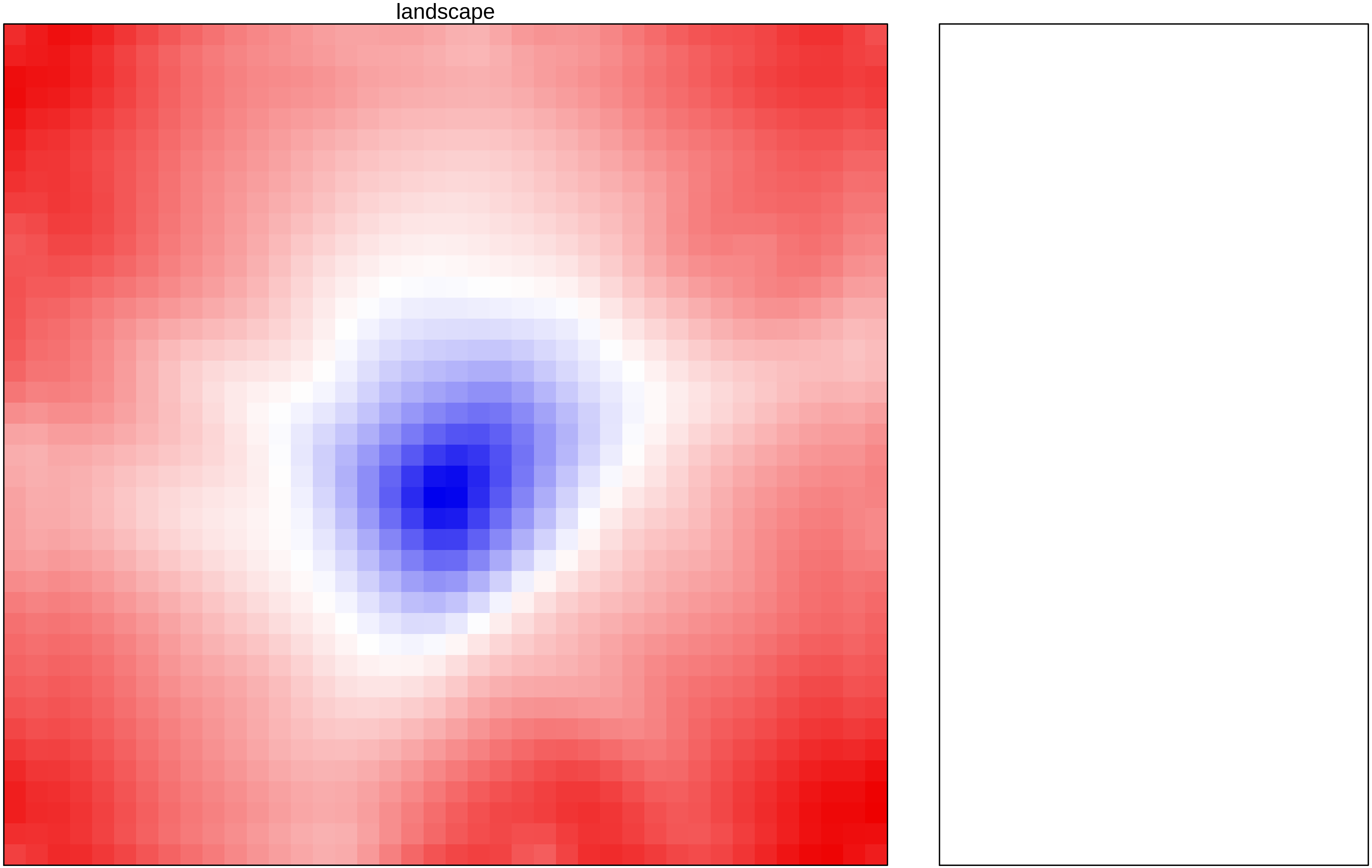
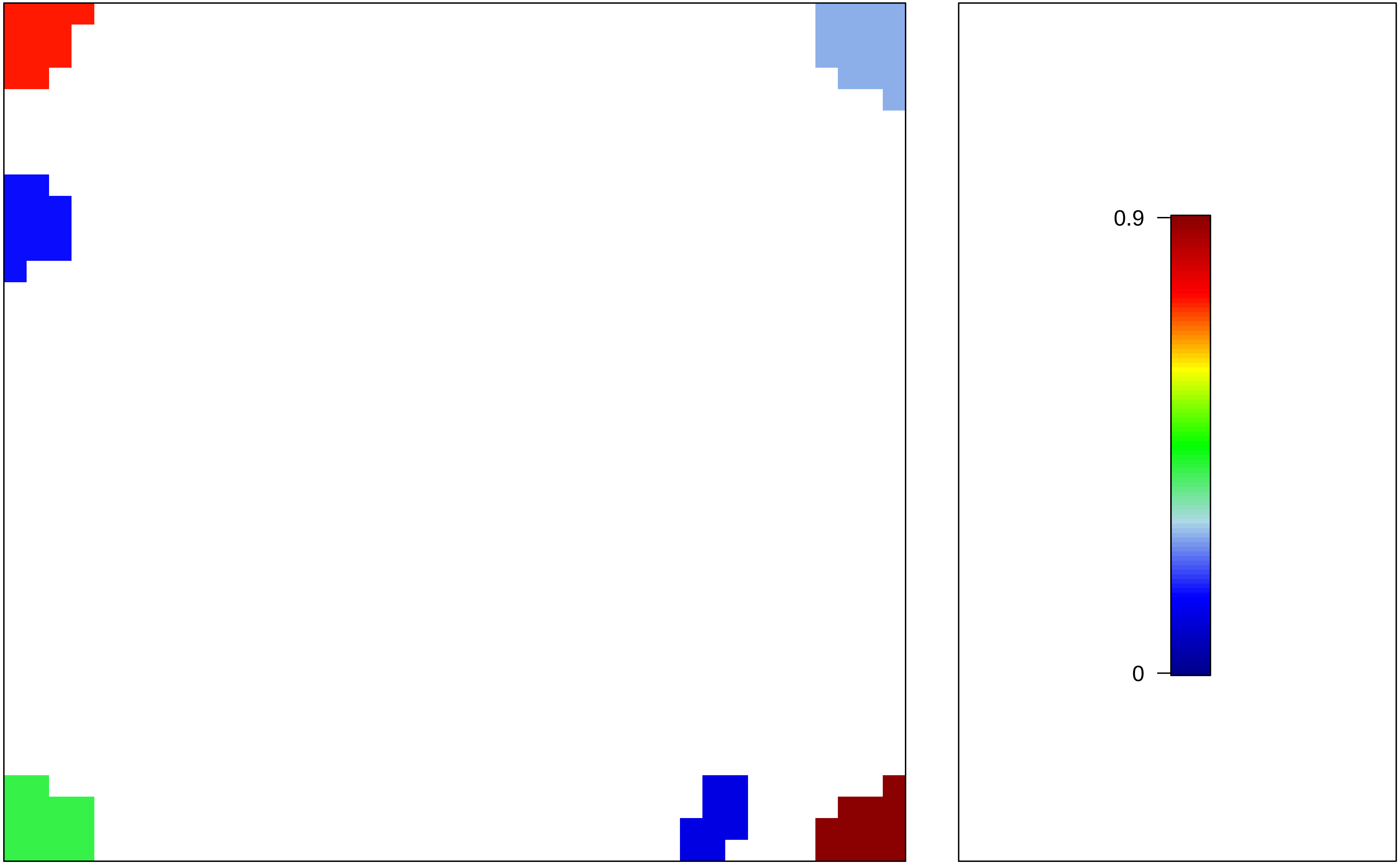
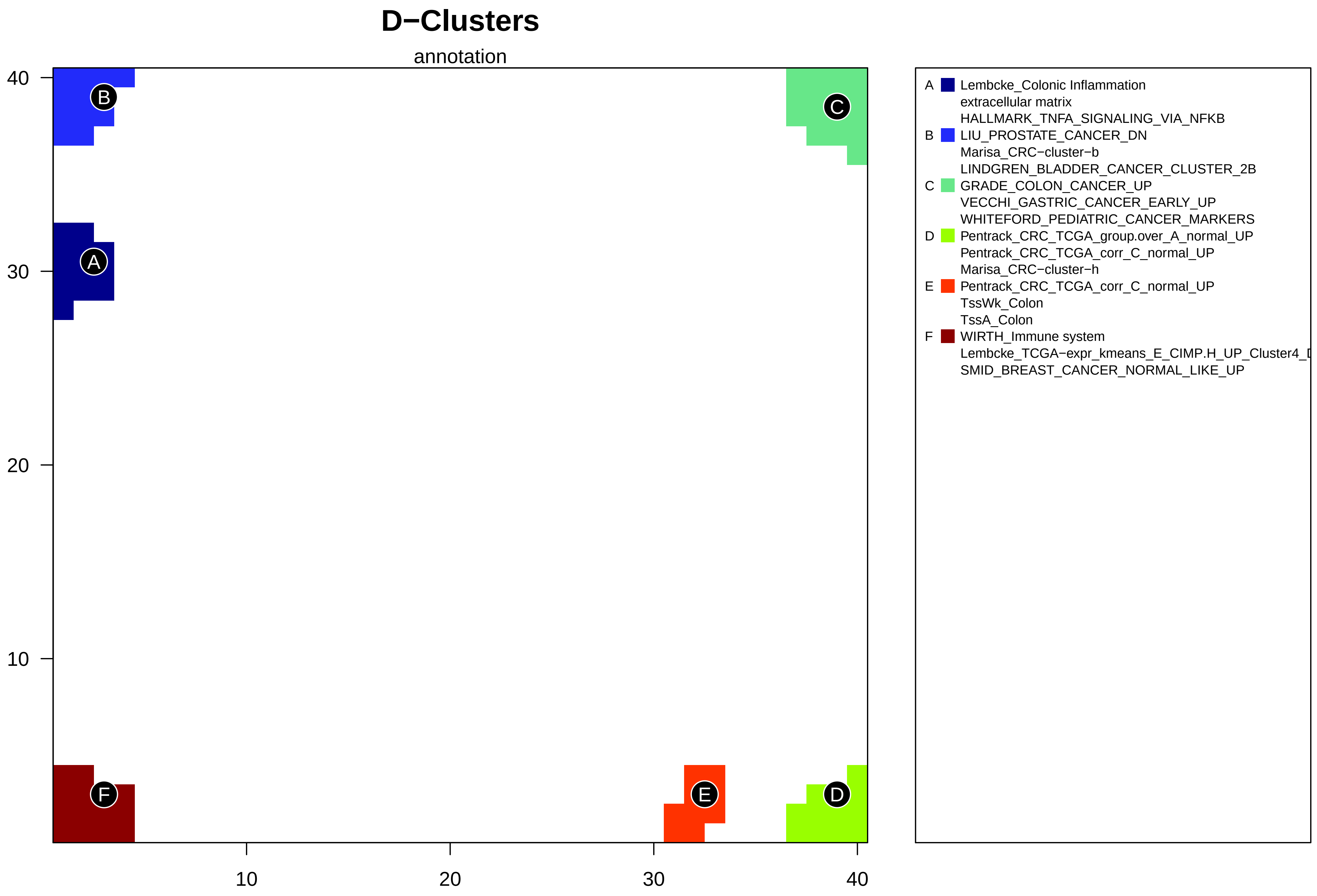
D−Clusters

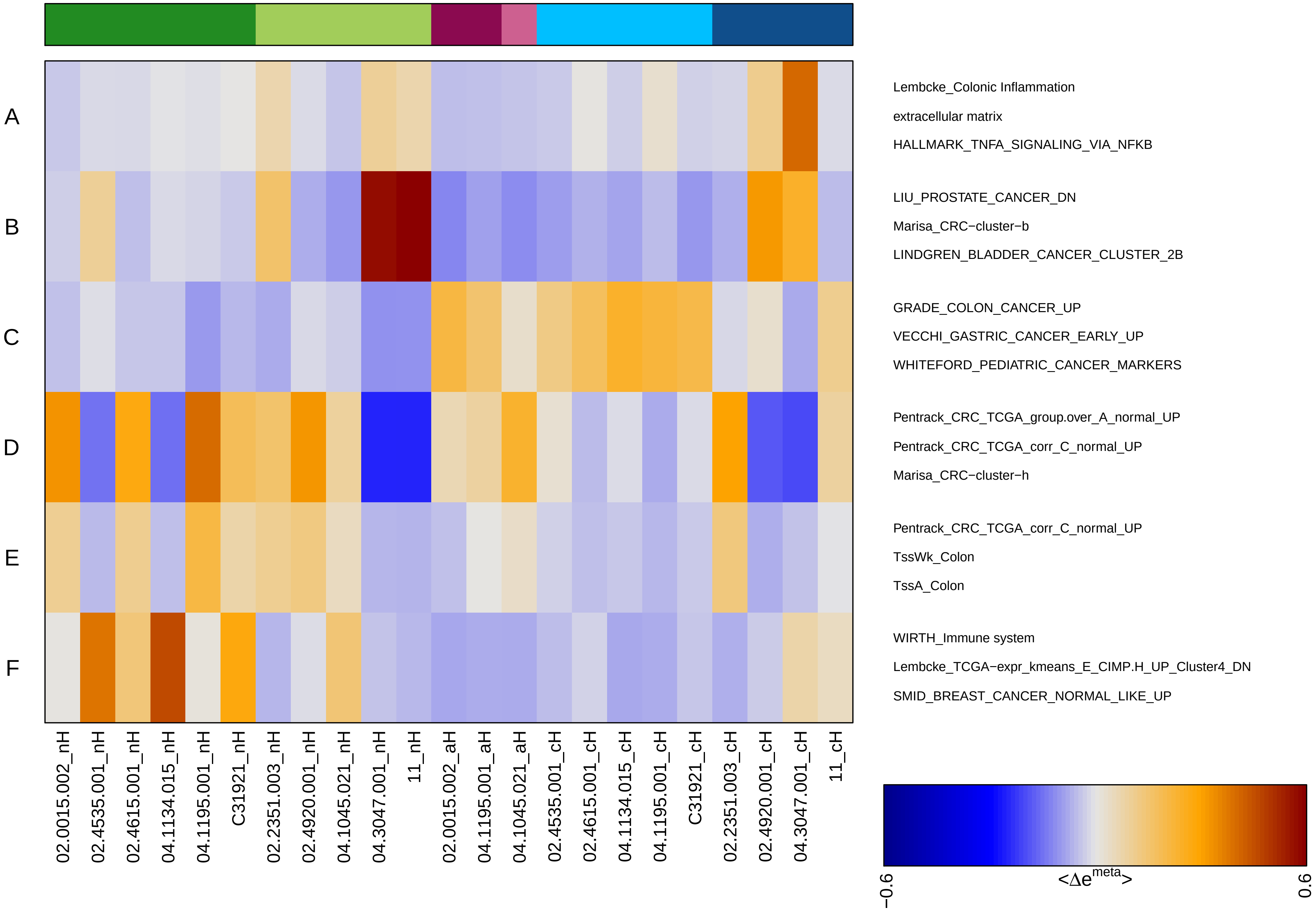


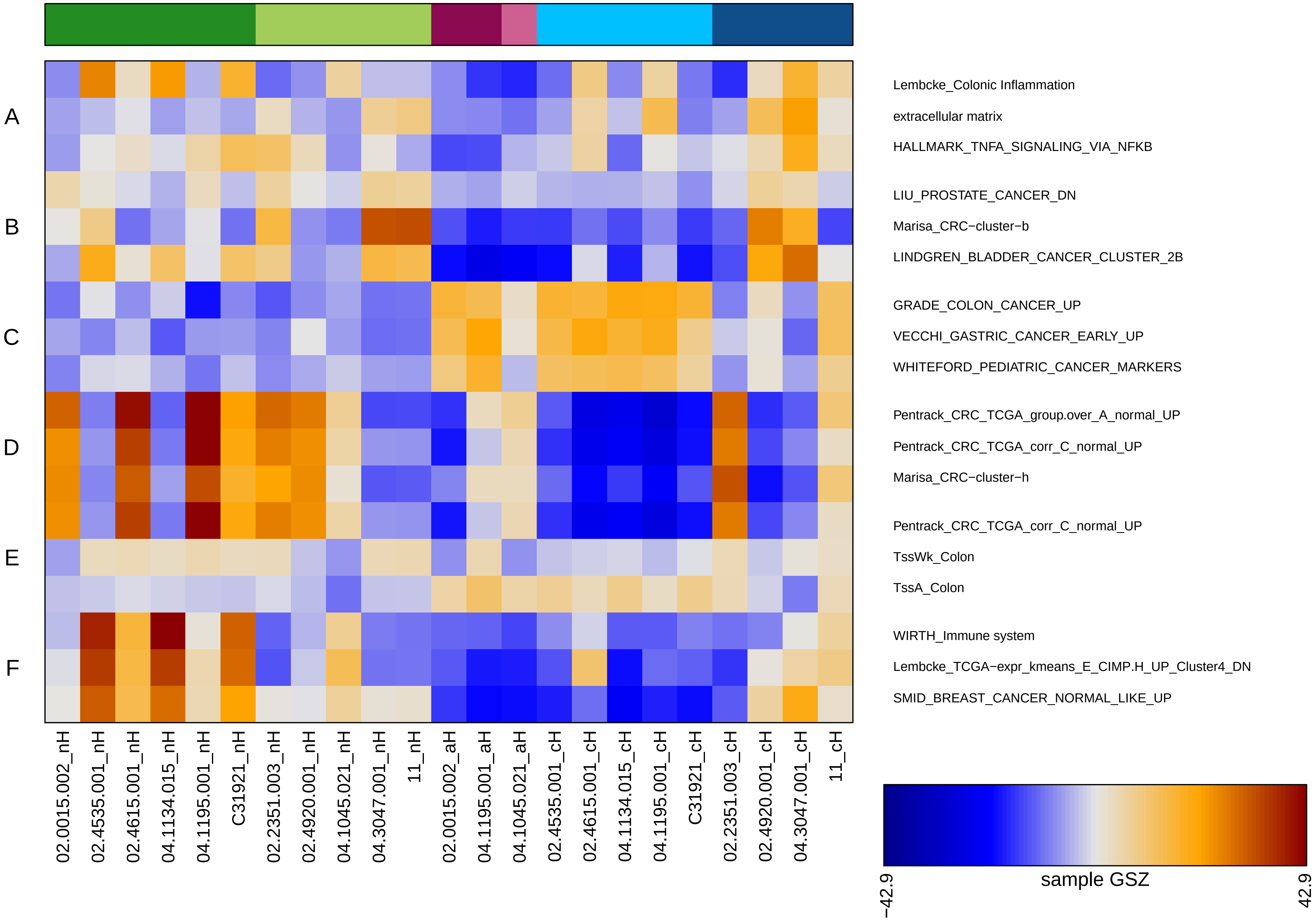


D−Clusters

beta−scores


D−Clusters
annotation
40
30
20
10
10
20
30
40
A
B
C
D
E
F
A 🟦 Lembcke_Colonic Inflammation
extracellular matrix
HALLMARK_TNFA_SIGNALING_VIA_NFKB
B 🟦 LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
LINDGREN_BLADDER_CANCER_CLUSTER_2B
C 🟩 GRADE_COLON_CANCER_UP
VECCHI_GASTRIC_CANCER_EARLY_UP
WHITEFORD_PEDIATRIC_CANCER_MARKERS
D 🟩 Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
E 🟥 Pentrack_CRC_TCGA_corr_C_normal_UP
TssWk_Colon
TssA_Colon
F 🟥 WIRTH_Immune system
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_
SMID_BREAST_CANCER_NORMAL_LIKE_UP


A
B
C
D
E
F
Lembcke_Colonic Inflammation
extracellular matrix
HALLMARK_TNFA_SIGNALING_VIA_NFKB
LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
LINDGREN_BLADDER_CANCER_CLUSTER_2B
GRADE_COLON_CANCER_UP
VECCHI_GASTRIC_CANCER_EARLY_UP
WHITEFORD_PEDIATRIC_CANCER_MARKERS
Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
Pentrack_CRC_TCGA_corr_C_normal_UP
TssWk_Colon
TssA_Colon
WIRTH_Immune system
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
SMID_BREAST_CANCER_NORMAL_LIKE_UP
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
<Δe^meta>
0.6


A
B
C
D
E
F
Lembcke_Colonic Inflammation
extracellular matrix
HALLMARK_TNFA_SIGNALING_VIA_NFKB
LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
LINDGREN_BLADDER_CANCER_CLUSTER_2B
GRADE_COLON_CANCER_UP
VECCHI_GASTRIC_CANCER_EARLY_UP
WHITEFORD_PEDIATRIC_CANCER_MARKERS
Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
Pentrack_CRC_TCGA_corr_C_normal_UP
TssWk_Colon
TssA_Colon
WIRTH_Immune system
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
SMID_BREAST_CANCER_NORMAL_LIKE_UP
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
sample GSZ
−42.9
42.9

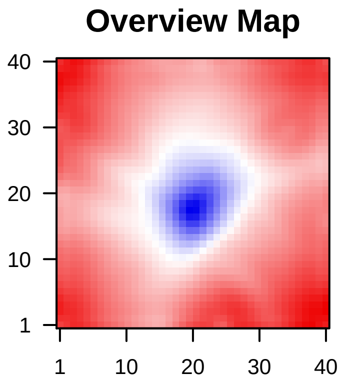
D−Clusters

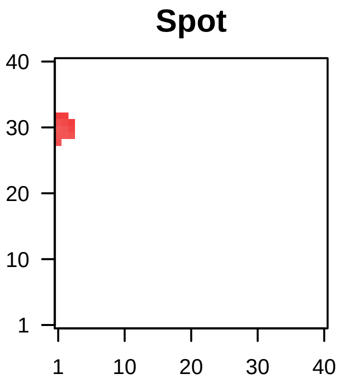
Spot Summary: A

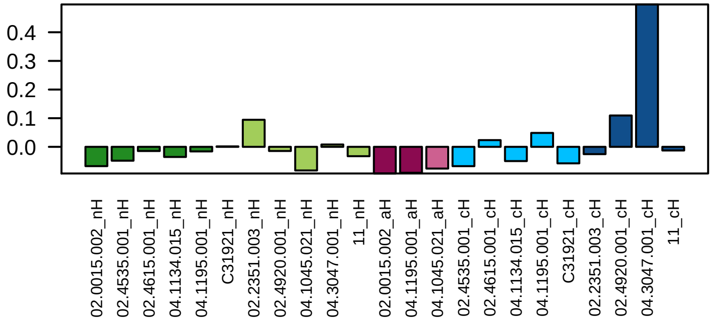
metagenes = 12
genes = 198

<r> metagenes = 0.99
<r> genes = 0.67
beta: r2= 0.17 / log p= −1.27

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





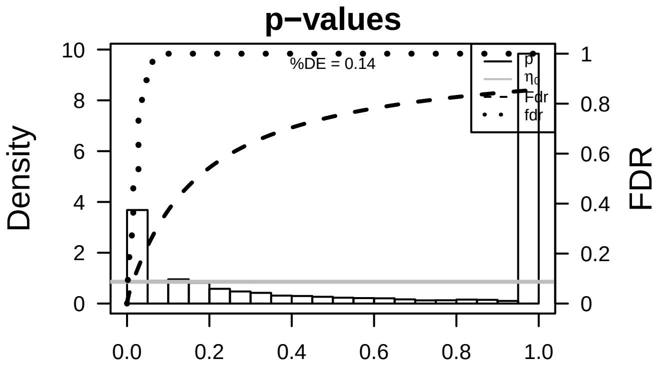


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.82	−0.23	0.9	FABP4	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
2	ENSG000002	1.31	−0.26	0.92	GPX3	glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:
3	ENSG000002	1.17	−0.14	0.35	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
4	ENSG000001	1.11	−0.22	0.93	SFRP2	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
5	ENSG000001	1.02	−0.41	0.88	CTGF	connective tissue growth factor [Source:HGNC Symbol;Acc:H
6	ENSG000001	1.01	−0.27	0.78	BGN	biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
7	ENSG000001	1	−0.16	0.92	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
8	ENSG000001	0.98	−0.25	0.66	SAA1	serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]
9	ENSG000001	0.95	−0.62	0.75	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:H
10	ENSG000001	0.9	−0.24	0.83	FOSB	FBJ murine osteosarcoma viral oncogene homolog B [Source
11	ENSG000001	0.89	−0.09	0.86	ADIPOQ	adiponectin, C1Q and collagen domain containing [Source:H
12	ENSG000001	0.87	−0.18	0.97	C11orf96	chromosome 11 open reading frame 96 [Source:HGNC Symb
13	ENSG000001	0.86	−0.22	0.82	C10orf10	chromosome 10 open reading frame 10 [Source:HGNC Symb
14	ENSG000001	0.86	−0.19	0.85	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	0.91	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	ENSG000002	0.82	−0.11	0.91	MUSTN1	musculoskeletal, embryonic nuclear protein 1 [Source:HGNC
18	ENSG000002	0.81	−0.2	0.83	ACKR1	atypical chemokine receptor 1 (Duffy blood group) [Source:H
19	ENSG000001	0.81	−0.07	0.91	PLIN1	perilipin 1 [Source:HGNC Symbol;Acc:HGNC:9076]
20	ENSG000001	0.78	−0.09	0.92	ID4	inhibitor of DNA binding 4, dominant negative helix−loop−heli

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−29	47 / 574	Canc	Lembcke_Colonic Inflammation
2	9e−29	32 / 202	CC	extracellular matrix
3	4e−28	31 / 192	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	7e−27	61 / 1176	CC	extracellular space
5	1e−26	36 / 326	GSE	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
6	3e−26	39 / 413	GSE	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
7	7e−26	37 / 368	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_2B
8	4e−25	29 / 198	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
9	2e−24	41 / 525	GSE	WEST_ADRENOCORTICAL_TUMOR_DN
10	7e−24	52 / 945	GSE	NABA_MATRISOME
11	2e−23	45 / 692	GSE	WONG_ADULT_TISSUE_STEM_MODULE
12	1e−22	32 / 314	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
13	1e−22	32 / 315	Lymp	WIRTH_lymphoma937_spot E
14	1e−21	38 / 522	GSE	SMID_BREAST_CANCER_LUMINAL_B_DN
15	5e−21	26 / 204	GSE	BOQUEST_STEM_CELL_DN
16	2e−20	28 / 261	Lymp	LENZ_Stromal signature 1
17	2e−19	56 / 1374	CC	extracellular region
18	5e−19	14 / 37	GSE	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
19	6e−19	19 / 101	GSE	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
20	7e−19	16 / 59	Lymp	LENZ_Stromal signature 2
21	8e−19	26 / 248	GSE	ONDER_CDH1_TARGETS_2_UP
22	8e−19	25 / 224	BP	angiogenesis
23	2e−18	16 / 62	GSE	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
24	3e−18	20 / 126	GSE	ZHU_CMV_ALL_DN
25	3e−18	26 / 261	GSE	NABA_CORE_MATRISOME
26	3e−18	17 / 78	GSE	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
27	7e−18	31 / 418	GSE	SWEET_LUNG_CANCER_KRAS_DN
28	7e−18	24 / 220	GSE	MCLACHLAN_DENTAL_CARIES_UP
29	1e−17	28 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
30	4e−17	17 / 90	GSE	ZHU_CMV_24_HR_DN
31	7e−17	14 / 50	GSE	BURTON_ADIPOGENESIS_PEAK_AT_2HR
32	3e−16	14 / 55	GSE	CROONQUIST_STROMAL_STIMULATION_UP
33	1e−15	21 / 196	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
34	1e−15	28 / 401	GSE	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
35	1e−15	23 / 249	GSE	BOQUEST_STEM_CELL_UP
36	2e−15	29 / 436	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
37	2e−15	30 / 478	GSE	LIM_MAMMARY_STEM_CELL_UP
38	6e−15	21 / 211	GSE	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
39	1e−14	18 / 144	GSE	IGLESIAS_E2F_TARGETS_UP
40	1e−14	19 / 167	GSE	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.1	2 / 57	TESCHENDORFF_age_hypermethylated
2	0.2	3 / 144	HORVATH_aging_genes meth UP
3	1.0	0 / 123	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−19	25 / 224	angiogenesis
2	1e−12	22 / 306	extracellular matrix organization
3	4e−11	16 / 175	response to hypoxia
4	1e−09	19 / 325	response to drug
5	6e−09	23 / 523	cell adhesion
6	3e−08	11 / 113	extracellular matrix disassembly
7	4e−08	14 / 209	platelet activation
8	7e−08	8 / 53	positive regulation of smooth muscle cell proliferation
9	2e−07	9 / 81	platelet degranulation
10	3e−07	11 / 143	response to organic cyclic compound
11	4e−07	8 / 65	fat cell differentiation
12	4e−07	10 / 118	leukocyte migration
13	9e−07	5 / 18	positive regulation of smooth muscle cell migration
14	9e−07	9 / 99	response to estradiol
15	1e−06	9 / 101	positive regulation of angiogenesis
16	1e−06	7 / 54	response to cAMP
17	1e−06	7 / 54	response to hydrogen peroxide
18	2e−06	18 / 466	blood coagulation
19	2e−06	11 / 175	response to lipopolysaccharide
20	2e−06	4 / 10	protein heterotrimerization

Brain

Rank	p−value	#in/all	Geneset
1	1e−11	41 / 1210	Fetal_TssP
2	9e−11	81 / 3977	Mid_Frontal_Lobe_ReprPC
3	3e−10	66 / 2956	Fetal_TssA
4	1e−09	52 / 2084	Mid_Frontal_Lobe_K9K27me3
5	3e−07	35 / 1327	Mid_Frontal_Lobe_TssP
6	2e−06	39 / 1713	Mid_Frontal_Lobe_ReprPCWk
7	2e−05	49 / 2603	Fetal_TxTrans
8	2e−05	48 / 2549	Fetal_TssF
9	8e−05	26 / 1108	Overlap_fetal_midbrain_TssA
10	3e−04	30 / 1478	Overlap_fetal_midbrain_TxTrans
11	1e−03	27 / 1394	Mid_Frontal_Lobe_Quies
12	1e−03	18 / 787	Overlap_fetal_midbrain_TssP
13	3e−03	18 / 840	Mid_Frontal_Lobe_TssF
14	6e−02	6 / 268	Mid_Frontal_Lobe_TssA
15	9e−02	5 / 232	Fetal_ReprPC
16	1e−01	6 / 317	Mid_Frontal_Lobe_Tx
17	1e−01	9 / 552	Fetal_Tx
18	3e−01	6 / 408	Mid_Frontal_Lobe_TxTrans
19	3e−01	11 / 865	Mid_Frontal_Lobe_Het
20	4e−01	21 / 1890	Overlap_fetal_midbrain_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	6e−29	47 / 574	Lembcke_Colonic Inflammation
2	2e−05	2 / 16	LIU_PROSTATE_CANCER_DN
3	1e−03	7 / 152	PanCan_MAPK_geneset_nanostring
4	2e−03	10 / 324	SPANG_BCL6−index2
5	5e−03	7 / 198	PanCan_PI3K_geneset_nanostring
6	1e−02	2 / 15	GENTLES_modul13
7	1e−02	2 / 15	GENTLES_modul17
8	1e−02	2 / 16	RHODES_CANCER_META_SIGNATURE
9	2e−02	3 / 51	PanCan_TGF−B_geneset_nanostring
10	2e−02	4 / 97	PanCan_TXmisReg_geneset_nanostring
11	5e−02	3 / 78	PanCan_Wnt_geneset_nanostring
12	6e−02	4 / 140	PanCan_RAS_geneset_nanostring
13	6e−02	3 / 86	PanCan_JAK−ST_geneset_nanostring
14	6e−02	1 / 6	ZHANG_MGUS up
15	1e−01	1 / 10	GENTLES_modul3
16	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
17	1e−01	1 / 14	BEN−PORATH_DN
18	1e−01	1 / 15	LIU_BREAST_CANCER
19	2e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
20	2e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	9e−29	32 / 202	extracellular matrix
2	7e−27	61 / 1176	extracellular space
3	2e−19	56 / 1374	extracellular region
4	8e−14	22 / 270	proteinaceous extracellular matrix
5	2e−11	64 / 2638	extracellular exosome
6	2e−10	25 / 523	cell surface
7	3e−08	8 / 48	platelet alpha granule lumen
8	2e−06	8 / 79	collagen trimer
9	8e−06	11 / 201	external side of plasma membrane
10	3e−05	60 / 3507	plasma membrane
11	2e−04	7 / 110	blood microparticle
12	3e−04	6 / 88	basement membrane
13	5e−04	3 / 15	platelet alpha granule
14	5e−04	16 / 596	perinuclear region of cytoplasm
15	6e−04	8 / 179	endoplasmic reticulum lumen
16	8e−04	8 / 190	membrane raft
17	1e−03	6 / 110	bicellular tight junction
18	2e−03	11 / 378	focal adhesion
19	3e−03	24 / 1250	integral component of plasma membrane
20	3e−03	4 / 59	lipid particle

Chr

Rank	p−value	#in/all	Geneset
1	0.008	17 / 859	Chr 7
2	0.138	4 / 191	Chr 21
3	0.138	14 / 976	Chr 6
4	0.236	9 / 651	Chr 8
5	0.287	13 / 1043	Chr 3
6	0.299	7 / 522	Chr 20
7	0.325	9 / 715	Chr 10
8	0.400	7 / 582	Chr 15
9	0.443	13 / 1172	Chr 11
10	0.474	5 / 436	Chr 22
11	0.511	13 / 1228	Chr 2
12	0.540	9 / 862	Chr 5
13	0.573	11 / 1083	Chr 17
14	0.621	19 / 1920	Chr 1
15	0.644	3 / 318	Chr 13
16	0.734	9 / 1017	Chr 12
17	0.766	5 / 613	Chr 14
18	0.779	6 / 735	Chr 4
19	0.790	6 / 745	Chr 9
20	0.881	11 / 1425	Chr 19

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−17	28 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
2	3e−12	16 / 148	Marisa_CRC−cluster−a
3	7e−12	22 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	1e−11	71 / 3109	TssP_Colon
5	1e−06	8 / 78	Ang_CRC_Hypermethylated
6	2e−06	44 / 2041	EnhP_Colon
7	3e−06	62 / 3406	ReprPC_Colon
8	4e−06	4 / 11	Kaneda_CIMP−group2
9	7e−05	16 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
10	8e−05	16 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
11	1e−04	6 / 73	Ang_CRC−CIMPH−vs−L_hyper
12	2e−04	14 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	4e−04	49 / 2947	ReprPCWk_Colon
14	7e−04	12 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	2e−03	17 / 754	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
16	5e−03	11 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
17	5e−03	9 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
18	2e−02	6 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
19	2e−02	4 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
20	5e−02	1 / 5	Kaneda_CIMP−group1

Disease

Rank	p−value	#in/all	Geneset
1	1e−06	17 / 399	GUDJ_psoriasis down
2	6e−04	16 / 608	GUDJ_psoriasis up
3	2e−01	1 / 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−13	22 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	4e−06	8 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
3	7e−06	10 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP
4	4e−05	9 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
5	8e−05	6 / 69	cultured astroglia vs. in vivo astrocytes
6	1e−04	7 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	1e−04	6 / 77	Weller_LGG_gradeII−vs−III_DOWN
8	2e−04	7 / 119	GIEZELT_GBM_WT_up_VS_mut
9	3e−04	7 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
10	4e−04	4 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
11	5e−04	4 / 36	Colman_survival_associated
12	5e−04	30 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
13	8e−04	5 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
14	1e−03	14 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
15	2e−03	6 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	2e−03	2 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expressio
17	3e−03	4 / 55	Gorovets_LGG_PG_subclass
18	3e−03	4 / 59	Christensen_hypomethylated_in_primary_glioblastoma
19	3e−03	4 / 59	developing astrocytes
20	3e−03	3 / 29	Christensen_hypomethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−26	36 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	3e−26	39 / 413	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
3	7e−26	37 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
4	2e−24	41 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
5	7e−24	52 / 945	NABA_MATRISOME
6	2e−23	45 / 692	WONG_ADULT_TISSUE_STEM_MODULE
7	1e−21	38 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
8	5e−21	26 / 204	BOQUEST_STEM_CELL_DN
9	5e−19	14 / 37	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
10	6e−19	19 / 101	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
11	8e−19	26 / 248	ONDER_CDH1_TARGETS_2_UP
12	2e−18	16 / 62	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
13	3e−18	20 / 126	ZHU_CMV_ALL_DN
14	3e−18	26 / 261	NABA_CORE_MATRISOME
15	3e−18	17 / 78	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
16	7e−18	31 / 418	SWEET_LUNG_CANCER_KRAS_DN
17	7e−18	24 / 220	MCLACHLAN_DENTAL_CARIES_UP
18	4e−17	17 / 90	ZHU_CMV_24_HR_DN
19	7e−17	14 / 50	BURTON_ADIPOGENESIS_PEAK_AT_2HR
20	3e−16	14 / 55	CROONQUIST_STROMAL_STIMULATION_UP

HM

Rank	p−value	#in/all	Geneset
1	4e−28	31 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	4e−25	29 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	5e−13	16 / 132	HALLMARK_COAGULATION
4	3e−12	18 / 198	HALLMARK_HYPOXIA
5	1e−11	17 / 189	HALLMARK_KRAS_SIGNALING_UP
6	8e−08	7 / 36	HALLMARK_ANGIOGENESIS
7	8e−07	11 / 157	HALLMARK_APOPTOSIS
8	6e−06	11 / 194	HALLMARK_INFLAMMATORY_RESPONSE
9	6e−06	11 / 195	HALLMARK_MYOGENESIS
10	2e−05	9 / 140	HALLMARK_UV_RESPONSE_DN
11	3e−05	10 / 190	HALLMARK_APICAL_JUNCTION
12	4e−05	10 / 199	HALLMARK_ADIPOGENESIS
13	2e−04	5 / 52	HALLMARK_TGF_BETA_SIGNALING
14	2e−04	8 / 155	HALLMARK_UV_RESPONSE_UP
15	3e−04	6 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
16	3e−03	7 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
17	4e−03	5 / 98	HALLMARK_ANDROGEN_RESPONSE
18	4e−03	7 / 192	HALLMARK_COMPLEMENT
19	5e−03	7 / 197	HALLMARK_IL2_STAT5_SIGNALING
20	1e−02	3 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	2 / 11	DUMEAUX_Smoking literature genes up
2	0.108	1 / 11	DUMEAUX_Women normal BMI literature genes up
3	0.614	1 / 91	DUMEAUX_Smoking enriched genes
4	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.000	0 / 7	DUMEAUX_Estrogen related in non 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 / 17	DUMEAUX_High bmi enriched genes
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−22	32 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
2	1e−22	32 / 315	WIRTH_lymphoma937_spot E
3	2e−20	28 / 261	LENZ_Stromal signature 1
4	7e−19	16 / 59	LENZ_Stromal signature 2
5	7e−12	97 / 5039	HOPP_Repressed
6	3e−09	62 / 2838	HOPP_Poised_promoter
7	6e−07	10 / 122	Subero_INT_hyper_meth
8	2e−06	10 / 138	Subero_DLBCL_hyper_meth
9	3e−05	15 / 414	TARTE_Mature plasma cell signature
10	6e−05	7 / 94	Subero_T−ALL_hyper_meth
11	1e−04	8 / 145	WIRTH_lymphoma937_spot F
12	1e−04	8 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
13	4e−04	6 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
14	7e−04	10 / 279	SPANG_IL21 DN
15	9e−04	5 / 71	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
16	1e−03	5 / 75	Subero_FL_hyper_meth
17	2e−03	4 / 49	Subero_DLBCL_hypo_meth
18	3e−03	6 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
19	4e−03	5 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
20	5e−03	4 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN

MF

Rank	p−value	#in/all	Geneset
1	2e−09	151 / 10693	protein binding
2	3e−09	13 / 142	heparin binding
3	1e−07	10 / 102	integrin binding
4	2e−07	8 / 60	collagen binding
5	2e−07	6 / 26	fibronectin binding
6	1e−06	7 / 53	extracellular matrix structural constituent
7	2e−06	22 / 672	calcium ion binding
8	3e−06	5 / 23	extracellular matrix binding
9	4e−06	4 / 11	platelet−derived growth factor binding
10	2e−05	4 / 16	transforming growth factor beta binding
11	2e−05	11 / 221	transcriptional activator activity, RNA polymerase II core promoter proximal re
12	4e−05	7 / 89	protease binding
13	9e−05	4 / 23	insulin−like growth factor binding
14	1e−04	4 / 26	coreceptor activity
15	2e−04	9 / 196	transmembrane signaling receptor activity
16	2e−04	16 / 556	sequence−specific DNA binding
17	5e−04	3 / 15	low−density lipoprotein particle binding
18	5e−04	3 / 15	platelet−derived growth factor receptor binding
19	9e−04	3 / 19	FK506 binding
20	1e−03	7 / 150	lipid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	10 / 246	hsa−miR−1252
2	1e−03	8 / 205	hsa−miR−181c
3	2e−03	8 / 225	hsa−miR−181a
4	5e−03	5 / 104	hsa−miR−600
5	9e−03	7 / 226	hsa−miR−181d
6	1e−02	3 / 43	hsa−miR−331−5p
7	1e−02	7 / 231	hsa−miR−181b
8	2e−02	6 / 209	hsa−miR−148b
9	2e−02	6 / 214	hsa−miR−148a
10	3e−02	3 / 66	hsa−miR−30e*
11	4e−02	5 / 175	hsa−miR−369−3p
12	4e−02	4 / 126	hsa−miR−421
13	4e−02	6 / 247	hsa−miR−152
14	4e−02	5 / 186	hsa−miR−1
15	6e−02	3 / 83	hsa−miR−30a*
16	6e−02	3 / 85	hsa−miR−582−3p
17	6e−02	2 / 38	hsa−miR−1269
18	6e−02	1 / 6	hsa−miR−937
19	6e−02	5 / 204	hsa−miR−206
20	6e−02	2 / 39	hsa−miR−484

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.009	2 / 14	GUSTAFSON_PI3K_UP
2	0.099	1 / 10	BENTINK_ras.4
3	0.136	1 / 14	BENTINK_myc.1
4	0.136	1 / 14	BENTINK_src.10
5	1.000	0 / 15	GUSTAFSON_PI3K_DN
6	1.000	0 / 14	BENTINK_e2f3.1
7	1.000	0 / 13	BENTINK_e2f3.2
8	1.000	0 / 12	BENTINK_ras.1
9	1.000	0 / 15	BENTINK_ras.6
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	9e−05	36 / 1798	HEBENSTREIT_low expression TF
2	3e−01	39 / 3511	ICGC_Rad21_targets
3	5e−01	16 / 1523	ICGC_P300_targets
4	7e−01	12 / 1294	KIM_MYC targets
5	7e−01	27 / 2827	ICGC_Bcl3_targets
6	7e−01	20 / 2149	ICGC_Mef2_targets
7	8e−01	16 / 1867	HEBENSTREIT_high expression TF
8	9e−01	28 / 3305	ICGC_BatfPcr1_targets
9	9e−01	11 / 1506	ICGC_Usf1_targets
10	9e−01	10 / 1472	ICGC_NrsfPcr1_targets
11	1e+00	18 / 2401	ICGC_Bcl11_targets
12	1e+00	15 / 2133	ICGC_Cebpbsc150_targets
13	1e+00	63 / 7202	ICGC_Runx3_targets
14	1e+00	20 / 2719	ICGC_Pbx3_targets
15	1e+00	24 / 3177	ICGC_Irf4_targets
16	1e+00	42 / 5135	ICGC_Ebfsc137065_targets
17	1e+00	54 / 6406	ICGC_Pax5_targets
18	1e+00	53 / 6313	ICGC_Pou2_targets
19	1e+00	51 / 6157	ICGC_Tcf3_targets
20	1e+00	3 / 731	ICGC_SrfPcr2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	2e−07	6 / 25	VAQUERIZAS_Adrenal cortex
2	1e−04	3 / 10	VAQUERIZAS_Skeletal.muscle.psoas
3	6e−04	3 / 16	VAQUERIZAS_Ovary
4	2e−03	3 / 24	VAQUERIZAS_Trachea
5	2e−03	2 / 7	VAQUERIZAS_Appendix
6	3e−03	2 / 8	VAQUERIZAS_Tongue
7	4e−03	4 / 64	VAQUERIZAS_Lung
8	1e−02	2 / 17	VAQUERIZAS_Adrenal gland
9	7e−02	2 / 42	VAQUERIZAS_Thyroid
10	2e−01	2 / 67	VAQUERIZAS_Whole blood
11	2e−01	1 / 17	VAQUERIZAS_Salivary gland
12	2e−01	1 / 20	VAQUERIZAS_Bone marrow
13	3e−01	1 / 31	VAQUERIZAS_Fetal lung
14	3e−01	1 / 41	VAQUERIZAS_Testis
15	4e−01	1 / 45	VAQUERIZAS_Placenta
16	4e−01	1 / 46	VAQUERIZAS_Whole brain
17	4e−01	1 / 49	VAQUERIZAS_Uterus
18	5e−01	2 / 155	VAQUERIZAS_General
19	1e+00	0 / 41	VAQUERIZAS_Fetal brain
20	1e+00	0 / 33	VAQUERIZAS_Liver

Tissue

Rank	p−value	#in/all	Geneset
1	7e−06	4 / 13	WIRTH_Sec. lymphoid organs
2	2e−03	9 / 259	PALMER_Granulocytes signature up
3	1e−02	2 / 15	WIRTH_Telencephalon
4	1e−01	1 / 13	WIRTH_Prim. lymphoid organs
5	2e−01	4 / 208	PALMER_B−Cell signature up
6	2e−01	3 / 140	PALMER_T−Cell signature up
7	7e−01	1 / 115	WIRTH_Liver
8	9e−01	2 / 427	WIRTH_Immune system
9	1e+00	0 / 6	WIRTH_Pituitary gland
10	1e+00	0 / 54	WIRTH_Pancreas
11	1e+00	0 / 14	WIRTH_B−cells
12	1e+00	0 / 12	WIRTH_Tonsil
13	1e+00	0 / 14	WIRTH_Thymus
14	1e+00	0 / 12	WIRTH_Lymphocytes
15	1e+00	0 / 14	WIRTH_Bone marrow
16	1e+00	0 / 476	WIRTH_Nervous System
17	1e+00	0 / 13	WIRTH_Globus pallidus
18	1e+00	0 / 13	WIRTH_Cortex cerebri
19	1e+00	0 / 16	WIRTH_Hippocampus
20	1e+00	0 / 14	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.02	68 / 5285	LU_BPDE 0.005 DN
2	0.90	10 / 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	

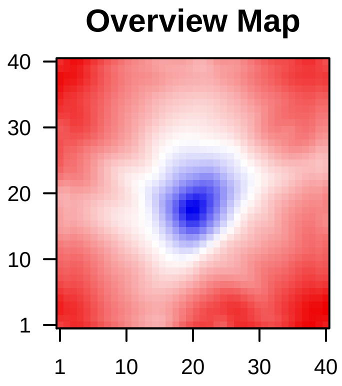
D−Clusters

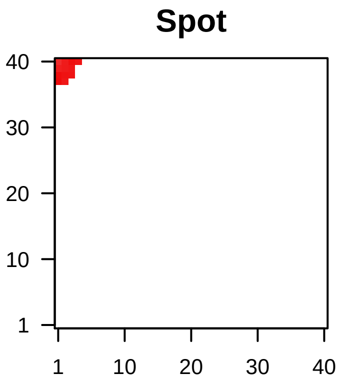
Spot Summary: B

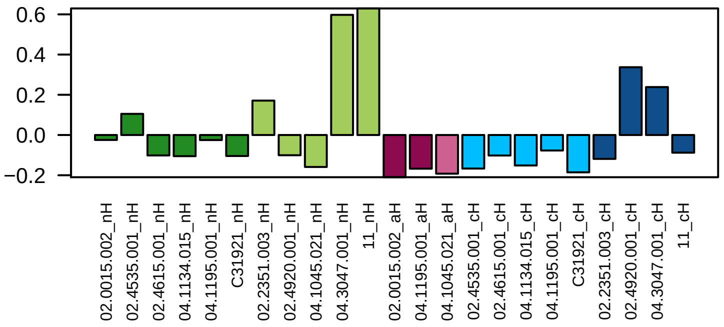
metagenes = 12
genes = 253

<r> metagenes = 1
<r> genes = 0.81
beta: r2= 0.77 / log p= −7.34

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


Overview Map


Spot

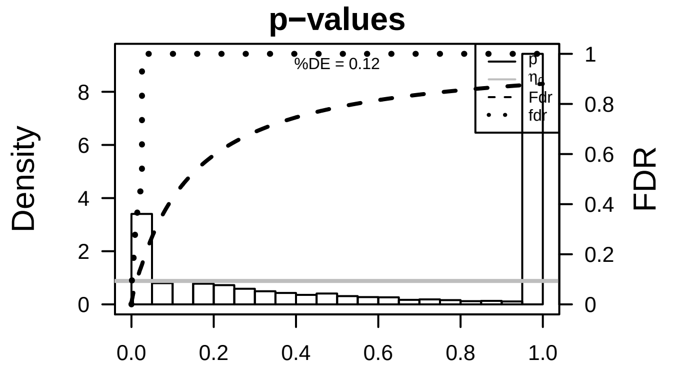


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.59	−0.8	0.88	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 Sym
3	ENSG000001	1.44	−0.52	0.94	CNN1	calponin 1, basic, smooth muscle [Source:HGNC Symbol;Acc
4	ENSG000001	1.42	−0.68	0.92	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
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	0.91	MYL9	myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:
7	ENSG000001	1.32	−0.37	0.97	SYNM	synemin, intermediate filament protein [Source:HGNC Symb
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;A
12	ENSG000001	1.2	−0.74	0.93	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	0.95	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:H
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	1e−69	4 / 16	Canc LIU_PROSTATE_CANCER_DN
2	1e−58	49 / 132	Colon Marisa_CRC−cluster−b
3	9e−46	58 / 368	GSE LINDGREN_BLADDER_CANCER_CLUSTER_2B
4	3e−44	53 / 303	GSE PASINI_SUZ12_TARGETS_DN
5	1e−42	61 / 478	GSE LIM_MAMMARY_STEM_CELL_UP
6	3e−40	43 / 196	GSE PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	2e−37	59 / 535	GSE CHICAS_RB1_TARGETS_CONFLUENT
8	2e−31	34 / 160	GSE BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
9	3e−31	42 / 294	GSE ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
10	2e−29	35 / 198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
11	2e−29	42 / 326	GSE SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
12	7e−28	46 / 445	GSE CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
13	9e−28	43 / 378	CC focal adhesion
14	9e−28	40 / 314	Lymp Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
15	1e−27	40 / 315	Lymp WIRTH_lymphoma937_spot E
16	2e−27	55 / 692	GSE WONG_ADULT_TISSUE_STEM_MODULE
17	3e−26	36 / 261	Lymp LENZ_Stromal signature 1
18	6e−26	43 / 418	GSE SWEET_LUNG_CANCER_KRAS_DN
19	1e−25	19 / 40	GSE TOMLINS_PROSTATE_CANCER_DN
20	2e−22	32 / 248	GSE ONDER_CDH1_TARGETS_2_UP
21	3e−22	29 / 195	HM HALLMARK_MYOGENESIS
22	8e−22	38 / 399	Disea GUDJ_psoriasis down
23	2e−20	31 / 267	GSE WANG_SMARCE1_TARGETS_UP
24	3e−20	16 / 40	GSE PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
25	3e−20	41 / 525	GSE WEST_ADRENOCORTICAL_TUMOR_DN
26	1e−19	13 / 22	GSE REACTOME_SMOOTH_MUSCLE_CONTRACTION
27	1e−18	45 / 711	GSE LEE_BMP2_TARGETS_UP
28	1e−18	23 / 144	GSE IGLESIAS_E2F_TARGETS_UP
29	3e−18	28 / 246	GSE DANG_REGULATED_BY_MYC_DN
30	1e−17	30 / 306	BP extracellular matrix organization
31	1e−17	25 / 195	GSE KEGG_FOCAL_ADHESION
32	4e−17	22 / 148	Colon Marisa_CRC−cluster−a
33	4e−17	33 / 401	GSE REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
34	5e−17	11 / 18	GSE NIELSEN_LEIOMYOSARCOMA_CNN1_UP
35	1e−16	19 / 105	BP muscle contraction
36	3e−16	24 / 202	CC extracellular matrix
37	3e−16	14 / 44	GSE REACTOME_MUSCLE_CONTRACTION
38	6e−16	26 / 254	GSE LU_AGING_BRAIN_UP
39	1e−15	26 / 261	GSE NABA_CORE_MATRISOME
40	1e−15	24 / 215	GSE SENESE_HDAC1_AND_HDAC2_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 144	HORVATH_aging_genes meth UP
2	0.2	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	1e−17	30 / 306	extracellular matrix organization
2	1e−16	19 / 105	muscle contraction
3	1e−11	30 / 523	cell adhesion
4	3e−10	14 / 113	extracellular matrix disassembly
5	3e−08	21 / 373	axon guidance
6	4e−08	11 / 93	cell−matrix adhesion
7	6e−08	6 / 17	regulation of muscle contraction
8	7e−07	7 / 39	platelet aggregation
9	1e−06	9 / 81	platelet degranulation
10	4e−06	8 / 71	collagen catabolic process
11	5e−06	8 / 73	actin filament organization
12	7e−06	6 / 36	muscle filament sliding
13	9e−06	4 / 11	negative regulation of neural precursor cell proliferation
14	9e−06	13 / 224	angiogenesis
15	2e−05	7 / 62	response to mechanical stimulus
16	2e−05	12 / 209	platelet activation
17	3e−05	5 / 28	endodermal cell differentiation
18	4e−05	5 / 30	sarcomere organization
19	5e−05	4 / 16	negative regulation of anoikis
20	5e−05	18 / 466	blood coagulation

Brain

Rank	p−value	#in/all	Geneset
1	7e−11	80 / 2956	Fetal_TssA
2	2e−06	37 / 1210	Fetal_TssP
3	9e−06	60 / 2603	Fetal_TxTrans
4	1e−05	51 / 2084	Mid_Frontal_Lobe_K9K27me3
5	5e−05	79 / 3977	Mid_Frontal_Lobe_ReprPC
6	8e−04	22 / 787	Overlap_fetal_midbrain_TssP
7	4e−03	49 / 2549	Fetal_TssF
8	1e−02	9 / 268	Mid_Frontal_Lobe_TssA
9	2e−02	14 / 552	Fetal_Tx
10	2e−02	27 / 1327	Mid_Frontal_Lobe_TssP
11	2e−02	11 / 408	Mid_Frontal_Lobe_TxTrans
12	7e−02	46 / 2820	Mid_Frontal_Lobe_HetRpts
13	9e−02	16 / 840	Mid_Frontal_Lobe_TssF
14	1e−01	16 / 855	Overlap_fetal_midbrain_ZNF
15	1e−01	24 / 1394	Mid_Frontal_Lobe_Quies
16	1e−01	52 / 3370	Mid_Frontal_Lobe_ZNF
17	1e−01	19 / 1108	Overlap_fetal_midbrain_TssA
18	2e−01	151 / 10800	Overlap_fetal_midbrain_Quies
19	2e−01	30 / 1890	Overlap_fetal_midbrain_TssF
20	2e−01	16 / 940	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	1e−69	4 / 16	LIU_PROSTATE_CANCER_DN
2	4e−10	7 / 15	GENTLES_modul17
3	8e−06	22 / 574	Lembcke_Colonic Inflammation
4	9e−04	3 / 15	BEN−PORATH_UP
5	1e−02	1 / 16	LIU_LIVER_CANCER
6	1e−02	7 / 191	SPANG_LPS−index2
7	2e−02	2 / 15	GENTLES_modul13
8	4e−02	1 / 15	LIU_BREAST_CANCER
9	5e−02	5 / 152	PanCan_MAPK_geneset_nanostring
10	1e−01	5 / 198	PanCan_PI3K_geneset_nanostring
11	1e−01	7 / 324	SPANG_BCL6−index2
12	2e−01	1 / 16	GENTLES_modul16
13	5e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	5e−01	1 / 51	PanCan_TGF−B_geneset_nanostring
15	6e−01	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
16	6e−01	1 / 71	SHAUGHNESSY_MM high risk
17	6e−01	1 / 78	PanCan_Wnt_geneset_nanostring
18	7e−01	0 / 14	LIU_PROSTATE_CANCER_UP
19	7e−01	1 / 97	PanCan_TXmisReg_geneset_nanostring
20	9e−01	4 / 550	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	9e−28	43 / 378	focal adhesion
2	3e−16	24 / 202	extracellular matrix
3	2e−14	82 / 2638	extracellular exosome
4	1e−12	16 / 109	Z disc
5	1e−11	14 / 91	sarcolemma
6	5e−11	11 / 51	stress fiber
7	8e−11	19 / 216	actin cytoskeleton
8	9e−11	45 / 1176	extracellular space
9	1e−10	13 / 88	basement membrane
10	1e−10	8 / 21	costamere
11	6e−10	20 / 270	proteinaceous extracellular matrix
12	4e−08	44 / 1374	extracellular region
13	2e−07	11 / 110	blood microparticle
14	4e−07	105 / 5185	cytoplasm
15	4e−07	10 / 93	ruffle
16	8e−07	12 / 151	lamellipodium
17	2e−06	22 / 523	cell surface
18	3e−06	18 / 381	cytoskeleton
19	3e−06	7 / 49	extracellular vesicle
20	4e−06	76 / 3507	plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.07	15 / 745	Chr 9
2	0.10	32 / 1920	Chr 1
3	0.11	5 / 191	Chr 21
4	0.12	14 / 746	Chr X
5	0.15	13 / 715	Chr 10
6	0.29	10 / 613	Chr 14
7	0.36	9 / 582	Chr 15
8	0.46	17 / 1228	Chr 2
9	0.47	12 / 862	Chr 5
10	0.54	7 / 522	Chr 20
11	0.57	14 / 1083	Chr 17
12	0.59	11 / 859	Chr 7
13	0.59	13 / 1017	Chr 12
14	0.63	8 / 651	Chr 8
15	0.64	9 / 735	Chr 4
16	0.64	12 / 976	Chr 6
17	0.73	12 / 1043	Chr 3
18	0.78	13 / 1172	Chr 11
19	0.88	2 / 272	Chr 18
20	0.93	2 / 318	Chr 13

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−58	49 / 132	Marisa_CRC−cluster−b
2	4e−17	22 / 148	Marisa_CRC−cluster−a
3	7e−12	30 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
4	2e−11	24 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	2e−11	24 / 337	Pentrack_CRC_TCGA_group.over_B_msi=h_UP
6	2e−08	199 / 11968	TssWk_Colon
7	5e−08	5 / 9	Budinska_D_Mesenchymal_UP
8	8e−08	195 / 11791	Enh_Colon
9	1e−07	74 / 3109	TssP_Colon
10	7e−07	72 / 3122	TxEnhG1_Colon
11	1e−06	114 / 5889	EnhWk1_Colon
12	5e−06	89 / 4379	TssD1_Colon
13	9e−06	21 / 532	K9acLow_Colon
14	1e−05	9 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
15	2e−05	67 / 3112	EnhA_Colon
16	2e−04	82 / 4327	EnhWk2_Colon
17	3e−04	22 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
18	8e−04	15 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
19	9e−04	12 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
20	1e−03	16 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Disease

Rank	p−value	#in/all	Geneset
1	8e−22	38 / 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	2e−10	21 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−08	8 / 36	Colman_survival_associated
3	1e−05	9 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
4	3e−05	9 / 119	GIEZELT_GBM_WT_up_VS_mut
5	4e−05	4 / 15	Mukasa_UP_in_GBM
6	5e−04	3 / 12	Phillips MES up vs Prolif & PN
7	9e−04	5 / 56	mature astrocytes
8	1e−03	5 / 63	OPC
9	2e−03	5 / 69	cultured astroglia vs. in vivo astrocytes
10	4e−03	5 / 77	Weller_LGG_gradeII−vs−III_DOWN
11	5e−03	7 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	6e−03	2 / 9	Colman_survival_robust
13	7e−03	4 / 58	OL vs. MOG− OL
14	9e−03	5 / 96	Weller_LGG_A_vs_O_UP
15	1e−02	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
16	1e−02	6 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
17	2e−02	4 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
18	2e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
19	2e−02	5 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
20	2e−02	5 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−69	4 / 16	LIU_PROSTATE_CANCER_DN
2	9e−46	58 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
3	3e−44	53 / 303	PASINI_SUZ12_TARGETS_DN
4	1e−42	61 / 478	LIM_MAMMARY_STEM_CELL_UP
5	3e−40	43 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	2e−37	59 / 535	CHICAS_RB1_TARGETS_CONFLUENT
7	2e−31	34 / 160	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
8	3e−31	42 / 294	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
9	2e−29	42 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	7e−28	46 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
11	2e−27	55 / 692	WONG_ADULT_TISSUE_STEM_MODULE
12	6e−26	43 / 418	SWEET_LUNG_CANCER_KRAS_DN
13	1e−25	19 / 40	TOMLINS_PROSTATE_CANCER_DN
14	2e−22	32 / 248	ONDER_CDH1_TARGETS_2_UP
15	2e−20	31 / 267	WANG_SMARCE1_TARGETS_UP
16	3e−20	16 / 40	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
17	3e−20	41 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
18	1e−19	13 / 22	REACTOME_SMOOTH_MUSCLE_CONTRACTION
19	1e−18	45 / 711	LEE_BMP2_TARGETS_UP
20	1e−18	23 / 144	IGLESIAS_E2F_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−29	35 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	3e−22	29 / 195	HALLMARK_MYOGENESIS
3	2e−07	14 / 190	HALLMARK_APICAL_JUNCTION
4	3e−06	11 / 140	HALLMARK_UV_RESPONSE_DN
5	5e−05	10 / 157	HALLMARK_APOPTOSIS
6	2e−04	10 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	3e−04	10 / 197	HALLMARK_IL2_STAT5_SIGNALING
8	3e−04	10 / 199	HALLMARK_ADIPOGENESIS
9	4e−03	8 / 192	HALLMARK_COMPLEMENT
10	4e−03	8 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	4e−03	8 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
12	5e−03	4 / 52	HALLMARK_TGF_BETA_SIGNALING
13	5e−03	8 / 198	HALLMARK_HYPOXIA
14	8e−03	6 / 132	HALLMARK_COAGULATION
15	4e−02	4 / 98	HALLMARK_ANDROGEN_RESPONSE
16	6e−02	5 / 155	HALLMARK_UV_RESPONSE_UP
17	8e−02	2 / 36	HALLMARK_ANGIOGENESIS
18	1e−01	2 / 44	HALLMARK_APICAL_SURFACE
19	1e−01	5 / 196	HALLMARK_P53_PATHWAY
20	1e−01	5 / 199	HALLMARK_MTORC1_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.06	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.34	2 / 91	DUMEAUX_Smoking enriched genes
4	0.36	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	9e−28	40 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
2	1e−27	40 / 315	WIRTH_lymphoma937_spot E
3	3e−26	36 / 261	LENZ_Stromal signature 1
4	1e−13	121 / 5039	HOPP_Repressed
5	6e−11	78 / 2838	HOPP_Poised_promoter
6	4e−08	12 / 115	ROSOLOWSKI_green total
7	3e−06	19 / 414	TARTE_Mature plasma cell signature
8	1e−05	7 / 59	LENZ_Stromal signature 2
9	9e−05	9 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
10	7e−04	8 / 145	WIRTH_lymphoma937_spot F
11	7e−04	8 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
12	8e−04	6 / 83	ROSOLOWSKI_green UP
13	9e−04	3 / 15	Subero_T−ALL_hypo_meth
14	1e−03	5 / 62	Subero_mBL_hyper_meth
15	1e−03	6 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
16	2e−03	6 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
17	2e−03	7 / 138	Subero_DLBCL_hyper_meth
18	3e−03	3 / 21	DAVE_Immune response 2
19	5e−03	9 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
20	6e−03	6 / 122	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	6e−10	21 / 301	actin binding
2	1e−09	187 / 10693	protein binding
3	2e−09	9 / 39	structural constituent of muscle
4	1e−07	11 / 102	integrin binding
5	3e−06	10 / 113	actin filament binding
6	6e−06	7 / 53	extracellular matrix structural constituent
7	4e−05	8 / 96	structural constituent of cytoskeleton
8	1e−04	6 / 58	cytoskeletal protein binding
9	1e−04	6 / 60	collagen binding
10	2e−04	4 / 22	laminin binding
11	2e−04	4 / 23	extracellular matrix binding
12	2e−04	4 / 23	insulin−like growth factor binding
13	3e−04	3 / 11	platelet−derived growth factor binding
14	3e−04	3 / 11	vinculin binding
15	4e−04	4 / 26	fibronectin binding
16	6e−04	8 / 142	heparin binding
17	2e−03	6 / 98	ion channel binding
18	2e−03	8 / 172	calmodulin binding
19	2e−03	3 / 20	myosin binding
20	4e−03	18 / 672	calcium ion binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	10 / 174	hsa−miR−520h
2	2e−04	17 / 480	hsa−miR−301a
3	3e−04	12 / 275	hsa−miR−449a
4	5e−04	9 / 172	hsa−miR−153
5	5e−04	12 / 291	hsa−miR−570
6	8e−04	7 / 113	hsa−miR−449b
7	8e−04	10 / 223	hsa−miR−548m
8	1e−03	8 / 153	hsa−miR−518a−5p
9	1e−03	6 / 88	hsa−miR−595
10	1e−03	10 / 233	hsa−miR−520g
11	1e−03	8 / 157	hsa−miR−527
12	2e−03	8 / 174	hsa−miR−7
13	2e−03	7 / 137	hsa−miR−199b−5p
14	2e−03	12 / 348	hsa−miR−548b−5p
15	3e−03	11 / 305	hsa−miR−202
16	3e−03	14 / 446	hsa−miR−19b
17	3e−03	8 / 180	hsa−miR−548k
18	3e−03	14 / 462	hsa−miR−130b
19	4e−03	6 / 112	hsa−miR−1271
20	4e−03	6 / 115	hsa−miR−491−3p

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	4e−06	4 / 9	MYC_Targets DOWN
2	9e−05	43 / 1798	HEBENSTREIT_low expression TF
3	2e−04	2 / 2	MYC_ECM cell adhesion DOWN
4	2e−02	83 / 5135	ICGC_Ebfsc137065_targets
5	3e−02	59 / 3511	ICGC_Rad21_targets
6	6e−02	1 / 5	MYC_TF and cofactors
7	2e−01	25 / 1523	ICGC_P300_targets
8	2e−01	80 / 5552	ICGC_Pol24_targets
9	3e−01	48 / 3305	ICGC_BatfPcr1_targets
10	3e−01	32 / 2149	ICGC_Mef2_targets
11	3e−01	67 / 4714	ICGC_Pu1_targets
12	3e−01	45 / 3177	ICGC_Irf4_targets
13	3e−01	22 / 1506	ICGC_Usf1_targets
14	3e−01	88 / 6406	ICGC_Pax5_targets
15	4e−01	19 / 1294	KIM_MYC targets
16	4e−01	34 / 2401	ICGC_Bcl11_targets
17	4e−01	11 / 731	ICGC_SrfPcr2_targets
18	5e−01	25 / 1867	HEBENSTREIT_high expression TF
19	5e−01	95 / 7202	ICGC_Runx3_targets
20	6e−01	37 / 2827	ICGC_Bcl3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.06	2 / 31	VAQUERIZAS_Fetal lung
2	0.12	2 / 45	VAQUERIZAS_Placenta
3	0.15	1 / 12	VAQUERIZAS_Kidney
4	0.20	1 / 17	VAQUERIZAS_Adrenal gland
5	0.21	2 / 64	VAQUERIZAS_Lung
6	0.21	1 / 18	VAQUERIZAS_Pancreas
7	0.26	1 / 23	VAQUERIZAS_Pituitary
8	0.27	1 / 24	VAQUERIZAS_Trachea
9	0.28	1 / 25	VAQUERIZAS_Adrenal cortex
10	0.43	1 / 42	VAQUERIZAS_Thymus
11	0.48	1 / 49	VAQUERIZAS_Uterus
12	0.61	2 / 155	VAQUERIZAS_General
13	1.00	0 / 41	VAQUERIZAS_Fetal brain
14	1.00	0 / 33	VAQUERIZAS_Liver
15	1.00	0 / 37	VAQUERIZAS_Prostate
16	1.00	0 / 30	VAQUERIZAS_Smooth muscle
17	1.00	0 / 25	VAQUERIZAS_Spinal cord
18	1.00	0 / 46	VAQUERIZAS_Whole brain
19	1.00	0 / 42	VAQUERIZAS_Thyroid
20	1.00	0 / 67	VAQUERIZAS_Whole blood

Tissue

Rank	p−value	#in/all	Geneset
1	5e−07	5 / 13	WIRTH_Sec. lymphoid organs
2	7e−03	8 / 208	PALMER_B−Cell signature up
3	1e−02	6 / 141	WIRTH_Muscle
4	4e−02	5 / 140	PALMER_T−Cell signature up
5	1e−01	6 / 259	PALMER_Granulocytes signature up
6	1e−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	2 / 54	WIRTH_Pancreas
10	2e−01	1 / 15	WIRTH_Telencephalon
11	2e−01	1 / 16	WIRTH_Hippocampus
12	5e−01	1 / 47	WIRTH_Placenta
13	8e−01	5 / 476	WIRTH_Nervous System
14	1e+00	0 / 6	WIRTH_Pituitary gland
15	1e+00	0 / 427	WIRTH_Immune system
16	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
17	1e+00	0 / 14	WIRTH_B−cells
18	1e+00	0 / 12	WIRTH_Tonsil
19	1e+00	0 / 14	WIRTH_Thymus
20	1e+00	0 / 14	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.07	81 / 5285	LU_BPDE 0.005 DN
2	0.12	23 / 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	

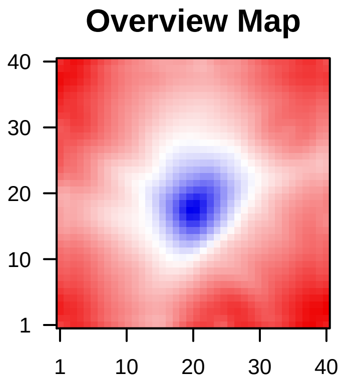
D−Clusters

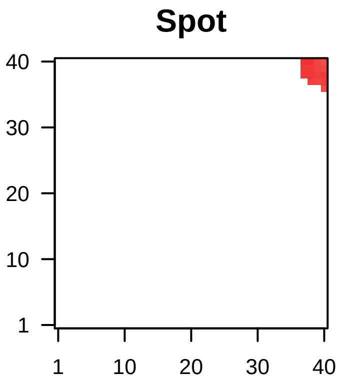
Spot Summary: C

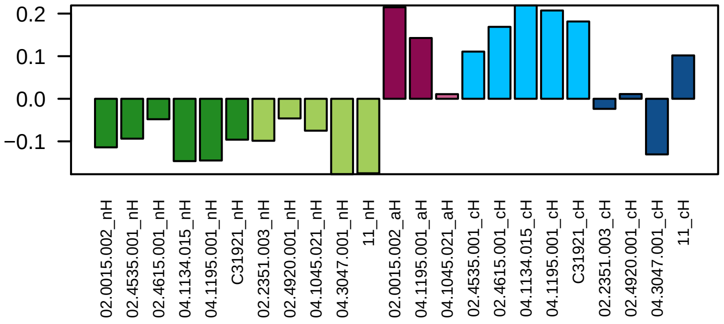
metagenes = 16
genes = 352

<r> metagenes = 0.98
<r> genes = 0.63
beta: r2= 0.28 / log p= −2.05

samples with spot = 4 (17.4 %)
MLH1_adenomaHNPCC : 1 (50 %)
MLH1_cancerHNPCC : 3 (60 %)





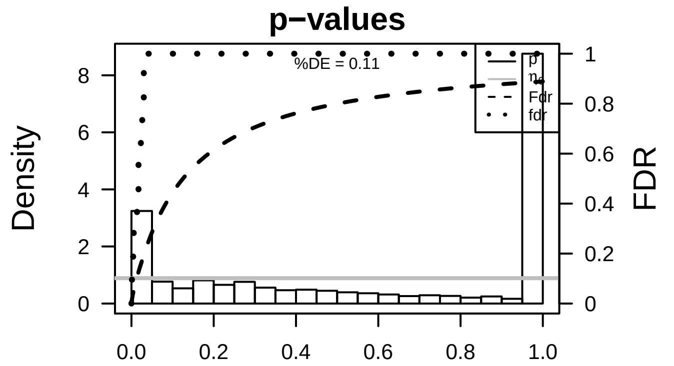


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.84	−0.57	0.57	REG1A	regenerating islet−derived 1 alpha [Source:HGNC Symbol;Ac
2	ENSG000001	1.71	−0.34	0.52	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	0.58	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	0.41	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) [Source
7	ENSG000001	1.31	−0.29	0.4	CXCL8	chemokine (C−X−C motif) ligand 8 [Source:HGNC Symbol;Ac
8	ENSG000001	1.27	−0.21	0.52	REG1B	regenerating islet−derived 1 beta [Source:HGNC Symbol;Acc
9	ENSG000001	1.25	−0.21	0.58	DMBT1	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
10	ENSG000001	1.17	−0.36	0.5	REG4	regenerating islet−derived family, member 4 [Source:HGNC S
11	ENSG000001	1.16	−0.2	0.6	MMP3	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC
12	ENSG000001	1.15	−0.44	0.74	SPINK1	serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symb
13	ENSG000000	1.15	−0.35	0.5	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
14	ENSG000002	1.1	−0.18	0.56	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy
15	ENSG000001	1.05	−0.66	0.85	LCN2	lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
16	ENSG000001	1.05	−0.87	0.79	AGR2	anterior gradient 2, protein disulphide isomerase family memb
17	ENSG000001	0.98	−0.17	0.41	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
18	ENSG000001	0.97	−0.41	0.65	SPINK4	serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symb
19	ENSG000001	0.91	−1	0.76	GPX2	glutathione peroxidase 2 [Source:HGNC Symbol;Acc:HGNC:
20	ENSG000001	0.87	−0.25	0.5	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−47	92 / 813	GSEA	GRADE_COLON_CANCER_UP
2	1e−41	64 / 400	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
3	2e−39	39 / 113	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
4	2e−37	67 / 519	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
5	9e−37	76 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	3e−35	68 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
7	3e−35	55 / 350	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
8	8e−34	41 / 174	GSEA	LI_AMPLIFIED_IN_LUNG_CANCER
9	8e−33	37 / 138	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	2e−32	81 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
11	1e−31	45 / 248	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
12	1e−30	73 / 807	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
13	7e−30	65 / 645	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
14	8e−29	71 / 811	Lymph	WIRTH_lymphoma937_spot D
15	2e−28	47 / 327	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
16	2e−27	70 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
17	1e−26	23 / 52	GSEA	ISHIDA_E2F_TARGETS
18	3e−26	65 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
19	8e−26	43 / 303	GSEA	HORIUCHI_WTAP_TARGETS_DN
20	1e−25	32 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
21	2e−25	41 / 275	GSEA	GRADE_COLON_AND_RECTAL_CANCER_UP
22	2e−25	5 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
23	3e−25	64 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
24	5e−25	26 / 85	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
25	8e−25	243 / 8123	Colon	TssF_Colon
26	8e−25	34 / 179	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
27	1e−24	35 / 195	HM	HALLMARK_MYC_TARGETS_V1
28	1e−24	43 / 323	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
29	1e−24	92 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
30	1e−24	67 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
31	2e−24	41 / 292	GSEA	MUELLER_PLURINET
32	2e−24	83 / 1298	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
33	3e−24	54 / 550	Cance	Lembcke_Normal vs Adenoma
34	7e−24	30 / 138	GSEA	DANG_MYC_TARGETS_UP
35	1e−23	26 / 95	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
36	3e−23	30 / 145	GSEA	BENPORATH_PROLIFERATION
37	4e−23	32 / 172	GSEA	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
38	9e−23	52 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
39	2e−22	33 / 197	HM	HALLMARK_E2F_TARGETS
40	4e−22	40 / 316	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	1e−17	32 / 259	translation
2	3e−14	44 / 633	cellular protein metabolic process
3	9e−14	19 / 108	SRP−dependent cotranslational protein targeting to membrane
4	1e−09	12 / 62	cell redox homeostasis
5	2e−09	42 / 820	gene expression
6	3e−09	28 / 410	mitotic cell cycle
7	3e−09	13 / 82	mitochondrial translational elongation
8	3e−09	14 / 98	mitochondrial translation
9	4e−09	18 / 174	protein folding
10	1e−08	12 / 77	nucleobase−containing small molecule metabolic process
11	3e−08	12 / 82	mitochondrial translational initiation
12	4e−08	13 / 101	translational elongation
13	4e−08	12 / 84	mitochondrial translational termination
14	5e−08	15 / 142	translational initiation
15	6e−08	13 / 104	endoplasmic reticulum unfolded protein response
16	6e−08	8 / 31	spliceosomal snRNP assembly
17	7e−08	12 / 88	translational termination
18	8e−07	12 / 109	viral transcription
19	8e−07	14 / 151	G1/S transition of mitotic cell cycle
20	1e−06	28 / 549	viral process

Brain

Rank	p−value	#in/all	Geneset
1	5e−07	227 / 9923	Overlap_fetal_midbrain_K9K27me3
2	8e−06	56 / 1680	Fetal_ReprPCWk
3	8e−05	70 / 2443	Fetal_Quies
4	7e−03	80 / 3370	Mid_Frontal_Lobe_ZNF
5	9e−03	26 / 865	Mid_Frontal_Lobe_Het
6	1e−02	27 / 939	Fetal_HetRpts
7	1e−02	25 / 855	Overlap_fetal_midbrain_ZNF
8	2e−02	8 / 191	Overlap_fetal_midbrain_Het
9	3e−02	205 / 10239	Overlap_fetal_midbrain_ReprPC
10	1e−01	11 / 400	Fetal_ZNF
11	1e−01	82 / 3977	Mid_Frontal_Lobe_ReprPC
12	1e−01	19 / 787	Overlap_fetal_midbrain_TssP
13	3e−01	203 / 10800	Overlap_fetal_midbrain_Quies
14	3e−01	34 / 1713	Mid_Frontal_Lobe_ReprPCWk
15	4e−01	5 / 232	Fetal_ReprPC
16	5e−01	38 / 2084	Mid_Frontal_Lobe_K9K27me3
17	7e−01	19 / 1108	Overlap_fetal_midbrain_TssA
18	7e−01	49 / 2820	Mid_Frontal_Lobe_HetRpts
19	8e−01	8 / 552	Fetal_Tx
20	9e−01	5 / 408	Mid_Frontal_Lobe_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	2e−25	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	3e−24	54 / 550	Lembcke_Normal vs Adenoma
3	1e−21	3 / 16	RHODES_CANCER_META_SIGNATURE
4	5e−21	6 / 16	RHODES_UNDIFFERENTIATED_CANCER
5	6e−13	3 / 14	LIU_PROSTATE_CANCER_UP
6	7e−07	8 / 41	ZHANG_MM up
7	7e−06	5 / 16	GENTLES_modul2
8	2e−04	4 / 16	GENTLES_modul7
9	7e−04	3 / 10	GENTLES_modul3
10	1e−03	22 / 574	Lembcke_Colonic Inflammation
11	2e−03	6 / 71	SHAUGHNESSY_MM high risk
12	2e−03	3 / 15	BEN−PORATH_UP
13	3e−03	3 / 16	WOLFER_overlap genes
14	3e−03	3 / 16	GENTLES_modul1
15	4e−03	8 / 136	PanCan_CC+Apop_geneset_nanostring
16	4e−03	10 / 198	PanCan_PI3K_geneset_nanostring
17	5e−03	4 / 37	KUIPER_MM good survival
18	1e−02	4 / 50	PanCan_DNARepair_geneset_nanostring
19	2e−02	4 / 52	KUIPER_MM poor survival
20	2e−02	2 / 11	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	1e−20	116 / 2638	extracellular exosome
2	5e−13	22 / 168	ribosome
3	2e−12	106 / 2974	cytosol
4	1e−09	29 / 425	mitochondrial inner membrane
5	2e−09	60 / 1441	mitochondrion
6	4e−09	7 / 15	U1 snRNP
7	7e−09	6 / 10	methylosome
8	4e−08	40 / 842	endoplasmic reticulum
9	5e−07	5 / 10	U4 snRNP
10	8e−07	5 / 11	endoplasmic reticulum chaperone complex
11	9e−07	9 / 57	endoplasmic reticulum−Golgi intermediate compartment
12	2e−06	11 / 97	melanosome
13	2e−06	45 / 1176	extracellular space
14	4e−06	6 / 24	small ribosomal subunit
15	5e−06	6 / 25	U12−type spliceosomal complex
16	5e−06	33 / 767	endoplasmic reticulum membrane
17	5e−06	77 / 2554	nucleoplasm
18	6e−06	14 / 179	endoplasmic reticulum lumen
19	1e−05	5 / 17	small nuclear ribonucleoprotein complex
20	1e−05	5 / 17	SMN−Sm protein complex

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	19 / 436	Chr 22
2	8e−04	35 / 1083	Chr 17
3	6e−02	20 / 745	Chr 9
4	1e−01	33 / 1425	Chr 19
5	2e−01	13 / 522	Chr 20
6	3e−01	13 / 582	Chr 15
7	4e−01	17 / 859	Chr 7
8	4e−01	19 / 976	Chr 6
9	5e−01	36 / 1920	Chr 1
10	5e−01	19 / 1017	Chr 12
11	7e−01	20 / 1172	Chr 11
12	7e−01	12 / 735	Chr 4
13	8e−01	13 / 847	Chr 16
14	8e−01	10 / 715	Chr 10
15	9e−01	18 / 1228	Chr 2
16	9e−01	2 / 191	Chr 21
17	9e−01	3 / 272	Chr 18
18	9e−01	14 / 1043	Chr 3
19	9e−01	7 / 613	Chr 14
20	1e+00	9 / 862	Chr 5

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−37	76 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	2e−27	70 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
3	8e−25	243 / 8123	TssF_Colon
4	5e−14	259 / 10475	TssA_Colon
5	2e−10	104 / 3122	TxEnhG1_Colon
6	4e−09	11 / 55	Marisa_CRC−cluster−e
7	3e−08	18 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
8	2e−07	229 / 9930	Tx_Colon
9	3e−07	22 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
10	4e−07	169 / 6761	TssD2_Colon
11	6e−07	259 / 11791	Enh_Colon
12	3e−05	29 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	8e−05	33 / 877	TxEnhG2_Colon
14	7e−03	2 / 7	Marisa_CRC−C5
15	1e−02	2 / 10	KIM_CRC−MSI−regulated_DN
16	1e−02	2 / 10	Marisa_CRC−C1
17	3e−02	236 / 11968	TssWk_Colon
18	4e−02	70 / 3112	EnhA_Colon
19	4e−02	189 / 9390	TxWk_Colon
20	5e−02	13 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	6e−17	47 / 608	GUDJ_psoriasis up
2	1e−01	2 / 37	BCHETNIA_EBM−DM up
3	3e−01	1 / 22	BCHETNIA_EBM up
4	6e−01	7 / 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	1e−25	32 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	4e−11	13 / 59	developing astrocytes
3	3e−10	13 / 69	cultured astroglia vs. in vivo astrocytes
4	1e−06	10 / 77	Weller_LGG_gradeII−vs−III_DOWN
5	1e−04	7 / 63	OPC
6	3e−04	9 / 119	GIEZELT_GBM_WT_up_VS_mut
7	5e−04	5 / 36	Colman_survival_associated
8	2e−03	2 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
9	2e−03	4 / 31	KIM prognostic signature LTS vs. STS
10	4e−03	7 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	6e−03	3 / 21	KIM deleted & downregulated in LTS
12	9e−03	5 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
13	9e−03	6 / 97	Weller_LGG_1p19qDel−vs−intact_UP
14	2e−02	4 / 55	Gorovets_LGG_PG_subclass
15	3e−02	12 / 344	Up
16	3e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
17	4e−02	3 / 40	Christensen_hypomethylated_in_ependymoma
18	4e−02	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
19	5e−02	46 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
20	7e−02	9 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−47	92 / 813	GRADE_COLON_CANCER_UP
2	1e−41	64 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
3	2e−39	39 / 113	WHITEFORD_PEDIATRIC_CANCER_MARKERS
4	2e−37	67 / 519	BERENJENO_TRANSFORMED_BY_RHOA_UP
5	3e−35	68 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	3e−35	55 / 350	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
7	8e−34	41 / 174	LI_AMPLIFIED_IN_LUNG_CANCER
8	8e−33	37 / 138	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	2e−32	81 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
10	1e−31	45 / 248	KOBAYASHI_EGFR_SIGNALING_24HR_DN
11	7e−30	65 / 645	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
12	2e−28	47 / 327	WONG_EMBRYONIC_STEM_CELL_CORE
13	1e−26	23 / 52	ISHIDA_E2F_TARGETS
14	3e−26	65 / 747	PUJANA_CHEK2_PCC_NETWORK
15	8e−26	43 / 303	HORIUCHI_WTAP_TARGETS_DN
16	2e−25	41 / 275	GRADE_COLON_AND_RECTAL_CANCER_UP
17	2e−25	5 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	3e−25	64 / 754	MARTENS_TRETINOIN_RESPONSE_DN
19	5e−25	26 / 85	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
20	8e−25	34 / 179	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−24	35 / 195	HALLMARK_MYC_TARGETS_V1
2	2e−22	33 / 197	HALLMARK_E2F_TARGETS
3	3e−19	30 / 196	HALLMARK_G2M_CHECKPOINT
4	2e−12	23 / 199	HALLMARK_MTORC1_SIGNALING
5	7e−10	20 / 198	HALLMARK_GLYCOLYSIS
6	9e−08	10 / 58	HALLMARK_MYC_TARGETS_V2
7	1e−07	13 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	3e−06	15 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
9	2e−05	12 / 146	HALLMARK_DNA_REPAIR
10	1e−03	11 / 197	HALLMARK_IL2_STAT5_SIGNALING
11	3e−03	10 / 193	HALLMARK_XENOBIOTIC_METABOLISM
12	8e−03	8 / 155	HALLMARK_UV_RESPONSE_UP
13	1e−02	4 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	1e−02	9 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	3e−02	8 / 196	HALLMARK_MITOTIC_SPINDLE
16	3e−02	8 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
17	4e−02	5 / 102	HALLMARK_PEROXISOME
18	4e−02	4 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
19	6e−02	7 / 192	HALLMARK_COMPLEMENT
20	7e−02	6 / 157	HALLMARK_APOPTOSIS

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	0.8	1 / 91	DUMEAUX_Smoking enriched genes
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_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	1e−30	73 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	8e−29	71 / 811	WIRTH_lymphoma937_spot D
3	3e−21	39 / 317	TARTE_Plasmablast signature
4	1e−11	15 / 78	TARTE_Plasma cell signature
5	4e−11	161 / 5643	HOPP_Txn_transition
6	2e−09	15 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
7	3e−09	15 / 116	WIRTH_lymphoma937_spot MM
8	3e−06	10 / 83	ROSOLOWSKI_green UP
9	3e−06	14 / 171	WIRTH_lymphoma937_spot C
10	1e−05	13 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
11	5e−05	10 / 115	ROSOLOWSKI_green total
12	1e−04	11 / 150	DAVE_BL−vs−DLBCL
13	5e−03	6 / 87	Aukema_BCL2 DN_BCL6 UP
14	1e−02	15 / 414	TARTE_Mature plasma cell signature
15	1e−02	6 / 105	ROSOLOWSKI_blue total
16	1e−02	10 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
17	1e−02	174 / 8358	HOPP_Active_promoter
18	2e−02	5 / 87	ROSOLOWSKI_red total
19	2e−02	156 / 7491	HOPP_Txn_elongation
20	3e−02	9 / 233	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_

MF

Rank	p−value	#in/all	Geneset
1	3e−15	24 / 162	structural constituent of ribosome
2	5e−14	59 / 1091	poly(A) RNA binding
3	1e−08	8 / 25	isomerase activity
4	1e−05	25 / 513	RNA binding
5	2e−05	4 / 10	U6 snRNA binding
6	3e−05	5 / 21	protein disulfide isomerase activity
7	5e−05	6 / 37	chemokine activity
8	6e−05	9 / 94	unfolded protein binding
9	8e−04	6 / 60	peptide binding
10	1e−03	7 / 89	histone deacetylase binding
11	1e−03	4 / 27	peptidase inhibitor activity
12	2e−03	7 / 93	mRNA binding
13	2e−03	21 / 578	identical protein binding
14	3e−03	14 / 328	enzyme binding
15	3e−03	6 / 80	chaperone binding
16	4e−03	3 / 18	cofactor binding
17	5e−03	3 / 19	nucleoside diphosphate kinase activity
18	6e−03	3 / 20	amino acid binding
19	6e−03	11 / 245	ubiquitin protein ligase binding
20	6e−03	4 / 40	ribosome binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 108	hsa−miR−605
2	3e−04	8 / 94	hsa−miR−378
3	7e−04	5 / 39	hsa−miR−593
4	7e−04	9 / 131	hsa−miR−145
5	2e−03	4 / 28	hsa−miR−519e*
6	3e−03	5 / 53	hsa−miR−337−3p
7	5e−03	4 / 37	hsa−miR−770−5p
8	6e−03	5 / 63	hsa−miR−324−3p
9	7e−03	4 / 41	hsa−miR−518f*
10	8e−03	3 / 23	hsa−miR−516a−5p
11	9e−03	5 / 70	hsa−miR−193b
12	9e−03	6 / 98	hsa−miR−133b
13	1e−02	7 / 129	hsa−miR−223
14	1e−02	6 / 99	hsa−miR−133a
15	1e−02	3 / 25	hsa−miR−99b
16	1e−02	2 / 9	hsa−miR−615−3p
17	1e−02	11 / 269	hsa−miR−548p
18	1e−02	6 / 102	hsa−miR−150
19	1e−02	12 / 307	hsa−miR−34c−5p
20	1e−02	5 / 76	hsa−miR−1254

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.002	5 / 14	BENTINK_myc.1
2	0.214	1 / 13	BENTINK_e2f3.2
3	0.228	1 / 14	GUSTAFSON_PI3K_UP
4	0.228	1 / 14	BENTINK_e2f3.1
5	1.000	0 / 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	2e−15	17 / 66	MYC_Targets UP
2	1e−09	56 / 1294	KIM_MYC targets
3	4e−08	7 / 20	MYC_Metabolism UP
4	5e−08	59 / 1549	ICGC_Myc_targets
5	5e−07	4 / 5	MYC_Cell growth and proliferation UP
6	7e−06	4 / 8	MYC_Cell cycle UP
7	2e−05	116 / 4470	ICGC_Creb1_targets
8	3e−04	55 / 1867	HEBENSTREIT_high expression TF
9	1e−03	2 / 3	MYC_DNA replication UP
10	1e−03	140 / 6157	ICGC_Tcf3_targets
11	2e−03	120 / 5173	ICGC_Taf1_targets
12	3e−03	124 / 5453	ICGC_Foxm1_targets
13	3e−03	3 / 17	MYC_Protein synthesis degradation UP
14	4e−03	150 / 6862	ICGC_Elf1_targets
15	4e−03	60 / 2342	ICGC_GabpPcr2_targets
16	9e−03	123 / 5578	ICGC_Stat5_targets
17	1e−02	41 / 1547	ICGC_Ets1_targets
18	1e−02	118 / 5393	ICGC_Sp1_targets
19	1e−02	120 / 5512	ICGC_Nficsc81335_targets
20	2e−02	116 / 5308	ICGC_Tcf12_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	0.12	2 / 33	VAQUERIZAS_Liver
4	0.15	2 / 37	VAQUERIZAS_Prostate
5	0.17	2 / 41	VAQUERIZAS_Testis
6	0.18	2 / 42	VAQUERIZAS_Thymus
7	0.20	2 / 45	VAQUERIZAS_Placenta
8	0.26	1 / 16	VAQUERIZAS_Fetal thyroid
9	0.28	1 / 18	VAQUERIZAS_Pancreas
10	0.31	1 / 20	VAQUERIZAS_Bone marrow
11	0.37	1 / 25	VAQUERIZAS_Spinal cord
12	0.43	1 / 30	VAQUERIZAS_Smooth muscle
13	0.53	1 / 41	VAQUERIZAS_Fetal brain
14	0.54	1 / 42	VAQUERIZAS_Thyroid
15	0.57	1 / 46	VAQUERIZAS_Whole brain
16	0.78	2 / 155	VAQUERIZAS_General
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	0.022	10 / 259	PALMER_Granulocytes signature up
3	0.023	2 / 13	WIRTH_Globus pallidus
4	0.026	2 / 14	WIRTH_B−cells
5	0.104	2 / 30	PALMER_Lymphocytes signature up
6	0.184	6 / 208	PALMER_B−Cell signature up
7	0.214	1 / 13	WIRTH_Cortex cerebri
8	0.228	1 / 14	WIRTH_Thyroid gland
9	0.242	1 / 15	WIRTH_Telencephalon
10	0.255	4 / 140	PALMER_T−Cell signature up
11	0.632	1 / 54	WIRTH_Pancreas
12	0.781	1 / 82	WIRTH_Homeostasis
13	1.000	1 / 427	WIRTH_Immune system
14	1.000	1 / 476	WIRTH_Nervous System
15	1.000	0 / 6	WIRTH_Pituitary gland
16	1.000	0 / 13	WIRTH_Sec. lymphoid organs
17	1.000	0 / 13	WIRTH_Prim. lymphoid organs
18	1.000	0 / 12	WIRTH_Tonsil
19	1.000	0 / 14	WIRTH_Thymus
20	1.000	0 / 14	WIRTH_Bone marrow

Toxic

Rank	p−value	#in/all	Geneset
1	0.5	25 / 1343	LU_BPDE 1n DN
2	1.0	67 / 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	

D−Clusters

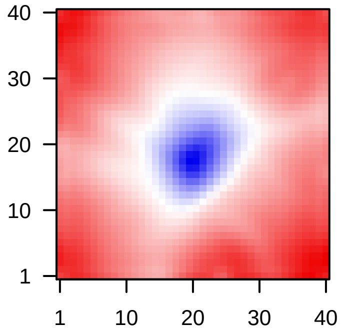
Spot Summary: D

metagenes = 12
genes = 234

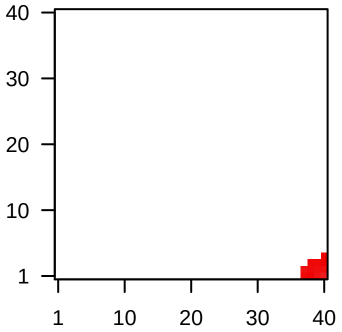
<r> metagenes = 0.99
<r> genes = 0.67
beta: r2= 0.94 / log p= −13.41

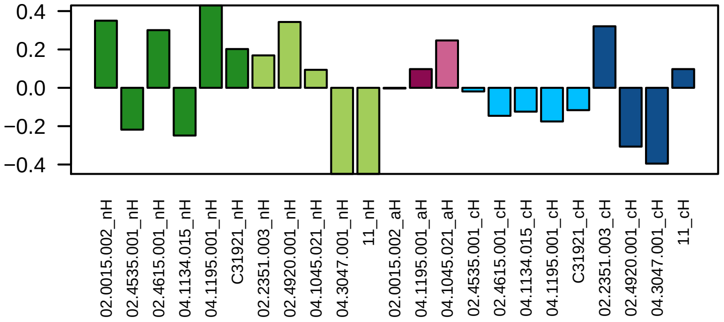
samples with spot = 7 (30.4 %)
MLH1_normHNPCC : 4 (66.7 %)
other_normHNPCC : 1 (20 %)
other_adenomaHNPCC : 1 (100 %)
other_cancerHNPCC : 1 (25 %)

Overview Map



Spot





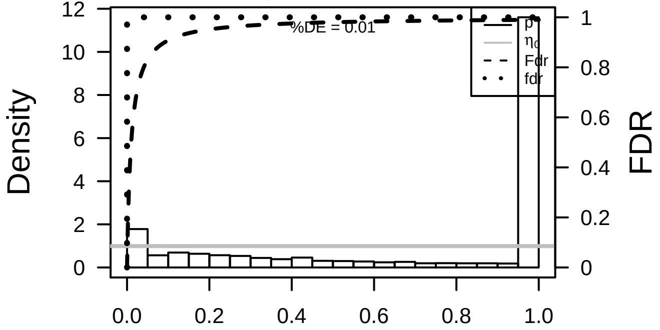
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	1.55	−0.86	0.89	PHGR1	proline/histidine/glycine−rich 1 [Source:HGNC Symbol;Acc:H
2	ENSG000001	1.42	−0.99	0.88	GUCA2A	guanylate cyclase activator 2A (guanylin) [Source:HGNC Syn
3	ENSG000001	1.33	−0.38	0.48	PP7080	uncharacterized LOC25845 [Source:EntrezGene;Acc:25845]
4	ENSG000001	1.3	−0.63	0.74	AQP8	aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG000001	1.28	−0.52	0.66	ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;A
6	ENSG000000	1.26	−0.59	0.72	CLCA4	chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
7	ENSG000000	1.24	−0.81	0.86	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 [
9	ENSG000001	1.24	−0.49	0.76	ZG16	zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGN
10	ENSG000000	1.22	−0.52	0.81	GUCA2B	guanylate cyclase activator 2B (uroguanylin) [Source:HGNC
11	ENSG000001	1.21	−0.51	0.64	TFF1	trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	−0.44	0.71	PRAP1	proline−rich acidic protein 1 [Source:HGNC Symbol;Acc:HGN
13	ENSG000002	1.15	−0.61	0.84		
14	ENSG000001	1.13	−1.09	0.9	FABP1	fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:
15	ENSG000001	1.12	−0.37	0.76	AKR1B10	aldo−keto reductase family 1, member B10 (aldose reductase
16	ENSG000001	1.1	−0.7	0.57	PI3	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
17	ENSG000001	1.06	−1.31	0.66	PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	ENSG000001	1.02	−1.15	0.7	CEACAM5	carcinoembryonic antigen−related cell adhesion molecule 5 [
19	ENSG000001	1	−0.96	0.91	KRT20	keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
20	ENSG000001	1	−0.35	0.79	C11orf86	chromosome 11 open reading frame 86 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−71	51 / 104	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	7e−61	75 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
3	3e−37	33 / 110	Colon	Marisa_CRC−cluster−h
4	3e−30	54 / 643	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	3e−27	50 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	9e−27	98 / 2638	CC	extracellular exosome
7	4e−21	38 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
8	4e−21	37 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
9	1e−20	30 / 262	GSEA	SABATES_COLORECTAL_ADENOMA_DN
10	1e−20	24 / 144	Lymph	WIRTH_lymphoma937_spot G
11	9e−20	35 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
12	1e−19	23 / 142	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil
13	2e−19	27 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
14	2e−18	65 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	3e−18	27 / 248	GSEA	JAEGER_METASTASIS_DN
16	9e−18	91 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
17	5e−17	20 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
18	1e−16	90 / 3122	Colon	TxEnhG1_Colon
19	1e−14	13 / 48	GSEA	KEGG_DRUG_METABOLISM_OTHER_ENZYMES
20	2e−14	13 / 49	Colon	Marisa_CRC−cluster−f
21	3e−14	13 / 51	GSEA	KEGG_STEROID_HORMONE_BIOSYNTHESIS
22	6e−14	10 / 23	BP	flavonoid biosynthetic process
23	6e−14	10 / 23	BP	flavonoid glucuronidation
24	6e−14	37 / 711	GSEA	LEE_BMP2_TARGETS_UP
25	7e−14	20 / 181	GSEA	WU_CELL_MIGRATION
26	9e−14	10 / 24	GSEA	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
27	3e−13	16 / 109	GSEA	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
28	4e−13	40 / 877	Colon	TxEnhG2_Colon
29	4e−13	10 / 27	GSEA	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS
30	4e−13	9 / 19	BP	cellular glucuronidation
31	4e−13	13 / 62	GSEA	KEGG_RETINOL_METABOLISM
32	8e−13	192 / 11791	Colon	Enh_Colon
33	1e−12	22 / 261	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
34	1e−12	10 / 30	MF	glucuronosyltransferase activity
35	2e−12	15 / 102	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
36	2e−12	34 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
37	3e−12	32 / 608	Disea	GUDJ_psoriasis up
38	3e−12	34 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
39	3e−12	28 / 467	GSEA	SWEET_LUNG_CANCER_KRAS_UP
40	6e−12	16 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	2 / 144	HORVATH_aging_genes meth UP
2	0.8	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−14	10 / 23	flavonoid biosynthetic process
2	6e−14	10 / 23	flavonoid glucuronidation
3	4e−13	9 / 19	cellular glucuronidation
4	9e−10	11 / 71	cellular response to hormone stimulus
5	4e−07	6 / 25	establishment of protein localization to plasma membrane
6	7e−07	34 / 1118	metabolic process
7	1e−06	6 / 29	one−carbon metabolic process
8	2e−06	6 / 33	bicarbonate transport
9	5e−06	8 / 79	epithelial cell differentiation
10	1e−05	4 / 12	microvillus assembly
11	1e−05	7 / 62	steroid metabolic process
12	2e−05	10 / 154	xenobiotic metabolic process
13	3e−05	4 / 16	retinoic acid metabolic process
14	6e−05	4 / 18	3'−phosphoadenosine 5'−phosphosulfate metabolic process
15	1e−04	4 / 22	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion
16	3e−04	3 / 11	intestinal absorption
17	3e−04	6 / 76	cell junction assembly
18	3e−04	4 / 28	positive regulation of establishment of protein localization to plasma membran
19	5e−04	32 / 1418	small molecule metabolic process
20	7e−04	4 / 34	negative regulation of cyclin−dependent protein kinase activity

Brain

Rank	p−value	#in/all	Geneset
1	1e−09	51 / 1713	Mid_Frontal_Lobe_ReprPCWk
2	2e−06	38 / 1394	Mid_Frontal_Lobe_Quies
3	3e−06	46 / 1890	Overlap_fetal_midbrain_TssF
4	1e−03	32 / 1478	Overlap_fetal_midbrain_TxTrans
5	1e−03	49 / 2603	Fetal_TxTrans
6	3e−03	52 / 2956	Fetal_TssA
7	9e−03	44 / 2549	Fetal_TssF
8	2e−02	17 / 805	Mid_Frontal_Lobe_EnhG
9	3e−02	17 / 840	Mid_Frontal_Lobe_TssF
10	4e−02	34 / 2084	Mid_Frontal_Lobe_K9K27me3
11	6e−02	6 / 232	Fetal_ReprPC
12	9e−02	57 / 3977	Mid_Frontal_Lobe_ReprPC
13	1e−01	8 / 408	Mid_Frontal_Lobe_TxTrans
14	1e−01	21 / 1327	Mid_Frontal_Lobe_TssP
15	1e−01	3 / 106	Overlap_fetal_midbrain_Tx
16	2e−01	15 / 940	Mid_Frontal_Lobe_Enh
17	2e−01	6 / 317	Mid_Frontal_Lobe_Tx
18	2e−01	5 / 268	Mid_Frontal_Lobe_TssA
19	3e−01	16 / 1108	Overlap_fetal_midbrain_TssA
20	6e−01	20 / 1680	Fetal_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	WANG_ER_UP
2	0.09	2 / 41	ZHANG_MM up
3	0.10	0 / 14	LIU_PROSTATE_CANCER_UP
4	0.18	1 / 16	LIU_PROSTATE_CANCER_DN
5	0.18	1 / 16	GENTLES_modul16
6	0.20	4 / 191	SPANG_LPS−index2
7	0.21	2 / 71	SHAUGHNESSY_MM high risk
8	0.33	2 / 97	PanCan_TXmisReg_geneset_nanostring
9	0.36	5 / 324	SPANG_BCL6−index2
10	0.44	2 / 123	PanCan_Driver_Gene_geneset_nanostring
11	0.46	1 / 50	PanCan_DNARepair_geneset_nanostring
12	0.46	1 / 51	PanCan_TGF−B_geneset_nanostring
13	0.49	2 / 136	PanCan_CC+Apop_geneset_nanostring
14	0.57	0 / 16	LIU_COMMON_CANCER_GENES
15	0.65	1 / 86	PanCan_JAK−ST_geneset_nanostring
16	0.69	2 / 198	PanCan_PI3K_geneset_nanostring
17	1.00	1 / 550	Lembcke_Normal vs Adenoma
18	1.00	1 / 574	Lembcke_Colonic Inflammation
19	1.00	0 / 16	RHODES_CANCER_META_SIGNATURE
20	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	9e−27	98 / 2638	extracellular exosome
2	1e−10	11 / 60	brush border
3	3e−08	17 / 268	apical plasma membrane
4	2e−06	72 / 3507	plasma membrane
5	2e−06	7 / 48	lateral plasma membrane
6	3e−06	12 / 185	basolateral plasma membrane
7	8e−06	9 / 110	bicellular tight junction
8	1e−05	8 / 91	apical part of cell
9	3e−05	6 / 51	cell periphery
10	4e−05	31 / 1176	extracellular space
11	8e−05	74 / 4052	integral component of membrane
12	2e−04	5 / 43	intercalated disc
13	2e−04	3 / 10	plasma membrane raft
14	3e−04	3 / 11	sodium:potassium−exchanging ATPase complex
15	3e−04	5 / 49	microvillus
16	8e−04	6 / 91	sarcolemma
17	1e−03	28 / 1250	integral component of plasma membrane
18	1e−03	16 / 558	intracellular membrane−bounded organelle
19	2e−03	3 / 21	desmosome
20	2e−03	8 / 190	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	0.002	16 / 582	Chr 15
2	0.053	16 / 847	Chr 16
3	0.060	31 / 1920	Chr 1
4	0.109	20 / 1228	Chr 2
5	0.299	8 / 522	Chr 20
6	0.365	19 / 1425	Chr 19
7	0.408	3 / 191	Chr 21
8	0.469	11 / 859	Chr 7
9	0.473	11 / 862	Chr 5
10	0.579	12 / 1017	Chr 12
11	0.640	8 / 715	Chr 10
12	0.640	11 / 976	Chr 6
13	0.643	3 / 272	Chr 18
14	0.666	12 / 1083	Chr 17
15	0.668	13 / 1172	Chr 11
16	0.685	8 / 745	Chr 9
17	0.777	4 / 436	Chr 22
18	0.791	7 / 735	Chr 4
19	0.804	6 / 651	Chr 8
20	0.972	7 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−71	51 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	7e−61	75 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
3	3e−37	33 / 110	Marisa_CRC−cluster−h
4	3e−30	54 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	3e−27	50 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	1e−16	90 / 3122	TxEnhG1_Colon
7	2e−14	13 / 49	Marisa_CRC−cluster−f
8	4e−13	40 / 877	TxEnhG2_Colon
9	8e−13	192 / 11791	Enh_Colon
10	3e−12	34 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
11	2e−11	79 / 3112	EnhA_Colon
12	1e−10	118 / 5889	EnhWk1_Colon
13	3e−08	161 / 9930	Tx_Colon
14	4e−06	177 / 11968	TssWk_Colon
15	5e−06	33 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
16	9e−05	3 / 8	Marisa_CRC−C6
17	3e−04	4 / 26	Ang_CRC−CIMPH−vs−L_hypo
18	4e−04	107 / 6761	TssD2_Colon
19	7e−04	151 / 10475	TssA_Colon
20	9e−04	4 / 36	Ang_CRC_Hypomethylated

Disease

Rank	p−value	#in/all	Geneset
1	3e−12	32 / 608	GUDJ_psoriasis up
2	1e−02	11 / 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	9e−18	91 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	2e−04	17 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
3	2e−04	22 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	2e−02	2 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
5	4e−02	3 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
6	5e−02	3 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
7	5e−02	17 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
8	6e−02	5 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
9	7e−02	2 / 36	Shaw_down_in_1p19q
10	7e−02	2 / 36	Colman_survival_associated
11	9e−02	3 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	1e−01	1 / 9	Colman_survival_robust
13	1e−01	9 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
14	1e−01	3 / 96	Weller_LGG_A_vs_O_UP
15	1e−01	6 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
16	1e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
17	1e−01	2 / 54	WILLSCHER_GBM_proteomics_wtOnly_SpotG
18	2e−01	1 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
19	2e−01	1 / 14	Christensen_hypermethylated_in_ependymoma
20	2e−01	1 / 15	Mukasa_UP_in_GBM

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−21	38 / 455	ONDER_CDH1_TARGETS_2_DN
2	4e−21	37 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
3	1e−20	30 / 262	SABATES_COLORECTAL_ADENOMA_DN
4	9e−20	35 / 412	LIM_MAMMARY_STEM_CELL_DN
5	2e−19	27 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
6	2e−18	65 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
7	3e−18	27 / 248	JAEGER_METASTASIS_DN
8	5e−17	20 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
9	1e−14	13 / 48	KEGG_DRUG_METABOLISM_OTHER_ENZYMES
10	3e−14	13 / 51	KEGG_STEROID_HORMONE_BIOSYNTHESIS
11	6e−14	37 / 711	LEE_BMP2_TARGETS_UP
12	7e−14	20 / 181	WU_CELL_MIGRATION
13	9e−14	10 / 24	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
14	3e−13	16 / 109	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
15	4e−13	10 / 27	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS
16	4e−13	13 / 62	KEGG_RETINOL_METABOLISM
17	1e−12	22 / 261	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
18	2e−12	15 / 102	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
19	2e−12	34 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
20	3e−12	28 / 467	SWEET_LUNG_CANCER_KRAS_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−09	16 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
2	1e−07	14 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	5e−06	12 / 196	HALLMARK_P53_PATHWAY
4	2e−05	11 / 189	HALLMARK_KRAS_SIGNALING_UP
5	1e−04	9 / 154	HALLMARK_FATTY_ACID_METABOLISM
6	6e−04	9 / 193	HALLMARK_XENOBIOTIC_METABOLISM
7	2e−03	8 / 192	HALLMARK_COMPLEMENT
8	7e−03	5 / 98	HALLMARK_ANDROGEN_RESPONSE
9	8e−03	5 / 102	HALLMARK_PEROXISOME
10	9e−03	7 / 190	HALLMARK_APICAL_JUNCTION
11	1e−02	6 / 157	HALLMARK_APOPTOSIS
12	3e−02	6 / 198	HALLMARK_HYPOXIA
13	3e−02	6 / 198	HALLMARK_GLYCOLYSIS
14	5e−02	4 / 112	HALLMARK_BILE_ACID_METABOLISM
15	5e−02	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
16	8e−02	5 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
17	9e−02	5 / 194	HALLMARK_INFLAMMATORY_RESPONSE
18	9e−02	5 / 197	HALLMARK_IL2_STAT5_SIGNALING
19	9e−02	5 / 199	HALLMARK_ADIPOGENESIS
20	1e−01	3 / 94	HALLMARK_PROTEIN_SECRETION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.177	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.187	1 / 17	DUMEAUX_High bmi enriched genes
4	0.671	1 / 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	24 / 144	WIRTH_lymphoma937_spot G
2	1e−19	23 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
3	3e−05	89 / 5039	HOPP_Repressed
4	1e−03	7 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
5	3e−03	3 / 23	SPANG_BAFF 9hrs UP
6	3e−03	6 / 115	ROSOLOWSKI_green total
7	1e−02	3 / 40	ROSOLOWSKI_blue DOWN
8	1e−02	9 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
9	1e−02	9 / 315	WIRTH_lymphoma937_spot E
10	2e−02	3 / 50	Subero_B−ALL_hyper_meth
11	3e−02	3 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
12	6e−02	3 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
13	6e−02	3 / 75	Subero_FL_hyper_meth
14	6e−02	3 / 75	WIRTH_lymphoma937_spot IM
15	7e−02	43 / 2838	HOPP_Poised_promoter
16	7e−02	1 / 6	DAVE_MHCCII BL DN
17	7e−02	6 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
18	8e−02	3 / 83	ROSOLOWSKI_green UP
19	1e−01	3 / 94	Subero_T−ALL_hyper_meth
20	1e−01	2 / 48	Subero_INT_hypo_meth

MF

Rank	p−value	#in/all	Geneset
1	1e−12	10 / 30	glucuronosyltransferase activity
2	1e−11	10 / 37	transferase activity, transferring hexosyl groups
3	3e−07	5 / 13	carbonate dehydratase activity
4	3e−05	4 / 15	retinoic acid binding
5	4e−05	11 / 204	structural molecule activity
6	1e−04	21 / 693	protein homodimerization activity
7	2e−04	3 / 10	sodium:potassium−exchanging ATPase activity
8	2e−04	20 / 672	calcium ion binding
9	5e−04	7 / 113	actin filament binding
10	9e−04	3 / 16	fatty acid binding
11	1e−03	3 / 17	sodium channel activity
12	1e−03	5 / 69	beta−catenin binding
13	3e−03	5 / 81	drug binding
14	5e−03	4 / 57	serine−type peptidase activity
15	5e−03	4 / 58	cell adhesion molecule binding
16	6e−03	2 / 10	potassium ion binding
17	6e−03	5 / 96	structural constituent of cytoskeleton
18	7e−03	2 / 11	estradiol 17−beta−dehydrogenase activity
19	7e−03	2 / 11	sulfate transmembrane transporter activity
20	7e−03	2 / 11	transferase activity, transferring phosphorus−containing groups

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	3 / 38	hsa−miR−1224−5p
2	0.03	5 / 147	hsa−miR−138
3	0.05	2 / 29	hsa−miR−591
4	0.07	2 / 36	hsa−miR−1287
5	0.08	4 / 136	hsa−miR−485−5p
6	0.09	2 / 41	hsa−miR−601
7	0.10	3 / 90	hsa−miR−587
8	0.10	2 / 44	hsa−miR−483−5p
9	0.13	1 / 11	hsa−miR−487b
10	0.13	3 / 104	hsa−miR−516b
11	0.13	2 / 53	hsa−miR−337−3p
12	0.14	7 / 352	hsa−miR−142−5p
13	0.14	4 / 164	hsa−miR−298
14	0.15	1 / 13	hsa−miR−1249
15	0.15	2 / 56	hsa−miR−208a
16	0.17	1 / 15	hsa−miR−671−3p
17	0.18	1 / 16	hsa−miR−598
18	0.18	4 / 184	hsa−miR−548e
19	0.18	4 / 184	hsa−miR−374a
20	0.19	1 / 17	hsa−miR−1298

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	5e−05	41 / 1798	HEBENSTREIT_low expression TF
2	2e−01	1 / 20	MYC_Metabolism UP
3	5e−01	43 / 3511	ICGC_Rad21_targets
4	6e−01	1 / 66	MYC_Targets UP
5	6e−01	18 / 1523	ICGC_P300_targets
6	8e−01	31 / 2827	ICGC_Bcl3_targets
7	8e−01	57 / 5135	ICGC_Ebfsc137065_targets
8	9e−01	24 / 2401	ICGC_Bcl11_targets
9	9e−01	5 / 619	ICGC_RxraPcr1_targets
10	9e−01	6 / 731	ICGC_SrfPcr2_targets
11	9e−01	6 / 745	ICGC_NrsfPcr2_targets
12	9e−01	32 / 3177	ICGC_Irf4_targets
13	9e−01	69 / 6406	ICGC_Pax5_targets
14	9e−01	33 / 3305	ICGC_BatfPcr1_targets
15	1e+00	18 / 2149	ICGC_Mef2_targets
16	1e+00	11 / 1506	ICGC_Usf1_targets
17	1e+00	44 / 4714	ICGC_Pu1_targets
18	1e+00	10 / 1472	ICGC_NrsfPcr1_targets
19	1e+00	8 / 1294	KIM_MYC targets
20	1e+00	52 / 5552	ICGC_Pol24_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.001	3 / 18	VAQUERIZAS_Pancreas
2	0.003	3 / 24	VAQUERIZAS_Trachea
3	0.010	2 / 13	VAQUERIZAS_Skin
4	0.043	3 / 64	VAQUERIZAS_Lung
5	0.054	2 / 31	VAQUERIZAS_Fetal lung
6	0.074	2 / 37	VAQUERIZAS_Prostate
7	0.093	1 / 8	VAQUERIZAS_Tongue
8	0.103	2 / 45	VAQUERIZAS_Placenta
9	0.207	1 / 19	VAQUERIZAS_Heart
10	0.235	1 / 22	VAQUERIZAS_Tonsil
11	0.331	1 / 33	VAQUERIZAS_Liver
12	0.401	1 / 42	VAQUERIZAS_Thyroid
13	1.000	0 / 41	VAQUERIZAS_Fetal brain
14	1.000	0 / 30	VAQUERIZAS_Smooth muscle
15	1.000	0 / 49	VAQUERIZAS_Uterus
16	1.000	0 / 155	VAQUERIZAS_General
17	1.000	0 / 12	VAQUERIZAS_Kidney
18	1.000	0 / 25	VAQUERIZAS_Spinal cord
19	1.000	0 / 46	VAQUERIZAS_Whole brain
20	1.000	0 / 42	VAQUERIZAS_Thymus

Tissue

Rank	p−value	#in/all	Geneset
1	1e−10	15 / 137	WIRTH_Mucosa
2	2e−07	5 / 12	WIRTH_Tonsil
3	2e−05	13 / 259	PALMER_Granulocytes signature up
4	5e−04	6 / 82	WIRTH_Homeostasis
5	1e−02	2 / 15	WIRTH_Telencephalon
6	1e−01	1 / 13	WIRTH_Prim. lymphoid organs
7	2e−01	1 / 14	WIRTH_Bone marrow
8	2e−01	1 / 14	WIRTH_Thalamus
9	2e−01	1 / 15	WIRTH_Cerebellum
10	2e−01	4 / 208	PALMER_B−Cell signature up
11	5e−01	1 / 54	WIRTH_Pancreas
12	5e−01	2 / 140	PALMER_T−Cell signature up
13	8e−01	1 / 115	WIRTH_Liver
14	9e−01	3 / 427	WIRTH_Immune system
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	0.7	60 / 5285	LU_BPDE 0.005 DN
2	1.0	8 / 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	

D−Clusters

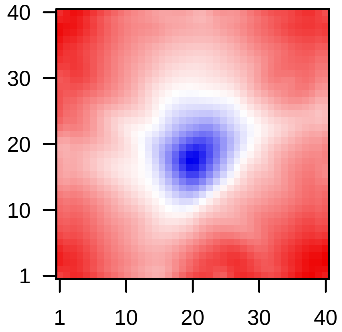
Spot Summary: E

\# metagenes = 9
\# genes = 97

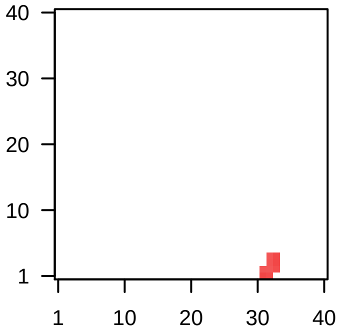
<r> metagenes = 0.99
<r> genes = 0.55
beta: r2= 0.12 / log p= −0.97

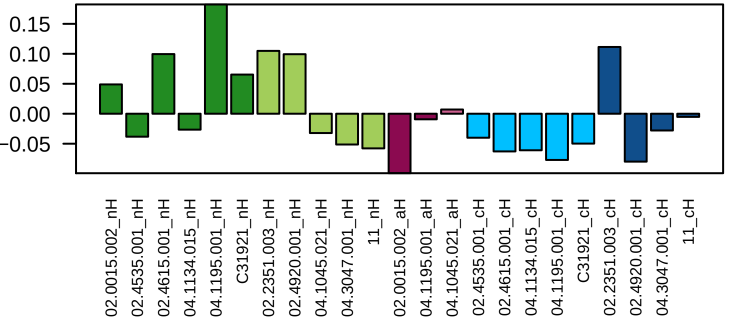
\# samples with spot = 1 (4.3 %)
MLH1_normHNPCC : 1 (16.7 %)

Overview Map



Spot





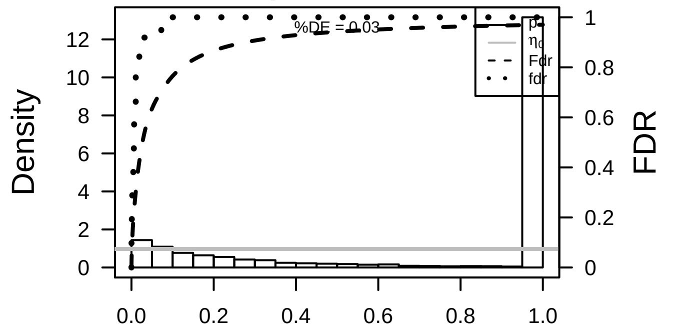
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	0.38	−0.17	0.5		
2	ENSG000001	0.38	−0.07	0.71	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:H
3	ENSG000001	0.38	−0.13	0.69	MT1F	metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]
4	ENSG000001	0.35	−0.2	0.62	CMPK1	cytidine monophosphate (UMP−CMP) kinase 1, cytosolic [So
5	ENSG000001	0.34	−0.18	0.59	CPT1A	carnitine palmitoyltransferase 1A (liver) [Source:HGNC Symb
6	ENSG000001	0.33	−0.28	0.59	CYCS	cytochrome c, somatic [Source:HGNC Symbol;Acc:HGNC:19
7	ENSG000001	0.33	−0.22	0.5	NDRG1	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:H
8	ENSG000001	0.32	−0.27	0.67	TNFRSF21	tumor necrosis factor receptor superfamily, member 21 [Sourc
9	ENSG000001	0.32	−0.24	0.62	RHOU	ras homolog family member U [Source:HGNC Symbol;Acc:HG
10	ENSG000000	0.31	−0.23	0.51	ACADVL	acyl−CoA dehydrogenase, very long chain [Source:HGNC Sy
11	ENSG000001	0.31	−0.11	0.58	ISG20	interferon stimulated exonuclease gene 20kDa [Source:HGNC
12	ENSG000001	0.3	−0.08	0.71	HEPACAM2	HEPACAM family member 2 [Source:HGNC Symbol;Acc:HGN
13	ENSG000002	0.28	−0.11	0.74		Tetraspanin [Source:UniProtKB/TrEMBL;Acc:B4E171]
14	ENSG000001	0.28	−0.15	0.87	WASL	Wiskott−Aldrich syndrome−like [Source:HGNC Symbol;Acc:H
15	ENSG000000	0.28	−0.11	0.58	EDN1	endothelin 1 [Source:HGNC Symbol;Acc:HGNC:3176]
16	ENSG000001	0.27	−0.19	0.79	CTNND1	catenin (cadherin−associated protein), delta 1 [Source:HGNC
17	ENSG000001	0.27	−0.19	0.6	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:HG
18	ENSG000001	0.27	−0.06	0.78	KRTAP13−2	keratin associated protein 13−2 [Source:HGNC Symbol;Acc:H
19	ENSG000001	0.27	−0.08	0.73	PTPRR	protein tyrosine phosphatase, receptor type, R [Source:HGNC
20	ENSG000000	0.27	−0.18	0.71	LXN	latexin [Source:HGNC Symbol;Acc:HGNC:13347]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−23	29 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
2	2e−11	88 / 11968	Colon	TssWk_Colon
3	8e−11	82 / 10475	Colon	TssA_Colon
4	3e−10	79 / 9930	Colon	Tx_Colon
5	7e−10	76 / 9390	Colon	TxWk_Colon
6	1e−09	76 / 9470	Colon	Quies3_Colon
7	1e−09	58 / 5889	Colon	EnhWk1_Colon
8	7e−09	14 / 385	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
9	6e−08	14 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
10	1e−07	20 / 1005	GSEA	NUYTTEN_EZH2_TARGETS_UP
11	2e−07	14 / 495	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
12	3e−07	11 / 296	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
13	6e−07	15 / 641	GSEA	FEVR_CTNNB1_TARGETS_UP
14	9e−07	14 / 568	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
15	1e−06	13 / 490	GSEA	ENK_UV_RESPONSE_EPIDERMIS_DN
16	2e−06	60 / 7491	Lymph	HOPP_Txn_elongation
17	5e−06	5 / 50	GSEA	PRAMOONJAGO_SOX4_TARGETS_UP
18	6e−06	12 / 493	miRN	hsa−miR−15b
19	7e−06	14 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
20	8e−06	10 / 342	miRN	hsa−let−7g
21	9e−06	11 / 424	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
22	1e−05	11 / 433	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
23	1e−05	8 / 211	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
24	1e−05	7 / 152	BP	actin cytoskeleton organization
25	1e−05	10 / 358	GSEA	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
26	1e−05	12 / 531	miRN	hsa−miR−15a
27	1e−05	11 / 444	miRN	hsa−let−7b
28	1e−05	8 / 218	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
29	1e−05	3 / 10	BP	viral budding via host ESCRT complex
30	2e−05	10 / 368	miRN	hsa−let−7i
31	2e−05	5 / 63	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
32	2e−05	8 / 224	GSEA	UDAYAKUMAR_MED1_TARGETS_DN
33	2e−05	12 / 547	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
34	2e−05	78 / 11791	Colon	Enh_Colon
35	2e−05	5 / 66	GSEA	DELPUECH_FOXO3_TARGETS_UP
36	2e−05	29 / 2638	CC	extracellular exosome
37	2e−05	73 / 10693	MF	protein binding
38	3e−05	8 / 238	GSEA	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP
39	3e−05	32 / 3122	Colon	TxEnhG1_Colon
40	3e−05	10 / 400	miRN	hsa−let−7c

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 123	HORVATH_aging_genes meth DOWN
2	0.5	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	1e−05	7 / 152	actin cytoskeleton organization
2	1e−05	3 / 10	viral budding via host ESCRT complex
3	3e−05	4 / 37	negative regulation of viral genome replication
4	8e−05	3 / 17	cell separation after cytokinesis
5	8e−05	3 / 17	regulation of centrosome duplication
6	1e−04	3 / 19	cellular response to fatty acid
7	2e−04	17 / 1279	signal transduction
8	2e−04	10 / 512	protein transport
9	1e−03	2 / 10	regulation of mitotic spindle assembly
10	1e−03	10 / 625	apoptotic process
11	1e−03	2 / 11	negative regulation of glucose import
12	2e−03	2 / 13	positive regulation of exosomal secretion
13	2e−03	4 / 106	response to virus
14	2e−03	3 / 50	negative regulation of ERK1 and ERK2 cascade
15	2e−03	6 / 272	neurotrophin TRK receptor signaling pathway
16	3e−03	4 / 117	cytoskeleton organization
17	4e−03	2 / 18	nucleus organization
18	4e−03	2 / 18	vasoconstriction
19	4e−03	2 / 20	carbohydrate transport
20	5e−03	2 / 21	negative regulation of peptidyl−serine phosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	4e−05	73 / 10800	Overlap_fetal_midbrain_Quies
2	8e−04	67 / 10278	Overlap_fetal_midbrain_ReprPCWk
3	1e−03	66 / 10239	Overlap_fetal_midbrain_ReprPC
4	3e−03	14 / 1210	Fetal_TssP
5	6e−03	8 / 552	Fetal_Tx
6	2e−02	42 / 6320	Overlap_fetal_midbrain_HetRpts
7	3e−02	11 / 1182	Fetal_EnhP
8	5e−02	58 / 9923	Overlap_fetal_midbrain_K9K27me3
9	5e−02	16 / 2084	Mid_Frontal_Lobe_K9K27me3
10	6e−02	21 / 2956	Fetal_TssA
11	6e−02	10 / 1137	Fetal_Enh
12	6e−02	20 / 2820	Mid_Frontal_Lobe_HetRpts
13	7e−02	23 / 3370	Mid_Frontal_Lobe_ZNF
14	8e−02	13 / 1713	Mid_Frontal_Lobe_ReprPCWk
15	9e−02	11 / 1394	Mid_Frontal_Lobe_Quies
16	9e−02	18 / 2603	Fetal_TxTrans
17	1e−01	10 / 1356	Fetal_K9K27me3
18	2e−01	7 / 939	Fetal_HetRpts
19	2e−01	7 / 940	Mid_Frontal_Lobe_Enh
20	2e−01	16 / 2549	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	4e−05	9 / 324	SPANG_BCL6−index2
2	5e−05	7 / 191	SPANG_LPS−index2
3	7e−03	4 / 152	PanCan_MAPK_geneset_nanostring
4	3e−02	2 / 52	KUIPER_MM poor survival
5	3e−02	3 / 136	PanCan_CC+Apop_geneset_nanostring
6	7e−02	1 / 14	LIU_PROSTATE_CANCER_UP
7	8e−02	1 / 16	GENTLES_modul1
8	8e−02	1 / 16	GENTLES_modul18
9	1e−01	2 / 123	PanCan_Driver_Gene_geneset_nanostring
10	1e−01	1 / 28	PanCan_HH_geneset_nanostring
11	2e−01	2 / 140	PanCan_RAS_geneset_nanostring
12	3e−01	1 / 78	PanCan_Wnt_geneset_nanostring
13	4e−01	1 / 97	PanCan_TXmisReg_geneset_nanostring
14	6e−01	1 / 198	PanCan_PI3K_geneset_nanostring
15	7e−01	0 / 16	LIU_PROSTATE_CANCER_DN
16	8e−01	2 / 574	Lembcke_Colonic Inflammation
17	1e+00	0 / 16	RHODES_CANCER_META_SIGNATURE
18	1e+00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
19	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−05	29 / 2638	extracellular exosome
2	2e−04	10 / 497	Golgi membrane
3	2e−04	29 / 2974	cytosol
4	6e−04	41 / 5185	cytoplasm
5	1e−03	3 / 39	recycling endosome membrane
6	3e−03	7 / 378	focal adhesion
7	3e−03	4 / 124	midbody
8	5e−03	7 / 425	mitochondrial inner membrane
9	6e−03	28 / 3507	plasma membrane
10	1e−02	8 / 596	perinuclear region of cytoplasm
11	1e−02	2 / 32	membrane coat
12	2e−02	2 / 46	cell−cell adherens junction
13	2e−02	4 / 216	actin cytoskeleton
14	3e−02	2 / 49	autophagosome
15	3e−02	9 / 864	Golgi apparatus
16	4e−02	4 / 246	endosome
17	5e−02	1 / 10	BBSome
18	5e−02	1 / 11	uropod
19	5e−02	3 / 171	cell−cell junction
20	6e−02	1 / 12	Arp2/3 protein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.008	13 / 1228	Chr 2
2	0.071	3 / 191	Chr 21
3	0.156	3 / 272	Chr 18
4	0.216	7 / 976	Chr 6
5	0.333	4 / 582	Chr 15
6	0.365	11 / 1920	Chr 1
7	0.373	3 / 436	Chr 22
8	0.400	6 / 1017	Chr 12
9	0.411	4 / 651	Chr 8
10	0.474	2 / 318	Chr 13
11	0.482	4 / 715	Chr 10
12	0.504	4 / 735	Chr 4
13	0.516	4 / 746	Chr X
14	0.628	4 / 859	Chr 7
15	0.637	5 / 1083	Chr 17
16	0.726	3 / 745	Chr 9
17	0.773	4 / 1043	Chr 3
18	0.816	2 / 613	Chr 14
19	0.845	4 / 1172	Chr 11
20	0.929	2 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−23	29 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
2	2e−11	88 / 11968	TssWk_Colon
3	8e−11	82 / 10475	TssA_Colon
4	3e−10	79 / 9930	Tx_Colon
5	7e−10	76 / 9390	TxWk_Colon
6	1e−09	76 / 9470	Quies3_Colon
7	1e−09	58 / 5889	EnhWk1_Colon
8	2e−05	78 / 11791	Enh_Colon
9	3e−05	32 / 3122	TxEnhG1_Colon
10	7e−05	31 / 3112	EnhA_Colon
11	1e−04	59 / 8123	TssF_Colon
12	2e−03	48 / 6761	TssD2_Colon
13	4e−03	11 / 877	TxEnhG2_Colon
14	2e−02	31 / 4379	TssD1_Colon
15	2e−02	8 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
16	3e−02	2 / 49	Marisa_CRC−cluster−f
17	4e−02	1 / 8	Budinska_A_Surface crypt−like_UP
18	5e−02	1 / 10	Juehling−MSI−enriched−in−7
19	6e−02	1 / 12	KIM_MSI−in−CRC
20	8e−02	1 / 17	TCGA_Mutated−in−CRC_non−hypermutated

Disease

Rank	p−value	#in/all	Geneset
1	0.03	7 / 608	GUDJ_psoriasis up
2	0.60	2 / 399	GUDJ_psoriasis down
3	1.00	0 / 22	BCHETNIA_EBM up
4	1.00	0 / 2	BCHETNIA_EBM down
5	1.00	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−04	8 / 344	Up
2	6e−03	6 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	3e−02	2 / 52	OL vs. OPC
4	3e−02	2 / 58	OL vs. MOG− OL
5	5e−02	2 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	5e−02	3 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	7e−02	5 / 434	Down_a
8	7e−02	8 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
9	8e−02	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
10	8e−02	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
11	8e−02	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
12	9e−02	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
13	1e−01	14 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
14	1e−01	1 / 27	Barbus_GBM_STS_vs._LTS
15	1e−01	1 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
16	2e−01	2 / 137	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
17	2e−01	4 / 436	Down_b
18	2e−01	2 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
19	2e−01	1 / 56	mature astrocytes
20	3e−01	1 / 59	Christensen_hypomethylated_in_primary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−09	14 / 385	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	6e−08	14 / 455	ONDER_CDH1_TARGETS_2_DN
3	1e−07	20 / 1005	NUYTTEN_EZH2_TARGETS_UP
4	2e−07	14 / 495	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
5	3e−07	11 / 296	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
6	6e−07	15 / 641	FEVR_CTNNB1_TARGETS_UP
7	9e−07	14 / 568	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
8	1e−06	13 / 490	ENK_UV_RESPONSE_EPIDERMIS_DN
9	5e−06	5 / 50	PRAMOONJAGO_SOX4_TARGETS_UP
10	7e−06	14 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
11	9e−06	11 / 424	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
12	1e−05	11 / 433	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
13	1e−05	8 / 211	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
14	1e−05	10 / 358	MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN
15	1e−05	8 / 218	RUTELLA_RESPONSE_TO_HGF_DN
16	2e−05	5 / 63	BROWNE_INTERFERON_RESPONSIVE_GENES
17	2e−05	8 / 224	UDAYAKUMAR_MED1_TARGETS_DN
18	2e−05	12 / 547	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
19	2e−05	5 / 66	DELPUECH_FOXO3_TARGETS_UP
20	3e−05	8 / 238	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP

HM

Rank	p−value	#in/all	Geneset
1	0.001	4 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	0.002	5 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.003	5 / 192	HALLMARK_COMPLEMENT
4	0.003	5 / 198	HALLMARK_HYPOXIA
5	0.015	3 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	0.016	4 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.017	4 / 197	HALLMARK_IL2_STAT5_SIGNALING
8	0.017	4 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
9	0.019	3 / 112	HALLMARK_BILE_ACID_METABOLISM
10	0.033	3 / 140	HALLMARK_UV_RESPONSE_DN
11	0.044	3 / 157	HALLMARK_APOPTOSIS
12	0.068	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	0.070	3 / 190	HALLMARK_APICAL_JUNCTION
14	0.073	3 / 193	HALLMARK_HEME_METABOLISM
15	0.073	3 / 193	HALLMARK_KRAS_SIGNALING_DN
16	0.074	3 / 194	HALLMARK_INFLAMMATORY_RESPONSE
17	0.075	3 / 196	HALLMARK_MITOTIC_SPINDLE
18	0.075	3 / 196	HALLMARK_P53_PATHWAY
19	0.077	3 / 198	HALLMARK_GLYCOLYSIS
20	0.078	3 / 199	HALLMARK_ADIPOGENESIS

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−06	60 / 7491	HOPP_Txn_elongation
2	1e−04	59 / 8147	HOPP_Weak_promoter
3	1e−04	60 / 8358	HOPP_Active_promoter
4	2e−04	45 / 5643	HOPP_Txn_transition
5	2e−04	49 / 6389	HOPP_Weak_txn
6	3e−03	4 / 123	SPANG_LPS 6hrs UP
7	4e−03	47 / 6784	HOPP_Weak_enhancer
8	6e−03	2 / 23	SPANG_BAFF 9hrs UP
9	6e−03	6 / 332	SPANG_CD40 6hrs UP
10	1e−02	5 / 279	SPANG_IL21 DN
11	1e−02	49 / 7592	HOPP_Strong_enhancer
12	2e−02	5 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
13	2e−02	5 / 315	WIRTH_lymphoma937_spot E
14	3e−02	4 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	7e−02	4 / 302	SPANG_IL21 UP
16	7e−02	19 / 2658	HOPP_Repetitive
17	7e−02	2 / 87	Aukema_BCL2 DN_BCL6 UP
18	8e−02	10 / 1215	SPANG_BCR DN
19	1e−01	5 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
20	1e−01	1 / 20	DAVE_BL Inter

MF

Rank	p−value	#in/all	Geneset
1	2e−05	73 / 10693	protein binding
2	1e−03	6 / 245	ubiquitin protein ligase binding
3	2e−03	2 / 12	ATPase activity, coupled
4	8e−03	5 / 250	GTPase activity
5	9e−03	2 / 28	cadherin binding
6	9e−03	2 / 28	epidermal growth factor receptor binding
7	9e−03	3 / 84	Rab GTPase binding
8	1e−02	6 / 371	GTP binding
9	2e−02	2 / 41	clathrin binding
10	3e−02	2 / 49	manganese ion binding
11	3e−02	7 / 578	identical protein binding
12	3e−02	2 / 53	GDP binding
13	3e−02	2 / 57	ubiquitin binding
14	4e−02	2 / 66	ATPase binding
15	5e−02	1 / 10	phospholipid scramblase activity
16	5e−02	1 / 10	type 1 angiotensin receptor binding
17	5e−02	1 / 10	type I transforming growth factor beta receptor binding
18	5e−02	1 / 11	acetylgalactosaminyltransferase activity
19	5e−02	1 / 11	I−SMAD binding
20	6e−02	1 / 12	activin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−06	12 / 493	hsa−miR−15b
2	8e−06	10 / 342	hsa−let−7g
3	1e−05	12 / 531	hsa−miR−15a
4	1e−05	11 / 444	hsa−let−7b
5	2e−05	10 / 368	hsa−let−7i
6	3e−05	10 / 400	hsa−let−7c
7	4e−05	9 / 330	hsa−let−7f
8	5e−05	6 / 129	hsa−miR−223
9	5e−05	7 / 194	hsa−miR−128
10	6e−05	10 / 431	hsa−miR−497
11	6e−05	8 / 270	hsa−miR−92b
12	6e−05	5 / 84	hsa−miR−365
13	7e−05	9 / 355	hsa−let−7e
14	8e−05	9 / 360	hsa−let−7a
15	9e−05	10 / 453	hsa−miR−424
16	2e−04	10 / 504	hsa−miR−16
17	2e−04	10 / 509	hsa−miR−107
18	3e−04	8 / 333	hsa−miR−32
19	5e−04	7 / 277	hsa−miR−363
20	5e−04	7 / 279	hsa−miR−92a

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.005	14 / 1294	KIM_MYC targets
2	0.011	17 / 1867	HEBENSTREIT_high expression TF
3	0.176	14 / 2133	ICGC_Cebpbsc150_targets
4	0.216	15 / 2401	ICGC_Bcl11_targets
5	0.303	5 / 731	ICGC_SrfPcr2_targets
6	0.338	5 / 766	ICGC_Atf3_targets
7	0.340	9 / 1506	ICGC_Usf1_targets
8	0.446	15 / 2827	ICGC_Bcl3_targets
9	0.492	17 / 3305	ICGC_BatfPcr1_targets
10	0.498	14 / 2719	ICGC_Pbx3_targets
11	0.524	23 / 4566	ICGC_Egr1_targets
12	0.589	31 / 6313	ICGC_Pou2_targets
13	0.594	23 / 4714	ICGC_Pu1_targets
14	0.602	25 / 5135	ICGC_Ebfsc137065_targets
15	0.603	3 / 619	ICGC_RxraPcr1_targets
16	0.619	25 / 5173	ICGC_Taf1_targets
17	0.640	15 / 3177	ICGC_Irf4_targets
18	0.647	7 / 1523	ICGC_P300_targets
19	0.664	7 / 1547	ICGC_Ets1_targets
20	0.676	30 / 6324	ICGC_Yy1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.02	2 / 42	VAQUERIZAS_Thyroid
2	0.02	2 / 46	VAQUERIZAS_Whole brain
3	0.08	1 / 16	VAQUERIZAS_Fetal liver
4	0.10	1 / 20	VAQUERIZAS_Bone marrow
5	0.11	1 / 23	VAQUERIZAS_Pituitary
6	0.12	1 / 25	VAQUERIZAS_Spinal cord
7	0.15	1 / 33	VAQUERIZAS_Liver
8	0.19	1 / 42	VAQUERIZAS_Thymus
9	0.20	1 / 45	VAQUERIZAS_Placenta
10	0.27	1 / 64	VAQUERIZAS_Lung
11	0.29	1 / 67	VAQUERIZAS_Whole blood
12	1.00	0 / 41	VAQUERIZAS_Fetal brain
13	1.00	0 / 37	VAQUERIZAS_Prostate
14	1.00	0 / 30	VAQUERIZAS_Smooth muscle
15	1.00	0 / 49	VAQUERIZAS_Uterus
16	1.00	0 / 155	VAQUERIZAS_General
17	1.00	0 / 12	VAQUERIZAS_Kidney
18	1.00	0 / 7	VAQUERIZAS_Appendix
19	1.00	0 / 31	VAQUERIZAS_Fetal lung
20	1.00	0 / 18	VAQUERIZAS_Pancreas

Tissue

Rank	p−value	#in/all	Geneset
1	0.01	5 / 259	PALMER_Granulocytes signature up
2	0.09	3 / 208	PALMER_B−Cell signature up
3	0.17	4 / 427	WIRTH_Immune system
4	0.51	1 / 140	PALMER_T−Cell signature up
5	1.00	0 / 6	WIRTH_Pituitary gland
6	1.00	0 / 54	WIRTH_Pancreas
7	1.00	0 / 13	WIRTH_Sec. lymphoid organs
8	1.00	0 / 13	WIRTH_Prim. lymphoid organs
9	1.00	0 / 14	WIRTH_B−cells
10	1.00	0 / 12	WIRTH_Tonsil
11	1.00	0 / 14	WIRTH_Thymus
12	1.00	0 / 12	WIRTH_Lymphocytes
13	1.00	0 / 14	WIRTH_Bone marrow
14	1.00	0 / 476	WIRTH_Nervous System
15	1.00	0 / 13	WIRTH_Globus pallidus
16	1.00	0 / 15	WIRTH_Telencephalon
17	1.00	0 / 13	WIRTH_Cortex cerebri
18	1.00	0 / 16	WIRTH_Hippocampus
19	1.00	0 / 14	WIRTH_Thalamus
20	1.00	0 / 15	WIRTH_Cerebellum

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	9 / 1343	LU_BPDE 1n DN
2	0.9	22 / 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	

D−Clusters

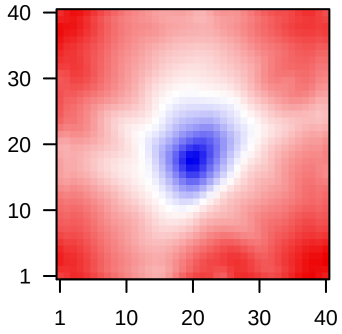
Spot Summary: F

metagenes = 14
genes = 280

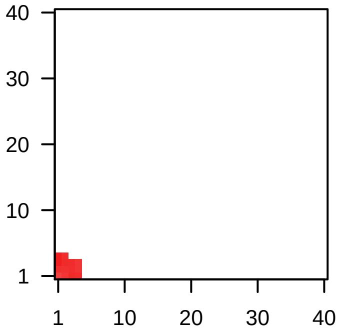
<r> metagenes = 0.99
<r> genes = 0.78
beta: r2= 0.42 / log p= −3.09

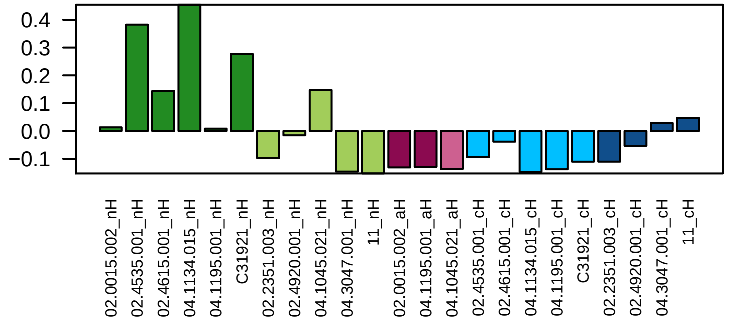
samples with spot = 3 (13 %)
MLH1_normHNPCC : 3 (50 %)

Overview Map



Spot



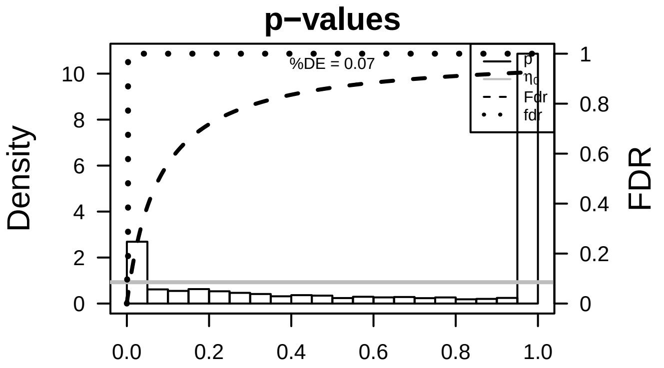


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.4	−0.53	0.84	FDCSP	follicular dendritic cell secreted protein [Source:HGNC Symbc
2	ENSG000001	1.34	−0.7	0.9	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	0.93	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	0.95	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	0.98	PTPRC	protein tyrosine phosphatase, receptor type, C [Source:HGNC
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	105 / 427	Tissu	WIRTH_Immune system
2	1e−99	152 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	7e−87	95 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	8e−79	98 / 574	Canc	Lembcke_Colonic Inflammation
5	4e−71	71 / 263	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
6	1e−63	58 / 175	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
7	1e−55	57 / 220	GSEA	MCLACHLAN_DENTAL_CARIES_UP
8	1e−52	58 / 259	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
9	8e−49	71 / 522	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
10	1e−46	50 / 210	GSEA	MCLACHLAN_DENTAL_CARIES_DN
11	1e−42	56 / 343	BP	immune response
12	9e−38	46 / 246	GSEA	QI_PLASMACYTOMA_UP
13	4e−35	210 / 7592	Lymp	HOPP_Strong_enhancer
14	6e−33	49 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
15	1e−30	36 / 181	HM	HALLMARK_ALLOGRAFT_REJECTION
16	2e−30	42 / 279	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
17	2e−29	49 / 435	GSEA	RODWELL_AGING_KIDNEY_UP
18	3e−29	23 / 51	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
19	1e−28	26 / 79	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
20	3e−27	15 / 16	CC	MHC class II protein complex
21	1e−26	77 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
22	5e−26	34 / 208	Tissu	PALMER_B−Cell signature up
23	7e−26	25 / 87	GSEA	BASSO_CD40_SIGNALING_UP
24	2e−25	21 / 53	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
25	1e−24	40 / 346	GSEA	SANSOM_APC_TARGETS_DN
26	1e−24	24 / 86	GSEA	WIELAND_UP_BY_HBV_INFECTION
27	4e−24	32 / 201	CC	external side of plasma membrane
28	2e−23	29 / 163	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
29	3e−23	21 / 64	BP	T cell costimulation
30	5e−23	32 / 218	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
31	1e−22	56 / 823	GSEA	REACTOME_IMMUNE_SYSTEM
32	5e−22	18 / 45	GSEA	YU_MYC_TARGETS_DN
33	1e−21	65 / 1165	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
34	6e−21	22 / 92	BP	T cell receptor signaling pathway
35	9e−21	21 / 82	GSEA	MORI_MATURE_B_LYMPHOCYTE_UP
36	1e−20	19 / 61	BP	antigen processing and presentation
37	4e−20	37 / 381	GSEA	KUMAR_TARGETS_OF_MLL_AF9_FUSION
38	7e−20	29 / 215	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
39	9e−20	40 / 466	Lymp	SPANG_CD40 6hrs DN
40	2e−19	40 / 475	GSEA	REACTOME_ADAPTIVE_IMMUNE_SYSTEM



Aging

Rank	p−value	#in/all	Geneset
1	0.2	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	1e−42	56 / 343	immune response
2	3e−23	21 / 64	T cell costimulation
3	6e−21	22 / 92	T cell receptor signaling pathway
4	1e−20	19 / 61	antigen processing and presentation
5	3e−18	14 / 31	B cell receptor signaling pathway
6	4e−18	10 / 11	antigen processing and presentation of peptide or polysaccharide antigen via
7	4e−17	18 / 78	regulation of immune response
8	3e−16	17 / 73	interferon−gamma−mediated signaling pathway
9	2e−13	18 / 122	adaptive immune response
10	6e−13	13 / 54	positive regulation of T cell proliferation
11	1e−12	24 / 270	cytokine−mediated signaling pathway
12	3e−12	38 / 707	innate immune response
13	5e−11	10 / 35	T cell differentiation
14	2e−10	9 / 29	B cell activation
15	4e−10	23 / 326	inflammatory response
16	5e−10	20 / 246	cell surface receptor signaling pathway
17	6e−10	13 / 90	antigen processing and presentation of exogenous peptide antigen via MHC c
18	3e−09	47 / 1279	signal transduction
19	5e−09	9 / 40	peptidyl−tyrosine autophosphorylation
20	8e−09	7 / 20	positive regulation of neutrophil chemotaxis

Brain

Rank	p−value	#in/all	Geneset
1	7e−06	55 / 2084	Mid_Frontal_Lobe_K9K27me3
2	2e−05	87 / 3977	Mid_Frontal_Lobe_ReprPC
3	2e−05	63 / 2603	Fetal_TxTrans
4	1e−04	38 / 1394	Mid_Frontal_Lobe_Quies
5	2e−04	39 / 1478	Overlap_fetal_midbrain_TxTrans
6	3e−04	46 / 1890	Overlap_fetal_midbrain_TssF
7	1e−03	55 / 2549	Fetal_TssF
8	5e−03	38 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	6e−03	31 / 1327	Mid_Frontal_Lobe_TssP
10	2e−02	56 / 2956	Fetal_TssA
11	3e−02	24 / 1108	Overlap_fetal_midbrain_TssA
12	6e−02	18 / 840	Mid_Frontal_Lobe_TssF
13	7e−02	4 / 106	Overlap_fetal_midbrain_Tx
14	1e−01	23 / 1210	Fetal_TssP
15	3e−01	10 / 552	Fetal_Tx
16	3e−01	19 / 1137	Fetal_Enh
17	3e−01	6 / 317	Mid_Frontal_Lobe_Tx
18	3e−01	27 / 1680	Fetal_ReprPCWk
19	7e−01	3 / 232	Fetal_ReprPC
20	7e−01	12 / 910	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	8e−79	98 / 574	Lembcke_Colonic Inflammation
2	8e−17	31 / 324	SPANG_BCL6−index2
3	1e−09	7 / 16	GENTLES_modul18
4	8e−07	14 / 191	SPANG_LPS−index2
5	5e−04	7 / 97	PanCan_TXmisReg_geneset_nanostring
6	1e−03	3 / 16	GENTLES_modul11
7	2e−03	6 / 86	PanCan_JAK−ST_geneset_nanostring
8	8e−03	8 / 198	PanCan_PI3K_geneset_nanostring
9	9e−03	6 / 123	PanCan_Driver_Gene_geneset_nanostring
10	2e−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	2 / 78	PanCan_Wnt_geneset_nanostring
18	3e−01	3 / 136	PanCan_CC+Apop_geneset_nanostring
19	4e−01	3 / 152	PanCan_MAPK_geneset_nanostring
20	4e−01	1 / 37	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	3e−27	15 / 16	MHC class II protein complex
2	4e−24	32 / 201	external side of plasma membrane
3	1e−15	107 / 3507	plasma membrane
4	1e−11	9 / 22	integral component of lumenal side of endoplasmic reticulum membrane
5	5e−11	10 / 35	ER to Golgi transport vesicle membrane
6	5e−10	9 / 32	immunological synapse
7	7e−10	7 / 15	T cell receptor complex
8	3e−09	83 / 3059	membrane
9	1e−08	27 / 523	cell surface
10	1e−08	8 / 32	transport vesicle membrane
11	2e−08	10 / 61	extrinsic component of cytoplasmic side of plasma membrane
12	7e−08	8 / 39	clathrin−coated endocytic vesicle membrane
13	3e−07	8 / 47	trans−Golgi network membrane
14	7e−07	41 / 1250	integral component of plasma membrane
15	9e−07	8 / 53	endocytic vesicle membrane
16	2e−06	67 / 2638	extracellular exosome
17	9e−06	71 / 2974	cytosol
18	1e−05	14 / 245	lysosomal membrane
19	2e−05	12 / 190	membrane raft
20	2e−04	12 / 235	lysosome

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	32 / 976	Chr 6
2	1e−01	15 / 746	Chr X
3	1e−01	22 / 1172	Chr 11
4	2e−01	33 / 1920	Chr 1
5	2e−01	9 / 436	Chr 22
6	3e−01	17 / 1017	Chr 12
7	6e−01	12 / 862	Chr 5
8	6e−01	9 / 651	Chr 8
9	6e−01	7 / 522	Chr 20
10	6e−01	10 / 745	Chr 9
11	7e−01	19 / 1425	Chr 19
12	7e−01	14 / 1083	Chr 17
13	8e−01	2 / 191	Chr 21
14	8e−01	15 / 1228	Chr 2
15	8e−01	10 / 859	Chr 7
16	8e−01	12 / 1043	Chr 3
17	8e−01	8 / 735	Chr 4
18	8e−01	3 / 318	Chr 13
19	9e−01	6 / 582	Chr 15
20	9e−01	9 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	152 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−19	34 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	6e−10	26 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	7e−09	33 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	2e−08	27 / 532	K9acLow_Colon
6	1e−07	20 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
7	5e−06	208 / 11968	TssWk_Colon
8	5e−04	18 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
9	8e−04	6 / 76	Marisa_CRC−cluster−g
10	1e−03	65 / 3112	EnhA_Colon
11	1e−03	3 / 15	Budinska_B_Lower crypt−like_DOWN
12	4e−03	83 / 4379	TssD1_Colon
13	1e−02	12 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
14	2e−02	78 / 4327	EnhWk2_Colon
15	2e−02	102 / 5889	EnhWk1_Colon
16	2e−02	5 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
17	5e−02	2 / 26	Ang_CRC−CIMPH−vs−L_hypo
18	6e−02	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
19	6e−02	1 / 4	Budinska_C_CIMP−H−like_DOWN
20	6e−02	5 / 148	Marisa_CRC−cluster−a

Disease

Rank	p−value	#in/all	Geneset
1	3e−10	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	2e−30	42 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	1e−08	12 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
3	2e−08	8 / 33	Donson−Misc immune function−associated with LTS in HGA
4	4e−08	26 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	9e−08	79 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	1e−07	11 / 96	Weller_LGG_A_vs_O_UP
7	3e−06	4 / 8	Donson−adaptive−immunity−associated with LTS in HGA
8	3e−06	4 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
9	1e−05	7 / 53	Donson−innate immunity−associated with LTS in HGA
10	7e−05	4 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
11	9e−05	4 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
12	2e−04	10 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	8e−04	4 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
14	2e−03	4 / 35	shaw_responders_down_in_oligo_glioma
15	1e−02	20 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
16	1e−02	4 / 59	Christensen_hypomethylated_in_primary_glioblastoma
17	1e−02	2 / 11	WILLSCHER_GBM_LTSwt_proteomics−G_UP
18	1e−02	5 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
19	1e−02	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
20	2e−02	2 / 14	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−87	95 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	4e−71	71 / 263	WALLACE_PROSTATE_CANCER_RACE_UP
3	1e−63	58 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE
4	1e−55	57 / 220	MCLACHLAN_DENTAL_CARIES_UP
5	1e−52	58 / 259	POOLA_INVASIVE_BREAST_CANCER_UP
6	8e−49	71 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
7	1e−46	50 / 210	MCLACHLAN_DENTAL_CARIES_DN
8	9e−38	46 / 246	QI_PLASMACYTOMA_UP
9	6e−33	49 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
10	2e−29	49 / 435	RODWELL_AGING_KIDNEY_UP
11	3e−29	23 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
12	1e−28	26 / 79	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
13	1e−26	77 / 1340	PUJANA_ATM_PCC_NETWORK
14	7e−26	25 / 87	BASSO_CD40_SIGNALING_UP
15	2e−25	21 / 53	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
16	1e−24	40 / 346	SANSOM_APC_TARGETS_DN
17	1e−24	24 / 86	WIELAND_UP_BY_HBV_INFECTION
18	2e−23	29 / 163	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
19	5e−23	32 / 218	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
20	1e−22	56 / 823	REACTOME_IMMUNE_SYSTEM

HM

Rank	p−value	#in/all	Geneset
1	1e−30	36 / 181	HALLMARK_ALLOGRAFT_REJECTION
2	3e−11	19 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	3e−10	18 / 189	HALLMARK_KRAS_SIGNALING_UP
4	2e−08	16 / 192	HALLMARK_COMPLEMENT
5	2e−08	16 / 194	HALLMARK_INFLAMMATORY_RESPONSE
6	1e−06	14 / 197	HALLMARK_IL2_STAT5_SIGNALING
7	2e−05	12 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	3e−05	8 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	2e−03	6 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	4e−03	6 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	7e−03	8 / 190	HALLMARK_APICAL_JUNCTION
12	9e−03	8 / 199	HALLMARK_MTORC1_SIGNALING
13	1e−02	6 / 132	HALLMARK_COAGULATION
14	7e−02	6 / 196	HALLMARK_P53_PATHWAY
15	7e−02	6 / 198	HALLMARK_HYPOXIA
16	1e−01	2 / 44	HALLMARK_APICAL_SURFACE
17	2e−01	5 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
18	2e−01	4 / 157	HALLMARK_APOPTOSIS
19	3e−01	2 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
20	3e−01	4 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	9e−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	4e−35	210 / 7592	HOPP_Strong_enhancer
2	9e−20	40 / 466	SPANG_CD40 6hrs DN
3	2e−19	153 / 5643	HOPP_Txn_transition
4	1e−17	23 / 145	WIRTH_lymphoma937_spot F
5	1e−17	23 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
6	1e−15	30 / 332	SPANG_CD40 6hrs UP
7	2e−15	29 / 315	WIRTH_lymphoma937_spot E
8	2e−14	28 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−c
9	6e−14	20 / 150	DAVE_BL−vs−DLBCL
10	1e−13	54 / 1215	SPANG_BCR DN
11	2e−13	10 / 22	DAVE_NFkB BL DN
12	2e−13	28 / 347	WIRTH_lymphoma937_spot H
13	2e−11	23 / 279	SPANG_IL21 DN
14	2e−11	25 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
15	1e−10	10 / 38	TARTE_B−cell signature
16	3e−10	15 / 123	SPANG_LPS 6hrs UP
17	2e−09	25 / 414	TARTE_Mature plasma cell signature
18	2e−09	7 / 17	WRIGHT_ABC UP
19	1e−08	167 / 8358	HOPP_Active_promoter
20	2e−08	11 / 79	SPANG_LPS 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	2e−11	8 / 16	MHC class II protein complex binding
2	7e−10	8 / 23	peptide antigen binding
3	2e−09	202 / 10693	protein binding
4	1e−08	9 / 45	non−membrane spanning protein tyrosine kinase activity
5	2e−07	15 / 196	transmembrane signaling receptor activity
6	2e−06	17 / 301	actin binding
7	1e−05	6 / 37	chemokine activity
8	5e−05	9 / 117	protein tyrosine kinase activity
9	5e−05	13 / 241	GTPase activator activity
10	9e−05	12 / 219	receptor activity
11	2e−04	4 / 20	antigen binding
12	2e−04	6 / 58	cell adhesion molecule binding
13	3e−04	8 / 114	SH3 domain binding
14	3e−04	3 / 10	profilin binding
15	4e−04	4 / 25	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
16	9e−04	5 / 52	SH3/SH2 adaptor activity
17	1e−03	14 / 370	receptor binding
18	1e−03	3 / 15	CCR chemokine receptor binding
19	1e−03	3 / 15	phosphotyrosine binding
20	3e−03	4 / 40	cytokine receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	3 / 29	hsa−miR−1292
2	0.059	3 / 61	hsa−miR−296−3p
3	0.061	3 / 62	hsa−miR−634
4	0.070	2 / 30	hsa−miR−486−5p
5	0.091	2 / 35	hsa−miR−1229
6	0.119	2 / 41	hsa−miR−758
7	0.134	5 / 186	hsa−miR−1
8	0.153	2 / 48	hsa−miR−623
9	0.174	2 / 52	hsa−miR−1224−3p
10	0.175	5 / 204	hsa−miR−206
11	0.180	3 / 101	hsa−miR−1299
12	0.185	4 / 154	hsa−miR−506
13	0.195	3 / 105	hsa−miR−613
14	0.205	2 / 58	hsa−miR−409−5p
15	0.233	4 / 170	hsa−miR−495
16	0.248	2 / 66	hsa−miR−30e*
17	0.253	1 / 20	hsa−miR−380*
18	0.253	2 / 67	hsa−miR−1285
19	0.275	3 / 126	hsa−miR−421
20	0.285	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−09	70 / 2401	ICGC_Bcl11_targets
2	7e−08	62 / 2149	ICGC_Mef2_targets
3	4e−06	102 / 4714	ICGC_Pu1_targets
4	2e−05	43 / 1523	ICGC_P300_targets
5	3e−05	54 / 2133	ICGC_Cebpbsc150_targets
6	5e−05	74 / 3305	ICGC_BatfPcr1_targets
7	7e−04	61 / 2827	ICGC_Bcl3_targets
8	1e−03	103 / 5512	ICGC_Nficsc81335_targets
9	3e−03	64 / 3177	ICGC_Irf4_targets
10	2e−02	76 / 4230	ICGC_Nfatc1_targets
11	4e−02	85 / 4969	ICGC_Atf2_targets
12	8e−02	103 / 6313	ICGC_Pou2_targets
13	9e−02	60 / 3511	ICGC_Rad21_targets
14	1e−01	34 / 1867	HEBENSTREIT_high expression TF
15	1e−01	28 / 1506	ICGC_Usf1_targets
16	1e−01	99 / 6157	ICGC_Tcf3_targets
17	1e−01	90 / 5578	ICGC_Stat5_targets
18	2e−01	87 / 5453	ICGC_Foxm1_targets
19	2e−01	80 / 4987	ICGC_Bclaf101388_targets
20	2e−01	88 / 5526	ICGC_Pmlsc71910_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	8e−05	5 / 31	VAQUERIZAS_Lymph node
2	3e−04	4 / 22	VAQUERIZAS_Tonsil
3	3e−04	5 / 42	VAQUERIZAS_Thymus
4	2e−03	5 / 64	VAQUERIZAS_Lung
5	3e−03	5 / 67	VAQUERIZAS_Whole blood
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	1e−01	2 / 37	VAQUERIZAS_Prostate
10	2e−01	1 / 18	VAQUERIZAS_Pancreas
11	4e−01	1 / 30	VAQUERIZAS_Smooth muscle
12	5e−01	1 / 42	VAQUERIZAS_Thyroid
13	5e−01	1 / 49	VAQUERIZAS_Uterus
14	7e−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	1e−99	105 / 427	WIRTH_Immune system
2	5e−26	34 / 208	PALMER_B−Cell signature up
3	8e−17	22 / 140	PALMER_T−Cell signature up
4	1e−03	11 / 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	0.08	26 / 1343	LU_BPDE 1h DN
2	1.00	48 / 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	