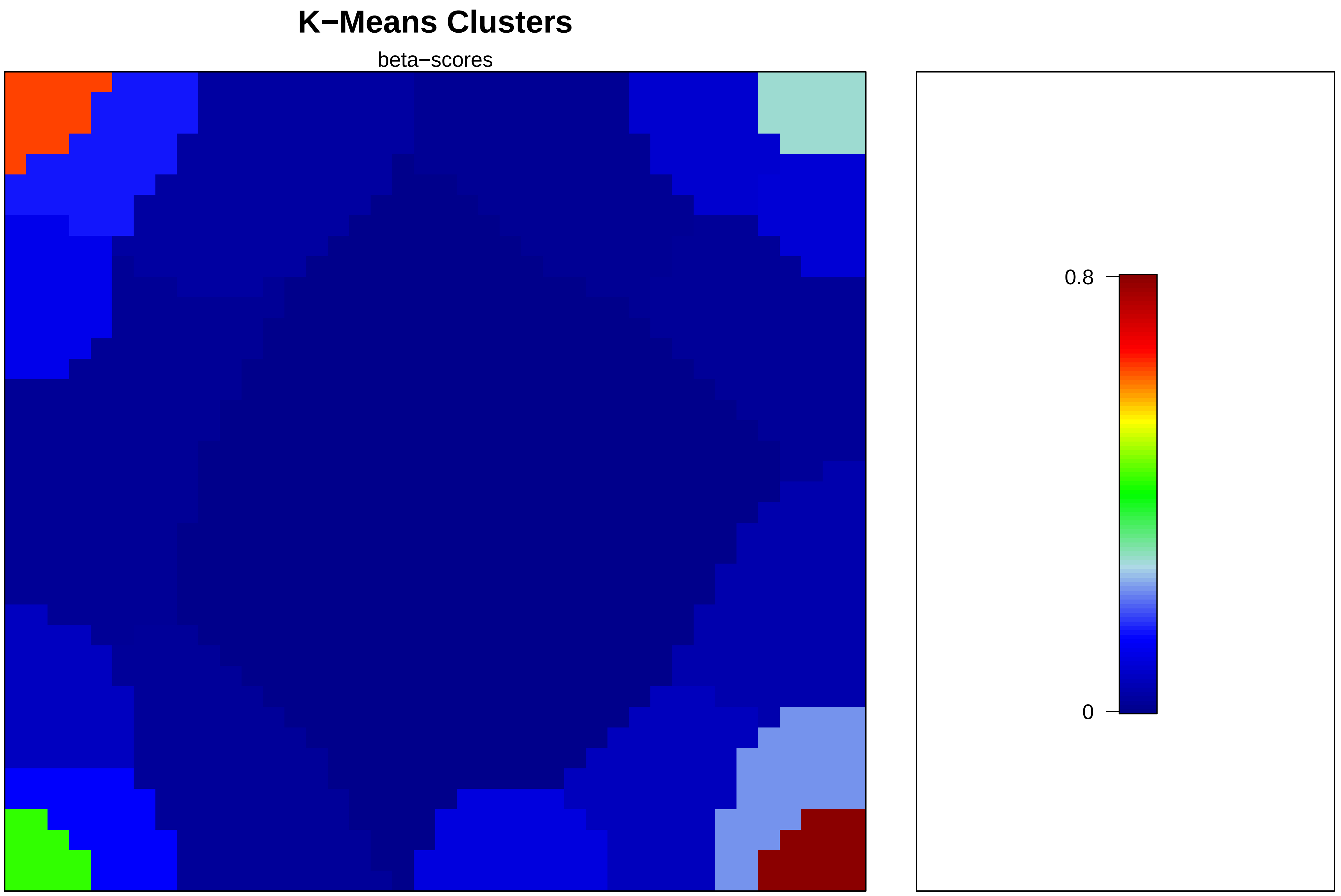
K−Means Clusters

landscape


K−Means Clusters
beta−scores
0.8
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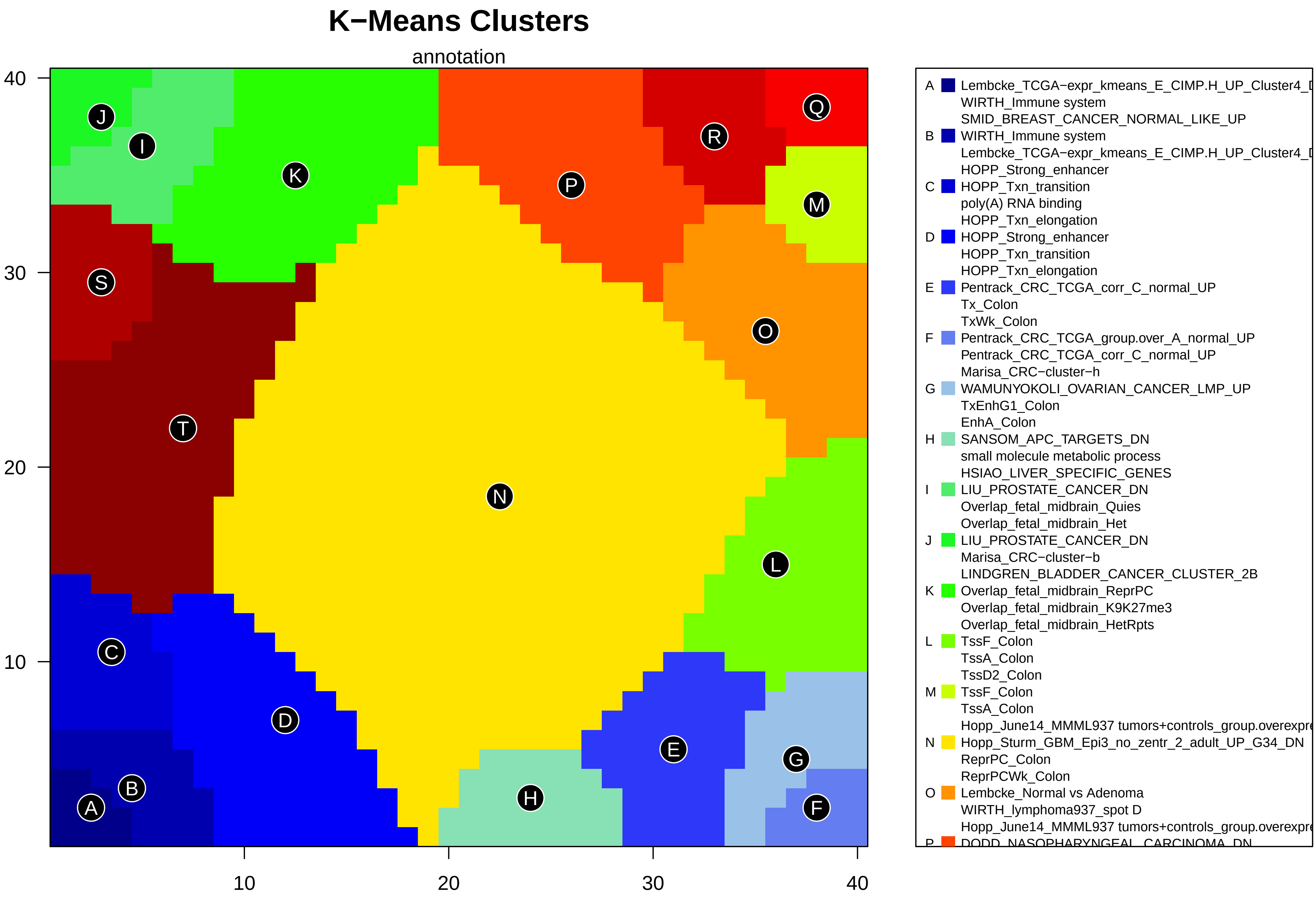
K−Means Clusters
annotation
40
30
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40
J
I
K
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Q
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S
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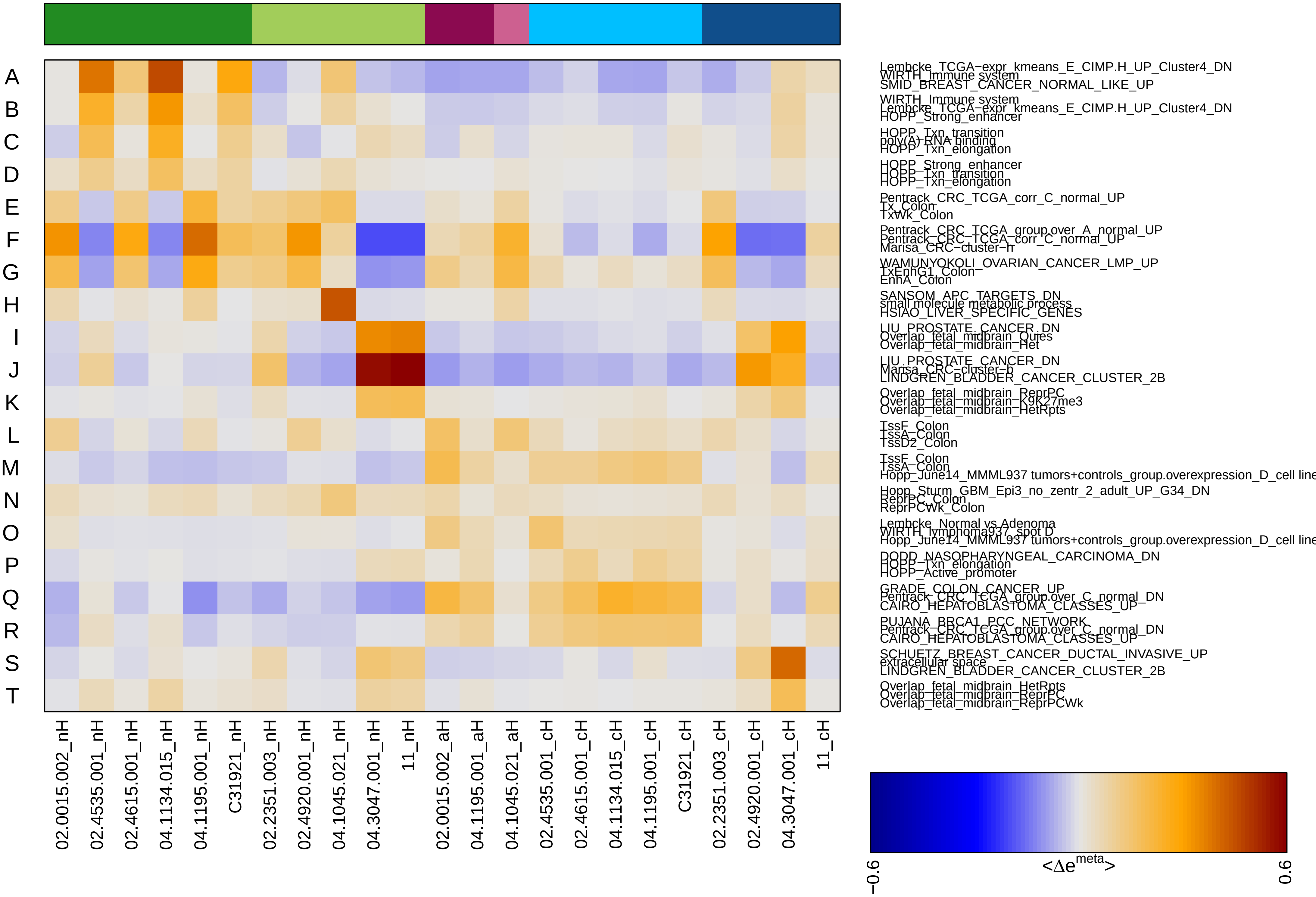
T
N
L
C
D
E
G
B
A
H
F
A Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_
WIRTH_Immune system
SMID_BREAST_CANCER_NORMAL_LIKE_UP
B WIRTH_Immune system
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_
HOPP_Strong_enhancer
C HOPP_Txn_transition
poly(A) RNA binding
HOPP_Txn_elongation
D HOPP_Strong_enhancer
HOPP_Txn_transition
HOPP_Txn_elongation
E Pentrack_CRC_TCGA_corr_C_normal_UP
Tx_Colon
TxWk_Colon
F Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
G WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
TxEnhG1_Colon
EnhA_Colon
H SANSOM_APC_TARGETS_DN
small molecule metabolic process
HSIAO_LIVER_SPECIFIC_GENES
I LIU_PROSTATE_CANCER_DN
Overlap_fetal_midbrain_Quies
Overlap_fetal_midbrain_Het
J LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
LINDGREN_BLADDER_CANCER_CLUSTER_2B
K Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_HetRpts
L TssF_Colon
TssA_Colon
TssD2_Colon
M TssF_Colon
TssA_Colon
Hopp_June14_MMML937 tumors+controls_group.overexpre
N Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
ReprPC_Colon
ReprPCWk_Colon
O Lembcke_Normal vs Adenoma
WIRTH_lymphoma937_spot D
Hopp_June14_MMML937 tumors+controls_group.overexpre
P DODD_NASOPHARYNGEAL_CARCINOMA_DN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Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
WIRTH_Immune system
SMID_BREAST_CANCER_NORMAL_LIKE_UP
WIRTH_Immune system
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
HOPP_Strong_enhancer
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poly(A) RNA binding
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Pentrack_CRC_TCGA_corr_C_normal_UP
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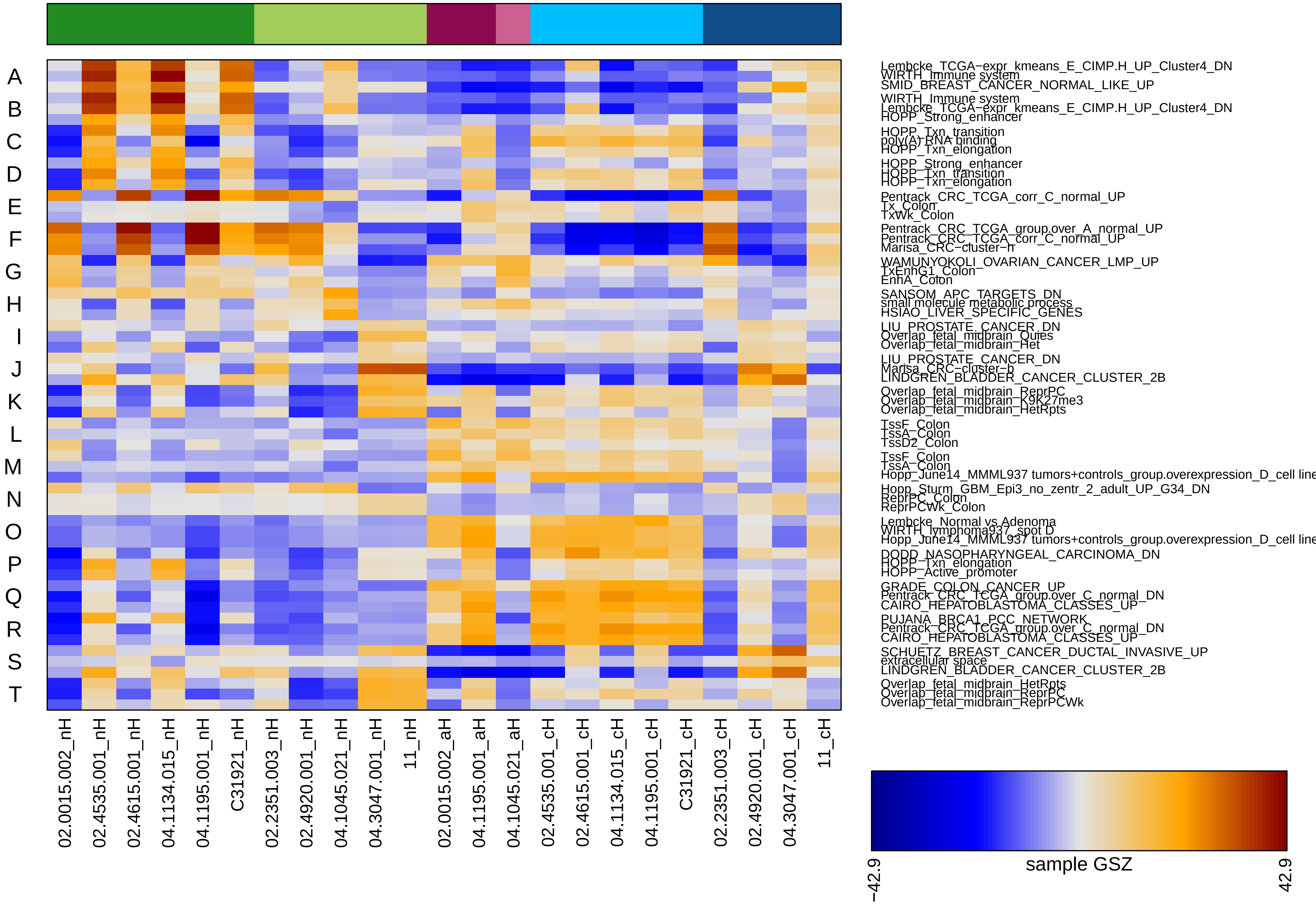
TssF_Colon
TssA_Colon
Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
ReprPC_Colon
ReprPCWk_Colon
Lembcke_Normal vs Adenoma
WIRTH_lymphoma937_spot D
Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
DODD_NASOPHARYNGEAL_CARCINOMA_DN
HOPP_Txn_elongation
HOPP_Active_promoter
GRADE_COLON_CANCER_UP
Pentrack_CRC_TCGA_group.over_C_normal_DN
CAIRO_HEPATOBLASTOMA_CLASSES_UP
PUJANA_BRCA1_PCC_NETWORK
Pentrack_CRC_TCGA_group.over_C_normal_DN
CAIRO_HEPATOBLASTOMA_CLASSES_UP
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
extracellular space
LINDGREN_BLADDER_CANCER_CLUSTER_2B
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_ReprPCWk
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
−0.6
$<\Delta e^{meta}>$
0.6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Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
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Pentrack_CRC_TCGA_corr_C_normal_UP
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Overlap_fetal_midbrain_K9K27me3
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HOPP_Active_promoter
GRADE_COLON_CANCER_UP
Pentrack_CRC_TCGA_group.over_C_normal_DN
CAIRO_HEPATOBLASTOMA_CLASSES_UP
PUJANA_BRCA1_PCC_NETWORK
Pentrack_CRC_TCGA_group.over_C_normal_DN
CAIRO_HEPATOBLASTOMA_CLASSES_UP
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
extracellular space
LINDGREN_BLADDER_CANCER_CLUSTER_2B
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_ReprPCWk
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
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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
−42.9
sample GSZ
42.9

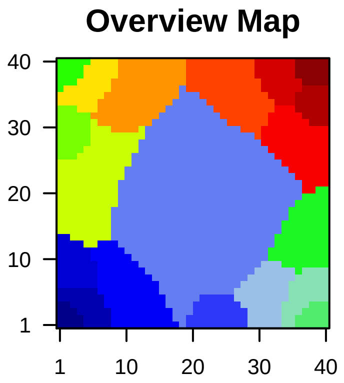
K−Means Clusters

Spot Summary: A

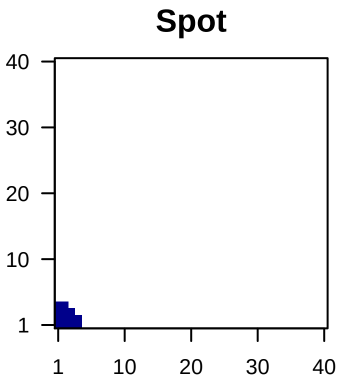
metagenes = 13
genes = 262

<r> metagenes = 0.99
<r> genes = 0.77
beta: r2= 0.44 / log p= −3.23

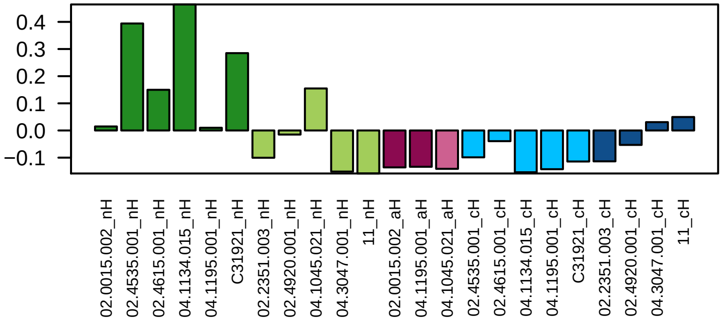
samples with spot = 5 (21.7 %)
MLH1_normHNPCC : 4 (66.7 %)
other_normHNPCC : 1 (20 %)



Overview Map



Spot

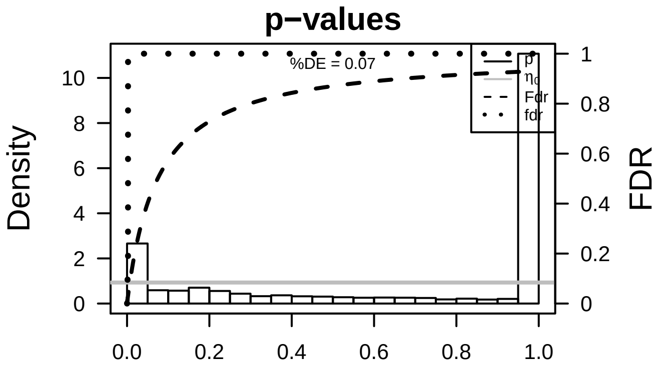


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.4	−0.53	0.84	FDCSP	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	ENSG000001	1.34	−0.7	0.91	CCL21	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
3	ENSG000001	1.14	−0.59	0.93	CCL19	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
4	ENSG000001	1.14	−0.52	0.93	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	0.94	CD52	CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
7	ENSG000001	0.95	−0.25	0.94	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	0.98	CCR7	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
10	ENSG000001	0.89	−0.51	0.94	CXCR4	chemokine (C−X−C motif) receptor 4 [Source:HGNC Symbol;
11	ENSG000001	0.85	−0.35	0.97	LCP1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
12	ENSG000002	0.85	−0.8	0.45		MT−RNR2−like 9 [Source:HGNC Symbol;Acc:HGNC:37166]
13	ENSG000001	0.85	−0.2	0.92	IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
14	ENSG000001	0.84	−0.29	0.97	MS4A1	membrane−spanning 4−domains, subfamily A, member 1 [So
15	ENSG000001	0.83	−0.25	0.94	GIMAP7	GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:
16	ENSG000001	0.82	−0.25	0.93	ETS1	v−ets avian erythroblastosis virus E26 oncogene homolog 1 [
17	ENSG000001	0.82	−0.39	0.93	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:HGN
19	ENSG000000	0.8	−0.2	0.97	PTPRC	protein tyrosine phosphatase, receptor type, C [Source:HGN
20	ENSG000001	0.79	−0.35	0.98	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	142 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−94	97 / 427	Tissu	WIRTH_Immune system
3	3e−81	89 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	4e−70	89 / 574	Canc	Lembcke_Colonic Inflammation
5	9e−69	68 / 263	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
6	6e−59	54 / 175	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
7	2e−51	53 / 220	GSEA	MCLACHLAN_DENTAL_CARIES_UP
8	4e−50	55 / 259	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
9	1e−48	69 / 522	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
10	6e−44	47 / 210	GSEA	MCLACHLAN_DENTAL_CARIES_DN
11	6e−42	54 / 343	BP	immune response
12	7e−38	45 / 246	GSEA	QI_PLASMACYTOMA_UP
13	8e−35	199 / 7592	Lymp	HOPP_Strong_enhancer
14	3e−33	48 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
15	5e−30	23 / 51	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
16	4e−29	34 / 181	HM	HALLMARK_ALLOGRAFT_REJECTION
17	7e−29	47 / 435	GSEA	RODWELL_AGING_KIDNEY_UP
18	3e−28	39 / 279	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
19	8e−28	25 / 79	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
20	1e−27	15 / 16	CC	MHC class II protein complex
21	5e−26	21 / 53	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
22	8e−26	33 / 208	Tissu	PALMER_B−Cell signature up
23	9e−24	23 / 86	GSEA	WIELAND_UP_BY_HBV_INFECTION
24	1e−23	23 / 87	GSEA	BASSO_CD40_SIGNALING_UP
25	1e−23	38 / 346	GSEA	SANSOM_APC_TARGETS_DN
26	5e−23	28 / 163	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
27	8e−23	31 / 218	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
28	1e−22	30 / 201	CC	external side of plasma membrane
29	2e−22	18 / 45	GSEA	YU_MYC_TARGETS_DN
30	2e−22	20 / 64	BP	T cell costimulation
31	4e−22	68 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
32	1e−21	22 / 92	BP	T cell receptor signaling pathway
33	2e−21	21 / 82	GSEA	MORI_MATURE_B_LYMPHOCYTE_UP
34	3e−21	19 / 61	BP	antigen processing and presentation
35	2e−20	61 / 1165	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
36	4e−20	51 / 823	GSEA	REACTOME_IMMUNE_SYSTEM
37	1e−19	28 / 215	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
38	3e−19	35 / 381	GSEA	KUMAR_TARGETS_OF_MLL_AF9_FUSION
39	3e−19	145 / 5643	Lymp	HOPP_Txn_transition
40	4e−19	38 / 466	Lymp	SPANG_CD40 6hrs DN



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 144	HORVATH_aging_genes meth UP
2	0.2	2 / 57	TESCHENDORFF_age_hypermethylated
3	0.8	1 / 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−42	54 / 343	immune response
2	2e−22	20 / 64	T cell costimulation
3	1e−21	22 / 92	T cell receptor signaling pathway
4	3e−21	19 / 61	antigen processing and presentation
5	2e−18	10 / 11	antigen processing and presentation of peptide or polysaccharide antigen via
6	6e−17	13 / 31	B cell receptor signaling pathway
7	3e−16	17 / 78	regulation of immune response
8	2e−15	16 / 73	interferon−gamma−mediated signaling pathway
9	3e−13	13 / 54	positive regulation of T cell proliferation
10	3e−13	38 / 707	innate immune response
11	7e−13	17 / 122	adaptive immune response
12	2e−11	10 / 35	T cell differentiation
13	1e−10	9 / 29	B cell activation
14	1e−10	21 / 270	cytokine−mediated signaling pathway
15	2e−10	20 / 246	cell surface receptor signaling pathway
16	2e−10	13 / 90	antigen processing and presentation of exogenous peptide antigen via MHC c
17	7e−10	22 / 326	inflammatory response
18	3e−09	9 / 40	peptidyl−tyrosine autophosphorylation
19	3e−09	45 / 1279	signal transduction
20	5e−09	7 / 20	positive regulation of neutrophil chemotaxis

Brain

Rank	p−value	#in/all	Geneset
1	4e−06	53 / 2084	Mid_Frontal_Lobe_K9K27me3
2	1e−05	83 / 3977	Mid_Frontal_Lobe_ReprPC
3	2e−05	60 / 2603	Fetal_TxTrans
4	6e−05	37 / 1394	Mid_Frontal_Lobe_Quies
5	8e−04	35 / 1478	Overlap_fetal_midbrain_TxTrans
6	1e−03	52 / 2549	Fetal_TssF
7	2e−03	41 / 1890	Overlap_fetal_midbrain_TssF
8	2e−03	38 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	1e−02	28 / 1327	Mid_Frontal_Lobe_TssP
10	3e−02	52 / 2956	Fetal_TssA
11	6e−02	17 / 840	Mid_Frontal_Lobe_TssF
12	8e−02	21 / 1108	Overlap_fetal_midbrain_TssA
13	1e−01	22 / 1210	Fetal_TssP
14	2e−01	3 / 106	Overlap_fetal_midbrain_Tx
15	2e−01	10 / 552	Fetal_Tx
16	3e−01	26 / 1680	Fetal_ReprPCWk
17	3e−01	18 / 1137	Fetal_Enh
18	4e−01	5 / 317	Mid_Frontal_Lobe_Tx
19	7e−01	10 / 805	Mid_Frontal_Lobe_EnhG
20	7e−01	4 / 342	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	4e−70	89 / 574	Lembcke_Colonic Inflammation
2	8e−16	29 / 324	SPANG_BCL6−index2
3	8e−10	7 / 16	GENTLES_modul18
4	2e−06	13 / 191	SPANG_LPS−index2
5	3e−04	7 / 97	PanCan_TXmisReg_geneset_nanostring
6	1e−03	6 / 86	PanCan_JAK−ST_geneset_nanostring
7	1e−03	3 / 16	GENTLES_modul11
8	6e−03	8 / 198	PanCan_PI3K_geneset_nanostring
9	7e−03	6 / 123	PanCan_Driver_Gene_geneset_nanostring
10	1e−02	2 / 14	GENTLES_modul12
11	8e−02	1 / 6	ZHANG_MGUS up
12	1e−01	4 / 140	PanCan_RAS_geneset_nanostring
13	2e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
14	2e−01	1 / 16	LIU_COMMON_CANCER_GENES
15	2e−01	1 / 16	WANG_ER_UP
16	3e−01	1 / 24	PanCan_Notch_geneset_nanostring
17	3e−01	3 / 136	PanCan_CC+Apop_geneset_nanostring
18	3e−01	2 / 78	PanCan_Wnt_geneset_nanostring
19	3e−01	3 / 152	PanCan_MAPK_geneset_nanostring
20	4e−01	1 / 37	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	1e−27	15 / 16	MHC class II protein complex
2	1e−22	30 / 201	external side of plasma membrane
3	3e−15	101 / 3507	plasma membrane
4	6e−12	9 / 22	integral component of lumenal side of endoplasmic reticulum membrane
5	2e−11	10 / 35	ER to Golgi transport vesicle membrane
6	3e−10	9 / 32	immunological synapse
7	4e−10	7 / 15	T cell receptor complex
8	3e−09	27 / 523	cell surface
9	8e−09	8 / 32	transport vesicle membrane
10	9e−09	10 / 61	extrinsic component of cytoplasmic side of plasma membrane
11	4e−08	8 / 39	clathrin−coated endocytic vesicle membrane
12	9e−08	75 / 3059	membrane
13	2e−07	8 / 47	trans−Golgi network membrane
14	3e−07	66 / 2638	extracellular exosome
15	5e−07	8 / 53	endocytic vesicle membrane
16	2e−06	38 / 1250	integral component of plasma membrane
17	7e−06	14 / 245	lysosomal membrane
18	1e−05	12 / 190	membrane raft
19	4e−05	65 / 2974	cytosol
20	9e−05	12 / 235	lysosome

Chr

Rank	p−value	#in/all	Geneset
1	2e−05	30 / 976	Chr 6
2	8e−02	22 / 1172	Chr 11
3	9e−02	33 / 1920	Chr 1
4	2e−01	17 / 1017	Chr 12
5	3e−01	12 / 746	Chr X
6	4e−01	7 / 436	Chr 22
7	6e−01	7 / 522	Chr 20
8	7e−01	18 / 1425	Chr 19
9	7e−01	9 / 745	Chr 9
10	7e−01	13 / 1083	Chr 17
11	7e−01	10 / 859	Chr 7
12	7e−01	2 / 191	Chr 21
13	7e−01	10 / 862	Chr 5
14	8e−01	7 / 651	Chr 8
15	8e−01	6 / 582	Chr 15
16	8e−01	3 / 318	Chr 13
17	8e−01	9 / 847	Chr 16
18	8e−01	11 / 1043	Chr 3
19	9e−01	13 / 1228	Chr 2
20	9e−01	7 / 735	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	142 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−18	32 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	7e−10	25 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	2e−08	31 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	7e−08	25 / 532	K9acLow_Colon
6	2e−07	19 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
7	1e−05	194 / 11968	TssWk_Colon
8	2e−04	18 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
9	6e−04	6 / 76	Marisa_CRC−cluster−g
10	1e−03	3 / 15	Budinska_B_Lower crypt−like_DOWN
11	2e−03	60 / 3112	EnhA_Colon
12	9e−03	76 / 4379	TssD1_Colon
13	1e−02	5 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	3e−02	94 / 5889	EnhWk1_Colon
15	4e−02	10 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
16	5e−02	18 / 877	TxEnhG2_Colon
17	5e−02	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
18	5e−02	1 / 4	Budinska_C_CIMP−H−like_DOWN
19	7e−02	1 / 5	Kaneda_CIMP−group1
20	8e−02	51 / 3122	TxEnhG1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	5e−11	32 / 608	GUDJ_psoriasis up
2	1e+00	1 / 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	3e−28	39 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	6e−09	12 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
3	1e−08	8 / 33	Donson−Misc immune function−associated with LTS in HGA
4	4e−08	25 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	7e−08	11 / 96	Weller_LGG_A_vs_O_UP
6	4e−07	73 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
7	2e−06	4 / 8	Donson−adaptive−immunity−associated with LTS in HGA
8	7e−06	7 / 53	Donson−innate immunity−associated with LTS in HGA
9	5e−05	4 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
10	1e−04	10 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
11	1e−04	3 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
12	6e−04	4 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
13	1e−03	4 / 35	shaw_responders_down_in_oligo_glioma
14	1e−03	3 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
15	8e−03	4 / 59	Christensen_hypomethylated_in_primary_glioblastoma
16	9e−03	2 / 11	WILLSCHER_GBM_LTSwt_proteomics−G_UP
17	9e−03	5 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
18	1e−02	19 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
19	1e−02	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
20	1e−02	2 / 14	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−81	89 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	9e−69	68 / 263	WALLACE_PROSTATE_CANCER_RACE_UP
3	6e−59	54 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE
4	2e−51	53 / 220	MCLACHLAN_DENTAL_CARIES_UP
5	4e−50	55 / 259	POOLA_INVASIVE_BREAST_CANCER_UP
6	1e−48	69 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
7	6e−44	47 / 210	MCLACHLAN_DENTAL_CARIES_DN
8	7e−38	45 / 246	QI_PLASMACYTOMA_UP
9	3e−33	48 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
10	5e−30	23 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
11	7e−29	47 / 435	RODWELL_AGING_KIDNEY_UP
12	8e−28	25 / 79	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
13	5e−26	21 / 53	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
14	9e−24	23 / 86	WIELAND_UP_BY_HBV_INFECTION
15	1e−23	23 / 87	BASSO_CD40_SIGNALING_UP
16	1e−23	38 / 346	SANSOM_APC_TARGETS_DN
17	5e−23	28 / 163	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
18	8e−23	31 / 218	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
19	2e−22	18 / 45	YU_MYC_TARGETS_DN
20	4e−22	68 / 1340	PUJANA_ATM_PCC_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	4e−29	34 / 181	HALLMARK_ALLOGRAFT_REJECTION
2	1e−10	18 / 189	HALLMARK_KRAS_SIGNALING_UP
3	7e−10	17 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
4	9e−09	16 / 194	HALLMARK_INFLAMMATORY_RESPONSE
5	4e−07	14 / 192	HALLMARK_COMPLEMENT
6	2e−05	12 / 197	HALLMARK_IL2_STAT5_SIGNALING
7	6e−05	11 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	2e−04	7 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	1e−03	6 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	4e−03	8 / 190	HALLMARK_APICAL_JUNCTION
11	9e−03	6 / 132	HALLMARK_COAGULATION
12	1e−02	5 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	2e−02	7 / 199	HALLMARK_MTORC1_SIGNALING
14	5e−02	6 / 196	HALLMARK_P53_PATHWAY
15	5e−02	6 / 198	HALLMARK_HYPOXIA
16	1e−01	2 / 44	HALLMARK_APICAL_SURFACE
17	1e−01	5 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
18	2e−01	4 / 157	HALLMARK_APOPTOSIS
19	2e−01	2 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	3e−01	4 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 17	DUMEAUX_High bmi enriched genes
2	1e−01	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	1e−01	1 / 11	DUMEAUX_Women normal BMI literature genes up
4	2e−01	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	7e−01	1 / 91	DUMEAUX_Smoking enriched genes
6	1e+00	0 / 11	DUMEAUX_Smoking 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	8e−35	199 / 7592	HOPP_Strong_enhancer
2	3e−19	145 / 5643	HOPP_Txn_transition
3	4e−19	38 / 466	SPANG_CD40 6hrs DN
4	4e−17	22 / 145	WIRTH_lymphoma937_spot F
5	4e−17	22 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
6	2e−16	30 / 332	SPANG_CD40 6hrs UP
7	3e−15	28 / 315	WIRTH_lymphoma937_spot E
8	2e−14	27 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
9	8e−14	52 / 1215	SPANG_BCR DN
10	2e−13	19 / 150	DAVE_BL−vs−DLBCL
11	6e−12	9 / 22	DAVE_NFkB BL DN
12	6e−11	10 / 38	TARTE_B−cell signature
13	7e−11	24 / 347	WIRTH_lymphoma937_spot H
14	1e−10	15 / 123	SPANG_LPS 6hrs UP
15	2e−10	21 / 279	SPANG_IL21 DN
16	2e−09	24 / 414	TARTE_Mature plasma cell signature
17	7e−09	21 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
18	1e−08	158 / 8358	HOPP_Active_promoter
19	6e−08	9 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
20	6e−08	6 / 17	YAMANE_AICDA_targets_recruited

MF

Rank	p−value	#in/all	Geneset
1	1e−11	8 / 16	MHC class II protein complex binding
2	4e−10	8 / 23	peptide antigen binding
3	6e−10	192 / 10693	protein binding
4	8e−09	9 / 45	non−membrane spanning protein tyrosine kinase activity
5	8e−08	15 / 196	transmembrane signaling receptor activity
6	9e−06	6 / 37	chemokine activity
7	2e−05	15 / 301	actin binding
8	3e−05	9 / 117	protein tyrosine kinase activity
9	1e−04	12 / 241	GTPase activator activity
10	1e−04	6 / 58	cell adhesion molecule binding
11	1e−04	4 / 20	antigen binding
12	2e−04	8 / 114	SH3 domain binding
13	2e−04	11 / 219	receptor activity
14	5e−04	14 / 370	receptor binding
15	1e−03	3 / 15	CCR chemokine receptor binding
16	1e−03	3 / 15	phosphotyrosine binding
17	2e−03	3 / 20	phosphatidylinositol 3−kinase binding
18	3e−03	6 / 102	integrin binding
19	4e−03	12 / 362	protein kinase binding
20	5e−03	3 / 25	cysteine−type endopeptidase inhibitor activity involved in apoptotic process

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	3 / 29	hsa−miR−1292
2	0.050	3 / 61	hsa−miR−296−3p
3	0.052	3 / 62	hsa−miR−634
4	0.062	2 / 30	hsa−miR−486−5p
5	0.081	2 / 35	hsa−miR−1229
6	0.106	2 / 41	hsa−miR−758
7	0.109	5 / 186	hsa−miR−1
8	0.138	2 / 48	hsa−miR−623
9	0.144	5 / 204	hsa−miR−206
10	0.156	2 / 52	hsa−miR−1224−3p
11	0.156	4 / 154	hsa−miR−506
12	0.170	3 / 105	hsa−miR−613
13	0.185	2 / 58	hsa−miR−409−5p
14	0.199	4 / 170	hsa−miR−495
15	0.225	2 / 66	hsa−miR−30e*
16	0.230	2 / 67	hsa−miR−1285
17	0.239	1 / 20	hsa−miR−380*
18	0.243	3 / 126	hsa−miR−421
19	0.260	2 / 73	hsa−miR−361−3p
20	0.269	1 / 23	hsa−miR−668

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	BENTINK_ras.4
2	0.2	1 / 12	BENTINK_ras.1
3	0.2	1 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 14	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 14	BENTINK_myc.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	5e−08	64 / 2401	ICGC_Bcl11_targets
2	2e−07	58 / 2149	ICGC_Mef2_targets
3	5e−06	96 / 4714	ICGC_Pu1_targets
4	2e−05	52 / 2133	ICGC_Cebpbsc150_targets
5	4e−05	40 / 1523	ICGC_P300_targets
6	2e−04	68 / 3305	ICGC_BatfPcr1_targets
7	6e−04	58 / 2827	ICGC_Bcl3_targets
8	3e−03	95 / 5512	ICGC_Nficsc81335_targets
9	4e−03	60 / 3177	ICGC_Irf4_targets
10	2e−02	72 / 4230	ICGC_Nfatc1_targets
11	4e−02	80 / 4969	ICGC_Atf2_targets
12	7e−02	33 / 1867	HEBENSTREIT_high expression TF
13	8e−02	57 / 3511	ICGC_Rad21_targets
14	9e−02	94 / 6157	ICGC_Tcf3_targets
15	9e−02	96 / 6313	ICGC_Pou2_targets
16	1e−01	85 / 5578	ICGC_Stat5_targets
17	1e−01	83 / 5453	ICGC_Foxm1_targets
18	1e−01	84 / 5526	ICGC_Pmlsc71910_targets
19	1e−01	26 / 1506	ICGC_Usf1_targets
20	1e−01	76 / 4987	ICGC_Bclaf101388_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 42	VAQUERIZAS_Thymus
2	8e−04	4 / 31	VAQUERIZAS_Lymph node
3	2e−03	5 / 64	VAQUERIZAS_Lung
4	2e−03	5 / 67	VAQUERIZAS_Whole blood
5	3e−03	3 / 22	VAQUERIZAS_Tonsil
6	2e−02	2 / 17	VAQUERIZAS_Salivary gland
7	3e−02	2 / 20	VAQUERIZAS_Bone marrow
8	7e−02	2 / 31	VAQUERIZAS_Fetal lung
9	9e−02	2 / 37	VAQUERIZAS_Prostate
10	2e−01	1 / 18	VAQUERIZAS_Pancreas
11	3e−01	1 / 30	VAQUERIZAS_Smooth muscle
12	4e−01	1 / 42	VAQUERIZAS_Thyroid
13	5e−01	1 / 49	VAQUERIZAS_Uterus
14	6e−01	2 / 155	VAQUERIZAS_General
15	1e+00	0 / 41	VAQUERIZAS_Fetal brain
16	1e+00	0 / 45	VAQUERIZAS_Placenta
17	1e+00	0 / 33	VAQUERIZAS_Liver
18	1e+00	0 / 12	VAQUERIZAS_Kidney
19	1e+00	0 / 25	VAQUERIZAS_Spinal cord
20	1e+00	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	4e−94	97 / 427	WIRTH_Immune system
2	8e−26	33 / 208	PALMER_B−Cell signature up
3	3e−16	21 / 140	PALMER_T−Cell signature up
4	9e−03	9 / 259	PALMER_Granulocytes signature up
5	2e−01	1 / 13	WIRTH_Cortex cerebri
6	2e−01	1 / 14	WIRTH_B−cells
7	2e−01	1 / 15	WIRTH_Cerebellum
8	2e−01	1 / 16	WIRTH_Hippocampus
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 / 12	WIRTH_Tonsil
14	1e+00	0 / 14	WIRTH_Thymus
15	1e+00	0 / 12	WIRTH_Lymphocytes
16	1e+00	0 / 14	WIRTH_Bone marrow
17	1e+00	0 / 476	WIRTH_Nervous System
18	1e+00	0 / 13	WIRTH_Globus pallidus
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 14	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	23 / 1343	LU_BPDE 1h DN
2	1.0	40 / 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	

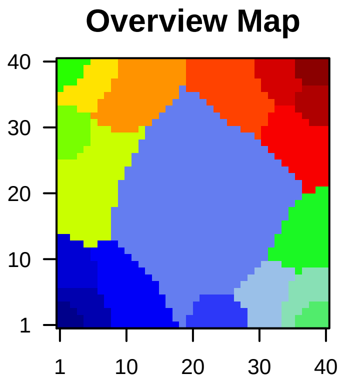
K−Means Clusters

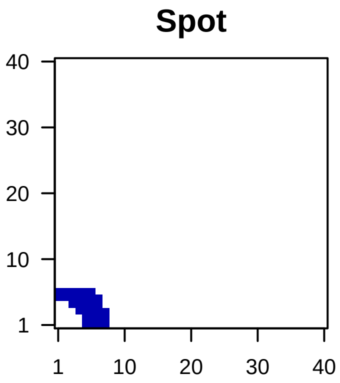
Spot Summary: B

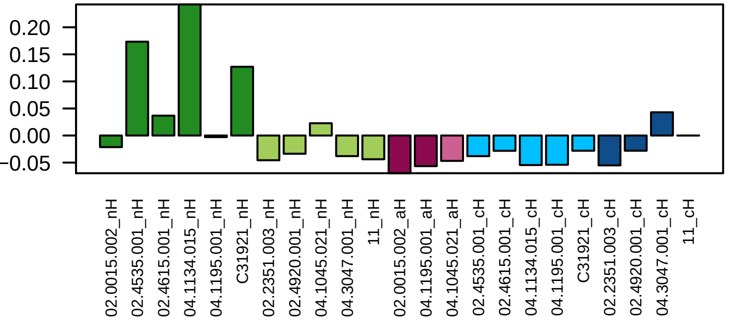
metagenes = 31
genes = 399

<r> metagenes = 0.96
<r> genes = 0.65
beta: r2= 0.14 / log p= −1.08

samples with spot = 3 (13 %)
MLH1_normHNPCC : 3 (50 %)


Overview Map


Spot

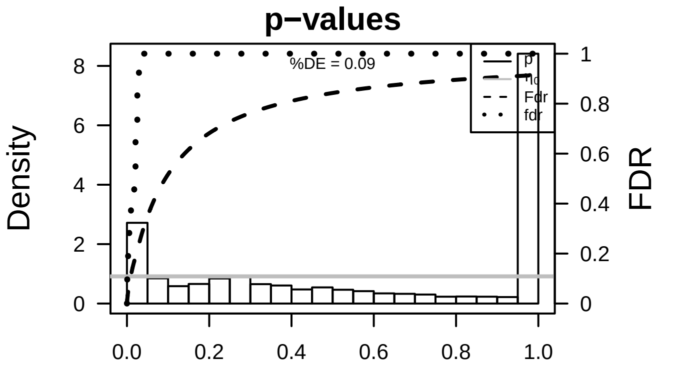


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.58	−0.12	0.41	IDO1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:I
2	ENSG000001	0.56	−0.14	0.71	S1PR1	sphingosine−1−phosphate receptor 1 [Source:HGNC Symbol
3	ENSG000002	0.51	−0.35	0.76		
4	ENSG000001	0.49	−0.07	0.91	LEF1	lymphoid enhancer−binding factor 1 [Source:HGNC Symbol;A
5	ENSG000001	0.49	−0.2	0.62	ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HG
6	ENSG000001	0.48	−0.24	0.65	GOLGA8A	golgin A8 family, member A [Source:HGNC Symbol;Acc:HGN
7	ENSG000001	0.46	−0.28	0.74		
8	ENSG000002	0.46	−0.19	0.76	GOLGA8B	golgin A8 family, member B [Source:HGNC Symbol;Acc:HGN
9	ENSG000001	0.44	−0.25	0.48	DUSP5	dual specificity phosphatase 5 [Source:HGNC Symbol;Acc:H
10	ENSG000001	0.44	−0.06	0.92	GPR15	G protein−coupled receptor 15 [Source:HGNC Symbol;Acc:H
11	ENSG000001	0.44	−0.29	0.28	TAP1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
12	ENSG000001	0.44	−0.23	0.47	STAT1	signal transducer and activator of transcription 1, 91kDa [Sou
13	ENSG000002	0.44	−0.4	0.57	NPIPB11	nuclear pore complex interacting protein family, member B11
14	ENSG000001	0.43	−0.17	0.75	OGT	O−linked N−acetylglucosamine (GlcNAc) transferase [Source
15	ENSG000000	0.42	−0.15	0.89	TRIB2	tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:3
16	ENSG000001	0.42	−0.21	0.8	DDX17	DEAD (Asp−Glu−Ala−Asp) box helicase 17 [Source:HGNC S
17	ENSG000001	0.42	−0.26	0.34	C1QB	complement component 1, q subcomponent, B chain [Source
18	ENSG000002	0.42	−0.33	0.72		
19	ENSG000001	0.42	−0.39	0.59	NPIPB4	Putative NPIP−like protein LOC613037 [Source:UniProtKB/S
20	ENSG000001	0.42	−0.38	0.6		nuclear pore complex interacting protein family, member B3 [S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−82	103 / 427	Tissu	WIRTH_Immune system
2	3e−66	118 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	6e−54	303 / 7592	Lympl	HOPP_Strong_enhancer
4	1e−40	241 / 5643	Lympl	HOPP_Txn_transition
5	6e−40	76 / 574	Canc	Lembcke_Colonic Inflammation
6	2e−37	109 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
7	2e−33	61 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
8	2e−29	39 / 175	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
9	1e−28	58 / 473	GSEA	ZHENG_BOUND_BY_FOXP3
10	1e−27	49 / 336	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−
11	5e−27	49 / 347	Lympl	WIRTH_lymphoma937_spot H
12	6e−26	128 / 2401	TF	ICGC_Bcl11_targets
13	8e−25	84 / 1165	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
14	2e−22	39 / 263	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
15	2e−21	245 / 7491	Lympl	HOPP_Txn_elongation
16	3e−21	91 / 1523	TF	ICGC_P300_targets
17	1e−19	35 / 246	GSEA	QI_PLASMACYTOMA_UP
18	2e−18	33 / 236	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
19	3e−18	105 / 2133	TF	ICGC_Cebpbsc150_targets
20	3e−18	174 / 4714	TF	ICGC_Pu1_targets
21	5e−18	105 / 2149	TF	ICGC_Mef2_targets
22	7e−18	36 / 297	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
23	1e−17	137 / 3305	TF	ICGC_BatfPcr1_targets
24	3e−17	59 / 823	GSEA	REACTOME_IMMUNE_SYSTEM
25	4e−17	96 / 1914	GSEA	PILON_KLF1_TARGETS_DN
26	4e−17	37 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
27	1e−16	17 / 51	GSEA	LEE_EARLY_T_LYMPHOCYTE_DN
28	2e−16	72 / 1215	Lympl	SPANG_BCR DN
29	3e−16	130 / 3177	TF	ICGC_Irf4_targets
30	3e−16	29 / 208	Tissu	PALMER_B−Cell signature up
31	7e−16	20 / 87	GSEA	BASSO_CD40_SIGNALING_UP
32	9e−16	156 / 4230	TF	ICGC_Nfatc1_targets
33	2e−15	186 / 5512	TF	ICGC_Nficsc81335_targets
34	2e−15	40 / 435	GSEA	RODWELL_AGING_KIDNEY_UP
35	3e−15	27 / 192	GSEA	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
36	5e−15	35 / 343	BP	immune response
37	2e−14	23 / 145	Lympl	WIRTH_lymphoma937_spot F
38	2e−14	23 / 145	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_to
39	5e−14	123 / 3122	Colon	TxEnhG1_Colon
40	6e−14	115 / 2827	TF	ICGC_Bcl3_targets


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 57	TESCHENDORFF_age_hypermethylated
2	0.7	2 / 123	HORVATH_aging_genes meth DOWN
3	0.8	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−15	35 / 343	immune response
2	6e−13	20 / 122	adaptive immune response
3	5e−12	17 / 92	T cell receptor signaling pathway
4	6e−11	63 / 1279	signal transduction
5	2e−10	43 / 707	innate immune response
6	4e−09	11 / 50	T cell activation
7	6e−09	12 / 64	T cell costimulation
8	2e−07	21 / 270	cytokine−mediated signaling pathway
9	2e−07	28 / 451	positive regulation of GTPase activity
10	5e−07	10 / 62	positive regulation of signal transduction
11	5e−07	11 / 78	regulation of immune response
12	8e−07	27 / 454	intracellular signal transduction
13	1e−06	22 / 326	inflammatory response
14	7e−06	28 / 539	small GTPase mediated signal transduction
15	8e−06	14 / 165	Fc−epsilon receptor signaling pathway
16	1e−05	8 / 53	humoral immune response
17	1e−05	5 / 16	negative regulation of T cell activation
18	1e−05	5 / 16	positive regulation of natural killer cell mediated cytotoxicity
19	1e−05	8 / 54	positive regulation of T cell proliferation
20	1e−05	9 / 71	Fc−gamma receptor signaling pathway involved in phagocytosis

Brain

Rank	p−value	#in/all	Geneset
1	6e−06	118 / 3977	Mid_Frontal_Lobe_ReprPC
2	2e−04	97 / 3370	Mid_Frontal_Lobe_ZNF
3	4e−03	72 / 2603	Fetal_TxTrans
4	5e−03	55 / 1890	Overlap_fetal_midbrain_TssF
5	6e−03	7 / 106	Overlap_fetal_midbrain_Tx
6	7e−03	50 / 1713	Mid_Frontal_Lobe_ReprPCWk
7	2e−02	67 / 2549	Fetal_TssF
8	2e−02	19 / 552	Fetal_Tx
9	2e−02	35 / 1210	Fetal_TssP
10	3e−02	39 / 1394	Mid_Frontal_Lobe_Quies
11	3e−02	26 / 855	Overlap_fetal_midbrain_ZNF
12	4e−02	8 / 191	Overlap_fetal_midbrain_Het
13	5e−02	27 / 940	Mid_Frontal_Lobe_Enh
14	1e−01	51 / 2084	Mid_Frontal_Lobe_K9K27me3
15	1e−01	70 / 2956	Fetal_TssA
16	2e−01	139 / 6320	Overlap_fetal_midbrain_HetRpts
17	2e−01	65 / 2820	Mid_Frontal_Lobe_HetRpts
18	2e−01	8 / 268	Mid_Frontal_Lobe_TssA
19	3e−01	227 / 10800	Overlap_fetal_midbrain_Quies
20	3e−01	33 / 1478	Overlap_fetal_midbrain_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	6e−40	76 / 574	Lembcke_Colonic Inflammation
2	3e−11	29 / 324	SPANG_BCL6−index2
3	2e−04	13 / 191	SPANG_LPS−index2
4	3e−04	4 / 16	GENTLES_modul18
5	3e−03	3 / 14	GENTLES_modul12
6	4e−03	3 / 16	GENTLES_modul14
7	8e−03	6 / 86	PanCan_JAK−ST_geneset_nanostring
8	1e−02	7 / 123	PanCan_Driver_Gene_geneset_nanostring
9	4e−02	2 / 16	GENTLES_modul11
10	9e−02	3 / 52	KUIPER_MM poor survival
11	9e−02	6 / 152	PanCan_MAPK_geneset_nanostring
12	1e−01	1 / 6	ZHANG_MGUS up
13	2e−01	6 / 198	PanCan_PI3K_geneset_nanostring
14	3e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	3e−01	1 / 15	GENTLES_modul13
16	3e−01	1 / 16	GENTLES_modul16
17	3e−01	4 / 136	PanCan_CC+Apop_geneset_nanostring
18	4e−01	1 / 24	PanCan_Notch_geneset_nanostring
19	5e−01	2 / 78	PanCan_Wnt_geneset_nanostring
20	5e−01	3 / 140	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−09	120 / 3507	plasma membrane
2	2e−08	105 / 3059	membrane
3	1e−06	97 / 2974	cytosol
4	4e−06	16 / 201	external side of plasma membrane
5	9e−06	5 / 15	T cell receptor complex
6	1e−05	14 / 171	cell−cell junction
7	1e−05	13 / 151	lamellipodium
8	5e−05	4 / 11	uropod
9	7e−05	4 / 12	Arp2/3 protein complex
10	1e−04	139 / 5185	cytoplasm
11	4e−04	5 / 32	immunological synapse
12	5e−04	5 / 33	COP9 signalosome
13	6e−04	8 / 93	ruffle
14	1e−03	6 / 60	brush border
15	2e−03	6 / 61	extrinsic component of cytoplasmic side of plasma membrane
16	2e−03	13 / 246	endosome
17	4e−03	8 / 122	cell cortex
18	5e−03	6 / 76	integral component of endoplasmic reticulum membrane
19	5e−03	16 / 378	focal adhesion
20	6e−03	39 / 1250	integral component of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.005	29 / 847	Chr 16
2	0.068	27 / 976	Chr 6
3	0.118	10 / 318	Chr 13
4	0.168	22 / 862	Chr 5
5	0.184	12 / 436	Chr 22
6	0.224	26 / 1083	Chr 17
7	0.314	32 / 1425	Chr 19
8	0.337	23 / 1017	Chr 12
9	0.374	27 / 1228	Chr 2
10	0.470	22 / 1043	Chr 3
11	0.608	38 / 1920	Chr 1
12	0.706	13 / 715	Chr 10
13	0.743	9 / 522	Chr 20
14	0.758	13 / 745	Chr 9
15	0.770	15 / 859	Chr 7
16	0.781	11 / 651	Chr 8
17	0.810	4 / 272	Chr 18
18	0.880	19 / 1172	Chr 11
19	0.936	8 / 613	Chr 14
20	0.936	10 / 735	Chr 4

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−66	118 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−17	37 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	5e−14	123 / 3122	TxEnhG1_Colon
4	7e−12	117 / 3112	EnhA_Colon
5	1e−10	264 / 9930	Tx_Colon
6	7e−10	251 / 9390	TxWk_Colon
7	8e−10	177 / 5889	EnhWk1_Colon
8	2e−08	33 / 532	K9acLow_Colon
9	3e−08	291 / 11791	Enh_Colon
10	4e−08	246 / 9470	Quies3_Colon
11	6e−08	265 / 10475	TssA_Colon
12	1e−07	24 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
13	2e−07	27 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	4e−07	37 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	1e−06	288 / 11968	TssWk_Colon
16	1e−05	207 / 8123	TssF_Colon
17	6e−05	36 / 877	TxEnhG2_Colon
18	3e−04	118 / 4327	EnhWk2_Colon
19	7e−04	169 / 6761	TssD2_Colon
20	3e−03	9 / 148	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	0.3	15 / 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	27 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	3e−09	19 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
3	4e−06	7 / 33	Donson−Misc immune function−associated with LTS in HGA
4	1e−05	8 / 53	Donson−innate immunity−associated with LTS in HGA
5	1e−04	9 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
6	3e−04	4 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
7	4e−04	3 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
8	3e−03	3 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
9	3e−03	7 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
10	5e−03	4 / 35	shaw_responders_down_in_oligo_glioma
11	6e−03	4 / 36	Shaw_down_in_1p19q
12	8e−03	7 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	8e−03	2 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
14	1e−02	2 / 8	Donson−adaptive−immunity−associated with LTS in HGA
15	1e−02	6 / 96	Weller_LGG_A_vs_O_UP
16	1e−02	5 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
17	2e−02	5 / 77	Weller_LGG_gradeII−vs−III_DOWN
18	3e−02	13 / 344	Up
19	4e−02	2 / 16	VERHAAK_PN subtype
20	7e−02	11 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−37	109 / 1340	PUJANA_ATM_PCC_NETWORK
2	2e−33	61 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	2e−29	39 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE
4	1e−28	58 / 473	ZHENG_BOUND_BY_FOXP3
5	8e−25	84 / 1165	CHEN_METABOLIC_SYNDROM_NETWORK
6	2e−22	39 / 263	WALLACE_PROSTATE_CANCER_RACE_UP
7	1e−19	35 / 246	QI_PLASMACYTOMA_UP
8	2e−18	33 / 236	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
9	7e−18	36 / 297	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
10	3e−17	59 / 823	REACTOME_IMMUNE_SYSTEM
11	4e−17	96 / 1914	PILON_KLF1_TARGETS_DN
12	1e−16	17 / 51	LEE_EARLY_T_LYMPHOCYTE_DN
13	7e−16	20 / 87	BASSO_CD40_SIGNALING_UP
14	2e−15	40 / 435	RODWELL_AGING_KIDNEY_UP
15	3e−15	27 / 192	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
16	9e−12	26 / 247	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM
17	3e−11	31 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
18	6e−11	26 / 269	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
19	7e−11	17 / 108	BOSCO_TH1_CYTOTOXIC_MODULE
20	9e−11	30 / 362	MULLIGHAN_MLL_SIGNATURE_1_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−12	23 / 181	HALLMARK_ALLOGRAFT_REJECTION
2	4e−11	22 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	4e−09	20 / 197	HALLMARK_IL2_STAT5_SIGNALING
4	2e−06	16 / 192	HALLMARK_COMPLEMENT
5	9e−06	10 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	5e−04	8 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	6e−04	12 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	7e−04	12 / 194	HALLMARK_INFLAMMATORY_RESPONSE
9	1e−03	8 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	2e−03	11 / 190	HALLMARK_APICAL_JUNCTION
11	2e−03	11 / 196	HALLMARK_MITOTIC_SPINDLE
12	5e−02	5 / 98	HALLMARK_ANDROGEN_RESPONSE
13	1e−01	7 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	1e−01	7 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
15	2e−01	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
16	2e−01	6 / 189	HALLMARK_KRAS_SIGNALING_UP
17	2e−01	6 / 196	HALLMARK_P53_PATHWAY
18	2e−01	5 / 157	HALLMARK_APOPTOSIS
19	2e−01	6 / 199	HALLMARK_MTORC1_SIGNALING
20	2e−01	2 / 44	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	DUMEAUX_Women normal BMI literature genes up
2	0.17	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.28	3 / 91	DUMEAUX_Smoking enriched genes
4	0.49	1 / 33	DUMEAUX_Fasting 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 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers 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	6e−54	303 / 7592	HOPP_Strong_enhancer
2	1e−40	241 / 5643	HOPP_Txn_transition
3	1e−27	49 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
4	5e−27	49 / 347	WIRTH_lymphoma937_spot H
5	2e−21	245 / 7491	HOPP_Txn_elongation
6	2e−16	72 / 1215	SPANG_BCR DN
7	2e−14	23 / 145	WIRTH_lymphoma937_spot F
8	2e−14	23 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
9	8e−13	39 / 500	WIRTH_lymphoma937_spot J
10	2e−12	37 / 466	SPANG_CD40 6hrs DN
11	4e−12	28 / 279	SPANG_IL21 DN
12	6e−12	37 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
13	5e−11	234 / 8358	HOPP_Active_promoter
14	3e−08	24 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−c
15	2e−07	23 / 315	WIRTH_lymphoma937_spot E
16	4e−07	23 / 332	SPANG_CD40 6hrs UP
17	7e−07	6 / 17	WRIGHT_ABC UP
18	1e−06	7 / 29	DAVE_Immune response 1
19	3e−06	14 / 150	DAVE_BL−vs−DLBCL
20	4e−06	6 / 22	DAVE_NFkB BL DN

MF

Rank	p−value	#in/all	Geneset
1	2e−10	278 / 10693	protein binding
2	5e−09	20 / 198	signal transducer activity
3	1e−06	9 / 52	SH3/SH2 adaptor activity
4	1e−05	7 / 40	cytokine receptor activity
5	5e−05	6 / 33	tumor necrosis factor receptor binding
6	5e−04	9 / 113	actin filament binding
7	6e−04	5 / 34	Rho GTPase binding
8	9e−04	8 / 98	protein N−terminus binding
9	2e−03	3 / 12	phospholipase C activity
10	2e−03	8 / 108	guanyl−nucleotide exchange factor activity
11	2e−03	8 / 114	SH3 domain binding
12	2e−03	6 / 67	protein phosphatase binding
13	3e−03	3 / 14	MHC class I protein binding
14	3e−03	3 / 14	thioesterase binding
15	4e−03	14 / 301	actin binding
16	4e−03	5 / 52	RNA polymerase II core promoter sequence−specific DNA binding
17	4e−03	12 / 241	GTPase activator activity
18	4e−03	12 / 243	transcription coactivator activity
19	6e−03	11 / 219	receptor activity
20	6e−03	11 / 221	transcriptional activator activity, RNA polymerase II core promoter proximal reg

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 41	hsa−miR−601
2	2e−04	13 / 197	hsa−miR−330−3p
3	2e−04	16 / 280	hsa−miR−30d
4	6e−04	12 / 190	hsa−miR−548a−3p
5	8e−04	10 / 145	hsa−miR−522
6	8e−04	20 / 442	hsa−miR−548n
7	1e−03	16 / 326	hsa−miR−30e
8	1e−03	8 / 105	hsa−miR−613
9	2e−03	15 / 304	hsa−miR−25
10	2e−03	20 / 471	hsa−miR−130a
11	2e−03	5 / 43	hsa−miR−518b
12	2e−03	14 / 277	hsa−miR−363
13	2e−03	6 / 64	hsa−miR−371−5p
14	2e−03	8 / 111	hsa−miR−376b
15	2e−03	11 / 196	hsa−miR−520d−5p
16	3e−03	24 / 631	hsa−miR−20a
17	3e−03	10 / 174	hsa−miR−520h
18	4e−03	15 / 333	hsa−miR−32
19	4e−03	6 / 73	hsa−miR−578
20	4e−03	11 / 208	hsa−miR−33a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 14	BENTINK_src.10
2	0.24	1 / 13	BENTINK_e2f3.2
3	0.27	1 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 14	BENTINK_e2f3.1
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.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−26	128 / 2401	ICGC_Bcl11_targets
2	3e−21	91 / 1523	ICGC_P300_targets
3	3e−18	105 / 2133	ICGC_Cebpbsc150_targets
4	3e−18	174 / 4714	ICGC_Pu1_targets
5	5e−18	105 / 2149	ICGC_Mef2_targets
6	1e−17	137 / 3305	ICGC_BatfPcr1_targets
7	3e−16	130 / 3177	ICGC_Irf4_targets
8	9e−16	156 / 4230	ICGC_Nfatc1_targets
9	2e−15	186 / 5512	ICGC_Nficsc81335_targets
10	6e−14	115 / 2827	ICGC_Bcl3_targets
11	3e−13	167 / 4969	ICGC_Atf2_targets
12	5e−13	170 / 5135	ICGC_Ebfsc137065_targets
13	5e−12	168 / 5173	ICGC_Taf1_targets
14	5e−12	176 / 5526	ICGC_Pmlsc71910_targets
15	6e−12	177 / 5578	ICGC_Stat5_targets
16	9e−12	193 / 6313	ICGC_Pou2_targets
17	2e−11	162 / 4987	ICGC_Bclaf101388_targets
18	3e−11	188 / 6157	ICGC_Tcf3_targets
19	8e−11	183 / 6005	ICGC_Mta3_targets
20	1e−10	170 / 5453	ICGC_Foxm1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	4e−13	12 / 31	VAQUERIZAS_Lymph node
2	2e−10	9 / 22	VAQUERIZAS_Tonsil
3	1e−06	10 / 67	VAQUERIZAS_Whole blood
4	2e−05	7 / 42	VAQUERIZAS_Thymus
5	7e−03	3 / 20	VAQUERIZAS_Bone marrow
6	1e−01	3 / 64	VAQUERIZAS_Lung
7	2e−01	2 / 41	VAQUERIZAS_Fetal brain
8	2e−01	2 / 41	VAQUERIZAS_Testis
9	2e−01	2 / 45	VAQUERIZAS_Placenta
10	2e−01	2 / 46	VAQUERIZAS_Whole brain
11	3e−01	1 / 16	VAQUERIZAS_Ovary
12	3e−01	1 / 16	VAQUERIZAS_Fetal thyroid
13	3e−01	1 / 17	VAQUERIZAS_Adrenal gland
14	3e−01	1 / 17	VAQUERIZAS_Salivary gland
15	3e−01	1 / 19	VAQUERIZAS_Heart
16	4e−01	1 / 25	VAQUERIZAS_Adrenal cortex
17	5e−01	1 / 30	VAQUERIZAS_Smooth muscle
18	5e−01	1 / 31	VAQUERIZAS_Fetal lung
19	5e−01	1 / 37	VAQUERIZAS_Prostate
20	6e−01	1 / 42	VAQUERIZAS_Thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	4e−82	103 / 427	WIRTH_Immune system
2	3e−16	29 / 208	PALMER_B−Cell signature up
3	6e−10	18 / 140	PALMER_T−Cell signature up
4	1e−04	4 / 13	PALMER_CD8+ T−Cell signature up
5	2e−01	1 / 12	WIRTH_Lymphocytes
6	3e−01	1 / 14	WIRTH_Thalamus
7	6e−01	5 / 259	PALMER_Granulocytes signature up
8	8e−01	1 / 82	WIRTH_Homeostasis
9	9e−01	1 / 141	WIRTH_Muscle
10	1e+00	3 / 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 / 13	WIRTH_Globus pallidus
20	1e+00	0 / 15	WIRTH_Telencephalon

Toxic

Rank	p−value	#in/all	Geneset
1	0.6	27 / 1343	LU_BPDE 1h DN
2	1.0	66 / 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	

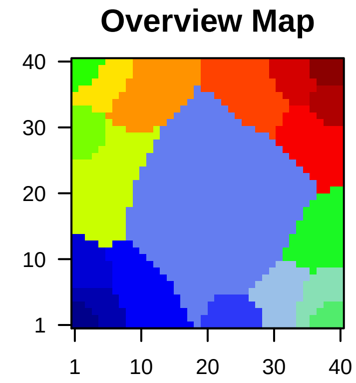
K−Means Clusters

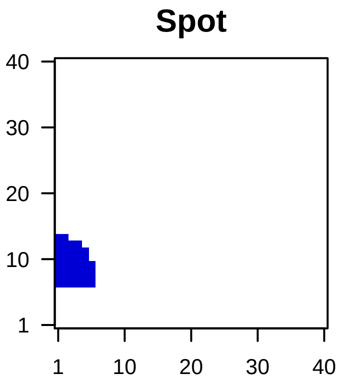
Spot Summary: C

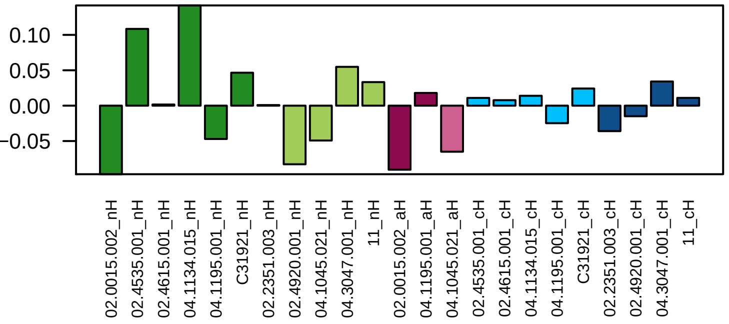
metagenes = 40
genes = 502

<r> metagenes = 0.93
<r> genes = 0.55
beta: r2= 0.06 / log p= −0.61

samples with spot = 2 (8.7 %)
MLH1_normHNPCC : 2 (33.3 %)





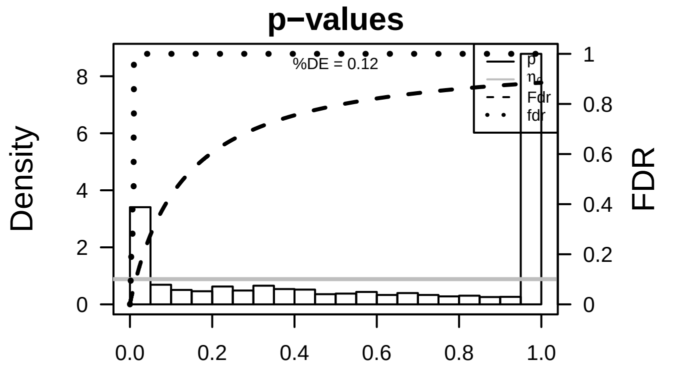


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.54	−0.37	0.72	BHLHE40	basic helix−loop−helix family, member e40 [Source:HGNC Sy
2	ENSG000002	0.52	−0.34	0.57		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:M0
3	ENSG000001	0.39	−0.24	0.77	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix−loop−he
4	ENSG000001	0.39	−0.34	0.89	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
5	ENSG000002	0.38	−0.2	0.79		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3I
6	ENSG000001	0.37	−0.23	0.47	CCNG1	cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
7	ENSG000001	0.37	−0.22	0.42	RPS15A	ribosomal protein S15a [Source:HGNC Symbol;Acc:HGNC:1(
8	ENSG000001	0.36	−0.26	0.88	HNRNPDL	heterogeneous nuclear ribonucleoprotein D−like [Source:HGN
9	ENSG000001	0.35	−0.2	0.42	TOMM7	translocase of outer mitochondrial membrane 7 homolog (yea
10	ENSG000001	0.35	−0.19	0.82	SLC38A1	solute carrier family 38, member 1 [Source:HGNC Symbol;Ac
11	ENSG000001	0.33	−0.16	0.74	SRSF11	serine/arginine−rich splicing factor 11 [Source:HGNC Symbol
12	ENSG000001	0.33	−0.34	0.43		
13	ENSG000000	0.33	−0.22	0.75	SYPL1	synaptophysin−like 1 [Source:HGNC Symbol;Acc:HGNC:115(
14	ENSG000001	0.32	−0.24	0.66	RPL10	ribosomal protein L10 [Source:HGNC Symbol;Acc:HGNC:102
15	ENSG000001	0.32	−0.23	0.86	EIF3L	eukaryotic translation initiation factor 3, subunit L [Source:HG
16	ENSG000000	0.32	−0.3	0.89	EIF4B	eukaryotic translation initiation factor 4B [Source:HGNC Syml
17	ENSG000001	0.32	−0.21	0.55	SNRNP70	small nuclear ribonucleoprotein 70kDa (U1) [Source:HGNC S
18	ENSG000000	0.31	−0.12	0.65	U2AF2	U2 small nuclear RNA auxiliary factor 2 [Source:HGNC Symb
19	ENSG000002	0.31	−0.19	0.54	C6orf48	chromosome 6 open reading frame 48 [Source:HGNC Symbo
20	ENSG000001	0.31	−0.3	0.75	RPS25	ribosomal protein S25 [Source:HGNC Symbol;Acc:HGNC:104

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−90	357 / 5643	Lympl	HOPP_Txn_transition
2	5e−87	168 / 1091	MF	poly(A) RNA binding
3	4e−71	382 / 7491	Lympl	HOPP_Txn_elongation
4	5e−68	437 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
5	3e−66	345 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
6	1e−63	426 / 9930	Colon	Tx_Colon
7	2e−57	407 / 9390	Colon	TxWk_Colon
8	4e−55	426 / 10475	Colon	TssA_Colon
9	3e−54	146 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
10	6e−54	157 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
11	9e−52	198 / 2554	CC	nucleoplasm
12	4e−50	373 / 8358	Lympl	HOPP_Active_promoter
13	3e−42	396 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
14	4e−39	57 / 237	BP	RNA splicing
15	5e−39	79 / 513	MF	RNA binding
16	3e−38	93 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
17	2e−37	124 / 1352	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
18	2e−37	50 / 182	BP	mRNA splicing, via spliceosome
19	2e−35	258 / 5101	CC	nucleus
20	3e−34	42 / 134	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
21	2e−33	91 / 820	BP	gene expression
22	5e−33	43 / 151	GSEA	REACTOME_MRNA_PROCESSING
23	2e−32	37 / 105	GSEA	REACTOME_MRNA_SPLICING
24	4e−27	98 / 1134	MF	nucleic acid binding
25	5e−27	41 / 183	BP	mRNA processing
26	2e−25	49 / 300	miRN	hsa−miR−186
27	3e−25	57 / 420	GSEA	SHEN_SMARCA2_TARGETS_UP
28	5e−25	320 / 8147	Lympl	HOPP_Weak_promoter
29	7e−25	72 / 685	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
30	1e−24	54 / 385	MF	nucleotide binding
31	3e−24	351 / 9470	Colon	Quies3_Colon
32	1e−22	123 / 1914	GSEA	PILON_KLF1_TARGETS_DN
33	2e−22	48 / 334	miRN	hsa−miR−590−3p
34	5e−22	60 / 539	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
35	5e−22	114 / 1713	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
36	8e−22	376 / 10800	Brain	Overlap_fetal_midbrain_Quies
37	8e−22	69 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
38	1e−21	76 / 855	Brain	Overlap_fetal_midbrain_ZNF
39	4e−21	55 / 475	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_DN
40	2e−20	73 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.8	2 / 123	HORVATH_aging_genes meth DOWN
2	0.9	2 / 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	4e−39	57 / 237	RNA splicing
2	2e−37	50 / 182	mRNA splicing, via spliceosome
3	2e−33	91 / 820	gene expression
4	5e−27	41 / 183	mRNA processing
5	8e−13	14 / 41	mRNA 3'−end processing
6	2e−12	14 / 44	termination of RNA polymerase II transcription
7	1e−11	18 / 90	protein sumoylation
8	2e−11	44 / 549	viral process
9	3e−11	29 / 259	translation
10	9e−11	21 / 142	translational initiation
11	2e−10	46 / 633	cellular protein metabolic process
12	3e−10	18 / 109	RNA processing
13	3e−10	9 / 19	mRNA splice site selection
14	1e−09	9 / 21	negative regulation of mRNA splicing, via spliceosome
15	1e−09	89 / 1807	transcription, DNA−templated
16	2e−08	16 / 108	SRP−dependent cotranslational protein targeting to membrane
17	3e−08	18 / 144	viral life cycle
18	5e−08	36 / 512	transcription from RNA polymerase II promoter
19	1e−07	15 / 109	viral transcription
20	2e−07	9 / 35	regulation of translational initiation

Brain

Rank	p−value	#in/all	Geneset
1	5e−68	437 / 10239	Overlap_fetal_midbrain_ReprPC
2	3e−66	345 / 6320	Overlap_fetal_midbrain_HetRpts
3	3e−42	396 / 9923	Overlap_fetal_midbrain_K9K27me3
4	8e−22	376 / 10800	Overlap_fetal_midbrain_Quies
5	1e−21	76 / 855	Overlap_fetal_midbrain_ZNF
6	2e−16	350 / 10278	Overlap_fetal_midbrain_ReprPCWk
7	8e−14	28 / 191	Overlap_fetal_midbrain_Het
8	2e−07	131 / 3370	Mid_Frontal_Lobe_ZNF
9	9e−06	24 / 342	Fetal_Het
10	7e−04	22 / 400	Fetal_ZNF
11	1e−02	33 / 865	Mid_Frontal_Lobe_Het
12	2e−01	36 / 1182	Fetal_EnhP
13	4e−01	26 / 939	Fetal_HetRpts
14	4e−01	45 / 1680	Fetal_ReprPCWk
15	5e−01	17 / 641	Mid_Frontal_Lobe_EnhP
16	6e−01	28 / 1137	Fetal_Enh
17	7e−01	21 / 910	Fetal_EnhG
18	8e−01	47 232	Fetal_ReprPC
19	1e+00	48 / 2443	Fetal_Quies
20	1e+00	23 / 1356	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	14 / 123	PanCan_Driver_Gene_geneset_nanostring
2	4e−05	5 / 16	GENTLES_modul14
3	3e−03	10 / 136	PanCan_CC+Apop_geneset_nanostring
4	1e−02	16 / 324	SPANG_BCL6−index2
5	1e−02	11 / 191	SPANG_LPS−index2
6	2e−02	4 / 41	ZHANG_MM up
7	3e−02	1 / 16	LIU_COMMON_CANCER_GENES
8	4e−02	6 / 97	PanCan_TXmisReg_geneset_nanostring
9	6e−02	2 / 15	LIU_BREAST_CANCER
10	6e−02	2 / 16	GENTLES_modul2
11	7e−02	3 / 37	KUIPER_MM good survival
12	1e−01	2 / 22	PanCan_ChromMod_geneset_nanostring
13	1e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1e−01	3 / 50	PanCan_DNARepair_geneset_nanostring
15	1e−01	4 / 78	PanCan_Wnt_geneset_nanostring
16	2e−01	0 / 16	RHODES_CANCER_META_SIGNATURE
17	2e−01	1 / 10	GENTLES_modul3
18	2e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
19	3e−01	1 / 14	LIU_PROSTATE_CANCER_UP
20	3e−01	1 / 15	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−52	198 / 2554	nucleoplasm
2	2e−35	258 / 5101	nucleus
3	2e−20	29 / 121	ribonucleoprotein complex
4	6e−18	24 / 92	spliceosomal complex
5	3e−17	31 / 180	nuclear speck
6	1e−15	63 / 799	nucleolus
7	1e−14	20 / 82	catalytic step 2 spliceosome
8	1e−10	11 / 31	cytoplasmic stress granule
9	6e−10	17 / 100	chromatin
10	2e−09	192 / 5185	cytoplasm
11	5e−08	14 / 88	chromosome
12	5e−08	6 / 10	nuclear inclusion body
13	5e−08	6 / 10	viral nucleocapsid
14	2e−06	115 / 2974	cytosol
15	2e−06	12 / 88	PML body
16	2e−05	9 / 58	chromosome, centromeric region
17	4e−05	5 / 16	eukaryotic translation initiation factor 3 complex
18	8e−05	26 / 442	protein complex
19	8e−05	13 / 143	nuclear envelope
20	9e−05	110 / 3059	membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.04	61 / 1920	Chr 1
2	0.05	20 / 522	Chr 20
3	0.07	25 / 715	Chr 10
4	0.12	33 / 1043	Chr 3
5	0.16	20 / 613	Chr 14
6	0.16	27 / 862	Chr 5
7	0.19	23 / 735	Chr 4
8	0.19	11 / 318	Chr 13
9	0.36	21 / 746	Chr X
10	0.45	26 / 976	Chr 6
11	0.45	27 / 1017	Chr 12
12	0.50	17 / 651	Chr 8
13	0.54	5 / 191	Chr 21
14	0.60	29 / 1172	Chr 11
15	0.66	26 / 1083	Chr 17
16	0.70	6 / 272	Chr 18
17	0.73	13 / 582	Chr 15
18	0.76	28 / 1228	Chr 2
19	0.88	17 / 847	Chr 16
20	0.93	16 / 859	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−63	426 / 9930	Tx_Colon
2	2e−57	407 / 9390	TxWk_Colon
3	4e−55	426 / 10475	TssA_Colon
4	3e−24	351 / 9470	Quies3_Colon
5	8e−22	69 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	4e−18	393 / 11968	TssWk_Colon
7	1e−09	273 / 8123	TssF_Colon
8	3e−08	127 / 3122	TxEnhG1_Colon
9	2e−06	45 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
10	2e−05	193 / 5889	EnhWk1_Colon
11	3e−05	344 / 11791	Enh_Colon
12	3e−04	145 / 4379	TssD1_Colon
13	2e−03	3 / 10	KIM_CRC−MSI−regulated_DN
14	3e−03	7 / 76	Marisa_CRC−cluster−g
15	6e−03	8 / 105	Marisa_CRC−cluster−d
16	6e−03	35 / 877	TxEnhG2_Colon
17	8e−03	199 / 6761	TssD2_Colon
18	3e−02	2 / 10	KIM_MSI−in−EC
19	3e−02	15 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
20	3e−02	10 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	1	9 / 608	GUDJ_psoriasis up
2	1	4 / 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	7e−19	128 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−15	110 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	4e−15	38 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	3e−08	51 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
5	4e−06	5 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
6	7e−06	5 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
7	1e−05	24 / 344	Up
8	6e−05	9 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	7e−05	9 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	9e−03	5 / 50	Vishal_subnetwork signature of survival in GBM
11	1e−02	10 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	6e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
13	6e−02	6 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	6e−02	2 / 16	VERHAAK_PN subtype
15	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
16	1e−01	3 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
17	2e−01	2 / 27	Barbus_GBM_STS_vs._LTS
18	2e−01	4 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
19	2e−01	3 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
20	2e−01	2 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−54	146 / 1340	PUJANA_ATM_PCC_NETWORK
2	6e−54	157 / 1563	PUJANA_BRCA1_PCC_NETWORK
3	3e−38	93 / 747	PUJANA_CHEK2_PCC_NETWORK
4	2e−37	124 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	3e−34	42 / 134	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
6	5e−33	43 / 151	REACTOME_MRNA_PROCESSING
7	2e−32	37 / 105	REACTOME_MRNA_SPLICING
8	3e−25	57 / 420	SHEN_SMARCA2_TARGETS_UP
9	7e−25	72 / 685	SCHLOSSER_SERUM_RESPONSE_DN
10	1e−22	123 / 1914	PILON_KLF1_TARGETS_DN
11	5e−22	60 / 539	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
12	5e−22	114 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
13	4e−21	55 / 475	ENK_UV_RESPONSE_KERATINOCYTE_DN
14	2e−20	73 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	6e−20	55 / 502	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
16	9e−19	48 / 408	PUJANA_BRCA2_PCC_NETWORK
17	1e−18	31 / 162	PUJANA_XPRSS_INT_NETWORK
18	3e−18	27 / 120	KEGG_SPLICEOSOME
19	4e−18	56 / 568	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
20	6e−18	78 / 1036	DANG_BOUND_BY_MYC

HM

Rank	p−value	#in/all	Geneset
1	9e−13	27 / 195	HALLMARK_MYC_TARGETS_V1
2	4e−11	25 / 197	HALLMARK_E2F_TARGETS
3	2e−10	24 / 196	HALLMARK_G2M_CHECKPOINT
4	5e−06	12 / 94	HALLMARK_PROTEIN_SECRETION
5	2e−02	7 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	4e−02	6 / 98	HALLMARK_ANDROGEN_RESPONSE
7	7e−02	9 / 199	HALLMARK_MTORC1_SIGNALING
8	8e−02	7 / 146	HALLMARK_DNA_REPAIR
9	1e−01	5 / 102	HALLMARK_PEROXISOME
10	1e−01	5 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	2e−01	6 / 140	HALLMARK_UV_RESPONSE_DN
12	3e−01	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	3e−01	6 / 181	HALLMARK_ALLOGRAFT_REJECTION
14	4e−01	6 / 192	HALLMARK_COMPLEMENT
15	4e−01	5 / 157	HALLMARK_APOPTOSIS
16	4e−01	2 / 52	HALLMARK_TGF_BETA_SIGNALING
17	4e−01	6 / 196	HALLMARK_P53_PATHWAY
18	4e−01	6 / 199	HALLMARK_ADIPOGENESIS
19	6e−01	5 / 195	HALLMARK_MYOGENESIS
20	6e−01	5 / 196	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 33	DUMEAUX_Fasting enriched genes
2	2e−01	1 / 11	DUMEAUX_Women normal BMI literature genes up
3	1e+00	0 / 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−90	357 / 5643	HOPP_Txn_transition
2	4e−71	382 / 7491	HOPP_Txn_elongation
3	4e−50	373 / 8358	HOPP_Active_promoter
4	5e−25	320 / 8147	HOPP_Weak_promoter
5	2e−17	286 / 7592	HOPP_Strong_enhancer
6	2e−16	49 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
7	3e−15	48 / 500	WIRTH_lymphoma937_spot J
8	7e−12	73 / 1215	SPANG_BCR DN
9	2e−04	212 / 6784	HOPP_Weak_enhancer
10	2e−04	20 / 317	TARTE_Plasmablast signature
11	7e−04	10 / 115	ROSOLOWSKI_green total
12	1e−03	3 / 9	MASCQUE_ABC UP
13	2e−03	35 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
14	2e−03	35 / 811	WIRTH_lymphoma937_spot D
15	5e−03	7 / 83	ROSOLOWSKI_green UP
16	6e−03	8 / 105	ROSOLOWSKI_blue total
17	7e−03	7 / 87	ROSOLOWSKI_red total
18	2e−02	20 / 466	SPANG_CD40 6hrs DN
19	4e−02	82 / 2658	HOPP_Repetitive
20	5e−02	14 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c

MF

Rank	p−value	#in/all	Geneset
1	5e−87	168 / 1091	poly(A) RNA binding
2	5e−39	79 / 513	RNA binding
3	4e−27	98 / 1134	nucleic acid binding
4	1e−24	54 / 385	nucleotide binding
5	4e−14	353 / 10693	protein binding
6	2e−12	38 / 394	chromatin binding
7	1e−08	7 / 13	poly(A) binding
8	2e−08	85 / 1803	DNA binding
9	7e−08	28 / 341	binding
10	6e−07	8 / 30	nucleosomal DNA binding
11	7e−07	13 / 93	mRNA binding
12	4e−06	11 / 76	helicase activity
13	4e−06	11 / 77	single−stranded DNA binding
14	4e−06	10 / 63	ATP−dependent RNA helicase activity
15	5e−06	20 / 243	transcription coactivator activity
16	7e−06	7 / 29	ATP−dependent DNA helicase activity
17	7e−06	9 / 53	translation initiation factor activity
18	2e−05	9 / 58	core promoter binding
19	3e−05	11 / 95	double−stranded DNA binding
20	1e−04	21 / 328	enzyme binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−25	49 / 300	hsa−miR−186
2	2e−22	48 / 334	hsa−miR−590−3p
3	7e−20	30 / 136	hsa−miR−200a
4	9e−20	32 / 160	hsa−miR−139−5p
5	4e−19	39 / 260	hsa−miR−548l
6	2e−18	38 / 257	hsa−miR−524−5p
7	1e−17	42 / 333	hsa−miR−302a
8	3e−17	36 / 248	hsa−miR−122
9	5e−17	31 / 183	hsa−miR−300
10	6e−17	42 / 348	hsa−miR−548d−5p
11	1e−16	39 / 307	hsa−miR−548c−3p
12	1e−16	35 / 246	hsa−miR−1252
13	4e−16	36 / 269	hsa−miR−548p
14	4e−16	31 / 196	hsa−miR−513a−3p
15	4e−16	31 / 196	hsa−miR−520d−5p
16	5e−16	38 / 303	hsa−miR−561
17	8e−16	30 / 187	hsa−miR−381
18	1e−15	36 / 279	hsa−miR−577
19	3e−15	45 / 442	hsa−miR−548n
20	6e−15	25 / 134	hsa−miR−335

Pathw Act

Rank	p−value	#in/all	Geneset
1	7e−07	6 / 14	BENTINK_src.2
2	6e−03	3 / 15	BENTINK_ras.6
3	3e−01	1 / 14	GUSTAFSON_PI3K_UP
4	3e−01	1 / 14	BENTINK_myc.1
5	3e−01	1 / 15	GUSTAFSON_PI3K_DN
6	1e+00	0 / 14	BENTINK_e2f3.1
7	1e+00	0 / 13	BENTINK_e2f3.2
8	1e+00	0 / 12	BENTINK_ras.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	

TF

Rank	p−value	#in/all	Geneset
1	5e−11	74 / 1294	KIM_MYC_targets
2	1e−08	189 / 5173	ICGC_Taf1_targets
3	2e−08	168 / 4470	ICGC_Creb1_targets
4	2e−08	76 / 1547	ICGC_Ets1_targets
5	1e−07	74 / 1549	ICGC_Myc_targets
6	8e−07	154 / 4230	ICGC_Nfatc1_targets
7	9e−07	97 / 2342	ICGC_GabpPcr2_targets
8	1e−06	174 / 4969	ICGC_Atf2_targets
9	4e−06	187 / 5512	ICGC_Nficsc81335_targets
10	8e−06	187 / 5578	ICGC_Stat5_targets
11	3e−05	168 / 4987	ICGC_Bclaf101388_targets
12	4e−05	84 / 2133	ICGC_Cebpbsc150_targets
13	8e−05	174 / 5308	ICGC_Tcf12_targets
14	9e−05	89 / 2354	ICGC_SrfV0416101_targets
15	2e−04	176 / 5453	ICGC_Foxm1_targets
16	2e−04	151 / 4566	ICGC_Egr1_targets
17	2e−04	177 / 5526	ICGC_Pmlsc71910_targets
18	3e−04	8 / 66	MYC_Targets UP
19	3e−04	198 / 6313	ICGC_Pou2_targets
20	4e−04	60 / 1503	ICGC_Six5_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	9 / 155	VAQUERIZAS_General
2	0.02	4 / 42	VAQUERIZAS_Thymus
3	0.04	3 / 30	VAQUERIZAS_Smooth muscle
4	0.09	3 / 41	VAQUERIZAS_Fetal brain
5	0.09	3 / 42	VAQUERIZAS_Thyroid
6	0.09	4 / 67	VAQUERIZAS_Whole blood
7	0.19	2 / 31	VAQUERIZAS_Lymph node
8	0.23	3 / 64	VAQUERIZAS_Lung
9	0.27	1 / 12	VAQUERIZAS_Kidney
10	0.34	1 / 16	VAQUERIZAS_Fetal liver
11	0.34	1 / 16	VAQUERIZAS_Fetal thyroid
12	0.36	1 / 17	VAQUERIZAS_Adrenal gland
13	0.36	1 / 17	VAQUERIZAS_Salivary gland
14	0.37	1 / 18	VAQUERIZAS_Pancreas
15	0.43	1 / 22	VAQUERIZAS_Tonsil
16	0.45	1 / 23	VAQUERIZAS_Pituitary
17	0.46	1 / 24	VAQUERIZAS_Trachea
18	0.55	1 / 31	VAQUERIZAS_Fetal lung
19	0.58	1 / 33	VAQUERIZAS_Liver
20	0.62	1 / 37	VAQUERIZAS_Prostate

Tissue

Rank	p−value	#in/all	Geneset
1	7e−07	30 / 427	WIRTH_Immune system
2	4e−02	3 / 30	PALMER_Lymphocytes signature up
3	4e−02	2 / 13	WIRTH_Globus pallidus
4	3e−01	1 / 13	WIRTH_Cortex cerebri
5	3e−01	1 / 14	WIRTH_B−cells
6	3e−01	1 / 15	WIRTH_Cerebellum
7	4e−01	6 / 208	PALMER_B−Cell signature up
8	1e+00	1 / 140	PALMER_T−Cell signature up
9	1e+00	2 / 259	PALMER_Granulocytes signature up
10	1e+00	0 / 6	WIRTH_Pituitary gland
11	1e+00	0 / 54	WIRTH_Pancreas
12	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
13	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
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 / 476	WIRTH_Nervous System
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	46 / 1343	LU_BPDE 1h DN
2	1.00	86 / 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	

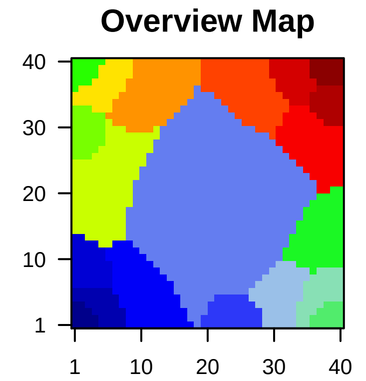
K−Means Clusters

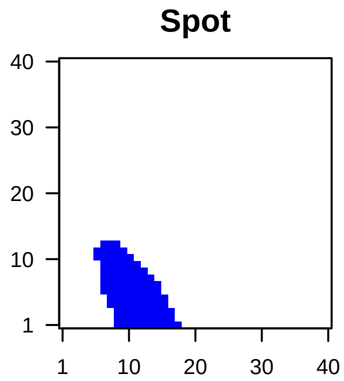
Spot Summary: D

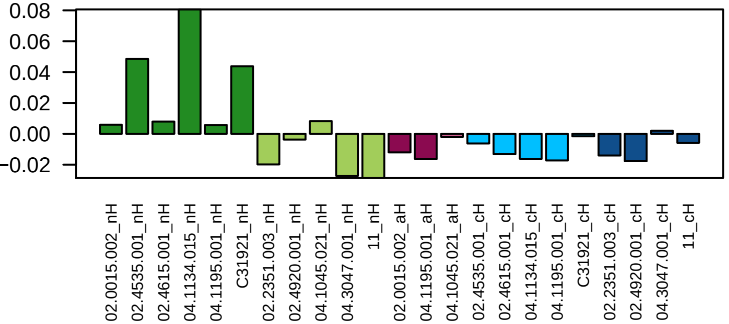
metagenes = 99
genes = 901

<r> metagenes = 0.83
<r> genes = 0.39
beta: r2= 0.02 / log p= −0.27

samples with spot = 0 (0 %)





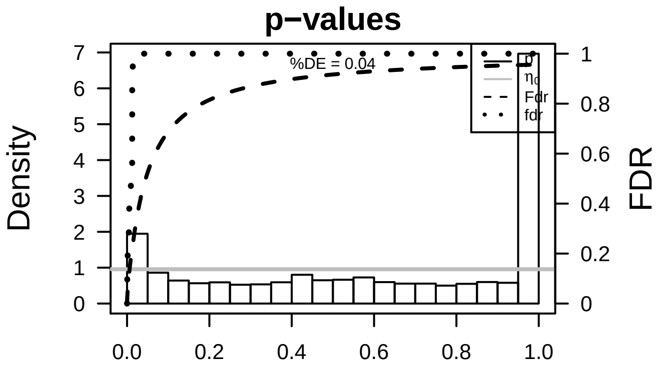


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.46	−0.14	0.36	CENPT	centromere protein T [Source:HGNC Symbol;Acc:HGNC:257
2	ENSG000001	0.39	−0.2	0.34	IRF1	interferon regulatory factor 1 [Source:HGNC Symbol;Acc:HG
3	ENSG000001	0.37	−0.11	0.2		
4	ENSG000001	0.35	−0.07	0.25	ABCC5	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
5	ENSG000000	0.33	−0.14	0.33	TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:HGNC:
6	ENSG000001	0.33	−0.1	0.2	OAS3	2'−5'−oligoadenylate synthetase 3, 100kDa [Source:HGNC S
7	ENSG000001	0.32	−0.21	0.44	CDK5RAP3	CDK5 regulatory subunit associated protein 3 [Source:HGNC
8	ENSG000002	0.31	−0.09	0.24	APOL6	apolipoprotein L, 6 [Source:HGNC Symbol;Acc:HGNC:14870
9	ENSG000001	0.31	−0.14	0.14	LDLR	low density lipoprotein receptor [Source:HGNC Symbol;Acc:
10	ENSG000000	0.3	−0.12	0.27	AKR1B1	aldo−keto reductase family 1, member B1 (aldose reductase)
11	ENSG000000	0.29	−0.18	0.26	TYROBP	TYRO protein tyrosine kinase binding protein [Source:HGNC
12	ENSG000001	0.29	−0.1	0.58	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1 [Sou
13	ENSG000001	0.29	−0.1	0.56	OTUD1	OTU deubiquitinase 1 [Source:HGNC Symbol;Acc:HGNC:27
14	ENSG000001	0.29	−0.13	0.5	CCDC88B	coiled−coil domain containing 88B [Source:HGNC Symbol;Ac
15	ENSG000001	0.28	−0.18	0.39	PFDN5	prefoldin subunit 5 [Source:HGNC Symbol;Acc:HGNC:8869]
16	ENSG000000	0.27	−0.02	0.29	DDX3Y	DEAD (Asp−Glu−Ala−Asp) box helicase 3, Y−linked [Source:
17	ENSG000000	0.27	−0.02	0.34	KDM5D	lysine (K)−specific demethylase 5D [Source:HGNC Symbol;A
18	ENSG000001	0.26	−0.1	0.26	PLEC	plectin [Source:HGNC Symbol;Acc:HGNC:9069]
19	ENSG000002	0.26	−0.14	0.51		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H0
20	ENSG000002	0.26	−0.16	0.42	IRF9	interferon regulatory factor 9 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−61	588 / 7592	Lymp	HOPP_Strong_enhancer
2	3e−56	481 / 5643	Lymp	HOPP_Txn_transition
3	1e−46	553 / 7491	Lymp	HOPP_Txn_elongation
4	1e−39	104 / 500	Lymp	WIRTH_lymphoma937_spot J
5	5e−34	95 / 484	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−
6	1e−33	128 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
7	2e−30	623 / 9930	Colon	Tx_Colon
8	1e−29	597 / 9390	Colon	TxWk_Colon
9	2e−24	76 / 427	Tissu	WIRTH_Immune system
10	8e−24	627 / 10475	Colon	TssA_Colon
11	4e−23	390 / 5512	TF	ICGC_Nficsc81335_targets
12	5e−20	338 / 4714	TF	ICGC_Pu1_targets
13	5e−20	519 / 8358	Lymp	HOPP_Active_promoter
14	7e−19	128 / 1215	Lymp	SPANG_BCR DN
15	9e−19	347 / 4969	TF	ICGC_Atf2_targets
16	4e−18	563 / 9470	Colon	Quies3_Colon
17	9e−18	354 / 5173	TF	ICGC_Taf1_targets
18	8e−17	250 / 3305	TF	ICGC_BatfPcr1_targets
19	1e−16	371 / 5578	TF	ICGC_Stat5_targets
20	2e−16	407 / 6313	TF	ICGC_Pou2_targets
21	2e−16	56 / 347	Lymp	WIRTH_lymphoma937_spot H
22	7e−16	492 / 8123	Colon	TssF_Colon
23	1e−15	54 / 336	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−
24	1e−15	239 / 3177	TF	ICGC_Irf4_targets
25	1e−15	309 / 4470	TF	ICGC_Creb1_targets
26	1e−15	314 / 4566	TF	ICGC_Egr1_targets
27	6e−15	192 / 2401	TF	ICGC_Bcl11_targets
28	6e−15	177 / 2149	TF	ICGC_Mef2_targets
29	6e−15	401 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
30	7e−15	49 / 297	GSE	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
31	8e−15	333 / 4987	TF	ICGC_Bclaf101388_targets
32	4e−14	354 / 5453	TF	ICGC_Foxm1_targets
33	5e−14	160 / 1914	GSE	PILON_KLF1_TARGETS_DN
34	1e−13	655 / 11968	Colon	TssWk_Colon
35	3e−13	386 / 6157	TF	ICGC_Tcf3_targets
36	4e−13	170 / 2133	TF	ICGC_Cebpbsc150_targets
37	5e−13	353 / 5526	TF	ICGC_Pmlsc71910_targets
38	6e−13	194 / 2554	CC	nucleoplasm
39	9e−13	46 / 301	GSE	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
40	1e−12	375 / 6005	TF	ICGC_Mta3_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.5	6 / 123	HORVATH_aging_genes meth DOWN
2	0.9	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	2e−09	70 / 707	innate immune response
2	2e−08	134 / 1807	transcription, DNA−templated
3	3e−07	10 / 28	cytokine production
4	3e−07	23 / 147	defense response to virus
5	5e−07	37 / 326	inflammatory response
6	2e−06	10 / 33	negative regulation of type I interferon production
7	2e−06	7 / 15	regulation of innate immune response
8	3e−06	125 / 1808	regulation of transcription, DNA−templated
9	9e−06	30 / 270	cytokine−mediated signaling pathway
10	1e−05	28 / 246	cell surface receptor signaling pathway
11	1e−05	18 / 122	adaptive immune response
12	1e−05	11 / 50	T cell activation
13	2e−05	49 / 560	positive regulation of transcription, DNA−templated
14	2e−05	9 / 35	T cell differentiation
15	3e−05	13 / 73	interferon−gamma−mediated signaling pathway
16	4e−05	16 / 109	toll−like receptor signaling pathway
17	6e−05	12 / 68	negative regulation of NF−kappaB transcription factor activity
18	8e−05	5 / 11	regulation of cytokine secretion
19	1e−04	11 / 63	type I interferon signaling pathway
20	1e−04	32 / 343	immune response

Brain

Rank	p−value	#in/all	Geneset
1	6e−15	401 / 6320	Overlap_fetal_midbrain_HetRpts
2	1e−09	546 / 9923	Overlap_fetal_midbrain_K9K27me3
3	2e−08	579 / 10800	Overlap_fetal_midbrain_Quies
4	5e−07	545 / 10239	Overlap_fetal_midbrain_ReprPC
5	5e−06	207 / 3370	Mid_Frontal_Lobe_ZNF
6	3e−05	535 / 10278	Overlap_fetal_midbrain_ReprPCWk
7	1e−04	64 / 855	Overlap_fetal_midbrain_ZNF
8	3e−02	55 / 910	Fetal_EnhG
9	3e−02	69 / 1182	Fetal_EnhP
10	3e−02	52 / 865	Mid_Frontal_Lobe_Het
11	5e−02	23 / 342	Fetal_Het
12	6e−02	64 / 1137	Fetal_Enh
13	6e−02	42 / 712	Overlap_fetal_midbrain_EnhP
14	2e−01	86 / 1680	Fetal_ReprPCWk
15	2e−01	140 / 2820	Mid_Frontal_Lobe_HetRpts
16	3e−01	33 / 641	Mid_Frontal_Lobe_EnhP
17	3e−01	69 / 1394	Mid_Frontal_Lobe_Quies
18	3e−01	17 / 317	Mid_Frontal_Lobe_Tx
19	4e−01	58 / 1210	Fetal_TssP
20	5e−01	80 / 1713	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	2e−10	63 / 574	Lembcke_Colonic Inflammation
2	1e−07	38 / 324	SPANG_BCL6−index2
3	4e−04	8 / 40	PanCan_HK_geneset_nanostring
4	5e−03	4 / 16	GENTLES_modul11
5	5e−03	4 / 16	GENTLES_modul14
6	1e−02	13 / 136	PanCan_CC+Apop_geneset_nanostring
7	2e−02	16 / 191	SPANG_LPS−index2
8	2e−02	3 / 14	GENTLES_modul12
9	3e−02	11 / 123	PanCan_Driver_Gene_geneset_nanostring
10	2e−01	2 / 15	LIU_BREAST_CANCER
11	2e−01	1 / 16	LIU_COMMON_CANCER_GENES
12	2e−01	1 / 6	ZHANG_MGUS up
13	3e−01	8 / 140	PanCan_RAS_geneset_nanostring
14	3e−01	1 / 9	WANG_ER_DN
15	4e−01	5 / 86	PanCan_JAK−ST_geneset_nanostring
16	4e−01	8 / 152	PanCan_MAPK_geneset_nanostring
17	4e−01	3 / 52	KUIPER_MM poor survival
18	5e−01	1 / 14	BEN−PORATH_DN
19	5e−01	1 / 15	BEN−PORATH_UP
20	5e−01	0 / 16	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	6e−13	194 / 2554	nucleoplasm
2	3e−12	328 / 5101	nucleus
3	6e−04	102 / 1604	intracellular
4	1e−03	4 / 11	CD40 receptor complex
5	1e−03	10 / 69	cytoplasmic mRNA processing body
6	1e−03	280 / 5185	cytoplasm
7	2e−03	5 / 21	mast cell granule
8	3e−03	10 / 77	ruffle membrane
9	3e−03	5 / 22	histone methyltransferase complex
10	6e−03	18 / 201	external side of plasma membrane
11	7e−03	10 / 88	PML body
12	1e−02	16 / 180	nuclear speck
13	1e−02	14 / 150	nuclear chromatin
14	1e−02	12 / 121	trans−Golgi network
15	2e−02	3 / 12	holo TFIIH complex
16	2e−02	3 / 12	phosphatidylinositol 3−kinase complex
17	2e−02	4 / 22	clathrin adaptor complex
18	2e−02	3 / 13	cell−cell contact zone
19	2e−02	3 / 13	low−density lipoprotein particle
20	2e−02	3 / 14	Golgi−associated vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.03	29 / 436	Chr 22
2	0.04	63 / 1083	Chr 17
3	0.04	51 / 859	Chr 7
4	0.04	57 / 976	Chr 6
5	0.05	50 / 847	Chr 16
6	0.13	33 / 582	Chr 15
7	0.18	12 / 191	Chr 21
8	0.21	54 / 1043	Chr 3
9	0.23	72 / 1425	Chr 19
10	0.33	31 / 613	Chr 14
11	0.41	2 / 30	Chr Y
12	0.49	13 / 272	Chr 18
13	0.59	46 / 1017	Chr 12
14	0.71	37 / 862	Chr 5
15	0.76	31 / 746	Chr X
16	0.77	52 / 1228	Chr 2
17	0.80	82 / 1920	Chr 1
18	0.84	48 / 1172	Chr 11
19	0.92	26 / 715	Chr 10
20	0.93	18 / 522	Chr 20

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−33	128 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−30	623 / 9930	Tx_Colon
3	1e−29	597 / 9390	TxWk_Colon
4	8e−24	627 / 10475	TssA_Colon
5	4e−18	563 / 9470	Quies3_Colon
6	7e−16	492 / 8123	TssF_Colon
7	1e−13	655 / 11968	TssWk_Colon
8	2e−11	220 / 3122	TxEnhG1_Colon
9	3e−10	632 / 11791	Enh_Colon
10	5e−10	357 / 5889	EnhWk1_Colon
11	1e−07	387 / 6761	TssD2_Colon
12	3e−06	195 / 3112	EnhA_Colon
13	7e−04	11 / 76	Marisa_CRC−cluster−g
14	8e−04	29 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
15	1e−03	41 / 532	K9acLow_Colon
16	1e−03	77 / 1178	ZNF_Colon
17	7e−03	4 / 17	TCGA−CRC_less−agressive−disease−markers
18	5e−02	9 / 105	Marisa_CRC−cluster−d
19	8e−02	2 / 10	Juehling−MSI−enriched−in−7
20	1e−01	218 / 4379	TssD1_Colon

Disease

Rank	p−value	#in/all	Geneset
1	0.01	41 / 608	GUDJ_psoriasis up
2	0.83	1 / 37	BCHETNIA_EBM−DM up
3	1.00	7 / 399	GUDJ_psoriasis down
4	1.00	0 / 22	BCHETNIA_EBM up
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	8e−04	5 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
2	1e−03	60 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−03	132 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	3e−03	8 / 53	Donson−innate immunity−associated with LTS in HGA
5	3e−03	4 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
6	4e−03	11 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
7	6e−03	23 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
8	6e−03	115 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	1e−02	10 / 96	Weller_LGG_A_vs_O_UP
10	2e−02	8 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	2e−02	5 / 33	Donson−Misc immune function−associated with LTS in HGA
12	2e−02	25 / 344	Up
13	3e−02	23 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	3e−02	3 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
15	3e−02	14 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
16	4e−02	3 / 16	VERHAAK_MES subtype
17	8e−02	7 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
18	9e−02	2 / 11	KIM amplified & overexpressed in LTS
19	9e−02	2 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
20	1e−01	11 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−15	49 / 297	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
2	5e−14	160 / 1914	PILON_KLF1_TARGETS_DN
3	9e−13	46 / 301	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	9e−12	30 / 150	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
5	2e−10	51 / 413	MITSIADES_RESPONSE_TO_APLIDIN_UP
6	2e−10	80 / 823	REACTOME_IMMUNE_SYSTEM
7	3e−09	30 / 189	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
8	4e−09	49 / 424	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
9	5e−09	109 / 1340	PUJANA_ATM_PCC_NETWORK
10	5e−09	18 / 74	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
11	7e−09	52 / 473	ZHENG_BOUND_BY_FOXP3
12	9e−09	49 / 435	RODWELL_AGING_KIDNEY_UP
13	5e−08	95 / 1168	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
14	7e−08	28 / 192	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
15	8e−08	82 / 967	MARSON_BOUND_BY_FOXP3_STIMULATED
16	1e−07	39 / 336	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
17	1e−07	46 / 433	MARTENS_BOUND_BY_PML_RARA_FUSION
18	1e−06	14 / 65	REACTOME_RIG_I_MDA5_MEDIATED_INDUCTION_OF_IFN_ALPHA_BET
19	1e−06	41 / 397	FOSTER_TOLERANT_MACROPHAGE_DN
20	2e−06	24 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE

HM

Rank	p−value	#in/all	Geneset
1	1e−10	32 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	7e−06	15 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	3e−05	22 / 181	HALLMARK_ALLOGRAFT_REJECTION
4	2e−03	19 / 194	HALLMARK_INFLAMMATORY_RESPONSE
5	4e−03	18 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	4e−03	18 / 192	HALLMARK_COMPLEMENT
7	8e−03	10 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	2e−02	6 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	2e−02	16 / 197	HALLMARK_IL2_STAT5_SIGNALING
10	3e−02	13 / 157	HALLMARK_APOPTOSIS
11	7e−02	14 / 196	HALLMARK_P53_PATHWAY
12	7e−02	9 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	2e−01	4 / 52	HALLMARK_TGF_BETA_SIGNALING
14	3e−01	9 / 155	HALLMARK_UV_RESPONSE_UP
15	3e−01	3 / 44	HALLMARK_APICAL_SURFACE
16	4e−01	10 / 193	HALLMARK_KRAS_SIGNALING_DN
17	4e−01	2 / 30	HALLMARK_NOTCH_SIGNALING
18	4e−01	10 / 196	HALLMARK_MITOTIC_SPINDLE
19	4e−01	10 / 198	HALLMARK_HYPOXIA
20	5e−01	7 / 140	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 17	DUMEAUX_High bmi enriched genes
2	0.3	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.4	1 / 11	DUMEAUX_Smoking literature genes up
4	0.4	1 / 11	DUMEAUX_Women normal BMI literature genes up
5	0.5	2 / 33	DUMEAUX_Fasting enriched genes
6	0.6	4 / 91	DUMEAUX_Smoking enriched genes
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−61	588 / 7592	HOPP_Strong_enhancer
2	3e−56	481 / 5643	HOPP_Txn_transition
3	1e−46	553 / 7491	HOPP_Txn_elongation
4	1e−39	104 / 500	WIRTH_lymphoma937_spot J
5	5e−34	95 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
6	5e−20	519 / 8358	HOPP_Active_promoter
7	7e−19	128 / 1215	SPANG_BCR DN
8	2e−16	56 / 347	WIRTH_lymphoma937_spot H
9	1e−15	54 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
10	9e−11	470 / 8147	HOPP_Weak_promoter
11	2e−09	38 / 279	SPANG_IL21 DN
12	2e−06	36 / 332	SPANG_CD40 6hrs UP
13	9e−06	356 / 6389	HOPP_Weak_txn
14	5e−04	88 / 1333	SPANG_BCR UP
15	9e−04	27 / 302	SPANG_IL21 UP
16	3e−03	353 / 6784	HOPP_Weak_enhancer
17	4e−03	11 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
18	6e−03	34 / 466	SPANG_CD40 6hrs DN
19	6e−03	25 / 315	WIRTH_lymphoma937_spot E
20	8e−03	6 / 38	TARTE_B−cell signature

MF

Rank	p−value	#in/all	Geneset
1	2e−11	590 / 10693	protein binding
2	1e−08	135 / 1803	DNA binding
3	6e−06	87 / 1164	zinc ion binding
4	9e−05	33 / 350	protein serine/threonine kinase activity
5	2e−04	35 / 394	chromatin binding
6	4e−04	24 / 243	transcription coactivator activity
7	4e−04	30 / 333	RNA polymerase II core promoter proximal region sequence−specific DNA bir
8	4e−04	5 / 15	hydrolase activity, acting on acid anhydrides
9	6e−04	67 / 962	transcription factor activity, sequence−specific DNA binding
10	7e−04	11 / 76	helicase activity
11	7e−04	76 / 1134	nucleic acid binding
12	8e−04	4 / 10	methyl−CpG binding
13	8e−04	93 / 1448	ATP binding
14	9e−04	41 / 527	protein kinase activity
15	9e−04	12 / 90	ubiquitin−specific protease activity
16	1e−03	21 / 219	receptor activity
17	2e−03	6 / 29	NF−kappaB binding
18	3e−03	9 / 64	cysteine−type peptidase activity
19	3e−03	5 / 22	ribonucleoprotein complex binding
20	3e−03	9 / 65	RNA polymerase II distal enhancer sequence−specific DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−05	50 / 591	hsa−miR−20b
2	8e−05	51 / 631	hsa−miR−20a
3	9e−05	45 / 536	hsa−miR−106b
4	1e−04	9 / 43	hsa−miR−541
5	2e−04	46 / 573	hsa−miR−93
6	2e−04	44 / 542	hsa−miR−106a
7	2e−04	27 / 278	hsa−miR−101
8	3e−04	22 / 208	hsa−miR−545
9	5e−04	24 / 245	hsa−miR−214
10	5e−04	37 / 447	hsa−miR−519d
11	8e−04	12 / 89	hsa−miR−496
12	8e−04	40 / 509	hsa−miR−103
13	9e−04	43 / 562	hsa−miR−17
14	1e−03	34 / 416	hsa−miR−519c−3p
15	2e−03	39 / 509	hsa−miR−107
16	2e−03	17 / 165	hsa−miR−512−3p
17	2e−03	14 / 125	hsa−miR−519e
18	2e−03	14 / 125	hsa−miR−380
19	2e−03	34 / 435	hsa−miR−372
20	2e−03	32 / 403	hsa−miR−519a

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	4e−23	390 / 5512	ICGC_Nficsc81335_targets
2	5e−20	338 / 4714	ICGC_Pu1_targets
3	9e−19	347 / 4969	ICGC_Atf2_targets
4	9e−18	354 / 5173	ICGC_Taf1_targets
5	8e−17	250 / 3305	ICGC_BatfPcr1_targets
6	1e−16	371 / 5578	ICGC_Stat5_targets
7	2e−16	407 / 6313	ICGC_Pou2_targets
8	1e−15	239 / 3177	ICGC_Irf4_targets
9	1e−15	309 / 4470	ICGC_Creb1_targets
10	1e−15	314 / 4566	ICGC_Egr1_targets
11	6e−15	192 / 2401	ICGC_Bcl11_targets
12	6e−15	177 / 2149	ICGC_Mef2_targets
13	8e−15	333 / 4987	ICGC_Bclaf101388_targets
14	4e−14	354 / 5453	ICGC_Foxm1_targets
15	3e−13	386 / 6157	ICGC_Tcf3_targets
16	4e−13	170 / 2133	ICGC_Cebpbsc150_targets
17	5e−13	353 / 5526	ICGC_Pmlsc71910_targets
18	1e−12	375 / 6005	ICGC_Mta3_targets
19	3e−12	432 / 7202	ICGC_Runx3_targets
20	5e−12	282 / 4230	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	5e−05	12 / 67	VAQUERIZAS_Whole blood
2	1e−04	19 / 155	VAQUERIZAS_General
3	1e−02	4 / 20	VAQUERIZAS_Bone marrow
4	1e−02	5 / 31	VAQUERIZAS_Lymph node
5	2e−02	4 / 22	VAQUERIZAS_Tonsil
6	4e−02	5 / 42	VAQUERIZAS_Thymus
7	1e−01	2 / 13	VAQUERIZAS_Skin
8	2e−01	2 / 16	VAQUERIZAS_Fetal liver
9	2e−01	5 / 64	VAQUERIZAS_Lung
10	2e−01	3 / 33	VAQUERIZAS_Liver
11	2e−01	2 / 19	VAQUERIZAS_Heart
12	3e−01	2 / 23	VAQUERIZAS_Pituitary
13	3e−01	3 / 42	VAQUERIZAS_Thyroid
14	4e−01	3 / 46	VAQUERIZAS_Whole brain
15	4e−01	1 / 12	VAQUERIZAS_Kidney
16	5e−01	1 / 16	VAQUERIZAS_Fetal thyroid
17	6e−01	2 / 41	VAQUERIZAS_Fetal brain
18	6e−01	2 / 45	VAQUERIZAS_Placenta
19	7e−01	1 / 24	VAQUERIZAS_Trachea
20	7e−01	1 / 25	VAQUERIZAS_Spinal cord

Tissue

Rank	p−value	#in/all	Geneset
1	2e−24	76 / 427	WIRTH_Immune system
2	2e−06	21 / 140	PALMER_T−Cell signature up
3	4e−06	26 / 208	PALMER_B−Cell signature up
4	1e−01	16 / 259	PALMER_Granulocytes signature up
5	5e−01	1 / 13	WIRTH_Globus pallidus
6	5e−01	1 / 13	WIRTH_Cortex cerebri
7	5e−01	1 / 13	PALMER_CD8+ T−Cell signature up
8	5e−01	1 / 14	WIRTH_Thalamus
9	5e−01	1 / 15	WIRTH_Cerebellum
10	9e−01	1 / 54	WIRTH_Pancreas
11	1e+00	2 / 141	WIRTH_Muscle
12	1e+00	10 / 476	WIRTH_Nervous System
13	1e+00	1 / 202	WIRTH_Testis
14	1e+00	0 / 6	WIRTH_Pituitary gland
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 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	64 / 1343	LU_BPDE 1h DN
2	1.0	158 / 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	

K−Means Clusters

Spot Summary: E

metagenes = 60
genes = 642

<r> metagenes = 0.9
<r> genes = 0.44
beta: r2= 0.06 / log p= −0.58

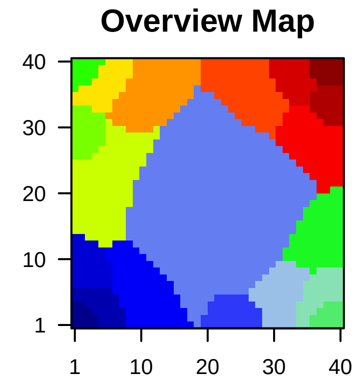
samples with spot = 1 (4.3 %)
MLH1_normHNPCC : 1 (16.7 %)

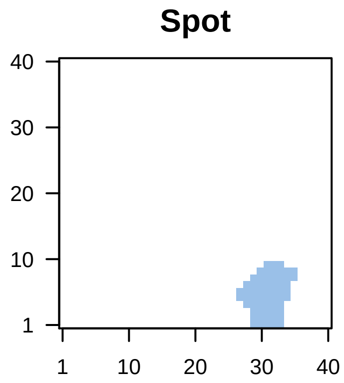
Spot Genelist

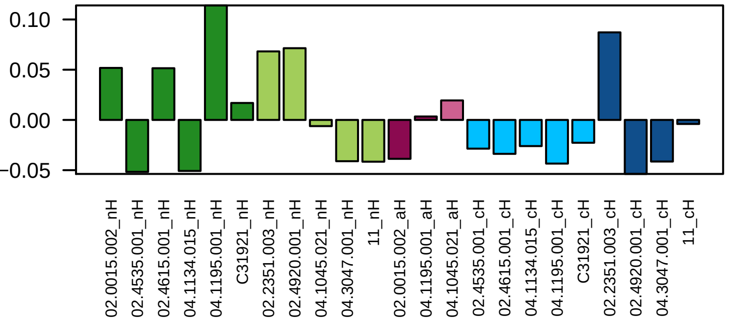
Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.64	−0.07	0.41	HSPB3	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:HGN
2	ENSG000001	0.62	−0.05	0.21	CSF3	colony stimulating factor 3 (granulocyte) [Source:HGNC Symb
3	ENSG000001	0.6	−0.11	0.41	RETNLB	resistin like beta [Source:HGNC Symbol;Acc:HGNC:20388]
4	ENSG000001	0.58	−0.49	0.48	MT1E	metallothionein 1E [Source:HGNC Symbol;Acc:HGNC:7397]
5	ENSG000001	0.49	−0.1	0.72	DDX60	DEAD (Asp−Glu−Ala−Asp) box polypeptide 60 [Source:HGN
6	ENSG000001	0.48	−0.09	0.38	ATOH1	atonal bHLH transcription factor 1 [Source:HGNC Symbol;Ac
7	ENSG000001	0.47	−0.08	0.6	SPINK5	serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
8	ENSG000001	0.45	−0.07	0.45	IL1R2	interleukin 1 receptor, type II [Source:HGNC Symbol;Acc:HG
9	ENSG000002	0.44	−0.12	0.67	SAMD9	sterile alpha motif domain containing 9 [Source:HGNC Symb
10	ENSG000001	0.43	−0.1	0.85	CLIC5	chloride intracellular channel 5 [Source:HGNC Symbol;Acc:H
11	ENSG000001	0.42	−0.2	0.76	MXI1	MAX interactor 1, dimerization protein [Source:HGNC Symbo
12	ENSG000001	0.42	−0.08	0.57	TPSG1	tryptase gamma 1 [Source:HGNC Symbol;Acc:HGNC:14134]
13	ENSG000001	0.41	−0.1	0.49	FFAR4	free fatty acid receptor 4 [Source:HGNC Symbol;Acc:HGNC:
14	ENSG000001	0.4	−0.07	0.2	CHGA	chromogranin A [Source:HGNC Symbol;Acc:HGNC:1929]
15	ENSG000001	0.4	−0.06	0.5	DISP2	dispatched homolog 2 (Drosophila) [Source:HGNC Symbol;A
16	ENSG000001	0.4	−0.08	0.58	CAPN9	calpain 9 [Source:HGNC Symbol;Acc:HGNC:1486]
17	ENSG000001	0.4	−0.18	0.31	RASL11A	RAS−like, family 11, member A [Source:HGNC Symbol;Acc:
18	ENSG000001	0.39	−0.33	0.46	ID3	inhibitor of DNA binding 3, dominant negative helix−loop−heli
19	ENSG000001	0.39	−0.09	0.59	ZFAND2A	zinc finger, AN1−type domain 2A [Source:HGNC Symbol;Acc
20	ENSG000001	0.39	−0.05	0.53	CMPK2	cytidine monophosphate (UMP−CMP) kinase 2, mitochondria

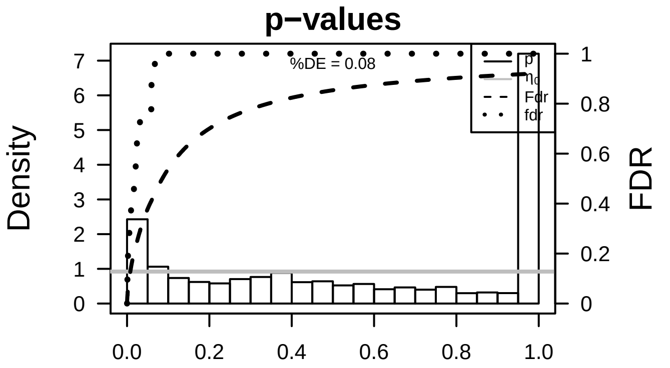
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−52	104 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
2	4e−46	501 / 9930	Colon	Tx_Colon
3	2e−45	484 / 9390	Colon	TxWk_Colon
4	2e−45	486 / 9470	Colon	Quies3_Colon
5	5e−37	348 / 5889	Colon	EnhWk1_Colon
6	9e−35	495 / 10475	Colon	TssA_Colon
7	3e−26	514 / 11791	Colon	Enh_Colon
8	1e−24	515 / 11968	Colon	TssWk_Colon
9	7e−22	78 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
10	4e−20	60 / 453	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
11	1e−18	449 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
12	1e−17	188 / 3112	Colon	EnhA_Colon
13	2e−17	188 / 3122	Colon	TxEnhG1_Colon
14	4e−16	457 / 10800	Brain	Overlap_fetal_midbrain_Quies
15	3e−14	364 / 8123	Colon	TssF_Colon
16	2e−13	314 / 6761	Colon	TssD2_Colon
17	2e−13	52 / 495	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
18	3e−13	55 / 549	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
19	5e−13	68 / 786	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
20	2e−12	365 / 8358	Lympl	HOPP_Active_promoter
21	2e−11	76 / 1005	GSEA	NUYTTEN_EZH2_TARGETS_UP
22	3e−11	65 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
23	8e−11	21 / 110	Colon	Marisa_CRC−cluster−h
24	1e−10	328 / 7491	Lympl	HOPP_Txn_elongation
25	2e−10	349 / 8147	Lympl	HOPP_Weak_promoter
26	2e−10	32 / 261	GSEA	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
27	2e−10	49 / 541	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
28	4e−10	54 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
29	4e−10	46 / 497	CC	Golgi membrane
30	4e−10	22 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
31	1e−09	38 / 377	GSEA	STEIN_ESRRA_TARGETS_UP
32	3e−09	44 / 490	GSEA	ENK_UV_RESPONSE_EPIDERMIS_DN
33	3e−09	413 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
34	4e−09	402 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
35	6e−09	29 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
36	2e−08	277 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
37	2e−08	41 / 468	GSEA	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
38	6e−08	54 / 740	GSEA	FORTSCHEGGER_PHF8_TARGETS_DN
39	6e−08	27 / 246	CC	endosome
40	1e−07	34 / 370	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 144	HORVATH_aging_genes meth UP
2	0.4	5 / 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	6e−07	40 / 512	protein transport
2	3e−06	18 / 150	endocytosis
3	3e−06	18 / 152	cellular lipid metabolic process
4	9e−06	5 / 10	regulation of mitotic spindle assembly
5	9e−06	5 / 10	viral budding via host ESCRT complex
6	1e−05	6 / 17	cell separation after cytokinesis
7	1e−05	6 / 17	regulation of centrosome duplication
8	1e−05	17 / 152	actin cytoskeleton organization
9	1e−05	77 / 1418	small molecule metabolic process
10	1e−04	25 / 329	intracellular protein transport
11	2e−04	6 / 27	vesicle organization
12	2e−04	11 / 91	ephrin receptor signaling pathway
13	2e−04	4 / 10	positive regulation of viral release from host cell
14	2e−04	5 / 18	nucleus organization
15	3e−04	21 / 272	neurotrophin TRK receptor signaling pathway
16	4e−04	9 / 68	endosomal transport
17	4e−04	7 / 42	fatty acid beta−oxidation
18	5e−04	6 / 31	mitotic metaphase plate congression
19	6e−04	9 / 71	Fc−gamma receptor signaling pathway involved in phagocytosis
20	7e−04	4 / 13	positive regulation of exosomal secretion

Brain

Rank	p−value	#in/all	Geneset
1	1e−18	449 / 10278	Overlap_fetal_midbrain_ReprPCWk
2	4e−16	457 / 10800	Overlap_fetal_midbrain_Quies
3	3e−09	413 / 10239	Overlap_fetal_midbrain_ReprPC
4	4e−09	402 / 9923	Overlap_fetal_midbrain_K9K27me3
5	2e−08	277 / 6320	Overlap_fetal_midbrain_HetRpts
6	7e−04	144 / 3370	Mid_Frontal_Lobe_ZNF
7	1e−03	60 / 1210	Fetal_TssP
8	2e−03	121 / 2820	Mid_Frontal_Lobe_HetRpts
9	2e−02	51 / 1137	Fetal_Enh
10	3e−02	102 / 2549	Fetal_TssF
11	3e−02	27 / 552	Fetal_Tx
12	3e−02	116 / 2956	Fetal_TssA
13	6e−02	29 / 641	Mid_Frontal_Lobe_EnhP
14	7e−02	40 / 939	Fetal_HetRpts
15	7e−02	148 / 3977	Mid_Frontal_Lobe_ReprPC
16	8e−02	55 / 1356	Fetal_K9K27me3
17	8e−02	56 / 1394	Mid_Frontal_Lobe_Quies
18	9e−02	34 / 805	Mid_Frontal_Lobe_EnhG
19	2e−01	33 / 855	Overlap_fetal_midbrain_ZNF
20	3e−01	14 / 342	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	4e−06	28 / 324	SPANG_BCL6−index2
2	2e−05	19 / 191	SPANG_LPS−index2
3	3e−03	1 / 14	LIU_PROSTATE_CANCER_UP
4	7e−03	14 / 198	PanCan_PI3K_geneset_nanostring
5	1e−02	11 / 152	PanCan_MAPK_geneset_nanostring
6	1e−02	3 / 16	GENTLES_modul6
7	2e−02	10 / 140	PanCan_RAS_geneset_nanostring
8	9e−02	8 / 136	PanCan_CC+Apop_geneset_nanostring
9	2e−01	3 / 51	PanCan_TGF−B_geneset_nanostring
10	3e−01	3 / 52	KUIPER_MM poor survival
11	3e−01	1 / 11	GENTLES_modul5
12	3e−01	4 / 86	PanCan_JAK−ST_geneset_nanostring
13	4e−01	1 / 14	BEN−PORATH_DN
14	4e−01	1 / 15	BEN−PORATH_UP
15	4e−01	4 / 97	PanCan_TXmisReg_geneset_nanostring
16	4e−01	1 / 16	LIU_LIVER_CANCER
17	4e−01	1 / 16	LIU_PROSTATE_CANCER_DN
18	4e−01	1 / 16	GENTLES_modul1
19	4e−01	1 / 16	GENTLES_modul7
20	4e−01	1 / 16	GENTLES_modul18

CC

Rank	p−value	#in/all	Geneset
1	4e−10	46 / 497	Golgi membrane
2	6e−08	27 / 246	endosome
3	1e−07	135 / 2638	extracellular exosome
4	3e−05	9 / 49	autophagosome
5	1e−04	30 / 425	mitochondrial inner membrane
6	1e−04	134 / 2974	cytosol
7	1e−04	11 / 87	late endosome membrane
8	2e−04	17 / 185	endosome membrane
9	2e−04	7 / 37	phagocytic vesicle
10	2e−04	37 / 596	perinuclear region of cytoplasm
11	3e−04	7 / 39	recycling endosome membrane
12	3e−04	171 / 4052	integral component of membrane
13	8e−04	12 / 122	cell cortex
14	9e−04	70 / 1441	mitochondrion
15	1e−03	17 / 216	actin cytoskeleton
16	1e−03	147 / 3507	plasma membrane
17	1e−03	16 / 204	early endosome
18	2e−03	18 / 245	lysosomal membrane
19	2e−03	15 / 190	membrane raft
20	2e−03	9 / 86	extrinsic component of membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	36 / 735	Chr 4
2	0.03	79 / 1920	Chr 1
3	0.03	53 / 1228	Chr 2
4	0.04	29 / 613	Chr 14
5	0.04	15 / 272	Chr 18
6	0.08	26 / 582	Chr 15
7	0.11	10 / 191	Chr 21
8	0.12	30 / 715	Chr 10
9	0.42	34 / 976	Chr 6
10	0.44	36 / 1043	Chr 3
11	0.49	11 / 318	Chr 13
12	0.59	33 / 1017	Chr 12
13	0.68	23 / 745	Chr 9
14	0.72	36 / 1172	Chr 11
15	0.76	25 / 847	Chr 16
16	0.79	25 / 859	Chr 7
17	0.79	12 / 436	Chr 22
18	0.79	25 / 862	Chr 5
19	0.84	31 / 1083	Chr 17
20	0.88	17 / 651	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−52	104 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
2	4e−46	501 / 9930	Tx_Colon
3	2e−45	484 / 9390	TxWk_Colon
4	2e−45	486 / 9470	Quies3_Colon
5	5e−37	348 / 5889	EnhWk1_Colon
6	9e−35	495 / 10475	TssA_Colon
7	3e−26	514 / 11791	Enh_Colon
8	1e−24	515 / 11968	TssWk_Colon
9	1e−17	188 / 3112	EnhA_Colon
10	2e−17	188 / 3122	TxEnhG1_Colon
11	3e−14	364 / 8123	TssF_Colon
12	2e−13	314 / 6761	TssD2_Colon
13	8e−11	21 / 110	Marisa_CRC−cluster−h
14	2e−07	50 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	5e−07	11 / 49	Marisa_CRC−cluster−f
16	5e−06	194 / 4379	TssD1_Colon
17	1e−05	67 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	8e−05	185 / 4327	EnhWk2_Colon
19	4e−04	8 / 55	Marisa_CRC−cluster−e
20	2e−03	3 / 8	Budinska_A_Surface crypt−like_UP

Disease

Rank	p−value	#in/all	Geneset
1	0.03	29 / 608	GUDJ_psoriasis up
2	0.05	20 / 399	GUDJ_psoriasis down
3	0.12	3 / 37	BCHETNIA_EBM−DM up
4	0.17	2 / 22	BCHETNIA_EBM up
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	4e−05	27 / 344	Up
2	4e−04	75 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	9e−04	47 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
4	6e−03	20 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	5e−02	8 / 119	GIEZELT_GBM_WT_up_VS_mut
6	5e−02	5 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	5e−02	2 / 11	KIM amplified & overexpressed in LTS
8	8e−02	2 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
9	8e−02	4 / 49	Noushmehr_Pron_GCIMP_hypermeth_DN
10	8e−02	3 / 31	KIM prognostic signature LTS vs. STS
11	9e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
12	9e−02	4 / 52	OL vs. OPC
13	1e−01	2 / 16	VERHAAK_MES subtype
14	1e−01	4 / 56	mature astrocytes
15	1e−01	4 / 58	OL vs. MOG− OL
16	1e−01	19 / 436	Down_b
17	1e−01	4 / 61	in vivo astrocytes vs. cultured astroglia
18	2e−01	4 / 63	Stuehler_Proteins_up_in_STS
19	2e−01	5 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
20	2e−01	14 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−22	78 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
2	4e−20	60 / 453	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
3	2e−13	52 / 495	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	3e−13	55 / 549	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
5	5e−13	68 / 786	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
6	2e−11	76 / 1005	NUYTTEN_EZH2_TARGETS_UP
7	3e−11	65 / 804	CUI_TCF21_TARGETS_2_DN
8	2e−10	32 / 261	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
9	2e−10	49 / 541	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
10	4e−10	54 / 641	FEVR_CTNNB1_TARGETS_UP
11	4e−10	22 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
12	1e−09	38 / 377	STEIN_ESRRA_TARGETS_UP
13	3e−09	44 / 490	ENK_UV_RESPONSE_EPIDERMIS_DN
14	6e−09	29 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
15	2e−08	41 / 468	ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
16	6e−08	54 / 740	FORTSCHEGGER_PHF8_TARGETS_DN
17	1e−07	34 / 370	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
18	2e−07	55 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
19	2e−07	41 / 513	STEIN_ESRRA_TARGETS
20	3e−07	92 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−06	21 / 193	HALLMARK_HEME_METABOLISM
2	8e−06	13 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	4e−04	17 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	4e−04	17 / 198	HALLMARK_GLYCOLYSIS
5	5e−04	16 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	1e−03	16 / 198	HALLMARK_HYPOXIA
7	2e−03	15 / 192	HALLMARK_COMPLEMENT
8	2e−03	10 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	3e−03	15 / 199	HALLMARK_ADIPOGENESIS
10	6e−03	12 / 154	HALLMARK_FATTY_ACID_METABOLISM
11	7e−03	6 / 52	HALLMARK_TGF_BETA_SIGNALING
12	1e−02	8 / 94	HALLMARK_PROTEIN_SECRETION
13	2e−02	8 / 98	HALLMARK_ANDROGEN_RESPONSE
14	3e−02	12 / 194	HALLMARK_INFLAMMATORY_RESPONSE
15	3e−02	8 / 112	HALLMARK_BILE_ACID_METABOLISM
16	5e−02	7 / 102	HALLMARK_PEROXISOME
17	6e−02	11 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
18	6e−02	11 / 193	HALLMARK_XENOBIOTIC_METABOLISM
19	6e−02	6 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
20	7e−02	11 / 197	HALLMARK_IL2_STAT5_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	3 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.21	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.26	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
4	0.26	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
5	0.95	1 / 91	DUMEAUX_Smoking enriched genes
6	1.00	0 / 11	DUMEAUX_Smoking 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 / 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	2e−12	365 / 8358	HOPP_Active_promoter
2	1e−10	328 / 7491	HOPP_Txn_elongation
3	2e−10	349 / 8147	HOPP_Weak_promoter
4	1e−07	317 / 7592	HOPP_Strong_enhancer
5	6e−07	271 / 6389	HOPP_Weak_txn
6	9e−06	278 / 6784	HOPP_Weak_enhancer
7	1e−04	65 / 1215	SPANG_BCR DN
8	4e−04	7 / 42	CARO_OxPhos_in_DLBCL_UP
9	5e−04	148 / 3457	HOPP_Heterochrom
10	8e−04	124 / 2838	HOPP_Poised_promoter
11	8e−04	9 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
12	8e−04	5 / 23	SPANG_BAFF 9hrs UP
13	8e−04	9 / 75	WIRTH_lymphoma937_spot IM
14	3e−03	220 / 5643	HOPP_Txn_transition
15	5e−03	62 / 1333	SPANG_BCR UP
16	6e−03	111 / 2658	HOPP_Repetitive
17	8e−03	10 / 123	SPANG_LPS 6hrs UP
18	1e−02	18 / 302	SPANG_IL21 UP
19	2e−02	19 / 332	SPANG_CD40 6hrs UP
20	2e−02	2 / 7	CARO_OxPhos_vs_BCR_UP

MF

Rank	p−value	#in/all	Geneset
1	4e−04	398 / 10693	protein binding
2	8e−04	5 / 23	galactosyltransferase activity
3	1e−03	9 / 79	phosphatidylinositol binding
4	2e−03	24 / 371	GTP binding
5	2e−03	8 / 67	flavin adenine dinucleotide binding
6	2e−03	7 / 53	GDP binding
7	2e−03	18 / 250	GTPase activity
8	2e−03	5 / 28	cadherin binding
9	2e−03	5 / 28	epidermal growth factor receptor binding
10	4e−03	3 / 10	1−acylglycerol−3−phosphate O−acyltransferase activity
11	5e−03	10 / 113	actin filament binding
12	6e−03	4 / 22	transferase activity, transferring acyl groups other than amino−acyl groups
13	6e−03	5 / 35	carboxylic ester hydrolase activity
14	6e−03	3 / 12	ATPase activity, coupled
15	1e−02	8 / 89	electron carrier activity
16	1e−02	9 / 108	guanyl−nucleotide exchange factor activity
17	1e−02	21 / 362	protein kinase binding
18	1e−02	6 / 57	ubiquitin binding
19	1e−02	13 / 191	magnesium ion binding
20	1e−02	3 / 15	cation transmembrane transporter activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−06	26 / 270	hsa−miR−92b
2	2e−06	26 / 277	hsa−miR−363
3	6e−06	34 / 444	hsa−let−7b
4	7e−06	34 / 446	hsa−miR−19b
5	1e−05	26 / 304	hsa−miR−25
6	2e−05	17 / 156	hsa−miR−142−3p
7	2e−05	14 / 112	hsa−miR−1271
8	2e−05	24 / 279	hsa−miR−92a
9	2e−05	33 / 452	hsa−miR−19a
10	2e−05	26 / 317	hsa−miR−548c−5p
11	4e−05	18 / 181	hsa−miR−199b−3p
12	6e−05	26 / 333	hsa−miR−32
13	6e−05	32 / 453	hsa−miR−424
14	6e−05	13 / 108	hsa−miR−33b
15	1e−04	35 / 531	hsa−miR−15a
16	1e−04	33 / 493	hsa−miR−15b
17	1e−04	25 / 332	hsa−miR−548a−5p
18	1e−04	18 / 201	hsa−miR−944
19	2e−04	16 / 168	hsa−miR−96
20	2e−04	23 / 297	hsa−miR−548j

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	2 / 12	BENTINK_ras.1
2	0.08	2 / 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	88 / 1867	HEBENSTREIT_high expression TF
2	3e−02	193 / 5135	ICGC_Ebfsc137065_targets
3	4e−02	206 / 5552	ICGC_Pol24_targets
4	8e−02	228 / 6324	ICGC_Yy1_targets
5	8e−02	217 / 6005	ICGC_Mta3_targets
6	9e−02	181 / 4969	ICGC_Atf2_targets
7	1e−01	129 / 3511	ICGC_Rad21_targets
8	1e−01	197 / 5512	ICGC_Nficsc81335_targets
9	1e−01	254 / 7202	ICGC_Runx3_targets
10	1e−01	242 / 6862	ICGC_Elf1_targets
11	2e−01	100 / 2719	ICGC_Pbx3_targets
12	2e−01	1 / 5	MYC_TF and cofactors
13	2e−01	184 / 5173	ICGC_Taf1_targets
14	2e−01	120 / 3305	ICGC_BatfPcr1_targets
15	2e−01	187 / 5308	ICGC_Tcf12_targets
16	2e−01	221 / 6322	ICGC_Pol2_targets
17	2e−01	194 / 5526	ICGC_Pmlsc71910_targets
18	2e−01	78 / 2133	ICGC_Cebpbsc150_targets
19	2e−01	219 / 6313	ICGC_Pou2_targets
20	2e−01	160 / 4566	ICGC_Egr1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	5 / 64	VAQUERIZAS_Lung
2	0.12	2 / 18	VAQUERIZAS_Pancreas
3	0.13	2 / 19	VAQUERIZAS_Heart
4	0.14	2 / 20	VAQUERIZAS_Bone marrow
5	0.16	3 / 42	VAQUERIZAS_Thyroid
6	0.20	3 / 46	VAQUERIZAS_Whole brain
7	0.35	2 / 37	VAQUERIZAS_Prostate
8	0.36	1 / 13	VAQUERIZAS_Skin
9	0.42	1 / 16	VAQUERIZAS_Fetal liver
10	0.45	2 / 45	VAQUERIZAS_Placenta
11	0.54	1 / 23	VAQUERIZAS_Pituitary
12	0.57	1 / 25	VAQUERIZAS_Spinal cord
13	0.64	1 / 30	VAQUERIZAS_Smooth muscle
14	0.66	2 / 67	VAQUERIZAS_Whole blood
15	0.67	1 / 33	VAQUERIZAS_Liver
16	0.75	1 / 41	VAQUERIZAS_Fetal brain
17	0.76	1 / 42	VAQUERIZAS_Thymus
18	0.81	1 / 49	VAQUERIZAS_Uterus
19	0.97	2 / 155	VAQUERIZAS_General
20	1.00	0 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	2e−04	21 / 259	PALMER_Granulocytes signature up
2	8e−02	2 / 14	WIRTH_Thyroid gland
3	9e−02	2 / 15	WIRTH_Cerebellum
4	3e−01	3 / 54	WIRTH_Pancreas
5	4e−01	1 / 13	PALMER_CD8+ T−Cell signature up
6	4e−01	1 / 14	WIRTH_Thymus
7	4e−01	8 / 208	PALMER_B−Cell signature up
8	5e−01	5 / 137	WIRTH_Mucosa
9	5e−01	3 / 82	WIRTH_Homeostasis
10	9e−01	3 / 141	WIRTH_Muscle
11	9e−01	9 / 427	WIRTH_Immune system
12	1e+00	1 / 115	WIRTH_Liver
13	1e+00	1 / 140	PALMER_T−Cell signature up
14	1e+00	6 / 476	WIRTH_Nervous System
15	1e+00	0 / 6	WIRTH_Pituitary gland
16	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
17	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
18	1e+00	0 / 14	WIRTH_B−cells
19	1e+00	0 / 12	WIRTH_Tonsil
20	1e+00	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	46 / 1343	LU_BPDE 1n DN
2	0.9	163 / 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	

K−Means Clusters

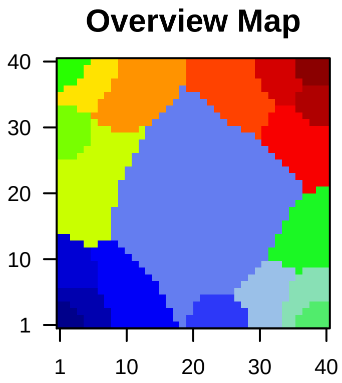
Spot Summary: F

metagenes = 17
genes = 299

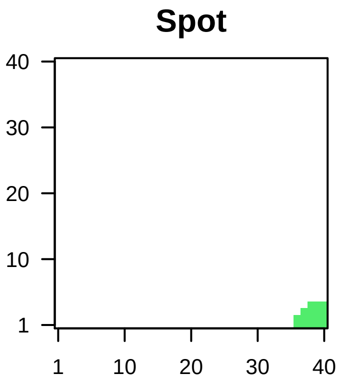
<r> metagenes = 0.98
<r> genes = 0.66
beta: r2= 0.82 / log p= −8.53

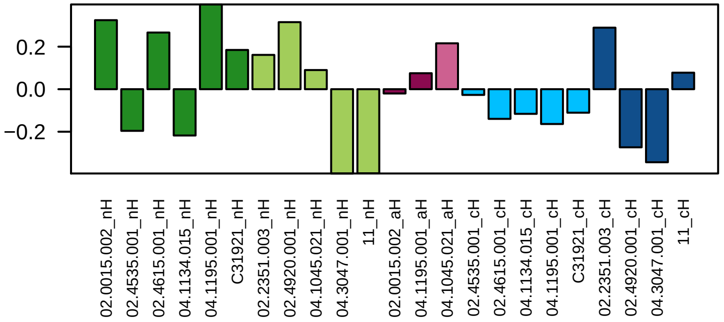
samples with spot = 8 (34.8 %)
MLH1_normHNPCC : 4 (66.7 %)
other_normHNPCC : 2 (40 %)
other_adenomaHNPCC : 1 (100 %)
other_cancerHNPCC : 1 (25 %)

Overview Map



Spot





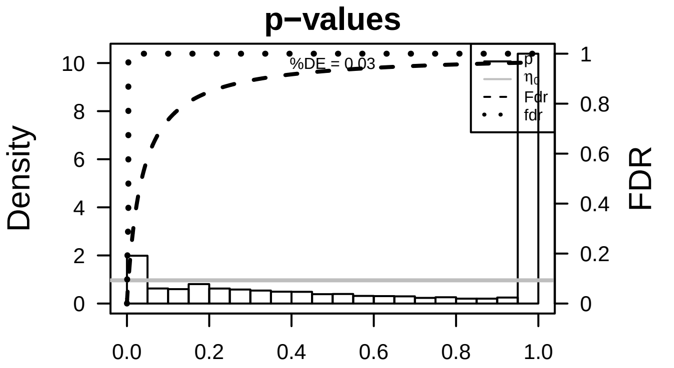
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	1.55	−0.86	0.89	PHGR1	proline/histidine/glycine−rich 1 [Source:HGNC Symbol;Acc:H
2	ENSG000001	1.42	−0.99	0.89	GUCA2A	guanylate cyclase activator 2A (guanylin) [Source:HGNC Syn
3	ENSG000001	1.33	−0.38	0.49	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	0.67	ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;A
6	ENSG000000	1.26	−0.59	0.74	CLCA4	chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
7	ENSG000000	1.24	−0.81	0.86	SLC26A3	solute carrier family 26 (anion exchanger), member 3 [Source
8	ENSG000000	1.24	−0.99	0.81	CEACAM7	carcinoembryonic antigen−related cell adhesion molecule 7 [S
9	ENSG000001	1.24	−0.49	0.77	ZG16	zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGN
10	ENSG000000	1.22	−0.52	0.83	GUCA2B	guanylate cyclase activator 2B (uroguanylin) [Source:HGNC S
11	ENSG000001	1.21	−0.51	0.63	TFF1	trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	−0.44	0.72	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	0.91	FABP1	fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:H
15	ENSG000001	1.12	−0.37	0.76	AKR1B10	aldo−keto reductase family 1, member B10 (aldose reductase
16	ENSG000001	1.1	−0.7	0.55	PI3	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
17	ENSG000001	1.06	−1.31	0.65	PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	ENSG000001	1.02	−1.15	0.69	CEACAM5	carcinoembryonic antigen−related cell adhesion molecule 5 [S
19	ENSG000001	1	−0.96	0.92	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	9e−83	60 / 104	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	3e−73	92 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
3	9e−40	37 / 110	Colon	Marisa_CRC−cluster−h
4	3e−29	118 / 2638	CC	extracellular exosome
5	3e−28	58 / 643	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
6	1e−25	54 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
7	9e−23	35 / 262	GSEA	SABATES_COLORECTAL_ADENOMA_DN
8	1e−22	82 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
9	1e−22	44 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
10	1e−21	41 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
11	4e−21	115 / 3122	Colon	TxEnhG1_Colon
12	6e−21	41 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
13	8e−21	31 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
14	1e−20	26 / 144	Lymph	WIRTH_lymphoma937_spot G
15	2e−19	25 / 142	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil
16	2e−19	31 / 248	GSEA	JAEGER_METASTASIS_DN
17	2e−18	23 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
18	1e−16	106 / 3112	Colon	EnhA_Colon
19	1e−16	46 / 711	GSEA	LEE_BMP2_TARGETS_UP
20	3e−16	104 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
21	5e−16	15 / 49	Colon	Marisa_CRC−cluster−f
22	1e−15	244 / 11791	Colon	Enh_Colon
23	2e−15	27 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
24	4e−15	49 / 877	Colon	TxEnhG2_Colon
25	1e−14	14 / 48	GSEA	KEGG_DRUG_METABOLISM_OTHER_ENZYMES
26	1e−14	154 / 5889	Colon	EnhWk1_Colon
27	3e−14	27 / 280	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
28	8e−14	41 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
29	1e−13	41 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
30	1e−13	32 / 424	GSEA	DELYS_THYROID_CANCER_UP
31	2e−13	19 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
32	3e−13	33 / 465	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
33	4e−13	25 / 261	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
34	5e−13	213 / 9930	Colon	Tx_Colon
35	6e−13	13 / 51	GSEA	KEGG_STEROID_HORMONE_BIOSYNTHESIS
36	6e−13	10 / 23	BP	flavonoid biosynthetic process
37	6e−13	10 / 23	BP	flavonoid glucuronidation
38	9e−13	17 / 109	GSEA	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
39	1e−12	37 / 608	Disea	GUDJ_psoriasis up
40	1e−12	10 / 24	GSEA	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.7	2 / 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	6e−13	10 / 23	flavonoid biosynthetic process
2	6e−13	10 / 23	flavonoid glucuronidation
3	4e−12	9 / 19	cellular glucuronidation
4	3e−09	45 / 1118	metabolic process
5	1e−08	11 / 71	cellular response to hormone stimulus
6	8e−07	13 / 154	xenobiotic metabolic process
7	2e−06	6 / 25	establishment of protein localization to plasma membrane
8	5e−06	6 / 29	one−carbon metabolic process
9	6e−06	5 / 18	3'−phosphoadenosine 5'−phosphosulfate metabolic process
10	1e−05	6 / 33	bicarbonate transport
11	2e−05	4 / 11	intestinal absorption
12	2e−05	5 / 22	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion
13	2e−05	4 / 12	microvillus assembly
14	3e−05	8 / 79	epithelial cell differentiation
15	3e−05	42 / 1418	small molecule metabolic process
16	5e−05	7 / 62	steroid metabolic process
17	9e−05	4 / 16	cellular sodium ion homeostasis
18	9e−05	4 / 16	retinoic acid metabolic process
19	2e−04	7 / 76	cell junction assembly
20	4e−04	5 / 40	excretion

Brain

Rank	p−value	#in/all	Geneset
1	1e−09	60 / 1713	Mid_Frontal_Lobe_ReprPCWk
2	3e−07	47 / 1394	Mid_Frontal_Lobe_Quies
3	2e−05	73 / 2956	Fetal_TssA
4	3e−05	52 / 1890	Overlap_fetal_midbrain_TssF
5	9e−05	64 / 2603	Fetal_TxTrans
6	4e−04	40 / 1478	Overlap_fetal_midbrain_TxTrans
7	8e−04	59 / 2549	Fetal_TssF
8	1e−03	50 / 2084	Mid_Frontal_Lobe_K9K27me3
9	2e−03	83 / 3977	Mid_Frontal_Lobe_ReprPC
10	2e−02	21 / 840	Mid_Frontal_Lobe_TssF
11	6e−02	28 / 1327	Mid_Frontal_Lobe_TssP
12	7e−02	7 / 232	Fetal_ReprPC
13	7e−02	18 / 805	Mid_Frontal_Lobe_EnhG
14	1e−01	22 / 1108	Overlap_fetal_midbrain_TssA
15	1e−01	19 / 940	Mid_Frontal_Lobe_Enh
16	2e−01	9 / 408	Mid_Frontal_Lobe_TxTrans
17	2e−01	7 / 317	Mid_Frontal_Lobe_Tx
18	2e−01	3 / 106	Overlap_fetal_midbrain_Tx
19	2e−01	22 / 1210	Fetal_TssP
20	4e−01	5 / 268	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	3 / 16	LIU_PROSTATE_CANCER_DN
2	0.025	2 / 16	WANG_ER_UP
3	0.044	3 / 51	PanCan_TGF−B_geneset_nanostring
4	0.051	0 / 14	LIU_PROSTATE_CANCER_UP
5	0.060	5 / 136	PanCan_CC+Apop_geneset_nanostring
6	0.076	6 / 191	SPANG_LPS−index2
7	0.130	8 / 324	SPANG_BCL6−index2
8	0.131	1 / 9	WANG_ER_DN
9	0.132	2 / 41	ZHANG_MM up
10	0.189	3 / 97	PanCan_TXmisReg_geneset_nanostring
11	0.192	5 / 198	PanCan_PI3K_geneset_nanostring
12	0.196	1 / 14	GENTLES_modul12
13	0.220	1 / 16	GENTLES_modul16
14	0.220	1 / 16	GENTLES_modul18
15	0.288	0 / 16	LIU_COMMON_CANCER_GENES
16	0.300	2 / 71	SHAUGHNESSY_MM high risk
17	0.541	1 / 50	PanCan_DNARepair_geneset_nanostring
18	0.568	2 / 123	PanCan_Driver_Gene_geneset_nanostring
19	0.639	2 / 140	PanCan_RAS_geneset_nanostring
20	0.738	1 / 86	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−29	118 / 2638	extracellular exosome
2	1e−10	12 / 60	brush border
3	3e−08	16 / 185	basolateral plasma membrane
4	2e−07	18 / 268	apical plasma membrane
5	1e−06	11 / 110	bicellular tight junction
6	2e−06	87 / 3507	plasma membrane
7	8e−06	7 / 48	lateral plasma membrane
8	2e−05	93 / 4052	integral component of membrane
9	8e−05	8 / 91	apical part of cell
10	1e−04	6 / 51	cell periphery
11	1e−04	35 / 1176	extracellular space
12	4e−04	3 / 10	plasma membrane raft
13	5e−04	5 / 43	intercalated disc
14	5e−04	3 / 11	sodium:potassium−exchanging ATPase complex
15	9e−04	5 / 49	microvillus
16	9e−04	5 / 49	myosin complex
17	1e−03	19 / 558	intracellular membrane−bounded organelle
18	2e−03	7 / 114	vesicle
19	3e−03	6 / 91	sarcolemma
20	4e−03	65 / 3059	membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.009	17 / 582	Chr 15
2	0.012	22 / 847	Chr 16
3	0.066	38 / 1920	Chr 1
4	0.139	24 / 1228	Chr 2
5	0.174	5 / 191	Chr 21
6	0.177	19 / 976	Chr 6
7	0.244	6 / 272	Chr 18
8	0.287	10 / 522	Chr 20
9	0.314	19 / 1083	Chr 17
10	0.531	22 / 1425	Chr 19
11	0.569	13 / 859	Chr 7
12	0.574	13 / 862	Chr 5
13	0.609	15 / 1017	Chr 12
14	0.639	17 / 1172	Chr 11
15	0.717	10 / 745	Chr 9
16	0.778	9 / 715	Chr 10
17	0.806	5 / 436	Chr 22
18	0.884	8 / 735	Chr 4
19	0.933	11 / 1043	Chr 3
20	0.939	6 / 651	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−83	60 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	3e−73	92 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
3	9e−40	37 / 110	Marisa_CRC−cluster−h
4	3e−28	58 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	1e−25	54 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	4e−21	115 / 3122	TxEnhG1_Colon
7	1e−16	106 / 3112	EnhA_Colon
8	5e−16	15 / 49	Marisa_CRC−cluster−f
9	1e−15	244 / 11791	Enh_Colon
10	4e−15	49 / 877	TxEnhG2_Colon
11	1e−14	154 / 5889	EnhWk1_Colon
12	1e−13	41 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	5e−13	213 / 9930	Tx_Colon
14	4e−09	46 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	3e−08	228 / 11968	TssWk_Colon
16	8e−07	186 / 9390	TxWk_Colon
17	1e−06	201 / 10475	TssA_Colon
18	2e−06	143 / 6761	TssD2_Colon
19	2e−04	177 / 9470	Quies3_Colon
20	2e−04	3 / 8	Marisa_CRC−C6

Disease

Rank	p−value	#in/all	Geneset
1	1e−12	37 / 608	GUDJ_psoriasis up
2	1e−03	15 / 399	GUDJ_psoriasis down
3	4e−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	3e−16	104 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e−04	19 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
3	2e−03	3 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
4	2e−03	23 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
5	8e−03	24 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
6	5e−02	3 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	5e−02	6 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	6e−02	12 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
9	7e−02	8 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
10	8e−02	3 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
11	9e−02	1 / 6	Martinez_Glio_hypometh
12	9e−02	3 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
13	1e−01	2 / 36	Shaw_down_in_1p19q
14	1e−01	2 / 36	Colman_survival_associated
15	1e−01	5 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
16	1e−01	1 / 9	oligodendrocytes_glio
17	1e−01	1 / 9	Colman_survival_robust
18	2e−01	3 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
19	2e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
20	2e−01	3 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−23	35 / 262	SABATES_COLORECTAL_ADENOMA_DN
2	1e−22	82 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
3	1e−22	44 / 455	ONDER_CDH1_TARGETS_2_DN
4	1e−21	41 / 412	LIM_MAMMARY_STEM_CELL_DN
5	6e−21	41 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
6	8e−21	31 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
7	2e−19	31 / 248	JAEGER_METASTASIS_DN
8	2e−18	23 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
9	1e−16	46 / 711	LEE_BMP2_TARGETS_UP
10	2e−15	27 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
11	1e−14	14 / 48	KEGG_DRUG_METABOLISM_OTHER_ENZYMES
12	3e−14	27 / 280	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
13	8e−14	41 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
14	1e−13	32 / 424	DELYS_THYROID_CANCER_UP
15	2e−13	19 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
16	3e−13	33 / 465	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
17	4e−13	25 / 261	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
18	6e−13	13 / 51	KEGG_STEROID_HORMONE_BIOSYNTHESIS
19	9e−13	17 / 109	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
20	1e−12	10 / 24	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM

HM

Rank	p−value	#in/all	Geneset
1	1e−09	18 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
2	6e−08	16 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	7e−08	16 / 196	HALLMARK_P53_PATHWAY
4	8e−06	13 / 189	HALLMARK_KRAS_SIGNALING_UP
5	3e−05	11 / 154	HALLMARK_FATTY_ACID_METABOLISM
6	5e−05	12 / 193	HALLMARK_XENOBIOTIC_METABOLISM
7	8e−04	9 / 157	HALLMARK_APOPTOSIS
8	1e−03	7 / 102	HALLMARK_PEROXISOME
9	2e−03	9 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	3e−03	9 / 190	HALLMARK_APICAL_JUNCTION
11	3e−03	8 / 155	HALLMARK_UV_RESPONSE_UP
12	3e−03	9 / 192	HALLMARK_COMPLEMENT
13	4e−03	9 / 197	HALLMARK_IL2_STAT5_SIGNALING
14	4e−03	9 / 199	HALLMARK_ADIPOGENESIS
15	4e−03	6 / 98	HALLMARK_ANDROGEN_RESPONSE
16	2e−02	4 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	3e−02	7 / 198	HALLMARK_HYPOXIA
18	3e−02	7 / 198	HALLMARK_GLYCOLYSIS
19	8e−02	6 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
20	8e−02	6 / 194	HALLMARK_INFLAMMATORY_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.005	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.220	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.232	1 / 17	DUMEAUX_High bmi enriched genes
4	0.411	2 / 91	DUMEAUX_Smoking enriched genes
5	1.000	0 / 11	DUMEAUX_Smoking literature genes up
6	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.000	0 / 9	DUMEAUX_Hormon therapy in non 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	1e−20	26 / 144	WIRTH_lymphoma937_spot G
2	2e−19	25 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
3	4e−05	109 / 5039	HOPP_Repressed
4	4e−04	14 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
5	4e−04	14 / 315	WIRTH_lymphoma937_spot E
6	2e−03	7 / 115	ROSOLOWSKI_green total
7	3e−03	2 / 6	DAVE_MHCCII BL DN
8	5e−03	3 / 23	SPANG_BAFF 9hrs UP
9	6e−03	7 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
10	2e−02	3 / 40	ROSOLOWSKI_blue DOWN
11	3e−02	4 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
12	3e−02	4 / 75	WIRTH_lymphoma937_spot IM
13	3e−02	8 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
14	4e−02	4 / 83	ROSOLOWSKI_green UP
15	4e−02	55 / 2838	HOPP_Poised_promoter
16	4e−02	3 / 50	Subero_B−ALL_hyper_meth
17	6e−02	3 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
18	1e−01	3 / 75	Subero_FL_hyper_meth
19	1e−01	61 / 3457	HOPP_Heterochrom
20	2e−01	3 / 87	Aukema_BCL2 DN_BCL6 UP

MF

Rank	p−value	#in/all	Geneset
1	2e−11	10 / 30	glucuronosyltransferase activity
2	2e−10	10 / 37	transferase activity, transferring hexosyl groups
3	1e−06	5 / 13	carbonate dehydratase activity
4	2e−05	13 / 204	structural molecule activity
5	7e−05	4 / 15	retinoic acid binding
6	2e−04	24 / 693	protein homodimerization activity
7	4e−04	3 / 10	sodium:potassium−exchanging ATPase activity
8	5e−04	13 / 287	oxidoreductase activity
9	1e−03	3 / 14	quinone binding
10	2e−03	3 / 16	fatty acid binding
11	2e−03	21 / 672	calcium ion binding
12	2e−03	7 / 113	actin filament binding
13	2e−03	3 / 17	sodium channel activity
14	3e−03	5 / 65	motor activity
15	4e−03	6 / 96	structural constituent of cytoskeleton
16	4e−03	5 / 69	beta−catenin binding
17	7e−03	3 / 25	steroid binding
18	8e−03	5 / 81	drug binding
19	1e−02	2 / 10	potassium ion binding
20	1e−02	9 / 232	hydrolase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 38	hsa−miR−1224−5p
2	0.03	6 / 147	hsa−miR−138
3	0.05	3 / 53	hsa−miR−337−3p
4	0.06	5 / 136	hsa−miR−485−5p
5	0.07	2 / 29	hsa−miR−591
6	0.08	3 / 67	hsa−miR−643
7	0.11	2 / 36	hsa−miR−1287
8	0.11	5 / 164	hsa−miR−298
9	0.13	2 / 40	hsa−miR−885−5p
10	0.13	2 / 41	hsa−miR−601
11	0.13	5 / 174	hsa−miR−7
12	0.14	3 / 84	hsa−miR−365
13	0.15	2 / 44	hsa−miR−483−5p
14	0.15	3 / 88	hsa−miR−134
15	0.16	5 / 184	hsa−miR−548e
16	0.16	5 / 184	hsa−miR−374a
17	0.16	1 / 11	hsa−miR−487b
18	0.16	3 / 90	hsa−miR−587
19	0.17	3 / 92	hsa−miR−362−5p
20	0.18	3 / 94	hsa−miR−216b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	BENTINK_ras.4
2	0.2	1 / 14	BENTINK_src.10
3	0.2	1 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 14	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 14	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 15	BENTINK_ras.6
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−04	46 / 1798	HEBENSTREIT_low expression TF
2	3e−02	1 / 2	MYC_Cell cycle DOWN
3	1e−01	1 / 9	MYC_Targets DOWN
4	2e−01	60 / 3511	ICGC_Rad21_targets
5	3e−01	1 / 20	MYC_Metabolism UP
6	4e−01	81 / 5135	ICGC_Ebfsc137065_targets
7	6e−01	1 / 66	MYC_Targets UP
8	7e−01	94 / 6406	ICGC_Pax5_targets
9	8e−01	39 / 2827	ICGC_Bcl3_targets
10	8e−01	20 / 1523	ICGC_P300_targets
11	9e−01	64 / 4714	ICGC_Pu1_targets
12	9e−01	41 / 3177	ICGC_Irf4_targets
13	9e−01	59 / 4436	ICGC_Zeb1_targets
14	9e−01	75 / 5552	ICGC_Pol24_targets
15	9e−01	42 / 3305	ICGC_BatfPcr1_targets
16	9e−01	17 / 1506	ICGC_Usf1_targets
17	9e−01	7 / 731	ICGC_SrfPcr2_targets
18	9e−01	29 / 2401	ICGC_Bcl11_targets
19	9e−01	7 / 745	ICGC_NrsfPcr2_targets
20	1e+00	7 / 766	ICGC_Atf3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.002	3 / 18	VAQUERIZAS_Pancreas
2	0.006	3 / 24	VAQUERIZAS_Trachea
3	0.017	2 / 13	VAQUERIZAS_Skin
4	0.076	3 / 64	VAQUERIZAS_Lung
5	0.082	2 / 31	VAQUERIZAS_Fetal lung
6	0.111	2 / 37	VAQUERIZAS_Prostate
7	0.117	1 / 8	VAQUERIZAS_Tongue
8	0.153	2 / 45	VAQUERIZAS_Placenta
9	0.170	1 / 12	VAQUERIZAS_Kidney
10	0.256	1 / 19	VAQUERIZAS_Heart
11	0.290	1 / 22	VAQUERIZAS_Tonsil
12	0.322	1 / 25	VAQUERIZAS_Adrenal cortex
13	0.402	1 / 33	VAQUERIZAS_Liver
14	0.480	1 / 42	VAQUERIZAS_Thyroid
15	1.000	0 / 41	VAQUERIZAS_Fetal brain
16	1.000	0 / 30	VAQUERIZAS_Smooth muscle
17	1.000	0 / 49	VAQUERIZAS_Uterus
18	1.000	0 / 155	VAQUERIZAS_General
19	1.000	0 / 25	VAQUERIZAS_Spinal cord
20	1.000	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	4e−11	17 / 137	WIRTH_Mucosa
2	6e−07	5 / 12	WIRTH_Tonsil
3	2e−04	13 / 259	PALMER_Granulocytes signature up
4	2e−03	6 / 82	WIRTH_Homeostasis
5	2e−02	2 / 14	WIRTH_Thalamus
6	2e−02	2 / 15	WIRTH_Telencephalon
7	2e−01	1 / 13	WIRTH_Prim. lymphoid organs
8	2e−01	1 / 14	WIRTH_Bone marrow
9	2e−01	1 / 15	WIRTH_Cerebellum
10	4e−01	4 / 208	PALMER_B−Cell signature up
11	6e−01	1 / 54	WIRTH_Pancreas
12	6e−01	2 / 140	PALMER_T−Cell signature up
13	8e−01	5 / 427	WIRTH_Immune system
14	8e−01	1 / 115	WIRTH_Liver
15	1e+00	1 / 476	WIRTH_Nervous System
16	1e+00	0 / 6	WIRTH_Pituitary gland
17	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
18	1e+00	0 / 14	WIRTH_B−cells
19	1e+00	0 / 14	WIRTH_Thymus
20	1e+00	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.8	76 / 5285	LU_BPDE 0.005 DN
2	1.0	12 / 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	

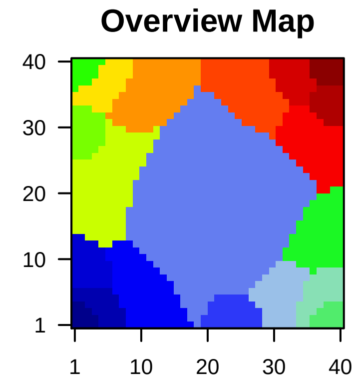
K−Means Clusters

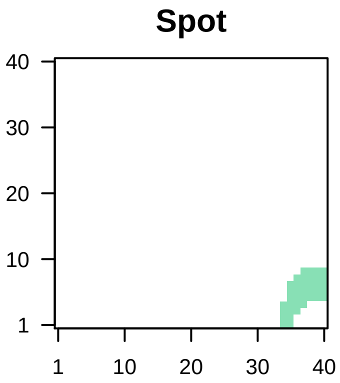
Spot Summary: G

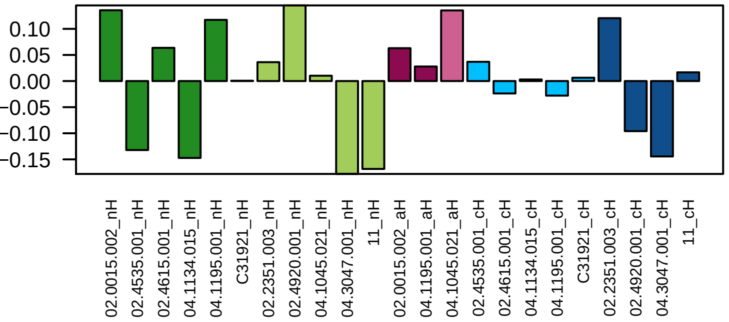
metagenes = 38
genes = 526

<r> metagenes = 0.9
<r> genes = 0.52
beta: r2= 0.23 / log p= −1.69

samples with spot = 5 (21.7 %)
MLH1_normHNPCC : 2 (33.3 %)
other_normHNPCC : 1 (20 %)
other_adenomaHNPCC : 1 (100 %)
other_cancerHNPCC : 1 (25 %)


Overview Map


Spot

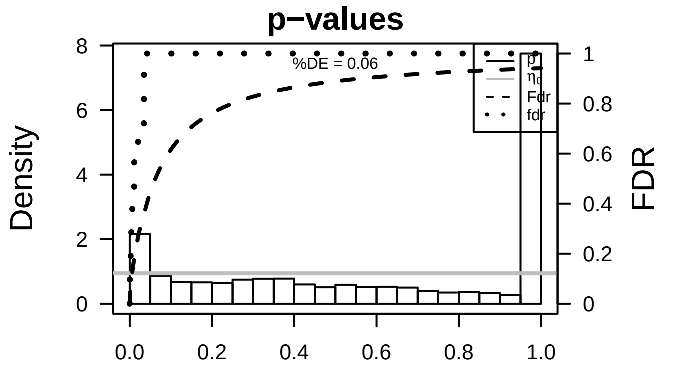


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.89	−0.51	0.64	SLPI	secretory leukocyte peptidase inhibitor [Source:HGNC Symbo
2	ENSG000000	0.88	−0.19	0.3	SLC9A3	solute carrier family 9, subfamily A (NHE3, cation proton antip
3	ENSG000002	0.86	−0.15	0.65	CAPN8	calpain 8 [Source:HGNC Symbol;Acc:HGNC:1485]
4	ENSG000002	0.83	−0.45	0.77		
5	ENSG000001	0.81	−0.17	0.57	B3GNT7	UDP−GlcNAc:betaGal beta−1,3−N−acetylglucosaminyltransfe
6	ENSG000001	0.8	−0.4	0.52		mucin 2, oligomeric mucus/gel−forming [Source:HGNC Symb
7	ENSG000001	0.79	−0.41	0.53	NQO1	NAD(P)H dehydrogenase, quinone 1 [Source:HGNC Symbol;
8	ENSG000001	0.73	−0.2	0.55	CDHR1	cadherin−related family member 1 [Source:HGNC Symbol;Ac
9	ENSG000001	0.71	−0.35	0.75	DGAT1	diacylglycerol O−acyltransferase 1 [Source:HGNC Symbol;Ac
10	ENSG000001	0.7	−0.27	0.56	AK1	adenylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:361]
11	ENSG000002	0.7	−0.25	0.63	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HG
12	ENSG000001	0.68	−0.4	0.64	DHCR24	24−dehydrocholesterol reductase [Source:HGNC Symbol;Acc
13	ENSG000001	0.66	−0.79	0.26	CKB	creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:199
14	ENSG000001	0.65	−0.16	0.5	HOXB5	homeobox B5 [Source:HGNC Symbol;Acc:HGNC:5116]
15	ENSG000001	0.63	−0.26	0.62	ROMO1	reactive oxygen species modulator 1 [Source:HGNC Symbol;
16	ENSG000001	0.62	−0.15	0.45	REP15	RAB15 effector protein [Source:HGNC Symbol;Acc:HGNC:33
17	ENSG000002	0.61	−0.17	0.45	HLA−G	major histocompatibility complex, class I, G [Source:HGNC S
18	ENSG000001	0.6	−0.4	0.64	BEST1	bestrophin 1 [Source:HGNC Symbol;Acc:HGNC:12703]
19	ENSG000001	0.57	−0.14	0.63	CASP5	caspase 5, apoptosis−related cysteine peptidase [Source:HG
20	ENSG000001	0.56	−0.11	0.57	INSL5	insulin−like 5 [Source:HGNC Symbol;Acc:HGNC:6088]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−48	68 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
2	3e−38	207 / 3122	Colon	TxEnhG1_Colon
3	1e−32	196 / 3112	Colon	EnhA_Colon
4	4e−32	354 / 8123	Colon	TssF_Colon
5	2e−29	48 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
6	1e−26	389 / 9930	Colon	Tx_Colon
7	1e−26	277 / 5889	Colon	EnhWk1_Colon
8	1e−26	61 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
9	2e−24	428 / 11791	Colon	Enh_Colon
10	7e−22	54 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
11	1e−21	80 / 877	Colon	TxEnhG2_Colon
12	4e−21	154 / 2638	CC	extracellular exosome
13	6e−20	67 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
14	4e−19	384 / 10475	Colon	TssA_Colon
15	4e−19	53 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
16	4e−19	56 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
17	6e−19	109 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
18	6e−18	280 / 6761	Colon	TssD2_Colon
19	2e−17	61 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
20	7e−17	52 / 495	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_UP
21	2e−16	189 / 3977	Brain	Mid_Frontal_Lobe_ReprPC
22	5e−15	92 / 1418	BP	small molecule metabolic process
23	9e−15	78 / 1103	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
24	5e−13	51 / 593	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
25	6e−13	22 / 115	GSEA	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
26	3e−12	23 / 137	Tissu	WIRTH_Mucosa
27	4e−12	22 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
28	4e−12	334 / 9390	Colon	TxWk_Colon
29	8e−11	21 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
30	4e−10	39 / 459	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
31	6e−10	30 / 292	GSEA	LI_INDUCED_T_TO_NATURAL_KILLER_UP
32	7e−10	39 / 467	GSEA	SWEET_LUNG_CANCER_KRAS_UP
33	8e−10	28 / 261	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
34	8e−10	27 / 244	GSEA	RICKMAN_METASTASIS_DN
35	2e−09	20 / 142	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil
36	3e−09	20 / 144	Lymph	WIRTH_lymphoma937_spot G
37	5e−09	22 / 181	GSEA	WU_CELL_MIGRATION
38	8e−09	17 / 110	Colon	Marisa_CRC−cluster−h
39	9e−09	45 / 643	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
40	1e−08	32 / 370	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	4 / 144	HORVATH_aging_genes meth UP
2	0.7	3 / 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	5e−15	92 / 1418	small molecule metabolic process
2	3e−07	11 / 57	hydrogen ion transmembrane transport
3	2e−06	13 / 96	respiratory electron transport chain
4	5e−06	15 / 136	cellular metabolic process
5	1e−05	7 / 29	actin filament bundle assembly
6	7e−05	5 / 17	very long−chain fatty acid metabolic process
7	1e−04	58 / 1279	signal transduction
8	1e−04	8 / 55	post−Golgi vesicle−mediated transport
9	2e−04	4 / 12	oligosaccharide biosynthetic process
10	3e−04	13 / 152	cellular lipid metabolic process
11	3e−04	4 / 13	immunoglobulin mediated immune response
12	3e−04	4 / 13	urea cycle
13	4e−04	4 / 14	vacuolar transport
14	6e−04	7 / 54	skin development
15	7e−04	9 / 88	response to glucocorticoid
16	7e−04	5 / 27	keratan sulfate biosynthetic process
17	7e−04	5 / 27	positive regulation of release of cytochrome c from mitochondria
18	9e−04	7 / 57	Rho protein signal transduction
19	1e−03	4 / 17	drug transmembrane transport
20	1e−03	9 / 93	glycerophospholipid biosynthetic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−16	189 / 3977	Mid_Frontal_Lobe_ReprPC
2	9e−08	122 / 2820	Mid_Frontal_Lobe_HetRpts
3	7e−07	94 / 2084	Mid_Frontal_Lobe_K9K27me3
4	1e−05	106 / 2603	Fetal_TxTrans
5	2e−05	117 / 2956	Fetal_TssA
6	2e−04	55 / 1210	Fetal_TssP
7	2e−04	72 / 1713	Mid_Frontal_Lobe_ReprPCWk
8	3e−04	98 / 2549	Fetal_TssF
9	2e−03	119 / 3370	Mid_Frontal_Lobe_ZNF
10	2e−03	54 / 1327	Mid_Frontal_Lobe_TssP
11	3e−03	46 / 1108	Overlap_fetal_midbrain_TssA
12	4e−02	52 / 1478	Overlap_fetal_midbrain_TxTrans
13	4e−02	64 / 1890	Overlap_fetal_midbrain_TssF
14	5e−02	32 / 865	Mid_Frontal_Lobe_Het
15	5e−02	57 / 1680	Fetal_ReprPCWk
16	1e−01	46 / 1394	Mid_Frontal_Lobe_Quies
17	3e−01	18 / 552	Fetal_Tx
18	3e−01	303 / 10800	Overlap_fetal_midbrain_Quies
19	3e−01	9 / 268	Mid_Frontal_Lobe_TssA
20	3e−01	13 / 408	Mid_Frontal_Lobe_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.009	3 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	0.012	2 / 14	LIU_PROSTATE_CANCER_UP
3	0.024	2 / 9	WANG_ER_DN
4	0.027	3 / 24	PanCan_Notch_geneset_nanostring
5	0.054	1 / 2	GENTLES_modul8
6	0.062	2 / 15	GENTLES_modul4
7	0.062	2 / 15	GENTLES_modul13
8	0.070	2 / 16	WANG_ER_UP
9	0.127	5 / 97	PanCan_TXmisReg_geneset_nanostring
10	0.153	1 / 6	ZHANG_MGUS up
11	0.155	8 / 191	SPANG_LPS−index2
12	0.170	3 / 52	KUIPER_MM poor survival
13	0.180	12 / 324	SPANG_BCL6−index2
14	0.186	6 / 140	PanCan_RAS_geneset_nanostring
15	0.248	5 / 123	PanCan_Driver_Gene_geneset_nanostring
16	0.263	1 / 11	GENTLES_modul5
17	0.269	0 / 16	LIU_LIVER_CANCER
18	0.293	1 / 16	LIU_COMMON_CANCER_GENES
19	0.300	7 / 198	PanCan_PI3K_geneset_nanostring
20	0.310	2 / 41	ZHANG_MM up

CC

Rank	p−value	#in/all	Geneset
1	4e−21	154 / 2638	extracellular exosome
2	1e−07	74 / 1441	mitochondrion
3	1e−06	48 / 842	endoplasmic reticulum
4	5e−06	22 / 268	apical plasma membrane
5	2e−05	28 / 425	mitochondrial inner membrane
6	3e−05	9 / 60	brush border
7	2e−04	18 / 245	lysosomal membrane
8	2e−04	5 / 21	desmosome
9	3e−04	14 / 171	cell−cell junction
10	3e−04	17 / 235	lysosome
11	3e−04	144 / 4052	integral component of membrane
12	8e−04	125 / 3507	plasma membrane
13	1e−03	30 / 596	perinuclear region of cytoplasm
14	2e−03	6 / 46	brush border membrane
15	2e−03	13 / 185	basolateral plasma membrane
16	2e−03	6 / 49	phagocytic vesicle membrane
17	2e−03	3 / 10	azurophil granule
18	2e−03	5 / 34	peroxisomal matrix
19	3e−03	6 / 51	stress fiber
20	4e−03	7 / 72	Golgi cisterna membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.006	36 / 847	Chr 16
2	0.030	51 / 1425	Chr 19
3	0.031	43 / 1172	Chr 11
4	0.097	37 / 1083	Chr 17
5	0.122	61 / 1920	Chr 1
6	0.189	18 / 522	Chr 20
7	0.234	24 / 745	Chr 9
8	0.417	13 / 436	Chr 22
9	0.425	6 / 191	Chr 21
10	0.438	29 / 1017	Chr 12
11	0.575	23 / 859	Chr 7
12	0.664	25 / 976	Chr 6
13	0.759	6 / 272	Chr 18
14	0.783	25 / 1043	Chr 3
15	0.829	16 / 715	Chr 10
16	0.856	14 / 651	Chr 8
17	0.858	16 / 735	Chr 4
18	0.871	6 / 318	Chr 13
19	0.926	11 / 582	Chr 15
20	0.941	17 / 862	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−38	207 / 3122	TxEnhG1_Colon
2	1e−32	196 / 3112	EnhA_Colon
3	4e−32	354 / 8123	TssF_Colon
4	1e−26	389 / 9930	Tx_Colon
5	1e−26	277 / 5889	EnhWk1_Colon
6	2e−24	428 / 11791	Enh_Colon
7	1e−21	80 / 877	TxEnhG2_Colon
8	4e−19	384 / 10475	TssA_Colon
9	4e−19	56 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
10	6e−18	280 / 6761	TssD2_Colon
11	4e−12	334 / 9390	TxWk_Colon
12	8e−09	17 / 110	Marisa_CRC−cluster−h
13	9e−09	45 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	2e−08	46 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	5e−06	13 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
16	6e−06	375 / 11968	TssWk_Colon
17	4e−05	35 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
18	1e−04	54 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
19	2e−04	3 / 5	Hewish_dMMR−secondary−mutations_Apoptosis
20	4e−04	7 / 49	Marisa_CRC−cluster−f

Disease

Rank	p−value	#in/all	Geneset
1	3e−07	40 / 608	GUDJ_psoriasis up
2	5e−01	1 / 22	BCHETNIA_EBM up
3	6e−01	1 / 37	BCHETNIA_EBM−DM up
4	8e−01	9 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	5e−07	75 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
2	2e−04	13 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	5e−04	11 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
4	9e−04	9 / 92	laffaire_hypermeth_LGG_vs_control
5	1e−03	9 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
6	1e−03	12 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	2e−03	7 / 63	Stuehler_Proteins_up_in_STS
8	3e−03	19 / 344	Up
9	4e−03	7 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
10	5e−03	6 / 58	OL vs. MOG− OL
11	5e−03	6 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
12	7e−03	9 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
13	1e−02	3 / 18	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
14	2e−02	8 / 119	GIEZELT_GBM_WT_up_VS_mut
15	2e−02	5 / 59	Christensen_hypomethylated_in_primary_glioblastoma
16	2e−02	4 / 40	Christensen_hypomethylated_in_ependymoma
17	4e−02	5 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
18	5e−02	4 / 50	WILLSCHER_GBM_Verhaak=PNwt_up
19	5e−02	3 / 31	KIM prognostic signature LTS vs. STS
20	5e−02	14 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−48	68 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
2	2e−29	48 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
3	1e−26	61 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
4	7e−22	54 / 412	LIM_MAMMARY_STEM_CELL_DN
5	6e−20	67 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
6	4e−19	53 / 455	ONDER_CDH1_TARGETS_2_DN
7	6e−19	109 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
8	2e−17	61 / 641	FEVR_CTNNB1_TARGETS_UP
9	7e−17	52 / 495	ENK_UV_RESPONSE_KERATINOCYTE_UP
10	9e−15	78 / 1103	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
11	5e−13	51 / 593	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
12	6e−13	22 / 115	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
13	4e−12	22 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
14	8e−11	21 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
15	4e−10	39 / 459	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
16	6e−10	30 / 292	LI_INDUCED_T_TO_NATURAL_KILLER_UP
17	7e−10	39 / 467	SWEET_LUNG_CANCER_KRAS_UP
18	8e−10	28 / 261	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
19	8e−10	27 / 244	RICKMAN_METASTASIS_DN
20	5e−09	22 / 181	WU_CELL_MIGRATION

HM

Rank	p−value	#in/all	Geneset
1	4e−07	20 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
2	5e−07	20 / 196	HALLMARK_P53_PATHWAY
3	6e−07	20 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	2e−06	19 / 193	HALLMARK_XENOBIOTIC_METABOLISM
5	2e−06	19 / 199	HALLMARK_ADIPOGENESIS
6	3e−05	15 / 157	HALLMARK_APOPTOSIS
7	9e−05	14 / 155	HALLMARK_UV_RESPONSE_UP
8	1e−04	16 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	1e−03	9 / 98	HALLMARK_ANDROGEN_RESPONSE
10	2e−03	9 / 102	HALLMARK_PEROXISOME
11	3e−03	13 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	3e−03	13 / 198	HALLMARK_HYPOXIA
13	3e−03	11 / 154	HALLMARK_FATTY_ACID_METABOLISM
14	4e−03	9 / 112	HALLMARK_BILE_ACID_METABOLISM
15	8e−03	5 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
16	1e−02	6 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	2e−02	11 / 190	HALLMARK_APICAL_JUNCTION
18	2e−02	9 / 146	HALLMARK_DNA_REPAIR
19	2e−02	11 / 198	HALLMARK_GLYCOLYSIS
20	4e−02	10 / 195	HALLMARK_MYOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	5 / 91	DUMEAUX_Smoking enriched genes
2	0.2	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.4	1 / 17	DUMEAUX_High bmi 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 / 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−09	20 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
2	3e−09	20 / 144	WIRTH_lymphoma937_spot G
3	4e−05	19 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
4	5e−03	21 / 414	TARTE_Mature plasma cell signature
5	6e−03	99 / 2838	HOPP_Poised_promoter
6	2e−02	2 / 8	MASCQUE_GCB UP
7	3e−02	3 / 24	Subero_mBL_hypo_meth
8	3e−02	4 / 42	CARO_OxPhos_in_DLBCL_UP
9	4e−02	243 / 8147	HOPP_Weak_promoter
10	4e−02	2 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
11	4e−02	4 / 48	Subero_INT_hypo_meth
12	4e−02	6 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	6e−02	2 / 15	Subero_B−ALL_hypo_meth
14	7e−02	4 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
15	7e−02	3 / 35	Subero_T−PLL_hypo_meth
16	8e−02	4 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
17	8e−02	12 / 279	SPANG_IL21 DN
18	9e−02	5 / 87	ROSOLOWSKI_red total
19	1e−01	6 / 116	WIRTH_lymphoma937_spot MM
20	1e−01	2 / 20	Subero_MCL_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	6e−05	6 / 26	cytochrome−c oxidase activity
2	5e−04	8 / 67	flavin adenine dinucleotide binding
3	6e−04	6 / 39	transmembrane receptor protein tyrosine kinase activity
4	9e−04	23 / 407	catalytic activity
5	1e−03	10 / 114	SH3 domain binding
6	2e−03	8 / 85	PDZ domain binding
7	3e−03	4 / 23	galactosyltransferase activity
8	3e−03	4 / 23	WW domain binding
9	3e−03	13 / 198	signal transducer activity
10	4e−03	3 / 12	fucosyltransferase activity
11	5e−03	6 / 57	calcium−dependent protein binding
12	5e−03	3 / 13	S100 protein binding
13	6e−03	16 / 287	oxidoreductase activity
14	9e−03	17 / 328	enzyme binding
15	1e−02	8 / 113	actin filament binding
16	1e−02	18 / 370	receptor binding
17	1e−02	4 / 35	NADP binding
18	2e−02	12 / 217	protein domain specific binding
19	2e−02	3 / 21	activating transcription factor binding
20	2e−02	3 / 21	antioxidant activity

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.008	12 / 197	hsa−miR−548d−3p
2	0.012	5 / 50	hsa−miR−302b*
3	0.027	5 / 62	hsa−miR−328
4	0.034	5 / 66	hsa−miR−618
5	0.035	6 / 89	hsa−miR−149
6	0.054	7 / 124	hsa−miR−579
7	0.055	5 / 75	hsa−miR−184
8	0.055	2 / 14	hsa−miR−574−3p
9	0.069	7 / 131	hsa−miR−145
10	0.070	3 / 35	hsa−miR−615−5p
11	0.071	6 / 106	hsa−miR−410
12	0.074	6 / 107	hsa−miR−377
13	0.074	9 / 188	hsa−miR−520f
14	0.078	4 / 59	hsa−miR−187
15	0.088	7 / 139	hsa−miR−198
16	0.090	6 / 113	hsa−miR−199a−5p
17	0.102	6 / 117	hsa−miR−875−3p
18	0.104	7 / 145	hsa−miR−522
19	0.109	17 / 447	hsa−miR−519d
20	0.119	3 / 44	hsa−miR−423−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	2 / 14	BENTINK_e2f3.1
2	0.32	1 / 14	GUSTAFSON_PI3K_UP
3	0.34	1 / 15	BENTINK_ras.6
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 / 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	0.001	151 / 4436	ICGC_Zeb1_targets
2	0.002	72 / 1867	HEBENSTREIT_high expression TF
3	0.004	100 / 2827	ICGC_Bcl3_targets
4	0.004	173 / 5308	ICGC_Tcf12_targets
5	0.006	174 / 5393	ICGC_Sp1_targets
6	0.009	165 / 5135	ICGC_Ebfsc137065_targets
7	0.009	214 / 6862	ICGC_Elf1_targets
8	0.010	194 / 6157	ICGC_Tcf3_targets
9	0.011	117 / 3511	ICGC_Rad21_targets
10	0.018	175 / 5578	ICGC_Stat5_targets
11	0.023	145 / 4566	ICGC_Egr1_targets
12	0.038	160 / 5173	ICGC_Taf1_targets
13	0.039	217 / 7202	ICGC_Runx3_targets
14	0.043	192 / 6324	ICGC_Yy1_targets
15	0.047	169 / 5526	ICGC_Pmlsc71910_targets
16	0.076	180 / 6005	ICGC_Mta3_targets
17	0.079	191 / 6406	ICGC_Pax5_targets
18	0.088	188 / 6322	ICGC_Pol2_targets
19	0.109	27 / 766	ICGC_Atf3_targets
20	0.120	141 / 4714	ICGC_Pu1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	4 / 45	VAQUERIZAS_Placenta
2	0.08	3 / 37	VAQUERIZAS_Prostate
3	0.09	2 / 18	VAQUERIZAS_Pancreas
4	0.09	2 / 19	VAQUERIZAS_Heart
5	0.10	4 / 64	VAQUERIZAS_Lung
6	0.14	2 / 24	VAQUERIZAS_Trachea
7	0.18	1 / 7	VAQUERIZAS_Appendix
8	0.20	1 / 8	VAQUERIZAS_Tongue
9	0.23	2 / 33	VAQUERIZAS_Liver
10	0.30	1 / 13	VAQUERIZAS_Skin
11	0.32	2 / 42	VAQUERIZAS_Thyroid
12	0.36	1 / 16	VAQUERIZAS_Ovary
13	0.36	1 / 16	VAQUERIZAS_Fetal thyroid
14	0.38	1 / 17	VAQUERIZAS_Salivary gland
15	0.46	1 / 22	VAQUERIZAS_Tonsil
16	0.55	2 / 67	VAQUERIZAS_Whole blood
17	0.58	1 / 31	VAQUERIZAS_Fetal lung
18	0.58	1 / 31	VAQUERIZAS_Lymph node
19	0.69	1 / 42	VAQUERIZAS_Thymus
20	0.80	3 / 155	VAQUERIZAS_General

Tissue

Rank	p−value	#in/all	Geneset
1	3e−12	23 / 137	WIRTH_Mucosa
2	4e−03	3 / 12	WIRTH_Tonsil
3	5e−02	2 / 14	WIRTH_B−cells
4	6e−02	4 / 54	WIRTH_Pancreas
5	1e−01	11 / 259	PALMER_Granulocytes signature up
6	3e−01	1 / 13	WIRTH_Sec. lymphoid organs
7	3e−01	1 / 13	WIRTH_Prim. lymphoid organs
8	3e−01	1 / 13	WIRTH_Cortex cerebri
9	3e−01	1 / 14	WIRTH_Thyroid gland
10	3e−01	7 / 208	PALMER_B−Cell signature up
11	4e−01	3 / 82	WIRTH_Homeostasis
12	5e−01	4 / 140	PALMER_T−Cell signature up
13	6e−01	3 / 115	WIRTH_Liver
14	1e+00	1 / 141	WIRTH_Muscle
15	1e+00	1 / 202	WIRTH_Testis
16	1e+00	4 / 476	WIRTH_Nervous System
17	1e+00	2 / 427	WIRTH_Immune system
18	1e+00	0 / 6	WIRTH_Pituitary gland
19	1e+00	0 / 14	WIRTH_Thymus
20	1e+00	0 / 12	WIRTH_Lymphocytes

Toxic

Rank	p−value	#in/all	Geneset
1	0.09	45 / 1343	LU_BPDE 1h DN
2	0.73	139 / 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	

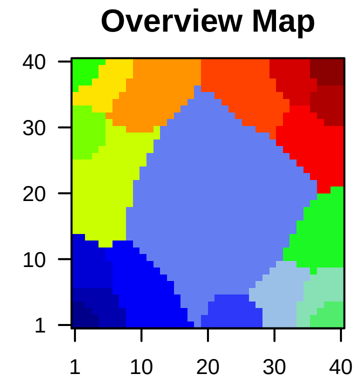
K−Means Clusters

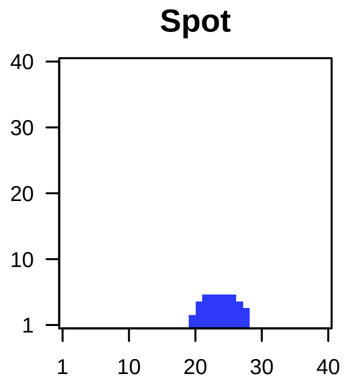
Spot Summary: H

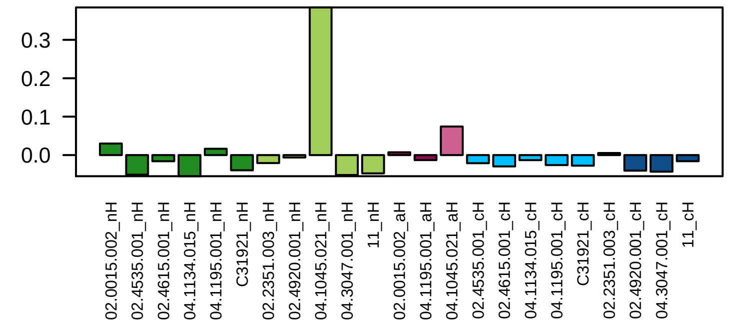
metagenes = 38
genes = 371

<r> metagenes = 0.95
<r> genes = 0.61
beta: r2= 0.1 / log p= −0.84

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





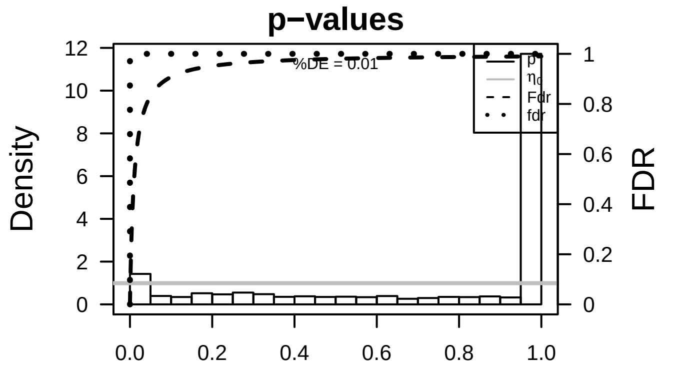


Spot Genelist

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	0.95	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	0.94	APOC3	apolipoprotein C−III [Source:HGNC Symbol;Acc:HGNC:610]
5	ENSG000001	1.38	−0.08	0.96	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4 [Sourc
6	ENSG000001	1.36	−0.06	0.94	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	0.95	APOA1	apolipoprotein A−I [Source:HGNC Symbol;Acc:HGNC:600]
9	ENSG000000	1.18	−0.06	0.95	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	0.95	GSTA1	glutathione S−transferase alpha 1 [Source:HGNC Symbol;Ac
12	ENSG000001	1.11	−0.06	0.94	CCL25	chemokine (C−C motif) ligand 25 [Source:HGNC Symbol;Acc
13	ENSG000001	1.09	−0.34	0.68	SERPINA1	serpin peptidase inhibitor, clade A (alpha−1 antiproteinase, a
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	0.85	DEFA5	defensin, alpha 5, Paneth cell−specific [Source:HGNC Symb
17	ENSG000000	0.98	−0.05	0.94	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	0.79	FABP2	fatty acid binding protein 2, intestinal [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−32	53 / 346	GSEA	SANSOM_APC_TARGETS_DN
2	2e−32	101 / 1418	BP	small molecule metabolic process
3	2e−31	44 / 229	GSEA	HSIAO_LIVER_SPECIFIC_GENES
4	5e−23	53 / 541	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
5	1e−21	121 / 2638	CC	extracellular exosome
6	3e−21	23 / 80	GSEA	WOO_LIVER_CANCER_RECURRENCE_DN
7	1e−19	28 / 154	BP	xenobiotic metabolic process
8	2e−18	26 / 141	GSEA	OHGUCHI_LIVER_HNF4A_TARGETS_DN
9	3e−18	51 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
10	4e−18	33 / 257	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
11	6e−18	29 / 193	HM	HALLMARK_XENOBIOTIC_METABOLISM
12	1e−17	19 / 67	GSEA	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
13	8e−17	49 / 640	BP	oxidation−reduction process
14	2e−16	26 / 170	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
15	3e−16	35 / 336	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
16	2e−15	17 / 64	BP	cholesterol homeostasis
17	7e−15	22 / 132	GSEA	REACTOME_BIOLOGICAL_OXIDATIONS
18	8e−15	24 / 164	GSEA	LEE_LIVER_CANCER_SURVIVAL_UP
19	2e−14	41 / 526	GSEA	ACEVEDO_LIVER_CANCER_DN
20	4e−14	44 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
21	3e−13	28 / 268	CC	apical plasma membrane
22	4e−13	45 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
23	6e−13	19 / 115	Tissu	WIRTH_Liver
24	4e−12	25 / 235	MF	transporter activity
25	7e−12	133 / 4052	CC	integral component of membrane
26	8e−12	14 / 62	GSEA	KEGG_RETINOL_METABOLISM
27	8e−12	14 / 62	GSEA	LEE_LIVER_CANCER_ACOX1_DN
28	8e−12	10 / 24	BP	triglyceride homeostasis
29	2e−11	25 / 255	GSEA	CAIRO_HEPATOBLASTOMA_DN
30	3e−11	31 / 396	GSEA	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECUL
31	3e−11	108 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
32	3e−11	14 / 68	GSEA	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
33	4e−11	44 / 753	BP	transmembrane transport
34	5e−11	26 / 287	MF	oxidoreductase activity
35	6e−11	25 / 268	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
36	1e−10	28 / 346	GSEA	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
37	3e−10	17 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
38	3e−10	12 / 54	BP	arachidonic acid metabolic process
39	5e−10	12 / 56	BP	retinoid metabolic process
40	6e−10	22 / 231	GSEA	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT



Aging

Rank	p−value	#in/all	Geneset
1	0.009	7 / 123	HORVATH_aging_genes meth DOWN
2	0.023	4 / 57	TESCHENDORFF_age_hypermethylated
3	0.140	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	2e−32	101 / 1418	small molecule metabolic process
2	1e−19	28 / 154	xenobiotic metabolic process
3	8e−17	49 / 640	oxidation−reduction process
4	2e−15	17 / 64	cholesterol homeostasis
5	8e−12	10 / 24	triglyceride homeostasis
6	4e−11	44 / 753	transmembrane transport
7	3e−10	12 / 54	arachidonic acid metabolic process
8	5e−10	12 / 56	retinoid metabolic process
9	3e−08	8 / 27	cholesterol efflux
10	5e−08	8 / 29	drug metabolic process
11	6e−08	25 / 375	carbohydrate metabolic process
12	7e−08	6 / 13	fructose metabolic process
13	7e−08	23 / 325	response to drug
14	9e−08	10 / 56	digestion
15	1e−07	48 / 1118	metabolic process
16	1e−07	9 / 44	cellular amino acid metabolic process
17	2e−07	17 / 191	lipid metabolic process
18	2e−07	10 / 62	steroid metabolic process
19	3e−07	28 / 491	transport
20	5e−07	8 / 38	lipoprotein metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.002	50 / 1713	Mid_Frontal_Lobe_ReprPCWk
2	0.006	40 / 1394	Mid_Frontal_Lobe_Quies
3	0.017	53 / 2084	Mid_Frontal_Lobe_K9K27me3
4	0.020	24 / 805	Mid_Frontal_Lobe_EnhG
5	0.062	88 / 3977	Mid_Frontal_Lobe_ReprPC
6	0.112	39 / 1680	Fetal_ReprPCWk
7	0.152	9 / 317	Mid_Frontal_Lobe_Tx
8	0.179	20 / 840	Mid_Frontal_Lobe_TssF
9	0.217	55 / 2603	Fetal_TxTrans
10	0.253	21 / 940	Mid_Frontal_Lobe_Enh
11	0.259	40 / 1890	Overlap_fetal_midbrain_TssF
12	0.308	50 / 2443	Fetal_Quies
13	0.327	3 / 106	Overlap_fetal_midbrain_Tx
14	0.452	5 / 232	Fetal_ReprPC
15	0.480	11 / 552	Fetal_Tx
16	0.581	16 / 865	Mid_Frontal_Lobe_Het
17	0.613	47 / 2549	Fetal_TssF
18	0.615	27 / 1478	Overlap_fetal_midbrain_TxTrans
19	0.648	54 / 2956	Fetal_TssA
20	0.678	11 / 641	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 16	LIU_LIVER_CANCER
2	0.24	0 / 14	LIU_PROSTATE_CANCER_UP
3	0.25	1 / 15	GENTLES_modul10
4	0.26	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	0.26	1 / 16	GENTLES_modul7
6	0.26	1 / 16	GENTLES_modul16
7	0.28	8 / 324	SPANG_BCL6−index2
8	0.51	1 / 37	KUIPER_MM good survival
9	0.53	11 / 574	Lembcke_Colonic Inflammation
10	0.63	0 / 16	LIU_PROSTATE_CANCER_DN
11	0.63	1 / 52	KUIPER_MM poor survival
12	0.82	8 / 550	Lembcke_Normal vs Adenoma
13	0.85	1 / 97	PanCan_TXmisReg_geneset_nanostring
14	0.88	2 / 191	SPANG_LPS−index2
15	0.98	1 / 198	PanCan_PI3K_geneset_nanostring
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_DN
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	1e−21	121 / 2638	extracellular exosome
2	3e−13	28 / 268	apical plasma membrane
3	7e−12	133 / 4052	integral component of membrane
4	1e−08	10 / 46	brush border membrane
5	2e−08	39 / 767	endoplasmic reticulum membrane
6	1e−07	6 / 14	chylomicron
7	1e−06	6 / 20	very−low−density lipoprotein particle
8	2e−06	9 / 60	brush border
9	3e−05	88 / 3059	membrane
10	3e−05	10 / 106	peroxisome
11	5e−05	49 / 1441	mitochondrion
12	2e−04	24 / 558	intracellular membrane−bounded organelle
13	3e−04	15 / 277	mitochondrial matrix
14	3e−04	4 / 18	microvillus membrane
15	5e−04	41 / 1250	integral component of plasma membrane
16	1e−03	3 / 11	secretory granule lumen
17	1e−03	18 / 425	mitochondrial inner membrane
18	4e−03	87 / 3507	plasma membrane
19	6e−03	3 / 20	high−density lipoprotein particle
20	8e−03	39 / 1374	extracellular region

Chr

Rank	p−value	#in/all	Geneset
1	0.001	26 / 715	Chr 10
2	0.174	27 / 1172	Chr 11
3	0.183	28 / 1228	Chr 2
4	0.183	25 / 1083	Chr 17
5	0.210	11 / 436	Chr 22
6	0.236	17 / 735	Chr 4
7	0.259	15 / 651	Chr 8
8	0.279	14 / 613	Chr 14
9	0.298	5 / 191	Chr 21
10	0.338	22 / 1043	Chr 3
11	0.468	17 / 859	Chr 7
12	0.547	16 / 847	Chr 16
13	0.551	11 / 582	Chr 15
14	0.587	18 / 976	Chr 6
15	0.663	13 / 745	Chr 9
16	0.726	5 / 318	Chr 13
17	0.756	33 / 1920	Chr 1
18	0.763	4 / 272	Chr 18
19	0.912	21 / 1425	Chr 19
20	0.941	11 / 862	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−14	44 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	4e−13	45 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
3	3e−08	35 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
4	5e−05	42 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
5	5e−04	159 / 6761	TssD2_Colon
6	2e−02	17 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
7	2e−02	6 / 110	Marisa_CRC−cluster−h
8	2e−02	99 / 4327	EnhWk2_Colon
9	5e−02	5 / 105	Marisa_CRC−cluster−d
10	6e−02	15 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
11	6e−02	239 / 11791	Enh_Colon
12	8e−02	125 / 5889	EnhWk1_Colon
13	8e−02	7 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
14	9e−02	3 / 55	Marisa_CRC−cluster−e
15	2e−01	1 / 9	Boland_CRC−MSI−TGC
16	2e−01	1 / 10	Marisa_CRC−C1
17	2e−01	66 / 3112	EnhA_Colon
18	3e−01	3 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
19	3e−01	1 / 20	Budinska_B_Lower crypt−like_UP
20	3e−01	9 / 389	K9K27me3_Colon

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	0.6	11 / 608	GUDJ_psoriasis up
4	0.8	6 / 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	3e−11	108 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e−04	29 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	5e−03	19 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	7e−03	5 / 63	Stuehler_Proteins_up_in_STS
5	7e−03	2 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
6	3e−02	5 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
7	5e−02	25 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
8	7e−02	3 / 49	Noushmehr_Pron_GCIMP_hypermeth_DN
9	8e−02	3 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	1e−01	3 / 59	Sturm_GBM_Meth_overexpression_F_IDH_UP
11	1e−01	1 / 6	laffaire_hypometh_LGG_vs_control
12	1e−01	3 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
13	2e−01	4 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
14	2e−01	1 / 11	WILLSCHER_GBM_LTSwt_proteomics−G_UP
15	2e−01	3 / 81	GIEZELT_GBM_STS_up_VS_LTS
16	2e−01	5 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
17	2e−01	1 / 13	VERHAAK_Brain
18	2e−01	1 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
19	2e−01	2 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
20	3e−01	1 / 16	VERHAAK_NL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−32	53 / 346	SANSOM_APC_TARGETS_DN
2	2e−31	44 / 229	HSIAO_LIVER_SPECIFIC_GENES
3	5e−23	53 / 541	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
4	3e−21	23 / 80	WOO_LIVER_CANCER_RECURRENCE_DN
5	2e−18	26 / 141	OHGUCHI_LIVER_HNF4A_TARGETS_DN
6	3e−18	51 / 641	FEVR_CTNNB1_TARGETS_UP
7	4e−18	33 / 257	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
8	1e−17	19 / 67	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
9	2e−16	26 / 170	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
10	3e−16	35 / 336	VECCHI_GASTRIC_CANCER_EARLY_DN
11	7e−15	22 / 132	REACTOME_BIOLOGICAL_OXIDATIONS
12	8e−15	24 / 164	LEE_LIVER_CANCER_SURVIVAL_UP
13	2e−14	41 / 526	ACEVEDO_LIVER_CANCER_DN
14	8e−12	14 / 62	KEGG_RETINOL_METABOLISM
15	8e−12	14 / 62	LEE_LIVER_CANCER_ACOX1_DN
16	2e−11	25 / 255	CAIRO_HEPATOBLASTOMA_DN
17	3e−11	31 / 396	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES
18	3e−11	14 / 68	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	6e−11	25 / 268	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
20	1e−10	28 / 346	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN

HM

Rank	p−value	#in/all	Geneset
1	6e−18	29 / 193	HALLMARK_XENOBIOTIC_METABOLISM
2	4e−08	16 / 154	HALLMARK_FATTY_ACID_METABOLISM
3	1e−06	16 / 199	HALLMARK_ADIPOGENESIS
4	1e−06	12 / 112	HALLMARK_BILE_ACID_METABOLISM
5	3e−05	14 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	1e−03	9 / 132	HALLMARK_COAGULATION
7	4e−03	10 / 193	HALLMARK_HEME_METABOLISM
8	4e−03	10 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	5e−03	4 / 37	HALLMARK_PANCREAS_BETA_CELLS
10	1e−02	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	1e−02	9 / 198	HALLMARK_HYPOXIA
12	5e−02	5 / 102	HALLMARK_PEROXISOME
13	8e−02	7 / 198	HALLMARK_GLYCOLYSIS
14	2e−01	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	2e−01	6 / 193	HALLMARK_KRAS_SIGNALING_DN
16	2e−01	6 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
17	2e−01	4 / 128	HALLMARK_SPERMATOGENESIS
18	2e−01	3 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
19	3e−01	5 / 189	HALLMARK_KRAS_SIGNALING_UP
20	3e−01	5 / 192	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.13	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.16	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.19	1 / 11	DUMEAUX_Smoking literature genes up
5	0.19	1 / 11	DUMEAUX_Women normal BMI literature genes up
6	0.28	1 / 17	DUMEAUX_High bmi enriched genes
7	0.83	1 / 91	DUMEAUX_Smoking 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 / 16	DUMEAUX_Red blood cells in non smokers 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	0.001	5 / 42	CARO_OxPhos_in_DLBCL_UP
2	0.007	4 / 40	ROSOLOWSKI_blue DOWN
3	0.009	2 / 8	MASCQUE_GCB UP
4	0.021	2 / 12	DAVE_BL_UP
5	0.045	2 / 18	Aukema_BCL2 UP_BCL6 DN
6	0.052	4 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
7	0.054	13 / 414	TARTE_Mature plasma cell signature
8	0.055	4 / 75	WIRTH_lymphoma937_spot IM
9	0.098	4 / 92	WIRTH_lymphoma937_spot A
10	0.102	3 / 59	LENZ_Stromal signature 2
11	0.104	4 / 94	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
12	0.114	75 / 3457	HOPP_Heterochrom
13	0.176	4 / 115	ROSOLOWSKI_green total
14	0.206	1 / 12	Subero_MM_hypo_meth
15	0.210	3 / 83	ROSOLOWSKI_green UP
16	0.230	3 / 87	ROSOLOWSKI_red total
17	0.236	1 / 14	DAVE_BL_DN
18	0.264	1 / 16	WRIGHT_GCB UP
19	0.306	1 / 19	DAVE_c−myc BL UP
20	0.309	2 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN

MF

Rank	p−value	#in/all	Geneset
1	4e−12	25 / 235	transporter activity
2	5e−11	26 / 287	oxidoreductase activity
3	3e−08	10 / 51	monooxygenase activity
4	1e−07	14 / 124	heme binding
5	2e−07	7 / 23	carboxypeptidase activity
6	6e−07	14 / 143	iron ion binding
7	1e−06	10 / 72	oxidoreductase activity, acting on paired donors, with incorporation or reductic
8	1e−06	24 / 407	catalytic activity
9	2e−06	5 / 12	dipeptidase activity
10	3e−06	6 / 22	steroid hydroxylase activity
11	3e−06	11 / 101	metallopeptidase activity
12	2e−05	5 / 18	cholesterol transporter activity
13	4e−05	4 / 11	aldo−keto reductase (NADP) activity
14	4e−05	5 / 21	lipid transporter activity
15	4e−05	5 / 21	oxidoreductase activity, acting on paired donors, with incorporation or reductic
16	6e−05	4 / 12	retinol binding
17	9e−05	5 / 25	steroid binding
18	2e−04	6 / 43	oxygen binding
19	2e−04	4 / 16	arachidonic acid epoxygenase activity
20	2e−04	4 / 16	retinol dehydrogenase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	3 / 44	hsa−miR−642
2	0.07	4 / 83	hsa−miR−562
3	0.08	3 / 54	hsa−miR−1279
4	0.10	5 / 131	hsa−miR−145
5	0.11	1 / 6	hsa−miR−937
6	0.14	2 / 34	hsa−miR−555
7	0.16	1 / 9	hsa−miR−615−3p
8	0.16	3 / 73	hsa−miR−548b−3p
9	0.18	3 / 77	hsa−miR−513c
10	0.19	1 / 11	hsa−miR−487b
11	0.21	1 / 12	hsa−miR−1180
12	0.22	2 / 46	hsa−miR−660
13	0.22	4 / 127	hsa−miR−204
14	0.22	4 / 127	hsa−miR−625
15	0.25	2 / 50	hsa−miR−549
16	0.25	1 / 15	hsa−miR−744
17	0.25	1 / 15	hsa−miR−452*
18	0.25	3 / 92	hsa−miR−362−5p
19	0.28	4 / 140	hsa−miR−488
20	0.28	1 / 17	hsa−miR−1298

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	0.006	49 / 1798	HEBENSTREIT_low expression TF
2	0.319	1 / 20	MYC_Metabolism UP
3	0.418	15 / 731	ICGC_SrfPcr2_targets
4	0.719	1 / 66	MYC_Targets UP
5	0.743	10 / 619	ICGC_RxraPcr1_targets
6	0.761	12 / 745	ICGC_NrsfPcr2_targets
7	0.927	28 / 1867	HEBENSTREIT_high expression TF
8	0.938	18 / 1294	KIM_MYC targets
9	0.959	20 / 1472	ICGC_NrsfPcr1_targets
10	0.969	20 / 1506	ICGC_Usf1_targets
11	0.971	90 / 5552	ICGC_Pol24_targets
12	0.980	8 / 766	ICGC_Atf3_targets
13	0.980	39 / 2719	ICGC_Pbx3_targets
14	0.984	19 / 1523	ICGC_P300_targets
15	0.984	29 / 2149	ICGC_Mef2_targets
16	0.985	33 / 2401	ICGC_Bcl11_targets
17	0.987	19 / 1549	ICGC_Myc_targets
18	0.990	79 / 5135	ICGC_Ebfsc137065_targets
19	0.991	116 / 7202	ICGC_Runx3_targets
20	0.992	71 / 4714	ICGC_Pu1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 33	VAQUERIZAS_Liver
2	0.08	2 / 25	VAQUERIZAS_Adrenal cortex
3	0.12	2 / 31	VAQUERIZAS_Lymph node
4	0.16	2 / 37	VAQUERIZAS_Prostate
5	0.18	2 / 41	VAQUERIZAS_Testis
6	0.21	1 / 12	VAQUERIZAS_Kidney
7	0.26	1 / 16	VAQUERIZAS_Fetal liver
8	0.28	1 / 17	VAQUERIZAS_Adrenal gland
9	0.31	1 / 19	VAQUERIZAS_Heart
10	0.55	1 / 42	VAQUERIZAS_Thyroid
11	0.57	3 / 155	VAQUERIZAS_General
12	0.58	1 / 45	VAQUERIZAS_Placenta
13	0.61	1 / 49	VAQUERIZAS_Uterus
14	1.00	0 / 41	VAQUERIZAS_Fetal brain
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_Thymus
19	1.00	0 / 67	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

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

Toxic

Rank	p−value	#in/all	Geneset
1	0.06	114 / 5285	LU_BPDE 0.005 DN
2	0.57	25 / 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	

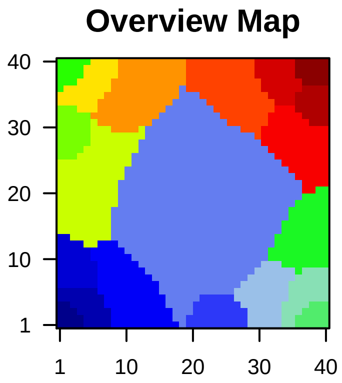
K−Means Clusters

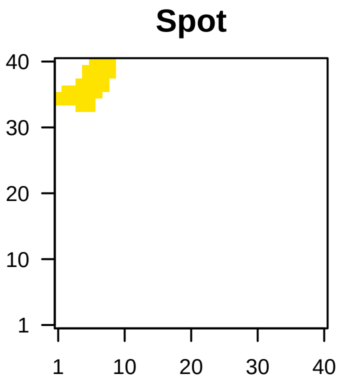
Spot Summary: I

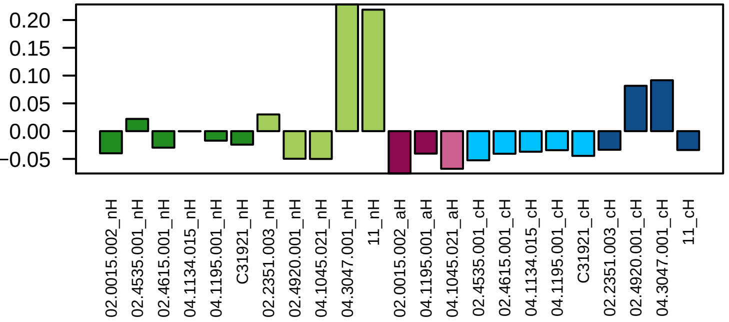
metagenes = 42
genes = 526

<r> metagenes = 0.94
<r> genes = 0.7
beta: r2= 0.15 / log p= −1.18

samples with spot = 2 (8.7 %)
other_normHNPCC : 2 (40 %)





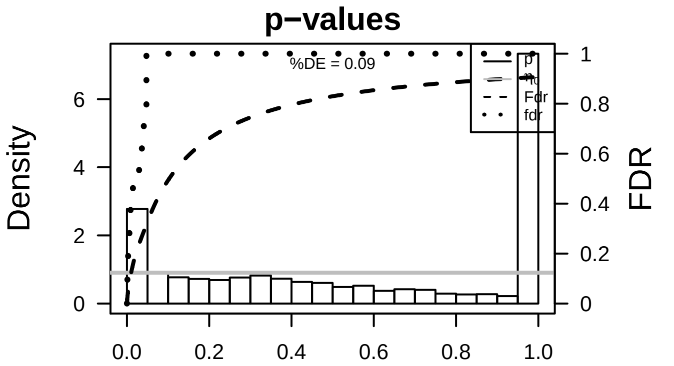


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	0.98	−0.1	0.41	CHRDL2	chordin−like 2 [Source:HGNC Symbol;Acc:HGNC:24168]
2	ENSG000001	0.66	−0.14	0.75	LHFP	lipoma HMGIC fusion partner [Source:HGNC Symbol;Acc:HG
3	ENSG000001	0.62	−0.35	0.36	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
4	ENSG000001	0.61	−0.32	0.55	C1R	complement component 1, r subcomponent [Source:HGNC S
5	ENSG000001	0.52	−0.06	0.86	NPTX1	neuronal pentraxin I [Source:HGNC Symbol;Acc:HGNC:7952
6	ENSG000001	0.5	−0.2	0.42	VIP	vasoactive intestinal peptide [Source:HGNC Symbol;Acc:HGN
7	ENSG000000	0.49	−0.24	0.49	CYBRD1	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:HGNC
8	ENSG000001	0.47	−0.36	0.71	CNN3	calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
9	ENSG000001	0.47	−0.18	0.67	FILIP1L	filamin A interacting protein 1−like [Source:HGNC Symbol;Ac
10	ENSG000001	0.47	−0.1	0.84	BTC	betacellulin [Source:HGNC Symbol;Acc:HGNC:1121]
11	ENSG000001	0.45	−0.22	0.8	CALM2	calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC S
12	ENSG000001	0.45	−0.06	0.92		
13	ENSG000001	0.45	−0.08	0.88	HACD1	3−hydroxyacyl−CoA dehydratase 1 [Source:HGNC Symbol;A
14	ENSG000000	0.44	−0.06	0.88	GPM6B	glycoprotein M6B [Source:HGNC Symbol;Acc:HGNC:4461]
15	ENSG000001	0.43	−0.13	0.79	HSPG2	heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:H
16	ENSG000001	0.42	−0.13	0.7	NFIL3	nuclear factor, interleukin 3 regulated [Source:HGNC Symbol
17	ENSG000001	0.42	−0.04	0.9	CHRM2	cholinergic receptor, muscarinic 2 [Source:HGNC Symbol;Ac
18	ENSG000001	0.41	−0.1	0.85	NT5DC3	5'−nucleotidase domain containing 3 [Source:HGNC Symbol;
19	ENSG000000	0.4	−0.16	0.82	PFN2	profilin 2 [Source:HGNC Symbol;Acc:HGNC:8882]
20	ENSG000001	0.4	−0.05	0.93	GPM6A	glycoprotein M6A [Source:HGNC Symbol;Acc:HGNC:4460]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−27	1 / 16	Canc	LIU_PROSTATE_CANCER_DN
2	3e−20	393 / 10800	Brain	Overlap_fetal_midbrain_Quies
3	2e−18	34 / 191	Brain	Overlap_fetal_midbrain_Het
4	6e−17	370 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
5	1e−16	370 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
6	3e−15	27 / 147	BP	homophilic cell adhesion via plasma membrane adhesion molecules
7	4e−15	257 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
8	1e−13	403 / 11968	Colon	TssWk_Colon
9	4e−13	40 / 384	GSE	BERENJENO_TRANSFORMED_BY_RHOA_DN
10	4e−13	45 / 478	GSE	LIM_MAMMARY_STEM_CELL_UP
11	7e−13	349 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
12	3e−12	55 / 711	GSE	LEE_BMP2_TARGETS_UP
13	4e−12	19 / 91	GSE	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
14	5e−12	334 / 9470	Colon	Quies3_Colon
15	1e−11	53 / 692	GSE	WONG_ADULT_TISSUE_STEM_MODULE
16	1e−11	55 / 736	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
17	1e−11	52 / 672	MF	calcium ion binding
18	1e−11	44 / 510	GSE	ONKEN_UVEAL_MELANOMA_DN
19	2e−11	19 / 99	Glio	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
20	2e−11	185 / 4379	Colon	TssD1_Colon
21	2e−11	22 / 138	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
22	2e−11	39 / 419	GSE	BAELDE_DIABETIC_NEPHROPATHY_DN
23	3e−11	200 / 4879	Colon	Quies1_Colon
24	5e−11	59 / 855	Brain	Overlap_fetal_midbrain_ZNF
25	6e−11	38 / 414	Lymp	TARTE_Mature plasma cell signature
26	9e−11	229 / 5889	Colon	EnhWk1_Colon
27	2e−10	57 / 834	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
28	2e−10	388 / 11791	Colon	Enh_Colon
29	2e−10	40 / 471	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
30	5e−10	20 / 132	Colon	Marisa_CRC−cluster−b
31	5e−10	38 / 445	GSE	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
32	7e−10	40 / 490	GSE	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
33	1e−09	36 / 418	GSE	SWEET_LUNG_CANCER_KRAS_DN
34	1e−09	36 / 420	GSE	SHEN_SMARCA2_TARGETS_UP
35	2e−09	23 / 189	GSE	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
36	2e−09	128 / 2838	Lymp	HOPP_Poised_promoter
37	3e−09	35 / 413	GSE	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
38	4e−09	20 / 148	Colon	Marisa_CRC−cluster−a
39	4e−09	50 / 745	TF	ICGC_NrsfPcr2_targets
40	4e−09	40 / 523	BP	cell adhesion



Aging

Rank	p−value	#in/all	Geneset
1	0.006	10 / 144	HORVATH_aging_genes meth UP
2	0.051	7 / 123	HORVATH_aging_genes meth DOWN
3	0.793	1 / 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−15	27 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
2	4e−09	40 / 523	cell adhesion
3	8e−06	6 / 19	regulation of cardiac muscle contraction by regulation of the release of seques
4	1e−04	24 / 373	axon guidance
5	2e−04	12 / 131	cell cycle arrest
6	3e−04	13 / 152	actin cytoskeleton organization
7	3e−04	6 / 34	positive regulation of Wnt signaling pathway
8	3e−04	6 / 34	regulation of heart rate
9	5e−04	5 / 25	adrenal gland development
10	7e−04	7 / 55	heart morphogenesis
11	8e−04	10 / 109	neuron migration
12	1e−03	25 / 466	blood coagulation
13	1e−03	5 / 30	developmental growth
14	1e−03	14 / 200	heart development
15	1e−03	6 / 45	adenylate cyclase−modulating G−protein coupled receptor signaling pathway
16	2e−03	19 / 325	response to drug
17	2e−03	4 / 20	semaphorin−plexin signaling pathway
18	2e−03	18 / 306	extracellular matrix organization
19	2e−03	7 / 66	positive regulation of endothelial cell proliferation
20	2e−03	9 / 104	chromatin modification

Brain

Rank	p−value	#in/all	Geneset
1	3e−20	393 / 10800	Overlap_fetal_midbrain_Quies
2	2e−18	34 / 191	Overlap_fetal_midbrain_Het
3	6e−17	370 / 10239	Overlap_fetal_midbrain_ReprPC
4	1e−16	370 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	4e−15	257 / 6320	Overlap_fetal_midbrain_HetRpts
6	7e−13	349 / 9923	Overlap_fetal_midbrain_K9K27me3
7	5e−11	59 / 855	Overlap_fetal_midbrain_ZNF
8	6e−09	27 / 268	Mid_Frontal_Lobe_TssA
9	1e−05	59 / 1210	Fetal_TssP
10	2e−05	57 / 1182	Fetal_EnhP
11	3e−05	128 / 3370	Mid_Frontal_Lobe_ZNF
12	9e−05	58 / 1279	Overlap_fetal_midbrain_Enh
13	3e−04	49 / 1084	Overlap_fetal_midbrain_EnhG
14	4e−04	41 / 865	Mid_Frontal_Lobe_Het
15	5e−04	21 / 342	Fetal_Het
16	7e−04	23 / 400	Fetal_ZNF
17	4e−03	32 / 712	Overlap_fetal_midbrain_EnhP
18	8e−03	45 / 1137	Fetal_Enh
19	8e−03	101 / 2956	Fetal_TssA
20	1e−02	38 / 939	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	5e−27	1 / 16	LIU_PROSTATE_CANCER_DN
2	8e−04	4 / 16	GENTLES_modul11
3	2e−03	19 / 324	SPANG_BCL6−index2
4	2e−03	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	2e−03	13 / 191	SPANG_LPS−index2
6	6e−02	2 / 15	GENTLES_modul17
7	7e−02	2 / 16	GENTLES_modul16
8	8e−02	3 / 37	KUIPER_MM good survival
9	9e−02	7 / 140	PanCan_RAS_geneset_nanostring
10	9e−02	9 / 198	PanCan_PI3K_geneset_nanostring
11	1e−01	7 / 152	PanCan_MAPK_geneset_nanostring
12	2e−01	4 / 78	PanCan_Wnt_geneset_nanostring
13	3e−01	1 / 16	LIU_LIVER_CANCER
14	3e−01	3 / 71	SHAUGHNESSY_MM high risk
15	3e−01	1 / 15	LIU_BREAST_CANCER
16	3e−01	1 / 15	BEN−PORATH_UP
17	4e−01	1 / 16	RHODES_CANCER_META_SIGNATURE
18	4e−01	1 / 16	LIU_COMMON_CANCER_GENES
19	4e−01	1 / 16	WANG_ER_UP
20	4e−01	1 / 16	GENTLES_modul18

CC

Rank	p−value	#in/all	Geneset
1	1e−05	107 / 2638	extracellular exosome
2	2e−05	133 / 3507	plasma membrane
3	4e−05	12 / 109	Z disc
4	4e−05	7 / 36	heterotrimeric G−protein complex
5	5e−05	7 / 37	microtubule associated complex
6	7e−05	6 / 27	cortical cytoskeleton
7	1e−04	10 / 88	basement membrane
8	3e−04	13 / 151	myelin sheath
9	3e−04	23 / 378	focal adhesion
10	8e−04	9 / 91	sarcolemma
11	3e−03	105 / 2974	cytosol
12	3e−03	3 / 11	apicolateral plasma membrane
13	3e−03	11 / 152	microtubule cytoskeleton
14	3e−03	16 / 270	proteinaceous extracellular matrix
15	4e−03	3 / 12	npBAF complex
16	4e−03	8 / 93	endomembrane system
17	4e−03	5 / 39	T−tubule
18	5e−03	3 / 13	axonal growth cone
19	6e−03	4 / 27	Cul3−RING ubiquitin ligase complex
20	6e−03	5 / 43	intercalated disc

Chr

Rank	p−value	#in/all	Geneset
1	0.01	35 / 862	Chr 5
2	0.03	45 / 1228	Chr 2
3	0.04	29 / 746	Chr X
4	0.12	21 / 582	Chr 15
5	0.15	25 / 735	Chr 4
6	0.31	56 / 1920	Chr 1
7	0.35	30 / 1017	Chr 12
8	0.47	21 / 745	Chr 9
9	0.48	24 / 859	Chr 7
10	0.48	20 / 715	Chr 10
11	0.49	30 / 1083	Chr 17
12	0.50	9 / 318	Chr 13
13	0.53	12 / 436	Chr 22
14	0.57	26 / 976	Chr 6
15	0.61	7 / 272	Chr 18
16	0.70	16 / 651	Chr 8
17	0.71	26 / 1043	Chr 3
18	0.79	28 / 1172	Chr 11
19	0.91	10 / 522	Chr 20
20	0.93	17 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−13	403 / 11968	TssWk_Colon
2	5e−12	334 / 9470	Quies3_Colon
3	2e−11	185 / 4379	TssD1_Colon
4	3e−11	200 / 4879	Quies1_Colon
5	9e−11	229 / 5889	EnhWk1_Colon
6	2e−10	388 / 11791	Enh_Colon
7	5e−10	20 / 132	Marisa_CRC−cluster−b
8	4e−09	20 / 148	Marisa_CRC−cluster−a
9	4e−08	29 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	2e−07	130 / 3109	TssP_Colon
11	6e−07	325 / 9930	Tx_Colon
12	9e−07	165 / 4327	EnhWk2_Colon
13	1e−06	309 / 9390	TxWk_Colon
14	2e−06	49 / 877	TxEnhG2_Colon
15	4e−06	34 / 532	K9acLow_Colon
16	9e−06	333 / 10475	TssA_Colon
17	1e−05	122 / 3112	EnhA_Colon
18	3e−05	60 / 1281	HetRpts_Colon
19	2e−04	22 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
20	4e−04	71 / 1753	Het_Colon

Disease

Rank	p−value	#in/all	Geneset
1	2e−08	33 / 399	GUDJ_psoriasis down
2	1e+00	6 / 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−11	19 / 99	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
2	8e−05	22 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	4e−04	26 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
4	4e−03	22 / 436	Down_b
5	7e−03	3 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
6	9e−03	3 / 16	VERHAAK_CL subtype
7	2e−02	20 / 434	Down_a
8	2e−02	4 / 36	Shaw_down_in_1p19q
9	2e−02	2 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
10	4e−02	6 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	4e−02	2 / 12	Phillips MES up vs Prolif & PN
12	5e−02	2 / 13	VERHAAK_Brain
13	7e−02	2 / 16	VERHAAK_MES subtype
14	7e−02	3 / 35	shaw_responders_down_in_oligo_glioma
15	8e−02	4 / 61	Christensen_hypermethylated_in_primary_glioblastoma
16	1e−01	6 / 119	GIEZELT_GBM_WT_up_VS_mut
17	1e−01	49 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
18	1e−01	2 / 24	Martinez_Glio_hypermeth
19	2e−01	3 / 50	Vishal_subnetwork signature of survival in GBM
20	2e−01	3 / 53	Donson−innate immunity−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−27	1 / 16	LIU_PROSTATE_CANCER_DN
2	4e−13	40 / 384	BERENJENO_TRANSFORMED_BY_RHOA_DN
3	4e−13	45 / 478	LIM_MAMMARY_STEM_CELL_UP
4	3e−12	55 / 711	LEE_BMP2_TARGETS_UP
5	4e−12	19 / 91	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G
6	1e−11	53 / 692	WONG_ADULT_TISSUE_STEM_MODULE
7	1e−11	55 / 736	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
8	1e−11	44 / 510	ONKEN_UVEAL_MELANOMA_DN
9	2e−11	22 / 138	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
10	2e−11	39 / 419	BAELDE_DIABETIC_NEPHROPATHY_DN
11	2e−10	57 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
12	2e−10	40 / 471	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
13	5e−10	38 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
14	7e−10	40 / 490	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
15	1e−09	36 / 418	SWEET_LUNG_CANCER_KRAS_DN
16	1e−09	36 / 420	SHEN_SMARCA2_TARGETS_UP
17	2e−09	23 / 189	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
18	3e−09	35 / 413	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
19	6e−09	23 / 200	KARLSSON_TGFB1_TARGETS_DN
20	7e−09	23 / 202	CHANG_CORE_SERUM_RESPONSE_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−04	15 / 195	HALLMARK_MYOGENESIS
2	5e−04	12 / 140	HALLMARK_UV_RESPONSE_DN
3	3e−03	13 / 198	HALLMARK_HYPOXIA
4	3e−03	13 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	1e−02	6 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	2e−02	11 / 193	HALLMARK_HEME_METABOLISM
7	2e−02	11 / 196	HALLMARK_MITOTIC_SPINDLE
8	2e−02	11 / 199	HALLMARK_ADIPOGENESIS
9	7e−02	3 / 36	HALLMARK_HEDGEHOG_SIGNALING
10	8e−02	9 / 190	HALLMARK_APICAL_JUNCTION
11	1e−01	5 / 94	HALLMARK_PROTEIN_SECRETION
12	1e−01	3 / 44	HALLMARK_APICAL_SURFACE
13	2e−01	6 / 132	HALLMARK_COAGULATION
14	2e−01	3 / 52	HALLMARK_TGF_BETA_SIGNALING
15	2e−01	8 / 198	HALLMARK_GLYCOLYSIS
16	3e−01	2 / 36	HALLMARK_ANGIOGENESIS
17	3e−01	7 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
18	3e−01	7 / 196	HALLMARK_G2M_CHECKPOINT
19	3e−01	7 / 197	HALLMARK_IL2_STAT5_SIGNALING
20	4e−01	3 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.6	1 / 33	DUMEAUX_Fasting enriched genes
2	0.7	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	6e−11	38 / 414	TARTE_Mature plasma cell signature
2	2e−09	128 / 2838	HOPP_Poised_promoter
3	8e−07	276 / 8147	HOPP_Weak_promoter
4	8e−07	23 / 261	LENZ_Stromal signature 1
5	1e−06	259 / 7592	HOPP_Strong_enhancer
6	6e−06	233 / 6784	HOPP_Weak_enhancer
7	8e−06	221 / 6389	HOPP_Weak_txn
8	4e−05	23 / 332	SPANG_CD40 6hrs UP
9	6e−05	271 / 8358	HOPP_Active_promoter
10	1e−04	22 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
11	2e−04	102 / 2658	HOPP_Repetitive
12	2e−04	22 / 347	WIRTH_lymphoma937_spot H
13	5e−04	171 / 5039	HOPP_Repressed
14	7e−04	19 / 302	SPANG_IL21 UP
15	2e−03	11 / 145	WIRTH_lymphoma937_spot F
16	2e−03	11 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
17	4e−03	53 / 1333	SPANG_BCR UP
18	9e−03	16 / 304	ZHANG_DLBCL mutated
19	1e−02	9 / 138	Subero_DLBCL_hyper_meth
20	1e−02	8 / 115	ROSOLOWSKI_green total

MF

Rank	p−value	#in/all	Geneset
1	1e−11	52 / 672	calcium ion binding
2	2e−07	347 / 10693	protein binding
3	6e−06	6 / 18	guanyl nucleotide binding
4	2e−04	4 / 11	glutathione binding
5	3e−04	5 / 22	G−protein beta/gamma−subunit complex binding
6	4e−04	35 / 693	protein homodimerization activity
7	5e−04	12 / 142	heparin binding
8	8e−04	4 / 16	phospholipase binding
9	8e−04	4 / 16	transforming growth factor beta binding
10	1e−03	7 / 58	cytoskeletal protein binding
11	1e−03	6 / 45	SMAD binding
12	1e−03	21 / 371	GTP binding
13	1e−03	16 / 250	GTPase activity
14	2e−03	18 / 301	actin binding
15	2e−03	7 / 66	ATPase binding
16	2e−03	13 / 189	transcription corepressor activity
17	5e−03	12 / 186	microtubule binding
18	7e−03	13 / 217	protein domain specific binding
19	7e−03	14 / 245	ubiquitin protein ligase binding
20	2e−02	12 / 219	receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−08	30 / 360	hsa−let−7a
2	1e−07	28 / 333	hsa−miR−32
3	2e−07	28 / 334	hsa−miR−590−3p
4	3e−07	26 / 304	hsa−miR−25
5	3e−07	11 / 57	hsa−miR−629
6	3e−07	26 / 307	hsa−miR−548c−3p
7	5e−07	20 / 197	hsa−miR−9
8	5e−07	33 / 462	hsa−miR−130b
9	6e−07	32 / 442	hsa−miR−548n
10	8e−07	33 / 471	hsa−miR−130a
11	2e−06	35 / 536	hsa−miR−106b
12	2e−06	26 / 337	hsa−miR−367
13	4e−06	18 / 187	hsa−miR−381
14	4e−06	25 / 330	hsa−let−7f
15	5e−06	35 / 562	hsa−miR−17
16	5e−06	23 / 291	hsa−miR−570
17	6e−06	34 / 542	hsa−miR−106a
18	6e−06	17 / 175	hsa−miR−369−3p
19	7e−06	30 / 452	hsa−miR−19a
20	8e−06	28 / 407	hsa−miR−301b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 10	BENTINK_ras.4
2	0.28	1 / 12	BENTINK_ras.1
3	0.30	1 / 13	BENTINK_e2f3.2
4	0.32	1 / 14	GUSTAFSON_PI3K_UP
5	0.32	1 / 14	BENTINK_e2f3.1
6	0.34	1 / 15	BENTINK_ras.6
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 14	BENTINK_myc.1
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−09	50 / 745	ICGC_NrsfPcr2_targets
2	7e−05	65 / 1472	ICGC_NrsfPcr1_targets
3	2e−04	107 / 2827	ICGC_Bcl3_targets
4	6e−04	83 / 2149	ICGC_Mef2_targets
5	9e−04	90 / 2401	ICGC_Bcl11_targets
6	2e−03	60 / 1506	ICGC_Usf1_targets
7	2e−03	122 / 3511	ICGC_Rad21_targets
8	6e−03	77 / 2133	ICGC_Cebpbsc150_targets
9	8e−03	58 / 1549	ICGC_Myc_targets
10	1e−02	146 / 4566	ICGC_Egr1_targets
11	2e−02	91 / 2719	ICGC_Pbx3_targets
12	5e−02	169 / 5552	ICGC_Pol24_targets
13	7e−02	143 / 4714	ICGC_Pu1_targets
14	9e−02	128 / 4230	ICGC_Nfatc1_targets
15	1e−01	201 / 6862	ICGC_Elf1_targets
16	1e−01	156 / 5308	ICGC_Tcf12_targets
17	1e−01	147 / 4987	ICGC_Bclaf101388_targets
18	1e−01	96 / 3177	ICGC_Irf4_targets
19	1e−01	151 / 5135	ICGC_Ebfsc137065_targets
20	1e−01	184 / 6324	ICGC_Yy1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	5e−05	8 / 49	VAQUERIZAS_Uterus
2	5e−05	5 / 16	VAQUERIZAS_Ovary
3	4e−03	4 / 25	VAQUERIZAS_Adrenal cortex
4	8e−03	6 / 64	VAQUERIZAS_Lung
5	2e−02	4 / 41	VAQUERIZAS_Fetal brain
6	4e−02	5 / 67	VAQUERIZAS_Whole blood
7	4e−02	4 / 46	VAQUERIZAS_Whole brain
8	5e−02	3 / 30	VAQUERIZAS_Smooth muscle
9	5e−02	3 / 31	VAQUERIZAS_Fetal lung
10	8e−02	2 / 17	VAQUERIZAS_Adrenal gland
11	8e−02	2 / 17	VAQUERIZAS_Salivary gland
12	8e−02	3 / 37	VAQUERIZAS_Prostate
13	9e−02	2 / 19	VAQUERIZAS_Heart
14	1e−01	2 / 23	VAQUERIZAS_Pituitary
15	1e−01	2 / 25	VAQUERIZAS_Spinal cord
16	2e−01	1 / 7	VAQUERIZAS_Appendix
17	2e−01	1 / 8	VAQUERIZAS_Tongue
18	2e−01	1 / 10	VAQUERIZAS_Skeletal.muscle.psoas
19	3e−01	2 / 42	VAQUERIZAS_Thyroid
20	4e−01	5 / 155	VAQUERIZAS_General

Tissue

Rank	p−value	#in/all	Geneset
1	0.006	23 / 476	WIRTH_Nervous System
2	0.015	9 / 140	PALMER_T−Cell signature up
3	0.054	2 / 14	WIRTH_B−cells
4	0.054	2 / 14	WIRTH_Thymus
5	0.054	2 / 14	WIRTH_Thyroid gland
6	0.171	10 / 259	PALMER_Granulocytes signature up
7	0.282	1 / 12	WIRTH_Tonsil
8	0.302	1 / 13	WIRTH_Prim. lymphoid organs
9	0.302	1 / 13	WIRTH_Globus pallidus
10	0.537	4 / 141	WIRTH_Muscle
11	0.821	4 / 208	PALMER_B−Cell signature up
12	0.891	2 / 137	WIRTH_Mucosa
13	0.896	1 / 82	WIRTH_Homeostasis
14	0.975	2 / 202	WIRTH_Testis
15	0.977	6 / 427	WIRTH_Immune system
16	1.000	0 / 6	WIRTH_Pituitary gland
17	1.000	0 / 54	WIRTH_Pancreas
18	1.000	0 / 13	WIRTH_Sec. lymphoid organs
19	1.000	0 / 12	WIRTH_Lymphocytes
20	1.000	0 / 14	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.01	167 / 5285	LU_BPDE 0.005 DN
2	0.05	47 / 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	

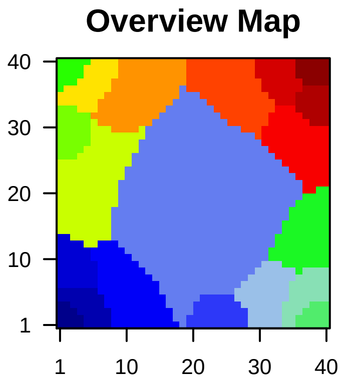
K−Means Clusters

Spot Summary: J

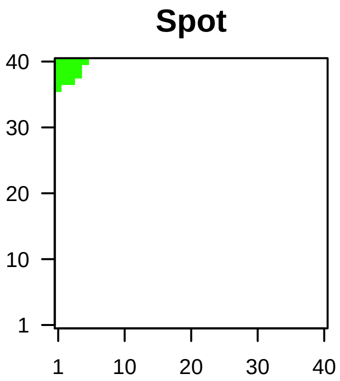
metagenes = 17
genes = 337

<r> metagenes = 0.99
<r> genes = 0.8
beta: r2= 0.65 / log p= −5.44

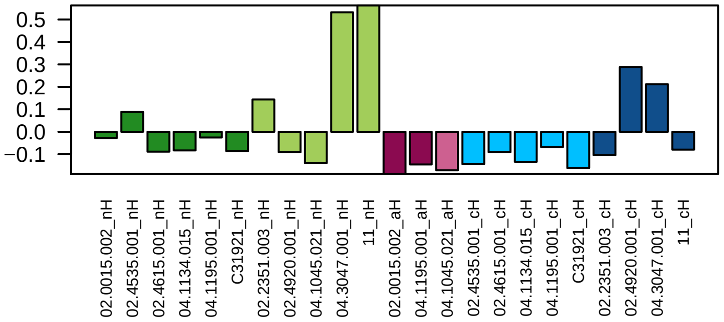
samples with spot = 5 (21.7 %)
other_normHNPCC : 3 (60 %)
other_cancerHNPCC : 2 (50 %)



Overview Map



Spot

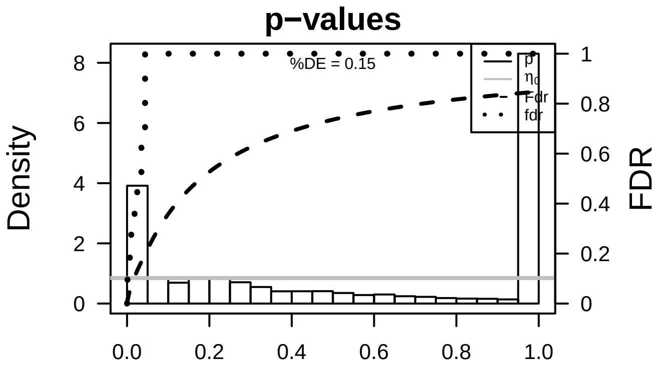


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.59	−0.8	0.87	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	ENSG000001	1.46	−0.53	0.95	MYH11	myosin, heavy chain 11, smooth muscle [Source:HGNC Symb
3	ENSG000001	1.44	−0.52	0.94	CNN1	calponin 1, basic, smooth muscle [Source:HGNC Symbol;Acc
4	ENSG000001	1.42	−0.68	0.91	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Symb
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	0.9	MYL9	myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:H
7	ENSG000001	1.32	−0.37	0.96	SYNM	synemin, intermediate filament protein [Source:HGNC Symbo
8	ENSG000001	1.3	−0.58	0.97	FLNA	filamin A, alpha [Source:HGNC Symbol;Acc:HGNC:3754]
9	ENSG000001	1.29	−0.49	0.95	TPM2	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
10	ENSG000001	1.24	−0.52	0.74	IGFBP7	insulin−like growth factor binding protein 7 [Source:HGNC Sy
11	ENSG000001	1.21	−0.38	0.98	CSRP1	cysteine and glycine−rich protein 1 [Source:HGNC Symbol;Ac
12	ENSG000001	1.2	−0.74	0.92	TAGLN	transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
13	ENSG000000	1.17	−0.45	0.95	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	0.99	CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
16	ENSG000000	1.17	−0.4	0.97	FHL1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:HG
17	ENSG000001	1.17	−0.36	0.98	LMOD1	leiomodin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
18	ENSG000001	1.14	−0.57	0.95	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	0.98	PLN	phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−72	5 / 16	Cance	LIU_PROSTATE_CANCER_DN
2	3e−67	58 / 132	Colon	Marisa_CRC−cluster−b
3	3e−51	69 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
4	7e−50	75 / 478	GSEA	LIM_MAMMARY_STEM_CELL_UP
5	3e−45	74 / 535	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
6	1e−44	59 / 303	GSEA	PASINI_SUZ12_TARGETS_DN
7	5e−40	47 / 196	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
8	8e−36	60 / 445	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
9	1e−33	51 / 326	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	2e−31	47 / 294	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
11	5e−31	67 / 692	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
12	2e−30	44 / 261	Lymph	LENZ_Stromal signature 1
13	9e−30	39 / 198	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	1e−29	36 / 160	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
15	2e−28	51 / 418	GSEA	SWEET_LUNG_CANCER_KRAS_DN
16	5e−28	45 / 314	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
17	5e−28	45 / 315	Lymph	WIRTH_lymphoma937_spot E
18	2e−27	48 / 378	CC	focal adhesion
19	3e−26	54 / 525	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
20	4e−25	20 / 40	GSEA	TOMLINS_PROSTATE_CANCER_DN
21	1e−24	60 / 711	GSEA	LEE_BMP2_TARGETS_UP
22	1e−23	45 / 399	Disea	GUDJ_psoriasis down
23	3e−23	39 / 292	GSEA	CHANDRAN_METASTASIS_DN
24	4e−23	33 / 195	HM	HALLMARK_MYOGENESIS
25	9e−23	36 / 248	GSEA	ONDER_CDH1_TARGETS_2_UP
26	1e−22	37 / 267	GSEA	WANG_SMARCE1_TARGETS_UP
27	3e−20	27 / 144	GSEA	IGLESIAS_E2F_TARGETS_UP
28	5e−20	27 / 148	Colon	Marisa_CRC−cluster−a
29	5e−20	14 / 22	GSEA	REACTOME_SMOOTH_MUSCLE_CONTRACTION
30	5e−20	17 / 40	GSEA	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
31	1e−19	33 / 249	GSEA	BOQUEST_STEM_CELL_UP
32	3e−19	36 / 313	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
33	2e−18	32 / 254	GSEA	LU_AGING_BRAIN_UP
34	7e−18	22 / 105	BP	muscle contraction
35	8e−18	39 / 413	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
36	8e−18	28 / 195	GSEA	KEGG_FOCAL_ADHESION
37	1e−17	16 / 44	GSEA	REACTOME_MUSCLE_CONTRACTION
38	1e−17	160 / 5039	Lymph	HOPP_Repressed
39	2e−17	38 / 401	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
40	2e−17	28 / 202	CC	extracellular matrix



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.04	6 / 144	HORVATH_aging_genes meth UP
2	0.06	5 / 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	7e−18	22 / 105	muscle contraction
2	6e−17	33 / 306	extracellular matrix organization
3	5e−11	34 / 523	cell adhesion
4	8e−10	14 / 93	cell−matrix adhesion
5	1e−08	25 / 373	axon guidance
6	1e−08	14 / 113	extracellular matrix disassembly
7	3e−07	6 / 17	regulation of muscle contraction
8	7e−07	7 / 30	sarcomere organization
9	8e−07	25 / 466	blood coagulation
10	1e−06	9 / 62	response to mechanical stimulus
11	3e−06	7 / 36	muscle filament sliding
12	3e−06	7 / 37	digestive tract development
13	3e−06	7 / 37	positive regulation of cell−substrate adhesion
14	4e−06	7 / 39	platelet aggregation
15	5e−06	9 / 73	actin filament organization
16	1e−05	15 / 224	angiogenesis
17	1e−05	25 / 539	small GTPase mediated signal transduction
18	1e−05	9 / 81	platelet degranulation
19	1e−05	9 / 83	integrin−mediated signaling pathway
20	2e−05	14 / 209	platelet activation

Brain

Rank	p−value	#in/all	Geneset
1	2e−14	107 / 2956	Fetal_TssA
2	4e−09	85 / 2603	Fetal_TxTrans
3	8e−08	48 / 1210	Fetal_TssP
4	6e−06	74 / 2549	Fetal_TssF
5	9e−06	103 / 3977	Mid_Frontal_Lobe_ReprPC
6	1e−05	63 / 2084	Mid_Frontal_Lobe_K9K27me3
7	3e−04	28 / 787	Overlap_fetal_midbrain_TssP
8	3e−03	14 / 342	Fetal_Het
9	4e−03	19 / 552	Fetal_Tx
10	5e−03	212 / 10800	Overlap_fetal_midbrain_Quies
11	2e−02	10 / 268	Mid_Frontal_Lobe_TssA
12	3e−02	73 / 3370	Mid_Frontal_Lobe_ZNF
13	4e−02	32 / 1327	Mid_Frontal_Lobe_TssP
14	4e−02	61 / 2820	Mid_Frontal_Lobe_HetRpts
15	1e−01	20 / 840	Mid_Frontal_Lobe_TssF
16	1e−01	11 / 408	Mid_Frontal_Lobe_TxTrans
17	1e−01	26 / 1182	Fetal_EnhP
18	1e−01	189 / 10239	Overlap_fetal_midbrain_ReprPC
19	2e−01	29 / 1356	Fetal_K9K27me3
20	2e−01	24 / 1108	Overlap_fetal_midbrain_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	2e−72	5 / 16	LIU_PROSTATE_CANCER_DN
2	3e−09	7 / 15	GENTLES_modul17
3	8e−05	24 / 574	Lembcke_Colonic Inflammation
4	2e−03	3 / 15	BEN−PORATH_UP
5	2e−03	3 / 15	GENTLES_modul13
6	5e−03	8 / 152	PanCan_MAPK_geneset_nanostring
7	7e−03	9 / 191	SPANG_LPS−index2
8	3e−02	1 / 16	LIU_LIVER_CANCER
9	3e−02	11 / 324	SPANG_BCL6−index2
10	7e−02	1 / 15	LIU_BREAST_CANCER
11	1e−01	6 / 198	PanCan_PI3K_geneset_nanostring
12	2e−01	2 / 51	PanCan_TGF−B_geneset_nanostring
13	2e−01	3 / 97	PanCan_TXmisReg_geneset_nanostring
14	2e−01	1 / 16	GENTLES_modul11
15	2e−01	1 / 16	GENTLES_modul16
16	3e−01	1 / 24	PanCan_Notch_geneset_nanostring
17	5e−01	0 / 14	LIU_PROSTATE_CANCER_UP
18	5e−01	1 / 37	KUIPER_MM good survival
19	6e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	6e−01	1 / 52	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	2e−27	48 / 378	focal adhesion
2	2e−17	28 / 202	extracellular matrix
3	1e−14	100 / 2638	extracellular exosome
4	2e−14	18 / 91	sarcolemma
5	5e−14	19 / 109	Z disc
6	3e−11	9 / 21	costamere
7	3e−11	22 / 216	actin cytoskeleton
8	6e−11	54 / 1176	extracellular space
9	1e−09	11 / 51	stress fiber
10	2e−09	22 / 270	proteinaceous extracellular matrix
11	4e−09	13 / 88	basement membrane
12	7e−08	13 / 110	blood microparticle
13	1e−07	52 / 1374	extracellular region
14	1e−07	100 / 3507	plasma membrane
15	2e−07	28 / 523	cell surface
16	5e−07	132 / 5185	cytoplasm
17	1e−06	22 / 381	cytoskeleton
18	1e−06	15 / 190	membrane raft
19	2e−06	85 / 2974	cytosol
20	2e−06	8 / 49	extracellular vesicle

Chr

Rank	p−value	#in/all	Geneset
1	8e−04	25 / 715	Chr 10
2	1e−02	22 / 745	Chr 9
3	4e−02	20 / 746	Chr X
4	2e−01	5 / 191	Chr 21
5	3e−01	13 / 613	Chr 14
6	4e−01	23 / 1228	Chr 2
7	4e−01	14 / 735	Chr 4
8	4e−01	19 / 1017	Chr 12
9	4e−01	35 / 1920	Chr 1
10	4e−01	16 / 859	Chr 7
11	6e−01	14 / 862	Chr 5
12	7e−01	19 / 1172	Chr 11
13	7e−01	9 / 582	Chr 15
14	7e−01	8 / 522	Chr 20
15	7e−01	17 / 1083	Chr 17
16	7e−01	15 / 976	Chr 6
17	7e−01	16 / 1043	Chr 3
18	8e−01	6 / 436	Chr 22
19	9e−01	8 / 651	Chr 8
20	1e+00	2 / 272	Chr 18

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−67	58 / 132	Marisa_CRC−cluster−b
2	5e−20	27 / 148	Marisa_CRC−cluster−a
3	2e−13	30 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	1e−11	28 / 337	Pentrack_CRC_TCGA_group.over_B_msi=h_UP
5	2e−11	265 / 11968	TssWk_Colon
6	9e−11	33 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
7	3e−09	256 / 11791	Enh_Colon
8	3e−08	150 / 5889	EnhWk1_Colon
9	4e−08	120 / 4379	TssD1_Colon
10	5e−08	93 / 3109	TssP_Colon
11	2e−07	5 / 9	Budinska_D_Mesenchymal_UP
12	5e−07	90 / 3122	TxEnhG1_Colon
13	8e−07	27 / 532	K9acLow_Colon
14	9e−07	89 / 3112	EnhA_Colon
15	9e−06	110 / 4327	EnhWk2_Colon
16	4e−05	21 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
17	9e−05	9 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
18	4e−04	148 / 6761	TssD2_Colon
19	5e−04	26 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
20	5e−04	20 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	1e−23	45 / 399	GUDJ_psoriasis down
2	1e+00	3 / 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	8e−10	23 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−07	8 / 36	Colman_survival_associated
3	3e−06	11 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
4	4e−06	5 / 15	Mukasa_UP_in_GBM
5	5e−06	8 / 56	mature astrocytes
6	2e−04	7 / 69	cultured astroglia vs. in vivo astrocytes
7	2e−04	9 / 119	GIEZELT_GBM_WT_up_VS_mut
8	7e−04	44 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
9	8e−04	6 / 63	OPC
10	9e−04	6 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
11	1e−03	3 / 12	Phillips MES up vs Prolif & PN
12	2e−03	5 / 52	OL vs. OPC
13	6e−03	8 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	1e−02	2 / 9	Colman_survival_robust
15	1e−02	5 / 77	Weller_LGG_gradeII−vs−III_DOWN
16	1e−02	7 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	2e−02	4 / 58	OL vs. MOG− OL
18	2e−02	3 / 34	WIRTH_PN subtype
19	2e−02	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
20	2e−02	4 / 61	in vivo astrocytes vs. cultured astroglia

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−72	5 / 16	LIU_PROSTATE_CANCER_DN
2	3e−51	69 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
3	7e−50	75 / 478	LIM_MAMMARY_STEM_CELL_UP
4	3e−45	74 / 535	CHICAS_RB1_TARGETS_CONFLUENT
5	1e−44	59 / 303	PASINI_SUZ12_TARGETS_DN
6	5e−40	47 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	8e−36	60 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
8	1e−33	51 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
9	2e−31	47 / 294	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
10	5e−31	67 / 692	WONG_ADULT_TISSUE_STEM_MODULE
11	1e−29	36 / 160	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
12	2e−28	51 / 418	SWEET_LUNG_CANCER_KRAS_DN
13	3e−26	54 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
14	4e−25	20 / 40	TOMLINS_PROSTATE_CANCER_DN
15	1e−24	60 / 711	LEE_BMP2_TARGETS_UP
16	3e−23	39 / 292	CHANDRAN_METASTASIS_DN
17	9e−23	36 / 248	ONDER_CDH1_TARGETS_2_UP
18	1e−22	37 / 267	WANG_SMARCE1_TARGETS_UP
19	3e−20	27 / 144	IGLESIAS_E2F_TARGETS_UP
20	5e−20	14 / 22	REACTOME_SMOOTH_MUSCLE_CONTRACTION

HM

Rank	p−value	#in/all	Geneset
1	9e−30	39 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	4e−23	33 / 195	HALLMARK_MYOGENESIS
3	7e−09	18 / 190	HALLMARK_APICAL_JUNCTION
4	7e−06	12 / 140	HALLMARK_UV_RESPONSE_DN
5	2e−04	12 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	5e−04	10 / 157	HALLMARK_APOPTOSIS
7	5e−04	9 / 132	HALLMARK_COAGULATION
8	6e−04	11 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	7e−04	11 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
10	7e−04	11 / 197	HALLMARK_IL2_STAT5_SIGNALING
11	3e−03	10 / 198	HALLMARK_HYPOXIA
12	3e−03	10 / 199	HALLMARK_ADIPOGENESIS
13	7e−03	9 / 192	HALLMARK_COMPLEMENT
14	1e−02	4 / 52	HALLMARK_TGF_BETA_SIGNALING
15	3e−02	5 / 98	HALLMARK_ANDROGEN_RESPONSE
16	4e−02	3 / 44	HALLMARK_APICAL_SURFACE
17	6e−02	6 / 155	HALLMARK_UV_RESPONSE_UP
18	6e−02	7 / 196	HALLMARK_MITOTIC_SPINDLE
19	1e−01	6 / 196	HALLMARK_P53_PATHWAY
20	1e−01	4 / 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	0.08	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.21	3 / 91	DUMEAUX_Smoking enriched genes
4	0.44	1 / 33	DUMEAUX_Fasting enriched genes
5	1.00	0 / 11	DUMEAUX_Smoking 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	2e−30	44 / 261	LENZ_Stromal signature 1
2	5e−28	45 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
3	5e−28	45 / 315	WIRTH_lymphoma937_spot E
4	1e−17	160 / 5039	HOPP_Repressed
5	4e−13	101 / 2838	HOPP_Poised_promoter
6	1e−07	13 / 115	ROSOLOWSKI_green total
7	8e−07	9 / 59	LENZ_Stromal signature 2
8	1e−06	23 / 414	TARTE_Mature plasma cell signature
9	1e−04	5 / 29	DAVE_Immune response 1
10	2e−04	10 / 145	WIRTH_lymphoma937_spot F
11	2e−04	10 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
12	6e−04	7 / 83	ROSOLOWSKI_green UP
13	7e−04	9 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
14	1e−03	12 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	1e−03	7 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
16	2e−03	3 / 15	Subero_T−ALL_hypo_meth
17	3e−03	8 / 138	Subero_DLBCL_hyper_meth
18	5e−03	5 / 62	Subero_mBL_hyper_meth
19	6e−03	3 / 21	DAVE_Immune response 2
20	6e−03	7 / 122	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	2e−10	242 / 10693	protein binding
2	9e−10	10 / 39	structural constituent of muscle
3	8e−08	21 / 301	actin binding
4	2e−07	12 / 102	integrin binding
5	9e−07	11 / 96	structural constituent of cytoskeleton
6	3e−05	10 / 113	actin filament binding
7	4e−05	7 / 53	extracellular matrix structural constituent
8	4e−05	5 / 23	insulin−like growth factor binding
9	7e−05	7 / 58	cytoskeletal protein binding
10	8e−05	4 / 14	transcription factor activity, RNA polymerase II transcription factor binding
11	8e−05	7 / 60	collagen binding
12	2e−04	10 / 142	heparin binding
13	2e−04	6 / 49	protein kinase C binding
14	2e−04	11 / 172	calmodulin binding
15	3e−04	17 / 371	GTP binding
16	5e−04	13 / 250	GTPase activity
17	5e−04	4 / 22	laminin binding
18	6e−04	4 / 23	extracellular matrix binding
19	7e−04	4 / 24	glycosaminoglycan binding
20	8e−04	3 / 11	platelet−derived growth factor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−05	22 / 480	hsa−miR−301a
2	6e−05	12 / 174	hsa−miR−520h
3	2e−04	16 / 324	hsa−miR−559
4	4e−04	16 / 348	hsa−miR−548b−5p
5	5e−04	6 / 57	hsa−miR−892a
6	6e−04	12 / 223	hsa−miR−548m
7	6e−04	7 / 83	hsa−miR−1179
8	6e−04	14 / 291	hsa−miR−570
9	7e−04	10 / 165	hsa−miR−802
10	8e−04	15 / 332	hsa−miR−548a−5p
11	8e−04	18 / 442	hsa−miR−548n
12	8e−04	8 / 113	hsa−miR−449b
13	9e−04	12 / 233	hsa−miR−520g
14	9e−04	18 / 446	hsa−miR−19b
15	1e−03	21 / 562	hsa−miR−17
16	1e−03	11 / 204	hsa−miR−206
17	1e−03	18 / 452	hsa−miR−19a
18	1e−03	13 / 275	hsa−miR−449a
19	1e−03	5 / 46	hsa−miR−636
20	1e−03	15 / 348	hsa−miR−548d−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_e2f3.1
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 / 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 / 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	1e−05	4 / 9	MYC_Targets DOWN
2	3e−05	55 / 1798	HEBENSTREIT_low expression TF
3	3e−04	2 / 2	MYC_ECM cell adhesion DOWN
4	3e−03	2 / 5	MYC_TF and cofactors
5	3e−02	106 / 5135	ICGC_Ebfsc137065_targets
6	6e−02	73 / 3511	ICGC_Rad21_targets
7	8e−02	34 / 1523	ICGC_P300_targets
8	2e−01	44 / 2149	ICGC_Mef2_targets
9	2e−01	65 / 3305	ICGC_BatfPcr1_targets
10	2e−01	62 / 3177	ICGC_Irf4_targets
11	2e−01	47 / 2401	ICGC_Bcl11_targets
12	3e−01	30 / 1506	ICGC_Usf1_targets
13	3e−01	36 / 1867	HEBENSTREIT_high expression TF
14	3e−01	87 / 4714	ICGC_Pu1_targets
15	4e−01	100 / 5552	ICGC_Pol24_targets
16	4e−01	115 / 6406	ICGC_Pax5_targets
17	4e−01	24 / 1294	KIM_MYC targets
18	5e−01	38 / 2133	ICGC_Cebpbsc150_targets
19	5e−01	41 / 2354	ICGC_SrfV0416101_targets
20	6e−01	125 / 7202	ICGC_Runx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.1	3 / 64	VAQUERIZAS_Lung
2	0.1	2 / 31	VAQUERIZAS_Fetal lung
3	0.2	2 / 45	VAQUERIZAS_Placenta
4	0.2	1 / 12	VAQUERIZAS_Kidney
5	0.2	2 / 49	VAQUERIZAS_Uterus
6	0.2	1 / 16	VAQUERIZAS_Fetal thyroid
7	0.3	1 / 17	VAQUERIZAS_Adrenal gland
8	0.3	1 / 18	VAQUERIZAS_Pancreas
9	0.3	1 / 23	VAQUERIZAS_Pituitary
10	0.3	1 / 24	VAQUERIZAS_Trachea
11	0.4	1 / 25	VAQUERIZAS_Adrenal cortex
12	0.5	1 / 42	VAQUERIZAS_Thymus
13	0.5	1 / 42	VAQUERIZAS_Thyroid
14	0.8	2 / 155	VAQUERIZAS_General
15	1.0	0 / 41	VAQUERIZAS_Fetal brain
16	1.0	0 / 33	VAQUERIZAS_Liver
17	1.0	0 / 37	VAQUERIZAS_Prostate
18	1.0	0 / 30	VAQUERIZAS_Smooth muscle
19	1.0	0 / 25	VAQUERIZAS_Spinal cord
20	1.0	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	2e−06	5 / 13	WIRTH_Sec. lymphoid organs
2	1e−02	7 / 141	WIRTH_Muscle
3	3e−02	8 / 208	PALMER_B−Cell signature up
4	4e−02	6 / 140	PALMER_T−Cell signature up
5	9e−02	8 / 259	PALMER_Granulocytes signature up
6	2e−01	1 / 12	WIRTH_Lymphocytes
7	2e−01	1 / 13	WIRTH_Globus pallidus
8	2e−01	1 / 13	PALMER_CD8+ T−Cell signature up
9	2e−01	1 / 14	WIRTH_B−cells
10	2e−01	1 / 14	WIRTH_Thymus
11	2e−01	1 / 15	WIRTH_Telencephalon
12	2e−01	2 / 54	WIRTH_Pancreas
13	2e−01	1 / 16	WIRTH_Hippocampus
14	3e−01	10 / 476	WIRTH_Nervous System
15	4e−01	1 / 30	PALMER_Lymphocytes signature up
16	6e−01	1 / 47	WIRTH_Placenta
17	1e+00	2 / 427	WIRTH_Immune system
18	1e+00	0 / 6	WIRTH_Pituitary gland
19	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
20	1e+00	0 / 12	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.001	39 / 1343	LU_BPDE 1n DN
2	0.003	116 / 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	

K−Means Clusters

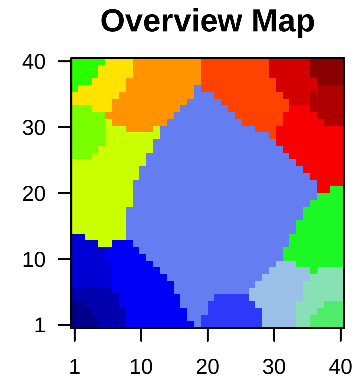
Spot Summary: K

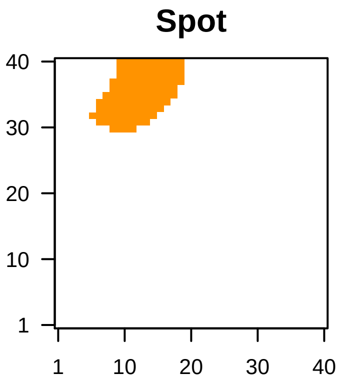
metagenes = 105
genes = 1170

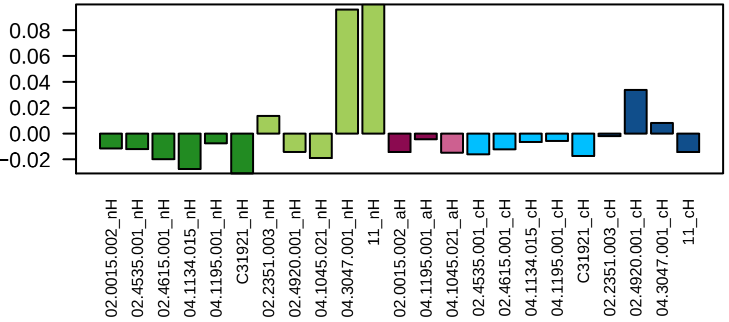
<r> metagenes = 0.87

beta: r2= 0.03 / log p= −0.34

samples with spot = 0 (0 %)


Overview Map


Spot

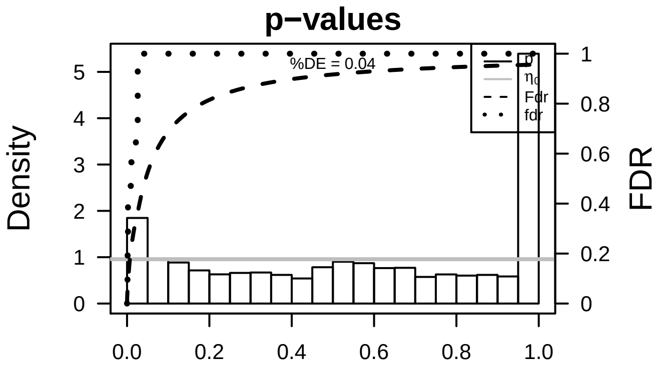


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.6	−0.03	0.23	SPINK13	serine peptidase inhibitor, Kazal type 13 (putative) [Source:H
2	ENSG000001	0.53	−0.03	0.24	SPINK6	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
3	ENSG000002	0.51	−0.06	0.33	LY6G6D	lymphocyte antigen 6 complex, locus G6D [Source:HGNC Sy
4	ENSG000001	0.43	−0.24	0.55	COPRS	coordinator of PRMT5, differentiation stimulator [Source:HGN
5	ENSG000001	0.43	−0.31	0.43	H1F0	H1 histone family, member 0 [Source:HGNC Symbol;Acc:HG
6	ENSG000000	0.42	−0.05	0.61	HSD17B6	hydroxysteroid (17−beta) dehydrogenase 6 [Source:HGNC S
7	ENSG000000	0.41	−0.14	0.45	P3H2	prolyl 3−hydroxylase 2 [Source:HGNC Symbol;Acc:HGNC:19
8	ENSG000001	0.39	−0.09	0.45	IFIT1	interferon−induced protein with tetratricopeptide repeats 1 [S
9	ENSG000001	0.37	−0.08	0.51	PLEKHA4	pleckstrin homology domain containing, family A (phosphoino
10	ENSG000001	0.36	−0.36	0.38	SDC4	syndecan 4 [Source:HGNC Symbol;Acc:HGNC:10661]
11	ENSG000001	0.34	−0.02	0.43	ASB5	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
12	ENSG000001	0.34	−0.11	0.52	IGFBP6	insulin−like growth factor binding protein 6 [Source:HGNC Sy
13	ENSG000001	0.34	−0.27	0.24	VASP	vasodilator−stimulated phosphoprotein [Source:HGNC Symb
14	ENSG000001	0.32	−0.14	0.33	PKDCC	protein kinase domain containing, cytoplasmic [Source:HGN
15	ENSG000001	0.31	−0.16	0.43	SLC16A1	solute carrier family 16 (monocarboxylate transporter), memb
16	ENSG000001	0.31	−0.09	0.48	STMN2	stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
17	ENSG000001	0.31	−0.13	0.54	SYNC	syncoilin, intermediate filament protein [Source:HGNC Symb
18	ENSG000001	0.29	−0.03	0.81	NTSR1	neurotensin receptor 1 (high affinity) [Source:HGNC Symbol;
19	ENSG000002	0.29	−0.42	0.4		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F8
20	ENSG000000	0.28	−0.07	0.51	PHGDH	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−46	856 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
2	7e−44	832 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
3	3e−41	602 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
4	4e−36	831 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
5	6e−36	860 / 10800	Brain	Overlap_fetal_midbrain_Quies
6	1e−22	883 / 11968	Colon	TssWk_Colon
7	4e−21	729 / 9390	Colon	TxWk_Colon
8	7e−21	158 / 1197	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
9	1e−20	81 / 420	GSEA	SHEN_SMARCA2_TARGETS_UP
10	5e−19	725 / 9470	Colon	Quies3_Colon
11	1e−18	796 / 10693	MF	protein binding
12	1e−18	751 / 9930	Colon	Tx_Colon
13	6e−17	776 / 10475	Colon	TssA_Colon
14	7e−17	635 / 8147	Lymph	HOPP_Weak_promoter
15	2e−14	307 / 3370	Brain	Mid_Frontal_Lobe_ZNF
16	4e−14	510 / 6389	Lymph	HOPP_Weak_txn
17	6e−12	366 / 4379	Colon	TssD1_Colon
18	1e−11	622 / 8358	Lymph	HOPP_Active_promoter
19	2e−11	417 / 5185	CC	cytoplasm
20	4e−11	520 / 6784	Lymph	HOPP_Weak_enhancer
21	2e−10	68 / 490	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
22	2e−09	59 / 421	GSEA	ROME_INSULIN_TARGETS_IN_MUSCLE_UP
23	5e−09	552 / 7491	Lymph	HOPP_Txn_elongation
24	1e−08	88 / 773	GSEA	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
25	1e−08	67 / 530	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
26	1e−08	62 / 476	Tissu	WIRTH_Nervous System
27	2e−08	109 / 1036	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
28	5e−08	585 / 8123	Colon	TssF_Colon
29	6e−08	239 / 2838	Lymph	HOPP_Poised_promoter
30	8e−08	805 / 11791	Colon	Enh_Colon
31	1e−07	56 / 435	miRN	hsa−miR−372
32	1e−07	157 / 1713	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
33	1e−07	92 / 864	CC	Golgi apparatus
34	2e−07	89 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
35	5e−07	371 / 4879	Colon	Quies1_Colon
36	6e−07	13 / 41	BP	mitochondrial electron transport, NADH to ubiquinone
37	6e−07	54 / 436	Glio	Down_b
38	7e−07	18 / 77	CC	primary cilium
39	8e−07	72 / 651	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
40	1e−06	59 / 503	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	8 / 123	HORVATH_aging_genes meth DOWN
2	0.5	9 / 144	HORVATH_aging_genes meth UP
3	0.7	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	6e−07	13 / 41	mitochondrial electron transport, NADH to ubiquinone
2	8e−06	23 / 136	cellular metabolic process
3	1e−04	12 / 56	retrograde transport, endosome to Golgi
4	1e−04	10 / 41	regulation of autophagy
5	1e−04	18 / 112	neuron projection development
6	2e−04	52 / 512	protein transport
7	3e−04	21 / 148	negative regulation of canonical Wnt signaling pathway
8	3e−04	8 / 30	tricarboxylic acid cycle
9	5e−04	6 / 18	intraciliary transport
10	6e−04	50 / 507	negative regulation of transcription, DNA−templated
11	6e−04	20 / 147	insulin receptor signaling pathway
12	7e−04	15 / 96	respiratory electron transport chain
13	7e−04	6 / 19	positive regulation of G1/S transition of mitotic cell cycle
14	7e−04	7 / 26	positive regulation of muscle cell differentiation
15	8e−04	12 / 68	smoothened signaling pathway
16	8e−04	106 / 1279	signal transduction
17	8e−04	9 / 42	lung alveolus development
18	1e−03	32 / 291	organelle organization
19	1e−03	22 / 174	Wnt signaling pathway
20	1e−03	34 / 316	nervous system development

Brain

Rank	p−value	#in/all	Geneset
1	5e−46	856 / 10239	Overlap_fetal_midbrain_ReprPC
2	7e−44	832 / 9923	Overlap_fetal_midbrain_K9K27me3
3	3e−41	602 / 6320	Overlap_fetal_midbrain_HetRpts
4	4e−36	831 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	6e−36	860 / 10800	Overlap_fetal_midbrain_Quies
6	2e−14	307 / 3370	Mid_Frontal_Lobe_ZNF
7	6e−06	48 / 400	Fetal_ZNF
8	4e−05	88 / 939	Fetal_HetRpts
9	2e−04	68 / 712	Overlap_fetal_midbrain_EnhP
10	2e−04	109 / 1279	Overlap_fetal_midbrain_Enh
11	4e−04	101 / 1182	Fetal_EnhP
12	4e−04	103 / 1210	Fetal_TssP
13	1e−03	36 / 342	Fetal_Het
14	1e−03	75 / 865	Mid_Frontal_Lobe_Het
15	3e−03	92 / 1137	Fetal_Enh
16	5e−03	75 / 910	Fetal_EnhG
17	8e−03	86 / 1084	Overlap_fetal_midbrain_EnhG
18	9e−03	104 / 1356	Fetal_K9K27me3
19	2e−02	67 / 855	Overlap_fetal_midbrain_ZNF
20	3e−02	51 / 641	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	0 / 16	LIU_PROSTATE_CANCER_DN
2	2e−03	5 / 16	GENTLES_modul16
3	9e−03	3 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	9e−02	13 / 140	PanCan_RAS_geneset_nanostring
5	9e−02	4 / 28	PanCan_HH_geneset_nanostring
6	1e−01	0 / 16	LIU_COMMON_CANCER_GENES
7	2e−01	7 / 78	PanCan_Wnt_geneset_nanostring
8	2e−01	2 / 15	GENTLES_modul4
9	2e−01	4 / 41	ZHANG_MM up
10	3e−01	2 / 16	GENTLES_modul1
11	3e−01	9 / 123	PanCan_Driver_Gene_geneset_nanostring
12	4e−01	4 / 51	PanCan_TGF−B_geneset_nanostring
13	4e−01	3 / 37	KUIPER_MM good survival
14	5e−01	10 / 152	PanCan_MAPK_geneset_nanostring
15	5e−01	1 / 14	LIU_PROSTATE_CANCER_UP
16	5e−01	1 / 11	GENTLES_modul5
17	5e−01	6 / 97	PanCan_TXmisReg_geneset_nanostring
18	6e−01	1 / 14	GENTLES_modul12
19	6e−01	1 / 15	GENTLES_modul10
20	6e−01	3 / 52	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	2e−11	417 / 5185	cytoplasm
2	1e−07	92 / 864	Golgi apparatus
3	7e−07	18 / 77	primary cilium
4	7e−06	12 / 43	ciliary tip
5	9e−06	12 / 44	mitochondrial respiratory chain complex I
6	1e−04	199 / 2554	nucleoplasm
7	2e−04	44 / 411	centrosome
8	3e−04	15 / 90	ciliary basal body
9	4e−04	18 / 121	trans−Golgi network
10	5e−04	5 / 12	AMP−activated protein kinase complex
11	5e−04	12 / 65	filopodium
12	6e−04	32 / 282	microtubule
13	7e−04	6 / 19	intraciliary transport particle B
14	8e−04	16 / 107	growth cone
15	8e−04	221 / 2974	cytosol
16	1e−03	19 / 142	cilium
17	1e−03	48 / 497	Golgi membrane
18	2e−03	5 / 15	cytoplasmic dynein complex
19	2e−03	33 / 317	neuron projection
20	2e−03	6 / 23	calcium channel complex

Chr

Rank	p−value	#in/all	Geneset
1	0.009	70 / 859	Chr 7
2	0.060	41 / 522	Chr 20
3	0.064	56 / 745	Chr 9
4	0.070	55 / 735	Chr 4
5	0.081	63 / 862	Chr 5
6	0.134	47 / 651	Chr 8
7	0.186	71 / 1043	Chr 3
8	0.222	49 / 715	Chr 10
9	0.228	20 / 272	Chr 18
10	0.231	23 / 318	Chr 13
11	0.252	81 / 1228	Chr 2
12	0.298	41 / 613	Chr 14
13	0.377	121 / 1920	Chr 1
14	0.585	65 / 1083	Chr 17
15	0.626	11 / 191	Chr 21
16	0.682	43 / 746	Chr X
17	0.698	68 / 1172	Chr 11
18	0.816	56 / 1017	Chr 12
19	0.871	52 / 976	Chr 6
20	0.932	20 / 436	Chr 22

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−22	883 / 11968	TssWk_Colon
2	4e−21	729 / 9390	TxWk_Colon
3	5e−19	725 / 9470	Quies3_Colon
4	1e−18	751 / 9930	Tx_Colon
5	6e−17	776 / 10475	TssA_Colon
6	6e−12	366 / 4379	TssD1_Colon
7	5e−08	585 / 8123	TssF_Colon
8	8e−08	805 / 11791	Enh_Colon
9	5e−07	371 / 4879	Quies1_Colon
10	2e−05	22 / 132	Marisa_CRC−cluster−b
11	2e−04	316 / 4327	EnhWk2_Colon
12	2e−04	53 / 525	Quies2_Colon
13	4e−04	468 / 6761	TssD2_Colon
14	4e−04	41 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	6e−04	411 / 5889	EnhWk1_Colon
16	2e−03	227 / 3109	TssP_Colon
17	1e−02	90 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	1e−02	39 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	3e−02	4 / 19	Vilar_non−hypermutated−in−CRC
20	6e−02	123 / 1753	Het_Colon

Disease

Rank	p−value	#in/all	Geneset
1	8e−04	41 / 399	GUDJ_psoriasis down
2	1e+00	18 / 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	6e−07	54 / 436	Down_b
2	2e−06	170 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	6e−06	187 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	2e−04	80 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
5	1e−03	43 / 434	Down_a
6	2e−03	21 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	3e−03	11 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	4e−03	7 / 34	WIRTH_PN subtype
9	5e−03	10 / 63	Stuehler_Proteins_up_in_STS
10	5e−03	32 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	1e−02	11 / 83	GIEZELT_GBM_WT_down_VS_mut
12	1e−02	4 / 16	VERHAAK_MES subtype
13	2e−02	4 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
14	2e−02	4 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	3e−02	5 / 28	Sturm_GBM_Meth_overexpression_H_K27_UP
16	4e−02	8 / 63	OPC
17	4e−02	3 / 13	Mukasa_UP_in_Astroglioma
18	4e−02	3 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
19	5e−02	7 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
20	5e−02	2 / 6	laffaire_hypometh_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−21	158 / 1197	BLALOCK_ALZHEIMERS_DISEASE_DN
2	1e−20	81 / 420	SHEN_SMARCA2_TARGETS_UP
3	2e−10	68 / 490	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
4	2e−09	59 / 421	ROME_INSULIN_TARGETS_IN_MUSCLE_UP
5	1e−08	88 / 773	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
6	1e−08	67 / 530	KIM_ALL_DISORDERS_CALB1_CORR_UP
7	2e−08	109 / 1036	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
8	1e−07	157 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
9	2e−07	89 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	8e−07	72 / 651	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
11	1e−06	59 / 503	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
12	1e−06	30 / 189	WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN
13	3e−06	41 / 313	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP
14	4e−06	141 / 1591	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
15	7e−06	67 / 631	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_8D
16	8e−06	122 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
17	1e−05	74 / 727	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
18	1e−05	12 / 45	ZHAN_MULTIPLE_MYELOMA_MS_UP
19	1e−05	20 / 111	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
20	1e−05	24 / 149	LU_AGING_BRAIN_DN

HM

Rank	p−value	#in/all	Geneset
1	5e−04	25 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	2e−03	23 / 195	HALLMARK_MYOGENESIS
3	1e−02	12 / 94	HALLMARK_PROTEIN_SECRETION
4	3e−02	19 / 193	HALLMARK_HEME_METABOLISM
5	5e−02	14 / 140	HALLMARK_UV_RESPONSE_DN
6	9e−02	17 / 196	HALLMARK_MITOTIC_SPINDLE
7	1e−01	10 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	1e−01	4 / 30	HALLMARK_NOTCH_SIGNALING
9	1e−01	16 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
10	2e−01	15 / 190	HALLMARK_APICAL_JUNCTION
11	2e−01	15 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	2e−01	9 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	3e−01	4 / 44	HALLMARK_APICAL_SURFACE
14	3e−01	14 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	4e−01	7 / 98	HALLMARK_ANDROGEN_RESPONSE
16	4e−01	7 / 102	HALLMARK_PEROXISOME
17	4e−01	13 / 199	HALLMARK_ADIPOGENESIS
18	4e−01	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
19	5e−01	7 / 112	HALLMARK_BILE_ACID_METABOLISM
20	5e−01	3 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	5 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.271	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.434	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.501	1 / 11	DUMEAUX_Smoking literature genes up
5	0.658	1 / 17	DUMEAUX_High bmi enriched genes
6	0.815	4 / 91	DUMEAUX_Smoking enriched genes
7	0.876	1 / 33	DUMEAUX_Fasting enriched genes
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 9	DUMEAUX_Hormon therapy_in non smokers literature genes up
11	1.000	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	7e−17	635 / 8147	HOPP_Weak_promoter
2	4e−14	510 / 6389	HOPP_Weak_txn
3	1e−11	622 / 8358	HOPP_Active_promoter
4	4e−11	520 / 6784	HOPP_Weak_enhancer
5	5e−09	552 / 7491	HOPP_Txn_elongation
6	6e−08	239 / 2838	HOPP_Poised_promoter
7	5e−05	209 / 2658	HOPP_Repetitive
8	2e−04	113 / 1333	SPANG_BCR UP
9	9e−04	355 / 5039	HOPP_Repressed
10	1e−02	7 / 42	CARO_OxPhos_in_DLBCL_UP
11	2e−02	10 / 75	Subero_FL_hyper_meth
12	3e−02	9 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
13	3e−02	24 / 261	LENZ_Stromal signature 1
14	4e−02	4 / 21	DAVE_Immune response 2
15	4e−02	14 / 138	Subero_DLBCL_hyper_meth
16	5e−02	233 / 3457	HOPP_Heterochrom
17	6e−02	3 / 15	BENTINK_mBL UP
18	6e−02	2 / 7	CARO_OxPhos_vs_BCR_UP
19	7e−02	12 / 122	Subero_INT_hyper_meth
20	8e−02	35 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-

MF

Rank	p−value	#in/all	Geneset
1	1e−18	796 / 10693	protein binding
2	2e−05	11 / 41	NADH dehydrogenase (ubiquinone) activity
3	6e−05	32 / 250	GTPase activity
4	1e−04	9 / 33	beta−tubulin binding
5	2e−04	41 / 371	GTP binding
6	3e−04	11 / 53	GDP binding
7	2e−03	5 / 16	dynein binding
8	5e−03	8 / 45	methylated histone binding
9	6e−03	5 / 20	enzyme regulator activity
10	6e−03	32 / 328	enzyme binding
11	7e−03	13 / 98	ion channel binding
12	7e−03	11 / 77	kinase binding
13	8e−03	5 / 21	ferrous iron binding
14	8e−03	5 / 21	protein phosphatase type 2A regulator activity
15	9e−03	4 / 14	insulin−like growth factor receptor binding
16	9e−03	6 / 30	ubiquitin conjugating enzyme activity
17	9e−03	6 / 30	Wnt−protein binding
18	1e−02	20 / 186	microtubule binding
19	1e−02	26 / 262	ubiquitin−protein transferase activity
20	1e−02	4 / 15	Wnt−activated receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−07	56 / 435	hsa−miR−372
2	2e−06	51 / 416	hsa−miR−519c−3p
3	3e−06	65 / 591	hsa−miR−20b
4	4e−06	63 / 573	hsa−miR−93
5	7e−06	46 / 378	hsa−miR−519b−3p
6	8e−06	48 / 403	hsa−miR−519a
7	3e−05	57 / 531	hsa−miR−15a
8	4e−05	44 / 381	hsa−miR−144
9	4e−05	54 / 504	hsa−miR−16
10	6e−05	22 / 144	hsa−miR−338−5p
11	7e−05	40 / 344	hsa−miR−302d
12	8e−05	13 / 62	hsa−miR−514
13	9e−05	63 / 631	hsa−miR−20a
14	2e−04	55 / 542	hsa−miR−106a
15	2e−04	44 / 407	hsa−miR−301b
16	2e−04	38 / 337	hsa−miR−367
17	2e−04	47 / 447	hsa−miR−519d
18	2e−04	54 / 536	hsa−miR−106b
19	2e−04	39 / 352	hsa−miR−142−5p
20	2e−04	37 / 328	hsa−miR−340

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	3 / 13	BENTINK_e2f3.2
2	0.05	3 / 14	BENTINK_e2f3.1
3	0.16	2 / 12	BENTINK_ras.1
4	0.47	1 / 10	BENTINK_ras.4
5	0.59	1 / 14	BENTINK_myc.1
6	0.59	1 / 14	BENTINK_src.2
7	0.61	1 / 15	BENTINK_ras.6
8	1.00	0 / 14	GUSTAFSON_PI3K_UP
9	1.00	0 / 15	GUSTAFSON_PI3K_DN
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	0.003	319 / 4566	ICGC_Egr1_targets
2	0.010	424 / 6324	ICGC_Yy1_targets
3	0.017	136 / 1867	HEBENSTREIT_high expression TF
4	0.023	452 / 6862	ICGC_Elf1_targets
5	0.027	110 / 1503	ICGC_Six5_targets
6	0.052	341 / 5173	ICGC_Taf1_targets
7	0.053	105 / 1472	ICGC_NrsfPcr1_targets
8	0.057	93 / 1294	KIM_MYC targets
9	0.076	390 / 6005	ICGC_Mta3_targets
10	0.078	294 / 4470	ICGC_Creb1_targets
11	0.084	361 / 5552	ICGC_Pol24_targets
12	0.088	359 / 5526	ICGC_Pmlsc71910_targets
13	0.111	231 / 3511	ICGC_Rad21_targets
14	0.112	181 / 2719	ICGC_Pbx3_targets
15	0.126	104 / 1523	ICGC_P300_targets
16	0.140	354 / 5512	ICGC_Nficsc81335_targets
17	0.144	52 / 731	ICGC_SrfPcr2_targets
18	0.168	155 / 2354	ICGC_SrfV0416101_targets
19	0.173	402 / 6322	ICGC_Pol2_targets
20	0.177	456 / 7202	ICGC_Runx3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.003	6 / 25	VAQUERIZAS_Spinal cord
2	0.007	18 / 155	VAQUERIZAS_General
3	0.060	6 / 46	VAQUERIZAS_Whole brain
4	0.082	3 / 17	VAQUERIZAS_Adrenal gland
5	0.103	5 / 41	VAQUERIZAS_Testis
6	0.163	3 / 23	VAQUERIZAS_Pituitary
7	0.254	4 / 42	VAQUERIZAS_Thyroid
8	0.294	3 / 31	VAQUERIZAS_Fetal lung
9	0.348	2 / 20	VAQUERIZAS_Bone marrow
10	0.352	4 / 49	VAQUERIZAS_Uterus
11	0.437	2 / 24	VAQUERIZAS_Trachea
12	0.458	2 / 25	VAQUERIZAS_Adrenal cortex
13	0.525	3 / 45	VAQUERIZAS_Placenta
14	0.531	1 / 12	VAQUERIZAS_Kidney
15	0.556	2 / 30	VAQUERIZAS_Smooth muscle
16	0.556	4 / 64	VAQUERIZAS_Lung
17	0.560	1 / 13	VAQUERIZAS_Skin
18	0.636	1 / 16	VAQUERIZAS_Fetal liver
19	0.636	1 / 16	VAQUERIZAS_Ovary
20	0.636	1 / 16	VAQUERIZAS_Fetal thyroid

Tissue

Rank	p−value	#in/all	Geneset
1	1e−08	62 / 476	WIRTH_Nervous System
2	2e−01	2 / 13	WIRTH_Prim. lymphoid organs
3	2e−01	2 / 13	WIRTH_Cortex cerebri
4	2e−01	2 / 14	WIRTH_Thyroid gland
5	4e−01	10 / 141	WIRTH_Muscle
6	5e−01	16 / 259	PALMER_Granulocytes signature up
7	6e−01	2 / 30	PALMER_Lymphocytes signature up
8	6e−01	1 / 13	WIRTH_Sec. lymphoid organs
9	6e−01	1 / 13	WIRTH_Globus pallidus
10	6e−01	1 / 14	WIRTH_Thalamus
11	6e−01	1 / 15	WIRTH_Telencephalon
12	6e−01	1 / 16	WIRTH_Hippocampus
13	7e−01	3 / 54	WIRTH_Pancreas
14	9e−01	6 / 140	PALMER_T−Cell signature up
15	9e−01	1 / 47	WIRTH_Placenta
16	1e+00	6 / 202	WIRTH_Testis
17	1e+00	6 / 208	PALMER_B−Cell signature up
18	1e+00	3 / 137	WIRTH_Mucosa
19	1e+00	1 / 82	WIRTH_Homeostasis
20	1e+00	4 / 427	WIRTH_Immune system

Toxic

Rank	p−value	#in/all	Geneset
1	0.01	358 / 5285	LU_BPDE 0.005 DN
2	0.04	98 / 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	

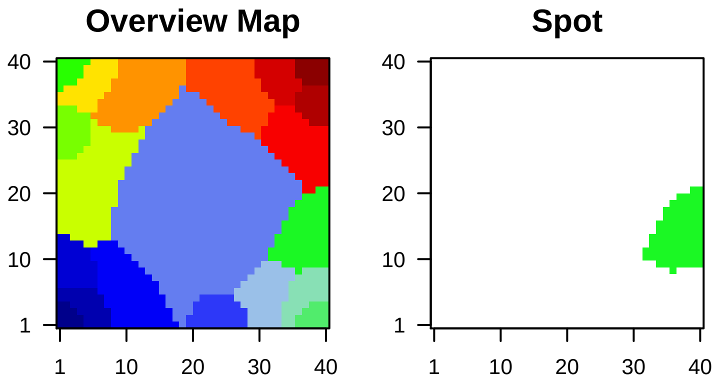
K−Means Clusters

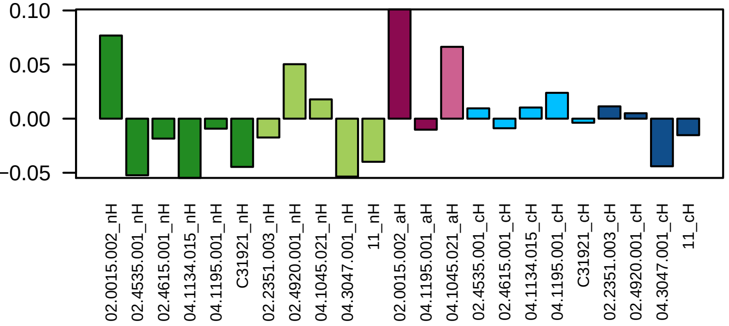
Spot Summary: L

metagenes = 79
genes = 943

<r> metagenes = 0.84
<r> genes = 0.43
beta: r2= 0.04 / log p= −0.45

samples with spot = 0 (0 %)



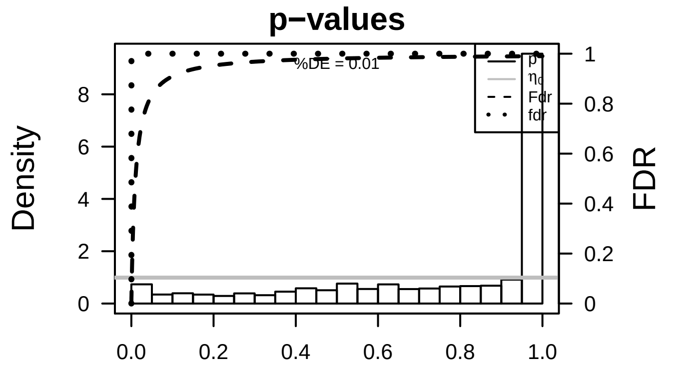


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.86	−0.35	0.6		cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
2	ENSG000002	0.8	−0.27	0.63	CRIP1	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
3	ENSG000001	0.7	−0.03	0.35	CTAG2	cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
4	ENSG000001	0.6	−0.09	0.6	FABP6	fatty acid binding protein 6, ileal [Source:HGNC Symbol;Acc:
5	ENSG000001	0.56	−0.1	0.72	TNNC2	troponin C type 2 (fast) [Source:HGNC Symbol;Acc:HGNC:11
6	ENSG000001	0.53	−0.22	0.66		ATP synthase, H+ transporting, mitochondrial F1 complex, ep
7	ENSG000001	0.49	−0.13	0.6	RCN3	reticulocalbin 3, EF−hand calcium binding domain [Source:H
8	ENSG000001	0.49	−0.42	0.55	RNASE1	ribonuclease, RNase A family, 1 (pancreatic) [Source:HGNC
9	ENSG000001	0.47	−0.11	0.44	URAD	ureidoimidazoline (2−oxo−4−hydroxy−4−carboxy−5−) decarb
10	ENSG000001	0.43	−0.19	0.65		
11	ENSG000001	0.41	−0.08	0.74	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type [Sou
12	ENSG000001	0.4	−0.23	0.87	NDUFS6	NADH dehydrogenase (ubiquinone) Fe−S protein 6, 13kDa (
13	ENSG000001	0.39	−0.1	0.43	HOXB6	homeobox B6 [Source:HGNC Symbol;Acc:HGNC:5117]
14	ENSG000001	0.39	−0.11	0.47	INSR	insulin receptor [Source:HGNC Symbol;Acc:HGNC:6091]
15	ENSG000001	0.38	−0.05	0.59	DUOXA1	dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:
16	ENSG000002	0.38	−0.05	0.57		
17	ENSG000001	0.38	−0.1	0.78	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U [Sou
18	ENSG000001	0.38	−0.15	0.85	FAM166A	family with sequence similarity 166, member A [Source:HGN
19	ENSG000001	0.37	−0.29	0.46	CYC1	cytochrome c−1 [Source:HGNC Symbol;Acc:HGNC:2579]
20	ENSG000002	0.37	−0.11	0.7	MROH6	maestro heat−like repeat family member 6 [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−78	666 / 8123	Colon	TssF_Colon
2	1e−59	736 / 10475	Colon	TssA_Colon
3	2e−51	546 / 6761	Colon	TssD2_Colon
4	9e−47	325 / 3122	Colon	TxEnhG1_Colon
5	2e−46	686 / 9930	Colon	Tx_Colon
6	2e−36	662 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
7	1e−33	311 / 3370	Brain	Mid_Frontal_Lobe_ZNF
8	5e−31	623 / 9390	Colon	TxWk_Colon
9	9e−29	723 / 11791	Colon	Enh_Colon
10	5e−24	427 / 5889	Colon	EnhWk1_Colon
11	4e−23	267 / 3112	Colon	EnhA_Colon
12	1e−17	103 / 865	Brain	Mid_Frontal_Lobe_Het
13	2e−14	61 / 425	CC	mitochondrial inner membrane
14	3e−14	631 / 10800	Brain	Overlap_fetal_midbrain_Quies
15	5e−14	27 / 96	BP	respiratory electron transport chain
16	7e−14	24 / 76	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES
17	7e−14	191 / 2342	TF	ICGC_GabpPcr2_targets
18	9e−14	66 / 499	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
19	1e−13	602 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
20	2e−13	133 / 1441	CC	mitochondrion
21	3e−13	31 / 136	BP	cellular metabolic process
22	1e−12	92 / 877	Colon	TxEnhG2_Colon
23	2e−12	27 / 111	GSEA	KEGG_OXIDATIVE_PHOSPHORYLATION
24	3e−12	20 / 60	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
25	3e−12	344 / 5173	TF	ICGC_Taf1_targets
26	5e−12	23 / 83	GSEA	MOOTHA_VOXPHOS
27	1e−11	26 / 111	GSEA	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSP
28	2e−11	302 / 4470	TF	ICGC_Creb1_targets
29	3e−11	16 / 41	MF	NADH dehydrogenase (ubiquinone) activity
30	3e−11	78 / 727	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
31	4e−11	49 / 356	GSEA	DAIRKEE_TERT_TARGETS_UP
32	7e−11	31 / 165	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
33	9e−11	35 / 207	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
34	9e−11	16 / 44	CC	mitochondrial respiratory chain complex I
35	1e−10	361 / 5643	Lymph	HOPP_Txn_transition
36	1e−10	207 / 2820	Brain	Mid_Frontal_Lobe_HetRpts
37	4e−10	355 / 5578	TF	ICGC_Stat5_targets
38	4e−10	113 / 1294	TF	KIM_MYC targets
39	5e−10	283 / 4230	TF	ICGC_Nfatc1_targets
40	5e−10	294 / 4436	TF	ICGC_Zeb1_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.07	10 / 123	HORVATH_aging_genes meth DOWN
2	0.83	5 / 144	HORVATH_aging_genes meth UP
3	0.94	1 / 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−14	27 / 96	respiratory electron transport chain
2	3e−13	31 / 136	cellular metabolic process
3	4e−09	14 / 41	mitochondrial electron transport, NADH to ubiquinone
4	3e−05	7 / 20	ATP synthesis coupled proton transport
5	6e−04	7 / 31	C−terminal protein lipidation
6	7e−04	95 / 1418	small molecule metabolic process
7	9e−04	7 / 33	retrograde vesicle−mediated transport, Golgi to ER
8	9e−04	8 / 43	autophagosome assembly
9	1e−03	5 / 17	mitochondrial ATP synthesis coupled proton transport
10	1e−03	6 / 26	GPI anchor biosynthetic process
11	2e−03	6 / 27	aerobic respiration
12	4e−03	11 / 89	vitamin metabolic process
13	5e−03	6 / 33	mitophagy
14	5e−03	4 / 15	glutathione biosynthetic process
15	5e−03	7 / 44	RNA phosphodiester bond hydrolysis, endonucleolytic
16	6e−03	19 / 207	cell cycle
17	6e−03	10 / 82	mitochondrial translational elongation
18	6e−03	10 / 82	mitochondrial translational initiation
19	7e−03	6 / 36	lysosome organization
20	7e−03	10 / 84	mitochondrial translational termination

Brain

Rank	p−value	#in/all	Geneset
1	2e−36	662 / 9923	Overlap_fetal_midbrain_K9K27me3
2	1e−33	311 / 3370	Mid_Frontal_Lobe_ZNF
3	1e−17	103 / 865	Mid_Frontal_Lobe_Het
4	3e−14	631 / 10800	Overlap_fetal_midbrain_Quies
5	1e−13	602 / 10239	Overlap_fetal_midbrain_ReprPC
6	1e−10	207 / 2820	Mid_Frontal_Lobe_HetRpts
7	1e−08	132 / 1680	Fetal_ReprPCWk
8	2e−02	55 / 855	Overlap_fetal_midbrain_ZNF
9	2e−02	101 / 1713	Mid_Frontal_Lobe_ReprPCWk
10	5e−02	213 / 3977	Mid_Frontal_Lobe_ReprPC
11	1e−01	53 / 939	Fetal_HetRpts
12	3e−01	19 / 342	Fetal_Het
13	3e−01	106 / 2084	Mid_Frontal_Lobe_K9K27me3
14	4e−01	120 / 2443	Fetal_Quies
15	5e−01	67 / 1394	Mid_Frontal_Lobe_Quies
16	6e−01	304 / 6320	Overlap_fetal_midbrain_HetRpts
17	7e−01	10 / 232	Fetal_ReprPC
18	8e−01	16 / 400	Fetal_ZNF
19	9e−01	3 / 106	Overlap_fetal_midbrain_Tx
20	9e−01	6 / 191	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	3 / 15	GENTLES_modul10
2	0.04	5 / 40	PanCan_HK_geneset_nanostring
3	0.10	2 / 11	GENTLES_modul5
4	0.14	2 / 14	GENTLES_modul12
5	0.18	2 / 16	LIU_LIVER_CANCER
6	0.18	2 / 16	WANG_ER_UP
7	0.22	4 / 50	PanCan_DNARepair_geneset_nanostring
8	0.29	2 / 22	PanCan_ChromMod_geneset_nanostring
9	0.36	1 / 9	WANG_ER_DN
10	0.52	1 / 15	GENTLES_modul4
11	0.55	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.55	1 / 16	LIU_COMMON_CANCER_GENES
13	0.55	1 / 16	GENTLES_modul1
14	0.55	1 / 16	GENTLES_modul7
15	0.58	9 / 191	SPANG_LPS−index2
16	0.61	15 / 324	SPANG_BCL6−index2
17	0.82	0 / 14	LIU_PROSTATE_CANCER_UP
18	0.83	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
19	0.84	1 / 37	KUIPER_MM good survival
20	0.86	5 / 152	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−14	61 / 425	mitochondrial inner membrane
2	2e−13	133 / 1441	mitochondrion
3	9e−11	16 / 44	mitochondrial respiratory chain complex I
4	2e−05	7 / 19	mitochondrial proton−transporting ATP synthase complex
5	8e−05	29 / 277	mitochondrial matrix
6	5e−04	15 / 116	late endosome
7	9e−04	12 / 87	late endosome membrane
8	2e−03	6 / 27	mitochondrial ribosome
9	3e−03	4 / 13	mitochondrial respiratory chain
10	4e−03	4 / 14	integral component of peroxisomal membrane
11	5e−03	21 / 235	lysosome
12	6e−03	53 / 767	endoplasmic reticulum membrane
13	7e−03	6 / 36	mediator complex
14	7e−03	5 / 26	pre−autophagosomal structure
15	8e−03	7 / 48	SNARE complex
16	1e−02	9 / 76	integral component of endoplasmic reticulum membrane
17	1e−02	11 / 106	peroxisome
18	2e−02	20 / 245	lysosomal membrane
19	2e−02	4 / 22	anaphase−promoting complex
20	2e−02	3 / 13	HOPS complex

Chr

Rank	p−value	#in/all	Geneset
1	2e−07	112 / 1425	Chr 19
2	4e−06	71 / 847	Chr 16
3	3e−04	78 / 1083	Chr 17
4	2e−03	41 / 522	Chr 20
5	6e−02	52 / 859	Chr 7
6	2e−01	64 / 1172	Chr 11
7	3e−01	39 / 745	Chr 9
8	4e−01	32 / 613	Chr 14
9	4e−01	23 / 436	Chr 22
10	5e−01	48 / 976	Chr 6
11	6e−01	31 / 651	Chr 8
12	7e−01	8 / 191	Chr 21
13	8e−01	44 / 1017	Chr 12
14	9e−01	10 / 272	Chr 18
15	9e−01	28 / 746	Chr X
16	9e−01	79 / 1920	Chr 1
17	1e+00	47 / 1228	Chr 2
18	1e+00	18 / 582	Chr 15
19	1e+00	26 / 862	Chr 5
20	1e+00	31 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−78	666 / 8123	TssF_Colon
2	1e−59	736 / 10475	TssA_Colon
3	2e−51	546 / 6761	TssD2_Colon
4	9e−47	325 / 3122	TxEnhG1_Colon
5	2e−46	686 / 9930	Tx_Colon
6	5e−31	623 / 9390	TxWk_Colon
7	9e−29	723 / 11791	Enh_Colon
8	5e−24	427 / 5889	EnhWk1_Colon
9	4e−23	267 / 3112	EnhA_Colon
10	1e−12	92 / 877	TxEnhG2_Colon
11	3e−04	509 / 9470	Quies3_Colon
12	9e−04	4 / 10	TCGA−CRC_agressive−disease−markers
13	5e−03	51 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	3e−02	8 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
15	8e−02	2 / 10	KIM_MSI−in−EC
16	3e−01	586 / 11968	TssWk_Colon
17	3e−01	34 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
18	4e−01	1 / 10	KIM_CRC−MSI−regulated_DN
19	5e−01	57 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
20	5e−01	3 / 55	Marisa_CRC−cluster−e

Disease

Rank	p−value	#in/all	Geneset
1	0.8	1 / 37	BCHETNIA_EBM−DM up
2	1.0	6 / 399	GUDJ_psoriasis down
3	1.0	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	2e−04	20 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
2	6e−04	9 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
3	2e−03	13 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	6e−03	9 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
5	1e−02	8 / 63	Stuehler_Proteins_up_in_STS
6	5e−02	6 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	5e−02	53 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
8	6e−02	6 / 58	OL vs. MOG− OL
9	6e−02	7 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
10	7e−02	8 / 91	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	7e−02	6 / 61	Christensen_hypermethylated_in_primary_glioblastoma
12	9e−02	21 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP
13	1e−01	108 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
14	1e−01	5 / 52	OL vs. OPC
15	1e−01	83 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
16	2e−01	7 / 92	laffaire_hypermeth_LGG_vs_control
17	2e−01	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
18	2e−01	117 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
19	2e−01	8 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
20	3e−01	9 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−14	24 / 76	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
2	9e−14	66 / 499	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
3	2e−12	27 / 111	KEGG_OXIDATIVE_PHOSPHORYLATION
4	3e−12	20 / 60	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
5	5e−12	23 / 83	MOOTHA_VOXPHOS
6	1e−11	26 / 111	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPOR
7	3e−11	78 / 727	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
8	4e−11	49 / 356	DAIRKEE_TERT_TARGETS_UP
9	7e−11	31 / 165	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
10	9e−11	35 / 207	WONG_MITOCHONDRIA_GENE_MODULE
11	2e−09	23 / 109	KEGG_PARKINSONS_DISEASE
12	3e−09	39 / 282	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
13	3e−08	48 / 420	MOOTHA_HUMAN_MITODB_6_2002
14	4e−08	49 / 437	MOOTHA_MITOCHONDRIA
15	1e−07	47 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
16	3e−07	62 / 651	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
17	5e−07	25 / 167	KEGG_HUNTINGTONS_DISEASE
18	5e−07	68 / 754	MARTENS_TRETINOIN_RESPONSE_DN
19	1e−06	23 / 151	KEGG_ALZHEIMERS_DISEASE
20	1e−06	47 / 459	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−09	32 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5e−03	15 / 146	HALLMARK_DNA_REPAIR
3	9e−02	14 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
4	1e−01	8 / 102	HALLMARK_PEROXISOME
5	1e−01	6 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	2e−01	7 / 94	HALLMARK_PROTEIN_SECRETION
7	2e−01	10 / 154	HALLMARK_FATTY_ACID_METABOLISM
8	3e−01	12 / 199	HALLMARK_ADIPOGENESIS
9	3e−01	7 / 112	HALLMARK_BILE_ACID_METABOLISM
10	3e−01	11 / 193	HALLMARK_HEME_METABOLISM
11	4e−01	6 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	4e−01	3 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
13	4e−01	2 / 30	HALLMARK_NOTCH_SIGNALING
14	5e−01	10 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	5e−01	10 / 196	HALLMARK_P53_PATHWAY
16	6e−01	9 / 190	HALLMARK_APICAL_JUNCTION
17	6e−01	9 / 196	HALLMARK_MITOTIC_SPINDLE
18	6e−01	5 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
19	7e−01	8 / 192	HALLMARK_COMPLEMENT
20	8e−01	3 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.4	1 / 11	DUMEAUX_Smoking literature genes up
3	0.5	5 / 91	DUMEAUX_Smoking enriched genes
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	1e−10	361 / 5643	HOPP_Txn_transition
2	5e−09	489 / 8358	HOPP_Active_promoter
3	1e−07	438 / 7491	HOPP_Txn_elongation
4	2e−03	437 / 8147	HOPP_Weak_promoter
5	1e−02	6 / 42	CARO_OxPhos_in_DLBCL_UP
6	3e−02	395 / 7592	HOPP_Strong_enhancer
7	6e−02	77 / 1333	SPANG_BCR UP
8	7e−02	7 / 75	WIRTH_lymphoma937_spot IM
9	8e−02	3 / 21	ROSOLOWSKI_red UP
10	8e−02	7 / 78	TARTE_Plasma cell signature
11	1e−01	7 / 87	ROSOLOWSKI_red total
12	1e−01	2 / 13	BENTINK_mBL DOWN
13	1e−01	6 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
14	2e−01	27 / 466	SPANG_CD40 6hrs DN
15	2e−01	3 / 35	Subero_T−PLL_hypo_meth
16	3e−01	19 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
17	3e−01	1 / 7	CARO_OxPhos_vs_BCR_UP
18	3e−01	3 / 40	ROSOLOWSKI_blue DOWN
19	3e−01	19 / 347	WIRTH_lymphoma937_spot H
20	4e−01	1 / 9	YAMANE_AICDA_targets_nonrecruited

MF

Rank	p−value	#in/all	Geneset
1	3e−11	16 / 41	NADH dehydrogenase (ubiquinone) activity
2	9e−05	5 / 11	NADH dehydrogenase activity
3	3e−03	6 / 30	hydrogen ion transmembrane transporter activity
4	3e−03	5 / 22	2 iron, 2 sulfur cluster binding
5	3e−03	5 / 22	protein disulfide oxidoreductase activity
6	7e−03	5 / 26	cytochrome−c oxidase activity
7	9e−03	20 / 232	hydrolase activity
8	1e−02	3 / 10	ribonuclease P activity
9	1e−02	10 / 89	electron carrier activity
10	1e−02	6 / 40	SNAP receptor activity
11	2e−02	4 / 21	calcium−dependent cysteine−type endopeptidase activity
12	2e−02	3 / 12	oxidoreductase activity, acting on NAD(P)H
13	2e−02	3 / 12	protein phosphatase type 1 regulator activity
14	2e−02	3 / 12	proton−transporting ATP synthase activity, rotational mechanism
15	2e−02	4 / 22	proton−transporting ATPase activity, rotational mechanism
16	2e−02	4 / 22	ribonucleoprotein complex binding
17	2e−02	4 / 23	polyubiquitin binding
18	3e−02	3 / 14	glutathione peroxidase activity
19	3e−02	5 / 36	hydrolase activity, hydrolyzing O−glycosyl compounds
20	3e−02	4 / 25	isomerase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	10 / 94	hsa−miR−378
2	0.06	7 / 72	hsa−miR−331−3p
3	0.06	4 / 31	hsa−miR−1293
4	0.06	3 / 19	hsa−miR−542−5p
5	0.07	4 / 33	hsa−miR−1296
6	0.07	4 / 33	hsa−miR−17*
7	0.08	7 / 77	hsa−miR−422a
8	0.10	2 / 11	hsa−miR−604
9	0.12	3 / 25	hsa−miR−1228
10	0.13	8 / 104	hsa−miR−516b
11	0.19	5 / 63	hsa−miR−671−5p
12	0.19	10 / 150	hsa−miR−491−5p
13	0.20	3 / 32	hsa−miR−296−5p
14	0.21	14 / 226	hsa−miR−185
15	0.23	2 / 19	hsa−miR−645
16	0.24	6 / 87	hsa−miR−339−5p
17	0.26	1 / 6	hsa−miR−937
18	0.26	1 / 6	hsa−miR−523
19	0.26	1 / 6	hsa−miR−886−5p
20	0.26	3 / 37	hsa−miR−769−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	2 / 15	GUSTAFSON_PI3K_DN
2	0.4	1 / 12	BENTINK_ras.1
3	0.5	1 / 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 / 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	7e−14	191 / 2342	ICGC_GabpPcr2_targets
2	3e−12	344 / 5173	ICGC_Taf1_targets
3	2e−11	302 / 4470	ICGC_Creb1_targets
4	4e−10	355 / 5578	ICGC_Stat5_targets
5	4e−10	113 / 1294	KIM_MYC_targets
6	5e−10	283 / 4230	ICGC_Nfatc1_targets
7	5e−10	294 / 4436	ICGC_Zeb1_targets
8	9e−10	321 / 4969	ICGC_Atf2_targets
9	5e−09	335 / 5308	ICGC_Tcf12_targets
10	6e−09	339 / 5393	ICGC_Sp1_targets
11	1e−08	172 / 2354	ICGC_SrfV0416101_targets
12	3e−08	292 / 4566	ICGC_Egr1_targets
13	3e−08	342 / 5526	ICGC_Pmlsc71910_targets
14	4e−08	366 / 6005	ICGC_Mta3_targets
15	3e−07	308 / 4987	ICGC_Bclaf101388_targets
16	3e−07	332 / 5453	ICGC_Foxm1_targets
17	3e−07	368 / 6157	ICGC_Tcf3_targets
18	6e−07	136 / 1867	HEBENSTREIT_high expression TF
19	8e−07	374 / 6324	ICGC_Yy1_targets
20	3e−06	329 / 5512	ICGC_Nficsc81335_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	3 / 19	VAQUERIZAS_Heart
2	0.21	3 / 33	VAQUERIZAS_Liver
3	0.43	2 / 30	VAQUERIZAS_Smooth muscle
4	0.55	1 / 16	VAQUERIZAS_Ovary
5	0.57	1 / 17	VAQUERIZAS_Adrenal gland
6	0.57	1 / 17	VAQUERIZAS_Salivary gland
7	0.66	2 / 46	VAQUERIZAS_Whole brain
8	0.71	1 / 25	VAQUERIZAS_Spinal cord
9	0.71	1 / 25	VAQUERIZAS_Adrenal cortex
10	0.77	6 / 155	VAQUERIZAS_General
11	0.79	1 / 31	VAQUERIZAS_Fetal lung
12	0.82	2 / 64	VAQUERIZAS_Lung
13	0.84	2 / 67	VAQUERIZAS_Whole blood
14	0.87	1 / 41	VAQUERIZAS_Fetal brain
15	0.87	1 / 41	VAQUERIZAS_Testis
16	0.88	1 / 42	VAQUERIZAS_Thymus
17	0.91	1 / 49	VAQUERIZAS_Uterus
18	1.00	0 / 45	VAQUERIZAS_Placenta
19	1.00	0 / 37	VAQUERIZAS_Prostate
20	1.00	0 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	3 / 13	WIRTH_Prim. lymphoid organs
2	0.05	4 / 30	PALMER_Lymphocytes signature up
3	0.12	17 / 259	PALMER_Granulocytes signature up
4	0.47	1 / 13	WIRTH_Sec. lymphoid organs
5	0.47	1 / 13	WIRTH_Globus pallidus
6	0.50	1 / 14	WIRTH_B−cells
7	0.50	1 / 14	WIRTH_Thymus
8	0.52	1 / 15	WIRTH_Telencephalon
9	0.90	4 / 137	WIRTH_Mucosa
10	0.90	1 / 47	WIRTH_Placenta
11	0.97	3 / 141	WIRTH_Muscle
12	0.98	1 / 82	WIRTH_Homeostasis
13	0.99	4 / 202	WIRTH_Testis
14	0.99	2 / 140	PALMER_T−Cell signature up
15	1.00	1 / 115	WIRTH_Liver
16	1.00	3 / 208	PALMER_B−Cell signature up
17	1.00	5 / 476	WIRTH_Nervous System
18	1.00	3 / 427	WIRTH_Immune system
19	1.00	0 / 6	WIRTH_Pituitary gland
20	1.00	0 / 54	WIRTH_Pancreas

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	65 / 1343	LU_BPDE 1h DN
2	1.0	173 / 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	

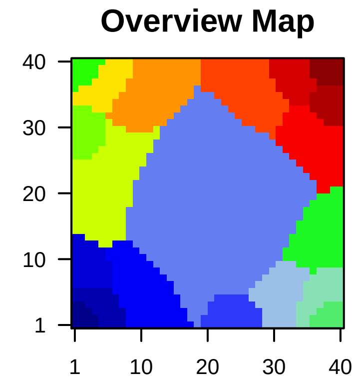
K−Means Clusters

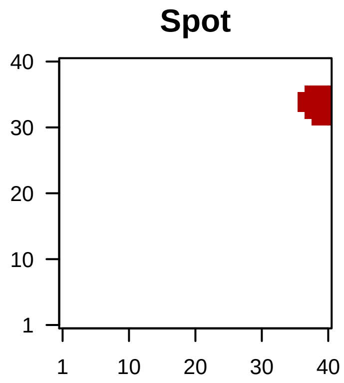
Spot Summary: M

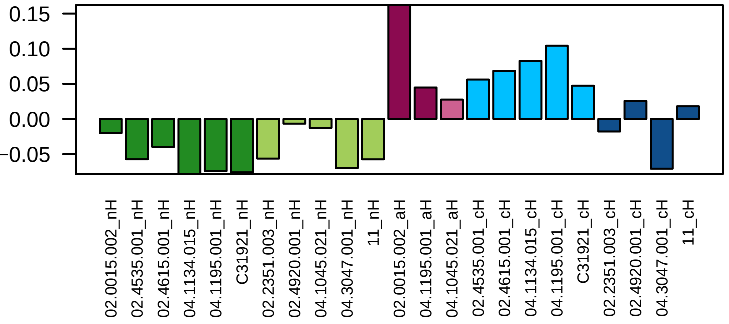
metagenes = 26
genes = 465

<r> metagenes = 0.97
<r> genes = 0.63
beta: r2= 0.09 / log p= −0.77

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





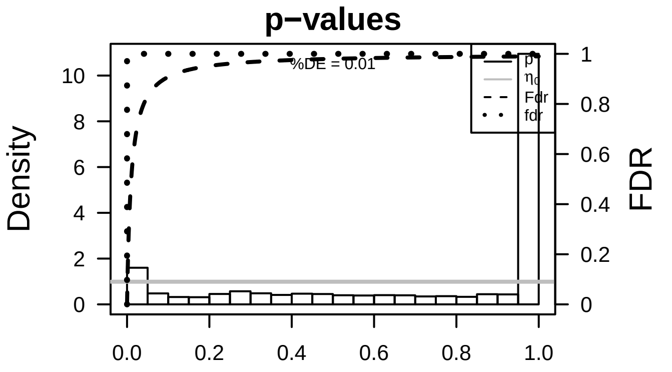


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	0.65	−0.08	0.52	TESC	tescalcin [Source:HGNC Symbol;Acc:HGNC:26065]
2	ENSG000001	0.62	−0.04	0.29	DUSP27	dual specificity phosphatase 27 (putative) [Source:HGNC Syr
3	ENSG000001	0.57	−0.3	0.64	RPLP2	ribosomal protein, large, P2 [Source:HGNC Symbol;Acc:HGN
4	ENSG000001	0.51	−0.3	0.8	NENF	neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HG
5	ENSG000001	0.48	−0.35	0.62	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
6	ENSG000002	0.47	−0.22	0.73		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3
7	ENSG000001	0.46	−0.1	0.62	DUOXA2	dual oxidase maturation factor 2 [Source:HGNC Symbol;Acc:
8	ENSG000001	0.46	−0.14	0.74	GCHFR	GTP cyclohydrolase I feedback regulator [Source:HGNC Sym
9	ENSG000001	0.46	−0.15	0.91	ZNF593	zinc finger protein 593 [Source:HGNC Symbol;Acc:HGNC:30
10	ENSG000001	0.44	−0.07	0.6	TACSTD2	tumor−associated calcium signal transducer 2 [Source:HGNC
11	ENSG000000	0.44	−0.08	0.62		RTEL1−TNFRSF6B readthrough (NMD candidate) [Source:H
12	ENSG000001	0.4	−0.15	0.86	LSMEM2	leucine−rich single−pass membrane protein 2 [Source:HGNC
13	ENSG000001	0.4	−0.18	0.83	NDUFB11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 1
14	ENSG000001	0.39	−0.13	0.78	ARSE	arylsulfatase E (chondrodysplasia punctata 1) [Source:HGNC
15	ENSG000001	0.39	−0.19	0.75	SEC61B	Sec61 beta subunit [Source:HGNC Symbol;Acc:HGNC:1699
16	ENSG000001	0.39	−0.08	0.61	CPNE7	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
17	ENSG000002	0.38	−0.21	0.74		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H0
18	ENSG000001	0.36	−0.07	0.76	NMU	neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
19	ENSG000001	0.36	−0.14	0.64	KCNE3	potassium channel, voltage gated subfamily E regulatory beta
20	ENSG000001	0.36	−0.04	0.68	PF4	platelet factor 4 [Source:HGNC Symbol;Acc:HGNC:8861]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−50	350 / 8123	Colon	TssF_Colon
2	7e−45	391 / 10475	Colon	TssA_Colon
3	8e−42	98 / 807	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
4	8e−41	97 / 811	Lymp	WIRTH_lymphoma937_spot D
5	4e−33	82 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	2e−31	92 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	5e−30	355 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
8	4e−29	84 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
9	2e−28	67 / 550	Canc	Lembcke_Normal vs Adenoma
10	8e−28	30 / 82	BP	mitochondrial translational elongation
11	8e−28	32 / 98	BP	mitochondrial translation
12	2e−27	30 / 84	BP	mitochondrial translational termination
13	2e−26	29 / 82	BP	mitochondrial translational initiation
14	2e−25	77 / 813	GSEA	GRADE_COLON_CANCER_UP
15	3e−25	60 / 499	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
16	4e−24	34 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
17	4e−23	101 / 1441	CC	mitochondrion
18	7e−23	42 / 259	BP	translation
19	1e−22	264 / 6761	Colon	TssD2_Colon
20	2e−21	51 / 425	CC	mitochondrial inner membrane
21	1e−20	2 / 16	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
22	5e−20	66 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
23	1e−19	57 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
24	2e−19	55 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
25	2e−18	329 / 9930	Colon	Tx_Colon
26	4e−18	41 / 327	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
27	5e−18	31 / 179	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
28	8e−18	66 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
29	2e−17	52 / 543	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_UP
30	2e−17	290 / 8358	Lymp	HOPP_Active_promoter
31	2e−17	29 / 162	MF	structural constituent of ribosome
32	3e−17	35 / 248	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
33	3e−17	30 / 177	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
34	7e−17	62 / 775	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
35	8e−17	57 / 668	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
36	3e−16	36 / 282	GSEA	MANALO_HYPOXIA_DN
37	4e−16	330 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
38	4e−16	45 / 446	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
39	2e−15	52 / 608	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
40	7e−15	67 / 975	GSEA	NUYTTEN_EZH2_TARGETS_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.3	5 / 144	HORVATH_aging_genes meth UP
2	0.3	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	

BP

Rank	p−value	#in/all	Geneset
1	8e−28	30 / 82	mitochondrial translational elongation
2	8e−28	32 / 98	mitochondrial translation
3	2e−27	30 / 84	mitochondrial translational termination
4	2e−26	29 / 82	mitochondrial translational initiation
5	7e−23	42 / 259	translation
6	3e−14	34 / 291	organelle organization
7	4e−10	34 / 410	mitotic cell cycle
8	4e−09	13 / 65	DNA damage response, signal transduction by p53 class mediator resulting in
9	4e−09	19 / 151	G1/S transition of mitotic cell cycle
10	9e−09	15 / 96	antigen processing and presentation of peptide antigen via MHC class I
11	1e−08	48 / 820	gene expression
12	2e−08	11 / 49	regulation of cellular amino acid metabolic process
13	2e−08	13 / 73	antigen processing and presentation of exogenous peptide antigen via MHC c
14	2e−08	23 / 239	mitotic nuclear division
15	2e−08	27 / 323	cell division
16	3e−08	13 / 77	antigen processing and presentation of exogenous peptide antigen via MHC c
17	4e−08	8 / 23	proteasomal ubiquitin−independent protein catabolic process
18	6e−08	13 / 80	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent p
19	1e−07	12 / 70	positive regulation of ubiquitin−protein ligase activity involved in regulation of m
20	2e−07	12 / 74	regulation of ubiquitin−protein ligase activity involved in mitotic cell cycle

Brain

Rank	p−value	#in/all	Geneset
1	5e−30	355 / 9923	Overlap_fetal_midbrain_K9K27me3
2	4e−16	330 / 10239	Overlap_fetal_midbrain_ReprPC
3	4e−07	46 / 865	Mid_Frontal_Lobe_Het
4	3e−06	307 / 10800	Overlap_fetal_midbrain_Quies
5	8e−06	118 / 3370	Mid_Frontal_Lobe_ZNF
6	5e−05	66 / 1680	Fetal_ReprPCWk
7	9e−05	42 / 939	Fetal_HetRpts
8	7e−04	83 / 2443	Fetal_Quies
9	8e−04	62 / 1713	Mid_Frontal_Lobe_ReprPCWk
10	3e−03	90 / 2820	Mid_Frontal_Lobe_HetRpts
11	2e−02	15 / 342	Fetal_Het
12	3e−01	12 / 400	Fetal_ZNF
13	3e−01	101 / 3977	Mid_Frontal_Lobe_ReprPC
14	3e−01	54 / 2084	Mid_Frontal_Lobe_K9K27me3
15	7e−01	5 / 232	Fetal_ReprPC
16	7e−01	19 / 855	Overlap_fetal_midbrain_ZNF
17	8e−01	3 / 191	Overlap_fetal_midbrain_Het
18	9e−01	7 / 408	Mid_Frontal_Lobe_TxTrans
19	1e+00	50 / 2549	Fetal_TssF
20	1e+00	3 / 268	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	2e−28	67 / 550	Lembcke_Normal vs Adenoma
2	1e−20	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	3e−06	5 / 16	RHODES_UNDIFFERENTIATED_CANCER
4	1e−04	4 / 11	GENTLES_modul5
5	6e−04	1 / 16	RHODES_CANCER_META_SIGNATURE
6	2e−02	8 / 136	PanCan_CC+Apop_geneset_nanostring
7	5e−02	2 / 15	GENTLES_modul4
8	6e−02	2 / 16	LIU_LIVER_CANCER
9	6e−02	2 / 16	GENTLES_modul1
10	6e−02	2 / 16	GENTLES_modul2
11	6e−02	2 / 16	GENTLES_modul6
12	6e−02	2 / 16	GENTLES_modul7
13	6e−02	3 / 37	KUIPER_MM good survival
14	7e−02	1 / 14	LIU_PROSTATE_CANCER_UP
15	9e−02	4 / 71	SHAUGHNESSY_MM high risk
16	3e−01	1 / 16	WANG_ER_UP
17	3e−01	1 / 16	WOLFER_overlap genes
18	3e−01	2 / 50	PanCan_DNARepair_geneset_nanostring
19	4e−01	1 / 24	PanCan_Notch_geneset_nanostring
20	5e−01	0 / 16	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	4e−23	101 / 1441	mitochondrion
2	2e−21	51 / 425	mitochondrial inner membrane
3	3e−12	12 / 31	mitochondrial large ribosomal subunit
4	9e−11	10 / 24	mitochondrial small ribosomal subunit
5	3e−10	10 / 27	mitochondrial ribosome
6	4e−09	20 / 168	ribosome
7	7e−09	12 / 56	proteasome complex
8	2e−08	25 / 277	mitochondrial matrix
9	4e−07	7 / 21	proteasome core complex
10	5e−07	112 / 2974	cytosol
11	2e−06	97 / 2554	nucleoplasm
12	4e−06	41 / 799	nucleolus
13	2e−05	38 / 767	endoplasmic reticulum membrane
14	4e−05	7 / 40	spindle microtubule
15	5e−05	5 / 18	U4/U6 x U5 tri−snRNP complex
16	6e−05	4 / 10	methylosome
17	6e−05	4 / 10	proteasome core complex, alpha−subunit complex
18	6e−05	4 / 10	U4 snRNP
19	9e−05	9 / 76	condensed chromosome kinetochore
20	3e−04	4 / 14	microtubule plus−end

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	36 / 847	Chr 16
2	1e−02	19 / 436	Chr 22
3	1e−02	36 / 1017	Chr 12
4	2e−02	21 / 522	Chr 20
5	1e−01	27 / 859	Chr 7
6	2e−01	40 / 1425	Chr 19
7	2e−01	33 / 1172	Chr 11
8	2e−01	18 / 613	Chr 14
9	3e−01	21 / 745	Chr 9
10	4e−01	28 / 1083	Chr 17
11	5e−01	14 / 582	Chr 15
12	7e−01	44 / 1920	Chr 1
13	9e−01	19 / 976	Chr 6
14	9e−01	14 / 746	Chr X
15	9e−01	5 / 318	Chr 13
16	9e−01	4 / 272	Chr 18
17	9e−01	11 / 651	Chr 8
18	9e−01	12 / 735	Chr 4
19	9e−01	2 / 191	Chr 21
20	1e+00	11 / 715	Chr 10

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−50	350 / 8123	TssF_Colon
2	7e−45	391 / 10475	TssA_Colon
3	4e−33	82 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	1e−22	264 / 6761	TssD2_Colon
5	2e−18	329 / 9930	Tx_Colon
6	8e−18	66 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
7	3e−11	295 / 9390	TxWk_Colon
8	4e−10	204 / 5889	EnhWk1_Colon
9	1e−08	340 / 11791	Enh_Colon
10	3e−06	334 / 11968	TssWk_Colon
11	5e−06	112 / 3122	TxEnhG1_Colon
12	5e−04	102 / 3112	EnhA_Colon
13	2e−03	259 / 9470	Quies3_Colon
14	4e−03	34 / 877	TxEnhG2_Colon
15	4e−02	4 / 55	Marisa_CRC−cluster−e
16	2e−01	11 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
17	2e−01	1 / 9	Marisa_CRC−C3
18	2e−01	2 / 36	Ang_CRC_Hypomethylated
19	4e−01	1 / 21	Juehling−MSI−enriched−in−6
20	5e−01	1 / 26	Ang_CRC−CIMPH−vs−L_hypo

Disease

Rank	p−value	#in/all	Geneset
1	0.1	20 / 608	GUDJ_psoriasis up
2	1.0	1 / 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	4e−24	34 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	5e−03	8 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	3e−02	4 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
4	9e−02	57 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	9e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
6	1e−01	1 / 5	Phillips Prolif up vs PN & MES
7	1e−01	12 / 344	Up
8	1e−01	1 / 6	Martinez_Glio_hypometh
9	2e−01	3 / 59	developing astrocytes
10	2e−01	61 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
11	2e−01	3 / 63	Stuehler_Proteins_up_in_STS
12	2e−01	2 / 35	shaw_responders_down_in_oligo_glioma
13	2e−01	25 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
14	2e−01	2 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	3e−01	2 / 40	Christensen_hypomethylated_in_ependymoma
16	3e−01	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
17	3e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
18	3e−01	1 / 15	Mukasa_UP_in_GBM
19	3e−01	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
20	3e−01	3 / 81	GIEZELT_GBM_STS_up_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−31	92 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	4e−29	84 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	2e−25	77 / 813	GRADE_COLON_CANCER_UP
4	3e−25	60 / 499	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
5	1e−20	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	5e−20	66 / 754	MARTENS_TRETINOIN_RESPONSE_DN
7	1e−19	57 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	2e−19	55 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
9	4e−18	41 / 327	WONG_EMBRYONIC_STEM_CELL_CORE
10	5e−18	31 / 179	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	2e−17	52 / 543	TIEN_INTESTINE_PROBIOTICS_24HR_UP
12	3e−17	35 / 248	KOBAYASHI_EGFR_SIGNALING_24HR_DN
13	3e−17	30 / 177	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
14	7e−17	62 / 775	WEI_MYCN_TARGETS_WITH_E_BOX
15	8e−17	57 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
16	3e−16	36 / 282	MANALO_HYPOXIA_DN
17	4e−16	45 / 446	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	2e−15	52 / 608	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
19	7e−15	67 / 975	NUYTTEN_EZH2_TARGETS_DN
20	9e−15	36 / 316	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−08	12 / 58	HALLMARK_MYC_TARGETS_V2
2	3e−07	19 / 197	HALLMARK_E2F_TARGETS
3	1e−06	18 / 195	HALLMARK_MYC_TARGETS_V1
4	6e−06	17 / 196	HALLMARK_G2M_CHECKPOINT
5	1e−04	15 / 199	HALLMARK_MTORC1_SIGNALING
6	2e−04	12 / 146	HALLMARK_DNA_REPAIR
7	3e−04	14 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	3e−04	14 / 198	HALLMARK_GLYCOLYSIS
9	2e−02	10 / 199	HALLMARK_ADIPOGENESIS
10	3e−02	5 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	8e−02	7 / 154	HALLMARK_FATTY_ACID_METABOLISM
12	8e−02	7 / 155	HALLMARK_UV_RESPONSE_UP
13	1e−01	8 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
14	1e−01	5 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	2e−01	7 / 196	HALLMARK_MITOTIC_SPINDLE
16	2e−01	7 / 197	HALLMARK_IL2_STAT5_SIGNALING
17	2e−01	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
18	3e−01	3 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
19	5e−01	3 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
20	5e−01	1 / 30	HALLMARK_NOTCH_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.6	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	8e−42	98 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	8e−41	97 / 811	WIRTH_lymphoma937_spot D
3	2e−17	290 / 8358	HOPP_Active_promoter
4	2e−11	250 / 7491	HOPP_Txn_elongation
5	1e−09	196 / 5643	HOPP_Txn_transition
6	4e−09	28 / 317	TARTE_Plasmablast signature
7	9e−07	17 / 171	WIRTH_lymphoma937_spot C
8	3e−06	16 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
9	1e−05	241 / 8147	HOPP_Weak_promoter
10	5e−05	17 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
11	1e−04	5 / 21	ROSOLOWSKI_red UP
12	2e−04	16 / 240	WIRTH_lymphoma937_spot B
13	2e−02	205 / 7592	HOPP_Strong_enhancer
14	2e−02	6 / 87	Aukema_BCL2 DN_BCL6 UP
15	2e−02	6 / 87	ROSOLOWSKI_red total
16	2e−02	7 / 116	WIRTH_lymphoma937_spot MM
17	5e−02	5 / 83	ROSOLOWSKI_green UP
18	5e−02	6 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
19	1e−01	4 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_C
20	1e−01	4 / 75	WIRTH_lymphoma937_spot IM

MF

Rank	p−value	#in/all	Geneset
1	2e−17	29 / 162	structural constituent of ribosome
2	1e−14	71 / 1091	poly(A) RNA binding
3	6e−07	7 / 22	threonine−type endopeptidase activity
4	1e−04	9 / 80	endopeptidase activity
5	1e−04	6 / 34	rRNA binding
6	2e−04	4 / 13	pseudouridine synthase activity
7	4e−04	6 / 41	NADH dehydrogenase (ubiquinone) activity
8	8e−04	5 / 31	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
9	2e−03	24 / 513	RNA binding
10	2e−03	4 / 22	snoRNA binding
11	2e−03	3 / 11	omega peptidase activity
12	7e−03	3 / 17	translation initiation factor binding
13	8e−03	7 / 94	unfolded protein binding
14	9e−03	3 / 18	ribonuclease activity
15	1e−02	18 / 407	catalytic activity
16	1e−02	12 / 232	hydrolase activity
17	2e−02	3 / 22	ribonucleoprotein complex binding
18	2e−02	5 / 63	transferase activity
19	2e−02	4 / 42	endonuclease activity
20	2e−02	2 / 10	ribonuclease P activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	4 / 38	hsa−miR−1224−5p
2	0.02	4 / 41	hsa−miR−95
3	0.02	7 / 115	hsa−miR−499−5p
4	0.02	5 / 68	hsa−miR−637
5	0.03	2 / 11	hsa−miR−604
6	0.04	3 / 32	hsa−miR−296−5p
7	0.04	3 / 33	hsa−miR−342−5p
8	0.04	3 / 33	hsa−miR−1296
9	0.05	3 / 35	hsa−miR−1229
10	0.07	3 / 40	hsa−miR−517*
11	0.07	5 / 92	hsa−miR−362−5p
12	0.08	5 / 97	hsa−miR−125b
13	0.08	5 / 97	hsa−miR−125a−5p
14	0.09	4 / 70	hsa−miR−193b
15	0.09	3 / 44	hsa−miR−661
16	0.10	4 / 72	hsa−miR−331−3p
17	0.10	3 / 46	hsa−miR−874
18	0.11	2 / 24	hsa−miR−451
19	0.11	3 / 49	hsa−miR−1291
20	0.11	4 / 77	hsa−miR−513c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 14	BENTINK_myc.1
2	0.25	1 / 12	BENTINK_ras.1
3	0.31	1 / 15	BENTINK_ras.6
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 15	GUSTAFSON_PI3K_DN
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	2e−12	74 / 1294	KIM_MYC targets
2	4e−09	75 / 1549	ICGC_Myc_targets
3	4e−08	177 / 5173	ICGC_Taf1_targets
4	3e−07	184 / 5578	ICGC_Stat5_targets
5	7e−07	153 / 4470	ICGC_Creb1_targets
6	2e−06	179 / 5512	ICGC_Nficsc81335_targets
7	3e−06	76 / 1867	HEBENSTREIT_high expression TF
8	5e−06	197 / 6313	ICGC_Pou2_targets
9	7e−06	89 / 2342	ICGC_GabpPcr2_targets
10	1e−05	209 / 6862	ICGC_Elf1_targets
11	1e−05	169 / 5308	ICGC_Tcf12_targets
12	2e−05	172 / 5453	ICGC_Foxm1_targets
13	3e−05	173 / 5526	ICGC_Pmlsc71910_targets
14	3e−05	189 / 6157	ICGC_Tcf3_targets
15	3e−05	185 / 6005	ICGC_Mta3_targets
16	5e−05	143 / 4436	ICGC_Zeb1_targets
17	2e−04	211 / 7202	ICGC_Runx3_targets
18	2e−04	83 / 2354	ICGC_SrfV0416101_targets
19	3e−04	187 / 6324	ICGC_Yy1_targets
20	3e−04	133 / 4230	ICGC_Nfatc1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.3	2 / 42	VAQUERIZAS_Thyroid
2	0.3	1 / 16	VAQUERIZAS_Fetal thyroid
3	0.4	1 / 24	VAQUERIZAS_Trachea
4	0.5	1 / 30	VAQUERIZAS_Smooth muscle
5	0.5	1 / 31	VAQUERIZAS_Fetal lung
6	0.6	1 / 33	VAQUERIZAS_Liver
7	0.6	1 / 37	VAQUERIZAS_Prostate
8	0.6	1 / 41	VAQUERIZAS_Fetal brain
9	0.6	1 / 42	VAQUERIZAS_Thymus
10	0.7	1 / 49	VAQUERIZAS_Uterus
11	0.8	1 / 64	VAQUERIZAS_Lung
12	0.9	2 / 155	VAQUERIZAS_General
13	1.0	0 / 45	VAQUERIZAS_Placenta
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 / 67	VAQUERIZAS_Whole blood
18	1.0	0 / 7	VAQUERIZAS_Appendix
19	1.0	0 / 18	VAQUERIZAS_Pancreas
20	1.0	0 / 16	VAQUERIZAS_Fetal liver

Tissue

Rank	p−value	#in/all	Geneset
1	0.2	5 / 137	WIRTH_Mucosa
2	0.3	1 / 12	WIRTH_Tonsil
3	0.3	1 / 13	WIRTH_Globus pallidus
4	0.3	1 / 14	WIRTH_Thymus
5	0.3	1 / 14	WIRTH_Bone marrow
6	0.3	1 / 14	WIRTH_Thalamus
7	0.9	1 / 115	WIRTH_Liver
8	1.0	1 / 140	PALMER_T−Cell signature up
9	1.0	1 / 141	WIRTH_Muscle
10	1.0	1 / 208	PALMER_B−Cell signature up
11	1.0	4 / 476	WIRTH_Nervous System
12	1.0	2 / 427	WIRTH_Immune system
13	1.0	0 / 6	WIRTH_Pituitary gland
14	1.0	0 / 54	WIRTH_Pancreas
15	1.0	0 / 13	WIRTH_Sec. lymphoid organs
16	1.0	0 / 13	WIRTH_Prim. lymphoid organs
17	1.0	0 / 14	WIRTH_B−cells
18	1.0	0 / 12	WIRTH_Lymphocytes
19	1.0	0 / 15	WIRTH_Telencephalon
20	1.0	0 / 13	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	40 / 1343	LU_BPDE 1h DN
2	1.0	85 / 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	

K−Means Clusters

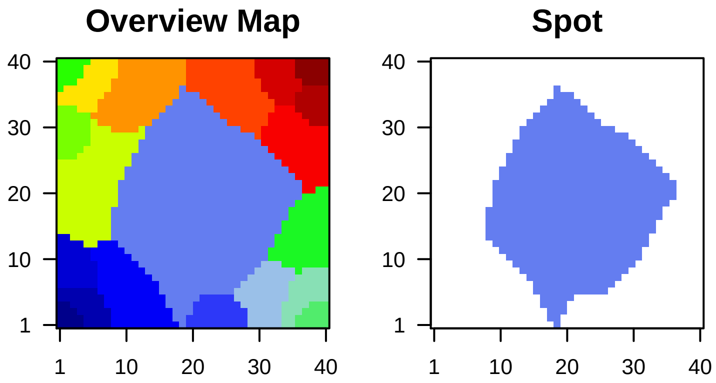
Spot Summary: N

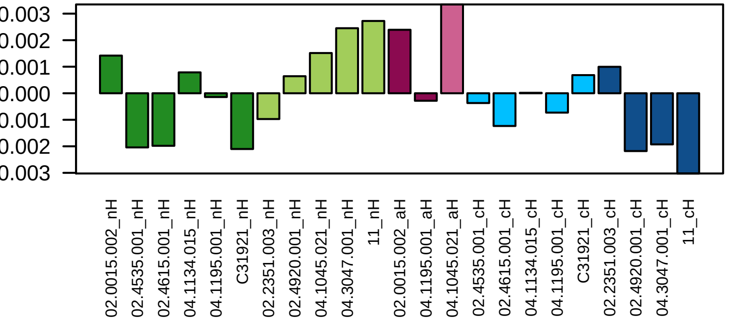
metagenes = 578
genes = 7452

<r> metagenes = 0.09

beta: r2= 0 / log p= −0.04

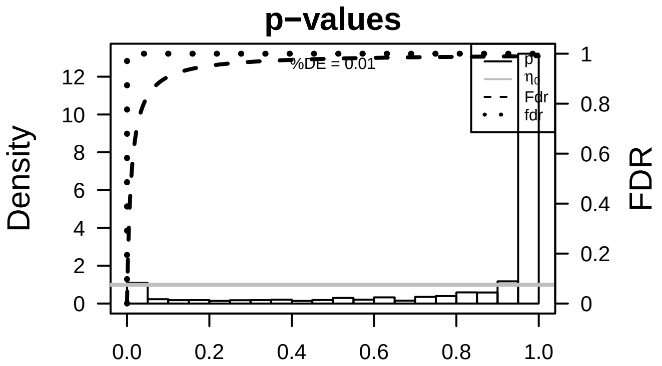
samples with spot = 0 (0 %)





Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	1723 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	1e−99	1960 / 3406	Colon	ReprPC_Colon
3	1e−99	1692 / 2947	Colon	ReprPCWk_Colon
4	2e−81	2440 / 5039	Lympl	HOPP_Repressed
5	5e−74	536 / 781	Glio	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
6	3e−71	1023 / 1798	TF	HEBENSTREIT_low expression TF
7	3e−71	408 / 551	MF	G−protein coupled receptor activity
8	5e−69	170 / 173	BP	detection of chemical stimulus involved in sensory perception of smell
9	1e−68	169 / 172	MF	olfactory receptor activity
10	6e−60	1101 / 2041	Colon	EnhP_Colon
11	7e−59	969 / 1753	Colon	Het_Colon
12	1e−51	178 / 202	Tissu	WIRTH_Testis
13	1e−50	133 / 138	GSEA	REACTOME_OLFACTORY_SIGNALING_PATHWAY
14	8e−49	161 / 180	GSEA	KEGG_OLFACTORY_TRANSDUCTION
15	1e−45	451 / 718	BP	G−protein coupled receptor signaling pathway
16	2e−43	360 / 546	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
17	4e−39	1481 / 3109	Colon	TssP_Colon
18	8e−39	966 / 1890	Brain	Overlap_fetal_midbrain_TssF
19	2e−38	2353 / 5285	Toxic	LU_BPDE 0.005 DN
20	2e−36	266 / 389	Colon	K9K27me3_Colon
21	2e−36	601 / 1084	Brain	Overlap_fetal_midbrain_EnhG
22	2e−36	690 / 1281	Colon	HetRpts_Colon
23	3e−33	107 / 119	BP	sensory perception of smell
24	4e−31	733 / 1418	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
25	2e−28	749 / 1478	Brain	Overlap_fetal_midbrain_TxTrans
26	2e−27	659 / 1279	Brain	Overlap_fetal_midbrain_Enh
27	5e−27	315 / 525	Colon	Quies2_Colon
28	5e−24	336 / 585	GSEA	REACTOME_GPCR_DOWNSTREAM_SIGNALING
29	2e−23	1542 / 3457	Lympl	HOPP_Heterochrom
30	3e−23	302 / 517	Glio	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
31	9e−23	662 / 1327	Brain	Mid_Frontal_Lobe_TssP
32	8e−22	430 / 805	Brain	Mid_Frontal_Lobe_EnhG
33	9e−22	247 / 410	GSEA	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
34	3e−21	337 / 604	GSEA	BENPORATH_PRC2_TARGETS
35	4e−21	2088 / 4879	Colon	Quies1_Colon
36	9e−21	168 / 255	GSEA	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
37	9e−21	276 / 476	Tissu	WIRTH_Nervous System
38	1e−20	374 / 689	GSEA	REACTOME_SIGNALING_BY_GPCR
39	2e−19	437 / 840	Brain	Mid_Frontal_Lobe_TssF
40	3e−19	108 / 147	Glio	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)



Aging

Rank	p−value	#in/all	Geneset
1	0.001	33 / 57	TESCHENDORFF_age_hypermethylated
2	0.698	51 / 144	HORVATH_aging_genes meth UP
3	0.999	30 / 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−69	170 / 173	detection of chemical stimulus involved in sensory perception of smell
2	1e−45	451 / 718	G−protein coupled receptor signaling pathway
3	3e−33	107 / 119	sensory perception of smell
4	5e−18	242 / 419	synaptic transmission
5	3e−16	42 / 44	detection of chemical stimulus involved in sensory perception
6	9e−15	121 / 186	visual perception
7	2e−13	81 / 114	regulation of membrane potential
8	4e−13	81 / 115	regulation of ion transmembrane transport
9	2e−10	169 / 308	ion transport
10	7e−10	40 / 50	neurological system process
11	2e−09	154 / 283	ion transmembrane transport
12	1e−08	67 / 104	potassium ion transmembrane transport
13	2e−08	61 / 93	neuropeptide signaling pathway
14	5e−08	27 / 32	sensory perception of taste
15	1e−07	38 / 52	response to stimulus
16	4e−07	23 / 27	detection of chemical stimulus involved in sensory perception of bitter taste
17	7e−07	37 / 52	sperm motility
18	1e−06	14 / 14	natural killer cell activation involved in immune response
19	3e−06	31 / 43	G−protein coupled receptor signaling pathway, coupled to cyclic nucleotide se
20	4e−06	169 / 345	spermatogenesis

Brain

Rank	p−value	#in/all	Geneset
1	8e−39	966 / 1890	Overlap_fetal_midbrain_TssF
2	2e−36	601 / 1084	Overlap_fetal_midbrain_EnhG
3	2e−28	749 / 1478	Overlap_fetal_midbrain_TxTrans
4	2e−27	659 / 1279	Overlap_fetal_midbrain_Enh
5	9e−23	662 / 1327	Mid_Frontal_Lobe_TssP
6	8e−22	430 / 805	Mid_Frontal_Lobe_EnhG
7	2e−19	437 / 840	Mid_Frontal_Lobe_TssF
8	1e−15	538 / 1108	Overlap_fetal_midbrain_TssA
9	7e−15	228 / 408	Mid_Frontal_Lobe_TxTrans
10	2e−12	179 / 317	Mid_Frontal_Lobe_Tx
11	7e−12	449 / 940	Mid_Frontal_Lobe_Enh
12	1e−07	363 / 787	Overlap_fetal_midbrain_TssP
13	8e−05	59 / 106	Overlap_fetal_midbrain_Tx
14	1e−04	1053 / 2603	Fetal_TxTrans
15	2e−04	128 / 268	Mid_Frontal_Lobe_TssA
16	3e−04	309 / 712	Overlap_fetal_midbrain_EnhP
17	1e−03	976 / 2443	Fetal_Quies
18	2e−03	1170 / 2956	Fetal_TssA
19	2e−03	1013 / 2549	Fetal_TssF
20	5e−02	533 / 1356	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	9 / 14	BEN−PORATH_DN
2	0.11	14 / 28	PanCan_HH_geneset_nanostring
3	0.71	3 / 9	WANG_ER_DN
4	0.72	2 / 15	LIU_BREAST_CANCER
5	0.77	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.77	5 / 16	LIU_COMMON_CANCER_GENES
7	0.78	4 / 16	LIU_LIVER_CANCER
8	0.91	49 / 152	PanCan_MAPK_geneset_nanostring
9	0.93	11 / 40	PanCan_HK_geneset_nanostring
10	0.94	1 / 6	ZHANG_MGUS up
11	0.95	14 / 51	PanCan_TGF−B_geneset_nanostring
12	0.95	5 / 22	PanCan_ChromMod_geneset_nanostring
13	0.95	43 / 140	PanCan_RAS_geneset_nanostring
14	0.96	22 / 78	PanCan_Wnt_geneset_nanostring
15	0.98	23 / 86	PanCan_JAK−ST_geneset_nanostring
16	0.99	2 / 14	LIU_PROSTATE_CANCER_UP
17	0.99	2 / 14	GENTLES_modul12
18	0.99	2 / 15	BEN−PORATH_UP
19	0.99	2 / 15	GENTLES_modul10
20	0.99	2 / 16	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−15	57 / 68	keratin filament
2	1e−13	639 / 1374	extracellular region
3	3e−10	117 / 198	postsynaptic membrane
4	5e−10	567 / 1250	integral component of plasma membrane
5	4e−09	1665 / 4052	integral component of membrane
6	2e−07	137 / 259	synapse
7	2e−06	41 / 61	motile cilium
8	9e−06	14 / 15	photoreceptor disc membrane
9	1e−05	44 / 70	axoneme
10	2e−05	15 / 17	GABA−A receptor complex
11	2e−05	27 / 38	photoreceptor inner segment
12	3e−05	50 / 84	voltage−gated potassium channel complex
13	3e−05	197 / 422	cell junction
14	5e−05	14 / 16	myosin filament
15	1e−04	54 / 96	intermediate filament
16	4e−04	73 / 142	cilium
17	7e−04	36 / 62	photoreceptor outer segment
18	7e−04	34 / 58	presynaptic membrane
19	1e−03	20 / 30	voltage−gated calcium channel complex
20	1e−03	25 / 40	myofibril

Chr

Rank	p−value	#in/all	Geneset
1	3e−08	26 / 30	Chr Y
2	1e−07	621 / 1425	Chr 19
3	4e−05	329 / 746	Chr X
4	1e−03	313 / 735	Chr 4
5	5e−02	115 / 272	Chr 18
6	1e−01	257 / 651	Chr 8
7	3e−01	443 / 1172	Chr 11
8	5e−01	377 / 1017	Chr 12
9	6e−01	264 / 715	Chr 10
10	6e−01	226 / 613	Chr 14
11	6e−01	451 / 1228	Chr 2
12	6e−01	69 / 191	Chr 21
13	7e−01	114 / 318	Chr 13
14	7e−01	188 / 522	Chr 20
15	7e−01	156 / 436	Chr 22
16	7e−01	378 / 1043	Chr 3
17	8e−01	265 / 745	Chr 9
18	9e−01	306 / 862	Chr 5
19	9e−01	346 / 976	Chr 6
20	9e−01	203 / 582	Chr 15

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	1960 / 3406	ReprPC_Colon
2	1e−99	1692 / 2947	ReprPCWk_Colon
3	6e−60	1101 / 2041	EnhP_Colon
4	7e−59	969 / 1753	Het_Colon
5	4e−39	1481 / 3109	TssP_Colon
6	2e−36	266 / 389	K9K27me3_Colon
7	2e−36	690 / 1281	HetRpts_Colon
8	5e−27	315 / 525	Quies2_Colon
9	4e−21	2088 / 4879	Quies1_Colon
10	2e−16	53 / 60	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
11	2e−15	47 / 52	Pentrack_CRC_TCGA_corr_S_normal_DN
12	2e−14	242 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
13	3e−11	172 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	5e−11	206 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	4e−10	362 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
16	1e−06	286 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
17	2e−04	300 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
18	4e−03	106 / 231	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
19	5e−02	204 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP
20	5e−02	174 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.005	22 / 37	BCHETNIA_EBM−DM up
2	0.073	12 / 22	BCHETNIA_EBM up
3	0.605	1 / 2	BCHETNIA_EBM down
4	1.000	111 / 399	GUDJ_psoriasis down
5	1.000	116 / 608	GUDJ_psoriasis 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	1e−99	1723 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e−74	536 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	3e−23	302 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	3e−19	108 / 147	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	3e−16	105 / 150	Sturm_GBM_Meth_overexpression_B_adult_UP
6	1e−15	456 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
7	1e−12	48 / 58	WILLSCHER_GBM_Verhaak−PNmut_down (G)
8	1e−11	123 / 204	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	5e−09	69 / 106	WIRTH_Normal Brain
10	2e−08	55 / 81	Weller_LGG_gradeII−vs−III_UP
11	1e−07	207 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
12	9e−06	54 / 90	Weller_LGG_A_vs_O_DOWN
13	1e−05	57 / 97	Weller_LGG_1p19qDel−vs−intact_UP
14	2e−05	75 / 137	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
15	3e−05	35 / 54	Hopp_Sturm_GBM_Epi3_B1_G34_DN
16	1e−03	192 / 434	Down_a
17	2e−03	47 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
18	2e−03	34 / 61	in vivo astrocytes vs. cultured astroglia
19	3e−03	14 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
20	3e−03	19 / 30	Gorovets_LGG_NB_subclass

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−50	133 / 138	REACTOME_OLFACTORY_SIGNALING_PATHWAY
2	8e−49	161 / 180	KEGG_OLFACTORY_TRANSDUCTION
3	2e−43	360 / 546	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
4	4e−31	733 / 1418	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
5	5e−24	336 / 585	REACTOME_GPCR_DOWNSTREAM_SIGNALING
6	9e−22	247 / 410	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
7	3e−21	337 / 604	BENPORATH_PRC2_TARGETS
8	9e−21	168 / 255	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
9	1e−20	374 / 689	REACTOME_SIGNALING_BY_GPCR
10	3e−18	140 / 210	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
11	1e−15	388 / 759	MARTENS_TRETINOIN_RESPONSE_UP
12	1e−15	509 / 1041	BENPORATH_ES_WITH_H3K27ME3
13	2e−14	193 / 335	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
14	3e−14	471 / 966	BENPORATH_EED_TARGETS
15	6e−14	472 / 971	BENPORATH_SUZ12_TARGETS
16	8e−14	186 / 324	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
17	6e−13	208 / 377	REACTOME_GPCR_LIGAND_BINDING
18	1e−12	107 / 167	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
19	1e−11	115 / 187	MIKKELSEN_MEF_ICP_WITH_H3K27ME3
20	1e−10	142 / 249	MEISSNER_BRAIN_HCP_WITH_H3K27ME3

HM

Rank	p−value	#in/all	Geneset
1	3e−09	112 / 193	HALLMARK_KRAS_SIGNALING_DN
2	4e−05	70 / 128	HALLMARK_SPERMATOGENESIS
3	3e−01	16 / 37	HALLMARK_PANCREAS_BETA_CELLS
4	6e−01	16 / 44	HALLMARK_APICAL_SURFACE
5	6e−01	13 / 36	HALLMARK_HEDGEHOG_SIGNALING
6	9e−01	12 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	9e−01	35 / 112	HALLMARK_BILE_ACID_METABOLISM
8	1e+00	35 / 132	HALLMARK_COAGULATION
9	1e+00	4 / 36	HALLMARK_ANGIOGENESIS
10	1e+00	48 / 195	HALLMARK_MYOGENESIS
11	1e+00	2 / 30	HALLMARK_NOTCH_SIGNALING
12	1e+00	5 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
13	1e+00	6 / 52	HALLMARK_TGF_BETA_SIGNALING
14	1e+00	15 / 94	HALLMARK_PROTEIN_SECRETION
15	1e+00	17 / 102	HALLMARK_PEROXISOME
16	1e+00	42 / 193	HALLMARK_HEME_METABOLISM
17	1e+00	17 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
18	1e+00	39 / 193	HALLMARK_XENOBIOTIC_METABOLISM
19	1e+00	11 / 98	HALLMARK_ANDROGEN_RESPONSE
20	1e+00	30 / 181	HALLMARK_ALLOGRAFT_REJECTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	6 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.07	41 / 91	DUMEAUX_Smoking enriched genes
3	0.84	10 / 33	DUMEAUX_Fasting enriched genes
4	0.95	2 / 11	DUMEAUX_Women normal BMI literature genes up
5	0.98	3 / 17	DUMEAUX_High bmi enriched genes
6	0.99	1 / 11	DUMEAUX_Smoking literature genes up
7	1.00	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−81	2440 / 5039	HOPP_Repressed
2	2e−23	1542 / 3457	HOPP_Heterochrom
3	2e−07	46 / 67	LEE_Developmental_regulators
4	2e−06	1166 / 2838	HOPP_Poised_promoter
5	8e−06	1089 / 2658	HOPP_Repetitive
6	7e−02	186 / 458	WIRTH_lymphoma937_spot I
7	9e−02	181 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
8	4e−01	19 / 48	Subero_INT_hypo_meth
9	5e−01	19 / 50	Subero_B−ALL_hyper_meth
10	5e−01	53 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
11	5e−01	8 / 21	Subero_MCL_hyper_meth
12	6e−01	53 / 144	WIRTH_lymphoma937_spot G
13	6e−01	2 / 5	Shaknovich_ABC_hyper_meth
14	7e−01	22 / 62	Subero_mBL_hyper_meth
15	7e−01	49 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
16	7e−01	4 / 12	DAVE_BL_UP
17	7e−01	8 / 24	Subero_mBL_hypo_meth
18	7e−01	8 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
19	7e−01	12 / 36	Subero_MM_hyper_meth
20	8e−01	3 / 10	Shaknovich_ABC_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	3e−71	408 / 551	G−protein coupled receptor activity
2	1e−68	169 / 172	olfactory receptor activity
3	3e−13	29 / 29	odorant binding
4	2e−10	37 / 44	extracellular ligand−gated ion channel activity
5	6e−10	84 / 132	ion channel activity
6	1e−09	68 / 102	hormone activity
7	1e−08	21 / 22	cytokine receptor binding
8	1e−07	33 / 43	voltage−gated calcium channel activity
9	1e−06	14 / 14	bitter taste receptor activity
10	3e−06	13 / 13	type I interferon receptor binding
11	6e−06	24 / 31	delayed rectifier potassium channel activity
12	1e−05	19 / 23	acetylcholine receptor activity
13	2e−05	34 / 51	voltage−gated potassium channel activity
14	2e−05	15 / 17	GABA−A receptor activity
15	2e−05	15 / 17	neuropeptide binding
16	2e−05	18 / 22	acetylcholine−activated cation−selective channel activity
17	5e−05	14 / 16	serotonin receptor activity
18	6e−05	12 / 13	taste receptor activity
19	1e−04	86 / 167	cytokine activity
20	2e−04	18 / 24	acetylcholine binding

miRNA Target

Rank	p−value	#in/all	Geneset
1	0.5	9 / 23	hsa−miR−151−5p
2	0.6	2 / 5	hsa−miR−1268
3	0.9	6 / 21	hsa−miR−554
4	0.9	2 / 8	hsa−miR−886−3p
5	0.9	4 / 16	hsa−miR−551b
6	0.9	4 / 16	hsa−miR−891a
7	0.9	2 / 9	hsa−miR−202*
8	0.9	6 / 23	hsa−miR−596
9	0.9	2 / 10	hsa−miR−933
10	0.9	2 / 10	hsa−miR−720
11	1.0	6 / 26	hsa−miR−943
12	1.0	4 / 19	hsa−miR−563
13	1.0	5 / 23	hsa−miR−323−5p
14	1.0	2 / 12	hsa−miR−369−5p
15	1.0	4 / 20	hsa−miR−380*
16	1.0	7 / 31	hsa−miR−1293
17	1.0	5 / 24	hsa−miR−451
18	1.0	1 / 8	hsa−miR−566
19	1.0	3 / 17	hsa−miR−551a
20	1.0	3 / 17	hsa−miR−302a*

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.9	3 / 14	BENTINK_src.10
2	1.0	2 / 14	BENTINK_e2f3.1
3	1.0	1 / 10	BENTINK_ras.4
4	1.0	1 / 13	BENTINK_e2f3.2
5	1.0	1 / 14	BENTINK_myc.1
6	1.0	1 / 15	GUSTAFSON_PI3K_DN
7	1.0	0 / 14	GUSTAFSON_PI3K_UP
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 15	BENTINK_ras.6
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−71	1023 / 1798	HEBENSTREIT_low expression TF
2	6e−02	298 / 745	ICGC_NrsfPcr2_targets
3	8e−01	1 / 3	MYC_Signal transduction UP
4	9e−01	4 / 16	NOWICK_TF
5	9e−01	1 / 5	MYC_TFs
6	1e+00	1 / 9	MYC_DNA repair UP
7	1e+00	2 / 20	MYC_Metabolism UP
8	1e+00	1 / 17	MYC_Protein synthesis degradation UP
9	1e+00	1171 / 3511	ICGC_Rad21_targets
10	1e+00	165 / 619	ICGC_RxraPcr1_targets
11	1e+00	200 / 731	ICGC_SrfPcr2_targets
12	1e+00	3 / 66	MYC_Targets UP
13	1e+00	448 / 1523	ICGC_P300_targets
14	1e+00	426 / 1472	ICGC_NrsfPcr1_targets
15	1e+00	190 / 766	ICGC_Atf3_targets
16	1e+00	305 / 1867	HEBENSTREIT_high expression TF
17	1e+00	175 / 1294	KIM_MYC targets
18	1e+00	0 / 9	MYC_Targets DOWN
19	1e+00	0 / 5	MYC_Apoptosis UP
20	1e+00	0 / 8	MYC_Cell cycle UP

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.3	5 / 10	VAQUERIZAS_Skeletal.muscle.psoas
2	0.6	17 / 46	VAQUERIZAS_Whole brain
3	0.6	9 / 25	VAQUERIZAS_Spinal cord
4	0.7	8 / 23	VAQUERIZAS_Pituitary
5	0.7	4 / 12	VAQUERIZAS_Kidney
6	0.8	2 / 7	VAQUERIZAS_Appendix
7	0.8	13 / 41	VAQUERIZAS_Fetal brain
8	0.8	13 / 41	VAQUERIZAS_Testis
9	0.9	2 / 8	VAQUERIZAS_Tongue
10	0.9	4 / 16	VAQUERIZAS_Fetal liver
11	0.9	3 / 13	VAQUERIZAS_Skin
12	1.0	4 / 19	VAQUERIZAS_Heart
13	1.0	3 / 16	VAQUERIZAS_Fetal thyroid
14	1.0	7 / 33	VAQUERIZAS_Liver
15	1.0	3 / 20	VAQUERIZAS_Bone marrow
16	1.0	7 / 37	VAQUERIZAS_Prostate
17	1.0	2 / 17	VAQUERIZAS_Salivary gland
18	1.0	9 / 45	VAQUERIZAS_Placenta
19	1.0	3 / 22	VAQUERIZAS_Tonsil
20	1.0	1 / 16	VAQUERIZAS_Ovary

Tissue

Rank	p−value	#in/all	Geneset
1	1e−51	178 / 202	WIRTH_Testis
2	9e−21	276 / 476	WIRTH_Nervous System
3	3e−13	95 / 141	WIRTH_Muscle
4	4e−13	81 / 115	WIRTH_Liver
5	2e−11	40 / 47	WIRTH_Placenta
6	1e−06	52 / 82	WIRTH_Homeostasis
7	3e−05	35 / 54	WIRTH_Pancreas
8	3e−03	6 / 6	WIRTH_Pituitary gland
9	1e−02	11 / 16	WIRTH_Hippocampus
10	4e−02	9 / 14	WIRTH_Bone marrow
11	2e−01	56 / 137	WIRTH_Mucosa
12	4e−01	6 / 14	WIRTH_Thalamus
13	9e−01	3 / 14	WIRTH_B−cells
14	9e−01	3 / 14	WIRTH_Thymus
15	1e+00	3 / 15	WIRTH_Telencephalon
16	1e+00	2 / 13	WIRTH_Prim. lymphoid organs
17	1e+00	2 / 13	PALMER_CD8+ T−Cell signature up
18	1e+00	1 / 12	WIRTH_Tonsil
19	1e+00	1 / 13	WIRTH_Globus pallidus
20	1e+00	1 / 13	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	2e−38	2353 / 5285	LU_BPDE 0.005 DN
2	1e+00	383 / 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	

K−Means Clusters

Spot Summary: O

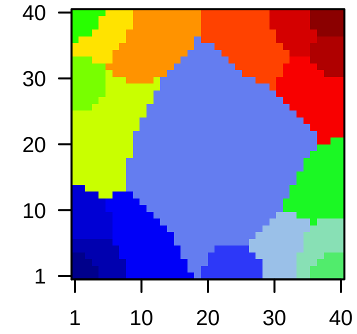
metagenes = 85
genes = 1004

<r> metagenes = 0.78

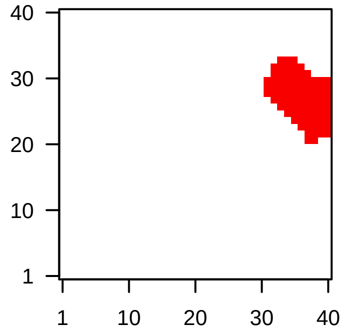
beta: r2= 0.02 / log p= −0.25

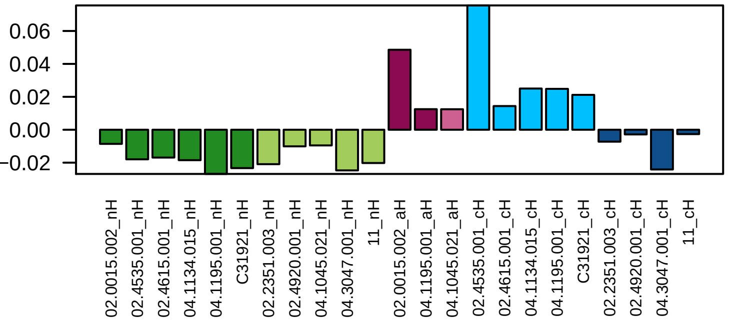
samples with spot = 0 (0 %)

Overview Map



Spot





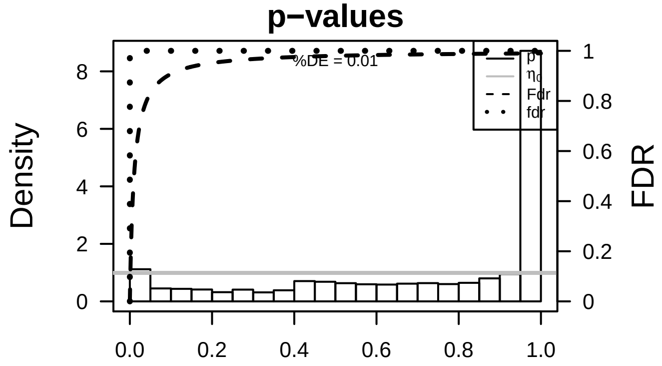
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	1.19	−0.05	0.63	PAGE1	P antigen family, member 1 (prostate associated) [Source:HG
2	ENSG000002	0.98	−0.05	0.63		
3	ENSG000002	0.93	−0.04	0.63	GAGE12G	G antigen 12G [Source:HGNC Symbol;Acc:HGNC:31907]
4	ENSG000002	0.93	−0.04	0.63	GAGE2D	G antigen 12F [Source:HGNC Symbol;Acc:HGNC:31906]
5	ENSG000002	0.86	−0.04	0.63		
6	ENSG000002	0.79	−0.04	0.63	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	ENSG000001	0.79	−0.13	0.52	RBP4	retinol binding protein 4, plasma [Source:HGNC Symbol;Acc:
8	ENSG000002	0.79	−0.04	0.63		
9	ENSG000002	0.78	−0.04	0.63		
10	ENSG000002	0.74	−0.03	0.63	GAGE12E	G antigen 12E [Source:HGNC Symbol;Acc:HGNC:31905]
11	ENSG000001	0.73	−0.17	0.3	EXOC3	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
12	ENSG000001	0.72	−0.07	0.62	GPC3	glypican 3 [Source:HGNC Symbol;Acc:HGNC:4451]
13	ENSG000001	0.72	−0.03	0.64	MAGEA6	melanoma antigen family A6 [Source:HGNC Symbol;Acc:HG
14	ENSG000002	0.71	−0.03	0.63	GAGE12C	G antigen 12C [Source:HGNC Symbol;Acc:HGNC:28402]
15	ENSG000002	0.71	−0.03	0.63	GAGE12D	G antigen 12D [Source:HGNC Symbol;Acc:HGNC:31904]
16	ENSG000002	0.7	−0.03	0.63		
17	ENSG000002	0.66	−0.03	0.64	MAGEA3	melanoma antigen family A3 [Source:HGNC Symbol;Acc:HG
18	ENSG000002	0.64	−0.03	0.63	GAGE12H	G antigen 12H [Source:HGNC Symbol;Acc:HGNC:31908]
19	ENSG000001	0.63	−0.09	0.6	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6 [Sourc
20	ENSG000001	0.63	−0.03	0.63	GAGE8	G antigen 2A [Source:HGNC Symbol;Acc:HGNC:4099]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−36	110 / 550	Canc	Lembcke_Normal vs Adenoma
2	2e−33	132 / 811	Lympl	WIRTH_lymphoma937_spot D
3	2e−32	130 / 807	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
4	5e−27	579 / 8123	Colon	TssF_Colon
5	2e−25	691 / 10475	Colon	TssA_Colon
6	6e−25	663 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
7	2e−21	87 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	2e−20	96 / 668	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	4e−20	620 / 9390	Colon	TxWk_Colon
10	1e−19	645 / 9930	Colon	Tx_Colon
11	4e−17	395 / 5393	TF	ICGC_Sp1_targets
12	1e−16	381 / 5173	TF	ICGC_Taf1_targets
13	1e−16	469 / 6761	Colon	TssD2_Colon
14	1e−16	340 / 4470	TF	ICGC_Creb1_targets
15	7e−16	335 / 4436	TF	ICGC_Zeb1_targets
16	8e−16	109 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	2e−15	399 / 5578	TF	ICGC_Stat5_targets
18	5e−15	394 / 5526	TF	ICGC_Pmlsc71910_targets
19	3e−14	464 / 6862	TF	ICGC_Elf1_targets
20	3e−13	51 / 316	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
21	3e−13	138 / 1441	CC	mitochondrion
22	5e−13	373 / 5308	TF	ICGC_Tcf12_targets
23	1e−12	659 / 10800	Brain	Overlap_fetal_midbrain_Quies
24	2e−12	258 / 3370	Brain	Mid_Frontal_Lobe_ZNF
25	3e−12	425 / 6313	TF	ICGC_Pou2_targets
26	3e−12	416 / 6157	TF	ICGC_Tcf3_targets
27	3e−12	425 / 6322	TF	ICGC_Pol2_targets
28	7e−12	406 / 6005	TF	ICGC_Mta3_targets
29	1e−11	90 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
30	1e−11	40 / 233	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell li
31	2e−11	469 / 7202	TF	ICGC_Runx3_targets
32	2e−11	421 / 6324	TF	ICGC_Yy1_targets
33	3e−11	624 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
34	4e−11	40 / 240	Lympl	WIRTH_lymphoma937_spot B
35	4e−11	90 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
36	1e−10	129 / 1425	Chr	Chr 19
37	2e−10	29 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
38	2e−10	136 / 1549	TF	ICGC_Myc_targets
39	6e−10	366 / 5453	TF	ICGC_Foxm1_targets
40	7e−10	578 / 9470	Colon	Quies3_Colon

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	6 / 123	HORVATH_aging_genes meth DOWN
2	0.6	7 / 144	HORVATH_aging_genes meth UP
3	0.8	2 / 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−09	42 / 304	DNA repair
2	1e−08	50 / 410	mitotic cell cycle
3	5e−06	22 / 145	DNA replication
4	1e−05	71 / 820	gene expression
5	2e−05	12 / 56	tRNA processing
6	6e−05	8 / 28	DNA−dependent DNA replication
7	7e−05	5 / 10	negative regulation of transcription elongation from RNA polymerase II promo
8	1e−04	7 / 23	telomere maintenance via semi−conservative replication
9	2e−04	8 / 33	DNA biosynthetic process
10	3e−04	7 / 27	telomere maintenance via recombination
11	3e−04	9 / 44	RNA phosphodiester bond hydrolysis, endonucleolytic
12	4e−04	12 / 74	nucleotide−excision repair
13	4e−04	9 / 45	tRNA aminoacylation for protein translation
14	6e−04	25 / 239	mitotic nuclear division
15	7e−04	9 / 48	transcription−coupled nucleotide−excision repair
16	8e−04	10 / 59	telomere maintenance
17	1e−03	51 / 640	oxidation−reduction process
18	1e−03	8 / 43	positive regulation of viral transcription
19	1e−03	6 / 25	RNA phosphodiester bond hydrolysis
20	2e−03	5 / 19	nucleotide−excision repair, DNA gap filling

Brain

Rank	p−value	#in/all	Geneset
1	6e−25	663 / 9923	Overlap_fetal_midbrain_K9K27me3
2	1e−12	659 / 10800	Overlap_fetal_midbrain_Quies
3	2e−12	258 / 3370	Mid_Frontal_Lobe_ZNF
4	3e−11	624 / 10239	Overlap_fetal_midbrain_ReprPC
5	2e−07	202 / 2820	Mid_Frontal_Lobe_HetRpts
6	4e−04	117 / 1680	Fetal_ReprPCWk
7	1e−03	70 / 939	Fetal_HetRpts
8	2e−03	367 / 6320	Overlap_fetal_midbrain_HetRpts
9	7e−03	61 / 865	Mid_Frontal_Lobe_Het
10	4e−02	104 / 1713	Mid_Frontal_Lobe_ReprPCWk
11	4e−02	554 / 10278	Overlap_fetal_midbrain_ReprPCWk
12	9e−02	17 / 232	Fetal_ReprPC
13	1e−01	220 / 3977	Mid_Frontal_Lobe_ReprPC
14	2e−01	24 / 400	Fetal_ZNF
15	5e−01	14 / 268	Mid_Frontal_Lobe_TssA
16	6e−01	60 / 1182	Fetal_EnhP
17	6e−01	16 / 317	Mid_Frontal_Lobe_Tx
18	6e−01	124 / 2443	Fetal_Quies
19	6e−01	105 / 2084	Mid_Frontal_Lobe_K9K27me3
20	7e−01	34 / 712	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	4e−36	110 / 550	Lembcke_Normal vs Adenoma
2	9e−07	13 / 50	PanCan_DNARepair_geneset_nanostring
3	6e−06	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	7e−02	7 / 71	SHAUGHNESSY_MM high risk
5	9e−02	2 / 10	GENTLES_modul3
6	1e−01	5 / 52	KUIPER_MM poor survival
7	2e−01	2 / 15	GENTLES_modul10
8	2e−01	2 / 16	GENTLES_modul6
9	3e−01	1 / 16	LIU_LIVER_CANCER
10	3e−01	2 / 22	PanCan_ChromMod_geneset_nanostring
11	4e−01	1 / 15	LIU_BREAST_CANCER
12	4e−01	2 / 24	PanCan_Notch_geneset_nanostring
13	4e−01	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
14	6e−01	7 / 136	PanCan_CC+Apop_geneset_nanostring
15	6e−01	1 / 16	LIU_COMMON_CANCER_GENES
16	6e−01	1 / 16	WANG_ER_UP
17	6e−01	1 / 16	WOLFER_overlap genes
18	6e−01	1 / 16	GENTLES_modul7
19	6e−01	1 / 16	GENTLES_modul16
20	6e−01	4 / 78	PanCan_Wnt_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	3e−13	138 / 1441	mitochondrion
2	8e−06	178 / 2554	nucleoplasm
3	2e−05	32 / 277	mitochondrial matrix
4	3e−04	5 / 13	Fanconi anaemia nuclear complex
5	8e−04	305 / 5101	nucleus
6	1e−03	5 / 16	replication fork
7	1e−03	37 / 425	mitochondrial inner membrane
8	1e−03	61 / 799	nucleolus
9	3e−03	4 / 13	TCTN−B9D complex
10	5e−03	35 / 431	cellular_component
11	5e−03	10 / 76	condensed chromosome kinetochore
12	1e−02	4 / 17	proteasome accessory complex
13	1e−02	32 / 411	centrosome
14	2e−02	3 / 11	Gemini of coiled bodies
15	2e−02	3 / 11	mRNA cleavage and polyadenylation specificity factor complex
16	2e−02	3 / 11	small nucleolar ribonucleoprotein complex
17	2e−02	7 / 53	kinesin complex
18	2e−02	4 / 21	retromer complex
19	2e−02	3 / 12	holo TFIIH complex
20	2e−02	3 / 12	SMN complex

Chr

Rank	p−value	#in/all	Geneset
1	1e−10	129 / 1425	Chr 19
2	1e−03	64 / 847	Chr 16
3	2e−02	52 / 746	Chr X
4	2e−01	49 / 859	Chr 7
5	2e−01	61 / 1083	Chr 17
6	3e−01	41 / 745	Chr 9
7	4e−01	24 / 436	Chr 22
8	4e−01	31 / 582	Chr 15
9	6e−01	30 / 613	Chr 14
10	7e−01	9 / 191	Chr 21
11	7e−01	57 / 1172	Chr 11
12	7e−01	31 / 651	Chr 8
13	7e−01	93 / 1920	Chr 1
14	8e−01	47 / 1017	Chr 12
15	8e−01	45 / 976	Chr 6
16	9e−01	22 / 522	Chr 20
17	9e−01	31 / 715	Chr 10
18	9e−01	36 / 862	Chr 5
19	9e−01	44 / 1043	Chr 3
20	9e−01	9 / 272	Chr 18

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−27	579 / 8123	TssF_Colon
2	2e−25	691 / 10475	TssA_Colon
3	4e−20	620 / 9390	TxWk_Colon
4	1e−19	645 / 9930	Tx_Colon
5	1e−16	469 / 6761	TssD2_Colon
6	1e−11	90 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
7	7e−10	578 / 9470	Quies3_Colon
8	3e−09	698 / 11968	TssWk_Colon
9	9e−09	687 / 11791	Enh_Colon
10	3e−07	69 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	6e−06	365 / 5889	EnhWk1_Colon
12	3e−04	200 / 3122	TxEnhG1_Colon
13	1e−02	186 / 3112	EnhA_Colon
14	2e−02	11 / 105	Marisa_CRC−cluster−d
15	2e−02	50 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
16	4e−02	8 / 75	Pentrack_CRC_TCGA_corr_N_msi−h_DN
17	8e−02	3 / 20	Budinska_B_Lower crypt−like_UP
18	1e−01	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
19	1e−01	1 / 2	Budinska_D_Mesenchymal_DOWN
20	1e−01	39 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	0.2	36 / 608	GUDJ_psoriasis up
2	1.0	14 / 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−10	29 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−04	70 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−02	5 / 30	Gorovets_LGG_NB_subclass
4	2e−02	11 / 108	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
5	3e−02	120 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	3e−02	3 / 14	Christensen_hypermethylated_in_ependymoma
7	4e−02	3 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
8	1e−01	7 / 77	Weller_LGG_gradeII−vs−III_DOWN
9	1e−01	5 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
10	1e−01	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
11	1e−01	12 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
12	1e−01	4 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
13	1e−01	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
14	2e−01	125 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
15	2e−01	1 / 4	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
16	3e−01	27 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
17	3e−01	4 / 53	Gorovets_LGG_EPL_subclass
18	3e−01	4 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
19	3e−01	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
20	3e−01	1 / 8	shaw_responders_up_in_oligo_glioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−21	87 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	2e−20	96 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
3	8e−16	109 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	3e−13	51 / 316	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	4e−11	90 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
6	2e−09	41 / 282	MANALO_HYPOXIA_DN
7	2e−09	51 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
8	4e−09	115 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	1e−08	20 / 86	ZHANG_TLX_TARGETS_UP
10	1e−08	109 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
11	2e−08	33 / 216	KAUFFMANN_DNA_REPAIR_GENES
12	4e−08	90 / 975	NUYTTEN_EZH2_TARGETS_DN
13	6e−08	98 / 1105	BRUINS_UVC_RESPONSE_LATE
14	7e−08	36 / 262	ZHANG_TLX_TARGETS_60HR_DN
15	7e−08	51 / 446	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
16	1e−07	44 / 366	REACTOME_CELL_CYCLE
17	2e−07	20 / 101	REACTOME_DNA_REPAIR
18	2e−07	28 / 182	REACTOME_DNA_REPLICATION
19	3e−07	70 / 731	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
20	4e−07	24 / 145	BENPORATH_PROLIFERATION

HM

Rank	p−value	#in/all	Geneset
1	9e−07	28 / 196	HALLMARK_G2M_CHECKPOINT
2	5e−06	22 / 146	HALLMARK_DNA_REPAIR
3	1e−03	21 / 198	HALLMARK_GLYCOLYSIS
4	6e−03	19 / 197	HALLMARK_E2F_TARGETS
5	9e−02	15 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	1e−01	14 / 196	HALLMARK_MITOTIC_SPINDLE
7	2e−01	5 / 58	HALLMARK_MYC_TARGETS_V2
8	2e−01	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	3e−01	10 / 154	HALLMARK_FATTY_ACID_METABOLISM
10	3e−01	5 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	4e−01	11 / 193	HALLMARK_HEME_METABOLISM
12	4e−01	6 / 102	HALLMARK_PEROXISOME
13	4e−01	11 / 199	HALLMARK_MTORC1_SIGNALING
14	5e−01	10 / 195	HALLMARK_MYC_TARGETS_V1
15	6e−01	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
16	6e−01	2 / 36	HALLMARK_ANGIOGENESIS
17	6e−01	10 / 199	HALLMARK_ADIPOGENESIS
18	6e−01	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
19	6e−01	6 / 128	HALLMARK_SPERMATOGENESIS
20	7e−01	9 / 193	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.38	1 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.50	5 / 91	DUMEAUX_Smoking enriched genes
4	0.59	1 / 17	DUMEAUX_High bmi enriched genes
5	0.82	1 / 33	DUMEAUX_Fasting enriched genes
6	1.00	0 / 11	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells 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	2e−33	132 / 811	WIRTH_lymphoma937_spot D
2	2e−32	130 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
3	1e−11	40 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line
4	4e−11	40 / 240	WIRTH_lymphoma937_spot B
5	8e−08	364 / 5643	HOPP_Txn_transition
6	1e−07	508 / 8358	HOPP_Active_promoter
7	2e−07	460 / 7491	HOPP_Txn_elongation
8	6e−06	105 / 1333	SPANG_BCR UP
9	1e−03	19 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line
10	2e−03	461 / 8147	HOPP_Weak_promoter
11	3e−03	18 / 171	WIRTH_lymphoma937_spot C
12	1e−02	10 / 87	Aukema_BCL2 DN_BCL6 UP
13	2e−02	25 / 317	TARTE_Plasmablast signature
14	6e−02	413 / 7592	HOPP_Strong_enhancer
15	7e−02	3 / 19	DAVE_c−myc BL UP
16	1e−01	9 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
17	1e−01	9 / 116	WIRTH_lymphoma937_spot MM
18	2e−01	5 / 63	SPANG_BAFF 9hrs DN
19	3e−01	1 / 6	MASCQUE_mBL UP
20	4e−01	331 / 6389	HOPP_Weak_txn

MF

Rank	p−value	#in/all	Geneset
1	8e−05	8 / 29	DNA−directed DNA polymerase activity
2	8e−05	9 / 37	aminoacyl−tRNA ligase activity
3	2e−04	11 / 61	damaged DNA binding
4	1e−03	8 / 41	4 iron, 4 sulfur cluster binding
5	1e−03	8 / 41	tRNA binding
6	1e−03	6 / 25	histone−lysine N−methyltransferase activity
7	2e−03	78 / 1091	poly(A) RNA binding
8	2e−03	4 / 12	protein−lysine N−methyltransferase activity
9	3e−03	5 / 20	S−adenosylmethionine−dependent methyltransferase activity
10	3e−03	6 / 29	nucleotidyltransferase activity
11	4e−03	5 / 21	lyase activity
12	5e−03	5 / 23	oxidoreductase activity, acting on the CH−CH group of donors
13	7e−03	25 / 287	oxidoreductase activity
14	1e−02	6 / 37	DNA−dependent ATPase activity
15	1e−02	3 / 10	ribonuclease P activity
16	1e−02	3 / 10	small protein activating enzyme activity
17	1e−02	93 / 1448	ATP binding
18	2e−02	6 / 40	heat shock protein binding
19	2e−02	4 / 20	enzyme regulator activity
20	2e−02	4 / 20	L−ascorbic acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	5 / 32	hsa−miR−631
2	0.12	6 / 65	hsa−miR−455−3p
3	0.12	3 / 24	hsa−miR−1225−5p
4	0.16	2 / 14	hsa−miR−147b
5	0.17	5 / 57	hsa−miR−940
6	0.18	4 / 43	hsa−miR−331−5p
7	0.18	3 / 29	hsa−miR−591
8	0.19	4 / 44	hsa−miR−483−5p
9	0.19	4 / 44	hsa−miR−661
10	0.19	6 / 76	hsa−miR−1304
11	0.19	6 / 76	hsa−miR−1254
12	0.20	6 / 77	hsa−miR−939
13	0.21	3 / 31	hsa−miR−371−3p
14	0.24	4 / 49	hsa−miR−518e*
15	0.24	4 / 49	hsa−miR−1291
16	0.28	9 / 139	hsa−miR−198
17	0.29	4 / 53	hsa−miR−370
18	0.29	8 / 122	hsa−miR−509−3p
19	0.32	7 / 108	hsa−miR−605
20	0.32	5 / 73	hsa−miR−361−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.5	1 / 14	GUSTAFSON_PI3K_UP
2	0.5	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	4e−17	395 / 5393	ICGC_Sp1_targets
2	1e−16	381 / 5173	ICGC_Taf1_targets
3	1e−16	340 / 4470	ICGC_Creb1_targets
4	7e−16	335 / 4436	ICGC_Zeb1_targets
5	2e−15	399 / 5578	ICGC_Stat5_targets
6	5e−15	394 / 5526	ICGC_Pmlsc71910_targets
7	3e−14	464 / 6862	ICGC_Elf1_targets
8	5e−13	373 / 5308	ICGC_Tcf12_targets
9	3e−12	425 / 6313	ICGC_Pou2_targets
10	3e−12	416 / 6157	ICGC_Tcf3_targets
11	3e−12	425 / 6322	ICGC_Pol2_targets
12	7e−12	406 / 6005	ICGC_Mta3_targets
13	2e−11	469 / 7202	ICGC_Runx3_targets
14	2e−11	421 / 6324	ICGC_Yy1_targets
15	2e−10	136 / 1549	ICGC_Myc_targets
16	6e−10	366 / 5453	ICGC_Foxm1_targets
17	1e−09	416 / 6406	ICGC_Pax5_targets
18	1e−09	338 / 4987	ICGC_Bclaf101388_targets
19	3e−09	183 / 2354	ICGC_SrfV0416101_targets
20	3e−09	182 / 2342	ICGC_GabpPcr2_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.02	6 / 41	VAQUERIZAS_Testis
2	0.06	13 / 155	VAQUERIZAS_General
3	0.20	2 / 16	VAQUERIZAS_Fetal liver
4	0.24	3 / 33	VAQUERIZAS_Liver
5	0.41	3 / 45	VAQUERIZAS_Placenta
6	0.47	1 / 12	VAQUERIZAS_Kidney
7	0.48	2 / 31	VAQUERIZAS_Fetal lung
8	0.57	1 / 16	VAQUERIZAS_Fetal thyroid
9	0.61	1 / 18	VAQUERIZAS_Pancreas
10	0.64	2 / 42	VAQUERIZAS_Thymus
11	0.72	1 / 24	VAQUERIZAS_Trachea
12	0.73	1 / 25	VAQUERIZAS_Adrenal cortex
13	0.79	1 / 30	VAQUERIZAS_Smooth muscle
14	0.85	2 / 64	VAQUERIZAS_Lung
15	0.86	1 / 37	VAQUERIZAS_Prostate
16	0.89	1 / 42	VAQUERIZAS_Thyroid
17	1.00	0 / 41	VAQUERIZAS_Fetal brain
18	1.00	0 / 49	VAQUERIZAS_Uterus
19	1.00	0 / 25	VAQUERIZAS_Spinal cord
20	1.00	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	0.04	3 / 15	WIRTH_Cerebellum
2	0.16	2 / 14	WIRTH_Thyroid gland
3	0.17	10 / 137	WIRTH_Mucosa
4	0.18	2 / 15	WIRTH_Telencephalon
5	0.47	1 / 12	WIRTH_Tonsil
6	0.47	1 / 12	WIRTH_Lymphocytes
7	0.52	1 / 14	WIRTH_B−cells
8	0.52	1 / 14	WIRTH_Bone marrow
9	0.77	2 / 54	WIRTH_Pancreas
10	0.85	4 / 115	WIRTH_Liver
11	0.92	1 / 47	WIRTH_Placenta
12	0.93	2 / 82	WIRTH_Homeostasis
13	0.96	17 / 476	WIRTH_Nervous System
14	0.98	5 / 202	WIRTH_Testis
15	0.99	12 / 427	WIRTH_Immune system
16	0.99	2 / 140	PALMER_T−Cell signature up
17	0.99	2 / 141	WIRTH_Muscle
18	1.00	4 / 259	PALMER_Granulocytes signature up
19	1.00	2 / 208	PALMER_B−Cell signature up
20	1.00	0 / 6	WIRTH_Pituitary gland

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	77 / 1343	LU_BPDE 1h DN
2	1.0	225 / 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	

K−Means Clusters

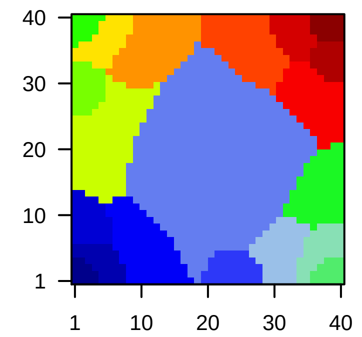
Spot Summary: P

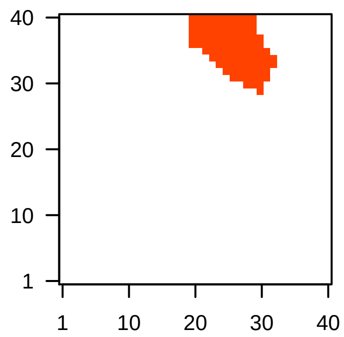
metagenes = 98
genes = 1048

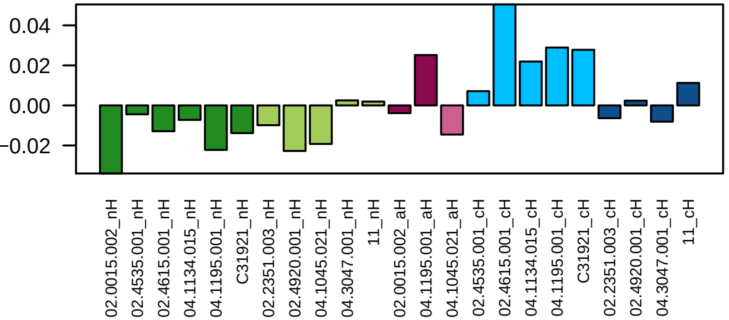
<r> metagenes = 0.75

beta: r2= 0.01 / log p= −0.2

samples with spot = 0 (0 %)


Overview Map


Spot

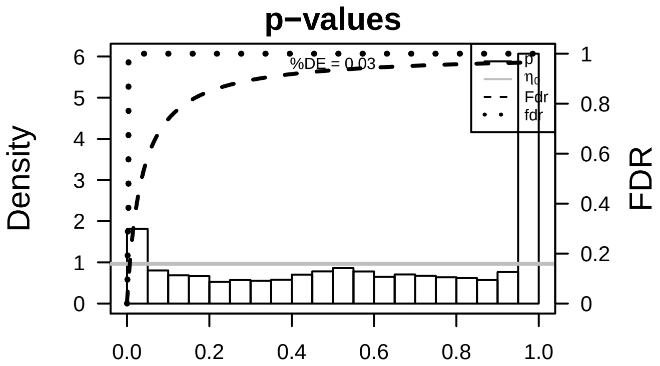


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.1	−0.2	0.26	HBA2	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:HGNC:4824
2	ENSG000002	1.08	−0.17	0.24	HBA1	hemoglobin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:4823
3	ENSG000001	0.84	−0.25	0.49	CXCL10	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
4	ENSG000001	0.73	−0.36	0.36	IFI6	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
5	ENSG000001	0.65	−0.17	0.28	APOE	apolipoprotein E [Source:HGNC Symbol;Acc:HGNC:613]
6	ENSG000001	0.63	−0.14	0.5	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:HGNC:5992]
7	ENSG000002	0.6	−0.19	0.33	GABBR1	gamma−aminobutyric acid (GABA) B receptor, 1 [Source:HGI
8	ENSG000001	0.59	−0.05	0.57	HCAR2	hydroxycarboxylic acid receptor 2 [Source:HGNC Symbol;Acc
9	ENSG000002	0.55	−0.04	0.62	HCAR3	hydroxycarboxylic acid receptor 3 [Source:HGNC Symbol;Acc
10	ENSG000001	0.47	−0.09	0.33	CXCL11	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;A
11	ENSG000001	0.46	−0.15	0.34	STMN3	stathmin−like 3 [Source:HGNC Symbol;Acc:HGNC:15926]
12	ENSG000001	0.45	−0.05	0.54	IL23A	interleukin 23, alpha subunit p19 [Source:HGNC Symbol;Acc:
13	ENSG000001	0.43	−0.03	0.14	SLC39A2	solute carrier family 39 (zinc transporter), member 2 [Source:
14	ENSG000001	0.42	−0.02	0.6	CALB1	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:HGNC:1434]
15	ENSG000002	0.42	−0.08	0.4		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:J3k
16	ENSG000000	0.4	−0.02	0.55	CYP24A1	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
17	ENSG000000	0.4	−0.03	0.64	OSM	oncostatin M [Source:HGNC Symbol;Acc:HGNC:8506]
18	ENSG000001	0.38	−0.26	0.36	UBE2L6	ubiquitin−conjugating enzyme E2L 6 [Source:HGNC Symbol;
19	ENSG000001	0.37	−0.04	0.38	COL7A1	collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:HGNC
20	ENSG000001	0.36	−0.03	0.2	EDAR	ectodysplasin A receptor [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−63	231 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
2	3e−61	658 / 7491	Lymph	HOPP_Txn_elongation
3	2e−43	664 / 8358	Lymph	HOPP_Active_promoter
4	1e−37	746 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
5	2e−37	147 / 859	GSEA	LEE_BMP2_TARGETS_DN
6	7e−36	529 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
7	2e−34	176 / 1228	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	9e−34	136 / 807	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
9	2e−32	134 / 811	Lymph	WIRTH_lymphoma937_spot D
10	2e−31	129 / 775	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
11	6e−27	99 / 550	Cance	Lembcke_Normal vs Adenoma
12	3e−26	104 / 610	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
13	2e−25	722 / 10475	Colon	TssA_Colon
14	3e−23	122 / 862	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
15	1e−22	590 / 8147	Lymph	HOPP_Weak_promoter
16	2e−22	660 / 9470	Colon	Quies3_Colon
17	3e−22	683 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
18	4e−22	117 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
19	5e−22	445 / 5643	Lymph	HOPP_Txn_transition
20	1e−21	653 / 9390	Colon	TxWk_Colon
21	3e−20	694 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
22	5e−19	774 / 11968	Colon	TssWk_Colon
23	1e−18	97 / 683	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
24	4e−18	57 / 284	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
25	2e−17	190 / 1914	GSEA	PILON_KLF1_TARGETS_DN
26	2e−17	665 / 9930	Colon	Tx_Colon
27	5e−17	42 / 171	Lymph	WIRTH_lymphoma937_spot C
28	1e−16	41 / 167	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell li
29	1e−15	155 / 1503	TF	ICGC_Six5_targets
30	1e−15	96 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
31	1e−15	112 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
32	4e−15	52 / 282	GSEA	MANALO_HYPOXIA_DN
33	1e−13	62 / 410	BP	mitotic cell cycle
34	6e−13	73 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
35	8e−13	83 / 668	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
36	1e−12	107 / 975	GSEA	NUYTTEN_EZH2_TARGETS_DN
37	3e−12	96 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
38	5e−12	74 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
39	6e−12	446 / 6389	Lymph	HOPP_Weak_txn
40	8e−12	59 / 415	GSEA	GARY_CD5_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	6 / 123	HORVATH_aging_genes meth DOWN
2	0.8	2 / 57	TESCHENDORFF_age_hypermethylated
3	1.0	4 / 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	1e−13	62 / 410	mitotic cell cycle
2	9e−09	21 / 90	protein sumoylation
3	4e−08	82 / 820	gene expression
4	3e−07	11 / 31	regulation of glucose transport
5	4e−07	39 / 303	post−translational protein modification
6	1e−06	12 / 41	hexose transport
7	1e−06	12 / 42	mitotic nuclear envelope disassembly
8	3e−06	14 / 61	glucose transport
9	4e−06	62 / 633	cellular protein metabolic process
10	2e−05	9 / 30	termination of RNA polymerase I transcription
11	2e−05	9 / 30	transcription elongation from RNA polymerase I promoter
12	2e−05	22 / 151	G1/S transition of mitotic cell cycle
13	4e−05	9 / 33	transcription initiation from RNA polymerase I promoter
14	6e−05	9 / 34	transcription from RNA polymerase I promoter
15	7e−05	15 / 88	regulation of gene expression, epigenetic
16	7e−05	13 / 69	regulation of cellular response to heat
17	1e−04	33 / 304	DNA repair
18	1e−04	11 / 55	ER−associated ubiquitin−dependent protein catabolic process
19	3e−04	33 / 323	cell division
20	3e−04	16 / 112	methylation

Brain

Rank	p−value	#in/all	Geneset
1	1e−37	746 / 10239	Overlap_fetal_midbrain_ReprPC
2	7e−36	529 / 6320	Overlap_fetal_midbrain_HetRpts
3	3e−22	683 / 9923	Overlap_fetal_midbrain_K9K27me3
4	3e−20	694 / 10278	Overlap_fetal_midbrain_ReprPCWk
5	2e−08	666 / 10800	Overlap_fetal_midbrain_Quies
6	8e−04	89 / 1182	Fetal_EnhP
7	3e−02	31 / 400	Fetal_ZNF
8	4e−02	63 / 939	Fetal_HetRpts
9	7e−02	148 / 2443	Fetal_Quies
10	2e−01	79 / 1356	Fetal_K9K27me3
11	4e−01	37 / 641	Mid_Frontal_Lobe_EnhP
12	5e−01	49 / 910	Fetal_EnhG
13	6e−01	12 / 232	Fetal_ReprPC
14	7e−01	72 / 1394	Mid_Frontal_Lobe_Quies
15	7e−01	17 / 342	Fetal_Het
16	8e−01	33 / 712	Overlap_fetal_midbrain_EnhP
17	9e−01	54 / 1137	Fetal_Enh
18	9e−01	169 / 3370	Mid_Frontal_Lobe_ZNF
19	9e−01	7 / 191	Overlap_fetal_midbrain_Het
20	9e−01	23 / 552	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	6e−27	99 / 550	Lembcke_Normal vs Adenoma
2	1e−03	11 / 71	SHAUGHNESSY_MM high risk
3	6e−03	7 / 41	ZHANG_MM up
4	8e−03	45 / 574	Lembcke_Colonic Inflammation
5	1e−02	2 / 16	LIU_COMMON_CANCER_GENES
6	2e−02	7 / 52	KUIPER_MM poor survival
7	3e−02	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	9e−02	8 / 86	PanCan_JAK−ST_geneset_nanostring
9	1e−01	1 / 16	RHODES_CANCER_META_SIGNATURE
10	1e−01	3 / 22	PanCan_ChromMod_geneset_nanostring
11	1e−01	5 / 50	PanCan_DNARepair_geneset_nanostring
12	2e−01	3 / 28	PanCan_HH_geneset_nanostring
13	2e−01	2 / 16	GENTLES_modul2
14	2e−01	2 / 16	GENTLES_modul6
15	4e−01	5 / 78	PanCan_Wnt_geneset_nanostring
16	4e−01	1 / 10	GENTLES_modul3
17	5e−01	7 / 123	PanCan_Driver_Gene_geneset_nanostring
18	6e−01	1 / 15	GENTLES_modul4
19	6e−01	1 / 15	GENTLES_modul10
20	6e−01	1 / 16	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	1e−10	88 / 799	nucleolus
2	2e−08	199 / 2554	nucleoplasm
3	9e−08	16 / 61	nuclear pore
4	7e−06	8 / 21	transcription elongation factor complex
5	3e−05	113 / 1441	mitochondrion
6	3e−05	9 / 32	small−subunit processome
7	5e−05	6 / 14	exosome (RNase complex)
8	1e−04	41 / 411	centrosome
9	2e−04	11 / 56	proteasome complex
10	4e−04	5 / 13	DNA−directed RNA polymerase I complex
11	4e−04	5 / 13	nuclear exosome (RNase complex)
12	9e−04	6 / 22	anaphase−promoting complex
13	1e−03	10 / 58	chromosome, centromeric region
14	1e−03	322 / 5185	cytoplasm
15	3e−03	314 / 5101	nucleus
16	4e−03	5 / 20	exon−exon junction complex
17	4e−03	19 / 179	endoplasmic reticulum lumen
18	4e−03	19 / 180	nuclear speck
19	4e−03	5 / 21	site of double−strand break
20	5e−03	12 / 95	centriole

Chr

Rank	p−value	#in/all	Geneset
1	0.001	31 / 318	Chr 13
2	0.004	88 / 1228	Chr 2
3	0.035	59 / 862	Chr 5
4	0.038	22 / 272	Chr 18
5	0.185	63 / 1043	Chr 3
6	0.253	44 / 735	Chr 4
7	0.283	44 / 745	Chr 9
8	0.291	109 / 1920	Chr 1
9	0.327	38 / 651	Chr 8
10	0.438	47 / 847	Chr 16
11	0.497	53 / 976	Chr 6
12	0.553	31 / 582	Chr 15
13	0.559	38 / 715	Chr 10
14	0.600	32 / 613	Chr 14
15	0.675	52 / 1017	Chr 12
16	0.681	60 / 1172	Chr 11
17	0.724	37 / 746	Chr X
18	0.733	21 / 436	Chr 22
19	0.810	1 / 30	Chr Y
20	0.887	39 / 859	Chr 7

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−25	722 / 10475	TssA_Colon
2	2e−22	660 / 9470	Quies3_Colon
3	4e−22	117 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
4	1e−21	653 / 9390	TxWk_Colon
5	5e−19	774 / 11968	TssWk_Colon
6	2e−17	665 / 9930	Tx_Colon
7	1e−11	84 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	9e−07	41 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
9	5e−05	14 / 76	Marisa_CRC−cluster−g
10	6e−05	25 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	5e−04	280 / 4379	TssD1_Colon
12	6e−04	488 / 8123	TssF_Colon
13	7e−03	29 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
14	2e−02	4 / 21	Juehling−MSI−enriched−in−6
15	4e−02	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
16	7e−02	2 / 8	Boland_CRC−MMR−system
17	7e−02	2 / 8	Marisa_CRC−C6
18	7e−02	2 / 8	Budinska_C_CIMP−H−like_UP
19	1e−01	2 / 10	Juehling−MSI−enriched−in−7
20	1e−01	2 / 10	Budinska_E_Mixed_UP

Disease

Rank	p−value	#in/all	Geneset
1	3e−05	57 / 608	GUDJ_psoriasis up
2	6e−01	2 / 37	BCHETNIA_EBM−DM up
3	7e−01	1 / 22	BCHETNIA_EBM up
4	1e+00	10 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	3e−10	188 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−08	163 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	8e−04	18 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
4	1e−03	31 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	8e−03	64 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
6	2e−02	3 / 12	WILLSCHER_GBM_LTSwt_proteomics−C_UP
7	7e−02	10 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	8e−02	2 / 9	Colman_survival_robust
9	1e−01	24 / 344	Up
10	1e−01	7 / 77	Weller_LGG_gradeII−vs−III_DOWN
11	1e−01	4 / 36	Colman_survival_associated
12	2e−01	4 / 39	WILLSCHER_GBM_proteomics_wtOnly_SpotH
13	2e−01	6 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
14	2e−01	19 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
15	2e−01	8 / 103	GIEZELT_GBM_STS_down_VS_LTS
16	2e−01	9 / 119	GIEZELT_GBM_WT_up_VS_mut
17	2e−01	1 / 5	Phillips Prolif up vs PN & MES
18	3e−01	2 / 18	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
19	3e−01	6 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
20	3e−01	3 / 35	shaw_responders_down_in_oligo_glioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−63	231 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
2	2e−37	147 / 859	LEE_BMP2_TARGETS_DN
3	2e−34	176 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	2e−31	129 / 775	WEI_MYCN_TARGETS_WITH_E_BOX
5	3e−26	104 / 610	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
6	3e−23	122 / 862	JOHNSTONE_PARVB_TARGETS_3_DN
7	1e−18	97 / 683	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
8	4e−18	57 / 284	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
9	2e−17	190 / 1914	PILON_KLF1_TARGETS_DN
10	1e−15	96 / 747	PUJANA_CHEK2_PCC_NETWORK
11	1e−15	112 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
12	4e−15	52 / 282	MANALO_HYPOXIA_DN
13	6e−13	73 / 546	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
14	8e−13	83 / 668	MARSON_BOUND_BY_E2F4_UNSTIMULATED
15	1e−12	107 / 975	NUYTTEN_EZH2_TARGETS_DN
16	3e−12	96 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
17	5e−12	74 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
18	8e−12	59 / 415	GARY_CD5_TARGETS_DN
19	9e−12	95 / 852	GEORGES_TARGETS_OF_MIR192_AND_MIR215
20	1e−11	147 / 1563	PUJANA_BRCA1_PCC_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	6e−06	27 / 194	HALLMARK_INFLAMMATORY_RESPONSE
2	1e−03	22 / 199	HALLMARK_MTORC1_SIGNALING
3	5e−03	20 / 197	HALLMARK_E2F_TARGETS
4	7e−03	13 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	8e−03	19 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	6e−02	16 / 196	HALLMARK_G2M_CHECKPOINT
7	9e−02	8 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
8	9e−02	6 / 58	HALLMARK_MYC_TARGETS_V2
9	1e−01	8 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	1e−01	14 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	1e−01	14 / 189	HALLMARK_KRAS_SIGNALING_UP
12	2e−01	14 / 198	HALLMARK_GLYCOLYSIS
13	2e−01	8 / 102	HALLMARK_PEROXISOME
14	2e−01	11 / 154	HALLMARK_FATTY_ACID_METABOLISM
15	2e−01	11 / 155	HALLMARK_UV_RESPONSE_UP
16	2e−01	3 / 30	HALLMARK_NOTCH_SIGNALING
17	3e−01	13 / 196	HALLMARK_P53_PATHWAY
18	3e−01	3 / 36	HALLMARK_HEDGEHOG_SIGNALING
19	3e−01	3 / 36	HALLMARK_ANGIOGENESIS
20	3e−01	5 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.05	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.12	2 / 11	DUMEAUX_Smoking literature genes up
4	0.12	2 / 11	DUMEAUX_Women normal BMI literature genes up
5	0.24	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	0.39	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
7	0.54	2 / 33	DUMEAUX_Fasting enriched genes
8	0.59	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	0.61	1 / 17	DUMEAUX_High bmi enriched genes
10	0.96	2 / 91	DUMEAUX_Smoking enriched genes
11	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−61	658 / 7491	HOPP_Txn_elongation
2	2e−43	664 / 8358	HOPP_Active_promoter
3	9e−34	136 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
4	2e−32	134 / 811	WIRTH_lymphoma937_spot D
5	1e−22	590 / 8147	HOPP_Weak_promoter
6	5e−22	445 / 5643	HOPP_Txn_transition
7	5e−17	42 / 171	WIRTH_lymphoma937_spot C
8	1e−16	41 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
9	6e−12	446 / 6389	HOPP_Weak_txn
10	2e−09	123 / 1333	SPANG_BCR UP
11	9e−09	451 / 6784	HOPP_Weak_enhancer
12	7e−07	33 / 240	WIRTH_lymphoma937_spot B
13	3e−06	31 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
14	2e−03	12 / 83	ROSOLOWSKI_green UP
15	4e−03	39 / 466	SPANG_CD40 6hrs DN
16	9e−03	13 / 115	ROSOLOWSKI_green total
17	2e−02	25 / 302	SPANG_IL21 UP
18	2e−02	440 / 7592	HOPP_Strong_enhancer
19	3e−02	81 / 1215	SPANG_BCR DN
20	3e−02	23 / 279	SPANG_IL21 DN

MF

Rank	p−value	#in/all	Geneset
1	7e−09	104 / 1091	poly(A) RNA binding
2	2e−06	7 / 13	nucleocytoplasmic transporter activity
3	3e−05	638 / 10693	protein binding
4	3e−05	18 / 113	methyltransferase activity
5	9e−05	5 / 10	IgG binding
6	9e−05	5 / 10	structural constituent of nuclear pore
7	2e−04	9 / 39	DNA−directed RNA polymerase activity
8	2e−04	109 / 1448	ATP binding
9	5e−04	11 / 63	ATP−dependent RNA helicase activity
10	9e−04	5 / 15	cation transmembrane transporter activity
11	1e−03	21 / 187	ATPase activity
12	2e−03	4 / 11	aminoacyl−tRNA editing activity
13	3e−03	4 / 12	RNA polymerase I activity
14	3e−03	7 / 37	aminoacyl−tRNA ligase activity
15	3e−03	7 / 37	DNA−dependent ATPase activity
16	4e−03	5 / 20	3'−5' exonuclease activity
17	4e−03	5 / 20	RNA polymerase II core binding
18	5e−03	42 / 513	RNA binding
19	5e−03	6 / 30	ATP−dependent helicase activity
20	5e−03	9 / 61	damaged DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	24 / 209	hsa−miR−221
2	4e−04	25 / 223	hsa−miR−203
3	4e−04	22 / 186	hsa−miR−196b
4	5e−04	15 / 105	hsa−miR−590−5p
5	8e−04	30 / 298	hsa−miR−34a
6	8e−04	21 / 181	hsa−miR−199b−3p
7	1e−03	39 / 431	hsa−miR−497
8	1e−03	19 / 164	hsa−miR−298
9	1e−03	14 / 105	hsa−miR−325
10	2e−03	39 / 442	hsa−miR−548n
11	2e−03	12 / 85	hsa−miR−630
12	2e−03	31 / 334	hsa−miR−590−3p
13	2e−03	28 / 293	hsa−miR−30c
14	3e−03	8 / 45	hsa−miR−411
15	3e−03	17 / 148	hsa−miR−409−3p
16	3e−03	21 / 200	hsa−miR−568
17	3e−03	21 / 202	hsa−miR−222
18	3e−03	42 / 504	hsa−miR−16
19	4e−03	29 / 317	hsa−miR−548c−5p
20	4e−03	9 / 59	hsa−miR−187

PathwAct

Rank	p−value	#in/all	Geneset
1	0.04	3 / 14	BENTINK_src.2
2	0.19	2 / 15	BENTINK_ras.6
3	0.54	1 / 14	BENTINK_src.10
4	0.56	1 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 14	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 14	BENTINK_myc.1
9	1.00	0 / 12	BENTINK_ras.1
10	1.00	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	1e−15	155 / 1503	ICGC_Six5_targets
2	2e−11	373 / 5173	ICGC_Taf1_targets
3	6e−11	393 / 5552	ICGC_Pol24_targets
4	3e−10	141 / 1549	ICGC_Myc_targets
5	4e−09	350 / 4987	ICGC_Bclaf101388_targets
6	5e−09	381 / 5526	ICGC_Pmlsc71910_targets
7	2e−08	117 / 1294	KIM_MYC targets
8	3e−07	415 / 6322	ICGC_Pol2_targets
9	6e−07	305 / 4436	ICGC_Zeb1_targets
10	8e−07	165 / 2133	ICGC_Cebpbsc150_targets
11	9e−07	366 / 5512	ICGC_Nficsc81335_targets
12	1e−06	178 / 2354	ICGC_SrfV0416101_targets
13	1e−06	305 / 4470	ICGC_Creb1_targets
14	2e−06	357 / 5393	ICGC_Sp1_targets
15	2e−06	409 / 6313	ICGC_Pou2_targets
16	2e−06	367 / 5578	ICGC_Stat5_targets
17	3e−06	308 / 4566	ICGC_Egr1_targets
18	4e−06	61 / 619	ICGC_RxraPcr1_targets
19	4e−06	350 / 5308	ICGC_Tcf12_targets
20	4e−06	124 / 1547	ICGC_Ets1_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.1	3 / 23	VAQUERIZAS_Pituitary
2	0.4	1 / 8	VAQUERIZAS_Tongue
3	0.5	3 / 49	VAQUERIZAS_Uterus
4	0.5	1 / 13	VAQUERIZAS_Skin
5	0.6	1 / 16	VAQUERIZAS_Ovary
6	0.6	1 / 16	VAQUERIZAS_Fetal thyroid
7	0.6	1 / 17	VAQUERIZAS_Salivary gland
8	0.7	2 / 41	VAQUERIZAS_Fetal brain
9	0.7	2 / 41	VAQUERIZAS_Testis
10	0.7	2 / 45	VAQUERIZAS_Placenta
11	0.7	1 / 24	VAQUERIZAS_Trachea
12	0.8	1 / 30	VAQUERIZAS_Smooth muscle
13	0.8	1 / 31	VAQUERIZAS_Fetal lung
14	0.8	1 / 33	VAQUERIZAS_Liver
15	0.9	1 / 42	VAQUERIZAS_Thyroid
16	0.9	5 / 155	VAQUERIZAS_General
17	1.0	1 / 64	VAQUERIZAS_Lung
18	1.0	1 / 67	VAQUERIZAS_Whole blood
19	1.0	0 / 37	VAQUERIZAS_Prostate
20	1.0	0 / 12	VAQUERIZAS_Kidney

Tissue

Rank	p−value	#in/all	Geneset
1	0.007	24 / 259	PALMER_Granulocytes signature up
2	0.153	2 / 13	WIRTH_Prim. lymphoid organs
3	0.172	2 / 14	WIRTH_Thymus
4	0.204	10 / 137	WIRTH_Mucosa
5	0.513	1 / 13	WIRTH_Cortex cerebri
6	0.513	1 / 13	PALMER_CD8+ T−Cell signature up
7	0.540	1 / 14	WIRTH_Bone marrow
8	0.540	1 / 14	WIRTH_Thalamus
9	0.564	1 / 15	WIRTH_Telencephalon
10	0.882	5 / 141	WIRTH_Muscle
11	0.926	1 / 47	WIRTH_Placenta
12	0.983	3 / 140	PALMER_T−Cell signature up
13	0.989	5 / 208	PALMER_B−Cell signature up
14	0.989	1 / 82	WIRTH_Homeostasis
15	0.998	1 / 115	WIRTH_Liver
16	0.999	3 / 202	WIRTH_Testis
17	0.999	10 / 427	WIRTH_Immune system
18	1.000	7 / 476	WIRTH_Nervous System
19	1.000	0 / 6	WIRTH_Pituitary gland
20	1.000	0 / 54	WIRTH_Pancreas

Toxic

Rank	p−value	#in/all	Geneset
1	0.03	88 / 1343	LU_BPDE 1h DN
2	0.94	264 / 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	

K−Means Clusters

Spot Summary: Q

metagenes = 19
genes = 360

<r> metagenes = 0.97
<r> genes = 0.62
beta: r2= 0.29 / log p= −2.07

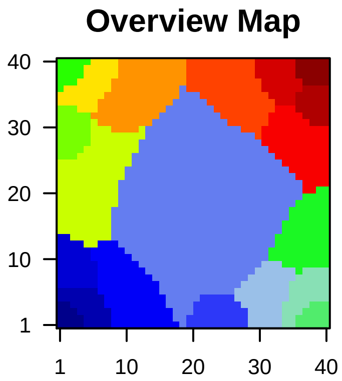
samples with spot = 8 (34.8 %)
MLH1_adenomaHNPCC : 2 (100 %)
MLH1_cancerHNPCC : 5 (100 %)
other_cancerHNPCC : 1 (25 %)

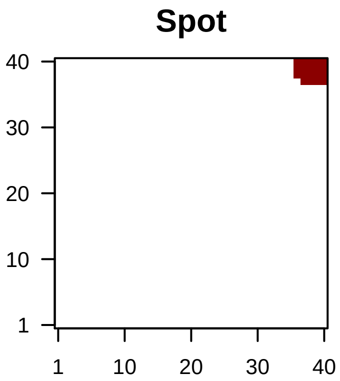
Spot Genelist

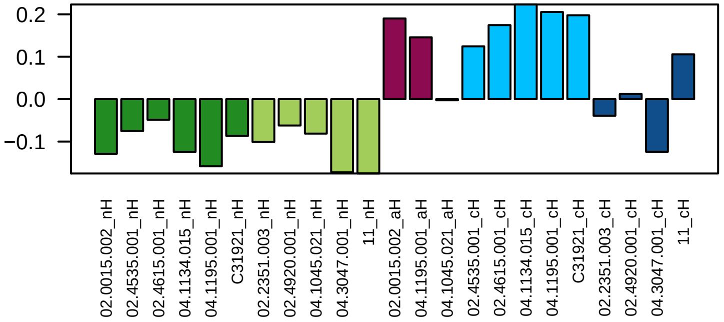
Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.84	−0.57	0.56	REG1A	regenerating islet−derived 1 alpha [Source:HGNC Symbol;Ac
2	ENSG000001	1.71	−0.34	0.52	ITLN1	intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
3	ENSG000001	1.65	−0.75	0.61	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
4	ENSG000001	1.57	−0.24	0.56	REG3A	regenerating islet−derived 3 alpha [Source:HGNC Symbol;Ac
5	ENSG000001	1.47	−0.28	0.62	MMP1	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
6	ENSG000001	1.33	−0.75	0.39	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) [Source
7	ENSG000001	1.31	−0.29	0.42	CXCL8	chemokine (C−X−C motif) ligand 8 [Source:HGNC Symbol;Ac
8	ENSG000001	1.27	−0.21	0.49	REG1B	regenerating islet−derived 1 beta [Source:HGNC Symbol;Acc
9	ENSG000001	1.25	−0.21	0.55	DMBT1	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
10	ENSG000001	1.17	−0.36	0.47	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	0.7	SPINK1	serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symb
13	ENSG000000	1.15	−0.35	0.51	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
14	ENSG000002	1.1	−0.18	0.55	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy
15	ENSG000001	1.05	−0.66	0.84	LCN2	lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
16	ENSG000001	1.05	−0.87	0.75	AGR2	anterior gradient 2, protein disulphide isomerase family memb
17	ENSG000001	0.98	−0.17	0.44	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
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	0.49	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc

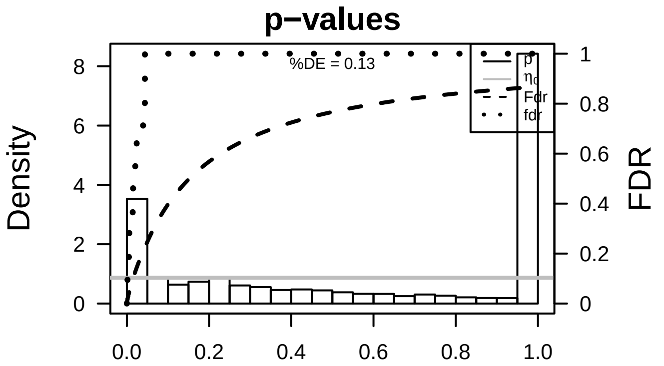
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−48	94 / 813	GSEA	GRADE_COLON_CANCER_UP
2	2e−44	85 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	3e−44	78 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
4	5e−42	41 / 113	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
5	6e−41	64 / 400	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
6	8e−41	59 / 327	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
7	8e−40	70 / 519	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
8	6e−38	58 / 350	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
9	5e−37	50 / 248	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
10	6e−36	43 / 174	GSEA	LI_AMPLIFIED_IN_LUNG_CANCER
11	4e−35	39 / 138	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
12	2e−34	76 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
13	1e−33	43 / 195	HM	HALLMARK_MYC_TARGETS_V1
14	3e−33	78 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
15	1e−32	69 / 645	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
16	2e−32	48 / 275	GSEA	GRADE_COLON_AND_RECTAL_CANCER_UP
17	2e−32	76 / 807	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
18	1e−31	49 / 303	GSEA	HORIUCHI_WTAP_TARGETS_DN
19	2e−31	75 / 811	Lymph	WIRTH_lymphoma937_spot D
20	5e−31	41 / 197	HM	HALLMARK_E2F_TARGETS
21	6e−31	103 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
22	4e−30	79 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
23	2e−28	34 / 138	GSEA	DANG_MYC_TARGETS_UP
24	2e−28	90 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
25	5e−28	68 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
26	2e−27	5 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
27	2e−27	49 / 370	GSEA	HSIAO_HOUSEKEEPING_GENES
28	3e−27	58 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
29	2e−26	33 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
30	2e−26	23 / 52	GSEA	ISHIDA_E2F_TARGETS
31	4e−26	27 / 85	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
32	4e−26	250 / 8123	Colon	TssF_Colon
33	2e−25	51 / 446	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
34	2e−25	56 / 550	Cance	Lembcke_Normal vs Adenoma
35	5e−25	42 / 292	GSEA	MUELLER_PLURINET
36	1e−24	27 / 95	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
37	1e−24	43 / 316	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
38	1e−24	75 / 1036	GSEA	DANG_BOUND_BY_MYC
39	2e−24	34 / 179	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
40	2e−24	28 / 108	BP	SRP−dependent cotranslational protein targeting to membrane









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−24	28 / 108	SRP−dependent cotranslational protein targeting to membrane
2	3e−23	57 / 633	cellular protein metabolic process
3	5e−23	38 / 259	translation
4	3e−20	23 / 88	translational termination
5	5e−20	24 / 101	translational elongation
6	1e−19	27 / 142	translational initiation
7	5e−18	23 / 109	viral transcription
8	2e−17	25 / 144	viral life cycle
9	3e−17	23 / 117	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
10	2e−15	43 / 549	viral process
11	2e−13	50 / 820	gene expression
12	1e−11	32 / 410	mitotic cell cycle
13	1e−10	13 / 62	cell redox homeostasis
14	7e−10	19 / 174	protein folding
15	9e−09	14 / 104	endoplasmic reticulum unfolded protein response
16	1e−08	24 / 323	cell division
17	1e−08	12 / 74	response to endoplasmic reticulum stress
18	6e−08	6 / 13	ribosomal small subunit biogenesis
19	2e−07	15 / 151	G1/S transition of mitotic cell cycle
20	2e−07	11 / 77	nucleobase−containing small molecule metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	1e−07	234 / 9923	Overlap_fetal_midbrain_K9K27me3
2	7e−07	16 / 191	Overlap_fetal_midbrain_Het
3	8e−07	38 / 855	Overlap_fetal_midbrain_ZNF
4	3e−05	73 / 2443	Fetal_Quies
5	6e−05	54 / 1680	Fetal_ReprPCWk
6	3e−04	224 / 10239	Overlap_fetal_midbrain_ReprPC
7	8e−04	32 / 939	Fetal_HetRpts
8	2e−03	29 / 865	Mid_Frontal_Lobe_Het
9	3e−03	84 / 3370	Mid_Frontal_Lobe_ZNF
10	1e−01	20 / 787	Overlap_fetal_midbrain_TssP
11	2e−01	210 / 10800	Overlap_fetal_midbrain_Quies
12	3e−01	9 / 400	Fetal_ZNF
13	6e−01	74 / 3977	Mid_Frontal_Lobe_ReprPC
14	6e−01	25 / 1356	Fetal_K9K27me3
15	6e−01	4 / 232	Fetal_ReprPC
16	7e−01	36 / 2084	Mid_Frontal_Lobe_K9K27me3
17	8e−01	48 / 2820	Mid_Frontal_Lobe_HetRpts
18	8e−01	8 / 552	Fetal_Tx
19	8e−01	17 / 1108	Overlap_fetal_midbrain_TssA
20	9e−01	3 / 268	Mid_Frontal_Lobe_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	2e−27	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	2e−25	56 / 550	Lembcke_Normal vs Adenoma
3	3e−22	6 / 16	RHODES_UNDIFFERENTIATED_CANCER
4	1e−18	3 / 16	RHODES_CANCER_META_SIGNATURE
5	6e−14	3 / 14	LIU_PROSTATE_CANCER_UP
6	5e−08	9 / 41	ZHANG_MM up
7	8e−06	5 / 16	GENTLES_modul2
8	8e−06	5 / 16	GENTLES_modul7
9	2e−04	4 / 16	GENTLES_modul1
10	2e−04	10 / 136	PanCan_CC+Apop_geneset_nanostring
11	4e−04	7 / 71	SHAUGHNESSY_MM high risk
12	7e−04	3 / 10	GENTLES_modul3
13	1e−03	11 / 198	PanCan_PI3K_geneset_nanostring
14	3e−03	3 / 15	BEN−PORATH_UP
15	3e−03	5 / 52	KUIPER_MM poor survival
16	3e−03	21 / 574	Lembcke_Colonic Inflammation
17	3e−03	3 / 16	WOLFER_overlap genes
18	5e−03	4 / 37	KUIPER_MM good survival
19	1e−02	4 / 50	PanCan_DNARepair_geneset_nanostring
20	2e−02	2 / 11	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	5e−22	31 / 168	ribosome
2	9e−21	118 / 2638	extracellular exosome
3	3e−16	117 / 2974	cytosol
4	3e−12	14 / 59	cytosolic large ribosomal subunit
5	3e−10	9 / 24	small ribosomal subunit
6	1e−09	102 / 3059	membrane
7	2e−09	10 / 39	cytosolic small ribosomal subunit
8	2e−08	6 / 11	endoplasmic reticulum chaperone complex
9	2e−08	41 / 842	endoplasmic reticulum
10	4e−08	27 / 425	mitochondrial inner membrane
11	6e−08	57 / 1441	mitochondrion
12	9e−08	10 / 57	endoplasmic reticulum−Golgi intermediate compartment
13	2e−07	24 / 378	focal adhesion
14	3e−07	12 / 97	melanosome
15	4e−07	37 / 799	nucleolus
16	5e−07	82 / 2554	nucleoplasm
17	9e−07	137 / 5101	nucleus
18	1e−06	35 / 767	endoplasmic reticulum membrane
19	1e−06	15 / 179	endoplasmic reticulum lumen
20	4e−06	45 / 1176	extracellular space

Chr

Rank	p−value	#in/all	Geneset
1	6e−04	36 / 1083	Chr 17
2	2e−02	15 / 436	Chr 22
3	7e−02	15 / 522	Chr 20
4	7e−02	20 / 745	Chr 9
5	9e−02	34 / 1425	Chr 19
6	4e−01	21 / 1017	Chr 12
7	4e−01	12 / 582	Chr 15
8	6e−01	18 / 976	Chr 6
9	6e−01	15 / 859	Chr 7
10	7e−01	34 / 1920	Chr 1
11	7e−01	12 / 715	Chr 10
12	7e−01	21 / 1228	Chr 2
13	7e−01	12 / 735	Chr 4
14	8e−01	17 / 1043	Chr 3
15	8e−01	19 / 1172	Chr 11
16	8e−01	13 / 847	Chr 16
17	9e−01	2 / 191	Chr 21
18	9e−01	3 / 272	Chr 18
19	9e−01	12 / 862	Chr 5
20	9e−01	7 / 613	Chr 14

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−44	85 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	3e−33	78 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
3	4e−26	250 / 8123	TssF_Colon
4	2e−15	268 / 10475	TssA_Colon
5	3e−14	116 / 3122	TxEnhG1_Colon
6	2e−08	42 / 877	TxEnhG2_Colon
7	2e−08	237 / 9930	Tx_Colon
8	3e−08	269 / 11791	Enh_Colon
9	4e−08	18 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
10	8e−07	9 / 55	Marisa_CRC−cluster−e
11	2e−06	21 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	2e−06	169 / 6761	TssD2_Colon
13	1e−04	28 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
14	7e−03	2 / 7	Marisa_CRC−C5
15	9e−03	246 / 11968	TssWk_Colon
16	1e−02	75 / 3112	EnhA_Colon
17	1e−02	2 / 10	KIM_CRC−MSI−regulated_DN
18	1e−02	2 / 10	Marisa_CRC−C1
19	3e−02	194 / 9390	TxWk_Colon
20	5e−02	5 / 105	Marisa_CRC−cluster−d

Disease

Rank	p−value	#in/all	Geneset
1	1e−16	47 / 608	GUDJ_psoriasis up
2	2e−01	2 / 37	BCHETNIA_EBM−DM up
3	3e−01	1 / 22	BCHETNIA_EBM up
4	8e−01	6 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	2e−26	33 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	3e−12	14 / 59	developing astrocytes
3	3e−11	14 / 69	cultured astroglia vs. in vivo astrocytes
4	2e−06	10 / 77	Weller_LGG_gradeII−vs−III_DOWN
5	5e−05	6 / 36	Colman_survival_associated
6	2e−04	7 / 63	OPC
7	4e−04	9 / 119	GIEZELT_GBM_WT_up_VS_mut
8	2e−03	2 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
9	3e−03	4 / 31	KIM prognostic signature LTS vs. STS
10	7e−03	3 / 21	KIM deleted & downregulated in LTS
11	1e−02	6 / 97	Weller_LGG_1p19qDel−vs−intact_UP
12	1e−02	51 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
13	2e−02	6 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	2e−02	4 / 55	Gorovets_LGG_PG_subclass
15	3e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
16	4e−02	3 / 40	Christensen_hypomethylated_in_ependymoma
17	4e−02	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
18	4e−02	4 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
19	5e−02	53 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
20	7e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−48	94 / 813	GRADE_COLON_CANCER_UP
2	3e−44	78 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
3	5e−42	41 / 113	WHITEFORD_PEDIATRIC_CANCER_MARKERS
4	6e−41	64 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
5	8e−41	59 / 327	WONG_EMBRYONIC_STEM_CELL_CORE
6	8e−40	70 / 519	BERENJENO_TRANSFORMED_BY_RHOA_UP
7	6e−38	58 / 350	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
8	5e−37	50 / 248	KOBAYASHI_EGFR_SIGNALING_24HR_DN
9	6e−36	43 / 174	LI_AMPLIFIED_IN_LUNG_CANCER
10	4e−35	39 / 138	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
11	2e−34	76 / 754	MARTENS_TRETINOIN_RESPONSE_DN
12	1e−32	69 / 645	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
13	2e−32	48 / 275	GRADE_COLON_AND_RECTAL_CANCER_UP
14	1e−31	49 / 303	HORIUCHI_WTAP_TARGETS_DN
15	6e−31	103 / 1563	PUJANA_BRCA1_PCC_NETWORK
16	4e−30	79 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	2e−28	34 / 138	DANG_MYC_TARGETS_UP
18	2e−28	90 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
19	5e−28	68 / 747	PUJANA_CHEK2_PCC_NETWORK
20	2e−27	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−33	43 / 195	HALLMARK_MYC_TARGETS_V1
2	5e−31	41 / 197	HALLMARK_E2F_TARGETS
3	4e−22	33 / 196	HALLMARK_G2M_CHECKPOINT
4	9e−19	30 / 199	HALLMARK_MTORC1_SIGNALING
5	7e−15	16 / 58	HALLMARK_MYC_TARGETS_V2
6	2e−13	19 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e−09	20 / 198	HALLMARK_GLYCOLYSIS
8	4e−06	15 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
9	4e−04	12 / 197	HALLMARK_IL2_STAT5_SIGNALING
10	4e−04	10 / 146	HALLMARK_DNA_REPAIR
11	4e−03	10 / 193	HALLMARK_XENOBIOTIC_METABOLISM
12	9e−03	8 / 155	HALLMARK_UV_RESPONSE_UP
13	1e−02	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	1e−02	5 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1e−02	9 / 196	HALLMARK_MITOTIC_SPINDLE
16	1e−02	9 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
17	1e−02	9 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
18	3e−02	8 / 196	HALLMARK_P53_PATHWAY
19	3e−02	8 / 198	HALLMARK_HYPOXIA
20	4e−02	5 / 102	HALLMARK_PEROXISOME

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	0.2	1 / 11	DUMEAUX_Smoking literature genes up
3	0.3	1 / 17	DUMEAUX_High bmi enriched genes
4	1.0	0 / 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	

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−32	76 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
2	2e−31	75 / 811	WIRTH_lymphoma937_spot D
3	1e−22	41 / 317	TARTE_Plasmablast signature
4	7e−19	185 / 5643	HOPP_Txn_transition
5	1e−12	16 / 78	TARTE_Plasma cell signature
6	3e−09	15 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
7	5e−09	15 / 116	WIRTH_lymphoma937_spot MM
8	5e−06	13 / 150	DAVE_BL−vs−DLBCL
9	1e−04	12 / 171	WIRTH_lymphoma937_spot C
10	2e−04	8 / 83	ROSOLOWSKI_green UP
11	3e−04	11 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line
12	3e−04	19 / 414	TARTE_Mature plasma cell signature
13	1e−03	186 / 8358	HOPP_Active_promoter
14	1e−03	8 / 115	ROSOLOWSKI_green total
15	2e−03	168 / 7491	HOPP_Txn_elongation
16	2e−03	12 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
17	4e−03	7 / 105	ROSOLOWSKI_blue total
18	5e−03	3 / 19	DAVE_c−myc BL UP
19	6e−03	6 / 87	Aukema_BCL2 DN_BCL6 UP
20	8e−03	165 / 7592	HOPP_Strong_enhancer

MF

Rank	p−value	#in/all	Geneset
1	1e−23	32 / 162	structural constituent of ribosome
2	3e−23	75 / 1091	poly(A) RNA binding
3	1e−08	8 / 25	isomerase activity
4	4e−08	30 / 513	RNA binding
5	2e−06	6 / 21	protein disulfide isomerase activity
6	1e−05	10 / 94	unfolded protein binding
7	9e−05	6 / 40	ribosome binding
8	2e−04	17 / 328	enzyme binding
9	4e−04	8 / 93	mRNA binding
10	6e−04	5 / 37	chemokine activity
11	7e−04	3 / 10	U6 snRNA binding
12	8e−04	7 / 80	chaperone binding
13	8e−04	13 / 245	ubiquitin protein ligase binding
14	1e−03	229 / 10693	protein binding
15	1e−03	7 / 89	histone deacetylase binding
16	2e−03	4 / 27	peptidase inhibitor activity
17	2e−03	3 / 13	misfolded protein binding
18	4e−03	4 / 34	rRNA binding
19	4e−03	3 / 17	translation initiation factor binding
20	4e−03	3 / 18	cofactor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−05	10 / 108	hsa−miR−605
2	2e−04	16 / 307	hsa−miR−34c−5p
3	6e−04	7 / 76	hsa−miR−1254
4	8e−04	5 / 39	hsa−miR−593
5	8e−04	9 / 131	hsa−miR−145
6	8e−04	11 / 187	hsa−miR−34b
7	2e−03	4 / 27	hsa−miR−1273
8	2e−03	4 / 28	hsa−miR−519e*
9	2e−03	13 / 269	hsa−miR−548p
10	2e−03	7 / 94	hsa−miR−378
11	2e−03	6 / 70	hsa−miR−193b
12	3e−03	5 / 53	hsa−miR−337−3p
13	4e−03	7 / 106	hsa−miR−525−5p
14	4e−03	7 / 108	hsa−miR−526b
15	5e−03	6 / 83	hsa−miR−30a*
16	5e−03	4 / 37	hsa−miR−770−5p
17	5e−03	7 / 112	hsa−miR−146a
18	6e−03	5 / 61	hsa−miR−492
19	6e−03	11 / 240	hsa−miR−27a
20	7e−03	5 / 63	hsa−miR−324−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.002	3 / 14	BENTINK_myc.1
2	0.218	1 / 13	BENTINK_e2f3.2
3	0.233	1 / 14	GUSTAFSON_PI3K_UP
4	0.233	1 / 14	BENTINK_e2f3.1
5	0.247	1 / 15	GUSTAFSON_PI3K_DN
6	1.000	0 / 12	BENTINK_ras.1
7	1.000	0 / 10	BENTINK_ras.4
8	1.000	0 / 15	BENTINK_ras.6
9	1.000	0 / 14	BENTINK_src.10
10	1.000	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−20	21 / 66	MYC_Targets UP
2	2e−12	63 / 1294	KIM_MYC targets
3	4e−09	63 / 1549	ICGC_Myc_targets
4	5e−08	7 / 20	MYC_Metabolism UP
5	1e−07	5 / 8	MYC_Cell cycle UP
6	1e−07	67 / 1867	HEBENSTREIT_high expression TF
7	6e−07	4 / 5	MYC_Cell growth and proliferation UP
8	1e−05	5 / 17	MYC_Protein synthesis degradation UP
9	6e−05	116 / 4470	ICGC_Creb1_targets
10	1e−04	50 / 1547	ICGC_Ets1_targets
11	1e−04	129 / 5173	ICGC_Taf1_targets
12	2e−04	134 / 5453	ICGC_Foxm1_targets
13	8e−04	144 / 6157	ICGC_Tcf3_targets
14	1e−03	132 / 5578	ICGC_Stat5_targets
15	1e−03	2 / 3	MYC_DNA replication UP
16	1e−03	128 / 5393	ICGC_Sp1_targets
17	1e−03	130 / 5512	ICGC_Nficsc81335_targets
18	1e−03	104 / 4230	ICGC_Nfatc1_targets
19	2e−03	156 / 6862	ICGC_Elf1_targets
20	3e−03	128 / 5526	ICGC_Pmlsc71910_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 17	VAQUERIZAS_Salivary gland
2	0.07	2 / 24	VAQUERIZAS_Trachea
3	0.15	2 / 37	VAQUERIZAS_Prostate
4	0.18	2 / 41	VAQUERIZAS_Testis
5	0.19	2 / 42	VAQUERIZAS_Thymus
6	0.21	2 / 45	VAQUERIZAS_Placenta
7	0.26	1 / 16	VAQUERIZAS_Fetal thyroid
8	0.29	1 / 18	VAQUERIZAS_Pancreas
9	0.32	1 / 20	VAQUERIZAS_Bone marrow
10	0.33	4 / 155	VAQUERIZAS_General
11	0.38	1 / 25	VAQUERIZAS_Spinal cord
12	0.43	1 / 30	VAQUERIZAS_Smooth muscle
13	0.46	1 / 33	VAQUERIZAS_Liver
14	0.54	1 / 41	VAQUERIZAS_Fetal brain
15	0.55	1 / 42	VAQUERIZAS_Thyroid
16	0.58	1 / 46	VAQUERIZAS_Whole brain
17	1.00	0 / 49	VAQUERIZAS_Uterus
18	1.00	0 / 12	VAQUERIZAS_Kidney
19	1.00	0 / 67	VAQUERIZAS_Whole blood
20	1.00	0 / 7	VAQUERIZAS_Appendix

Tissue

Rank	p−value	#in/all	Geneset
1	0.001	3 / 12	WIRTH_Lymphocytes
2	0.002	4 / 30	PALMER_Lymphocytes signature up
3	0.024	2 / 13	WIRTH_Globus pallidus
4	0.025	10 / 259	PALMER_Granulocytes signature up
5	0.027	2 / 14	WIRTH_B−cells
6	0.097	7 / 208	PALMER_B−Cell signature up
7	0.123	5 / 140	PALMER_T−Cell signature up
8	0.218	1 / 13	WIRTH_Cortex cerebri
9	0.233	1 / 14	WIRTH_Thyroid gland
10	0.247	1 / 15	WIRTH_Telencephalon
11	0.247	1 / 15	WIRTH_Cerebellum
12	0.641	1 / 54	WIRTH_Pancreas
13	0.789	1 / 82	WIRTH_Homeostasis
14	0.997	2 / 427	WIRTH_Immune system
15	1.000	1 / 476	WIRTH_Nervous System
16	1.000	0 / 6	WIRTH_Pituitary gland
17	1.000	0 / 13	WIRTH_Sec. lymphoid organs
18	1.000	0 / 13	WIRTH_Prim. lymphoid organs
19	1.000	0 / 12	WIRTH_Tonsil
20	1.000	0 / 14	WIRTH_Thymus

Toxic

Rank	p−value	#in/all	Geneset
1	0.4	27 / 1343	LU_BPDE 1h DN
2	1.0	65 / 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	

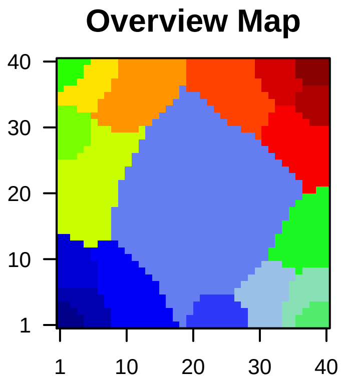
K−Means Clusters

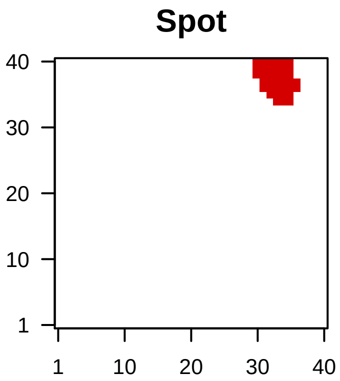
Spot Summary: R

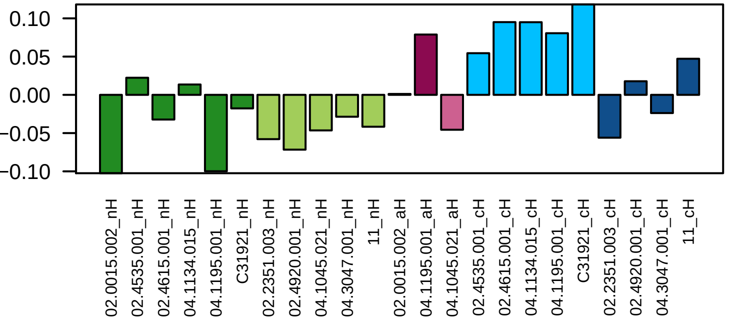
metagenes = 37
genes = 559

<r> metagenes = 0.93
<r> genes = 0.48
beta: r2= 0.08 / log p= −0.72

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





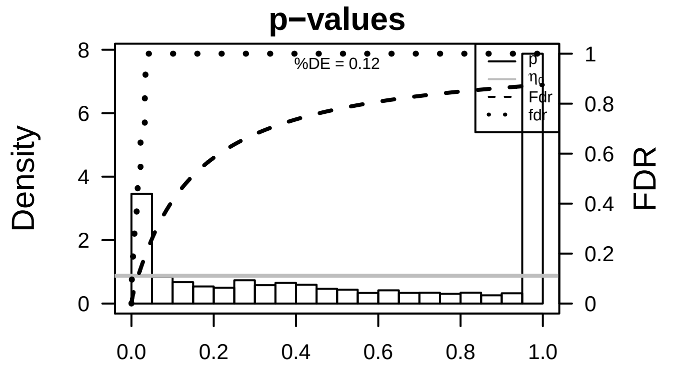


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.95	−0.08	0.28	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
2	ENSG000001	0.75	−0.13	0.33	FAM83D	family with sequence similarity 83, member D [Source:HGNC
3	ENSG000001	0.71	−0.63	0.6	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC S
4	ENSG000001	0.68	−0.21	0.48	WARS	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
5	ENSG000001	0.66	−0.21	0.25	NPIPB15	nuclear pore complex interacting protein family, member B15
6	ENSG000001	0.63	−0.11	0.4	LRP4	low density lipoprotein receptor−related protein 4 [Source:HG
7	ENSG000001	0.62	−0.43	0.61	IFITM2	interferon induced transmembrane protein 2 [Source:HGNC S
8	ENSG000001	0.58	−0.04	0.39	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family
9	ENSG000001	0.57	−0.35	0.55	HSPA8	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
10	ENSG000000	0.54	−0.26	0.52	FXYD5	FXYD domain containing ion transport regulator 5 [Source:HG
11	ENSG000001	0.54	−0.07	0.5	CST1	cystatin SN [Source:HGNC Symbol;Acc:HGNC:2473]
12	ENSG000002	0.54	−0.06	0.48	L1TD1	LINE−1 type transposase domain containing 1 [Source:HGNC
13	ENSG000001	0.53	−0.27	0.41	ETS2	v−ets avian erythroblastosis virus E26 oncogene homolog 2 [
14	ENSG000000	0.53	−0.29	0.61	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1
15	ENSG000001	0.51	−0.34	0.59	ALDH1B1	aldehyde dehydrogenase 1 family, member B1 [Source:HGNC
16	ENSG000002	0.48	−0.31	0.73		RPL36A−HNRNPH2 readthrough [Source:HGNC Symbol;Acc
17	ENSG000001	0.48	−0.33	0.71	TUBA1B	tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
18	ENSG000001	0.45	−0.14	0.52	TGFBI	transforming growth factor, beta−induced, 68kDa [Source:HG
19	ENSG000001	0.43	−0.36	0.67	RPS16	ribosomal protein S16 [Source:HGNC Symbol;Acc:HGNC:10
20	ENSG000002	0.42	−0.1	0.56	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) [Source

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−85	207 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
2	2e−78	141 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	8e−77	128 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
4	1e−73	139 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
5	3e−64	354 / 5643	Lympl	HOPP_Txn_transition
6	3e−56	144 / 1091	MF	poly(A) RNA binding
7	3e−52	66 / 195	HM	HALLMARK_MYC_TARGETS_V1
8	2e−51	123 / 859	GSEA	LEE_BMP2_TARGETS_DN
9	5e−49	147 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
10	7e−48	70 / 259	BP	translation
11	4e−46	461 / 10475	Colon	TssA_Colon
12	1e−45	447 / 9930	Colon	Tx_Colon
13	1e−45	79 / 370	GSEA	HSIAO_HOUSEKEEPING_GENES
14	6e−45	82 / 412	GSEA	REACTOME_METABOLISM_OF_PROTEINS
15	7e−45	113 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
16	3e−44	403 / 8358	Lympl	HOPP_Active_promoter
17	9e−44	111 / 820	BP	gene expression
18	2e−43	46 / 102	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
19	3e−43	52 / 142	GSEA	REACTOME_TRANSLATION
20	4e−43	376 / 7491	Lympl	HOPP_Txn_elongation
21	2e−42	54 / 162	MF	structural constituent of ribosome
22	5e−42	51 / 142	BP	translational initiation
23	2e−41	44 / 98	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
24	2e−41	54 / 168	CC	ribosome
25	9e−41	44 / 101	BP	translational elongation
26	1e−40	45 / 108	BP	SRP−dependent cotranslational protein targeting to membrane
27	2e−40	131 / 1228	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
28	7e−40	48 / 132	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
29	8e−40	44 / 105	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
30	1e−39	40 / 82	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
31	1e−39	41 / 88	BP	translational termination
32	4e−39	40 / 84	GSEA	KEGG_RIBOSOME
33	1e−37	43 / 109	BP	viral transcription
34	6e−37	90 / 633	BP	cellular protein metabolic process
35	1e−36	132 / 1352	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
36	2e−36	65 / 317	Lympl	TARTE_Plasmablast signature
37	9e−36	415 / 9390	Colon	TxWk_Colon
38	6e−35	64 / 323	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
39	6e−35	40 / 102	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
40	7e−35	99 / 813	GSEA	GRADE_COLON_CANCER_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	5 / 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	7e−48	70 / 259	translation
2	9e−44	111 / 820	gene expression
3	5e−42	51 / 142	translational initiation
4	9e−41	44 / 101	translational elongation
5	1e−40	45 / 108	SRP−dependent cotranslational protein targeting to membrane
6	1e−39	41 / 88	translational termination
7	1e−37	43 / 109	viral transcription
8	6e−37	90 / 633	cellular protein metabolic process
9	1e−34	42 / 117	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
10	7e−33	44 / 144	viral life cycle
11	5e−32	78 / 549	viral process
12	8e−14	44 / 410	mitotic cell cycle
13	2e−13	12 / 22	cytoplasmic translation
14	1e−12	27 / 174	protein folding
15	3e−10	13 / 45	tRNA aminoacylation for protein translation
16	1e−08	16 / 95	rRNA processing
17	7e−08	14 / 80	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent p
18	9e−08	19 / 151	G1/S transition of mitotic cell cycle
19	9e−08	10 / 38	'de novo' posttranslational protein folding
20	2e−07	18 / 145	DNA replication

Brain

Rank	p−value	#in/all	Geneset
1	1e−34	435 / 10239	Overlap_fetal_midbrain_ReprPC
2	3e−27	411 / 9923	Overlap_fetal_midbrain_K9K27me3
3	4e−14	68 / 855	Overlap_fetal_midbrain_ZNF
4	8e−12	260 / 6320	Overlap_fetal_midbrain_HetRpts
5	9e−09	23 / 191	Overlap_fetal_midbrain_Het
6	1e−08	378 / 10800	Overlap_fetal_midbrain_Quies
7	3e−06	53 / 939	Fetal_HetRpts
8	9e−04	42 / 865	Mid_Frontal_Lobe_Het
9	3e−03	332 / 10278	Overlap_fetal_midbrain_ReprPCWk
10	5e−03	122 / 3370	Mid_Frontal_Lobe_ZNF
11	6e−03	19 / 342	Fetal_Het
12	2e−02	63 / 1680	Fetal_ReprPCWk
13	3e−02	87 / 2443	Fetal_Quies
14	5e−02	18 / 400	Fetal_ZNF
15	2e−01	45 / 1356	Fetal_K9K27me3
16	4e−01	84 / 2820	Mid_Frontal_Lobe_HetRpts
17	5e−01	7 / 232	Fetal_ReprPC
18	9e−01	42 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	9e−01	33 / 1394	Mid_Frontal_Lobe_Quies
20	1e+00	12 / 641	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	4e−20	62 / 550	Lembcke_Normal vs Adenoma
2	3e−17	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	1e−10	9 / 16	WOLFER_overlap genes
4	2e−10	5 / 16	RHODES_CANCER_META_SIGNATURE
5	4e−09	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
6	7e−05	5 / 16	GENTLES_modul1
7	2e−04	9 / 71	SHAUGHNESSY_MM high risk
8	8e−04	4 / 15	GENTLES_modul4
9	1e−03	4 / 16	GENTLES_modul6
10	1e−03	6 / 41	ZHANG_MM up
11	9e−03	3 / 15	LIU_BREAST_CANCER
12	9e−03	3 / 15	BEN−PORATH_UP
13	9e−03	3 / 15	GENTLES_modul10
14	1e−02	3 / 16	GENTLES_modul2
15	1e−02	3 / 16	GENTLES_modul7
16	1e−02	5 / 50	PanCan_DNARepair_geneset_nanostring
17	2e−02	5 / 52	KUIPER_MM poor survival
18	2e−02	4 / 37	KUIPER_MM good survival
19	3e−02	2 / 10	GENTLES_modul3
20	5e−02	8 / 136	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−41	54 / 168	ribosome
2	4e−29	29 / 59	cytosolic large ribosomal subunit
3	2e−24	83 / 799	nucleolus
4	5e−22	176 / 2974	cytosol
5	1e−17	152 / 2638	extracellular exosome
6	4e−15	16 / 39	cytosolic small ribosomal subunit
7	1e−13	138 / 2554	nucleoplasm
8	5e−13	155 / 3059	membrane
9	7e−13	23 / 121	ribonucleoprotein complex
10	2e−12	40 / 378	focal adhesion
11	2e−12	226 / 5185	cytoplasm
12	4e−07	201 / 5101	nucleus
13	1e−06	74 / 1441	mitochondrion
14	4e−06	7 / 24	small ribosomal subunit
15	5e−06	13 / 97	melanosome
16	8e−06	5 / 11	large ribosomal subunit
17	2e−05	10 / 65	cell body
18	4e−05	8 / 45	mitochondrial nucleoid
19	5e−05	5 / 15	eukaryotic 48S preinitiation complex
20	1e−04	4 / 10	mitochondrial outer membrane translocase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.04	26 / 613	Chr 14
2	0.05	15 / 318	Chr 13
3	0.05	44 / 1172	Chr 11
4	0.07	45 / 1228	Chr 2
5	0.13	31 / 862	Chr 5
6	0.18	21 / 582	Chr 15
7	0.20	26 / 745	Chr 9
8	0.22	34 / 1017	Chr 12
9	0.39	14 / 436	Chr 22
10	0.48	29 / 976	Chr 6
11	0.59	1 / 30	Chr Y
12	0.63	54 / 1920	Chr 1
13	0.63	29 / 1043	Chr 3
14	0.64	30 / 1083	Chr 17
15	0.66	14 / 522	Chr 20
16	0.68	7 / 272	Chr 18
17	0.69	19 / 715	Chr 10
18	0.79	16 / 651	Chr 8
19	0.81	18 / 735	Chr 4
20	0.81	4 / 191	Chr 21

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−78	141 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	4e−46	461 / 10475	TssA_Colon
3	1e−45	447 / 9930	Tx_Colon
4	7e−45	113 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
5	9e−36	415 / 9390	TxWk_Colon
6	4e−20	342 / 8123	TssF_Colon
7	1e−14	431 / 11968	TssWk_Colon
8	7e−09	143 / 3122	TxEnhG1_Colon
9	3e−08	339 / 9470	Quies3_Colon
10	3e−06	248 / 6761	TssD2_Colon
11	2e−05	48 / 877	TxEnhG2_Colon
12	5e−05	167 / 4379	TssD1_Colon
13	1e−04	23 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
14	2e−04	16 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	6e−03	199 / 5889	EnhWk1_Colon
16	2e−02	366 / 11791	Enh_Colon
17	3e−02	2 / 10	Budinska_E_Mixed_UP
18	3e−02	7 / 105	Marisa_CRC−cluster−d
19	1e−01	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
20	1e−01	1 / 4	Budinska_C_CIMP−H−like_DOWN

Disease

Rank	p−value	#in/all	Geneset
1	1e−04	35 / 608	GUDJ_psoriasis up
2	3e−01	2 / 37	BCHETNIA_EBM−DM up
3	5e−01	1 / 22	BCHETNIA_EBM up
4	6e−01	11 / 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	

Glio

Rank	p−value	#in/all	Geneset
1	3e−11	23 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	2e−06	103 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	7e−06	91 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	7e−06	10 / 59	developing astrocytes
5	5e−04	22 / 344	Up
6	6e−04	7 / 50	Vishal_subnetwork signature of survival in GBM
7	4e−03	3 / 12	WILLSCHER__GBM_LTSwt_proteomics−C_UP
8	7e−03	18 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	7e−03	7 / 77	Weller_LGG_gradeII−vs−III_DOWN
10	2e−02	4 / 36	Colman_survival_associated
11	2e−02	36 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
12	3e−02	6 / 83	GIEZELT_GBM_WT_down_VS_mut
13	4e−02	2 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
14	5e−02	5 / 69	cultured astroglia vs. in vivo astrocytes
15	8e−02	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
16	8e−02	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
17	1e−01	6 / 111	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
18	1e−01	3 / 40	Christensen_hypomethylated_in_ependymoma
19	1e−01	4 / 63	Stuehler_Proteins_up_in_STS
20	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−85	207 / 1563	PUJANA_BRCA1_PCC_NETWORK
2	8e−77	128 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
3	1e−73	139 / 747	PUJANA_CHEK2_PCC_NETWORK
4	2e−51	123 / 859	LEE_BMP2_TARGETS_DN
5	5e−49	147 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
6	1e−45	79 / 370	HSIAO_HOUSEKEEPING_GENES
7	6e−45	82 / 412	REACTOME_METABOLISM_OF_PROTEINS
8	2e−43	46 / 102	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
9	3e−43	52 / 142	REACTOME_TRANSLATION
10	2e−41	44 / 98	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
11	2e−40	131 / 1228	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	7e−40	48 / 132	REACTOME_INFLUENZA_LIFE_CYCLE
13	8e−40	44 / 105	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
14	1e−39	40 / 82	REACTOME_PEPTIDE_CHAIN_ELONGATION
15	4e−39	40 / 84	KEGG_RIBOSOME
16	1e−36	132 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
17	6e−35	64 / 323	PENG_GLUTAMINE_DEPRIVATION_DN
18	6e−35	40 / 102	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
19	7e−35	99 / 813	GRADE_COLON_CANCER_UP
20	2e−34	80 / 536	FEVR_CTNNB1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−52	66 / 195	HALLMARK_MYC_TARGETS_V1
2	9e−20	37 / 197	HALLMARK_E2F_TARGETS
3	9e−14	30 / 196	HALLMARK_G2M_CHECKPOINT
4	9e−13	29 / 199	HALLMARK_MTORC1_SIGNALING
5	3e−09	18 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	8e−07	11 / 58	HALLMARK_MYC_TARGETS_V2
7	5e−05	15 / 155	HALLMARK_UV_RESPONSE_UP
8	7e−04	15 / 198	HALLMARK_GLYCOLYSIS
9	4e−03	11 / 146	HALLMARK_DNA_REPAIR
10	6e−03	5 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	1e−02	12 / 196	HALLMARK_MITOTIC_SPINDLE
12	2e−02	6 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	4e−02	9 / 154	HALLMARK_FATTY_ACID_METABOLISM
14	5e−02	6 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	5e−02	10 / 190	HALLMARK_APICAL_JUNCTION
16	8e−02	9 / 181	HALLMARK_ALLOGRAFT_REJECTION
17	1e−01	9 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
18	2e−01	5 / 98	HALLMARK_ANDROGEN_RESPONSE
19	2e−01	7 / 157	HALLMARK_APOPTOSIS
20	2e−01	6 / 132	HALLMARK_COAGULATION

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	

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−64	354 / 5643	HOPP_Txn_transition
2	3e−44	403 / 8358	HOPP_Active_promoter
3	4e−43	376 / 7491	HOPP_Txn_elongation
4	2e−36	65 / 317	TARTE_Plasmablast signature
5	1e−24	84 / 811	WIRTH_lymphoma937_spot D
6	2e−23	82 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	8e−19	339 / 8147	HOPP_Weak_promoter
8	2e−08	21 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
9	3e−08	21 / 171	WIRTH_lymphoma937_spot C
10	3e−07	279 / 7592	HOPP_Strong_enhancer
11	4e−07	13 / 78	TARTE_Plasma cell signature
12	6e−07	7 / 19	DAVE_c−myc BL UP
13	6e−06	63 / 1215	SPANG_BCR DN
14	3e−05	15 / 150	DAVE_BL−vs−DLBCL
15	5e−05	12 / 105	ROSOLOWSKI_blue total
16	8e−05	4 / 9	YAMANE_AICDA_targets_nonrecruited
17	3e−03	4 / 21	ROSOLOWSKI_red UP
18	1e−02	7 / 87	Aukema_BCL2 DN_BCL6 UP
19	2e−02	8 / 116	WIRTH_lymphoma937_spot MM
20	3e−02	219 / 6784	HOPP_Weak_enhancer

MF

Rank	p−value	#in/all	Geneset
1	3e−56	144 / 1091	poly(A) RNA binding
2	2e−42	54 / 162	structural constituent of ribosome
3	1e−21	62 / 513	RNA binding
4	2e−11	19 / 94	unfolded protein binding
5	3e−09	35 / 385	nucleotide binding
6	5e−09	11 / 37	aminoacyl−tRNA ligase activity
7	5e−07	14 / 93	mRNA binding
8	1e−06	74 / 1448	ATP binding
9	2e−06	9 / 41	tRNA binding
10	2e−06	12 / 77	single−stranded DNA binding
11	5e−06	8 / 34	rRNA binding
12	2e−05	9 / 53	translation initiation factor activity
13	2e−04	353 / 10693	protein binding
14	2e−04	4 / 11	aminoacyl−tRNA editing activity
15	3e−04	5 / 21	DNA helicase activity
16	3e−04	4 / 12	neutral amino acid transmembrane transporter activity
17	4e−04	5 / 22	threonine−type endopeptidase activity
18	4e−04	8 / 61	damaged DNA binding
19	4e−04	32 / 578	identical protein binding
20	1e−03	5 / 29	Ran GTPase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−08	31 / 348	hsa−miR−548b−5p
2	1e−07	30 / 348	hsa−miR−548d−5p
3	5e−07	27 / 312	hsa−miR−548i
4	5e−07	28 / 332	hsa−miR−548a−5p
5	1e−06	27 / 324	hsa−miR−559
6	2e−06	25 / 297	hsa−miR−548j
7	7e−06	25 / 317	hsa−miR−548c−5p
8	1e−05	14 / 122	hsa−miR−509−3p
9	2e−05	20 / 237	hsa−miR−124
10	3e−05	30 / 452	hsa−miR−19a
11	3e−05	17 / 184	hsa−miR−548e
12	3e−05	17 / 186	hsa−miR−1
13	4e−05	13 / 118	hsa−miR−376c
14	4e−05	14 / 136	hsa−miR−28−5p
15	4e−05	16 / 172	hsa−miR−548g
16	5e−05	16 / 173	hsa−miR−323b−5p
17	6e−05	12 / 106	hsa−miR−210
18	7e−05	10 / 76	hsa−miR−708
19	1e−04	13 / 129	hsa−miR−223
20	1e−04	17 / 204	hsa−miR−206

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	1e−26	113 / 1294	KIM_MYC targets
2	3e−21	115 / 1549	ICGC_Myc_targets
3	5e−11	16 / 66	MYC_Targets UP
4	2e−08	210 / 5173	ICGC_Taf1_targets
5	2e−07	79 / 1503	ICGC_Six5_targets
6	3e−07	7 / 17	MYC_Protein synthesis degradation UP
7	3e−07	80 / 1547	ICGC_Ets1_targets
8	4e−07	181 / 4470	ICGC_Creb1_targets
9	4e−07	214 / 5512	ICGC_Nficsc81335_targets
10	1e−06	90 / 1867	HEBENSTREIT_high expression TF
11	8e−06	201 / 5308	ICGC_Tcf12_targets
12	9e−06	96 / 2133	ICGC_Cebpbsc150_targets
13	1e−05	103 / 2342	ICGC_GabpPcr2_targets
14	2e−05	188 / 4969	ICGC_Atf2_targets
15	3e−05	164 / 4230	ICGC_Nfatc1_targets
16	3e−05	188 / 4987	ICGC_Bclaf101388_targets
17	3e−05	224 / 6157	ICGC_Tcf3_targets
18	3e−05	200 / 5393	ICGC_Sp1_targets
19	5e−05	128 / 3177	ICGC_Irf4_targets
20	5e−05	203 / 5526	ICGC_Pmlsc71910_targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.08	2 / 16	VAQUERIZAS_Fetal liver
2	0.10	2 / 18	VAQUERIZAS_Pancreas
3	0.25	2 / 33	VAQUERIZAS_Liver
4	0.30	1 / 12	VAQUERIZAS_Kidney
5	0.32	1 / 13	VAQUERIZAS_Skin
6	0.40	1 / 17	VAQUERIZAS_Adrenal gland
7	0.45	1 / 20	VAQUERIZAS_Bone marrow
8	0.52	1 / 25	VAQUERIZAS_Adrenal cortex
9	0.59	1 / 30	VAQUERIZAS_Smooth muscle
10	0.60	1 / 31	VAQUERIZAS_Fetal lung
11	0.67	1 / 37	VAQUERIZAS_Prostate
12	0.71	1 / 42	VAQUERIZAS_Thymus
13	0.74	1 / 46	VAQUERIZAS_Whole brain
14	0.77	1 / 49	VAQUERIZAS_Uterus
15	0.85	1 / 64	VAQUERIZAS_Lung
16	0.86	1 / 67	VAQUERIZAS_Whole blood
17	1.00	0 / 41	VAQUERIZAS_Fetal brain
18	1.00	0 / 45	VAQUERIZAS_Placenta
19	1.00	0 / 155	VAQUERIZAS_General
20	1.00	0 / 25	VAQUERIZAS_Spinal cord

Tissue

Rank	p−value	#in/all	Geneset
1	1e−07	9 / 30	PALMER_Lymphocytes signature up
2	3e−04	4 / 12	WIRTH_Lymphocytes
3	5e−02	2 / 13	WIRTH_Cortex cerebri
4	6e−02	2 / 14	WIRTH_Thyroid gland
5	8e−02	12 / 259	PALMER_Granulocytes signature up
6	3e−01	15 / 427	WIRTH_Immune system
7	3e−01	1 / 13	WIRTH_Globus pallidus
8	3e−01	1 / 14	WIRTH_Thymus
9	4e−01	1 / 15	WIRTH_Telencephalon
10	4e−01	5 / 140	PALMER_T−Cell signature up
11	9e−01	4 / 208	PALMER_B−Cell signature up
12	1e+00	1 / 137	WIRTH_Mucosa
13	1e+00	1 / 141	WIRTH_Muscle
14	1e+00	2 / 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 / 14	WIRTH_B−cells
20	1e+00	0 / 12	WIRTH_Tonsil

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	47 / 1343	LU_BPDE 1h DN
2	1.0	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	

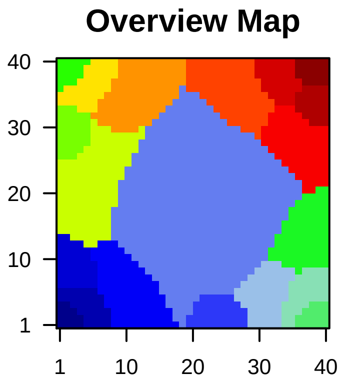
K−Means Clusters

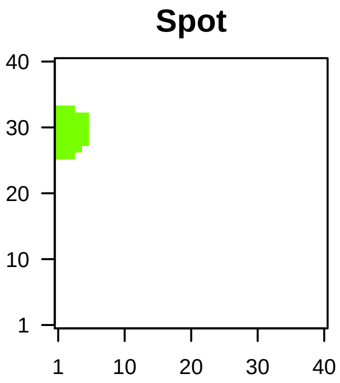
Spot Summary: S

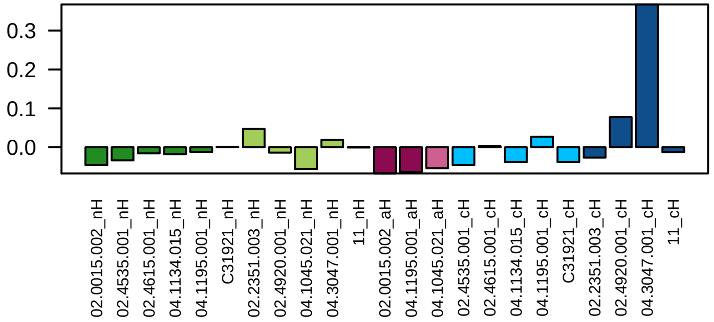
metagenes = 35
genes = 434

<r> metagenes = 0.95
<r> genes = 0.61
beta: r2= 0.11 / log p= −0.94

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


Overview Map


Spot

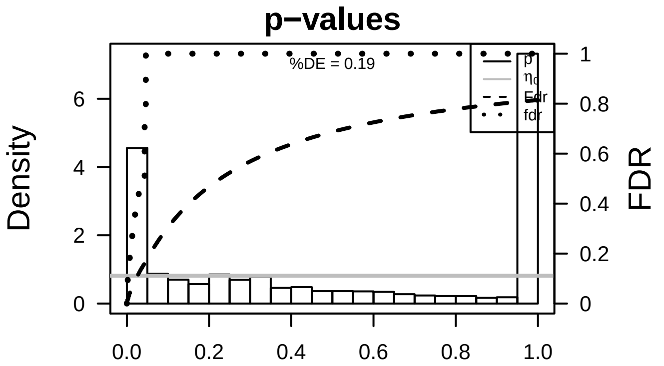


Spot Genelist

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	0.29	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
4	ENSG000001	1.11	−0.22	0.92	SFRP2	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
5	ENSG000001	1.02	−0.41	0.87	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	0.93	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
8	ENSG000001	0.98	−0.25	0.63	SAA1	serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]
9	ENSG000001	0.95	−0.62	0.74	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:H
10	ENSG000001	0.9	−0.24	0.82	FOSB	FBJ murine osteosarcoma viral oncogene homolog B [Source
11	ENSG000001	0.89	−0.09	0.85	ADIPOQ	adiponectin, C1Q and collagen domain containing [Source:H
12	ENSG000001	0.87	−0.18	0.95	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	0.82	G0S2	G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]
15	ENSG000001	0.84	−0.09	0.95	RBP7	retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:
16	ENSG000001	0.83	−0.15	0.88	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	ENSG000001	0.83	−0.21	0.8	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide [Source
18	ENSG000002	0.82	−0.11	0.92	MUSTN1	musculoskeletal, embryonic nuclear protein 1 [Source:HGNC
19	ENSG000002	0.81	−0.2	0.83	ACKR1	atypical chemokine receptor 1 (Duffy blood group) [Source:H
20	ENSG000001	0.81	−0.07	0.91	PLIN1	perilipin 1 [Source:HGNC Symbol;Acc:HGNC:9076]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−48	70 / 326	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	2e−36	106 / 1176	CC	extracellular space
3	2e−36	62 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
4	2e−34	70 / 522	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
5	2e−34	73 / 574	Cance	Lembcke_Colonic Inflammation
6	3e−34	47 / 202	CC	extracellular matrix
7	4e−34	47 / 204	GSEA	BOQUEST_STEM_CELL_DN
8	2e−32	61 / 413	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
9	3e−32	77 / 692	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
10	4e−31	60 / 418	GSEA	SWEET_LUNG_CANCER_KRAS_DN
11	2e−30	87 / 945	GSEA	NABA_MATRISOME
12	4e−30	43 / 198	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	3e−29	27 / 59	Lymph	LENZ_Stromal signature 2
14	5e−29	47 / 261	Lymph	LENZ_Stromal signature 1
15	1e−28	103 / 1374	CC	extracellular region
16	9e−28	43 / 224	BP	angiogenesis
17	2e−27	40 / 192	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
18	5e−27	50 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
19	1e−26	28 / 78	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
20	1e−26	56 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
21	3e−26	58 / 478	GSEA	LIM_MAMMARY_STEM_CELL_UP
22	8e−25	38 / 196	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
23	2e−24	46 / 314	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
24	2e−24	46 / 315	Lymph	WIRTH_lymphoma937_spot E
25	4e−24	58 / 525	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
26	7e−24	41 / 248	GSEA	ONDER_CDH1_TARGETS_2_UP
27	7e−24	34 / 158	GSEA	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
28	8e−24	41 / 249	GSEA	BOQUEST_STEM_CELL_UP
29	9e−23	26 / 85	GSEA	SANA_TNF_SIGNALING_DN
30	2e−22	23 / 62	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
31	1e−21	68 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
32	4e−21	39 / 261	GSEA	NABA_CORE_MATRISOME
33	6e−21	84 / 1210	Brain	Fetal_TssP
34	1e−20	26 / 101	GSEA	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
35	3e−20	22 / 67	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
36	6e−20	46 / 401	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
37	1e−19	199 / 5039	Lymph	HOPP_Repressed
38	1e−19	145 / 3109	Colon	TssP_Colon
39	2e−19	140 / 2956	Brain	Fetal_TssA
40	2e−19	29 / 148	Colon	Marisa_CRC−cluster−a


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.009	5 / 57	TESCHENDORFF_age_hypermethylated
2	0.221	5 / 144	HORVATH_aging_genes meth UP
3	0.297	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	9e−28	43 / 224	angiogenesis
2	2e−15	35 / 306	extracellular matrix organization
3	9e−12	25 / 209	platelet activation
4	6e−11	14 / 61	vasculogenesis
5	2e−10	13 / 56	negative regulation of angiogenesis
6	3e−10	15 / 81	platelet degranulation
7	4e−10	21 / 175	response to hypoxia
8	8e−10	16 / 101	positive regulation of angiogenesis
9	2e−09	34 / 466	blood coagulation
10	3e−09	20 / 175	response to lipopolysaccharide
11	5e−09	12 / 58	blood vessel development
12	5e−09	50 / 913	positive regulation of transcription from RNA polymerase II promoter
13	9e−09	30 / 402	negative regulation of cell proliferation
14	1e−08	10 / 39	collagen fibril organization
15	2e−08	11 / 53	positive regulation of smooth muscle cell proliferation
16	2e−08	17 / 143	response to organic cyclic compound
17	5e−08	13 / 85	positive regulation of MAPK cascade
18	2e−07	11 / 65	response to wounding
19	2e−07	11 / 66	positive regulation of endothelial cell proliferation
20	2e−07	14 / 113	extracellular matrix disassembly

Brain

Rank	p−value	#in/all	Geneset
1	6e−21	84 / 1210	Fetal_TssP
2	2e−19	140 / 2956	Fetal_TssA
3	2e−17	108 / 2084	Mid_Frontal_Lobe_K9K27me3
4	5e−16	161 / 3977	Mid_Frontal_Lobe_ReprPC
5	1e−10	107 / 2603	Fetal_TxTrans
6	9e−10	103 / 2549	Fetal_TssF
7	2e−06	57 / 1327	Mid_Frontal_Lobe_TssP
8	2e−06	68 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	8e−06	38 / 787	Overlap_fetal_midbrain_TssP
10	2e−04	44 / 1108	Overlap_fetal_midbrain_TssA
11	1e−03	51 / 1478	Overlap_fetal_midbrain_TxTrans
12	2e−03	48 / 1394	Mid_Frontal_Lobe_Quies
13	7e−03	22 / 552	Fetal_Tx
14	7e−03	82 / 2820	Mid_Frontal_Lobe_HetRpts
15	8e−03	30 / 840	Mid_Frontal_Lobe_TssF
16	8e−02	10 / 268	Mid_Frontal_Lobe_TssA
17	1e−01	13 / 408	Mid_Frontal_Lobe_TxTrans
18	2e−01	24 / 865	Mid_Frontal_Lobe_Het
19	2e−01	12 / 400	Fetal_ZNF
20	2e−01	48 / 1890	Overlap_fetal_midbrain_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	2e−34	73 / 574	Lembcke_Colonic Inflammation
2	1e−11	2 / 16	LIU_PROSTATE_CANCER_DN
3	1e−08	7 / 15	GENTLES_modul13
4	3e−04	4 / 15	GENTLES_modul17
5	6e−04	11 / 152	PanCan_MAPK_geneset_nanostring
6	1e−03	17 / 324	SPANG_BCL6−index2
7	1e−03	8 / 97	PanCan_TXmisReg_geneset_nanostring
8	2e−03	12 / 198	PanCan_PI3K_geneset_nanostring
9	1e−02	8 / 140	PanCan_RAS_geneset_nanostring
10	3e−02	4 / 51	PanCan_TGF−B_geneset_nanostring
11	3e−02	5 / 78	PanCan_Wnt_geneset_nanostring
12	4e−02	2 / 14	LIU_PROSTATE_CANCER_UP
13	4e−02	2 / 14	BEN−PORATH_DN
14	5e−02	2 / 16	RHODES_CANCER_META_SIGNATURE
15	5e−02	2 / 16	LIU_LIVER_CANCER
16	9e−02	6 / 136	PanCan_CC+Apop_geneset_nanostring
17	1e−01	2 / 24	PanCan_Notch_geneset_nanostring
18	1e−01	4 / 86	PanCan_JAK−ST_geneset_nanostring
19	1e−01	1 / 6	ZHANG_MGUS up
20	1e−01	7 / 191	SPANG_LPS−index2

CC

Rank	p−value	#in/all	Geneset
1	2e−36	106 / 1176	extracellular space
2	3e−34	47 / 202	extracellular matrix
3	1e−28	103 / 1374	extracellular region
4	4e−17	35 / 270	proteinaceous extracellular matrix
5	4e−14	44 / 523	cell surface
6	3e−11	13 / 48	platelet alpha granule lumen
7	1e−10	108 / 2638	extracellular exosome
8	3e−07	18 / 190	membrane raft
9	8e−07	119 / 3507	plasma membrane
10	1e−06	13 / 110	blood microparticle
11	3e−06	17 / 201	external side of plasma membrane
12	5e−06	53 / 1250	integral component of plasma membrane
13	7e−05	9 / 79	collagen trimer
14	8e−05	29 / 596	perinuclear region of cytoplasm
15	3e−04	4 / 15	platelet alpha granule
16	4e−04	20 / 378	focal adhesion
17	5e−04	4 / 17	anchored component of external side of plasma membrane
18	9e−04	12 / 184	transcription factor complex
19	1e−03	15 / 268	apical plasma membrane
20	4e−03	7 / 88	basement membrane

Chr

Rank	p−value	#in/all	Geneset
1	4e−04	29 / 651	Chr 8
2	2e−02	29 / 859	Chr 7
3	1e−01	25 / 862	Chr 5
4	1e−01	7 / 191	Chr 21
5	1e−01	32 / 1172	Chr 11
6	2e−01	27 / 1043	Chr 3
7	3e−01	25 / 976	Chr 6
8	4e−01	13 / 522	Chr 20
9	4e−01	24 / 1017	Chr 12
10	5e−01	43 / 1920	Chr 1
11	6e−01	24 / 1083	Chr 17
12	6e−01	7 / 318	Chr 13
13	6e−01	16 / 735	Chr 4
14	6e−01	15 / 715	Chr 10
15	7e−01	25 / 1228	Chr 2
16	7e−01	12 / 613	Chr 14
17	8e−01	11 / 582	Chr 15
18	8e−01	8 / 436	Chr 22
19	9e−01	13 / 745	Chr 9
20	1e+00	2 / 272	Chr 18

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−27	50 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
2	1e−19	145 / 3109	TssP_Colon
3	2e−19	29 / 148	Marisa_CRC−cluster−a
4	2e−16	38 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	3e−06	114 / 3406	ReprPC_Colon
6	3e−06	29 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
7	6e−06	76 / 2041	EnhP_Colon
8	9e−06	10 / 78	Ang_CRC_Hypermethylated
9	2e−05	20 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
10	3e−05	28 / 532	K9acLow_Colon
11	7e−05	4 / 11	Kaneda_CIMP−group2
12	1e−04	95 / 2947	ReprPCWk_Colon
13	2e−04	8 / 73	Ang_CRC−CIMPH−vs−L_hyper
14	2e−04	22 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
15	3e−04	4 / 15	Budinska_B_Lower crypt−like_DOWN
16	4e−04	22 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
17	9e−04	31 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
18	1e−03	19 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
19	3e−03	123 / 4379	TssD1_Colon
20	5e−03	11 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Disease

Rank	p−value	#in/all	Geneset
1	8e−09	30 / 399	GUDJ_psoriasis down
2	3e−03	25 / 608	GUDJ_psoriasis up
3	4e−02	1 / 2	BCHETNIA_EBM down
4	9e−02	2 / 22	BCHETNIA_EBM up
5	6e−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	3e−19	38 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	4e−10	20 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
3	9e−09	14 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
4	7e−07	14 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	4e−06	13 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
6	7e−06	11 / 92	laffaire_hypermeth_LGG_vs_control
7	8e−06	10 / 77	Weller_LGG_gradeII−vs−III_DOWN
8	2e−05	9 / 69	cultured astroglia vs. in vivo astrocytes
9	3e−05	13 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
10	2e−04	4 / 13	Mukasa_UP_in_Astroglioma
11	3e−04	4 / 15	Mukasa_UP_in_GBM
12	3e−04	12 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
13	3e−04	10 / 119	GIEZELT_GBM_WT_up_VS_mut
14	7e−04	24 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
15	8e−04	9 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
16	1e−03	6 / 53	Donson−innate immunity−associated with LTS in HGA
17	1e−03	5 / 36	Colman_survival_associated
18	1e−03	7 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
19	2e−03	52 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
20	2e−03	11 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−48	70 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	2e−36	62 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
3	2e−34	70 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
4	4e−34	47 / 204	BOQUEST_STEM_CELL_DN
5	2e−32	61 / 413	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
6	3e−32	77 / 692	WONG_ADULT_TISSUE_STEM_MODULE
7	4e−31	60 / 418	SWEET_LUNG_CANCER_KRAS_DN
8	2e−30	87 / 945	NABA_MATRISOME
9	1e−26	28 / 78	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
10	1e−26	56 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
11	3e−26	58 / 478	LIM_MAMMARY_STEM_CELL_UP
12	8e−25	38 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
13	4e−24	58 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
14	7e−24	41 / 248	ONDER_CDH1_TARGETS_2_UP
15	7e−24	34 / 158	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
16	8e−24	41 / 249	BOQUEST_STEM_CELL_UP
17	9e−23	26 / 85	SANA_TNF_SIGNALING_DN
18	2e−22	23 / 62	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
19	1e−21	68 / 804	CUI_TCF21_TARGETS_2_DN
20	4e−21	39 / 261	NABA_CORE_MATRISOME

HM

Rank	p−value	#in/all	Geneset
1	4e−30	43 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	2e−27	40 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	7e−15	28 / 198	HALLMARK_HYPOXIA
4	1e−13	26 / 189	HALLMARK_KRAS_SIGNALING_UP
5	1e−10	19 / 132	HALLMARK_COAGULATION
6	2e−10	11 / 36	HALLMARK_ANGIOGENESIS
7	2e−09	18 / 140	HALLMARK_UV_RESPONSE_DN
8	5e−07	16 / 157	HALLMARK_APOPTOSIS
9	2e−06	9 / 52	HALLMARK_TGF_BETA_SIGNALING
10	8e−06	16 / 194	HALLMARK_INFLAMMATORY_RESPONSE
11	4e−05	15 / 197	HALLMARK_IL2_STAT5_SIGNALING
12	8e−05	14 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	2e−04	14 / 199	HALLMARK_ADIPOGENESIS
14	5e−04	13 / 195	HALLMARK_MYOGENESIS
15	6e−04	8 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
16	3e−03	10 / 155	HALLMARK_UV_RESPONSE_UP
17	4e−03	11 / 190	HALLMARK_APICAL_JUNCTION
18	1e−02	10 / 192	HALLMARK_COMPLEMENT
19	1e−02	10 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
20	2e−02	6 / 98	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	DUMEAUX_Smoking literature genes up
2	0.18	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.22	1 / 11	DUMEAUX_Women normal BMI literature genes up
4	0.30	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.33	3 / 91	DUMEAUX_Smoking enriched genes
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 / 7	DUMEAUX_Estrogen related in non 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	3e−29	27 / 59	LENZ_Stromal signature 2
2	5e−29	47 / 261	LENZ_Stromal signature 1
3	2e−24	46 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
4	2e−24	46 / 315	WIRTH_lymphoma937_spot E
5	1e−19	199 / 5039	HOPP_Repressed
6	3e−16	129 / 2838	HOPP_Poised_promoter
7	1e−11	21 / 145	WIRTH_lymphoma937_spot F
8	1e−11	21 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
9	2e−10	18 / 122	Subero_INT_hyper_meth
10	8e−08	16 / 138	Subero_DLBCL_hyper_meth
11	2e−07	13 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
12	8e−07	27 / 414	TARTE_Mature plasma cell signature
13	8e−06	11 / 94	Subero_T−ALL_hyper_meth
14	2e−04	8 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	2e−04	17 / 279	SPANG_IL21 DN
16	5e−04	7 / 62	Subero_mBL_hyper_meth
17	1e−03	7 / 75	Subero_FL_hyper_meth
18	2e−03	8 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
19	2e−03	4 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
20	2e−03	6 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN

MF

Rank	p−value	#in/all	Geneset
1	6e−11	20 / 142	heparin binding
2	9e−11	303 / 10693	protein binding
3	1e−10	13 / 53	extracellular matrix structural constituent
4	8e−09	15 / 102	integrin binding
5	6e−08	39 / 672	calcium ion binding
6	8e−08	11 / 60	collagen binding
7	8e−07	6 / 16	transforming growth factor beta binding
8	1e−06	7 / 26	fibronectin binding
9	2e−06	7 / 28	growth factor binding
10	3e−06	7 / 30	Wnt−protein binding
11	5e−06	6 / 21	hyaluronic acid binding
12	9e−06	6 / 23	extracellular matrix binding
13	9e−06	30 / 556	sequence−specific DNA binding
14	9e−06	16 / 196	transmembrane signaling receptor activity
15	1e−05	14 / 155	growth factor activity
16	1e−05	17 / 221	transcriptional activator activity, RNA polymerase II core promoter proximal re
17	7e−05	4 / 11	platelet−derived growth factor binding
18	2e−04	5 / 26	coreceptor activity
19	5e−04	18 / 333	RNA polymerase II core promoter proximal region sequence−specific DNA bi
20	6e−04	4 / 18	HMG box domain binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	10 / 104	hsa−miR−600
2	2e−03	11 / 175	hsa−miR−369−3p
3	2e−03	9 / 125	hsa−miR−380
4	2e−03	12 / 205	hsa−miR−181c
5	3e−03	10 / 157	hsa−miR−429
6	4e−03	13 / 246	hsa−miR−1252
7	7e−03	17 / 391	hsa−miR−454
8	8e−03	19 / 462	hsa−miR−130b
9	8e−03	24 / 631	hsa−miR−20a
10	9e−03	9 / 158	hsa−miR−200c
11	1e−02	14 / 307	hsa−miR−34c−5p
12	1e−02	4 / 38	hsa−miR−1269
13	1e−02	19 / 471	hsa−miR−130a
14	1e−02	17 / 407	hsa−miR−301b
15	1e−02	9 / 162	hsa−miR−200b
16	1e−02	9 / 165	hsa−miR−802
17	1e−02	17 / 416	hsa−miR−519c−3p
18	2e−02	7 / 117	hsa−miR−875−3p
19	2e−02	20 / 536	hsa−miR−106b
20	2e−02	2 / 10	hsa−miR−887

Pathw Act

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 14	GUSTAFSON_PI3K_UP
2	4e−02	2 / 14	BENTINK_src.10
3	2e−01	1 / 10	BENTINK_ras.4
4	3e−01	1 / 13	BENTINK_e2f3.2
5	3e−01	1 / 14	BENTINK_e2f3.1
6	3e−01	1 / 14	BENTINK_myc.1
7	1e+00	0 / 15	GUSTAFSON_PI3K_DN
8	1e+00	0 / 12	BENTINK_ras.1
9	1e+00	0 / 15	BENTINK_ras.6
10	1e+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−08	76 / 1798	HEBENSTREIT_low expression TF
2	3e−01	1 / 16	NOWICK_TF
3	4e−01	82 / 3511	ICGC_Rad21_targets
4	4e−01	1 / 20	MYC_Metabolism UP
5	8e−01	1 / 66	MYC_Targets UP
6	8e−01	58 / 2827	ICGC_Bcl3_targets
7	8e−01	29 / 1523	ICGC_P300_targets
8	9e−01	45 / 2401	ICGC_Bcl11_targets
9	9e−01	39 / 2149	ICGC_Mef2_targets
10	1e+00	21 / 1294	KIM_MYC targets
11	1e+00	25 / 1506	ICGC_Usf1_targets
12	1e+00	37 / 2133	ICGC_Cebpbsc150_targets
13	1e+00	24 / 1472	ICGC_NrsfPcr1_targets
14	1e+00	10 / 731	ICGC_SrfPcr2_targets
15	1e+00	60 / 3305	ICGC_BatfPcr1_targets
16	1e+00	31 / 1867	HEBENSTREIT_high expression TF
17	1e+00	7 / 619	ICGC_RxraPcr1_targets
18	1e+00	9 / 745	ICGC_NrsfPcr2_targets
19	1e+00	51 / 3177	ICGC_Irf4_targets
20	1e+00	90 / 5135	ICGC_Ebfsc137065_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	2e−08	12 / 64	VAQUERIZAS_Lung
2	3e−07	8 / 31	VAQUERIZAS_Fetal lung
3	9e−07	7 / 25	VAQUERIZAS_Adrenal cortex
4	1e−05	6 / 24	VAQUERIZAS_Trachea
5	5e−04	6 / 45	VAQUERIZAS_Placenta
6	1e−03	3 / 10	VAQUERIZAS_Skeletal.muscle.psoas
7	2e−03	5 / 42	VAQUERIZAS_Thyroid
8	4e−03	4 / 30	VAQUERIZAS_Smooth muscle
9	5e−03	5 / 49	VAQUERIZAS_Uterus
10	5e−03	3 / 16	VAQUERIZAS_Ovary
11	6e−03	3 / 17	VAQUERIZAS_Salivary gland
12	9e−03	4 / 37	VAQUERIZAS_Prostate
13	1e−02	2 / 7	VAQUERIZAS_Appendix
14	1e−02	2 / 8	VAQUERIZAS_Tongue
15	5e−02	2 / 17	VAQUERIZAS_Adrenal gland
16	2e−01	2 / 41	VAQUERIZAS_Fetal brain
17	3e−01	5 / 155	VAQUERIZAS_General
18	3e−01	2 / 46	VAQUERIZAS_Whole brain
19	3e−01	1 / 16	VAQUERIZAS_Fetal thyroid
20	3e−01	1 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	6e−06	5 / 13	WIRTH_Sec. lymphoid organs
2	8e−04	15 / 259	PALMER_Granulocytes signature up
3	4e−02	2 / 15	WIRTH_Telencephalon
4	1e−01	2 / 30	PALMER_Lymphocytes signature up
5	2e−01	5 / 140	PALMER_T−Cell signature up
6	2e−01	1 / 12	WIRTH_Lymphocytes
7	3e−01	1 / 13	WIRTH_Prim. lymphoid organs
8	3e−01	1 / 16	WIRTH_Hippocampus
9	3e−01	6 / 208	PALMER_B−Cell signature up
10	7e−01	1 / 54	WIRTH_Pancreas
11	7e−01	2 / 115	WIRTH_Liver
12	8e−01	2 / 141	WIRTH_Muscle
13	1e+00	2 / 427	WIRTH_Immune system
14	1e+00	2 / 476	WIRTH_Nervous System
15	1e+00	0 / 6	WIRTH_Pituitary gland
16	1e+00	0 / 14	WIRTH_B−cells
17	1e+00	0 / 12	WIRTH_Tonsil
18	1e+00	0 / 14	WIRTH_Thymus
19	1e+00	0 / 14	WIRTH_Bone marrow
20	1e+00	0 / 13	WIRTH_Globus pallidus

Toxic

Rank	p−value	#in/all	Geneset
1	1e−05	158 / 5285	LU_BPDE 0.005 DN
2	1e+00	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	

K−Means Clusters

Spot Summary: T

metagenes = 143
genes = 1421

<r> metagenes = 0.69

beta: r2= 0.01 / log p= −0.22

samples with spot = 0 (0 %)

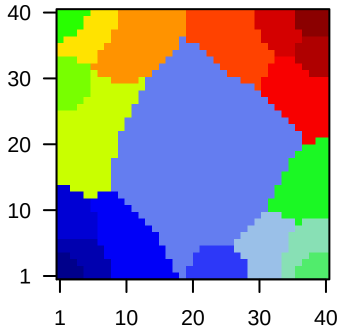
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000000	0.5	−0.11	0.24	RAB27A	RAB27A, member RAS oncogene family [Source:HGNC Sym
2	ENSG000000	0.33	−0.04	0.27	SELE	selectin E [Source:HGNC Symbol;Acc:HGNC:10718]
3	ENSG000002	0.3	−0.11	0.81	RGL2	ral guanine nucleotide dissociation stimulator−like 2 [Source:
4	ENSG000001	0.27	−0.1	0.14	PARP9	poly (ADP−ribose) polymerase family, member 9 [Source:HG
5	ENSG000001	0.25	−0.13	0.52	TRAFD1	TRAF−type zinc finger domain containing 1 [Source:HGNC S
6	ENSG000001	0.25	−0.14	0.45	FAM193B	family with sequence similarity 193, member B [Source:HGN
7	ENSG000001	0.24	−0.09	0.51	FOLR2	folate receptor 2 (fetal) [Source:HGNC Symbol;Acc:HGNC:37
8	ENSG000001	0.24	−0.1	0.5	RALGDS	ral guanine nucleotide dissociation stimulator [Source:HGNC
9	ENSG000001	0.23	−0.09	0.83	PPP1R2	protein phosphatase 1, regulatory (inhibitor) subunit 2 [Sourc
10	ENSG000001	0.23	−0.15	0.5	RAP1B	RAP1B, member of RAS oncogene family [Source:HGNC Sy
11	ENSG000001	0.23	−0.11	0.43	MAN2C1	mannosidase, alpha, class 2C, member 1 [Source:HGNC Sy
12	ENSG000001	0.22	−0.05	0.41	ANO1	anoctamin 1, calcium activated chloride channel [Source:HG
13	ENSG000001	0.22	−0.09	0.76	ARID5B	AT rich interactive domain 5B (MRF1−like) [Source:HGNC Sy
14	ENSG000001	0.22	−0.08	0.53	GPX7	glutathione peroxidase 7 [Source:HGNC Symbol;Acc:HGNC:
15	ENSG000000	0.22	−0.06	0.58	NTN4	netrin 4 [Source:HGNC Symbol;Acc:HGNC:13658]
16	ENSG000001	0.21	−0.07	0.75	TMEM204	transmembrane protein 204 [Source:HGNC Symbol;Acc:HGN
17	ENSG000002	0.21	−0.05	0.68		
18	ENSG000001	0.21	−0.11	0.75	PTEN	phosphatase and tensin homolog [Source:HGNC Symbol;Acc
19	ENSG000001	0.21	−0.07	0.47	PCGF3	polycomb group ring finger 3 [Source:HGNC Symbol;Acc:HG
20	ENSG000000	0.21	−0.03	0.46	SUSD2	sushi domain containing 2 [Source:HGNC Symbol;Acc:HGNC

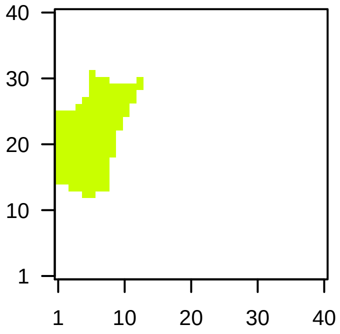
Geneset Overrepresentation

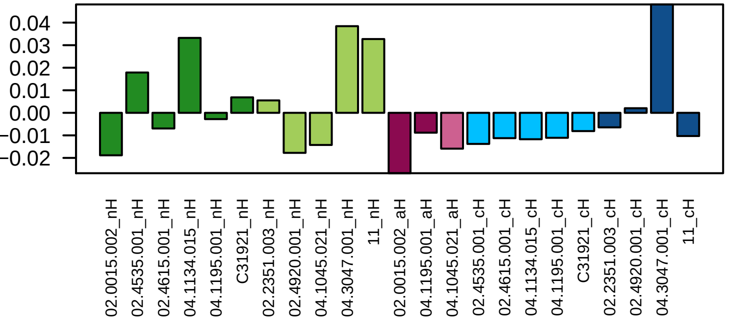
Rank	p−value	#in/all	Geneset	
1	6e−89	815 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
2	3e−64	1048 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
3	2e−60	1042 / 10278	Brain	Overlap_fetal_midbrain_ReprPCWk
4	5e−52	960 / 9390	Colon	TxWk_Colon
5	9e−51	1128 / 11968	Colon	TssWk_Colon
6	8e−49	812 / 7491	Lympl	HOPP_Txn_elongation
7	4e−48	955 / 9470	Colon	Quies3_Colon
8	1e−44	1037 / 10800	Brain	Overlap_fetal_midbrain_Quies
9	1e−43	974 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
10	5e−43	973 / 9930	Colon	Tx_Colon
11	4e−37	842 / 8358	Lympl	HOPP_Active_promoter
12	1e−35	170 / 834	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
13	5e−31	611 / 5643	Lympl	HOPP_Txn_transition
14	4e−28	963 / 10475	Colon	TssA_Colon
15	1e−26	107 / 471	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
16	1e−24	251 / 1807	BP	transcription, DNA−templated
17	3e−24	780 / 8147	Lympl	HOPP_Weak_promoter
18	7e−21	109 / 568	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
19	5e−19	716 / 7592	Lympl	HOPP_Strong_enhancer
20	6e−19	623 / 6389	Lympl	HOPP_Weak_txn
21	6e−18	85 / 420	GSEA	SHEN_SMARCA2_TARGETS_UP
22	3e−17	117 / 705	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
23	1e−16	65 / 286	GSEA	GABRIELY_MIR21_TARGETS
24	9e−16	131 / 866	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
25	1e−15	124 / 804	GSEA	CUI_TCF21_TARGETS_2_DN
26	2e−15	162 / 1178	Colon	ZNF_Colon
27	4e−15	89 / 500	Lympl	WIRTH_lymphoma937_spot J
28	5e−15	923 / 10693	MF	protein binding
29	5e−15	121 / 791	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
30	1e−14	483 / 4879	Colon	Quies1_Colon
31	1e−14	70 / 352	miRN	hsa−miR−142−5p
32	3e−14	440 / 4379	Colon	TssD1_Colon
33	3e−14	64 / 311	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
34	3e−14	85 / 484	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
35	2e−13	71 / 381	miRN	hsa−miR−144
36	3e−13	93 / 573	miRN	hsa−miR−93
37	6e−13	88 / 536	miRN	hsa−miR−106b
38	6e−13	280 / 2554	CC	nucleoplasm
39	7e−13	213 / 1803	MF	DNA binding
40	7e−13	289 / 2658	Lympl	HOPP_Repetitive

Overview Map

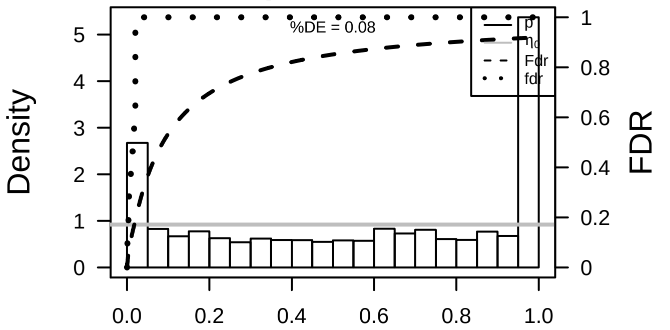


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	12 / 144	HORVATH_aging_genes meth UP
2	0.4	10 / 123	HORVATH_aging_genes meth DOWN
3	0.9	2 / 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	251 / 1807	transcription, DNA−templated
2	3e−11	207 / 1808	regulation of transcription, DNA−templated
3	3e−07	64 / 451	positive regulation of GTPase activity
4	6e−07	13 / 35	histone acetylation
5	1e−06	16 / 54	phosphatidylinositol biosynthetic process
6	3e−06	19 / 78	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
7	3e−06	35 / 208	chromatin organization
8	2e−05	50 / 366	protein ubiquitination
9	6e−05	99 / 913	positive regulation of transcription from RNA polymerase II promoter
10	7e−05	8 / 21	phosphatidylinositol dephosphorylation
11	1e−04	6 / 12	regulation of cell motility
12	1e−04	71 / 617	protein phosphorylation
13	2e−04	14 / 64	Golgi organization
14	2e−04	8 / 24	nonmotile primary cilium assembly
15	3e−04	7 / 19	protein targeting to Golgi
16	3e−04	19 / 107	vascular endothelial growth factor receptor signaling pathway
17	5e−04	28 / 194	epidermal growth factor receptor signaling pathway
18	5e−04	61 / 539	small GTPase mediated signal transduction
19	5e−04	24 / 158	Notch signaling pathway
20	7e−04	5 / 11	regulation of protein kinase B signaling

Brain

Rank	p−value	#in/all	Geneset
1	6e−89	815 / 6320	Overlap_fetal_midbrain_HetRpts
2	3e−64	1048 / 10239	Overlap_fetal_midbrain_ReprPC
3	2e−60	1042 / 10278	Overlap_fetal_midbrain_ReprPCWk
4	1e−44	1037 / 10800	Overlap_fetal_midbrain_Quies
5	1e−43	974 / 9923	Overlap_fetal_midbrain_K9K27me3
6	6e−12	97 / 641	Mid_Frontal_Lobe_EnhP
7	3e−10	141 / 1137	Fetal_Enh
8	1e−09	98 / 712	Overlap_fetal_midbrain_EnhP
9	6e−09	115 / 910	Fetal_EnhG
10	8e−09	140 / 1182	Fetal_EnhP
11	4e−07	318 / 3370	Mid_Frontal_Lobe_ZNF
12	2e−05	96 / 855	Overlap_fetal_midbrain_ZNF
13	8e−03	117 / 1279	Overlap_fetal_midbrain_Enh
14	1e−02	110 / 1210	Fetal_TssP
15	2e−02	36 / 342	Fetal_Het
16	8e−02	113 / 1356	Fetal_K9K27me3
17	2e−01	35 / 400	Fetal_ZNF
18	2e−01	18 / 191	Overlap_fetal_midbrain_Het
19	2e−01	217 / 2820	Mid_Frontal_Lobe_HetRpts
20	2e−01	86 / 1084	Overlap_fetal_midbrain_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	7 / 24	PanCan_Notch_geneset_nanostring
2	0.001	15 / 86	PanCan_JAK−ST_geneset_nanostring
3	0.004	18 / 123	PanCan_Driver_Gene_geneset_nanostring
4	0.006	25 / 198	PanCan_PI3K_geneset_nanostring
5	0.025	7 / 40	PanCan_HK_geneset_nanostring
6	0.052	16 / 140	PanCan_RAS_geneset_nanostring
7	0.059	10 / 78	PanCan_Wnt_geneset_nanostring
8	0.069	52 / 574	Lembcke_Colonic Inflammation
9	0.078	7 / 51	PanCan_TGF−B_geneset_nanostring
10	0.108	3 / 16	GENTLES_modul14
11	0.126	14 / 136	PanCan_CC+Apop_geneset_nanostring
12	0.149	8 / 71	SHAUGHNESSY_MM high risk
13	0.167	1 / 16	LIU_PROSTATE_CANCER_DN
14	0.217	3 / 22	PanCan_ChromMod_geneset_nanostring
15	0.291	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	0.303	2 / 15	GENTLES_modul13
17	0.442	12 / 152	PanCan_MAPK_geneset_nanostring
18	0.497	1 / 9	WANG_ER_DN
19	0.535	1 / 15	LIU_BREAST_CANCER
20	0.601	23 / 324	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	6e−13	280 / 2554	nucleoplasm
2	1e−12	490 / 5101	nucleus
3	4e−06	454 / 5185	cytoplasm
4	4e−05	26 / 151	lamellipodium
5	2e−04	17 / 88	PML body
6	3e−04	91 / 864	Golgi apparatus
7	6e−04	10 / 41	chromosome, telomeric region
8	1e−03	7 / 23	histone acetyltransferase complex
9	2e−03	19 / 125	receptor complex
10	2e−03	14 / 81	ubiquitin ligase complex
11	3e−03	7 / 27	Cul3−RING ubiquitin ligase complex
12	3e−03	21 / 150	nuclear chromatin
13	4e−03	30 / 246	endosome
14	5e−03	145 / 1604	intracellular
15	5e−03	17 / 116	late endosome
16	6e−03	5 / 17	pericentriolar material
17	6e−03	52 / 497	Golgi membrane
18	7e−03	23 / 180	nuclear speck
19	9e−03	4 / 12	phosphatidylinositol 3−kinase complex
20	1e−02	9 / 51	transcriptional repressor complex

Chr

Rank	p−value	#in/all	Geneset
1	7e−05	110 / 1043	Chr 3
2	2e−04	42 / 318	Chr 13
3	3e−03	61 / 582	Chr 15
4	7e−03	83 / 862	Chr 5
5	4e−02	21 / 191	Chr 21
6	4e−02	65 / 715	Chr 10
7	1e−01	57 / 651	Chr 8
8	2e−01	97 / 1228	Chr 2
9	3e−01	48 / 613	Chr 14
10	4e−01	144 / 1920	Chr 1
11	5e−01	76 / 1017	Chr 12
12	6e−01	54 / 745	Chr 9
13	8e−01	50 / 746	Chr X
14	8e−01	49 / 735	Chr 4
15	8e−01	17 / 272	Chr 18
16	9e−01	64 / 976	Chr 6
17	9e−01	55 / 847	Chr 16
18	9e−01	55 / 859	Chr 7
19	9e−01	30 / 522	Chr 20
20	1e+00	64 / 1083	Chr 17

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−52	960 / 9390	TxWk_Colon
2	9e−51	1128 / 11968	TssWk_Colon
3	4e−48	955 / 9470	Quies3_Colon
4	5e−43	973 / 9930	Tx_Colon
5	4e−28	963 / 10475	TssA_Colon
6	2e−15	162 / 1178	ZNF_Colon
7	1e−14	483 / 4879	Quies1_Colon
8	3e−14	440 / 4379	TssD1_Colon
9	3e−07	396 / 4327	EnhWk2_Colon
10	7e−05	64 / 532	K9acLow_Colon
11	3e−04	7 / 19	Vilar_hypermutated−in−CRC
12	8e−04	4 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
13	1e−03	920 / 11791	Enh_Colon
14	4e−03	158 / 1753	Het_Colon
15	1e−02	15 / 105	Marisa_CRC−cluster−d
16	1e−02	471 / 5889	EnhWk1_Colon
17	1e−02	5 / 20	Vilar_mutated−in−CRC−CampP
18	2e−02	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
19	2e−02	114 / 1281	HetRpts_Colon
20	2e−02	6 / 30	Marisa_CRC−cluster−c

Disease

Rank	p−value	#in/all	Geneset
1	0.7	27 / 399	GUDJ_psoriasis down
2	0.8	1 / 22	BCHETNIA_EBM up
3	1.0	20 / 608	GUDJ_psoriasis 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	1e−09	56 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	2e−06	102 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−05	215 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	1e−04	15 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	1e−04	187 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	2e−03	41 / 344	Up
7	2e−03	14 / 81	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	6e−03	4 / 11	KIM amplified & overexpressed in LTS
9	7e−03	13 / 83	GIEZELT_GBM_WT_down_VS_mut
10	3e−02	12 / 90	Weller_LGG_A_vs_O_DOWN
11	6e−02	11 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	7e−02	3 / 13	VERHAAK_Brain
13	7e−02	5 / 31	KIM prognostic signature LTS vs. STS
14	1e−01	7 / 56	mature astrocytes
15	2e−01	10 / 103	GIEZELT_GBM_STS_down_VS_LTS
16	2e−01	35 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
17	3e−01	6 / 58	OL vs. MOG− OL
18	3e−01	6 / 61	Christensen_hypermethylated_in_primary_glioblastoma
19	3e−01	6 / 61	in vivo astrocytes vs. cultured astroglia
20	3e−01	26 / 316	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−35	170 / 834	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	1e−26	107 / 471	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
3	7e−21	109 / 568	HAMAI_APOPTOSIS_VIA_TRAIL_UP
4	6e−18	85 / 420	SHEN_SMARCA2_TARGETS_UP
5	3e−17	117 / 705	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
6	1e−16	65 / 286	GABRIELY_MIR21_TARGETS
7	9e−16	131 / 866	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
8	1e−15	124 / 804	CUI_TCF21_TARGETS_2_DN
9	5e−15	121 / 791	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
10	3e−14	64 / 311	DAZARD_RESPONSE_TO_UV_NHEK_DN
11	3e−12	69 / 383	OSMAN_BLADDER_CANCER_UP
12	1e−11	106 / 736	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
13	6e−10	193 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
14	1e−09	104 / 773	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
15	9e−09	177 / 1591	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
16	1e−08	205 / 1914	PILON_KLF1_TARGETS_DN
17	3e−08	25 / 99	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER
18	4e−08	40 / 215	CHEN_HOXA5_TARGETS_9HR_UP
19	5e−08	90 / 685	SCHLOSSER_SERUM_RESPONSE_DN
20	8e−08	71 / 503	MILI_PSEUDOPODIA_HAPTOTAXIS_UP

HM

Rank	p−value	#in/all	Geneset
1	8e−07	35 / 196	HALLMARK_MITOTIC_SPINDLE
2	1e−02	9 / 52	HALLMARK_TGF_BETA_SIGNALING
3	2e−02	22 / 190	HALLMARK_APICAL_JUNCTION
4	3e−02	17 / 140	HALLMARK_UV_RESPONSE_DN
5	8e−02	11 / 94	HALLMARK_PROTEIN_SECRETION
6	2e−01	18 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	2e−01	10 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	3e−01	9 / 98	HALLMARK_ANDROGEN_RESPONSE
9	3e−01	4 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
10	4e−01	3 / 30	HALLMARK_NOTCH_SIGNALING
11	5e−01	10 / 128	HALLMARK_SPERMATOGENESIS
12	5e−01	12 / 155	HALLMARK_UV_RESPONSE_UP
13	6e−01	14 / 196	HALLMARK_G2M_CHECKPOINT
14	6e−01	14 / 196	HALLMARK_P53_PATHWAY
15	6e−01	14 / 198	HALLMARK_HYPOXIA
16	6e−01	10 / 146	HALLMARK_DNA_REPAIR
17	6e−01	6 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
18	7e−01	13 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	7e−01	13 / 192	HALLMARK_COMPLEMENT
20	7e−01	13 / 193	HALLMARK_HEME_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.009	7 / 33	DUMEAUX_Fasting enriched genes
2	0.414	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.507	7 / 91	DUMEAUX_Smoking enriched genes
4	0.568	1 / 11	DUMEAUX_Smoking literature genes up
5	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.000	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.000	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	8e−49	812 / 7491	HOPP_Txn_elongation
2	4e−37	842 / 8358	HOPP_Active_promoter
3	5e−31	611 / 5643	HOPP_Txn_transition
4	3e−24	780 / 8147	HOPP_Weak_promoter
5	5e−19	716 / 7592	HOPP_Strong_enhancer
6	6e−19	623 / 6389	HOPP_Weak_txn
7	4e−15	89 / 500	WIRTH_lymphoma937_spot J
8	3e−14	85 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
9	7e−13	289 / 2658	HOPP_Repetitive
10	7e−11	611 / 6784	HOPP_Weak_enhancer
11	1e−06	50 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
12	4e−06	50 / 347	WIRTH_lymphoma937_spot H
13	7e−06	130 / 1215	SPANG_BCR DN
14	1e−04	134 / 1333	SPANG_BCR UP
15	1e−03	52 / 458	WIRTH_lymphoma937_spot I
16	2e−03	50 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
17	5e−03	33 / 279	SPANG_IL21 DN
18	1e−02	34 / 304	ZHANG_DLBCL mutated
19	1e−02	48 / 466	SPANG_CD40 6hrs DN
20	2e−02	14 / 105	ROSOLOWSKI_blue total

MF

Rank	p−value	#in/all	Geneset
1	5e−15	923 / 10693	protein binding
2	7e−13	213 / 1803	DNA binding
3	2e−08	215 / 2040	metal ion binding
4	6e−08	132 / 1134	nucleic acid binding
5	2e−07	133 / 1164	zinc ion binding
6	2e−07	14 / 38	histone acetyltransferase activity
7	4e−07	46 / 286	ligase activity
8	5e−07	43 / 262	ubiquitin−protein transferase activity
9	9e−07	51 / 341	binding
10	1e−05	107 / 962	transcription factor activity, sequence−specific DNA binding
11	3e−05	21 / 108	guanyl−nucleotide exchange factor activity
12	7e−05	18 / 89	histone deacetylase binding
13	4e−04	38 / 291	transcription factor binding
14	4e−04	33 / 241	GTPase activator activity
15	5e−04	60 / 527	protein kinase activity
16	6e−04	15 / 79	phosphatidylinositol binding
17	6e−04	29 / 207	RNA polymerase II regulatory region sequence−specific DNA binding
18	7e−04	11 / 49	SNARE binding
19	1e−03	7 / 23	bHLH transcription factor binding
20	1e−03	12 / 61	transcription cofactor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−14	70 / 352	hsa−miR−142−5p
2	2e−13	71 / 381	hsa−miR−144
3	3e−13	93 / 573	hsa−miR−93
4	6e−13	88 / 536	hsa−miR−106b
5	1e−12	90 / 562	hsa−miR−17
6	7e−12	75 / 442	hsa−miR−548n
7	1e−11	91 / 591	hsa−miR−20b
8	3e−11	94 / 631	hsa−miR−20a
9	7e−11	59 / 324	hsa−miR−559
10	8e−11	68 / 403	hsa−miR−519a
11	2e−10	66 / 391	hsa−miR−454
12	3e−10	82 / 542	hsa−miR−106a
13	3e−10	67 / 407	hsa−miR−301b
14	4e−10	75 / 480	hsa−miR−301a
15	7e−10	63 / 378	hsa−miR−519b−3p
16	3e−09	69 / 446	hsa−miR−19b
17	4e−09	50 / 280	hsa−miR−548h
18	5e−09	69 / 452	hsa−miR−19a
19	5e−09	32 / 139	hsa−miR−155
20	6e−09	67 / 435	hsa−miR−372

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	4 / 15	GUSTAFSON_PI3K_DN
2	0.22	2 / 12	BENTINK_ras.1
3	0.25	2 / 13	BENTINK_e2f3.2
4	0.28	2 / 14	BENTINK_src.10
5	0.30	2 / 15	BENTINK_ras.6
6	0.53	1 / 10	BENTINK_ras.4
7	0.66	1 / 14	GUSTAFSON_PI3K_UP
8	0.66	1 / 14	BENTINK_e2f3.1
9	0.66	1 / 14	BENTINK_myc.1
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−09	474 / 5173	ICGC_Taf1_targets
2	7e−08	169 / 1547	ICGC_Ets1_targets
3	8e−07	404 / 4470	ICGC_Creb1_targets
4	4e−06	542 / 6324	ICGC_Yy1_targets
5	5e−06	156 / 1503	ICGC_Six5_targets
6	1e−05	403 / 4566	ICGC_Egr1_targets
7	1e−05	207 / 2133	ICGC_Cebpbsc150_targets
8	2e−05	432 / 4969	ICGC_Atf2_targets
9	3e−05	252 / 2719	ICGC_Pbx3_targets
10	7e−05	428 / 4987	ICGC_Bclaf101388_targets
11	1e−04	470 / 5552	ICGC_Pol24_targets
12	1e−04	466 / 5512	ICGC_Nficsc81335_targets
13	1e−04	217 / 2342	ICGC_GabpPcr2_targets
14	1e−04	461 / 5453	ICGC_Foxm1_targets
15	2e−04	200 / 2149	ICGC_Mef2_targets
16	3e−04	453 / 5393	ICGC_Sp1_targets
17	3e−04	467 / 5578	ICGC_Stat5_targets
18	4e−04	462 / 5526	ICGC_Pmlsc71910_targets
19	5e−04	289 / 3305	ICGC_BatfPcr1_targets
20	7e−04	360 / 4230	ICGC_Nfatc1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	7e−06	14 / 49	VAQUERIZAS_Uterus
2	2e−03	22 / 155	VAQUERIZAS_General
3	2e−02	6 / 30	VAQUERIZAS_Smooth muscle
4	2e−02	10 / 67	VAQUERIZAS_Whole blood
5	3e−02	7 / 41	VAQUERIZAS_Fetal brain
6	1e−01	3 / 17	VAQUERIZAS_Adrenal gland
7	2e−01	5 / 41	VAQUERIZAS_Testis
8	2e−01	4 / 31	VAQUERIZAS_Lymph node
9	2e−01	5 / 42	VAQUERIZAS_Thyroid
10	3e−01	3 / 25	VAQUERIZAS_Spinal cord
11	3e−01	3 / 25	VAQUERIZAS_Adrenal cortex
12	3e−01	2 / 16	VAQUERIZAS_Fetal liver
13	3e−01	2 / 16	VAQUERIZAS_Ovary
14	3e−01	2 / 16	VAQUERIZAS_Fetal thyroid
15	4e−01	4 / 42	VAQUERIZAS_Thymus
16	4e−01	1 / 7	VAQUERIZAS_Appendix
17	4e−01	4 / 46	VAQUERIZAS_Whole brain
18	4e−01	3 / 33	VAQUERIZAS_Liver
19	5e−01	2 / 23	VAQUERIZAS_Pituitary
20	5e−01	3 / 37	VAQUERIZAS_Prostate

Tissue

Rank	p−value	#in/all	Geneset
1	0.02	4 / 15	WIRTH_Cerebellum
2	0.07	3 / 13	PALMER_CD8+ T−Cell signature up
3	0.23	13 / 140	PALMER_T−Cell signature up
4	0.25	2 / 13	WIRTH_Cortex cerebri
5	0.36	17 / 208	PALMER_B−Cell signature up
6	0.39	37 / 476	WIRTH_Nervous System
7	0.63	1 / 13	WIRTH_Globus pallidus
8	0.66	1 / 14	WIRTH_Thymus
9	0.66	1 / 14	WIRTH_Thalamus
10	0.66	1 / 14	WIRTH_Thyroid gland
11	0.71	1 / 16	WIRTH_Hippocampus
12	0.87	2 / 47	WIRTH_Placenta
13	0.90	1 / 30	PALMER_Lymphocytes signature up
14	0.91	14 / 259	PALMER_Granulocytes signature up
15	0.96	23 / 427	WIRTH_Immune system
16	0.99	4 / 141	WIRTH_Muscle
17	1.00	1 / 115	WIRTH_Liver
18	1.00	2 / 202	WIRTH_Testis
19	1.00	0 / 6	WIRTH_Pituitary gland
20	1.00	0 / 54	WIRTH_Pancreas

Toxic

Rank	p−value	#in/all	Geneset
1	0.008	122 / 1343	LU_BPDE 1h DN
2	0.620	384 / 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	