ENSG000001	0.53	−0.22	0.85		ATP synthase, H+ transporting, mitochondrial F1 complex, ep
5	ENSG000001	0.49	−0.13	0.63	RCN3	reticulocalbin 3, EF−hand calcium binding domain [Source:H
6	ENSG000001	0.49	−0.42	0.55	RNASE1	ribonuclease, RNase A family, 1 (pancreatic) [Source:HGNC
7	ENSG000001	0.47	−0.11	0.44	URAD	ureidoimidazoline (2−oxo−4−hydroxy−4−carboxy−5−) decarb
8	ENSG000001	0.43	−0.19	0.68		
9	ENSG000001	0.41	−0.08	0.8	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type [Sou
10	ENSG000001	0.4	−0.23	0.94	NDUFS6	NADH dehydrogenase (ubiquinone) Fe−S protein 6, 13kDa (
11	ENSG000001	0.38	−0.05	0.62	DUOXA1	dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:
12	ENSG000001	0.38	−0.1	0.83	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U [Sou
13	ENSG000001	0.38	−0.15	0.92	FAM166A	family with sequence similarity 166, member A [Source:HGN
14	ENSG000001	0.37	−0.27	0.73	DUSP23	dual specificity phosphatase 23 [Source:HGNC Symbol;Acc:
15	ENSG000001	0.37	−0.15	0.85	CDC26	cell division cycle 26 [Source:HGNC Symbol;Acc:HGNC:178
16	ENSG000002	0.36	−0.19	0.79	FIS1	fission, mitochondrial 1 [Source:HGNC Symbol;Acc:HGNC:21
17	ENSG000001	0.35	−0.18	0.59	RAB24	RAB24, member RAS oncogene family [Source:HGNC Symb
18	ENSG000001	0.35	−0.19	0.93	MRPL27	mitochondrial ribosomal protein L27 [Source:HGNC Symbol;
19	ENSG000000	0.34	−0.17	0.89	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8k
20	ENSG000001	0.34	−0.17	0.54	VKORC1	vitamin K epoxide reductase complex, subunit 1 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−62	504 / 8123	Colon	TssF_Colon
2	1e−57	572 / 10475	Colon	TssA_Colon
3	3e−48	539 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
4	2e−39	410 / 6761	Colon	TssD2_Colon
5	9e−35	512 / 9930	Colon	Tx_Colon
6	7e−29	241 / 3370	Brain	Mid_Frontal_Lobe_ZNF
7	2e−26	502 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
8	3e−26	473 / 9390	Colon	TxWk_Colon
9	4e−18	497 / 10800	Brain	Overlap_fetal_midbrain_Quies
10	7e−17	198 / 3122	Colon	TxEnhG1_Colon
11	2e−16	60 / 499	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
12	3e−15	81 / 865	Brain	Mid_Frontal_Lobe_Het
13	3e−13	301 / 5889	Colon	EnhWk1_Colon
14	6e−13	512 / 11791	Colon	Enh_Colon
15	2e−12	391 / 8358	Lympl	HOPP_Active_promoter
16	1e−11	146 / 2342	TF	ICGC_GabpPcr2_targets
17	2e−11	265 / 5173	TF	ICGC_Taf1_targets
18	8e−11	352 / 7491	Lympl	HOPP_Txn_elongation
19	1e−10	143 / 2354	TF	ICGC_SrfV0416101_targets
20	2e−10	26 / 165	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
21	3e−10	62 / 727	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
22	3e−10	99 / 1441	CC	mitochondrion
23	5e−10	231 / 4470	TF	ICGC_Creb1_targets
24	2e−09	108 / 1680	Brain	Fetal_ReprPCWk
25	1e−08	269 / 5578	TF	ICGC_Stat5_targets
26	1e−08	87 / 1294	TF	KIM_MYC targets
27	1e−08	271 / 5643	Lympl	HOPP_Txn_transition
28	5e−08	17 / 96	BP	respiratory electron transport chain
29	6e−08	45 / 522	Chr	Chr 20
30	7e−08	15 / 76	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
31	8e−08	35 / 356	GSEA	DAIRKEE_TERT_TARGETS_UP
32	9e−08	94 / 1503	TF	ICGC_Six5_targets
33	1e−07	39 / 425	CC	mitochondrial inner membrane
34	3e−07	11 / 44	CC	mitochondrial respiratory chain complex I
35	4e−07	237 / 4969	TF	ICGC_Atf2_targets
36	4e−07	19 / 136	BP	cellular metabolic process
37	4e−07	258 / 5512	TF	ICGC_Nficsc81335_targets
38	5e−07	207 / 4230	TF	ICGC_Nfatc1_targets
39	5e−07	258 / 5526	TF	ICGC_Pmlsc71910_targets
40	6e−07	220 / 4566	TF	ICGC_Egr1_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 123	HORVATH_aging_genes meth DOWN
2	0.6	5 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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−08	17 / 96	respiratory electron transport chain
2	4e−07	19 / 136	cellular metabolic process
3	3e−06	21 / 182	mRNA splicing, via spliceosome
4	1e−05	9 / 41	mitochondrial electron transport, NADH to ubiquinone
5	2e−04	24 / 291	organelle organization
6	6e−04	17 / 191	vesicle−mediated transport
7	7e−04	10 / 82	mitochondrial translational elongation
8	7e−04	10 / 82	mitochondrial translational initiation
9	8e−04	7 / 43	autophagosome assembly
10	8e−04	11 / 98	mitochondrial translation
11	8e−04	8 / 56	tRNA processing
12	9e−04	10 / 84	mitochondrial translational termination
13	1e−03	6 / 33	mitophagy
14	3e−03	4 / 17	iron−sulfur cluster assembly
15	4e−03	14 / 174	protein folding
16	4e−03	8 / 72	double−strand break repair via homologous recombination
17	5e−03	3 / 10	viral budding via host ESCRT complex
18	5e−03	5 / 31	C−terminal protein lipidation
19	5e−03	4 / 20	ATP synthesis coupled proton transport
20	6e−03	33 / 575	biological_process

Brain

Rank	p−value	#in/all	Geneset
1	3e−48	539 / 9923	Overlap_fetal_midbrain_K9K27me3
2	7e−29	241 / 3370	Mid_Frontal_Lobe_ZNF
3	2e−26	502 / 10239	Overlap_fetal_midbrain_ReprPC
4	4e−18	497 / 10800	Overlap_fetal_midbrain_Quies
5	3e−15	81 / 865	Mid_Frontal_Lobe_Het
6	2e−09	108 / 1680	Fetal_ReprPCWk
7	2e−05	141 / 2820	Mid_Frontal_Lobe_HetRpts
8	6e−03	259 / 6320	Overlap_fetal_midbrain_HetRpts
9	7e−02	18 / 342	Fetal_Het
10	9e−02	42 / 939	Fetal_HetRpts
11	9e−02	20 / 400	Fetal_ZNF
12	1e−01	38 / 855	Overlap_fetal_midbrain_ZNF
13	2e−01	95 / 2443	Fetal_Quies
14	3e−01	67 / 1713	Mid_Frontal_Lobe_ReprPCWk
15	8e−01	5 / 191	Overlap_fetal_midbrain_Het
16	8e−01	6 / 232	Fetal_ReprPC
17	9e−01	43 / 1394	Mid_Frontal_Lobe_Quies
18	9e−01	34 / 1182	Fetal_EnhP
19	1e+00	124 / 3977	Mid_Frontal_Lobe_ReprPC
20	1e+00	345 / 10278	Overlap_fetal_midbrain_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	5 / 40	PanCan_HK_geneset_nanostring
2	0.02	3 / 16	LIU_LIVER_CANCER
3	0.10	2 / 15	GENTLES_modul10
4	0.11	4 / 50	PanCan_DNARepair_geneset_nanostring
5	0.19	2 / 22	PanCan_ChromMod_geneset_nanostring
6	0.28	1 / 9	WANG_ER_DN
7	0.33	1 / 11	GENTLES_modul5
8	0.38	8 / 191	SPANG_LPS−index2
9	0.40	1 / 14	GENTLES_modul12
10	0.44	1 / 16	RHODES_CANCER_META_SIGNATURE
11	0.44	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.44	1 / 16	GENTLES_modul7
13	0.55	2 / 51	PanCan_TGF−B_geneset_nanostring
14	0.69	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	0.72	0 / 16	LIU_COMMON_CANCER_GENES
16	0.73	4 / 136	PanCan_CC+Apop_geneset_nanostring
17	0.74	10 / 324	SPANG_BCL6−index2
18	0.78	17 / 550	Lembcke_Normal vs Adenoma
19	0.78	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	0.87	2 / 97	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−10	99 / 1441	mitochondrion
2	1e−07	39 / 425	mitochondrial inner membrane
3	3e−07	11 / 44	mitochondrial respiratory chain complex I
4	4e−05	12 / 82	catalytic step 2 spliceosome
5	6e−05	5 / 13	Prp19 complex
6	7e−05	12 / 87	late endosome membrane
7	7e−05	14 / 116	late endosome
8	3e−04	7 / 36	mediator complex
9	5e−04	5 / 19	mitochondrial proton−transporting ATP synthase complex
10	6e−04	222 / 5101	nucleus
11	2e−03	7 / 48	SNARE complex
12	2e−03	4 / 15	Ada2/Gcn5/Ada3 transcription activator complex
13	2e−03	5 / 26	pre−autophagosomal structure
14	4e−03	4 / 19	mitochondrial envelope
15	6e−03	8 / 76	integral component of endoplasmic reticulum membrane
16	7e−03	4 / 22	anaphase−promoting complex
17	8e−03	17 / 245	lysosomal membrane
18	1e−02	3 / 13	HOPS complex
19	1e−02	16 / 235	lysosome
20	2e−02	4 / 27	mitochondrial ribosome

Chr

Rank	p−value	#in/all	Geneset
1	6e−08	45 / 522	Chr 20
2	2e−06	86 / 1425	Chr 19
3	1e−04	52 / 847	Chr 16
4	1e−03	49 / 859	Chr 7
5	5e−03	27 / 436	Chr 22
6	8e−02	48 / 1083	Chr 17
7	8e−02	29 / 613	Chr 14
8	2e−01	25 / 582	Chr 15
9	5e−01	42 / 1172	Chr 11
10	6e−01	35 / 1017	Chr 12
11	7e−01	24 / 745	Chr 9
12	8e−01	31 / 976	Chr 6
13	9e−01	60 / 1920	Chr 1
14	9e−01	36 / 1228	Chr 2
15	1e+00	5 / 272	Chr 18
16	1e+00	18 / 746	Chr X
17	1e+00	14 / 651	Chr 8
18	1e+00	2 / 191	Chr 21
19	1e+00	23 / 1043	Chr 3
20	1e+00	4 / 318	Chr 13

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−62	504 / 8123	TssF_Colon
2	1e−57	572 / 10475	TssA_Colon
3	2e−39	410 / 6761	TssD2_Colon
4	9e−35	512 / 9930	Tx_Colon
5	3e−26	473 / 9390	TxWk_Colon
6	7e−17	198 / 3122	TxEnhG1_Colon
7	3e−13	301 / 5889	EnhWk1_Colon
8	6e−13	512 / 11791	Enh_Colon
9	1e−06	160 / 3112	EnhA_Colon
10	6e−06	398 / 9470	Quies3_Colon
11	3e−04	4 / 10	TCGA−CRC_agressive−disease−markers
12	2e−03	49 / 877	TxEnhG2_Colon
13	5e−02	2 / 10	KIM_MSI−in−EC
14	5e−02	35 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	1e−01	5 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
16	2e−01	2 / 20	Budinska_B_Lower crypt−like_UP
17	3e−01	1 / 10	KIM_CRC−MSI−regulated_DN
18	4e−01	29 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
19	4e−01	435 / 11968	TssWk_Colon
20	4e−01	1 / 15	Budinska_B_Lower crypt−like_DOWN

Disease

Rank	p−value	#in/all	Geneset
1	1	9 / 608	GUDJ_psoriasis up
2	1	3 / 399	GUDJ_psoriasis down
3	1	0 / 22	BCHETNIA_EBM up
4	1	0 / 2	BCHETNIA_EBM down
5	1	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	7 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
2	0.003	14 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
3	0.010	45 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	0.038	6 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
5	0.038	86 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	0.042	8 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.045	5 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
8	0.058	95 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
9	0.077	5 / 63	Stuehler_Proteins_up_in_STS
10	0.165	3 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
11	0.201	6 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	0.335	4 / 81	GIEZELT_GBM_STS_up_VS_LTS
13	0.357	1 / 12	Phillips PN up vs MES & Prolif
14	0.357	1 / 12	WILLSCHER__GBM_LTSwt_proteomics−C_UP
15	0.357	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
16	0.378	3 / 61	Christensen_hypermethylated_in_primary_glioblastoma
17	0.380	1 / 13	Mukasa_UP_in_Astroglioma
18	0.402	1 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
19	0.406	17 / 436	Down_b
20	0.418	3 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−16	60 / 499	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	2e−10	26 / 165	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
3	3e−10	62 / 727	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
4	7e−08	15 / 76	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
5	8e−08	35 / 356	DAIRKEE_TERT_TARGETS_UP
6	1e−06	12 / 60	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
7	1e−06	14 / 83	MOOTHA_VOXPHOS
8	1e−06	37 / 437	MOOTHA_MITOCHONDRIA
9	2e−06	36 / 420	MOOTHA_HUMAN_MITODB_6_2002
10	5e−06	47 / 651	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
11	6e−06	53 / 773	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
12	6e−06	22 / 207	WONG_MITOCHONDRIA_GENE_MODULE
13	1e−05	25 / 263	LU_EZH2_TARGETS_UP
14	1e−05	15 / 111	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
15	1e−05	17 / 140	KIM_ALL_DISORDERS_DURATION_CORR_DN
16	2e−05	21 / 206	SANSOM_APC_MYC_TARGETS
17	4e−05	14 / 109	KEGG_PARKINSONS_DISEASE
18	4e−05	8 / 37	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
19	5e−05	14 / 111	KEGG_OXIDATIVE_PHOSPHORYLATION
20	6e−05	12 / 86	LI_DCP2_BOUND_MRNA

HM

Rank	p−value	#in/all	Geneset
1	8e−04	14 / 146	HALLMARK_DNA_REPAIR
2	2e−03	16 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	8e−02	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	2e−01	6 / 102	HALLMARK_PEROXISOME
5	3e−01	9 / 193	HALLMARK_HEME_METABOLISM
6	3e−01	2 / 30	HALLMARK_NOTCH_SIGNALING
7	4e−01	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	5e−01	6 / 154	HALLMARK_FATTY_ACID_METABOLISM
9	6e−01	7 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
10	7e−01	3 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	7e−01	6 / 199	HALLMARK_ADIPOGENESIS
12	7e−01	2 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	7e−01	1 / 36	HALLMARK_ANGIOGENESIS
14	8e−01	3 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	8e−01	3 / 112	HALLMARK_BILE_ACID_METABOLISM
16	8e−01	5 / 193	HALLMARK_KRAS_SIGNALING_DN
17	8e−01	3 / 128	HALLMARK_SPERMATOGENESIS
18	9e−01	2 / 94	HALLMARK_PROTEIN_SECRETION
19	9e−01	1 / 58	HALLMARK_MYC_TARGETS_V2
20	9e−01	4 / 190	HALLMARK_APICAL_JUNCTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.3	1 / 11	DUMEAUX_Smoking literature genes up
3	0.4	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	1.0	1 / 91	DUMEAUX_Smoking enriched genes
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−12	391 / 8358	HOPP_Active_promoter
2	8e−11	352 / 7491	HOPP_Txn_elongation
3	1e−08	271 / 5643	HOPP_Txn_transition
4	6e−02	314 / 8147	HOPP_Weak_promoter
5	8e−02	58 / 1333	SPANG_BCR UP
6	2e−01	2 / 21	ROSOLOWSKI_red UP
7	3e−01	1 / 9	YAMANE_AICDA_targets_nonrecruited
8	3e−01	4 / 75	WIRTH_lymphoma937_spot IM
9	3e−01	280 / 7592	HOPP_Strong_enhancer
10	3e−01	3 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
11	4e−01	10 / 240	WIRTH_lymphoma937_spot B
12	4e−01	1 / 13	BENTINK_mBL DOWN
13	4e−01	1 / 13	Subero_B−CLL_hypo_meth
14	4e−01	4 / 87	Aukema_BCL2 DN_BCL6 UP
15	4e−01	31 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
16	4e−01	31 / 811	WIRTH_lymphoma937_spot D
17	5e−01	2 / 42	CARO_OxPhos_in_DLBCL_UP
18	5e−01	1 / 17	YAMANE_AICDA_targets_recruited
19	5e−01	9 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
20	5e−01	1 / 18	Aukema_BCL2 UP_BCL6 DN

MF

Rank	p−value	#in/all	Geneset
1	1e−06	10 / 41	NADH dehydrogenase (ubiquinone) activity
2	5e−04	7 / 40	SNAP receptor activity
3	7e−04	6 / 31	oxidoreductase activity, acting on paired donors, with incorporation or reductic
4	2e−03	14 / 161	ubiquitin protein ligase activity
5	3e−03	6 / 39	DNA−directed RNA polymerase activity
6	5e−03	3 / 10	ribonuclease P activity
7	5e−03	4 / 20	L−ascorbic acid binding
8	6e−03	3 / 11	NADH dehydrogenase activity
9	6e−03	3 / 11	ubiquitin−ubiquitin ligase activity
10	7e−03	17 / 243	transcription coactivator activity
11	7e−03	4 / 22	2 iron, 2 sulfur cluster binding
12	9e−03	5 / 36	RNA polymerase II transcription cofactor activity
13	1e−02	8 / 89	electron carrier activity
14	2e−02	4 / 30	ubiquitin conjugating enzyme activity
15	4e−02	12 / 187	ATPase activity
16	4e−02	33 / 667	molecular_function
17	4e−02	14 / 232	hydrolase activity
18	4e−02	3 / 22	protein disulfide oxidoreductase activity
19	5e−02	2 / 10	protein kinase regulator activity
20	5e−02	15 / 262	ubiquitin−protein transferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	3 / 19	hsa−miR−542−5p
2	0.05	6 / 72	hsa−miR−331−3p
3	0.05	3 / 23	hsa−miR−151−5p
4	0.05	7 / 94	hsa−miR−378
5	0.06	6 / 77	hsa−miR−422a
6	0.06	7 / 97	hsa−miR−125a−3p
7	0.07	3 / 27	hsa−miR−1273
8	0.09	3 / 29	hsa−miR−1225−3p
9	0.11	3 / 33	hsa−miR−1296
10	0.11	3 / 33	hsa−miR−17*
11	0.12	12 / 226	hsa−miR−185
12	0.14	5 / 77	hsa−miR−939
13	0.15	3 / 37	hsa−miR−518e
14	0.16	3 / 38	hsa−miR−760
15	0.16	3 / 38	hsa−miR−127−3p
16	0.17	3 / 40	hsa−miR−517*
17	0.19	4 / 63	hsa−miR−671−5p
18	0.20	1 / 6	hsa−miR−937
19	0.20	4 / 64	hsa−miR−1275
20	0.20	2 / 23	hsa−miR−668

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	1e−11	146 / 2342	ICGC_GabpPcr2_targets
2	2e−11	265 / 5173	ICGC_Taf1_targets
3	1e−10	143 / 2354	ICGC_SrfV0416101_targets
4	5e−10	231 / 4470	ICGC_Creb1_targets
5	1e−08	269 / 5578	ICGC_Stat5_targets
6	1e−08	87 / 1294	KIM_MYC targets
7	9e−08	94 / 1503	ICGC_Six5_targets
8	4e−07	237 / 4969	ICGC_Atf2_targets
9	4e−07	258 / 5512	ICGC_Nficsc81335_targets
10	5e−07	207 / 4230	ICGC_Nfatc1_targets
11	5e−07	258 / 5526	ICGC_Pmlsc71910_targets
12	6e−07	220 / 4566	ICGC_Egr1_targets
13	1e−06	275 / 6005	ICGC_Mta3_targets
14	1e−06	235 / 4987	ICGC_Bclaf101388_targets
15	3e−06	245 / 5308	ICGC_Tcf12_targets
16	4e−06	250 / 5453	ICGC_Foxm1_targets
17	4e−06	104 / 1867	HEBENSTREIT_high expression TF
18	5e−06	303 / 6862	ICGC_Elf1_targets
19	1e−05	245 / 5393	ICGC_Sp1_targets
20	2e−05	206 / 4436	ICGC_Zeb1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	2 / 19	VAQUERIZAS_Heart
2	0.4	1 / 13	VAQUERIZAS_Skin
3	0.4	2 / 41	VAQUERIZAS_Fetal brain
4	0.4	2 / 41	VAQUERIZAS_Testis
5	0.5	2 / 42	VAQUERIZAS_Thymus
6	0.5	2 / 46	VAQUERIZAS_Whole brain
7	0.6	1 / 25	VAQUERIZAS_Spinal cord
8	0.7	5 / 155	VAQUERIZAS_General
9	0.7	1 / 33	VAQUERIZAS_Liver
10	0.8	1 / 42	VAQUERIZAS_Thyroid
11	0.9	1 / 64	VAQUERIZAS_Lung
12	0.9	1 / 67	VAQUERIZAS_Whole blood
13	1.0	0 / 45	VAQUERIZAS_Placenta
14	1.0	0 / 37	VAQUERIZAS_Prostate
15	1.0	0 / 30	VAQUERIZAS_Smooth muscle
16	1.0	0 / 49	VAQUERIZAS_Uterus
17	1.0	0 / 12	VAQUERIZAS_Kidney
18	1.0	0 / 7	VAQUERIZAS_Appendix
19	1.0	0 / 31	VAQUERIZAS_Fetal lung
20	1.0	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.09	3 / 30	PALMER_Lymphocytes signature up
2	0.10	2 / 15	WIRTH_Telencephalon
3	0.36	1 / 12	WIRTH_Tonsil
4	0.38	1 / 13	WIRTH_Globus pallidus
5	0.40	1 / 14	WIRTH_Thyroid gland
6	0.73	4 / 137	WIRTH_Mucosa
7	0.82	1 / 47	WIRTH_Placenta
8	0.89	3 / 141	WIRTH_Muscle
9	0.94	4 / 202	WIRTH_Testis
10	0.95	4 / 208	PALMER_B−Cell signature up
11	0.96	5 / 259	PALMER_Granulocytes signature up
12	0.99	1 / 115	WIRTH_Liver
13	0.99	1 / 140	PALMER_T−Cell signature up
14	1.00	3 / 427	WIRTH_Immune system
15	1.00	3 / 476	WIRTH_Nervous System
16	1.00	0 / 6	WIRTH_Pituitary gland
17	1.00	0 / 54	WIRTH_Pancreas
18	1.00	0 / 13	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_Prim. lymphoid organs
20	1.00	0 / 14	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	44 / 1343	LU_BPDE 1n DN
2	1.0	115 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

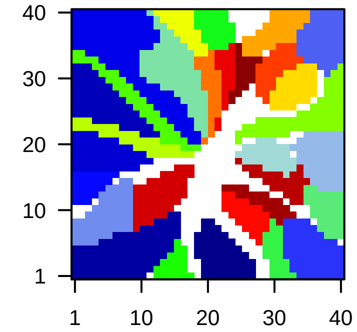
Spot Summary: R

metagenes = 65
genes = 943

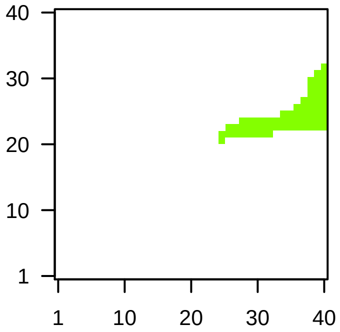
<r> metagenes = 0.94
<r> genes = 0.48
beta: r2= 0.01 / log p= −0.18

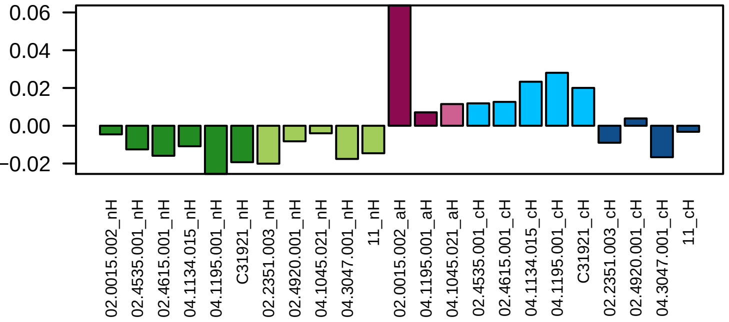
samples with spot = 1 (4.3 %)
MLH1_adenomaHNPCC : 1 (50 %)

Overview Map



Spot





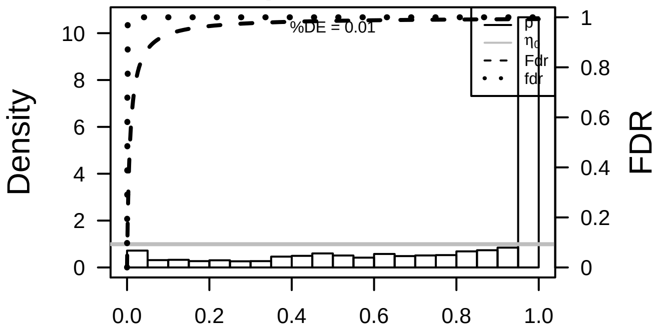
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.36	−0.04	0.77	PF4	platelet factor 4 [Source:HGNC Symbol;Acc:HGNC:8861]
2	ENSG000001	0.35	−0.07	0.47	TMEM74B	transmembrane protein 74B [Source:HGNC Symbol;Acc:HGN
3	ENSG000001	0.28	−0.06	0.91	LOC100507424	integrin alpha FG−GAP repeat containing 2 [Source:HGNC S
4	ENSG000001	0.28	−0.11	0.68	USP5	ubiquitin specific peptidase 5 (isopeptidase T) [Source:HGNC
5	ENSG000001	0.27	−0.07	0.82	NMB	neuromedin B [Source:HGNC Symbol;Acc:HGNC:7842]
6	ENSG000001	0.27	−0.07	0.89	LSM5	LSM5 homolog, U6 small nuclear RNA and mRNA degradatic
7	ENSG000001	0.26	−0.25	0.61	RPL38	ribosomal protein L38 [Source:HGNC Symbol;Acc:HGNC:103
8	ENSG000002	0.26	−0.07	0.72	RTEL1	regulator of telomere elongation helicase 1 [Source:HGNC Sy
9	ENSG000000	0.25	−0.04	0.52	WNT11	wingless−type MMTV integration site family, member 11 [Sou
10	ENSG000001	0.24	−0.09	0.51	PLCB4	phospholipase C, beta 4 [Source:HGNC Symbol;Acc:HGNC:
11	ENSG000001	0.24	−0.05	0.9	F12	coagulation factor XII (Hageman factor) [Source:HGNC Symb
12	ENSG000001	0.23	−0.12	0.73	C20orf27	chromosome 20 open reading frame 27 [Source:HGNC Symb
13	ENSG000001	0.23	−0.1	0.81	PELP1	proline, glutamate and leucine rich protein 1 [Source:HGNC S
14	ENSG000000	0.23	−0.19	0.67	ERP29	endoplasmic reticulum protein 29 [Source:HGNC Symbol;Acc
15	ENSG000001	0.22	−0.13	0.82	EIF3B	eukaryotic translation initiation factor 3, subunit B [Source:HG
16	ENSG000001	0.22	−0.06	0.64	LYG1	lysozyme G−like 1 [Source:HGNC Symbol;Acc:HGNC:27014]
17	ENSG000001	0.22	−0.14	0.79	JMJD8	jumonji domain containing 8 [Source:HGNC Symbol;Acc:HGN
18	ENSG000001	0.22	−0.14	0.63	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucle
19	ENSG000002	0.21	−0.13	0.8	CKLF	chemokine−like factor [Source:HGNC Symbol;Acc:HGNC:132
20	ENSG000001	0.21	−0.09	0.9	WDR74	WD repeat domain 74 [Source:HGNC Symbol;Acc:HGNC:25

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−28	95 / 550	Cance	Lembcke_Normal vs Adenoma
2	1e−13	496 / 8123	Colon	TssF_Colon
3	6e−13	77 / 668	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
4	1e−11	84 / 807	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
5	2e−11	84 / 811	Lymph	WIRTH_lymphoma937_spot D
6	2e−09	60 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	2e−09	408 / 6761	Colon	TssD2_Colon
8	3e−09	125 / 1549	TF	ICGC_Myc_targets
9	6e−09	34 / 233	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell li
10	3e−08	84 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
11	7e−08	552 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
12	1e−07	476 / 8358	Lymph	HOPP_Active_promoter
13	2e−07	32 / 240	Lymph	WIRTH_lymphoma937_spot B
14	2e−07	35 / 282	GSEA	MANALO_HYPOXIA_DN
15	3e−07	73 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
16	4e−07	68 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
17	5e−07	277 / 4470	TF	ICGC_Creb1_targets
18	5e−07	29 / 216	GSEA	KAUFFMANN_DNA_REPAIR_GENES
19	5e−07	36 / 304	BP	DNA repair
20	8e−07	113 / 1503	TF	ICGC_Six5_targets
21	2e−06	272 / 4436	TF	ICGC_Zeb1_targets
22	3e−06	329 / 5578	TF	ICGC_Stat5_targets
23	3e−06	567 / 10475	Colon	TssA_Colon
24	4e−06	627 / 11791	Colon	Enh_Colon
25	4e−06	6 / 11	BP	RNA methylation
26	6e−06	21 / 145	BP	DNA replication
27	6e−06	313 / 5308	TF	ICGC_Tcf12_targets
28	7e−06	18 / 113	MF	methyltransferase activity
29	8e−06	156 / 2342	TF	ICGC_GabpPcr2_targets
30	9e−06	34 / 316	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
31	9e−06	305 / 5173	TF	ICGC_Taf1_targets
32	1e−05	30 / 263	GSEA	LU_EZH2_TARGETS_UP
33	1e−05	16 / 95	GSEA	REACTOME_CHROMOSOME_MAINTENANCE
34	2e−05	210 / 3370	Brain	Mid_Frontal_Lobe_ZNF
35	2e−05	6 / 13	CC	Fanconi anaemia nuclear complex
36	2e−05	10 / 41	MF	tRNA binding
37	2e−05	68 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
38	3e−05	313 / 5393	TF	ICGC_Sp1_targets
39	3e−05	11 / 52	GSEA	REACTOME_TELOMERE_MAINTENANCE
40	4e−05	10 / 45	GSEA	PID_FANCONI_PATHWAY

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.04	12 / 144	HORVATH_aging_genes meth UP
2	0.37	7 / 123	HORVATH_aging_genes meth DOWN
3	0.52	3 / 57	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−07	36 / 304	DNA repair
2	4e−06	6 / 11	RNA methylation
3	6e−06	21 / 145	DNA replication
4	6e−05	11 / 56	tRNA processing
5	1e−04	11 / 59	telomere maintenance
6	3e−04	15 / 112	methylation
7	6e−04	13 / 96	nucleosome assembly
8	7e−04	5 / 16	RNA modification
9	2e−03	6 / 28	DNA replication initiation
10	3e−03	4 / 13	mannosylation
11	3e−03	5 / 21	histone lysine methylation
12	4e−03	4 / 14	DNA replication−dependent nucleosome assembly
13	4e−03	5 / 23	telomere maintenance via semi−conservative replication
14	5e−03	4 / 15	replication fork processing
15	5e−03	4 / 15	tRNA methylation
16	5e−03	19 / 208	cellular response to DNA damage stimulus
17	6e−03	11 / 95	rRNA processing
18	6e−03	4 / 16	pseudouridine synthesis
19	7e−03	4 / 17	iron−sulfur cluster assembly
20	8e−03	5 / 27	telomere maintenance via recombination

Brain

Rank	p−value	#in/all	Geneset
1	7e−08	552 / 9923	Overlap_fetal_midbrain_K9K27me3
2	2e−05	210 / 3370	Mid_Frontal_Lobe_ZNF
3	7e−04	537 / 10239	Overlap_fetal_midbrain_ReprPC
4	3e−03	165 / 2820	Mid_Frontal_Lobe_HetRpts
5	2e−02	139 / 2443	Fetal_Quies
6	2e−02	547 / 10800	Overlap_fetal_midbrain_Quies
7	2e−02	59 / 939	Fetal_HetRpts
8	4e−02	53 / 865	Mid_Frontal_Lobe_Het
9	9e−02	94 / 1713	Mid_Frontal_Lobe_ReprPCWk
10	2e−01	89 / 1680	Fetal_ReprPCWk
11	2e−01	108 / 2084	Mid_Frontal_Lobe_K9K27me3
12	3e−01	22 / 408	Mid_Frontal_Lobe_TxTrans
13	3e−01	196 / 3977	Mid_Frontal_Lobe_ReprPC
14	4e−01	12 / 232	Fetal_ReprPC
15	5e−01	20 / 400	Fetal_ZNF
16	5e−01	67 / 1394	Mid_Frontal_Lobe_Quies
17	6e−01	39 / 855	Overlap_fetal_midbrain_ZNF
18	7e−01	28 / 641	Mid_Frontal_Lobe_EnhP
19	8e−01	60 / 1356	Fetal_K9K27me3
20	8e−01	480 / 10278	Overlap_fetal_midbrain_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	2e−28	95 / 550	Lembcke_Normal vs Adenoma
2	1e−04	10 / 50	PanCan_DNARepair_geneset_nanostring
3	2e−01	2 / 15	GENTLES_modul10
4	2e−01	6 / 78	PanCan_Wnt_geneset_nanostring
5	3e−01	5 / 71	SHAUGHNESSY_MM high risk
6	3e−01	1 / 16	LIU_LIVER_CANCER
7	4e−01	1 / 10	GENTLES_modul3
8	4e−01	2 / 28	PanCan_HH_geneset_nanostring
9	5e−01	1 / 14	GENTLES_modul12
10	5e−01	7 / 140	PanCan_RAS_geneset_nanostring
11	5e−01	1 / 16	GENTLES_modul2
12	5e−01	1 / 16	GENTLES_modul6
13	6e−01	0 / 14	LIU_PROSTATE_CANCER_UP
14	7e−01	1 / 22	PanCan_ChromMod_geneset_nanostring
15	7e−01	0 / 15	LIU_BREAST_CANCER
16	7e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	7e−01	6 / 152	PanCan_MAPK_geneset_nanostring
18	8e−01	5 / 136	PanCan_CC+Apop_geneset_nanostring
19	8e−01	4 / 123	PanCan_Driver_Gene_geneset_nanostring
20	8e−01	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	2e−05	6 / 13	Fanconi anaemia nuclear complex
2	6e−05	101 / 1441	mitochondrion
3	2e−04	10 / 53	nucleosome
4	7e−04	5 / 16	replication fork
5	1e−03	5 / 18	U4/U6 x U5 tri−snRNP complex
6	2e−03	35 / 431	cellular_component
7	3e−03	4 / 13	TCTN−B9D complex
8	3e−03	7 / 41	chromosome, telomeric region
9	3e−03	6 / 31	mitochondrial large ribosomal subunit
10	4e−03	11 / 92	spliceosomal complex
11	9e−03	4 / 18	DNA−directed RNA polymerase III complex
12	1e−02	53 / 799	nucleolus
13	1e−02	3 / 10	cytoplasmic exosome (RNase complex)
14	1e−02	3 / 11	Gemini of coiled bodies
15	1e−02	3 / 11	mRNA cleavage and polyadenylation specificity factor complex
16	1e−02	3 / 11	small nucleolar ribonucleoprotein complex
17	2e−02	5 / 32	small−subunit processome
18	2e−02	3 / 12	SMN complex
19	2e−02	3 / 13	integrator complex
20	3e−02	4 / 26	synaptonemal complex

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	63 / 847	Chr 16
2	9e−04	71 / 1017	Chr 12
3	1e−02	56 / 859	Chr 7
4	1e−02	49 / 745	Chr 9
5	5e−02	64 / 1083	Chr 17
6	1e−01	31 / 522	Chr 20
7	1e−01	26 / 436	Chr 22
8	3e−01	98 / 1920	Chr 1
9	3e−01	37 / 715	Chr 10
10	4e−01	31 / 613	Chr 14
11	5e−01	57 / 1172	Chr 11
12	5e−01	47 / 976	Chr 6
13	5e−01	28 / 582	Chr 15
14	7e−01	28 / 651	Chr 8
15	8e−01	7 / 191	Chr 21
16	9e−01	41 / 1043	Chr 3
17	1e+00	8 / 272	Chr 18
18	1e+00	55 / 1425	Chr 19
19	1e+00	29 / 862	Chr 5
20	1e+00	22 / 746	Chr X

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−13	496 / 8123	TssF_Colon
2	2e−09	408 / 6761	TssD2_Colon
3	3e−07	73 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
4	3e−06	567 / 10475	TssA_Colon
5	4e−06	627 / 11791	Enh_Colon
6	1e−03	519 / 9930	Tx_Colon
7	2e−03	493 / 9390	TxWk_Colon
8	2e−03	50 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
9	2e−02	48 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
10	2e−02	47 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	9e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
12	1e−01	5 / 52	Pentrack_CRC_TCGA_corr_S_normal_DN
13	1e−01	299 / 5889	EnhWk1_Colon
14	1e−01	470 / 9470	Quies3_Colon
15	1e−01	43 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
16	2e−01	5 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
17	2e−01	35 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
18	2e−01	158 / 3122	TxEnhG1_Colon
19	2e−01	3 / 36	Ang_CRC_Hypomethylated
20	3e−01	4 / 55	Marisa_CRC−cluster−e

Disease

Rank	p−value	#in/all	Geneset
1	0.5	29 / 608	GUDJ_psoriasis up
2	0.7	1 / 22	BCHETNIA_EBM up
3	0.8	1 / 37	BCHETNIA_EBM−DM up
4	1.0	11 / 399	GUDJ_psoriasis down
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	6e−04	14 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	6e−03	8 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
3	2e−02	14 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
4	3e−02	2 / 6	Martinez_Glio_hypometh
5	6e−02	52 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
6	9e−02	11 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
7	9e−02	5 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
8	1e−01	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
9	1e−01	9 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
10	1e−01	2 / 14	Christensen_hypermethylated_in_ependymoma
11	2e−01	5 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
12	2e−01	5 / 61	Christensen_hypermethylated_in_primary_glioblastoma
13	2e−01	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
14	2e−01	1 / 5	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
15	2e−01	8 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	2e−01	4 / 53	Gorovets_LGG_EPL_subclass
17	3e−01	4 / 59	Christensen_hypomethylated_in_primary_glioblastoma
18	3e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
19	3e−01	47 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
20	3e−01	17 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−13	77 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
2	2e−09	60 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	3e−08	84 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	2e−07	35 / 282	MANALO_HYPOXIA_DN
5	4e−07	68 / 754	MARTENS_TRETINOIN_RESPONSE_DN
6	5e−07	29 / 216	KAUFFMANN_DNA_REPAIR_GENES
7	9e−06	34 / 316	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	1e−05	30 / 263	LU_EZH2_TARGETS_UP
9	1e−05	16 / 95	REACTOME_CHROMOSOME_MAINTENANCE
10	2e−05	68 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
11	3e−05	11 / 52	REACTOME_TELOMERE_MAINTENANCE
12	4e−05	10 / 45	PID_FANCONI_PATHWAY
13	5e−05	45 / 505	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
14	9e−05	15 / 101	REACTOME_DNA_REPAIR
15	9e−05	23 / 200	SANSOM_APC_TARGETS_REQUIRE_MYC
16	1e−04	20 / 163	REACTOME_TRANSCRIPTION
17	2e−04	34 / 366	REACTOME_CELL_CYCLE
18	2e−04	7 / 27	REACTOME_EXTENSION_OF_TELOMERES
19	4e−04	26 / 262	ZHANG_TLX_TARGETS_60HR_DN
20	4e−04	16 / 128	SABATES_COLORECTAL_ADENOMA_UP

HM

Rank	p−value	#in/all	Geneset
1	0.004	15 / 146	HALLMARK_DNA_REPAIR
2	0.013	17 / 196	HALLMARK_G2M_CHECKPOINT
3	0.143	5 / 58	HALLMARK_MYC_TARGETS_V2
4	0.234	12 / 197	HALLMARK_E2F_TARGETS
5	0.259	3 / 37	HALLMARK_PANCREAS_BETA_CELLS
6	0.269	8 / 128	HALLMARK_SPERMATOGENESIS
7	0.349	11 / 198	HALLMARK_GLYCOLYSIS
8	0.579	9 / 193	HALLMARK_KRAS_SIGNALING_DN
9	0.695	4 / 98	HALLMARK_ANDROGEN_RESPONSE
10	0.709	8 / 193	HALLMARK_HEME_METABOLISM
11	0.762	5 / 132	HALLMARK_COAGULATION
12	0.789	4 / 112	HALLMARK_BILE_ACID_METABOLISM
13	0.821	7 / 193	HALLMARK_XENOBIOTIC_METABOLISM
14	0.829	1 / 36	HALLMARK_ANGIOGENESIS
15	0.844	7 / 199	HALLMARK_MTORC1_SIGNALING
16	0.860	2 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	0.865	5 / 154	HALLMARK_FATTY_ACID_METABOLISM
18	0.872	3 / 102	HALLMARK_PEROXISOME
19	0.876	3 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
20	0.895	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.4	5 / 91	DUMEAUX_Smoking enriched genes
3	0.6	1 / 17	DUMEAUX_High bmi enriched genes
4	0.8	1 / 33	DUMEAUX_Fasting enriched genes
5	1.0	0 / 11	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 11	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−11	84 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	2e−11	84 / 811	WIRTH_lymphoma937_spot D
3	6e−09	34 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
4	1e−07	476 / 8358	HOPP_Active_promoter
5	2e−07	32 / 240	WIRTH_lymphoma937_spot B
6	7e−04	405 / 7491	HOPP_Txn_elongation
7	1e−03	88 / 1333	SPANG_BCR UP
8	5e−03	428 / 8147	HOPP_Weak_promoter
9	3e−02	14 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
10	7e−02	13 / 171	WIRTH_lymphoma937_spot C
11	2e−01	2 / 18	Aukema_BCL2 UP_BCL6 DN
12	2e−01	2 / 19	DAVE_c−myc BL UP
13	2e−01	6 / 87	Aukema_BCL2 DN_BCL6 UP
14	3e−01	1 / 6	MASCQUE_mBL UP
15	3e−01	2 / 21	Subero_MCL_hyper_meth
16	3e−01	7 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
17	3e−01	7 / 116	WIRTH_lymphoma937_spot MM
18	4e−01	3 / 50	Subero_B−ALL_hyper_meth
19	4e−01	1 / 12	DAVE_BL UP
20	5e−01	5 / 94	Subero_T−ALL_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	7e−06	18 / 113	methyltransferase activity
2	2e−05	10 / 41	tRNA binding
3	5e−05	8 / 29	nucleotidyltransferase activity
4	2e−03	7 / 37	DNA−dependent ATPase activity
5	2e−03	5 / 20	S−adenosylmethionine−dependent methyltransferase activity
6	2e−03	6 / 29	DNA−directed DNA polymerase activity
7	3e−03	4 / 13	pseudouridine synthase activity
8	6e−03	5 / 25	histone−lysine N−methyltransferase activity
9	6e−03	4 / 16	exonuclease activity
10	8e−03	8 / 61	damaged DNA binding
11	9e−03	4 / 18	RNA polymerase III activity
12	1e−02	4 / 19	FK506 binding
13	1e−02	6 / 41	4 iron, 4 sulfur cluster binding
14	1e−02	14 / 151	serine−type endopeptidase activity
15	1e−02	5 / 31	iron−sulfur cluster binding
16	2e−02	4 / 21	lyase activity
17	2e−02	3 / 12	four−way junction DNA binding
18	2e−02	3 / 12	protein−lysine N−methyltransferase activity
19	2e−02	3 / 13	mannosyltransferase activity
20	3e−02	66 / 1091	poly(A) RNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.1	2 / 14	hsa−miR−147b
2	0.2	4 / 44	hsa−miR−483−5p
3	0.2	4 / 44	hsa−miR−661
4	0.2	3 / 32	hsa−miR−631
5	0.2	4 / 49	hsa−miR−1291
6	0.2	2 / 18	hsa−miR−564
7	0.3	3 / 37	hsa−miR−588
8	0.3	4 / 58	hsa−miR−409−5p
9	0.3	2 / 24	hsa−miR−1225−5p
10	0.4	4 / 65	hsa−miR−612
11	0.4	1 / 11	hsa−miR−487b
12	0.4	4 / 69	hsa−miR−518c*
13	0.4	2 / 30	hsa−miR−486−5p
14	0.5	4 / 72	hsa−miR−1266
15	0.5	2 / 32	hsa−miR−654−5p
16	0.5	1 / 13	hsa−miR−1249
17	0.5	4 / 77	hsa−miR−939
18	0.5	2 / 36	hsa−miR−1287
19	0.5	2 / 36	hsa−miR−34c−3p
20	0.5	1 / 16	hsa−miR−891a

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	3e−09	125 / 1549	ICGC_Myc_targets
2	5e−07	277 / 4470	ICGC_Creb1_targets
3	8e−07	113 / 1503	ICGC_Six5_targets
4	2e−06	272 / 4436	ICGC_Zeb1_targets
5	3e−06	329 / 5578	ICGC_Stat5_targets
6	6e−06	313 / 5308	ICGC_Tcf12_targets
7	8e−06	156 / 2342	ICGC_GabpPcr2_targets
8	9e−06	305 / 5173	ICGC_Taf1_targets
9	3e−05	313 / 5393	ICGC_Sp1_targets
10	6e−05	107 / 1547	ICGC_Ets1_targets
11	8e−05	151 / 2354	ICGC_SrfV0416101_targets
12	1e−04	248 / 4230	ICGC_Nfatc1_targets
13	2e−04	315 / 5552	ICGC_Pol24_targets
14	2e−04	345 / 6157	ICGC_Tcf3_targets
15	2e−04	59 / 766	ICGC_Atf3_targets
16	3e−04	311 / 5526	ICGC_Pmlsc71910_targets
17	3e−04	89 / 1294	KIM_MYC targets
18	3e−04	377 / 6862	ICGC_Elf1_targets
19	4e−04	350 / 6322	ICGC_Pol2_targets
20	4e−04	334 / 6005	ICGC_Mta3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.5	2 / 33	VAQUERIZAS_Liver
2	0.5	1 / 16	VAQUERIZAS_Fetal liver
3	0.6	1 / 18	VAQUERIZAS_Pancreas
4	0.6	2 / 41	VAQUERIZAS_Testis
5	0.6	7 / 155	VAQUERIZAS_General
6	0.6	1 / 20	VAQUERIZAS_Bone marrow
7	0.6	2 / 45	VAQUERIZAS_Placenta
8	0.7	1 / 24	VAQUERIZAS_Trachea
9	0.9	1 / 42	VAQUERIZAS_Thymus
10	1.0	0 / 41	VAQUERIZAS_Fetal brain
11	1.0	0 / 37	VAQUERIZAS_Prostate
12	1.0	0 / 30	VAQUERIZAS_Smooth muscle
13	1.0	0 / 49	VAQUERIZAS_Uterus
14	1.0	0 / 12	VAQUERIZAS_Kidney
15	1.0	0 / 25	VAQUERIZAS_Spinal cord
16	1.0	0 / 46	VAQUERIZAS_Whole brain
17	1.0	0 / 42	VAQUERIZAS_Thyroid
18	1.0	0 / 67	VAQUERIZAS_Whole blood
19	1.0	0 / 7	VAQUERIZAS_Appendix
20	1.0	0 / 31	VAQUERIZAS_Fetal lung

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	16 / 202	WIRTH_Testis
2	0.16	2 / 15	WIRTH_Cerebellum
3	0.25	1 / 6	WIRTH_Pituitary gland
4	0.26	4 / 54	WIRTH_Pancreas
5	0.44	1 / 12	WIRTH_Lymphocytes
6	0.47	1 / 13	WIRTH_Globus pallidus
7	0.47	6 / 115	WIRTH_Liver
8	0.50	1 / 14	WIRTH_B−cells
9	0.50	1 / 14	WIRTH_Bone marrow
10	0.64	6 / 137	WIRTH_Mucosa
11	0.97	7 / 259	PALMER_Granulocytes signature up
12	0.97	3 / 141	WIRTH_Muscle
13	0.98	1 / 82	WIRTH_Homeostasis
14	1.00	11 / 476	WIRTH_Nervous System
15	1.00	1 / 140	PALMER_T−Cell signature up
16	1.00	8 / 427	WIRTH_Immune system
17	1.00	1 / 208	PALMER_B−Cell signature up
18	1.00	0 / 13	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_Prim. lymphoid organs
20	1.00	0 / 12	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	64 / 1343	LU_BPDE 1h DN
2	0.8	243 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

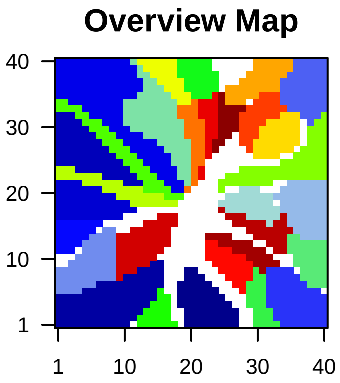
Correlation Clusters

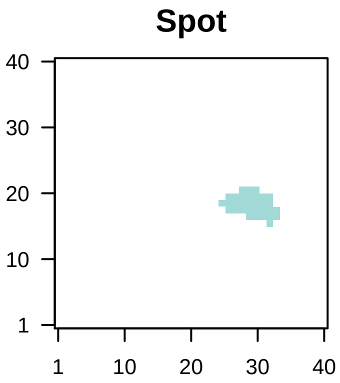
Spot Summary: S

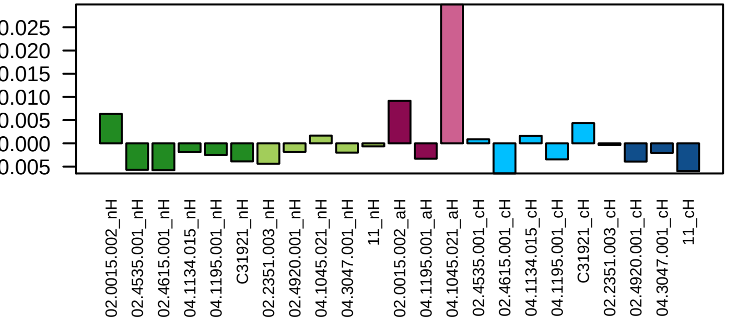
metagenes = 32
genes = 390

<r> metagenes = 0.93
<r> genes = 0.44
beta: r2= 0 / log p= −0.05

samples with spot = 0 (0 %)





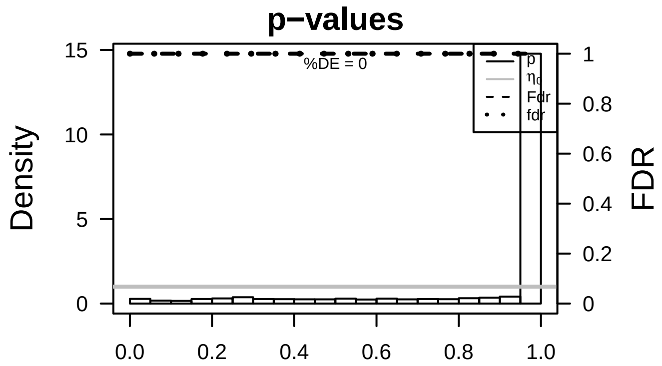


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.16	−0.04	0.74	NSUN6	NOP2/Sun domain family, member 6 [Source:HGNC Symbol;
2	ENSG000002	0.15	−0.05	0.86		MROH7−TTC4 readthrough (NMD candidate) [Source:HGNC
3	ENSG000001	0.14	−0.06	0.77	GALNT10	polypeptide N−acetylgalactosaminyltransferase 10 [Source:H
4	ENSG000001	0.14	−0.07	0.51	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4 [Source:HGN
5	ENSG000001	0.14	−0.04	0.68	MMEL1	membrane metallo−endopeptidase−like 1 [Source:HGNC Syr
6	ENSG000001	0.13	−0.03	0.79	TMEM178A	transmembrane protein 178A [Source:HGNC Symbol;Acc:HG
7	ENSG000001	0.12	−0.03	0.76		
8	ENSG000001	0.11	−0.02	0.82	ADAMTSL5	ADAMTS−like 5 [Source:HGNC Symbol;Acc:HGNC:27912]
9	ENSG000001	0.11	−0.1	0.64	ECHDC2	enoyl CoA hydratase domain containing 2 [Source:HGNC Syr
10	ENSG000001	0.1	−0.02	0.82	C6orf52	chromosome 6 open reading frame 52 [Source:HGNC Symbo
11	ENSG000001	0.1	−0.01	0.72	SERPINA4	serpin peptidase inhibitor, clade A (alpha−1 antiproteinase, ar
12	ENSG000001	0.1	−0.04	0.67	SAMD14	sterile alpha motif domain containing 14 [Source:HGNC Syml
13	ENSG000002	0.1	−0.03	0.73	AMY2A	amylase, alpha 2A (pancreatic) [Source:HGNC Symbol;Acc:H
14	ENSG000001	0.1	−0.02	0.97	DCST2	DC−STAMP domain containing 2 [Source:HGNC Symbol;Acc
15	ENSG000001	0.1	−0.06	0.67	STK25	serine/threonine kinase 25 [Source:HGNC Symbol;Acc:HGN
16	ENSG000001	0.09	−0.04	0.88	ZNF789	zinc finger protein 789 [Source:HGNC Symbol;Acc:HGNC:27
17	ENSG000001	0.09	−0.03	0.77	RNF123	ring finger protein 123 [Source:HGNC Symbol;Acc:HGNC:21
18	ENSG000002	0.09	−0.04	0.58	COLCA2	colorectal cancer associated 2 [Source:HGNC Symbol;Acc:H
19	ENSG000001	0.09	−0.02	0.43	GALNT14	polypeptide N−acetylgalactosaminyltransferase 14 [Source:H
20	ENSG000000	0.09	−0.01	0.8	TNMD	tenomodulin [Source:HGNC Symbol;Acc:HGNC:17757]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−06	91 / 2947	Colon	ReprPCWk_Colon
2	8e−06	99 / 3406	Colon	ReprPC_Colon
3	9e−06	4 / 8	GSEA	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
4	2e−05	8 / 60	Colon	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	3e−05	22 / 431	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
6	1e−04	63 / 2041	Colon	EnhP_Colon
7	2e−04	13 / 202	Tissu	WIRTH_Testis
8	4e−04	4 / 19	MF	cation binding
9	4e−04	4 / 19	CC	sperm principal piece
10	4e−04	10 / 142	CC	cilium
11	6e−04	83 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
12	8e−04	3 / 10	Colon	Juehling_HNPCC−mutated−in−5
13	1e−03	6 / 62	GSEA	MIKKELSEN_MEF_LCP_WITH_H3K27ME3
14	1e−03	44 / 1425	Chr	Chr 19
15	1e−03	4 / 26	GSEA	REACTOME_STRIATED_MUSCLE_CONTRACTION
16	2e−03	15 / 326	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	2e−03	5 / 46	GSEA	DOANE_BREAST_CANCER_ESR1_DN
18	2e−03	6 / 68	CC	keratin filament
19	2e−03	37 / 1178	Colon	ZNF_Colon
20	3e−03	39 / 1281	Colon	HetRpts_Colon
21	3e−03	26 / 754	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
22	3e−03	51 / 1798	TF	HEBENSTREIT_low expression TF
23	3e−03	5 / 52	Colon	Pentrack_CRC_TCGA_corr_S_normal_DN
24	3e−03	53 / 1890	Brain	Overlap_fetal_midbrain_TssF
25	3e−03	42 / 1418	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
26	4e−03	6 / 78	BP	protein O−linked glycosylation
27	4e−03	3 / 17	MF	sodium channel activity
28	4e−03	4 / 34	GSEA	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP
29	4e−03	22 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
30	5e−03	4 / 36	BP	muscle filament sliding
31	5e−03	46 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
32	5e−03	2 / 6	GSEA	WEBER_METHYLATED_LCP_IN_SPERM_DN
33	5e−03	2 / 6	GSEA	BERGER_MBD2_TARGETS
34	6e−03	33 / 1084	Brain	Overlap_fetal_midbrain_EnhG
35	6e−03	72 / 2820	Brain	Mid_Frontal_Lobe_HetRpts
36	7e−03	7 / 117	BP	cytoskeleton organization
37	8e−03	48 / 1753	Colon	Het_Colon
38	8e−03	3 / 22	BP	gamete generation
39	8e−03	4 / 42	BP	fertilization
40	9e−03	3 / 23	GSEA	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.7	2 / 123	HORVATH_aging_genes meth DOWN
2	1.0	0 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.004	6 / 78	protein O−linked glycosylation
2	0.005	4 / 36	muscle filament sliding
3	0.007	7 / 117	cytoskeleton organization
4	0.008	3 / 22	gamete generation
5	0.008	4 / 42	fertilization
6	0.011	4 / 45	social behavior
7	0.011	7 / 126	calcium ion transmembrane transport
8	0.015	3 / 27	bile acid and bile salt transport
9	0.015	2 / 10	histone monoubiquitination
10	0.015	2 / 10	protein deacetylation
11	0.015	2 / 10	sexual reproduction
12	0.018	4 / 52	O−glycan processing
13	0.019	3 / 30	sarcomere organization
14	0.021	3 / 31	associative learning
15	0.021	2 / 12	auditory receptor cell stereocilium organization
16	0.021	2 / 12	sensory perception
17	0.021	2 / 12	sperm−egg recognition
18	0.021	2 / 12	sulfate transmembrane transport
19	0.023	3 / 32	sensory perception of taste
20	0.025	2 / 13	ammonium transmembrane transport

Brain

Rank	p−value	#in/all	Geneset
1	0.003	53 / 1890	Overlap_fetal_midbrain_TssF
2	0.006	33 / 1084	Overlap_fetal_midbrain_EnhG
3	0.006	72 / 2820	Mid_Frontal_Lobe_HetRpts
4	0.018	40 / 1478	Overlap_fetal_midbrain_TxTrans
5	0.029	44 / 1713	Mid_Frontal_Lobe_ReprPCWk
6	0.037	30 / 1108	Overlap_fetal_midbrain_TssA
7	0.114	17 / 641	Mid_Frontal_Lobe_EnhP
8	0.145	18 / 712	Overlap_fetal_midbrain_EnhP
9	0.159	9 / 317	Mid_Frontal_Lobe_Tx
10	0.169	32 / 1394	Mid_Frontal_Lobe_Quies
11	0.202	29 / 1279	Overlap_fetal_midbrain_Enh
12	0.239	54 / 2549	Fetal_TssF
13	0.266	13 / 552	Fetal_Tx
14	0.289	6 / 232	Fetal_ReprPC
15	0.292	54 / 2603	Fetal_TxTrans
16	0.352	20 / 940	Mid_Frontal_Lobe_Enh
17	0.527	8 / 408	Mid_Frontal_Lobe_TxTrans
18	0.586	15 / 805	Mid_Frontal_Lobe_EnhG
19	0.607	2 / 106	Overlap_fetal_midbrain_Tx
20	0.652	24 / 1327	Mid_Frontal_Lobe_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	0.18	2 / 40	PanCan_HK_geneset_nanostring
3	0.25	1 / 15	GENTLES_modul10
4	0.27	1 / 16	LIU_LIVER_CANCER
5	0.27	1 / 16	WANG_ER_UP
6	0.42	1 / 28	PanCan_HH_geneset_nanostring
7	0.78	1 / 78	PanCan_Wnt_geneset_nanostring
8	0.81	1 / 86	PanCan_JAK−ST_geneset_nanostring
9	0.93	1 / 140	PanCan_RAS_geneset_nanostring
10	0.95	1 / 152	PanCan_MAPK_geneset_nanostring
11	0.98	1 / 198	PanCan_PI3K_geneset_nanostring
12	0.99	2 / 324	SPANG_BCL6−index2
13	0.99	0 / 16	LIU_PROSTATE_CANCER_DN
14	1.00	1 / 550	Lembcke_Normal vs Adenoma
15	1.00	1 / 574	Lembcke_Colonic Inflammation
16	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
17	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
18	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	1.00	0 / 15	LIU_BREAST_CANCER
20	1.00	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 19	sperm principal piece
2	4e−04	10 / 142	cilium
3	2e−03	6 / 68	keratin filament
4	1e−02	3 / 27	stereocilium
5	1e−02	2 / 10	sperm midpiece
6	1e−02	2 / 10	striated muscle thin filament
7	2e−02	37 / 1374	extracellular region
8	2e−02	2 / 13	condensed nuclear chromosome, centromeric region
9	3e−02	2 / 14	nBAF complex
10	3e−02	4 / 61	motile cilium
11	4e−02	8 / 198	postsynaptic membrane
12	4e−02	2 / 17	acrosomal membrane
13	5e−02	2 / 19	intraciliary transport particle B
14	5e−02	11 / 329	neuronal cell body
15	6e−02	3 / 46	brush border membrane
16	6e−02	3 / 47	axon terminus
17	7e−02	2 / 22	I band
18	7e−02	4 / 80	perikaryon
19	7e−02	2 / 23	calcium channel complex
20	7e−02	2 / 23	dynein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.001	44 / 1425	Chr 19
2	0.015	21 / 651	Chr 8
3	0.067	30 / 1172	Chr 11
4	0.125	44 / 1920	Chr 1
5	0.201	20 / 847	Chr 16
6	0.297	19 / 859	Chr 7
7	0.398	13 / 613	Chr 14
8	0.425	6 / 272	Chr 18
9	0.443	12 / 582	Chr 15
10	0.445	21 / 1043	Chr 3
11	0.497	24 / 1228	Chr 2
12	0.510	14 / 715	Chr 10
13	0.603	8 / 436	Chr 22
14	0.714	3 / 191	Chr 21
15	0.789	8 / 522	Chr 20
16	0.837	17 / 1083	Chr 17
17	0.852	11 / 745	Chr 9
18	0.863	4 / 318	Chr 13
19	0.903	10 / 735	Chr 4
20	0.946	11 / 862	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	91 / 2947	ReprPCWk_Colon
2	8e−06	99 / 3406	ReprPC_Colon
3	2e−05	8 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
4	1e−04	63 / 2041	EnhP_Colon
5	8e−04	3 / 10	Juehling_HNPCC−mutated−in−5
6	2e−03	37 / 1178	ZNF_Colon
7	3e−03	39 / 1281	HetRpts_Colon
8	3e−03	26 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	3e−03	5 / 52	Pentrack_CRC_TCGA_corr_S_normal_DN
10	4e−03	22 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	8e−03	48 / 1753	Het_Colon
12	1e−02	113 / 4879	Quies1_Colon
13	1e−02	21 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	3e−02	32 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	6e−02	4 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
16	7e−02	12 / 389	K9K27me3_Colon
17	7e−02	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
18	8e−02	8 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
19	2e−01	13 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
20	2e−01	1 / 10	Juehling−MSI−enriched−in−7

Disease

Rank	p−value	#in/all	Geneset
1	0.2	10 / 399	GUDJ_psoriasis down
2	0.5	1 / 37	BCHETNIA_EBM−DM up
3	0.6	11 / 608	GUDJ_psoriasis up
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	6e−04	83 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	1e−02	3 / 27	Barbus_GBM_STS_vs._LTS
3	2e−02	3 / 30	Gorovets_LGG_NB_subclass
4	3e−02	26 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
5	7e−02	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
6	1e−01	3 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	1e−01	14 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
8	1e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
9	3e−01	1 / 16	VERHAAK_NL subtype
10	3e−01	4 / 137	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
11	3e−01	2 / 54	Hopp_Sturm_GBM_Epi3_B1_G34_DN
12	3e−01	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
13	3e−01	10 / 434	Down_a
14	3e−01	4 / 150	Sturm_GBM_Meth_overexpression_B_adult_UP
15	3e−01	3 / 106	WIRTH_Normal Brain
16	3e−01	3 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
17	4e−01	1 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
18	5e−01	2 / 81	GIEZELT_GBM_STS_up_VS_LTS
19	5e−01	2 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
20	5e−01	9 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−06	4 / 8	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
2	3e−05	22 / 431	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
3	1e−03	6 / 62	MIKKELSEN_MEF_LCP_WITH_H3K27ME3
4	1e−03	4 / 26	REACTOME_STRIATED_MUSCLE_CONTRACTION
5	2e−03	15 / 326	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
6	2e−03	5 / 46	DOANE_BREAST_CANCER_ESR1_DN
7	3e−03	42 / 1418	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
8	4e−03	4 / 34	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP
9	5e−03	46 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
10	5e−03	2 / 6	WEBER_METHYLATED_LCP_IN_SPERM_DN
11	5e−03	2 / 6	BERGER_MBD2_TARGETS
12	9e−03	3 / 23	STAMBOLSKY_RESPONSE_TO_VITAMIN_D3_DN
13	1e−02	2 / 8	KHETCHOUMIAN_TRIM24_TARGETS_DN
14	1e−02	4 / 44	REACTOME_MUSCLE_CONTRACTION
15	1e−02	6 / 97	REN_ALVEOLAR_RHABDOMYOSARCOMA_UP
16	1e−02	3 / 25	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN
17	1e−02	2 / 9	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS
18	1e−02	2 / 9	WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN
19	1e−02	4 / 49	KEGG_STARCH_AND_SUCROSE_METABOLISM
20	1e−02	3 / 27	ABE_VEGFA_TARGETS_30MIN

HM

Rank	p−value	#in/all	Geneset
1	0.3	3 / 102	HALLMARK_PEROXISOME
2	0.3	5 / 193	HALLMARK_KRAS_SIGNALING_DN
3	0.3	5 / 195	HALLMARK_MYOGENESIS
4	0.4	3 / 112	HALLMARK_BILE_ACID_METABOLISM
5	0.4	3 / 128	HALLMARK_SPERMATOGENESIS
6	0.6	1 / 44	HALLMARK_APICAL_SURFACE
7	0.6	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	0.7	3 / 193	HALLMARK_HEME_METABOLISM
9	0.7	3 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.7	3 / 198	HALLMARK_GLYCOLYSIS
11	0.8	2 / 154	HALLMARK_FATTY_ACID_METABOLISM
12	0.9	1 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	0.9	2 / 196	HALLMARK_P53_PATHWAY
14	0.9	1 / 132	HALLMARK_COAGULATION
15	0.9	1 / 140	HALLMARK_UV_RESPONSE_DN
16	1.0	1 / 155	HALLMARK_UV_RESPONSE_UP
17	1.0	1 / 189	HALLMARK_KRAS_SIGNALING_UP
18	1.0	1 / 190	HALLMARK_APICAL_JUNCTION
19	1.0	1 / 192	HALLMARK_COMPLEMENT
20	1.0	1 / 193	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 33	DUMEAUX_Fasting enriched genes
2	1.0	0 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	16 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
2	0.01	116 / 5039	HOPP_Repressed
3	0.02	16 / 458	WIRTH_lymphoma937_spot I
4	0.05	79 / 3457	HOPP_Heterochrom
5	0.10	60 / 2658	HOPP_Repetitive
6	0.29	4 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
7	0.30	4 / 144	WIRTH_lymphoma937_spot G
8	0.42	2 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
9	0.42	2 / 75	WIRTH_lymphoma937_spot IM
10	0.50	1 / 36	Subero_MM_hyper_meth
11	0.61	1 / 48	Subero_INT_hypo_meth
12	0.61	1 / 49	Subero_DLBCL_hypo_meth
13	0.70	1 / 62	Subero_mBL_hyper_meth
14	0.71	1 / 63	SPANG_BAFF 9hrs DN
15	0.72	1 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
16	0.73	1 / 67	LEE_Developmental_regulators
17	0.77	50 / 2838	HOPP_Poised_promoter
18	0.78	1 / 79	SPANG_LPS 6hrs DN
19	0.80	5 / 347	WIRTH_lymphoma937_spot H
20	0.81	6 / 414	TARTE_Mature plasma cell signature

MF

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 19	cation binding
2	4e−03	3 / 17	sodium channel activity
3	1e−02	22 / 667	molecular_function
4	2e−02	2 / 12	secondary active sulfate transmembrane transporter activity
5	2e−02	2 / 13	calcium activated cation channel activity
6	2e−02	2 / 13	NAD+ binding
7	3e−02	2 / 14	intracellular calcium activated chloride channel activity
8	3e−02	2 / 14	tropomyosin binding
9	3e−02	51 / 2040	metal ion binding
10	3e−02	2 / 15	oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as
11	4e−02	2 / 16	acyl−CoA dehydrogenase activity
12	4e−02	5 / 96	structural constituent of cytoskeleton
13	5e−02	2 / 19	microfilament motor activity
14	6e−02	2 / 20	polypeptide N−acetylgalactosaminyltransferase activity
15	6e−02	2 / 21	inward rectifier potassium channel activity
16	6e−02	2 / 21	lyase activity
17	7e−02	5 / 113	actin filament binding
18	7e−02	3 / 49	SNARE binding
19	7e−02	2 / 23	oxidoreductase activity, acting on the CH−CH group of donors
20	8e−02	2 / 25	substrate−specific transmembrane transporter activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.1	3 / 57	hsa−miR−940
2	0.2	2 / 43	hsa−miR−192
3	0.2	2 / 44	hsa−miR−483−5p
4	0.3	1 / 20	hsa−miR−380*
5	0.4	3 / 113	hsa−miR−199a−5p
6	0.4	1 / 25	hsa−miR−609
7	0.4	1 / 25	hsa−miR−99b
8	0.4	1 / 26	hsa−miR−99a
9	0.4	1 / 26	hsa−miR−100
10	0.4	2 / 72	hsa−miR−1266
11	0.4	2 / 73	hsa−miR−127−5p
12	0.4	2 / 77	hsa−miR−939
13	0.4	1 / 30	hsa−miR−193a−5p
14	0.5	1 / 31	hsa−miR−1293
15	0.5	1 / 34	hsa−miR−1178
16	0.5	1 / 35	hsa−miR−615−5p
17	0.5	1 / 35	hsa−miR−1274b
18	0.5	1 / 37	hsa−miR−770−5p
19	0.5	1 / 38	hsa−miR−215
20	0.5	1 / 38	hsa−miR−760

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.003	51 / 1798	HEBENSTREIT_low expression TF
2	0.267	1 / 16	NOWICK_TF
3	0.268	17 / 745	ICGC_NrsfPcr2_targets
4	0.298	32 / 1503	ICGC_Six5_targets
5	0.336	71 / 3511	ICGC_Rad21_targets
6	0.498	122 / 6322	ICGC_Pol2_targets
7	0.525	45 / 2342	ICGC_GabpPcr2_targets
8	0.602	28 / 1506	ICGC_Usf1_targets
9	0.655	120 / 6406	ICGC_Pax5_targets
10	0.659	28 / 1547	ICGC_Ets1_targets
11	0.666	115 / 6157	ICGC_Tcf3_targets
12	0.703	134 / 7202	ICGC_Runx3_targets
13	0.716	13 / 766	ICGC_Atf3_targets
14	0.821	40 / 2354	ICGC_SrfV0416101_targets
15	0.830	99 / 5552	ICGC_Pol24_targets
16	0.845	9 / 619	ICGC_RxraPcr1_targets
17	0.846	46 / 2719	ICGC_Pbx3_targets
18	0.869	56 / 3305	ICGC_BatfPcr1_targets
19	0.870	98 / 5578	ICGC_Stat5_targets
20	0.884	94 / 5393	ICGC_Sp1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 41	VAQUERIZAS_Fetal brain
2	0.3	1 / 16	VAQUERIZAS_Fetal liver
3	0.3	1 / 16	VAQUERIZAS_Fetal thyroid
4	0.3	1 / 17	VAQUERIZAS_Salivary gland
5	0.3	1 / 19	VAQUERIZAS_Heart
6	0.4	1 / 23	VAQUERIZAS_Pituitary
7	0.4	1 / 24	VAQUERIZAS_Trachea
8	0.4	1 / 25	VAQUERIZAS_Spinal cord
9	0.5	1 / 33	VAQUERIZAS_Liver
10	0.5	1 / 37	VAQUERIZAS_Prostate
11	0.5	1 / 41	VAQUERIZAS_Testis
12	0.6	1 / 42	VAQUERIZAS_Thyroid
13	0.6	1 / 45	VAQUERIZAS_Placenta
14	0.6	1 / 46	VAQUERIZAS_Whole brain
15	1.0	1 / 155	VAQUERIZAS_General
16	1.0	0 / 30	VAQUERIZAS_Smooth muscle
17	1.0	0 / 49	VAQUERIZAS_Uterus
18	1.0	0 / 12	VAQUERIZAS_Kidney
19	1.0	0 / 42	VAQUERIZAS_Thymus
20	1.0	0 / 67	VAQUERIZAS_Whole blood

Tissue

Rank	p−value	#in/all	Geneset
1	2e−04	13 / 202	WIRTH_Testis
2	1e−02	4 / 47	WIRTH_Placenta
3	4e−02	2 / 16	WIRTH_Hippocampus
4	7e−02	5 / 115	WIRTH_Liver
5	1e−01	5 / 137	WIRTH_Mucosa
6	1e−01	5 / 141	WIRTH_Muscle
7	3e−01	2 / 54	WIRTH_Pancreas
8	5e−01	2 / 82	WIRTH_Homeostasis
9	7e−01	8 / 476	WIRTH_Nervous System
10	1e+00	1 / 259	PALMER_Granulocytes signature up
11	1e+00	0 / 6	WIRTH_Pituitary gland
12	1e+00	0 / 427	WIRTH_Immune system
13	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
14	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
15	1e+00	0 / 14	WIRTH_B−cells
16	1e+00	0 / 12	WIRTH_Tonsil
17	1e+00	0 / 14	WIRTH_Thymus
18	1e+00	0 / 12	WIRTH_Lymphocytes
19	1e+00	0 / 14	WIRTH_Bone marrow
20	1e+00	0 / 13	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	105 / 5285	LU_BPDE 0.005 DN
2	0.8	22 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

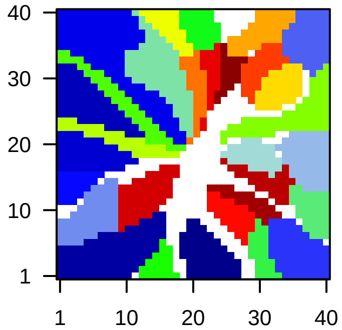
Spot Summary: T

metagenes = 35
genes = 463

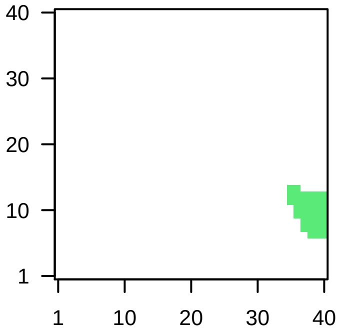
<r> metagenes = 0.96
<r> genes = 0.54
beta: r2= 0.11 / log p= −0.91

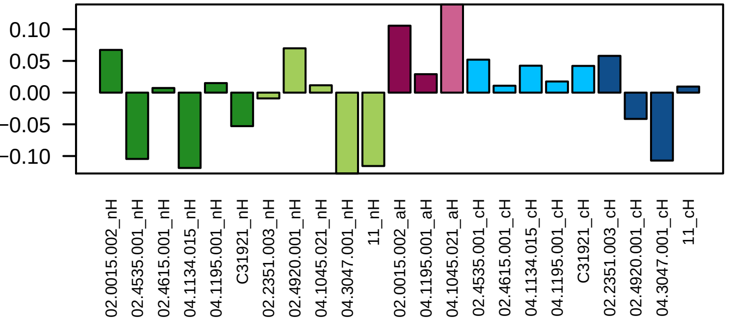
samples with spot = 6 (26.1 %)
MLH1_normHNPCC : 1 (16.7 %)
other_normHNPCC : 1 (20 %)
MLH1_adenomaHNPCC : 1 (50 %)
other_adenomaHNPCC : 1 (100 %)
MLH1_cancerHNPCC : 1 (20 %)
other_cancerHNPCC : 1 (25 %)

Overview Map



Spot





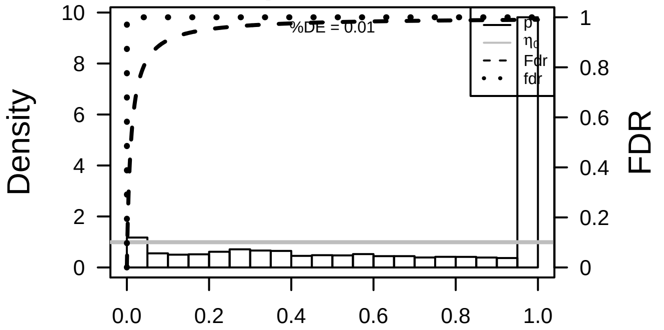
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.7	−0.03	0.41	CTAG2	cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
2	ENSG000001	0.65	−0.16	0.69	HOXB5	homeobox B5 [Source:HGNC Symbol;Acc:HGNC:5116]
3	ENSG000001	0.63	−0.26	0.78	ROMO1	reactive oxygen species modulator 1 [Source:HGNC Symbol;
4	ENSG000001	0.6	−0.09	0.61	FABP6	fatty acid binding protein 6, ileal [Source:HGNC Symbol;Acc:
5	ENSG000001	0.56	−0.24	0.57	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble [Source:HGNC
6	ENSG000000	0.5	−0.23	0.52	NOX1	NADPH oxidase 1 [Source:HGNC Symbol;Acc:HGNC:7889]
7	ENSG000001	0.5	−0.39	0.7	COX6B1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
8	ENSG000001	0.47	−0.18	0.59	SPDEF	SAM pointed domain containing ETS transcription factor [Sou
9	ENSG000001	0.46	−0.42	0.43	MAOA	monoamine oxidase A [Source:HGNC Symbol;Acc:HGNC:68
10	ENSG000001	0.46	−0.24	0.73	GJB1	gap junction protein, beta 1, 32kDa [Source:HGNC Symbol;A
11	ENSG000001	0.45	−0.26	0.73	LAMTOR4	late endosomal/lysosomal adaptor, MAPK and MTOR activat
12	ENSG000000	0.45	−0.2	0.62	CFTR	cystic fibrosis transmembrane conductance regulator (ATP−bi
13	ENSG000001	0.43	−0.33	0.55	MDK	midkine (neurite growth−promoting factor 2) [Source:HGNC S
14	ENSG000001	0.42	−0.35	0.77	ANXA2	annexin A2 [Source:HGNC Symbol;Acc:HGNC:537]
15	ENSG000001	0.41	−0.37	0.91	UQCRQ	ubiquinol−cytochrome c reductase, complex III subunit VII, 9.
16	ENSG000001	0.41	−0.23	0.65	HOXB9	homeobox B9 [Source:HGNC Symbol;Acc:HGNC:5120]
17	ENSG000001	0.41	−0.34	0.83	ECHS1	enoyl CoA hydratase, short chain, 1, mitochondrial [Source:H
18	ENSG000001	0.4	−0.26	0.72	FOXH1	forkhead box H1 [Source:HGNC Symbol;Acc:HGNC:3814]
19	ENSG000001	0.4	−0.27	0.96	NAPRT	nicotinate phosphoribosyltransferase [Source:HGNC Symbol;
20	ENSG000001	0.4	−0.25	0.69	UBXN11	UBX domain protein 11 [Source:HGNC Symbol;Acc:HGNC:3

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−33	320 / 8123	Colon	TssF_Colon
2	2e−29	173 / 3122	Colon	TxEnhG1_Colon
3	2e−25	165 / 3112	Colon	EnhA_Colon
4	3e−24	353 / 10475	Colon	TssA_Colon
5	7e−22	336 / 9930	Colon	Tx_Colon
6	4e−21	259 / 6761	Colon	TssD2_Colon
7	1e−20	39 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
8	5e−20	95 / 1441	CC	mitochondrion
9	2e−19	369 / 11791	Colon	Enh_Colon
10	3e−19	48 / 425	CC	mitochondrial inner membrane
11	1e−18	33 / 198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	1e−17	25 / 111	GSEA	KEGG_OXIDATIVE_PHOSPHORYLATION
13	1e−17	46 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
14	7e−16	22 / 96	BP	respiratory electron transport chain
15	1e−15	221 / 5889	Colon	EnhWk1_Colon
16	2e−15	25 / 136	BP	cellular metabolic process
17	5e−15	20 / 83	GSEA	MOOTHA_VOXPHOS
18	6e−15	84 / 1418	BP	small molecule metabolic process
19	1e−14	19 / 76	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
20	2e−14	22 / 111	GSEA	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSP
21	5e−14	61 / 877	Colon	TxEnhG2_Colon
22	1e−13	21 / 109	GSEA	KEGG_PARKINSONS_DISEASE
23	2e−13	25 / 167	GSEA	KEGG_HUNTINGTONS_DISEASE
24	5e−13	16 / 60	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
25	2e−12	23 / 151	GSEA	KEGG_ALZHEIMERS_DISEASE
26	5e−12	26 / 207	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
27	5e−12	37 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
28	7e−12	38 / 437	GSEA	MOOTHA_MITOCHONDRIA
29	9e−12	37 / 420	GSEA	MOOTHA_HUMAN_MITODB_6_2002
30	2e−11	294 / 9390	Colon	TxWk_Colon
31	2e−10	113 / 2638	CC	extracellular exosome
32	4e−10	36 / 459	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
33	9e−10	150 / 3977	Brain	Mid_Frontal_Lobe_ReprPC
34	9e−10	33 / 404	GSEA	MOOTHA_PGC
35	3e−09	20 / 165	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
36	1e−08	35 / 495	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_UP
37	2e−08	158 / 4436	TF	ICGC_Zeb1_targets
38	2e−08	17 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
39	4e−08	180 / 5308	TF	ICGC_Tcf12_targets
40	4e−08	111 / 2820	Brain	Mid_Frontal_Lobe_HetRpts

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 57	TESCHENDORFF_age_hypermethylated
2	0.8	2 / 123	HORVATH_aging_genes meth DOWN
3	0.9	2 / 144	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−16	22 / 96	respiratory electron transport chain
2	2e−15	25 / 136	cellular metabolic process
3	6e−15	84 / 1418	small molecule metabolic process
4	9e−08	11 / 57	hydrogen ion transmembrane transport
5	5e−05	7 / 41	mitochondrial electron transport, NADH to ubiquinone
6	2e−04	31 / 640	oxidation−reduction process
7	3e−04	6 / 38	cholesterol biosynthetic process
8	4e−04	4 / 15	fatty acid transport
9	5e−04	6 / 43	glycosphingolipid metabolic process
10	6e−04	4 / 17	mitochondrial ATP synthesis coupled proton transport
11	9e−04	5 / 32	response to axon injury
12	9e−04	4 / 19	2−oxoglutarate metabolic process
13	1e−03	11 / 152	cellular lipid metabolic process
14	1e−03	4 / 20	ATP synthesis coupled proton transport
15	1e−03	4 / 21	heme biosynthetic process
16	1e−03	3 / 10	mitochondrial calcium ion transport
17	3e−03	42 / 1118	metabolic process
18	3e−03	3 / 12	oxidative phosphorylation
19	3e−03	5 / 42	fatty acid beta−oxidation
20	4e−03	4 / 27	aerobic respiration

Brain

Rank	p−value	#in/all	Geneset
1	9e−10	150 / 3977	Mid_Frontal_Lobe_ReprPC
2	4e−08	111 / 2820	Mid_Frontal_Lobe_HetRpts
3	1e−06	121 / 3370	Mid_Frontal_Lobe_ZNF
4	6e−05	278 / 9923	Overlap_fetal_midbrain_K9K27me3
5	1e−04	39 / 865	Mid_Frontal_Lobe_Het
6	1e−03	290 / 10800	Overlap_fetal_midbrain_Quies
7	1e−02	66 / 2084	Mid_Frontal_Lobe_K9K27me3
8	1e−02	55 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	3e−02	86 / 2956	Fetal_TssA
10	3e−02	52 / 1680	Fetal_ReprPCWk
11	5e−02	38 / 1210	Fetal_TssP
12	1e−01	26 / 855	Overlap_fetal_midbrain_ZNF
13	3e−01	30 / 1108	Overlap_fetal_midbrain_TssA
14	3e−01	67 / 2603	Fetal_TxTrans
15	3e−01	63 / 2443	Fetal_Quies
16	3e−01	39 / 1478	Overlap_fetal_midbrain_TxTrans
17	4e−01	35 / 1394	Mid_Frontal_Lobe_Quies
18	4e−01	63 / 2549	Fetal_TssF
19	5e−01	3 / 106	Overlap_fetal_midbrain_Tx
20	6e−01	22 / 939	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	3 / 16	WANG_ER_UP
2	0.047	1 / 2	GENTLES_modul8
3	0.055	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	0.065	0 / 14	LIU_PROSTATE_CANCER_UP
5	0.112	2 / 24	PanCan_Notch_geneset_nanostring
6	0.128	3 / 52	KUIPER_MM poor survival
7	0.196	1 / 9	WANG_ER_DN
8	0.234	1 / 11	GENTLES_modul5
9	0.257	2 / 41	ZHANG_MM up
10	0.287	1 / 14	GENTLES_modul12
11	0.304	1 / 15	LIU_BREAST_CANCER
12	0.304	1 / 15	GENTLES_modul10
13	0.321	1 / 16	LIU_COMMON_CANCER_GENES
14	0.321	1 / 16	LIU_LIVER_CANCER
15	0.321	1 / 16	GENTLES_modul1
16	0.321	1 / 16	GENTLES_modul7
17	0.339	4 / 123	PanCan_Driver_Gene_geneset_nanostring
18	0.592	1 / 37	KUIPER_MM good survival
19	0.702	1 / 50	PanCan_DNARepair_geneset_nanostring
20	0.768	11 / 550	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	5e−20	95 / 1441	mitochondrion
2	3e−19	48 / 425	mitochondrial inner membrane
3	2e−10	113 / 2638	extracellular exosome
4	1e−05	20 / 277	mitochondrial matrix
5	7e−05	5 / 19	mitochondrial proton−transporting ATP synthase complex
6	8e−05	7 / 44	mitochondrial respiratory chain complex I
7	2e−04	16 / 235	lysosome
8	2e−04	35 / 767	endoplasmic reticulum membrane
9	6e−04	36 / 842	endoplasmic reticulum
10	1e−03	3 / 10	NADPH oxidase complex
11	1e−03	3 / 10	proton−transporting V−type ATPase, V0 domain
12	3e−03	3 / 13	mitochondrial respiratory chain
13	4e−03	9 / 130	mitochondrial outer membrane
14	6e−03	6 / 68	mitochondrial intermembrane space
15	7e−03	119 / 4052	integral component of membrane
16	1e−02	32 / 864	Golgi apparatus
17	1e−02	10 / 185	basolateral plasma membrane
18	2e−02	3 / 24	vesicle membrane
19	2e−02	7 / 117	cytoplasmic vesicle membrane
20	3e−02	3 / 27	cortical cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	38 / 847	Chr 16
2	7e−03	39 / 1083	Chr 17
3	4e−02	23 / 651	Chr 8
4	9e−02	42 / 1425	Chr 19
5	1e−01	23 / 745	Chr 9
6	2e−01	33 / 1172	Chr 11
7	4e−01	12 / 436	Chr 22
8	4e−01	22 / 859	Chr 7
9	5e−01	13 / 522	Chr 20
10	5e−01	5 / 191	Chr 21
11	6e−01	17 / 746	Chr X
12	6e−01	22 / 976	Chr 6
13	7e−01	16 / 735	Chr 4
14	8e−01	18 / 862	Chr 5
15	8e−01	5 / 272	Chr 18
16	9e−01	13 / 715	Chr 10
17	9e−01	39 / 1920	Chr 1
18	9e−01	5 / 318	Chr 13
19	9e−01	19 / 1017	Chr 12
20	9e−01	19 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−33	320 / 8123	TssF_Colon
2	2e−29	173 / 3122	TxEnhG1_Colon
3	2e−25	165 / 3112	EnhA_Colon
4	3e−24	353 / 10475	TssA_Colon
5	7e−22	336 / 9930	Tx_Colon
6	4e−21	259 / 6761	TssD2_Colon
7	2e−19	369 / 11791	Enh_Colon
8	1e−15	221 / 5889	EnhWk1_Colon
9	5e−14	61 / 877	TxEnhG2_Colon
10	2e−11	294 / 9390	TxWk_Colon
11	2e−02	10 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
12	2e−02	24 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	3e−02	25 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
14	3e−02	4 / 49	Marisa_CRC−cluster−f
15	3e−02	38 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
16	4e−02	4 / 55	Marisa_CRC−cluster−e
17	6e−02	2 / 17	TCGA−CRC_less−agressive−disease−markers
18	6e−02	243 / 9470	Quies3_Colon
19	8e−02	301 / 11968	TssWk_Colon
20	1e−01	4 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.1	19 / 608	GUDJ_psoriasis up
2	0.2	2 / 37	BCHETNIA_EBM−DM up
3	0.8	7 / 399	GUDJ_psoriasis down
4	1.0	0 / 22	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−05	10 / 92	laffaire_hypermeth_LGG_vs_control
2	1e−04	8 / 63	Stuehler_Proteins_up_in_STS
3	4e−04	9 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
4	5e−04	57 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	1e−03	11 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	3e−03	10 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	3e−03	9 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
8	8e−03	10 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
9	8e−03	6 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
10	9e−03	8 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
11	1e−02	5 / 58	OL vs. MOG− OL
12	1e−02	5 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
13	2e−02	5 / 61	Christensen_hypermethylated_in_primary_glioblastoma
14	2e−02	14 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	2e−02	6 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
16	5e−02	6 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
17	6e−02	16 / 436	Down_b
18	7e−02	6 / 119	GIEZELT_GBM_WT_up_VS_mut
19	7e−02	2 / 18	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
20	7e−02	3 / 40	Christensen_hypomethylated_in_ependymoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−20	39 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
2	1e−17	25 / 111	KEGG_OXIDATIVE_PHOSPHORYLATION
3	1e−17	46 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
4	5e−15	20 / 83	MOOTHA_VOXPHOS
5	1e−14	19 / 76	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
6	2e−14	22 / 111	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
7	1e−13	21 / 109	KEGG_PARKINSONS_DISEASE
8	2e−13	25 / 167	KEGG_HUNTINGTONS_DISEASE
9	5e−13	16 / 60	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
10	2e−12	23 / 151	KEGG_ALZHEIMERS_DISEASE
11	5e−12	26 / 207	WONG_MITOCHONDRIA_GENE_MODULE
12	5e−12	37 / 412	LIM_MAMMARY_STEM_CELL_DN
13	7e−12	38 / 437	MOOTHA_MITOCHONDRIA
14	9e−12	37 / 420	MOOTHA_HUMAN_MITODB_6_2002
15	4e−10	36 / 459	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
16	9e−10	33 / 404	MOOTHA_PGC
17	3e−09	20 / 165	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
18	1e−08	35 / 495	ENK_UV_RESPONSE_KERATINOCYTE_UP
19	2e−08	17 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
20	6e−08	16 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−18	33 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	3e−07	19 / 199	HALLMARK_ADIPOGENESIS
3	3e−04	14 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
4	7e−03	6 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	8e−03	11 / 196	HALLMARK_P53_PATHWAY
6	9e−03	11 / 199	HALLMARK_MTORC1_SIGNALING
7	1e−02	9 / 154	HALLMARK_FATTY_ACID_METABOLISM
8	2e−02	10 / 193	HALLMARK_XENOBIOTIC_METABOLISM
9	2e−02	10 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	3e−02	3 / 30	HALLMARK_NOTCH_SIGNALING
11	4e−02	6 / 102	HALLMARK_PEROXISOME
12	8e−02	7 / 157	HALLMARK_APOPTOSIS
13	9e−02	8 / 190	HALLMARK_APICAL_JUNCTION
14	1e−01	8 / 198	HALLMARK_GLYCOLYSIS
15	2e−01	4 / 94	HALLMARK_PROTEIN_SECRETION
16	2e−01	7 / 198	HALLMARK_HYPOXIA
17	2e−01	4 / 98	HALLMARK_ANDROGEN_RESPONSE
18	2e−01	4 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
19	3e−01	5 / 146	HALLMARK_DNA_REPAIR
20	3e−01	4 / 112	HALLMARK_BILE_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	5 / 91	DUMEAUX_Smoking enriched genes
2	0.32	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.34	1 / 17	DUMEAUX_High bmi enriched genes
4	1.00	0 / 11	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−04	233 / 8147	HOPP_Weak_promoter
2	5e−04	6 / 42	CARO_OxPhos_in_DLBCL_UP
3	5e−03	7 / 87	ROSOLOWSKI_red total
4	5e−03	13 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
5	9e−03	4 / 35	Subero_T−PLL_hypo_meth
6	1e−02	3 / 21	ROSOLOWSKI_red UP
7	4e−02	5 / 78	TARTE_Plasma cell signature
8	5e−02	218 / 8358	HOPP_Active_promoter
9	6e−02	6 / 116	WIRTH_lymphoma937_spot MM
10	6e−02	198 / 7592	HOPP_Strong_enhancer
11	7e−02	3 / 40	ROSOLOWSKI_blue DOWN
12	9e−02	16 / 466	SPANG_CD40 6hrs DN
13	1e−01	3 / 49	Subero_DLBCL_hypo_meth
14	1e−01	3 / 50	Subero_B−ALL_hyper_meth
15	1e−01	6 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
16	1e−01	6 / 144	WIRTH_lymphoma937_spot G
17	2e−01	4 / 87	Aukema_BCL2 DN_BCL6 UP
18	2e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
19	2e−01	3 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
20	2e−01	1 / 8	MASCQUE_GCB UP

MF

Rank	p−value	#in/all	Geneset
1	1e−07	8 / 26	cytochrome−c oxidase activity
2	5e−05	7 / 41	NADH dehydrogenase (ubiquinone) activity
3	7e−05	6 / 30	hydrogen ion transmembrane transporter activity
4	1e−03	4 / 21	calcium−dependent cysteine−type endopeptidase activity
5	2e−03	5 / 36	hydrolase activity, hydrolyzing O−glycosyl compounds
6	2e−03	3 / 11	NADH dehydrogenase activity
7	2e−03	3 / 11	transferase activity, transferring phosphorus−containing groups
8	4e−03	3 / 14	glutathione peroxidase activity
9	4e−03	19 / 407	catalytic activity
10	9e−03	27 / 693	protein homodimerization activity
11	9e−03	4 / 35	NADP binding
12	1e−02	4 / 39	Rac GTPase binding
13	1e−02	3 / 22	proton−transporting ATPase activity, rotational mechanism
14	2e−02	11 / 217	protein domain specific binding
15	2e−02	10 / 191	magnesium ion binding
16	2e−02	25 / 667	molecular_function
17	2e−02	3 / 24	glutathione transferase activity
18	2e−02	7 / 114	kinase activity
19	2e−02	22 / 578	identical protein binding
20	2e−02	2 / 10	carboxylic acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	3 / 31	hsa−miR−1293
2	0.05	6 / 108	hsa−miR−526b
3	0.07	3 / 39	hsa−miR−593
4	0.08	3 / 42	hsa−miR−525−3p
5	0.08	6 / 127	hsa−miR−204
6	0.10	2 / 23	hsa−miR−662
7	0.11	3 / 48	hsa−miR−524−3p
8	0.11	6 / 136	hsa−miR−200a
9	0.13	5 / 111	hsa−miR−211
10	0.13	4 / 81	hsa−miR−584
11	0.14	1 / 6	hsa−miR−523
12	0.14	2 / 27	hsa−miR−483−3p
13	0.15	4 / 86	hsa−miR−433
14	0.18	1 / 8	hsa−miR−886−3p
15	0.18	1 / 8	hsa−miR−566
16	0.18	2 / 32	hsa−miR−1237
17	0.18	2 / 32	hsa−miR−296−5p
18	0.18	4 / 93	hsa−miR−608
19	0.19	2 / 33	hsa−miR−17*
20	0.19	5 / 128	hsa−miR−515−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 12	BENTINK_ras.1
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 14	BENTINK_myc.1
7	1.0	0 / 10	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 14	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−08	158 / 4436	ICGC_Zeb1_targets
2	4e−08	180 / 5308	ICGC_Tcf12_targets
3	8e−07	196 / 6157	ICGC_Tcf3_targets
4	1e−06	154 / 4566	ICGC_Egr1_targets
5	2e−06	169 / 5173	ICGC_Taf1_targets
6	2e−06	179 / 5578	ICGC_Stat5_targets
7	6e−06	172 / 5393	ICGC_Sp1_targets
8	2e−05	215 / 7202	ICGC_Runx3_targets
9	3e−05	162 / 5135	ICGC_Ebfsc137065_targets
10	4e−05	205 / 6862	ICGC_Elf1_targets
11	7e−05	190 / 6324	ICGC_Yy1_targets
12	8e−05	84 / 2342	ICGC_GabpPcr2_targets
13	1e−04	169 / 5526	ICGC_Pmlsc71910_targets
14	1e−04	167 / 5453	ICGC_Foxm1_targets
15	1e−04	191 / 6406	ICGC_Pax5_targets
16	2e−04	179 / 6005	ICGC_Mta3_targets
17	3e−04	186 / 6322	ICGC_Pol2_targets
18	4e−04	185 / 6313	ICGC_Pou2_targets
19	8e−04	111 / 3511	ICGC_Rad21_targets
20	1e−03	49 / 1294	KIM_MYC targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 8	VAQUERIZAS_Tongue
2	0.2	2 / 37	VAQUERIZAS_Prostate
3	0.3	1 / 13	VAQUERIZAS_Skin
4	0.3	1 / 16	VAQUERIZAS_Ovary
5	0.3	1 / 16	VAQUERIZAS_Fetal thyroid
6	0.3	1 / 17	VAQUERIZAS_Adrenal gland
7	0.4	1 / 19	VAQUERIZAS_Heart
8	0.5	1 / 25	VAQUERIZAS_Adrenal cortex
9	0.5	2 / 64	VAQUERIZAS_Lung
10	0.5	1 / 30	VAQUERIZAS_Smooth muscle
11	0.5	1 / 31	VAQUERIZAS_Fetal lung
12	0.6	1 / 42	VAQUERIZAS_Thyroid
13	0.7	1 / 45	VAQUERIZAS_Placenta
14	0.7	1 / 49	VAQUERIZAS_Uterus
15	1.0	1 / 155	VAQUERIZAS_General
16	1.0	0 / 41	VAQUERIZAS_Fetal brain
17	1.0	0 / 33	VAQUERIZAS_Liver
18	1.0	0 / 12	VAQUERIZAS_Kidney
19	1.0	0 / 25	VAQUERIZAS_Spinal cord
20	1.0	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 13	WIRTH_Prim. lymphoid organs
2	0.05	11 / 259	PALMER_Granulocytes signature up
3	0.11	6 / 137	WIRTH_Mucosa
4	0.25	1 / 12	WIRTH_Tonsil
5	0.27	1 / 13	WIRTH_Sec. lymphoid organs
6	0.27	1 / 13	WIRTH_Cortex cerebri
7	0.29	1 / 14	WIRTH_B−cells
8	0.29	1 / 14	WIRTH_Thymus
9	0.29	1 / 14	WIRTH_Thyroid gland
10	0.52	1 / 30	PALMER_Lymphocytes signature up
11	0.73	1 / 54	WIRTH_Pancreas
12	0.88	3 / 208	PALMER_B−Cell signature up
13	0.96	2 / 202	WIRTH_Testis
14	0.97	1 / 140	PALMER_T−Cell signature up
15	0.97	1 / 141	WIRTH_Muscle
16	1.00	3 / 476	WIRTH_Nervous System
17	1.00	1 / 427	WIRTH_Immune system
18	1.00	0 / 6	WIRTH_Pituitary gland
19	1.00	0 / 12	WIRTH_Lymphocytes
20	1.00	0 / 14	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	38 / 1343	LU_BPDE 1n DN
2	0.9	112 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

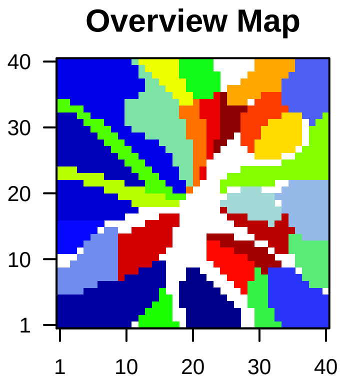
Spot Summary: U

metagenes = 37
genes = 404

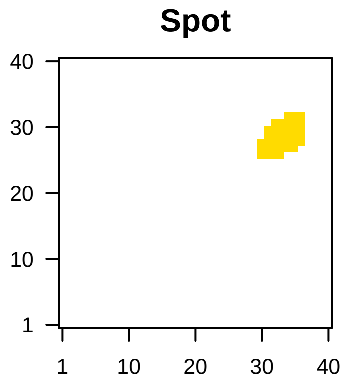
<r> metagenes = 0.95
<r> genes = 0.52
beta: r2= 0.01 / log p= −0.22

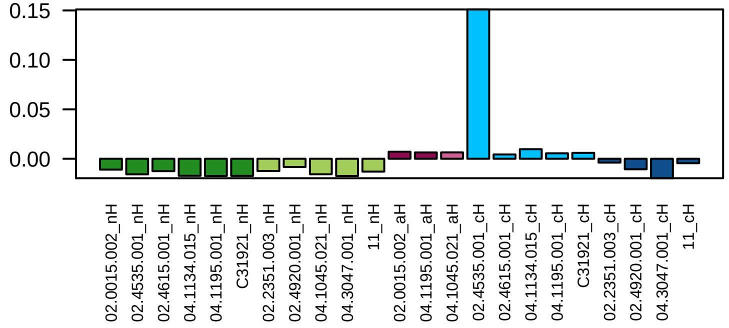
samples with spot = 1 (4.3 %)
MLH1_cancerHNPCC : 1 (20 %)

Overview Map



Spot





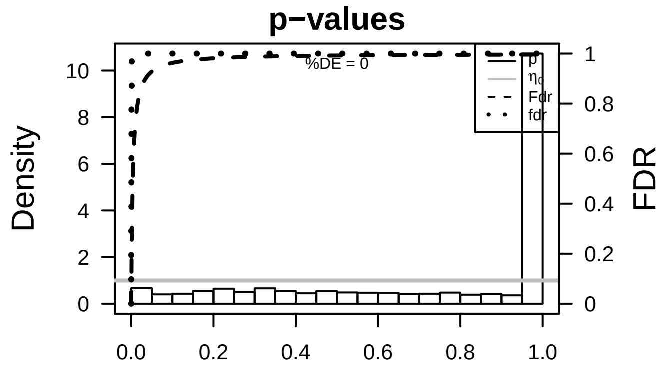
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	1.19	−0.05	0.96	PAGE1	P antigen family, member 1 (prostate associated) [Source:HG
2	ENSG000002	0.98	−0.05	0.96		
3	ENSG000002	0.93	−0.04	0.96	GAGE12G	G antigen 12G [Source:HGNC Symbol;Acc:HGNC:31907]
4	ENSG000002	0.93	−0.04	0.96	GAGE2D	G antigen 12F [Source:HGNC Symbol;Acc:HGNC:31906]
5	ENSG000002	0.86	−0.04	0.96		
6	ENSG000002	0.79	−0.04	0.96	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	ENSG000001	0.79	−0.13	0.76	RBP4	retinol binding protein 4, plasma [Source:HGNC Symbol;Acc:
8	ENSG000002	0.79	−0.04	0.96		
9	ENSG000002	0.78	−0.04	0.96		
10	ENSG000002	0.74	−0.03	0.96	GAGE12E	G antigen 12E [Source:HGNC Symbol;Acc:HGNC:31905]
11	ENSG000001	0.73	−0.17	0.68	EXOC3	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
12	ENSG000001	0.72	−0.07	0.91	GPC3	glypican 3 [Source:HGNC Symbol;Acc:HGNC:4451]
13	ENSG000001	0.72	−0.03	0.96	MAGEA6	melanoma antigen family A6 [Source:HGNC Symbol;Acc:HG
14	ENSG000002	0.71	−0.03	0.96	GAGE12C	G antigen 12C [Source:HGNC Symbol;Acc:HGNC:28402]
15	ENSG000002	0.71	−0.03	0.96	GAGE12D	G antigen 12D [Source:HGNC Symbol;Acc:HGNC:31904]
16	ENSG000002	0.7	−0.03	0.96		
17	ENSG000002	0.66	−0.03	0.96	MAGEA3	melanoma antigen family A3 [Source:HGNC Symbol;Acc:HG
18	ENSG000002	0.64	−0.03	0.96	GAGE12H	G antigen 12H [Source:HGNC Symbol;Acc:HGNC:31908]
19	ENSG000001	0.63	−0.09	0.84	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6 [Sourc
20	ENSG000001	0.63	−0.03	0.96	GAGE8	G antigen 2A [Source:HGNC Symbol;Acc:HGNC:4099]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−29	100 / 1425	Chr	Chr 19
2	5e−10	164 / 5393	TF	ICGC_Sp1_targets
3	2e−08	190 / 6862	TF	ICGC_Elf1_targets
4	9e−08	176 / 6322	TF	ICGC_Pol2_targets
5	2e−07	175 / 6324	TF	ICGC_Yy1_targets
6	2e−07	133 / 4436	TF	ICGC_Zeb1_targets
7	2e−07	158 / 5578	TF	ICGC_Stat5_targets
8	4e−07	192 / 7202	TF	ICGC_Runx3_targets
9	4e−07	173 / 6313	TF	ICGC_Pou2_targets
10	5e−07	100 / 3109	Colon	TssP_Colon
11	1e−06	32 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
12	1e−06	36 / 746	Chr	Chr X
13	1e−06	154 / 5526	TF	ICGC_Pmlsc71910_targets
14	2e−06	132 / 4566	TF	ICGC_Egr1_targets
15	5e−06	17 / 233	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell li
16	7e−06	65 / 1867	TF	HEBENSTREIT_high expression TF
17	8e−06	105 / 3511	TF	ICGC_Rad21_targets
18	9e−06	169 / 6406	TF	ICGC_Pax5_targets
19	1e−05	142 / 5173	TF	ICGC_Taf1_targets
20	1e−05	163 / 6157	TF	ICGC_Tcf3_targets
21	1e−05	126 / 4470	TF	ICGC_Creb1_targets
22	2e−05	137 / 4987	TF	ICGC_Bclaf101388_targets
23	2e−05	159 / 6005	TF	ICGC_Mta3_targets
24	3e−05	139 / 5135	TF	ICGC_Ebfsc137065_targets
25	3e−05	16 / 240	Lymp	WIRTH_lymphoma937_spot B
26	8e−05	32 / 766	TF	ICGC_Atf3_targets
27	8e−05	13 / 182	GSE	REACTOME_DNA_REPLICATION
28	1e−04	65 / 2041	Colon	EnhP_Colon
29	1e−04	10 / 117	GSE	YEGNASUBRAMANIAN_PROSTATE_CANCER
30	1e−04	13 / 193	GSE	WANG_CISPLATIN_RESPONSE_AND_XPC_UP
31	2e−04	139 / 5308	TF	ICGC_Tcf12_targets
32	2e−04	12 / 175	GSE	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
33	2e−04	4 / 16	GSE	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
34	3e−04	24 / 546	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
35	3e−04	8 / 85	GSE	PYEON_HPV_POSITIVE_TUMORS_UP
36	3e−04	272 / 11968	Colon	TssWk_Colon
37	3e−04	95 / 3406	Colon	ReprPC_Colon
38	4e−04	140 / 5453	TF	ICGC_Foxm1_targets
39	5e−04	6 / 50	BP	base−excision repair
40	5e−04	31 / 811	Lymp	WIRTH_lymphoma937_spot D

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	3 / 57	TESCHENDORFF_age_hypermethylated
2	0.8	2 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 123	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	6 / 50	base−excision repair
2	1e−03	25 / 640	oxidation−reduction process
3	1e−03	11 / 186	cellular nitrogen compound metabolic process
4	1e−03	4 / 25	RNA phosphodiester bond hydrolysis
5	2e−03	18 / 410	mitotic cell cycle
6	3e−03	4 / 30	eye development
7	3e−03	3 / 15	neurotransmitter biosynthetic process
8	3e−03	22 / 575	biological_process
9	3e−03	53 / 1808	regulation of transcription, DNA−templated
10	4e−03	8 / 126	anatomical structure morphogenesis
11	5e−03	3 / 18	branched−chain amino acid catabolic process
12	5e−03	3 / 18	double−strand break repair via nonhomologous end joining
13	8e−03	3 / 21	nucleotide−excision repair, DNA damage removal
14	9e−03	6 / 89	nucleic acid phosphodiester bond hydrolysis
15	9e−03	3 / 22	positive regulation of blood pressure
16	1e−02	3 / 23	telomere maintenance via semi−conservative replication
17	1e−02	4 / 44	RNA phosphodiester bond hydrolysis, endonucleolytic
18	1e−02	50 / 1807	transcription, DNA−templated
19	1e−02	4 / 45	positive regulation of cell differentiation
20	1e−02	4 / 45	tRNA aminoacylation for protein translation

Brain

Rank	p−value	#in/all	Geneset
1	0.002	78 / 2820	Mid_Frontal_Lobe_HetRpts
2	0.008	12 / 268	Mid_Frontal_Lobe_TssA
3	0.018	51 / 1890	Overlap_fetal_midbrain_TssF
4	0.024	74 / 2956	Fetal_TssA
5	0.024	28 / 939	Fetal_HetRpts
6	0.030	22 / 712	Overlap_fetal_midbrain_EnhP
7	0.035	217 / 9923	Overlap_fetal_midbrain_K9K27me3
8	0.043	94 / 3977	Mid_Frontal_Lobe_ReprPC
9	0.053	24 / 840	Mid_Frontal_Lobe_TssF
10	0.059	30 / 1108	Overlap_fetal_midbrain_TssA
11	0.078	51 / 2084	Mid_Frontal_Lobe_K9K27me3
12	0.092	78 / 3370	Mid_Frontal_Lobe_ZNF
13	0.093	25 / 940	Mid_Frontal_Lobe_Enh
14	0.096	37 / 1478	Overlap_fetal_midbrain_TxTrans
15	0.108	61 / 2603	Fetal_TxTrans
16	0.118	33 / 1327	Mid_Frontal_Lobe_TssP
17	0.120	218 / 10278	Overlap_fetal_midbrain_ReprPCWk
18	0.135	41 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	0.152	227 / 10800	Overlap_fetal_midbrain_Quies
20	0.166	20 / 787	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	21 / 550	Lembcke_Normal vs Adenoma
2	0.012	3 / 24	PanCan_Notch_geneset_nanostring
3	0.020	4 / 52	KUIPER_MM poor survival
4	0.076	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	0.142	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
6	0.183	1 / 10	GENTLES_modul3
7	0.262	1 / 15	LIU_BREAST_CANCER
8	0.277	1 / 16	LIU_LIVER_CANCER
9	0.277	1 / 16	GENTLES_modul6
10	0.309	3 / 97	PanCan_TXmisReg_geneset_nanostring
11	0.360	1 / 22	PanCan_ChromMod_geneset_nanostring
12	0.418	2 / 71	SHAUGHNESSY_MM high risk
13	0.516	3 / 136	PanCan_CC+Apop_geneset_nanostring
14	0.528	1 / 37	KUIPER_MM good survival
15	0.542	0 / 14	LIU_PROSTATE_CANCER_UP
16	0.565	1 / 41	ZHANG_MM up
17	0.591	3 / 152	PanCan_MAPK_geneset_nanostring
18	0.637	1 / 50	PanCan_DNARepair_geneset_nanostring
19	0.645	1 / 51	PanCan_TGF−B_geneset_nanostring
20	0.710	0 / 16	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	0.004	7 / 99	dendritic spine
2	0.004	5 / 53	kinesin complex
3	0.004	3 / 17	proteasome accessory complex
4	0.007	3 / 20	inclusion body
5	0.010	123 / 5101	nucleus
6	0.010	12 / 277	mitochondrial matrix
7	0.023	2 / 12	holo TFIIH complex
8	0.028	15 / 431	cellular_component
9	0.033	3 / 35	mitotic spindle
10	0.034	4 / 61	transport vesicle
11	0.035	39 / 1441	mitochondrion
12	0.050	2 / 18	dendrite membrane
13	0.050	2 / 18	extrinsic component of plasma membrane
14	0.050	4 / 69	cytoplasmic mRNA processing body
15	0.054	4 / 71	kinetochore
16	0.055	3 / 43	intercellular bridge
17	0.060	2 / 20	protein phosphatase type 2A complex
18	0.061	3 / 45	mitochondrial nucleoid
19	0.066	2 / 21	desmosome
20	0.066	2 / 21	retromer complex

Chr

Rank	p−value	#in/all	Geneset
1	1e−29	100 / 1425	Chr 19
2	1e−06	36 / 746	Chr X
3	2e−01	6 / 191	Chr 21
4	4e−01	10 / 436	Chr 22
5	5e−01	17 / 847	Chr 16
6	6e−01	5 / 272	Chr 18
7	7e−01	10 / 582	Chr 15
8	8e−01	15 / 862	Chr 5
9	8e−01	35 / 1920	Chr 1
10	8e−01	5 / 318	Chr 13
11	8e−01	12 / 715	Chr 10
12	8e−01	14 / 859	Chr 7
13	8e−01	8 / 522	Chr 20
14	9e−01	9 / 613	Chr 14
15	9e−01	11 / 745	Chr 9
16	9e−01	14 / 976	Chr 6
17	1e+00	14 / 1043	Chr 3
18	1e+00	15 / 1228	Chr 2
19	1e+00	14 / 1172	Chr 11
20	1e+00	6 / 651	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−07	100 / 3109	TssP_Colon
2	1e−06	32 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	1e−04	65 / 2041	EnhP_Colon
4	3e−04	272 / 11968	TssWk_Colon
5	3e−04	95 / 3406	ReprPC_Colon
6	1e−03	8 / 105	Marisa_CRC−cluster−d
7	1e−03	39 / 1178	ZNF_Colon
8	3e−03	4 / 30	Marisa_CRC−cluster−c
9	4e−03	79 / 2947	ReprPCWk_Colon
10	1e−02	27 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
11	1e−02	49 / 1753	Het_Colon
12	2e−02	105 / 4379	TssD1_Colon
13	2e−02	17 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	3e−02	181 / 8123	TssF_Colon
15	3e−02	254 / 11791	Enh_Colon
16	4e−02	35 / 1281	HetRpts_Colon
17	5e−02	101 / 4327	EnhWk2_Colon
18	6e−02	2 / 20	Budinska_B_Lower crypt−like_UP
19	7e−02	16 / 525	Quies2_Colon
20	8e−02	21 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.3	14 / 608	GUDJ_psoriasis up
2	1.0	4 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	4 / 30	Gorovets_LGG_NB_subclass
2	0.009	8 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
3	0.018	27 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	0.031	2 / 14	Christensen_hypermethylated_in_ependymoma
5	0.059	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
6	0.062	5 / 106	WIRTH_Normal Brain
7	0.150	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
8	0.150	1 / 8	shaw_responders_up_in_oligo_glioma
9	0.172	4 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	0.184	2 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
11	0.216	1 / 12	Phillips PN up vs MES & Prolif
12	0.217	4 / 119	GIEZELT_GBM_WT_up_VS_mut
13	0.222	3 / 81	Weller_LGG_gradeII−vs−III_UP
14	0.223	5 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
15	0.262	1 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
16	0.265	2 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
17	0.277	1 / 16	VERHAAK_NL subtype
18	0.277	1 / 16	astrocytes_glio
19	0.287	34 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
20	0.288	2 / 53	Gorovets_LGG_EPL_subclass

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−05	13 / 182	REACTOME_DNA_REPLICATION
2	1e−04	10 / 117	YEGNASUBRAMANIAN_PROSTATE_CANCER
3	1e−04	13 / 193	WANG_CISPLATIN_RESPONSE_AND_XPC_UP
4	2e−04	12 / 175	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
5	2e−04	4 / 16	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
6	3e−04	24 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	3e−04	8 / 85	PYEON_HPV_POSITIVE_TUMORS_UP
8	6e−04	11 / 168	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
9	7e−04	20 / 446	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	1e−03	4 / 23	REACTOME_KINESINS
11	1e−03	16 / 329	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
12	1e−03	15 / 298	REACTOME_CELL_CYCLE_MITOTIC
13	1e−03	11 / 185	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES
14	2e−03	42 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
15	2e−03	5 / 43	NAKAMURA_METASTASIS
16	2e−03	10 / 162	REACTOME_MITOTIC_M_M_G1_PHASES
17	2e−03	4 / 26	BIOCARTA_PROTEASOME_PATHWAY
18	2e−03	4 / 28	KUUSELO_PANCREATIC_CANCER_19Q13_AMPLIFICATION
19	2e−03	10 / 171	BROWNE_HCMV_INFECTION_48HR_UP
20	3e−03	5 / 48	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER

HM

Rank	p−value	#in/all	Geneset
1	0.007	10 / 198	HALLMARK_GLYCOLYSIS
2	0.101	7 / 196	HALLMARK_MITOTIC_SPINDLE
3	0.162	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
4	0.171	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	0.191	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.202	6 / 196	HALLMARK_G2M_CHECKPOINT
7	0.208	6 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	0.236	2 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.337	4 / 146	HALLMARK_DNA_REPAIR
10	0.362	5 / 197	HALLMARK_E2F_TARGETS
11	0.366	5 / 198	HALLMARK_HYPOXIA
12	0.370	5 / 199	HALLMARK_MTORC1_SIGNALING
13	0.378	4 / 155	HALLMARK_UV_RESPONSE_UP
14	0.475	3 / 128	HALLMARK_SPERMATOGENESIS
15	0.518	1 / 36	HALLMARK_ANGIOGENESIS
16	0.527	4 / 189	HALLMARK_KRAS_SIGNALING_UP
17	0.544	4 / 193	HALLMARK_HEME_METABOLISM
18	0.552	4 / 195	HALLMARK_MYOGENESIS
19	0.560	4 / 197	HALLMARK_IL2_STAT5_SIGNALING
20	0.600	3 / 154	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.5	2 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	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−06	17 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
2	3e−05	16 / 240	WIRTH_lymphoma937_spot B
3	5e−04	31 / 811	WIRTH_lymphoma937_spot D
4	2e−03	29 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
5	5e−03	76 / 2838	HOPP_Poised_promoter
6	2e−02	8 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
7	2e−02	8 / 171	WIRTH_lymphoma937_spot C
8	1e−01	10 / 317	TARTE_Plasmablast signature
9	1e−01	8 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
10	1e−01	112 / 5039	HOPP_Repressed
11	2e−01	3 / 67	LEE_Developmental_regulators
12	2e−01	4 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
13	2e−01	12 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
14	2e−01	4 / 116	WIRTH_lymphoma937_spot MM
15	2e−01	1 / 13	BENTINK_mBL DOWN
16	3e−01	3 / 94	Subero_T−ALL_hyper_meth
17	3e−01	11 / 458	WIRTH_lymphoma937_spot I
18	3e−01	4 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
19	3e−01	1 / 19	DAVE_c−myc BL UP
20	3e−01	4 / 144	WIRTH_lymphoma937_spot G

MF

Rank	p−value	#in/all	Geneset
1	0.002	60 / 2040	metal ion binding
2	0.004	36 / 1134	nucleic acid binding
3	0.006	4 / 37	aminoacyl−tRNA ligase activity
4	0.008	5 / 61	damaged DNA binding
5	0.008	4 / 40	heat shock protein binding
6	0.011	30 / 962	transcription factor activity, sequence−specific DNA binding
7	0.013	7 / 124	heme binding
8	0.016	2 / 10	small protein activating enzyme activity
9	0.017	4 / 49	protein serine/threonine phosphatase activity
10	0.019	8 / 166	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
11	0.020	3 / 29	SH2 domain binding
12	0.020	5 / 78	microtubule motor activity
13	0.027	2 / 13	glutamate receptor activity
14	0.033	3 / 35	NADP binding
15	0.038	47 / 1803	DNA binding
16	0.040	2 / 16	transmembrane receptor protein tyrosine phosphatase activity
17	0.049	3 / 41	4 iron, 4 sulfur cluster binding
18	0.050	2 / 18	Notch binding
19	0.055	3 / 43	oxygen binding
20	0.055	2 / 19	aldehyde dehydrogenase (NAD) activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	13 / 333	hsa−miR−302a
2	0.03	2 / 13	hsa−miR−614
3	0.03	12 / 321	hsa−miR−302b
4	0.04	12 / 330	hsa−miR−302c
5	0.06	3 / 44	hsa−miR−483−5p
6	0.06	4 / 73	hsa−miR−127−5p
7	0.07	11 / 326	hsa−miR−30e
8	0.08	2 / 23	hsa−miR−662
9	0.09	3 / 52	hsa−miR−362−3p
10	0.09	11 / 344	hsa−miR−302d
11	0.09	2 / 25	hsa−miR−1228
12	0.09	7 / 191	hsa−miR−302e
13	0.10	7 / 194	hsa−miR−128
14	0.10	3 / 56	hsa−miR−208a
15	0.10	11 / 355	hsa−let−7e
16	0.11	3 / 57	hsa−miR−940
17	0.12	3 / 61	hsa−miR−296−3p
18	0.13	2 / 31	hsa−miR−371−3p
19	0.13	2 / 32	hsa−miR−1237
20	0.13	2 / 32	hsa−miR−631

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	GUSTAFSON_PI3K_UP
2	0.2	1 / 14	BENTINK_e2f3.1
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 14	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 10	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 14	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	164 / 5393	ICGC_Sp1_targets
2	2e−08	190 / 6862	ICGC_Elf1_targets
3	9e−08	176 / 6322	ICGC_Pol2_targets
4	2e−07	175 / 6324	ICGC_Yy1_targets
5	2e−07	133 / 4436	ICGC_Zeb1_targets
6	2e−07	158 / 5578	ICGC_Stat5_targets
7	4e−07	192 / 7202	ICGC_Runx3_targets
8	4e−07	173 / 6313	ICGC_Pou2_targets
9	1e−06	154 / 5526	ICGC_Pmlsc71910_targets
10	2e−06	132 / 4566	ICGC_Egr1_targets
11	7e−06	65 / 1867	HEBENSTREIT_high expression TF
12	8e−06	105 / 3511	ICGC_Rad21_targets
13	9e−06	169 / 6406	ICGC_Pax5_targets
14	1e−05	142 / 5173	ICGC_Taf1_targets
15	1e−05	163 / 6157	ICGC_Tcf3_targets
16	1e−05	126 / 4470	ICGC_Creb1_targets
17	2e−05	137 / 4987	ICGC_Bclaf101388_targets
18	2e−05	159 / 6005	ICGC_Mta3_targets
19	3e−05	139 / 5135	ICGC_Ebfsc137065_targets
20	8e−05	32 / 766	ICGC_Atf3_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.001	5 / 41	VAQUERIZAS_Testis
2	0.037	7 / 155	VAQUERIZAS_General
3	0.128	2 / 31	VAQUERIZAS_Fetal lung
4	0.199	2 / 41	VAQUERIZAS_Fetal brain
5	0.277	1 / 16	VAQUERIZAS_Fetal liver
6	0.277	1 / 16	VAQUERIZAS_Fetal thyroid
7	0.369	2 / 64	VAQUERIZAS_Lung
8	0.398	1 / 25	VAQUERIZAS_Adrenal cortex
9	0.456	1 / 30	VAQUERIZAS_Smooth muscle
10	0.488	1 / 33	VAQUERIZAS_Liver
11	0.573	1 / 42	VAQUERIZAS_Thymus
12	0.573	1 / 42	VAQUERIZAS_Thyroid
13	0.599	1 / 45	VAQUERIZAS_Placenta
14	0.607	1 / 46	VAQUERIZAS_Whole brain
15	1.000	0 / 37	VAQUERIZAS_Prostate
16	1.000	0 / 49	VAQUERIZAS_Uterus
17	1.000	0 / 12	VAQUERIZAS_Kidney
18	1.000	0 / 25	VAQUERIZAS_Spinal cord
19	1.000	0 / 67	VAQUERIZAS_Whole blood
20	1.000	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.06	6 / 137	WIRTH_Mucosa
2	0.16	13 / 476	WIRTH_Nervous System
3	0.25	1 / 14	WIRTH_Bone marrow
4	0.25	1 / 14	WIRTH_Thyroid gland
5	0.26	1 / 15	WIRTH_Telencephalon
6	0.26	1 / 15	WIRTH_Cerebellum
7	0.41	3 / 115	WIRTH_Liver
8	0.49	2 / 82	WIRTH_Homeostasis
9	0.58	4 / 202	WIRTH_Testis
10	0.61	1 / 47	WIRTH_Placenta
11	0.67	1 / 54	WIRTH_Pancreas
12	0.78	2 / 141	WIRTH_Muscle
13	0.89	3 / 259	PALMER_Granulocytes signature up
14	0.92	2 / 208	PALMER_B−Cell signature up
15	0.94	1 / 140	PALMER_T−Cell signature up
16	0.97	4 / 427	WIRTH_Immune system
17	1.00	0 / 6	WIRTH_Pituitary gland
18	1.00	0 / 13	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_Prim. lymphoid organs
20	1.00	0 / 14	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	31 / 1343	LU_BPDE 1h DN
2	0.9	95 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

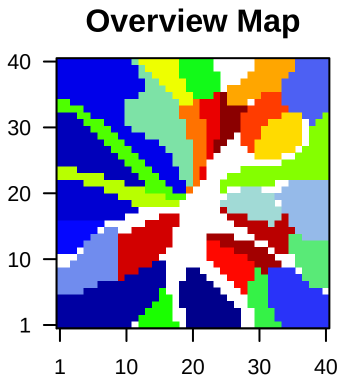
Correlation Clusters

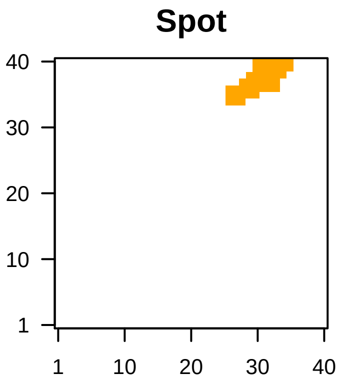
Spot Summary: V

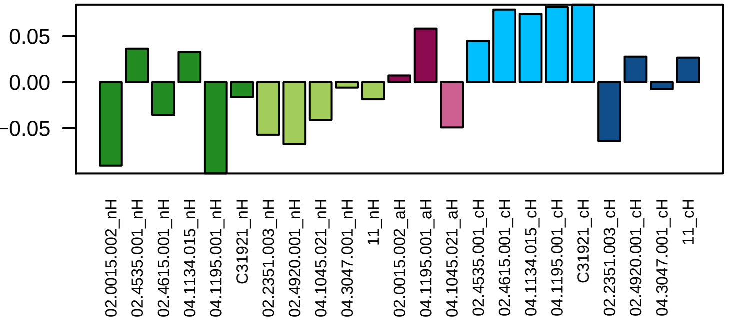
metagenes = 40
genes = 544

<r> metagenes = 0.96
<r> genes = 0.54
beta: r2= 0.06 / log p= −0.56

samples with spot = 5 (21.7 %)
MLH1_adenomaHNPCC : 1 (50 %)
MLH1_cancerHNPCC : 4 (80 %)


Overview Map


Spot

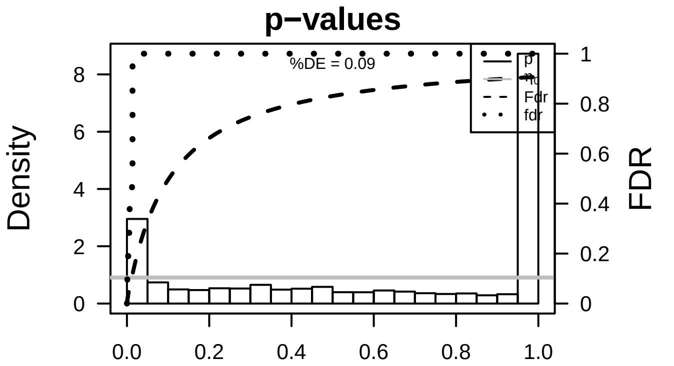


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.95	−0.08	0.22	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
2	ENSG000001	0.75	−0.13	0.36	FAM83D	family with sequence similarity 83, member D [Source:HGNC
3	ENSG000001	0.71	−0.63	0.63	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC
4	ENSG000001	0.68	−0.21	0.52	WARS	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
5	ENSG000001	0.62	−0.43	0.62	IFITM2	interferon induced transmembrane protein 2 [Source:HGNC
6	ENSG000001	0.58	−0.04	0.41	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family
7	ENSG000001	0.57	−0.35	0.57	HSPA8	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
8	ENSG000000	0.54	−0.26	0.56	FXYD5	FXYD domain containing ion transport regulator 5 [Source:H
9	ENSG000000	0.53	−0.29	0.61	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member
10	ENSG000001	0.51	−0.34	0.59	ALDH1B1	aldehyde dehydrogenase 1 family, member B1 [Source:HGN
11	ENSG000002	0.48	−0.31	0.75		RPL36A−HNRNPH2 readthrough [Source:HGNC Symbol;Acc
12	ENSG000001	0.48	−0.33	0.73	TUBA1B	tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
13	ENSG000001	0.45	−0.14	0.57	TGFBI	transforming growth factor, beta−induced, 68kDa [Source:HG
14	ENSG000001	0.43	−0.36	0.73	RPS16	ribosomal protein S16 [Source:HGNC Symbol;Acc:HGNC:10
15	ENSG000002	0.42	−0.1	0.53	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) [Source
16	ENSG000002	0.42	−0.24	0.49	RPS29	ribosomal protein S29 [Source:HGNC Symbol;Acc:HGNC:10
17	ENSG000001	0.41	−0.09	0.54	WDR45B	WD repeat domain 45B [Source:HGNC Symbol;Acc:HGNC:2
18	ENSG000002	0.4	−0.4	0.4		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3
19	ENSG000002	0.4	−0.22	0.64	RPL36A	ribosomal protein L36a [Source:HGNC Symbol;Acc:HGNC:1
20	ENSG000001	0.39	−0.2	0.68	LY6E	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−72	189 / 1563	GSE	PUJANA_BRCA1_PCC_NETWORK
2	5e−72	144 / 859	GSE	LEE_BMP2_TARGETS_DN
3	4e−71	132 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	4e−71	412 / 7491	Lymp	HOPP_Txn_elongation
5	4e−70	158 / 1091	MF	poly(A) RNA binding
6	2e−68	169 / 1298	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	1e−63	114 / 582	GSE	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	7e−62	343 / 5643	Lymp	HOPP_Txn_transition
9	2e−58	417 / 8358	Lymp	HOPP_Active_promoter
10	6e−58	126 / 820	BP	gene expression
11	3e−56	119 / 747	GSE	PUJANA_CHEK2_PCC_NETWORK
12	1e−54	123 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
13	2e−52	454 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
14	1e−47	69 / 259	BP	translation
15	2e−47	439 / 9930	Colon	Tx_Colon
16	9e−47	49 / 109	BP	viral transcription
17	6e−46	52 / 132	GSE	REACTOME_INFLUENZA_LIFE_CYCLE
18	3e−44	59 / 195	HM	HALLMARK_MYC_TARGETS_V1
19	5e−44	46 / 102	GSE	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
20	6e−44	64 / 242	GSE	REACTOME_METABOLISM_OF_RNA
21	3e−43	445 / 10475	Colon	TssA_Colon
22	1e−42	51 / 142	BP	translational initiation
23	1e−42	51 / 142	GSE	REACTOME_TRANSLATION
24	8e−42	53 / 162	MF	structural constituent of ribosome
25	2e−41	105 / 799	CC	nucleolus
26	3e−41	44 / 101	BP	translational elongation
27	6e−41	103 / 775	GSE	WEI_MYCN_TARGETS_WITH_E_BOX
28	6e−41	50 / 144	BP	viral life cycle
29	7e−41	53 / 168	CC	ribosome
30	1e−40	414 / 9390	Colon	TxWk_Colon
31	1e−40	43 / 98	GSE	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
32	4e−40	40 / 82	GSE	REACTOME_PEPTIDE_CHAIN_ELONGATION
33	4e−40	41 / 88	BP	translational termination
34	9e−40	44 / 108	BP	SRP−dependent cotranslational protein targeting to membrane
35	1e−39	40 / 84	GSE	KEGG_RIBOSOME
36	4e−39	55 / 198	GSE	REACTOME_METABOLISM_OF_MRNA
37	6e−39	43 / 105	GSE	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
38	1e−37	70 / 370	GSE	HSIAO_HOUSEKEEPING_GENES
39	3e−37	89 / 633	BP	cellular protein metabolic process
40	8e−37	41 / 102	GSE	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	5 / 123	HORVATH_aging_genes meth DOWN
2	0.4	5 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 57	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	9e−19	59 / 550	Lembcke_Normal vs Adenoma
2	4e−09	8 / 16	WOLFER_overlap genes
3	4e−08	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	6e−07	12 / 71	SHAUGHNESSY_MM high risk
5	1e−06	47 / 16	RHODES_CANCER_META_SIGNATURE
6	6e−05	5 / 16	GENTLES_modul1
7	1e−04	7 / 41	ZHANG_MM up
8	5e−04	7 / 50	PanCan_DNARepair_geneset_nanostring
9	9e−04	4 / 16	GENTLES_modul2
10	9e−04	4 / 16	GENTLES_modul6
11	8e−03	3 / 15	LIU_BREAST_CANCER
12	8e−03	3 / 15	GENTLES_modul4
13	8e−03	3 / 15	GENTLES_modul10
14	1e−02	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	3e−02	2 / 10	GENTLES_modul3
16	7e−02	2 / 16	GENTLES_modul7
17	9e−02	3 / 37	KUIPER_MM good survival
18	9e−02	7 / 136	PanCan_CC+Apop_geneset_nanostring
19	9e−02	9 / 191	SPANG_LPS−index2
20	1e−01	3 / 40	PanCan_HK_geneset_nanostring

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−71	132 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	1e−54	123 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
3	2e−47	439 / 9930	Tx_Colon
4	3e−43	445 / 10475	TssA_Colon
5	1e−40	414 / 9390	TxWk_Colon
6	9e−17	426 / 11968	TssWk_Colon
7	6e−13	311 / 8123	TssF_Colon
8	1e−11	344 / 9470	Quies3_Colon
9	5e−07	173 / 4379	TssD1_Colon
10	6e−03	38 / 877	TxEnhG2_Colon
11	1e−02	108 / 3122	TxEnhG1_Colon
12	1e−02	216 / 6761	TssD2_Colon
13	2e−02	2 / 8	Marisa_CRC−C6
14	3e−02	2 / 10	Budinska_E_Mixed_UP
15	5e−02	10 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
16	6e−02	15 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
17	9e−02	181 / 5889	EnhWk1_Colon
18	2e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
19	2e−01	4 / 76	Marisa_CRC−cluster−g
20	2e−01	25 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−72	189 / 1563	PUJANA_BRCA1_PCC_NETWORK
2	5e−72	144 / 859	LEE_BMP2_TARGETS_DN
3	2e−68	169 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	1e−63	114 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
5	3e−56	119 / 747	PUJANA_CHEK2_PCC_NETWORK
6	6e−46	52 / 132	REACTOME_INFLUENZA_LIFE_CYCLE
7	5e−44	46 / 102	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
8	6e−44	64 / 242	REACTOME_METABOLISM_OF_RNA
9	1e−42	51 / 142	REACTOME_TRANSLATION
10	6e−41	103 / 775	WEI_MYCN_TARGETS_WITH_E_BOX
11	1e−40	43 / 98	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
12	4e−40	40 / 82	REACTOME_PEPTIDE_CHAIN_ELONGATION
13	1e−39	40 / 84	KEGG_RIBOSOME
14	4e−39	55 / 198	REACTOME_METABOLISM_OF_MRNA
15	6e−39	43 / 105	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
16	1e−37	70 / 370	HSIAO_HOUSEKEEPING_GENES
17	8e−37	41 / 102	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
18	2e−36	72 / 412	REACTOME_METABOLISM_OF_PROTEINS
19	2e−36	123 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
20	1e−33	83 / 610	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−71	412 / 7491	HOPP_Txn_elongation
2	7e−62	343 / 5643	HOPP_Txn_transition
3	2e−58	417 / 8358	HOPP_Active_promoter
4	2e−29	358 / 8147	HOPP_Weak_promoter
5	6e−23	80 / 811	WIRTH_lymphoma937_spot D
6	3e−21	77 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	3e−19	45 / 317	TARTE_Plasmablast signature
8	6e−17	31 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
9	1e−16	31 / 171	WIRTH_lymphoma937_spot C
10	2e−06	244 / 6784	HOPP_Weak_enhancer
11	5e−06	62 / 1215	SPANG_BCR_DN
12	2e−05	262 / 7592	HOPP_Strong_enhancer
13	2e−05	226 / 6389	HOPP_Weak_txn
14	3e−04	13 / 150	DAVE_BL−vs−DLBCL
15	3e−04	9 / 78	TARTE_Plasma cell signature
16	2e−03	3 / 9	YAMANE_AICDA_targets_nonrecruited
17	3e−03	4 / 21	ROSOLOWSKI_red UP
18	4e−03	3 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
19	9e−03	14 / 240	WIRTH_lymphoma937_spot B
20	1e−02	8 / 105	ROSOLOWSKI_blue total

Pathw Act

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

Tissue

Rank	p−value	#in/all	Geneset
1	9e−08	9 / 30	PALMER_Lymphocytes signature up
2	4e−03	3 / 12	WIRTH_Lymphocytes
3	5e−02	2 / 13	WIRTH_Cortex cerebri
4	2e−01	10 / 259	PALMER_Granulocytes signature up
5	3e−01	1 / 13	WIRTH_Globus pallidus
6	3e−01	1 / 14	WIRTH_Thyroid gland
7	8e−01	3 / 141	WIRTH_Muscle
8	9e−01	2 / 140	PALMER_T−Cell signature up
9	9e−01	3 / 208	PALMER_B−Cell signature up
10	1e+00	7 / 427	WIRTH_Immune system
11	1e+00	1 / 202	WIRTH_Testis
12	1e+00	1 / 476	WIRTH_Nervous System
13	1e+00	0 / 6	WIRTH_Pituitary gland
14	1e+00	0 / 54	WIRTH_Pancreas
15	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
16	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
17	1e+00	0 / 14	WIRTH_B−cells
18	1e+00	0 / 12	WIRTH_Tonsil
19	1e+00	0 / 14	WIRTH_Thymus
20	1e+00	0 / 14	WIRTH_Bone marrow

BP

Rank	p−value	#in/all	Geneset
1	6e−58	126 / 820	gene expression
2	1e−47	69 / 259	translation
3	9e−47	49 / 109	viral transcription
4	1e−42	51 / 142	translational initiation
5	3e−41	44 / 101	translational elongation
6	6e−41	50 / 144	viral life cycle
7	4e−40	41 / 88	translational termination
8	9e−40	44 / 108	SRP−dependent cotranslational protein targeting to membrane
9	3e−37	89 / 633	cellular protein metabolic process
10	1e−36	43 / 117	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
11	7e−33	78 / 549	viral process
12	2e−18	50 / 410	mitotic cell cycle
13	1e−13	12 / 22	cytoplasmic translation
14	2e−13	21 / 95	rRNA processing
15	8e−13	15 / 45	tRNA aminoacylation for protein translation
16	2e−11	25 / 174	protein folding
17	2e−09	21 / 151	G1/S transition of mitotic cell cycle
18	1e−08	29 / 304	DNA repair
19	7e−08	10 / 38	'de novo' posttranslational protein folding
20	9e−08	8 / 22	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r

CC

Rank	p−value	#in/all	Geneset
1	2e−41	105 / 799	nucleolus
2	7e−41	53 / 168	ribosome
3	2e−29	29 / 59	cytosolic large ribosomal subunit
4	9e−20	151 / 2554	nucleoplasm
5	5e−19	165 / 2974	cytosol
6	3e−15	16 / 39	cytosolic small ribosomal subunit
7	5e−15	25 / 121	ribonucleoprotein complex
8	5e−14	226 / 5185	cytoplasm
9	6e−14	223 / 5101	nucleus
10	3e−12	134 / 2638	extracellular exosome
11	6e−10	11 / 32	small−subunit processome
12	3e−09	34 / 378	focal adhesion
13	1e−07	12 / 61	nuclear pore
14	2e−07	8 / 24	small ribosomal subunit
15	4e−07	74 / 1441	mitochondrion
16	1e−06	129 / 3059	membrane
17	7e−06	5 / 11	large ribosomal subunit
18	2e−05	12 / 97	melanosome
19	3e−05	7 / 32	polysome
20	4e−05	5 / 15	eukaryotic 48S preinitiation complex

Disease

Rank	p−value	#in/all	Geneset
1	0.5	18 / 608	GUDJ_psoriasis up
2	0.5	1 / 22	BCHETNIA_EBM up
3	0.7	1 / 37	BCHETNIA_EBM−DM up
4	1.0	4 / 399	GUDJ_psoriasis down
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	3e−44	59 / 195	HALLMARK_MYC_TARGETS_V1
2	2e−12	28 / 197	HALLMARK_E2F_TARGETS
3	3e−10	19 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	2e−09	24 / 196	HALLMARK_G2M_CHECKPOINT
5	1e−05	18 / 199	HALLMARK_MTORC1_SIGNALING
6	3e−05	9 / 58	HALLMARK_MYC_TARGETS_V2
7	1e−04	14 / 155	HALLMARK_UV_RESPONSE_UP
8	1e−02	11 / 181	HALLMARK_ALLOGRAFT_REJECTION
9	6e−02	8 / 146	HALLMARK_DNA_REPAIR
10	8e−02	8 / 157	HALLMARK_APOPTOSIS
11	1e−01	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	1e−01	7 / 154	HALLMARK_FATTY_ACID_METABOLISM
13	2e−01	8 / 196	HALLMARK_MITOTIC_SPINDLE
14	2e−01	4 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	3e−01	7 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
16	3e−01	4 / 98	HALLMARK_ANDROGEN_RESPONSE
17	3e−01	7 / 198	HALLMARK_GLYCOLYSIS
18	4e−01	3 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	5e−01	6 / 194	HALLMARK_INFLAMMATORY_RESPONSE
20	5e−01	6 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

MF

Rank	p−value	#in/all	Geneset
1	4e−70	158 / 1091	poly(A) RNA binding
2	8e−42	53 / 162	structural constituent of ribosome
3	4e−23	63 / 513	RNA binding
4	1e−13	21 / 94	unfolded protein binding
5	4e−09	11 / 37	aminoacyl−tRNA ligase activity
6	5e−09	34 / 385	nucleotide binding
7	1e−08	11 / 41	tRNA binding
8	2e−08	10 / 34	rRNA binding
9	2e−07	13 / 77	single−stranded DNA binding
10	3e−07	14 / 93	mRNA binding
11	2e−06	72 / 1448	ATP binding
12	6e−06	352 / 10693	protein binding
13	7e−06	5 / 11	aminoacyl−tRNA editing activity
14	2e−05	9 / 53	translation initiation factor activity
15	5e−05	9 / 61	damaged DNA binding
16	1e−04	4 / 10	ligase activity, forming aminoacyl−tRNA and related compounds
17	1e−04	6 / 29	Ran GTPase binding
18	3e−04	5 / 22	snoRNA binding
19	6e−04	17 / 245	ubiquitin protein ligase binding
20	7e−04	5 / 26	N−acetyltransferase activity

TF

Rank	p−value	#in/all	Geneset
1	1e−34	124 / 1294	KIM_MYC targets
2	4e−26	122 / 1549	ICGC_Myc_targets
3	3e−15	98 / 1503	ICGC_Six5_targets
4	2e−10	213 / 5173	ICGC_Taf1_targets
5	4e−10	87 / 1547	ICGC_Ets1_targets
6	4e−09	14 / 66	MYC_Targets UP
7	7e−09	217 / 5512	ICGC_Nficsc81335_targets
8	8e−09	105 / 2133	ICGC_Cebpbsc150_targets
9	1e−08	112 / 2342	ICGC_GabpPcr2_targets
10	5e−08	207 / 5308	ICGC_Tcf12_targets
11	7e−08	213 / 5526	ICGC_Pmlsc71910_targets
12	1e−07	195 / 4987	ICGC_Bclaf101388_targets
13	2e−07	212 / 5552	ICGC_Pol24_targets
14	2e−07	178 / 4470	ICGC_Creb1_targets
15	3e−07	193 / 4969	ICGC_Atf2_targets
16	6e−07	168 / 4230	ICGC_Nfatc1_targets
17	2e−06	230 / 6313	ICGC_Pou2_targets
18	2e−06	225 / 6157	ICGC_Tcf3_targets
19	5e−06	6 / 17	MYC_Protein synthesis degradation UP
20	6e−06	205 / 5578	ICGC_Stat5_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	44 / 1343	LU_BPDE 1h DN
2	1.0	96 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	2e−52	454 / 10239	Overlap_fetal_midbrain_ReprPC
2	2e−31	410 / 9923	Overlap_fetal_midbrain_K9K27me3
3	2e−22	287 / 6320	Overlap_fetal_midbrain_HetRpts
4	3e−11	61 / 855	Overlap_fetal_midbrain_ZNF
5	2e−09	371 / 10800	Overlap_fetal_midbrain_Quies
6	1e−07	21 / 191	Overlap_fetal_midbrain_Het
7	6e−06	51 / 939	Fetal_HetRpts
8	2e−05	338 / 10278	Overlap_fetal_midbrain_ReprPCWk
9	8e−04	21 / 342	Fetal_Het
10	1e−02	20 / 400	Fetal_ZNF
11	1e−02	87 / 2443	Fetal_Quies
12	5e−02	33 / 865	Mid_Frontal_Lobe_Het
13	6e−02	48 / 1356	Fetal_K9K27me3
14	2e−01	103 / 3370	Mid_Frontal_Lobe_ZNF
15	2e−01	53 / 1680	Fetal_ReprPCWk
16	6e−01	6 / 232	Fetal_ReprPC
17	7e−01	31 / 1182	Fetal_EnhP
18	8e−01	44 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	9e−01	33 / 1394	Mid_Frontal_Lobe_Quies
20	9e−01	69 / 2820	Mid_Frontal_Lobe_HetRpts

Chr

Rank	p−value	#in/all	Geneset
1	0.02	47 / 1228	Chr 2
2	0.07	24 / 613	Chr 14
3	0.07	65 / 1920	Chr 1
4	0.08	28 / 745	Chr 9
5	0.10	31 / 862	Chr 5
6	0.28	31 / 976	Chr 6
7	0.29	11 / 318	Chr 13
8	0.30	21 / 651	Chr 8
9	0.33	36 / 1172	Chr 11
10	0.34	23 / 735	Chr 4
11	0.48	17 / 582	Chr 15
12	0.58	1 / 30	Chr Y
13	0.58	12 / 436	Chr 22
14	0.61	23 / 847	Chr 16
15	0.65	7 / 272	Chr 18
16	0.66	27 / 1017	Chr 12
17	0.78	27 / 1083	Chr 17
18	0.83	25 / 1043	Chr 3
19	0.84	20 / 859	Chr 7
20	0.86	16 / 715	Chr 10

Glio

Rank	p−value	#in/all	Geneset
1	1e−15	129 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−11	107 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	1e−03	41 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	4e−03	3 / 12	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
5	4e−03	19 / 344	Up
6	2e−02	9 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
7	4e−02	2 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
8	4e−02	15 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	5e−02	2 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
10	5e−02	9 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	5e−02	4 / 50	Vishal_subnetwork signature of survival in GBM
12	7e−02	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
13	8e−02	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
14	9e−02	5 / 83	GIEZELT_GBM_WT_down_VS_mut
15	1e−01	4 / 63	Stuehler_Proteins_up_in_STS
16	1e−01	3 / 40	Christensen_hypomethylated_in_ependymoma
17	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
18	2e−01	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
19	2e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
20	2e−01	1 / 9	Colman_survival_robust

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.4	1 / 17	DUMEAUX_High bmi enriched genes
3	0.6	1 / 33	DUMEAUX_Fasting enriched genes
4	1.0	0 / 91	DUMEAUX_Smoking enriched genes
5	1.0	0 / 11	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 11	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	

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−08	30 / 348	hsa−miR−548b−5p
2	2e−07	29 / 348	hsa−miR−548d−5p
3	3e−07	27 / 312	hsa−miR−548i
4	4e−07	27 / 317	hsa−miR−548c−5p
5	4e−06	24 / 297	hsa−miR−548j
6	6e−06	14 / 118	hsa−miR−376c
7	2e−05	14 / 130	hsa−miR−646
8	3e−05	24 / 332	hsa−miR−548a−5p
9	5e−05	21 / 280	hsa−miR−548h
10	6e−05	14 / 145	hsa−miR−522
11	8e−05	21 / 289	hsa−miR−320a
12	1e−04	10 / 83	hsa−miR−1179
13	1e−04	7 / 41	hsa−miR−182*
14	1e−04	22 / 324	hsa−miR−559
15	2e−04	16 / 197	hsa−miR−330−3p
16	2e−04	11 / 104	hsa−miR−1301
17	2e−04	12 / 123	hsa−miR−543
18	3e−04	9 / 76	hsa−miR−708
19	5e−04	15 / 195	hsa−miR−382
20	5e−04	12 / 136	hsa−miR−28−5p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.3	1 / 12	VAQUERIZAS_Kidney
2	0.3	1 / 13	VAQUERIZAS_Skin
3	0.4	1 / 16	VAQUERIZAS_Fetal liver
4	0.4	1 / 18	VAQUERIZAS_Pancreas
5	0.4	1 / 20	VAQUERIZAS_Bone marrow
6	0.6	1 / 33	VAQUERIZAS_Liver
7	0.7	1 / 37	VAQUERIZAS_Prostate
8	0.8	1 / 49	VAQUERIZAS_Uterus
9	0.8	3 / 155	VAQUERIZAS_General
10	0.9	1 / 67	VAQUERIZAS_Whole blood
11	1.0	0 / 41	VAQUERIZAS_Fetal brain
12	1.0	0 / 45	VAQUERIZAS_Placenta
13	1.0	0 / 30	VAQUERIZAS_Smooth muscle
14	1.0	0 / 25	VAQUERIZAS_Spinal cord
15	1.0	0 / 46	VAQUERIZAS_Whole brain
16	1.0	0 / 42	VAQUERIZAS_Thymus
17	1.0	0 / 42	VAQUERIZAS_Thyroid
18	1.0	0 / 7	VAQUERIZAS_Appendix
19	1.0	0 / 31	VAQUERIZAS_Fetal lung
20	1.0	0 / 64	VAQUERIZAS_Lung

Correlation Clusters

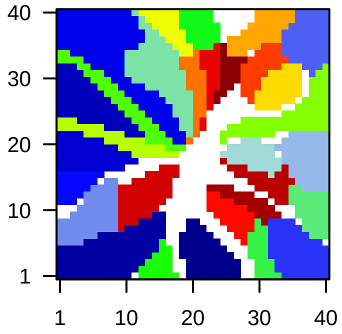
Spot Summary: W

metagenes = 54
genes = 906

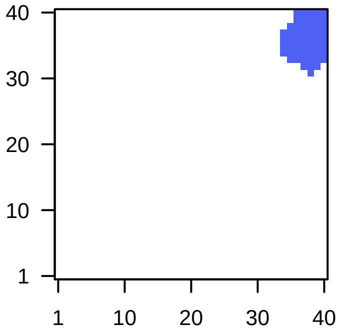
<r> metagenes = 0.93
<r> genes = 0.57
beta: r2= 0.15 / log p= −1.2

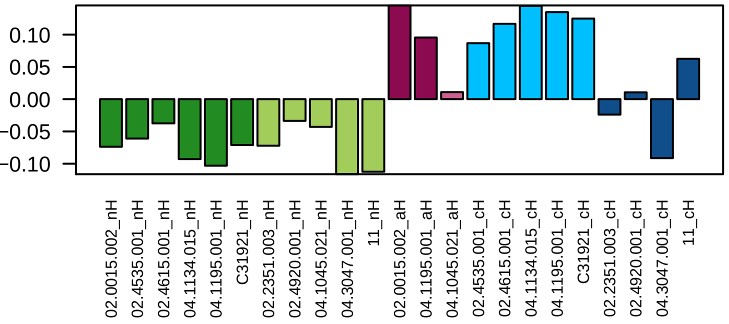
samples with spot = 8 (34.8 %)
MLH1_adenomaHNPCC : 2 (100 %)
MLH1_cancerHNPCC : 5 (100 %)
other_cancerHNPCC : 1 (25 %)

Overview Map



Spot





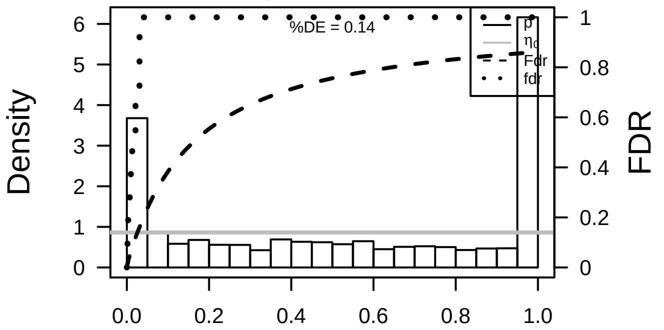
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.84	−0.57	0.57	REG1A	regenerating islet−derived 1 alpha [Source:HGNC Symbol;Ac
2	ENSG000001	1.71	−0.34	0.49	ITLN1	intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
3	ENSG000001	1.65	−0.75	0.6	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
4	ENSG000001	1.57	−0.24	0.58	REG3A	regenerating islet−derived 3 alpha [Source:HGNC Symbol;Ac
5	ENSG000001	1.47	−0.28	0.63	MMP1	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
6	ENSG000001	1.33	−0.75	0.38	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) [Source
7	ENSG000001	1.31	−0.29	0.4	CXCL8	chemokine (C−X−C motif) ligand 8 [Source:HGNC Symbol;Ac
8	ENSG000001	1.27	−0.21	0.52	REG1B	regenerating islet−derived 1 beta [Source:HGNC Symbol;Acc
9	ENSG000001	1.25	−0.21	0.58	DMBT1	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
10	ENSG000001	1.17	−0.36	0.48	REG4	regenerating islet−derived family, member 4 [Source:HGNC S
11	ENSG000001	1.16	−0.2	0.61	MMP3	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC
12	ENSG000001	1.15	−0.44	0.74	SPINK1	serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symb
13	ENSG000000	1.15	−0.35	0.48	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
14	ENSG000002	1.1	−0.18	0.56	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy
15	ENSG000001	1.05	−0.66	0.85	LCN2	lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
16	ENSG000001	1.05	−0.87	0.76	AGR2	anterior gradient 2, protein disulphide isomerase family memb
17	ENSG000001	0.98	−0.17	0.41	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC
18	ENSG000001	0.97	−0.41	0.62	SPINK4	serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symb
19	ENSG000001	0.91	−1	0.73	GPX2	glutathione peroxidase 2 [Source:HGNC Symbol;Acc:HGNC:
20	ENSG000001	0.87	−0.25	0.53	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−98	207 / 807	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
2	9e−96	205 / 811	Lympl	WIRTH_lymphoma937_spot D
3	1e−91	189 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	4e−84	91 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
5	2e−83	164 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	2e−79	110 / 248	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	1e−78	9 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	2e−76	121 / 327	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
9	6e−76	84 / 138	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	9e−76	152 / 550	Cance	Lembcke_Normal vs Adenoma
11	1e−71	178 / 813	GSEA	GRADE_COLON_CANCER_UP
12	3e−68	634 / 8123	Colon	TssF_Colon
13	7e−68	124 / 400	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
14	5e−65	140 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
15	1e−62	125 / 446	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	3e−60	720 / 10475	Colon	TssA_Colon
17	8e−60	131 / 519	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
18	1e−59	104 / 316	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
19	1e−59	67 / 113	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	2e−59	81 / 179	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
21	9e−59	175 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
22	7e−56	225 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
23	3e−55	202 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
24	7e−55	70 / 141	GSEA	CHANG_CYCLING_GENES
25	2e−54	139 / 645	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
26	2e−53	96 / 303	GSEA	HORIUCHI_WTAP_TARGETS_DN
27	7e−53	156 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
28	6e−51	90 / 278	GSEA	BASAKI_YBX1_TARGETS_UP
29	7e−51	100 / 350	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
30	2e−50	89 / 275	GSEA	GRADE_COLON_AND_RECTAL_CANCER_UP
31	2e−49	143 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
32	3e−48	55 / 95	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
33	7e−48	151 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
34	3e−47	74 / 197	HM	HALLMARK_E2F_TARGETS
35	2e−46	91 / 317	Lympl	TARTE_Plasmablast signature
36	1e−45	181 / 1228	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
37	3e−45	138 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
38	8e−45	90 / 323	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
39	5e−43	84 / 292	GSEA	MUELLER_PLURINET
40	2e−42	90 / 343	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	[illegible]	[illegible]	HORVATH_aging_genes meth UP
2	0.8	4 / 123	HORVATH_aging_genes meth DOWN
3	1.0	0 / 57	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	1e−78	9 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	9e−76	152 / 550	Lembcke_Normal vs Adenoma
3	7e−37	11 / 16	RHODES_UNDIFFERENTIATED_CANCER
4	5e−24	5 / 16	RHODES_CANCER_META_SIGNATURE
5	2e−12	4 / 14	LIU_PROSTATE_CANCER_UP
6	9e−09	9 / 16	GENTLES_modul7
7	2e−06	21 / 136	PanCan_CC+Apop_geneset_nanostring
8	4e−06	7 / 16	WOLFER_overlap genes
9	4e−06	7 / 16	GENTLES_modul2
10	4e−06	6 / 11	GENTLES_modul5
11	4e−05	9 / 37	KUIPER_MM good survival
12	6e−05	6 / 16	GENTLES_modul1
13	1e−04	9 / 41	ZHANG_MM up
14	1e−04	12 / 71	SHAUGHNESSY_MM high risk
15	1e−04	10 / 52	KUIPER_MM poor survival
16	5e−04	5 / 15	BEN−PORATH_UP
17	8e−04	4 / 10	GENTLES_modul3
18	4e−03	4 / 15	GENTLES_modul4
19	2e−02	16 / 198	PanCan_PI3K_geneset_nanostring
20	3e−02	6 / 50	PanCan_DNARepair_geneset_nanostring

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−91	189 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	3e−68	634 / 8123	TssF_Colon
3	3e−60	720 / 10475	TssA_Colon
4	7e−53	156 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
5	1e−26	470 / 6761	TssD2_Colon
6	1e−25	617 / 9930	Tx_Colon
7	4e−20	253 / 3122	TxEnhG1_Colon
8	2e−14	659 / 11791	Enh_Colon
9	1e−11	539 / 9390	TxWk_Colon
10	2e−11	654 / 11968	TssWk_Colon
11	7e−10	361 / 5889	EnhWk1_Colon
12	9e−09	80 / 877	TxEnhG2_Colon
13	1e−08	30 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
14	2e−08	15 / 55	Marisa_CRC−cluster−e
15	3e−08	41 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
16	3e−05	192 / 3112	EnhA_Colon
17	2e−03	487 / 9470	Quies3_Colon
18	7e−03	47 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
19	4e−02	2 / 7	Marisa_CRC−C5
20	4e−02	3 / 17	TCGA−CRC_less−agressive−disease−markers

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−83	164 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
2	2e−79	110 / 248	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	1e−78	9 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	2e−76	121 / 327	WONG_EMBRYONIC_STEM_CELL_CORE
5	6e−76	84 / 138	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	1e−71	178 / 813	GRADE_COLON_CANCER_UP
7	7e−68	124 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
8	5e−65	140 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
9	1e−62	125 / 446	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	8e−60	131 / 519	BERENJENO_TRANSFORMED_BY_RHOA_UP
11	1e−59	104 / 316	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
12	1e−59	67 / 113	WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	2e−59	81 / 179	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
14	9e−59	175 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
15	7e−56	225 / 1563	PUJANA_BRCA1_PCC_NETWORK
16	3e−55	202 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
17	7e−55	70 / 141	CHANG_CYCLING_GENES
18	2e−54	139 / 645	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
19	2e−53	96 / 303	HORIUCHI_WTAP_TARGETS_DN
20	6e−51	90 / 278	BASAKI_YBX1_TARGETS_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−98	207 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	9e−96	205 / 811	WIRTH_lymphoma937_spot D
3	2e−46	91 / 317	TARTE_Plasmablast signature
4	2e−34	435 / 5643	HOPP_Txn_transition
5	1e−19	524 / 8358	HOPP_Active_promoter
6	6e−15	464 / 7491	HOPP_Txn_elongation
7	6e−12	22 / 78	TARTE_Plasma cell signature
8	4e−09	23 / 116	WIRTH_lymphoma937_spot MM
9	1e−08	22 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
10	3e−08	27 / 171	WIRTH_lymphoma937_spot C
11	3e−07	25 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
12	2e−06	22 / 150	DAVE_BL−vs−DLBCL
13	3e−06	423 / 7592	HOPP_Strong_enhancer
14	6e−06	447 / 8147	HOPP_Weak_promoter
15	1e−05	15 / 87	Aukema_BCL2 DN_BCL6 UP
16	1e−04	15 / 105	ROSOLOWSKI_blue total
17	2e−04	6 / 19	DAVE_c−myc BL UP
18	2e−04	25 / 240	WIRTH_lymphoma937_spot B
19	3e−04	24 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
20	5e−04	12 / 83	ROSOLOWSKI_green UP

PathwACT

Rank	p−value	#in/all	Geneset
1	1e−06	7 / 14	BENTINK_myc.1
2	3e−02	3 / 14	GUSTAFSON_PI3K_UP
3	4e−01	1 / 10	BENTINK_ras.4
4	4e−01	1 / 12	BENTINK_ras.1
5	5e−01	1 / 13	BENTINK_e2f3.2
6	5e−01	1 / 14	BENTINK_e2f3.1
7	5e−01	1 / 14	BENTINK_src.2
8	5e−01	1 / 15	GUSTAFSON_PI3K_DN
9	5e−01	1 / 15	BENTINK_ras.6
10	1e+00	0 / 14	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 12	WIRTH_Lymphocytes
2	0.05	4 / 30	PALMER_Lymphocytes signature up
3	0.12	2 / 13	WIRTH_Globus pallidus
4	0.14	2 / 14	WIRTH_B−cells
5	0.14	2 / 14	WIRTH_Thymus
6	0.14	2 / 14	WIRTH_Thyroid gland
7	0.16	2 / 15	WIRTH_Telencephalon
8	0.21	9 / 140	PALMER_T−Cell signature up
9	0.44	1 / 12	WIRTH_Tonsil
10	0.45	13 / 259	PALMER_Granulocytes signature up
11	0.47	1 / 13	WIRTH_Cortex cerebri
12	0.49	1 / 14	WIRTH_Thalamus
13	0.51	1 / 15	WIRTH_Cerebellum
14	0.77	8 / 208	PALMER_B−Cell signature up
15	0.78	5 / 137	WIRTH_Mucosa
16	0.93	1 / 54	WIRTH_Pancreas
17	0.98	1 / 82	WIRTH_Homeostasis
18	0.99	11 / 427	WIRTH_Immune system
19	1.00	1 / 115	WIRTH_Liver
20	1.00	1 / 141	WIRTH_Muscle

BP

Rank	p−value	#in/all	Geneset
1	1e−38	75 / 259	translation
2	2e−30	83 / 410	mitotic cell cycle
3	2e−26	39 / 98	mitochondrial translation
4	2e−25	97 / 633	cellular protein metabolic process
5	4e−25	35 / 82	mitochondrial translational elongation
6	6e−24	34 / 82	mitochondrial translational initiation
7	2e−23	34 / 84	mitochondrial translational termination
8	1e−21	62 / 323	cell division
9	2e−20	35 / 108	SRP−dependent cotranslational protein targeting to membrane
10	3e−19	101 / 820	gene expression
11	8e−18	48 / 239	mitotic nuclear division
12	5e−17	37 / 151	G1/S transition of mitotic cell cycle
13	2e−15	27 / 88	translational termination
14	2e−15	72 / 549	viral process
15	1e−14	28 / 101	translational elongation
16	1e−14	33 / 142	translational initiation
17	1e−13	24 / 80	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent p
18	4e−13	46 / 291	organelle organization
19	7e−13	27 / 109	viral transcription
20	2e−11	29 / 144	viral life cycle

CC

Rank	p−value	#in/all	Geneset
1	6e−26	261 / 2974	cytosol
2	7e−26	161 / 1441	mitochondrion
3	9e−26	49 / 168	ribosome
4	3e−22	73 / 425	mitochondrial inner membrane
5	5e−17	215 / 2638	extracellular exosome
6	1e−14	202 / 2554	nucleoplasm
7	2e−12	82 / 767	endoplasmic reticulum membrane
8	8e−12	13 / 24	mitochondrial small ribosomal subunit
9	8e−12	83 / 799	nucleolus
10	2e−10	20 / 76	condensed chromosome kinetochore
11	2e−10	40 / 277	mitochondrial matrix
12	3e−10	82 / 842	endoplasmic reticulum
13	1e−09	8 / 10	methylosome
14	3e−09	11 / 24	small ribosomal subunit
15	3e−09	8 / 11	endoplasmic reticulum chaperone complex
16	6e−09	316 / 5101	nucleus
17	7e−09	12 / 31	mitochondrial large ribosomal subunit
18	7e−09	320 / 5185	cytoplasm
19	8e−09	16 / 59	cytosolic large ribosomal subunit
20	2e−08	13 / 40	spindle microtubule

Disease

Rank	p−value	#in/all	Geneset
1	1e−22	90 / 608	GUDJ_psoriasis up
2	5e−01	2 / 37	BCHETNIA_EBM−DM up
3	7e−01	1 / 22	BCHETNIA_EBM up
4	1e+00	12 / 399	GUDJ_psoriasis down
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	3e−47	74 / 197	HALLMARK_E2F_TARGETS
2	5e−42	69 / 195	HALLMARK_MYC_TARGETS_V1
3	1e−34	62 / 196	HALLMARK_G2M_CHECKPOINT
4	1e−25	53 / 199	HALLMARK_MTORC1_SIGNALING
5	3e−22	28 / 58	HALLMARK_MYC_TARGETS_V2
6	2e−17	43 / 198	HALLMARK_GLYCOLYSIS
7	1e−12	27 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	4e−09	26 / 146	HALLMARK_DNA_REPAIR
9	5e−06	14 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	5e−06	25 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
11	6e−06	25 / 196	HALLMARK_MITOTIC_SPINDLE
12	6e−05	23 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	2e−03	19 / 197	HALLMARK_IL2_STAT5_SIGNALING
14	3e−03	16 / 155	HALLMARK_UV_RESPONSE_UP
15	1e−02	17 / 199	HALLMARK_ADIPOGENESIS
16	3e−02	13 / 154	HALLMARK_FATTY_ACID_METABOLISM
17	4e−02	11 / 128	HALLMARK_SPERMATOGENESIS
18	4e−02	15 / 196	HALLMARK_P53_PATHWAY
19	6e−02	5 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
20	7e−02	14 / 193	HALLMARK_XENOBIOTIC_METABOLISM

MF

Rank	p−value	#in/all	Geneset
1	8e−36	58 / 162	structural constituent of ribosome
2	2e−28	140 / 1091	poly(A) RNA binding
3	9e−08	10 / 25	isomerase activity
4	3e−07	9 / 22	threonine−type endopeptidase activity
5	2e−06	17 / 94	unfolded protein binding
6	2e−06	49 / 513	RNA binding
7	1e−05	10 / 40	ribosome binding
8	2e−05	14 / 80	endopeptidase activity
9	2e−05	9 / 34	rRNA binding
10	5e−05	7 / 22	snoRNA binding
11	7e−05	8 / 31	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
12	3e−04	6 / 21	protein disulfide isomerase activity
13	3e−04	12 / 80	chaperone binding
14	4e−04	46 / 578	identical protein binding
15	4e−04	35 / 407	catalytic activity
16	7e−04	10 / 63	transferase activity
17	8e−04	4 / 10	U6 snRNA binding
18	9e−04	5 / 17	translation initiation factor binding
19	1e−03	548 / 10693	protein binding
20	1e−03	12 / 93	mRNA binding

TF

Rank	p−value	#in/all	Geneset
1	5e−22	142 / 1294	KIM_MYC targets
2	4e−19	27 / 66	MYC_Targets UP
3	4e−15	142 / 1549	ICGC_Myc_targets
4	4e−13	156 / 1867	HEBENSTREIT_high expression TF
5	1e−10	328 / 5173	ICGC_Taf1_targets
6	3e−10	290 / 4470	ICGC_Creb1_targets
7	4e−09	7 / 8	MYC_Cell cycle UP
8	2e−08	331 / 5453	ICGC_Foxm1_targets
9	3e−08	333 / 5512	ICGC_Nficsc81335_targets
10	3e−08	336 / 5578	ICGC_Stat5_targets
11	3e−07	394 / 6862	ICGC_Elf1_targets
12	3e−07	359 / 6157	ICGC_Tcf3_targets
13	6e−07	365 / 6313	ICGC_Pou2_targets
14	1e−06	324 / 5526	ICGC_Pmlsc71910_targets
15	2e−06	8 / 20	MYC_Metabolism UP
16	2e−06	257 / 4230	ICGC_Nfatc1_targets
17	2e−06	267 / 4436	ICGC_Zeb1_targets
18	3e−06	311 / 5308	ICGC_Tcf12_targets
19	4e−06	111 / 1547	ICGC_Ets1_targets
20	8e−06	312 / 5393	ICGC_Sp1_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	78 / 1343	LU_BPDE 1n DN
2	1.00	164 / 5285	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	5e−32	635 / 9923	Overlap_fetal_midbrain_K9K27me3
2	1e−16	600 / 10239	Overlap_fetal_midbrain_ReprPC
3	3e−10	135 / 1680	Fetal_ReprPCWk
4	9e−09	84 / 939	Fetal_HetRpts
5	1e−07	76 / 865	Mid_Frontal_Lobe_Het
6	4e−07	166 / 2443	Fetal_Quies
7	3e−06	573 / 10800	Overlap_fetal_midbrain_Quies
8	1e−05	208 / 3370	Mid_Frontal_Lobe_ZNF
9	3e−04	21 / 191	Overlap_fetal_midbrain_Het
10	1e−03	60 / 855	Overlap_fetal_midbrain_ZNF
11	2e−02	154 / 2820	Mid_Frontal_Lobe_HetRpts
12	3e−02	97 / 1713	Mid_Frontal_Lobe_ReprPCWk
13	2e−01	199 / 3977	Mid_Frontal_Lobe_ReprPC
14	3e−01	19 / 342	Fetal_Het
15	3e−01	103 / 2084	Mid_Frontal_Lobe_K9K27me3
16	4e−01	12 / 232	Fetal_ReprPC
17	4e−01	20 / 400	Fetal_ZNF
18	9e−01	31 / 787	Overlap_fetal_midbrain_TssP
19	9e−01	55 / 1356	Fetal_K9K27me3
20	1e+00	12 / 408	Mid_Frontal_Lobe_TxTrans

Chr

Rank	p−value	#in/all	Geneset
1	0.002	35 / 436	Chr 22
2	0.004	70 / 1083	Chr 17
3	0.005	38 / 522	Chr 20
4	0.055	80 / 1425	Chr 19
5	0.096	43 / 745	Chr 9
6	0.154	33 / 582	Chr 15
7	0.192	54 / 1017	Chr 12
8	0.322	43 / 847	Chr 16
9	0.414	57 / 1172	Chr 11
10	0.437	30 / 613	Chr 14
11	0.735	37 / 859	Chr 7
12	0.778	84 / 1920	Chr 1
13	0.797	41 / 976	Chr 6
14	0.866	28 / 715	Chr 10
15	0.873	42 / 1043	Chr 3
16	0.898	97 272	Chr 18
17	0.928	27 / 735	Chr 4
18	0.940	27 / 746	Chr X
19	0.942	23 / 651	Chr 8
20	0.945	47 / 1228	Chr 2

Glio

Rank	p−value	#in/all	Geneset
1	4e−84	91 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	2e−19	26 / 59	developing astrocytes
3	2e−09	19 / 77	Weller_LGG_gradeII−vs−III_DOWN
4	1e−08	17 / 69	cultured astroglia vs. in vivo astrocytes
5	2e−04	8 / 36	Colman_survival_associated
6	1e−03	14 / 119	GIEZELT_GBM_WT_up_VS_mut
7	2e−03	120 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
8	4e−03	4 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
9	8e−03	7 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
10	1e−02	2 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
11	1e−02	2 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
12	2e−02	2 / 5	Phillips Prolif up vs PN & MES
13	2e−02	126 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
14	3e−02	7 / 63	OPC
15	4e−02	7 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
16	6e−02	4 / 31	KIM prognostic signature LTS vs. STS
17	7e−02	9 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
18	7e−02	3 / 21	KIM deleted & downregulated in LTS
19	8e−02	6 / 63	Stuehler_Proteins_up_in_STS
20	8e−02	9 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	0.4	1 / 11	DUMEAUX_Smoking literature genes up
3	0.6	1 / 17	DUMEAUX_High bmi enriched genes
4	0.9	2 / 91	DUMEAUX_Smoking enriched genes
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	18 / 122	hsa−miR−509−3p
2	7e−05	22 / 187	hsa−miR−34b
3	3e−04	15 / 115	hsa−miR−499−5p
4	4e−04	11 / 70	hsa−miR−193b
5	6e−04	13 / 97	hsa−miR−125b
6	1e−03	10 / 68	hsa−miR−637
7	2e−03	15 / 136	hsa−miR−28−5p
8	2e−03	12 / 97	hsa−miR−125a−5p
9	4e−03	9 / 66	hsa−miR−30e*
10	6e−03	12 / 110	hsa−miR−146b−5p
11	6e−03	25 / 307	hsa−miR−34c−5p
12	6e−03	12 / 111	hsa−miR−376b
13	6e−03	11 / 98	hsa−miR−133b
14	6e−03	12 / 112	hsa−miR−146a
15	7e−03	11 / 99	hsa−miR−133a
16	8e−03	16 / 173	hsa−miR−323b−5p
17	8e−03	5 / 27	hsa−miR−1273
18	9e−03	10 / 89	hsa−miR−188−3p
19	9e−03	8 / 63	hsa−miR−324−3p
20	9e−03	6 / 39	hsa−miR−593

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	3 / 24	VAQUERIZAS_Trachea
2	0.1	4 / 42	VAQUERIZAS_Thymus
3	0.2	3 / 30	VAQUERIZAS_Smooth muscle
4	0.2	2 / 16	VAQUERIZAS_Fetal thyroid
5	0.2	2 / 17	VAQUERIZAS_Salivary gland
6	0.2	3 / 33	VAQUERIZAS_Liver
7	0.2	2 / 18	VAQUERIZAS_Pancreas
8	0.3	3 / 37	VAQUERIZAS_Prostate
9	0.3	3 / 42	VAQUERIZAS_Thyroid
10	0.4	2 / 31	VAQUERIZAS_Fetal lung
11	0.5	1 / 16	VAQUERIZAS_Fetal liver
12	0.6	1 / 17	VAQUERIZAS_Adrenal gland
13	0.6	2 / 41	VAQUERIZAS_Fetal brain
14	0.6	2 / 41	VAQUERIZAS_Testis
15	0.6	1 / 20	VAQUERIZAS_Bone marrow
16	0.6	2 / 45	VAQUERIZAS_Placenta
17	0.6	2 / 46	VAQUERIZAS_Whole brain
18	0.7	1 / 25	VAQUERIZAS_Spinal cord
19	0.7	1 / 25	VAQUERIZAS_Adrenal cortex
20	0.7	6 / 155	VAQUERIZAS_General

Correlation Clusters

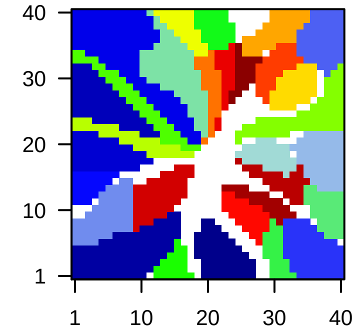
Spot Summary: X

metagenes = 32
genes = 375

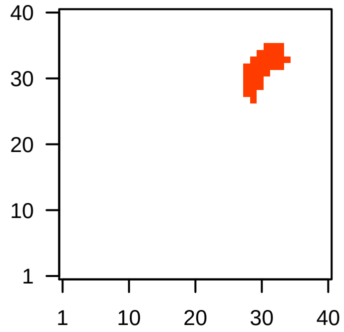
<r> metagenes = 0.96
<r> genes = 0.42
beta: r2= 0.01 / log p= −0.22

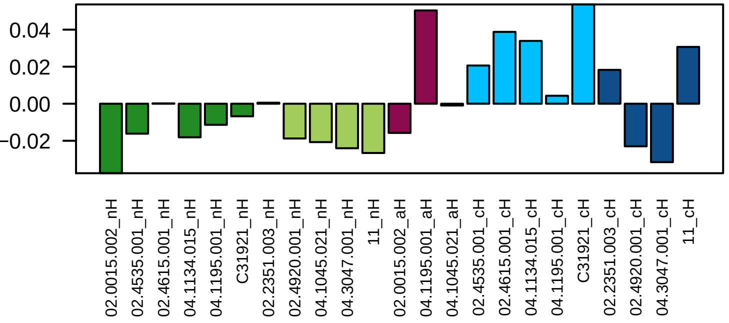
samples with spot = 2 (8.7 %)
MLH1_adenomaHNPCC : 1 (50 %)
MLH1_cancerHNPCC : 1 (20 %)

Overview Map



Spot





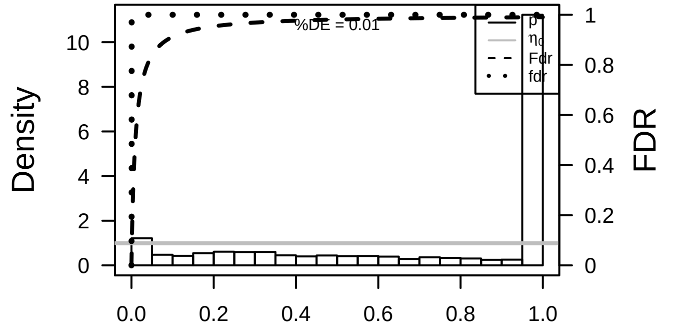
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.66	−0.21	0.31	NPIPB15	nuclear pore complex interacting protein family, member B15
2	ENSG000001	0.43	−0.03	0.27	SLC39A2	solute carrier family 39 (zinc transporter), member 2 [Source:
3	ENSG000002	0.42	−0.08	0.58		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:J3
4	ENSG000001	0.38	−0.29	0.55	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, be
5	ENSG000001	0.38	−0.09	0.36	FAM118A	family with sequence similarity 118, member A [Source:HGN
6	ENSG000001	0.36	−0.03	0.32	EDAR	ectodysplasin A receptor [Source:HGNC Symbol;Acc:HGNC:
7	ENSG000001	0.36	−0.16	0.72	GOLIM4	golgi integral membrane protein 4 [Source:HGNC Symbol;Ac
8	ENSG000001	0.32	−0.14	0.55	KIAA0226L	KIAA0226−like [Source:HGNC Symbol;Acc:HGNC:20420]
9	ENSG000000	0.32	−0.17	0.55	FAT1	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:HGNC:3
10	ENSG000000	0.3	−0.17	0.69	TFRC	transferrin receptor [Source:HGNC Symbol;Acc:HGNC:1176
11	ENSG000002	0.28	−0.13	0.59	SRXN1	sulfiredoxin 1 [Source:HGNC Symbol;Acc:HGNC:16132]
12	ENSG000001	0.28	−0.08	0.56	PRKRIR	protein−kinase, interferon−inducible double stranded RNA de
13	ENSG000002	0.28	−0.13	0.59		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:S4
14	ENSG000001	0.27	−0.15	0.47	INSIG1	insulin induced gene 1 [Source:HGNC Symbol;Acc:HGNC:60
15	ENSG000001	0.26	−0.07	0.78	SLC18A2	solute carrier family 18 (vesicular monoamine transporter), m
16	ENSG000001	0.25	−0.31	0.55	ARF4	ADP−ribosylation factor 4 [Source:HGNC Symbol;Acc:HGNC
17	ENSG000001	0.24	−0.15	0.43	GAS6	growth arrest−specific 6 [Source:HGNC Symbol;Acc:HGNC:4
18	ENSG000001	0.23	−0.08	0.52	CCDC14	coiled−coil domain containing 14 [Source:HGNC Symbol;Acc
19	ENSG000001	0.23	−0.06	0.64	SYBU	syntabulin (syntaxin−interacting) [Source:HGNC Symbol;Acc:
20	ENSG000002	0.23	−0.21	0.74		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H0

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−24	83 / 1228	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	4e−20	230 / 7491	Lymp	HOPP_Txn_elongation
3	1e−17	57 / 807	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
4	6e−17	62 / 975	GSE	NUYTTEN_EZH2_TARGETS_DN
5	6e−17	56 / 811	Lymp	WIRTH_lymphoma937_spot D
6	2e−15	70 / 1298	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	4e−14	53 / 852	GSE	GEORGES_TARGETS_OF_MIR192_AND_MIR215
8	5e−13	173 / 5643	Lymp	HOPP_Txn_transition
9	6e−13	228 / 8358	Lymp	HOPP_Active_promoter
10	3e−12	265 / 10475	Colon	TssA_Colon
11	3e−11	182 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
12	1e−10	47 / 862	GSE	JOHNSTONE_PARVB_TARGETS_3_DN
13	1e−10	36 / 546	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
14	4e−10	18 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
15	5e−10	26 / 316	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
16	6e−10	35 / 550	Canc	Lembcke_Normal vs Adenoma
17	9e−10	239 / 9470	Colon	Quies3_Colon
18	1e−09	253 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
19	1e−09	237 / 9390	Colon	TxWk_Colon
20	1e−09	283 / 11968	Colon	TssWk_Colon
21	2e−09	41 / 747	GSE	PUJANA_CHEK2_PCC_NETWORK
22	5e−09	211 / 8147	Lymp	HOPP_Weak_promoter
23	8e−09	37 / 668	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
24	3e−08	22 / 284	GSE	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
25	5e−08	241 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
26	9e−08	25 / 377	miRN	hsa−let−7d
27	1e−07	240 / 9930	Colon	Tx_Colon
28	2e−07	27 / 446	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
29	2e−07	17 / 192	GSE	FUJII_YBX1_TARGETS_DN
30	2e−07	245 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
31	5e−07	53 / 1352	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
32	6e−07	39 / 859	GSE	LEE_BMP2_TARGETS_DN
33	8e−07	13 / 124	GSE	ODONNELL_TFRC_TARGETS_DN
34	9e−07	15 / 168	GSE	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
35	9e−07	31 / 610	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
36	1e−06	24 / 400	GSE	VECCHI_GASTRIC_CANCER_EARLY_UP
37	1e−06	33 / 683	GSE	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
38	1e−06	56 / 1503	TF	ICGC_Six5_targets
39	1e−06	14 / 152	GSE	WHITFIELD_CELL_CYCLE_S
40	2e−06	15 / 175	GSE	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	3 / 144	HORVATH_aging_genes meth UP
2	0.7	2 / 123	HORVATH_aging_genes meth DOWN
3	1.0	0 / 57	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−04	20 / 410	mitotic cell cycle
2	5e−04	4 / 20	G2 DNA damage checkpoint
3	2e−03	3 / 13	trophoblast giant cell differentiation
4	2e−03	12 / 239	mitotic nuclear division
5	2e−03	4 / 30	tricarboxylic acid cycle
6	3e−03	3 / 15	isoprenoid biosynthetic process
7	3e−03	3 / 16	intracellular steroid hormone receptor signaling pathway
8	4e−03	10 / 191	vesicle−mediated transport
9	4e−03	14 / 323	cell division
10	5e−03	3 / 19	zinc II ion transport
11	1e−02	5 / 69	chromosome segregation
12	1e−02	4 / 45	tRNA aminoacylation for protein translation
13	1e−02	6 / 98	mitochondrial translation
14	1e−02	4 / 48	biosynthetic process
15	1e−02	3 / 27	release of sequestered calcium ion into cytosol
16	2e−02	32 / 1118	metabolic process
17	2e−02	7 / 136	cellular metabolic process
18	2e−02	8 / 170	proteasome−mediated ubiquitin−dependent protein catabolic process
19	2e−02	2 / 11	acrosome assembly
20	2e−02	2 / 11	cellular response to cholesterol

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	182 / 6320	Overlap_fetal_midbrain_HetRpts
2	1e−09	253 / 10239	Overlap_fetal_midbrain_ReprPC
3	5e−08	241 / 9923	Overlap_fetal_midbrain_K9K27me3
4	2e−07	245 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	4e−03	36 / 1182	Fetal_EnhP
6	5e−03	232 / 10800	Overlap_fetal_midbrain_Quies
7	1e−01	32 / 1356	Fetal_K9K27me3
8	2e−01	52 / 2443	Fetal_Quies
9	3e−01	69 / 3370	Mid_Frontal_Lobe_ZNF
10	4e−01	20 / 939	Fetal_HetRpts
11	4e−01	9 / 400	Fetal_ZNF
12	4e−01	19 / 910	Fetal_EnhG
13	5e−01	5 / 232	Fetal_ReprPC
14	5e−01	13 / 641	Mid_Frontal_Lobe_EnhP
15	5e−01	14 / 712	Overlap_fetal_midbrain_EnhP
16	6e−01	26 / 1394	Mid_Frontal_Lobe_Quies
17	6e−01	2 / 106	Overlap_fetal_midbrain_Tx
18	6e−01	20 / 1108	Overlap_fetal_midbrain_TssA
19	7e−01	16 / 940	Mid_Frontal_Lobe_Enh
20	8e−01	13 / 787	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	6e−10	35 / 550	Lembcke_Normal vs Adenoma
2	2e−03	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	4e−02	1 / 2	GENTLES_modul8
4	4e−02	0 / 16	LIU_COMMON_CANCER_GENES
5	4e−02	3 / 41	ZHANG_MM up
6	5e−02	4 / 71	SHAUGHNESSY_MM high risk
7	8e−02	3 / 52	KUIPER_MM poor survival
8	3e−01	1 / 15	GENTLES_modul4
9	3e−01	1 / 16	RHODES_CANCER_META_SIGNATURE
10	3e−01	1 / 16	WANG_ER_UP
11	3e−01	1 / 16	GENTLES_modul6
12	3e−01	1 / 16	GENTLES_modul16
13	3e−01	1 / 22	PanCan_ChromMod_geneset_nanostring
14	4e−01	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	4e−01	3 / 123	PanCan_Driver_Gene_geneset_nanostring
16	5e−01	1 / 37	KUIPER_MM good survival
17	5e−01	0 / 14	LIU_PROSTATE_CANCER_UP
18	6e−01	2 / 97	PanCan_TXmisReg_geneset_nanostring
19	6e−01	1 / 50	PanCan_DNARepair_geneset_nanostring
20	7e−01	3 / 191	SPANG_LPS−index2

CC

Rank	p−value	#in/all	Geneset
1	3e−05	17 / 277	mitochondrial matrix
2	5e−04	46 / 1441	mitochondrion
3	5e−03	5 / 58	chromosome, centromeric region
4	7e−03	3 / 21	transcription elongation factor complex
5	8e−03	18 / 497	Golgi membrane
6	9e−03	12 / 282	microtubule
7	1e−02	24 / 767	endoplasmic reticulum membrane
8	1e−02	2 / 10	mRNA cap binding complex
9	1e−02	2 / 10	pericentric heterochromatin
10	2e−02	5 / 76	condensed chromosome kinetochore
11	2e−02	4 / 51	transcriptional repressor complex
12	2e−02	4 / 53	kinesin complex
13	2e−02	63 / 2554	nucleoplasm
14	2e−02	2 / 13	chromocenter
15	3e−02	7 / 152	microtubule cytoskeleton
16	3e−02	14 / 411	centrosome
17	3e−02	3 / 36	mediator complex
18	4e−02	14 / 425	mitochondrial inner membrane
19	4e−02	5 / 95	centriole
20	4e−02	2 / 16	Cul4−RING E3 ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.08	20 / 735	Chr 4
2	0.08	20 / 745	Chr 9
3	0.09	10 / 318	Chr 13
4	0.10	29 / 1172	Chr 11
5	0.15	18 / 715	Chr 10
6	0.27	15 / 651	Chr 8
7	0.33	10 / 436	Chr 22
8	0.38	39 / 1920	Chr 1
9	0.40	21 / 1017	Chr 12
10	0.41	25 / 1228	Chr 2
11	0.42	6 / 272	Chr 18
12	0.46	17 / 847	Chr 16
13	0.49	17 / 862	Chr 5
14	0.55	10 / 522	Chr 20
15	0.63	11 / 613	Chr 14
16	0.68	13 / 746	Chr X
17	0.72	18 / 1043	Chr 3
18	0.78	16 / 976	Chr 6
19	0.84	17 / 1083	Chr 17
20	0.88	2 / 191	Chr 21

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−12	265 / 10475	TssA_Colon
2	9e−10	239 / 9470	Quies3_Colon
3	1e−09	237 / 9390	TxWk_Colon
4	1e−09	283 / 11968	TssWk_Colon
5	1e−07	240 / 9930	Tx_Colon
6	5e−05	30 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	2e−04	32 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
8	3e−04	189 / 8123	TssF_Colon
9	4e−03	36 / 1178	ZNF_Colon
10	2e−02	101 / 4379	TssD1_Colon
11	4e−02	1 / 2	Budinska_D_Mesenchymal_DOWN
12	4e−02	19 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	6e−02	2 / 20	Budinska_B_Lower crypt−like_UP
14	7e−02	1 / 4	Budinska_C_CIMP−H−like_DOWN
15	1e−01	141 / 6761	TssD2_Colon
16	1e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
17	1e−01	1 / 8	Boland_CRC−MMR−system
18	2e−01	18 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
19	2e−01	1 / 10	Juehling−MSI−enriched−in−7
20	2e−01	6 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.1	16 / 608	GUDJ_psoriasis up
2	0.2	2 / 37	BCHETNIA_EBM−DM up
3	0.3	1 / 22	BCHETNIA_EBM up
4	0.5	8 / 399	GUDJ_psoriasis down
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	18 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−05	65 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−05	70 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	4e−03	2 / 5	Phillips Prolif up vs PN & MES
5	1e−02	3 / 24	Martinez_Glio_hypermeth
6	2e−02	16 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
7	2e−02	12 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	6e−02	2 / 21	KIM deleted & downregulated in LTS
9	6e−02	4 / 77	Weller_LGG_gradeII−vs−III_DOWN
10	1e−01	6 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	1e−01	2 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
12	1e−01	1 / 8	shaw_responders_up_in_oligo_glioma
13	2e−01	1 / 9	Shaw_up_in_1p19qdel
14	2e−01	21 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
15	2e−01	3 / 81	GIEZELT_GBM_STS_up_VS_LTS
16	2e−01	3 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
17	2e−01	1 / 13	Mukasa_UP_in_Astroglioma
18	2e−01	3 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
19	2e−01	3 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
20	3e−01	1 / 16	astrocytes_glio

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−24	83 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	6e−17	62 / 975	NUYTTEN_EZH2_TARGETS_DN
3	2e−15	70 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	4e−14	53 / 852	GEORGES_TARGETS_OF_MIR192_AND_MIR215
5	1e−10	47 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
6	1e−10	36 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	5e−10	26 / 316	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	2e−09	41 / 747	PUJANA_CHEK2_PCC_NETWORK
9	8e−09	37 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	3e−08	22 / 284	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
11	2e−07	27 / 446	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	2e−07	17 / 192	FUJII_YBX1_TARGETS_DN
13	5e−07	53 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
14	6e−07	39 / 859	LEE_BMP2_TARGETS_DN
15	8e−07	13 / 124	ODONNELL_TFRC_TARGETS_DN
16	9e−07	15 / 168	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
17	9e−07	31 / 610	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
18	1e−06	24 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
19	1e−06	33 / 683	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
20	1e−06	14 / 152	WHITFIELD_CELL_CYCLE_S

HM

Rank	p−value	#in/all	Geneset
1	0.005	10 / 196	HALLMARK_G2M_CHECKPOINT
2	0.015	9 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	0.037	8 / 197	HALLMARK_E2F_TARGETS
4	0.039	8 / 199	HALLMARK_MTORC1_SIGNALING
5	0.047	5 / 102	HALLMARK_PEROXISOME
6	0.077	6 / 154	HALLMARK_FATTY_ACID_METABOLISM
7	0.101	3 / 58	HALLMARK_MYC_TARGETS_V2
8	0.156	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.174	6 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.271	3 / 94	HALLMARK_PROTEIN_SECRETION
11	0.291	3 / 98	HALLMARK_ANDROGEN_RESPONSE
12	0.321	5 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.325	5 / 196	HALLMARK_MITOTIC_SPINDLE
14	0.333	5 / 198	HALLMARK_GLYCOLYSIS
15	0.365	3 / 112	HALLMARK_BILE_ACID_METABOLISM
16	0.506	3 / 140	HALLMARK_UV_RESPONSE_DN
17	0.510	4 / 193	HALLMARK_HEME_METABOLISM
18	0.534	4 / 199	HALLMARK_ADIPOGENESIS
19	0.591	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
20	0.633	2 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.47	1 / 33	DUMEAUX_Fasting enriched genes
3	1.00	0 / 91	DUMEAUX_Smoking enriched genes
4	1.00	0 / 11	DUMEAUX_Smoking literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−20	230 / 7491	HOPP_Txn_elongation
2	1e−17	57 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
3	6e−17	56 / 811	WIRTH_lymphoma937_spot D
4	5e−13	173 / 5643	HOPP_Txn_transition
5	6e−13	228 / 8358	HOPP_Active_promoter
6	5e−09	211 / 8147	HOPP_Weak_promoter
7	1e−04	12 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
8	1e−04	12 / 171	WIRTH_lymphoma937_spot C
9	2e−04	45 / 1333	SPANG_BCR UP
10	6e−04	13 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
11	8e−04	13 / 240	WIRTH_lymphoma937_spot B
12	2e−03	14 / 302	SPANG_IL21 UP
13	1e−02	144 / 6389	HOPP_Weak_txn
14	1e−02	35 / 1215	SPANG_BCR DN
15	1e−02	151 / 6784	HOPP_Weak_enhancer
16	2e−02	12 / 317	TARTE_Plasmablast signature
17	2e−02	6 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
18	2e−02	6 / 116	WIRTH_lymphoma937_spot MM
19	3e−02	2 / 15	BENTINK_mBL UP
20	5e−02	2 / 19	DAVE_c−myc BL UP

MF

Rank	p−value	#in/all	Geneset
1	0.005	42 / 1448	ATP binding
2	0.005	4 / 37	aminoacyl−tRNA ligase activity
3	0.005	3 / 19	aldehyde dehydrogenase (NAD) activity
4	0.009	3 / 23	phosphatidylserine binding
5	0.010	9 / 187	ATPase activity
6	0.012	32 / 1091	poly(A) RNA binding
7	0.013	8 / 161	ubiquitin protein ligase activity
8	0.014	4 / 49	ligand−dependent nuclear receptor transcription coactivator activity
9	0.015	2 / 10	structural constituent of nuclear pore
10	0.016	3 / 28	protein phosphatase 2A binding
11	0.018	2 / 11	mismatched DNA binding
12	0.021	2 / 12	proton−transporting ATP synthase activity, rotational mechanism
13	0.029	3 / 35	kinesin binding
14	0.030	4 / 61	damaged DNA binding
15	0.031	3 / 36	RNA polymerase II transcription cofactor activity
16	0.033	2 / 15	cation transmembrane transporter activity
17	0.033	2 / 15	coenzyme binding
18	0.034	3 / 37	DNA−dependent ATPase activity
19	0.036	5 / 95	double−stranded DNA binding
20	0.037	2 / 16	vitamin D receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−08	25 / 377	hsa−let−7d
2	3e−05	10 / 105	hsa−miR−613
3	6e−05	14 / 212	hsa−miR−432
4	9e−05	18 / 334	hsa−miR−590−3p
5	1e−04	11 / 148	hsa−miR−409−3p
6	4e−04	13 / 223	hsa−miR−548m
7	6e−04	11 / 174	hsa−miR−580
8	6e−04	17 / 360	hsa−let−7a
9	8e−04	12 / 209	hsa−miR−221
10	8e−04	11 / 181	hsa−miR−199b−3p
11	8e−04	13 / 241	hsa−miR−26a
12	9e−04	15 / 305	hsa−miR−202
13	9e−04	10 / 156	hsa−miR−338−3p
14	1e−03	11 / 186	hsa−miR−196b
15	1e−03	11 / 186	hsa−miR−1
16	1e−03	19 / 442	hsa−miR−548n
17	1e−03	13 / 250	hsa−miR−26b
18	1e−03	9 / 139	hsa−miR−155
19	2e−03	8 / 113	hsa−miR−449b
20	2e−03	11 / 200	hsa−miR−568

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_src.10
2	0.2	1 / 14	BENTINK_src.2
3	0.3	1 / 15	BENTINK_ras.6
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 14	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_e2f3.2
8	1.0	0 / 14	BENTINK_myc.1
9	1.0	0 / 12	BENTINK_ras.1
10	1.0	0 / 10	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	1e−06	56 / 1503	ICGC_Six5_targets
2	3e−06	139 / 5173	ICGC_Taf1_targets
3	7e−05	118 / 4470	ICGC_Creb1_targets
4	1e−04	51 / 1549	ICGC_Myc_targets
5	1e−04	128 / 4987	ICGC_Bclaf101388_targets
6	1e−04	116 / 4436	ICGC_Zeb1_targets
7	2e−04	139 / 5552	ICGC_Pol24_targets
8	2e−04	138 / 5526	ICGC_Pmlsc71910_targets
9	3e−04	68 / 2342	ICGC_GabpPcr2_targets
10	6e−04	136 / 5578	ICGC_Stat5_targets
11	7e−04	132 / 5393	ICGC_Sp1_targets
12	1e−03	47 / 1547	ICGC_Ets1_targets
13	1e−03	149 / 6322	ICGC_Pol2_targets
14	2e−03	65 / 2354	ICGC_SrfV0416101_targets
15	2e−03	132 / 5512	ICGC_Nficsc81335_targets
16	3e−03	129 / 5453	ICGC_Foxm1_targets
17	3e−03	119 / 4969	ICGC_Atf2_targets
18	3e−03	140 / 6005	ICGC_Mta3_targets
19	4e−03	71 / 2719	ICGC_Pbx3_targets
20	4e−03	110 / 4566	ICGC_Egr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	3 / 33	VAQUERIZAS_Liver
2	0.21	1 / 12	VAQUERIZAS_Kidney
3	0.27	1 / 16	VAQUERIZAS_Fetal liver
4	0.29	1 / 18	VAQUERIZAS_Pancreas
5	0.37	1 / 24	VAQUERIZAS_Trachea
6	0.45	1 / 31	VAQUERIZAS_Fetal lung
7	0.51	1 / 37	VAQUERIZAS_Prostate
8	0.55	1 / 41	VAQUERIZAS_Fetal brain
9	0.55	1 / 41	VAQUERIZAS_Testis
10	0.56	1 / 42	VAQUERIZAS_Thymus
11	0.58	1 / 45	VAQUERIZAS_Placenta
12	0.61	1 / 49	VAQUERIZAS_Uterus
13	0.71	1 / 64	VAQUERIZAS_Lung
14	0.80	2 / 155	VAQUERIZAS_General
15	1.00	0 / 30	VAQUERIZAS_Smooth muscle
16	1.00	0 / 25	VAQUERIZAS_Spinal cord
17	1.00	0 / 46	VAQUERIZAS_Whole brain
18	1.00	0 / 42	VAQUERIZAS_Thyroid
19	1.00	0 / 67	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	WIRTH_Lymphocytes
2	0.2	1 / 14	WIRTH_Thymus
3	0.4	6 / 259	PALMER_Granulocytes signature up
4	0.5	3 / 137	WIRTH_Mucosa
5	0.6	1 / 47	WIRTH_Placenta
6	0.8	3 / 208	PALMER_B−Cell signature up
7	0.8	1 / 82	WIRTH_Homeostasis
8	0.8	6 / 427	WIRTH_Immune system
9	0.9	6 / 476	WIRTH_Nervous System
10	0.9	1 / 140	PALMER_T−Cell signature up
11	1.0	1 / 202	WIRTH_Testis
12	1.0	0 / 6	WIRTH_Pituitary gland
13	1.0	0 / 54	WIRTH_Pancreas
14	1.0	0 / 13	WIRTH_Sec. lymphoid organs
15	1.0	0 / 13	WIRTH_Prim. lymphoid organs
16	1.0	0 / 14	WIRTH_B−cells
17	1.0	0 / 12	WIRTH_Tonsil
18	1.0	0 / 14	WIRTH_Bone marrow
19	1.0	0 / 13	WIRTH_Globus pallidus
20	1.0	0 / 15	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	34 / 1343	LU_BPDE 1h DN
2	0.92	90 / 5285	LU_BPDE 0.005 DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Correlation Clusters

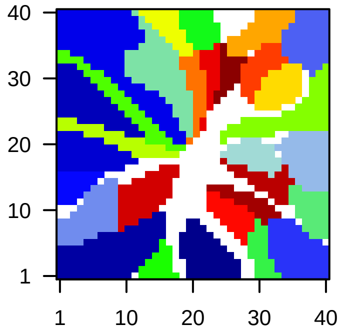
Spot Summary: Y

metagenes = 21
genes = 204

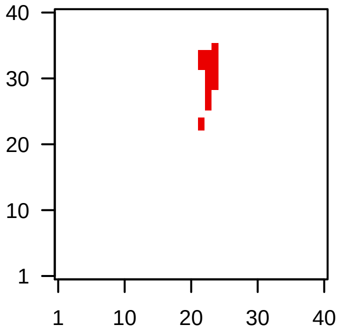
<r> metagenes = 0.94
<r> genes = 0.41
beta: r2= 0 / log p= −0.06

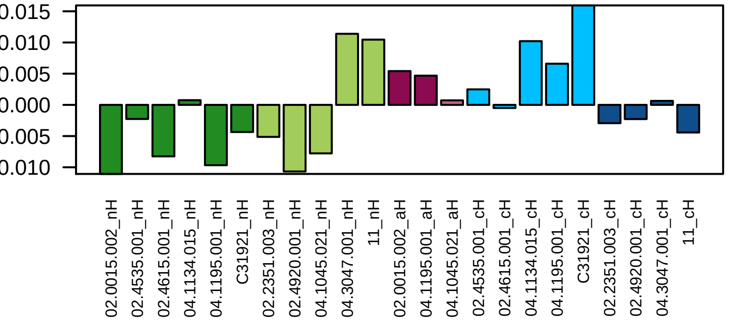
samples with spot = 0 (0 %)

Overview Map



Spot





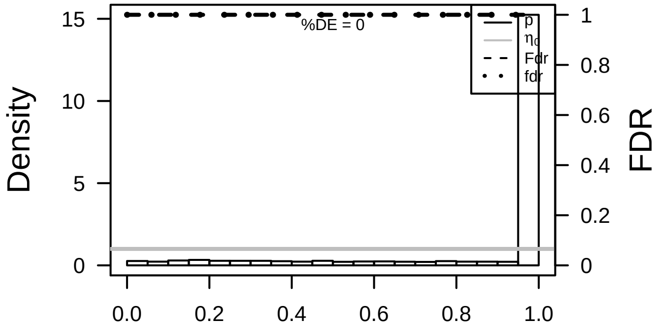
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	0.19	−0.02	0.34	CHGB	chromogranin B [Source:HGNC Symbol;Acc:HGNC:1930]
2	ENSG000001	0.1	−0.04	0.5	TRMT12	tRNA methyltransferase 12 homolog (S. cerevisiae) [Source:H
3	ENSG000001	0.09	−0.02	0.75	PGAP1	post−GPI attachment to proteins 1 [Source:HGNC Symbol;Ac
4	ENSG000002	0.08	−0.02	0.47		Coiled−coil domain−containing protein 144A; Uncharacterized
5	ENSG000001	0.08	−0.03	0.63	STK36	serine/threonine kinase 36 [Source:HGNC Symbol;Acc:HGNC
6	ENSG000001	0.08	−0.04	0.55	DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 [
7	ENSG000001	0.07	−0.03	0.48	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane d
8	ENSG000001	0.06	−0.01	0.52	ITGB8	integrin, beta 8 [Source:HGNC Symbol;Acc:HGNC:6163]
9	ENSG000002	0.06	−0.01	0.7		
10	ENSG000001	0.06	−0.04	0.72	TBC1D16	TBC1 domain family, member 16 [Source:HGNC Symbol;Acc
11	ENSG000001	0.06	−0.03	0.58	ZNF300	zinc finger protein 300 [Source:HGNC Symbol;Acc:HGNC:13
12	ENSG000001	0.06	−0.01	0.44	UBQLNL	ubiquilin−like [Source:HGNC Symbol;Acc:HGNC:28294]
13	ENSG000001	0.05	−0.03	0.51	PGM2L1	phosphoglucomutase 2−like 1 [Source:HGNC Symbol;Acc:HG
14	ENSG000001	0.05	−0.02	0.46	KBTBD12	kelch repeat and BTB (POZ) domain containing 12 [Source:H
15	ENSG000001	0.05	0	0.54	GALNT13	polypeptide N−acetylgalactosaminyltransferase 13 [Source:H
16	ENSG000002	0.05	−0.02	0.67	DFNB59	deafness, autosomal recessive 59 [Source:HGNC Symbol;Ac
17	ENSG000001	0.05	−0.03	0.64	TCAIM	T cell activation inhibitor, mitochondrial [Source:HGNC Symbo
18	ENSG000001	0.05	−0.02	0.51	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1 [Sour
19	ENSG000002	0.05	−0.01	0.66	C4orf47	chromosome 4 open reading frame 47 [Source:HGNC Symbo
20	ENSG000001	0.05	−0.03	0.67	NMNAT3	nicotinamide nucleotide adenylyltransferase 3 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−08	142 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
2	2e−07	140 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
3	3e−06	101 / 6784	Lymph	HOPP_Weak_enhancer
4	1e−05	28 / 1134	MF	nucleic acid binding
5	2e−05	24 / 910	Brain	Fetal_EnhG
6	3e−05	6 / 60	Colon	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
7	6e−05	75 / 4879	Colon	Quies1_Colon
8	7e−05	4 / 22	BP	cilium movement
9	2e−04	111 / 8358	Lymph	HOPP_Active_promoter
10	2e−04	10 / 240	Lymph	WIRTH_lymphoma937_spot B
11	3e−04	3 / 13	BP	head development
12	3e−04	108 / 8147	Lymph	HOPP_Weak_promoter
13	4e−04	88 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
14	5e−04	33 / 1753	Colon	Het_Colon
15	5e−04	3 / 16	BP	axoneme assembly
16	7e−04	3 / 17	BP	retinal ganglion cell axon guidance
17	7e−04	65 / 4379	Colon	TssD1_Colon
18	7e−04	26 / 1281	Colon	HetRpts_Colon
19	7e−04	9 / 233	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell li
20	1e−03	53 / 3457	Lymph	HOPP_Heterochrom
21	1e−03	6 / 118	BP	cilium assembly
22	2e−03	12 / 431	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
23	2e−03	3 / 25	CC	ciliary base
24	2e−03	4 / 53	GSEA	OUILLETTE_CLL_13Q14_DELETION_DN
25	2e−03	85 / 6389	Lymph	HOPP_Weak_txn
26	2e−03	3 / 26	miRN	hsa−miR−943
27	2e−03	5 / 90	CC	ciliary basal body
28	2e−03	23 / 1182	Brain	Fetal_EnhP
29	3e−03	37 / 2253	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
30	3e−03	16 / 712	Brain	Overlap_fetal_midbrain_EnhP
31	3e−03	4 / 58	BP	determination of left/right symmetry
32	3e−03	38 / 2354	TF	ICGC_SrfV0416101_targets
33	3e−03	22 / 1137	Brain	Fetal_Enh
34	3e−03	18 / 859	Chr	Chr 7
35	4e−03	11 / 411	CC	centrosome
36	4e−03	83 / 6324	TF	ICGC_Yy1_targets
37	4e−03	2 / 10	BP	regulation of cilium assembly
38	5e−03	4 / 66	BP	cilium morphogenesis
39	5e−03	4 / 68	BP	protein localization
40	5e−03	5 / 109	BP	neuron migration

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 124	HORVATH_aging_genes meth DOWN
2	1	0 / 144	HORVATH_aging_genes meth UP
3	1	0 / 57	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 22	cilium movement
2	3e−04	3 / 13	head development
3	5e−04	3 / 16	axoneme assembly
4	7e−04	3 / 17	retinal ganglion cell axon guidance
5	1e−03	6 / 118	cilium assembly
6	3e−03	4 / 58	determination of left/right symmetry
7	4e−03	2 / 10	regulation of cilium assembly
8	5e−03	4 / 66	cilium morphogenesis
9	5e−03	4 / 68	protein localization
10	5e−03	5 / 109	neuron migration
11	5e−03	2 / 11	establishment of planar polarity
12	6e−03	30 / 1808	regulation of transcription, DNA−templated
13	6e−03	2 / 12	outer dynein arm assembly
14	6e−03	2 / 12	regulation of cell−cell adhesion
15	1e−02	2 / 15	multicellular organismal aging
16	1e−02	3 / 44	skeletal system morphogenesis
17	1e−02	2 / 17	positive regulation of G2/M transition of mitotic cell cycle
18	1e−02	2 / 18	intraciliary transport
19	2e−02	2 / 20	response to vitamin A
20	2e−02	2 / 21	embryonic pattern specification

Brain

Rank	p−value	#in/all	Geneset
1	5e−08	142 / 10278	Overlap_fetal_midbrain_ReprPCWk
2	2e−07	140 / 10239	Overlap_fetal_midbrain_ReprPC
3	2e−05	24 / 910	Fetal_EnhG
4	4e−04	88 / 6320	Overlap_fetal_midbrain_HetRpts
5	2e−03	23 / 1182	Fetal_EnhP
6	3e−03	16 / 712	Overlap_fetal_midbrain_EnhP
7	3e−03	22 / 1137	Fetal_Enh
8	6e−03	38 / 2443	Fetal_Quies
9	1e−02	22 / 1279	Overlap_fetal_midbrain_Enh
10	1e−02	23 / 1356	Fetal_K9K27me3
11	3e−02	12 / 641	Mid_Frontal_Lobe_EnhP
12	6e−02	15 / 939	Fetal_HetRpts
13	8e−02	121 / 10800	Overlap_fetal_midbrain_Quies
14	8e−02	112 / 9923	Overlap_fetal_midbrain_K9K27me3
15	9e−02	16 / 1084	Overlap_fetal_midbrain_EnhG
16	2e−01	4 / 232	Fetal_ReprPC
17	2e−01	33 / 2820	Mid_Frontal_Lobe_HetRpts
18	4e−01	11 / 940	Mid_Frontal_Lobe_Enh
19	5e−01	27 / 2549	Fetal_TssF
20	5e−01	4 / 342	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	9 / 550	Lembcke_Normal vs Adenoma
2	0.3	3 / 198	PanCan_PI3K_geneset_nanostring
3	0.6	1 / 78	PanCan_Wnt_geneset_nanostring
4	0.6	1 / 86	PanCan_JAK−ST_geneset_nanostring
5	0.7	1 / 123	PanCan_Driver_Gene_geneset_nanostring
6	0.8	1 / 140	PanCan_RAS_geneset_nanostring
7	0.9	1 / 191	SPANG_LPS−index2
8	1.0	1 / 324	SPANG_BCL6−index2
9	1.0	0 / 16	LIU_PROSTATE_CANCER_DN
10	1.0	1 / 574	Lembcke_Colonic Inflammation
11	1.0	0 / 16	RHODES_CANCER_META_SIGNATURE
12	1.0	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
13	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.0	0 / 15	LIU_BREAST_CANCER
16	1.0	0 / 16	LIU_COMMON_CANCER_GENES
17	1.0	0 / 16	LIU_LIVER_CANCER
18	1.0	0 / 14	LIU_PROSTATE_CANCER_UP
19	1.0	0 / 16	WANG_ER_UP
20	1.0	0 / 9	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	0.002	3 / 25	ciliary base
2	0.002	5 / 90	ciliary basal body
3	0.004	11 / 411	centrosome
4	0.006	4 / 70	axoneme
5	0.006	3 / 36	photoreceptor connecting cilium
6	0.016	2 / 19	nonmotile primary cilium
7	0.019	2 / 21	ciliary transition zone
8	0.029	2 / 26	presynaptic active zone
9	0.040	24 / 1604	intracellular
10	0.051	3 / 81	ubiquitin ligase complex
11	0.054	7 / 329	neuronal cell body
12	0.059	4 / 142	cilium
13	0.067	3 / 91	apical part of cell
14	0.072	2 / 43	ciliary tip
15	0.072	2 / 43	intercellular bridge
16	0.074	3 / 95	centriole
17	0.098	1 / 10	axon initial segment
18	0.098	1 / 10	sperm midpiece
19	0.098	1 / 10	spindle pole centrosome
20	0.107	1 / 11	mRNA cleavage and polyadenylation specificity factor complex

Chr

Rank	p−value	#in/all	Geneset
1	0.003	18 / 859	Chr 7
2	0.044	16 / 976	Chr 6
3	0.136	11 / 735	Chr 4
4	0.177	12 / 862	Chr 5
5	0.186	14 / 1043	Chr 3
6	0.195	16 / 1228	Chr 2
7	0.531	3 / 272	Chr 18
8	0.559	11 / 1083	Chr 17
9	0.586	2 / 191	Chr 21
10	0.604	7 / 715	Chr 10
11	0.637	3 / 318	Chr 13
12	0.648	7 / 745	Chr 9
13	0.717	5 / 582	Chr 15
14	0.723	9 / 1017	Chr 12
15	0.758	5 / 613	Chr 14
16	0.775	17 / 1920	Chr 1
17	0.803	5 / 651	Chr 8
18	0.857	9 / 1172	Chr 11
19	0.874	11 / 1425	Chr 19
20	0.907	3 / 522	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	6 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
2	6e−05	75 / 4879	Quies1_Colon
3	5e−04	33 / 1753	Het_Colon
4	7e−04	65 / 4379	TssD1_Colon
5	7e−04	26 / 1281	HetRpts_Colon
6	1e−02	21 / 1178	ZNF_Colon
7	2e−02	2 / 20	Juehling_HNPCC−mutated−in−4
8	5e−02	109 / 9470	Quies3_Colon
9	7e−02	118 / 10475	TssA_Colon
10	8e−02	1 / 8	Boland_CRC−MMR−system
11	9e−02	9 / 525	Quies2_Colon
12	1e−01	1 / 15	TCGA_Mutated−in−CRC_hypermutated
13	2e−01	7 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
14	2e−01	1 / 19	Vilar_hypermutated−in−CRC
15	2e−01	1 / 21	Juehling−MSI−enriched−in−6
16	2e−01	4 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
17	3e−01	127 / 11968	TssWk_Colon
18	4e−01	1 / 52	Pentrack_CRC_TCGA_corr_S_normal_DN
19	5e−01	6 / 532	K9acLow_Colon
20	5e−01	9 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.9	4 / 608	GUDJ_psoriasis up
2	0.9	2 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	37 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.006	32 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	0.066	14 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	0.067	8 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
5	0.100	2 / 52	OL vs. OPC
6	0.117	1 / 12	Phillips PN up vs MES & Prolif
7	0.117	1 / 12	WILLSCHER_GBM_LTSwt_proteomics−C_UP
8	0.162	2 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.187	1 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
10	0.195	1 / 21	KIM deleted & downregulated in LTS
11	0.202	2 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.230	3 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
13	0.236	2 / 90	Weller_LGG_A_vs_O_DOWN
14	0.243	1 / 27	Barbus_GBM_STS_vs._LTS
15	0.274	1 / 31	KIM prognostic signature LTS vs. STS
16	0.279	5 / 344	Up
17	0.286	2 / 103	GIEZELT_GBM_STS_down_VS_LTS
18	0.292	6 / 436	Down_b
19	0.338	6 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
20	0.342	11 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	12 / 431	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
2	0.002	4 / 53	OUILLETTE_CLL_13Q14_DELETION_DN
3	0.006	4 / 69	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN
4	0.007	4 / 74	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA
5	0.008	7 / 219	ZWANG_DOWN_BY_2ND_EGF_PULSE
6	0.009	7 / 228	WANG_CLIM2_TARGETS_UP
7	0.010	2 / 15	ZHANG_GATA6_TARGETS_UP
8	0.011	4 / 83	GAUSSMANN_MLL_AF4_FUSION_TARGETS_A_DN
9	0.013	2 / 17	PID_SMAD2_3PATHWAY
10	0.016	19 / 1084	PEREZ_TP53_TARGETS
11	0.018	2 / 20	VERRECCHIA_RESPONSE_TO_TGFB1_C5
12	0.019	3 / 55	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
13	0.019	2 / 21	OKAWA_NEUROBLASTOMA_1P36_31_DELETION
14	0.020	8 / 326	RICKMAN_METASTASIS_UP
15	0.024	4 / 106	BROWNE_HCMV_INFECTION_12HR_UP
16	0.030	4 / 114	HOOI_ST7_TARGETS_DN
17	0.030	3 / 66	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP
18	0.033	3 / 68	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
19	0.043	7 / 312	GRESHOCK_CANCER_COPY_NUMBER_UP
20	0.045	3 / 77	KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION

HM

Rank	p−value	#in/all	Geneset
1	0.07	2 / 44	HALLMARK_APICAL_SURFACE
2	0.31	1 / 36	HALLMARK_HEDGEHOG_SIGNALING
3	0.59	2 / 193	HALLMARK_KRAS_SIGNALING_DN
4	0.60	2 / 196	HALLMARK_G2M_CHECKPOINT
5	0.62	1 / 94	HALLMARK_PROTEIN_SECRETION
6	0.68	1 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.69	1 / 112	HALLMARK_BILE_ACID_METABOLISM
8	0.78	1 / 146	HALLMARK_DNA_REPAIR
9	0.80	1 / 155	HALLMARK_UV_RESPONSE_UP
10	0.86	1 / 189	HALLMARK_KRAS_SIGNALING_UP
11	0.86	1 / 192	HALLMARK_COMPLEMENT
12	0.86	1 / 193	HALLMARK_XENOBIOTIC_METABOLISM
13	0.87	1 / 194	HALLMARK_INFLAMMATORY_RESPONSE
14	0.87	1 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.87	1 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
16	0.87	1 / 196	HALLMARK_MITOTIC_SPINDLE
17	0.87	1 / 197	HALLMARK_IL2_STAT5_SIGNALING
18	0.87	1 / 198	HALLMARK_GLYCOLYSIS
19	1.00	0 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	1.00	0 / 198	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 91	DUMEAUX_Smoking enriched genes
2	1	0 / 11	DUMEAUX_Smoking literature genes up
3	1	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 17	DUMEAUX_High bmi enriched genes
11	1	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−06	101 / 6784	HOPP_Weak_enhancer
2	2e−04	111 / 8358	HOPP_Active_promoter
3	2e−04	10 / 240	WIRTH_lymphoma937_spot B
4	3e−04	108 / 8147	HOPP_Weak_promoter
5	7e−04	9 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
6	1e−03	53 / 3457	HOPP_Heterochrom
7	2e−03	85 / 6389	HOPP_Weak_txn
8	5e−02	36 / 2658	HOPP_Repetitive
9	5e−02	38 / 2838	HOPP_Poised_promoter
10	9e−02	4 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
11	1e−01	4 / 171	WIRTH_lymphoma937_spot C
12	2e−01	11 / 811	WIRTH_lymphoma937_spot D
13	2e−01	57 / 5039	HOPP_Repressed
14	3e−01	10 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
15	3e−01	2 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_t
16	3e−01	2 / 116	WIRTH_lymphoma937_spot MM
17	4e−01	80 / 7491	HOPP_Txn_elongation
18	5e−01	14 / 1333	SPANG_BCR UP
19	6e−01	3 / 302	SPANG_IL21 UP
20	6e−01	1 / 92	WIRTH_lymphoma937_spot A

MF

Rank	p−value	#in/all	Geneset
1	1e−05	28 / 1134	nucleic acid binding
2	1e−02	2 / 15	K63−linked polyubiquitin binding
3	1e−02	4 / 90	ubiquitin−specific protease activity
4	1e−02	3 / 49	manganese ion binding
5	2e−02	2 / 21	protein kinase activator activity
6	3e−02	2 / 26	nuclease activity
7	4e−02	3 / 73	ubiquitinyl hydrolase activity
8	5e−02	2 / 35	kinesin binding
9	7e−02	28 / 2040	metal ion binding
10	7e−02	2 / 42	protein complex scaffold
11	7e−02	15 / 962	transcription factor activity, sequence−specific DNA binding
12	7e−02	2 / 43	symporter activity
13	8e−02	25 / 1803	DNA binding
14	1e−01	1 / 10	1−acylglycerol−3−phosphate O−acyltransferase activity
15	1e−01	1 / 10	chemorepellent activity
16	1e−01	1 / 10	phospholipid transporter activity
17	1e−01	1 / 10	potassium ion binding
18	1e−01	1 / 10	signaling adaptor activity
19	1e−01	1 / 10	small protein activating enzyme activity
20	1e−01	1 / 11	mismatched DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 26	hsa−miR−943
2	0.011	5 / 131	hsa−miR−145
3	0.016	9 / 377	hsa−let−7d
4	0.023	2 / 23	hsa−miR−596
5	0.032	3 / 67	hsa−miR−1285
6	0.050	1 / 5	hsa−miR−1268
7	0.052	5 / 196	hsa−miR−513a−3p
8	0.054	3 / 83	hsa−miR−1179
9	0.055	8 / 400	hsa−let−7c
10	0.056	5 / 200	hsa−miR−568
11	0.068	5 / 212	hsa−miR−432
12	0.070	4 / 151	hsa−miR−143
13	0.071	3 / 93	hsa−miR−425
14	0.078	2 / 45	hsa−miR−518d−3p
15	0.078	3 / 97	hsa−miR−125a−3p
16	0.079	7 / 360	hsa−let−7a
17	0.087	2 / 48	hsa−miR−623
18	0.088	8 / 444	hsa−let−7b
19	0.089	1 / 9	hsa−miR−202*
20	0.093	2 / 50	hsa−miR−1201

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.003	38 / 2354	ICGC_SrfV0416101_targets
2	0.004	83 / 6324	ICGC_Yy1_targets
3	0.006	26 / 1503	ICGC_Six5_targets
4	0.006	82 / 6322	ICGC_Pol2_targets
5	0.009	15 / 731	ICGC_SrfPcr2_targets
6	0.018	71 / 5552	ICGC_Pol24_targets
7	0.019	85 / 6862	ICGC_Elf1_targets
8	0.030	65 / 5135	ICGC_Ebfsc137065_targets
9	0.034	63 / 4987	ICGC_Bclaf101388_targets
10	0.035	68 / 5453	ICGC_Foxm1_targets
11	0.039	58 / 4566	ICGC_Egr1_targets
12	0.040	69 / 5578	ICGC_Stat5_targets
13	0.044	68 / 5512	ICGC_Nficsc81335_targets
14	0.046	30 / 2133	ICGC_Cebpbsc150_targets
15	0.048	56 / 4436	ICGC_Zeb1_targets
16	0.049	64 / 5173	ICGC_Taf1_targets
17	0.055	43 / 3305	ICGC_BatfPcr1_targets
18	0.063	67 / 5526	ICGC_Pmlsc71910_targets
19	0.063	36 / 2719	ICGC_Pbx3_targets
20	0.074	65 / 5393	ICGC_Sp1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 41	VAQUERIZAS_Fetal brain
2	1	0 / 45	VAQUERIZAS_Placenta
3	1	0 / 33	VAQUERIZAS_Liver
4	1	0 / 37	VAQUERIZAS_Prostate
5	1	0 / 30	VAQUERIZAS_Smooth muscle
6	1	0 / 49	VAQUERIZAS_Uterus
7	1	0 / 155	VAQUERIZAS_General
8	1	0 / 12	VAQUERIZAS_Kidney
9	1	0 / 25	VAQUERIZAS_Spinal cord
10	1	0 / 46	VAQUERIZAS_Whole brain
11	1	0 / 42	VAQUERIZAS_Thymus
12	1	0 / 42	VAQUERIZAS_Thyroid
13	1	0 / 67	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 31	VAQUERIZAS_Fetal lung
16	1	0 / 64	VAQUERIZAS_Lung
17	1	0 / 18	VAQUERIZAS_Pancreas
18	1	0 / 24	VAQUERIZAS_Trachea
19	1	0 / 16	VAQUERIZAS_Fetal liver
20	1	0 / 22	VAQUERIZAS_Tonsil

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	8 / 478	WIRTH_Nervous System
2	0.2	4 / 202	WIRTH_Testis
3	0.4	1 / 47	WIRTH_Placenta
4	0.6	1 / 82	WIRTH_Homeostasis
5	0.8	1 / 140	PALMER_T−Cell signature up
6	0.8	1 / 141	WIRTH_Muscle
7	1.0	0 / 6	WIRTH_Pituitary gland
8	1.0	0 / 54	WIRTH_Pancreas
9	1.0	0 / 427	WIRTH_Immune system
10	1.0	0 / 13	WIRTH_Sec. lymphoid organs
11	1.0	0 / 13	WIRTH_Prim. lymphoid organs
12	1.0	0 / 14	WIRTH_B−cells
13	1.0	0 / 14	WIRTH_Tonsil
14	1.0	0 / 14	WIRTH_Thymus
15	1.0	0 / 12	WIRTH_Lymphocytes
16	1.0	0 / 14	WIRTH_Bone marrow
17	1.0	0 / 13	WIRTH_Globus pallidus
18	1.0	0 / 15	WIRTH_Telencephalon
19	1.0	0 / 12	WIRTH_Cortex cerebri
20	1.0	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.005	71 / 5285	LU_BPDE 0.005 DN
2	0.987	7 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

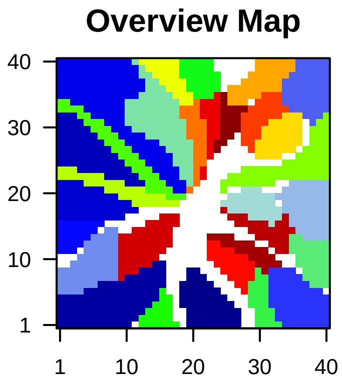
Correlation Clusters

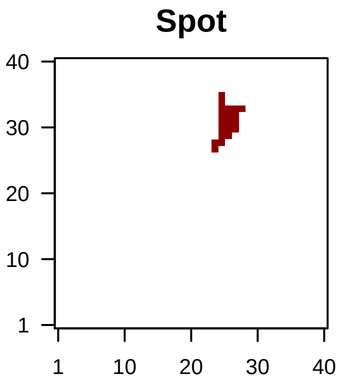
Spot Summary: Z

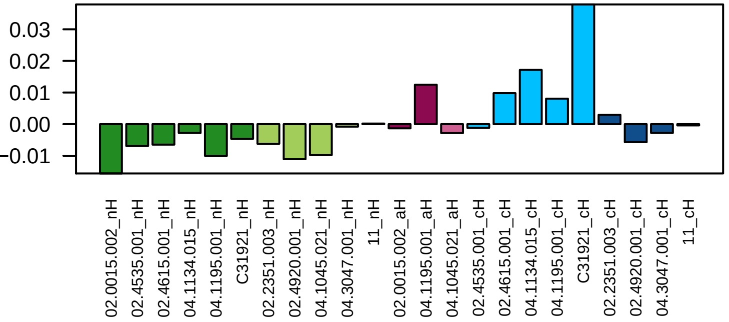
metagenes = 20
genes = 176

<r> metagenes = 0.94
<r> genes = 0.42
beta: r2= 0 / log p= −0.09

samples with spot = 0 (0 %)





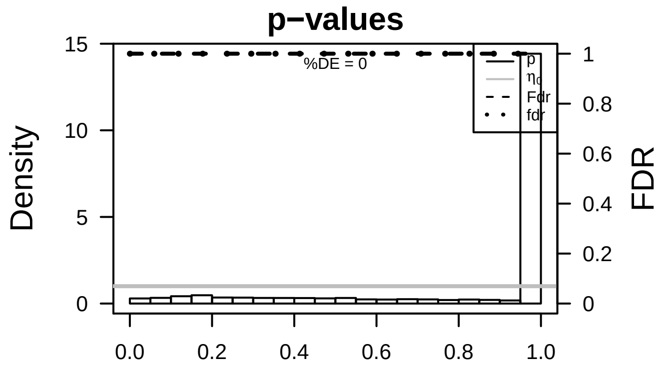


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.2	−0.02	0.73	SLITRK6	SLIT and NTRK−like family, member 6 [Source:HGNC Symbo
2	ENSG000001	0.19	−0.04	0.73	ODF2L	outer dense fiber of sperm tails 2−like [Source:HGNC Symbo
3	ENSG000001	0.17	−0.03	0.73	LRP5L	low density lipoprotein receptor−related protein 5−like [Sourc
4	ENSG000001	0.17	−0.01	0.44	GIF	gastric intrinsic factor (vitamin B synthesis) [Source:HGNC S
5	ENSG000001	0.16	−0.04	0.73	SLC2A10	solute carrier family 2 (facilitated glucose transporter), membe
6	ENSG000001	0.15	−0.02	0.68	ALDH1A2	aldehyde dehydrogenase 1 family, member A2 [Source:HGN
7	ENSG000001	0.15	−0.05	0.63	SHF	Src homology 2 domain containing F [Source:HGNC Symbol;
8	ENSG000001	0.14	−0.01	0.5	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H
9	ENSG000001	0.12	−0.06	0.67	MTA1	metastasis associated 1 [Source:HGNC Symbol;Acc:HGNC:
10	ENSG000001	0.12	−0.03	0.71	ANKRD36	ankyrin repeat domain 36 [Source:HGNC Symbol;Acc:HGNC
11	ENSG000000	0.11	−0.02	0.6	MT3	metallothionein 3 [Source:HGNC Symbol;Acc:HGNC:7408]
12	ENSG000001	0.1	−0.01	0.67	WT1	Wilms tumor 1 [Source:HGNC Symbol;Acc:HGNC:12796]
13	ENSG000001	0.1	−0.01	0.77	HAPLN1	hyaluronan and proteoglycan link protein 1 [Source:HGNC S
14	ENSG000001	0.09	−0.06	0.52	FANCF	Fanconi anemia, complementation group F [Source:HGNC S
15	ENSG000001	0.09	−0.02	0.68	CYP4X1	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
16	ENSG000001	0.09	−0.01	0.75	NBPF4	neuroblastoma breakpoint family, member 4 [Source:HGNC
17	ENSG000001	0.09	−0.01	0.65	SLCO1B3	solute carrier organic anion transporter family, member 1B3 [
18	ENSG000000	0.09	−0.01	0.8	SLC11A1	solute carrier family 11 (proton−coupled divalent metal ion tra
19	ENSG000001	0.09	−0.07	0.42	MCEE	methylmalonyl CoA epimerase [Source:HGNC Symbol;Acc:H
20	ENSG000001	0.08	0	0.33	TTC29	tetratricopeptide repeat domain 29 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−05	18 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
2	4e−04	22 / 1084	Brain	Overlap_fetal_midbrain_EnhG
3	4e−04	16 / 668	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
4	6e−04	14 / 550	Canc	Lembcke_Normal vs Adenoma
5	9e−04	18 / 859	GSE	LEE_BMP2_TARGETS_DN
6	1e−03	11 / 396	GSE	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECUL
7	1e−03	7 / 175	GSE	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
8	1e−03	6 / 128	GSE	SABATES_COLORECTAL_ADENOMA_UP
9	1e−03	2 / 6	GSE	PALOMERO_GSI_SENSITIVITY_UP
10	2e−03	16 / 753	BP	transmembrane transport
11	3e−03	28 / 1753	Colon	Het_Colon
12	3e−03	3 / 31	MF	antiporter activity
13	3e−03	4 / 65	BP	camera−type eye development
14	3e−03	22 / 1279	Brain	Overlap_fetal_midbrain_Enh
15	3e−03	127 / 11968	Colon	TssWk_Colon
16	4e−03	3 / 34	BP	embryonic forelimb morphogenesis
17	4e−03	1 / 16	Canc	LIU_COMMON_CANCER_GENES
18	4e−03	5 / 113	MF	methyltransferase activity
19	4e−03	3 / 35	GSE	SHIPP_DLBCL_CURED_VS_FATAL_UP
20	4e−03	16 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
21	4e−03	2 / 11	GSE	MATHEW_FANCONI_ANEMIA_GENES
22	4e−03	6 / 167	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell li
23	5e−03	6 / 171	Lymp	WIRTH_lymphoma937_spot C
24	5e−03	2 / 12	MF	fucosyltransferase activity
25	6e−03	7 / 231	GSE	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
26	6e−03	11 / 491	BP	transport
27	6e−03	17 / 944	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
28	6e−03	2 / 13	CC	Fanconi anaemia nuclear complex
29	6e−03	2 / 13	BP	fucosylation
30	7e−03	4 / 81	CC	ubiquitin ligase complex
31	7e−03	5 / 129	BP	sensory perception of sound
32	7e−03	12 / 578	GSE	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
33	8e−03	4 / 85	BP	chloride transmembrane transport
34	8e−03	21 / 1298	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
35	8e−03	3 / 45	BP	anion transmembrane transport
36	8e−03	3 / 45	GSE	PID_FANCONI_PATHWAY
37	8e−03	2 / 15	MF	cation transmembrane transporter activity
38	9e−03	2 / 16	BP	nucleotide biosynthetic process
39	1e−02	3 / 50	MF	chloride channel activity
40	1e−02	2 / 18	CC	DNA−directed RNA polymerase III complex



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 57	TESCHENDORFF_age_hypermethylated
2	1.0	0 / 123	HORVATH_aging_genes meth DOWN
3	1.0	0 / 144	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	6e−04	14 / 550	Lembcke_Normal vs Adenoma
2	4e−03	1 / 16	LIU_COMMON_CANCER_GENES
3	5e−02	0 / 14	LIU_PROSTATE_CANCER_UP
4	5e−02	1 / 6	ZHANG_MGUS up
5	4e−01	1 / 50	PanCan_DNARepair_geneset_nanostring
6	4e−01	1 / 52	KUIPER_MM poor survival
7	5e−01	1 / 86	PanCan_JAK−ST_geneset_nanostring
8	6e−01	1 / 97	PanCan_TXmisReg_geneset_nanostring
9	7e−01	1 / 123	PanCan_Driver_Gene_geneset_nanostring
10	7e−01	1 / 136	PanCan_CC+Apop_geneset_nanostring
11	8e−01	1 / 198	PanCan_PI3K_geneset_nanostring
12	9e−01	3 / 574	Lembcke_Colonic Inflammation
13	1e+00	0 / 16	RHODES_CANCER_META_SIGNATURE
14	1e+00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	1e+00	0 / 15	LIU_BREAST_CANCER
18	1e+00	0 / 16	LIU_LIVER_CANCER
19	1e+00	0 / 16	LIU_PROSTATE_CANCER_DN
20	1e+00	0 / 16	WANG_ER_UP

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−05	18 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
2	3e−03	28 / 1753	Het_Colon
3	3e−03	127 / 11968	TssWk_Colon
4	4e−03	16 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
5	1e−02	58 / 4879	Quies1_Colon
6	2e−02	2 / 21	Juehling−MSI−enriched−in−6
7	3e−02	19 / 1281	HetRpts_Colon
8	7e−02	1 / 8	Marisa_CRC−C6
9	7e−02	1 / 8	Budinska_C_CIMP−H−like_UP
10	8e−02	48 / 4327	EnhWk2_Colon
11	9e−02	1 / 10	Juehling−HNPCC−mutated−in−5
12	9e−02	1 / 10	Juehling−MSI−enriched−in−7
13	1e−01	2 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
14	1e−01	9 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
15	2e−01	2 / 76	Marisa_CRC−cluster−g
16	2e−01	10 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
17	2e−01	2 / 78	Ang_CRC_Hypermethylated
18	2e−01	1 / 19	Vilar_hypermutated−in−CRC
19	2e−01	7 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
20	3e−01	2 / 110	Marisa_CRC−cluster−h

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	16 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
2	9e−04	18 / 859	LEE_BMP2_TARGETS_DN
3	1e−03	11 / 396	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES
4	1e−03	7 / 175	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
5	1e−03	6 / 128	SABATES_COLORECTAL_ADENOMA_UP
6	1e−03	2 / 6	PALOMERO_GSI_SENSITIVITY_UP
7	4e−03	1 / 16	LIU_COMMON_CANCER_GENES
8	4e−03	3 / 35	SHIPP_DLBCL_CURED_VS_FATAL_UP
9	4e−03	2 / 11	MATHEW_FANCONI_ANEMIA_GENES
10	6e−03	7 / 231	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
11	6e−03	17 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
12	7e−03	12 / 578	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
13	8e−03	21 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	8e−03	3 / 45	PID_FANCONI_PATHWAY
15	1e−02	15 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
16	1e−02	4 / 97	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN
17	1e−02	3 / 53	ROVERSI_GLIOMA_COPY_NUMBER_DN
18	1e−02	2 / 19	OUYANG_PROSTATE_CANCER_MARKERS
19	1e−02	3 / 54	REACTOME_ION_CHANNEL_TRANSPORT
20	1e−02	3 / 55	HOQUE_METHYLATED_IN_CANCER

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.004	6 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
2	0.005	6 / 171	WIRTH_lymphoma937_spot C
3	0.017	14 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
4	0.019	72 / 6389	HOPP_Weak_txn
5	0.036	13 / 811	WIRTH_lymphoma937_spot D
6	0.037	19 / 1333	SPANG_BCR UP
7	0.042	4 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
8	0.044	4 / 144	WIRTH_lymphoma937_spot G
9	0.070	72 / 6784	HOPP_Weak_enhancer
10	0.072	3 / 105	ROSOLOWSKI_blue total
11	0.086	86 / 8358	HOPP_Active_promoter
12	0.114	83 / 8147	HOPP_Weak_promoter
13	0.123	2 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	0.138	2 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	0.151	2 / 75	Subero_FL_hyper_meth
16	0.176	1 / 21	ROSOLOWSKI_red UP
17	0.178	52 / 5039	HOPP_Repressed
18	0.190	2 / 87	ROSOLOWSKI_red total
19	0.213	2 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
20	0.224	30 / 2838	HOPP_Poised_promoter

Pathw Act

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

Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	WIRTH_Bone marrow
2	0.1	3 / 137	WIRTH_Mucosa
3	0.2	1 / 30	PALMER_Lymphocytes signature up
4	0.5	1 / 82	WIRTH_Homeostasis
5	0.7	1 / 115	WIRTH_Liver
6	0.7	1 / 141	WIRTH_Muscle
7	0.8	3 / 476	WIRTH_Nervous System
8	0.8	1 / 202	WIRTH_Testis
9	0.9	1 / 259	PALMER_Granulocytes signature up
10	1.0	1 / 427	WIRTH_Immune system
11	1.0	0 / 6	WIRTH_Pituitary gland
12	1.0	0 / 54	WIRTH_Pancreas
13	1.0	0 / 13	WIRTH_Sec. lymphoid organs
14	1.0	0 / 13	WIRTH_Prim. lymphoid organs
15	1.0	0 / 14	WIRTH_B−cells
16	1.0	0 / 12	WIRTH_Tonsil
17	1.0	0 / 14	WIRTH_Thymus
18	1.0	0 / 12	WIRTH_Lymphocytes
19	1.0	0 / 13	WIRTH_Globus pallidus
20	1.0	0 / 15	WIRTH_Telencephalon

BP

Rank	p−value	#in/all	Geneset
1	0.002	16 / 753	transmembrane transport
2	0.003	4 / 65	camera−type eye development
3	0.004	3 / 34	embryonic forelimb morphogenesis
4	0.006	11 / 491	transport
5	0.006	2 / 13	fucosylation
6	0.007	5 / 129	sensory perception of sound
7	0.008	4 / 85	chloride transmembrane transport
8	0.008	3 / 45	anion transmembrane transport
9	0.009	2 / 16	nucleotide biosynthetic process
10	0.012	2 / 18	innervation
11	0.012	2 / 18	termination of RNA polymerase III transcription
12	0.012	2 / 18	transcription elongation from RNA polymerase III promoter
13	0.012	5 / 148	phosphorylation
14	0.013	2 / 19	positive regulation of innate immune response
15	0.014	2 / 20	inflammatory response to antigenic stimulus
16	0.014	2 / 20	negative regulation of reactive oxygen species metabolic process
17	0.014	2 / 20	startle response
18	0.016	2 / 21	cochlea development
19	0.017	3 / 59	chloride transport
20	0.017	3 / 59	positive regulation of protein ubiquitination

CC

Rank	p−value	#in/all	Geneset
1	0.006	2 / 13	Fanconi anaemia nuclear complex
2	0.007	4 / 81	ubiquitin ligase complex
3	0.012	2 / 18	DNA−directed RNA polymerase III complex
4	0.014	9 / 411	centrosome
5	0.028	14 / 864	Golgi apparatus
6	0.033	10 / 558	intracellular membrane−bounded organelle
7	0.038	18 / 1250	integral component of plasma membrane
8	0.043	4 / 143	nuclear envelope
9	0.043	2 / 36	SCF ubiquitin ligase complex
10	0.043	47 / 4052	integral component of membrane
11	0.057	2 / 42	cis−Golgi network
12	0.057	3 / 95	centriole
13	0.069	2 / 47	chloride channel complex
14	0.084	4 / 180	nuclear speck
15	0.087	8 / 497	Golgi membrane
16	0.088	1 / 10	inhibitory synapse
17	0.088	1 / 10	RISC complex
18	0.093	3 / 117	cytoplasmic vesicle membrane
19	0.096	1 / 11	mRNA cleavage and polyadenylation specificity factor complex
20	0.113	1 / 13	STAGA complex

Disease

Rank	p−value	#in/all	Geneset
1	0.7	5 / 608	GUDJ_psoriasis up
2	0.9	2 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	0.03	5 / 189	HALLMARK_KRAS_SIGNALING_UP
2	0.10	2 / 58	HALLMARK_MYC_TARGETS_V2
3	0.10	4 / 194	HALLMARK_INFLAMMATORY_RESPONSE
4	0.11	4 / 198	HALLMARK_GLYCOLYSIS
5	0.33	2 / 128	HALLMARK_SPERMATOGENESIS
6	0.54	2 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
7	0.54	2 / 196	HALLMARK_P53_PATHWAY
8	0.54	2 / 197	HALLMARK_E2F_TARGETS
9	0.55	2 / 199	HALLMARK_MTORC1_SIGNALING
10	0.70	1 / 132	HALLMARK_COAGULATION
11	0.73	1 / 140	HALLMARK_UV_RESPONSE_DN
12	0.74	1 / 146	HALLMARK_DNA_REPAIR
13	0.76	1 / 154	HALLMARK_FATTY_ACID_METABOLISM
14	0.83	1 / 192	HALLMARK_COMPLEMENT
15	0.83	1 / 193	HALLMARK_HEME_METABOLISM
16	0.83	1 / 193	HALLMARK_KRAS_SIGNALING_DN
17	0.84	1 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	0.84	1 / 196	HALLMARK_G2M_CHECKPOINT
19	0.84	1 / 198	HALLMARK_HYPOXIA
20	0.84	1 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 31	antiporter activity
2	0.004	5 / 113	methyltransferase activity
3	0.005	2 / 12	fucosyltransferase activity
4	0.008	2 / 15	cation transmembrane transporter activity
5	0.011	3 / 50	chloride channel activity
6	0.012	2 / 18	RNA polymerase III activity
7	0.022	2 / 25	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
8	0.022	2 / 25	Hsp90 protein binding
9	0.043	2 / 36	core promoter sequence−specific DNA binding
10	0.050	2 / 39	DNA−directed RNA polymerase activity
11	0.061	2 / 44	extracellular ligand−gated ion channel activity
12	0.065	5 / 235	transporter activity
13	0.073	5 / 243	transcription coactivator activity
14	0.088	1 / 10	1−acylglycerol−3−phosphate O−acyltransferase activity
15	0.088	1 / 10	glucose binding
16	0.096	2 / 57	serine−type peptidase activity
17	0.096	1 / 11	anion transmembrane transporter activity
18	0.096	1 / 11	inhibitory extracellular ligand−gated ion channel activity
19	0.096	1 / 11	omega peptidase activity
20	0.096	1 / 11	peptidoglycan binding

TF

Rank	p−value	#in/all	Geneset
1	0.03	53 / 4566	ICGC_Egr1_targets
2	0.04	1 / 5	MYC_TFs
3	0.13	50 / 4714	ICGC_Pu1_targets
4	0.14	35 / 3177	ICGC_Irf4_targets
5	0.21	20 / 1798	HEBENSTREIT_low expression TF
6	0.22	56 / 5552	ICGC_Pol24_targets
7	0.23	9 / 731	ICGC_SrfPcr2_targets
8	0.23	63 / 6324	ICGC_Yy1_targets
9	0.25	53 / 5308	ICGC_Tcf12_targets
10	0.29	51 / 5173	ICGC_Taf1_targets
11	0.31	16 / 1506	ICGC_Usf1_targets
12	0.32	33 / 3305	ICGC_BatfPcr1_targets
13	0.32	62 / 6406	ICGC_Pax5_targets
14	0.34	66 / 6862	ICGC_Elf1_targets
15	0.36	24 / 2401	ICGC_Bcl11_targets
16	0.36	53 / 5512	ICGC_Nficsc81335_targets
17	0.39	60 / 6313	ICGC_Pou2_targets
18	0.39	23 / 2342	ICGC_GabpPcr2_targets
19	0.40	49 / 5135	ICGC_Ebfsc137065_targets
20	0.40	8 / 766	ICGC_Atf3_targets

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	48 / 5285	LU_BPDE 0.005 DN
2	0.9	9 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	4e−04	22 / 1084	Overlap_fetal_midbrain_EnhG
2	3e−03	22 / 1279	Overlap_fetal_midbrain_Enh
3	2e−02	15 / 910	Fetal_EnhG
4	3e−02	11 / 641	Mid_Frontal_Lobe_EnhP
5	3e−02	8 / 408	Mid_Frontal_Lobe_TxTrans
6	6e−02	105 / 10278	Overlap_fetal_midbrain_ReprPCWk
7	6e−02	30 / 2443	Fetal_Quies
8	7e−02	104 / 10239	Overlap_fetal_midbrain_ReprPC
9	7e−02	6 / 317	Mid_Frontal_Lobe_Tx
10	1e−01	11 / 840	Mid_Frontal_Lobe_TssF
11	2e−01	32 / 2956	Fetal_TssA
12	2e−01	16 / 1356	Fetal_K9K27me3
13	2e−01	14 / 1210	Fetal_TssP
14	2e−01	63 / 6320	Overlap_fetal_midbrain_HetRpts
15	2e−01	11 / 939	Fetal_HetRpts
16	2e−01	13 / 1137	Fetal_Enh
17	2e−01	11 / 940	Mid_Frontal_Lobe_Enh
18	4e−01	11 / 1108	Overlap_fetal_midbrain_TssA
19	4e−01	13 / 1327	Mid_Frontal_Lobe_TssP
20	4e−01	20 / 2084	Mid_Frontal_Lobe_K9K27me3

Chr

Rank	p−value	#in/all	Geneset
1	0.02	19 / 1228	Chr 2
2	0.03	14 / 862	Chr 5
3	0.03	2 / 30	Chr Y
4	0.06	14 / 976	Chr 6
5	0.16	11 / 847	Chr 16
6	0.17	5 / 318	Chr 13
7	0.20	8 / 613	Chr 14
8	0.26	3 / 191	Chr 21
9	0.39	7 / 651	Chr 8
10	0.46	3 / 272	Chr 18
11	0.53	7 / 746	Chr X
12	0.57	4 / 436	Chr 22
13	0.64	10 / 1172	Chr 11
14	0.67	6 / 735	Chr 4
15	0.71	4 / 522	Chr 20
16	0.72	8 / 1017	Chr 12
17	0.78	4 / 582	Chr 15
18	0.80	6 / 859	Chr 7
19	0.87	7 / 1083	Chr 17
20	0.91	13 / 1920	Chr 1

Glio

Rank	p−value	#in/all	Geneset
1	0.02	2 / 23	Shinawi_with_increased_methylation_in_STS
2	0.04	21 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	0.08	2 / 50	Vishal_subnetwork signature of survival in GBM
4	0.08	3 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
5	0.10	2 / 58	WILLSCHER_GBM_Verhaak=PNmut_down (G)
6	0.10	1 / 12	WILLSCHER_GBM_LTSwt_proteomics−C_UP
7	0.14	1 / 16	VERHAAK_NL subtype
8	0.16	3 / 150	Sturm_GBM_Meth_overexpression_B_adult_UP
9	0.18	25 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
10	0.18	3 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
11	0.24	2 / 103	GIEZELT_GBM_STS_down_VS_LTS
12	0.26	2 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	0.31	1 / 40	Christensen_hypomethylated_in_ependymoma
14	0.36	2 / 137	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
15	0.37	5 / 434	Down_a
16	0.38	1 / 52	OL vs. OPC
17	0.39	1 / 53	Donson−innate immunity−associated with LTS in HGA
18	0.40	1 / 55	Gorovets_LGG_PG_subclass
19	0.40	1 / 56	mature astrocytes
20	0.41	9 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.08	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.26	1 / 33	DUMEAUX_Fasting enriched genes
4	1.00	0 / 91	DUMEAUX_Smoking enriched genes
5	1.00	0 / 11	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	7 / 297	hsa−miR−548j
2	0.02	9 / 442	hsa−miR−548n
3	0.03	7 / 317	hsa−miR−548c−5p
4	0.04	4 / 136	hsa−miR−200a
5	0.04	7 / 348	hsa−miR−548d−5p
6	0.04	7 / 348	hsa−miR−548b−5p
7	0.05	1 / 6	hsa−miR−937
8	0.06	3 / 100	hsa−miR−1259
9	0.07	6 / 312	hsa−miR−548i
10	0.08	3 / 107	hsa−miR−377
11	0.08	1 / 9	hsa−miR−202*
12	0.08	4 / 180	hsa−miR−548k
13	0.09	6 / 332	hsa−miR−548a−5p
14	0.09	3 / 117	hsa−miR−875−3p
15	0.11	3 / 124	hsa−miR−1248
16	0.11	3 / 124	hsa−miR−579
17	0.11	1 / 13	hsa−miR−1234
18	0.12	5 / 280	hsa−miR−548h
19	0.12	2 / 64	hsa−miR−1243
20	0.12	1 / 14	hsa−miR−574−3p

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	VAQUERIZAS_Skin
2	0.1	1 / 16	VAQUERIZAS_Ovary
3	0.1	1 / 17	VAQUERIZAS_Salivary gland
4	0.3	1 / 41	VAQUERIZAS_Testis
5	0.3	1 / 45	VAQUERIZAS_Placenta
6	0.4	1 / 49	VAQUERIZAS_Uterus
7	1.0	0 / 41	VAQUERIZAS_Fetal brain
8	1.0	0 / 33	VAQUERIZAS_Liver
9	1.0	0 / 37	VAQUERIZAS_Prostate
10	1.0	0 / 30	VAQUERIZAS_Smooth muscle
11	1.0	0 / 155	VAQUERIZAS_General
12	1.0	0 / 12	VAQUERIZAS_Kidney
13	1.0	0 / 25	VAQUERIZAS_Spinal cord
14	1.0	0 / 46	VAQUERIZAS_Whole brain
15	1.0	0 / 42	VAQUERIZAS_Thymus
16	1.0	0 / 42	VAQUERIZAS_Thyroid
17	1.0	0 / 67	VAQUERIZAS_Whole blood
18	1.0	0 / 7	VAQUERIZAS_Appendix
19	1.0	0 / 31	VAQUERIZAS_Fetal lung
20	1.0	0 / 64	VAQUERIZAS_Lung

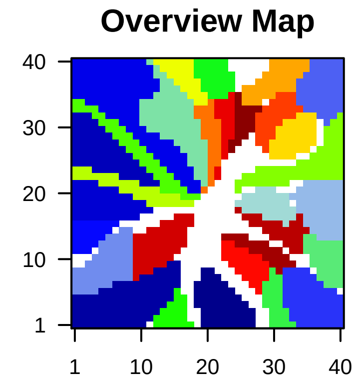
Correlation Clusters

Spot Summary: A1

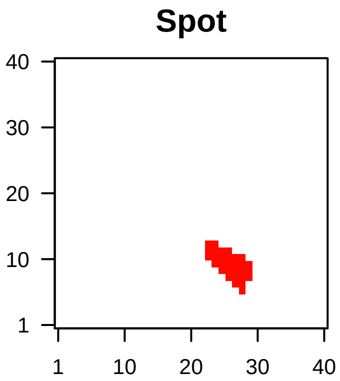
metagenes = 30
genes = 321

<r> metagenes = 0.96
<r> genes = 0.36
beta: r2= 0.01 / log p= −0.13

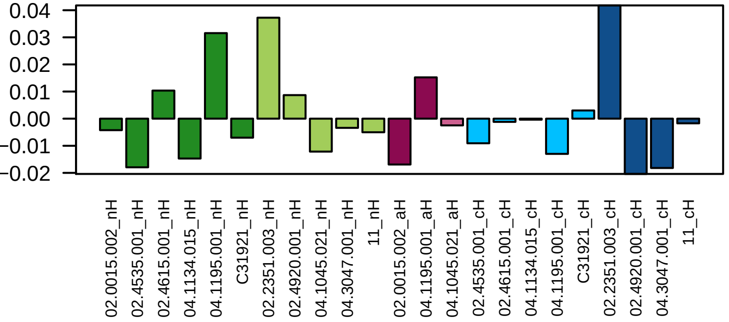
samples with spot = 0 (0 %)



Overview Map



Spot

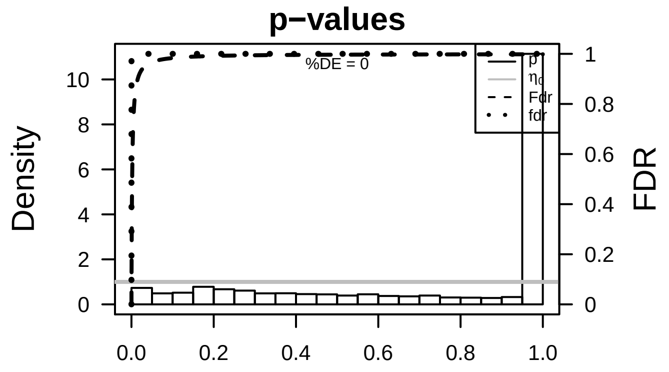


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.62	−0.05	0.4	CSF3	colony stimulating factor 3 (granulocyte) [Source:HGNC Symb
2	ENSG000001	0.3	−0.11	0.37	TXNRD1	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
3	ENSG000001	0.23	−0.05	0.56	STXBP5	syntaxin binding protein 5 (tomosyn) [Source:HGNC Symbol;
4	ENSG000000	0.23	−0.06	0.55	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
5	ENSG000001	0.23	−0.4	0.36	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HG
6	ENSG000001	0.23	−0.13	0.75	SNX4	sorting nexin 4 [Source:HGNC Symbol;Acc:HGNC:11175]
7	ENSG000001	0.22	−0.04	0.67	MB	myoglobin [Source:HGNC Symbol;Acc:HGNC:6915]
8	ENSG000001	0.22	−0.06	0.67	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12 [Source:HG
9	ENSG000000	0.2	−0.13	0.59	NEO1	neogenin 1 [Source:HGNC Symbol;Acc:HGNC:7754]
10	ENSG000001	0.19	−0.1	0.68	LOC102724985	pyridoxal−dependent decarboxylase domain containing 1 [So
11	ENSG000002	0.19	−0.02	0.76	FER1L6	fer−1−like family member 6 [Source:HGNC Symbol;Acc:HGN
12	ENSG000001	0.17	−0.05	0.66	USP38	ubiquitin specific peptidase 38 [Source:HGNC Symbol;Acc:H
13	ENSG000001	0.17	−0.04	0.51	FAM177B	family with sequence similarity 177, member B [Source:HGN
14	ENSG000001	0.17	−0.02	0.25	GCG	glucagon [Source:HGNC Symbol;Acc:HGNC:4191]
15	ENSG000001	0.17	−0.04	0.62	CLIC6	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:H
16	ENSG000001	0.17	−0.06	0.64	XRCC6BP1	XRCC6 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:
17	ENSG000002	0.17	−0.03	0.25		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3
18	ENSG000001	0.16	−0.04	0.31	PTPRD	protein tyrosine phosphatase, receptor type, D [Source:HGN
19	ENSG000001	0.16	−0.07	0.63	TOR1B	torsin family 1, member B (torsin B) [Source:HGNC Symbol;A
20	ENSG000000	0.16	−0.07	0.77	BRPF3	bromodomain and PHD finger containing, 3 [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−09	222 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
2	6e−09	208 / 9470	Colon	Quies3_Colon
3	8e−09	23 / 329	BP	intracellular protein transport
4	2e−08	245 / 11968	Colon	TssWk_Colon
5	5e−08	217 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
6	5e−07	31 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
7	1e−06	147 / 6389	Lymp	HOPP_Weak_txn
8	1e−06	30 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
9	4e−06	10 / 94	HM	HALLMARK_PROTEIN_SECRETION
10	4e−06	196 / 9390	Colon	TxWk_Colon
11	5e−06	143 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
12	7e−06	20 / 383	GSEA	OSMAN_BLADDER_CANCER_UP
13	9e−06	116 / 4879	Colon	Quies1_Colon
14	1e−05	211 / 10475	Colon	TssA_Colon
15	4e−05	147 / 6784	Lymp	HOPP_Weak_enhancer
16	7e−05	199 / 9930	Colon	Tx_Colon
17	7e−05	7 / 62	BP	ER to Golgi vesicle−mediated transport
18	1e−04	15 / 286	GSEA	GABRIELY_MIR21_TARGETS
19	1e−04	101 / 4327	Colon	EnhWk2_Colon
20	1e−04	168 / 8147	Lymp	HOPP_Weak_promoter
21	1e−04	5 / 31	GSEA	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
22	2e−04	29 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
23	2e−04	11 / 176	GSEA	KEGG_ENDOCYTOSIS
24	2e−04	25 / 685	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
25	2e−04	9 / 124	miRN	hsa−miR−579
26	3e−04	5 / 35	GSEA	BIOCARTA_TOLL_PATHWAY
27	3e−04	67 / 2658	Lymp	HOPP_Repetitive
28	3e−04	35 / 1137	Brain	Fetal_Enh
29	4e−04	4 / 21	miRN	hsa−miR−554
30	4e−04	21 / 549	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
31	4e−04	20 / 512	BP	protein transport
32	6e−04	4 / 24	GSEA	REACTOME_EGFR_DOWNREGULATION
33	6e−04	29 / 910	Brain	Fetal_EnhG
34	9e−04	167 / 8358	Lymp	HOPP_Active_promoter
35	1e−03	18 / 471	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
36	1e−03	152 / 7491	Lymp	HOPP_Txn_elongation
37	1e−03	5 / 47	CC	chloride channel complex
38	1e−03	6 / 71	BP	Rab protein signal transduction
39	1e−03	11 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
40	1e−03	8 / 127	GSEA	KEGG_TIGHT_JUNCTION



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 123	HORVATH_aging_genes meth DOWN
2	0.6	1 / 57	TESCHENDORFF_age_hypermethylated
3	0.9	1 / 144	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	8e−09	23 / 329	intracellular protein transport
2	7e−05	7 / 62	ER to Golgi vesicle−mediated transport
3	4e−04	20 / 512	protein transport
4	1e−03	6 / 71	Rab protein signal transduction
5	2e−03	3 / 15	COPII vesicle coating
6	2e−03	6 / 78	protein ubiquitination involved in ubiquitin−dependent protein catabolic process
7	2e−03	7 / 110	nucleocytoplasmic transport
8	3e−03	35 / 1279	signal transduction
9	3e−03	4 / 35	vesicle docking involved in exocytosis
10	3e−03	4 / 36	negative regulation of neuron death
11	4e−03	5 / 62	cell morphogenesis
12	4e−03	4 / 39	bicellular tight junction assembly
13	5e−03	9 / 191	vesicle−mediated transport
14	5e−03	3 / 21	positive regulation of exocytosis
15	5e−03	9 / 194	epidermal growth factor receptor signaling pathway
16	6e−03	3 / 23	regulation of nitric−oxide synthase activity
17	1e−02	3 / 28	intra−Golgi vesicle−mediated transport
18	1e−02	2 / 10	morphogenesis of an epithelial sheet
19	1e−02	2 / 10	negative regulation of appetite
20	1e−02	2 / 10	negative regulation of glycolytic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−09	222 / 10278	Overlap_fetal_midbrain_ReprPCWk
2	5e−08	217 / 10239	Overlap_fetal_midbrain_ReprPC
3	5e−06	143 / 6320	Overlap_fetal_midbrain_HetRpts
4	3e−04	35 / 1137	Fetal_Enh
5	6e−04	29 / 910	Fetal_EnhG
6	2e−03	37 / 1356	Fetal_K9K27me3
7	2e−03	205 / 10800	Overlap_fetal_midbrain_Quies
8	3e−03	21 / 641	Mid_Frontal_Lobe_EnhP
9	3e−03	35 / 1279	Overlap_fetal_midbrain_Enh
10	1e−02	185 / 9923	Overlap_fetal_midbrain_K9K27me3
11	1e−02	30 / 1182	Fetal_EnhP
12	5e−02	28 / 1210	Fetal_TssP
13	6e−02	25 / 1084	Overlap_fetal_midbrain_EnhG
14	1e−01	19 / 840	Mid_Frontal_Lobe_TssF
15	1e−01	50 / 2549	Fetal_TssF
16	2e−01	19 / 940	Mid_Frontal_Lobe_Enh
17	3e−01	45 / 2443	Fetal_Quies
18	3e−01	16 / 805	Mid_Frontal_Lobe_EnhG
19	3e−01	18 / 939	Fetal_HetRpts
20	4e−01	45 / 2603	Fetal_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	5 / 140	PanCan_RAS_geneset_nanostring
2	0.11	5 / 152	PanCan_MAPK_geneset_nanostring
3	0.17	3 / 86	PanCan_JAK−ST_geneset_nanostring
4	0.21	2 / 51	PanCan_TGF−B_geneset_nanostring
5	0.23	5 / 198	PanCan_PI3K_geneset_nanostring
6	0.24	1 / 16	LIU_PROSTATE_CANCER_DN
7	0.24	1 / 16	GENTLES_modul1
8	0.24	1 / 16	GENTLES_modul16
9	0.31	1 / 22	PanCan_ChromMod_geneset_nanostring
10	0.33	2 / 71	SHAUGHNESSY_MM high risk
11	0.33	0 / 15	LIU_BREAST_CANCER
12	0.38	1 / 28	PanCan_HH_geneset_nanostring
13	0.44	0 / 14	LIU_PROSTATE_CANCER_UP
14	0.46	0 / 16	LIU_LIVER_CANCER
15	0.61	2 / 123	PanCan_Driver_Gene_geneset_nanostring
16	0.63	5 / 324	SPANG_BCL6−index2
17	0.69	0 / 16	LIU_COMMON_CANCER_GENES
18	0.80	1 / 97	PanCan_TXmisReg_geneset_nanostring
19	0.83	2 / 191	SPANG_LPS−index2
20	0.90	1 / 136	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.001	5 / 47	chloride channel complex
2	0.001	3 / 14	Golgi transport complex
3	0.002	18 / 497	Golgi membrane
4	0.002	12 / 268	apical plasma membrane
5	0.002	4 / 32	membrane coat
6	0.002	7 / 110	bicellular tight junction
7	0.005	4 / 42	cis−Golgi network
8	0.005	25 / 864	Golgi apparatus
9	0.007	3 / 24	secretory granule membrane
10	0.008	4 / 48	SNARE complex
11	0.010	3 / 27	Cul3−RING ubiquitin ligase complex
12	0.011	2 / 10	AP−3 adaptor complex
13	0.014	2 / 11	AP−2 adaptor complex
14	0.014	2 / 11	CD40 receptor complex
15	0.017	38 / 1604	intracellular
16	0.022	2 / 14	apical junction complex
17	0.022	9 / 246	endosome
18	0.023	5 / 97	melanosome
19	0.023	3 / 37	phagocytic vesicle
20	0.027	3 / 39	T−tubule

Chr

Rank	p−value	#in/all	Geneset
1	0.06	28 / 1228	Chr 2
2	0.11	14 / 582	Chr 15
3	0.13	15 / 651	Chr 8
4	0.14	21 / 976	Chr 6
5	0.14	16 / 715	Chr 10
6	0.17	16 / 735	Chr 4
7	0.29	20 / 1043	Chr 3
8	0.30	6 / 272	Chr 18
9	0.36	14 / 745	Chr 9
10	0.39	4 / 191	Chr 21
11	0.44	6 / 318	Chr 13
12	0.46	15 / 859	Chr 7
13	0.47	15 / 862	Chr 5
14	0.70	9 / 613	Chr 14
15	0.70	11 / 746	Chr X
16	0.72	15 / 1017	Chr 12
17	0.74	6 / 436	Chr 22
18	0.76	17 / 1172	Chr 11
19	0.80	28 / 1920	Chr 1
20	0.84	11 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−09	208 / 9470	Quies3_Colon
2	2e−08	245 / 11968	TssWk_Colon
3	5e−07	31 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
4	4e−06	196 / 9390	TxWk_Colon
5	9e−06	116 / 4879	Quies1_Colon
6	1e−05	211 / 10475	TssA_Colon
7	7e−05	199 / 9930	Tx_Colon
8	1e−04	101 / 4327	EnhWk2_Colon
9	2e−03	6 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
10	1e−02	6 / 110	Marisa_CRC−cluster−h
11	1e−02	90 / 4379	TssD1_Colon
12	2e−02	18 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
13	2e−02	41 / 1753	Het_Colon
14	5e−02	1 / 3	Budinska_E_Mixed_DOWN
15	8e−02	1 / 5	Hewish_dMMR−secondary−mutations_Apoptosis
16	1e−01	3 / 73	Ang_CRC−CIMPH−vs−L_hyper
17	1e−01	27 / 1281	HetRpts_Colon
18	1e−01	1 / 8	Marisa_CRC−C6
19	1e−01	1 / 8	Budinska_C_CIMP−H−like_UP
20	1e−01	3 / 78	Ang_CRC_Hypermethylated

Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 22	BCHETNIA_EBM up
2	0.5	1 / 37	BCHETNIA_EBM−DM up
3	0.7	6 / 399	GUDJ_psoriasis down
4	0.7	9 / 608	GUDJ_psoriasis up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.007	2 / 8	shaw_responders_up_in_oligo_glioma
2	0.015	14 / 436	Down_b
3	0.025	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	0.030	49 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	0.035	22 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.041	43 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	0.044	10 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	0.050	4 / 83	GIEZELT_GBM_WT_down_VS_mut
9	0.050	3 / 50	Vishal_subnetwork signature of survival in GBM
10	0.055	7 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
11	0.065	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_down (A)
12	0.096	1 / 6	Martinez_Glio_hypometh
13	0.108	3 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	0.111	3 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
15	0.140	1 / 9	Shaw_up_in_1p19qdel
16	0.189	3 / 90	Weller_LGG_A_vs_O_DOWN
17	0.223	1 / 15	neurons_glio
18	0.228	3 / 99	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
19	0.229	4 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
20	0.245	2 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−06	30 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
2	7e−06	20 / 383	OSMAN_BLADDER_CANCER_UP
3	1e−04	15 / 286	GABRIELY_MIR21_TARGETS
4	1e−04	5 / 31	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
5	2e−04	29 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
6	2e−04	11 / 176	KEGG_ENDOCYTOSIS
7	2e−04	25 / 685	SCHLOSSER_SERUM_RESPONSE_DN
8	3e−04	5 / 35	BIOCARTA_TOLL_PATHWAY
9	4e−04	21 / 549	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
10	6e−04	4 / 24	REACTOME_EGFR_DOWNREGULATION
11	1e−03	18 / 471	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
12	1e−03	11 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
13	1e−03	8 / 127	KEGG_TIGHT_JUNCTION
14	2e−03	6 / 76	WALLACE_PROSTATE_CANCER_RACE_DN
15	2e−03	7 / 106	BROWNE_HCMV_INFECTION_12HR_UP
16	2e−03	25 / 804	CUI_TCF21_TARGETS_2_DN
17	4e−03	24 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
18	4e−03	3 / 19	REACTOME_TRAF6_MEDIATED_NFKB_ACTIVATION
19	4e−03	5 / 62	KIM_GERMINAL_CENTER_T_HELPER_UP
20	4e−03	4 / 40	GENTILE_UV_RESPONSE_CLUSTER_D2

HM

Rank	p−value	#in/all	Geneset
1	4e−06	10 / 94	HALLMARK_PROTEIN_SECRETION
2	6e−02	3 / 52	HALLMARK_TGF_BETA_SIGNALING
3	9e−02	4 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
4	1e−01	6 / 189	HALLMARK_KRAS_SIGNALING_UP
5	1e−01	6 / 190	HALLMARK_APICAL_JUNCTION
6	1e−01	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
7	2e−01	2 / 44	HALLMARK_APICAL_SURFACE
8	4e−01	3 / 128	HALLMARK_SPERMATOGENESIS
9	4e−01	3 / 132	HALLMARK_COAGULATION
10	4e−01	4 / 193	HALLMARK_KRAS_SIGNALING_DN
11	4e−01	4 / 196	HALLMARK_MITOTIC_SPINDLE
12	4e−01	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	4e−01	4 / 199	HALLMARK_ADIPOGENESIS
14	4e−01	2 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	5e−01	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
16	5e−01	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
17	6e−01	2 / 112	HALLMARK_BILE_ACID_METABOLISM
18	6e−01	3 / 181	HALLMARK_ALLOGRAFT_REJECTION
19	6e−01	3 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	6e−01	3 / 193	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	DUMEAUX_Hormon therapy_in non smokers literature genes up
2	0.2	1 / 11	DUMEAUX_Women normal BMI literature genes up
3	0.4	1 / 33	DUMEAUX_Fasting enriched genes
4	1.0	0 / 91	DUMEAUX_Smoking enriched genes
5	1.0	0 / 11	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 17	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−06	147 / 6389	HOPP_Weak_txn
2	4e−05	147 / 6784	HOPP_Weak_enhancer
3	1e−04	168 / 8147	HOPP_Weak_promoter
4	3e−04	67 / 2658	HOPP_Repetitive
5	9e−04	167 / 8358	HOPP_Active_promoter
6	1e−03	152 / 7491	HOPP_Txn_elongation
7	1e−03	3 / 14	DAVE_BL_DN
8	5e−03	5 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
9	2e−02	4 / 62	Subero_mBL_hyper_meth
10	3e−02	2 / 15	BENTINK_mBL_UP
11	3e−02	10 / 302	SPANG_IL21 UP
12	4e−02	4 / 75	Subero_FL_hyper_meth
13	4e−02	2 / 20	Subero_MCL_hypo_meth
14	5e−02	3 / 49	Subero_DLBCL_hypo_meth
15	5e−02	3 / 50	Subero_B−ALL_hyper_meth
16	6e−02	2 / 24	Subero_mBL_hypo_meth
17	7e−02	4 / 94	Subero_T−ALL_hyper_meth
18	8e−02	139 / 7592	HOPP_Strong_enhancer
19	8e−02	5 / 138	Subero_DLBCL_hyper_meth
20	8e−02	29 / 1333	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	0.001	15 / 371	GTP binding
2	0.003	11 / 250	GTPase activity
3	0.004	3 / 20	protein kinase A binding
4	0.005	5 / 67	protein transporter activity
5	0.006	3 / 22	ligand−dependent nuclear receptor binding
6	0.007	5 / 71	syntaxin binding
7	0.010	5 / 79	phosphatidylinositol binding
8	0.012	4 / 53	GDP binding
9	0.012	11 / 301	actin binding
10	0.014	2 / 11	I−SMAD binding
11	0.014	2 / 11	voltage−gated chloride channel activity
12	0.015	3 / 31	hydrolase activity, acting on ester bonds
13	0.019	2 / 13	carboxy−lyase activity
14	0.019	2 / 13	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in linear
15	0.022	2 / 14	oxygen transporter activity
16	0.028	2 / 16	protein kinase A regulatory subunit binding
17	0.028	2 / 16	transmembrane receptor protein tyrosine phosphatase activity
18	0.032	2 / 17	cysteine−type endopeptidase activator activity involved in apoptotic process
19	0.032	2 / 17	fibroblast growth factor receptor binding
20	0.032	2 / 17	myosin V binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 124	hsa−miR−579
2	4e−04	4 / 21	hsa−miR−554
3	4e−03	6 / 90	hsa−miR−587
4	6e−03	3 / 23	hsa−miR−323−5p
5	8e−03	6 / 105	hsa−miR−325
6	9e−03	8 / 173	hsa−miR−374b
7	9e−03	16 / 493	hsa−miR−15b
8	9e−03	12 / 326	hsa−miR−30e
9	9e−03	7 / 140	hsa−miR−488
10	1e−02	2 / 10	hsa−miR−1306
11	1e−02	8 / 184	hsa−miR−374a
12	1e−02	7 / 149	hsa−miR−494
13	2e−02	11 / 317	hsa−miR−548c−5p
14	2e−02	10 / 282	hsa−miR−30b
15	2e−02	7 / 170	hsa−miR−137
16	3e−02	10 / 293	hsa−miR−30c
17	3e−02	6 / 136	hsa−miR−28−5p
18	3e−02	12 / 381	hsa−miR−144
19	3e−02	6 / 137	hsa−miR−576−3p
20	3e−02	5 / 102	hsa−miR−500

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_src.10
2	0.2	1 / 15	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 14	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 14	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 10	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	0.07	48 / 2342	ICGC_GabpPcr2_targets
2	0.12	32 / 1547	ICGC_Ets1_targets
3	0.13	31 / 1503	ICGC_Six5_targets
4	0.22	92 / 5135	ICGC_Ebfsc137065_targets
5	0.25	1 / 17	MYC_Protein synthesis degradation UP
6	0.25	84 / 4714	ICGC_Pu1_targets
7	0.29	57 / 3177	ICGC_Irf4_targets
8	0.30	33 / 1798	HEBENSTREIT_low expression TF
9	0.38	33 / 1867	HEBENSTREIT_high expression TF
10	0.39	42 / 2401	ICGC_Bcl11_targets
11	0.39	95 / 5552	ICGC_Pol24_targets
12	0.41	57 / 3305	ICGC_BatfPcr1_targets
13	0.41	47 / 2719	ICGC_Pbx3_targets
14	0.47	87 / 5173	ICGC_Taf1_targets
15	0.48	106 / 6322	ICGC_Pol2_targets
16	0.51	74 / 4436	ICGC_Zeb1_targets
17	0.56	91 / 5512	ICGC_Nficsc81335_targets
18	0.58	113 / 6862	ICGC_Elf1_targets
19	0.61	118 / 7202	ICGC_Runx3_targets
20	0.61	81 / 4969	ICGC_Atf2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.3	1 / 23	VAQUERIZAS_Pituitary
2	0.5	3 / 155	VAQUERIZAS_General
3	1.0	0 / 41	VAQUERIZAS_Fetal brain
4	1.0	0 / 45	VAQUERIZAS_Placenta
5	1.0	0 / 33	VAQUERIZAS_Liver
6	1.0	0 / 37	VAQUERIZAS_Prostate
7	1.0	0 / 30	VAQUERIZAS_Smooth muscle
8	1.0	0 / 49	VAQUERIZAS_Uterus
9	1.0	0 / 12	VAQUERIZAS_Kidney
10	1.0	0 / 25	VAQUERIZAS_Spinal cord
11	1.0	0 / 46	VAQUERIZAS_Whole brain
12	1.0	0 / 42	VAQUERIZAS_Thymus
13	1.0	0 / 42	VAQUERIZAS_Thyroid
14	1.0	0 / 67	VAQUERIZAS_Whole blood
15	1.0	0 / 7	VAQUERIZAS_Appendix
16	1.0	0 / 31	VAQUERIZAS_Fetal lung
17	1.0	0 / 64	VAQUERIZAS_Lung
18	1.0	0 / 18	VAQUERIZAS_Pancreas
19	1.0	0 / 24	VAQUERIZAS_Trachea
20	1.0	0 / 16	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 15	WIRTH_Telencephalon
2	0.06	3 / 54	WIRTH_Pancreas
3	0.16	3 / 82	WIRTH_Homeostasis
4	0.20	1 / 13	WIRTH_Cortex cerebri
5	0.21	4 / 141	WIRTH_Muscle
6	0.21	1 / 14	WIRTH_Thyroid gland
7	0.24	1 / 16	WIRTH_Hippocampus
8	0.26	6 / 259	PALMER_Granulocytes signature up
9	0.40	1 / 30	PALMER_Lymphocytes signature up
10	0.54	8 / 476	WIRTH_Nervous System
11	0.55	1 / 47	WIRTH_Placenta
12	0.57	2 / 115	WIRTH_Liver
13	0.67	2 / 137	WIRTH_Mucosa
14	0.68	3 / 208	PALMER_B−Cell signature up
15	0.91	1 / 140	PALMER_T−Cell signature up
16	0.97	3 / 427	WIRTH_Immune system
17	1.00	0 / 6	WIRTH_Pituitary gland
18	1.00	0 / 13	WIRTH_Sec. lymphoid organs
19	1.00	0 / 13	WIRTH_Prim. lymphoid organs
20	1.00	0 / 14	WIRTH_B−cells

Toxic

Rank	p−value	#in/all	Geneset
1	0.002	112 / 5285	LU_BPDE 0.005 DN
2	0.178	27 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

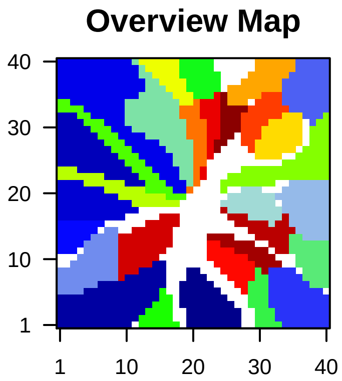
Correlation Clusters

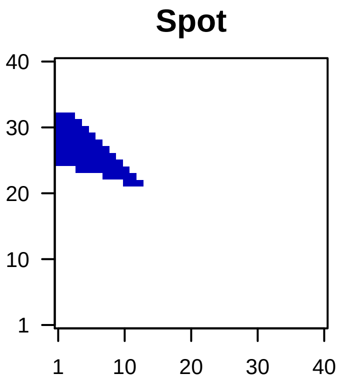
Spot Summary: B1

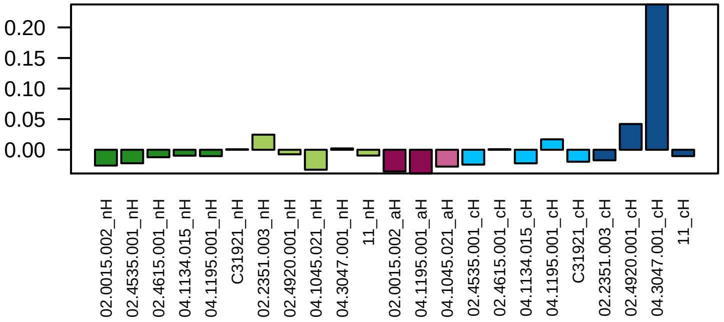
metagenes = 68
genes = 751

<r> metagenes = 0.96
<r> genes = 0.61
beta: r2= 0.05 / log p= −0.51

samples with spot = 1 (4.3 %)
other_cancerHNPCC : 1 (25 %)


Overview Map


Spot

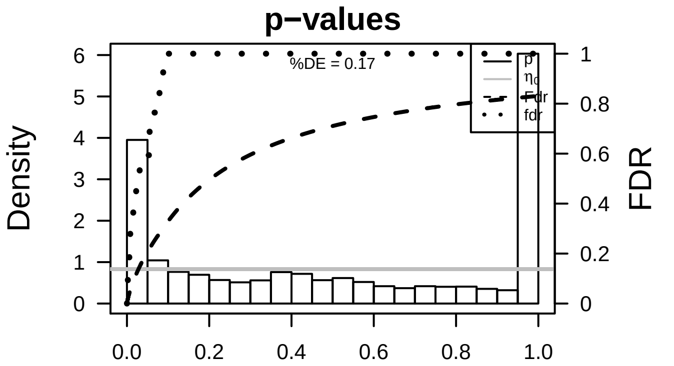


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.82	−0.23	0.89	FABP4	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
2	ENSG000002	1.31	−0.26	0.91	GPX3	glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:
3	ENSG000002	1.17	−0.14	0.27	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
4	ENSG000001	1.11	−0.22	0.91	SFRP2	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
5	ENSG000001	1.02	−0.41	0.84	CTGF	connective tissue growth factor [Source:HGNC Symbol;Acc:H
6	ENSG000001	1.01	−0.27	0.77	BGN	biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
7	ENSG000001	1	−0.16	0.92	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
8	ENSG000001	0.98	−0.25	0.64	SAA1	serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]
9	ENSG000001	0.95	−0.62	0.71	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:H
10	ENSG000001	0.9	−0.24	0.81	FOSB	FBJ murine osteosarcoma viral oncogene homolog B [Source
11	ENSG000001	0.89	−0.09	0.86	ADIPOQ	adiponectin, C1Q and collagen domain containing [Source:H
12	ENSG000001	0.87	−0.18	0.94	C11orf96	chromosome 11 open reading frame 96 [Source:HGNC Symb
13	ENSG000001	0.86	−0.22	0.8	C10orf10	chromosome 10 open reading frame 10 [Source:HGNC Symb
14	ENSG000001	0.86	−0.19	0.83	G0S2	G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]
15	ENSG000001	0.84	−0.09	0.96	RBP7	retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:
16	ENSG000001	0.83	−0.15	0.89	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	ENSG000002	0.82	−0.11	0.94	MUSTN1	musculoskeletal, embryonic nuclear protein 1 [Source:HGNC
18	ENSG000002	0.81	−0.2	0.83	ACKR1	atypical chemokine receptor 1 (Duffy blood group) [Source:H
19	ENSG000001	0.81	−0.07	0.92	PLIN1	perilipin 1 [Source:HGNC Symbol;Acc:HGNC:9076]
20	ENSG000001	0.78	−0.09	0.95	ID4	inhibitor of DNA binding 4, dominant negative helix−loop−heli

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−47	70 / 204	GSEA	BOQUEST_STEM_CELL_DN
2	1e−44	275 / 3109	Colon	TssP_Colon
3	1e−36	353 / 5039	Lympl	HOPP_Repressed
4	4e−35	73 / 326	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	1e−34	125 / 945	GSEA	NABA_MATRISOME
6	4e−31	91 / 574	Canc	Lembcke_Colonic Inflammation
7	1e−29	75 / 413	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
8	1e−29	235 / 2956	Brain	Fetal_TssA
9	3e−29	228 / 2838	Lympl	HOPP_Poised_promoter
10	5e−28	254 / 3406	Colon	ReprPC_Colon
11	3e−27	56 / 249	GSEA	BOQUEST_STEM_CELL_UP
12	5e−27	72 / 418	GSEA	SWEET_LUNG_CANCER_KRAS_DN
13	6e−27	53 / 224	BP	angiogenesis
14	2e−26	50 / 202	CC	extracellular matrix
15	3e−25	137 / 1374	CC	extracellular region
16	5e−25	48 / 198	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
17	5e−25	124 / 1176	CC	extracellular space
18	1e−23	31 / 78	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
19	1e−23	42 / 158	GSEA	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
20	3e−23	219 / 2947	Colon	ReprPCWk_Colon
21	1e−22	52 / 261	Lympl	LENZ_Stromal signature 1
22	1e−22	71 / 478	GSEA	LIM_MAMMARY_STEM_CELL_UP
23	2e−22	74 / 522	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
24	4e−22	50 / 248	GSEA	ONDER_CDH1_TARGETS_2_UP
25	4e−22	61 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
26	5e−22	94 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
27	6e−22	56 / 314	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
28	7e−22	56 / 315	Lympl	WIRTH_lymphoma937_spot E
29	9e−22	41 / 167	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
30	2e−21	26 / 59	Lympl	LENZ_Stromal signature 2
31	8e−21	26 / 62	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
32	3e−20	71 / 525	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
33	3e−20	42 / 192	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
34	5e−20	55 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
35	8e−20	42 / 196	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
36	8e−20	42 / 196	GSEA	MANALO_HYPOXIA_UP
37	2e−19	81 / 684	GSEA	NABA_MATRISOME_ASSOCIATED
38	5e−19	49 / 279	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
39	1e−18	25 / 67	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAI
40	1e−18	113 / 1210	Brain	Fetal_TssP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.07	5 / 57	TESCHENDORFF_age_hypermethylated
2	0.20	8 / 144	HORVATH_aging_genes meth UP
3	0.20	7 / 123	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−27	53 / 224	angiogenesis
2	8e−15	26 / 101	positive regulation of angiogenesis
3	1e−12	42 / 306	extracellular matrix organization
4	2e−11	55 / 523	cell adhesion
5	5e−10	19 / 85	positive regulation of MAPK cascade
6	9e−10	16 / 61	vasculogenesis
7	3e−09	29 / 209	platelet activation
8	4e−09	15 / 58	blood vessel development
9	4e−09	26 / 175	response to lipopolysaccharide
10	2e−08	45 / 466	blood coagulation
11	5e−08	21 / 134	receptor−mediated endocytosis
12	6e−08	44 / 467	positive regulation of cell proliferation
13	7e−08	16 / 81	platelet degranulation
14	8e−08	24 / 175	response to hypoxia
15	8e−08	22 / 150	skeletal system development
16	2e−07	13 / 56	negative regulation of angiogenesis
17	2e−07	11 / 39	collagen fibril organization
18	2e−07	9 / 25	endothelial cell migration
19	6e−07	21 / 155	positive regulation of cell migration
20	7e−07	20 / 143	positive regulation of ERK1 and ERK2 cascade

Brain

Rank	p−value	#in/all	Geneset
1	1e−29	235 / 2956	Fetal_TssA
2	1e−18	113 / 1210	Fetal_TssP
3	1e−17	252 / 3977	Mid_Frontal_Lobe_ReprPC
4	3e−15	179 / 2603	Fetal_TxTrans
5	3e−14	150 / 2084	Mid_Frontal_Lobe_K9K27me3
6	2e−13	116 / 1478	Overlap_fetal_midbrain_TxTrans
7	1e−12	93 / 1108	Overlap_fetal_midbrain_TssA
8	2e−12	105 / 1327	Mid_Frontal_Lobe_TssP
9	2e−11	164 / 2549	Fetal_TssF
10	1e−09	67 / 787	Overlap_fetal_midbrain_TssP
11	2e−06	113 / 1890	Overlap_fetal_midbrain_TssF
12	6e−06	44 / 552	Fetal_Tx
13	1e−05	101 / 1713	Mid_Frontal_Lobe_ReprPCWk
14	2e−05	85 / 1394	Mid_Frontal_Lobe_Quies
15	4e−05	149 / 2820	Mid_Frontal_Lobe_HetRpts
16	2e−04	54 / 840	Mid_Frontal_Lobe_TssF
17	3e−02	42 / 805	Mid_Frontal_Lobe_EnhG
18	4e−02	44 / 865	Mid_Frontal_Lobe_Het
19	5e−02	8 / 106	Overlap_fetal_midbrain_Tx
20	9e−02	32 / 641	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	4e−31	91 / 574	Lembcke_Colonic Inflammation
2	6e−08	3 / 16	LIU_PROSTATE_CANCER_DN
3	6e−07	7 / 15	GENTLES_modul13
4	8e−07	24 / 198	PanCan_PI3K_geneset_nanostring
5	1e−04	16 / 140	PanCan_RAS_geneset_nanostring
6	5e−04	11 / 86	PanCan_JAK−ST_geneset_nanostring
7	1e−03	11 / 97	PanCan_TXmisReg_geneset_nanostring
8	2e−03	4 / 14	BEN−PORATH_DN
9	2e−03	4 / 15	GENTLES_modul17
10	2e−03	14 / 152	PanCan_MAPK_geneset_nanostring
11	1e−02	4 / 24	PanCan_Notch_geneset_nanostring
12	2e−02	11 / 136	PanCan_CC+Apop_geneset_nanostring
13	2e−02	3 / 16	RHODES_CANCER_META_SIGNATURE
14	5e−02	5 / 51	PanCan_TGF−B_geneset_nanostring
15	8e−02	18 / 324	SPANG_BCL6−index2
16	8e−02	6 / 78	PanCan_Wnt_geneset_nanostring
17	1e−01	2 / 14	LIU_PROSTATE_CANCER_UP
18	1e−01	2 / 15	LIU_BREAST_CANCER
19	1e−01	2 / 16	LIU_LIVER_CANCER
20	2e−01	1 / 6	ZHANG_MGUS up

CC

Rank	p−value	#in/all	Geneset
1	2e−26	50 / 202	extracellular matrix
2	3e−25	137 / 1374	extracellular region
3	5e−25	124 / 1176	extracellular space
4	3e−15	43 / 270	proteinaceous extracellular matrix
5	6e−11	54 / 523	cell surface
6	9e−10	202 / 3507	plasma membrane
7	2e−09	14 / 48	platelet alpha granule lumen
8	2e−06	82 / 1250	integral component of plasma membrane
9	7e−06	17 / 125	receptor complex
10	1e−05	33 / 378	focal adhesion
11	5e−05	12 / 79	collagen trimer
12	9e−05	14 / 110	blood microparticle
13	1e−04	20 / 201	external side of plasma membrane
14	3e−04	23 / 268	apical plasma membrane
15	4e−04	5 / 17	anchored component of external side of plasma membrane
16	8e−04	15 / 151	lamellipodium
17	2e−03	4 / 14	interstitial matrix
18	2e−03	10 / 88	basement membrane
19	2e−03	4 / 15	platelet alpha granule
20	3e−03	129 / 2638	extracellular exosome

Chr

Rank	p−value	#in/all	Geneset
1	0.002	41 / 651	Chr 8
2	0.008	48 / 862	Chr 5
3	0.017	14 / 191	Chr 21
4	0.097	49 / 1043	Chr 3
5	0.135	40 / 859	Chr 7
6	0.176	52 / 1172	Chr 11
7	0.297	23 / 522	Chr 20
8	0.466	13 / 318	Chr 13
9	0.505	48 / 1228	Chr 2
10	0.511	28 / 715	Chr 10
11	0.529	42 / 1083	Chr 17
12	0.559	39 / 1017	Chr 12
13	0.598	73 / 1920	Chr 1
14	0.669	21 / 582	Chr 15
15	0.715	35 / 976	Chr 6
16	0.743	26 / 745	Chr 9
17	0.870	48 / 1425	Chr 19
18	0.884	23 / 735	Chr 4
19	0.915	26 / 847	Chr 16
20	0.955	11 / 436	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−44	275 / 3109	TssP_Colon
2	5e−28	254 / 3406	ReprPC_Colon
3	3e−23	219 / 2947	ReprPCWk_Colon
4	5e−20	55 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	1e−15	152 / 2041	EnhP_Colon
6	3e−12	28 / 148	Marisa_CRC−cluster−a
7	5e−09	36 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
8	6e−09	17 / 78	Ang_CRC_Hypermethylated
9	4e−08	36 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
10	9e−08	229 / 4327	EnhWk2_Colon
11	1e−07	15 / 73	Ang_CRC−CIMPH−vs−L_hyper
12	3e−07	41 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	9e−07	45 / 532	K9acLow_Colon
14	1e−06	43 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
15	6e−06	55 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
16	8e−06	34 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
17	5e−05	34 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
18	3e−04	231 / 4879	Quies1_Colon
19	6e−04	4 / 11	Kaneda_CIMP−group2
20	2e−03	50 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN

Disease

Rank	p−value	#in/all	Geneset
1	4e−07	38 / 399	GUDJ_psoriasis down
2	2e−02	34 / 608	GUDJ_psoriasis up
3	8e−02	1 / 2	BCHETNIA_EBM down
4	2e−01	2 / 22	BCHETNIA_EBM up
5	8e−01	1 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	5e−19	49 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−11	21 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
3	4e−08	23 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
4	8e−08	101 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	1e−06	18 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
6	4e−06	19 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	5e−06	17 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
8	8e−06	13 / 77	Weller_LGG_gradeII−vs−III_DOWN
9	6e−05	15 / 119	GIEZELT_GBM_WT_up_VS_mut
10	7e−05	11 / 69	cultured astroglia vs. in vivo astrocytes
11	1e−04	9 / 49	Noushmehr_Pron_GCIMP_hypermeth_DN
12	2e−04	12 / 92	laffaire_hypermeth_LGG_vs_control
13	3e−04	12 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
14	6e−04	25 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	1e−03	12 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
16	1e−03	4 / 13	Mukasa_UP_in_Astroglioma
17	1e−03	150 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
18	2e−03	9 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
19	2e−03	4 / 15	Mukasa_UP_in_GBM
20	3e−03	15 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−47	70 / 204	BOQUEST_STEM_CELL_DN
2	4e−35	73 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	1e−34	125 / 945	NABA_MATRISOME
4	1e−29	75 / 413	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
5	3e−27	56 / 249	BOQUEST_STEM_CELL_UP
6	5e−27	72 / 418	SWEET_LUNG_CANCER_KRAS_DN
7	1e−23	31 / 78	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
8	1e−23	42 / 158	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
9	1e−22	71 / 478	LIM_MAMMARY_STEM_CELL_UP
10	2e−22	74 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
11	4e−22	50 / 248	ONDER_CDH1_TARGETS_2_UP
12	4e−22	61 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
13	5e−22	94 / 804	CUI_TCF21_TARGETS_2_DN
14	9e−22	41 / 167	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
15	8e−21	26 / 62	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
16	3e−20	71 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
17	8e−20	42 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
18	8e−20	42 / 196	MANALO_HYPOXIA_UP
19	2e−19	81 / 684	NABA_MATRISOME_ASSOCIATED
20	1e−18	25 / 67	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_

HM

Rank	p−value	#in/all	Geneset
1	5e−25	48 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	3e−20	42 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	2e−12	32 / 189	HALLMARK_KRAS_SIGNALING_UP
4	3e−11	31 / 198	HALLMARK_HYPOXIA
5	8e−09	22 / 132	HALLMARK_COAGULATION
6	1e−07	25 / 190	HALLMARK_APICAL_JUNCTION
7	6e−07	24 / 194	HALLMARK_INFLAMMATORY_RESPONSE
8	8e−07	10 / 36	HALLMARK_ANGIOGENESIS
9	1e−05	19 / 157	HALLMARK_APOPTOSIS
10	1e−04	20 / 199	HALLMARK_ADIPOGENESIS
11	1e−04	16 / 140	HALLMARK_UV_RESPONSE_DN
12	2e−04	9 / 52	HALLMARK_TGF_BETA_SIGNALING
13	2e−04	19 / 195	HALLMARK_MYOGENESIS
14	3e−04	19 / 197	HALLMARK_IL2_STAT5_SIGNALING
15	3e−03	14 / 155	HALLMARK_UV_RESPONSE_UP
16	3e−03	16 / 192	HALLMARK_COMPLEMENT
17	4e−03	16 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
18	6e−03	9 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	1e−02	14 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	2e−02	14 / 193	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	8 / 91	DUMEAUX_Smoking enriched genes
2	0.07	2 / 11	DUMEAUX_Smoking literature genes up
3	0.24	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	0.30	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
5	0.35	1 / 11	DUMEAUX_Women normal BMI literature genes up
6	0.47	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 17	DUMEAUX_High bmi enriched genes
11	1.00	0 / 33	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−36	353 / 5039	HOPP_Repressed
2	3e−29	228 / 2838	HOPP_Poised_promoter
3	1e−22	52 / 261	LENZ_Stromal signature 1
4	6e−22	56 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
5	7e−22	56 / 315	WIRTH_lymphoma937_spot E
6	2e−21	26 / 59	LENZ_Stromal signature 2
7	1e−13	27 / 122	Subero_INT_hyper_meth
8	2e−11	26 / 138	Subero_DLBCL_hyper_meth
9	6e−11	26 / 145	WIRTH_lymphoma937_spot F
10	6e−11	26 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
11	2e−09	19 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
12	3e−09	19 / 94	Subero_T−ALL_hyper_meth
13	4e−08	41 / 414	TARTE_Mature plasma cell signature
14	2e−05	12 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	2e−05	11 / 62	Subero_mBL_hyper_meth
16	4e−05	11 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
17	5e−05	176 / 3457	HOPP_Heterochrom
18	2e−04	6 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
19	6e−04	10 / 75	Subero_FL_hyper_meth
20	2e−03	11 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP

MF

Rank	p−value	#in/all	Geneset
1	2e−10	25 / 142	heparin binding
2	5e−08	14 / 60	collagen binding
3	7e−08	18 / 102	integrin binding
4	8e−08	13 / 53	extracellular matrix structural constituent
5	2e−07	483 / 10693	protein binding
6	5e−07	17 / 104	metalloendopeptidase activity
7	6e−07	21 / 155	growth factor activity
8	8e−07	53 / 672	calcium ion binding
9	1e−06	7 / 16	transforming growth factor beta binding
10	9e−06	7 / 21	hyaluronic acid binding
11	2e−05	43 / 556	sequence−specific DNA binding
12	3e−05	21 / 196	transmembrane signaling receptor activity
13	5e−05	15 / 117	protein tyrosine kinase activity
14	5e−05	9 / 45	scavenger receptor activity
15	8e−05	7 / 28	growth factor binding
16	1e−04	8 / 39	transmembrane receptor protein tyrosine kinase activity
17	2e−04	12 / 89	serine−type endopeptidase inhibitor activity
18	2e−04	5 / 15	low−density lipoprotein particle binding
19	2e−04	5 / 15	platelet−derived growth factor receptor binding
20	3e−04	7 / 34	endopeptidase inhibitor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	11 / 104	hsa−miR−600
2	0.009	14 / 175	hsa−miR−369−3p
3	0.011	4 / 23	hsa−miR−517a
4	0.014	2 / 5	hsa−miR−1268
5	0.015	3 / 14	hsa−miR−638
6	0.035	11 / 152	hsa−miR−655
7	0.037	8 / 98	hsa−miR−133b
8	0.039	8 / 99	hsa−miR−133a
9	0.057	14 / 225	hsa−miR−181a
10	0.057	13 / 205	hsa−miR−181c
11	0.059	4 / 38	hsa−miR−215
12	0.059	4 / 38	hsa−miR−1269
13	0.059	8 / 108	hsa−miR−33b
14	0.071	3 / 25	hsa−miR−517c
15	0.076	12 / 194	hsa−miR−128
16	0.077	2 / 12	hsa−miR−369−5p
17	0.079	4 / 42	hsa−miR−129−3p
18	0.083	6 / 78	hsa−miR−1827
19	0.083	6 / 78	hsa−miR−890
20	0.083	5 / 60	hsa−miR−379

PathwAct

Rank	p−value	#in/all	Geneset
1	0.06	2 / 10	BENTINK_ras.4
2	0.10	2 / 14	GUSTAFSON_PI3K_UP
3	0.10	2 / 14	BENTINK_src.10
4	0.40	1 / 13	BENTINK_e2f3.2
5	0.43	1 / 14	BENTINK_myc.1
6	0.45	1 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 14	BENTINK_e2f3.1
8	1.00	0 / 12	BENTINK_ras.1
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	1e−08	117 / 1798	HEBENSTREIT_low expression TF
2	3e−02	156 / 3511	ICGC_Rad21_targets
3	1e−01	1 / 3	MYC_Signal transduction UP
4	5e−01	1 / 16	NOWICK_TF
5	6e−01	27 / 731	ICGC_SrfPcr2_targets
6	7e−01	105 / 2827	ICGC_Bcl3_targets
7	8e−01	25 / 745	ICGC_NrsfPcr2_targets
8	9e−01	51 / 1523	ICGC_P300_targets
9	9e−01	50 / 1506	ICGC_Usf1_targets
10	9e−01	1 / 66	MYC_Targets UP
11	1e+00	46 / 1472	ICGC_NrsfPcr1_targets
12	1e+00	76 / 2401	ICGC_Bcl11_targets
13	1e+00	63 / 2149	ICGC_Mef2_targets
14	1e+00	102 / 3305	ICGC_BatfPcr1_targets
15	1e+00	60 / 2133	ICGC_Cebpbsc150_targets
16	1e+00	150 / 4714	ICGC_Pu1_targets
17	1e+00	11 / 619	ICGC_RxraPcr1_targets
18	1e+00	49 / 1867	HEBENSTREIT_high expression TF
19	1e+00	163 / 5135	ICGC_Ebfsc137065_targets
20	1e+00	208 / 6406	ICGC_Pax5_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	3e−06	8 / 25	VAQUERIZAS_Adrenal cortex
2	2e−05	8 / 31	VAQUERIZAS_Fetal lung
3	3e−05	11 / 64	VAQUERIZAS_Lung
4	5e−05	9 / 45	VAQUERIZAS_Placenta
5	6e−04	8 / 49	VAQUERIZAS_Uterus
6	2e−03	5 / 24	VAQUERIZAS_Trachea
7	3e−03	4 / 16	VAQUERIZAS_Ovary
8	4e−03	4 / 17	VAQUERIZAS_Adrenal gland
9	6e−03	3 / 10	VAQUERIZAS_Skeletal.muscle.psoas
10	3e−02	4 / 30	VAQUERIZAS_Smooth.muscle
11	3e−02	2 / 7	VAQUERIZAS_Appendix
12	4e−02	2 / 8	VAQUERIZAS_Tongue
13	5e−02	4 / 37	VAQUERIZAS_Prostate
14	8e−02	4 / 42	VAQUERIZAS_Thyroid
15	1e−01	2 / 17	VAQUERIZAS_Salivary gland
16	2e−01	2 / 20	VAQUERIZAS_Bone marrow
17	2e−01	3 / 41	VAQUERIZAS_Fetal brain
18	3e−01	2 / 25	VAQUERIZAS_Spinal cord
19	3e−01	3 / 46	VAQUERIZAS_Whole brain
20	4e−01	1 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.001	4 / 13	WIRTH_Sec. lymphoid organs
2	0.113	2 / 15	WIRTH_Telencephalon
3	0.126	2 / 16	WIRTH_Hippocampus
4	0.134	14 / 259	PALMER_Granulocytes signature up
5	0.179	8 / 140	PALMER_T−Cell signature up
6	0.184	8 / 141	WIRTH_Muscle
7	0.230	22 / 476	WIRTH_Nervous System
8	0.403	1 / 13	WIRTH_Prim. lymphoid organs
9	0.403	1 / 13	PALMER_CD8+ T−Cell signature up
10	0.562	8 / 208	PALMER_B−Cell signature up
11	0.696	1 / 30	PALMER_Lymphocytes signature up
12	0.829	3 / 115	WIRTH_Liver
13	0.845	1 / 47	WIRTH_Placenta
14	0.883	1 / 54	WIRTH_Pancreas
15	1.000	3 / 427	WIRTH_Immune system
16	1.000	0 / 6	WIRTH_Pituitary gland
17	1.000	0 / 14	WIRTH_B−cells
18	1.000	0 / 12	WIRTH_Tonsil
19	1.000	0 / 14	WIRTH_Thymus
20	1.000	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	3e−04	248 / 5285	LU_BPDE 0.005 DN
2	8e−01	48 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

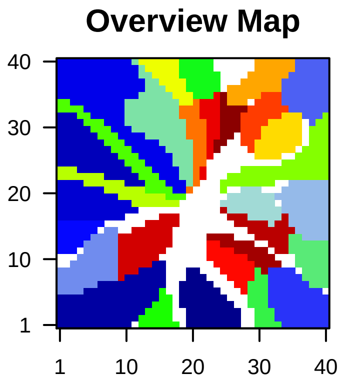
Correlation Clusters

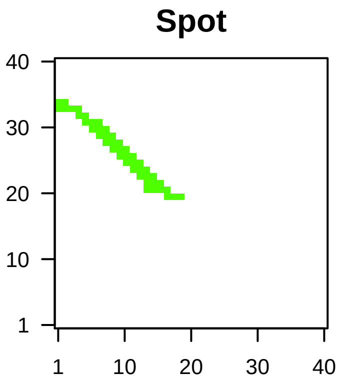
Spot Summary: C1

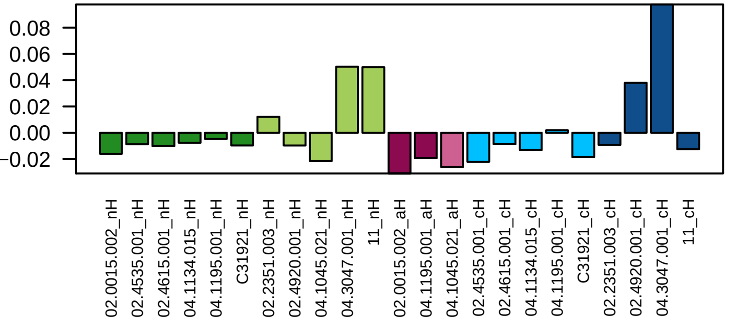
metagenes = 45
genes = 419

<r> metagenes = 0.95
<r> genes = 0.51
beta: r2= 0.02 / log p= −0.27

samples with spot = 3 (13 %)
other_normHNPCC : 2 (40 %)
other_cancerHNPCC : 1 (25 %)





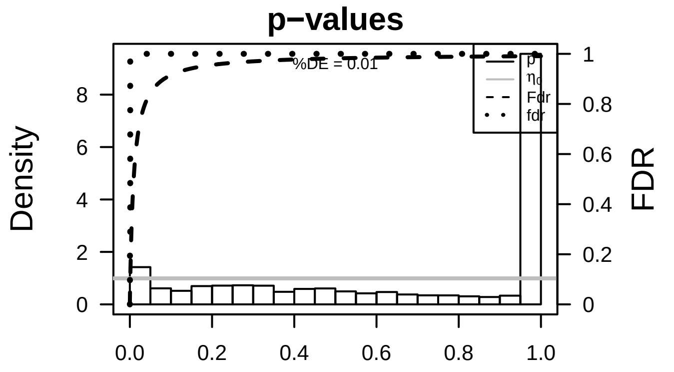


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.83	−0.21	0.83	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide [Source
2	ENSG000001	0.73	−0.29	0.87	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [S
3	ENSG000001	0.67	−0.26	0.4	GREM1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbo
4	ENSG000001	0.66	−0.14	0.98	LHFP	lipoma HMGIC fusion partner [Source:HGNC Symbol;Acc:HG
5	ENSG000001	0.64	−0.45	0.66	LUM	lumican [Source:HGNC Symbol;Acc:HGNC:6724]
6	ENSG000001	0.63	−0.23	0.85	LDLRAD2	low density lipoprotein receptor class A domain containing 2 [
7	ENSG000001	0.62	−0.35	0.47	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
8	ENSG000001	0.61	−0.32	0.77	C1R	complement component 1, r subcomponent [Source:HGNC S
9	ENSG000001	0.51	−0.17	0.76	IL33	interleukin 33 [Source:HGNC Symbol;Acc:HGNC:16028]
10	ENSG000001	0.49	−0.17	0.87	PLS3	plastin 3 [Source:HGNC Symbol;Acc:HGNC:9091]
11	ENSG000001	0.47	−0.19	0.69	WSB1	WD repeat and SOCS box containing 1 [Source:HGNC Symb
12	ENSG000000	0.46	−0.19	0.79	LAMB1	laminin, beta 1 [Source:HGNC Symbol;Acc:HGNC:6486]
13	ENSG000001	0.42	−0.11	0.83	PER1	period circadian clock 1 [Source:HGNC Symbol;Acc:HGNC:8
14	ENSG000001	0.42	−0.13	0.82	NFIL3	nuclear factor, interleukin 3 regulated [Source:HGNC Symbol
15	ENSG000001	0.41	−0.24	0.67	VAMP5	vesicle−associated membrane protein 5 [Source:HGNC Symb
16	ENSG000002	0.4	−0.14	0.74	COL5A2	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:HGNC:
17	ENSG000001	0.4	−0.19	0.75	KCTD12	potassium channel tetramerization domain containing 12 [Sou
18	ENSG000001	0.4	−0.09	0.97	TNS2	tensin 2 [Source:HGNC Symbol;Acc:HGNC:19737]
19	ENSG000001	0.39	−0.07	0.95	FZD4	frizzled class receptor 4 [Source:HGNC Symbol;Acc:HGNC:4
20	ENSG000001	0.39	−0.11	0.95	CRISPLD2	cysteine−rich secretory protein LCCL domain containing 2 [S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−29	158 / 3109	Colon	TssP_Colon
2	5e−20	191 / 5039	Lympl	HOPP_Repressed
3	1e−14	120 / 2838	Lympl	HOPP_Poised_promoter
4	5e−13	32 / 326	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	1e−11	127 / 3406	Colon	ReprPC_Colon
6	3e−11	114 / 2956	Brain	Fetal_TssA
7	5e−10	85 / 2041	Colon	EnhP_Colon
8	3e−09	23 / 249	GSEA	BOQUEST_STEM_CELL_UP
9	4e−09	58 / 1210	Brain	Fetal_TssP
10	7e−09	31 / 445	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
11	1e−08	49 / 966	GSEA	BENPORATH_EED_TARGETS
12	3e−08	31 / 478	GSEA	LIM_MAMMARY_STEM_CELL_UP
13	4e−08	1 / 16	Canc	LIU_PROSTATE_CANCER_DN
14	4e−08	104 / 2947	Colon	ReprPCWk_Colon
15	4e−08	47 / 945	GSEA	NABA_MATRISOME
16	5e−08	50 / 1041	GSEA	BENPORATH_ES_WITH_H3K27ME3
17	1e−07	22 / 281	GSEA	WANG_MLL_TARGETS
18	3e−07	28 / 442	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	3e−07	18 / 202	CC	extracellular matrix
20	6e−07	15 / 148	Colon	Marisa_CRC−cluster−a
21	6e−07	22 / 306	BP	extracellular matrix organization
22	8e−07	20 / 261	Lympl	LENZ_Stromal signature 1
23	8e−07	20 / 261	GSEA	NABA_CORE_MATRISOME
24	1e−06	36 / 711	GSEA	LEE_BMP2_TARGETS_UP
25	1e−06	20 / 270	CC	proteinaceous extracellular matrix
26	1e−06	155 / 5285	Toxic	LU_BPDE 0.005 DN
27	1e−06	19 / 248	GSEA	ONDER_CDH1_TARGETS_2_UP
28	2e−06	22 / 329	GSEA	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN
29	3e−06	21 / 310	Colon	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
30	3e−06	17 / 215	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
31	4e−06	43 / 971	GSEA	BENPORATH_SUZ12_TARGETS
32	4e−06	45 / 1040	GSEA	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
33	5e−06	34 / 692	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
34	7e−06	54 / 1374	CC	extracellular region
35	1e−05	8 / 53	MF	extracellular matrix structural constituent
36	1e−05	30 / 604	GSEA	BENPORATH_PRC2_TARGETS
37	2e−05	36 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
38	2e−05	24 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
39	3e−05	15 / 203	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_DN
40	3e−05	35 / 787	Brain	Overlap_fetal_midbrain_TssP



Aging

Rank	p−value	#in/all	Geneset
1	0.03	4 / 57	TESCHENDORFF_age_hypermethylated
2	0.03	7 / 144	HORVATH_aging_genes meth UP
3	0.26	4 / 123	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−07	22 / 306	extracellular matrix organization
2	8e−05	4 / 12	ear development
3	4e−04	7 / 64	positive regulation of epithelial cell proliferation
4	4e−04	17 / 316	nervous system development
5	7e−04	9 / 113	extracellular matrix disassembly
6	1e−03	3 / 10	adenylate cyclase−activating adrenergic receptor signaling pathway
7	1e−03	18 / 373	axon guidance
8	1e−03	8 / 97	peptidyl−tyrosine dephosphorylation
9	1e−03	5 / 39	collagen fibril organization
10	1e−03	3 / 11	activation of transmembrane receptor protein tyrosine kinase activity
11	1e−03	3 / 11	negative regulation of pathway−restricted SMAD protein phosphorylation
12	2e−03	7 / 80	positive regulation of protein kinase B signaling
13	2e−03	20 / 454	intracellular signal transduction
14	2e−03	3 / 12	extracellular fibril organization
15	2e−03	3 / 12	positive regulation of potassium ion transport
16	2e−03	5 / 43	embryo implantation
17	2e−03	20 / 469	cell differentiation
18	3e−03	5 / 46	cellular response to amino acid stimulus
19	3e−03	4 / 30	cellular response to BMP stimulus
20	4e−03	5 / 49	negative regulation of Wnt signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	114 / 2956	Fetal_TssA
2	4e−09	58 / 1210	Fetal_TssP
3	3e−05	35 / 787	Overlap_fetal_midbrain_TssP
4	6e−05	83 / 2603	Fetal_TxTrans
5	2e−03	109 / 3977	Mid_Frontal_Lobe_ReprPC
6	4e−03	73 / 2549	Fetal_TssF
7	5e−03	79 / 2820	Mid_Frontal_Lobe_HetRpts
8	6e−03	32 / 940	Mid_Frontal_Lobe_Enh
9	8e−03	45 / 1478	Overlap_fetal_midbrain_TxTrans
10	9e−03	241 / 10278	Overlap_fetal_midbrain_ReprPCWk
11	9e−03	55 / 1890	Overlap_fetal_midbrain_TssF
12	1e−02	27 / 805	Mid_Frontal_Lobe_EnhG
13	1e−02	39 / 1279	Overlap_fetal_midbrain_Enh
14	2e−02	36 / 1182	Fetal_EnhP
15	3e−02	19 / 552	Fetal_Tx
16	5e−02	55 / 2084	Mid_Frontal_Lobe_K9K27me3
17	5e−02	20 / 641	Mid_Frontal_Lobe_EnhP
18	6e−02	10 / 268	Mid_Frontal_Lobe_TssA
19	1e−01	35 / 1327	Mid_Frontal_Lobe_TssP
20	1e−01	29 / 1108	Overlap_fetal_midbrain_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	4e−08	1 / 16	LIU_PROSTATE_CANCER_DN
2	1e−02	10 / 198	PanCan_PI3K_geneset_nanostring
3	2e−02	5 / 71	SHAUGHNESSY_MM high risk
4	3e−02	2 / 14	BEN−PORATH_DN
5	4e−02	2 / 15	GENTLES_modul13
6	1e−01	6 / 152	PanCan_MAPK_geneset_nanostring
7	2e−01	5 / 140	PanCan_RAS_geneset_nanostring
8	2e−01	2 / 37	KUIPER_MM good survival
9	3e−01	1 / 15	GENTLES_modul10
10	3e−01	1 / 15	GENTLES_modul17
11	3e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	4e−01	5 / 191	SPANG_LPS−index2
13	4e−01	13 / 574	Lembcke_Colonic Inflammation
14	5e−01	2 / 86	PanCan_JAK−ST_geneset_nanostring
15	7e−01	1 / 51	PanCan_TGF−B_geneset_nanostring
16	7e−01	1 / 52	KUIPER_MM poor survival
17	8e−01	0 / 16	LIU_COMMON_CANCER_GENES
18	8e−01	2 / 136	PanCan_CC+Apop_geneset_nanostring
19	8e−01	1 / 78	PanCan_Wnt_geneset_nanostring
20	1e+00	3 / 324	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	3e−07	18 / 202	extracellular matrix
2	1e−06	20 / 270	proteinaceous extracellular matrix
3	7e−06	54 / 1374	extracellular region
4	8e−05	8 / 67	neuronal postsynaptic density
5	1e−04	8 / 70	caveola
6	2e−03	7 / 84	voltage−gated potassium channel complex
7	3e−03	7 / 88	basement membrane
8	3e−03	5 / 47	axon terminus
9	4e−03	3 / 16	dendrite cytoplasm
10	5e−03	7 / 99	dendritic spine
11	8e−03	20 / 523	cell surface
12	8e−03	3 / 20	podosome
13	9e−03	3 / 21	autophagosome membrane
14	1e−02	14 / 329	neuronal cell body
15	1e−02	4 / 43	sarcomere
16	1e−02	92 / 3507	plasma membrane
17	1e−02	9 / 179	endoplasmic reticulum lumen
18	2e−02	6 / 97	synaptic vesicle
19	2e−02	3 / 26	pre−autophagosomal structure
20	2e−02	2 / 10	juxtaparanode region of axon

Chr

Rank	p−value	#in/all	Geneset
1	0.02	20 / 582	Chr 15
2	0.04	12 / 318	Chr 13
3	0.04	30 / 1017	Chr 12
4	0.06	33 / 1172	Chr 11
5	0.09	33 / 1228	Chr 2
6	0.15	18 / 651	Chr 8
7	0.18	19 / 715	Chr 10
8	0.21	12 / 436	Chr 22
9	0.31	13 / 522	Chr 20
10	0.32	15 / 613	Chr 14
11	0.41	17 / 745	Chr 9
12	0.51	16 / 746	Chr X
13	0.62	21 / 1043	Chr 3
14	0.73	16 / 859	Chr 7
15	0.76	18 / 976	Chr 6
16	0.77	3 / 191	Chr 21
17	0.80	36 / 1920	Chr 1
18	0.86	12 / 735	Chr 4
19	0.88	14 / 862	Chr 5
20	0.95	12 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−29	158 / 3109	TssP_Colon
2	1e−11	127 / 3406	ReprPC_Colon
3	5e−10	85 / 2041	EnhP_Colon
4	4e−08	104 / 2947	ReprPCWk_Colon
5	3e−07	28 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
6	6e−07	15 / 148	Marisa_CRC−cluster−a
7	3e−06	21 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
8	1e−04	11 / 132	Marisa_CRC−cluster−b
9	7e−04	132 / 4879	Quies1_Colon
10	2e−03	118 / 4379	TssD1_Colon
11	2e−03	21 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
12	3e−03	28 / 754	Lembcke_TCGA=expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	6e−03	113 / 4327	EnhWk2_Colon
14	1e−02	51 / 1753	Het_Colon
15	2e−02	3 / 30	Marisa_CRC−cluster−c
16	3e−02	18 / 525	Quies2_Colon
17	4e−02	4 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
18	6e−02	12 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
19	1e−01	11 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
20	1e−01	13 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	1e−04	21 / 399	GUDJ_psoriasis down
2	4e−01	1 / 22	BCHETNIA_EBM up
3	5e−01	1 / 37	BCHETNIA_EBM−DM up
4	1e+00	2 / 608	GUDJ_psoriasis up
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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−04	9 / 92	laffaire_hypermeth_LGG_vs_control
2	8e−03	5 / 59	developing astrocytes
3	1e−02	3 / 23	Shinawi_with_increased_methylation_in_STS
4	2e−02	16 / 434	Down_a
5	3e−02	15 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
6	3e−02	3 / 34	WIRTH_PN subtype
7	4e−02	4 / 61	Christensen_hypermethylated_in_primary_glioblastoma
8	5e−02	6 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	5e−02	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
10	5e−02	7 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	5e−02	5 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
12	5e−02	2 / 18	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
13	6e−02	7 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	7e−02	2 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
15	7e−02	11 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP
16	9e−02	6 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	1e−01	3 / 52	OL vs. OPC
18	1e−01	3 / 53	Donson−innate immunity−associated with LTS in HGA
19	1e−01	74 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
20	1e−01	5 / 122	Christensen_hypermethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−13	32 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	3e−09	23 / 249	BOQUEST_STEM_CELL_UP
3	7e−09	31 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
4	1e−08	49 / 966	BENPORATH_EED_TARGETS
5	3e−08	31 / 478	LIM_MAMMARY_STEM_CELL_UP
6	4e−08	17 / 16	LIU_PROSTATE_CANCER_DN
7	4e−08	47 / 945	NABA_MATRISOME
8	5e−08	50 / 1041	BENPORATH_ES_WITH_H3K27ME3
9	1e−07	22 / 281	WANG_MLL_TARGETS
10	8e−07	20 / 261	NABA_CORE_MATRISOME
11	1e−06	36 / 711	LEE_BMP2_TARGETS_UP
12	1e−06	19 / 248	ONDER_CDH1_TARGETS_2_UP
13	2e−06	22 / 329	IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN
14	3e−06	17 / 215	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
15	4e−06	43 / 971	BENPORATH_SUZ12_TARGETS
16	4e−06	45 / 1040	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
17	5e−06	34 / 692	WONG_ADULT_TISSUE_STEM_MODULE
18	1e−05	30 / 604	BENPORATH_PRC2_TARGETS
19	2e−05	36 / 804	CUI_TCF21_TARGETS_2_DN
20	2e−05	24 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP

HM

Rank	p−value	#in/all	Geneset
1	8e−05	14 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	2e−04	11 / 140	HALLMARK_UV_RESPONSE_DN
3	2e−02	4 / 52	HALLMARK_TGF_BETA_SIGNALING
4	6e−02	8 / 198	HALLMARK_HYPOXIA
5	1e−01	6 / 154	HALLMARK_FATTY_ACID_METABOLISM
6	1e−01	7 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	1e−01	7 / 199	HALLMARK_ADIPOGENESIS
8	2e−01	4 / 102	HALLMARK_PEROXISOME
9	2e−01	2 / 36	HALLMARK_ANGIOGENESIS
10	2e−01	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
11	2e−01	6 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	2e−01	6 / 192	HALLMARK_COMPLEMENT
13	4e−01	5 / 190	HALLMARK_APICAL_JUNCTION
14	4e−01	5 / 193	HALLMARK_XENOBIOTIC_METABOLISM
15	4e−01	5 / 196	HALLMARK_P53_PATHWAY
16	4e−01	3 / 112	HALLMARK_BILE_ACID_METABOLISM
17	5e−01	3 / 132	HALLMARK_COAGULATION
18	6e−01	4 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	6e−01	4 / 195	HALLMARK_MYOGENESIS
20	6e−01	2 / 94	HALLMARK_PROTEIN_SECRETION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	1 / 33	DUMEAUX_Fasting enriched genes
2	0.6	2 / 91	DUMEAUX_Smoking enriched genes
3	1.0	0 / 11	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−20	191 / 5039	HOPP_Repressed
2	1e−14	120 / 2838	HOPP_Poised_promoter
3	8e−07	20 / 261	LENZ_Stromal signature 1
4	2e−04	7 / 59	LENZ_Stromal signature 2
5	9e−04	4 / 21	Subero_MCL_hyper_meth
6	9e−04	79 / 2658	HOPP_Repetitive
7	1e−03	7 / 75	Subero_FL_hyper_meth
8	3e−03	9 / 138	Subero_DLBCL_hyper_meth
9	4e−03	5 / 50	Subero_B−ALL_hyper_meth
10	8e−03	5 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
11	1e−02	5 / 62	Subero_mBL_hyper_meth
12	1e−02	8 / 145	WIRTH_lymphoma937_spot F
13	1e−02	8 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
14	1e−02	5 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
15	1e−02	7 / 122	Subero_INT_hyper_meth
16	2e−02	5 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
17	7e−02	85 / 3457	HOPP_Heterochrom
18	7e−02	5 / 105	ROSOLOWSKI_blue total
19	1e−01	1 / 6	MASCQUE_mBL UP
20	1e−01	4 / 92	WIRTH_lymphoma937_spot A

MF

Rank	p−value	#in/all	Geneset
1	1e−05	8 / 53	extracellular matrix structural constituent
2	1e−03	8 / 97	protein tyrosine phosphatase activity
3	1e−03	7 / 79	phosphatidylinositol binding
4	1e−03	8 / 102	integrin binding
5	2e−03	3 / 13	polysaccharide binding
6	3e−03	3 / 14	transcription factor activity, transcription factor binding
7	3e−03	9 / 142	heparin binding
8	4e−03	4 / 31	cation channel activity
9	4e−03	3 / 16	transmembrane receptor protein tyrosine phosphatase activity
10	5e−03	7 / 98	ion channel binding
11	5e−03	3 / 17	fibroblast growth factor receptor binding
12	6e−03	6 / 77	kinase binding
13	6e−03	12 / 245	ubiquitin protein ligase binding
14	7e−03	3 / 19	G−protein alpha−subunit binding
15	7e−03	4 / 37	transcription regulatory region sequence−specific DNA binding
16	1e−02	4 / 42	ATPase activity, coupled to transmembrane movement of substances
17	1e−02	3 / 23	R−SMAD binding
18	1e−02	7 / 118	phosphatase activity
19	1e−02	3 / 24	3',5'−cyclic−nucleotide phosphodiesterase activity
20	1e−02	4 / 44	phosphatase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	9 / 125	hsa−miR−105
2	0.002	23 / 562	hsa−miR−17
3	0.003	23 / 573	hsa−miR−93
4	0.003	19 / 447	hsa−miR−519d
5	0.004	23 / 591	hsa−miR−20b
6	0.007	4 / 36	hsa−miR−1287
7	0.008	17 / 416	hsa−miR−519c−3p
8	0.008	23 / 631	hsa−miR−20a
9	0.010	9 / 170	hsa−miR−190
10	0.010	20 / 536	hsa−miR−106b
11	0.011	9 / 173	hsa−miR−374b
12	0.012	16 / 403	hsa−miR−519a
13	0.013	16 / 407	hsa−miR−301b
14	0.014	17 / 446	hsa−miR−19b
15	0.016	4 / 46	hsa−miR−874
16	0.016	12 / 279	hsa−miR−92a
17	0.016	17 / 452	hsa−miR−19a
18	0.016	9 / 184	hsa−miR−374a
19	0.017	7 / 125	hsa−miR−380
20	0.018	9 / 187	hsa−miR−34b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 13	BENTINK_e2f3.2
2	0.03	2 / 14	GUSTAFSON_PI3K_UP
3	0.03	2 / 14	BENTINK_e2f3.1
4	0.23	1 / 12	BENTINK_ras.1
5	0.26	1 / 14	BENTINK_src.10
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 14	BENTINK_myc.1
8	1.00	0 / 10	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	1e−04	61 / 1798	HEBENSTREIT_low expression TF
2	3e−01	1 / 20	MYC_Metabolism UP
3	5e−01	74 / 3511	ICGC_Rad21_targets
4	8e−01	1 / 66	MYC_Targets UP
5	8e−01	46 / 2401	ICGC_Bcl11_targets
6	8e−01	13 / 745	ICGC_NrsfPcr2_targets
7	8e−01	27 / 1506	ICGC_Usf1_targets
8	9e−01	9 / 619	ICGC_RxraPcr1_targets
9	9e−01	24 / 1472	ICGC_NrsfPcr1_targets
10	9e−01	59 / 3305	ICGC_BatfPcr1_targets
11	1e+00	10 / 766	ICGC_Atf3_targets
12	1e+00	21 / 1523	ICGC_P300_targets
13	1e+00	32 / 2354	ICGC_SrfV0416101_targets
14	1e+00	28 / 2133	ICGC_Cebpbsc150_targets
15	1e+00	28 / 2149	ICGC_Mef2_targets
16	1e+00	46 / 3177	ICGC_Irf4_targets
17	1e+00	23 / 1867	HEBENSTREIT_high expression TF
18	1e+00	74 / 4714	ICGC_Pu1_targets
19	1e+00	90 / 5552	ICGC_Pol24_targets
20	1e+00	13 / 1294	KIM_MYC targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 25	VAQUERIZAS_Adrenal cortex
2	0.02	4 / 49	VAQUERIZAS_Uterus
3	0.04	2 / 16	VAQUERIZAS_Ovary
4	0.05	2 / 17	VAQUERIZAS_Adrenal gland
5	0.13	2 / 30	VAQUERIZAS_Smooth muscle
6	0.14	2 / 31	VAQUERIZAS_Fetal lung
7	0.15	3 / 64	VAQUERIZAS_Lung
8	0.17	3 / 67	VAQUERIZAS_Whole blood
9	0.18	2 / 37	VAQUERIZAS_Prostate
10	0.22	2 / 42	VAQUERIZAS_Thyroid
11	0.23	1 / 12	VAQUERIZAS_Kidney
12	0.25	2 / 46	VAQUERIZAS_Whole brain
13	0.29	1 / 16	VAQUERIZAS_Fetal thyroid
14	0.30	1 / 17	VAQUERIZAS_Salivary gland
15	0.32	1 / 18	VAQUERIZAS_Pancreas
16	0.39	1 / 23	VAQUERIZAS_Pituitary
17	0.40	1 / 24	VAQUERIZAS_Trachea
18	0.41	1 / 25	VAQUERIZAS_Spinal cord
19	0.58	1 / 41	VAQUERIZAS_Fetal brain
20	0.58	1 / 41	VAQUERIZAS_Testis

Tissue

Rank	p−value	#in/all	Geneset
1	0.004	3 / 15	WIRTH_Cerebellum
2	0.025	3 / 30	PALMER_Lymphocytes signature up
3	0.046	16 / 476	WIRTH_Nervous System
4	0.178	5 / 141	WIRTH_Muscle
5	0.226	1 / 12	WIRTH_Lymphocytes
6	0.242	1 / 13	WIRTH_Sec. lymphoid organs
7	0.242	1 / 13	WIRTH_Prim. lymphoid organs
8	0.242	1 / 13	WIRTH_Cortex cerebri
9	0.242	1 / 13	PALMER_CD8+ T−Cell signature up
10	0.258	1 / 14	WIRTH_B−cells
11	0.258	1 / 14	WIRTH_Thalamus
12	0.258	1 / 14	WIRTH_Thyroid gland
13	0.308	7 / 259	PALMER_Granulocytes signature up
14	0.570	3 / 140	PALMER_T−Cell signature up
15	0.634	1 / 47	WIRTH_Placenta
16	0.929	2 / 202	WIRTH_Testis
17	0.936	2 / 208	PALMER_B−Cell signature up
18	0.947	1 / 137	WIRTH_Mucosa
19	1.000	1 / 427	WIRTH_Immune system
20	1.000	0 / 6	WIRTH_Pituitary gland

Toxic

Rank	p−value	#in/all	Geneset
1	1e−06	155 / 5285	LU_BPDE 0.005 DN
2	6e−01	27 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

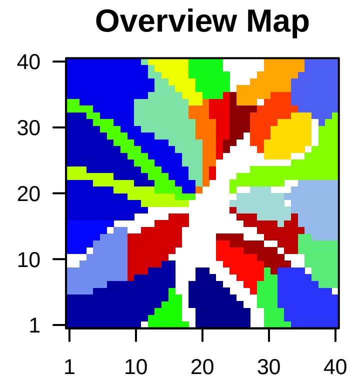
Correlation Clusters

Spot Summary: D1

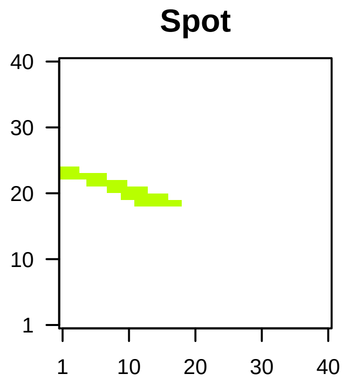
metagenes = 36
genes = 318

<r> metagenes = 0.96
<r> genes = 0.48
beta: r2= 0 / log p= −0.1

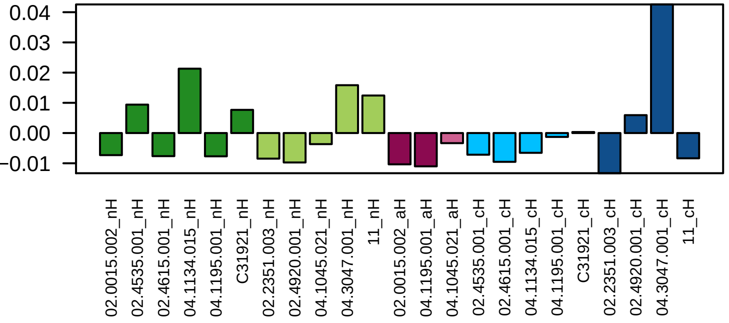
samples with spot = 0 (0 %)



Overview Map



Spot

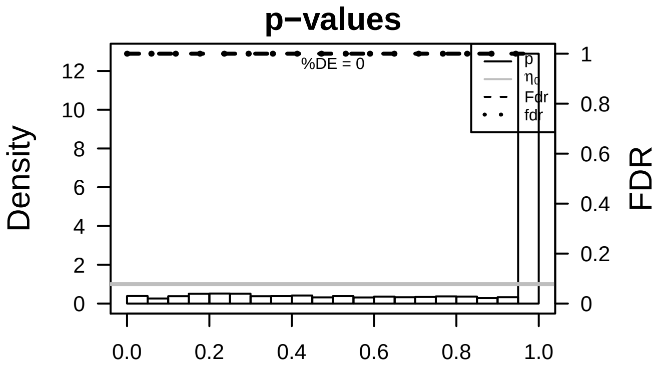


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.22	−0.08	0.57	GPX7	glutathione peroxidase 7 [Source:HGNC Symbol;Acc:HGNC:
2	ENSG000001	0.2	−0.15	0.6	SLC25A28	solute carrier family 25 (mitochondrial iron transporter), memb
3	ENSG000001	0.2	−0.14	0.41	APOL2	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:HGNC:619]
4	ENSG000001	0.18	−0.1	0.84	INTS3	integrator complex subunit 3 [Source:HGNC Symbol;Acc:HGN
5	ENSG000001	0.18	−0.1	0.74	WBP1L	WW domain binding protein 1−like [Source:HGNC Symbol;Ac
6	ENSG000002	0.18	−0.07	0.87	S1PR3	sphingosine−1−phosphate receptor 3 [Source:HGNC Symbol
7	ENSG000001	0.18	−0.1	0.78	ZNF337	zinc finger protein 337 [Source:HGNC Symbol;Acc:HGNC:15
8	ENSG000001	0.18	−0.11	0.86	NXF1	nuclear RNA export factor 1 [Source:HGNC Symbol;Acc:HGN
9	ENSG000002	0.17	−0.08	0.83	ACAD11	acyl−CoA dehydrogenase family, member 11 [Source:HGNC
10	ENSG000001	0.16	−0.06	0.92	SENP7	SUMO1/sentrin specific peptidase 7 [Source:HGNC Symbol;
11	ENSG000002	0.16	−0.08	0.8	RING1	ring finger protein 1 [Source:HGNC Symbol;Acc:HGNC:1001
12	ENSG000001	0.16	−0.08	0.66	RASSF4	Ras association (RalGDS/AF−6) domain family member 4 [So
13	ENSG000002	0.16	−0.11	0.59	WBP1	WW domain binding protein 1 [Source:HGNC Symbol;Acc:HG
14	ENSG000001	0.16	−0.09	0.66	AMT	aminomethyltransferase [Source:HGNC Symbol;Acc:HGNC:4
15	ENSG000001	0.16	−0.05	0.9	TCF4	transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:116
16	ENSG000001	0.16	−0.12	0.69	SIRPA	signal−regulatory protein alpha [Source:HGNC Symbol;Acc:H
17	ENSG000001	0.15	−0.07	0.82	CSF1	colony stimulating factor 1 (macrophage) [Source:HGNC Sym
18	ENSG000000	0.15	−0.14	0.72	RBM5	RNA binding motif protein 5 [Source:HGNC Symbol;Acc:HGN
19	ENSG000002	0.15	−0.04	0.86	LOC100128108	
20	ENSG000000	0.15	−0.07	0.89	NISCH	nischarin [Source:HGNC Symbol;Acc:HGNC:18006]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−06	118 / 5039	Lymph	HOPP_Repressed
2	2e−06	82 / 3109	Colon	TssP_Colon
3	2e−05	84 / 3406	Colon	ReprPC_Colon
4	7e−05	73 / 2947	Colon	ReprPCWk_Colon
5	1e−04	19 / 442	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
6	2e−04	4 / 19	BP	regulation of cardiac muscle contraction
7	1e−03	29 / 971	GSEA	BENPORATH_SUZ12_TARGETS
8	1e−03	3 / 13	BP	cardiac muscle cell proliferation
9	1e−03	3 / 14	BP	cAMP catabolic process
10	1e−03	3 / 14	BP	sulfate transport
11	1e−03	30 / 1041	GSEA	BENPORATH_ES_WITH_H3K27ME3
12	1e−03	15 / 386	Colon	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
13	1e−03	19 / 551	MF	G−protein coupled receptor activity
14	2e−03	6 / 79	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2
15	2e−03	10 / 204	Glio	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
16	2e−03	6 / 82	BP	hemopoiesis
17	2e−03	3 / 17	GSEA	KEGG_ASTHMA
18	2e−03	13 / 326	BP	inflammatory response
19	2e−03	2 / 5	GSEA	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_DN
20	3e−03	3 / 18	GSEA	BIOCARTA_ETS_PATHWAY
21	3e−03	22 / 718	BP	G−protein coupled receptor signaling pathway
22	3e−03	14 / 374	GSEA	HATADA_METHYLATED_IN_LUNG_CANCER_UP
23	4e−03	15 / 429	GSEA	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
24	4e−03	4 / 42	BP	outflow tract morphogenesis
25	5e−03	34 / 1327	Brain	Mid_Frontal_Lobe_TssP
26	5e−03	3 / 22	GSEA	BIOCARTA_DC_PATHWAY
27	6e−03	3 / 23	MF	carboxypeptidase activity
28	6e−03	98 / 4879	Colon	Quies1_Colon
29	6e−03	18 / 582	Chr	Chr 15
30	6e−03	34 / 1356	Brain	Fetal_K9K27me3
31	6e−03	3 / 24	MF	3',5'−cyclic−nucleotide phosphodiesterase activity
32	6e−03	3 / 24	BP	artery morphogenesis
33	7e−03	2 / 8	GSEA	BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
34	8e−03	14 / 417	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
35	8e−03	14 / 419	BP	synaptic transmission
36	8e−03	9 / 215	miRN	hsa−miR−196a
37	8e−03	3 / 26	GSEA	BIOCARTA_INFLAM_PATHWAY
38	9e−03	2 / 9	GSEA	BUDHU_LIVER_CANCER_METASTASIS_UP
39	9e−03	2 / 9	GSEA	SEIKE_LUNG_CANCER_POOR_SURVIVAL
40	9e−03	61 / 2838	Lymph	HOPP_Poised_promoter



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.06	3 / 57	TESCHENDORFF_age_hypermethylated
2	0.14	4 / 123	HORVATH_aging_genes meth DOWN
3	0.90	1 / 144	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	4 / 19	regulation of cardiac muscle contraction
2	1e−03	3 / 13	cardiac muscle cell proliferation
3	1e−03	3 / 14	cAMP catabolic process
4	1e−03	3 / 14	sulfate transport
5	2e−03	6 / 82	hemopoiesis
6	2e−03	13 / 326	inflammatory response
7	3e−03	22 / 718	G−protein coupled receptor signaling pathway
8	4e−03	4 / 42	outflow tract morphogenesis
9	6e−03	3 / 24	artery morphogenesis
10	8e−03	14 / 419	synaptic transmission
11	1e−02	4 / 53	skeletal muscle tissue development
12	1e−02	2 / 10	embryonic viscerocranium morphogenesis
13	1e−02	2 / 10	negative regulation of NF−kappaB import into nucleus
14	1e−02	2 / 10	regulation of dopamine metabolic process
15	1e−02	4 / 54	positive regulation of protein binding
16	1e−02	3 / 29	intracellular transport
17	1e−02	11 / 308	ion transport
18	1e−02	2 / 11	adenylate cyclase−activating dopamine receptor signaling pathway
19	1e−02	2 / 11	negative regulation of interleukin−12 production
20	1e−02	2 / 11	regulation of organ growth

Brain

Rank	p−value	#in/all	Geneset
1	0.005	34 / 1327	Mid_Frontal_Lobe_TssP
2	0.006	34 / 1356	Fetal_K9K27me3
3	0.026	54 / 2603	Fetal_TxTrans
4	0.028	41 / 1890	Overlap_fetal_midbrain_TssF
5	0.050	32 / 1478	Overlap_fetal_midbrain_TxTrans
6	0.054	16 / 641	Mid_Frontal_Lobe_EnhP
7	0.086	27 / 1279	Overlap_fetal_midbrain_Enh
8	0.097	18 / 805	Mid_Frontal_Lobe_EnhG
9	0.098	56 / 2956	Fetal_TssA
10	0.151	22 / 1084	Overlap_fetal_midbrain_EnhG
11	0.169	6 / 232	Fetal_ReprPC
12	0.225	23 / 1210	Fetal_TssP
13	0.241	3 / 106	Overlap_fetal_midbrain_Tx
14	0.242	21 / 1108	Overlap_fetal_midbrain_TssA
15	0.246	7 / 317	Mid_Frontal_Lobe_Tx
16	0.261	45 / 2549	Fetal_TssF
17	0.280	21 / 1137	Fetal_Enh
18	0.329	30 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	0.339	67 / 3977	Mid_Frontal_Lobe_ReprPC
20	0.342	21 / 1182	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 14	BEN−PORATH_DN
2	0.16	3 / 86	PanCan_JAK−ST_geneset_nanostring
3	0.18	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.21	12 / 574	Lembcke_Colonic Inflammation
5	0.22	1 / 15	LIU_BREAST_CANCER
6	0.22	1 / 15	BEN−PORATH_UP
7	0.30	1 / 22	PanCan_ChromMod_geneset_nanostring
8	0.66	2 / 140	PanCan_RAS_geneset_nanostring
9	0.70	2 / 152	PanCan_MAPK_geneset_nanostring
10	0.72	1 / 78	PanCan_Wnt_geneset_nanostring
11	0.79	1 / 97	PanCan_TXmisReg_geneset_nanostring
12	0.83	2 / 198	PanCan_PI3K_geneset_nanostring
13	0.86	1 / 123	PanCan_Driver_Gene_geneset_nanostring
14	0.95	1 / 191	SPANG_LPS−index2
15	0.97	2 / 324	SPANG_BCL6−index2
16	0.98	0 / 16	LIU_PROSTATE_CANCER_DN
17	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
18	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
19	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	1.00	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	0.02	4 / 67	acrosomal vesicle
2	0.02	3 / 39	T−tubule
3	0.04	69 / 3507	plasma membrane
4	0.04	2 / 19	basal lamina
5	0.04	2 / 19	nonmotile primary cilium
6	0.05	2 / 23	anchored component of plasma membrane
7	0.07	76 / 4052	integral component of membrane
8	0.08	6 / 184	transcription factor complex
9	0.08	2 / 29	RNA polymerase II transcription factor complex
10	0.08	2 / 30	voltage−gated calcium channel complex
11	0.10	19 / 864	Golgi apparatus
12	0.10	3 / 70	caveola
13	0.11	2 / 36	nuclear inner membrane
14	0.12	2 / 37	dendritic shaft
15	0.13	3 / 79	collagen trimer
16	0.15	25 / 1250	integral component of plasma membrane
17	0.15	1 / 10	junctional sarcoplasmic reticulum membrane
18	0.15	1 / 10	sperm midpiece
19	0.15	2 / 43	intercellular bridge
20	0.16	1 / 11	NMDA selective glutamate receptor complex

Chr

Rank	p−value	#in/all	Geneset
1	0.006	18 / 582	Chr 15
2	0.013	26 / 1017	Chr 12
3	0.040	18 / 715	Chr 10
4	0.114	22 / 1043	Chr 3
5	0.148	7 / 272	Chr 18
6	0.152	18 / 862	Chr 5
7	0.186	13 / 613	Chr 14
8	0.211	21 / 1083	Chr 17
9	0.246	13 / 651	Chr 8
10	0.400	6 / 318	Chr 13
11	0.409	21 / 1228	Chr 2
12	0.599	8 / 522	Chr 20
13	0.622	13 / 859	Chr 7
14	0.744	10 / 735	Chr 4
15	0.830	5 / 436	Chr 22
16	0.847	9 / 745	Chr 9
17	0.881	18 / 1425	Chr 19
18	0.948	23 / 1920	Chr 1
19	0.954	10 / 976	Chr 6
20	0.964	8 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	82 / 3109	TssP_Colon
2	2e−05	84 / 3406	ReprPC_Colon
3	7e−05	73 / 2947	ReprPCWk_Colon
4	1e−04	19 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
5	1e−03	15 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
6	6e−03	98 / 4879	Quies1_Colon
7	9e−03	23 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	2e−02	12 / 389	K9K27me3_Colon
9	3e−02	44 / 2041	EnhP_Colon
10	3e−02	14 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
11	3e−02	19 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	4e−02	14 / 525	Quies2_Colon
13	5e−02	37 / 1753	Het_Colon
14	6e−02	9 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
15	9e−02	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
16	1e−01	3 / 73	Ang_CRC−CIMPH−vs−L_hyper
17	1e−01	2 / 36	Ang_CRC_Hypomethylated
18	1e−01	26 / 1281	HetRpts_Colon
19	1e−01	3 / 78	Ang_CRC_Hypermethylated
20	1e−01	1 / 9	Marisa_CRC−C3

Disease

Rank	p−value	#in/all	Geneset
1	0.1	10 / 399	GUDJ_psoriasis down
2	0.1	2 / 37	BCHETNIA_EBM−DM up
3	0.3	1 / 22	BCHETNIA_EBM up
4	1.0	3 / 608	GUDJ_psoriasis up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
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	10 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
2	0.008	14 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
3	0.016	4 / 61	in vivo astrocytes vs. cultured astroglia
4	0.023	23 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
5	0.041	4 / 81	Weller_LGG_gradeII−vs−III_UP
6	0.052	2 / 23	Shinawi_with_increased_methylation_in_STS
7	0.092	1 / 6	Sturm_GBM_Meth_overexpression_K_mesenchymal_UP
8	0.102	3 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.121	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
10	0.142	30 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
11	0.148	3 / 83	GIEZELT_GBM_WT_down_VS_mut
12	0.176	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
13	0.199	3 / 96	Weller_LGG_A_vs_O_UP
14	0.208	2 / 53	Donson−innate immunity−associated with LTS in HGA
15	0.220	2 / 55	Gorovets_LGG_PG_subclass
16	0.220	4 / 150	Sturm_GBM_Meth_overexpression_B_adult_UP
17	0.226	2 / 56	mature astrocytes
18	0.228	1 / 16	VERHAAK_PN subtype
19	0.228	1 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
20	0.241	3 / 106	WIRTH_Normal Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	29 / 971	BENPORATH_SUZ12_TARGETS
2	0.001	30 / 1041	BENPORATH_ES_WITH_H3K27ME3
3	0.002	6 / 79	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2
4	0.002	3 / 17	KEGG_ASTHMA
5	0.002	2 / 5	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_DN
6	0.003	3 / 18	BIOCARTA_ETS_PATHWAY
7	0.003	14 / 374	HATADA_METHYLATED_IN_LUNG_CANCER_UP
8	0.004	15 / 429	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
9	0.005	3 / 22	BIOCARTA_DC_PATHWAY
10	0.007	2 / 8	BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
11	0.008	3 / 26	BIOCARTA_INFLAM_PATHWAY
12	0.009	2 / 9	BUDHU_LIVER_CANCER_METASTASIS_UP
13	0.009	2 / 9	SEIKE_LUNG_CANCER_POOR_SURVIVAL
14	0.011	2 / 10	BRUNEAU_SEPTATION_VENTRICULAR
15	0.012	4 / 55	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
16	0.013	25 / 966	BENPORATH_EED_TARGETS
17	0.015	9 / 238	SENESE_HDAC1_TARGETS_DN
18	0.015	19 / 686	MIKKELSEN_ES_ICP_WITH_H3K4ME3
19	0.015	2 / 12	REACTOME_PYRIMIDINE_CATABOLISM
20	0.015	2 / 12	KINNEY_DNMT1_METHYLATION_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 128	HALLMARK_SPERMATOGENESIS
2	0.2	2 / 44	HALLMARK_APICAL_SURFACE
3	0.3	4 / 181	HALLMARK_ALLOGRAFT_REJECTION
4	0.4	4 / 193	HALLMARK_XENOBIOTIC_METABOLISM
5	0.4	4 / 194	HALLMARK_INFLAMMATORY_RESPONSE
6	0.4	2 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	0.4	1 / 36	HALLMARK_ANGIOGENESIS
8	0.4	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
9	0.5	3 / 155	HALLMARK_UV_RESPONSE_UP
10	0.5	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.6	3 / 193	HALLMARK_HEME_METABOLISM
12	0.6	3 / 197	HALLMARK_IL2_STAT5_SIGNALING
13	0.6	3 / 198	HALLMARK_HYPOXIA
14	0.6	3 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	0.7	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
16	0.8	1 / 98	HALLMARK_ANDROGEN_RESPONSE
17	0.8	2 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
18	0.8	2 / 190	HALLMARK_APICAL_JUNCTION
19	0.8	2 / 195	HALLMARK_MYOGENESIS
20	0.8	2 / 196	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.8	1 / 91	DUMEAUX_Smoking enriched genes
2	1.0	0 / 11	DUMEAUX_Smoking literature genes up
3	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.0	0 / 11	DUMEAUX_Women normal BMI literature genes up
10	1.0	0 / 17	DUMEAUX_High bmi enriched genes
11	1.0	0 / 33	DUMEAUX_Fasting enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−06	118 / 5039	HOPP_Repressed
2	9e−03	61 / 2838	HOPP_Poised_promoter
3	2e−02	11 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
4	3e−02	55 / 2658	HOPP_Repetitive
5	5e−02	10 / 347	WIRTH_lymphoma937_spot H
6	1e−01	11 / 458	WIRTH_lymphoma937_spot I
7	1e−01	7 / 261	LENZ_Stromal signature 1
8	1e−01	1 / 9	MASCQUE_ABC UP
9	1e−01	63 / 3457	HOPP_Heterochrom
10	2e−01	4 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
11	2e−01	10 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC−
12	2e−01	3 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
13	2e−01	1 / 15	Subero_B−ALL_hypo_meth
14	2e−01	1 / 15	Subero_T−ALL_hypo_meth
15	2e−01	1 / 17	WRIGHT_ABC UP
16	2e−01	2 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
17	3e−01	1 / 21	DAVE_Immune response 2
18	3e−01	6 / 279	SPANG_IL21 DN
19	3e−01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
20	4e−01	9 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−

MF

Rank	p−value	#in/all	Geneset
1	0.001	19 / 551	G−protein coupled receptor activity
2	0.006	3 / 23	carboxypeptidase activity
3	0.006	3 / 24	3',5'−cyclic−nucleotide phosphodiesterase activity
4	0.011	2 / 10	3',5'−cyclic−AMP phosphodiesterase activity
5	0.011	7 / 150	lipid binding
6	0.012	5 / 85	transcriptional activator activity, RNA polymerase II transcription regulatory re
7	0.012	8 / 192	carbohydrate binding
8	0.013	2 / 11	high voltage−gated calcium channel activity
9	0.013	2 / 11	sulfate transmembrane transporter activity
10	0.013	2 / 11	transaminase activity
11	0.015	2 / 12	secondary active sulfate transmembrane transporter activity
12	0.018	2 / 13	anion:anion antiporter activity
13	0.018	2 / 13	mannosyltransferase activity
14	0.020	6 / 132	ion channel activity
15	0.020	4 / 65	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
16	0.033	2 / 18	HMG box domain binding
17	0.037	2 / 19	alpha−tubulin binding
18	0.037	2 / 19	voltage−gated sodium channel activity
19	0.040	2 / 20	amino acid binding
20	0.040	2 / 20	cytokine binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	9 / 215	hsa−miR−196a
2	0.010	8 / 186	hsa−miR−196b
3	0.075	5 / 140	hsa−miR−488
4	0.081	6 / 187	hsa−miR−34b
5	0.095	4 / 108	hsa−miR−33b
6	0.095	4 / 108	hsa−miR−526b
7	0.103	4 / 111	hsa−miR−190b
8	0.107	1 / 7	hsa−miR−339−3p
9	0.113	4 / 115	hsa−miR−154
10	0.125	9 / 360	hsa−let−7a
11	0.126	5 / 165	hsa−miR−1297
12	0.129	3 / 78	hsa−miR−619
13	0.129	3 / 78	hsa−miR−890
14	0.129	3 / 78	hsa−miR−1305
15	0.134	2 / 40	hsa−miR−885−5p
16	0.140	2 / 41	hsa−miR−601
17	0.145	2 / 42	hsa−miR−525−3p
18	0.151	2 / 43	hsa−miR−518b
19	0.161	8 / 330	hsa−miR−98
20	0.161	8 / 330	hsa−let−7f

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.03	39 / 1798	HEBENSTREIT_low expression TF
2	0.73	42 / 2827	ICGC_Bcl3_targets
3	0.80	26 / 1867	HEBENSTREIT_high expression TF
4	0.80	51 / 3511	ICGC_Rad21_targets
5	0.85	9 / 745	ICGC_NrsfPcr2_targets
6	0.85	20 / 1523	ICGC_P300_targets
7	0.86	68 / 4714	ICGC_Pu1_targets
8	0.88	37 / 2719	ICGC_Pbx3_targets
9	0.89	32 / 2401	ICGC_Bcl11_targets
10	0.89	28 / 2133	ICGC_Cebpbsc150_targets
11	0.90	28 / 2149	ICGC_Mef2_targets
12	0.93	44 / 3305	ICGC_BatfPcr1_targets
13	0.93	8 / 766	ICGC_Atf3_targets
14	0.93	6 / 619	ICGC_RxraPcr1_targets
15	0.96	40 / 3177	ICGC_Irf4_targets
16	0.96	69 / 5135	ICGC_Ebfsc137065_targets
17	0.98	86 / 6406	ICGC_Pax5_targets
18	0.98	73 / 5552	ICGC_Pol24_targets
19	0.98	15 / 1503	ICGC_Six5_targets
20	0.99	14 / 1472	ICGC_NrsfPcr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	3 / 41	VAQUERIZAS_Fetal brain
2	0.04	3 / 49	VAQUERIZAS_Uterus
3	0.15	1 / 10	VAQUERIZAS_Skeletal.muscle.psoas
4	0.26	1 / 19	VAQUERIZAS_Heart
5	0.29	2 / 67	VAQUERIZAS_Whole blood
6	0.33	1 / 25	VAQUERIZAS_Spinal cord
7	0.45	3 / 155	VAQUERIZAS_General
8	0.48	1 / 41	VAQUERIZAS_Testis
9	1.00	0 / 45	VAQUERIZAS_Placenta
10	1.00	0 / 33	VAQUERIZAS_Liver
11	1.00	0 / 37	VAQUERIZAS_Prostate
12	1.00	0 / 30	VAQUERIZAS_Smooth muscle
13	1.00	0 / 12	VAQUERIZAS_Kidney
14	1.00	0 / 46	VAQUERIZAS_Whole brain
15	1.00	0 / 42	VAQUERIZAS_Thymus
16	1.00	0 / 42	VAQUERIZAS_Thyroid
17	1.00	0 / 7	VAQUERIZAS_Appendix
18	1.00	0 / 31	VAQUERIZAS_Fetal lung
19	1.00	0 / 64	VAQUERIZAS_Lung
20	1.00	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.01	6 / 115	WIRTH_Liver
2	0.14	11 / 476	WIRTH_Nervous System
3	0.17	2 / 47	WIRTH_Placenta
4	0.19	1 / 13	PALMER_CD8+ T−Cell signature up
5	0.19	4 / 141	WIRTH_Muscle
6	0.20	1 / 14	WIRTH_Thalamus
7	0.38	2 / 82	WIRTH_Homeostasis
8	0.43	4 / 208	PALMER_B−Cell signature up
9	0.58	1 / 54	WIRTH_Pancreas
10	0.63	3 / 202	WIRTH_Testis
11	0.89	1 / 137	WIRTH_Mucosa
12	0.90	1 / 140	PALMER_T−Cell signature up
13	0.99	1 / 259	PALMER_Granulocytes signature up
14	1.00	0 / 6	WIRTH_Pituitary gland
15	1.00	0 / 427	WIRTH_Immune system
16	1.00	0 / 13	WIRTH_Sec. lymphoid organs
17	1.00	0 / 13	WIRTH_Prim. lymphoid organs
18	1.00	0 / 14	WIRTH_B−cells
19	1.00	0 / 12	WIRTH_Tonsil
20	1.00	0 / 14	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.08	96 / 5285	LU_BPDE 0.005 DN
2	0.66	20 / 1343	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	