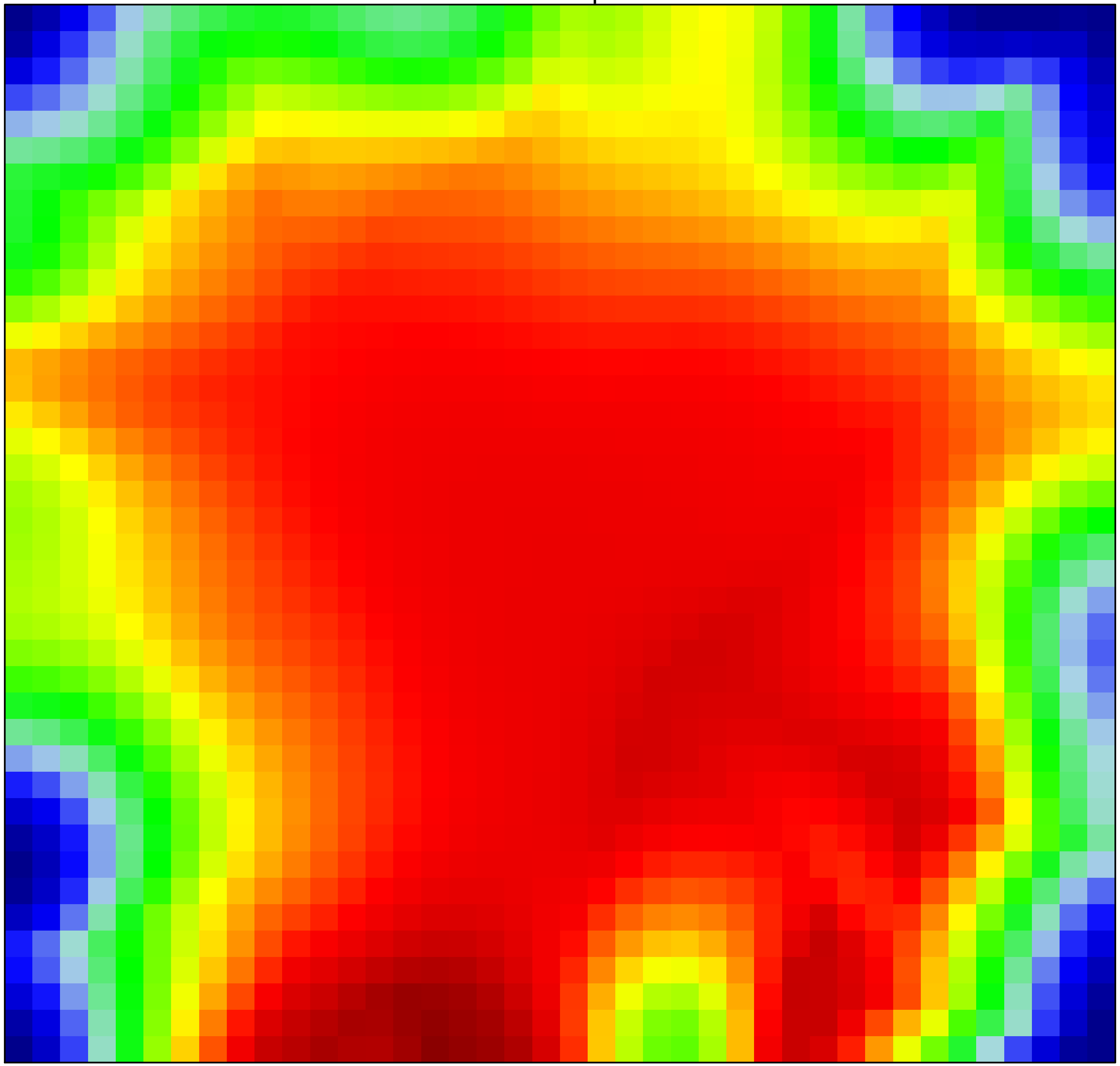
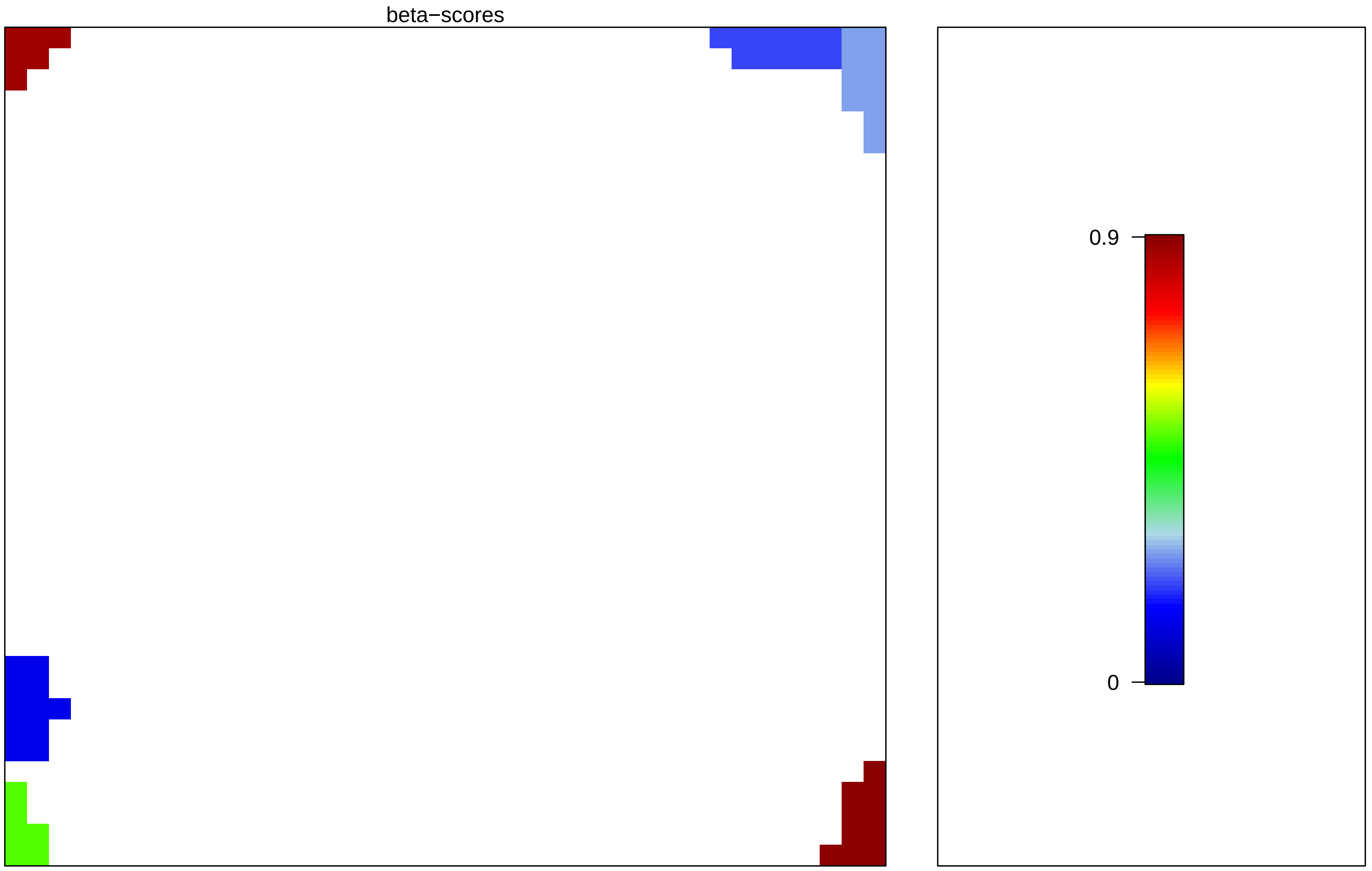
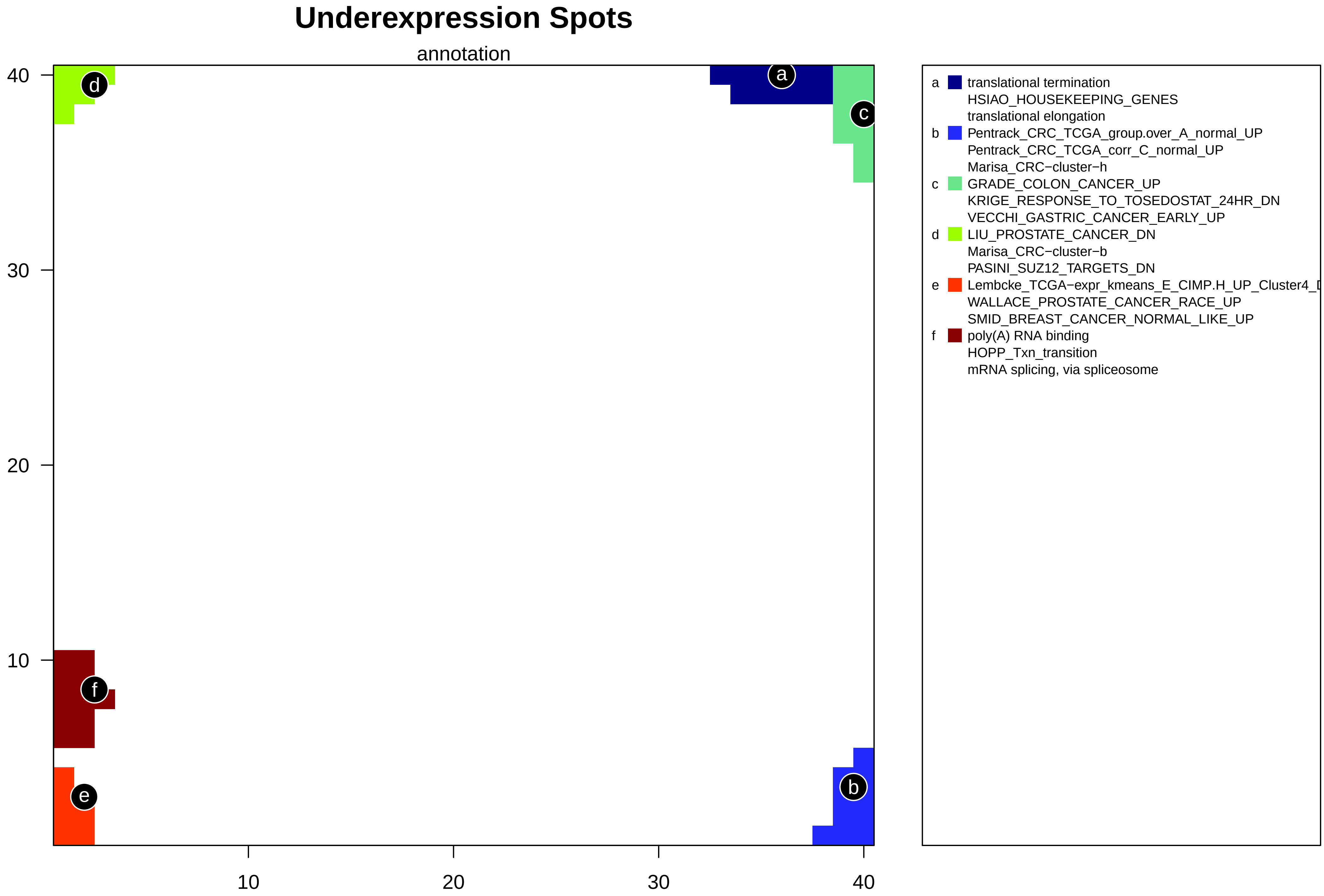
Underexpression Spots

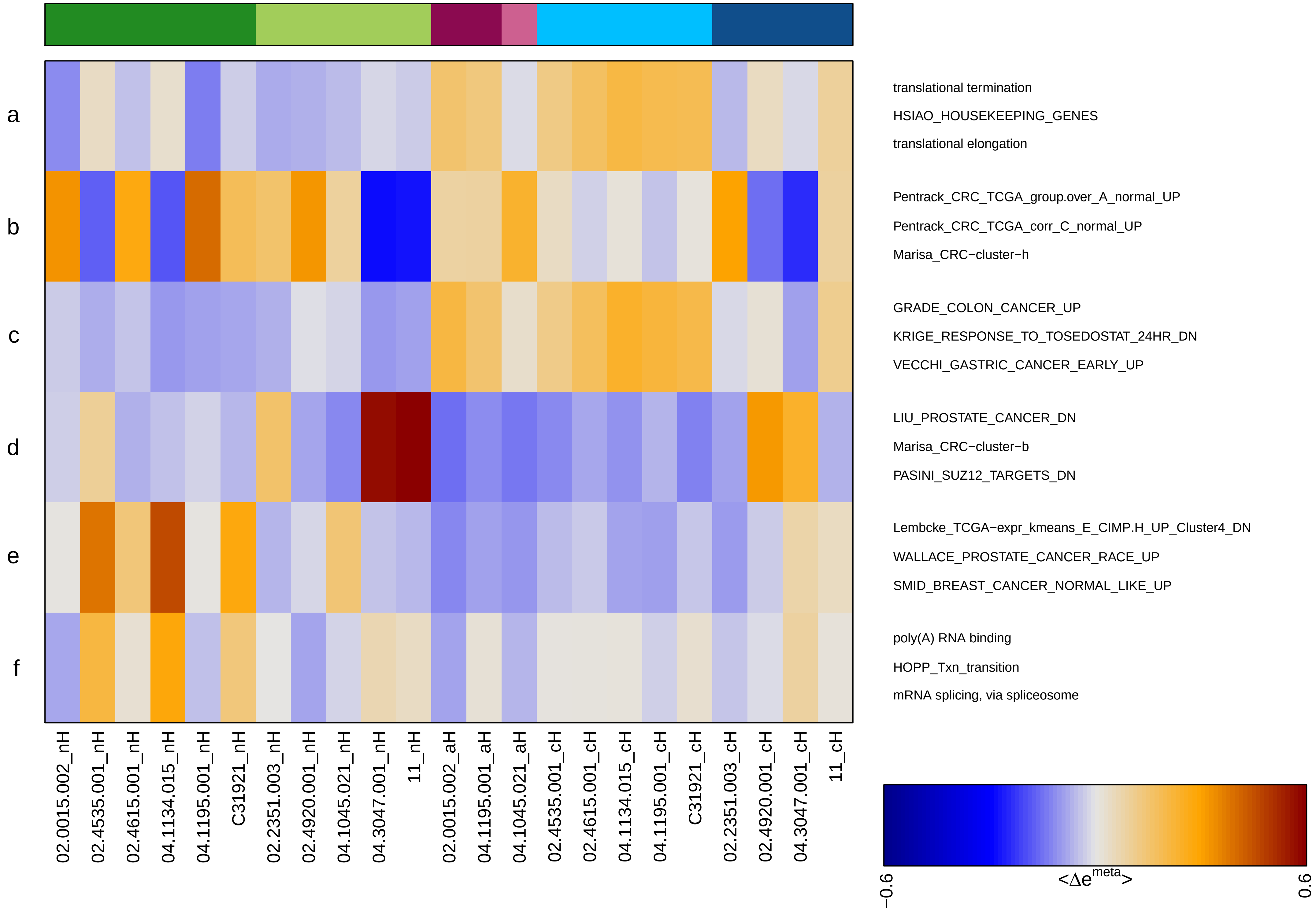
landscape

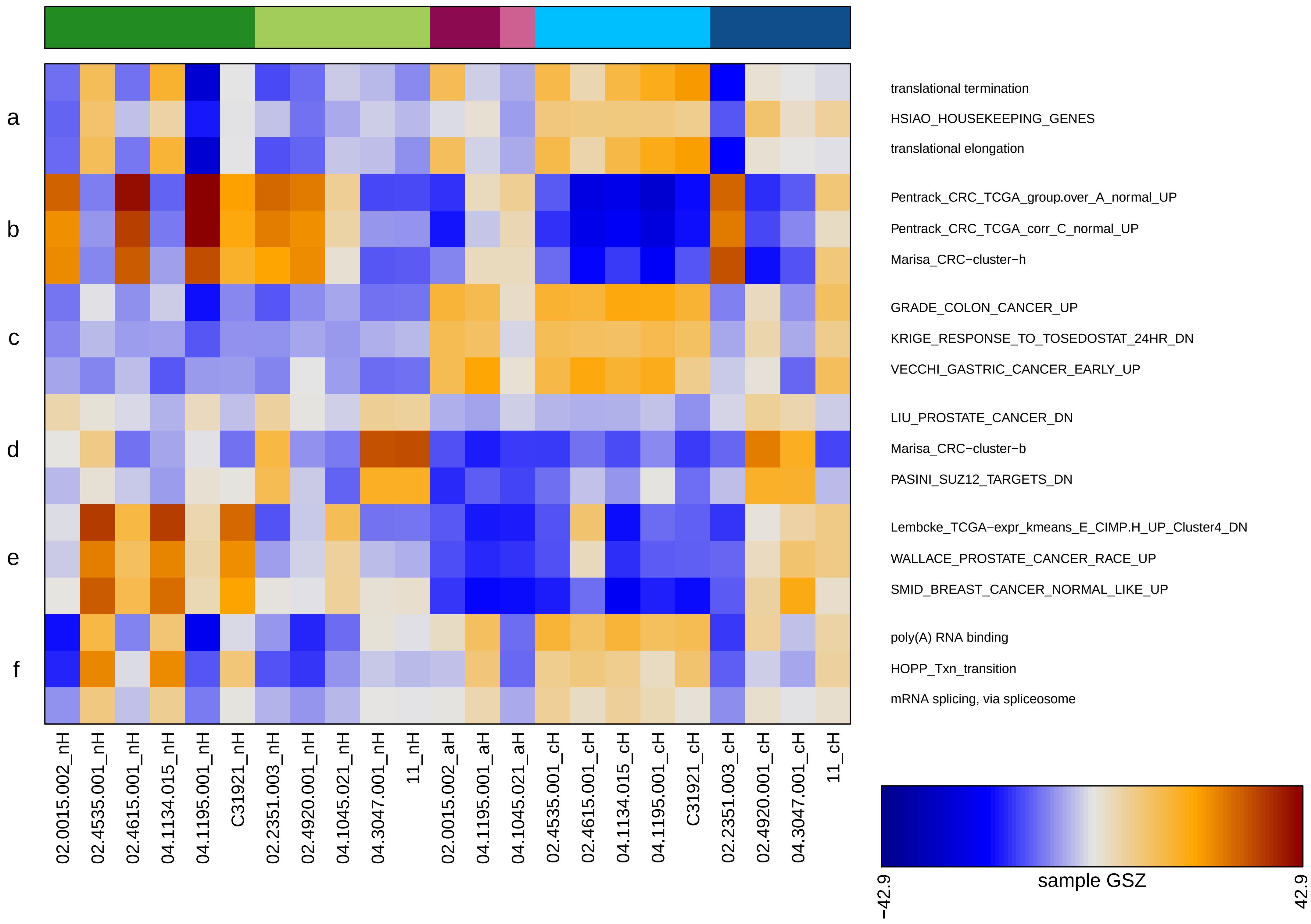


Underexpression Spots




Underexpression Spots
annotation
40
30
20
10
10
20
30
40
a
b
c
d
e
f
a translational termination
HSIAO_HOUSEKEEPING_GENES
translational elongation
b Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
c GRADE_COLON_CANCER_UP
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
VECCHI_GASTRIC_CANCER_EARLY_UP
d LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
PASINI_SUZ12_TARGETS_DN
e Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_
WALLACE_PROSTATE_CANCER_RACE_UP
SMID_BREAST_CANCER_NORMAL_LIKE_UP
f poly(A) RNA binding
HOPP_Txn_transition
mRNA splicing, via spliceosome


a
b
c
d
e
f
translational termination
HSIAO_HOUSEKEEPING_GENES
translational elongation
Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
GRADE_COLON_CANCER_UP
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
VECCHI_GASTRIC_CANCER_EARLY_UP
LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
PASINI_SUZ12_TARGETS_DN
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
WALLACE_PROSTATE_CANCER_RACE_UP
SMID_BREAST_CANCER_NORMAL_LIKE_UP
poly(A) RNA binding
HOPP_Txn_transition
mRNA splicing, via spliceosome
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
$\langle\Delta e^{meta}\rangle$
0.6


a
b
c
d
e
f
translational termination
HSIAO_HOUSEKEEPING_GENES
translational elongation
Pentrack_CRC_TCGA_group.over_A_normal_UP
Pentrack_CRC_TCGA_corr_C_normal_UP
Marisa_CRC−cluster−h
GRADE_COLON_CANCER_UP
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
VECCHI_GASTRIC_CANCER_EARLY_UP
LIU_PROSTATE_CANCER_DN
Marisa_CRC−cluster−b
PASINI_SUZ12_TARGETS_DN
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
WALLACE_PROSTATE_CANCER_RACE_UP
SMID_BREAST_CANCER_NORMAL_LIKE_UP
poly(A) RNA binding
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mRNA splicing, via spliceosome
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11_nH
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04.1195.001_aH
04.1045.021_aH
02.4535.001_cH
02.4615.001_cH
04.1134.015_cH
04.1195.001_cH
C31921_cH
02.2351.003_cH
02.4920.001_cH
04.3047.001_cH
11_cH
−42.9
sample GSZ
42.9

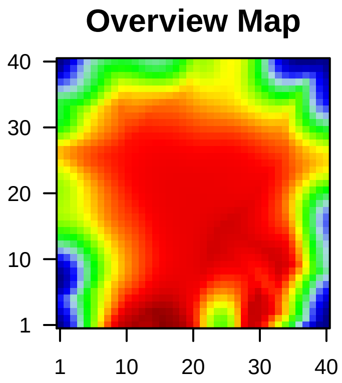
Underexpression Spots

Spot Summary: a

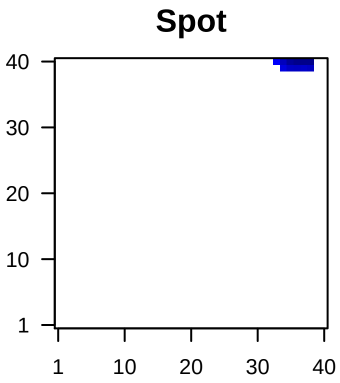
metagenes = 11
genes = 242

<r> metagenes = 0.97
<r> genes = 0.61
beta: r2= 0.2 / log p= −1.5

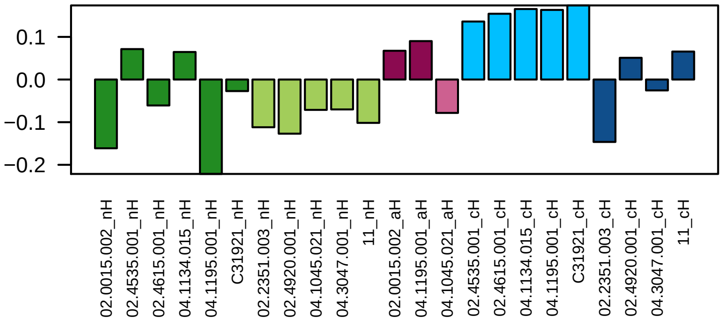
samples with spot = 0 (0 %)



Overview Map



Spot

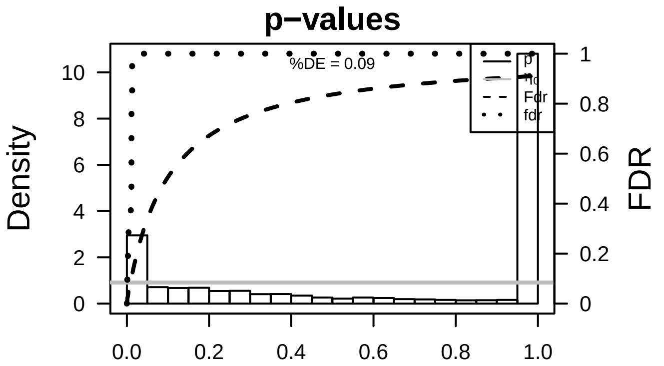


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.31	−0.29	0.44	CXCL8	chemokine (C−X−C motif) ligand 8 [Source:HGNC Symbol;Ac
2	ENSG000001	0.98	−0.17	0.47	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
3	ENSG000001	0.84	−0.29	0.58	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
4	ENSG000001	0.78	−0.58	0.61	IFITM1	interferon induced transmembrane protein 1 [Source:HGNC S
5	ENSG000000	0.73	−0.07	0.45	CLDN18	claudin 18 [Source:HGNC Symbol;Acc:HGNC:2039]
6	ENSG000001	0.71	−0.63	0.56	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC S
7	ENSG000001	0.62	−0.43	0.61	IFITM2	interferon induced transmembrane protein 2 [Source:HGNC S
8	ENSG000001	0.59	−0.18	0.73	PSAT1	phosphoserine aminotransferase 1 [Source:HGNC Symbol;Ac
9	ENSG000002	0.57	−0.12	0.6		
10	ENSG000001	0.57	−0.35	0.44	HSPA8	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
11	ENSG000000	0.56	−0.34	0.51	CXCL2	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
12	ENSG000000	0.54	−0.26	0.66	FXYD5	FXYD domain containing ion transport regulator 5 [Source:HC
13	ENSG000000	0.53	−0.29	0.52	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member
14	ENSG000001	0.52	−0.27	0.74	ODC1	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:HGNC
15	ENSG000001	0.51	−0.34	0.51	ALDH1B1	aldehyde dehydrogenase 1 family, member B1 [Source:HGNC
16	ENSG000001	0.5	−0.46	0.91	RPS2	ribosomal protein S2 [Source:HGNC Symbol;Acc:HGNC:104
17	ENSG000001	0.49	−0.33	0.8	MYC	v−myc avian myelocytomatosis viral oncogene homolog [Sou
18	ENSG000001	0.49	−0.44	0.71	RPS21	ribosomal protein S21 [Source:HGNC Symbol;Acc:HGNC:10
19	ENSG000001	0.49	−0.34	0.8	RPS19	ribosomal protein S19 [Source:HGNC Symbol;Acc:HGNC:10
20	ENSG000000	0.48	−0.31	0.79	RPL18	ribosomal protein L18 [Source:HGNC Symbol;Acc:HGNC:10

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	62 / 88	BP	translational termination
2	1e−99	95 / 370	GSEA	HSIAO_HOUSEKEEPING_GENES
3	1e−98	64 / 101	BP	translational elongation
4	3e−98	64 / 102	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
5	4e−96	59 / 82	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	7e−96	64 / 108	BP	SRP−dependent cotranslational protein targeting to membrane
7	3e−93	68 / 142	GSEA	REACTOME_TRANSLATION
8	1e−92	58 / 84	GSEA	KEGG_RIBOSOME
9	3e−91	67 / 142	BP	translational initiation
10	3e−91	62 / 109	BP	viral transcription
11	5e−91	60 / 98	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
12	2e−90	61 / 105	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
13	2e−88	62 / 117	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	3e−88	68 / 162	MF	structural constituent of ribosome
15	3e−87	59 / 102	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
16	8e−87	65 / 144	BP	viral life cycle
17	9e−85	76 / 259	BP	translation
18	4e−84	62 / 132	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
19	4e−83	66 / 168	CC	ribosome
20	5e−77	114 / 1091	MF	poly(A) RNA binding
21	4e−75	81 / 412	GSEA	REACTOME_METABOLISM_OF_PROTEINS
22	8e−73	126 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
23	2e−72	67 / 242	GSEA	REACTOME_METABOLISM_OF_RNA
24	3e−72	63 / 198	GSEA	REACTOME_METABOLISM_OF_MRNA
25	2e−69	61 / 195	HM	HALLMARK_MYC_TARGETS_V1
26	4e−67	83 / 549	BP	viral process
27	6e−67	87 / 633	BP	cellular protein metabolic process
28	4e−63	92 / 820	BP	gene expression
29	7e−61	39 / 59	CC	cytosolic large ribosomal subunit
30	7e−60	89 / 813	GSEA	GRADE_COLON_CANCER_UP
31	6e−55	75 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
32	9e−54	37 / 66	GSEA	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
33	1e−53	81 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
34	2e−53	81 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
35	3e−46	73 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
36	1e−43	43 / 174	GSEA	LI_AMPLIFIED_IN_LUNG_CANCER
37	9e−41	28 / 50	GSEA	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
38	1e−40	126 / 2974	CC	cytosol
39	4e−40	27 / 46	GSEA	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
40	2e−39	28 / 54	GSEA	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	2 / 123	HORVATH_aging_genes meth DOWN
2	0.8	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−99	62 / 88	translational termination
2	1e−98	64 / 101	translational elongation
3	7e−96	64 / 108	SRP−dependent cotranslational protein targeting to membrane
4	3e−91	67 / 142	translational initiation
5	3e−91	62 / 109	viral transcription
6	2e−88	62 / 117	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
7	8e−87	65 / 144	viral life cycle
8	9e−85	76 / 259	translation
9	4e−67	83 / 549	viral process
10	6e−67	87 / 633	cellular protein metabolic process
11	4e−63	92 / 820	gene expression
12	1e−20	21 / 95	rRNA processing
13	8e−20	11 / 13	ribosomal small subunit biogenesis
14	7e−18	12 / 22	cytoplasmic translation
15	7e−14	20 / 174	protein folding
16	1e−10	7 / 14	ribosomal small subunit assembly
17	8e−10	7 / 17	ribosomal large subunit biogenesis
18	4e−08	6 / 17	ribosomal large subunit assembly
19	2e−07	6 / 22	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
20	3e−07	20 / 410	mitotic cell cycle

Brain

Rank	p−value	#in/all	Geneset
1	6e−33	65 / 855	Overlap_fetal_midbrain_ZNF
2	1e−25	31 / 191	Overlap_fetal_midbrain_Het
3	1e−22	200 / 10239	Overlap_fetal_midbrain_ReprPC
4	2e−14	182 / 9923	Overlap_fetal_midbrain_K9K27me3
5	5e−07	30 / 865	Mid_Frontal_Lobe_Het
6	3e−04	50 / 2443	Fetal_Quies
7	8e−04	24 / 939	Fetal_HetRpts
8	2e−03	13 / 400	Fetal_ZNF
9	4e−03	11 / 342	Fetal_Het
10	3e−02	30 / 1680	Fetal_ReprPCWk
11	1e−01	50 / 3370	Mid_Frontal_Lobe_ZNF
12	2e−01	87 / 6320	Overlap_fetal_midbrain_HetRpts
13	2e−01	143 / 10800	Overlap_fetal_midbrain_Quies
14	4e−01	18 / 1356	Fetal_K9K27me3
15	7e−01	16 / 1394	Mid_Frontal_Lobe_Quies
16	8e−01	31 / 2820	Mid_Frontal_Lobe_HetRpts
17	9e−01	2 / 268	Mid_Frontal_Lobe_TssA
18	9e−01	16 / 1713	Mid_Frontal_Lobe_ReprPCWk
19	9e−01	1 / 232	Fetal_ReprPC
20	1e+00	3 / 552	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	1e−11	4 / 16	RHODES_CANCER_META_SIGNATURE
2	3e−11	2 / 16	RHODES_UNDIFFERENTIATED_CANCER
3	3e−08	6 / 16	WOLFER_overlap genes
4	4e−08	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	7e−07	7 / 41	ZHANG_MM up
6	1e−06	5 / 16	GENTLES_modul1
7	9e−05	5 / 37	KUIPER_MM good survival
8	1e−03	3 / 16	GENTLES_modul7
9	2e−03	16 / 550	Lembcke_Normal vs Adenoma
10	2e−03	7 / 136	PanCan_CC+Apop_geneset_nanostring
11	2e−03	5 / 71	SHAUGHNESSY_MM high risk
12	7e−03	2 / 10	GENTLES_modul3
13	1e−02	2 / 15	LIU_BREAST_CANCER
14	1e−02	2 / 15	BEN−PORATH_UP
15	1e−02	2 / 15	GENTLES_modul4
16	2e−02	3 / 50	PanCan_DNARepair_geneset_nanostring
17	6e−02	0 / 16	LIU_COMMON_CANCER_GENES
18	1e−01	0 / 14	LIU_PROSTATE_CANCER_UP
19	1e−01	5 / 198	PanCan_PI3K_geneset_nanostring
20	1e−01	2 / 52	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	4e−83	66 / 168	ribosome
2	7e−61	39 / 59	cytosolic large ribosomal subunit
3	1e−40	126 / 2974	cytosol
4	1e−38	25 / 39	cytosolic small ribosomal subunit
5	5e−35	112 / 2638	extracellular exosome
6	4e−29	59 / 799	nucleolus
7	1e−28	43 / 378	focal adhesion
8	4e−27	109 / 3059	membrane
9	2e−25	16 / 24	small ribosomal subunit
10	8e−21	23 / 121	ribonucleoprotein complex
11	4e−15	122 / 5185	cytoplasm
12	3e−14	59 / 1604	intracellular
13	9e−12	113 / 5101	nucleus
14	1e−10	70 / 2554	nucleoplasm
15	7e−09	14 / 151	myelin sheath
16	9e−09	7 / 23	cytoplasmic ribonucleoprotein granule
17	4e−08	11 / 97	melanosome
18	1e−07	9 / 65	cell body
19	1e−07	5 / 11	large ribosomal subunit
20	5e−06	4 / 10	methylosome

Chr

Rank	p−value	#in/all	Geneset
1	0.09	21 / 1228	Chr 2
2	0.19	22 / 1425	Chr 19
3	0.21	16 / 1017	Chr 12
4	0.22	12 / 735	Chr 4
5	0.34	8 / 522	Chr 20
6	0.34	11 / 745	Chr 9
7	0.34	11 / 746	Chr X
8	0.35	14 / 976	Chr 6
9	0.37	5 / 318	Chr 13
10	0.41	16 / 1172	Chr 11
11	0.45	4 / 272	Chr 18
12	0.55	13 / 1043	Chr 3
13	0.61	13 / 1083	Chr 17
14	0.65	10 / 862	Chr 5
15	0.74	6 / 582	Chr 15
16	0.79	6 / 613	Chr 14
17	0.84	20 / 1920	Chr 1
18	0.85	8 / 859	Chr 7
19	0.89	6 / 715	Chr 10
20	0.91	1 / 191	Chr 21

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−46	73 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	1e−34	66 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
3	3e−27	209 / 10475	TssA_Colon
4	6e−23	177 / 8123	TssF_Colon
5	4e−22	196 / 9930	Tx_Colon
6	5e−17	93 / 3122	TxEnhG1_Colon
7	6e−16	45 / 877	TxEnhG2_Colon
8	1e−07	158 / 9390	TxWk_Colon
9	6e−05	177 / 11791	Enh_Colon
10	8e−04	174 / 11968	TssWk_Colon
11	4e−02	4 / 105	Marisa_CRC−cluster−d
12	6e−02	97 / 6761	TssD2_Colon
13	1e−01	1 / 10	Marisa_CRC−C1
14	1e−01	7 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
15	2e−01	1 / 17	TCGA−CRC_less−agressive−disease−markers
16	2e−01	61 / 4379	TssD1_Colon
17	2e−01	4 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
18	3e−01	1 / 26	Ang_CRC−CIMPH−vs=L_hypo
19	3e−01	42 / 3112	EnhA_Colon
20	4e−01	1 / 36	Ang_CRC_Hypomethylated

Disease

Rank	p−value	#in/all	Geneset
1	0.04	13 / 608	GUDJ_psoriasis up
2	0.99	1 / 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	1e−05	52 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	3e−05	46 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−03	7 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
4	7e−03	3 / 31	KIM prognostic signature LTS vs. STS
5	1e−02	3 / 36	Colman_survival_associated
6	1e−02	5 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	2e−02	4 / 77	Weller_LGG_gradeII−vs−III_DOWN
8	2e−02	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
9	2e−02	3 / 50	Vishal_subnetwork signature of survival in GBM
10	3e−02	2 / 21	KIM deleted & downregulated in LTS
11	4e−02	3 / 59	developing astrocytes
12	5e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
13	5e−02	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
14	6e−02	4 / 119	GIEZELT_GBM_WT_up_VS_mut
15	7e−02	2 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotC
16	7e−02	1 / 6	Martinez_Glio_hypometh
17	8e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expressio
18	9e−02	3 / 83	GIEZELT_GBM_WT_down_VS_mut
19	1e−01	1 / 11	KIM amplified & overexpressed in LTS
20	1e−01	1 / 12	Phillips MES up vs Prolif & PN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	95 / 370	HSIAO_HOUSEKEEPING_GENES
2	3e−98	64 / 102	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
3	4e−96	59 / 82	REACTOME_PEPTIDE_CHAIN_ELONGATION
4	3e−93	68 / 142	REACTOME_TRANSLATION
5	1e−92	58 / 84	KEGG_RIBOSOME
6	5e−91	60 / 98	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
7	2e−90	61 / 105	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
8	3e−87	59 / 102	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
9	4e−84	62 / 132	REACTOME_INFLUENZA_LIFE_CYCLE
10	4e−75	81 / 412	REACTOME_METABOLISM_OF_PROTEINS
11	8e−73	126 / 1563	PUJANA_BRCA1_PCC_NETWORK
12	2e−72	67 / 242	REACTOME_METABOLISM_OF_RNA
13	3e−72	63 / 198	REACTOME_METABOLISM_OF_MRNA
14	7e−60	89 / 813	GRADE_COLON_CANCER_UP
15	6e−55	75 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP
16	9e−54	37 / 66	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
17	1e−53	81 / 747	PUJANA_CHEK2_PCC_NETWORK
18	2e−53	81 / 754	MARTENS_TRETINOIN_RESPONSE_DN
19	1e−43	43 / 174	LI_AMPLIFIED_IN_LUNG_CANCER
20	9e−41	28 / 50	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−69	61 / 195	HALLMARK_MYC_TARGETS_V1
2	6e−16	23 / 197	HALLMARK_E2F_TARGETS
3	6e−15	22 / 196	HALLMARK_G2M_CHECKPOINT
4	6e−12	12 / 58	HALLMARK_MYC_TARGETS_V2
5	9e−12	15 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	4e−08	15 / 199	HALLMARK_MTORC1_SIGNALING
7	5e−04	8 / 146	HALLMARK_DNA_REPAIR
8	4e−03	7 / 155	HALLMARK_UV_RESPONSE_UP
9	1e−02	7 / 197	HALLMARK_IL2_STAT5_SIGNALING
10	1e−02	7 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	1e−02	6 / 157	HALLMARK_APOPTOSIS
12	3e−02	4 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	3e−02	6 / 181	HALLMARK_ALLOGRAFT_REJECTION
14	4e−02	6 / 196	HALLMARK_P53_PATHWAY
15	4e−02	6 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	4e−02	6 / 198	HALLMARK_GLYCOLYSIS
17	5e−02	5 / 154	HALLMARK_FATTY_ACID_METABOLISM
18	8e−02	2 / 36	HALLMARK_ANGIOGENESIS
19	9e−02	5 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	9e−02	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−38	167 / 5643	HOPP_Txn_transition
2	4e−19	173 / 8358	HOPP_Active_promoter
3	7e−18	30 / 317	TARTE_Plasmablast signature
4	1e−10	25 / 414	TARTE_Mature plasma cell signature
5	4e−09	140 / 7592	HOPP_Strong_enhancer
6	1e−08	146 / 8147	HOPP_Weak_promoter
7	3e−08	31 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
8	4e−08	31 / 811	WIRTH_lymphoma937_spot D
9	1e−06	131 / 7491	HOPP_Txn_elongation
10	8e−05	4 / 19	DAVE_c−myc BL UP
11	3e−04	9 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
12	3e−04	9 / 171	WIRTH_lymphoma937_spot C
13	6e−04	8 / 150	DAVE_BL−vs−DLBCL
14	2e−03	6 / 105	ROSOLOWSKI_blue total
15	3e−03	5 / 78	TARTE_Plasma cell signature
16	4e−03	5 / 83	ROSOLOWSKI_green UP
17	2e−02	5 / 115	ROSOLOWSKI_green total
18	2e−02	2 / 17	YAMANE_AICDA_targets_recruited
19	2e−02	24 / 1215	SPANG_BCR DN
20	5e−02	1 / 4	MASCQUE_mBL DOWN

MF

Rank	p−value	#in/all	Geneset
1	3e−88	68 / 162	structural constituent of ribosome
2	5e−77	114 / 1091	poly(A) RNA binding
3	1e−37	57 / 513	RNA binding
4	6e−18	19 / 94	unfolded protein binding
5	8e−12	10 / 34	rRNA binding
6	3e−07	10 / 93	mRNA binding
7	5e−06	168 / 10693	protein binding
8	8e−06	17 / 385	nucleotide binding
9	3e−05	5 / 30	nucleosomal DNA binding
10	4e−05	4 / 16	MHC class II protein complex binding
11	5e−05	7 / 77	single−stranded DNA binding
12	9e−05	6 / 58	double−stranded RNA binding
13	1e−04	6 / 61	damaged DNA binding
14	1e−04	4 / 22	snoRNA binding
15	3e−04	11 / 245	ubiquitin protein ligase binding
16	3e−04	3 / 11	RAGE receptor binding
17	5e−04	5 / 53	translation initiation factor activity
18	2e−03	4 / 40	ribosome binding
19	2e−03	3 / 21	DNA helicase activity
20	2e−03	3 / 21	fibroblast growth factor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	7 / 102	hsa−miR−150
2	6e−04	13 / 355	hsa−let−7e
3	6e−04	11 / 269	hsa−miR−548p
4	7e−04	9 / 190	hsa−miR−548a−3p
5	1e−03	5 / 61	hsa−miR−492
6	1e−03	6 / 93	hsa−miR−425
7	1e−03	7 / 129	hsa−miR−223
8	2e−03	14 / 444	hsa−let−7b
9	2e−03	4 / 40	hsa−miR−490−5p
10	2e−03	7 / 136	hsa−miR−28−5p
11	2e−03	4 / 41	hsa−miR−1308
12	2e−03	11 / 307	hsa−miR−34c−5p
13	2e−03	9 / 226	hsa−miR−185
14	2e−03	8 / 184	hsa−miR−582−5p
15	2e−03	8 / 184	hsa−miR−548e
16	3e−03	8 / 186	hsa−miR−196b
17	3e−03	6 / 111	hsa−miR−376b
18	3e−03	7 / 151	hsa−miR−548f
19	4e−03	10 / 289	hsa−miR−320a
20	4e−03	6 / 118	hsa−miR−376c

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	1e−27	23 / 66	MYC_Targets UP
2	3e−24	67 / 1294	KIM_MYC targets
3	2e−15	60 / 1549	ICGC_Myc_targets
4	1e−11	8 / 17	MYC_Protein synthesis degradation UP
5	2e−07	44 / 1547	ICGC_Ets1_targets
6	1e−06	41 / 1472	ICGC_NrsfPcr1_targets
7	2e−06	4 / 8	MYC_Cell cycle UP
8	3e−06	4 / 9	MYC_RNA processing binding UP
9	4e−06	5 / 20	MYC_Metabolism UP
10	2e−05	3 / 5	MYC_Cell growth and proliferation UP
11	2e−05	81 / 4230	ICGC_Nfatc1_targets
12	3e−05	38 / 1503	ICGC_Six5_targets
13	3e−05	52 / 2342	ICGC_GabpPcr2_targets
14	8e−05	97 / 5512	ICGC_Nficsc81335_targets
15	9e−05	47 / 2133	ICGC_Cebpbsc150_targets
16	1e−04	42 / 1867	HEBENSTREIT_high expression TF
17	2e−04	3 / 9	MYC_DNA repair UP
18	2e−04	91 / 5173	ICGC_Taf1_targets
19	2e−04	88 / 4969	ICGC_Atf2_targets
20	3e−04	87 / 4987	ICGC_Bclaf101388_targets

TF Tissue

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

Tissue

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

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	20 / 1343	LU_BPDE 1h DN
2	1.0	25 / 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	

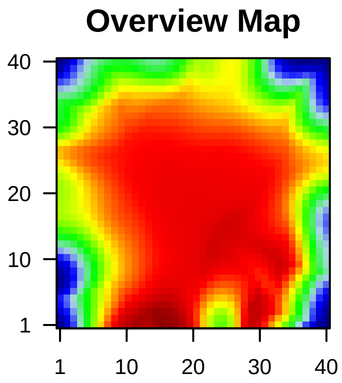
Underexpression Spots

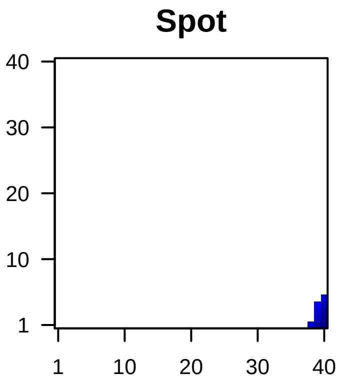
Spot Summary: b

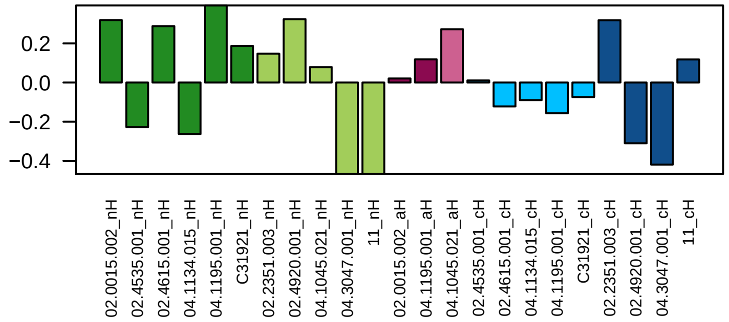
metagenes = 10
genes = 231

<r> metagenes = 0.98
<r> genes = 0.65
beta: r2= 0.91 / log p= −11.8

samples with spot = 6 (26.1 %)
MLH1_normHNPCC : 3 (50 %)
other_normHNPCC : 1 (20 %)
other_adenomaHNPCC : 1 (100 %)
other_cancerHNPCC : 1 (25 %)





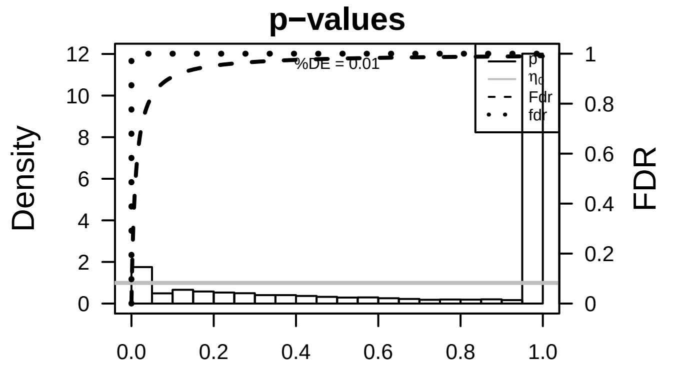


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000002	1.55	−0.86	0.88	PHGR1	proline/histidine/glycine−rich 1 [Source:HGNC Symbol;Acc:H
2	ENSG000001	1.42	−0.99	0.85	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	0.71	AQP8	aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG000001	1.28	−0.52	0.64	ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;A
6	ENSG000000	1.26	−0.59	0.69	CLCA4	chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
7	ENSG000000	1.24	−0.81	0.84	SLC26A3	solute carrier family 26 (anion exchanger), member 3 [Source
8	ENSG000000	1.24	−0.99	0.8	CEACAM7	carcinoembryonic antigen−related cell adhesion molecule 7 [
9	ENSG000001	1.24	−0.49	0.73	ZG16	zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGN
10	ENSG000000	1.22	−0.52	0.77	GUCA2B	guanylate cyclase activator 2B (uroguanylin) [Source:HGNC
11	ENSG000001	1.21	−0.51	0.66	TFF1	trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	−0.44	0.69	PRAP1	proline−rich acidic protein 1 [Source:HGNC Symbol;Acc:HGN
13	ENSG000002	1.15	−0.61	0.82		
14	ENSG000001	1.13	−1.09	0.89	FABP1	fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:
15	ENSG000001	1.12	−0.37	0.73	AKR1B10	aldo−keto reductase family 1, member B10 (aldose reductase
16	ENSG000001	1.1	−0.7	0.6	PI3	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
17	ENSG000001	1.06	−1.31	0.69	PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	ENSG000001	1.02	−1.15	0.73	CEACAM5	carcinoembryonic antigen−related cell adhesion molecule 5 [
19	ENSG000001	1	−0.96	0.9	KRT20	keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
20	ENSG000001	1	−0.35	0.75	C11orf86	chromosome 11 open reading frame 86 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−63	47 / 104	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	2e−53	69 / 507	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
3	4e−34	31 / 110	Colon	Marisa_CRC−cluster−h
4	2e−29	53 / 643	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	1e−27	99 / 2638	CC	extracellular exosome
6	4e−27	44 / 455	GSEA	ONDER_CDH1_TARGETS_2_DN
7	6e−26	28 / 144	Lymp	WIRTH_lymphoma937_spot G
8	8e−25	27 / 142	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsi
9	9e−25	40 / 412	GSEA	LIM_MAMMARY_STEM_CELL_DN
10	2e−24	47 / 616	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	4e−24	40 / 429	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
12	4e−24	31 / 222	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
13	9e−24	32 / 248	GSEA	JAEGER_METASTASIS_DN
14	3e−21	69 / 1624	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	4e−20	96 / 3122	Colon	TxEnhG1_Colon
16	6e−19	48 / 877	Colon	TxEnhG2_Colon
17	2e−18	92 / 3064	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
18	3e−18	24 / 181	GSEA	WU_CELL_MIGRATION
19	5e−17	20 / 126	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
20	6e−17	38 / 608	Disea	GUDJ_psoriasis up
21	7e−17	40 / 682	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
22	1e−16	20 / 132	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
23	1e−16	19 / 115	GSEA	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
24	2e−16	198 / 11791	Colon	Enh_Colon
25	3e−16	20 / 137	Tissu	WIRTH_Mucosa
26	5e−16	25 / 251	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
27	1e−15	25 / 261	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
28	2e−15	39 / 711	GSEA	LEE_BMP2_TARGETS_UP
29	1e−14	24 / 262	GSEA	SABATES_COLORECTAL_ADENOMA_DN
30	3e−14	26 / 326	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
31	7e−14	84 / 3112	Colon	EnhA_Colon
32	2e−13	124 / 5889	Colon	EnhWk1_Colon
33	3e−13	16 / 109	GSEA	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
34	4e−13	29 / 465	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
35	3e−12	19 / 195	HM	HALLMARK_ESTROGEN_RESPONSE_LATE
36	4e−12	18 / 174	GSEA	LI_AMPLIFIED_IN_LUNG_CANCER
37	4e−12	22 / 280	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
38	1e−11	11 / 49	Colon	Marisa_CRC−cluster−f
39	1e−11	33 / 688	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
40	2e−11	27 / 467	GSEA	SWEET_LUNG_CANCER_KRAS_UP



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	2e−10	8 / 23	flavonoid biosynthetic process
2	2e−10	8 / 23	flavonoid glucuronidation
3	2e−09	7 / 19	cellular glucuronidation
4	2e−07	9 / 71	cellular response to hormone stimulus
5	4e−07	6 / 25	establishment of protein localization to plasma membrane
6	2e−06	33 / 1118	metabolic process
7	9e−06	4 / 12	microvillus assembly
8	3e−05	4 / 16	retinoic acid metabolic process
9	4e−05	7 / 76	cell junction assembly
10	4e−05	5 / 33	bicarbonate transport
11	5e−05	7 / 79	epithelial cell differentiation
12	7e−05	4 / 19	epithelial cell morphogenesis
13	1e−04	4 / 22	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion
14	3e−04	3 / 11	intestinal absorption
15	3e−04	6 / 77	negative regulation of cysteine−type endopeptidase activity involved in apopto
16	3e−04	4 / 28	positive regulation of establishment of protein localization to plasma membran
17	4e−04	16 / 496	proteolysis
18	4e−04	4 / 29	actin filament bundle assembly
19	4e−04	4 / 29	one−carbon metabolic process
20	4e−04	5 / 52	O−glycan processing

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	49 / 1890	Overlap_fetal_midbrain_TssF
2	5e−07	45 / 1713	Mid_Frontal_Lobe_ReprPCWk
3	4e−05	59 / 2956	Fetal_TssA
4	9e−05	35 / 1478	Overlap_fetal_midbrain_TxTrans
5	1e−04	52 / 2603	Fetal_TxTrans
6	1e−03	41 / 2084	Mid_Frontal_Lobe_K9K27me3
7	1e−03	30 / 1394	Mid_Frontal_Lobe_Quies
8	3e−03	46 / 2549	Fetal_TssF
9	7e−03	64 / 3977	Mid_Frontal_Lobe_ReprPC
10	3e−02	17 / 840	Mid_Frontal_Lobe_TssF
11	4e−02	8 / 317	Mid_Frontal_Lobe_Tx
12	5e−02	23 / 1327	Mid_Frontal_Lobe_TssP
13	6e−02	9 / 408	Mid_Frontal_Lobe_TxTrans
14	1e−01	6 / 268	Mid_Frontal_Lobe_TssA
15	1e−01	14 / 805	Mid_Frontal_Lobe_EnhG
16	1e−01	18 / 1108	Overlap_fetal_midbrain_TssA
17	1e−01	3 / 106	Overlap_fetal_midbrain_Tx
18	1e−01	5 / 232	Fetal_ReprPC
19	2e−01	15 / 940	Mid_Frontal_Lobe_Enh
20	3e−01	8 / 552	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	LIU_PROSTATE_CANCER_DN
2	0.08	5 / 191	SPANG_LPS−index2
3	0.10	0 / 14	LIU_PROSTATE_CANCER_UP
4	0.10	1 / 9	WANG_ER_DN
5	0.18	1 / 16	LIU_COMMON_CANCER_GENES
6	0.18	1 / 16	WANG_ER_UP
7	0.18	1 / 16	GENTLES_modul16
8	0.18	1 / 16	GENTLES_modul18
9	0.21	2 / 71	SHAUGHNESSY_MM high risk
10	0.35	5 / 324	SPANG_BCL6−index2
11	0.39	1 / 41	ZHANG_MM up
12	0.44	2 / 123	PanCan_Driver_Gene_geneset_nanostring
13	0.46	1 / 50	PanCan_DNARepair_geneset_nanostring
14	0.46	1 / 51	PanCan_TGF−B_geneset_nanostring
15	0.65	1 / 86	PanCan_JAK−ST_geneset_nanostring
16	0.69	2 / 198	PanCan_PI3K_geneset_nanostring
17	0.69	1 / 97	PanCan_TXmisReg_geneset_nanostring
18	0.81	1 / 136	PanCan_CC+Apop_geneset_nanostring
19	0.83	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	0.99	2 / 550	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	1e−27	99 / 2638	extracellular exosome
2	3e−08	17 / 268	apical plasma membrane
3	4e−08	9 / 60	brush border
4	9e−07	10 / 110	bicellular tight junction
5	2e−06	7 / 48	lateral plasma membrane
6	3e−06	12 / 185	basolateral plasma membrane
7	3e−06	71 / 3507	plasma membrane
8	5e−06	33 / 1176	extracellular space
9	3e−05	6 / 51	cell periphery
10	4e−05	75 / 4052	integral component of membrane
11	2e−04	5 / 43	intercalated disc
12	2e−04	3 / 10	plasma membrane raft
13	3e−04	5 / 49	microvillus
14	4e−04	57 / 3059	membrane
15	5e−04	7 / 114	vesicle
16	5e−04	29 / 1250	integral component of plasma membrane
17	8e−04	6 / 91	apical part of cell
18	8e−04	6 / 91	sarcolemma
19	2e−03	3 / 21	desmosome
20	2e−03	8 / 190	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	0.005	15 / 582	Chr 15
2	0.037	32 / 1920	Chr 1
3	0.089	15 / 847	Chr 16
4	0.159	19 / 1228	Chr 2
5	0.198	21 / 1425	Chr 19
6	0.249	17 / 1172	Chr 11
7	0.327	15 / 1083	Chr 17
8	0.397	13 / 976	Chr 6
9	0.406	3 / 191	Chr 21
10	0.416	4 / 272	Chr 18
11	0.442	7 / 522	Chr 20
12	0.463	11 / 859	Chr 7
13	0.607	5 / 436	Chr 22
14	0.717	9 / 862	Chr 5
15	0.801	6 / 651	Chr 8
16	0.866	6 / 715	Chr 10
17	0.870	9 / 1017	Chr 12
18	0.890	6 / 745	Chr 9
19	0.899	2 / 318	Chr 13
20	0.939	8 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−63	47 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	2e−53	69 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
3	4e−34	31 / 110	Marisa_CRC−cluster−h
4	2e−29	53 / 643	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	2e−24	47 / 616	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	4e−20	96 / 3122	TxEnhG1_Colon
7	6e−19	48 / 877	TxEnhG2_Colon
8	2e−16	198 / 11791	Enh_Colon
9	7e−14	84 / 3112	EnhA_Colon
10	2e−13	124 / 5889	EnhWk1_Colon
11	1e−11	11 / 49	Marisa_CRC−cluster−f
12	1e−11	33 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	6e−10	165 / 9930	Tx_Colon
14	1e−07	181 / 11968	TssWk_Colon
15	3e−06	160 / 10475	TssA_Colon
16	7e−05	110 / 6761	TssD2_Colon
17	8e−05	30 / 1169	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
18	9e−05	3 / 8	Marisa_CRC−C6
19	2e−04	125 / 8123	TssF_Colon
20	2e−04	4 / 26	Ang_CRC−CIMPH−vs−L_hypo

Disease

Rank	p−value	#in/all	Geneset
1	6e−17	38 / 608	GUDJ_psoriasis up
2	2e−02	10 / 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	2e−18	92 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	6e−05	18 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
3	8e−05	23 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	8e−03	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
5	1e−02	4 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
6	1e−02	12 / 462	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
7	2e−02	8 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
8	2e−02	4 / 88	GIEZELT_GBM_STSwt_down_VS_LTSwt
9	7e−02	2 / 36	Colman_survival_associated
10	7e−02	3 / 81	GIEZELT_GBM_STS_up_VS_LTS
11	8e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expressio
12	9e−02	16 / 917	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
13	1e−01	1 / 9	Colman_survival_robust
14	1e−01	3 / 99	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
15	1e−01	3 / 103	GIEZELT_GBM_STS_down_VS_LTS
16	1e−01	2 / 55	Gorovets_LGG_PG_subclass
17	2e−01	2 / 57	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
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	23 / 1527	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−27	44 / 455	ONDER_CDH1_TARGETS_2_DN
2	9e−25	40 / 412	LIM_MAMMARY_STEM_CELL_DN
3	4e−24	40 / 429	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
4	4e−24	31 / 222	COLDREN_GEFITINIB_RESISTANCE_DN
5	9e−24	32 / 248	JAEGER_METASTASIS_DN
6	3e−21	69 / 1624	DODD_NASOPHARYNGEAL_CARCINOMA_UP
7	3e−18	24 / 181	WU_CELL_MIGRATION
8	5e−17	20 / 126	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
9	7e−17	40 / 682	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
10	1e−16	20 / 132	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
11	1e−16	19 / 115	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
12	5e−16	25 / 251	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
13	1e−15	25 / 261	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
14	2e−15	39 / 711	LEE_BMP2_TARGETS_UP
15	1e−14	24 / 262	SABATES_COLORECTAL_ADENOMA_DN
16	3e−14	26 / 326	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	3e−13	16 / 109	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
18	4e−13	29 / 465	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
19	4e−12	18 / 174	LI_AMPLIFIED_IN_LUNG_CANCER
20	4e−12	22 / 280	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−12	19 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
2	2e−08	15 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	3e−06	12 / 189	HALLMARK_KRAS_SIGNALING_UP
4	2e−05	11 / 193	HALLMARK_XENOBIOTIC_METABOLISM
5	1e−04	10 / 196	HALLMARK_P53_PATHWAY
6	6e−04	8 / 154	HALLMARK_FATTY_ACID_METABOLISM
7	1e−03	6 / 98	HALLMARK_ANDROGEN_RESPONSE
8	2e−03	8 / 190	HALLMARK_APICAL_JUNCTION
9	2e−03	8 / 192	HALLMARK_COMPLEMENT
10	8e−03	5 / 102	HALLMARK_PEROXISOME
11	1e−02	7 / 198	HALLMARK_GLYCOLYSIS
12	1e−02	4 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	2e−02	5 / 132	HALLMARK_COAGULATION
14	8e−02	5 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	9e−02	5 / 198	HALLMARK_HYPOXIA
16	1e−01	3 / 94	HALLMARK_PROTEIN_SECRETION
17	1e−01	4 / 155	HALLMARK_UV_RESPONSE_UP
18	1e−01	2 / 52	HALLMARK_TGF_BETA_SIGNALING
19	2e−01	3 / 112	HALLMARK_BILE_ACID_METABOLISM
20	2e−01	4 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.176	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.186	1 / 17	DUMEAUX_High bmi enriched genes
4	0.669	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	6e−26	28 / 144	WIRTH_lymphoma937_spot G
2	8e−25	27 / 142	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
3	3e−07	96 / 5039	HOPP_Repressed
4	3e−04	8 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
5	2e−03	2 / 6	DAVE_MHCCII BL DN
6	1e−02	47 / 2838	HOPP_Poised_promoter
7	2e−02	3 / 48	Subero_INT_hypo_meth
8	2e−02	3 / 50	Subero_B−ALL_hyper_meth
9	2e−02	2 / 20	Subero_MCL_hypo_meth
10	3e−02	2 / 23	SPANG_BAFF 9hrs UP
11	3e−02	4 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
12	4e−02	8 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−(
13	4e−02	8 / 315	WIRTH_lymphoma937_spot E
14	6e−02	3 / 75	Subero_FL_hyper_meth
15	8e−02	7 / 304	ZHANG_DLBCL mutated
16	8e−02	2 / 40	ROSOLOWSKI_blue DOWN
17	9e−02	9 / 449	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
18	1e−01	9 / 458	WIRTH_lymphoma937_spot I
19	1e−01	3 / 94	Subero_T−ALL_hyper_meth
20	1e−01	49 / 3457	HOPP_Heterochrom

MF

Rank	p−value	#in/all	Geneset
1	4e−10	9 / 37	transferase activity, transferring hexosyl groups
2	2e−09	8 / 30	glucuronosyltransferase activity
3	7e−06	12 / 204	structural molecule activity
4	1e−05	4 / 13	carbonate dehydratase activity
5	3e−05	4 / 15	retinoic acid binding
6	2e−04	20 / 672	calcium ion binding
7	4e−04	7 / 113	actin filament binding
8	7e−04	6 / 89	serine−type endopeptidase inhibitor activity
9	8e−04	19 / 693	protein homodimerization activity
10	9e−04	3 / 16	fatty acid binding
11	3e−03	3 / 23	peptide antigen binding
12	3e−03	5 / 81	drug binding
13	5e−03	4 / 57	serine−type peptidase activity
14	5e−03	4 / 58	cell adhesion molecule binding
15	6e−03	2 / 10	potassium ion binding
16	6e−03	2 / 10	sodium:potassium−exchanging ATPase activity
17	7e−03	2 / 11	sulfate transmembrane transporter activity
18	7e−03	2 / 11	transferase activity, transferring phosphorus−containing groups
19	8e−03	5 / 101	metallopeptidase activity
20	8e−03	4 / 65	motor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.07	2 / 36	hsa−miR−1287
2	0.08	2 / 38	hsa−miR−1224−5p
3	0.08	2 / 39	hsa−miR−484
4	0.10	4 / 147	hsa−miR−138
5	0.12	1 / 11	hsa−miR−487b
6	0.13	2 / 53	hsa−miR−337−3p
7	0.15	1 / 13	hsa−miR−1249
8	0.16	1 / 14	hsa−miR−574−3p
9	0.17	1 / 15	hsa−miR−671−3p
10	0.18	4 / 184	hsa−miR−374a
11	0.19	1 / 17	hsa−miR−1298
12	0.20	2 / 68	hsa−miR−499−3p
13	0.23	2 / 75	hsa−miR−657
14	0.23	2 / 75	hsa−miR−184
15	0.25	1 / 24	hsa−miR−1225−5p
16	0.25	1 / 24	hsa−miR−1250
17	0.28	2 / 87	hsa−miR−510
18	0.30	2 / 90	hsa−miR−587
19	0.30	1 / 29	hsa−miR−591
20	0.32	1 / 32	hsa−miR−654−5p

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	2e−06	45 / 1798	HEBENSTREIT_low expression TF
2	2e−01	1 / 20	MYC_Metabolism UP
3	6e−01	42 / 3511	ICGC_Rad21_targets
4	6e−01	1 / 66	MYC_Targets UP
5	7e−01	32 / 2827	ICGC_Bcl3_targets
6	7e−01	59 / 5135	ICGC_Ebfsc137065_targets
7	7e−01	73 / 6406	ICGC_Pax5_targets
8	8e−01	48 / 4436	ICGC_Zeb1_targets
9	9e−01	6 / 745	ICGC_NrsfPcr2_targets
10	9e−01	13 / 1523	ICGC_P300_targets
11	1e+00	56 / 5552	ICGC_Pol24_targets
12	1e+00	30 / 3305	ICGC_BatfPcr1_targets
13	1e+00	11 / 1472	ICGC_NrsfPcr1_targets
14	1e+00	61 / 6157	ICGC_Tcf3_targets
15	1e+00	28 / 3177	ICGC_Irf4_targets
16	1e+00	3 / 619	ICGC_RxraPcr1_targets
17	1e+00	11 / 1549	ICGC_Myc_targets
18	1e+00	19 / 2401	ICGC_Bcl11_targets
19	1e+00	61 / 6322	ICGC_Pol2_targets
20	1e+00	43 / 4714	ICGC_Pu1_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	0.042	3 / 64	VAQUERIZAS_Lung
5	0.054	2 / 31	VAQUERIZAS_Fetal lung
6	0.073	2 / 37	VAQUERIZAS_Prostate
7	0.093	1 / 8	VAQUERIZAS_Tongue
8	0.102	2 / 45	VAQUERIZAS_Placenta
9	0.206	1 / 19	VAQUERIZAS_Heart
10	0.234	1 / 22	VAQUERIZAS_Tonsil
11	0.330	1 / 33	VAQUERIZAS_Liver
12	0.400	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	3e−16	20 / 137	WIRTH_Mucosa
2	2e−07	5 / 12	WIRTH_Tonsil
3	6e−07	15 / 259	PALMER_Granulocytes signature up
4	3e−03	5 / 82	WIRTH_Homeostasis
5	1e−02	2 / 13	WIRTH_Prim. lymphoid organs
6	1e−02	2 / 15	WIRTH_Telencephalon
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	0 / 6	WIRTH_Pituitary gland
16	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
17	1e+00	0 / 14	WIRTH_B−cells
18	1e+00	0 / 14	WIRTH_Thymus
19	1e+00	0 / 12	WIRTH_Lymphocytes
20	1e+00	0 / 476	WIRTH_Nervous System

Toxic

Rank	p−value	#in/all	Geneset
1	0.9	56 / 5285	LU_BPDE 0.005 DN
2	1.0	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	

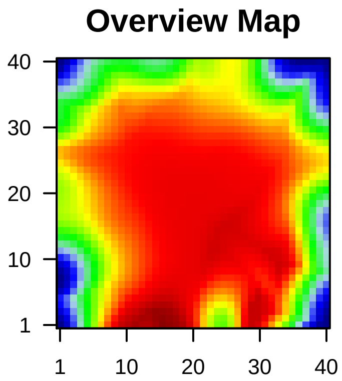
Underexpression Spots

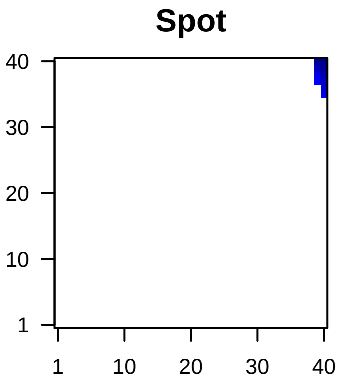
Spot Summary: c

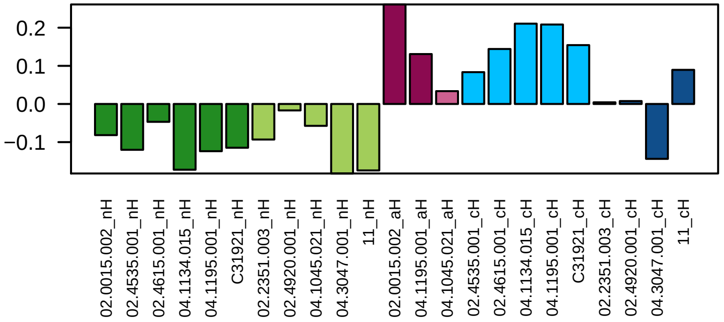
metagenes = 10
genes = 295

<r> metagenes = 0.99
<r> genes = 0.64
beta: r2= 0.27 / log p= −1.93

samples with spot = 3 (13 %)
MLH1_adenomaHNPCC : 1 (50 %)
MLH1_cancerHNPCC : 2 (40 %)


Overview Map


Spot

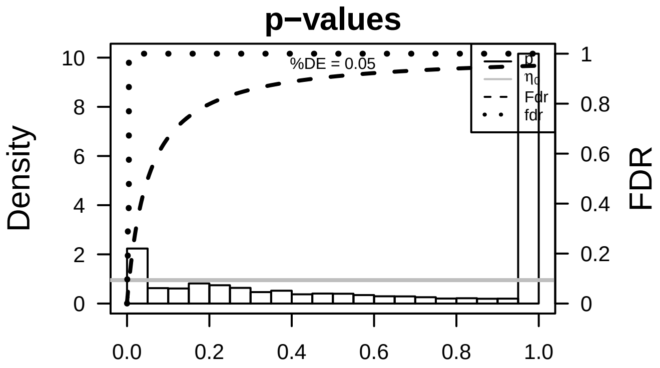


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.84	−0.57	0.6	REG1A	regenerating islet−derived 1 alpha [Source:HGNC Symbol;Ac
2	ENSG000001	1.71	−0.34	0.5	ITLN1	intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;
3	ENSG000001	1.65	−0.75	0.6	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
4	ENSG000001	1.57	−0.24	0.61	REG3A	regenerating islet−derived 3 alpha [Source:HGNC Symbol;Ac
5	ENSG000001	1.47	−0.28	0.59	MMP1	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
6	ENSG000001	1.33	−0.75	0.43	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) [Source
7	ENSG000001	1.27	−0.21	0.57	REG1B	regenerating islet−derived 1 beta [Source:HGNC Symbol;Acc
8	ENSG000001	1.25	−0.21	0.65	DMBT1	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
9	ENSG000001	1.17	−0.36	0.55	REG4	regenerating islet−derived family, member 4 [Source:HGNC S
10	ENSG000001	1.16	−0.2	0.57	MMP3	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC
11	ENSG000001	1.15	−0.44	0.8	SPINK1	serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symb
12	ENSG000000	1.15	−0.35	0.47	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
13	ENSG000002	1.1	−0.18	0.56	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy
14	ENSG000001	1.05	−0.66	0.86	LCN2	lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
15	ENSG000001	1.05	−0.87	0.84	AGR2	anterior gradient 2, protein disulphide isomerase family memb
16	ENSG000001	0.97	−0.41	0.7	SPINK4	serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symb
17	ENSG000001	0.91	−1	0.8	GPX2	glutathione peroxidase 2 [Source:HGNC Symbol;Acc:HGNC:
18	ENSG000001	0.87	−0.25	0.52	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc
19	ENSG000001	0.79	−0.11	0.61	CLDN2	claudin 2 [Source:HGNC Symbol;Acc:HGNC:2041]
20	ENSG000001	0.78	−0.25	0.6	WFDC2	WAP four−disulfide core domain 2 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−33	70 / 813	GSEA	GRADE_COLON_CANCER_UP
2	1e−26	67 / 944	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	4e−24	43 / 400	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
4	3e−22	58 / 850	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	7e−22	205 / 8123	Colon	TssF_Colon
6	2e−20	51 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	7e−20	25 / 138	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8	1e−19	27 / 174	GSEA	LI_AMPLIFIED_IN_LUNG_CANCER
9	2e−19	44 / 550	Cance	Lembcke_Normal vs Adenoma
10	2e−19	51 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
11	3e−18	24 / 145	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
12	3e−17	40 / 519	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
13	4e−17	21 / 113	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
14	7e−17	32 / 327	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
15	4e−16	31 / 323	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
16	4e−16	43 / 645	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
17	5e−16	48 / 807	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
18	6e−16	48 / 811	Lymph	WIRTH_lymphoma937_spot D
19	3e−15	31 / 350	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
20	7e−15	20 / 128	GSEA	SABATES_COLORECTAL_ADENOMA_UP
21	1e−14	4 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
22	1e−14	28 / 292	GSEA	MUELLER_PLURINET
23	2e−14	20 / 135	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
24	1e−13	25 / 248	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
25	1e−13	45 / 830	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
26	2e−13	16 / 85	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
27	2e−13	37 / 582	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
28	2e−13	21 / 172	GSEA	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
29	3e−13	2 / 16	Cance	RHODES_CANCER_META_SIGNATURE
30	3e−13	15 / 74	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
31	8e−13	15 / 78	Lymph	TARTE_Plasma cell signature
32	9e−13	5 / 16	Cance	RHODES_UNDIFFERENTIATED_CANCER
33	3e−12	23 / 239	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
34	3e−12	21 / 197	HM	HALLMARK_E2F_TARGETS
35	4e−12	34 / 546	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
36	6e−12	18 / 141	GSEA	CHANG_CYCLING_GENES
37	6e−12	17 / 123	GSEA	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
38	7e−12	2 / 14	Cance	LIU_PROSTATE_CANCER_UP
39	1e−11	14 / 77	GSEA	MORI_PRE_BI_LYMPHOCYTE_UP
40	1e−11	19 / 168	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	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−11	23 / 259	translation
2	2e−11	15 / 98	mitochondrial translation
3	2e−11	14 / 82	mitochondrial translational elongation
4	3e−10	13 / 82	mitochondrial translational initiation
5	5e−10	13 / 84	mitochondrial translational termination
6	5e−08	30 / 633	cellular protein metabolic process
7	6e−07	11 / 104	endoplasmic reticulum unfolded protein response
8	2e−06	21 / 410	mitotic cell cycle
9	2e−06	8 / 56	IRE1−mediated unfolded protein response
10	3e−06	17 / 291	organelle organization
11	2e−05	12 / 174	protein folding
12	3e−05	8 / 80	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent
13	4e−05	9 / 108	SRP−dependent cotranslational protein targeting to membrane
14	4e−05	7 / 62	cell redox homeostasis
15	1e−04	4 / 18	nucleobase−containing small molecule interconversion
16	1e−04	15 / 323	cell division
17	2e−04	4 / 19	cellular response to fatty acid
18	2e−04	7 / 77	nucleobase−containing small molecule metabolic process
19	4e−04	4 / 23	negative regulation of peptidase activity
20	4e−04	3 / 10	pentose−phosphate shunt

Brain

Rank	p−value	#in/all	Geneset
1	1e−05	64 / 2443	Fetal_Quies
2	6e−05	185 / 9923	Overlap_fetal_midbrain_K9K27me3
3	8e−05	46 / 1680	Fetal_ReprPCWk
4	4e−03	24 / 865	Mid_Frontal_Lobe_Het
5	9e−03	68 / 3370	Mid_Frontal_Lobe_ZNF
6	3e−02	22 / 939	Fetal_HetRpts
7	5e−02	73 / 3977	Mid_Frontal_Lobe_ReprPC
8	1e−01	32 / 1713	Mid_Frontal_Lobe_ReprPCWk
9	1e−01	38 / 2084	Mid_Frontal_Lobe_K9K27me3
10	2e−01	166 / 10239	Overlap_fetal_midbrain_ReprPC
11	2e−01	15 / 787	Overlap_fetal_midbrain_TssP
12	4e−01	7 / 400	Fetal_ZNF
13	5e−01	4 / 232	Fetal_ReprPC
14	5e−01	43 / 2820	Mid_Frontal_Lobe_HetRpts
15	6e−01	5 / 342	Fetal_Het
16	6e−01	8 / 552	Fetal_Tx
17	6e−01	16 / 1108	Overlap_fetal_midbrain_TssA
18	7e−01	12 / 855	Overlap_fetal_midbrain_ZNF
19	7e−01	162 / 10800	Overlap_fetal_midbrain_Quies
20	8e−01	2 / 191	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	2e−19	44 / 550	Lembcke_Normal vs Adenoma
2	1e−14	4 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	3e−13	2 / 16	RHODES_CANCER_META_SIGNATURE
4	9e−13	5 / 16	RHODES_UNDIFFERENTIATED_CANCER
5	7e−12	2 / 14	LIU_PROSTATE_CANCER_UP
6	2e−05	4 / 11	GENTLES_modul5
7	2e−03	3 / 16	GENTLES_modul2
8	2e−03	3 / 16	GENTLES_modul7
9	4e−03	4 / 41	ZHANG_MM up
10	8e−03	17 / 574	Lembcke_Colonic Inflammation
11	2e−02	4 / 71	SHAUGHNESSY_MM high risk
12	5e−02	3 / 52	KUIPER_MM poor survival
13	6e−02	5 / 136	PanCan_CC+Apop_geneset_nanostring
14	8e−02	6 / 198	PanCan_PI3K_geneset_nanostring
15	2e−01	2 / 50	PanCan_DNARepair_geneset_nanostring
16	2e−01	3 / 97	PanCan_TXmisReg_geneset_nanostring
17	2e−01	1 / 15	BEN−PORATH_UP
18	2e−01	1 / 16	LIU_COMMON_CANCER_GENES
19	2e−01	1 / 16	WANG_ER_UP
20	2e−01	1 / 16	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	2e−11	84 / 2638	extracellular exosome
2	1e−10	28 / 425	mitochondrial inner membrane
3	5e−09	52 / 1441	mitochondrion
4	9e−08	35 / 842	endoplasmic reticulum
5	9e−08	33 / 767	endoplasmic reticulum membrane
6	1e−06	6 / 24	mitochondrial small ribosomal subunit
7	2e−06	13 / 168	ribosome
8	2e−06	8 / 57	endoplasmic reticulum−Golgi intermediate compartment
9	2e−05	4 / 11	small nucleolar ribonucleoprotein complex
10	4e−05	72 / 2974	cytosol
11	5e−05	5 / 27	mitochondrial ribosome
12	1e−04	8 / 97	melanosome
13	1e−04	35 / 1176	extracellular space
14	2e−04	5 / 35	endoplasmic reticulum−Golgi intermediate compartment membrane
15	5e−04	10 / 179	endoplasmic reticulum lumen
16	5e−04	3 / 11	endoplasmic reticulum chaperone complex
17	5e−04	9 / 151	myelin sheath
18	6e−04	4 / 26	smooth endoplasmic reticulum
19	1e−03	6 / 76	condensed chromosome kinetochore
20	1e−03	3 / 15	U1 snRNP

Chr

Rank	p−value	#in/all	Geneset
1	4e−04	17 / 436	Chr 22
2	1e−03	30 / 1083	Chr 17
3	1e−02	20 / 745	Chr 9
4	1e−01	18 / 859	Chr 7
5	1e−01	23 / 1172	Chr 11
6	3e−01	25 / 1425	Chr 19
7	3e−01	10 / 522	Chr 20
8	3e−01	11 / 582	Chr 15
9	4e−01	17 / 1017	Chr 12
10	4e−01	16 / 976	Chr 6
11	5e−01	13 / 847	Chr 16
12	6e−01	9 / 613	Chr 14
13	8e−01	25 / 1920	Chr 1
14	9e−01	14 / 1228	Chr 2
15	9e−01	9 / 862	Chr 5
16	9e−01	7 / 715	Chr 10
17	9e−01	7 / 746	Chr X
18	1e+00	2 / 318	Chr 13
19	1e+00	5 / 651	Chr 8
20	1e+00	9 / 1043	Chr 3

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−22	205 / 8123	TssF_Colon
2	2e−20	51 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	1e−13	45 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
4	2e−11	215 / 10475	TssA_Colon
5	6e−10	11 / 55	Marisa_CRC−cluster−e
6	2e−08	150 / 6761	TssD2_Colon
7	7e−08	84 / 3122	TxEnhG1_Colon
8	7e−08	16 / 197	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	1e−05	215 / 11791	Enh_Colon
10	1e−05	31 / 877	TxEnhG2_Colon
11	2e−05	17 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	2e−05	187 / 9930	Tx_Colon
13	2e−05	26 / 688	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
14	5e−03	2 / 7	Marisa_CRC−C5
15	1e−02	2 / 10	KIM_CRC−MSI−regulated_DN
16	1e−02	109 / 5889	EnhWk1_Colon
17	5e−02	1 / 3	Budinska_E_Mixed_DOWN
18	6e−02	11 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
19	1e−01	1 / 7	Hewish_dMMR−secondary−mutations_Signal_transduction
20	1e−01	194 / 11968	TssWk_Colon

Disease

Rank	p−value	#in/all	Geneset
1	5e−09	31 / 608	GUDJ_psoriasis up
2	1e−01	2 / 37	BCHETNIA_EBM−DM up
3	3e−01	1 / 22	BCHETNIA_EBM up
4	7e−01	5 / 399	GUDJ_psoriasis down
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−18	24 / 145	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−05	8 / 69	cultured astroglia vs. in vivo astrocytes
3	3e−05	7 / 59	developing astrocytes
4	2e−02	5 / 97	Weller_LGG_1p19qDel−vs−intact_UP
5	2e−02	11 / 344	Up
6	4e−02	5 / 119	GIEZELT_GBM_WT_up_VS_mut
7	5e−02	3 / 54	Hopp_Sturm_GBM_Epi3_B1_G34_DN
8	6e−02	1 / 4	WILLSCHER_GBM_STSwt_proteomics−L_UP
9	7e−02	3 / 63	Stuehler_Proteins_up_in_STS
10	7e−02	3 / 63	OPC
11	9e−02	3 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	1e−01	2 / 36	Colman_survival_associated
13	1e−01	5 / 169	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
14	1e−01	4 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	1e−01	2 / 40	Christensen_hypomethylated_in_ependymoma
16	1e−01	1 / 9	Colman_survival_robust
17	1e−01	7 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
18	2e−01	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
19	2e−01	1 / 12	Phillips PN up vs MES & Prolif
20	2e−01	4 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−33	70 / 813	GRADE_COLON_CANCER_UP
2	1e−26	67 / 944	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	4e−24	43 / 400	VECCHI_GASTRIC_CANCER_EARLY_UP
4	3e−22	58 / 850	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	7e−20	25 / 138	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	1e−19	27 / 174	LI_AMPLIFIED_IN_LUNG_CANCER
7	2e−19	51 / 754	MARTENS_TRETINOIN_RESPONSE_DN
8	3e−17	40 / 519	BERENJENO_TRANSFORMED_BY_RHOA_UP
9	4e−17	21 / 113	WHITEFORD_PEDIATRIC_CANCER_MARKERS
10	7e−17	32 / 327	WONG_EMBRYONIC_STEM_CELL_CORE
11	4e−16	31 / 323	PENG_GLUTAMINE_DEPRIVATION_DN
12	4e−16	43 / 645	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
13	3e−15	31 / 350	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
14	7e−15	20 / 128	SABATES_COLORECTAL_ADENOMA_UP
15	1e−14	4 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	1e−14	28 / 292	MUELLER_PLURINET
17	2e−14	20 / 135	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
18	1e−13	25 / 248	KOBAYASHI_EGFR_SIGNALING_24HR_DN
19	2e−13	16 / 85	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
20	2e−13	37 / 582	CAIRO_HEPATOBLASTOMA_CLASSES_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−12	21 / 197	HALLMARK_E2F_TARGETS
2	1e−08	17 / 196	HALLMARK_G2M_CHECKPOINT
3	4e−07	15 / 198	HALLMARK_GLYCOLYSIS
4	1e−06	11 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	5e−05	12 / 195	HALLMARK_MYC_TARGETS_V1
6	6e−05	12 / 199	HALLMARK_MTORC1_SIGNALING
7	8e−04	10 / 193	HALLMARK_XENOBIOTIC_METABOLISM
8	3e−03	9 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
9	3e−03	9 / 197	HALLMARK_IL2_STAT5_SIGNALING
10	4e−03	9 / 198	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	1e−02	5 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	1e−02	4 / 58	HALLMARK_MYC_TARGETS_V2
13	7e−02	5 / 146	HALLMARK_DNA_REPAIR
14	8e−02	2 / 30	HALLMARK_NOTCH_SIGNALING
15	8e−02	6 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
16	1e−01	3 / 71	HALLMARK_CHOLESTEROL_HOMEOSTASIS
17	1e−01	4 / 132	HALLMARK_COAGULATION
18	2e−01	2 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
19	2e−01	5 / 189	HALLMARK_KRAS_SIGNALING_UP
20	2e−01	5 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	0.2	1 / 17	DUMEAUX_High bmi enriched genes
3	0.4	2 / 91	DUMEAUX_Smoking enriched genes
4	1.0	0 / 11	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_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	5e−16	48 / 807	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	6e−16	48 / 811	WIRTH_lymphoma937_spot D
3	8e−13	15 / 78	TARTE_Plasma cell signature
4	1e−10	24 / 317	TARTE_Plasmablast signature
5	3e−09	14 / 116	WIRTH_lymphoma937_spot MM
6	2e−08	13 / 112	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
7	5e−04	9 / 150	DAVE_BL−vs−DLBCL
8	2e−03	6 / 83	ROSOLOWSKI_green UP
9	2e−03	6 / 87	Aukema_BCL2 DN_BCL6 UP
10	4e−03	108 / 5643	HOPP_Txn_transition
11	5e−03	8 / 171	WIRTH_lymphoma937_spot C
12	9e−03	6 / 115	ROSOLOWSKI_green total
13	1e−02	7 / 167	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
14	3e−02	145 / 8358	HOPP_Active_promoter
15	3e−02	8 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
16	4e−02	2 / 21	ROSOLOWSKI_red UP
17	4e−02	4 / 87	ROSOLOWSKI_red total
18	6e−02	128 / 7491	HOPP_Txn_elongation
19	7e−02	1 / 5	Shaknovich_ABC_hyper_meth
20	1e−01	3 / 74	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_

MF

Rank	p−value	#in/all	Geneset
1	4e−09	16 / 162	structural constituent of ribosome
2	5e−06	37 / 1091	poly(A) RNA binding
3	1e−05	4 / 10	U6 snRNA binding
4	3e−05	5 / 25	isomerase activity
5	2e−04	4 / 20	amino acid binding
6	7e−04	4 / 27	peptidase inhibitor activity
7	1e−03	4 / 31	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
8	1e−03	3 / 15	coenzyme binding
9	2e−03	4 / 37	chemokine activity
10	3e−03	3 / 19	nucleoside diphosphate kinase activity
11	3e−03	9 / 192	carbohydrate binding
12	4e−03	3 / 21	protein disulfide isomerase activity
13	5e−03	12 / 328	enzyme binding
14	8e−03	5 / 80	chaperone binding
15	1e−02	2 / 10	deoxyribonuclease activity
16	1e−02	7 / 155	growth factor activity
17	1e−02	3 / 30	cysteine−type endopeptidase inhibitor activity
18	1e−02	3 / 30	ubiquitin conjugating enzyme activity
19	1e−02	4 / 60	peptide binding
20	1e−02	5 / 94	unfolded protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 28	hsa−miR−519e*
2	3e−03	6 / 93	hsa−miR−608
3	4e−03	5 / 68	hsa−miR−637
4	5e−03	4 / 46	hsa−miR−874
5	7e−03	5 / 77	hsa−miR−877
6	1e−02	5 / 94	hsa−miR−378
7	2e−02	4 / 66	hsa−miR−30e*
8	2e−02	2 / 14	hsa−miR−574−3p
9	2e−02	3 / 39	hsa−miR−593
10	2e−02	3 / 39	hsa−miR−484
11	2e−02	3 / 40	hsa−miR−517*
12	2e−02	3 / 41	hsa−miR−518f*
13	3e−02	4 / 74	hsa−miR−622
14	3e−02	4 / 76	hsa−miR−1254
15	3e−02	3 / 44	hsa−miR−661
16	3e−02	5 / 115	hsa−miR−154
17	3e−02	4 / 79	hsa−miR−205
18	5e−02	3 / 53	hsa−miR−337−3p
19	5e−02	2 / 23	hsa−miR−516a−5p
20	5e−02	5 / 131	hsa−miR−145

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.2
2	0.2	1 / 14	BENTINK_e2f3.1
3	0.2	1 / 14	BENTINK_myc.1
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
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	1e−07	51 / 1549	ICGC_Myc_targets
2	7e−07	9 / 66	MYC_Targets UP
3	1e−06	43 / 1294	KIM_MYC targets
4	4e−04	94 / 4470	ICGC_Creb1_targets
5	1e−03	119 / 6157	ICGC_Tcf3_targets
6	1e−03	105 / 5308	ICGC_Tcf12_targets
7	1e−03	45 / 1867	HEBENSTREIT_high expression TF
8	2e−03	2 / 5	MYC_Cell growth and proliferation UP
9	3e−03	128 / 6862	ICGC_Elf1_targets
10	3e−03	3 / 20	MYC_Metabolism UP
11	6e−03	99 / 5173	ICGC_Taf1_targets
12	7e−03	103 / 5453	ICGC_Foxm1_targets
13	1e−02	104 / 5578	ICGC_Stat5_targets
14	1e−02	85 / 4436	ICGC_Zeb1_targets
15	1e−02	87 / 4566	ICGC_Egr1_targets
16	1e−02	49 / 2342	ICGC_GabpPcr2_targets
17	1e−02	81 / 4230	ICGC_Nfatc1_targets
18	2e−02	99 / 5393	ICGC_Sp1_targets
19	3e−02	113 / 6313	ICGC_Pou2_targets
20	3e−02	108 / 6005	ICGC_Mta3_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	2 / 17	VAQUERIZAS_Salivary gland
2	0.05	2 / 24	VAQUERIZAS_Trachea
3	0.09	2 / 33	VAQUERIZAS_Liver
4	0.11	2 / 37	VAQUERIZAS_Prostate
5	0.13	2 / 41	VAQUERIZAS_Testis
6	0.14	2 / 42	VAQUERIZAS_Thymus
7	0.22	1 / 16	VAQUERIZAS_Fetal thyroid
8	0.24	1 / 18	VAQUERIZAS_Pancreas
9	0.27	1 / 20	VAQUERIZAS_Bone marrow
10	0.32	1 / 25	VAQUERIZAS_Spinal cord
11	0.47	1 / 41	VAQUERIZAS_Fetal brain
12	0.48	1 / 42	VAQUERIZAS_Thyroid
13	0.51	1 / 46	VAQUERIZAS_Whole brain
14	0.69	2 / 155	VAQUERIZAS_General
15	1.00	0 / 45	VAQUERIZAS_Placenta
16	1.00	0 / 30	VAQUERIZAS_Smooth muscle
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	0.02	2 / 14	WIRTH_B−cells
2	0.10	7 / 259	PALMER_Granulocytes signature up
3	0.17	1 / 12	WIRTH_Lymphocytes
4	0.18	1 / 13	WIRTH_Cortex cerebri
5	0.21	1 / 15	WIRTH_Telencephalon
6	0.37	1 / 30	PALMER_Lymphocytes signature up
7	0.40	4 / 208	PALMER_B−Cell signature up
8	0.57	1 / 54	WIRTH_Pancreas
9	0.64	2 / 140	PALMER_T−Cell signature up
10	0.72	1 / 82	WIRTH_Homeostasis
11	1.00	1 / 476	WIRTH_Nervous System
12	1.00	0 / 6	WIRTH_Pituitary gland
13	1.00	0 / 427	WIRTH_Immune system
14	1.00	0 / 13	WIRTH_Sec. lymphoid organs
15	1.00	0 / 13	WIRTH_Prim. lymphoid organs
16	1.00	0 / 12	WIRTH_Tonsil
17	1.00	0 / 14	WIRTH_Thymus
18	1.00	0 / 14	WIRTH_Bone marrow
19	1.00	0 / 13	WIRTH_Globus pallidus
20	1.00	0 / 16	WIRTH_Hippocampus

Toxic

Rank	p−value	#in/all	Geneset
1	0.3	23 / 1343	LU_BPDE 1h DN
2	1.0	62 / 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	

Underexpression Spots

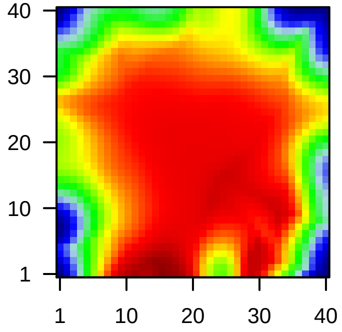
Spot Summary: d

metagenes = 6
genes = 183

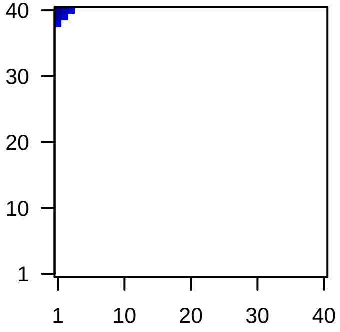
<r> metagenes = 1
<r> genes = 0.83
beta: r2= 0.89 / log p= −10.66

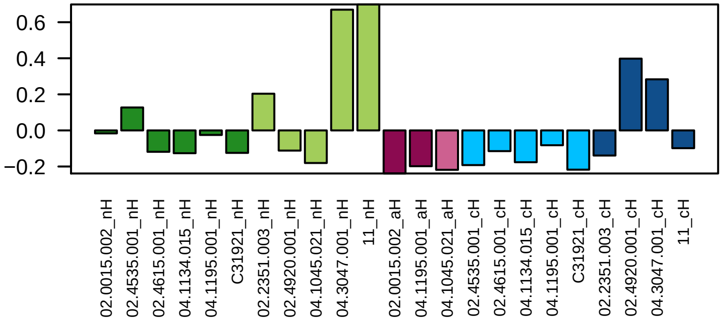
samples with spot = 5 (21.7 %)
other_normHNPCC : 3 (60 %)
other_cancerHNPCC : 2 (50 %)

Overview Map



Spot





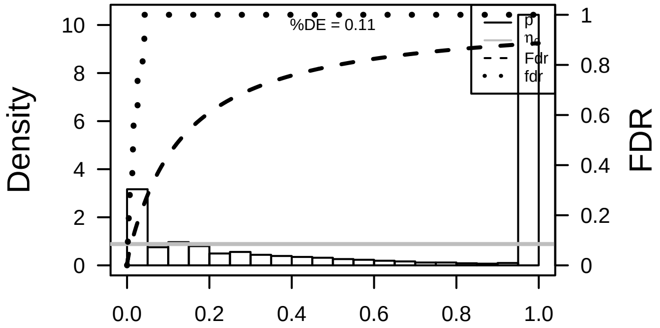
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.59	−0.8	0.89	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	ENSG000001	1.46	−0.53	0.96	MYH11	myosin, heavy chain 11, smooth muscle [Source:HGNC Sym
3	ENSG000001	1.44	−0.52	0.95	CNN1	calponin 1, basic, smooth muscle [Source:HGNC Symbol;Ac
4	ENSG000001	1.42	−0.68	0.93	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
5	ENSG000002	1.37	−0.24	0.44	MTRNR2L1	MT−RNR2−like 1 [Source:HGNC Symbol;Acc:HGNC:37155]
6	ENSG000001	1.35	−0.91	0.92	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	0.96	TPM2	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
10	ENSG000001	1.24	−0.52	0.75	IGFBP7	insulin−like growth factor binding protein 7 [Source:HGNC Sy
11	ENSG000001	1.21	−0.38	0.99	CSRP1	cysteine and glycine−rich protein 1 [Source:HGNC Symbol;A
12	ENSG000001	1.2	−0.74	0.94	TAGLN	transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
13	ENSG000000	1.17	−0.45	0.96	HSPB6	heat shock protein, alpha−crystallin−related, B6 [Source:HG
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	0.99	LMOD1	leiomodin 1 (smooth muscle) [Source:HGNC Symbol;Acc:HG
18	ENSG000001	1.14	−0.57	0.96	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	8e−65	3 / 16	Canc	LIU_PROSTATE_CANCER_DN
2	3e−53	42 / 132	Colon	Marisa_CRC−cluster−b
3	1e−43	47 / 303	GSE	PASINI_SUZ12_TARGETS_DN
4	8e−41	48 / 368	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_2B
5	1e−36	51 / 535	GSE	CHICAS_RB1_TARGETS_CONFLUENT
6	2e−35	48 / 478	GSE	LIM_MAMMARY_STEM_CELL_UP
7	1e−34	35 / 196	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
8	3e−33	32 / 160	GSE	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
9	2e−29	36 / 294	GSE	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
10	4e−29	39 / 378	CC	focal adhesion
11	5e−29	49 / 692	GSE	WONG_ADULT_TISSUE_STEM_MODULE
12	2e−27	30 / 198	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	2e−26	18 / 40	GSE	TOMLINS_PROSTATE_CANCER_DN
14	2e−25	38 / 445	GSE	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
15	7e−25	33 / 314	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
16	7e−25	33 / 315	Lymp	WIRTH_lymphoma937_spot E
17	4e−24	36 / 418	GSE	SWEET_LUNG_CANCER_KRAS_DN
18	4e−22	31 / 326	GSE	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
19	2e−21	13 / 22	GSE	REACTOME_SMOOTH_MUSCLE_CONTRACTION
20	2e−21	28 / 261	Lymp	LENZ_Stromal signature 1
21	2e−20	32 / 399	Disea	GUDJ_psoriasis down
22	6e−20	24 / 195	HM	HALLMARK_MYOGENESIS
23	1e−19	26 / 248	GSE	ONDER_CDH1_TARGETS_2_UP
24	1e−18	11 / 18	GSE	NIELSEN_LEIOMYOSARCOMA_CNN1_UP
25	3e−18	14 / 44	GSE	REACTOME_MUSCLE_CONTRACTION
26	6e−18	33 / 525	GSE	WEST_ADRENOCORTICAL_TUMOR_DN
27	8e−18	18 / 105	BP	muscle contraction
28	2e−17	24 / 246	GSE	DANG_REGULATED_BY_MYC_DN
29	4e−17	13 / 40	GSE	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
30	1e−16	24 / 267	GSE	WANG_SMARCE1_TARGETS_UP
31	1e−16	16 / 86	GSE	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
32	1e−16	19 / 144	GSE	IGLESIAS_E2F_TARGETS_UP
33	2e−16	19 / 148	Colon	Marisa_CRC−cluster−a
34	3e−16	23 / 249	GSE	BOQUEST_STEM_CELL_UP
35	1e−15	15 / 81	GSE	SWEET_KRAS_TARGETS_UP
36	2e−15	24 / 306	BP	extracellular matrix organization
37	3e−15	20 / 195	GSE	KEGG_FOCAL_ADHESION
38	7e−15	34 / 711	GSE	LEE_BMP2_TARGETS_UP
39	1e−14	14 / 76	GSE	FRIDMAN_SENESCENCE_UP
40	2e−14	20 / 215	GSE	SENESE_HDAC1_AND_HDAC2_TARGETS_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	3 / 123	HORVATH_aging_genes meth DOWN
2	0.2	3 / 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	8e−18	18 / 105	muscle contraction
2	2e−15	24 / 306	extracellular matrix organization
3	8e−09	6 / 17	regulation of muscle contraction
4	1e−08	11 / 113	extracellular matrix disassembly
5	2e−08	10 / 93	cell−matrix adhesion
6	3e−08	21 / 523	cell adhesion
7	8e−08	7 / 39	platelet aggregation
8	1e−07	17 / 373	axon guidance
9	5e−07	8 / 73	actin filament organization
10	1e−06	8 / 81	platelet degranulation
11	3e−06	4 / 11	negative regulation of neural precursor cell proliferation
12	5e−06	7 / 71	collagen catabolic process
13	6e−06	11 / 209	platelet activation
14	6e−06	5 / 28	endodermal cell differentiation
15	8e−06	7 / 76	cell junction assembly
16	9e−06	5 / 30	sarcomere organization
17	1e−05	16 / 466	blood coagulation
18	1e−05	4 / 16	negative regulation of anoikis
19	2e−05	17 / 539	small GTPase mediated signal transduction
20	2e−05	7 / 87	negative regulation of cell migration

Brain

Rank	p−value	#in/all	Geneset
1	7e−08	57 / 2956	Fetal_TssA
2	3e−05	27 / 1210	Fetal_TssP
3	7e−05	38 / 2084	Mid_Frontal_Lobe_K9K27me3
4	2e−04	19 / 787	Overlap_fetal_midbrain_TssP
5	4e−04	42 / 2603	Fetal_TxTrans
6	3e−03	54 / 3977	Mid_Frontal_Lobe_ReprPC
7	1e−02	7 / 268	Mid_Frontal_Lobe_TssA
8	2e−02	9 / 408	Mid_Frontal_Lobe_TxTrans
9	2e−02	11 / 552	Fetal_Tx
10	3e−02	37 / 2820	Mid_Frontal_Lobe_HetRpts
11	4e−02	14 / 855	Overlap_fetal_midbrain_ZNF
12	4e−02	42 / 3370	Mid_Frontal_Lobe_ZNF
13	4e−02	33 / 2549	Fetal_TssF
14	6e−02	23 / 1713	Mid_Frontal_Lobe_ReprPCWk
15	7e−02	5 / 232	Fetal_ReprPC
16	8e−02	19 / 1394	Mid_Frontal_Lobe_Quies
17	8e−02	22 / 1680	Fetal_ReprPCWk
18	1e−01	12 / 840	Mid_Frontal_Lobe_TssF
19	1e−01	4 / 191	Overlap_fetal_midbrain_Het
20	1e−01	23 / 1890	Overlap_fetal_midbrain_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	8e−65	3 / 16	LIU_PROSTATE_CANCER_DN
2	4e−11	7 / 15	GENTLES_modul17
3	4e−05	17 / 574	Lembcke_Colonic Inflammation
4	9e−03	2 / 15	BEN−PORATH_UP
5	9e−03	2 / 15	GENTLES_modul13
6	2e−02	5 / 152	PanCan_MAPK_geneset_nanostring
7	2e−02	1 / 15	LIU_BREAST_CANCER
8	5e−02	1 / 16	LIU_LIVER_CANCER
9	1e−01	4 / 198	PanCan_PI3K_geneset_nanostring
10	1e−01	1 / 16	GENTLES_modul16
11	3e−01	3 / 191	SPANG_LPS−index2
12	4e−01	1 / 51	PanCan_TGF−B_geneset_nanostring
13	5e−01	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
14	5e−01	1 / 71	SHAUGHNESSY_MM high risk
15	5e−01	1 / 78	PanCan_Wnt_geneset_nanostring
16	6e−01	3 / 324	SPANG_BCL6−index2
17	6e−01	1 / 97	PanCan_TXmisReg_geneset_nanostring
18	1e+00	2 / 550	Lembcke_Normal vs Adenoma
19	1e+00	0 / 16	RHODES_CANCER_META_SIGNATURE
20	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	4e−29	39 / 378	focal adhesion
2	8e−14	19 / 202	extracellular matrix
3	9e−14	65 / 2638	extracellular exosome
4	1e−13	15 / 109	Z disc
5	3e−12	18 / 216	actin cytoskeleton
6	5e−11	10 / 51	stress fiber
7	7e−11	12 / 91	sarcolemma
8	7e−10	7 / 21	costamere
9	6e−09	34 / 1176	extracellular space
10	8e−09	16 / 270	proteinaceous extracellular matrix
11	2e−07	17 / 381	cytoskeleton
12	2e−07	82 / 5185	cytoplasm
13	4e−07	7 / 49	extracellular vesicle
14	8e−07	33 / 1374	extracellular region
15	1e−06	9 / 110	blood microparticle
16	1e−06	54 / 2974	cytosol
17	1e−06	17 / 442	protein complex
18	2e−06	10 / 151	lamellipodium
19	2e−06	8 / 88	basement membrane
20	3e−06	8 / 93	ruffle

Chr

Rank	p−value	#in/all	Geneset
1	0.06	12 / 745	Chr 9
2	0.07	25 / 1920	Chr 1
3	0.27	12 / 1017	Chr 12
4	0.28	3 / 191	Chr 21
5	0.29	14 / 1228	Chr 2
6	0.38	8 / 715	Chr 10
7	0.42	8 / 746	Chr X
8	0.44	9 / 862	Chr 5
9	0.47	11 / 1083	Chr 17
10	0.49	6 / 582	Chr 15
11	0.54	6 / 613	Chr 14
12	0.56	7 / 735	Chr 4
13	0.56	5 / 522	Chr 20
14	0.57	11 / 1172	Chr 11
15	0.60	6 / 651	Chr 8
16	0.72	7 / 859	Chr 7
17	0.72	8 / 976	Chr 6
18	0.79	3 / 436	Chr 22
19	0.81	2 / 318	Chr 13
20	0.91	5 / 847	Chr 16

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−53	42 / 132	Marisa_CRC−cluster−b
2	2e−16	19 / 148	Marisa_CRC−cluster−a
3	2e−11	25 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
4	4e−09	18 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	9e−09	5 / 9	Budinska_D_Mesenchymal_UP
6	2e−08	17 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
7	5e−07	57 / 3122	TxEnhG1_Colon
8	8e−07	145 / 11968	TssWk_Colon
9	1e−06	56 / 3109	TssP_Colon
10	1e−06	143 / 11791	Enh_Colon
11	6e−05	7 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
12	1e−04	64 / 4379	TssD1_Colon
13	2e−04	15 / 532	K9acLow_Colon
14	3e−04	79 / 5889	EnhWk1_Colon
15	3e−04	14 / 499	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
16	4e−04	48 / 3112	EnhA_Colon
17	8e−04	19 / 877	TxEnhG2_Colon
18	1e−03	12 / 442	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
19	3e−03	9 / 310	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN_
20	3e−03	2 / 9	Marisa_CRC−C3

Disease

Rank	p−value	#in/all	Geneset
1	2e−20	32 / 399	GUDJ_psoriasis down
2	1e+00	1 / 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	1e−08	16 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	4e−08	7 / 36	Colman_survival_associated
3	2e−04	3 / 12	Phillips MES up vs Prolif & PN
4	4e−04	3 / 15	Mukasa_UP_in_GBM
5	5e−04	5 / 69	cultured astroglia vs. in vivo astrocytes
6	9e−04	5 / 77	Weller_LGG_gradeII−vs−III_DOWN
7	2e−03	4 / 56	mature astrocytes
8	2e−03	5 / 96	Weller_LGG_A_vs_O_UP
9	4e−03	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
10	4e−03	5 / 109	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	4e−03	6 / 157	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	5e−03	4 / 73	Christensen_hypermethylated_in_grade2_astrocytoma
13	6e−03	5 / 119	GIEZELT_GBM_WT_up_VS_mut
14	6e−03	5 / 122	Christensen_hypermethylated_in_grade3_astrocytoma
15	7e−03	5 / 123	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	9e−03	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
17	1e−02	4 / 95	Christensen_hypermethylated_in_secondary_glioblastoma
18	1e−02	5 / 146	Christensen_hypermethylated_in_grade3_oligoastrocytoma
19	2e−02	3 / 58	OL vs. MOG− OL
20	2e−02	5 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−65	3 / 16	LIU_PROSTATE_CANCER_DN
2	1e−43	47 / 303	PASINI_SUZ12_TARGETS_DN
3	8e−41	48 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
4	1e−36	51 / 535	CHICAS_RB1_TARGETS_CONFLUENT
5	2e−35	48 / 478	LIM_MAMMARY_STEM_CELL_UP
6	1e−34	35 / 196	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	3e−33	32 / 160	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
8	2e−29	36 / 294	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
9	5e−29	49 / 692	WONG_ADULT_TISSUE_STEM_MODULE
10	2e−26	18 / 40	TOMLINS_PROSTATE_CANCER_DN
11	2e−25	38 / 445	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
12	4e−24	36 / 418	SWEET_LUNG_CANCER_KRAS_DN
13	4e−22	31 / 326	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
14	2e−21	13 / 22	REACTOME_SMOOTH_MUSCLE_CONTRACTION
15	1e−19	26 / 248	ONDER_CDH1_TARGETS_2_UP
16	1e−18	11 / 18	NIELSEN_LEIOMYOSARCOMA_CNN1_UP
17	3e−18	14 / 44	REACTOME_MUSCLE_CONTRACTION
18	6e−18	33 / 525	WEST_ADRENOCORTICAL_TUMOR_DN
19	2e−17	24 / 246	DANG_REGULATED_BY_MYC_DN
20	4e−17	13 / 40	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−27	30 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	6e−20	24 / 195	HALLMARK_MYOGENESIS
3	6e−05	8 / 140	HALLMARK_UV_RESPONSE_DN
4	9e−05	9 / 190	HALLMARK_APICAL_JUNCTION
5	1e−04	9 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	1e−04	9 / 199	HALLMARK_ADIPOGENESIS
7	1e−04	8 / 157	HALLMARK_APOPTOSIS
8	2e−03	6 / 132	HALLMARK_COAGULATION
9	3e−03	7 / 192	HALLMARK_COMPLEMENT
10	3e−03	7 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
11	1e−02	6 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	1e−02	6 / 197	HALLMARK_IL2_STAT5_SIGNALING
13	1e−02	6 / 198	HALLMARK_HYPOXIA
14	5e−02	2 / 36	HALLMARK_ANGIOGENESIS
15	6e−02	4 / 155	HALLMARK_UV_RESPONSE_UP
16	7e−02	3 / 98	HALLMARK_ANDROGEN_RESPONSE
17	9e−02	2 / 52	HALLMARK_TGF_BETA_SIGNALING
18	1e−01	4 / 189	HALLMARK_KRAS_SIGNALING_UP
19	1e−01	4 / 196	HALLMARK_MITOTIC_SPINDLE
20	1e−01	4 / 199	HALLMARK_MTORC1_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.27	1 / 33	DUMEAUX_Fasting enriched genes
3	0.58	1 / 91	DUMEAUX_Smoking enriched genes
4	1.00	0 / 11	DUMEAUX_Smoking literature genes up
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 11	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 17	DUMEAUX_High bmi enriched genes
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−25	33 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
2	7e−25	33 / 315	WIRTH_lymphoma937_spot E
3	2e−21	28 / 261	LENZ_Stromal signature 1
4	8e−11	89 / 5039	HOPP_Repressed
5	3e−10	61 / 2838	HOPP_Poised_promoter
6	5e−07	17 / 414	TARTE_Mature plasma cell signature
7	1e−06	7 / 59	LENZ_Stromal signature 2
8	2e−06	9 / 115	ROSOLOWSKI_green total
9	6e−05	8 / 138	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
10	8e−05	8 / 145	WIRTH_lymphoma937_spot F
11	8e−05	8 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
12	3e−04	6 / 93	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	4e−04	3 / 15	Subero_T−ALL_hypo_meth
14	4e−04	6 / 99	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
15	1e−03	3 / 21	DAVE_Immune response 2
16	2e−03	6 / 138	Subero_DLBCL_hyper_meth
17	2e−03	4 / 59	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
18	3e−03	3 / 29	DAVE_Immune response 1
19	3e−03	4 / 62	Subero_mBL_hyper_meth
20	6e−03	5 / 122	Subero_INT_hyper_meth

MF

Rank	p−value	#in/all	Geneset
1	9e−11	9 / 39	structural constituent of muscle
2	7e−10	18 / 301	actin binding
3	5e−09	140 / 10693	protein binding
4	1e−07	10 / 113	actin filament binding
5	6e−07	9 / 102	integrin binding
6	4e−06	8 / 96	structural constituent of cytoskeleton
7	2e−05	6 / 58	cytoskeletal protein binding
8	5e−05	4 / 22	laminin binding
9	6e−05	4 / 23	insulin−like growth factor binding
10	1e−04	3 / 11	platelet−derived growth factor binding
11	1e−04	3 / 11	vinculin binding
12	2e−04	5 / 53	extracellular matrix structural constituent
13	3e−04	8 / 172	calmodulin binding
14	3e−04	5 / 60	collagen binding
15	4e−04	6 / 98	ion channel binding
16	9e−04	11 / 371	GTP binding
17	1e−03	4 / 49	protein kinase C binding
18	1e−03	3 / 23	extracellular matrix binding
19	1e−03	14 / 578	identical protein binding
20	2e−03	5 / 89	protease binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	7 / 174	hsa−miR−520h
2	0.002	6 / 137	hsa−miR−199b−5p
3	0.002	2 / 8	hsa−miR−566
4	0.003	4 / 62	hsa−miR−1236
5	0.004	5 / 112	hsa−miR−1271
6	0.006	6 / 168	hsa−miR−96
7	0.006	7 / 223	hsa−miR−548m
8	0.006	4 / 77	hsa−miR−651
9	0.007	8 / 291	hsa−miR−570
10	0.007	7 / 233	hsa−miR−520g
11	0.008	6 / 180	hsa−miR−548k
12	0.010	4 / 87	hsa−miR−767−5p
13	0.010	4 / 88	hsa−miR−595
14	0.012	3 / 49	hsa−miR−346
15	0.015	8 / 333	hsa−miR−302a
16	0.016	5 / 153	hsa−miR−518a−5p
17	0.018	6 / 215	hsa−miR−196a
18	0.018	5 / 157	hsa−miR−527
19	0.020	2 / 23	hsa−miR−516a−5p
20	0.020	2 / 23	hsa−miR−596

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	BENTINK_e2f3.1
2	0.1	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	9e−05	2 / 2	MYC_ECM cell adhesion DOWN
2	2e−03	30 / 1798	HEBENSTREIT_low expression TF
3	3e−03	2 / 9	MYC_Targets DOWN
4	1e−02	63 / 5135	ICGC_Ebfsc137065_targets
5	5e−02	43 / 3511	ICGC_Rad21_targets
6	9e−02	20 / 1523	ICGC_P300_targets
7	2e−01	28 / 2401	ICGC_Bcl11_targets
8	2e−01	68 / 6406	ICGC_Pax5_targets
9	2e−01	25 / 2149	ICGC_Mef2_targets
10	2e−01	59 / 5552	ICGC_Pol24_targets
11	2e−01	35 / 3177	ICGC_Irf4_targets
12	2e−01	50 / 4714	ICGC_Pu1_targets
13	3e−01	17 / 1506	ICGC_Usf1_targets
14	3e−01	73 / 7202	ICGC_Runx3_targets
15	3e−01	20 / 1867	HEBENSTREIT_high expression TF
16	4e−01	34 / 3305	ICGC_BatfPcr1_targets
17	4e−01	8 / 731	ICGC_SrfPcr2_targets
18	4e−01	24 / 2354	ICGC_SrfV0416101_targets
19	4e−01	62 / 6324	ICGC_Yy1_targets
20	5e−01	13 / 1294	KIM_MYC targets

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.04	2 / 31	VAQUERIZAS_Fetal lung
2	0.11	1 / 12	VAQUERIZAS_Kidney
3	0.13	2 / 64	VAQUERIZAS_Lung
4	0.15	1 / 17	VAQUERIZAS_Adrenal gland
5	0.16	1 / 18	VAQUERIZAS_Pancreas
6	0.20	1 / 23	VAQUERIZAS_Pituitary
7	0.21	1 / 24	VAQUERIZAS_Trachea
8	0.21	1 / 25	VAQUERIZAS_Adrenal cortex
9	0.33	1 / 42	VAQUERIZAS_Thymus
10	0.35	1 / 45	VAQUERIZAS_Placenta
11	0.44	2 / 155	VAQUERIZAS_General
12	1.00	0 / 41	VAQUERIZAS_Fetal brain
13	1.00	0 / 33	VAQUERIZAS_Liver
14	1.00	0 / 37	VAQUERIZAS_Prostate
15	1.00	0 / 30	VAQUERIZAS_Smooth muscle
16	1.00	0 / 49	VAQUERIZAS_Uterus
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	9e−08	5 / 13	WIRTH_Sec. lymphoid organs
2	4e−03	7 / 208	PALMER_B−Cell signature up
3	1e−01	5 / 259	PALMER_Granulocytes signature up
4	1e−01	1 / 13	WIRTH_Globus pallidus
5	1e−01	1 / 15	WIRTH_Telencephalon
6	1e−01	1 / 16	WIRTH_Hippocampus
7	2e−01	3 / 141	WIRTH_Muscle
8	4e−01	1 / 47	WIRTH_Placenta
9	4e−01	2 / 140	PALMER_T−Cell signature up
10	4e−01	1 / 54	WIRTH_Pancreas
11	7e−01	4 / 476	WIRTH_Nervous System
12	1e+00	0 / 6	WIRTH_Pituitary gland
13	1e+00	0 / 427	WIRTH_Immune system
14	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
15	1e+00	0 / 14	WIRTH_B−cells
16	1e+00	0 / 12	WIRTH_Tonsil
17	1e+00	0 / 14	WIRTH_Thymus
18	1e+00	0 / 12	WIRTH_Lymphocytes
19	1e+00	0 / 14	WIRTH_Bone marrow
20	1e+00	0 / 13	WIRTH_Cortex cerebri

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	59 / 5285	LU_BPDE 0.005 DN
2	0.2	16 / 1343	LU_BPDE 1h DN
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Underexpression Spots

Spot Summary: e

metagenes = 6
genes = 172

<r> metagenes = 0.99
<r> genes = 0.77
beta: r2= 0.51 / log p= −3.85

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

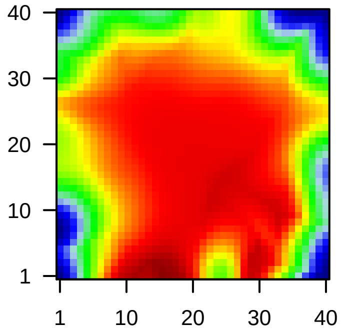
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	1.4	−0.53	0.84	FDCSP	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	ENSG000001	1.34	−0.7	0.92	CCL21	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
3	ENSG000001	1.14	−0.59	0.94	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	0.49		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	0.95	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	0.44		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	0.97	PTPRC	protein tyrosine phosphatase, receptor type, C [Source:HGN
20	ENSG000001	0.79	−0.35	0.98	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]

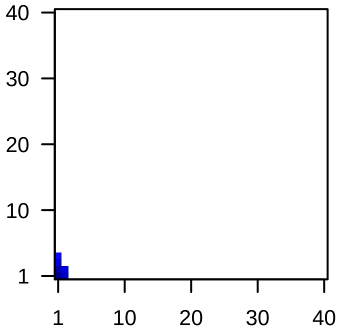
Geneset Overrepresentation

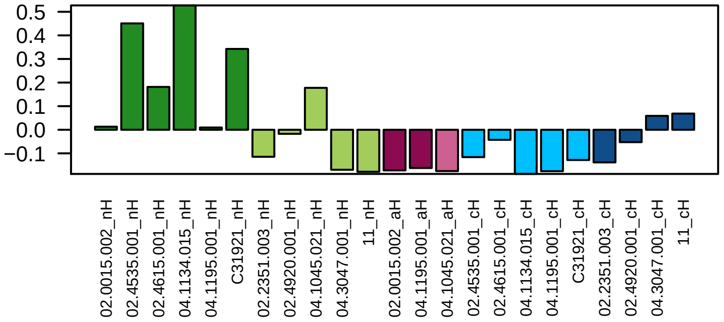
Rank	p−value	#in/all	Geneset	
1	4e−90	99 / 844	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	9e−63	56 / 263	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
3	8e−60	63 / 436	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	1e−54	59 / 427	Tissu	WIRTH_Immune system
5	9e−51	62 / 574	Canc	Lembcke_Colonic Inflammation
6	1e−47	44 / 220	GSEA	MCLACHLAN_DENTAL_CARIES_UP
7	9e−46	45 / 259	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
8	1e−40	39 / 210	GSEA	MCLACHLAN_DENTAL_CARIES_DN
9	8e−38	50 / 522	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
10	1e−37	35 / 175	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
11	2e−37	43 / 343	BP	immune response
12	3e−32	35 / 246	GSEA	QI_PLASMACYTOMA_UP
13	1e−27	14 / 16	CC	MHC class II protein complex
14	2e−27	22 / 79	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
15	2e−27	36 / 368	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
16	1e−26	19 / 51	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
17	5e−24	30 / 279	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
18	3e−23	20 / 86	GSEA	WIELAND_UP_BY_HBV_INFECTION
19	5e−23	26 / 201	CC	external side of plasma membrane
20	1e−22	24 / 163	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
21	1e−22	34 / 435	GSEA	RODWELL_AGING_KIDNEY_UP
22	1e−22	17 / 53	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
23	2e−22	129 / 7592	Lympl	HOPP_Strong_enhancer
24	2e−21	24 / 181	HM	HALLMARK_ALLOGRAFT_REJECTION
25	8e−21	25 / 218	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
26	1e−19	16 / 61	BP	antigen processing and presentation
27	9e−18	15 / 64	BP	T cell costimulation
28	1e−17	9 / 11	BP	antigen processing and presentation of peptide or polysaccharide antigen v
29	2e−17	16 / 82	GSEA	MORI_MATURE_B_LYMPHOCYTE_UP
30	5e−17	26 / 346	GSEA	SANSOM_APC_TARGETS_DN
31	1e−16	13 / 46	GSEA	WINTER_HYPOXIA_DN
32	1e−16	16 / 92	BP	T cell receptor signaling pathway
33	2e−16	25 / 332	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
34	5e−16	46 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
35	6e−16	22 / 251	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
36	7e−16	24 / 315	Lympl	WIRTH_lymphoma937_spot E
37	1e−15	15 / 87	GSEA	BASSO_CD40_SIGNALING_UP
38	2e−15	20 / 208	Tissu	PALMER_B−Cell signature up
39	2e−15	14 / 73	BP	interferon−gamma−mediated signaling pathway
40	2e−15	42 / 1165	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK

Overview Map

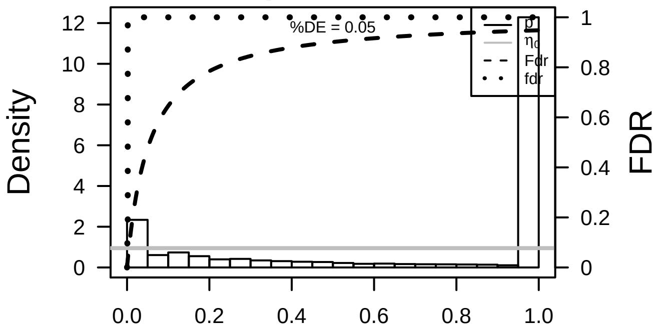


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.04	4 / 144	HORVATH_aging_genes meth UP
2	0.09	2 / 57	TESCHENDORFF_age_hypermethylated
3	1.00	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	2e−37	43 / 343	immune response
2	1e−19	16 / 61	antigen processing and presentation
3	9e−18	15 / 64	T cell costimulation
4	1e−17	9 / 11	antigen processing and presentation of peptide or polysaccharide antigen via
5	1e−16	16 / 92	T cell receptor signaling pathway
6	2e−15	14 / 73	interferon−gamma−mediated signaling pathway
7	1e−12	11 / 54	positive regulation of T cell proliferation
8	2e−11	12 / 90	antigen processing and presentation of exogenous peptide antigen via MHC c
9	3e−11	18 / 270	cytokine−mediated signaling pathway
10	6e−10	16 / 246	cell surface receptor signaling pathway
11	2e−09	10 / 78	regulation of immune response
12	8e−09	11 / 118	leukocyte migration
13	2e−08	6 / 20	positive regulation of neutrophil chemotaxis
14	3e−08	6 / 22	positive regulation of T cell activation
15	2e−07	15 / 326	inflammatory response
16	3e−07	6 / 31	B cell receptor signaling pathway
17	4e−07	5 / 18	lymph node development
18	1e−06	7 / 60	chemokine−mediated signaling pathway
19	1e−06	4 / 10	positive thymic T cell selection
20	1e−06	21 / 707	innate immune response

Brain

Rank	p−value	#in/all	Geneset
1	6e−04	39 / 2603	Fetal_TxTrans
2	8e−04	53 / 3977	Mid_Frontal_Lobe_ReprPC
3	1e−03	24 / 1394	Mid_Frontal_Lobe_Quies
4	3e−03	31 / 2084	Mid_Frontal_Lobe_K9K27me3
5	2e−02	24 / 1713	Mid_Frontal_Lobe_ReprPCWk
6	2e−02	21 / 1478	Overlap_fetal_midbrain_TxTrans
7	2e−02	32 / 2549	Fetal_TssF
8	3e−02	25 / 1890	Overlap_fetal_midbrain_TssF
9	7e−02	16 / 1210	Fetal_TssP
10	2e−01	7 / 552	Fetal_Tx
11	2e−01	18 / 1680	Fetal_ReprPCWk
12	2e−01	30 / 2956	Fetal_TssA
13	3e−01	24 / 2443	Fetal_Quies
14	4e−01	11 / 1108	Overlap_fetal_midbrain_TssA
15	4e−01	13 / 1327	Mid_Frontal_Lobe_TssP
16	4e−01	11 / 1137	Fetal_Enh
17	5e−01	8 / 840	Mid_Frontal_Lobe_TssF
18	5e−01	7 / 787	Overlap_fetal_midbrain_TssP
19	6e−01	3 / 342	Fetal_Het
20	6e−01	1 / 106	Overlap_fetal_midbrain_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	9e−51	62 / 574	Lembcke_Colonic Inflammation
2	1e−14	23 / 324	SPANG_BCL6−index2
3	2e−07	5 / 16	GENTLES_modul18
4	3e−04	8 / 191	SPANG_LPS−index2
5	7e−03	2 / 14	GENTLES_modul12
6	2e−02	4 / 123	PanCan_Driver_Gene_geneset_nanostring
7	3e−02	5 / 198	PanCan_PI3K_geneset_nanostring
8	4e−02	3 / 86	PanCan_JAK−ST_geneset_nanostring
9	5e−02	1 / 6	ZHANG_MGUS up
10	5e−02	3 / 97	PanCan_TXmisReg_geneset_nanostring
11	1e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
12	1e−01	1 / 16	LIU_COMMON_CANCER_GENES
13	1e−01	1 / 16	WANG_ER_UP
14	1e−01	1 / 16	GENTLES_modul11
15	3e−01	1 / 37	KUIPER_MM good survival
16	3e−01	2 / 136	PanCan_CC+Apop_geneset_nanostring
17	4e−01	2 / 140	PanCan_RAS_geneset_nanostring
18	4e−01	2 / 152	PanCan_MAPK_geneset_nanostring
19	4e−01	0 / 16	RHODES_CANCER_META_SIGNATURE
20	5e−01	1 / 71	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	1e−27	14 / 16	MHC class II protein complex
2	5e−23	26 / 201	external side of plasma membrane
3	9e−12	8 / 22	integral component of lumenal side of endoplasmic reticulum membrane
4	2e−11	9 / 35	ER to Golgi transport vesicle membrane
5	3e−10	8 / 32	transport vesicle membrane
6	6e−10	65 / 3507	plasma membrane
7	2e−09	8 / 39	clathrin−coated endocytic vesicle membrane
8	7e−09	8 / 47	trans−Golgi network membrane
9	8e−09	21 / 523	cell surface
10	2e−08	8 / 53	endocytic vesicle membrane
11	4e−08	14 / 245	lysosomal membrane
12	3e−07	6 / 32	immunological synapse
13	1e−06	47 / 2638	extracellular exosome
14	1e−05	27 / 1250	integral component of plasma membrane
15	1e−05	49 / 3059	membrane
16	4e−05	9 / 185	endosome membrane
17	7e−05	27 / 1374	extracellular region
18	1e−04	24 / 1176	extracellular space
19	1e−04	5 / 55	actin filament
20	3e−04	9 / 235	lysosome

Chr

Rank	p−value	#in/all	Geneset
1	2e−05	23 / 976	Chr 6
2	5e−02	24 / 1920	Chr 1
3	6e−02	16 / 1172	Chr 11
4	3e−01	11 / 1017	Chr 12
5	3e−01	8 / 746	Chr X
6	3e−01	5 / 436	Chr 22
7	5e−01	11 / 1228	Chr 2
8	5e−01	3 / 318	Chr 13
9	6e−01	9 / 1043	Chr 3
10	6e−01	5 / 613	Chr 14
11	6e−01	7 / 862	Chr 5
12	7e−01	4 / 522	Chr 20
13	8e−01	6 / 847	Chr 16
14	8e−01	1 / 191	Chr 21
15	9e−01	7 / 1083	Chr 17
16	9e−01	4 / 715	Chr 10
17	9e−01	5 / 859	Chr 7
18	9e−01	4 / 735	Chr 4
19	9e−01	8 / 1425	Chr 19
20	1e+00	3 / 745	Chr 9

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−90	99 / 844	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−16	25 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	2e−10	21 / 423	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	5e−08	16 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	5e−06	17 / 532	K9acLow_Colon
6	2e−05	19 / 728	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
7	5e−05	15 / 507	Pentrack_CRC_TCGA_corr_C_normal_UP
8	9e−05	129 / 11968	TssWk_Colon
9	2e−03	5 / 104	Pentrack_CRC_TCGA_group.over_A_normal_UP
10	8e−03	2 / 15	Budinska_B_Lower crypt−like_DOWN
11	2e−02	51 / 4379	TssD1_Colon
12	2e−02	14 / 877	TxEnhG2_Colon
13	3e−02	3 / 76	Marisa_CRC−cluster−g
14	3e−02	1 / 4	Juehling_HNPCC−mutated−in−6−to−8
15	3e−02	1 / 4	Budinska_C_CIMP−H−like_DOWN
16	4e−02	4 / 148	Marisa_CRC−cluster−a
17	9e−02	1 / 10	KIM_MSI−in−EC
18	9e−02	1 / 11	Kaneda_CIMP−group2
19	1e−01	34 / 3112	EnhA_Colon
20	1e−01	6 / 386	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN

Disease

Rank	p−value	#in/all	Geneset
1	8e−10	24 / 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	5e−24	30 / 279	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−07	9 / 95	Weller_LGG_1p19qDel−vs−intact_DOWN
3	1e−06	52 / 3064	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
4	2e−06	8 / 96	Weller_LGG_A_vs_O_UP
5	1e−05	4 / 16	Donson−chemokines/cytokines−associated with LTS in HGA
6	1e−05	5 / 33	Donson−Misc immune function−associated with LTS in HGA
7	1e−05	16 / 517	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
8	4e−05	3 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
9	9e−04	7 / 173	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
10	1e−03	4 / 53	Donson−innate immunity−associated with LTS in HGA
11	2e−03	16 / 781	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
12	2e−03	3 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
13	2e−03	2 / 8	Donson−adaptive−immunity−associated with LTS in HGA
14	3e−03	4 / 65	Sturm_GBM_Meth_overexpression_D_G34_UP
15	4e−03	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
16	7e−03	2 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
17	1e−02	2 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
18	2e−02	3 / 59	Christensen_hypomethylated_in_primary_glioblastoma
19	2e−02	3 / 70	Christensen_hypomethylated_in_secondary_glioblastoma
20	5e−02	1 / 6	Martinez_Glio_hypometh

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−63	56 / 263	WALLACE_PROSTATE_CANCER_RACE_UP
2	8e−60	63 / 436	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	1e−47	44 / 220	MCLACHLAN_DENTAL_CARIES_UP
4	9e−46	45 / 259	POOLA_INVASIVE_BREAST_CANCER_UP
5	1e−40	39 / 210	MCLACHLAN_DENTAL_CARIES_DN
6	8e−38	50 / 522	SMID_BREAST_CANCER_LUMINAL_B_DN
7	1e−37	35 / 175	LEE_DIFFERENTIATING_T_LYMPHOCYTE
8	3e−32	35 / 246	QI_PLASMACYTOMA_UP
9	2e−27	22 / 79	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
10	2e−27	36 / 368	LINDGREN_BLADDER_CANCER_CLUSTER_2B
11	1e−26	19 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
12	3e−23	20 / 86	WIELAND_UP_BY_HBV_INFECTION
13	1e−22	24 / 163	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
14	1e−22	34 / 435	RODWELL_AGING_KIDNEY_UP
15	1e−22	17 / 53	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
16	8e−21	25 / 218	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
17	2e−17	16 / 82	MORI_MATURE_B_LYMPHOCYTE_UP
18	5e−17	26 / 346	SANSOM_APC_TARGETS_DN
19	1e−16	13 / 46	WINTER_HYPOXIA_DN
20	5e−16	46 / 1340	PUJANA_ATM_PCC_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	2e−21	24 / 181	HALLMARK_ALLOGRAFT_REJECTION
2	1e−12	17 / 189	HALLMARK_KRAS_SIGNALING_UP
3	1e−08	13 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
4	2e−08	13 / 194	HALLMARK_INFLAMMATORY_RESPONSE
5	8e−06	10 / 192	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	8e−06	10 / 192	HALLMARK_COMPLEMENT
7	7e−05	9 / 197	HALLMARK_IL2_STAT5_SIGNALING
8	1e−04	6 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	2e−03	7 / 190	HALLMARK_APICAL_JUNCTION
10	6e−03	5 / 132	HALLMARK_COAGULATION
11	8e−03	4 / 89	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	1e−02	4 / 103	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	3e−02	5 / 198	HALLMARK_HYPOXIA
14	3e−02	5 / 199	HALLMARK_MTORC1_SIGNALING
15	5e−02	4 / 157	HALLMARK_APOPTOSIS
16	1e−01	4 / 195	HALLMARK_ESTROGEN_RESPONSE_LATE
17	1e−01	4 / 198	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
18	2e−01	3 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
19	3e−01	1 / 44	HALLMARK_APICAL_SURFACE
20	3e−01	1 / 46	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	2 / 17	DUMEAUX_High bmi enriched genes
2	0.08	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.09	1 / 11	DUMEAUX_Women normal BMI literature genes up
4	0.56	1 / 91	DUMEAUX_Smoking enriched genes
5	1.00	0 / 11	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 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−22	129 / 7592	HOPP_Strong_enhancer
2	7e−16	24 / 315	WIRTH_lymphoma937_spot E
3	7e−15	23 / 314	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−c
4	6e−14	26 / 466	SPANG_CD40 6hrs DN
5	3e−12	15 / 145	WIRTH_lymphoma937_spot F
6	3e−12	15 / 145	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
7	5e−12	15 / 150	DAVE_BL−vs−DLBCL
8	1e−10	36 / 1215	SPANG_BCR DN
9	1e−10	19 / 332	SPANG_CD40 6hrs UP
10	6e−10	88 / 5643	HOPP_Txn_transition
11	1e−09	8 / 38	TARTE_B−cell signature
12	5e−09	19 / 414	TARTE_Mature plasma cell signature
13	2e−07	14 / 279	SPANG_IL21 DN
14	5e−07	106 / 8358	HOPP_Active_promoter
15	5e−07	8 / 79	SPANG_LPS 6hrs DN
16	1e−06	5 / 22	DAVE_NFkB BL DN
17	1e−06	9 / 123	SPANG_LPS 6hrs UP
18	3e−04	3 / 16	WRIGHT_GCB UP
19	4e−04	3 / 17	WRIGHT_ABC UP
20	5e−04	10 / 317	TARTE_Plasmablast signature

MF

Rank	p−value	#in/all	Geneset
1	4e−13	8 / 16	MHC class II protein complex binding
2	8e−10	7 / 23	peptide antigen binding
3	8e−07	125 / 10693	protein binding
4	1e−05	10 / 196	transmembrane signaling receptor activity
5	2e−05	12 / 301	actin binding
6	2e−05	5 / 37	chemokine activity
7	2e−04	5 / 58	cell adhesion molecule binding
8	7e−04	3 / 20	antigen binding
9	2e−03	4 / 60	glycoprotein binding
10	3e−03	5 / 113	actin filament binding
11	3e−03	2 / 10	profilin binding
12	3e−03	7 / 219	receptor activity
13	3e−03	5 / 114	SH3 domain binding
14	5e−03	9 / 362	protein kinase binding
15	5e−03	3 / 40	cytokine receptor activity
16	7e−03	3 / 45	non−membrane spanning protein tyrosine kinase activity
17	8e−03	2 / 15	CCR chemokine receptor binding
18	1e−02	2 / 20	cytokine binding
19	1e−02	2 / 20	phosphatidylinositol 3−kinase binding
20	2e−02	8 / 371	GTP binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 61	hsa−miR−296−3p
2	0.03	2 / 29	hsa−miR−1292
3	0.04	2 / 35	hsa−miR−1229
4	0.05	2 / 41	hsa−miR−758
5	0.06	4 / 170	hsa−miR−495
6	0.07	2 / 48	hsa−miR−623
7	0.08	2 / 52	hsa−miR−1224−3p
8	0.10	3 / 126	hsa−miR−421
9	0.10	4 / 201	hsa−miR−944
10	0.11	5 / 282	hsa−miR−30b
11	0.11	4 / 204	hsa−miR−448
12	0.12	2 / 66	hsa−miR−30e*
13	0.12	5 / 293	hsa−miR−30c
14	0.14	3 / 144	hsa−miR−338−5p
15	0.15	2 / 78	hsa−miR−890
16	0.16	3 / 154	hsa−miR−506
17	0.16	1 / 20	hsa−miR−380*
18	0.18	2 / 87	hsa−miR−767−5p
19	0.18	1 / 23	hsa−miR−668
20	0.18	1 / 23	hsa−miR−151−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	1 / 10	BENTINK_ras.4
2	0.10	1 / 12	BENTINK_ras.1
3	1.00	0 / 14	GUSTAFSON_PI3K_UP
4	1.00	0 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 14	BENTINK_e2f3.1
6	1.00	0 / 13	BENTINK_e2f3.2
7	1.00	0 / 14	BENTINK_myc.1
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 14	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−05	37 / 2149	ICGC_Mef2_targets
2	1e−04	39 / 2401	ICGC_Bcl11_targets
3	2e−04	28 / 1523	ICGC_P300_targets
4	3e−04	62 / 4714	ICGC_Pu1_targets
5	1e−03	33 / 2133	ICGC_Cebpbsc150_targets
6	1e−02	41 / 3305	ICGC_BatfPcr1_targets
7	2e−02	62 / 5512	ICGC_Nficsc81335_targets
8	2e−02	39 / 3177	ICGC_Irf4_targets
9	4e−02	34 / 2827	ICGC_Bcl3_targets
10	7e−02	46 / 4230	ICGC_Nfatc1_targets
11	9e−02	52 / 4969	ICGC_Atf2_targets
12	1e−01	38 / 3511	ICGC_Rad21_targets
13	1e−01	51 / 4987	ICGC_Bclaf101388_targets
14	1e−01	56 / 5578	ICGC_Stat5_targets
15	2e−01	21 / 1867	HEBENSTREIT_high expression TF
16	2e−01	61 / 6157	ICGC_Tcf3_targets
17	2e−01	62 / 6313	ICGC_Pou2_targets
18	2e−01	54 / 5526	ICGC_Pmlsc71910_targets
19	2e−01	53 / 5453	ICGC_Foxm1_targets
20	3e−01	50 / 5173	ICGC_Taf1_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.002	4 / 64	VAQUERIZAS_Lung
2	0.003	3 / 31	VAQUERIZAS_Lymph node
3	0.003	4 / 67	VAQUERIZAS_Whole blood
4	0.006	3 / 42	VAQUERIZAS_Thymus
5	0.016	2 / 22	VAQUERIZAS_Tonsil
6	0.031	2 / 31	VAQUERIZAS_Fetal lung
7	0.042	2 / 37	VAQUERIZAS_Prostate
8	0.140	1 / 17	VAQUERIZAS_Salivary gland
9	0.148	1 / 18	VAQUERIZAS_Pancreas
10	0.163	1 / 20	VAQUERIZAS_Bone marrow
11	0.234	1 / 30	VAQUERIZAS_Smooth muscle
12	0.312	1 / 42	VAQUERIZAS_Thyroid
13	0.353	1 / 49	VAQUERIZAS_Uterus
14	0.749	1 / 155	VAQUERIZAS_General
15	1.000	0 / 41	VAQUERIZAS_Fetal brain
16	1.000	0 / 45	VAQUERIZAS_Placenta
17	1.000	0 / 33	VAQUERIZAS_Liver
18	1.000	0 / 12	VAQUERIZAS_Kidney
19	1.000	0 / 25	VAQUERIZAS_Spinal cord
20	1.000	0 / 46	VAQUERIZAS_Whole brain

Tissue

Rank	p−value	#in/all	Geneset
1	1e−54	59 / 427	WIRTH_Immune system
2	2e−15	20 / 208	PALMER_B−Cell signature up
3	4e−09	12 / 140	PALMER_T−Cell signature up
4	8e−02	5 / 259	PALMER_Granulocytes signature up
5	1e−01	1 / 13	WIRTH_Cortex cerebri
6	1e−01	1 / 14	WIRTH_B−cells
7	1e−01	1 / 15	WIRTH_Cerebellum
8	1e−01	1 / 16	WIRTH_Hippocampus
9	1e+00	0 / 6	WIRTH_Pituitary gland
10	1e+00	0 / 54	WIRTH_Pancreas
11	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
12	1e+00	0 / 13	WIRTH_Prim. lymphoid organs
13	1e+00	0 / 12	WIRTH_Tonsil
14	1e+00	0 / 14	WIRTH_Thymus
15	1e+00	0 / 12	WIRTH_Lymphocytes
16	1e+00	0 / 14	WIRTH_Bone marrow
17	1e+00	0 / 476	WIRTH_Nervous System
18	1e+00	0 / 13	WIRTH_Globus pallidus
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 14	WIRTH_Thalamus

Toxic

Rank	p−value	#in/all	Geneset
1	0.1	16 / 1343	LU_BPDE 1h DN
2	1.0	29 / 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	

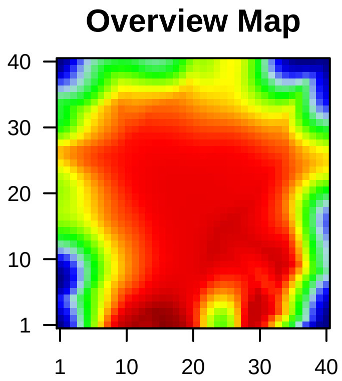
Underexpression Spots

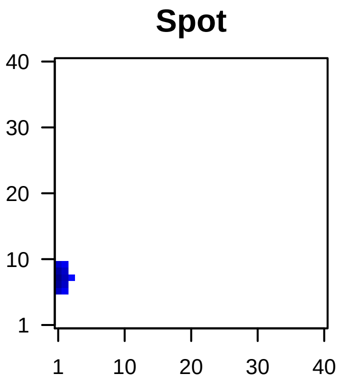
Spot Summary: f

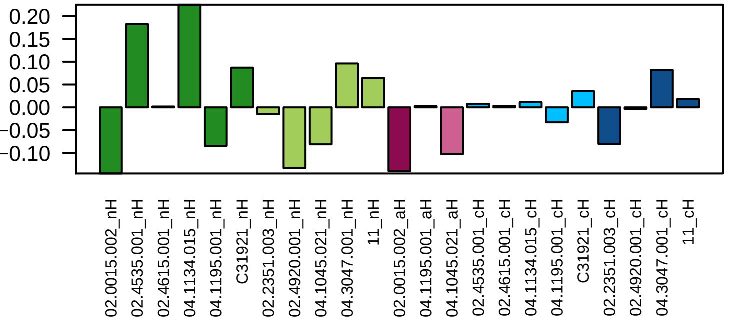
metagenes = 11
genes = 195

<r> metagenes = 0.97
<r> genes = 0.65
beta: r2= 0.13 / log p= −1.02

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


Overview Map


Spot

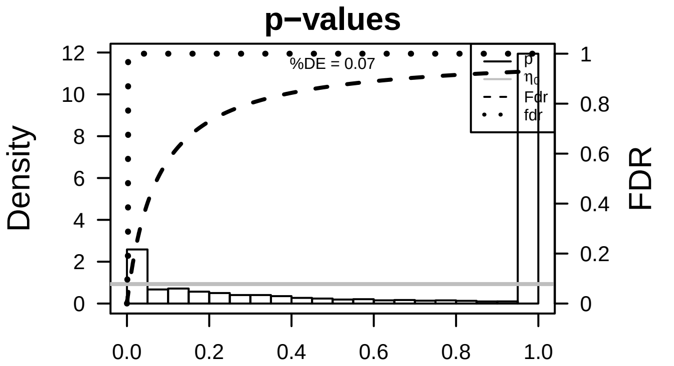


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ENSG000001	0.54	−0.37	0.75	BHLHE40	basic helix−loop−helix family, member e40 [Source:HGNC Sy
2	ENSG000002	0.52	−0.34	0.58		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:M0
3	ENSG000002	0.51	−0.35	0.91		
4	ENSG000001	0.49	−0.2	0.7	ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HG
5	ENSG000001	0.48	−0.24	0.76	GOLGA8A	golgin A8 family, member A [Source:HGNC Symbol;Acc:HGN
6	ENSG000001	0.46	−0.28	0.92		
7	ENSG000002	0.46	−0.19	0.84	GOLGA8B	golgin A8 family, member B [Source:HGNC Symbol;Acc:HGN
8	ENSG000001	0.44	−0.23	0.51	STAT1	signal transducer and activator of transcription 1, 91kDa [Sou
9	ENSG000002	0.42	−0.33	0.91		
10	ENSG000001	0.4	−0.43	0.75	PABPC3	poly(A) binding protein, cytoplasmic 3 [Source:HGNC Symbol
11	ENSG000002	0.4	−0.28	0.92		
12	ENSG000001	0.39	−0.24	0.77	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix−loop−he
13	ENSG000001	0.39	−0.34	0.87	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
14	ENSG000001	0.39	−0.21	0.87	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
15	ENSG000002	0.38	−0.2	0.78		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H3I
16	ENSG000001	0.37	−0.08	0.83	SLFN5	schlafen family member 5 [Source:HGNC Symbol;Acc:HGNC
17	ENSG000000	0.36	−0.15	0.45	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3
18	ENSG000001	0.36	−0.26	0.92	HNRNPDL	heterogeneous nuclear ribonucleoprotein D−like [Source:HGN
19	ENSG000001	0.36	−0.21	0.9		
20	ENSG000001	0.36	−0.22	0.82	SRRM2	serine/arginine repetitive matrix 2 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−68	94 / 1091	MF	poly(A) RNA binding
2	2e−35	134 / 5643	Lymph	HOPP_Txn_transition
3	2e−34	34 / 182	BP	mRNA splicing, via spliceosome
4	4e−33	36 / 237	BP	RNA splicing
5	1e−31	27 / 105	GSEA	REACTOME_MRNA_SPLICING
6	6e−30	28 / 134	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
7	8e−30	29 / 151	GSEA	REACTOME_MRNA_PROCESSING
8	3e−28	85 / 2554	CC	nucleoplasm
9	4e−27	62 / 1340	GSEA	PUJANA_ATM_PCC_NETWORK
10	1e−26	66 / 1563	GSEA	PUJANA_BRCA1_PCC_NETWORK
11	2e−26	41 / 513	MF	RNA binding
12	3e−24	160 / 10239	Brain	Overlap_fetal_midbrain_ReprPC
13	5e−24	47 / 820	BP	gene expression
14	1e−23	161 / 10475	Colon	TssA_Colon
15	4e−23	53 / 1134	MF	nucleic acid binding
16	8e−23	156 / 9930	Colon	Tx_Colon
17	7e−21	108 / 5101	CC	nucleus
18	3e−20	41 / 747	GSEA	PUJANA_CHEK2_PCC_NETWORK
19	4e−19	30 / 385	MF	nucleotide binding
20	5e−19	23 / 191	Brain	Overlap_fetal_midbrain_Het
21	4e−18	19 / 121	CC	ribonucleoprotein complex
22	2e−17	37 / 713	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
23	3e−17	40 / 855	Brain	Overlap_fetal_midbrain_ZNF
24	8e−17	18 / 120	GSEA	KEGG_SPLICEOSOME
25	8e−17	126 / 7491	Lymph	HOPP_Txn_elongation
26	8e−17	134 / 8358	Lymph	HOPP_Active_promoter
27	1e−16	49 / 1352	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
28	7e−16	36 / 754	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
29	8e−16	20 / 183	BP	mRNA processing
30	1e−15	141 / 9390	Colon	TxWk_Colon
31	1e−15	57 / 1914	GSEA	PILON_KLF1_TARGETS_DN
32	1e−15	15 / 82	CC	catalytic step 2 spliceosome
33	4e−15	30 / 539	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
34	2e−14	21 / 246	miRN	hsa−miR−1252
35	4e−14	18 / 170	GSEA	JISON_SICKLE_CELL_DISEASE_DN
36	5e−14	16 / 124	miRN	hsa−miR−515−5p
37	5e−14	109 / 6320	Brain	Overlap_fetal_midbrain_HetRpts
38	9e−14	142 / 9923	Brain	Overlap_fetal_midbrain_K9K27me3
39	1e−13	15 / 109	BP	RNA processing
40	5e−13	18 / 196	miRN	hsa−miR−513a−3p



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	2e−34	34 / 182	mRNA splicing, via spliceosome
2	4e−33	36 / 237	RNA splicing
3	5e−24	47 / 820	gene expression
4	8e−16	20 / 183	mRNA processing
5	1e−13	15 / 109	RNA processing
6	5e−11	18 / 259	translation
7	8e−11	14 / 142	translational initiation
8	6e−10	7 / 21	negative regulation of mRNA splicing, via spliceosome
9	4e−09	8 / 41	mRNA 3'−end processing
10	7e−09	8 / 44	termination of RNA polymerase II transcription
11	2e−08	6 / 19	mRNA splice site selection
12	9e−08	20 / 512	transcription from RNA polymerase II promoter
13	2e−07	22 / 633	cellular protein metabolic process
14	2e−07	8 / 64	mRNA export from nucleus
15	2e−07	7 / 44	RNA secondary structure unwinding
16	5e−06	6 / 47	DNA duplex unwinding
17	5e−06	8 / 101	translational elongation
18	9e−06	8 / 108	SRP−dependent cotranslational protein targeting to membrane
19	2e−05	8 / 117	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
20	2e−05	5 / 35	regulation of translational initiation

Brain

Rank	p−value	#in/all	Geneset
1	3e−24	160 / 10239	Overlap_fetal_midbrain_ReprPC
2	5e−19	23 / 191	Overlap_fetal_midbrain_Het
3	3e−17	40 / 855	Overlap_fetal_midbrain_ZNF
4	5e−14	109 / 6320	Overlap_fetal_midbrain_HetRpts
5	9e−14	142 / 9923	Overlap_fetal_midbrain_K9K27me3
6	1e−06	133 / 10800	Overlap_fetal_midbrain_Quies
7	1e−03	18 / 865	Mid_Frontal_Lobe_Het
8	2e−03	10 / 342	Fetal_Het
9	5e−03	46 / 3370	Mid_Frontal_Lobe_ZNF
10	8e−03	17 / 939	Fetal_HetRpts
11	4e−02	8 / 400	Fetal_ZNF
12	5e−02	23 / 1680	Fetal_ReprPCWk
13	9e−02	107 / 10278	Overlap_fetal_midbrain_ReprPCWk
14	2e−01	15 / 1182	Fetal_EnhP
15	4e−01	3 / 232	Fetal_ReprPC
16	4e−01	14 / 1356	Fetal_K9K27me3
17	8e−01	9 / 1137	Fetal_Enh
18	8e−01	7 / 910	Fetal_EnhG
19	8e−01	2 / 317	Mid_Frontal_Lobe_Tx
20	9e−01	19 / 2443	Fetal_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	1 / 16	LIU_COMMON_CANCER_GENES
2	0.009	2 / 15	LIU_BREAST_CANCER
3	0.010	2 / 16	GENTLES_modul14
4	0.011	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.036	5 / 191	SPANG_LPS−index2
6	0.065	3 / 97	PanCan_TXmisReg_geneset_nanostring
7	0.087	2 / 52	KUIPER_MM poor survival
8	0.091	1 / 10	GENTLES_modul3
9	0.112	3 / 123	PanCan_Driver_Gene_geneset_nanostring
10	0.125	1 / 14	LIU_PROSTATE_CANCER_UP
11	0.125	1 / 14	GENTLES_modul12
12	0.126	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
13	0.133	1 / 15	BEN−PORATH_UP
14	0.139	3 / 136	PanCan_CC+Apop_geneset_nanostring
15	0.141	1 / 16	WOLFER_overlap genes
16	0.141	1 / 16	GENTLES_modul2
17	0.189	1 / 22	PanCan_ChromMod_geneset_nanostring
18	0.196	2 / 86	PanCan_JAK−ST_geneset_nanostring
19	0.369	4 / 324	SPANG_BCL6−index2
20	0.441	0 / 16	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	3e−28	85 / 2554	nucleoplasm
2	7e−21	108 / 5101	nucleus
3	4e−18	19 / 121	ribonucleoprotein complex
4	1e−15	15 / 82	catalytic step 2 spliceosome
5	1e−12	17 / 180	nuclear speck
6	7e−11	12 / 92	spliceosomal complex
7	4e−10	8 / 31	cytoplasmic stress granule
8	1e−09	62 / 3059	membrane
9	4e−08	26 / 799	nucleolus
10	1e−06	79 / 5185	cytoplasm
11	2e−06	4 / 10	viral nucleocapsid
12	1e−05	4 / 16	eukaryotic translation initiation factor 3 complex
13	5e−05	7 / 100	chromatin
14	2e−04	8 / 168	ribosome
15	4e−04	3 / 15	eukaryotic 43S preinitiation complex
16	4e−04	3 / 15	eukaryotic 48S preinitiation complex
17	4e−04	3 / 15	U1 snRNP
18	8e−04	3 / 20	exon−exon junction complex
19	1e−03	3 / 23	cytoplasmic ribonucleoprotein granule
20	2e−03	4 / 59	cytosolic large ribosomal subunit

Chr

Rank	p−value	#in/all	Geneset
1	0.02	16 / 976	Chr 6
2	0.05	16 / 1083	Chr 17
3	0.10	24 / 1920	Chr 1
4	0.10	14 / 1017	Chr 12
5	0.14	10 / 715	Chr 10
6	0.23	7 / 522	Chr 20
7	0.36	4 / 318	Chr 13
8	0.40	11 / 1043	Chr 3
9	0.54	2 / 191	Chr 21
10	0.56	7 / 746	Chr X
11	0.58	8 / 862	Chr 5
12	0.60	4 / 436	Chr 22
13	0.62	11 / 1228	Chr 2
14	0.71	6 / 745	Chr 9
15	0.83	6 / 859	Chr 7
16	0.83	5 / 735	Chr 4
17	0.84	4 / 613	Chr 14
18	0.88	10 / 1425	Chr 19
19	0.93	7 / 1172	Chr 11
20	0.95	3 / 651	Chr 8

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−23	161 / 10475	TssA_Colon
2	8e−23	156 / 9930	Tx_Colon
3	2e−17	37 / 713	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	1e−15	141 / 9390	TxWk_Colon
5	1e−09	117 / 8123	TssF_Colon
6	1e−07	58 / 3122	TxEnhG1_Colon
7	1e−06	24 / 830	Pentrack_CRC_TCGA_corr_R_normal_DN
8	3e−06	24 / 877	TxEnhG2_Colon
9	7e−06	141 / 11968	TssWk_Colon
10	9e−05	12 / 337	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
11	3e−04	11 / 332	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
12	3e−03	130 / 11791	Enh_Colon
13	4e−03	108 / 9470	Quies3_Colon
14	6e−03	4 / 76	Marisa_CRC−cluster−g
15	4e−02	76 / 6761	TssD2_Colon
16	6e−02	66 / 5889	EnhWk1_Colon
17	7e−02	1 / 8	Budinska_C_CIMP−H−like_UP
18	8e−02	3 / 105	Marisa_CRC−cluster−d
19	8e−02	37 / 3112	EnhA_Colon
20	9e−02	1 / 10	KIM_MSI−in−EC

Disease

Rank	p−value	#in/all	Geneset
1	0.9	3 / 608	GUDJ_psoriasis up
2	1.0	0 / 399	GUDJ_psoriasis down
3	1.0	0 / 22	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 37	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−08	17 / 344	Up
2	3e−08	5 / 11	WILLSCHER_GBM_LTSmut_proteomics−A_UP
3	5e−07	15 / 322	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	4e−06	4 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
5	3e−05	41 / 2253	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	2e−04	35 / 1978	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	1e−02	2 / 16	VERHAAK_PN subtype
8	3e−02	3 / 69	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	4e−02	14 / 873	Sturm_GBM_Meth_overexpression_E_G34_UP
10	4e−02	2 / 35	shaw_responders_down_in_oligo_glioma
11	8e−02	2 / 50	WILLSCHER_GBM_Verhaak−PNwt_up
12	1e−01	1 / 12	Phillips PN up vs MES & Prolif
13	1e−01	1 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
14	1e−01	1 / 16	VERHAAK_MES subtype
15	1e−01	2 / 70	WILLSCHER_GBM_Verhaak−PNwt & MES_up
16	2e−01	1 / 27	Barbus_GBM_STS_vs._LTS
17	3e−01	1 / 36	Shaw_down_in_1p19q
18	4e−01	5 / 417	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
19	4e−01	1 / 49	Noushmehr_Pron_GCIMP_hypermeth_DN
20	5e−01	2 / 161	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−31	27 / 105	REACTOME_MRNA_SPLICING
2	6e−30	28 / 134	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
3	8e−30	29 / 151	REACTOME_MRNA_PROCESSING
4	4e−27	62 / 1340	PUJANA_ATM_PCC_NETWORK
5	1e−26	66 / 1563	PUJANA_BRCA1_PCC_NETWORK
6	3e−20	41 / 747	PUJANA_CHEK2_PCC_NETWORK
7	8e−17	18 / 120	KEGG_SPLICEOSOME
8	1e−16	49 / 1352	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
9	7e−16	36 / 754	MARTENS_TRETINOIN_RESPONSE_DN
10	1e−15	57 / 1914	PILON_KLF1_TARGETS_DN
11	4e−15	30 / 539	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
12	4e−14	18 / 170	JISON_SICKLE_CELL_DISEASE_DN
13	5e−13	26 / 475	ENK_UV_RESPONSE_KERATINOCYTE_DN
14	1e−12	23 / 370	HSIAO_HOUSEKEEPING_GENES
15	1e−12	49 / 1713	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
16	1e−12	33 / 813	GRADE_COLON_CANCER_UP
17	2e−12	37 / 1036	DANG_BOUND_BY_MYC
18	5e−12	18 / 225	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
19	5e−12	41 / 1298	DODD_NASOPHARYNGEAL_CARCINOMA_DN
20	6e−12	15 / 142	REACTOME_TRANSLATION

HM

Rank	p−value	#in/all	Geneset
1	5e−12	17 / 195	HALLMARK_MYC_TARGETS_V1
2	6e−10	15 / 197	HALLMARK_E2F_TARGETS
3	5e−08	13 / 196	HALLMARK_G2M_CHECKPOINT
4	4e−03	5 / 111	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	1e−02	4 / 94	HALLMARK_PROTEIN_SECRETION
6	1e−02	4 / 98	HALLMARK_ANDROGEN_RESPONSE
7	3e−02	5 / 181	HALLMARK_ALLOGRAFT_REJECTION
8	5e−02	2 / 36	HALLMARK_HEDGEHOG_SIGNALING
9	7e−02	3 / 102	HALLMARK_PEROXISOME
10	1e−01	4 / 186	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	1e−01	3 / 140	HALLMARK_UV_RESPONSE_DN
12	2e−01	3 / 155	HALLMARK_UV_RESPONSE_UP
13	2e−01	3 / 157	HALLMARK_APOPTOSIS
14	3e−01	3 / 195	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	3e−01	3 / 195	HALLMARK_MYOGENESIS
16	3e−01	3 / 197	HALLMARK_IL2_STAT5_SIGNALING
17	3e−01	3 / 198	HALLMARK_HYPOXIA
18	3e−01	1 / 36	HALLMARK_ANGIOGENESIS
19	3e−01	3 / 199	HALLMARK_MTORC1_SIGNALING
20	3e−01	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−35	134 / 5643	HOPP_Txn_transition
2	8e−17	126 / 7491	HOPP_Txn_elongation
3	8e−17	134 / 8358	HOPP_Active_promoter
4	9e−11	120 / 8147	HOPP_Weak_promoter
5	2e−10	23 / 484	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
6	4e−10	23 / 500	WIRTH_lymphoma937_spot J
7	8e−06	101 / 7592	HOPP_Strong_enhancer
8	3e−05	27 / 1215	SPANG_BCR DN
9	1e−02	8 / 317	TARTE_Plasmablast signature
10	1e−02	2 / 19	DAVE_c−myc BL UP
11	2e−02	7 / 279	SPANG_IL21 DN
12	4e−02	3 / 79	SPANG_LPS 6hrs DN
13	5e−02	3 / 87	ROSOLOWSKI_red total
14	6e−02	1 / 6	WRIGHT_custom ABC−DLBCL UP
15	8e−02	74 / 6784	HOPP_Weak_enhancer
16	8e−02	8 / 466	SPANG_CD40 6hrs DN
17	8e−02	5 / 240	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
18	8e−02	1 / 9	MASCQUE_ABC UP
19	1e−01	6 / 336	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
20	1e−01	6 / 347	WIRTH_lymphoma937_spot H

MF

Rank	p−value	#in/all	Geneset
1	4e−68	94 / 1091	poly(A) RNA binding
2	2e−26	41 / 513	RNA binding
3	4e−23	53 / 1134	nucleic acid binding
4	4e−19	30 / 385	nucleotide binding
5	1e−11	7 / 13	poly(A) binding
6	8e−09	9 / 63	ATP−dependent RNA helicase activity
7	2e−08	137 / 10693	protein binding
8	3e−07	6 / 29	ATP−dependent DNA helicase activity
9	6e−07	8 / 76	helicase activity
10	8e−06	7 / 77	single−stranded DNA binding
11	9e−06	5 / 30	ATP−dependent helicase activity
12	1e−05	6 / 53	translation initiation factor activity
13	1e−04	13 / 394	chromatin binding
14	2e−04	33 / 1803	DNA binding
15	2e−04	3 / 12	RNA helicase activity
16	2e−04	3 / 13	poly(U) RNA binding
17	3e−04	6 / 93	mRNA binding
18	3e−04	6 / 95	double−stranded DNA binding
19	4e−04	4 / 38	single−stranded RNA binding
20	1e−03	10 / 328	enzyme binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−14	21 / 246	hsa−miR−1252
2	5e−14	16 / 124	hsa−miR−515−5p
3	5e−13	18 / 196	hsa−miR−513a−3p
4	2e−12	21 / 307	hsa−miR−548c−3p
5	6e−12	17 / 197	hsa−miR−548d−3p
6	9e−12	20 / 300	hsa−miR−186
7	4e−11	19 / 289	hsa−miR−320a
8	5e−11	18 / 257	hsa−miR−524−5p
9	2e−10	14 / 149	hsa−miR−135a
10	2e−10	15 / 179	hsa−miR−607
11	5e−10	19 / 334	hsa−miR−590−3p
12	7e−10	18 / 303	hsa−miR−561
13	1e−09	14 / 174	hsa−miR−452
14	1e−09	13 / 145	hsa−miR−135b
15	2e−09	14 / 184	hsa−miR−582−5p
16	3e−09	17 / 291	hsa−miR−570
17	3e−09	18 / 332	hsa−miR−548a−5p
18	4e−09	14 / 192	hsa−miR−129−5p
19	5e−09	11 / 105	hsa−miR−224
20	5e−09	14 / 195	hsa−miR−382

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.008	2 / 14	BENTINK_src.2
2	0.125	1 / 14	GUSTAFSON_PI3K_UP
3	0.125	1 / 14	BENTINK_myc.1
4	0.133	1 / 15	GUSTAFSON_PI3K_DN
5	0.133	1 / 15	BENTINK_ras.6
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 / 10	BENTINK_ras.4
10	1.000	0 / 14	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−10	38 / 1294	KIM_MYC targets
2	1e−08	39 / 1549	ICGC_Myc_targets
3	2e−06	78 / 5173	ICGC_Taf1_targets
4	7e−06	80 / 5512	ICGC_Nficsc81335_targets
5	4e−05	6 / 66	MYC_Targets UP
6	5e−05	31 / 1547	ICGC_Ets1_targets
7	6e−05	63 / 4230	ICGC_Nfatc1_targets
8	6e−05	35 / 1867	HEBENSTREIT_high expression TF
9	7e−05	3 / 9	MYC_RNA processing binding UP
10	8e−05	77 / 5578	ICGC_Stat5_targets
11	1e−04	66 / 4566	ICGC_Egr1_targets
12	2e−04	69 / 4969	ICGC_Atf2_targets
13	3e−04	72 / 5308	ICGC_Tcf12_targets
14	3e−04	63 / 4470	ICGC_Creb1_targets
15	6e−04	73 / 5526	ICGC_Pmlsc71910_targets
16	6e−04	81 / 6313	ICGC_Pou2_targets
17	7e−04	72 / 5453	ICGC_Foxm1_targets
18	8e−04	67 / 4987	ICGC_Bclaf101388_targets
19	8e−04	35 / 2133	ICGC_Cebpbsc150_targets
20	2e−03	34 / 2149	ICGC_Mef2_targets

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.003	3 / 30	VAQUERIZAS_Smooth muscle
2	0.018	2 / 22	VAQUERIZAS_Tonsil
3	0.035	2 / 31	VAQUERIZAS_Lymph node
4	0.108	1 / 12	VAQUERIZAS_Kidney
5	0.133	2 / 67	VAQUERIZAS_Whole blood
6	0.150	1 / 17	VAQUERIZAS_Salivary gland
7	0.174	1 / 20	VAQUERIZAS_Bone marrow
8	0.204	1 / 24	VAQUERIZAS_Trachea
9	0.324	1 / 41	VAQUERIZAS_Testis
10	0.330	1 / 42	VAQUERIZAS_Thymus
11	0.349	1 / 45	VAQUERIZAS_Placenta
12	0.457	1 / 64	VAQUERIZAS_Lung
13	0.773	1 / 155	VAQUERIZAS_General
14	1.000	0 / 41	VAQUERIZAS_Fetal brain
15	1.000	0 / 33	VAQUERIZAS_Liver
16	1.000	0 / 37	VAQUERIZAS_Prostate
17	1.000	0 / 49	VAQUERIZAS_Uterus
18	1.000	0 / 25	VAQUERIZAS_Spinal cord
19	1.000	0 / 46	VAQUERIZAS_Whole brain
20	1.000	0 / 42	VAQUERIZAS_Thyroid

Tissue

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

Toxic

Rank	p−value	#in/all	Geneset
1	0.2	16 / 1343	LU_BPDE 1h DN
2	1.0	28 / 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	