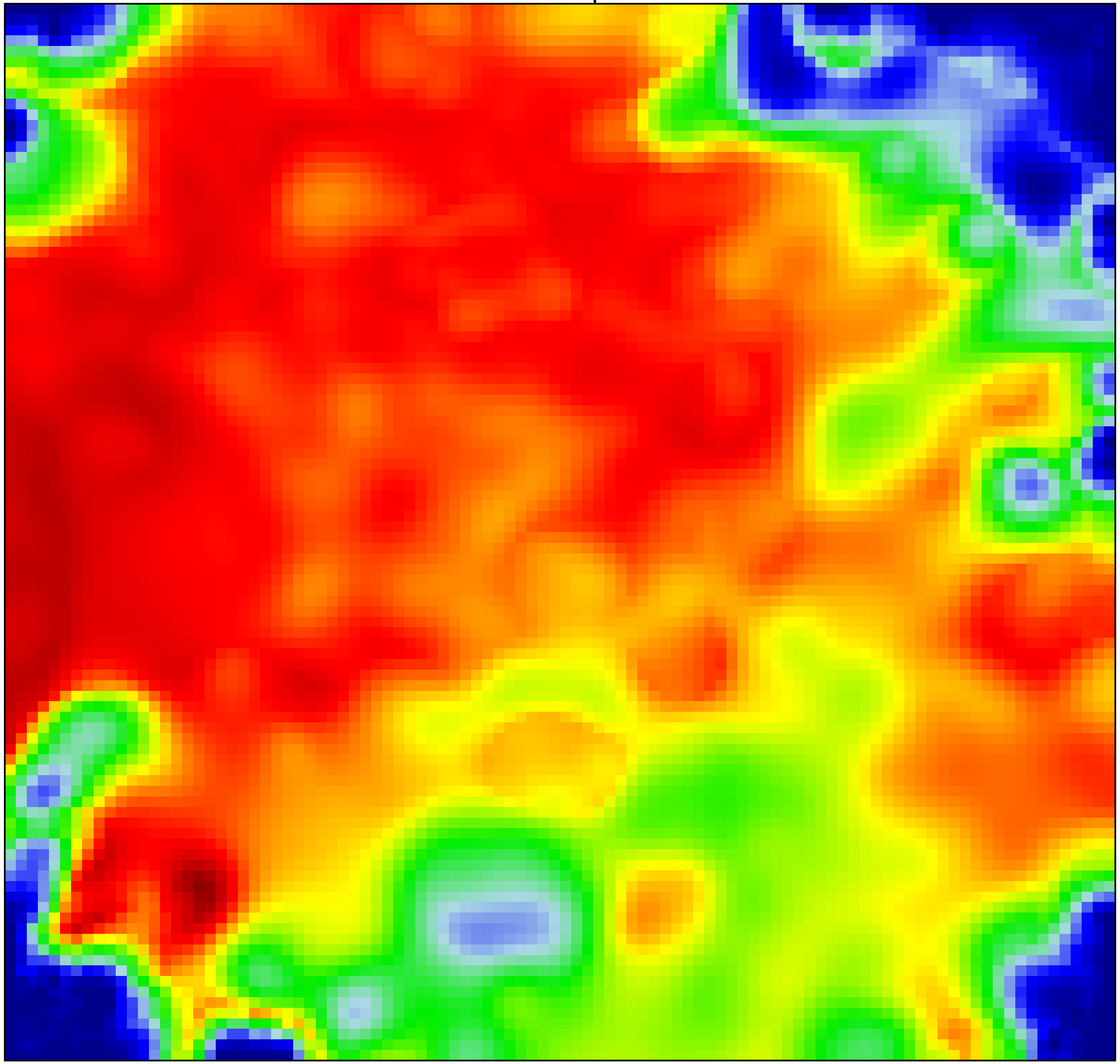
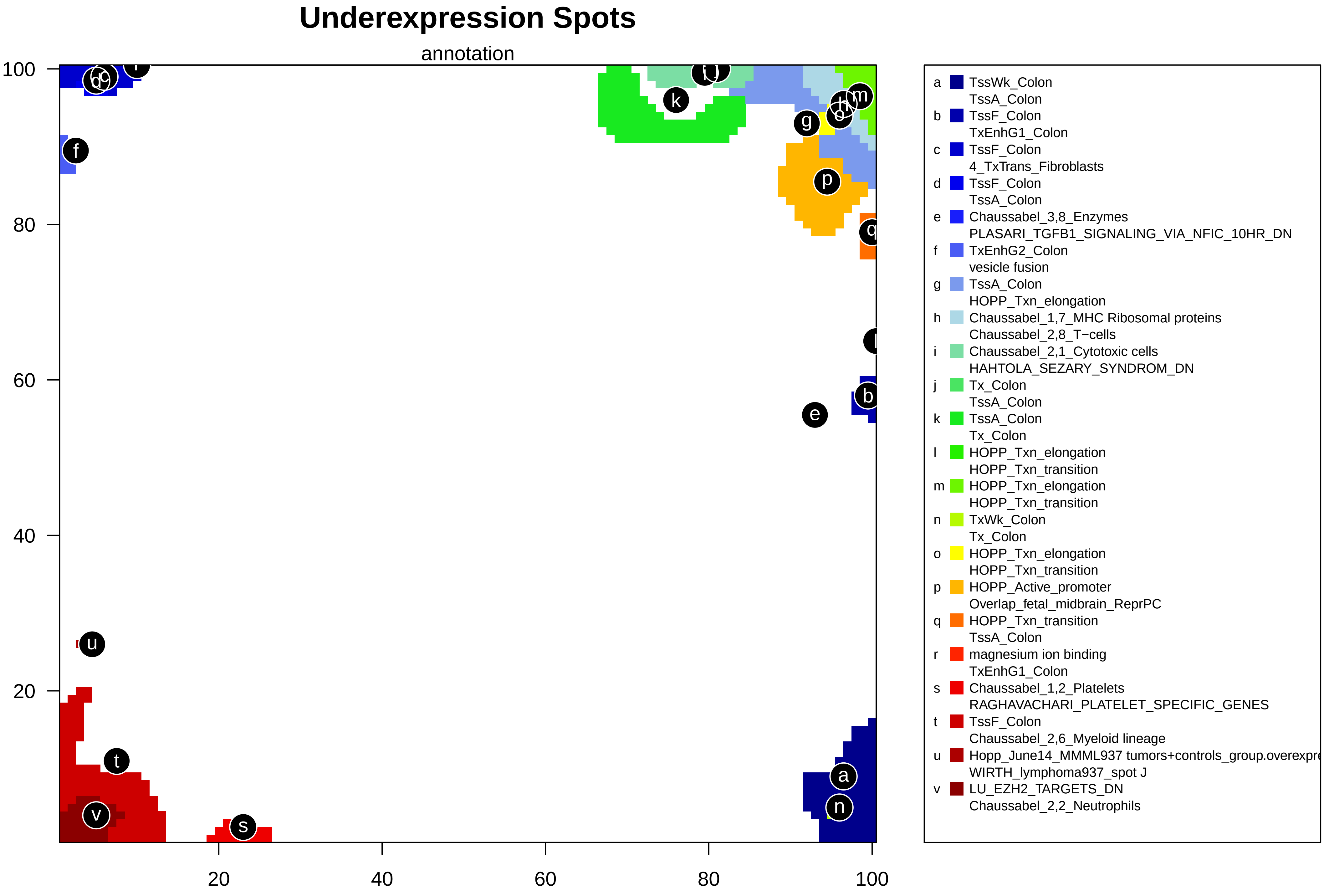
Underexpression Spots

landscape




Underexpression Spots
annotation
100
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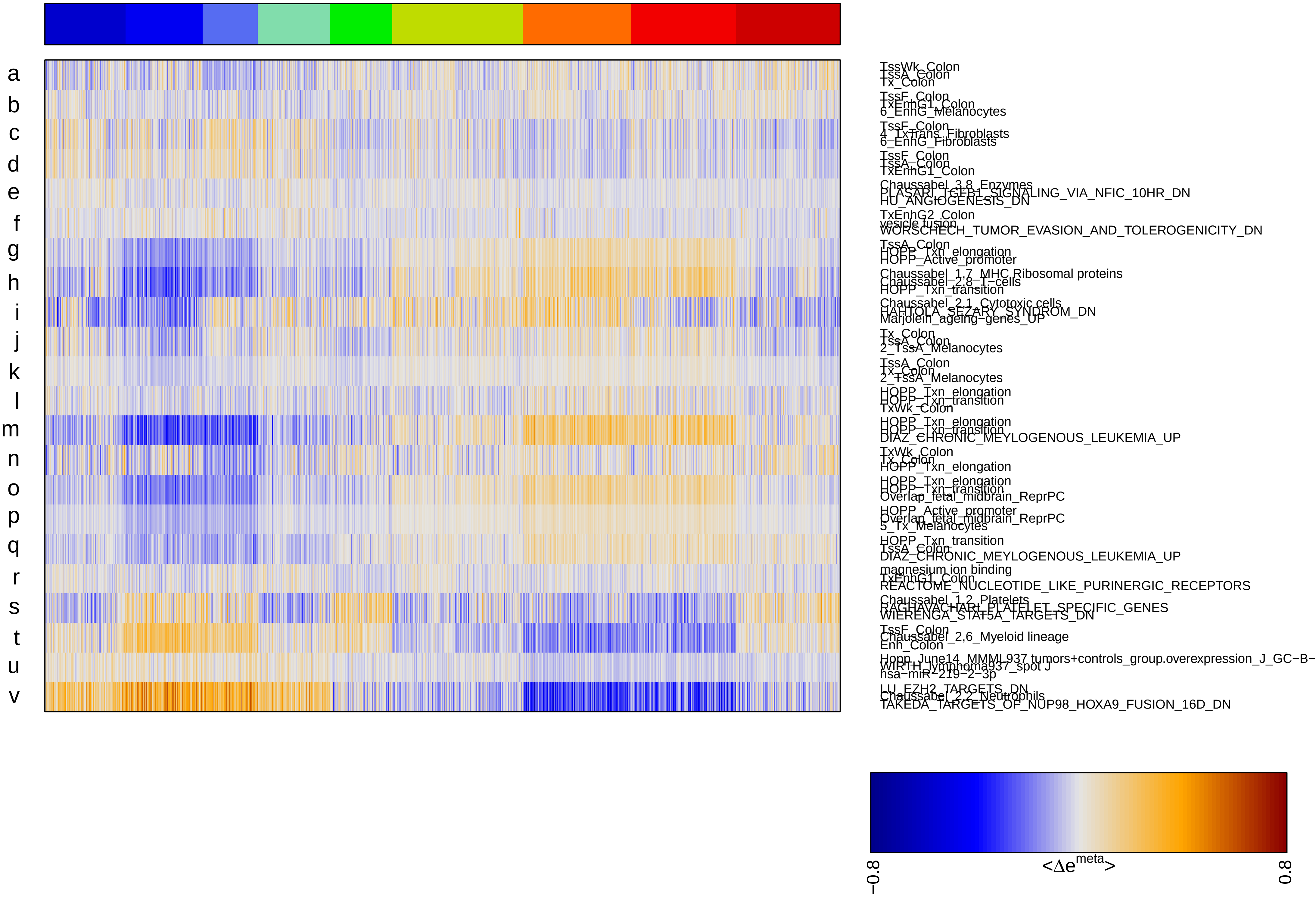
u
v
a TssWk_Colon
TssA_Colon
b TssF_Colon
TxEnhG1_Colon
c TssF_Colon
4_TxTrans_Fibroblasts
d TssF_Colon
TssA_Colon
e Chaussabel_3,8_Enzymes
PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN
f TxEnhG2_Colon
vesicle fusion
g TssA_Colon
HOPP_Txn_elongation
h Chaussabel_1,7_MHC Ribosomal proteins
Chaussabel_2,8_T−cells
i Chaussabel_2,1_Cytotoxic cells
HAHTOLA_SEZARY_SYNDROM_DN
j Tx_Colon
TssA_Colon
k TssA_Colon
Tx_Colon
l HOPP_Txn_elongation
HOPP_Txn_transition
m HOPP_Txn_elongation
HOPP_Txn_transition
n TxWk_Colon
Tx_Colon
o HOPP_Txn_elongation
HOPP_Txn_transition
p HOPP_Active_promoter
Overlap_fetal_midbrain_ReprPC
q HOPP_Txn_transition
TssA_Colon
r magnesium ion binding
TxEnhG1_Colon
s Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
t TssF_Colon
Chaussabel_2,6_Myeloid lineage
u Hopp_June14_MMML937 tumors+controls_group.overexpre
WIRTH_lymphoma937_spot J
v LU_EZH2_TARGETS_DN
Chaussabel_2,2_Neutrophils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TssWk_Colon
TssA_Colon
Tx_Colon
TssF_Colon
TxEnhG1_Colon
6_EnhG_Melanocytes
TssF_Colon
4_TxTrans_Fibroblasts
6_EnhG_Fibroblasts
TssF_Colon
TssA_Colon
TxEnhG1_Colon
Chaussabel_3,8_Enzymes
PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN
HU_ANGIOGENESIS_DN
TxEnhG2_Colon
vesicle fusion
WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
TssA_Colon
HOPP_Txn_elongation
HOPP_Active_promoter
Chaussabel_1,7_MHC Ribosomal proteins
Chaussabel_2,8_T−cells
HOPP_Txn_transition
Chaussabel_2,1_Cytotoxic cells
HAHTOLA_SEZARY_SYNDROM_DN
Marjolein_ageing−genes_UP
Tx_Colon
TssA_Colon
2_TssA_Melanocytes
TssA_Colon
Tx_Colon
2_TssA_Melanocytes
HOPP_Txn_elongation
HOPP_Txn_transition
TxWk_Colon
HOPP_Txn_elongation
HOPP_Txn_transition
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
TxWk_Colon
Tx_Colon
HOPP_Txn_elongation
HOPP_Txn_elongation
HOPP_Txn_transition
Overlap_fetal_midbrain_ReprPC
HOPP_Active_promoter
Overlap_fetal_midbrain_ReprPC
5_Tx_Melanocytes
HOPP_Txn_transition
TssA_Colon
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
magnesium ion binding
TxEnhG1_Colon
REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS
Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
WIERENGA_STAT5A_TARGETS_DN
TssF_Colon
Chaussabel_2,6_Myeloid lineage
Enh_Colon
Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
WIRTH_lymphoma937_spot J
hsa−miR−219−2−3p
LU_EZH2_TARGETS_DN
Chaussabel_2,2_Neutrophils
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
−0.8
<Δe^meta>
0.8

Underexpression Spots

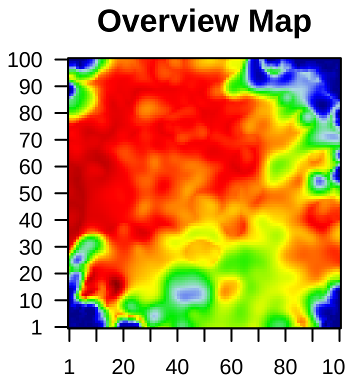
Spot Summary: a

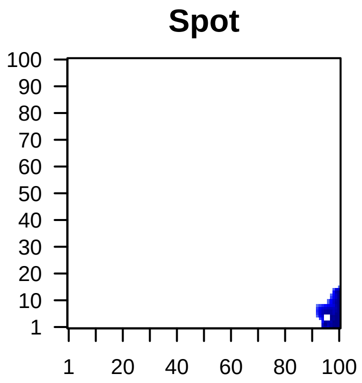
metagenes = 95
genes = 1247

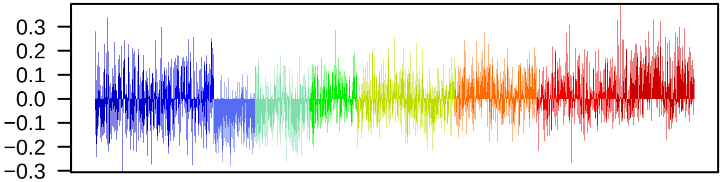
<r> metagenes = 0.73

beta: r2= 33.29 / log p= −Inf

samples with spot = 394 (11.6 %)
A * : 36 (10.5 %)
A C * : 53 (16.2 %)
A C F * : 1 (0.4 %)
A F * : 12 (3.9 %)
C F * : 19 (7.2 %)
F * : 38 (6.8 %)
F J * : 60 (13 %)
J * : 61 (13.6 %)
N * : 114 (25.7 %)





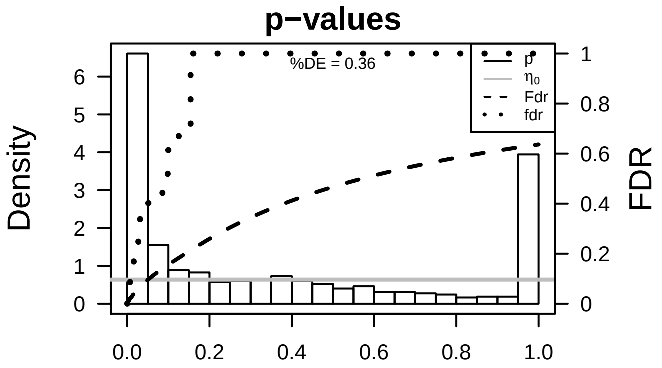


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_170769	2.95	−1.6	0.41	IFIT1	interferon induced protein with tetratricopeptide repeats 1 [So
2	ILMN_205878	2.77	−0.73	0.14	IFI27	interferon alpha inducible protein 27 [Source:HGNC Symbol;/
3	ILMN_180575	2.64	−2.03	0.31	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC S
4	ILMN_172391	2.52	−1.06	0.41	IFI44L	interferon induced protein 44 like [Source:HGNC Symbol;Acc
5	ILMN_170178	2.51	−1.31	0.37	IFIT3	interferon induced protein with tetratricopeptide repeats 3 [So
6	ILMN_165787	2.46	−0.83	0.41	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:I
7	ILMN_181520	2.38	−5.09	0.22		
8	ILMN_205401	2.34	−1	0.17	ISG15	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:HG
9	ILMN_172974	2.3	−1.14	0.35	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase
10	ILMN_238854	2.22	−1.39	0.39	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
11	ILMN_174539	2.13	−1.15	0.44	OAS3	2'−5'−oligoadenylate synthetase 3 [Source:HGNC Symbol;Ac
12	ILMN_166235	2.12	−1.32	0.33	MX1	MX dynamin like GTPase 1 [Source:HGNC Symbol;Acc:HGN
13	ILMN_176006	2.1	−1.07	0.39	IFI44	interferon induced protein 44 [Source:HGNC Symbol;Acc:HG
14	ILMN_324640	2.08	−1.52	0.28	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HG
15	ILMN_166314	1.94	−1.51	0.14	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Sy
16	ILMN_168738	1.93	−1.08	0.29	IFI6	interferon alpha inducible protein 6 [Source:HGNC Symbol;Ac
17	ILMN_173942	1.91	−1.24	0.61	IFIT2	interferon induced protein with tetratricopeptide repeats 2 [So
18	ILMN_172311	1.86	−0.84	0.19	AMFR	autocrine motility factor receptor [Source:HGNC Symbol;Acc:
19	ILMN_324306	1.85	−2.53	0.26	SIGLEC14	sialic acid binding Ig like lectin 14 [Source:HGNC Symbol;Acc
20	ILMN_167481	1.79	−0.91	0.35	OASL	2'−5'−oligoadenylate synthetase like [Source:HGNC Symbol;/

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	770 / 10999	Colon	TssWk_Colon
2	1e−97	708 / 9555	Colon	TssA_Colon
3	5e−96	685 / 9054	Colon	Tx_Colon
4	6e−92	608 / 7448	Lympl	HOPP_Strong_enhancer
5	1e−88	657 / 8678	Colon	Quies3_Colon
6	9e−87	649 / 8568	Colon	TxWk_Colon
7	2e−84	630 / 8226	Lympl	HOPP_Active_promoter
8	3e−82	583 / 7275	Lympl	HOPP_Txn_elongation
9	2e−73	741 / 11455	Chror	2_TssA_Fibroblasts
10	2e−69	249 / 1797	GSEA	PILON_KLF1_TARGETS_DN
11	2e−65	457 / 5356	Lympl	HOPP_Txn_transition
12	3e−65	64 / 96	Refer	Chaussabel_3,1_Interferon−inducible
13	1e−64	117 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
14	1e−63	754 / 12298	Chror	2_TssA_Melanocytes
15	1e−62	735 / 11836	Chror	3_TssF_Melanocytes
16	1e−61	170 / 960	GSEA	NUYTTEN_EZH2_TARGETS_UP
17	3e−60	578 / 8098	Lympl	HOPP_Weak_promoter
18	5e−60	607 / 8771	Chror	5_Tx_Melanocytes
19	7e−60	154 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	3e−56	643 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
21	2e−55	599 / 8818	MF	protein binding
22	3e−55	606 / 8990	Chror	15_Quies_Fibroblasts
23	6e−55	753 / 12741	Chror	7_Enh_Melanocytes
24	1e−54	555 / 7854	Chror	5_Tx_Fibroblasts
25	2e−52	71 / 172	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
26	5e−50	578 / 8613	Chror	7_Enh_Fibroblasts
27	1e−48	51 / 85	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
28	6e−48	51 / 87	GSEA	HECKER_IFNB1_TARGETS
29	5e−45	83 / 301	Canc	SPANG_BCL6−index2
30	5e−45	75 / 240	Refer	Chaussabel_3,3_Inflammation II
31	7e−45	621 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
32	2e−44	283 / 2979	CC	cytosol
33	9e−43	437 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
34	2e−42	664 / 11130	Chror	15_Quies_Melanocytes
35	6e−42	649 / 10779	Colon	Enh_Colon
36	2e−40	730 / 12983	Chror	2_TssA_Neuronal_Progenitor
37	3e−40	51 / 113	Refer	Chaussabel_1,5_Myeloid lineage
38	8e−40	148 / 1069	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
39	1e−38	38 / 58	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
40	1e−38	415 / 5699	Chror	6_EnhG_Melanocytes



Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 111	HORVATH_aging_genes meth DOWN
2	0.9	1 / 58	TESCHENDORFF_age_hypermethylated
3	1.0	2 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	5e−45	83 / 301	SPANG_BCL6−index2
2	5e−34	56 / 178	SPANG_LPS−index2
3	4e−19	74 / 554	Lembcke_Colonic Inflammation
4	2e−05	17 / 125	PanCan_CC+Apop_geneset_nanostring
5	3e−04	14 / 117	PanCan_Driver_Gene_geneset_nanostring
6	4e−04	5 / 16	GENTLES_modul14
7	3e−03	7 / 46	PanCan_TGF−B_geneset_nanostring
8	3e−03	9 / 73	SHAUGHNESSY_MM high risk
9	7e−03	9 / 82	PanCan_JAK−ST_geneset_nanostring
10	1e−02	8 / 76	PanCan_Wnt_geneset_nanostring
11	1e−02	3 / 13	GENTLES_modul12
12	2e−02	4 / 24	PanCan_Notch_geneset_nanostring
13	2e−02	12 / 150	PanCan_MAPK_geneset_nanostring
14	2e−02	2 / 6	ZHANG_MGUS up
15	3e−02	1 / 15	LIU_PROSTATE_CANCER_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−73	741 / 11455	2_TssA_Fibroblasts
2	1e−63	754 / 12298	2_TssA_Melanocytes
3	1e−62	735 / 11836	3_TssF_Melanocytes
4	5e−60	607 / 8771	5_Tx_Melanocytes
5	3e−55	606 / 8990	15_Quies_Fibroblasts
6	6e−55	753 / 12741	7_Enh_Melanocytes
7	1e−54	555 / 7854	5_Tx_Fibroblasts
8	5e−50	578 / 8613	7_Enh_Fibroblasts
9	2e−42	664 / 11130	15_Quies_Melanocytes
10	2e−40	730 / 12983	2_TssA_Neuronal_Progenitor
11	1e−38	415 / 5699	6_EnhG_Melanocytes
12	1e−36	588 / 9635	3_TssF_Fibroblasts
13	4e−29	449 / 6970	5_Tx_Neuronal_Progenitor
14	1e−28	676 / 12393	15_Quies_Neuronal_Progenitor
15	5e−21	630 / 11847	7_Enh_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−69	249 / 1797	PILON_KLF1_TARGETS_DN
2	1e−64	117 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
3	1e−61	170 / 960	NUYTTEN_EZH2_TARGETS_UP
4	6e−48	51 / 87	HECKER_IFNB1_TARGETS
5	1e−38	38 / 58	BROWNE_INTERFERON_RESPONSIVE_GENES
6	2e−38	97 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
7	3e−38	28 / 29	MOSERLE_IFNA_RESPONSE
8	1e−36	72 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
9	3e−36	143 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
10	1e−35	55 / 161	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
11	5e−35	104 / 622	SCHLOSSER_SERUM_RESPONSE_DN
12	5e−33	114 / 774	REACTOME_IMMUNE_SYSTEM
13	6e−33	106 / 680	ONKEN_UVEAL_MELANOMA_UP
14	4e−32	76 / 366	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
15	4e−31	75 / 368	OSMAN_BLADDER_CANCER_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−92	608 / 7448	HOPP_Strong_enhancer
2	2e−84	630 / 8226	HOPP_Active_promoter
3	3e−82	583 / 7275	HOPP_Txn_elongation
4	2e−65	457 / 5356	HOPP_Txn_transition
5	3e−60	578 / 8098	HOPP_Weak_promoter
6	5e−36	74 / 306	WIRTH_lymphoma937_spot E
7	1e−35	73 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
8	2e−33	461 / 6959	HOPP_Weak_enhancer
9	3e−32	66 / 272	SPANG_IL21 DN
10	2e−31	437 / 6559	HOPP_Weak_txn
11	4e−20	119 / 1169	SPANG_BCR DN
12	5e−14	20 / 57	Monti_Host_response_cluster
13	5e−13	46 / 331	SPANG_CD40 6hrs UP
14	3e−10	19 / 78	Sha_DLBCL UP
15	4e−10	40 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−65	64 / 96	Chaussabel_3,1_Interferon−inducible
2	5e−45	75 / 240	Chaussabel_3,3_Inflammation II
3	3e−40	51 / 113	Chaussabel_1,5_Myeloid lineage
4	2e−38	44 / 84	Chaussabel_2,10_Immune related cell surface molecules
5	3e−24	70 / 412	WIRTH_Immune system
6	3e−18	46 / 242	Chaussabel_3,2_Inflammation I
7	5e−18	36 / 150	Chaussabel_2,6_Myeloid lineage
8	2e−14	32 / 153	Chaussabel_2,9_Cytosceleton
9	3e−13	72 / 681	PROTEINATLAS_lung
10	2e−12	60 / 535	PROTEINATLAS_spleen
11	1e−10	18 / 66	VAQUERIZAS_Whole blood_TF
12	2e−10	68 / 724	PROTEINATLAS_lymph node
13	3e−10	39 / 302	Chaussabel_3,4_Protein phosphatases
14	8e−08	81 / 1063	PROTEINATLAS_tonsil
15	9e−08	20 / 119	Chaussabel_2,11_Replication

BP

Rank	p−value	#in/all	Geneset
1	6e−24	28 / 57	type I interferon signaling pathway
2	4e−23	35 / 102	response to virus
3	2e−21	40 / 153	defense response to virus
4	7e−18	54 / 335	innate immune response
5	4e−13	16 / 37	negative regulation of viral genome replication
6	2e−12	19 / 60	interferon−gamma−mediated signaling pathway
7	2e−11	51 / 434	protein phosphorylation
8	4e−11	28 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
9	9e−11	55 / 511	apoptotic process
10	6e−10	41 / 336	inflammatory response
11	2e−09	23 / 127	regulation of cell shape
12	5e−09	36 / 292	positive regulation of apoptotic process
13	1e−08	11 / 30	negative regulation of type I interferon production
14	7e−08	31 / 254	cell−cell adhesion
15	8e−08	16 / 77	movement of cell or subcellular component

CC

Rank	p−value	#in/all	Geneset
1	2e−44	283 / 2979	cytosol
2	4e−35	362 / 4822	cytoplasm
3	1e−31	225 / 2464	extracellular exosome
4	4e−19	166 / 1979	membrane
5	1e−12	77 / 777	Golgi apparatus
6	6e−12	34 / 207	lysosome
7	4e−11	283 / 4828	nucleus
8	5e−11	59 / 561	intracellular membrane−bounded organelle
9	6e−11	44 / 352	focal adhesion
10	8e−10	57 / 571	perinuclear region of cytoplasm
11	1e−09	165 / 2535	nucleoplasm
12	3e−09	219 / 3662	plasma membrane
13	7e−09	36 / 295	cell−cell adherens junction
14	3e−08	27 / 194	membrane raft
15	4e−08	66 / 788	endoplasmic reticulum membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	770 / 10999	TssWk_Colon
2	1e−97	708 / 9555	TssA_Colon
3	5e−96	685 / 9054	Tx_Colon
4	1e−88	657 / 8678	Quies3_Colon
5	9e−87	649 / 8568	TxWk_Colon
6	7e−60	154 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
7	6e−42	649 / 10779	Enh_Colon
8	8e−40	148 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	3e−31	71 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	2e−30	377 / 5373	EnhWk1_Colon
11	5e−28	68 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	4e−27	141 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	2e−25	455 / 7354	TssF_Colon
14	2e−19	277 / 4034	TssD1_Colon
15	2e−18	134 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a

HM

Rank	p−value	#in/all	Geneset
1	2e−52	71 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	1e−48	51 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	6e−12	32 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	1e−11	32 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	4e−11	31 / 187	HALLMARK_COMPLEMENT
6	3e−09	28 / 185	HALLMARK_MTORC1_SIGNALING
7	1e−08	24 / 151	HALLMARK_APOPTOSIS
8	6e−08	24 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	2e−07	16 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	7e−06	22 / 183	HALLMARK_APICAL_JUNCTION
11	9e−06	22 / 185	HALLMARK_P53_PATHWAY
12	1e−05	22 / 189	HALLMARK_HYPOXIA
13	3e−05	21 / 186	HALLMARK_IL2_STAT5_SIGNALING
14	6e−05	13 / 87	HALLMARK_PROTEIN_SECRETION
15	1e−04	16 / 132	HALLMARK_UV_RESPONSE_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.008	6 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.286	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.680	1 / 27	Hugo_melanoma−all−LEF1_UP
4	0.718	1 / 30	Hugo_melanoma−all−MET_UP
5	0.898	1 / 54	Hugo_melanoma−all−MET_DN
6	1.000	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−24	86 / 602	hsa−miR−20a
2	2e−22	80 / 561	hsa−miR−20b
3	2e−21	75 / 520	hsa−miR−106a
4	9e−21	50 / 250	hsa−miR−548l
5	1e−20	76 / 546	hsa−miR−93
6	1e−20	58 / 336	hsa−miR−142−5p
7	2e−20	65 / 416	hsa−miR−372
8	2e−20	73 / 513	hsa−miR−106b
9	8e−20	74 / 540	hsa−miR−17
10	2e−19	66 / 449	hsa−miR−130b
11	4e−19	66 / 455	hsa−miR−130a
12	1e−18	66 / 463	hsa−miR−301a
13	4e−18	63 / 438	hsa−miR−19a
14	6e−18	62 / 428	hsa−miR−519d
15	6e−18	62 / 429	hsa−miR−548n

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	2 / 27	Nabetani_alt len telomeres_genes_ko
2	0.4	1 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	3e−56	643 / 9815	Overlap_fetal_midbrain_ReprPC
2	7e−45	621 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	9e−43	437 / 5936	Overlap_fetal_midbrain_HetRpts
4	5e−37	622 / 10430	Overlap_fetal_midbrain_Quies
5	3e−28	558 / 9504	Overlap_fetal_midbrain_K9K27me3
6	3e−11	100 / 1213	Fetal_TssP
7	7e−06	178 / 3164	Mid_Frontal_Lobe_ZNF
8	1e−04	55 / 796	Overlap_fetal_midbrain_ZNF
9	5e−04	72 / 1171	Fetal_EnhP
10	6e−04	27 / 328	Fetal_Het
11	7e−04	141 / 2630	Fetal_TssF
12	2e−03	141 / 2709	Mid_Frontal_Lobe_HetRpts
13	3e−03	81 / 1436	Fetal_K9K27me3
14	3e−03	16 / 180	Overlap_fetal_midbrain_Het
15	4e−03	112 / 2127	Mid_Frontal_Lobe_K9K27me3

Chr

Rank	p−value	#in/all	Geneset
1	6e−04	58 / 902	Chr 4
2	3e−03	83 / 1492	Chr 2
3	8e−02	20 / 342	Chr 18
4	8e−02	58 / 1160	Chr 12
5	8e−02	60 / 1211	Chr 6
6	2e−01	57 / 1217	Chr 3
7	2e−01	36 / 769	Chr 15
8	3e−01	47 / 1060	Chr 5
9	4e−01	34 / 768	Chr 14
10	4e−01	56 / 1318	Chr 17
11	5e−01	18 / 422	Chr 13
12	5e−01	40 / 954	Chr 9
13	5e−01	96 / 2323	Chr 1
14	5e−01	12 / 289	Chr 21
15	6e−01	47 / 1170	Chr 7

Glio

Rank	p−value	#in/all	Geneset
1	5e−31	64 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−20	56 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	8e−20	55 / 315	Up
4	3e−10	15 / 47	Donson−innate immunity−associated with LTS in HGA
5	8e−08	133 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	2e−06	16 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
7	2e−06	21 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	3e−06	113 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	7e−06	61 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
10	4e−05	8 / 32	Donson−Misc immune function−associated with LTS in HGA
11	1e−04	5 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
12	2e−04	14 / 113	GIEZELT_GBM_WT_up_VS_mut
13	5e−04	12 / 94	Weller_LGG_A_vs_O_UP
14	8e−04	6 / 28	KIM prognostic signature LTS vs. STS
15	2e−03	15 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−11	34 / 211	Homuth_BMI−associated−genes_DN
2	6e−06	5 / 8	DUMEAUX_Monocytes in smokers literature genes up
3	3e−05	6 / 16	Huan_blood−pressure_DBP−signature
4	6e−05	6 / 18	Huan_blood−pressure_SBP−signature
5	5e−04	4 / 10	DUMEAUX_Smoking literature genes up
6	7e−04	3 / 5	Huan_blood−pressure_HTN−signature
7	2e−01	2 / 17	DUMEAUX_High bmi enriched genes
8	2e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	3e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
10	3e−01	5 / 94	DUMEAUX_Smoking enriched genes
11	5e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	6e−01	6 / 147	Homuth_BMI−associated−genes_UP
13	7e−01	1 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
15	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	2e−55	599 / 8818	protein binding
2	4e−10	36 / 265	cadherin binding involved in cell−cell adhesion
3	4e−09	100 / 1329	ATP binding
4	3e−08	36 / 311	enzyme binding
5	1e−07	28 / 217	protein kinase activity
6	1e−07	35 / 315	protein serine/threonine kinase activity
7	2e−07	27 / 213	GTPase activity
8	1e−06	25 / 204	protein domain specific binding
9	2e−06	12 / 54	double−stranded RNA binding
10	2e−06	23 / 182	signal transducer activity
11	3e−06	73 / 1013	poly(A) RNA binding
12	4e−06	48 / 580	identical protein binding
13	7e−06	9 / 34	phosphatidylinositol−3,4,5−trisphosphate binding
14	2e−05	32 / 350	protein kinase binding
15	3e−05	49 / 646	protein homodimerization activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	4e−05	5 / 11	BENTINK_ras.4
2	2e−03	4 / 13	BENTINK_src.10
3	9e−02	2 / 12	BENTINK_ras.1
4	1e−01	2 / 14	BENTINK_ras.6
5	4e−01	1 / 13	BENTINK_e2f3.1
6	4e−01	1 / 14	GUSTAFSON_PI3K_UP
7	5e−01	1 / 15	GUSTAFSON_PI3K_DN
8	1e+00	0 / 13	BENTINK_e2f3.2
9	1e+00	0 / 13	BENTINK_myc.1
10	1e+00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−21	318 / 4735	ICGC_Pu1_targets
2	7e−20	329 / 5067	ICGC_Taf1_targets
3	3e−19	346 / 5466	ICGC_Nficsc81335_targets
4	9e−17	309 / 4881	ICGC_Atf2_targets
5	1e−16	168 / 2133	ICGC_Mef2_targets
6	7e−16	306 / 4890	ICGC_Bclaf101388_targets
7	1e−15	335 / 5518	ICGC_Stat5_targets
8	7e−15	160 / 2087	ICGC_Cebpbsc150_targets
9	3e−14	263 / 4131	ICGC_Nfatc1_targets
10	3e−14	180 / 2497	ICGC_Bcl11_targets
11	4e−14	325 / 5442	ICGC_Pmlsc71910_targets
12	5e−14	407 / 7247	ICGC_Runx3_targets
13	1e−13	136 / 1723	HEBENSTREIT_high expression TF
14	3e−13	345 / 5961	ICGC_Pol24_targets
15	4e−13	346 / 5984	ICGC_Mta3_targets

Underexpression Spots

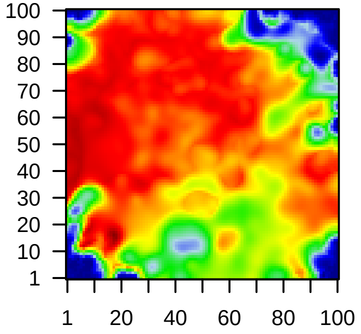
Spot Summary: b

metagenes = 14
genes = 128

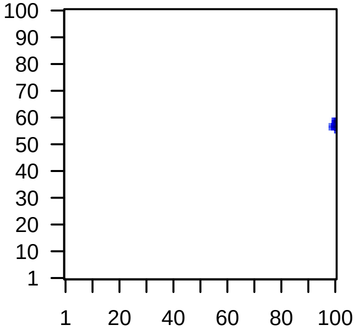
<r> metagenes = 0.93
<r> genes = 0.19
beta: r2= 4.88 / log p= −Inf

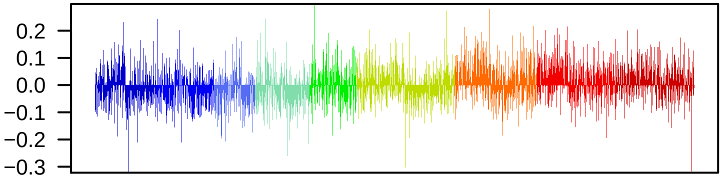
samples with spot = 173 (5.1 %)
A * : 13 (3.8 %)
A C * : 5 (1.5 %)
A C F * : 5 (2.1 %)
A F * : 7 (2.3 %)
C F * : 15 (5.7 %)
F * : 19 (3.4 %)
F J * : 44 (9.5 %)
J * : 34 (7.6 %)
N * : 31 (7 %)

Overview Map



Spot





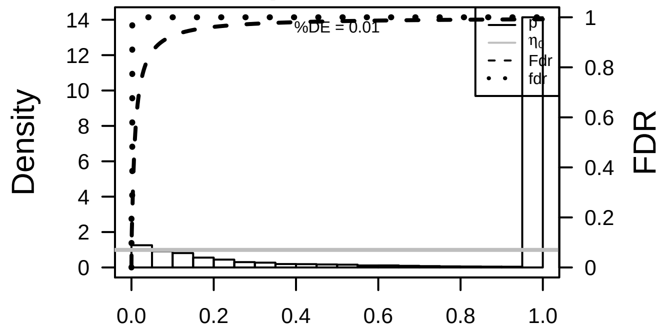
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_215969	2.92	−1.39	0.33		
2	ILMN_216575	2.67	−3.76	0.41		
3	ILMN_179153	2.13	−0.79	0.33		
4	ILMN_324215	1.9	−0.58	0.27		
5	ILMN_166607	1.73	−2.16	0.43		
6	ILMN_210557	1.53	−0.75	0.15	CCL3L3	C−C motif chemokine ligand 3 like 3 [Source:HGNC Symbol;
7	ILMN_324371	1.44	−1.23	0.4		
8	ILMN_165667	0.98	−0.73	0.38	HLA−G	major histocompatibility complex, class I, G [Source:HGNC S
9	ILMN_166813	0.93	−0.56	0.2	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
10	ILMN_166092	0.92	−0.81	0.63	LOC554223	major histocompatibility complex, class I, V (pseudogene) [Sc
11	ILMN_173324	0.91	−0.52	0.49		
12	ILMN_176286	0.88	−0.93	0.34	HLA−F	major histocompatibility complex, class I, F [Source:HGNC Sy
13	ILMN_169180	0.83	−0.57	0.43		
14	ILMN_167888	0.83	−0.55	0.46	LOC105379645	killer cell immunoglobulin like receptor, two Ig domains and lo
15	ILMN_176225	0.8	−0.41	0.16	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
16	ILMN_237582	0.79	−0.86	0.45	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
17	ILMN_208259	0.79	−0.51	0.47	KIR3DL3	killer cell immunoglobulin like receptor, three Ig domains and
18	ILMN_172728	0.69	−0.63	0.36	CD4	CD4 molecule [Source:HGNC Symbol;Acc:HGNC:1678]
19	ILMN_232467	0.64	−0.67	0.55	USF2	upstream transcription factor 2, c−fos interacting [Source:HG
20	ILMN_170457	0.63	−0.75	0.51	FAM53B	family with sequence similarity 53 member B [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−10	58 / 7354	Colon	TssF_Colon
2	8e−10	34 / 2845	Colon	TxEnhG1_Colon
3	2e−09	49 / 5699	Chror	6_EnhG_Melanocytes
4	3e−09	44 / 4795	Chror	6_EnhG_Fibroblasts
5	1e−08	32 / 2810	Colon	EnhA_Colon
6	1e−08	34 / 3164	Brain	Mid_Frontal_Lobe_ZNF
7	8e−08	48 / 6138	Colon	TssD2_Colon
8	4e−07	33 / 3450	Chror	4_TxTrans_Fibroblasts
9	4e−07	66 / 10779	Colon	Enh_Colon
10	4e−07	19 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran
11	5e−07	59 / 9054	Colon	Tx_Colon
12	6e−07	11 / 412	Refer	WIRTH_Immune system
13	1e−06	42 / 5356	Lympl	HOPP_Txn_transition
14	2e−06	60 / 9555	Colon	TssA_Colon
15	2e−06	23 / 2028	Chror	4_TxTrans_Melanocytes
16	6e−06	69 / 12298	Chror	2_TssA_Melanocytes
17	7e−06	17 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
18	8e−06	67 / 11836	Chror	3_TssF_Melanocytes
19	9e−06	40 / 5373	Colon	EnhWk1_Colon
20	1e−05	16 / 1169	Lympl	SPANG_BCR DN
21	2e−05	7 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
22	3e−05	53 / 8568	Colon	TxWk_Colon
23	3e−05	48 / 7448	Lympl	HOPP_Strong_enhancer
24	6e−05	3 / 20	MF	peptide antigen binding
25	7e−05	3 / 21	MF	14−3−3 protein binding
26	7e−05	3 / 21	CC	integral component of lumenal side of endoplasmic reticulum membrane
27	8e−05	3 / 22	BP	antigen processing and presentation of peptide antigen via MHC class I
28	9e−05	17 / 1535	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
29	9e−05	4 / 60	BP	interferon−gamma−mediated signaling pathway
30	1e−04	6 / 190	GSEA	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
31	1e−04	52 / 8771	Chror	5_Tx_Melanocytes
32	2e−04	2 / 5	Lympl	DAVE_MHCCII BL DN
33	2e−04	5 / 136	GSEA	ELVIDGE_HYPOXIA_DN
34	2e−04	55 / 9635	Chror	3_TssF_Fibroblasts
35	2e−04	3 / 30	miRN	hsa−miR−371−3p
36	3e−04	6 / 232	GSEA	RICKMAN_METASTASIS_DN
37	3e−04	16 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
38	3e−04	33 / 4735	TF	ICGC_Pu1_targets
39	3e−04	5 / 152	GSEA	AMIT_EGF_RESPONSE_480_HELA
40	4e−04	2 / 8	GSEA	RUNNE_GENDER_EFFECT_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	2 / 13	GENTLES_modul18
2	0.003	4 / 150	PanCan_MAPK_geneset_nanostring
3	0.022	6 / 554	Lembcke_Colonic Inflammation
4	0.033	3 / 178	SPANG_LPS−index2
5	0.041	2 / 82	PanCan_JAK−ST_geneset_nanostring
6	0.050	1 / 13	GENTLES_modul2
7	0.086	2 / 125	PanCan_CC+Apop_geneset_nanostring
8	0.100	2 / 136	PanCan_RAS_geneset_nanostring
9	0.115	3 / 301	SPANG_BCL6−index2
10	0.118	0 / 13	LIU_LIVER_CANCER
11	0.169	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.175	2 / 193	PanCan_PI3K_geneset_nanostring
13	0.301	1 / 91	PanCan_TXmisReg_geneset_nanostring
14	0.369	1 / 117	PanCan_Driver_Gene_geneset_nanostring
15	0.519	0 / 15	LIU_PROSTATE_CANCER_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−09	49 / 5699	6_EnhG_Melanocytes
2	3e−09	44 / 4795	6_EnhG_Fibroblasts
3	4e−07	33 / 3450	4_TxTrans_Fibroblasts
4	2e−06	23 / 2028	4_TxTrans_Melanocytes
5	6e−06	69 / 12298	2_TssA_Melanocytes
6	8e−06	67 / 11836	3_TssF_Melanocytes
7	1e−04	52 / 8771	5_Tx_Melanocytes
8	2e−04	55 / 9635	3_TssF_Fibroblasts
9	5e−04	61 / 11455	2_TssA_Fibroblasts
10	7e−04	46 / 7854	5_Tx_Fibroblasts
11	8e−04	13 / 1206	6_EnhG_Neuronal_Progenitor
12	8e−04	42 / 6970	5_Tx_Neuronal_Progenitor
13	2e−03	64 / 12741	7_Enh_Melanocytes
14	2e−03	36 / 5956	3_TssF_Neuronal_Progenitor
15	6e−03	63 / 12983	2_TssA_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−06	17 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	2e−05	7 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
3	9e−05	17 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
4	1e−04	6 / 190	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
5	2e−04	5 / 136	ELVIDGE_HYPOXIA_DN
6	3e−04	6 / 232	RICKMAN_METASTASIS_DN
7	3e−04	5 / 152	AMIT_EGF_RESPONSE_480_HELA
8	4e−04	2 / 8	RUNNE_GENDER_EFFECT_UP
9	5e−04	4 / 93	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY
10	5e−04	6 / 259	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
11	6e−04	4 / 100	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR
12	7e−04	5 / 179	MCBRYAN_PUBERTAL_BREAST_6_7WK_UP
13	8e−04	3 / 46	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
14	9e−04	10 / 774	REACTOME_IMMUNE_SYSTEM
15	1e−03	2 / 12	BIOCARTA_AKAP95_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−06	42 / 5356	HOPP_Txn_transition
2	1e−05	16 / 1169	SPANG_BCR DN
3	3e−05	48 / 7448	HOPP_Strong_enhancer
4	2e−04	2 / 5	DAVE_MHCCII BL DN
5	2e−03	6 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
6	4e−03	41 / 7275	HOPP_Txn_elongation
7	4e−03	45 / 8226	HOPP_Active_promoter
8	1e−02	5 / 331	WIRTH_lymphoma937_spot H
9	2e−02	42 / 8098	HOPP_Weak_promoter
10	2e−02	2 / 60	SPANG_BAFF 9hrs DN
11	3e−02	5 / 455	SPANG_CD40 6hrs DN
12	4e−02	2 / 75	SPANG_LPS 6hrs DN
13	4e−02	2 / 78	Sha_DLBCL UP
14	5e−02	2 / 88	ROSOLOWSKI_red total
15	6e−02	1 / 15	Subero_B−ALL_hypo_meth

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−07	11 / 412	WIRTH_Immune system
2	2e−03	9 / 724	PROTEINATLAS_lymph node
3	6e−03	10 / 1003	PROTEINATLAS_appendix
4	9e−03	10 / 1063	PROTEINATLAS_tonsil
5	2e−02	7 / 681	PROTEINATLAS_lung
6	2e−02	6 / 535	PROTEINATLAS_spleen
7	3e−02	8 / 912	PROTEINATLAS_urinary bladder
8	3e−02	9 / 1118	PROTEINATLAS_placenta
9	3e−02	7 / 782	PROTEINATLAS_thyroid gland
10	5e−02	1 / 14	WIRTH_Thyroid gland
11	5e−02	1 / 14	JONGENEEL_Peripheral Blood Lymphocytes
12	6e−02	3 / 221	Chaussabel_3,8_Enzymes
13	6e−02	9 / 1268	PROTEINATLAS_colon
14	7e−02	3 / 242	Chaussabel_3,2_Inflammation I
15	8e−02	7 / 960	PROTEINATLAS_cerebellum

BP

Rank	p−value	#in/all	Geneset
1	8e−05	3 / 22	antigen processing and presentation of peptide antigen via MHC class I
2	9e−05	4 / 60	interferon−gamma−mediated signaling pathway
3	7e−04	2 / 10	regulation of release of sequestered calcium ion into cytosol
4	2e−03	4 / 126	T cell receptor signaling pathway
5	2e−03	2 / 16	nucleosome disassembly
6	3e−03	3 / 73	liver development
7	3e−03	2 / 21	ATP−dependent chromatin remodeling
8	3e−03	2 / 22	positive regulation of T cell activation
9	4e−03	2 / 24	cellular response to interleukin−4
10	4e−03	2 / 25	protein import into nucleus, translocation
11	5e−03	3 / 86	response to organic substance
12	5e−03	2 / 27	glycogen metabolic process
13	5e−03	2 / 27	glycolytic process
14	6e−03	7 / 550	positive regulation of transcription, DNA−templated
15	8e−03	3 / 103	covalent chromatin modification

CC

Rank	p−value	#in/all	Geneset
1	7e−05	3 / 21	integral component of lumenal side of endoplasmic reticulum membrane
2	6e−04	18 / 1979	membrane
3	8e−04	2 / 11	transcription factor TFTC complex
4	9e−04	3 / 49	transcriptional repressor complex
5	1e−03	2 / 12	BAF−type complex
6	1e−03	3 / 51	phagocytic vesicle membrane
7	1e−03	2 / 13	SWI/SNF complex
8	1e−03	7 / 422	protein complex
9	2e−03	20 / 2535	nucleoplasm
10	2e−03	4 / 133	microtubule organizing center
11	3e−03	9 / 775	endoplasmic reticulum
12	5e−03	4 / 170	cell−cell junction
13	5e−03	21 / 2979	cytosol
14	5e−03	7 / 539	Golgi membrane
15	6e−03	2 / 30	immunological synapse

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−10	58 / 7354	TssF_Colon
2	8e−10	34 / 2845	TxEnhG1_Colon
3	1e−08	32 / 2810	EnhA_Colon
4	8e−08	48 / 6138	TssD2_Colon
5	4e−07	66 / 10779	Enh_Colon
6	4e−07	19 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
7	5e−07	59 / 9054	Tx_Colon
8	2e−06	60 / 9555	TssA_Colon
9	9e−06	40 / 5373	EnhWk1_Colon
10	3e−05	53 / 8568	TxWk_Colon
11	3e−04	16 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
12	2e−03	57 / 10999	TssWk_Colon
13	4e−03	9 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
14	1e−02	12 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	1e−02	8 / 789	TxEnhG2_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.007	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
2	0.016	2 / 50	HALLMARK_TGF_BETA_SIGNALING
3	0.036	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	0.037	3 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.039	3 / 191	HALLMARK_INFLAMMATORY_RESPONSE
6	0.062	2 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.108	1 / 29	HALLMARK_NOTCH_SIGNALING
8	0.118	2 / 151	HALLMARK_APOPTOSIS
9	0.133	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
10	0.139	2 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	0.145	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	0.150	2 / 175	HALLMARK_XENOBIOTIC_METABOLISM
13	0.156	2 / 179	HALLMARK_G2M_CHECKPOINT
14	0.161	2 / 183	HALLMARK_GLYCOLYSIS
15	0.164	2 / 185	HALLMARK_MTORC1_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 30	hsa−miR−371−3p
2	6e−04	4 / 100	hsa−miR−150
3	2e−03	3 / 61	hsa−miR−296−3p
4	2e−03	4 / 144	hsa−miR−491−5p
5	4e−03	2 / 23	hsa−miR−1227
6	5e−03	3 / 88	hsa−miR−188−3p
7	6e−03	5 / 294	hsa−miR−503
8	6e−03	5 / 299	hsa−miR−548c−3p
9	8e−03	2 / 34	hsa−miR−1231
10	1e−02	2 / 39	hsa−miR−525−3p
11	1e−02	4 / 216	hsa−miR−182
12	1e−02	2 / 41	hsa−miR−532−3p
13	2e−02	2 / 48	hsa−miR−346
14	2e−02	2 / 52	hsa−miR−508−5p
15	2e−02	3 / 148	hsa−miR−409−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	1e−08	34 / 3164	Mid_Frontal_Lobe_ZNF
2	7e−04	29 / 4112	Mid_Frontal_Lobe_ReprPC
3	1e−03	56 / 10430	Overlap_fetal_midbrain_Quies
4	1e−03	52 / 9504	Overlap_fetal_midbrain_K9K27me3
5	5e−03	35 / 5936	Overlap_fetal_midbrain_HetRpts
6	7e−03	14 / 1728	Fetal_ReprPCWk
7	1e−02	18 / 2630	Fetal_TssF
8	3e−02	17 / 2709	Mid_Frontal_Lobe_HetRpts
9	6e−02	7 / 906	Fetal_HetRpts
10	7e−02	13 / 2127	Mid_Frontal_Lobe_K9K27me3
11	1e−01	6 / 818	Mid_Frontal_Lobe_Het
12	2e−01	44 / 9917	Overlap_fetal_midbrain_ReprPCWk
13	2e−01	7 / 1171	Fetal_EnhP
14	2e−01	5 / 796	Overlap_fetal_midbrain_ZNF
15	2e−01	8 / 1506	Mid_Frontal_Lobe_Quies

Chr

Rank	p−value	#in/all	Geneset
1	0.003	13 / 1411	Chr 11
2	0.046	2 / 87	Chr Y
3	0.102	8 / 1211	Chr 6
4	0.200	7 / 1217	Chr 3
5	0.302	6 / 1160	Chr 12
6	0.319	5 / 954	Chr 9
7	0.323	5 / 959	Chr 16
8	0.351	3 / 536	Chr 22
9	0.352	7 / 1467	Chr 19
10	0.415	4 / 836	Chr 8
11	0.475	4 / 904	Chr 10
12	0.583	3 / 768	Chr 14
13	0.594	5 / 1318	Chr 17
14	0.681	1 / 289	Chr 21
15	0.817	7 / 2323	Chr 1

Glio

Rank	p−value	#in/all	Geneset
1	0.001	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
2	0.009	12 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	0.024	3 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	0.031	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
5	0.035	1 / 9	Colman_survival_robust
6	0.036	4 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.055	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
8	0.057	1 / 15	Mukasa_UP_in_GBM
9	0.057	1 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
10	0.073	2 / 113	GIEZELT_GBM_WT_up_VS_mut
11	0.088	3 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
12	0.103	6 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.126	3 / 315	Up
14	0.128	1 / 35	WIRTH_PN subtype
15	0.128	1 / 35	Colman_survival_associated

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	4 / 147	Homuth_BMI−associated−genes_UP
2	0.016	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
3	0.038	1 / 10	DUMEAUX_Women normal BMI literature genes up
4	0.050	3 / 211	Homuth_BMI−associated−genes_DN
5	1.000	0 / 94	DUMEAUX_Smoking enriched genes
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.000	0 / 17	DUMEAUX_High bmi enriched genes
13	1.000	0 / 31	DUMEAUX_Fasting enriched genes
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	6e−05	3 / 20	peptide antigen binding
2	7e−05	3 / 21	14−3−3 protein binding
3	7e−04	2 / 10	dipeptidyl−peptidase activity
4	7e−04	50 / 8818	protein binding
5	1e−03	6 / 311	enzyme binding
6	2e−03	3 / 59	RNA polymerase II distal enhancer sequence−specific DNA binding
7	2e−03	2 / 17	ligand−dependent nuclear receptor binding
8	4e−03	8 / 646	protein homodimerization activity
9	5e−03	2 / 26	nucleosomal DNA binding
10	5e−03	2 / 26	retinoic acid receptor binding
11	7e−03	2 / 31	ADP binding
12	8e−03	5 / 314	RNA polymerase II core promoter proximal region sequence−specific DNA bi
13	1e−02	5 / 350	protein kinase binding
14	1e−02	4 / 227	transcription coactivator activity
15	1e−02	2 / 45	protein kinase C binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	1 / 13	BENTINK_src.10
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−04	33 / 4735	ICGC_Pu1_targets
2	7e−04	15 / 1498	ICGC_Ets1_targets
3	2e−03	29 / 4345	ICGC_Zeb1_targets
4	2e−03	34 / 5442	ICGC_Pmlsc71910_targets
5	3e−03	18 / 2255	ICGC_SrfV0416101_targets
6	3e−03	29 / 4468	ICGC_Egr1_targets
7	4e−03	32 / 5188	ICGC_Ebfsc137065_targets
8	4e−03	37 / 6322	ICGC_Tcf3_targets
9	5e−03	33 / 5518	ICGC_Stat5_targets
10	5e−03	32 / 5312	ICGC_Tcf12_targets
11	5e−03	30 / 4881	ICGC_Atf2_targets
12	5e−03	14 / 1669	ICGC_P300_targets
13	6e−03	13 / 1501	ICGC_Usf1_targets
14	6e−03	36 / 6267	ICGC_Yy1_targets
15	6e−03	32 / 5383	ICGC_Sp1_targets

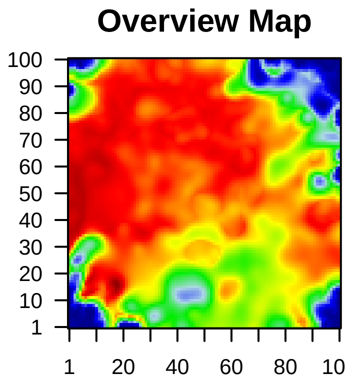
Underexpression Spots

Spot Summary: c

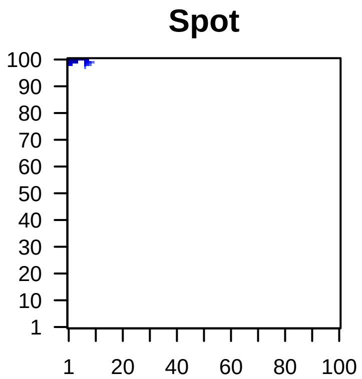
metagenes = 22
genes = 490

<r> metagenes = 0.9
<r> genes = 0.35
beta: r2= 24.2 / log p= −Inf

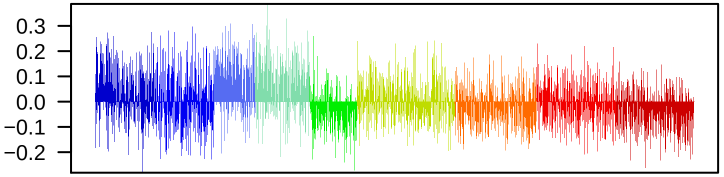
samples with spot = 440 (13 %)
A * : 81 (23.5 %)
A C * : 53 (16.2 %)
A C F * : 95 (40.4 %)
A F * : 96 (31.2 %)
C F * : 6 (2.3 %)
F * : 52 (9.4 %)
F J * : 19 (4.1 %)
J * : 30 (6.7 %)
N * : 8 (1.8 %)



Overview Map



Spot

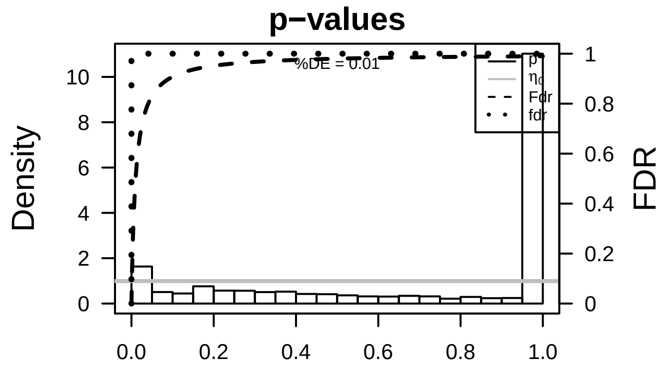


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_220158	1.9	−1.61	0.22		
2	ILMN_239186	1.67	−1.5	0.24	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:H
3	ILMN_168730	1.63	−1.3	0.19	LGALS2	galectin 2 [Source:HGNC Symbol;Acc:HGNC:6562]
4	ILMN_219323	1.52	−0.67	0.32	MZB1	marginal zone B and B1 cell specific protein [Source:HGNC S
5	ILMN_210941	1.44	−1.31	0.31	NAPSB	napsin B aspartic peptidase, pseudogene [Source:HGNC Syr
6	ILMN_231260	1.31	−1.1	0.17	IRF5	interferon regulatory factor 5 [Source:HGNC Symbol;Acc:HGI
7	ILMN_168610	1.27	−0.47	0.27	CCL23	C−C motif chemokine ligand 23 [Source:HGNC Symbol;Acc:H
8	ILMN_180537	1.13	−0.9	0.25		
9	ILMN_240803	1.03	−0.72	0.68	EEF1D	eukaryotic translation elongation factor 1 delta [Source:HGNC
10	ILMN_168817	0.98	−1.06	0.45	RRP7A	ribosomal RNA processing 7 homolog A [Source:HGNC Syml
11	ILMN_178404	0.93	−0.68	0.4		
12	ILMN_173683	0.93	−0.53	0.29	PRSS33	protease, serine 33 [Source:HGNC Symbol;Acc:HGNC:3040
13	ILMN_325914	0.92	−0.7	0.48	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
14	ILMN_166258	0.92	−0.62	0.5		
15	ILMN_211204	0.92	−0.7	0.46	CARD9	caspase recruitment domain family member 9 [Source:HGNC
16	ILMN_172348	0.92	−0.72	0.53	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
17	ILMN_169531	0.89	−0.72	0.39	HLA−DMA	major histocompatibility complex, class II, DM alpha [Source:I
18	ILMN_178254	0.89	−0.74	0.45	EEF1D	eukaryotic translation elongation factor 1 delta [Source:HGNC
19	ILMN_174921	0.87	−0.57	0.68	SDF2L1	stromal cell derived factor 2 like 1 [Source:HGNC Symbol;Acc
20	ILMN_170332	0.87	−0.55	0.27	PTGDR2	prostaglandin D2 receptor 2 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−82	321 / 7354	Colon	TssF_Colon
2	1e−67	211 / 3450	Chror	4_TxTrans_Fibroblasts
3	2e−57	233 / 4795	Chror	6_EnhG_Fibroblasts
4	3e−57	329 / 9555	Colon	TssA_Colon
5	2e−52	358 / 11836	Chror	3_TssF_Melanocytes
6	9e−52	246 / 5699	Chror	6_EnhG_Melanocytes
7	7e−48	307 / 9054	Colon	Tx_Colon
8	9e−47	357 / 12298	Chror	2_TssA_Melanocytes
9	1e−39	236 / 6138	Colon	TssD2_Colon
10	2e−39	323 / 10779	Colon	Enh_Colon
11	2e−38	128 / 2028	Chror	4_TxTrans_Melanocytes
12	7e−38	152 / 2845	Colon	TxEnhG1_Colon
13	7e−38	354 / 12983	Chror	2_TssA_Neuronal_Progenitor
14	9e−36	295 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
15	7e−35	156 / 3164	Brain	Mid_Frontal_Lobe_ZNF
16	3e−34	325 / 11455	Chror	2_TssA_Fibroblasts
17	5e−34	222 / 5956	Chror	3_TssF_Neuronal_Progenitor
18	1e−33	274 / 8568	Colon	TxWk_Colon
19	2e−32	291 / 9635	Chror	3_TssF_Fibroblasts
20	7e−29	136 / 2810	Colon	EnhA_Colon
21	2e−26	194 / 5373	Colon	EnhWk1_Colon
22	2e−21	86 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
23	1e−19	172 / 5067	TF	ICGC_Taf1_targets
24	1e−18	275 / 10430	Brain	Overlap_fetal_midbrain_Quies
25	3e−18	244 / 8771	Chror	5_Tx_Melanocytes
26	4e−18	226 / 7854	Chror	5_Tx_Fibroblasts
27	1e−17	151 / 4345	TF	ICGC_Zeb1_targets
28	1e−16	48 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
29	2e−16	174 / 5518	TF	ICGC_Stat5_targets
30	2e−16	143 / 4131	TF	ICGC_Nfatc1_targets
31	2e−16	56 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
32	3e−16	170 / 5356	Lympl	HOPP_Txn_transition
33	4e−16	190 / 6322	TF	ICGC_Tcf3_targets
34	4e−16	201 / 6868	TF	ICGC_Elf1_targets
35	5e−16	53 / 818	Brain	Mid_Frontal_Lobe_Het
36	5e−16	171 / 5442	TF	ICGC_Pmlsc71910_targets
37	7e−16	68 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
38	1e−15	107 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
39	2e−15	168 / 5383	TF	ICGC_Sp1_targets
40	2e−14	51 / 831	GSEA	LOPEZ_MBD_TARGETS



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	3 / 111	HORVATH_aging_genes meth DOWN
2	0.5	3 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	19 / 527	Lembcke_Normal vs Adenoma
2	0.022	2 / 13	GENTLES_modul2
3	0.025	2 / 14	LIU_PROSTATE_CANCER_UP
4	0.033	2 / 16	GENTLES_modul7
5	0.046	10 / 301	SPANG_BCL6−index2
6	0.107	1 / 14	LIU_COMMON_CANCER_GENES
7	0.136	2 / 36	PanCan_HK_geneset_nanostring
8	0.150	1 / 9	GENTLES_modul3
9	0.150	1 / 9	GENTLES_modul5
10	0.199	2 / 46	PanCan_DNARepair_geneset_nanostring
11	0.209	1 / 13	GENTLES_modul12
12	0.215	5 / 178	SPANG_LPS−index2
13	0.224	1 / 14	GENTLES_modul1
14	0.224	1 / 14	GENTLES_modul10
15	0.237	1 / 15	WANG_ER_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−67	211 / 3450	4_TxTrans_Fibroblasts
2	2e−57	233 / 4795	6_EnhG_Fibroblasts
3	2e−52	358 / 11836	3_TssF_Melanocytes
4	9e−52	246 / 5699	6_EnhG_Melanocytes
5	9e−47	357 / 12298	2_TssA_Melanocytes
6	2e−38	128 / 2028	4_TxTrans_Melanocytes
7	7e−38	354 / 12983	2_TssA_Neuronal_Progenitor
8	3e−34	325 / 11455	2_TssA_Fibroblasts
9	5e−34	222 / 5956	3_TssF_Neuronal_Progenitor
10	2e−32	291 / 9635	3_TssF_Fibroblasts
11	3e−18	244 / 8771	5_Tx_Melanocytes
12	4e−18	226 / 7854	5_Tx_Fibroblasts
13	4e−12	191 / 6970	5_Tx_Neuronal_Progenitor
14	8e−10	273 / 11847	7_Enh_Neuronal_Progenitor
15	7e−09	285 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−16	48 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
2	2e−16	56 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	2e−14	51 / 831	LOPEZ_MBD_TARGETS
4	2e−14	47 / 723	GRADE_COLON_CANCER_UP
5	2e−13	16 / 73	LI_DCP2_BOUND_MRNA
6	4e−13	35 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
7	1e−11	45 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
8	6e−11	37 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
9	6e−11	23 / 237	LU_EZH2_TARGETS_UP
10	3e−10	16 / 117	WELCSH_BRCA1_TARGETS_DN
11	3e−10	29 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
12	4e−10	36 / 607	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
13	7e−10	17 / 141	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
14	7e−10	16 / 123	KIM_ALL_DISORDERS_DURATION_CORR_DN
15	8e−10	35 / 593	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−16	170 / 5356	HOPP_Txn_transition
2	3e−13	219 / 8226	HOPP_Active_promoter
3	4e−10	190 / 7275	HOPP_Txn_elongation
4	2e−07	183 / 7448	HOPP_Strong_enhancer
5	1e−06	192 / 8098	HOPP_Weak_promoter
6	4e−06	33 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
7	3e−05	31 / 777	WIRTH_lymphoma937_spot D
8	2e−04	7 / 66	TARTE_Plasma cell signature
9	2e−04	16 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	1e−03	15 / 331	WIRTH_lymphoma937_spot H
11	5e−03	4 / 39	CARO_OxPhos_in_DLBCL_UP
12	6e−03	3 / 21	ROSOLOWSKI_red UP
13	2e−02	5 / 88	ROSOLOWSKI_red total
14	2e−02	9 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	2e−02	2 / 13	Subero_B−CLL_hypo_meth

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−09	23 / 275	Chaussabel_3,7_Spliceosome
2	5e−09	45 / 963	PROTEINATLAS_pancreas
3	6e−08	33 / 640	PROTEINATLAS_parathyroid gland
4	9e−08	34 / 681	PROTEINATLAS_lung
5	1e−07	46 / 1118	PROTEINATLAS_placenta
6	2e−07	47 / 1176	PROTEINATLAS_duodenum
7	4e−07	35 / 759	PROTEINATLAS_epididymis
8	4e−07	47 / 1194	PROTEINATLAS_stomach
9	4e−07	48 / 1239	PROTEINATLAS_testis
10	1e−06	45 / 1167	PROTEINATLAS_gallbladder
11	1e−06	45 / 1173	PROTEINATLAS_rectum
12	1e−06	43 / 1097	PROTEINATLAS_kidney
13	1e−06	42 / 1063	PROTEINATLAS_tonsil
14	2e−06	47 / 1268	PROTEINATLAS_colon
15	2e−06	38 / 933	PROTEINATLAS_adrenal gland

BP

Rank	p−value	#in/all	Geneset
1	1e−06	7 / 32	mitochondrial electron transport, NADH to ubiquinone
2	1e−06	8 / 46	mitochondrial respiratory chain complex I assembly
3	2e−05	7 / 47	proton transport
4	3e−05	8 / 69	mitochondrial translational elongation
5	4e−05	8 / 71	mitochondrial translational termination
6	6e−05	13 / 196	mRNA splicing, via spliceosome
7	1e−04	23 / 530	biological_process
8	1e−04	8 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
9	2e−04	10 / 137	ER to Golgi vesicle−mediated transport
10	2e−04	6 / 48	negative regulation of protein binding
11	3e−04	6 / 52	IRE1−mediated unfolded protein response
12	8e−04	3 / 11	sphingosine−1−phosphate signaling pathway
13	1e−03	4 / 25	canonical glycolysis
14	1e−03	4 / 26	ATP biosynthetic process
15	1e−03	4 / 26	proteolysis involved in cellular protein catabolic process

CC

Rank	p−value	#in/all	Geneset
1	1e−13	96 / 2464	extracellular exosome
2	2e−11	78 / 1979	membrane
3	5e−11	59 / 1304	mitochondrion
4	2e−10	28 / 374	mitochondrial inner membrane
5	5e−09	96 / 2979	cytosol
6	1e−06	17 / 234	lysosomal membrane
7	2e−06	7 / 33	mitochondrial respiratory chain complex I
8	5e−06	18 / 287	mitochondrial matrix
9	8e−06	8 / 57	endoplasmic reticulum−Golgi intermediate compartment
10	1e−05	11 / 119	vesicle
11	3e−05	73 / 2535	nucleoplasm
12	8e−05	119 / 4822	cytoplasm
13	1e−04	30 / 788	endoplasmic reticulum membrane
14	4e−04	28 / 775	endoplasmic reticulum
15	4e−04	11 / 178	endoplasmic reticulum lumen

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−82	321 / 7354	TssF_Colon
2	3e−57	329 / 9555	TssA_Colon
3	7e−48	307 / 9054	Tx_Colon
4	1e−39	236 / 6138	TssD2_Colon
5	2e−39	323 / 10779	Enh_Colon
6	7e−38	152 / 2845	TxEnhG1_Colon
7	1e−33	274 / 8568	TxWk_Colon
8	7e−29	136 / 2810	EnhA_Colon
9	2e−26	194 / 5373	EnhWk1_Colon
10	2e−21	86 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	7e−16	68 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	3e−11	44 / 789	TxEnhG2_Colon
13	7e−07	68 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e−06	245 / 10999	TssWk_Colon
15	3e−06	201 / 8678	Quies3_Colon

HM

Rank	p−value	#in/all	Geneset
1	2e−06	14 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	4e−06	12 / 130	HALLMARK_DNA_REPAIR
3	3e−03	5 / 54	HALLMARK_MYC_TARGETS_V2
4	5e−03	9 / 176	HALLMARK_ADIPOGENESIS
5	2e−02	8 / 183	HALLMARK_GLYCOLYSIS
6	4e−02	5 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e−01	6 / 175	HALLMARK_XENOBIOTIC_METABOLISM
8	1e−01	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	2e−01	5 / 162	HALLMARK_ALLOGRAFT_REJECTION
10	2e−01	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	2e−01	5 / 170	HALLMARK_MYC_TARGETS_V1
12	2e−01	5 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	2e−01	5 / 177	HALLMARK_MITOTIC_SPINDLE
14	2e−01	4 / 137	HALLMARK_UV_RESPONSE_UP
15	2e−01	4 / 138	HALLMARK_FATTY_ACID_METABOLISM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 30	Hugo_melanoma−all−MET_UP
2	1.0	0 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 30	hsa−miR−371−3p
2	0.02	5 / 88	hsa−miR−608
3	0.03	2 / 14	hsa−miR−574−3p
4	0.03	3 / 39	hsa−miR−517*
5	0.04	2 / 18	hsa−miR−542−5p
6	0.04	3 / 43	hsa−miR−661
7	0.07	4 / 85	hsa−miR−220c
8	0.10	3 / 61	hsa−miR−1236
9	0.10	3 / 63	hsa−miR−518c*
10	0.10	3 / 63	hsa−miR−612
11	0.11	2 / 31	hsa−miR−654−5p
12	0.11	3 / 66	hsa−miR−550
13	0.12	1 / 7	hsa−miR−566
14	0.12	1 / 7	hsa−miR−339−3p
15	0.12	2 / 34	hsa−miR−1226

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	9e−36	295 / 9504	Overlap_fetal_midbrain_K9K27me3
2	7e−35	156 / 3164	Mid_Frontal_Lobe_ZNF
3	1e−18	275 / 10430	Overlap_fetal_midbrain_Quies
4	5e−16	53 / 818	Mid_Frontal_Lobe_Het
5	1e−15	107 / 2709	Mid_Frontal_Lobe_HetRpts
6	4e−12	245 / 9815	Overlap_fetal_midbrain_ReprPC
7	5e−12	73 / 1728	Fetal_ReprPCWk
8	4e−08	118 / 4112	Mid_Frontal_Lobe_ReprPC
9	6e−04	28 / 796	Overlap_fetal_midbrain_ZNF
10	2e−02	62 / 2654	Fetal_Quies
11	2e−02	51 / 2127	Mid_Frontal_Lobe_K9K27me3
12	2e−02	125 / 5936	Overlap_fetal_midbrain_HetRpts
13	2e−02	25 / 906	Fetal_HetRpts
14	8e−02	40 / 1784	Mid_Frontal_Lobe_ReprPCWk
15	2e−01	5 / 180	Overlap_fetal_midbrain_Het

Chr

Rank	p−value	#in/all	Geneset
1	9e−11	63 / 1467	Chr 19
2	1e−05	37 / 959	Chr 16
3	2e−03	41 / 1411	Chr 11
4	8e−03	36 / 1318	Chr 17
5	6e−02	15 / 536	Chr 22
6	6e−02	24 / 954	Chr 9
7	1e−01	15 / 619	Chr 20
8	6e−01	20 / 1170	Chr 7
9	7e−01	39 / 2323	Chr 1
10	8e−01	13 / 904	Chr 10
11	9e−01	16 / 1160	Chr 12
12	9e−01	3 / 289	Chr 21
13	9e−01	16 / 1211	Chr 6
14	9e−01	9 / 768	Chr 14
15	1e+00	14 / 1217	Chr 3

Glio

Rank	p−value	#in/all	Geneset
1	1e−06	8 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	5e−06	11 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	3e−05	12 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	5e−05	55 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	2e−03	27 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	2e−03	5 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	4e−03	53 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
8	6e−03	5 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	2e−02	6 / 113	GIEZELT_GBM_WT_up_VS_mut
10	2e−02	3 / 32	Donson−Misc immune function−associated with LTS in HGA
11	2e−02	10 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
12	2e−02	7 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	3e−02	11 / 315	Up
14	3e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	3e−02	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−04	10 / 147	Homuth_BMI−associated−genes_UP
2	1e−01	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
3	2e−01	1 / 10	Marjolein_ageing−genes_UP
4	3e−01	5 / 211	Homuth_BMI−associated−genes_DN
5	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
6	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	5e−11	223 / 8818	protein binding
2	8e−05	36 / 1013	poly(A) RNA binding
3	2e−04	25 / 627	molecular_function
4	2e−04	5 / 32	NADH dehydrogenase (ubiquinone) activity
5	7e−04	4 / 23	proton−transporting ATPase activity, rotational mechanism
6	8e−04	4 / 24	transmembrane transporter activity
7	7e−03	3 / 22	polyubiquitin binding
8	9e−03	4 / 46	motor activity
9	9e−03	8 / 163	serine−type endopeptidase activity
10	1e−02	7 / 133	ATPase activity
11	1e−02	2 / 10	glutathione binding
12	1e−02	2 / 10	very long−chain fatty acid−CoA ligase activity
13	2e−02	2 / 11	glucose transmembrane transporter activity
14	2e−02	2 / 11	ion transmembrane transporter activity
15	2e−02	2 / 11	sugar:proton symporter activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 12	BENTINK_ras.1
2	0.02	2 / 13	BENTINK_myc.1
3	0.18	1 / 11	BENTINK_ras.4
4	0.24	1 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−19	172 / 5067	ICGC_Taf1_targets
2	1e−17	151 / 4345	ICGC_Zeb1_targets
3	2e−16	174 / 5518	ICGC_Stat5_targets
4	2e−16	143 / 4131	ICGC_Nfatc1_targets
5	4e−16	190 / 6322	ICGC_Tcf3_targets
6	4e−16	201 / 6868	ICGC_Elf1_targets
7	5e−16	171 / 5442	ICGC_Pmlsc71910_targets
8	2e−15	168 / 5383	ICGC_Sp1_targets
9	2e−14	164 / 5312	ICGC_Tcf12_targets
10	2e−14	167 / 5466	ICGC_Nficsc81335_targets
11	4e−14	183 / 6267	ICGC_Yy1_targets
12	5e−14	189 / 6578	ICGC_Pou2_targets
13	5e−14	160 / 5188	ICGC_Ebfsc137065_targets
14	2e−13	201 / 7247	ICGC_Runx3_targets
15	2e−13	152 / 4881	ICGC_Atf2_targets

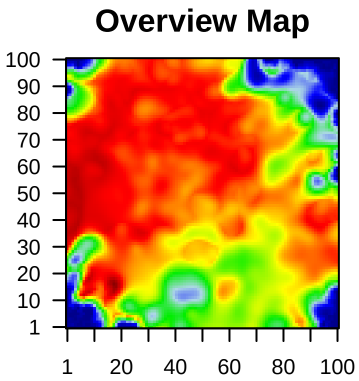
Underexpression Spots

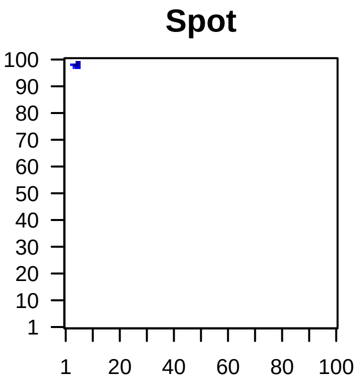
Spot Summary: d

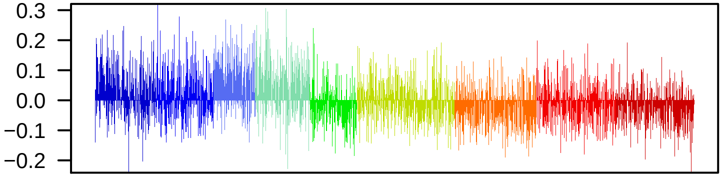
metagenes = 9
genes = 103

<r> metagenes = 0.98
<r> genes = 0.38
beta: r2= 15.15 / log p= −Inf

samples with spot = 292 (8.6 %)
- A * : 57 (16.6 %)
- A C * : 44 (13.4 %)
- A C F * : 63 (26.8 %)
- A F * : 61 (19.8 %)
- C F * : 8 (3 %)
- F * : 27 (4.9 %)
- F J * : 11 (2.4 %)
- J * : 18 (4 %)
- N * : 3 (0.7 %)





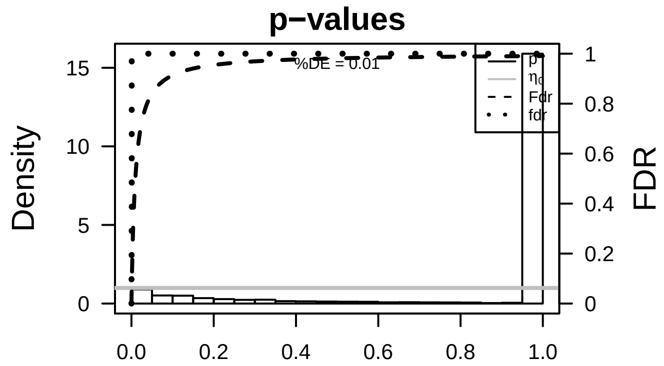


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_182151	1.46	−1.14	0.31		
2	ILMN_213367	0.68	−0.67	0.46	SGSH	N−sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;A
3	ILMN_212574	0.67	−0.6	0.53	CORO1A	coronin 1A [Source:HGNC Symbol;Acc:HGNC:2252]
4	ILMN_179472	0.67	−0.57	0.43	RNF167	ring finger protein 167 [Source:HGNC Symbol;Acc:HGNC:24
5	ILMN_324695	0.64	−0.39	0.44	CMTR1	cap methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:2
6	ILMN_175175	0.63	−0.49	0.53	IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial [Source
7	ILMN_177396	0.63	−0.58	0.47	H1FX	H1 histone family member X [Source:HGNC Symbol;Acc:HG
8	ILMN_174026	0.62	−0.42	0.42	ACOT7	acyl−CoA thioesterase 7 [Source:HGNC Symbol;Acc:HGNC:
9	ILMN_174870	0.61	−0.5	0.49	CRELD2	cysteine rich with EGF like domains 2 [Source:HGNC Symbol
10	ILMN_167568	0.61	−0.52	0.62	APOBEC3C	apolipoprotein B mRNA editing enzyme catalytic subunit 3C [
11	ILMN_181132	0.6	−0.45	0.72	DPP7	dipeptidyl peptidase 7 [Source:HGNC Symbol;Acc:HGNC:14
12	ILMN_234413	0.59	−0.69	0.57		
13	ILMN_179114	0.57	−0.49	0.64		
14	ILMN_172835	0.57	−0.68	0.55		
15	ILMN_177507	0.55	−0.55	0.69		
16	ILMN_177511	0.54	−0.52	0.48	SND1	staphylococcal nuclease and tudor domain containing 1 [Sou
17	ILMN_169061	0.54	−0.6	0.73	RALY	RALY heterogeneous nuclear ribonucleoprotein [Source:HGN
18	ILMN_166882	0.54	−0.4	0.56	BATF	basic leucine zipper ATF−like transcription factor [Source:HG
19	ILMN_180270	0.54	−0.53	0.78		
20	ILMN_215742	0.53	−0.52	0.62		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−25	75 / 7354	Colon	TssF_Colon
2	5e−25	82 / 9555	Colon	TssA_Colon
3	2e−23	50 / 2845	Colon	TxEnhG1_Colon
4	3e−22	65 / 5699	Chrom	6_EnhG_Melanocytes
5	4e−20	76 / 9054	Colon	Tx_Colon
6	5e−19	83 / 11836	Chrom	3_TssF_Melanocytes
7	7e−19	84 / 12298	Chrom	2_TssA_Melanocytes
8	1e−18	76 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
9	9e−17	78 / 10779	Colon	Enh_Colon
10	2e−16	46 / 3450	Chrom	4_TxTrans_Fibroblasts
11	2e−15	59 / 6138	Colon	TssD2_Colon
12	3e−15	35 / 2028	Chrom	4_TxTrans_Melanocytes
13	2e−12	75 / 11455	Chrom	2_TssA_Fibroblasts
14	3e−12	48 / 4795	Chrom	6_EnhG_Fibroblasts
15	4e−12	79 / 12983	Chrom	2_TssA_Neuronal_Progenitor
16	4e−11	67 / 9635	Chrom	3_TssF_Fibroblasts
17	1e−10	51 / 5956	Chrom	3_TssF_Neuronal_Progenitor
18	2e−10	62 / 8568	Colon	TxWk_Colon
19	1e−09	35 / 3164	Brain	Mid_Frontal_Lobe_ZNF
20	4e−09	32 / 2810	Colon	EnhA_Colon
21	9e−09	60 / 8818	MF	protein binding
22	1e−07	64 / 10430	Brain	Overlap_fetal_midbrain_Quies
23	1e−07	43 / 5373	Colon	EnhWk1_Colon
24	2e−07	21 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
25	4e−07	13 / 594	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_U
26	4e−07	17 / 1063	Refer	PROTEINATLAS_tonsil
27	4e−07	10 / 325	GSEA	DAIRKEE_TERT_TARGETS_UP
28	8e−07	60 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
29	1e−06	18 / 1268	Refer	PROTEINATLAS_colon
30	1e−06	13 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
31	1e−06	16 / 1013	MF	poly(A) RNA binding
32	2e−06	14 / 789	Colon	TxEnhG2_Colon
33	2e−06	17 / 1167	Refer	PROTEINATLAS_gallbladder
34	2e−06	38 / 4822	CC	cytoplasm
35	2e−06	39 / 5067	TF	ICGC_Taf1_targets
36	2e−06	14 / 818	Brain	Mid_Frontal_Lobe_Het
37	3e−06	40 / 5356	Lymp	HOPP_Txn_transition
38	3e−06	15 / 963	Refer	PROTEINATLAS_pancreas
39	4e−06	14 / 850	Refer	PROTEINATLAS_skin
40	4e−06	35 / 4362	TF	ICGC_Creb1_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
2	0.13	1 / 36	PanCan_HK_geneset_nanostring
3	0.15	2 / 178	SPANG_LPS−index2
4	0.32	3 / 527	Lembcke_Normal vs Adenoma
5	0.36	1 / 117	PanCan_Driver_Gene_geneset_nanostring
6	0.38	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	0.40	1 / 136	PanCan_RAS_geneset_nanostring
8	0.62	2 / 554	Lembcke_Colonic Inflammation
9	0.68	1 / 301	SPANG_BCL6−index2
10	0.82	0 / 15	LIU_PROSTATE_CANCER_DN
11	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
12	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1.00	0 / 12	LIU_BREAST_CANCER
14	1.00	0 / 14	LIU_COMMON_CANCER_GENES
15	1.00	0 / 13	LIU_LIVER_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−22	65 / 5699	6_EnhG_Melanocytes
2	5e−19	83 / 11836	3_TssF_Melanocytes
3	7e−19	84 / 12298	2_TssA_Melanocytes
4	2e−16	46 / 3450	4_TxTrans_Fibroblasts
5	3e−15	35 / 2028	4_TxTrans_Melanocytes
6	2e−12	75 / 11455	2_TssA_Fibroblasts
7	3e−12	48 / 4795	6_EnhG_Fibroblasts
8	4e−12	79 / 12983	2_TssA_Neuronal_Progenitor
9	4e−11	67 / 9635	3_TssF_Fibroblasts
10	1e−10	51 / 5956	3_TssF_Neuronal_Progenitor
11	3e−04	42 / 6970	5_Tx_Neuronal_Progenitor
12	4e−04	61 / 11847	7_Enh_Neuronal_Progenitor
13	4e−04	64 / 12741	7_Enh_Melanocytes
14	6e−04	13 / 1206	6_EnhG_Neuronal_Progenitor
15	1e−03	44 / 7854	5_Tx_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−07	13 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
2	4e−07	10 / 325	DAIRKEE_TERT_TARGETS_UP
3	1e−06	13 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
4	2e−05	6 / 141	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
5	2e−05	12 / 723	GRADE_COLON_CANCER_UP
6	3e−05	7 / 237	LU_EZH2_TARGETS_UP
7	1e−04	5 / 123	KIM_ALL_DISORDERS_DURATION_CORR_DN
8	1e−04	9 / 515	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
9	1e−04	13 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
10	2e−04	4 / 71	REACTOME_UNFOLDED_PROTEIN_RESPONSE
11	2e−04	6 / 217	PENG_RAPAMYCIN_RESPONSE_DN
12	3e−04	8 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
13	4e−04	9 / 593	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
14	5e−04	3 / 40	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S
15	7e−04	5 / 184	FOSTER_KDM1A_TARGETS_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−06	40 / 5356	HOPP_Txn_transition
2	1e−05	51 / 8226	HOPP_Active_promoter
3	3e−03	12 / 1270	SPANG_BCR UP
4	4e−03	40 / 7275	HOPP_Txn_elongation
5	4e−03	5 / 283	TARTE_Plasmablast signature
6	5e−03	43 / 8098	HOPP_Weak_promoter
7	6e−03	40 / 7448	HOPP_Strong_enhancer
8	8e−03	6 / 455	SPANG_CD40 6hrs DN
9	1e−02	2 / 39	CARO_OxPhos_in_DLBCL_UP
10	3e−02	1 / 8	MASCQUE_ABC UP
11	6e−02	1 / 16	WRIGHT_ABC UP
12	6e−02	1 / 17	YAMANE_AICDA_targets_recruited
13	7e−02	6 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
14	7e−02	6 / 777	WIRTH_lymphoma937_spot D
15	8e−02	3 / 272	SPANG_IL21 DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−07	17 / 1063	PROTEINATLAS_tonsil
2	1e−06	18 / 1268	PROTEINATLAS_colon
3	2e−06	17 / 1167	PROTEINATLAS_gallbladder
4	3e−06	15 / 963	PROTEINATLAS_pancreas
5	4e−06	14 / 850	PROTEINATLAS_skin
6	9e−06	16 / 1194	PROTEINATLAS_stomach
7	1e−05	13 / 816	PROTEINATLAS_endometrium
8	1e−05	14 / 959	PROTEINATLAS_nasopharynx
9	3e−05	14 / 1016	PROTEINATLAS_cerebral cortex
10	3e−05	12 / 759	PROTEINATLAS_epididymis
11	3e−05	15 / 1176	PROTEINATLAS_duodenum
12	6e−05	13 / 960	PROTEINATLAS_cerebellum
13	8e−05	14 / 1118	PROTEINATLAS_placenta
14	9e−05	14 / 1138	PROTEINATLAS_small intestine
15	1e−04	11 / 740	PROTEINATLAS_esophagus

BP

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 69	mitochondrial translational elongation
2	2e−04	4 / 71	mitochondrial translational termination
3	6e−04	2 / 10	proteasome assembly
4	8e−04	2 / 11	negative regulation of transcription elongation from RNA polymerase II promo
5	1e−03	3 / 52	IRE1−mediated unfolded protein response
6	1e−03	3 / 59	regulation of protein stability
7	2e−03	3 / 63	transcription elongation from RNA polymerase II promoter
8	3e−03	2 / 22	positive regulation of viral transcription
9	3e−03	2 / 23	mitochondrial translation
10	3e−03	2 / 23	nucleotide−binding oligomerization domain containing signaling pathway
11	5e−03	4 / 184	translation
12	7e−03	2 / 32	MyD88−dependent toll−like receptor signaling pathway
13	7e−03	3 / 103	activation of MAPK activity
14	9e−03	3 / 113	Fc−epsilon receptor signaling pathway
15	1e−02	3 / 122	positive regulation of NF−kappaB transcription factor activity

CC

Rank	p−value	#in/all	Geneset
1	2e−06	38 / 4822	cytoplasm
2	1e−04	15 / 1304	mitochondrion
3	6e−04	7 / 374	mitochondrial inner membrane
4	2e−03	2 / 18	phagocytic cup
5	3e−03	30 / 4828	nucleus
6	3e−03	2 / 20	mitochondrial small ribosomal subunit
7	3e−03	3 / 78	catalytic step 2 spliceosome
8	4e−03	2 / 24	mitochondrial ribosome
9	5e−03	5 / 287	mitochondrial matrix
10	6e−03	18 / 2535	nucleoplasm
11	7e−03	4 / 202	early endosome
12	8e−03	4 / 207	lysosome
13	1e−02	19 / 2979	cytosol
14	2e−02	2 / 51	proteasome complex
15	2e−02	14 / 1979	membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−25	75 / 7354	TssF_Colon
2	5e−25	82 / 9555	TssA_Colon
3	2e−23	50 / 2845	TxEnhG1_Colon
4	4e−20	76 / 9054	Tx_Colon
5	9e−17	78 / 10779	Enh_Colon
6	2e−15	59 / 6138	TssD2_Colon
7	2e−10	62 / 8568	TxWk_Colon
8	4e−09	32 / 2810	EnhA_Colon
9	1e−07	43 / 5373	EnhWk1_Colon
10	2e−07	21 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	2e−06	14 / 789	TxEnhG2_Colon
12	1e−03	13 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	4e−03	13 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	1e−02	53 / 10999	TssWk_Colon
15	1e−02	44 / 8678	Quies3_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.002	4 / 130	HALLMARK_DNA_REPAIR
2	0.004	4 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	0.007	3 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.096	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
5	0.136	2 / 170	HALLMARK_MYC_TARGETS_V1
6	0.153	2 / 183	HALLMARK_APICAL_JUNCTION
7	0.155	2 / 185	HALLMARK_P53_PATHWAY
8	0.157	2 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.186	1 / 54	HALLMARK_MYC_TARGETS_V2
10	0.231	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	0.276	1 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	0.293	1 / 91	HALLMARK_ANDROGEN_RESPONSE
13	0.293	1 / 91	HALLMARK_PEROXISOME
14	0.324	1 / 103	HALLMARK_BILE_ACID_METABOLISM
15	0.383	1 / 127	HALLMARK_COAGULATION

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 86	hsa−miR−339−5p
2	4e−03	3 / 84	hsa−miR−486−3p
3	5e−03	3 / 93	hsa−miR−378
4	6e−03	3 / 97	hsa−miR−125a−3p
5	1e−02	2 / 48	hsa−miR−146b−3p
6	4e−02	2 / 88	hsa−miR−423−5p
7	5e−02	1 / 13	hsa−miR−452*
8	7e−02	1 / 18	hsa−miR−542−5p
9	8e−02	1 / 23	hsa−miR−668
10	8e−02	1 / 23	hsa−miR−596
11	1e−01	2 / 143	hsa−miR−548f
12	1e−01	2 / 144	hsa−miR−24
13	1e−01	2 / 144	hsa−miR−491−5p
14	1e−01	1 / 29	hsa−miR−17*
15	1e−01	1 / 33	hsa−miR−615−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	1e−18	76 / 9504	Overlap_fetal_midbrain_K9K27me3
2	1e−09	35 / 3164	Mid_Frontal_Lobe_ZNF
3	1e−07	64 / 10430	Overlap_fetal_midbrain_Quies
4	8e−07	60 / 9815	Overlap_fetal_midbrain_ReprPC
5	2e−06	14 / 818	Mid_Frontal_Lobe_Het
6	5e−03	14 / 1728	Fetal_ReprPCWk
7	6e−03	19 / 2709	Mid_Frontal_Lobe_HetRpts
8	1e−02	8 / 796	Overlap_fetal_midbrain_ZNF
9	2e−02	8 / 906	Fetal_HetRpts
10	5e−02	30 / 5936	Overlap_fetal_midbrain_HetRpts
11	5e−02	22 / 4112	Mid_Frontal_Lobe_ReprPC
12	6e−02	4 / 386	Fetal_ZNF
13	1e−01	14 / 2654	Fetal_Quies
14	1e−01	3 / 328	Fetal_Het
15	1e−01	2 / 180	Overlap_fetal_midbrain_Het

Chr

Rank	p−value	#in/all	Geneset
1	0.02	6 / 536	Chr 22
2	0.03	10 / 1318	Chr 17
3	0.05	10 / 1467	Chr 19
4	0.07	7 / 959	Chr 16
5	0.21	4 / 619	Chr 20
6	0.29	5 / 954	Chr 9
7	0.32	5 / 994	Chr X
8	0.49	5 / 1211	Chr 6
9	0.50	6 / 1492	Chr 2
10	0.52	9 / 2323	Chr 1
11	0.56	3 / 768	Chr 14
12	0.83	3 / 1170	Chr 7
13	0.83	2 / 836	Chr 8
14	0.85	3 / 1217	Chr 3
15	0.86	2 / 904	Chr 10

Glio

Rank	p−value	#in/all	Geneset
1	0.001	3 / 55	Stuehler_Proteins_up_in_STS
2	0.008	3 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.012	2 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
4	0.030	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
5	0.055	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
6	0.091	6 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	0.173	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
8	0.207	1 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
9	0.212	3 / 419	Down_a
10	0.231	1 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
11	0.303	1 / 95	Weller_LGG_1p19qDel−vs−intact_UP
12	0.311	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	0.337	2 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	0.381	1 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
15	0.395	1 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 31	DUMEAUX_Fasting enriched genes
2	0.4	1 / 147	Homuth_BMI−associated−genes_UP
3	1.0	0 / 94	DUMEAUX_Smoking enriched genes
4	1.0	0 / 10	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 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 211	Homuth_BMI−associated−genes_DN
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	9e−09	60 / 8818	protein binding
2	1e−06	16 / 1013	poly(A) RNA binding
3	4e−03	2 / 24	fatty−acyl−CoA binding
4	4e−03	4 / 169	structural constituent of ribosome
5	6e−03	7 / 580	identical protein binding
6	1e−02	2 / 49	protein serine/threonine phosphatase activity
7	2e−02	3 / 145	nucleic acid binding
8	2e−02	2 / 54	serine−type peptidase activity
9	2e−02	2 / 57	transcription cofactor activity
10	2e−02	4 / 283	nucleotide binding
11	2e−02	2 / 62	virus receptor activity
12	2e−02	2 / 63	phosphatidylinositol binding
13	4e−02	1 / 10	dipeptidyl−peptidase activity
14	4e−02	1 / 10	peptide alpha−N−acetyltransferase activity
15	4e−02	1 / 10	proteasome binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	1 / 13	BENTINK_myc.1
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 12	BENTINK_ras.1
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−06	39 / 5067	ICGC_Taf1_targets
2	4e−06	35 / 4362	ICGC_Creb1_targets
3	6e−06	40 / 5518	ICGC_Stat5_targets
4	1e−05	44 / 6578	ICGC_Pou2_targets
5	2e−05	45 / 6868	ICGC_Elf1_targets
6	2e−05	36 / 4890	ICGC_Bclaf101388_targets
7	2e−05	22 / 2215	ICGC_GabpPcr2_targets
8	3e−05	46 / 7247	ICGC_Runx3_targets
9	3e−05	38 / 5442	ICGC_Pmlsc71910_targets
10	6e−05	34 / 4735	ICGC_Pu1_targets
11	6e−05	37 / 5383	ICGC_Sp1_targets
12	7e−05	18 / 1723	HEBENSTREIT_high expression TF
13	8e−05	41 / 6322	ICGC_Tcf3_targets
14	9e−05	37 / 5466	ICGC_Nficsc81335_targets
15	1e−04	34 / 4881	ICGC_Atf2_targets

Underexpression Spots

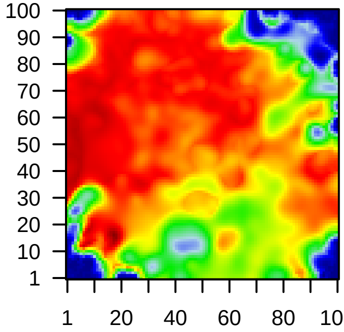
Spot Summary: e

metagenes = 2
genes = 38

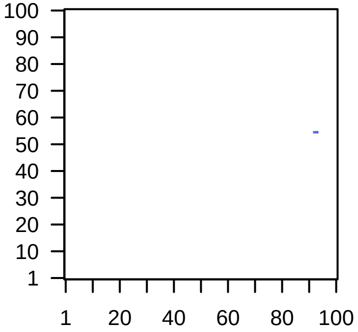
<r> metagenes = 1
<r> genes = 0.24
beta: r2= 2.13 / log p= −Inf

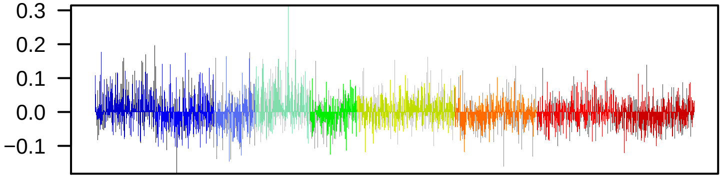
samples with spot = 63 (1.9 %)
- A * : 17 (4.9 %)
- A C * : 9 (2.7 %)
- A C F * : 5 (2.1 %)
- A F * : 18 (5.8 %)
- C F * : 1 (0.4 %)
- F * : 7 (1.3 %)
- F J * : 2 (0.4 %)
- J * : 2 (0.4 %)
- N * : 2 (0.5 %)

Overview Map



Spot





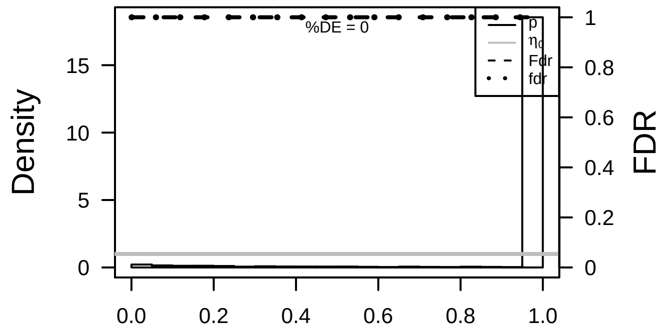
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178823	0.84	−0.38	0.27		
2	ILMN_241003	0.58	−0.47	0.45	FAM111A	family with sequence similarity 111 member A [Source:HGNC
3	ILMN_179938	0.54	−0.29	0.33	SNORD14A	small nucleolar RNA, C/D box 14A [Source:HGNC Symbol;Ac
4	ILMN_171863	0.48	−0.41	0.51	LRP5L	LDL receptor related protein 5 like [Source:HGNC Symbol;Ac
5	ILMN_168203	0.46	−0.37	0.64	SNORA32	small nucleolar RNA, H/ACA box 32 [Source:HGNC Symbol;A
6	ILMN_239537	0.44	−0.37	0.56	GABBR1	gamma−aminobutyric acid type B receptor subunit 1 [Source:
7	ILMN_207315	0.44	−0.33	0.58	AMY2B	amylase, alpha 2B (pancreatic) [Source:HGNC Symbol;Acc:H
8	ILMN_180146	0.42	−0.26	0.56	ANKFY1	ankyrin repeat and FYVE domain containing 1 [Source:HGNC
9	ILMN_229161	0.41	−0.27	0.33		
10	ILMN_170922	0.41	−0.3	0.63	CCDC84	coiled−coil domain containing 84 [Source:HGNC Symbol;Acc
11	ILMN_165526	0.41	−0.34	0.47	ERP27	endoplasmic reticulum protein 27 [Source:HGNC Symbol;Acc
12	ILMN_184394	0.4	−0.34	0.61	HMBOX1	homeobox containing 1 [Source:HGNC Symbol;Acc:HGNC:2
13	ILMN_170285	0.4	−0.3	0.54	ADHFE1	alcohol dehydrogenase, iron containing 1 [Source:HGNC Syn
14	ILMN_206843	0.4	−0.33	0.57	ZNF700	zinc finger protein 700 [Source:HGNC Symbol;Acc:HGNC:25
15	ILMN_178868	0.37	−0.46	0.49	PHIP	pleckstrin homology domain interacting protein [Source:HGN
16	ILMN_165511	0.36	−0.32	0.48	WDR19	WD repeat domain 19 [Source:HGNC Symbol;Acc:HGNC:18
17	ILMN_190413	0.35	−0.32	0.57		
18	ILMN_172222	0.35	−0.23	0.41		
19	ILMN_210870	0.35	−0.32	0.5		
20	ILMN_171511	0.34	−0.34	0.45	HARS2	histidyl−tRNA synthetase 2, mitochondrial [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	4 / 221	Refer	Chaussabel_3,8_Enzymes
2	7e−04	2 / 28	GSEA	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN
3	7e−04	2 / 29	GSEA	HU_ANGIOGENESIS_DN
4	9e−04	2 / 32	BP	embryonic cranial skeleton morphogenesis
5	2e−03	4 / 407	GSEA	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
6	3e−03	3 / 221	GSEA	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4
7	4e−03	3 / 228	GSEA	PLASARI_TGFB1_TARGETS_10HR_DN
8	4e−03	2 / 72	BP	insulin receptor signaling pathway
9	7e−03	4 / 550	BP	positive regulation of transcription, DNA−templated
10	7e−03	3 / 287	CC	mitochondrial matrix
11	8e−03	2 / 97	miRN	hsa−miR−1301
12	9e−03	2 / 103	Colon	Marisa_CRC−cluster−d
13	1e−02	1 / 7	GSEA	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
14	1e−02	4 / 644	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3
15	1e−02	1 / 10	BP	lysine catabolic process
16	1e−02	1 / 10	BP	regulation of dendrite development
17	1e−02	6 / 1468	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
18	2e−02	1 / 11	BP	gonad development
19	2e−02	1 / 11	BP	lymphangiogenesis
20	2e−02	1 / 12	BP	embryonic camera−type eye development
21	2e−02	1 / 12	BP	lymph vessel development
22	2e−02	1 / 12	BP	neurological system process
23	2e−02	1 / 12	Glio	Phillips PN up vs MES & Prolif
24	2e−02	1 / 13	BP	cardiac muscle cell proliferation
25	2e−02	1 / 13	CC	nBAF complex
26	2e−02	1 / 13	MF	oxidoreductase activity, acting on the CH−CH group of donors, with a flavin
27	2e−02	1 / 13	BP	positive regulation of cell adhesion mediated by integrin
28	2e−02	1 / 13	BP	positive regulation of insulin−like growth factor receptor signaling pathway
29	2e−02	1 / 14	miRN	hsa−miR−574−3p
30	2e−02	1 / 15	BP	fatty acid beta−oxidation using acyl−CoA dehydrogenase
31	2e−02	1 / 15	BP	fatty acid oxidation
32	2e−02	1 / 15	MF	structural constituent of eye lens
33	2e−02	1 / 16	BP	neural crest cell development
34	2e−02	1 / 16	GSEA	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION
35	2e−02	1 / 17	BP	2−oxoglutarate metabolic process
36	2e−02	1 / 17	BP	acyl−CoA metabolic process
37	2e−02	1 / 17	MF	lysine−acetylated histone binding
38	2e−02	1 / 17	BP	positive regulation of dendrite morphogenesis
39	2e−02	1 / 17	Refer	JONGENEEL_Pancreas
40	2e−02	1 / 17	GSEA	STREICHER_LSM1_TARGETS_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
2	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
3	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	1.00	0 / 12	LIU_BREAST_CANCER
6	1.00	0 / 14	LIU_COMMON_CANCER_GENES
7	1.00	0 / 13	LIU_LIVER_CANCER
8	1.00	0 / 15	LIU_PROSTATE_CANCER_DN
9	1.00	0 / 14	LIU_PROSTATE_CANCER_UP
10	1.00	0 / 15	WANG_ER_UP
11	1.00	0 / 13	WANG_ER_DN
12	1.00	0 / 15	WOLFER_overlap genes
13	1.00	0 / 16	BEN−PORATH_DN
14	1.00	0 / 14	BEN−PORATH_UP
15	1.00	0 / 14	GENTLES_modul1

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.04	16 / 7854	5_Tx_Fibroblasts
2	0.11	16 / 8771	5_Tx_Melanocytes
3	0.13	13 / 6970	5_Tx_Neuronal_Progenitor
4	0.20	9 / 4795	6_EnhG_Fibroblasts
5	0.22	8 / 4237	14_ZNF_Neuronal_Progenitor
6	0.34	14 / 8990	15_Quies_Fibroblasts
7	0.34	17 / 11130	15_Quies_Melanocytes
8	0.40	17 / 11455	2_TssA_Fibroblasts
9	0.44	1 / 416	4_TxTrans_Neuronal_Progenitor
10	0.44	9 / 5956	3_TssF_Neuronal_Progenitor
11	0.46	14 / 9635	3_TssF_Fibroblasts
12	0.50	2 / 1206	6_EnhG_Neuronal_Progenitor
13	0.54	8 / 5699	6_EnhG_Melanocytes
14	0.56	17 / 12298	2_TssA_Melanocytes
15	0.59	1 / 630	14_ZNF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 28	PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN
2	7e−04	2 / 29	HU_ANGIOGENESIS_DN
3	2e−03	4 / 407	MIKKELSEN_NPC_ICP_WITH_H3K4ME3
4	3e−03	3 / 221	SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4
5	4e−03	3 / 228	PLASARI_TGFB1_TARGETS_10HR_DN
6	1e−02	1 / 7	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE
7	1e−02	4 / 644	MIKKELSEN_ES_ICP_WITH_H3K4ME3
8	2e−02	1 / 16	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION
9	2e−02	1 / 17	STREICHER_LSM1_TARGETS_DN
10	2e−02	1 / 17	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP
11	2e−02	2 / 174	ZHANG_TLX_TARGETS_36HR_DN
12	3e−02	3 / 466	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
13	3e−02	1 / 21	SAGIV_CD24_TARGETS_UP
14	3e−02	1 / 21	WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG
15	3e−02	1 / 24	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.03	3 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
2	0.03	3 / 493	WIRTH_lymphoma937_spot J
3	0.05	12 / 5356	HOPP_Txn_transition
4	0.05	15 / 7275	HOPP_Txn_elongation
5	0.06	2 / 290	SPANG_IL21 UP
6	0.11	1 / 88	WIRTH_lymphoma937_spot A
7	0.12	1 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_c
8	0.15	1 / 121	SPANG_LPS 6hrs UP
9	0.33	1 / 286	ZHANG_DLBCL mutated
10	0.37	1 / 331	SPANG_CD40 6hrs UP
11	0.45	11 / 7448	HOPP_Strong_enhancer
12	0.47	1 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
13	0.48	1 / 464	WIRTH_lymphoma937_spot I
14	0.57	9 / 6559	HOPP_Weak_txn
15	0.65	9 / 6959	HOPP_Weak_enhancer

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 221	Chaussabel_3,8_Enzymes
2	2e−02	1 / 17	JONGENEEL_Pancreas
3	6e−02	1 / 43	VAQUERIZAS_Placenta_TF
4	1e−01	3 / 963	PROTEINATLAS_pancreas
5	1e−01	2 / 490	PROTEINATLAS_heart muscle
6	2e−01	1 / 119	Chaussabel_2,4_Ribosomal proteins
7	2e−01	1 / 153	Chaussabel_2,9_Cytosceleton
8	4e−01	2 / 929	PROTEINATLAS_bronchus
9	4e−01	2 / 959	PROTEINATLAS_nasopharynx
10	5e−01	2 / 1097	PROTEINATLAS_kidney
11	5e−01	1 / 465	PROTEINATLAS_liver
12	5e−01	2 / 1194	PROTEINATLAS_stomach
13	5e−01	1 / 535	PROTEINATLAS_spleen
14	6e−01	1 / 598	PROTEINATLAS_prostate
15	6e−01	1 / 619	PROTEINATLAS_salivary gland

BP

Rank	p−value	#in/all	Geneset
1	9e−04	2 / 32	embryonic cranial skeleton morphogenesis
2	4e−03	2 / 72	insulin receptor signaling pathway
3	7e−03	4 / 550	positive regulation of transcription, DNA−templated
4	1e−02	1 / 10	lysine catabolic process
5	1e−02	1 / 10	regulation of dendrite development
6	2e−02	1 / 11	gonad development
7	2e−02	1 / 11	lymphangiogenesis
8	2e−02	1 / 12	embryonic camera−type eye development
9	2e−02	1 / 12	lymph vessel development
10	2e−02	1 / 12	neurological system process
11	2e−02	1 / 13	cardiac muscle cell proliferation
12	2e−02	1 / 13	positive regulation of cell adhesion mediated by integrin
13	2e−02	1 / 13	positive regulation of insulin−like growth factor receptor signaling pathway
14	2e−02	1 / 15	fatty acid beta−oxidation using acyl−CoA dehydrogenase
15	2e−02	1 / 15	fatty acid oxidation

CC

Rank	p−value	#in/all	Geneset
1	0.007	3 / 287	mitochondrial matrix
2	0.018	1 / 13	nBAF complex
3	0.025	1 / 18	telomerase holoenzyme complex
4	0.027	1 / 20	retromer complex
5	0.031	1 / 23	nonmotile primary cilium
6	0.043	1 / 32	photoreceptor connecting cilium
7	0.047	1 / 35	nuclear body
8	0.051	1 / 38	ciliary tip
9	0.071	1 / 53	photoreceptor outer segment
10	0.078	1 / 59	presynaptic membrane
11	0.079	1 / 60	motile cilium
12	0.091	1 / 69	primary cilium
13	0.092	1 / 70	kinetochore
14	0.098	1 / 75	condensed chromosome kinetochore
15	0.117	1 / 90	chromatin

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.009	2 / 103	Marisa_CRC−cluster−d
2	0.014	6 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	0.100	1 / 76	Pentrack_CRC_TCGA_corr_N_msi−h_DN
4	0.118	1 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	0.146	3 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
6	0.186	3 / 1083	ZNF_Colon
7	0.200	16 / 9555	TssA_Colon
8	0.203	11 / 6138	TssD2_Colon
9	0.264	14 / 8568	TxWk_Colon
10	0.283	14 / 8678	Quies3_Colon
11	0.318	2 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	0.340	1 / 299	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	0.351	14 / 9054	Tx_Colon
14	0.408	1 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	0.425	1 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	1 / 91	HALLMARK_ANDROGEN_RESPONSE
2	0.2	1 / 138	HALLMARK_FATTY_ACID_METABOLISM
3	0.2	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM
4	0.2	1 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	1.0	0 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	1.0	0 / 189	HALLMARK_HYPOXIA
7	1.0	0 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	1.0	0 / 177	HALLMARK_MITOTIC_SPINDLE
9	1.0	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
10	1.0	0 / 50	HALLMARK_TGF_BETA_SIGNALING
11	1.0	0 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	1.0	0 / 130	HALLMARK_DNA_REPAIR
13	1.0	0 / 179	HALLMARK_G2M_CHECKPOINT
14	1.0	0 / 151	HALLMARK_APOPTOSIS
15	1.0	0 / 29	HALLMARK_NOTCH_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	2 / 97	hsa−miR−1301
2	0.019	1 / 14	hsa−miR−574−3p
3	0.027	1 / 20	hsa−miR−380*
4	0.036	2 / 216	hsa−miR−182
5	0.060	1 / 45	hsa−miR−766
6	0.063	1 / 47	hsa−miR−875−5p
7	0.064	1 / 48	hsa−miR−654−3p
8	0.065	1 / 49	hsa−miR−556−3p
9	0.078	1 / 59	hsa−miR−526b*
10	0.090	1 / 68	hsa−miR−649
11	0.095	1 / 72	hsa−miR−489
12	0.097	1 / 74	hsa−miR−877
13	0.102	1 / 78	hsa−miR−562
14	0.134	1 / 104	hsa−miR−325
15	0.135	2 / 467	hsa−miR−195

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	0.1	3 / 796	Overlap_fetal_midbrain_ZNF
2	0.2	11 / 5936	Overlap_fetal_midbrain_HetRpts
3	0.2	2 / 630	Mid_Frontal_Lobe_EnhP
4	0.2	3 / 1171	Fetal_EnhP
5	0.2	2 / 681	Overlap_fetal_midbrain_EnhP
6	0.3	15 / 9504	Overlap_fetal_midbrain_K9K27me3
7	0.3	2 / 818	Mid_Frontal_Lobe_Het
8	0.4	1 / 328	Fetal_Het
9	0.5	1 / 465	Mid_Frontal_Lobe_TxTrans
10	0.5	14 / 9815	Overlap_fetal_midbrain_ReprPC
11	0.5	4 / 2654	Fetal_Quies
12	0.7	4 / 3164	Mid_Frontal_Lobe_ZNF
13	0.7	13 / 9917	Overlap_fetal_midbrain_ReprPCWk
14	0.7	2 / 1728	Fetal_ReprPCWk
15	0.7	3 / 2709	Mid_Frontal_Lobe_HetRpts

Chr

Rank	p−value	#in/all	Geneset
1	0.03	4 / 836	Chr 8
2	0.13	4 / 1411	Chr 11
3	0.33	3 / 1467	Chr 19
4	0.35	2 / 902	Chr 4
5	0.38	1 / 342	Chr 18
6	0.43	2 / 1060	Chr 5
7	0.50	2 / 1211	Chr 6
8	0.51	2 / 1217	Chr 3
9	0.53	1 / 536	Chr 22
10	0.55	2 / 1318	Chr 17
11	0.58	1 / 619	Chr 20
12	0.74	1 / 954	Chr 9
13	0.74	1 / 959	Chr 16
14	0.75	1 / 994	Chr X
15	0.81	1 / 1160	Chr 12

Glio

Rank	p−value	#in/all	Geneset
1	0.02	1 / 12	Phillips PN up vs MES & Prolif
2	0.05	1 / 35	WIRTH_PN subtype
3	0.05	1 / 35	Colman_survival_associated
4	0.11	3 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
5	0.12	1 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
6	0.13	1 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
7	0.20	1 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.23	1 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	0.31	4 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
10	0.35	1 / 315	Up
11	0.36	1 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
12	0.42	1 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
13	0.45	3 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
14	0.68	1 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
15	1.00	0 / 15	VERHAAK_CL subtype

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 94	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 10	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 17	DUMEAUX_High bmi enriched genes
11	1	0 / 31	DUMEAUX_Fasting enriched genes
12	1	0 / 147	Homuth_BMI−associated−genes_UP
13	1	0 / 211	Homuth_BMI−associated−genes_DN
14	1	0 / 18	Huan_blood−pressure_SBP−signature
15	1	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.02	1 / 13	oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as
2	0.02	1 / 15	structural constituent of eye lens
3	0.02	1 / 17	lysine−acetylated histone binding
4	0.02	1 / 18	protein disulfide isomerase activity
5	0.02	1 / 18	telomeric DNA binding
6	0.03	1 / 20	Wnt−activated receptor activity
7	0.03	1 / 24	fatty−acyl−CoA binding
8	0.04	1 / 30	insulin receptor binding
9	0.04	1 / 30	Wnt−protein binding
10	0.06	1 / 47	chromatin DNA binding
11	0.07	1 / 54	flavin adenine dinucleotide binding
12	0.08	1 / 64	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
13	0.10	1 / 77	electron carrier activity
14	0.14	1 / 112	Rab GTPase binding
15	0.21	4 / 1717	metal ion binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.2	4 / 1753	HEBENSTREIT_low expression TF
2	0.3	6 / 3348	ICGC_BatfPcr1_targets
3	0.3	3 / 1478	ICGC_Myc_targets
4	0.4	9 / 5961	ICGC_Pol24_targets
5	0.5	4 / 2497	ICGC_Bcl11_targets
6	0.5	8 / 5466	ICGC_Nficsc81335_targets
7	0.5	2 / 1231	KIM_MYC targets
8	0.5	6 / 4131	ICGC_Nfatc1_targets
9	0.5	7 / 4881	ICGC_Atf2_targets
10	0.6	7 / 5067	ICGC_Taf1_targets
11	0.6	3 / 2133	ICGC_Mef2_targets
12	0.6	9 / 6578	ICGC_Pou2_targets
13	0.6	6 / 4468	ICGC_Egr1_targets
14	0.6	8 / 5984	ICGC_Mta3_targets
15	0.6	1 / 733	ICGC_Atf3_targets

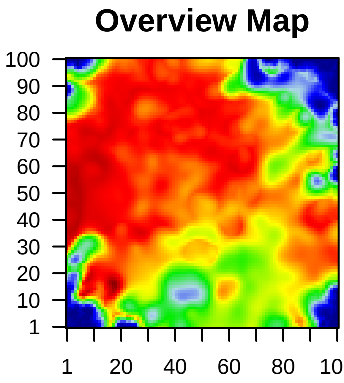
Underexpression Spots

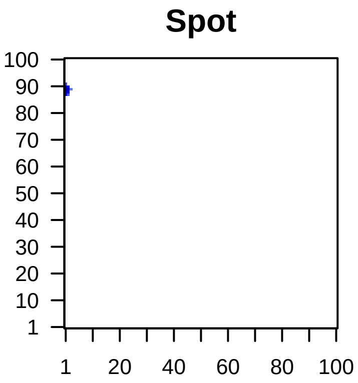
Spot Summary: f

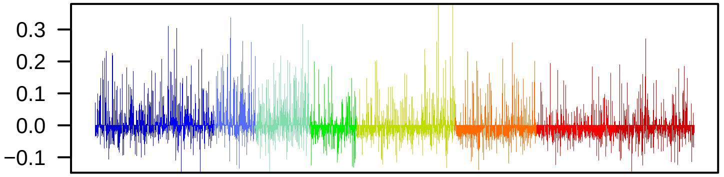
\# metagenes = 10
\# genes = 259

<r> metagenes = 0.99
<r> genes = 0.29
beta: r2= 7.38 / log p= −Inf

\# samples with spot = 186 (5.5 %)
A * : 25 (7.3 %)
A C * : 26 (7.9 %)
A C F * : 32 (13.6 %)
A F * : 30 (9.7 %)
C F * : 6 (2.3 %)
F * : 22 (4 %)
F J * : 22 (4.8 %)
J * : 8 (1.8 %)
N * : 15 (3.4 %)





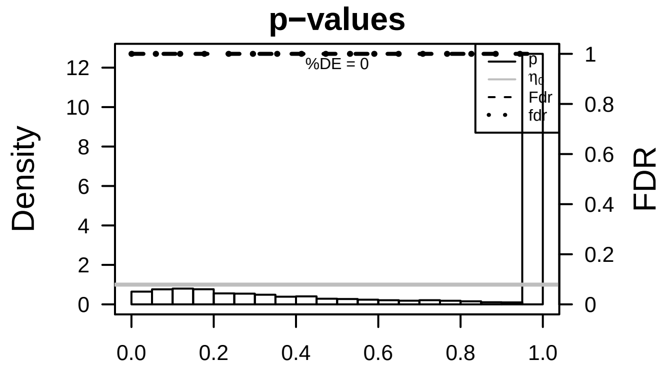


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166406	0.86	−0.57	0.47	ERGIC1	endoplasmic reticulum−golgi intermediate compartment 1 [So
2	ILMN_324781	0.75	−0.41	0.31		RAS p21 protein activator 4CD, pseudogene [Source:HGNC S
3	ILMN_168507	0.72	−0.49	0.28	TELO2	telomere maintenance 2 [Source:HGNC Symbol;Acc:HGNC:2
4	ILMN_326869	0.72	−0.54	0.25		
5	ILMN_330822	0.69	−0.43	0.34	MIR1282	microRNA 1282 [Source:HGNC Symbol;Acc:HGNC:35360]
6	ILMN_324665	0.68	−0.42	0.33		
7	ILMN_186927	0.68	−0.4	0.32		
8	ILMN_165761	0.65	−0.35	0.71	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
9	ILMN_180048	0.61	−0.38	0.36	CT47B1	cancer/testis antigen family 47, member B1 [Source:HGNC S
10	ILMN_224967	0.57	−0.36	0.66	LSR	lipolysis stimulated lipoprotein receptor [Source:HGNC Symb
11	ILMN_328824	0.57	−0.43	0.53		
12	ILMN_183964	0.56	−0.31	0.64	LINC00323	long intergenic non−protein coding RNA 323 [Source:HGNC S
13	ILMN_176111	0.56	−0.35	0.66	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
14	ILMN_178092	0.56	−0.32	0.68	SLC43A1	solute carrier family 43 member 1 [Source:HGNC Symbol;Acc
15	ILMN_190200	0.55	−0.35	0.43		
16	ILMN_165712	0.55	−0.34	0.39	PTPRU	protein tyrosine phosphatase, receptor type U [Source:HGNC
17	ILMN_324766	0.55	−0.36	0.7		
18	ILMN_181169	0.54	−0.31	0.6	FDXR	ferredoxin reductase [Source:HGNC Symbol;Acc:HGNC:3642
19	ILMN_168140	0.53	−0.31	0.61		
20	ILMN_235880	0.53	−0.3	0.68	PLEKHG5	pleckstrin homology and RhoGEF domain containing G5 [Sou

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	19 / 789	Colon	TxEnhG2_Colon
2	3e−05	5 / 46	BP	vesicle fusion
3	1e−04	3 / 13	GSEA	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
4	3e−04	107 / 10779	Colon	Enh_Colon
5	3e−04	3 / 18	BP	B cell homeostasis
6	4e−04	2 / 4	GSEA	COURTOIS_SENESCENCE_TRIGGERS
7	4e−04	18 / 933	Refer	PROTEINATLAS_adrenal gland
8	4e−04	37 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
9	5e−04	3 / 21	GSEA	PID_HEDGEHOG_2PATHWAY
10	6e−04	78 / 7354	Colon	TssF_Colon
11	8e−04	37 / 2810	Colon	EnhA_Colon
12	9e−04	4 / 55	BP	cellular response to growth factor stimulus
13	1e−03	89 / 8818	MF	protein binding
14	1e−03	40 / 3164	Brain	Mid_Frontal_Lobe_ZNF
15	1e−03	4 / 59	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
16	1e−03	3 / 27	GSEA	MATZUK_MALE_REPRODUCTION_SERTOLI
17	1e−03	8 / 268	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
18	1e−03	9 / 336	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
19	1e−03	3 / 28	BP	cellular response to nerve growth factor stimulus
20	1e−03	3 / 28	GSEA	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
21	1e−03	3 / 28	GSEA	JAZAG_TGFB1_SIGNALING_DN
22	1e−03	6 / 156	BP	negative regulation of gene expression
23	1e−03	44 / 3639	Chrom	1_TssP_Fibroblasts
24	2e−03	2 / 8	GSEA	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
25	2e−03	48 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
26	2e−03	10 / 425	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
27	2e−03	3 / 32	miRN	hsa−miR−1229
28	2e−03	28 / 2028	Chrom	4_TxTrans_Melanocytes
29	3e−03	2 / 10	BP	negative regulation of cell size
30	3e−03	2 / 10	BP	negative regulation of interleukin−10 production
31	3e−03	18 / 1118	Refer	PROTEINATLAS_placenta
32	3e−03	61 / 5699	Chrom	6_EnhG_Melanocytes
33	3e−03	3 / 37	BP	positive regulation of nitric oxide biosynthetic process
34	3e−03	3 / 37	GSEA	BIOCARTA_IL2RB_PATHWAY
35	3e−03	7 / 244	GSEA	ROZANOV_MMP14_TARGETS_UP
36	3e−03	2 / 11	BP	cytoplasmic sequestering of transcription factor
37	3e−03	2 / 11	BP	male sex determination
38	3e−03	6 / 185	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
39	3e−03	11 / 539	CC	Golgi membrane
40	3e−03	3 / 39	MF	clathrin binding



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 142	HORVATH_aging_genes meth UP
2	0.4	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.6	1 / 111	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	3 / 125	PanCan_CC+Apop_geneset_nanostring
2	0.11	3 / 150	PanCan_MAPK_geneset_nanostring
3	0.12	1 / 16	GENTLES_modul11
4	0.13	2 / 82	PanCan_JAK−ST_geneset_nanostring
5	0.14	0 / 14	LIU_PROSTATE_CANCER_UP
6	0.16	2 / 91	PanCan_TXmisReg_geneset_nanostring
7	0.28	2 / 136	PanCan_RAS_geneset_nanostring
8	0.30	1 / 46	PanCan_DNARepair_geneset_nanostring
9	0.33	0 / 13	RHODES_CANCER_META_SIGNATURE
10	0.44	2 / 193	PanCan_PI3K_geneset_nanostring
11	0.59	4 / 527	Lembcke_Normal vs Adenoma
12	0.60	1 / 117	PanCan_Driver_Gene_geneset_nanostring
13	0.62	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	0.63	4 / 554	Lembcke_Colonic Inflammation
15	0.67	0 / 15	LIU_PROSTATE_CANCER_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.001	44 / 3639	1_TssP_Fibroblasts
2	0.002	28 / 2028	4_TxTrans_Melanocytes
3	0.003	61 / 5699	6_EnhG_Melanocytes
4	0.005	62 / 5956	3_TssF_Neuronal_Progenitor
5	0.007	36 / 3068	8_EnhP_Fibroblasts
6	0.013	17 / 1206	6_EnhG_Neuronal_Progenitor
7	0.028	105 / 11836	3_TssF_Melanocytes
8	0.028	105 / 11847	7_Enh_Neuronal_Progenitor
9	0.036	29 / 2660	8_EnhP_Melanocytes
10	0.037	21 / 1789	8_EnhP_Neuronal_Progenitor
11	0.055	35 / 3450	4_TxTrans_Fibroblasts
12	0.058	41 / 4169	10_ReprPC_Fibroblasts
13	0.067	111 / 12983	2_TssA_Neuronal_Progenitor
14	0.070	35 / 3523	1_TssP_Melanocytes
15	0.077	34 / 3438	10_ReprPC_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 13	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
2	4e−04	2 / 4	COURTOIS_SENESCENCE_TRIGGERS
3	5e−04	3 / 21	PID_HEDGEHOG_2PATHWAY
4	1e−03	4 / 59	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
5	1e−03	3 / 27	MATZUK_MALE_REPRODUCTION_SERTOLI
6	1e−03	8 / 268	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
7	1e−03	9 / 336	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
8	1e−03	3 / 28	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
9	1e−03	3 / 28	JAZAG_TGFB1_SIGNALING_DN
10	2e−03	2 / 8	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
11	2e−03	10 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
12	3e−03	3 / 37	BIOCARTA_IL2RB_PATHWAY
13	3e−03	7 / 244	ROZANOV_MMP14_TARGETS_UP
14	3e−03	6 / 185	HOLLMANN_APOPTOSIS_VIA_CD40_UP
15	3e−03	3 / 39	PID_HNF3B_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.03	8 / 455	SPANG_CD40 6hrs DN
2	0.09	50 / 5384	HOPP_Repressed
3	0.09	3 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
4	0.09	4 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
5	0.09	3 / 138	WIRTH_lymphoma937_spot G
6	0.10	2 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
7	0.11	4 / 232	WIRTH_lymphoma937_spot B
8	0.11	1 / 15	Subero_B−ALL_hypo_meth
9	0.15	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
10	0.16	4 / 272	SPANG_IL21 DN
11	0.16	1 / 23	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
12	0.17	2 / 94	Sha_BL UP
13	0.18	64 / 7448	HOPP_Strong_enhancer
14	0.19	2 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
15	0.20	2 / 105	WIRTH_lymphoma937_spot MM

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 30	Systemic lupus erythematosus (SLE)
2	0.4	1 / 73	Stroke, susceptibility to
3	0.4	1 / 76	Muscular
4	0.7	1 / 142	Lung cancer
5	1.0	0 / 7	Thyroid carcinoma, papillary
6	1.0	0 / 123	Pancreatic cancer
7	1.0	0 / 68	Glioblastoma multiforme, somatic
8	1.0	0 / 63	Gastrointestinal
9	1.0	0 / 3	Pituitary adenoma
10	1.0	0 / 116	Cancer
11	1.0	0 / 95	Colorectal cancer
12	1.0	0 / 2	Adenomas, multiple colorectal
13	1.0	0 / 124	Prostate cancer
14	1.0	0 / 48	Alzheimer disease, susceptibility to
15	1.0	0 / 7	Schizophrenia, susceptibility to

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−04	18 / 933	PROTEINATLAS_adrenal gland
2	3e−03	18 / 1118	PROTEINATLAS_placenta
3	5e−03	15 / 912	PROTEINATLAS_fallopian tube
4	1e−02	17 / 1173	PROTEINATLAS_rectum
5	1e−02	15 / 1003	PROTEINATLAS_appendix
6	2e−02	16 / 1167	PROTEINATLAS_gallbladder
7	2e−02	17 / 1268	PROTEINATLAS_colon
8	2e−02	2 / 30	VAQUERIZAS_Smooth muscle_TF
9	2e−02	15 / 1097	PROTEINATLAS_kidney
10	3e−02	16 / 1239	PROTEINATLAS_testis
11	3e−02	12 / 850	PROTEINATLAS_skin
12	3e−02	11 / 759	PROTEINATLAS_epididymis
13	4e−02	13 / 960	PROTEINATLAS_cerebellum
14	4e−02	13 / 963	PROTEINATLAS_pancreas
15	4e−02	15 / 1176	PROTEINATLAS_duodenum

BP

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 46	vesicle fusion
2	3e−04	3 / 18	B cell homeostasis
3	9e−04	4 / 55	cellular response to growth factor stimulus
4	1e−03	3 / 28	cellular response to nerve growth factor stimulus
5	1e−03	6 / 156	negative regulation of gene expression
6	3e−03	2 / 10	negative regulation of cell size
7	3e−03	2 / 10	negative regulation of interleukin−10 production
8	3e−03	3 / 37	positive regulation of nitric oxide biosynthetic process
9	3e−03	2 / 11	cytoplasmic sequestering of transcription factor
10	3e−03	2 / 11	male sex determination
11	4e−03	2 / 12	trophoblast giant cell differentiation
12	4e−03	2 / 13	positive regulation of monocyte chemotaxis
13	4e−03	2 / 13	striated muscle cell differentiation
14	5e−03	2 / 14	positive regulation of glycogen biosynthetic process
15	5e−03	3 / 45	intrinsic apoptotic signaling pathway in response to DNA damage

CC

Rank	p−value	#in/all	Geneset
1	0.003	11 / 539	Golgi membrane
2	0.003	14 / 788	endoplasmic reticulum membrane
3	0.008	13 / 775	endoplasmic reticulum
4	0.014	4 / 119	vesicle
5	0.014	3 / 65	caveola
6	0.018	2 / 27	intrinsic component of plasma membrane
7	0.022	39 / 3662	plasma membrane
8	0.029	5 / 221	endosome
9	0.034	16 / 1252	integral component of plasma membrane
10	0.041	4 / 167	external side of plasma membrane
11	0.055	22 / 1979	membrane
12	0.057	2 / 50	SNARE complex
13	0.066	4 / 196	postsynaptic membrane
14	0.068	2 / 55	synaptic vesicle membrane
15	0.070	4 / 200	nuclear membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−05	19 / 789	TxEnhG2_Colon
2	3e−04	107 / 10779	Enh_Colon
3	6e−04	78 / 7354	TssF_Colon
4	8e−04	37 / 2810	EnhA_Colon
5	6e−03	3 / 47	Marisa_CRC−cluster−f
6	7e−03	34 / 2845	TxEnhG1_Colon
7	9e−03	17 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	2e−02	60 / 6138	TssD2_Colon
9	4e−02	31 / 2894	TssP_Colon
10	4e−02	15 / 1186	HetRpts_Colon
11	5e−02	85 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	8e−02	7 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	1e−01	20 / 1895	EnhP_Colon
14	1e−01	83 / 9555	TssA_Colon
15	1e−01	9 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN

HM

Rank	p−value	#in/all	Geneset
1	0.004	4 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
2	0.040	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.056	4 / 185	HALLMARK_P53_PATHWAY
4	0.057	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.091	3 / 137	HALLMARK_UV_RESPONSE_UP
6	0.170	3 / 183	HALLMARK_APICAL_JUNCTION
7	0.174	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	0.181	3 / 189	HALLMARK_HYPOXIA
9	0.227	1 / 33	HALLMARK_ANGIOGENESIS
10	0.227	2 / 116	HALLMARK_SPERMATOGENESIS
11	0.273	2 / 132	HALLMARK_UV_RESPONSE_DN
12	0.290	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
13	0.399	2 / 177	HALLMARK_KRAS_SIGNALING_DN
14	0.405	2 / 179	HALLMARK_G2M_CHECKPOINT
15	0.421	2 / 185	HALLMARK_MTORC1_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	1.00	0 / 30	Hugo_melanoma−all−MET_UP
3	1.00	0 / 54	Hugo_melanoma−all−MET_DN
4	1.00	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 32	hsa−miR−1229
2	0.018	2 / 27	hsa−miR−1292
3	0.037	2 / 39	hsa−miR−484
4	0.040	3 / 97	hsa−miR−125a−3p
5	0.042	2 / 42	hsa−miR−885−3p
6	0.043	3 / 100	hsa−miR−147
7	0.059	4 / 188	hsa−miR−548d−3p
8	0.078	3 / 128	hsa−miR−335
9	0.079	2 / 60	hsa−miR−1200
10	0.082	1 / 11	hsa−miR−604
11	0.089	1 / 12	hsa−miR−652
12	0.096	1 / 13	hsa−miR−1249
13	0.096	1 / 13	hsa−miR−452*
14	0.103	1 / 14	hsa−miR−574−3p
15	0.105	2 / 71	hsa−miR−1266

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	4e−04	37 / 2709	Mid_Frontal_Lobe_HetRpts
2	1e−03	40 / 3164	Mid_Frontal_Lobe_ZNF
3	2e−03	48 / 4112	Mid_Frontal_Lobe_ReprPC
4	5e−03	14 / 818	Mid_Frontal_Lobe_Het
5	2e−02	18 / 1360	Mid_Frontal_Lobe_TssP
6	3e−02	6 / 304	Mid_Frontal_Lobe_TssA
7	5e−02	85 / 9504	Overlap_fetal_midbrain_K9K27me3
8	6e−02	21 / 1893	Overlap_fetal_midbrain_TssF
9	6e−02	20 / 1784	Mid_Frontal_Lobe_ReprPCWk
10	7e−02	7 / 465	Mid_Frontal_Lobe_TxTrans
11	1e−01	11 / 924	Mid_Frontal_Lobe_TssF
12	1e−01	16 / 1506	Mid_Frontal_Lobe_Quies
13	2e−01	12 / 1119	Overlap_fetal_midbrain_TssA
14	2e−01	17 / 1728	Fetal_ReprPCWk
15	2e−01	87 / 10430	Overlap_fetal_midbrain_Quies

Chr

Rank	p−value	#in/all	Geneset
1	0.09	14 / 1211	Chr 6
2	0.14	14 / 1318	Chr 17
3	0.19	12 / 1160	Chr 12
4	0.21	10 / 959	Chr 16
5	0.24	10 / 994	Chr X
6	0.25	14 / 1467	Chr 19
7	0.30	11 / 1170	Chr 7
8	0.39	3 / 289	Chr 21
9	0.44	19 / 2323	Chr 1
10	0.49	1 / 87	Chr Y
11	0.55	6 / 768	Chr 14
12	0.55	7 / 902	Chr 4
13	0.75	2 / 342	Chr 18
14	0.75	6 / 954	Chr 9
15	0.77	9 / 1411	Chr 11

Glio

Rank	p−value	#in/all	Geneset
1	0.008	7 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
2	0.021	4 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	0.029	3 / 86	laffaire_hypermeth_LGG_vs_control
4	0.046	1 / 6	laffaire_hypometh_LGG_vs_control
5	0.054	3 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
6	0.057	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	0.089	1 / 12	Mukasa_UP_in_Astroglioma
8	0.096	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
9	0.106	3 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	0.110	1 / 15	VERHAAK_PN subtype
11	0.124	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
12	0.124	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
13	0.124	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
14	0.131	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	0.137	1 / 19	KIM deleted & downregulated in LTS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 94	DUMEAUX_Smoking enriched genes
2	0.3	2 / 147	Homuth_BMI−associated−genes_UP
3	0.5	2 / 211	Homuth_BMI−associated−genes_DN
4	1.0	0 / 10	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 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.001	89 / 8818	protein binding
2	0.003	3 / 39	clathrin binding
3	0.004	2 / 12	insulin−like growth factor I binding
4	0.008	3 / 52	SNARE binding
5	0.008	2 / 18	peroxidase activity
6	0.011	2 / 21	insulin−like growth factor binding
7	0.012	3 / 62	syntaxin binding
8	0.016	2 / 25	protein phosphatase 2A binding
9	0.020	7 / 350	protein kinase binding
10	0.020	2 / 28	transmembrane receptor protein tyrosine kinase activity
11	0.023	3 / 78	phospholipid binding
12	0.032	2 / 36	protein complex scaffold
13	0.033	2 / 37	SNAP receptor activity
14	0.036	4 / 160	protein C−terminus binding
15	0.040	2 / 41	calcium−dependent phospholipid binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.02	25 / 2087	ICGC_Cebpbsc150_targets
2	0.03	37 / 3507	ICGC_Rad21_targets
3	0.03	20 / 1669	ICGC_P300_targets
4	0.04	1 / 5	MYC_TFs
5	0.06	15 / 1231	KIM_MYC targets
6	0.07	28 / 2704	ICGC_Pbx3_targets
7	0.07	32 / 3194	ICGC_Irf4_targets
8	0.10	48 / 5188	ICGC_Ebfsc137065_targets
9	0.15	48 / 5383	ICGC_Sp1_targets
10	0.16	15 / 1452	ICGC_Six5_targets
11	0.16	24 / 2497	ICGC_Bcl11_targets
12	0.17	15 / 1466	ICGC_NrsfPcr1_targets
13	0.17	26 / 2759	ICGC_Bcl3_targets
14	0.19	15 / 1498	ICGC_Ets1_targets
15	0.21	8 / 733	ICGC_Atf3_targets

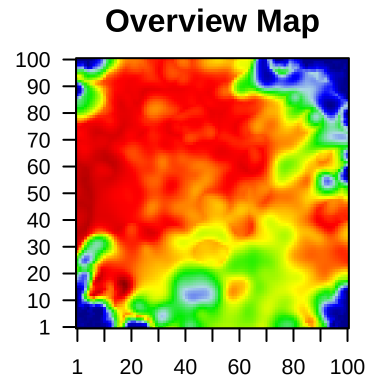
Underexpression Spots

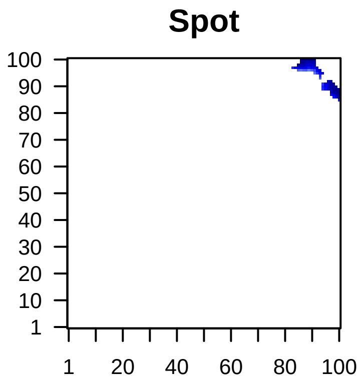
Spot Summary: g

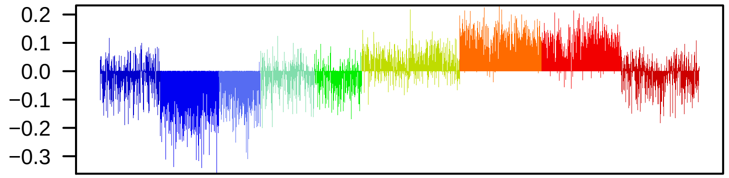
metagenes = 76
genes = 975

<r> metagenes = 0.76
<r> genes = 0.31
beta: r2= 34.86 / log p= −Inf

samples with spot = 351 (10.4 %)
A * : 1 (0.3 %)
A F * : 1 (0.3 %)
F * : 16 (2.9 %)
F J * : 187 (40.4 %)
J * : 146 (32.7 %)





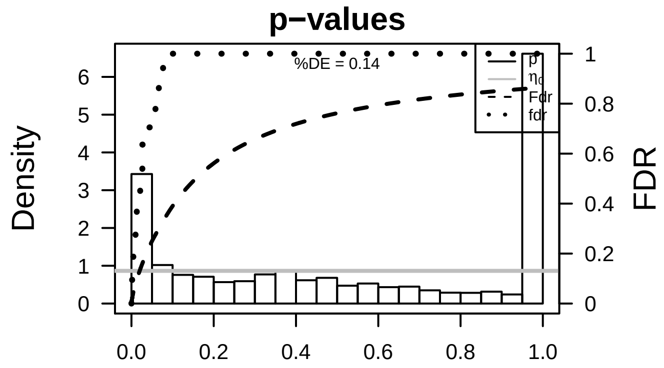


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_206606	2.72	−3.26	0.1	HLA−DRB6	major histocompatibility complex, class II, DR beta 6 (pseudo
2	ILMN_179817	2.09	−1.22	0.09	CHURC1	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
3	ILMN_174314	1.89	−2.07	0.13	ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Sym
4	ILMN_178270	1.6	−1.28	0.27		
5	ILMN_169169	1.35	−1.04	0.43	FCRL3	Fc receptor like 3 [Source:HGNC Symbol;Acc:HGNC:18506]
6	ILMN_236621	1.34	−1.34	0.41	CD79B	CD79b molecule [Source:HGNC Symbol;Acc:HGNC:1699]
7	ILMN_224608	1.32	−1.59	0.09	CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis
8	ILMN_178543	1.28	−0.95	0.31	CD79B	CD79b molecule [Source:HGNC Symbol;Acc:HGNC:1699]
9	ILMN_236853	1.27	−1.19	0.34	IL32	interleukin 32 [Source:HGNC Symbol;Acc:HGNC:16830]
10	ILMN_236604	1.22	−0.87	0.45	ITM2C	integral membrane protein 2C [Source:HGNC Symbol;Acc:HG
11	ILMN_166245	1.21	−0.72	0.29	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HG
12	ILMN_168045	1.19	−0.91	0.41	ITM2C	integral membrane protein 2C [Source:HGNC Symbol;Acc:HG
13	ILMN_177262	1.14	−1.22	0.39	NSG1	Neuron−specific protein family member 1 [Source:UniProtKB
14	ILMN_165907	1.12	−0.85	0.47	HLA−DOA	major histocompatibility complex, class II, DO alpha [Source:H
15	ILMN_232550	1.11	−0.89	0.4	BCAS4	breast carcinoma amplified sequence 4 [Source:HGNC Symb
16	ILMN_167241	1.08	−0.97	0.45	CORO1B	coronin 1B [Source:HGNC Symbol;Acc:HGNC:2253]
17	ILMN_177801	1.07	−1	0.52	IL32	interleukin 32 [Source:HGNC Symbol;Acc:HGNC:16830]
18	ILMN_174525	1.06	−0.75	0.39	CXXC5	CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26
19	ILMN_173979	1.05	−0.97	0.49	CD3E	CD3e molecule [Source:HGNC Symbol;Acc:HGNC:1674]
20	ILMN_166133	1.03	−0.8	0.23	SPTBN1	spectrin beta, non−erythrocytic 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−89	621 / 9555	Colon	TssA_Colon
2	4e−85	529 / 7275	Lympl	HOPP_Txn_elongation
3	6e−78	554 / 8226	Lympl	HOPP_Active_promoter
4	1e−71	424 / 5356	Lympl	HOPP_Txn_transition
5	5e−70	598 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
6	1e−69	652 / 11455	Chror	2_TssA_Fibroblasts
7	5e−69	677 / 12298	Chror	2_TssA_Melanocytes
8	2e−63	575 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
9	5e−63	558 / 9054	Colon	Tx_Colon
10	7e−60	534 / 8568	Colon	TxWk_Colon
11	3e−58	535 / 8678	Colon	Quies3_Colon
12	4e−58	679 / 12983	Chror	2_TssA_Neuronal_Progenitor
13	4e−55	532 / 8771	Chror	5_Tx_Melanocytes
14	2e−52	501 / 8098	Lympl	HOPP_Weak_promoter
15	5e−50	451 / 6970	Chror	5_Tx_Neuronal_Progenitor
16	6e−49	484 / 7854	Chror	5_Tx_Fibroblasts
17	2e−47	595 / 10999	Colon	TssWk_Colon
18	2e−45	177 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
19	1e−43	394 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
20	2e−43	614 / 11836	Chror	3_TssF_Melanocytes
21	4e−35	528 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
22	3e−34	544 / 10430	Brain	Overlap_fetal_midbrain_Quies
23	1e−32	618 / 12741	Chror	7_Enh_Melanocytes
24	6e−32	605 / 12393	Chror	15_Quies_Neuronal_Progenitor
25	5e−31	135 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
26	1e−29	322 / 5067	TF	ICGC_Taf1_targets
27	9e−29	414 / 7354	Colon	TssF_Colon
28	8e−28	160 / 1797	GSEA	PILON_KLF1_TARGETS_DN
29	6e−27	465 / 8818	MF	protein binding
30	1e−26	136 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
31	2e−26	411 / 7448	Lympl	HOPP_Strong_enhancer
32	3e−25	109 / 1013	MF	poly(A) RNA binding
33	1e−23	538 / 11130	Chror	15_Quies_Melanocytes
34	6e−23	110 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
35	1e−22	458 / 8990	Chror	15_Quies_Fibroblasts
36	7e−22	92 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
37	8e−22	326 / 5699	Chror	6_EnhG_Melanocytes
38	2e−21	315 / 5466	TF	ICGC_Nficsc81335_targets
39	3e−21	375 / 6959	Lympl	HOPP_Weak_enhancer
40	1e−20	437 / 8613	Chror	7_Enh_Fibroblasts



Aging

Rank	p−value	#in/all	Geneset
1	0.02	9 / 111	HORVATH_aging_genes meth DOWN
2	0.75	4 / 142	HORVATH_aging_genes meth UP
3	0.88	1 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 13	GENTLES_modul6
2	1e−03	4 / 14	GENTLES_modul1
3	4e−03	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	7e−03	3 / 12	LIU_BREAST_CANCER
5	1e−02	1 / 13	RHODES_CANCER_META_SIGNATURE
6	1e−02	19 / 301	SPANG_BCL6−index2
7	1e−02	3 / 15	WOLFER_overlap genes
8	2e−02	3 / 16	GENTLES_modul7
9	4e−02	2 / 9	GENTLES_modul5
10	4e−02	5 / 54	KUIPER_MM poor survival
11	5e−02	4 / 38	KUIPER_MM good survival
12	5e−02	4 / 39	ZHANG_MM up
13	5e−02	6 / 76	PanCan_Wnt_geneset_nanostring
14	7e−02	27 / 554	Lembcke_Colonic Inflammation
15	8e−02	2 / 13	GENTLES_modul18

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−69	652 / 11455	2_TssA_Fibroblasts
2	5e−69	677 / 12298	2_TssA_Melanocytes
3	4e−58	679 / 12983	2_TssA_Neuronal_Progenitor
4	4e−55	532 / 8771	5_Tx_Melanocytes
5	5e−50	451 / 6970	5_Tx_Neuronal_Progenitor
6	6e−49	484 / 7854	5_Tx_Fibroblasts
7	2e−43	614 / 11836	3_TssF_Melanocytes
8	1e−32	618 / 12741	7_Enh_Melanocytes
9	6e−32	605 / 12393	15_Quies_Neuronal_Progenitor
10	1e−23	538 / 11130	15_Quies_Melanocytes
11	1e−22	458 / 8990	15_Quies_Fibroblasts
12	8e−22	326 / 5699	6_EnhG_Melanocytes
13	1e−20	437 / 8613	7_Enh_Fibroblasts
14	8e−20	472 / 9635	3_TssF_Fibroblasts
15	3e−08	500 / 11847	7_Enh_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−31	135 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	8e−28	160 / 1797	PILON_KLF1_TARGETS_DN
3	1e−26	136 / 1417	PUJANA_BRCA1_PCC_NETWORK
4	6e−23	110 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
5	7e−22	92 / 841	ACEVEDO_LIVER_CANCER_UP
6	2e−17	106 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	9e−17	76 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
8	3e−16	79 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
9	3e−16	66 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
10	3e−15	45 / 317	HSIAO_HOUSEKEEPING_GENES
11	3e−15	58 / 500	KIM_ALL_DISORDERS_CALB1_CORR_UP
12	4e−15	50 / 388	SHEN_SMARCA2_TARGETS_UP
13	5e−15	77 / 811	LEE_BMP2_TARGETS_DN
14	7e−15	68 / 666	BENPORATH_MYC_MAX_TARGETS
15	3e−14	80 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−85	529 / 7275	HOPP_Txn_elongation
2	6e−78	554 / 8226	HOPP_Active_promoter
3	1e−71	424 / 5356	HOPP_Txn_transition
4	2e−52	501 / 8098	HOPP_Weak_promoter
5	2e−26	411 / 7448	HOPP_Strong_enhancer
6	3e−21	375 / 6959	HOPP_Weak_enhancer
7	3e−20	356 / 6559	HOPP_Weak_txn
8	3e−11	88 / 1169	SPANG_BCR DN
9	7e−10	34 / 283	TARTE_Plasmablast signature
10	2e−08	85 / 1270	SPANG_BCR UP
11	4e−08	59 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
12	3e−07	57 / 777	WIRTH_lymphoma937_spot D
13	3e−06	37 / 455	SPANG_CD40 6hrs DN
14	6e−06	14 / 94	Sha_BL UP
15	1e−05	17 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−12	95 / 1239	PROTEINATLAS_testis
2	7e−12	87 / 1118	PROTEINATLAS_placenta
3	9e−12	46 / 412	WIRTH_Immune system
4	1e−11	81 / 1016	PROTEINATLAS_cerebral cortex
5	2e−11	83 / 1063	PROTEINATLAS_tonsil
6	5e−11	75 / 933	PROTEINATLAS_adrenal gland
7	7e−11	76 / 960	PROTEINATLAS_cerebellum
8	8e−11	87 / 1173	PROTEINATLAS_rectum
9	9e−11	83 / 1097	PROTEINATLAS_kidney
10	2e−10	63 / 740	PROTEINATLAS_esophagus
11	5e−10	86 / 1194	PROTEINATLAS_stomach
12	1e−09	82 / 1138	PROTEINATLAS_small intestine
13	1e−09	21 / 119	Chaussabel_2,8_T−cells
14	1e−09	60 / 724	PROTEINATLAS_lymph node
15	1e−09	65 / 816	PROTEINATLAS_endometrium

BP

Rank	p−value	#in/all	Geneset
1	2e−07	24 / 196	mRNA splicing, via spliceosome
2	2e−06	26 / 255	viral process
3	6e−06	19 / 163	rRNA processing
4	1e−05	20 / 184	translation
5	1e−05	16 / 126	T cell receptor signaling pathway
6	1e−04	8 / 43	T cell activation
7	3e−04	6 / 26	exonucleolytic nuclear−transcribed mRNA catabolic process involved in deade
8	4e−04	9 / 63	T cell costimulation
9	5e−04	6 / 29	B cell receptor signaling pathway
10	5e−04	31 / 457	regulation of transcription from RNA polymerase II promoter
11	6e−04	4 / 12	anterograde synaptic vesicle transport
12	6e−04	4 / 12	maturation of LSU−rRNA
13	8e−04	9 / 69	mitochondrial translational elongation
14	8e−04	15 / 163	protein polyubiquitination
15	8e−04	6 / 32	tRNA aminoacylation for protein translation

CC

Rank	p−value	#in/all	Geneset
1	3e−18	175 / 2535	nucleoplasm
2	4e−18	112 / 1304	mitochondrion
3	3e−15	187 / 2979	cytosol
4	6e−14	136 / 1979	membrane
5	3e−13	68 / 721	nucleolus
6	4e−12	44 / 374	mitochondrial inner membrane
7	4e−12	255 / 4828	nucleus
8	1e−11	253 / 4822	cytoplasm
9	7e−11	149 / 2464	extracellular exosome
10	6e−08	20 / 134	myelin sheath
11	2e−06	18 / 138	mitochondrial outer membrane
12	3e−05	6 / 18	telomerase holoenzyme complex
13	4e−05	25 / 287	mitochondrial matrix
14	7e−05	6 / 21	U4/U6 x U5 tri−snRNP complex
15	1e−04	11 / 78	catalytic step 2 spliceosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−89	621 / 9555	TssA_Colon
2	5e−63	558 / 9054	Tx_Colon
3	7e−60	534 / 8568	TxWk_Colon
4	3e−58	535 / 8678	Quies3_Colon
5	2e−47	595 / 10999	TssWk_Colon
6	2e−45	177 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	9e−29	414 / 7354	TssF_Colon
8	1e−17	505 / 10779	Enh_Colon
9	2e−14	112 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	2e−13	75 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	2e−12	279 / 5373	EnhWk1_Colon
12	4e−11	77 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
13	2e−10	300 / 6138	TssD2_Colon
14	2e−09	78 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	2e−09	211 / 4034	TssD1_Colon

HM

Rank	p−value	#in/all	Geneset
1	7e−14	31 / 170	HALLMARK_MYC_TARGETS_V1
2	5e−11	27 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	2e−04	14 / 130	HALLMARK_DNA_REPAIR
4	1e−03	16 / 185	HALLMARK_MTORC1_SIGNALING
5	3e−03	12 / 132	HALLMARK_UV_RESPONSE_DN
6	4e−03	10 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	4e−03	12 / 138	HALLMARK_FATTY_ACID_METABOLISM
8	5e−03	14 / 177	HALLMARK_MITOTIC_SPINDLE
9	6e−03	13 / 162	HALLMARK_ALLOGRAFT_REJECTION
10	9e−03	13 / 173	HALLMARK_E2F_TARGETS
11	1e−02	6 / 54	HALLMARK_MYC_TARGETS_V2
12	2e−02	8 / 91	HALLMARK_PEROXISOME
13	2e−02	13 / 186	HALLMARK_IL2_STAT5_SIGNALING
14	2e−02	8 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
15	2e−02	12 / 176	HALLMARK_ADIPOGENESIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.8	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.9	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−09	46 / 493	hsa−miR−103
2	1e−08	46 / 516	hsa−miR−15a
3	2e−08	43 / 467	hsa−miR−195
4	2e−08	44 / 491	hsa−miR−107
5	3e−08	41 / 441	hsa−miR−424
6	4e−08	16 / 84	hsa−miR−433
7	5e−08	24 / 184	hsa−miR−129−5p
8	1e−07	32 / 317	hsa−miR−559
9	2e−07	42 / 489	hsa−miR−16
10	2e−07	29 / 272	hsa−miR−577
11	2e−07	14 / 72	hsa−miR−890
12	3e−07	25 / 216	hsa−miR−548m
13	3e−07	30 / 295	hsa−miR−561
14	4e−07	15 / 87	hsa−miR−299−3p
15	5e−07	23 / 193	hsa−miR−513a−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	Alternative lengthening of telomeres
2	0.6	1 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	5e−70	598 / 9815	Overlap_fetal_midbrain_ReprPC
2	2e−63	575 / 9504	Overlap_fetal_midbrain_K9K27me3
3	1e−43	394 / 5936	Overlap_fetal_midbrain_HetRpts
4	4e−35	528 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	3e−34	544 / 10430	Overlap_fetal_midbrain_Quies
6	2e−08	67 / 906	Fetal_HetRpts
7	1e−06	162 / 3164	Mid_Frontal_Lobe_ZNF
8	3e−04	28 / 386	Fetal_ZNF
9	8e−03	48 / 937	Fetal_EnhG
10	1e−02	41 / 796	Overlap_fetal_midbrain_ZNF
11	1e−02	13 / 180	Overlap_fetal_midbrain_Het
12	8e−02	51 / 1171	Fetal_EnhP
13	1e−01	50 / 1162	Fetal_Enh
14	1e−01	107 / 2709	Mid_Frontal_Lobe_HetRpts
15	2e−01	27 / 630	Mid_Frontal_Lobe_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	0.007	60 / 1211	Chr 6
2	0.016	45 / 902	Chr 4
3	0.018	24 / 422	Chr 13
4	0.055	48 / 1060	Chr 5
5	0.104	52 / 1217	Chr 3
6	0.127	49 / 1160	Chr 12
7	0.130	39 / 904	Chr 10
8	0.178	48 / 1170	Chr 7
9	0.185	60 / 1492	Chr 2
10	0.236	13 / 289	Chr 21
11	0.302	33 / 836	Chr 8
12	0.628	21 / 619	Chr 20
13	0.698	79 / 2323	Chr 1
14	0.715	25 / 769	Chr 15
15	0.800	30 / 959	Chr 16

Glio

Rank	p−value	#in/all	Geneset
1	7e−14	126 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	6e−12	133 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	4e−07	12 / 55	Stuehler_Proteins_up_in_STS
4	9e−07	20 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	1e−05	54 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	8e−05	26 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	6e−04	28 / 401	Down_b
8	2e−03	4 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
9	2e−03	7 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	8e−03	7 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	1e−02	7 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	2e−02	2 / 7	Donson−adaptive−immunity−associated with LTS in HGA
13	6e−02	3 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
14	9e−02	2 / 14	Christensen_hypermethylated_in_ependymoma
15	9e−02	6 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−05	16 / 147	Homuth_BMI−associated−genes_UP
2	1e−04	7 / 32	Marjolein_ageing−genes_DN
3	2e−02	3 / 17	DUMEAUX_High bmi enriched genes
4	1e−01	2 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	3e−01	1 / 10	DUMEAUX_Smoking literature genes up
6	3e−01	1 / 10	Marjolein_ageing−genes_UP
7	4e−01	1 / 16	Huan_blood−pressure_DBP−signature
8	5e−01	1 / 18	Huan_blood−pressure_SBP−signature
9	6e−01	7 / 211	Homuth_BMI−associated−genes_DN
10	9e−01	2 / 94	DUMEAUX_Smoking enriched genes
11	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
13	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
14	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	6e−27	465 / 8818	protein binding
2	3e−25	109 / 1013	poly(A) RNA binding
3	3e−06	20 / 169	structural constituent of ribosome
4	6e−05	40 / 580	identical protein binding
5	9e−05	5 / 14	telomerase RNA binding
6	3e−04	72 / 1329	ATP binding
7	6e−04	28 / 399	RNA binding
8	6e−04	21 / 265	cadherin binding involved in cell−cell adhesion
9	8e−04	9 / 70	ATPase binding
10	9e−04	20 / 256	ubiquitin protein ligase binding
11	2e−03	24 / 351	GTP binding
12	2e−03	4 / 16	amino acid binding
13	3e−03	4 / 18	snoRNA binding
14	3e−03	17 / 227	transcription coactivator activity
15	4e−03	5 / 30	Rab guanyl−nucleotide exchange factor activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	3 / 13	BENTINK_myc.1
2	0.09	2 / 14	BENTINK_ras.6
3	0.38	1 / 13	BENTINK_e2f3.1
4	0.38	1 / 13	BENTINK_e2f3.2
5	0.40	1 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−29	322 / 5067	ICGC_Taf1_targets
2	2e−21	315 / 5466	ICGC_Nficsc81335_targets
3	2e−20	314 / 5518	ICGC_Stat5_targets
4	4e−20	310 / 5442	ICGC_Pmlsc71910_targets
5	3e−19	266 / 4468	ICGC_Egr1_targets
6	7e−19	260 / 4362	ICGC_Creb1_targets
7	2e−18	281 / 4890	ICGC_Bclaf101388_targets
8	3e−18	280 / 4881	ICGC_Atf2_targets
9	1e−17	335 / 6267	ICGC_Yy1_targets
10	1e−17	296 / 5312	ICGC_Tcf12_targets
11	6e−17	253 / 4345	ICGC_Zeb1_targets
12	8e−17	131 / 1723	HEBENSTREIT_high expression TF
13	1e−16	320 / 5984	ICGC_Mta3_targets
14	6e−16	341 / 6578	ICGC_Pou2_targets
15	7e−16	116 / 1478	ICGC_Myc_targets

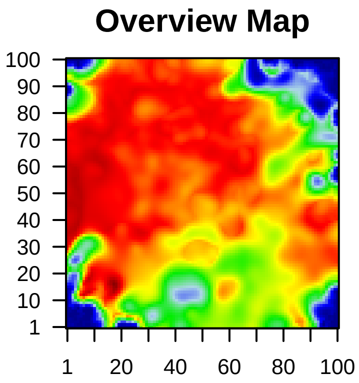
Underexpression Spots

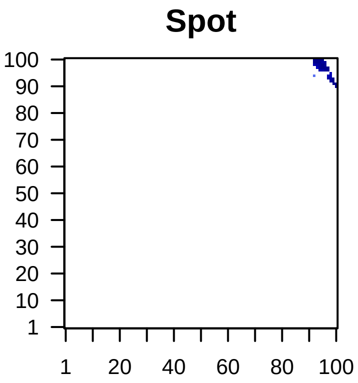
Spot Summary: h

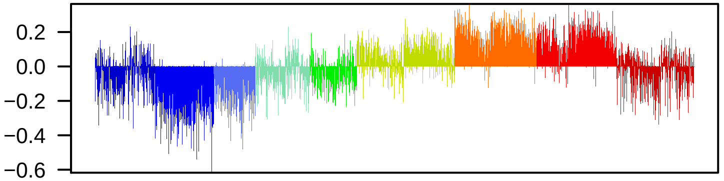
metagenes = 35
genes = 621

<r> metagenes = 0.87
<r> genes = 0.46
beta: r2= 70.26 / log p= −Inf

samples with spot = 795 (23.5 %)
A * : 19 (5.5 %)
A F * : 13 (4.2 %)
C F * : 5 (1.9 %)
F * : 128 (23.1 %)
F J * : 340 (73.4 %)
J * : 270 (60.4 %)
N * : 20 (4.5 %)


Overview Map


Spot

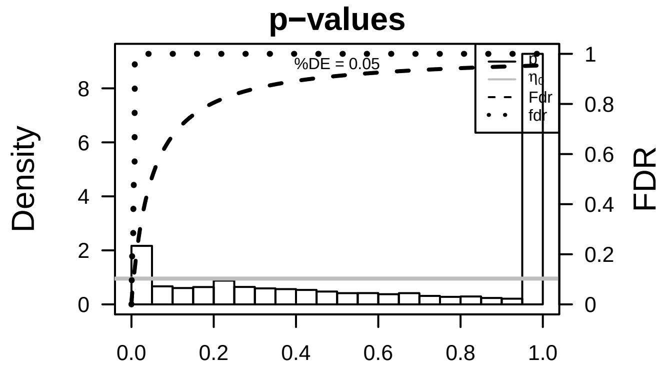


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169749	5.33	−1.74	0.06	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	ILMN_171516	4.62	−2.25	0.07		
3	ILMN_239376	2.36	−2.48	0.29	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
4	ILMN_324037	2.04	−1.35	0.36		immunoglobulin kappa variable 1D−17 [Source:HGNC Symbo
5	ILMN_169921	1.89	−1.18	0.29		
6	ILMN_178810	1.79	−0.92	0.36		BLOC1S5−TXNDC5 readthrough (NMD candidate) [Source:H
7	ILMN_177365	1.78	−1.17	0.5	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
8	ILMN_169107	1.77	−1.46	0.49	FCRLA	Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]
9	ILMN_177245	1.73	−2.05	0.4	RPS23	ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_168027	1.73	−0.94	0.35		immunoglobulin kappa variable 1−33 [Source:HGNC Symbol;
11	ILMN_240485	1.7	−1.35	0.32	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10
12	ILMN_173487	1.64	−1.96	0.53	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
13	ILMN_165379	1.59	−1.31	0.27		
14	ILMN_233792	1.41	−1.24	0.58	CXCR5	C−X−C motif chemokine receptor 5 [Source:HGNC Symbol;A
15	ILMN_165303	1.4	−1.48	0.39		
16	ILMN_170014	1.38	−1.08	0.42	VPREB3	pre−B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271
17	ILMN_169022	1.38	−0.68	0.43	CNTNAP2	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
18	ILMN_171513	1.34	−1.58	0.75	CCR7	C−C motif chemokine receptor 7 [Source:HGNC Symbol;Acc:
19	ILMN_321438	1.33	−1.23	0.25		
20	ILMN_230275	1.33	−1.08	0.44	FCGBP	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−40	44 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
2	3e−27	33 / 119	Refer	Chaussabel_2,8_T−cells
3	1e−22	215 / 5356	Lymph	HOPP_Txn_transition
4	2e−22	70 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
5	4e−20	257 / 7275	Lymph	HOPP_Txn_elongation
6	3e−19	40 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
7	2e−18	24 / 101	GSEA	REACTOME_TRANSLATION
8	3e−18	28 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
9	5e−18	20 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
10	4e−17	271 / 8226	Lymph	HOPP_Active_promoter
11	5e−17	67 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
12	8e−17	20 / 74	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
13	9e−17	18 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
14	1e−16	24 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
15	4e−16	82 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
16	5e−16	67 / 1013	MF	poly(A) RNA binding
17	5e−16	53 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
18	1e−15	75 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
19	2e−15	14 / 32	Lifesty	Marjolein_ageing−genes_DN
20	3e−15	21 / 99	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
21	6e−15	18 / 69	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
22	9e−15	19 / 81	BP	viral transcription
23	2e−14	293 / 9555	Colon	TssA_Colon
24	7e−14	17 / 68	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
25	7e−14	16 / 58	GSEA	KEGG_RIBOSOME
26	1e−13	29 / 242	Refer	Chaussabel_3,9_Kinases
27	2e−13	19 / 96	BP	translational initiation
28	4e−13	255 / 8098	Lymph	HOPP_Weak_promoter
29	5e−13	88 / 1797	GSEA	PILON_KLF1_TARGETS_DN
30	1e−12	79 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
31	2e−12	35 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
32	3e−12	23 / 170	HM	HALLMARK_MYC_TARGETS_V1
33	4e−12	16 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
34	5e−12	17 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
35	6e−12	13 / 44	GSEA	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
36	1e−11	22 / 163	BP	rRNA processing
37	1e−11	40 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
38	2e−11	60 / 1063	Refer	PROTEINATLAS_tonsil
39	2e−11	61 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
40	3e−11	259 / 8568	Colon	TxWk_Colon


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	3 / 111	HORVATH_aging_genes meth DOWN
2	0.6	3 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 13	RHODES_CANCER_META_SIGNATURE
2	2e−03	5 / 39	ZHANG_MM up
3	2e−02	9 / 178	SPANG_LPS−index2
4	3e−02	2 / 13	WANG_ER_DN
5	3e−02	2 / 13	GENTLES_modul6
6	3e−02	2 / 13	GENTLES_modul12
7	4e−02	2 / 14	LIU_COMMON_CANCER_GENES
8	4e−02	2 / 14	GENTLES_modul10
9	4e−02	2 / 15	WOLFER_overlap genes
10	5e−02	2 / 16	GENTLES_modul7
11	5e−02	2 / 16	GENTLES_modul11
12	5e−02	2 / 16	GENTLES_modul16
13	6e−02	18 / 554	Lembcke_Colonic Inflammation
14	7e−02	11 / 301	SPANG_BCL6−index2
15	8e−02	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−09	212 / 6970	5_Tx_Neuronal_Progenitor
2	6e−08	250 / 8771	5_Tx_Melanocytes
3	6e−06	219 / 7854	5_Tx_Fibroblasts
4	1e−05	316 / 12298	2_TssA_Melanocytes
5	2e−05	296 / 11455	2_TssA_Fibroblasts
6	1e−04	22 / 416	4_TxTrans_Neuronal_Progenitor
7	1e−03	230 / 8990	15_Quies_Fibroblasts
8	5e−03	312 / 12983	2_TssA_Neuronal_Progenitor
9	1e−02	39 / 1206	6_EnhG_Neuronal_Progenitor
10	1e−02	146 / 5699	6_EnhG_Melanocytes
11	1e−02	112 / 4237	14_ZNF_Neuronal_Progenitor
12	3e−02	279 / 11836	3_TssF_Melanocytes
13	1e−01	48 / 1846	14_ZNF_Melanocytes
14	2e−01	114 / 4795	6_EnhG_Fibroblasts
15	3e−01	277 / 12393	15_Quies_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−19	40 / 317	HSIAO_HOUSEKEEPING_GENES
2	2e−18	24 / 101	REACTOME_TRANSLATION
3	3e−18	28 / 151	JISON_SICKLE_CELL_DISEASE_DN
4	8e−17	20 / 74	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
5	9e−17	18 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	4e−16	82 / 1417	PUJANA_BRCA1_PCC_NETWORK
7	5e−16	53 / 669	PUJANA_CHEK2_PCC_NETWORK
8	1e−15	75 / 1241	PUJANA_ATM_PCC_NETWORK
9	3e−15	21 / 99	REACTOME_INFLUENZA_LIFE_CYCLE
10	6e−15	18 / 69	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
11	7e−14	17 / 68	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
12	7e−14	16 / 58	KEGG_RIBOSOME
13	5e−13	88 / 1797	PILON_KLF1_TARGETS_DN
14	2e−12	35 / 388	SHEN_SMARCA2_TARGETS_UP
15	4e−12	16 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−22	215 / 5356	HOPP_Txn_transition
2	4e−20	257 / 7275	HOPP_Txn_elongation
3	4e−17	271 / 8226	HOPP_Active_promoter
4	4e−13	255 / 8098	HOPP_Weak_promoter
5	2e−06	212 / 7448	HOPP_Strong_enhancer
6	1e−05	24 / 408	TARTE_Mature plasma cell signature
7	1e−04	6 / 35	TARTE_B−cell signature
8	1e−04	24 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
9	6e−04	23 / 493	WIRTH_lymphoma937_spot J
10	2e−03	5 / 43	Monti_OxPhos_cluster
11	3e−03	9 / 134	DAVE_BL−vs−DLBCL
12	3e−03	7 / 88	WIRTH_lymphoma937_spot A
13	3e−03	40 / 1169	SPANG_BCR DN
14	4e−03	9 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
15	4e−03	9 / 141	WIRTH_lymphoma937_spot F

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−40	44 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	3e−27	33 / 119	Chaussabel_2,8_T−cells
3	1e−16	24 / 119	Chaussabel_2,4_Ribosomal proteins
4	1e−13	29 / 242	Chaussabel_3,9_Kinases
5	2e−11	60 / 1063	PROTEINATLAS_tonsil
6	3e−09	53 / 1003	PROTEINATLAS_appendix
7	3e−09	43 / 724	PROTEINATLAS_lymph node
8	9e−09	35 / 535	PROTEINATLAS_spleen
9	1e−08	45 / 816	PROTEINATLAS_endometrium
10	1e−07	36 / 623	PROTEINATLAS_seminal vesicle
11	1e−07	46 / 912	PROTEINATLAS_urinary bladder
12	2e−07	55 / 1194	PROTEINATLAS_stomach
13	3e−07	43 / 850	PROTEINATLAS_skin
14	7e−07	38 / 726	PROTEINATLAS_cervix, uterine
15	3e−06	51 / 1176	PROTEINATLAS_duodenum

BP

Rank	p−value	#in/all	Geneset
1	5e−18	20 / 65	SRP−dependent cotranslational protein targeting to membrane
2	9e−15	19 / 81	viral transcription
3	2e−13	19 / 96	translational initiation
4	5e−12	17 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
5	1e−11	22 / 163	rRNA processing
6	2e−08	19 / 184	translation
7	2e−07	21 / 254	cell−cell adhesion
8	1e−05	18 / 255	viral process
9	2e−05	5 / 17	mitochondrial ATP synthesis coupled proton transport
10	3e−05	5 / 18	cytoplasmic translation
11	2e−04	5 / 26	ATP biosynthetic process
12	2e−03	3 / 12	maturation of SSU−rRNA
13	2e−03	3 / 12	nucleotide metabolic process
14	2e−03	4 / 26	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
15	3e−03	4 / 27	odontogenesis

CC

Rank	p−value	#in/all	Geneset
1	2e−10	12 / 45	cytosolic large ribosomal subunit
2	5e−08	10 / 46	ribosome
3	3e−07	13 / 101	intracellular ribonucleoprotein complex
4	6e−07	38 / 721	nucleolus
5	6e−07	22 / 295	cell−cell adherens junction
6	6e−06	100 / 2979	cytosol
7	2e−05	144 / 4822	cytoplasm
8	3e−05	6 / 28	cytosolic small ribosomal subunit
9	4e−05	5 / 19	mitochondrial proton−transporting ATP synthase complex
10	7e−05	69 / 1979	membrane
11	2e−04	82 / 2535	nucleoplasm
12	4e−04	15 / 248	extracellular matrix
13	4e−04	137 / 4828	nucleus
14	5e−04	78 / 2464	extracellular exosome
15	2e−03	3 / 12	COPI vesicle coat

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−22	70 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	5e−17	67 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	2e−14	293 / 9555	TssA_Colon
4	1e−12	79 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	3e−11	259 / 8568	TxWk_Colon
6	2e−10	267 / 9054	Tx_Colon
7	1e−07	56 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
8	4e−07	80 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
9	2e−06	240 / 8678	Quies3_Colon
10	5e−05	284 / 10999	TssWk_Colon
11	9e−05	14 / 193	Kosinski_lower−crypt−long−list
12	3e−04	197 / 7354	TssF_Colon
13	7e−04	40 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	2e−02	106 / 4034	TssD1_Colon
15	2e−02	18 / 489	K9acLow_Colon

HM

Rank	p−value	#in/all	Geneset
1	3e−12	23 / 170	HALLMARK_MYC_TARGETS_V1
2	8e−05	13 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	4e−04	9 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	5e−03	10 / 176	HALLMARK_ADIPOGENESIS
5	9e−03	9 / 162	HALLMARK_ALLOGRAFT_REJECTION
6	4e−02	5 / 87	HALLMARK_PROTEIN_SECRETION
7	9e−02	7 / 177	HALLMARK_MITOTIC_SPINDLE
8	1e−01	7 / 179	HALLMARK_G2M_CHECKPOINT
9	1e−01	7 / 185	HALLMARK_MTORC1_SIGNALING
10	1e−01	3 / 54	HALLMARK_MYC_TARGETS_V2
11	2e−01	6 / 173	HALLMARK_E2F_TARGETS
12	2e−01	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
13	2e−01	6 / 176	HALLMARK_KRAS_SIGNALING_UP
14	2e−01	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
15	2e−01	6 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−06	28 / 463	hsa−miR−301a
2	3e−06	20 / 272	hsa−miR−577
3	5e−06	16 / 190	hsa−miR−330−3p
4	9e−06	20 / 295	hsa−miR−561
5	9e−06	23 / 374	hsa−miR−144
6	1e−05	31 / 602	hsa−miR−20a
7	2e−05	15 / 187	hsa−miR−586
8	2e−05	24 / 416	hsa−miR−372
9	2e−05	19 / 291	hsa−miR−186
10	2e−05	28 / 540	hsa−miR−17
11	3e−05	10 / 91	hsa−miR−10b
12	3e−05	22 / 377	hsa−miR−373
13	4e−05	26 / 493	hsa−miR−103
14	5e−05	6 / 31	hsa−miR−617
15	5e−05	17 / 256	hsa−miR−520a−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	4e−11	196 / 5936	Overlap_fetal_midbrain_HetRpts
2	1e−10	285 / 9815	Overlap_fetal_midbrain_ReprPC
3	5e−08	43 / 796	Overlap_fetal_midbrain_ZNF
4	8e−07	261 / 9504	Overlap_fetal_midbrain_K9K27me3
5	5e−05	22 / 386	Fetal_ZNF
6	2e−04	13 / 180	Overlap_fetal_midbrain_Het
7	2e−03	16 / 328	Fetal_Het
8	2e−02	239 / 9917	Overlap_fetal_midbrain_ReprPCWk
9	6e−02	27 / 906	Fetal_HetRpts
10	1e−01	241 / 10430	Overlap_fetal_midbrain_Quies
11	2e−01	30 / 1171	Fetal_EnhP
12	3e−01	29 / 1162	Fetal_Enh
13	5e−01	21 / 937	Fetal_EnhG
14	6e−01	26 / 1213	Fetal_TssP
15	6e−01	14 / 681	Overlap_fetal_midbrain_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	0.003	40 / 1160	Chr 12
2	0.011	39 / 1217	Chr 3
3	0.026	33 / 1060	Chr 5
4	0.121	22 / 769	Chr 15
5	0.133	25 / 902	Chr 4
6	0.191	57 / 2323	Chr 1
7	0.197	26 / 994	Chr X
8	0.214	12 / 422	Chr 13
9	0.289	36 / 1492	Chr 2
10	0.369	20 / 836	Chr 8
11	0.606	6 / 289	Chr 21
12	0.643	25 / 1211	Chr 6
13	0.689	18 / 904	Chr 10
14	0.727	28 / 1411	Chr 11
15	0.760	6 / 342	Chr 18

Glio

Rank	p−value	#in/all	Geneset
1	0.001	65 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.002	16 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.019	52 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.022	13 / 315	Up
5	0.032	3 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
6	0.035	3 / 33	Shaw_responders_down_in_oligo_glioma
7	0.038	3 / 34	Shaw_down_in_1p19q
8	0.067	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
9	0.087	3 / 48	Vishal_subnetwork signature of survival in GBM
10	0.103	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
11	0.118	3 / 55	Stuehler_Proteins_up_in_STS
12	0.143	1 / 7	Donson−adaptive−immunity−associated with LTS in HGA
13	0.146	4 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
14	0.154	2 / 32	Donson−Misc immune function−associated with LTS in HGA
15	0.162	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−15	14 / 32	Marjolein_ageing−genes_DN
2	2e−05	13 / 147	Homuth_BMI−associated−genes_UP
3	2e−02	10 / 211	Homuth_BMI−associated−genes_DN
4	5e−02	2 / 16	Huan_blood−pressure_DBP−signature
5	1e−01	2 / 31	DUMEAUX_Fasting enriched genes
6	3e−01	1 / 17	DUMEAUX_High bmi enriched genes
7	9e−01	1 / 94	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
15	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up

MF

Rank	p−value	#in/all	Geneset
1	5e−16	67 / 1013	poly(A) RNA binding
2	3e−08	18 / 169	structural constituent of ribosome
3	1e−07	22 / 265	cadherin binding involved in cell−cell adhesion
4	2e−07	27 / 399	RNA binding
5	6e−06	241 / 8818	protein binding
6	1e−04	4 / 12	proton−transporting ATP synthase activity, rotational mechanism
7	3e−04	19 / 351	GTP binding
8	2e−03	4 / 24	transmembrane transporter activity
9	5e−03	5 / 51	GDP binding
10	1e−02	3 / 22	transferase activity
11	1e−02	3 / 23	proton−transporting ATPase activity, rotational mechanism
12	2e−02	4 / 45	tRNA binding
13	2e−02	3 / 25	RNA polymerase II transcription corepressor activity
14	2e−02	4 / 46	helicase activity
15	2e−02	4 / 48	SH3/SH2 adaptor activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 12	BENTINK_ras.1
2	0.23	1 / 12	BENTINK_src.2
3	0.25	1 / 13	BENTINK_e2f3.1
4	0.25	1 / 13	BENTINK_e2f3.2
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 13	BENTINK_myc.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−09	61 / 1231	KIM_MYC targets
2	3e−06	5 / 12	MYC_Protein synthesis degradation UP
3	2e−04	7 / 55	MYC_Targets UP
4	5e−04	52 / 1478	ICGC_Myc_targets
5	1e−03	66 / 2087	ICGC_Cebpbsc150_targets
6	2e−03	159 / 5961	ICGC_Pol24_targets
7	4e−03	136 / 5067	ICGC_Taf1_targets
8	1e−02	52 / 1723	HEBENSTREIT_high expression TF
9	1e−02	46 / 1498	ICGC_Ets1_targets
10	2e−02	127 / 4881	ICGC_Atf2_targets
11	2e−02	164 / 6578	ICGC_Pou2_targets
12	3e−02	138 / 5466	ICGC_Nficsc81335_targets
13	4e−02	84 / 3194	ICGC_Irf4_targets
14	4e−02	123 / 4890	ICGC_Bclaf101388_targets
15	5e−02	105 / 4131	ICGC_Nfatc1_targets

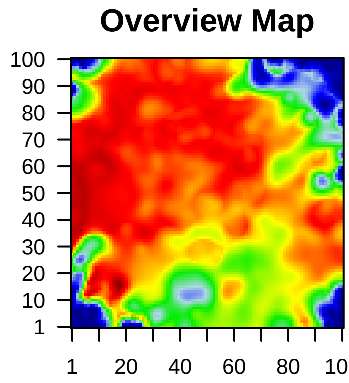
Underexpression Spots

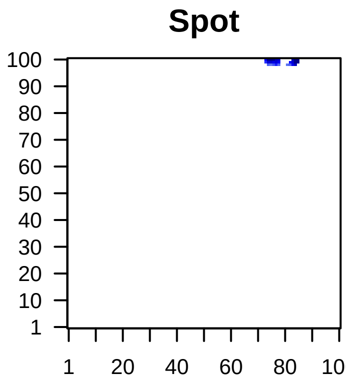
Spot Summary: i

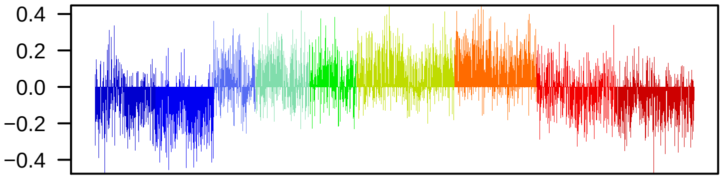
metagenes = 28
genes = 245

<r> metagenes = 0.7
<r> genes = 0.22
beta: r2= 29.96 / log p= −Inf

samples with spot = 761 (22.5 %)
A * : 21 (6.1 %)
A C * : 5 (1.5 %)
A C F * : 49 (20.9 %)
A F * : 103 (33.4 %)
C F * : 72 (27.2 %)
F * : 199 (35.9 %)
F J * : 239 (51.6 %)
J * : 53 (11.9 %)
N * : 20 (4.5 %)





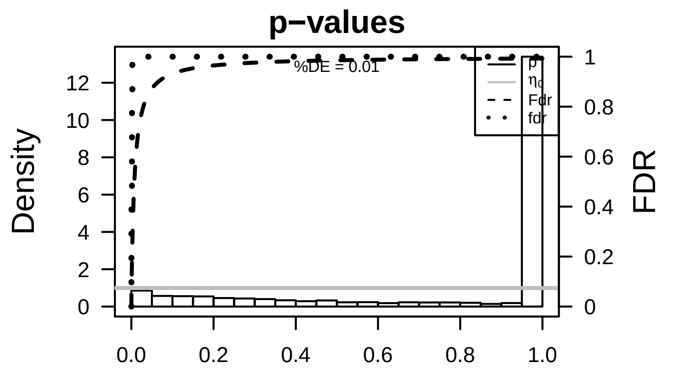


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_171673	3.14	−1.47	0.16	MYOM2	myomesin 2 [Source:HGNC Symbol;Acc:HGNC:7614]
2	ILMN_175063	2.47	−2.69	0.55		
3	ILMN_218086	2.33	−2.64	0.54		ribosomal protein S26 pseudogene 11 [Source:HGNC Symbo
4	ILMN_172664	2.23	−2.64	0.54		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
5	ILMN_324883	2.2	−2.25	0.54		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
6	ILMN_231070	2.2	−2.41	0.54		
7	ILMN_320919	2.15	−2.18	0.54	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
8	ILMN_167852	2.13	−2.24	0.54		
9	ILMN_220902	2.12	−2.29	0.53	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_169558	2.09	−2.34	0.54	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
11	ILMN_329699	2.07	−2.21	0.54		
12	ILMN_329001	2.01	−1.81	0.52		ribosomal protein S26 pseudogene 2 [Source:HGNC Symbol;
13	ILMN_167769	2.01	−2.28	0.55		ribosomal protein S26 pseudogene 35 [Source:HGNC Symbo
14	ILMN_178681	2.01	−1.2	0.31	LOC105379645	killer cell immunoglobulin like receptor, two Ig domains and lo
15	ILMN_328515	1.94	−2.25	0.55	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
16	ILMN_324228	1.92	−2.21	0.54	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
17	ILMN_325449	1.92	−1.96	0.52		ribosomal protein S26 pseudogene 55 [Source:HGNC Symbo
18	ILMN_173123	1.91	−2.04	0.62	GZMH	granzyme H [Source:HGNC Symbol;Acc:HGNC:4710]
19	ILMN_173975	1.64	−1.34	0.45		
20	ILMN_179069	1.63	−1.97	0.64		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−74	46 / 84	Refer	Chaussabel_2,1_Cytotoxic cells
2	1e−22	15 / 34	GSEA	HAHTOLA_SEZARY_SYNDROM_DN
3	2e−21	10 / 10	Lifesty	Marjolein_ageing−genes_UP
4	4e−20	27 / 288	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
5	2e−17	38 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	1e−15	8 / 10	GSEA	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL
7	2e−14	19 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
8	8e−12	13 / 105	BP	regulation of immune response
9	3e−11	22 / 425	GSEA	MATSUDA_NATURAL_KILLER_DIFFERENTIATION
10	5e−11	18 / 277	GSEA	LI_INDUCED_T_TO_NATURAL_KILLER_UP
11	2e−10	18 / 306	Lymph	WIRTH_lymphoma937_spot E
12	5e−10	7 / 22	GSEA	ONO_AML1_TARGETS_UP
13	1e−09	9 / 55	GSEA	PID_IL12_2PATHWAY
14	1e−09	17 / 301	GSEA	GOLDRATH_ANTIGEN_RESPONSE
15	8e−09	8 / 48	BP	cellular defense response
16	1e−08	16 / 300	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−E
17	1e−08	5 / 10	Lifesty	DUMEAUX_Women normal BMI literature genes up
18	2e−08	12 / 162	HM	HALLMARK_ALLOGRAFT_REJECTION
19	2e−08	10 / 103	GSEA	BOSCO_TH1_CYTOTOXIC_MODULE
20	3e−08	10 / 106	GSEA	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
21	1e−07	17 / 412	Refer	WIRTH_Immune system
22	2e−07	8 / 70	GSEA	GRABARCZYK_BCL11B_TARGETS_UP
23	2e−07	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
24	2e−07	5 / 16	GSEA	KEGG_GRAFT_VERSUS_HOST_DISEASE
25	3e−07	10 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
26	3e−07	5 / 17	BP	cytolysis
27	4e−07	5 / 18	Lifesty	Huan_blood−pressure_SBP−signature
28	6e−07	7 / 57	GSEA	PID_CD8_TCR_DOWNSTREAM_PATHWAY
29	1e−06	4 / 10	GSEA	BIOCARTA_CTL_PATHWAY
30	2e−06	10 / 167	CC	external side of plasma membrane
31	3e−06	3 / 4	Lifesty	DUMEAUX_Exercising non smoker literature enriched genes
32	1e−05	12 / 293	BP	immune response
33	1e−05	14 / 402	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
34	2e−05	11 / 253	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
35	2e−05	11 / 254	BP	cell surface receptor signaling pathway
36	2e−05	4 / 18	GSEA	KEGG_ALLOGRAFT_REJECTION
37	2e−05	5 / 37	GSEA	ONO_FOXP3_TARGETS_DN
38	2e−05	6 / 62	BP	positive regulation of phosphatidylinositol 3−kinase signaling
39	2e−05	3 / 7	GSEA	FARDIN_HYPOXIA_9
40	4e−05	4 / 22	GSEA	KEGG_TYPE_I_DIABETES_MELLITUS



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 111	HORVATH_aging_genes meth DOWN
2	0.7	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	8e−12	13 / 105	regulation of immune response
2	8e−09	8 / 48	cellular defense response
3	3e−07	5 / 17	cytolysis
4	1e−05	12 / 293	immune response
5	2e−05	11 / 254	cell surface receptor signaling pathway
6	2e−05	6 / 62	positive regulation of phosphatidylinositol 3−kinase signaling
7	2e−04	3 / 13	positive regulation of Rho protein signal transduction
8	3e−04	3 / 16	natural killer cell mediated cytotoxicity
9	7e−04	4 / 46	positive regulation of cell adhesion
10	8e−04	4 / 48	cellular response to interferon−gamma
11	9e−04	3 / 22	positive regulation of calcium ion transport
12	1e−03	4 / 52	chemokine−mediated signaling pathway
13	1e−03	4 / 54	positive regulation of smooth muscle cell proliferation
14	1e−03	4 / 56	neutrophil chemotaxis
15	2e−03	6 / 153	defense response to virus

Brain

Rank	p−value	#in/all	Geneset
1	0.1	6 / 383	Mid_Frontal_Lobe_Tx
2	0.2	10 / 818	Mid_Frontal_Lobe_Het
3	0.2	7 / 578	Fetal_Tx
4	0.2	5 / 386	Fetal_ZNF
5	0.3	27 / 2700	Fetal_TxTrans
6	0.3	10 / 937	Fetal_EnhG
7	0.4	18 / 1893	Overlap_fetal_midbrain_TssF
8	0.4	8 / 796	Overlap_fetal_midbrain_ZNF
9	0.4	24 / 2630	Fetal_TssF
10	0.5	19 / 2127	Mid_Frontal_Lobe_K9K27me3
11	0.5	12 / 1329	Overlap_fetal_midbrain_Enh
12	0.5	10 / 1119	Overlap_fetal_midbrain_TssA
13	0.5	36 / 4112	Mid_Frontal_Lobe_ReprPC
14	0.5	13 / 1476	Overlap_fetal_midbrain_TxTrans
15	0.5	15 / 1728	Fetal_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	6 / 193	PanCan_PI3K_geneset_nanostring
2	0.010	11 / 554	Lembcke_Colonic Inflammation
3	0.046	3 / 91	PanCan_TXmisReg_geneset_nanostring
4	0.061	2 / 46	PanCan_TGF−B_geneset_nanostring
5	0.108	1 / 13	WANG_ER_DN
6	0.108	1 / 13	GENTLES_modul18
7	0.117	3 / 136	PanCan_RAS_geneset_nanostring
8	0.123	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	0.161	2 / 82	PanCan_JAK−ST_geneset_nanostring
10	0.176	0 / 12	LIU_BREAST_CANCER
11	0.273	2 / 117	PanCan_Driver_Gene_geneset_nanostring
12	0.284	1 / 38	KUIPER_MM good survival
13	0.378	2 / 150	PanCan_MAPK_geneset_nanostring
14	0.462	2 / 178	SPANG_LPS−index2
15	0.474	1 / 73	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	2e−06	10 / 167	external side of plasma membrane
2	6e−04	6 / 119	vesicle
3	1e−03	22 / 1252	integral component of plasma membrane
4	4e−03	5 / 121	receptor complex
5	5e−03	2 / 12	small ribosomal subunit
6	2e−02	26 / 1979	membrane
7	2e−02	2 / 28	cytosolic small ribosomal subunit
8	3e−02	5 / 194	membrane raft
9	3e−02	2 / 30	immunological synapse
10	3e−02	5 / 202	early endosome
11	3e−02	3 / 81	late endosome membrane
12	4e−02	5 / 207	lysosome
13	4e−02	9 / 524	intracellular
14	6e−02	3 / 99	recycling endosome
15	7e−02	2 / 48	integral component of Golgi membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.03	17 / 1160	Chr 12
2	0.05	28 / 2323	Chr 1
3	0.18	5 / 342	Chr 18
4	0.21	16 / 1467	Chr 19
5	0.23	16 / 1492	Chr 2
6	0.25	15 / 1411	Chr 11
7	0.33	6 / 536	Chr 22
8	0.48	12 / 1318	Chr 17
9	0.51	7 / 769	Chr 15
10	0.53	8 / 902	Chr 4
11	0.60	8 / 954	Chr 9
12	0.70	9 / 1170	Chr 7
13	0.72	3 / 422	Chr 13
14	0.72	2 / 289	Chr 21
15	0.74	7 / 959	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.05	46 / 4169	10_ReprPC_Fibroblasts
2	0.06	35 / 3068	8_EnhP_Fibroblasts
3	0.06	16 / 1206	6_EnhG_Neuronal_Progenitor
4	0.07	7 / 416	4_TxTrans_Neuronal_Progenitor
5	0.14	14 / 1154	11_K9K27me3_Neuronal_Progenitor
6	0.18	9 / 717	11_K9K27me3_Fibroblasts
7	0.18	28 / 2682	12_Het_Neuronal_Progenitor
8	0.20	41 / 4107	9_ReprPCWk_Fibroblasts
9	0.27	14 / 1324	13_HetRpts_Fibroblasts
10	0.29	23 / 2315	13_HetRpts_Melanocytes
11	0.29	35 / 3639	1_TssP_Fibroblasts
12	0.36	40 / 4304	9_ReprPCWk_Melanocytes
13	0.38	25 / 2660	8_EnhP_Melanocytes
14	0.40	34 / 3691	9_ReprPCWk_Neuronal_Progenitor
15	0.42	30 / 3272	13_HetRpts_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−17	38 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−04	13 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
3	6e−04	41 / 2810	EnhA_Colon
4	8e−04	11 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
5	2e−02	8 / 366	K9K27me3_Colon
6	2e−02	3 / 64	Marisa_CRC−cluster−g
7	3e−02	7 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	3e−02	1 / 3	Kaneda_CIMP−group1
9	3e−02	7 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
10	3e−02	13 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	4e−02	14 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	7e−02	8 / 489	K9acLow_Colon
13	7e−02	1 / 8	Marisa_CRC−C6
14	7e−02	10 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	8e−02	1 / 10	Marisa_CRC−C1

Glio

Rank	p−value	#in/all	Geneset
1	2e−07	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
2	3e−03	3 / 32	Donson−Misc immune function−associated with LTS in HGA
3	3e−03	4 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
4	2e−02	4 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
5	2e−02	4 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
6	3e−02	4 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	4e−02	3 / 86	laffaire_hypermeth_LGG_vs_control
8	4e−02	4 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	4e−02	3 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
10	9e−02	2 / 59	Christensen_hypermethylated_in_primary_glioblastoma
11	1e−01	1 / 12	Phillips PN up vs MES & Prolif
12	1e−01	1 / 14	Christensen_hypermethylated_in_ependymoma
13	1e−01	1 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
14	1e−01	2 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
15	1e−01	3 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−22	15 / 34	HAHTOLA_SEZARY_SYNDROM_DN
2	4e−20	27 / 288	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
3	1e−15	8 / 10	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL
4	2e−14	19 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	3e−11	22 / 425	MATSUDA_NATURAL_KILLER_DIFFERENTIATION
6	5e−11	18 / 277	LI_INDUCED_T_TO_NATURAL_KILLER_UP
7	5e−10	7 / 22	ONO_AML1_TARGETS_UP
8	1e−09	9 / 55	PID_IL12_2PATHWAY
9	1e−09	17 / 301	GOLDRATH_ANTIGEN_RESPONSE
10	2e−08	10 / 103	BOSCO_TH1_CYTOTOXIC_MODULE
11	3e−08	10 / 106	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
12	2e−07	8 / 70	GRABARCZYK_BCL11B_TARGETS_UP
13	2e−07	5 / 16	KEGG_GRAFT_VERSUS_HOST_DISEASE
14	6e−07	7 / 57	PID_CD8_TCR_DOWNSTREAM_PATHWAY
15	1e−06	4 / 10	BIOCARTA_CTL_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	2e−08	12 / 162	HALLMARK_ALLOGRAFT_REJECTION
2	6e−05	8 / 151	HALLMARK_APOPTOSIS
3	1e−03	7 / 185	HALLMARK_MTORC1_SIGNALING
4	6e−03	6 / 185	HALLMARK_P53_PATHWAY
5	6e−03	6 / 186	HALLMARK_IL2_STAT5_SIGNALING
6	2e−02	5 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	2e−02	5 / 183	HALLMARK_GLYCOLYSIS
8	2e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	2e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
10	3e−02	5 / 189	HALLMARK_HYPOXIA
11	3e−02	4 / 132	HALLMARK_UV_RESPONSE_DN
12	5e−02	2 / 41	HALLMARK_APICAL_SURFACE
13	7e−02	2 / 50	HALLMARK_TGF_BETA_SIGNALING
14	2e−01	3 / 175	HALLMARK_XENOBIOTIC_METABOLISM
15	2e−01	3 / 187	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−21	10 / 10	Marjolein_ageing−genes_UP
2	1e−08	5 / 10	DUMEAUX_Women normal BMI literature genes up
3	4e−07	5 / 18	Huan_blood−pressure_SBP−signature
4	3e−06	3 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	8e−03	2 / 16	Huan_blood−pressure_DBP−signature
6	4e−02	4 / 147	Homuth_BMI−associated−genes_UP
7	4e−02	1 / 5	Huan_blood−pressure_HTN−signature
8	1e−01	1 / 17	DUMEAUX_High bmi enriched genes
9	2e−01	1 / 32	Marjolein_ageing−genes_DN
10	6e−01	2 / 211	Homuth_BMI−associated−genes_DN
11	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
12	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
13	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
14	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
15	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−10	18 / 306	WIRTH_lymphoma937_spot E
2	1e−08	16 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
3	1e−04	4 / 31	Care_Extended T−cell
4	4e−03	5 / 121	SPANG_LPS 6hrs UP
5	6e−03	2 / 13	Care_Polarized immune response
6	9e−03	8 / 331	SPANG_CD40 6hrs UP
7	1e−02	3 / 57	Monti_Host_response_cluster
8	2e−02	2 / 28	DAVE_Immune response 1
9	3e−02	1 / 3	WRIGHT_custom GCB−DLBCL UP
10	4e−02	2 / 36	Subero_MM_hyper_meth
11	4e−02	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
12	5e−02	5 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
13	6e−02	1 / 7	MASCQUE_GCB UP
14	7e−02	2 / 48	Subero_B−ALL_hyper_meth
15	8e−02	3 / 118	Subero_INT_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Hugo_melanoma−all−LEF1_UP
2	0.4	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−04	8 / 174	transmembrane signaling receptor activity
2	1e−03	7 / 188	receptor activity
3	2e−03	3 / 30	antigen binding
4	5e−03	2 / 12	activin binding
5	5e−03	3 / 39	chemokine activity
6	5e−03	3 / 39	clathrin binding
7	7e−03	2 / 15	MHC class I protein binding
8	7e−03	2 / 15	platelet−derived growth factor receptor binding
9	9e−03	2 / 17	phosphatidylinositol 3−kinase binding
10	1e−02	3 / 54	serine−type peptidase activity
11	1e−02	2 / 19	chemokine receptor activity
12	1e−02	2 / 20	phosphatidylinositol−4−phosphate binding
13	1e−02	5 / 160	carbohydrate binding
14	1e−02	2 / 21	cytokine receptor activity
15	1e−02	5 / 163	serine−type endopeptidase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 20	Parkinson disease
2	0.2	1 / 22	Pigmented adrenocortical disease, primary isolated
3	0.2	1 / 27	Duchenne muscular dystrophy
4	0.2	1 / 28	Miyoshi myopathy
5	0.2	1 / 29	Myelofibrosis, idiopathic
6	0.3	1 / 40	Muscular dystrophy
7	0.3	1 / 47	Cervical cancer, somatic
8	0.3	1 / 48	Multiple myeloma
9	0.4	1 / 56	Myopathy, nemaline, 3
10	0.4	1 / 57	Cardiomyopathy, dilated
11	0.4	1 / 65	Hepatocellular carcinoma
12	0.4	1 / 68	Glioblastoma multiforme, somatic
13	0.5	1 / 73	Stroke, susceptibility to
14	0.5	1 / 76	Muscular
15	0.6	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	3 / 85	hsa−miR−510
2	0.06	4 / 164	hsa−miR−153
3	0.11	3 / 135	hsa−miR−576−3p
4	0.16	3 / 160	hsa−miR−512−3p
5	0.17	2 / 86	hsa−miR−339−5p
6	0.18	1 / 23	hsa−miR−596
7	0.20	1 / 25	hsa−miR−432*
8	0.21	1 / 27	hsa−miR−483−3p
9	0.23	1 / 30	hsa−miR−626
10	0.24	1 / 31	hsa−miR−654−5p
11	0.24	5 / 382	hsa−let−7c
12	0.25	1 / 32	hsa−miR−631
13	0.25	3 / 198	hsa−miR−181c
14	0.26	1 / 35	hsa−miR−769−5p
15	0.27	1 / 36	hsa−miR−34c−3p

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−74	46 / 84	Chaussabel_2,1_Cytotoxic cells
2	1e−07	17 / 412	WIRTH_Immune system
3	3e−07	10 / 132	Chaussabel_1,7_MHC Ribosomal proteins
4	6e−03	2 / 14	JONGENEEL_Peripheral Blood Lymphocytes
5	1e−02	2 / 19	VAQUERIZAS_Bone marrow_TF
6	1e−02	2 / 21	VAQUERIZAS_Tonsil_TF
7	5e−02	2 / 41	VAQUERIZAS_Thymus_TF
8	1e−01	2 / 66	VAQUERIZAS_Whole blood_TF
9	1e−01	1 / 17	VAQUERIZAS_Salivary gland_TF
10	1e−01	1 / 17	JONGENEEL_Lung
11	2e−01	7 / 535	PROTEINATLAS_spleen
12	2e−01	1 / 30	VAQUERIZAS_Lymph node_TF
13	2e−01	6 / 478	WIRTH_Nervous System
14	3e−01	2 / 119	Chaussabel_2,4_Ribosomal proteins
15	3e−01	1 / 43	VAQUERIZAS_Placenta_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	0.002	36 / 2497	ICGC_Bcl11_targets
2	0.006	25 / 1669	ICGC_P300_targets
3	0.019	54 / 4735	ICGC_Pu1_targets
4	0.039	67 / 6322	ICGC_Tcf3_targets
5	0.053	38 / 3348	ICGC_BatfPcr1_targets
6	0.060	68 / 6578	ICGC_Pou2_targets
7	0.280	62 / 6616	ICGC_Pax5_targets
8	0.288	56 / 5961	ICGC_Pol24_targets
9	0.316	21 / 2133	ICGC_Mef2_targets
10	0.330	8 / 747	ICGC_NrsfPcr2_targets
11	0.359	60 / 6552	ICGC_Pol2_targets
12	0.438	16 / 1723	HEBENSTREIT_high expression TF
13	0.483	46 / 5188	ICGC_Ebfsc137065_targets
14	0.500	24 / 2704	ICGC_Pbx3_targets
15	0.530	47 / 5383	ICGC_Sp1_targets

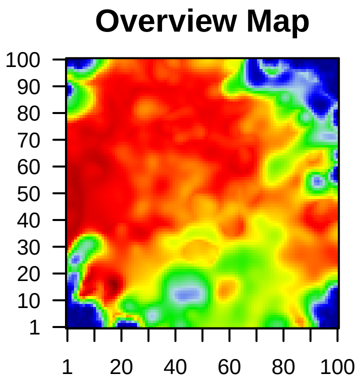
Underexpression Spots

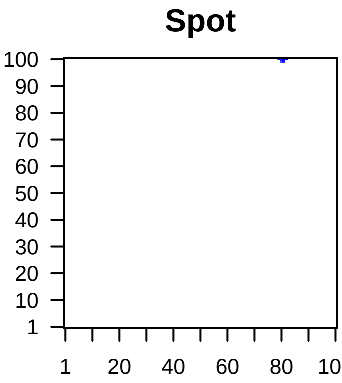
Spot Summary: j

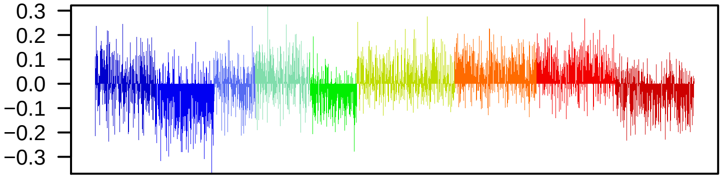
metagenes = 6
genes = 148

<r> metagenes = 0.96
<r> genes = 0.4
beta: r2= 18.97 / log p= −Inf

samples with spot = 339 (10 %)
- A * : 51 (14.8 %)
- A C * : 6 (1.8 %)
- A C F * : 13 (5.5 %)
- A F * : 48 (15.6 %)
- C F * : 3 (1.1 %)
- F * : 61 (11 %)
- F J * : 77 (16.6 %)
- J * : 77 (17.2 %)
- N * : 3 (0.7 %)





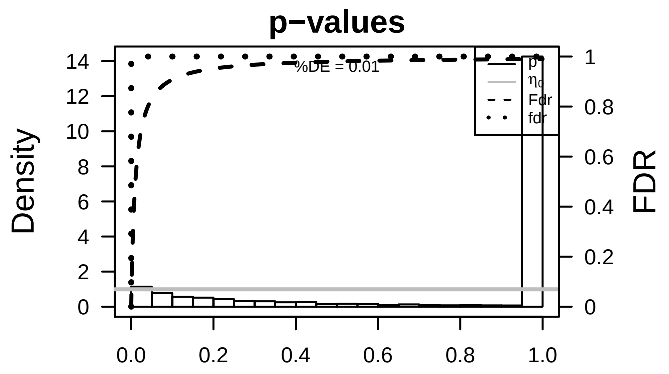


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_171876	0.82	−0.83	0.47	MT1F	metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]
2	ILMN_323043	0.75	−0.69	0.4	VOPP1	vesicular, overexpressed in cancer, prosurvival protein 1 [Sou
3	ILMN_218351	0.74	−0.49	0.55	MANF	mesencephalic astrocyte derived neurotrophic factor [Source:
4	ILMN_224901	0.68	−0.5	0.32	MIR3621	microRNA 3621 [Source:HGNC Symbol;Acc:HGNC:38930]
5	ILMN_214511	0.66	−0.62	0.55	TMEM173	transmembrane protein 173 [Source:HGNC Symbol;Acc:HGN
6	ILMN_239795	0.65	−0.51	0.47	PARP3	poly(ADP−ribose) polymerase family member 3 [Source:HGN
7	ILMN_324385	0.64	−0.57	0.7	NDUFB9	NADH:ubiquinone oxidoreductase subunit B9 [Source:HGNC
8	ILMN_181266	0.62	−0.71	0.36	DNAJC15	DnaJ heat shock protein family (Hsp40) member C15 [Source
9	ILMN_177593	0.62	−0.5	0.59	DDB1	damage specific DNA binding protein 1 [Source:HGNC Symb
10	ILMN_169098	0.62	−0.65	0.54	DDTL	D−dopachrome tautomerase [Source:HGNC Symbol;Acc:HG
11	ILMN_168792	0.61	−0.45	0.74	RP9	retinitis pigmentosa 9 (autosomal dominant) [Source:HGNC S
12	ILMN_167704	0.6	−0.7	0.66	AKR7A2	aldo−keto reductase family 7 member A2 [Source:HGNC Syn
13	ILMN_173423	0.6	−0.48	0.61	PINK1−AS	PINK1 antisense RNA [Source:HGNC Symbol;Acc:HGNC:38
14	ILMN_216092	0.6	−0.43	0.6	FEN1	flap structure−specific endonuclease 1 [Source:HGNC Symbo
15	ILMN_320702	0.59	−0.68	0.54		
16	ILMN_166300	0.58	−0.51	0.67	STOML2	stomatin like 2 [Source:HGNC Symbol;Acc:HGNC:14559]
17	ILMN_167980	0.58	−0.68	0.58	GSTP1	glutathione S−transferase pi 1 [Source:HGNC Symbol;Acc:HC
18	ILMN_179095	0.57	−0.43	0.49	TBCB	tubulin folding cofactor B [Source:HGNC Symbol;Acc:HGNC:
19	ILMN_230984	0.57	−0.74	0.51	FXYD5	FXYD domain containing ion transport regulator 5 [Source:HC
20	ILMN_211563	0.57	−0.46	0.57	CD320	CD320 molecule [Source:HGNC Symbol;Acc:HGNC:16692]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−27	114 / 9054	Colon	Tx_Colon
2	2e−26	116 / 9555	Colon	TssA_Colon
3	3e−25	127 / 12298	Chror	2_TssA_Melanocytes
4	3e−23	112 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
5	2e−21	67 / 3450	Chror	4_TxTrans_Fibroblasts
6	3e−21	121 / 11836	Chror	3_TssF_Melanocytes
7	1e−20	125 / 12983	Chror	2_TssA_Neuronal_Progenitor
8	3e−20	118 / 11455	Chror	2_TssA_Fibroblasts
9	3e−19	94 / 7354	Colon	TssF_Colon
10	4e−18	107 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	7e−18	78 / 5356	Lympl	HOPP_Txn_transition
12	2e−17	80 / 5699	Chror	6_EnhG_Melanocytes
13	4e−16	37 / 1304	CC	mitochondrion
14	1e−15	96 / 8568	Colon	TxWk_Colon
15	9e−15	52 / 2845	Colon	TxEnhG1_Colon
16	6e−14	85 / 7275	Lympl	HOPP_Txn_elongation
17	9e−14	67 / 4795	Chror	6_EnhG_Fibroblasts
18	2e−12	35 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
19	3e−12	101 / 10430	Brain	Overlap_fetal_midbrain_Quies
20	9e−12	102 / 10779	Colon	Enh_Colon
21	2e−11	95 / 9635	Chror	3_TssF_Fibroblasts
22	3e−11	86 / 8226	Lympl	HOPP_Active_promoter
23	1e−10	71 / 6138	Colon	TssD2_Colon
24	2e−10	18 / 450	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
25	4e−10	100 / 10999	Colon	TssWk_Colon
26	7e−10	16 / 374	CC	mitochondrial inner membrane
27	8e−10	27 / 1167	Refer	PROTEINATLAS_gallbladder
28	1e−09	24 / 933	Refer	PROTEINATLAS_adrenal gland
29	2e−09	23 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
30	7e−09	8 / 69	BP	mitochondrial translational elongation
31	1e−08	34 / 2028	Chror	4_TxTrans_Melanocytes
32	2e−08	25 / 1176	Refer	PROTEINATLAS_duodenum
33	2e−08	23 / 1013	MF	poly(A) RNA binding
34	3e−08	10 / 154	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
35	4e−08	14 / 371	GSEA	MOOTHA_HUMAN_MITODB_6_2002
36	5e−08	71 / 6970	Chror	5_Tx_Neuronal_Progenitor
37	5e−08	43 / 3164	Brain	Mid_Frontal_Lobe_ZNF
38	7e−08	14 / 388	GSEA	MOOTHA_MITOCHONDRIA
39	1e−07	76 / 7854	Chror	5_Tx_Fibroblasts
40	1e−07	6 / 39	GSEA	CHEN_HOXA5_TARGETS_9HR_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	7e−09	8 / 69	mitochondrial translational elongation
2	2e−07	7 / 71	mitochondrial translational termination
3	4e−05	4 / 32	mitochondrial electron transport, NADH to ubiquinone
4	2e−04	4 / 46	mitochondrial respiratory chain complex I assembly
5	4e−04	6 / 163	rRNA processing
6	7e−04	6 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
7	1e−03	3 / 36	cellular response to UV
8	1e−03	2 / 10	negative regulation of intrinsic apoptotic signaling pathway in response to DN
9	2e−03	2 / 11	positive regulation of transcription from RNA polymerase II promoter in respon
10	2e−03	2 / 12	maturation of LSU−rRNA
11	2e−03	2 / 12	PERK−mediated unfolded protein response
12	3e−03	2 / 13	alternative mRNA splicing, via spliceosome
13	3e−03	2 / 13	cerebellar Purkinje cell layer development
14	3e−03	2 / 14	cellular response to interferon−beta
15	3e−03	2 / 14	positive regulation of telomerase RNA localization to Cajal body

Brain

Rank	p−value	#in/all	Geneset
1	3e−23	112 / 9504	Overlap_fetal_midbrain_K9K27me3
2	4e−18	107 / 9815	Overlap_fetal_midbrain_ReprPC
3	3e−12	101 / 10430	Overlap_fetal_midbrain_Quies
4	5e−08	43 / 3164	Mid_Frontal_Lobe_ZNF
5	4e−06	59 / 5936	Overlap_fetal_midbrain_HetRpts
6	2e−05	16 / 796	Overlap_fetal_midbrain_ZNF
7	3e−04	14 / 818	Mid_Frontal_Lobe_Het
8	3e−03	20 / 1728	Fetal_ReprPCWk
9	2e−02	11 / 906	Fetal_HetRpts
10	4e−02	5 / 328	Fetal_Het
11	5e−02	68 / 9917	Overlap_fetal_midbrain_ReprPCWk
12	3e−01	2 / 180	Overlap_fetal_midbrain_Het
13	4e−01	17 / 2654	Fetal_Quies
14	4e−01	3 / 386	Fetal_ZNF
15	5e−01	1 / 110	Overlap_fetal_midbrain_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	5 / 301	SPANG_BCL6−index2
2	0.05	1 / 9	GENTLES_modul5
3	0.07	2 / 73	SHAUGHNESSY_MM high risk
4	0.08	1 / 14	GENTLES_modul10
5	0.08	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.09	3 / 178	SPANG_LPS−index2
7	0.17	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.20	1 / 39	ZHANG_MM up
9	0.24	1 / 46	PanCan_DNARepair_geneset_nanostring
10	0.26	0 / 13	RHODES_CANCER_META_SIGNATURE
11	0.37	4 / 527	Lembcke_Normal vs Adenoma
12	0.40	0 / 14	LIU_PROSTATE_CANCER_UP
13	0.50	1 / 117	PanCan_Driver_Gene_geneset_nanostring
14	0.52	1 / 125	PanCan_CC+Apop_geneset_nanostring
15	0.55	1 / 136	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	4e−16	37 / 1304	mitochondrion
2	7e−10	16 / 374	mitochondrial inner membrane
3	7e−07	5 / 29	mitochondrial large ribosomal subunit
4	5e−06	51 / 4828	nucleus
5	4e−05	4 / 33	mitochondrial respiratory chain complex I
6	5e−05	31 / 2535	nucleoplasm
7	3e−04	13 / 721	nucleolus
8	1e−03	3 / 36	condensed nuclear chromosome
9	2e−03	12 / 775	endoplasmic reticulum
10	3e−03	3 / 51	proteasome complex
11	4e−03	2 / 16	proteasome core complex
12	4e−03	25 / 2464	extracellular exosome
13	5e−03	4 / 115	nuclear chromosome, telomeric region
14	5e−03	2 / 18	telomerase holoenzyme complex
15	6e−03	2 / 20	mitochondrial small ribosomal subunit

Chr

Rank	p−value	#in/all	Geneset
1	0.04	7 / 536	Chr 22
2	0.07	7 / 619	Chr 20
3	0.11	9 / 954	Chr 9
4	0.11	9 / 959	Chr 16
5	0.12	12 / 1411	Chr 11
6	0.15	10 / 1170	Chr 7
7	0.17	9 / 1060	Chr 5
8	0.32	3 / 342	Chr 18
9	0.36	10 / 1467	Chr 19
10	0.51	8 / 1318	Chr 17
11	0.52	7 / 1160	Chr 12
12	0.70	5 / 994	Chr X
13	0.71	2 / 422	Chr 13
14	0.72	6 / 1211	Chr 6
15	0.78	4 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−25	127 / 12298	2_TssA_Melanocytes
2	2e−21	67 / 3450	4_TxTrans_Fibroblasts
3	3e−21	121 / 11836	3_TssF_Melanocytes
4	1e−20	125 / 12983	2_TssA_Neuronal_Progenitor
5	3e−20	118 / 11455	2_TssA_Fibroblasts
6	2e−17	80 / 5699	6_EnhG_Melanocytes
7	9e−14	67 / 4795	6_EnhG_Fibroblasts
8	2e−11	95 / 9635	3_TssF_Fibroblasts
9	1e−08	34 / 2028	4_TxTrans_Melanocytes
10	5e−08	71 / 6970	5_Tx_Neuronal_Progenitor
11	1e−07	76 / 7854	5_Tx_Fibroblasts
12	1e−06	79 / 8771	5_Tx_Melanocytes
13	6e−06	12 / 416	4_TxTrans_Neuronal_Progenitor
14	1e−05	58 / 5956	3_TssF_Neuronal_Progenitor
15	3e−05	98 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−27	114 / 9054	Tx_Colon
2	2e−26	116 / 9555	TssA_Colon
3	3e−19	94 / 7354	TssF_Colon
4	1e−15	96 / 8568	TxWk_Colon
5	9e−15	52 / 2845	TxEnhG1_Colon
6	2e−12	35 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	9e−12	102 / 10779	Enh_Colon
8	1e−10	71 / 6138	TssD2_Colon
9	4e−10	100 / 10999	TssWk_Colon
10	7e−07	79 / 8678	Quies3_Colon
11	8e−06	17 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
12	1e−05	54 / 5373	EnhWk1_Colon
13	6e−05	20 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	5e−04	15 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
15	3e−03	15 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Glio

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 55	Stuehler_Proteins_up_in_STS
2	1e−02	6 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	2e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
4	4e−02	5 / 315	Up
5	6e−02	16 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	9e−02	2 / 84	GIEZELT_GBM_STS_up_VS_LTS
7	1e−01	2 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	1e−01	1 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
9	2e−01	1 / 32	Donson−Misc immune function−associated with LTS in HGA
10	2e−01	1 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
11	2e−01	7 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
12	2e−01	15 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
13	2e−01	2 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	2e−01	1 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
15	2e−01	2 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−10	18 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	2e−09	23 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	3e−08	10 / 154	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
4	4e−08	14 / 371	MOOTHA_HUMAN_MITODB_6_2002
5	7e−08	14 / 388	MOOTHA_MITOCHONDRIA
6	1e−07	6 / 39	CHEN_HOXA5_TARGETS_9HR_DN
7	5e−07	13 / 389	GARY_CD5_TARGETS_DN
8	6e−07	10 / 217	PENG_RAPAMYCIN_RESPONSE_DN
9	7e−07	25 / 1417	PUJANA_BRCA1_PCC_NETWORK
10	2e−06	16 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
11	2e−06	16 / 669	PUJANA_CHEK2_PCC_NETWORK
12	5e−06	16 / 723	GRADE_COLON_CANCER_UP
13	7e−06	10 / 282	PENG_GLUTAMINE_DEPRIVATION_DN
14	8e−06	8 / 171	BURTON_ADIPOGENESIS_6
15	8e−06	13 / 499	TIEN_INTESTINE_PROBIOTICS_24HR_UP

HM

Rank	p−value	#in/all	Geneset
1	6e−07	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	6e−04	6 / 176	HALLMARK_ADIPOGENESIS
3	3e−03	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	7e−03	4 / 130	HALLMARK_DNA_REPAIR
5	2e−02	4 / 179	HALLMARK_G2M_CHECKPOINT
6	4e−02	2 / 54	HALLMARK_MYC_TARGETS_V2
7	8e−02	3 / 170	HALLMARK_MYC_TARGETS_V1
8	8e−02	3 / 173	HALLMARK_E2F_TARGETS
9	9e−02	3 / 183	HALLMARK_GLYCOLYSIS
10	2e−01	2 / 137	HALLMARK_UV_RESPONSE_UP
11	2e−01	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
12	3e−01	2 / 185	HALLMARK_MTORC1_SIGNALING
13	3e−01	2 / 189	HALLMARK_HYPOXIA
14	5e−01	1 / 132	HALLMARK_UV_RESPONSE_DN
15	6e−01	1 / 162	HALLMARK_ALLOGRAFT_REJECTION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.008	5 / 211	Homuth_BMI−associated−genes_DN
2	0.213	2 / 147	Homuth_BMI−associated−genes_UP
3	1.000	0 / 94	DUMEAUX_Smoking enriched genes
4	1.000	0 / 10	DUMEAUX_Smoking literature genes up
5	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.000	0 / 17	DUMEAUX_High bmi enriched genes
13	1.000	0 / 31	DUMEAUX_Fasting enriched genes
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−18	78 / 5356	HOPP_Txn_transition
2	6e−14	85 / 7275	HOPP_Txn_elongation
3	3e−11	86 / 8226	HOPP_Active_promoter
4	1e−06	75 / 8098	HOPP_Weak_promoter
5	5e−05	15 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	5e−05	15 / 777	WIRTH_lymphoma937_spot D
7	8e−05	4 / 39	CARO_OxPhos_in_DLBCL_UP
8	4e−04	4 / 60	SPANG_BAFF 9hrs DN
9	1e−03	9 / 455	SPANG_CD40 6hrs DN
10	2e−03	6 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
11	2e−03	6 / 232	WIRTH_lymphoma937_spot B
12	5e−03	4 / 115	ROSOLOWSKI_green total
13	5e−03	2 / 18	Aukema_BCL2 UP_BCL6 DN
14	6e−03	58 / 7448	HOPP_Strong_enhancer
15	7e−03	6 / 283	TARTE_Plasmablast signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−08	23 / 1013	poly(A) RNA binding
2	1e−07	82 / 8818	protein binding
3	4e−05	4 / 32	NADH dehydrogenase (ubiquinone) activity
4	4e−04	4 / 59	damaged DNA binding
5	5e−04	6 / 169	structural constituent of ribosome
6	2e−03	2 / 12	exonuclease activity
7	2e−03	3 / 46	ligand−dependent nuclear receptor transcription coactivator activity
8	3e−03	2 / 14	telomerase RNA binding
9	5e−03	5 / 185	magnesium ion binding
10	5e−03	2 / 18	threonine−type endopeptidase activity
11	6e−03	3 / 62	p53 binding
12	6e−03	3 / 62	syntaxin binding
13	1e−02	3 / 77	electron carrier activity
14	1e−02	3 / 82	unfolded protein binding
15	1e−02	2 / 29	rRNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−05	11 / 425	hsa−let−7b
2	2e−04	6 / 144	hsa−miR−140−5p
3	4e−04	4 / 58	hsa−miR−379
4	8e−04	4 / 71	hsa−miR−939
5	9e−04	8 / 342	hsa−let−7e
6	2e−03	4 / 85	hsa−miR−510
7	2e−03	8 / 382	hsa−let−7c
8	2e−03	3 / 46	hsa−miR−658
9	2e−03	3 / 46	hsa−miR−575
10	3e−03	7 / 316	hsa−let−7f
11	4e−03	3 / 52	hsa−miR−940
12	4e−03	7 / 343	hsa−let−7a
13	5e−03	5 / 191	hsa−miR−222
14	7e−03	3 / 66	hsa−miR−550
15	8e−03	3 / 71	hsa−miR−1266

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−10	27 / 1167	PROTEINATLAS_gallbladder
2	1e−09	24 / 933	PROTEINATLAS_adrenal gland
3	2e−08	25 / 1176	PROTEINATLAS_duodenum
4	2e−07	21 / 959	PROTEINATLAS_nasopharynx
5	4e−07	23 / 1194	PROTEINATLAS_stomach
6	7e−07	16 / 619	PROTEINATLAS_salivary gland
7	8e−07	23 / 1239	PROTEINATLAS_testis
8	1e−06	21 / 1063	PROTEINATLAS_tonsil
9	1e−06	14 / 490	PROTEINATLAS_heart muscle
10	1e−06	23 / 1268	PROTEINATLAS_colon
11	1e−06	22 / 1173	PROTEINATLAS_rectum
12	1e−06	18 / 816	PROTEINATLAS_endometrium
13	2e−06	19 / 912	PROTEINATLAS_urinary bladder
14	2e−06	17 / 740	PROTEINATLAS_esophagus
15	2e−06	20 / 1003	PROTEINATLAS_appendix

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

TF

Rank	p−value	#in/all	Geneset
1	7e−07	55 / 5067	ICGC_Taf1_targets
2	4e−06	24 / 1452	ICGC_Six5_targets
3	6e−06	24 / 1498	ICGC_Ets1_targets
4	8e−06	47 / 4345	ICGC_Zeb1_targets
5	1e−05	30 / 2215	ICGC_GabpPcr2_targets
6	1e−05	64 / 6868	ICGC_Elf1_targets
7	2e−05	54 / 5518	ICGC_Stat5_targets
8	3e−05	20 / 1231	KIM_MYC targets
9	4e−05	53 / 5442	ICGC_Pmlsc71910_targets
10	6e−05	56 / 5984	ICGC_Mta3_targets
11	8e−05	64 / 7247	ICGC_Runx3_targets
12	1e−04	44 / 4362	ICGC_Creb1_targets
13	1e−04	57 / 6267	ICGC_Yy1_targets
14	1e−04	51 / 5383	ICGC_Sp1_targets
15	3e−04	49 / 5312	ICGC_Tcf12_targets

Underexpression Spots

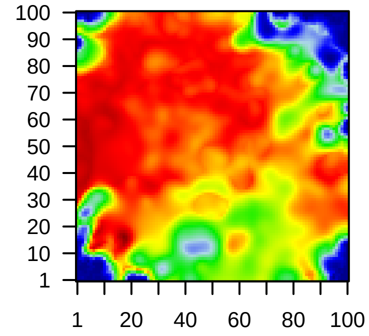
Spot Summary: k

metagenes = 102
genes = 731

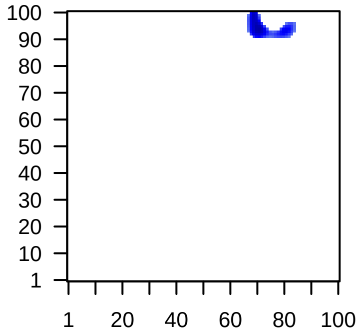
<r> metagenes = 0.88
<r> genes = 0.21
beta: r2= 6.44 / log p= −Inf

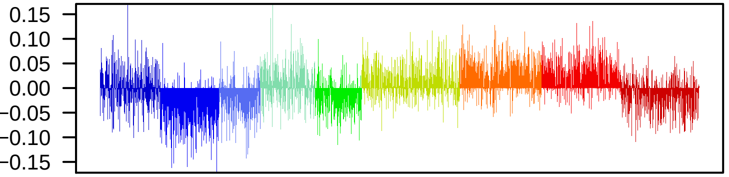
samples with spot = 13 (0.4 %)
A * : 1 (0.3 %)
A F * : 3 (1 %)
F * : 2 (0.4 %)
F J * : 4 (0.9 %)
J * : 3 (0.7 %)

Overview Map



Spot





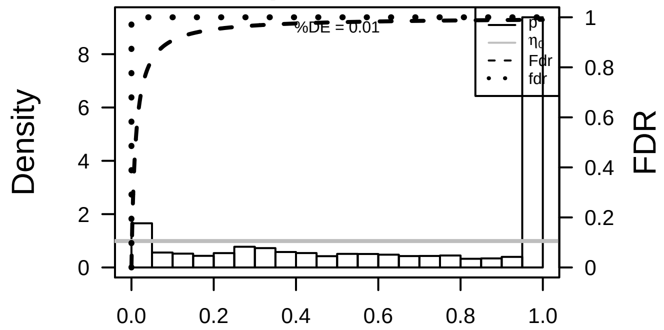
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166126	1.62	−1.38	0.16		
2	ILMN_324366	0.8	−0.75	0.24	LOC613037	Homo sapiens nuclear pore complex interacting protein meml
3	ILMN_175378	0.76	−0.58	0.34	ZNF266	zinc finger protein 266 [Source:HGNC Symbol;Acc:HGNC:13
4	ILMN_179985	0.75	−0.61	0.25	NOMO3	NODAL modulator 3 [Source:HGNC Symbol;Acc:HGNC:2524
5	ILMN_173623	0.69	−0.52	0.4	CHTOP	chromatin target of PRMT1 [Source:HGNC Symbol;Acc:HGN
6	ILMN_172598	0.69	−0.36	0.27	EIF3CL	eukaryotic translation initiation factor 3 subunit C−like [Source
7	ILMN_166733	0.66	−0.74	0.15		
8	ILMN_323697	0.64	−0.41	0.23	LINC00667	long intergenic non−protein coding RNA 667 [Source:HGNC
9	ILMN_173005	0.63	−0.55	0.1		
10	ILMN_322859	0.63	−0.45	0.44		
11	ILMN_172524	0.61	−0.6	0.55	GSTK1	glutathione S−transferase kappa 1 [Source:HGNC Symbol;Ac
12	ILMN_185990	0.61	−0.37	0.35	TRAPPC2L	trafficking protein particle complex 2 like [Source:HGNC Syml
13	ILMN_206932	0.6	−0.4	0.21		
14	ILMN_167183	0.6	−0.54	0.34	TAF1C	TATA−box binding protein associated factor, RNA polymerase
15	ILMN_323822	0.6	−0.43	0.22		
16	ILMN_323532	0.6	−0.39	0.25		Small nucleolar RNA SNORA71 [Source:RFAM;Acc:RF0005
17	ILMN_172804	0.59	−0.52	0.58		
18	ILMN_176479	0.58	−0.45	0.6	PSMB2	proteasome subunit beta 2 [Source:HGNC Symbol;Acc:HGN
19	ILMN_173786	0.56	−0.5	0.65	PSMB4	proteasome subunit beta 4 [Source:HGNC Symbol;Acc:HGN
20	ILMN_323798	0.55	−0.4	0.46	CARNS1	carnosine synthase 1 [Source:HGNC Symbol;Acc:HGNC:292

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−84	486 / 9555	Colon	TssA_Colon
2	7e−83	471 / 9054	Colon	Tx_Colon
3	8e−80	541 / 12298	Chror	2_TssA_Melanocytes
4	2e−78	452 / 8568	Colon	TxWk_Colon
5	1e−69	542 / 12983	Chror	2_TssA_Neuronal_Progenitor
6	1e−69	510 / 11455	Chror	2_TssA_Fibroblasts
7	3e−69	463 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
8	3e−67	515 / 11836	Chror	3_TssF_Melanocytes
9	3e−64	396 / 7354	Colon	TssF_Colon
10	1e−55	449 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	7e−51	413 / 8771	Chror	5_Tx_Melanocytes
12	1e−50	370 / 7275	Lympl	HOPP_Txn_elongation
13	3e−49	395 / 8226	Lympl	HOPP_Active_promoter
14	1e−48	357 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	1e−48	383 / 7854	Chror	5_Tx_Fibroblasts
16	2e−46	313 / 5699	Chror	6_EnhG_Melanocytes
17	2e−44	279 / 4795	Chror	6_EnhG_Fibroblasts
18	5e−42	312 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
19	2e−41	418 / 9635	Chror	3_TssF_Fibroblasts
20	4e−39	434 / 10430	Brain	Overlap_fetal_midbrain_Quies
21	6e−39	312 / 6138	Colon	TssD2_Colon
22	4e−37	383 / 8678	Colon	Quies3_Colon
23	7e−37	438 / 10779	Colon	Enh_Colon
24	4e−36	281 / 5356	Lympl	HOPP_Txn_transition
25	1e−33	276 / 5373	Colon	EnhWk1_Colon
26	2e−33	209 / 3450	Chror	4_TxTrans_Fibroblasts
27	2e−31	194 / 3164	Brain	Mid_Frontal_Lobe_ZNF
28	2e−29	461 / 12393	Chror	15_Quies_Neuronal_Progenitor
29	8e−29	255 / 5067	TF	ICGC_Taf1_targets
30	4e−26	225 / 4362	TF	ICGC_Creb1_targets
31	2e−25	275 / 5956	Chror	3_TssF_Neuronal_Progenitor
32	2e−24	336 / 8098	Lympl	HOPP_Weak_promoter
33	2e−24	414 / 10999	Colon	TssWk_Colon
34	2e−24	167 / 2845	Colon	TxEnhG1_Colon
35	6e−22	252 / 5518	TF	ICGC_Stat5_targets
36	2e−21	73 / 772	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
37	3e−21	449 / 12741	Chror	7_Enh_Melanocytes
38	3e−21	73 / 777	Lympl	WIRTH_lymphoma937_spot D
39	2e−20	203 / 4131	TF	ICGC_Nfatc1_targets
40	6e−20	244 / 5442	TF	ICGC_Pmlsc71910_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.7	3 / 142	HORVATH_aging_genes meth UP
2	0.8	2 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	3e−07	9 / 36	PanCan_HK_geneset_nanostring
2	7e−04	8 / 73	SHAUGHNESSY_MM high risk
3	9e−04	27 / 527	Lembcke_Normal vs Adenoma
4	4e−02	2 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	4e−02	2 / 13	LIU_LIVER_CANCER
6	5e−02	4 / 54	KUIPER_MM poor survival
7	7e−02	2 / 16	GENTLES_modul7
8	1e−01	3 / 46	PanCan_DNARepair_geneset_nanostring
9	1e−01	2 / 24	PanCan_Notch_geneset_nanostring
10	2e−01	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
11	2e−01	1 / 9	GENTLES_modul5
12	2e−01	5 / 125	PanCan_CC+Apop_geneset_nanostring
13	3e−01	1 / 13	WANG_ER_DN
14	3e−01	1 / 14	GENTLES_modul4
15	3e−01	1 / 14	GENTLES_modul10

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−80	541 / 12298	2_TssA_Melanocytes
2	1e−69	542 / 12983	2_TssA_Neuronal_Progenitor
3	1e−69	510 / 11455	2_TssA_Fibroblasts
4	3e−67	515 / 11836	3_TssF_Melanocytes
5	7e−51	413 / 8771	5_Tx_Melanocytes
6	1e−48	357 / 6970	5_Tx_Neuronal_Progenitor
7	1e−48	383 / 7854	5_Tx_Fibroblasts
8	2e−46	313 / 5699	6_EnhG_Melanocytes
9	2e−44	279 / 4795	6_EnhG_Fibroblasts
10	2e−41	418 / 9635	3_TssF_Fibroblasts
11	2e−33	209 / 3450	4_TxTrans_Fibroblasts
12	2e−29	461 / 12393	15_Quies_Neuronal_Progenitor
13	2e−25	275 / 5956	3_TssF_Neuronal_Progenitor
14	3e−21	449 / 12741	7_Enh_Melanocytes
15	3e−19	421 / 11847	7_Enh_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−17	71 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	9e−15	63 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	1e−13	33 / 262	MANALO_HYPOXIA_DN
4	4e−13	46 / 509	PARENT_MTOR_SIGNALING_UP
5	3e−12	42 / 459	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
6	8e−12	64 / 952	DANG_BOUND_BY_MYC
7	4e−11	81 / 1417	PUJANA_BRCA1_PCC_NETWORK
8	5e−10	29 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
9	1e−09	48 / 693	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
10	3e−09	40 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
11	1e−08	48 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
12	2e−08	40 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
13	8e−08	43 / 666	BENPORATH_MYC_MAX_TARGETS
14	2e−07	77 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
15	3e−07	21 / 217	PENG_RAPAMYCIN_RESPONSE_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−50	370 / 7275	HOPP_Txn_elongation
2	3e−49	395 / 8226	HOPP_Active_promoter
3	4e−36	281 / 5356	HOPP_Txn_transition
4	2e−24	336 / 8098	HOPP_Weak_promoter
5	2e−21	73 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	3e−21	73 / 777	WIRTH_lymphoma937_spot D
7	1e−18	300 / 7448	HOPP_Strong_enhancer
8	8e−10	72 / 1270	SPANG_BCR UP
9	8e−07	228 / 6559	HOPP_Weak_txn
10	1e−06	33 / 493	WIRTH_lymphoma937_spot J
11	4e−06	31 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
12	1e−05	19 / 232	WIRTH_lymphoma937_spot B
13	2e−05	18 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
14	6e−04	50 / 1169	SPANG_BCR DN
15	1e−03	219 / 6959	HOPP_Weak_enhancer

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−08	23 / 221	Chaussabel_3,8_Enzymes
2	9e−08	25 / 275	Chaussabel_3,7_Spliceosome
3	2e−07	45 / 740	PROTEINATLAS_esophagus
4	7e−07	61 / 1194	PROTEINATLAS_stomach
5	7e−07	60 / 1167	PROTEINATLAS_gallbladder
6	8e−07	51 / 929	PROTEINATLAS_bronchus
7	2e−06	59 / 1173	PROTEINATLAS_rectum
8	3e−06	57 / 1138	PROTEINATLAS_small intestine
9	4e−06	55 / 1097	PROTEINATLAS_kidney
10	1e−05	60 / 1268	PROTEINATLAS_colon
11	2e−05	47 / 933	PROTEINATLAS_adrenal gland
12	2e−05	46 / 912	PROTEINATLAS_fallopian tube
13	3e−05	55 / 1176	PROTEINATLAS_duodenum
14	5e−05	45 / 912	PROTEINATLAS_urinary bladder
15	6e−05	48 / 1003	PROTEINATLAS_appendix

BP

Rank	p−value	#in/all	Geneset
1	4e−06	25 / 335	protein transport
2	5e−06	74 / 1643	transcription, DNA−templated
3	1e−05	10 / 67	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
4	1e−05	17 / 187	DNA repair
5	2e−05	10 / 71	mitochondrial translational termination
6	2e−05	9 / 57	NIK/NF−kappaB signaling
7	3e−05	9 / 62	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
8	4e−05	30 / 511	apoptotic process
9	5e−05	19 / 255	viral process
10	6e−05	9 / 66	anaphase−promoting complex−dependent catabolic process
11	8e−05	9 / 69	mitochondrial translational elongation
12	9e−05	10 / 86	mRNA export from nucleus
13	1e−04	7 / 43	regulation of cellular amino acid metabolic process
14	2e−04	15 / 196	mRNA splicing, via spliceosome
15	3e−04	7 / 48	antigen processing and presentation of exogenous peptide antigen via MHC c

CC

Rank	p−value	#in/all	Geneset
1	2e−13	82 / 1304	mitochondrion
2	1e−12	126 / 2535	nucleoplasm
3	2e−11	197 / 4828	nucleus
4	1e−08	128 / 2979	cytosol
5	3e−07	29 / 374	mitochondrial inner membrane
6	7e−07	43 / 721	nucleolus
7	9e−06	22 / 287	mitochondrial matrix
8	2e−05	170 / 4822	cytoplasm
9	5e−05	8 / 51	proteasome complex
10	2e−04	8 / 60	nuclear pore
11	4e−04	5 / 24	mitochondrial ribosome
12	9e−04	11 / 135	cilium
13	1e−03	6 / 44	Cajal body
14	1e−03	28 / 561	intracellular membrane−bounded organelle
15	1e−03	8 / 79	spliceosomal complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−84	486 / 9555	TssA_Colon
2	7e−83	471 / 9054	Tx_Colon
3	2e−78	452 / 8568	TxWk_Colon
4	3e−64	396 / 7354	TssF_Colon
5	6e−39	312 / 6138	TssD2_Colon
6	4e−37	383 / 8678	Quies3_Colon
7	7e−37	438 / 10779	Enh_Colon
8	1e−33	276 / 5373	EnhWk1_Colon
9	2e−24	414 / 10999	TssWk_Colon
10	2e−24	167 / 2845	TxEnhG1_Colon
11	2e−15	72 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	1e−09	126 / 2810	EnhA_Colon
13	1e−09	79 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	4e−08	96 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
15	2e−07	49 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−07	11 / 54	HALLMARK_MYC_TARGETS_V2
2	2e−04	12 / 130	HALLMARK_DNA_REPAIR
3	1e−03	11 / 138	HALLMARK_FATTY_ACID_METABOLISM
4	4e−03	12 / 185	HALLMARK_MTORC1_SIGNALING
5	6e−03	11 / 173	HALLMARK_E2F_TARGETS
6	6e−02	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	8e−02	8 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	8e−02	8 / 170	HALLMARK_MYC_TARGETS_V1
9	9e−02	5 / 91	HALLMARK_PEROXISOME
10	9e−02	8 / 175	HALLMARK_XENOBIOTIC_METABOLISM
11	2e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
12	2e−01	7 / 177	HALLMARK_MITOTIC_SPINDLE
13	3e−01	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	3e−01	5 / 137	HALLMARK_UV_RESPONSE_UP
15	4e−01	6 / 183	HALLMARK_GLYCOLYSIS

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	17 / 288	hsa−miR−34a
2	0.003	6 / 54	hsa−miR−28−3p
3	0.003	10 / 134	hsa−miR−198
4	0.004	8 / 97	hsa−miR−526a
5	0.005	6 / 61	hsa−miR−671−5p
6	0.006	5 / 45	hsa−miR−524−3p
7	0.011	5 / 51	hsa−miR−519b−5p
8	0.011	5 / 51	hsa−miR−519c−5p
9	0.014	5 / 54	hsa−miR−330−5p
10	0.014	7 / 97	hsa−miR−1301
11	0.016	4 / 37	hsa−miR−518e
12	0.016	5 / 56	hsa−miR−518d−5p
13	0.016	5 / 56	hsa−miR−520c−5p
14	0.016	9 / 147	hsa−miR−506
15	0.017	8 / 124	hsa−miR−515−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	3 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	3e−69	463 / 9504	Overlap_fetal_midbrain_K9K27me3
2	1e−55	449 / 9815	Overlap_fetal_midbrain_ReprPC
3	5e−42	312 / 5936	Overlap_fetal_midbrain_HetRpts
4	4e−39	434 / 10430	Overlap_fetal_midbrain_Quies
5	2e−31	194 / 3164	Mid_Frontal_Lobe_ZNF
6	2e−15	358 / 9917	Overlap_fetal_midbrain_ReprPCWk
7	4e−09	87 / 1728	Fetal_ReprPCWk
8	6e−07	47 / 818	Mid_Frontal_Lobe_Het
9	9e−06	43 / 796	Overlap_fetal_midbrain_ZNF
10	5e−04	99 / 2709	Mid_Frontal_Lobe_HetRpts
11	1e−03	32 / 681	Overlap_fetal_midbrain_EnhP
12	2e−03	39 / 906	Fetal_HetRpts
13	2e−02	26 / 630	Mid_Frontal_Lobe_EnhP
14	2e−02	10 / 180	Overlap_fetal_midbrain_Het
15	8e−02	39 / 1171	Fetal_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	50 / 959	Chr 16
2	2e−03	26 / 536	Chr 22
3	1e−02	37 / 954	Chr 9
4	6e−02	47 / 1411	Chr 11
5	1e−01	39 / 1217	Chr 3
6	1e−01	21 / 619	Chr 20
7	3e−01	43 / 1467	Chr 19
8	4e−01	42 / 1492	Chr 2
9	4e−01	64 / 2323	Chr 1
10	5e−01	21 / 768	Chr 14
11	5e−01	31 / 1170	Chr 7
12	6e−01	7 / 289	Chr 21
13	7e−01	33 / 1318	Chr 17
14	7e−01	18 / 769	Chr 15
15	8e−01	27 / 1160	Chr 12

Glio

Rank	p−value	#in/all	Geneset
1	3e−07	92 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−06	46 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	7e−06	78 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−03	18 / 315	Up
5	2e−03	6 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	2e−02	9 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	7e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
8	8e−02	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
9	8e−02	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
10	8e−02	13 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	1e−01	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	1e−01	2 / 25	Barbus_GBM_STS_vs._LTS
13	1e−01	4 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	1e−01	15 / 419	Down_a
15	2e−01	3 / 55	Stuehler_Proteins_up_in_STS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.009	4 / 31	DUMEAUX_Fasting enriched genes
2	0.027	2 / 10	DUMEAUX_Smoking literature genes up
3	0.073	2 / 17	DUMEAUX_High bmi enriched genes
4	0.348	5 / 147	Homuth_BMI−associated−genes_UP
5	0.454	3 / 94	DUMEAUX_Smoking enriched genes
6	0.659	5 / 211	Homuth_BMI−associated−genes_DN
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−09	61 / 1013	poly(A) RNA binding
2	1e−08	301 / 8818	protein binding
3	1e−06	79 / 1717	metal ion binding
4	1e−05	62 / 1329	ATP binding
5	1e−05	9 / 56	ATP−dependent RNA helicase activity
6	8e−05	5 / 18	DNA helicase activity
7	2e−04	17 / 232	ligase activity
8	9e−04	4 / 17	S−adenosylmethionine−dependent methyltransferase activity
9	2e−03	17 / 283	nucleotide binding
10	2e−03	4 / 21	translation initiation factor binding
11	3e−03	3 / 12	phosphatidic acid binding
12	3e−03	3 / 12	pseudouridine synthase activity
13	4e−03	17 / 311	enzyme binding
14	5e−03	10 / 145	nucleic acid binding
15	6e−03	5 / 44	methylated histone binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	8e−29	255 / 5067	ICGC_Taf1_targets
2	4e−26	225 / 4362	ICGC_Creb1_targets
3	6e−22	252 / 5518	ICGC_Stat5_targets
4	2e−20	203 / 4131	ICGC_Nfatc1_targets
5	6e−20	244 / 5442	ICGC_Pmlsc71910_targets
6	1e−19	270 / 6322	ICGC_Tcf3_targets
7	2e−19	243 / 5466	ICGC_Nficsc81335_targets
8	3e−19	102 / 1478	ICGC_Myc_targets
9	7e−19	223 / 4881	ICGC_Atf2_targets
10	4e−18	273 / 6578	ICGC_Pou2_targets
11	7e−18	281 / 6868	ICGC_Elf1_targets
12	1e−17	206 / 4468	ICGC_Egr1_targets
13	3e−17	127 / 2215	ICGC_GabpPcr2_targets
14	6e−17	233 / 5383	ICGC_Sp1_targets
15	9e−17	217 / 4890	ICGC_Bclaf101388_targets

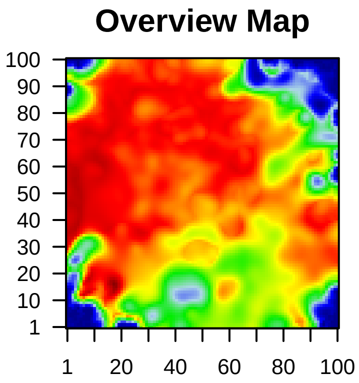
Underexpression Spots

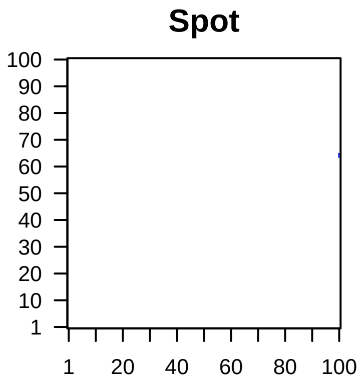
Spot Summary: I

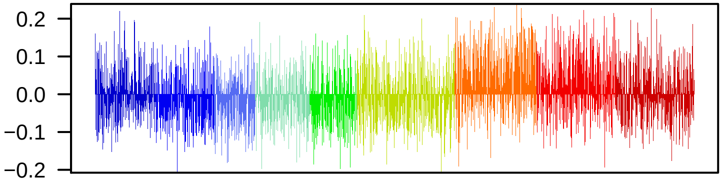
metagenes = 2
genes = 140

<r> metagenes = 1
<r> genes = 0.29
beta: r2= 6.08 / log p= −Inf

samples with spot = 273 (8.1 %)
A * : 24 (7 %)
A C * : 12 (3.7 %)
A C F * : 3 (1.3 %)
A F * : 7 (2.3 %)
C F * : 10 (3.8 %)
F * : 27 (4.9 %)
F J * : 97 (21 %)
J * : 65 (14.5 %)
N * : 28 (6.3 %)





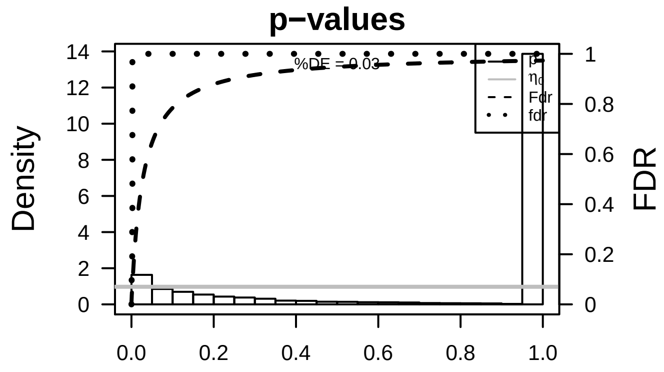


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324359	1.46	−0.55	0.42		
2	ILMN_167657	1.42	−1.17	0.43	IKZF1	IKAROS family zinc finger 1 [Source:HGNC Symbol;Acc:HGN
3	ILMN_234913	1.35	−0.37	0.3	CDC42SE1	CDC42 small effector 1 [Source:HGNC Symbol;Acc:HGNC:1
4	ILMN_180478	0.87	−0.92	0.57	CCAR2	cell cycle and apoptosis regulator 2 [Source:HGNC Symbol;A
5	ILMN_166703	0.85	−0.74	0.28	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit [So
6	ILMN_323500	0.81	−0.62	0.46	LINC00869	long intergenic non−protein coding RNA 869 [Source:HGNC
7	ILMN_174282	0.78	−0.67	0.45	SPATA13	spermatogenesis associated 13 [Source:HGNC Symbol;Acc:
8	ILMN_168010	0.77	−0.56	0.53	COL4A3BP	collagen type IV alpha 3 binding protein [Source:HGNC Sym
9	ILMN_235777	0.73	−0.64	0.46	TCEA1	transcription elongation factor A1 [Source:HGNC Symbol;Acc
10	ILMN_175710	0.73	−0.58	0.63	MARCH6	membrane associated ring−CH−type finger 6 [Source:HGNC
11	ILMN_177315	0.7	−0.71	0.38		
12	ILMN_168831	0.7	−0.7	0.37		FSHD region gene 1 family member B, pseudogene [Source:
13	ILMN_175051	0.69	−0.39	0.62	ALYREF	Aly/REF export factor [Source:HGNC Symbol;Acc:HGNC:190
14	ILMN_174205	0.67	−0.32	0.59	SERPINB9	serpin family B member 9 [Source:HGNC Symbol;Acc:HGNC
15	ILMN_174857	0.66	−0.57	0.61		
16	ILMN_169140	0.63	−0.73	0.71	LOC645513	
17	ILMN_170333	0.62	−0.25	0.33		
18	ILMN_226956	0.62	−0.71	0.66	ARID4B	AT−rich interaction domain 4B [Source:HGNC Symbol;Acc:H
19	ILMN_180943	0.62	−0.51	0.66		high mobility group box 1 pseudogene 1 [Source:HGNC Sym
20	ILMN_209584	0.62	−0.66	0.61	KAT6A	lysine acetyltransferase 6A [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−32	98 / 7275	Lymp	HOPP_Txn_elongation
2	6e−29	84 / 5356	Lymp	HOPP_Txn_transition
3	9e−23	95 / 8568	Colon	TxWk_Colon
4	2e−22	91 / 7854	Chro	5_Tx_Fibroblasts
5	1e−21	96 / 9054	Colon	Tx_Colon
6	2e−19	92 / 8771	Chro	5_Tx_Melanocytes
7	9e−18	87 / 8226	Lymp	HOPP_Active_promoter
8	2e−17	93 / 9555	Colon	TssA_Colon
9	4e−16	87 / 8678	Colon	Quies3_Colon
10	1e−15	46 / 2535	CC	nucleoplasm
11	3e−15	102 / 12298	Chro	2_TssA_Melanocytes
12	4e−15	70 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
13	5e−14	103 / 12983	Chro	2_TssA_Neuronal_Progenitor
14	1e−13	74 / 6970	Chro	5_Tx_Neuronal_Progenitor
15	2e−13	94 / 10999	Colon	TssWk_Colon
16	9e−13	12 / 119	Refer	Chaussabel_2,11_Replication
17	2e−12	96 / 11836	Chro	3_TssF_Melanocytes
18	4e−12	94 / 11455	Chro	2_TssA_Fibroblasts
19	7e−12	34 / 1797	GSE	PILON_KLF1_TARGETS_DN
20	2e−11	85 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
21	2e−10	82 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
22	6e−10	83 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
23	6e−10	25 / 1168	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
24	1e−09	85 / 10430	Brain	Overlap_fetal_midbrain_Quies
25	1e−09	73 / 8098	Lymp	HOPP_Weak_promoter
26	1e−09	59 / 5699	Chro	6_EnhG_Melanocytes
27	2e−09	28 / 1535	GSE	BLALOCK_ALZHEIMERS_DISEASE_UP
28	3e−09	77 / 8990	Chro	15_Quies_Fibroblasts
29	3e−09	75 / 8613	Chro	7_Enh_Fibroblasts
30	5e−09	68 / 7448	Lymp	HOPP_Strong_enhancer
31	1e−08	92 / 12393	Chro	15_Quies_Neuronal_Progenitor
32	1e−08	26 / 1468	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
33	2e−08	10 / 178	miRN	hsa−miR−300
34	3e−08	10 / 181	miRN	hsa−miR−381
35	3e−08	21 / 1013	MF	poly(A) RNA binding
36	4e−08	14 / 433	miRN	hsa−miR−19b
37	5e−08	50 / 4795	Chro	6_EnhG_Fibroblasts
38	1e−07	22 / 1194	Refer	PROTEINATLAS_stomach
39	2e−07	8 / 120	miRN	hsa−miR−664
40	2e−07	91 / 12741	Chro	7_Enh_Melanocytes



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 59	cell morphogenesis
2	5e−04	10 / 550	positive regulation of transcription, DNA−templated
3	8e−04	9 / 486	negative regulation of transcription, DNA−templated
4	1e−03	2 / 11	microtubule anchoring
5	1e−03	2 / 11	regulation of DNA−templated transcription, elongation
6	2e−03	8 / 435	negative regulation of apoptotic process
7	2e−03	12 / 889	positive regulation of transcription from RNA polymerase II promoter
8	2e−03	3 / 49	regulation of circadian rhythm
9	2e−03	2 / 14	DNA damage response, signal transduction by p53 class mediator
10	2e−03	8 / 457	regulation of transcription from RNA polymerase II promoter
11	3e−03	2 / 15	DNA damage response, signal transduction by p53 class mediator resulting in
12	3e−03	4 / 115	regulation of signal transduction by p53 class mediator
13	3e−03	2 / 16	erythrocyte development
14	5e−03	4 / 134	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
15	5e−03	2 / 21	ATP−dependent chromatin remodeling

Brain

Rank	p−value	#in/all	Geneset
1	4e−15	70 / 5936	Overlap_fetal_midbrain_HetRpts
2	2e−11	85 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−10	82 / 9504	Overlap_fetal_midbrain_K9K27me3
4	6e−10	83 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	1e−09	85 / 10430	Overlap_fetal_midbrain_Quies
6	4e−03	27 / 3164	Mid_Frontal_Lobe_ZNF
7	2e−02	9 / 796	Overlap_fetal_midbrain_ZNF
8	5e−02	20 / 2709	Mid_Frontal_Lobe_HetRpts
9	6e−02	7 / 681	Overlap_fetal_midbrain_EnhP
10	7e−02	10 / 1171	Fetal_EnhP
11	1e−01	6 / 630	Mid_Frontal_Lobe_EnhP
12	1e−01	7 / 818	Mid_Frontal_Lobe_Het
13	2e−01	8 / 1162	Fetal_Enh
14	3e−01	6 / 906	Fetal_HetRpts
15	3e−01	3 / 386	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	2 / 16	GENTLES_modul14
2	0.003	4 / 117	PanCan_Driver_Gene_geneset_nanostring
3	0.077	2 / 91	PanCan_TXmisReg_geneset_nanostring
4	0.131	2 / 125	PanCan_CC+Apop_geneset_nanostring
5	0.179	1 / 39	ZHANG_MM up
6	0.194	3 / 301	SPANG_BCL6−index2
7	0.309	1 / 73	SHAUGHNESSY_MM high risk
8	0.319	1 / 76	PanCan_Wnt_geneset_nanostring
9	0.353	0 / 14	LIU_PROSTATE_CANCER_UP
10	0.532	1 / 150	PanCan_MAPK_geneset_nanostring
11	0.594	1 / 178	SPANG_LPS−index2
12	0.624	1 / 193	PanCan_PI3K_geneset_nanostring
13	0.941	1 / 554	Lembcke_Colonic Inflammation
14	1.000	0 / 13	RHODES_CANCER_META_SIGNATURE
15	1.000	0 / 14	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	1e−15	46 / 2535	nucleoplasm
2	3e−06	15 / 721	nucleolus
3	9e−06	45 / 4822	cytoplasm
4	9e−06	45 / 4828	nucleus
5	1e−04	3 / 18	exon−exon junction complex
6	2e−03	5 / 173	nuclear chromatin
7	6e−03	7 / 422	protein complex
8	8e−03	8 / 561	intracellular membrane−bounded organelle
9	8e−03	2 / 27	heterochromatin
10	1e−02	3 / 87	PML body
11	1e−02	2 / 35	nuclear body
12	2e−02	5 / 287	mitochondrial matrix
13	2e−02	9 / 777	Golgi apparatus
14	3e−02	2 / 49	transcriptional repressor complex
15	3e−02	2 / 53	photoreceptor outer segment

Chr

Rank	p−value	#in/all	Geneset
1	0.009	11 / 959	Chr 16
2	0.023	19 / 2323	Chr 1
3	0.129	7 / 836	Chr 8
4	0.131	9 / 1160	Chr 12
5	0.220	9 / 1318	Chr 17
6	0.358	3 / 422	Chr 13
7	0.376	7 / 1170	Chr 7
8	0.445	6 / 1060	Chr 5
9	0.545	4 / 769	Chr 15
10	0.575	6 / 1211	Chr 6
11	0.671	4 / 902	Chr 4
12	0.713	4 / 954	Chr 9
13	0.740	5 / 1217	Chr 3
14	0.748	3 / 768	Chr 14
15	0.770	1 / 289	Chr 21

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−22	91 / 7854	5_Tx_Fibroblasts
2	2e−19	92 / 8771	5_Tx_Melanocytes
3	3e−15	102 / 12298	2_TssA_Melanocytes
4	5e−14	103 / 12983	2_TssA_Neuronal_Progenitor
5	1e−13	74 / 6970	5_Tx_Neuronal_Progenitor
6	2e−12	96 / 11836	3_TssF_Melanocytes
7	4e−12	94 / 11455	2_TssA_Fibroblasts
8	1e−09	59 / 5699	6_EnhG_Melanocytes
9	3e−09	77 / 8990	15_Quies_Fibroblasts
10	3e−09	75 / 8613	7_Enh_Fibroblasts
11	1e−08	92 / 12393	15_Quies_Neuronal_Progenitor
12	5e−08	50 / 4795	6_EnhG_Fibroblasts
13	2e−07	91 / 12741	7_Enh_Melanocytes
14	9e−07	82 / 11130	15_Quies_Melanocytes
15	1e−04	38 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−23	95 / 8568	TxWk_Colon
2	1e−21	96 / 9054	Tx_Colon
3	2e−17	93 / 9555	TssA_Colon
4	4e−16	87 / 8678	Quies3_Colon
5	2e−13	94 / 10999	TssWk_Colon
6	6e−10	25 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
7	1e−08	26 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
8	1e−06	23 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	7e−06	78 / 10779	Enh_Colon
10	8e−06	60 / 7354	TssF_Colon
11	2e−05	39 / 4034	TssD1_Colon
12	3e−05	21 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
13	9e−05	24 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	4e−04	3 / 29	Marisa_CRC−cluster−c
15	1e−03	14 / 1083	ZNF_Colon

Glio

Rank	p−value	#in/all	Geneset
1	9e−04	12 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	3e−03	20 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−02	3 / 92	Weller_LGG_A_vs_O_DOWN
4	1e−02	14 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	2e−02	5 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	6e−02	14 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	7e−02	1 / 14	Christensen_hypermethylated_in_ependymoma
8	7e−02	1 / 15	VERHAAK_MES subtype
9	7e−02	1 / 15	VERHAAK_NL subtype
10	7e−02	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
11	8e−02	4 / 315	Up
12	1e−01	1 / 24	Martinez_Glio_hypermeth
13	1e−01	1 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
14	2e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	2e−01	1 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−12	34 / 1797	PILON_KLF1_TARGETS_DN
2	2e−09	28 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
3	5e−07	17 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
4	2e−06	16 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	3e−06	19 / 1104	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
6	3e−06	11 / 368	OSMAN_BLADDER_CANCER_UP
7	8e−06	11 / 411	GARY_CD5_TARGETS_UP
8	2e−05	19 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
9	2e−05	11 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
10	3e−05	11 / 471	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN
11	3e−05	7 / 177	MCBRYAN_PUBERTAL_BREAST_4_5WK_DN
12	7e−05	11 / 527	HAMAI_APOPTOSIS_VIA_TRAIL_UP
13	1e−04	10 / 454	SENESE_HDAC3_TARGETS_UP
14	1e−04	8 / 288	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
15	1e−04	8 / 291	DAZARD_RESPONSE_TO_UV_NHEK_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	4 / 185	HALLMARK_HEME_METABOLISM
2	0.07	3 / 189	HALLMARK_HYPOXIA
3	0.07	2 / 87	HALLMARK_PROTEIN_SECRETION
4	0.14	2 / 130	HALLMARK_DNA_REPAIR
5	0.14	2 / 132	HALLMARK_UV_RESPONSE_DN
6	0.18	2 / 151	HALLMARK_APOPTOSIS
7	0.18	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.19	1 / 41	HALLMARK_APICAL_SURFACE
9	0.19	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	0.22	2 / 176	HALLMARK_ADIPOGENESIS
11	0.22	2 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.22	1 / 50	HALLMARK_TGF_BETA_SIGNALING
13	0.22	2 / 177	HALLMARK_KRAS_SIGNALING_DN
14	0.24	2 / 185	HALLMARK_MTORC1_SIGNALING
15	0.24	2 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.7	1 / 211	Homuth_BMI−associated−genes_DN
2	1.0	0 / 94	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	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 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 147	Homuth_BMI−associated−genes_UP
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−32	98 / 7275	HOPP_Txn_elongation
2	6e−29	84 / 5356	HOPP_Txn_transition
3	9e−18	87 / 8226	HOPP_Active_promoter
4	1e−09	73 / 8098	HOPP_Weak_promoter
5	5e−09	68 / 7448	HOPP_Strong_enhancer
6	2e−05	6 / 109	ROSOLOWSKI_blue total
7	3e−05	54 / 6559	HOPP_Weak_txn
8	6e−04	52 / 6959	HOPP_Weak_enhancer
9	7e−04	9 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
10	9e−04	9 / 493	WIRTH_lymphoma937_spot J
11	6e−03	13 / 1169	SPANG_BCR DN
12	2e−02	22 / 2701	HOPP_Repetitive
13	2e−02	2 / 40	Monti_BCR_cluster
14	3e−02	6 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
15	3e−02	6 / 464	WIRTH_lymphoma937_spot I

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	1 / 30	Hugo_melanoma−all−MET_UP
2	0.2	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	3e−08	21 / 1013	poly(A) RNA binding
2	7e−06	68 / 8818	protein binding
3	2e−05	9 / 301	ubiquitin−protein transferase activity
4	2e−05	8 / 232	ligase activity
5	1e−04	3 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
6	3e−04	15 / 1065	zinc ion binding
7	8e−04	6 / 215	transcription regulatory region DNA binding
8	1e−03	2 / 11	ion transmembrane transporter activity
9	3e−03	2 / 15	aldehyde dehydrogenase (NAD) activity
10	3e−03	6 / 274	transcription factor binding
11	3e−03	16 / 1475	DNA binding
12	5e−03	6 / 314	RNA polymerase II core promoter proximal region sequence−specific DNA bi
13	5e−03	2 / 22	transferase activity
14	8e−03	2 / 26	nucleosomal DNA binding
15	8e−03	2 / 26	thyroid hormone receptor binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−08	10 / 178	hsa−miR−300
2	3e−08	10 / 181	hsa−miR−381
3	4e−08	14 / 433	hsa−miR−19b
4	2e−07	8 / 120	hsa−miR−664
5	3e−07	13 / 438	hsa−miR−19a
6	4e−07	8 / 132	hsa−miR−28−5p
7	4e−07	15 / 602	hsa−miR−20a
8	7e−07	12 / 394	hsa−miR−301b
9	2e−06	9 / 217	hsa−miR−185
10	4e−06	13 / 546	hsa−miR−93
11	4e−06	12 / 463	hsa−miR−301a
12	5e−06	8 / 186	hsa−miR−520d−5p
13	7e−06	10 / 332	hsa−miR−302d
14	1e−05	9 / 272	hsa−miR−101
15	1e−05	6 / 100	hsa−miR−516b

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−13	12 / 119	Chaussabel_2,11_Replication
2	1e−07	22 / 1194	PROTEINATLAS_stomach
3	1e−06	20 / 1167	PROTEINATLAS_gallbladder
4	2e−06	20 / 1173	PROTEINATLAS_rectum
5	2e−06	15 / 695	PROTEINATLAS_bone marrow
6	3e−06	17 / 912	PROTEINATLAS_urinary bladder
7	4e−06	17 / 929	PROTEINATLAS_bronchus
8	5e−06	9 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
9	5e−06	20 / 1268	PROTEINATLAS_colon
10	2e−05	13 / 640	PROTEINATLAS_parathyroid gland
11	2e−05	17 / 1063	PROTEINATLAS_tonsil
12	3e−05	16 / 959	PROTEINATLAS_nasopharynx
13	3e−05	16 / 963	PROTEINATLAS_pancreas
14	8e−05	13 / 726	PROTEINATLAS_cervix, uterine
15	9e−05	13 / 740	PROTEINATLAS_esophagus

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	8e−07	49 / 5067	ICGC_Taf1_targets
2	1e−05	21 / 1452	ICGC_Six5_targets
3	1e−05	34 / 3194	ICGC_Irf4_targets
4	1e−05	45 / 4890	ICGC_Bclaf101388_targets
5	2e−05	41 / 4362	ICGC_Creb1_targets
6	3e−05	26 / 2215	ICGC_GabpPcr2_targets
7	4e−05	50 / 5961	ICGC_Pol24_targets
8	5e−05	46 / 5312	ICGC_Tcf12_targets
9	6e−05	20 / 1498	ICGC_Ets1_targets
10	6e−05	47 / 5518	ICGC_Stat5_targets
11	7e−05	46 / 5383	ICGC_Sp1_targets
12	8e−05	46 / 5410	ICGC_Foxm1_targets
13	9e−05	40 / 4468	ICGC_Egr1_targets
14	1e−04	52 / 6552	ICGC_Pol2_targets
15	1e−04	52 / 6578	ICGC_Pou2_targets

Underexpression Spots

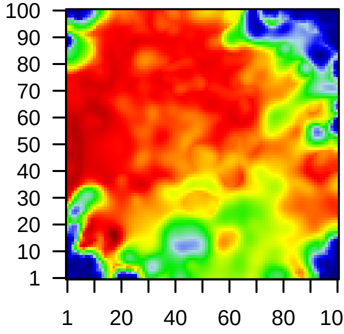
Spot Summary: m

metagenes = 25
genes = 584

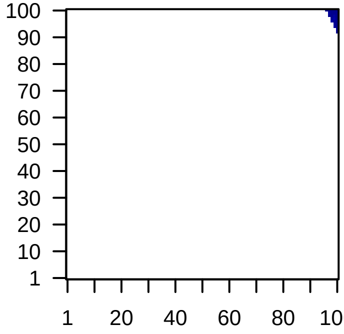
<r> metagenes = 0.95
<r> genes = 0.55
beta: r2= 81.89 / log p= −Inf

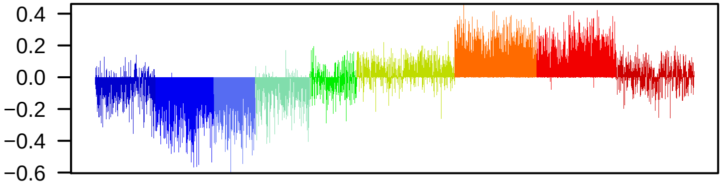
samples with spot = 928 (27.4 %)
A * : 3 (0.9 %)
A F * : 1 (0.3 %)
C F * : 13 (4.9 %)
F * : 112 (20.2 %)
F J * : 426 (92 %)
J * : 325 (72.7 %)
N * : 48 (10.8 %)

Overview Map



Spot





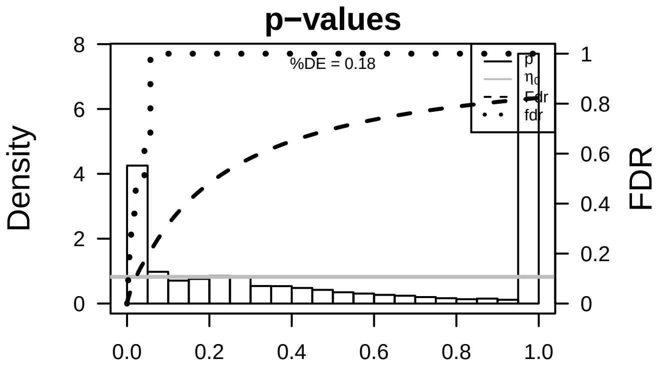
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_210544	2.45	−1.45	0.34	JCHAIN	joining chain of multimeric IgA and IgM [Source:HGNC Symb
2	ILMN_165219	2.24	−1.63	0.27		
3	ILMN_173950	2.08	−1.34	0.3		
4	ILMN_324966	1.89	−1.85	0.35		
5	ILMN_181589	1.69	−2.79	0.17		
6	ILMN_180840	1.68	−1.68	0.37	HLA−DQA1	major histocompatibility complex, class II, DQ alpha 1 [Source
7	ILMN_175259	1.47	−1.51	0.4		
8	ILMN_171073	1.39	−1.44	0.46	GZMK	granzyme K [Source:HGNC Symbol;Acc:HGNC:4711]
9	ILMN_170496	1.38	−1.61	0.65		
10	ILMN_166708	1.34	−1.65	0.73	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
11	ILMN_234257	1.32	−1.58	0.56	IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
12	ILMN_238175	1.25	−1.46	0.37	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
13	ILMN_207965	1.24	−1.4	0.59	KLRB1	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
14	ILMN_206765	1.22	−1.32	0.76	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
15	ILMN_176037	1.22	−0.81	0.52	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
16	ILMN_187303	1.2	−1.66	0.81		
17	ILMN_328411	1.18	−0.87	0.76		nucleophosmin 1 pseudogene 25 [Source:HGNC Symbol;Acc
18	ILMN_172413	1.15	−1.15	0.78	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
19	ILMN_167918	1.15	−1.53	0.72	LEF1	lymphoid enhancer binding factor 1 [Source:HGNC Symbol;A
20	ILMN_236546	1.13	−0.95	0.8	XBP1	X−box binding protein 1 [Source:HGNC Symbol;Acc:HGNC:1

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−55	313 / 7275	Lympl	HOPP_Txn_elongation
2	3e−53	263 / 5356	Lympl	HOPP_Txn_transition
3	4e−53	127 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	2e−52	133 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
5	7e−48	143 / 1797	GSEA	PILON_KLF1_TARGETS_DN
6	9e−46	319 / 8226	Lympl	HOPP_Active_promoter
7	2e−34	245 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
8	2e−33	324 / 9555	Colon	TssA_Colon
9	2e−32	99 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
10	3e−32	327 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	3e−32	73 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
12	4e−32	311 / 9054	Colon	Tx_Colon
13	1e−31	92 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
14	2e−30	297 / 8568	Colon	TxWk_Colon
15	1e−29	61 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
16	2e−28	84 / 1013	MF	poly(A) RNA binding
17	2e−28	105 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
18	3e−28	342 / 10999	Colon	TssWk_Colon
19	3e−27	280 / 8098	Lympl	HOPP_Weak_promoter
20	8e−27	64 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
21	4e−26	292 / 8771	Chror	5_Tx_Melanocytes
22	2e−25	250 / 6970	Chror	5_Tx_Neuronal_Progenitor
23	7e−25	287 / 8678	Colon	Quies3_Colon
24	9e−24	43 / 302	Refer	Chaussabel_3,4_Protein phosphatases
25	8e−23	264 / 7854	Chror	5_Tx_Fibroblasts
26	2e−22	63 / 724	Refer	PROTEINATLAS_lymph node
27	9e−22	336 / 11455	Chror	2_TssA_Fibroblasts
28	6e−21	250 / 7448	Lympl	HOPP_Strong_enhancer
29	1e−20	48 / 455	GSEA	ZHENG_BOUND_BY_FOXP3
30	1e−20	31 / 170	HM	HALLMARK_MYC_TARGETS_V1
31	4e−20	51 / 532	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
32	6e−20	73 / 1063	Refer	PROTEINATLAS_tonsil
33	9e−20	49 / 500	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
34	9e−20	64 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
35	1e−19	79 / 1239	Refer	PROTEINATLAS_testis
36	2e−19	276 / 8818	MF	protein binding
37	1e−18	44 / 429	miRN	hsa−miR−548n
38	1e−17	37 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
39	1e−17	100 / 1979	CC	membrane
40	1e−17	38 / 338	miRN	hsa−miR−548d−5p

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 111	HORVATH_aging_genes meth DOWN
2	0.7	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.9	1 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−10	17 / 126	T cell receptor signaling pathway
2	5e−08	16 / 145	mRNA processing
3	8e−08	13 / 96	translational initiation
4	2e−07	15 / 139	RNA splicing
5	1e−06	19 / 255	viral process
6	2e−06	5 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
7	3e−06	16 / 196	mRNA splicing, via spliceosome
8	4e−06	25 / 435	negative regulation of apoptotic process
9	2e−05	6 / 28	regulation of translational initiation
10	2e−05	17 / 254	cell−cell adhesion
11	3e−05	7 / 44	gene expression
12	7e−05	5 / 22	positive regulation of T cell activation
13	7e−05	9 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	1e−04	10 / 115	leukocyte migration
15	2e−04	4 / 15	formation of translation preinitiation complex

Brain

Rank	p−value	#in/all	Geneset
1	2e−34	245 / 5936	Overlap_fetal_midbrain_HetRpts
2	3e−32	327 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−16	282 / 9504	Overlap_fetal_midbrain_K9K27me3
4	3e−15	287 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	2e−11	285 / 10430	Overlap_fetal_midbrain_Quies
6	5e−07	39 / 796	Overlap_fetal_midbrain_ZNF
7	2e−04	20 / 386	Fetal_ZNF
8	3e−04	12 / 180	Overlap_fetal_midbrain_Het
9	5e−04	17 / 328	Fetal_Het
10	5e−04	41 / 1162	Fetal_Enh
11	2e−03	39 / 1171	Fetal_EnhP
12	2e−02	29 / 937	Fetal_EnhG
13	1e−01	24 / 906	Fetal_HetRpts
14	1e−01	36 / 1436	Fetal_K9K27me3
15	3e−01	68 / 3164	Mid_Frontal_Lobe_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	9e−08	2 / 13	RHODES_CANCER_META_SIGNATURE
2	1e−04	4 / 13	GENTLES_modul12
3	2e−04	17 / 301	SPANG_BCL6−index2
4	3e−03	3 / 14	GENTLES_modul1
5	3e−03	8 / 117	PanCan_Driver_Gene_geneset_nanostring
6	4e−03	10 / 178	SPANG_LPS−index2
7	4e−03	3 / 16	GENTLES_modul11
8	4e−03	3 / 16	GENTLES_modul14
9	7e−03	6 / 82	PanCan_JAK−ST_geneset_nanostring
10	1e−02	7 / 125	PanCan_CC+Apop_geneset_nanostring
11	3e−02	2 / 13	GENTLES_modul18
12	4e−02	2 / 15	WANG_ER_UP
13	4e−02	2 / 15	WOLFER_overlap genes
14	4e−02	18 / 554	Lembcke_Colonic Inflammation
15	4e−02	2 / 16	GENTLES_modul7

CC

Rank	p−value	#in/all	Geneset
1	1e−17	100 / 1979	membrane
2	3e−16	175 / 4822	cytoplasm
3	4e−13	106 / 2535	nucleoplasm
4	2e−12	102 / 2464	extracellular exosome
5	3e−12	116 / 2979	cytosol
6	3e−12	163 / 4828	nucleus
7	1e−09	42 / 721	nucleolus
8	7e−09	10 / 41	ER to Golgi transport vesicle membrane
9	1e−07	6 / 13	MHC class II protein complex
10	3e−07	24 / 352	focal adhesion
11	1e−06	12 / 101	intracellular ribonucleoprotein complex
12	3e−06	6 / 21	integral component of lumenal side of endoplasmic reticulum membrane
13	4e−06	7 / 33	transport vesicle membrane
14	9e−06	7 / 37	clathrin−coated endocytic vesicle membrane
15	1e−05	19 / 295	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	0.004	31 / 904	Chr 10
2	0.025	13 / 342	Chr 18
3	0.027	35 / 1217	Chr 3
4	0.030	31 / 1060	Chr 5
5	0.032	27 / 902	Chr 4
6	0.072	22 / 768	Chr 14
7	0.084	32 / 1211	Chr 6
8	0.158	12 / 422	Chr 13
9	0.207	28 / 1160	Chr 12
10	0.222	35 / 1492	Chr 2
11	0.229	24 / 994	Chr X
12	0.264	52 / 2323	Chr 1
13	0.542	6 / 289	Chr 21
14	0.544	17 / 836	Chr 8
15	0.608	23 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−26	292 / 8771	5_Tx_Melanocytes
2	2e−25	250 / 6970	5_Tx_Neuronal_Progenitor
3	8e−23	264 / 7854	5_Tx_Fibroblasts
4	9e−22	336 / 11455	2_TssA_Fibroblasts
5	2e−17	341 / 12298	2_TssA_Melanocytes
6	8e−17	352 / 12983	2_TssA_Neuronal_Progenitor
7	1e−15	269 / 8990	15_Quies_Fibroblasts
8	2e−13	188 / 5699	6_EnhG_Melanocytes
9	5e−10	319 / 12393	15_Quies_Neuronal_Progenitor
10	2e−08	287 / 11130	15_Quies_Melanocytes
11	8e−08	232 / 8613	7_Enh_Fibroblasts
12	1e−07	298 / 11836	3_TssF_Melanocytes
13	5e−07	313 / 12741	7_Enh_Melanocytes
14	2e−03	229 / 9635	3_TssF_Fibroblasts
15	6e−03	38 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−33	324 / 9555	TssA_Colon
2	4e−32	311 / 9054	Tx_Colon
3	2e−30	297 / 8568	TxWk_Colon
4	2e−28	105 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	3e−28	342 / 10999	TssWk_Colon
6	7e−25	287 / 8678	Quies3_Colon
7	3e−16	58 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	8e−13	92 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	1e−12	65 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
10	5e−08	129 / 4034	TssD1_Colon
11	7e−07	44 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	9e−06	44 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	4e−05	53 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	5e−05	147 / 5373	EnhWk1_Colon
15	9e−04	3 / 10	KIM_MSI−in−EC

Glio

Rank	p−value	#in/all	Geneset
1	2e−09	26 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	8e−09	73 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−07	23 / 315	Up
4	9e−07	74 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	2e−04	9 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	4e−04	7 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	4e−04	32 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
8	2e−03	3 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
9	5e−03	9 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	8e−03	6 / 84	GIEZELT_GBM_WT_down_VS_mut
11	9e−03	16 / 401	Down_b
12	2e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
13	3e−02	4 / 55	Stuehler_Proteins_up_in_STS
14	4e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
15	4e−02	5 / 92	Weller_LGG_A_vs_O_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−53	127 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	2e−52	133 / 1417	PUJANA_BRCA1_PCC_NETWORK
3	7e−48	143 / 1797	PILON_KLF1_TARGETS_DN
4	2e−32	99 / 1241	PUJANA_ATM_PCC_NETWORK
5	3e−32	73 / 669	PUJANA_CHEK2_PCC_NETWORK
6	1e−31	92 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
7	1e−29	61 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
8	8e−27	64 / 622	SCHLOSSER_SERUM_RESPONSE_DN
9	1e−20	48 / 455	ZHENG_BOUND_BY_FOXP3
10	4e−20	51 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
11	9e−20	49 / 500	KIM_ALL_DISORDERS_CALB1_CORR_UP
12	9e−20	64 / 841	ACEVEDO_LIVER_CANCER_UP
13	1e−17	37 / 317	HSIAO_HOUSEKEEPING_GENES
14	3e−17	44 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
15	4e−17	39 / 368	OSMAN_BLADDER_CANCER_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−20	31 / 170	HALLMARK_MYC_TARGETS_V1
2	1e−06	16 / 185	HALLMARK_MTORC1_SIGNALING
3	3e−05	13 / 162	HALLMARK_ALLOGRAFT_REJECTION
4	6e−05	13 / 173	HALLMARK_E2F_TARGETS
5	7e−05	9 / 87	HALLMARK_PROTEIN_SECRETION
6	1e−04	13 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	3e−04	9 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	5e−04	12 / 187	HALLMARK_COMPLEMENT
9	6e−04	10 / 138	HALLMARK_FATTY_ACID_METABOLISM
10	2e−03	10 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	5e−03	10 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
12	1e−02	9 / 179	HALLMARK_G2M_CHECKPOINT
13	1e−02	9 / 183	HALLMARK_GLYCOLYSIS
14	1e−02	9 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	1e−02	9 / 186	HALLMARK_IL2_STAT5_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−04	14 / 211	Homuth_BMI−associated−genes_DN
2	4e−04	5 / 32	Marjolein_ageing−genes_DN
3	1e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	6e−01	3 / 147	Homuth_BMI−associated−genes_UP
5	9e−01	1 / 94	DUMEAUX_Smoking enriched genes
6	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−55	313 / 7275	HOPP_Txn_elongation
2	3e−53	263 / 5356	HOPP_Txn_transition
3	9e−46	319 / 8226	HOPP_Active_promoter
4	3e−27	280 / 8098	HOPP_Weak_promoter
5	6e−21	250 / 7448	HOPP_Strong_enhancer
6	8e−09	55 / 1169	SPANG_BCR DN
7	1e−08	191 / 6559	HOPP_Weak_txn
8	5e−08	197 / 6959	HOPP_Weak_enhancer
9	4e−06	5 / 13	Care_Polarized immune response
10	6e−06	13 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
11	7e−06	13 / 141	WIRTH_lymphoma937_spot F
12	2e−04	5 / 28	DAVE_Immune response 1
13	2e−04	14 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
14	8e−04	15 / 283	TARTE_Plasmablast signature
15	9e−04	7 / 75	SPANG_LPS 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−28	84 / 1013	poly(A) RNA binding
2	2e−19	276 / 8818	protein binding
3	7e−08	27 / 399	RNA binding
4	3e−06	19 / 265	cadherin binding involved in cell−cell adhesion
5	1e−05	7 / 39	translation initiation factor activity
6	2e−05	18 / 283	nucleotide binding
7	4e−05	5 / 20	peptide antigen binding
8	8e−05	16 / 256	ubiquitin protein ligase binding
9	1e−04	48 / 1329	ATP binding
10	1e−04	4 / 14	MHC class II protein complex binding
11	3e−04	8 / 82	unfolded protein binding
12	5e−04	11 / 160	protein C−terminus binding
13	6e−04	15 / 274	transcription factor binding
14	8e−04	6 / 54	double−stranded RNA binding
15	1e−03	6 / 56	ATP−dependent RNA helicase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−18	44 / 429	hsa−miR−548n
2	1e−17	38 / 338	hsa−miR−548d−5p
3	1e−17	38 / 338	hsa−miR−548b−5p
4	8e−17	35 / 299	hsa−miR−548c−3p
5	1e−16	36 / 323	hsa−miR−548a−5p
6	1e−15	34 / 307	hsa−miR−548c−5p
7	2e−15	33 / 295	hsa−miR−561
8	5e−15	34 / 321	hsa−miR−590−3p
9	6e−15	24 / 150	hsa−miR−633
10	3e−14	23 / 146	hsa−miR−548o
11	5e−14	24 / 164	hsa−miR−548g
12	5e−14	31 / 287	hsa−miR−548j
13	9e−14	39 / 463	hsa−miR−301a
14	1e−13	24 / 170	hsa−miR−580
15	1e−13	25 / 187	hsa−miR−586

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 12	BENTINK_src.2
2	0.03	2 / 14	BENTINK_ras.6
3	0.20	1 / 11	BENTINK_ras.4
4	0.24	1 / 13	BENTINK_e2f3.2
5	0.24	1 / 13	BENTINK_myc.1
6	1.00	0 / 14	GUSTAFSON_PI3K_UP
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	BENTINK_e2f3.1
9	1.00	0 / 12	BENTINK_ras.1
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−24	43 / 302	Chaussabel_3,4_Protein phosphatases
2	2e−22	63 / 724	PROTEINATLAS_lymph node
3	6e−20	73 / 1063	PROTEINATLAS_tonsil
4	1e−19	79 / 1239	PROTEINATLAS_testis
5	4e−17	72 / 1167	PROTEINATLAS_gallbladder
6	5e−17	55 / 726	PROTEINATLAS_cervix, uterine
7	9e−17	56 / 759	PROTEINATLAS_epididymis
8	1e−16	58 / 816	PROTEINATLAS_endometrium
9	2e−16	59 / 850	PROTEINATLAS_skin
10	3e−16	23 / 119	Chaussabel_2,4_Ribosomal proteins
11	3e−16	63 / 963	PROTEINATLAS_pancreas
12	7e−16	68 / 1118	PROTEINATLAS_placenta
13	9e−16	62 / 959	PROTEINATLAS_nasopharynx
14	1e−15	51 / 681	PROTEINATLAS_lung
15	1e−15	60 / 912	PROTEINATLAS_urinary bladder

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	1.0	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	2e−12	65 / 1231	KIM_MYC targets
2	1e−08	71 / 1723	HEBENSTREIT_high expression TF
3	1e−07	152 / 5067	ICGC_Taf1_targets
4	3e−06	57 / 1478	ICGC_Myc_targets
5	5e−06	57 / 1498	ICGC_Ets1_targets
6	1e−05	71 / 2087	ICGC_Cebpbsc150_targets
7	2e−05	74 / 2215	ICGC_GabpPcr2_targets
8	2e−05	86 / 2704	ICGC_Pbx3_targets
9	3e−05	125 / 4362	ICGC_Creb1_targets
10	3e−05	161 / 5961	ICGC_Pol24_targets
11	4e−05	136 / 4881	ICGC_Atf2_targets
12	7e−05	135 / 4890	ICGC_Bclaf101388_targets
13	8e−05	149 / 5518	ICGC_Stat5_targets
14	9e−05	72 / 2255	ICGC_SrfV0416101_targets
15	1e−04	124 / 4468	ICGC_Egr1_targets

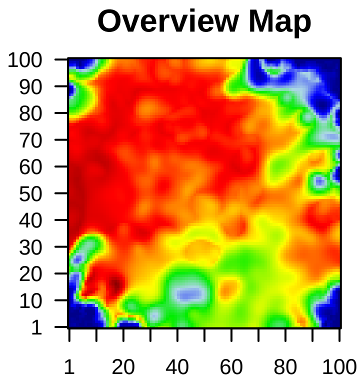
Underexpression Spots

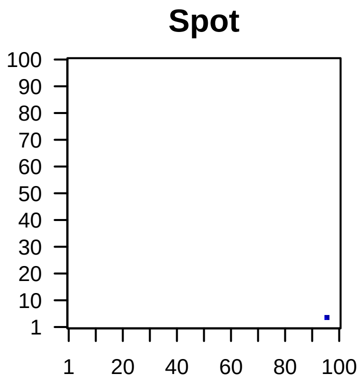
Spot Summary: n

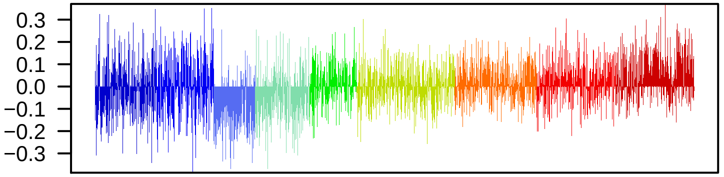
metagenes = 4
genes = 40

<r> metagenes = 0.99
<r> genes = 0.43
beta: r2= 28.03 / log p= −Inf

samples with spot = 481 (14.2 %)
A * : 49 (14.2 %)
A C * : 67 (20.4 %)
A C F * : 3 (1.3 %)
A F * : 21 (6.8 %)
C F * : 38 (14.3 %)
F * : 60 (10.8 %)
F J * : 63 (13.6 %)
J * : 55 (12.3 %)
N * : 125 (28.2 %)





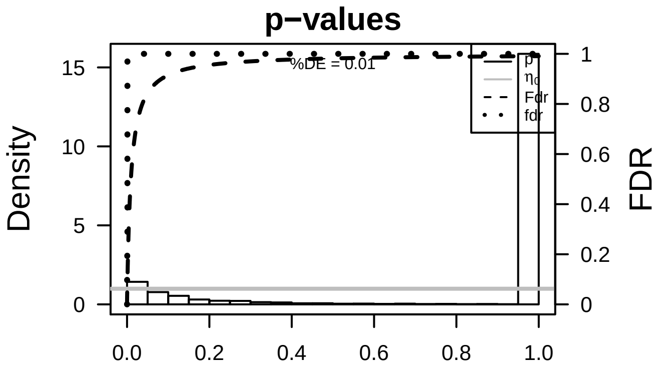


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_177844	1.16	−0.92	0.3	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3
2	ILMN_168870	0.83	−1.13	0.52	PJA2	praja ring finger ubiquitin ligase 2 [Source:HGNC Symbol;Acc
3	ILMN_178245	0.79	−0.67	0.58	OSBPL8	oxysterol binding protein like 8 [Source:HGNC Symbol;Acc:H
4	ILMN_170224	0.78	−0.58	0.65	CCNDBP1	cyclin D1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC
5	ILMN_234025	0.66	−0.6	0.6	PDE4B	phosphodiesterase 4B [Source:HGNC Symbol;Acc:HGNC:87
6	ILMN_178893	0.64	−0.72	0.68	DOCK8	dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:HGNC
7	ILMN_218196	0.6	−0.6	0.74	CBL	Cbl proto−oncogene [Source:HGNC Symbol;Acc:HGNC:1541
8	ILMN_232992	0.6	−0.53	0.51	ABCG1	ATP binding cassette subfamily G member 1 [Source:HGNC
9	ILMN_215932	0.6	−0.49	0.69	SLK	STE20 like kinase [Source:HGNC Symbol;Acc:HGNC:11088]
10	ILMN_173331	0.59	−0.56	0.57	PIGB	phosphatidylinositol glycan anchor biosynthesis class B [Sour
11	ILMN_166896	0.58	−0.59	0.52	MID1IP1	MID1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC
12	ILMN_174218	0.57	−0.44	0.59	MAN1A1	mannosidase alpha class 1A member 1 [Source:HGNC Symb
13	ILMN_210376	0.57	−0.62	0.77		
14	ILMN_178244	0.56	−0.59	0.72	YIPF4	Yip1 domain family member 4 [Source:HGNC Symbol;Acc:H
15	ILMN_240408	0.56	−0.63	0.71	CLIP1	CAP−Gly domain containing linker protein 1 [Source:HGNC
16	ILMN_167266	0.56	−0.54	0.61	MBP	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
17	ILMN_173679	0.54	−0.49	0.8	RB1CC1	RB1 inducible coiled−coil 1 [Source:HGNC Symbol;Acc:HGN
18	ILMN_174115	0.53	−0.49	0.67	MAP3K8	mitogen−activated protein kinase kinase kinase 8 [Source:HG
19	ILMN_174750	0.53	−0.49	0.57	AHCTF1	AT−hook containing transcription factor 1 [Source:HGNC Sym
20	ILMN_170275	0.53	−0.47	0.55	TMX4	thioredoxin related transmembrane protein 4 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−13	37 / 8568	Colon	TxWk_Colon
2	2e−12	37 / 9054	Colon	Tx_Colon
3	3e−11	33 / 7275	Lympl	HOPP_Txn_elongation
4	7e−11	35 / 8678	Colon	Quies3_Colon
5	2e−08	36 / 10999	Colon	TssWk_Colon
6	2e−08	9 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
7	2e−08	33 / 8990	Chror	15_Quies_Fibroblasts
8	2e−08	31 / 7854	Chror	5_Tx_Fibroblasts
9	2e−08	38 / 12741	Chror	7_Enh_Melanocytes
10	3e−08	27 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
11	4e−08	34 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
12	6e−08	32 / 8771	Chror	5_Tx_Melanocytes
13	2e−07	34 / 10430	Brain	Overlap_fetal_midbrain_Quies
14	3e−07	4 / 33	GSEA	PID_IL8_CXCR2_PATHWAY
15	4e−07	30 / 8226	Lympl	HOPP_Active_promoter
16	4e−07	35 / 11455	Chror	2_TssA_Fibroblasts
17	6e−07	36 / 12298	Chror	2_TssA_Melanocytes
18	6e−07	32 / 9555	Colon	TssA_Colon
19	6e−07	10 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
20	7e−07	4 / 40	GSEA	SHIPP_DLBCL_CURED_VS_FATAL_DN
21	7e−07	7 / 301	Cance	SPANG_BCL6−index2
22	1e−06	10 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
23	1e−06	30 / 8613	Chror	7_Enh_Fibroblasts
24	1e−06	32 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
25	1e−06	35 / 11836	Chror	3_TssF_Melanocytes
26	2e−06	6 / 211	GSEA	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_DN
27	3e−06	36 / 12983	Chror	2_TssA_Neuronal_Progenitor
28	5e−06	9 / 770	GSEA	CUI_TCF21_TARGETS_2_DN
29	7e−06	33 / 11130	Chror	15_Quies_Melanocytes
30	1e−05	22 / 5356	Lympl	HOPP_Txn_transition
31	2e−05	7 / 492	GSEA	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
32	3e−05	5 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
33	3e−05	5 / 211	Lifest	Homuth_BMI−associated−genes_DN
34	4e−05	7 / 559	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
35	5e−05	3 / 42	CC	cell leading edge
36	5e−05	21 / 5373	Colon	EnhWk1_Colon
37	6e−05	3 / 44	GSEA	PID_CD8_TCR_PATHWAY
38	6e−05	5 / 245	GSEA	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
39	6e−05	4 / 125	GSEA	UDAYAKUMAR_MED1_TARGETS_UP
40	7e−05	15 / 2979	CC	cytosol



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 511	apoptotic process
2	3e−04	2 / 14	regulation of I−kappaB kinase/NF−kappaB signaling
3	6e−04	2 / 21	bone resorption
4	7e−04	2 / 23	microtubule bundle formation
5	8e−04	2 / 24	activation of protein kinase B activity
6	8e−04	2 / 25	glycogen biosynthetic process
7	1e−03	2 / 27	phagosome acidification
8	1e−03	2 / 28	cytoplasmic microtubule organization
9	2e−03	2 / 43	cytokinesis
10	3e−03	2 / 44	activation of MAPKK activity
11	3e−03	2 / 51	epidermal growth factor receptor signaling pathway
12	4e−03	3 / 185	cell cycle
13	5e−03	2 / 63	T cell costimulation
14	5e−03	3 / 207	small GTPase mediated signal transduction
15	6e−03	2 / 70	macroautophagy

Brain

Rank	p−value	#in/all	Geneset
1	3e−08	27 / 5936	Overlap_fetal_midbrain_HetRpts
2	4e−08	34 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	2e−07	34 / 10430	Overlap_fetal_midbrain_Quies
4	1e−06	32 / 9815	Overlap_fetal_midbrain_ReprPC
5	2e−04	28 / 9504	Overlap_fetal_midbrain_K9K27me3
6	2e−02	11 / 3164	Mid_Frontal_Lobe_ZNF
7	5e−02	5 / 1171	Fetal_EnhP
8	5e−02	4 / 818	Mid_Frontal_Lobe_Het
9	1e−01	2 / 328	Fetal_Het
10	1e−01	4 / 1162	Fetal_Enh
11	1e−01	8 / 3046	Fetal_TssA
12	2e−01	4 / 1213	Fetal_TssP
13	2e−01	6 / 2127	Mid_Frontal_Lobe_K9K27me3
14	2e−01	3 / 796	Overlap_fetal_midbrain_ZNF
15	2e−01	7 / 2630	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	7e−07	7 / 301	SPANG_BCL6−index2
2	2e−04	2 / 13	GENTLES_modul12
3	2e−03	3 / 150	PanCan_MAPK_geneset_nanostring
4	2e−02	1 / 14	GENTLES_modul4
5	6e−02	1 / 38	KUIPER_MM good survival
6	7e−02	3 / 554	Lembcke_Colonic Inflammation
7	9e−02	1 / 54	KUIPER_MM poor survival
8	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
9	1e−01	1 / 76	PanCan_Wnt_geneset_nanostring
10	1e−01	1 / 82	PanCan_JAK−ST_geneset_nanostring
11	2e−01	1 / 117	PanCan_Driver_Gene_geneset_nanostring
12	2e−01	1 / 136	PanCan_RAS_geneset_nanostring
13	3e−01	1 / 178	SPANG_LPS−index2
14	5e−01	0 / 15	LIU_PROSTATE_CANCER_DN
15	1e+00	0 / 13	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	5e−05	3 / 42	cell leading edge
2	7e−05	15 / 2979	cytosol
3	9e−05	3 / 51	phagocytic vesicle membrane
4	3e−04	2 / 16	pre−autophagosomal structure membrane
5	4e−04	4 / 200	nuclear membrane
6	5e−04	18 / 4822	cytoplasm
7	2e−03	3 / 139	microtubule cytoskeleton
8	2e−03	6 / 777	Golgi apparatus
9	2e−03	6 / 788	endoplasmic reticulum membrane
10	2e−03	11 / 2464	extracellular exosome
11	3e−03	5 / 561	intracellular membrane−bounded organelle
12	3e−03	4 / 352	focal adhesion
13	5e−03	2 / 63	lipid particle
14	6e−03	3 / 221	endosome
15	9e−03	2 / 83	ruffle

Chr

Rank	p−value	#in/all	Geneset
1	0.1	2 / 342	Chr 18
2	0.1	3 / 769	Chr 15
3	0.2	2 / 536	Chr 22
4	0.3	3 / 1160	Chr 12
5	0.3	3 / 1211	Chr 6
6	0.3	3 / 1217	Chr 3
7	0.4	1 / 289	Chr 21
8	0.5	2 / 902	Chr 4
9	0.5	2 / 904	Chr 10
10	0.5	3 / 1492	Chr 2
11	0.5	2 / 954	Chr 9
12	0.6	2 / 1060	Chr 5
13	0.7	1 / 619	Chr 20
14	0.7	2 / 1318	Chr 17
15	0.7	2 / 1411	Chr 11

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−08	33 / 8990	15_Quies_Fibroblasts
2	2e−08	31 / 7854	5_Tx_Fibroblasts
3	2e−08	38 / 12741	7_Enh_Melanocytes
4	6e−08	32 / 8771	5_Tx_Melanocytes
5	4e−07	35 / 11455	2_TssA_Fibroblasts
6	6e−07	36 / 12298	2_TssA_Melanocytes
7	1e−06	30 / 8613	7_Enh_Fibroblasts
8	1e−06	35 / 11836	3_TssF_Melanocytes
9	3e−06	36 / 12983	2_TssA_Neuronal_Progenitor
10	7e−06	33 / 11130	15_Quies_Melanocytes
11	8e−05	24 / 6970	5_Tx_Neuronal_Progenitor
12	1e−04	33 / 12393	15_Quies_Neuronal_Progenitor
13	3e−04	17 / 4237	14_ZNF_Neuronal_Progenitor
14	1e−03	19 / 5699	6_EnhG_Melanocytes
15	2e−03	26 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−13	37 / 8568	TxWk_Colon
2	2e−12	37 / 9054	Tx_Colon
3	7e−11	35 / 8678	Quies3_Colon
4	2e−08	36 / 10999	TssWk_Colon
5	6e−07	32 / 9555	TssA_Colon
6	5e−05	21 / 5373	EnhWk1_Colon
7	6e−04	16 / 4034	TssD1_Colon
8	7e−04	29 / 10779	Enh_Colon
9	2e−03	10 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
10	4e−03	8 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	4e−03	7 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	4e−02	5 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	5e−02	4 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
14	6e−02	5 / 1224	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
15	7e−02	11 / 4018	EnhWk2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	4e−04	7 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	2e−02	1 / 11	VERHAAK_Brain
3	2e−02	8 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	3e−02	1 / 15	VERHAAK_NL subtype
5	3e−02	1 / 15	VERHAAK_PN subtype
6	6e−02	1 / 33	Shaw_responders_down_in_oligo_glioma
7	7e−02	1 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
8	8e−02	2 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
9	9e−02	1 / 52	OL vs. OPC
10	1e−01	1 / 58	in vivo astrocytes vs. cultured astroglia
11	1e−01	1 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	1e−01	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	1e−01	1 / 92	Weller_LGG_A_vs_O_DOWN
14	2e−01	2 / 401	Down_b
15	2e−01	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−08	9 / 388	SHEN_SMARCA2_TARGETS_UP
2	3e−07	4 / 33	PID_IL8_CXCR2_PATHWAY
3	6e−07	10 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
4	7e−07	4 / 40	SHIPP_DLBCL_CURED_VS_FATAL_DN
5	1e−06	10 / 841	ACEVEDO_LIVER_CANCER_UP
6	2e−06	6 / 211	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_DN
7	5e−06	9 / 770	CUI_TCF21_TARGETS_2_DN
8	2e−05	7 / 492	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
9	3e−05	5 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
10	4e−05	7 / 559	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
11	6e−05	3 / 44	PID_CD8_TCR_PATHWAY
12	6e−05	5 / 245	DURCHDEWALD_SKIN_CARCINOGENESIS_DN
13	6e−05	4 / 125	UDAYAKUMAR_MED1_TARGETS_UP
14	7e−05	4 / 128	LIU_SOX4_TARGETS_UP
15	1e−04	6 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN

HM

Rank	p−value	#in/all	Geneset
1	0.003	3 / 177	HALLMARK_MITOTIC_SPINDLE
2	0.004	3 / 189	HALLMARK_HYPOXIA
3	0.009	2 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	0.021	2 / 130	HALLMARK_DNA_REPAIR
5	0.040	2 / 183	HALLMARK_APICAL_JUNCTION
6	0.040	2 / 183	HALLMARK_GLYCOLYSIS
7	0.040	2 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	0.041	2 / 186	HALLMARK_IL2_STAT5_SIGNALING
9	0.057	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
10	0.068	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	0.145	1 / 91	HALLMARK_ANDROGEN_RESPONSE
12	0.251	1 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	0.257	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.259	1 / 173	HALLMARK_E2F_TARGETS
15	0.261	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 211	Homuth_BMI−associated−genes_DN
2	4e−04	2 / 18	Huan_blood−pressure_SBP−signature
3	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
5	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
13	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 147	Homuth_BMI−associated−genes_UP
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−11	33 / 7275	HOPP_Txn_elongation
2	4e−07	30 / 8226	HOPP_Active_promoter
3	1e−05	22 / 5356	HOPP_Txn_transition
4	8e−04	23 / 7448	HOPP_Strong_enhancer
5	1e−03	24 / 8098	HOPP_Weak_promoter
6	7e−03	19 / 6559	HOPP_Weak_txn
7	8e−03	2 / 78	Sha_DLBCL UP
8	1e−02	2 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
9	2e−02	3 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	2e−02	3 / 331	WIRTH_lymphoma937_spot H
11	2e−02	6 / 1270	SPANG_BCR UP
12	2e−02	2 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
13	4e−02	9 / 2701	HOPP_Repetitive
14	6e−02	17 / 6959	HOPP_Weak_enhancer
15	7e−02	1 / 45	Subero_INT_hypo_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.00	0 / 30	Hugo_melanoma−all−MET_UP
3	1.00	0 / 54	Hugo_melanoma−all−MET_DN
4	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	8e−05	3 / 48	receptor signaling protein serine/threonine kinase activity
2	1e−04	27 / 8818	protein binding
3	2e−04	2 / 12	phospholipid transporter activity
4	1e−03	2 / 31	ADP binding
5	2e−03	2 / 38	cholesterol binding
6	7e−03	7 / 1329	ATP binding
7	1e−02	3 / 265	cadherin binding involved in cell−cell adhesion
8	1e−02	2 / 103	guanyl−nucleotide exchange factor activity
9	2e−02	3 / 315	protein serine/threonine kinase activity
10	2e−02	1 / 10	microtubule plus−end binding
11	2e−02	1 / 11	mannosyltransferase activity
12	2e−02	1 / 12	actin−dependent ATPase activity
13	2e−02	1 / 12	MAP kinase kinase activity
14	2e−02	1 / 12	phosphotyrosine binding
15	2e−02	1 / 13	cholesterol transporter activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	5 / 294	hsa−miR−503
2	9e−04	4 / 250	hsa−miR−548l
3	2e−03	3 / 143	hsa−miR−135a
4	2e−03	4 / 315	hsa−miR−30e
5	2e−03	3 / 152	hsa−miR−583
6	2e−03	5 / 546	hsa−miR−93
7	3e−03	3 / 158	hsa−miR−802
8	3e−03	2 / 44	hsa−miR−1256
9	3e−03	3 / 164	hsa−miR−96
10	3e−03	3 / 176	hsa−miR−199b−3p
11	4e−03	3 / 179	hsa−miR−539
12	4e−03	3 / 184	hsa−miR−129−5p
13	4e−03	4 / 379	hsa−miR−454
14	5e−03	2 / 61	hsa−miR−627
15	6e−03	2 / 67	hsa−miR−1262

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	1 / 13	BENTINK_src.10
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 640	PROTEINATLAS_parathyroid gland
2	1e−04	9 / 1173	PROTEINATLAS_rectum
3	1e−04	7 / 681	PROTEINATLAS_lung
4	2e−04	8 / 933	PROTEINATLAS_adrenal gland
5	3e−04	8 / 1016	PROTEINATLAS_cerebral cortex
6	3e−04	7 / 782	PROTEINATLAS_thyroid gland
7	5e−04	6 / 598	PROTEINATLAS_prostate
8	8e−04	8 / 1194	PROTEINATLAS_stomach
9	9e−04	4 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
10	1e−03	8 / 1239	PROTEINATLAS_testis
11	1e−03	8 / 1268	PROTEINATLAS_colon
12	2e−03	7 / 1063	PROTEINATLAS_tonsil
13	2e−03	5 / 535	PROTEINATLAS_spleen
14	2e−03	7 / 1097	PROTEINATLAS_kidney
15	3e−03	7 / 1167	PROTEINATLAS_gallbladder

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	1e−04	11 / 1723	HEBENSTREIT_high expression TF
2	1e−02	14 / 4362	ICGC_Creb1_targets
3	2e−02	14 / 4735	ICGC_Pu1_targets
4	2e−02	11 / 3348	ICGC_BatfPcr1_targets
5	2e−02	1 / 14	NOWICK_TF
6	3e−02	14 / 4890	ICGC_Bclaf101388_targets
7	3e−02	13 / 4468	ICGC_Egr1_targets
8	3e−02	15 / 5466	ICGC_Nficsc81335_targets
9	4e−02	14 / 5067	ICGC_Taf1_targets
10	6e−02	17 / 6868	ICGC_Elf1_targets
11	6e−02	5 / 1231	KIM_MYC targets
12	7e−02	14 / 5442	ICGC_Pmlsc71910_targets
13	7e−02	14 / 5518	ICGC_Stat5_targets
14	7e−02	16 / 6578	ICGC_Pou2_targets
15	9e−02	17 / 7247	ICGC_Runx3_targets

Underexpression Spots

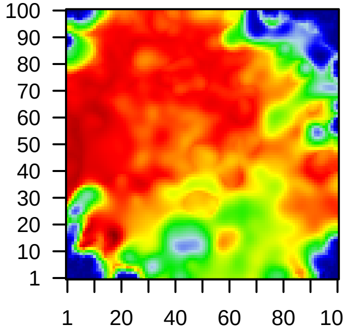
Spot Summary: o

metagenes = 11
genes = 167

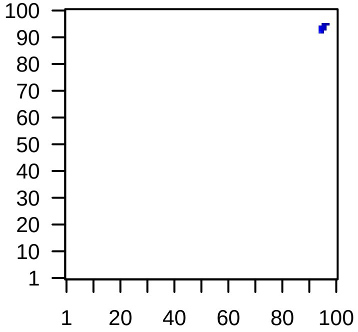
<r> metagenes = 0.99
<r> genes = 0.52
beta: r2= 41.51 / log p= −Inf

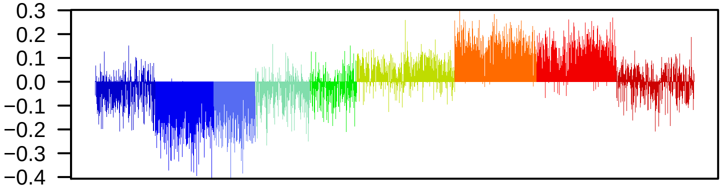
samples with spot = 584 (17.2 %)
- A * : 2 (0.6 %)
- A F * : 2 (0.6 %)
- C F * : 5 (1.9 %)
- F * : 42 (7.6 %)
- F J * : 306 (66.1 %)
- J * : 223 (49.9 %)
- N * : 4 (0.9 %)

Overview Map



Spot





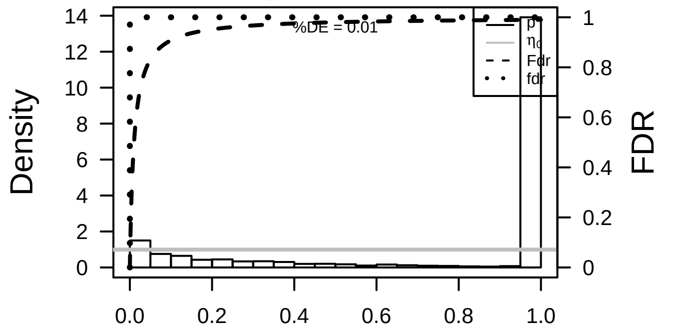
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_168842	1.05	−1.38	0.31	FCER1A	Fc fragment of IgE receptor Ia [Source:HGNC Symbol;Acc:H
2	ILMN_165302	0.91	−0.71	0.6	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254
3	ILMN_175424	0.79	−0.69	0.4		
4	ILMN_176520	0.78	−0.6	0.66	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 in
5	ILMN_169342	0.77	−0.67	0.52		
6	ILMN_179865	0.76	−0.64	0.65	MCM6	minichromosome maintenance complex component 6 [Source
7	ILMN_323188	0.76	−0.65	0.5		
8	ILMN_205367	0.74	−0.66	0.81	ACADM	acyl−CoA dehydrogenase, C−4 to C−12 straight chain [Sourc
9	ILMN_169417	0.72	−0.62	0.76	PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:
10	ILMN_224355	0.72	−0.54	0.55	LOC105378378	zinc finger protein 275 [Source:HGNC Symbol;Acc:HGNC:13
11	ILMN_205460	0.7	−0.81	0.46	CYP4V2	cytochrome P450 family 4 subfamily V member 2 [Source:HG
12	ILMN_236702	0.69	−0.59	0.69	SEC61G	Sec61 translocon gamma subunit [Source:HGNC Symbol;Acc
13	ILMN_213613	0.68	−0.71	0.6	MIR7705	poly(A) binding protein cytoplasmic 1 [Source:HGNC Symbol;
14	ILMN_166963	0.68	−0.6	0.72	ACP1	acid phosphatase 1, soluble [Source:HGNC Symbol;Acc:HGN
15	ILMN_171962	0.67	−0.72	0.57	RABEP1	rabaptin, RAB GTPase binding effector protein 1 [Source:HG
16	ILMN_217513	0.66	−0.66	0.57		
17	ILMN_180948	0.64	−0.47	0.69	SPCS2	signal peptidase complex subunit 2 [Source:HGNC Symbol;A
18	ILMN_168356	0.63	−0.56	0.73		small nuclear ribonucleoprotein polypeptide G pseudogene 5
19	ILMN_173161	0.63	−0.53	0.73	DAD1	defender against cell death 1 [Source:HGNC Symbol;Acc:HG
20	ILMN_174590	0.63	−0.56	0.69	CCDC6	coiled−coil domain containing 6 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	9e−29	110 / 7275	Lympl	HOPP_Txn_elongation
2	2e−26	93 / 5356	Lympl	HOPP_Txn_transition
3	4e−25	121 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
4	3e−22	130 / 12298	Chror	2_TssA_Melanocytes
5	2e−21	125 / 11455	Chror	2_TssA_Fibroblasts
6	9e−21	106 / 8226	Lympl	HOPP_Active_promoter
7	1e−20	114 / 9555	Colon	TssA_Colon
8	1e−19	96 / 6970	Chror	5_Tx_Neuronal_Progenitor
9	1e−18	129 / 12983	Chror	2_TssA_Neuronal_Progenitor
10	2e−18	106 / 8771	Chror	5_Tx_Melanocytes
11	2e−17	104 / 8678	Colon	Quies3_Colon
12	3e−17	103 / 8568	Colon	TxWk_Colon
13	8e−17	108 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
14	5e−16	104 / 9054	Colon	Tx_Colon
15	9e−16	115 / 10999	Colon	TssWk_Colon
16	1e−15	28 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
17	1e−15	82 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
18	4e−15	40 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
19	7e−15	38 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
20	1e−14	28 / 737	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
21	3e−14	117 / 11836	Chror	3_TssF_Melanocytes
22	3e−13	93 / 8098	Lympl	HOPP_Weak_promoter
23	6e−13	107 / 10430	Brain	Overlap_fetal_midbrain_Quies
24	1e−12	70 / 5067	TF	ICGC_Taf1_targets
25	2e−12	39 / 1797	GSEA	PILON_KLF1_TARGETS_DN
26	3e−12	97 / 8990	Chror	15_Quies_Fibroblasts
27	4e−12	31 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
28	2e−11	101 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
29	5e−11	87 / 7854	Chror	5_Tx_Fibroblasts
30	9e−11	114 / 12393	Chror	15_Quies_Neuronal_Progenitor
31	4e−10	68 / 5466	TF	ICGC_Nficsc81335_targets
32	4e−10	24 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
33	7e−10	63 / 4881	TF	ICGC_Atf2_targets
34	7e−10	63 / 4890	TF	ICGC_Bclaf101388_targets
35	8e−10	29 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
36	8e−10	38 / 2087	TF	ICGC_Cebpbsc150_targets
37	2e−09	67 / 5518	TF	ICGC_Stat5_targets
38	3e−09	66 / 5442	TF	ICGC_Pmlsc71910_targets
39	4e−09	74 / 6578	TF	ICGC_Pou2_targets
40	5e−09	57 / 4362	TF	ICGC_Creb1_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 142	HORVATH_aging_genes meth UP
2	0.5	1 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	2 / 16	GENTLES_modul11
2	0.004	2 / 16	GENTLES_modul16
3	0.023	2 / 38	KUIPER_MM good survival
4	0.024	2 / 39	ZHANG_MM up
5	0.041	0 / 13	RHODES_CANCER_META_SIGNATURE
6	0.049	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
7	0.118	4 / 301	SPANG_BCL6−index2
8	0.249	1 / 46	PanCan_DNARepair_geneset_nanostring
9	0.415	0 / 14	LIU_PROSTATE_CANCER_UP
10	0.433	1 / 91	PanCan_TXmisReg_geneset_nanostring
11	0.518	1 / 117	PanCan_Driver_Gene_geneset_nanostring
12	0.541	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	0.541	1 / 125	PanCan_CC+Apop_geneset_nanostring
14	0.638	3 / 527	Lembcke_Normal vs Adenoma
15	0.762	0 / 15	LIU_PROSTATE_CANCER_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−22	130 / 12298	2_TssA_Melanocytes
2	2e−21	125 / 11455	2_TssA_Fibroblasts
3	1e−19	96 / 6970	5_Tx_Neuronal_Progenitor
4	1e−18	129 / 12983	2_TssA_Neuronal_Progenitor
5	2e−18	106 / 8771	5_Tx_Melanocytes
6	3e−14	117 / 11836	3_TssF_Melanocytes
7	3e−12	97 / 8990	15_Quies_Fibroblasts
8	5e−11	87 / 7854	5_Tx_Fibroblasts
9	9e−11	114 / 12393	15_Quies_Neuronal_Progenitor
10	6e−08	110 / 12741	7_Enh_Melanocytes
11	8e−07	98 / 11130	15_Quies_Melanocytes
12	4e−06	60 / 5699	6_EnhG_Melanocytes
13	4e−05	77 / 8613	7_Enh_Fibroblasts
14	4e−04	80 / 9635	3_TssF_Fibroblasts
15	1e−02	87 / 11847	7_Enh_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−15	28 / 669	PUJANA_CHEK2_PCC_NETWORK
2	7e−15	38 / 1417	PUJANA_BRCA1_PCC_NETWORK
3	1e−14	28 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
4	2e−12	39 / 1797	PILON_KLF1_TARGETS_DN
5	4e−12	31 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
6	4e−10	24 / 841	ACEVEDO_LIVER_CANCER_UP
7	8e−10	29 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
8	3e−08	26 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	3e−08	17 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
10	4e−08	26 / 1241	PUJANA_ATM_PCC_NETWORK
11	7e−08	24 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
12	2e−07	12 / 276	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
13	2e−07	12 / 282	PENG_GLUTAMINE_DEPRIVATION_DN
14	3e−07	18 / 693	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
15	5e−07	28 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−29	110 / 7275	HOPP_Txn_elongation
2	2e−26	93 / 5356	HOPP_Txn_transition
3	9e−21	106 / 8226	HOPP_Active_promoter
4	3e−13	93 / 8098	HOPP_Weak_promoter
5	4e−07	69 / 6559	HOPP_Weak_txn
6	2e−06	70 / 6959	HOPP_Weak_enhancer
7	3e−05	70 / 7448	HOPP_Strong_enhancer
8	6e−05	7 / 158	WIRTH_lymphoma937_spot C
9	6e−05	7 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
10	5e−04	31 / 2701	HOPP_Repetitive
11	3e−03	4 / 94	Sha_BL UP
12	3e−03	12 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
13	3e−03	12 / 777	WIRTH_lymphoma937_spot D
14	8e−03	8 / 455	SPANG_CD40 6hrs DN
15	9e−03	6 / 283	TARTE_Plasmablast signature

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−08	23 / 933	PROTEINATLAS_adrenal gland
2	9e−08	18 / 639	PROTEINATLAS_breast
3	6e−07	18 / 724	PROTEINATLAS_lymph node
4	6e−07	24 / 1239	PROTEINATLAS_testis
5	7e−07	22 / 1063	PROTEINATLAS_tonsil
6	1e−06	21 / 1003	PROTEINATLAS_appendix
7	2e−06	16 / 619	PROTEINATLAS_salivary gland
8	2e−06	22 / 1138	PROTEINATLAS_small intestine
9	2e−06	16 / 640	PROTEINATLAS_parathyroid gland
10	3e−06	11 / 302	Chaussabel_3,4_Protein phosphatases
11	4e−06	22 / 1194	PROTEINATLAS_stomach
12	1e−05	21 / 1176	PROTEINATLAS_duodenum
13	2e−05	20 / 1118	PROTEINATLAS_placenta
14	2e−05	17 / 850	PROTEINATLAS_skin
15	3e−05	15 / 695	PROTEINATLAS_bone marrow

BP

Rank	p−value	#in/all	Geneset
1	6e−05	3 / 13	positive regulation of mRNA splicing, via spliceosome
2	7e−05	5 / 69	mitochondrial translational elongation
3	1e−04	4 / 39	mitotic nuclear envelope disassembly
4	2e−04	5 / 86	mRNA export from nucleus
5	2e−04	7 / 196	mRNA splicing, via spliceosome
6	4e−04	3 / 23	tRNA methylation
7	8e−04	3 / 29	regulation of glucose transport
8	8e−04	3 / 29	tRNA export from nucleus
9	9e−04	4 / 69	dephosphorylation
10	1e−03	4 / 71	mitochondrial translational termination
11	2e−03	4 / 81	viral transcription
12	2e−03	2 / 10	maturation of 5.8S rRNA
13	2e−03	2 / 12	maturation of LSU−rRNA
14	2e−03	2 / 12	postreplication repair
15	2e−03	6 / 219	mitotic nuclear division

CC

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 25	preribosome, large subunit precursor
2	4e−05	6 / 101	intracellular ribonucleoprotein complex
3	7e−05	32 / 2535	nucleoplasm
4	1e−04	5 / 78	catalytic step 2 spliceosome
5	2e−04	14 / 721	nucleolus
6	2e−04	20 / 1304	mitochondrion
7	2e−04	26 / 1979	membrane
8	3e−04	7 / 200	nuclear membrane
9	3e−04	48 / 4828	nucleus
10	4e−03	12 / 788	endoplasmic reticulum membrane
11	5e−03	2 / 17	pericentriolar material
12	6e−03	3 / 60	nuclear pore
13	7e−03	2 / 20	cytoplasmic ribonucleoprotein granule
14	9e−03	6 / 287	mitochondrial matrix
15	1e−02	4 / 138	mitochondrial outer membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−20	114 / 9555	TssA_Colon
2	2e−17	104 / 8678	Quies3_Colon
3	3e−17	103 / 8568	TxWk_Colon
4	5e−16	104 / 9054	Tx_Colon
5	9e−16	115 / 10999	TssWk_Colon
6	4e−15	40 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	1e−07	22 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
8	7e−05	68 / 7354	TssF_Colon
9	2e−04	15 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	7e−04	20 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	9e−04	25 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	1e−03	40 / 4034	TssD1_Colon
13	9e−03	15 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	1e−02	81 / 10779	Enh_Colon
15	3e−02	49 / 6138	TssD2_Colon

HM

Rank	p−value	#in/all	Geneset
1	1e−06	9 / 170	HALLMARK_MYC_TARGETS_V1
2	5e−03	5 / 173	HALLMARK_E2F_TARGETS
3	6e−03	5 / 185	HALLMARK_MTORC1_SIGNALING
4	2e−02	4 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	3e−02	4 / 179	HALLMARK_G2M_CHECKPOINT
6	4e−02	2 / 54	HALLMARK_MYC_TARGETS_V2
7	1e−01	3 / 176	HALLMARK_ADIPOGENESIS
8	1e−01	3 / 185	HALLMARK_P53_PATHWAY
9	1e−01	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	1e−01	2 / 91	HALLMARK_PEROXISOME
11	1e−01	2 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	2e−01	2 / 130	HALLMARK_DNA_REPAIR
13	2e−01	1 / 41	HALLMARK_APICAL_SURFACE
14	3e−01	2 / 176	HALLMARK_KRAS_SIGNALING_UP
15	3e−01	2 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−05	8 / 176	hsa−miR−199b−3p
2	3e−05	7 / 143	hsa−miR−922
3	3e−05	10 / 321	hsa−miR−590−3p
4	6e−05	8 / 215	hsa−miR−199a−3p
5	8e−05	4 / 37	hsa−miR−518e
6	1e−04	8 / 233	hsa−miR−1252
7	2e−04	6 / 140	hsa−miR−338−5p
8	3e−04	6 / 149	hsa−miR−142−3p
9	4e−04	5 / 102	hsa−miR−1284
10	5e−04	5 / 104	hsa−miR−325
11	6e−04	9 / 374	hsa−miR−144
12	6e−04	9 / 379	hsa−miR−454
13	6e−04	10 / 463	hsa−miR−301a
14	8e−04	4 / 67	hsa−miR−1184
15	8e−04	3 / 30	hsa−miR−626

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	4e−25	121 / 9815	Overlap_fetal_midbrain_ReprPC
2	8e−17	108 / 9504	Overlap_fetal_midbrain_K9K27me3
3	1e−15	82 / 5936	Overlap_fetal_midbrain_HetRpts
4	6e−13	107 / 10430	Overlap_fetal_midbrain_Quies
5	2e−11	101 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	3e−03	16 / 1171	Fetal_EnhP
7	1e−02	11 / 796	Overlap_fetal_midbrain_ZNF
8	2e−02	26 / 2709	Mid_Frontal_Lobe_HetRpts
9	3e−02	6 / 386	Fetal_ZNF
10	1e−01	9 / 937	Fetal_EnhG
11	1e−01	4 / 328	Fetal_Het
12	2e−01	10 / 1162	Fetal_Enh
13	4e−01	10 / 1436	Fetal_K9K27me3
14	4e−01	21 / 3164	Mid_Frontal_Lobe_ZNF
15	6e−01	4 / 630	Mid_Frontal_Lobe_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	0.08	14 / 1492	Chr 2
2	0.08	20 / 2323	Chr 1
3	0.11	11 / 1160	Chr 12
4	0.12	5 / 422	Chr 13
5	0.16	4 / 342	Chr 18
6	0.22	10 / 1217	Chr 3
7	0.27	3 / 289	Chr 21
8	0.28	8 / 994	Chr X
9	0.33	7 / 902	Chr 4
10	0.48	8 / 1211	Chr 6
11	0.58	8 / 1318	Chr 17
12	0.59	7 / 1170	Chr 7
13	0.60	5 / 836	Chr 8
14	0.65	6 / 1060	Chr 5
15	0.85	2 / 536	Chr 22

Glio

Rank	p−value	#in/all	Geneset
1	1e−07	31 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	8e−07	32 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	8e−04	8 / 315	Up
4	4e−03	7 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	5e−02	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
6	7e−02	9 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	1e−01	5 / 401	Down_b
8	2e−01	1 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
9	3e−01	1 / 55	developing astrocytes
10	4e−01	1 / 74	Weller_LGG_gradeII−vs−III_DOWN
11	4e−01	1 / 84	GIEZELT_GBM_STS_up_VS_LTS
12	4e−01	1 / 84	Weller_LGG_gradeII−vs−III_UP
13	4e−01	1 / 92	Weller_LGG_A_vs_O_DOWN
14	4e−01	3 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
15	5e−01	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 31	DUMEAUX_Fasting enriched genes
2	0.10	1 / 17	DUMEAUX_High bmi enriched genes
3	0.44	1 / 94	DUMEAUX_Smoking enriched genes
4	0.60	1 / 147	Homuth_BMI−associated−genes_UP
5	0.73	1 / 211	Homuth_BMI−associated−genes_DN
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	1e−06	21 / 1013	poly(A) RNA binding
2	1e−05	10 / 283	nucleotide binding
3	1e−04	3 / 17	structural constituent of nuclear pore
4	2e−03	2 / 10	poly(A) binding
5	2e−03	72 / 8818	protein binding
6	3e−03	2 / 14	5'−nucleotidase activity
7	3e−03	4 / 99	mRNA binding
8	5e−03	2 / 17	translation elongation factor activity
9	6e−03	2 / 19	nucleocytoplasmic transporter activity
10	1e−02	2 / 29	Hsp70 protein binding
11	2e−02	2 / 33	phosphatase activity
12	2e−02	3 / 94	double−stranded DNA binding
13	2e−02	2 / 36	single−stranded RNA binding
14	2e−02	4 / 169	structural constituent of ribosome
15	4e−02	6 / 399	RNA binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	BENTINK_src.2
2	0.083	1 / 14	BENTINK_ras.6
3	1.000	0 / 14	GUSTAFSON_PI3K_UP
4	1.000	0 / 15	GUSTAFSON_PI3K_DN
5	1.000	0 / 13	BENTINK_e2f3.1
6	1.000	0 / 13	BENTINK_e2f3.2
7	1.000	0 / 13	BENTINK_myc.1
8	1.000	0 / 12	BENTINK_ras.1
9	1.000	0 / 11	BENTINK_ras.4
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−12	70 / 5067	ICGC_Taf1_targets
2	4e−10	68 / 5466	ICGC_Nficsc81335_targets
3	7e−10	63 / 4881	ICGC_Atf2_targets
4	7e−10	63 / 4890	ICGC_Bclaf101388_targets
5	8e−10	38 / 2087	ICGC_Cebpbsc150_targets
6	2e−09	67 / 5518	ICGC_Stat5_targets
7	3e−09	66 / 5442	ICGC_Pmlsc71910_targets
8	4e−09	74 / 6578	ICGC_Pou2_targets
9	5e−09	57 / 4362	ICGC_Creb1_targets
10	6e−09	65 / 5410	ICGC_Foxm1_targets
11	9e−09	71 / 6267	ICGC_Yy1_targets
12	9e−09	30 / 1498	ICGC_Ets1_targets
13	2e−08	54 / 4131	ICGC_Nfatc1_targets
14	5e−08	67 / 5961	ICGC_Pol24_targets
15	6e−08	71 / 6552	ICGC_Pol2_targets

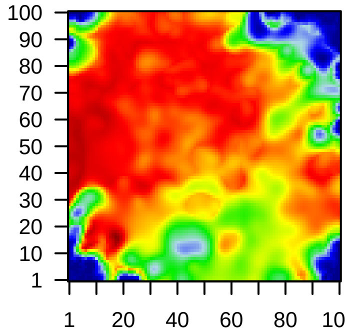
Underexpression Spots

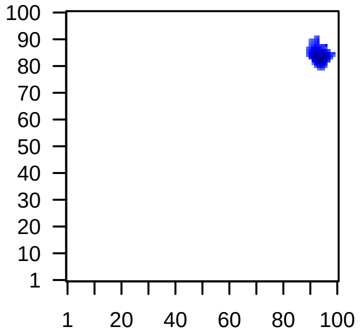
Spot Summary: p

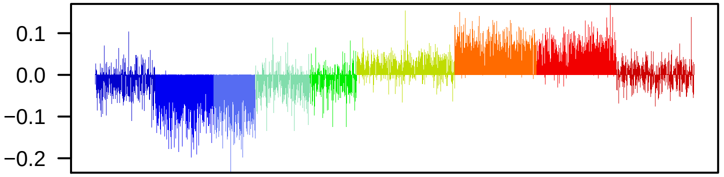
metagenes = 86
genes = 732

<r> metagenes = 0.95
<r> genes = 0.33
beta: r2= 11.93 / log p= −Inf

samples with spot = 41 (1.2 %)
F * : 1 (0.2 %)
F J * : 26 (5.6 %)
J * : 13 (2.9 %)
N * : 1 (0.2 %)


Overview Map


Spot

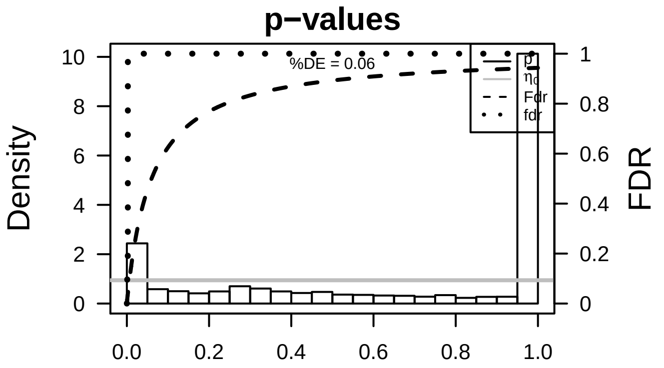


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_208622	0.94	−0.81	0.21	WDR11	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:138
2	ILMN_165936	0.82	−0.62	0.2		
3	ILMN_175316	0.77	−0.9	0.16	IPO8	importin 8 [Source:HGNC Symbol;Acc:HGNC:9853]
4	ILMN_180713	0.73	−0.66	0.39		ciliary rootlet coiled−coil, rootletin pseudogene 2 [Source:HGI
5	ILMN_240021	0.65	−0.5	0.36	SRI	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
6	ILMN_180026	0.64	−0.56	0.43	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
7	ILMN_181512	0.6	−0.63	0.39	CHCHD2	coiled−coil−helix−coiled−coil−helix domain containing 2 [Sour
8	ILMN_180502	0.58	−0.44	0.34		
9	ILMN_171813	0.57	−0.72	0.52	UQCRHL	ubiquinol−cytochrome c reductase hinge protein like [Source:
10	ILMN_179734	0.57	−0.57	0.49	ARID1A	AT−rich interaction domain 1A [Source:HGNC Symbol;Acc:H
11	ILMN_170816	0.57	−0.55	0.57	EIF3A	eukaryotic translation initiation factor 3 subunit A [Source:HGI
12	ILMN_219168	0.56	−0.66	0.32	CHCHD2	coiled−coil−helix−coiled−coil−helix domain containing 2 [Sour
13	ILMN_233086	0.55	−0.46	0.62	SMC4	structural maintenance of chromosomes 4 [Source:HGNC Sy
14	ILMN_172085	0.55	−0.56	0.43	ABRACL	ABRA C−terminal like [Source:HGNC Symbol;Acc:HGNC:212
15	ILMN_168035	0.55	−0.44	0.54	NSF	N−ethylmaleimide sensitive factor, vesicle fusing ATPase [Sou
16	ILMN_175592	0.54	−0.51	0.36		
17	ILMN_219041	0.54	−0.58	0.48	ZNF83	zinc finger protein 83 [Source:HGNC Symbol;Acc:HGNC:131
18	ILMN_169089	0.53	−0.38	0.59		heat shock protein 90 beta family member 3, pseudogene [Sc
19	ILMN_170326	0.52	−0.36	0.49	SP140	SP140 nuclear body protein [Source:HGNC Symbol;Acc:HGN
20	ILMN_170129	0.52	−0.42	0.43		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	469 / 8226	Lympl	HOPP_Active_promoter
2	1e−99	526 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
3	7e−99	478 / 8771	Chror	5_Tx_Melanocytes
4	3e−94	549 / 12298	Chror	2_TssA_Melanocytes
5	9e−93	430 / 7275	Lympl	HOPP_Txn_elongation
6	7e−90	528 / 11455	Chror	2_TssA_Fibroblasts
7	3e−85	480 / 9555	Colon	TssA_Colon
8	2e−84	551 / 12983	Chror	2_TssA_Neuronal_Progenitor
9	3e−84	454 / 8568	Colon	TxWk_Colon
10	1e−81	374 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
11	2e−81	431 / 7854	Chror	5_Tx_Fibroblasts
12	1e−80	452 / 8678	Colon	Quies3_Colon
13	4e−78	458 / 9054	Colon	Tx_Colon
14	8e−66	382 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	1e−65	438 / 8990	Chror	15_Quies_Fibroblasts
16	4e−63	483 / 10999	Colon	TssWk_Colon
17	6e−60	442 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
18	3e−58	402 / 8098	Lympl	HOPP_Weak_promoter
19	1e−56	447 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
20	5e−50	465 / 11130	Chror	15_Quies_Melanocytes
21	3e−49	480 / 11836	Chror	3_TssF_Melanocytes
22	6e−45	485 / 12393	Chror	15_Quies_Neuronal_Progenitor
23	9e−42	487 / 12741	Chror	7_Enh_Melanocytes
24	5e−36	277 / 5356	Lympl	HOPP_Txn_transition
25	1e−33	111 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
26	6e−33	113 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
27	9e−33	91 / 811	GSEA	LEE_BMP2_TARGETS_DN
28	2e−32	413 / 10430	Brain	Overlap_fetal_midbrain_Quies
29	7e−29	298 / 6559	Lympl	HOPP_Weak_txn
30	4e−24	240 / 5067	TF	ICGC_Taf1_targets
31	7e−24	297 / 6959	Lympl	HOPP_Weak_enhancer
32	8e−23	76 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
33	9e−23	121 / 1797	GSEA	PILON_KLF1_TARGETS_DN
34	2e−22	209 / 4237	Chror	14_ZNF_Neuronal_Progenitor
35	4e−21	336 / 8613	Chror	7_Enh_Fibroblasts
36	1e−20	340 / 8818	MF	protein binding
37	2e−20	197 / 4034	Colon	TssD1_Colon
38	2e−20	126 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
39	2e−20	54 / 465	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
40	3e−20	115 / 1777	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.07	6 / 111	HORVATH_aging_genes meth DOWN
2	0.31	5 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	3 / 13	GENTLES_modul6
2	0.005	3 / 14	GENTLES_modul4
3	0.018	4 / 39	ZHANG_MM up
4	0.036	21 / 527	Lembcke_Normal vs Adenoma
5	0.043	2 / 13	RHODES_CANCER_META_SIGNATURE
6	0.051	4 / 54	KUIPER_MM poor survival
7	0.057	2 / 15	WOLFER_overlap genes
8	0.117	3 / 46	PanCan_DNARepair_geneset_nanostring
9	0.122	4 / 73	SHAUGHNESSY_MM high risk
10	0.122	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.184	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
12	0.188	5 / 117	PanCan_Driver_Gene_geneset_nanostring
13	0.211	1 / 9	GENTLES_modul3
14	0.211	1 / 9	GENTLES_modul5
15	0.240	2 / 36	PanCan_HK_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−99	478 / 8771	5_Tx_Melanocytes
2	3e−94	549 / 12298	2_TssA_Melanocytes
3	7e−90	528 / 11455	2_TssA_Fibroblasts
4	2e−84	551 / 12983	2_TssA_Neuronal_Progenitor
5	2e−81	431 / 7854	5_Tx_Fibroblasts
6	8e−66	382 / 6970	5_Tx_Neuronal_Progenitor
7	1e−65	438 / 8990	15_Quies_Fibroblasts
8	5e−50	465 / 11130	15_Quies_Melanocytes
9	3e−49	480 / 11836	3_TssF_Melanocytes
10	6e−45	485 / 12393	15_Quies_Neuronal_Progenitor
11	9e−42	487 / 12741	7_Enh_Melanocytes
12	2e−22	209 / 4237	14_ZNF_Neuronal_Progenitor
13	4e−21	336 / 8613	7_Enh_Fibroblasts
14	4e−17	111 / 1846	14_ZNF_Melanocytes
15	1e−15	346 / 9635	3_TssF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−33	111 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	6e−33	113 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	9e−33	91 / 811	LEE_BMP2_TARGETS_DN
4	8e−23	76 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
5	9e−23	121 / 1797	PILON_KLF1_TARGETS_DN
6	2e−20	54 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
7	2e−18	47 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
8	9e−18	46 / 389	GARY_CD5_TARGETS_DN
9	1e−17	95 / 1417	PUJANA_BRCA1_PCC_NETWORK
10	2e−15	63 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
11	2e−15	53 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
12	4e−15	65 / 841	ACEVEDO_LIVER_CANCER_UP
13	9e−15	96 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
14	3e−14	41 / 388	SHEN_SMARCA2_TARGETS_UP
15	2e−13	47 / 527	HAMAI_APOPTOSIS_VIA_TRAIL_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	469 / 8226	HOPP_Active_promoter
2	9e−93	430 / 7275	HOPP_Txn_elongation
3	3e−58	402 / 8098	HOPP_Weak_promoter
4	5e−36	277 / 5356	HOPP_Txn_transition
5	7e−29	298 / 6559	HOPP_Weak_txn
6	7e−24	297 / 6959	HOPP_Weak_enhancer
7	8e−20	93 / 1270	SPANG_BCR UP
8	3e−16	64 / 777	WIRTH_lymphoma937_spot D
9	9e−16	63 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
10	2e−11	23 / 158	WIRTH_lymphoma937_spot C
11	3e−11	23 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line
12	2e−09	262 / 7448	HOPP_Strong_enhancer
13	2e−05	29 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
14	1e−04	28 / 493	WIRTH_lymphoma937_spot J
15	4e−04	25 / 455	SPANG_CD40 6hrs DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−12	30 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
2	1e−11	22 / 139	Chaussabel_1,8_Metabolism Biosynthesis
3	2e−10	27 / 242	Chaussabel_3,9_Kinases
4	4e−10	30 / 302	Chaussabel_3,4_Protein phosphatases
5	6e−09	66 / 1194	PROTEINATLAS_stomach
6	4e−08	54 / 933	PROTEINATLAS_adrenal gland
7	9e−08	62 / 1173	PROTEINATLAS_rectum
8	2e−07	57 / 1063	PROTEINATLAS_tonsil
9	3e−07	24 / 275	Chaussabel_3,7_Spliceosome
10	4e−07	60 / 1167	PROTEINATLAS_gallbladder
11	5e−07	52 / 959	PROTEINATLAS_nasopharynx
12	8e−07	53 / 1003	PROTEINATLAS_appendix
13	1e−06	51 / 963	PROTEINATLAS_pancreas
14	2e−06	42 / 740	PROTEINATLAS_esophagus
15	2e−06	38 / 640	PROTEINATLAS_parathyroid gland

BP

Rank	p−value	#in/all	Geneset
1	2e−07	78 / 1643	transcription, DNA−templated
2	4e−07	11 / 61	snRNA transcription from RNA polymerase II promoter
3	1e−06	62 / 1272	regulation of transcription, DNA−templated
4	4e−06	12 / 91	sister chromatid cohesion
5	5e−06	10 / 63	transcription elongation from RNA polymerase II promoter
6	6e−06	9 / 51	stem cell population maintenance
7	1e−05	11 / 86	mRNA export from nucleus
8	2e−05	17 / 196	mRNA splicing, via spliceosome
9	2e−05	5 / 14	preassembly of GPI anchor in ER membrane
10	4e−05	21 / 300	cell division
11	6e−05	6 / 27	transcription elongation from RNA polymerase I promoter
12	7e−05	6 / 28	termination of RNA polymerase I transcription
13	7e−05	22 / 335	protein transport
14	1e−04	6 / 30	transcription initiation from RNA polymerase I promoter
15	1e−04	5 / 20	GPI anchor biosynthetic process

CC

Rank	p−value	#in/all	Geneset
1	7e−19	141 / 2535	nucleoplasm
2	5e−13	200 / 4828	nucleus
3	2e−08	69 / 1304	mitochondrion
4	2e−08	46 / 721	nucleolus
5	2e−05	113 / 2979	cytosol
6	4e−05	166 / 4822	cytoplasm
7	6e−05	24 / 379	centrosome
8	7e−05	13 / 139	microtubule cytoskeleton
9	3e−04	22 / 374	mitochondrial inner membrane
10	5e−04	9 / 90	spindle pole
11	7e−04	8 / 75	condensed chromosome kinetochore
12	1e−03	4 / 18	exon−exon junction complex
13	2e−03	4 / 21	U4/U6 x U5 tri−snRNP complex
14	2e−03	3 / 11	mRNA cleavage and polyadenylation specificity factor complex
15	3e−03	4 / 23	precatalytic spliceosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−85	480 / 9555	TssA_Colon
2	3e−84	454 / 8568	TxWk_Colon
3	1e−80	452 / 8678	Quies3_Colon
4	4e−78	458 / 9054	Tx_Colon
5	4e−63	483 / 10999	TssWk_Colon
6	2e−20	197 / 4034	TssD1_Colon
7	6e−19	103 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
8	5e−14	112 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	5e−13	274 / 7354	TssF_Colon
10	2e−11	68 / 1083	ZNF_Colon
11	1e−06	165 / 4526	Quies1_Colon
12	4e−06	65 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
13	3e−05	10 / 76	Pentrack_CRC_TCGA_corr_N_msi−h_DN
14	3e−05	56 / 1224	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
15	3e−05	64 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

HM

Rank	p−value	#in/all	Geneset
1	1e−04	14 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−04	14 / 173	HALLMARK_E2F_TARGETS
3	7e−03	9 / 130	HALLMARK_DNA_REPAIR
4	7e−03	11 / 179	HALLMARK_G2M_CHECKPOINT
5	1e−02	10 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	2e−02	10 / 185	HALLMARK_MTORC1_SIGNALING
7	8e−02	5 / 87	HALLMARK_PROTEIN_SECRETION
8	9e−02	8 / 177	HALLMARK_MITOTIC_SPINDLE
9	1e−01	6 / 132	HALLMARK_UV_RESPONSE_DN
10	2e−01	6 / 138	HALLMARK_FATTY_ACID_METABOLISM
11	3e−01	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	3e−01	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	3e−01	6 / 176	HALLMARK_KRAS_SIGNALING_UP
14	4e−01	2 / 54	HALLMARK_MYC_TARGETS_V2
15	5e−01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	0.5	1 / 30	Hugo_melanoma−all−MET_UP
2	0.7	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−09	32 / 382	hsa−let−7c
2	1e−08	38 / 516	hsa−miR−15a
3	3e−08	33 / 425	hsa−let−7b
4	3e−08	36 / 491	hsa−miR−107
5	3e−08	36 / 493	hsa−miR−103
6	9e−08	20 / 186	hsa−miR−520d−5p
7	2e−07	30 / 394	hsa−miR−301b
8	2e−07	24 / 272	hsa−miR−101
9	3e−07	25 / 295	hsa−miR−561
10	4e−07	26 / 321	hsa−miR−590−3p
11	4e−07	27 / 343	hsa−let−7a
12	4e−07	28 / 366	hsa−let−7d
13	4e−07	33 / 480	hsa−miR−15b
14	6e−07	32 / 463	hsa−miR−301a
15	7e−07	22 / 249	hsa−miR−524−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.5	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	1e−99	526 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−81	374 / 5936	Overlap_fetal_midbrain_HetRpts
3	6e−60	442 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−56	447 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	2e−32	413 / 10430	Overlap_fetal_midbrain_Quies
6	4e−11	50 / 681	Overlap_fetal_midbrain_EnhP
7	7e−09	65 / 1171	Fetal_EnhP
8	6e−07	69 / 1436	Fetal_K9K27me3
9	1e−05	46 / 906	Fetal_HetRpts
10	3e−05	46 / 937	Fetal_EnhG
11	2e−03	47 / 1162	Fetal_Enh
12	8e−03	27 / 630	Mid_Frontal_Lobe_EnhP
13	4e−02	29 / 796	Overlap_fetal_midbrain_ZNF
14	5e−02	82 / 2654	Fetal_Quies
15	6e−02	44 / 1329	Overlap_fetal_midbrain_Enh

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	24 / 422	Chr 13
2	7e−03	41 / 1060	Chr 5
3	3e−02	51 / 1492	Chr 2
4	5e−02	32 / 902	Chr 4
5	7e−02	27 / 768	Chr 14
6	7e−02	31 / 904	Chr 10
7	1e−01	13 / 342	Chr 18
8	1e−01	37 / 1160	Chr 12
9	2e−01	10 / 289	Chr 21
10	2e−01	36 / 1217	Chr 3
11	3e−01	35 / 1211	Chr 6
12	3e−01	24 / 836	Chr 8
13	3e−01	27 / 954	Chr 9
14	5e−01	31 / 1170	Chr 7
15	8e−01	17 / 769	Chr 15

Glio

Rank	p−value	#in/all	Geneset
1	2e−20	126 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	3e−20	115 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−11	57 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	9e−06	23 / 315	Up
5	4e−03	4 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
6	1e−02	6 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	2e−02	4 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
8	2e−02	2 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
9	2e−02	15 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	4e−02	2 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
11	1e−01	15 / 401	Down_b
12	1e−01	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
13	1e−01	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	1e−01	1 / 5	Phillips Prolif up vs PN & MES
15	2e−01	3 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 31	DUMEAUX_Fasting enriched genes
2	0.5	6 / 211	Homuth_BMI−associated−genes_DN
3	0.7	3 / 147	Homuth_BMI−associated−genes_UP
4	1.0	0 / 94	DUMEAUX_Smoking enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	1e−20	340 / 8818	protein binding
2	5e−11	64 / 1013	poly(A) RNA binding
3	2e−06	77 / 1717	metal ion binding
4	2e−05	26 / 399	RNA binding
5	7e−05	6 / 28	DNA−dependent ATPase activity
6	4e−04	4 / 14	RNA polymerase II carboxy−terminal domain kinase activity
7	5e−04	18 / 283	nucleotide binding
8	8e−04	5 / 29	repressing transcription factor binding
9	1e−03	6 / 45	tRNA binding
10	1e−03	9 / 99	mRNA binding
11	2e−03	52 / 1329	ATP binding
12	2e−03	4 / 22	polyubiquitin binding
13	2e−03	17 / 301	ubiquitin−protein transferase activity
14	4e−03	3 / 13	GTPase regulator activity
15	4e−03	55 / 1475	DNA binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 13	BENTINK_e2f3.2
2	0.25	1 / 11	BENTINK_ras.4
3	0.27	1 / 12	BENTINK_ras.1
4	0.27	1 / 12	BENTINK_src.2
5	0.29	1 / 13	BENTINK_myc.1
6	0.31	1 / 14	GUSTAFSON_PI3K_UP
7	0.31	1 / 14	BENTINK_ras.6
8	0.33	1 / 15	GUSTAFSON_PI3K_DN
9	1.00	0 / 13	BENTINK_e2f3.1
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−24	240 / 5067	ICGC_Taf1_targets
2	2e−16	213 / 4881	ICGC_Atf2_targets
3	2e−16	230 / 5442	ICGC_Pmlsc71910_targets
4	5e−16	195 / 4362	ICGC_Creb1_targets
5	1e−14	207 / 4890	ICGC_Bclaf101388_targets
6	1e−13	98 / 1723	HEBENSTREIT_high expression TF
7	1e−13	116 / 2215	ICGC_GabpPcr2_targets
8	1e−13	245 / 6267	ICGC_Yy1_targets
9	3e−13	220 / 5466	ICGC_Nficsc81335_targets
10	1e−12	213 / 5312	ICGC_Tcf12_targets
11	2e−12	219 / 5518	ICGC_Stat5_targets
12	2e−12	76 / 1231	KIM_MYC targets
13	5e−12	113 / 2255	ICGC_SrfV0416101_targets
14	2e−11	229 / 5984	ICGC_Mta3_targets
15	3e−11	211 / 5410	ICGC_Foxm1_targets

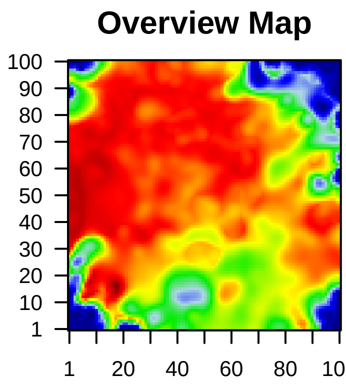
Underexpression Spots

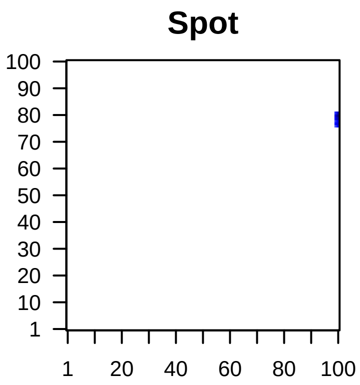
Spot Summary: q

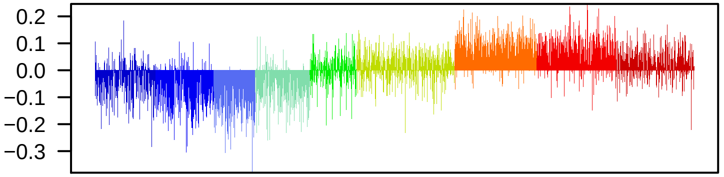
metagenes = 12
genes = 273

<r> metagenes = 0.98
<r> genes = 0.42
beta: r2= 15.64 / log p= −Inf

samples with spot = 249 (7.3 %)
A * : 2 (0.6 %)
A F * : 2 (0.6 %)
C F * : 6 (2.3 %)
F * : 8 (1.4 %)
F J * : 116 (25.1 %)
J * : 95 (21.3 %)
N * : 20 (4.5 %)


Overview Map


Spot

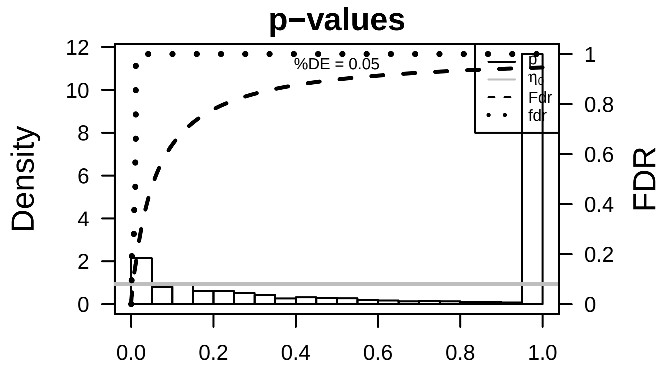


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_176146	0.96	−0.79	0.55	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
2	ILMN_166860	0.89	−0.76	0.43		
3	ILMN_178617	0.85	−0.97	0.47	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
4	ILMN_165798	0.82	−0.55	0.53	TERF2IP	TERF2 interacting protein [Source:HGNC Symbol;Acc:HGNC
5	ILMN_174216	0.79	−0.89	0.68	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
6	ILMN_232088	0.78	−0.79	0.46	CXCR4	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
7	ILMN_228556	0.76	−0.7	0.42		
8	ILMN_177801	0.75	−0.6	0.31	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit [So
9	ILMN_235945	0.72	−0.67	0.39	ERGIC3	ERGIC and golgi 3 [Source:HGNC Symbol;Acc:HGNC:15927
10	ILMN_173185	0.71	−0.59	0.55		
11	ILMN_177279	0.7	−0.49	0.59	ARPP19	cAMP regulated phosphoprotein 19 [Source:HGNC Symbol;A
12	ILMN_324439	0.68	−0.68	0.57		
13	ILMN_169579	0.67	−0.52	0.49	CUL4A	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
14	ILMN_170684	0.66	−0.72	0.64	PGAM4	phosphoglycerate mutase family member 4 [Source:HGNC S
15	ILMN_225118	0.65	−0.74	0.77	ERP29	endoplasmic reticulum protein 29 [Source:HGNC Symbol;Acc
16	ILMN_165588	0.64	−0.59	0.75	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
17	ILMN_237416	0.64	−0.6	0.71		
18	ILMN_177602	0.64	−0.65	0.69	EIF4H	eukaryotic translation initiation factor 4H [Source:HGNC Sym
19	ILMN_237415	0.62	−0.57	0.66	HERPUD1	homocysteine inducible ER protein with ubiquitin like domain
20	ILMN_166289	0.61	−0.55	0.56	WDR11	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:13

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−30	128 / 5356	Lymph	HOPP_Txn_transition
2	6e−28	167 / 9555	Colon	TssA_Colon
3	1e−26	60 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	2e−26	143 / 7275	Lymph	HOPP_Txn_elongation
5	1e−25	159 / 9054	Colon	Tx_Colon
6	1e−24	153 / 8568	Colon	TxWk_Colon
7	4e−22	150 / 8678	Colon	Quies3_Colon
8	1e−21	132 / 6970	Chror	5_Tx_Neuronal_Progenitor
9	1e−20	158 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
10	1e−19	117 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
11	5e−19	176 / 12298	Chror	2_TssA_Melanocytes
12	1e−17	58 / 1797	GSEA	PILON_KLF1_TARGETS_DN
13	2e−16	135 / 8226	Lymph	HOPP_Active_promoter
14	4e−16	27 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
15	1e−15	139 / 8771	Chror	5_Tx_Melanocytes
16	1e−15	163 / 11455	Chror	2_TssA_Fibroblasts
17	3e−15	129 / 7854	Chror	5_Tx_Fibroblasts
18	1e−14	157 / 10999	Colon	TssWk_Colon
19	2e−13	171 / 12983	Chror	2_TssA_Neuronal_Progenitor
20	3e−13	47 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
21	5e−13	144 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
22	9e−13	21 / 302	Refer	Chaussabel_3,4_Protein phosphatases
23	2e−12	100 / 5699	Chror	6_EnhG_Melanocytes
24	4e−12	60 / 2535	CC	nucleoplasm
25	4e−12	138 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
26	6e−11	115 / 7448	Lymph	HOPP_Strong_enhancer
27	7e−11	89 / 5067	TF	ICGC_Taf1_targets
28	8e−10	39 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
29	1e−09	153 / 11836	Chror	3_TssF_Melanocytes
30	2e−09	146 / 11130	Chror	15_Quies_Melanocytes
31	2e−09	157 / 12393	Chror	15_Quies_Neuronal_Progenitor
32	2e−09	33 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
33	3e−09	122 / 8613	Chror	7_Enh_Fibroblasts
34	4e−09	139 / 10430	Brain	Overlap_fetal_midbrain_Quies
35	6e−09	125 / 8990	Chror	15_Quies_Fibroblasts
36	8e−09	10 / 87	miRN	hsa−miR−496
37	9e−09	21 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
38	1e−08	19 / 412	Refer	WIRTH_Immune system
39	1e−08	158 / 12741	Chror	7_Enh_Melanocytes
40	1e−08	34 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	3e−06	5 / 25	tricarboxylic acid cycle
2	2e−04	3 / 12	response to arsenic−containing substance
3	2e−04	6 / 90	regulation of mRNA stability
4	3e−04	8 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
5	3e−04	5 / 64	microtubule cytoskeleton organization
6	3e−04	7 / 140	ubiquitin−dependent protein catabolic process
7	5e−04	3 / 17	nucleotide−excision repair, DNA incision, 3'−to lesion
8	5e−04	3 / 17	nucleotide−excision repair, preincision complex stabilization
9	9e−04	4 / 46	endoplasmic reticulum unfolded protein response
10	2e−03	3 / 25	nucleotide−excision repair, preincision complex assembly
11	2e−03	5 / 92	cellular calcium ion homeostasis
12	2e−03	3 / 27	protein secretion
13	2e−03	9 / 300	cell division
14	2e−03	3 / 28	regulation of translational initiation
15	2e−03	3 / 28	spindle assembly

Brain

Rank	p−value	#in/all	Geneset
1	1e−20	158 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−19	117 / 5936	Overlap_fetal_midbrain_HetRpts
3	5e−13	144 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	4e−12	138 / 9504	Overlap_fetal_midbrain_K9K27me3
5	4e−09	139 / 10430	Overlap_fetal_midbrain_Quies
6	3e−04	48 / 3164	Mid_Frontal_Lobe_ZNF
7	7e−03	15 / 796	Overlap_fetal_midbrain_ZNF
8	3e−02	5 / 180	Overlap_fetal_midbrain_Het
9	3e−02	8 / 386	Fetal_ZNF
10	7e−02	19 / 1436	Fetal_K9K27me3
11	8e−02	16 / 1171	Fetal_EnhP
12	9e−02	6 / 328	Fetal_Het
13	1e−01	15 / 1162	Fetal_Enh
14	1e−01	12 / 906	Fetal_HetRpts
15	2e−01	9 / 681	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	0 / 13	RHODES_CANCER_META_SIGNATURE
2	0.005	5 / 117	PanCan_Driver_Gene_geneset_nanostring
3	0.017	0 / 12	LIU_BREAST_CANCER
4	0.029	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	0.034	10 / 554	Lembcke_Colonic Inflammation
6	0.084	4 / 178	SPANG_LPS−index2
7	0.114	1 / 13	GENTLES_modul2
8	0.119	0 / 14	LIU_COMMON_CANCER_GENES
9	0.122	1 / 14	GENTLES_modul1
10	0.122	1 / 14	GENTLES_modul10
11	0.130	1 / 15	WOLFER_overlap genes
12	0.138	1 / 16	GENTLES_modul14
13	0.147	2 / 73	SHAUGHNESSY_MM high risk
14	0.156	2 / 76	PanCan_Wnt_geneset_nanostring
15	0.285	1 / 36	PanCan_HK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	4e−12	60 / 2535	nucleoplasm
2	5e−07	76 / 4822	cytoplasm
3	1e−04	68 / 4828	nucleus
4	1e−04	3 / 11	proteasome regulatory particle, base subcomplex
5	3e−04	8 / 179	nuclear speck
6	3e−04	34 / 1979	membrane
7	5e−04	14 / 539	Golgi membrane
8	6e−04	45 / 2979	cytosol
9	1e−03	4 / 49	cytoplasmic microtubule
10	1e−03	4 / 49	transcriptional repressor complex
11	1e−03	16 / 721	nucleolus
12	1e−03	4 / 51	proteasome complex
13	1e−03	5 / 88	melanosome
14	2e−03	4 / 60	nuclear pore
15	3e−03	3 / 30	cytoplasmic stress granule

Chr

Rank	p−value	#in/all	Geneset
1	0.02	19 / 1217	Chr 3
2	0.04	7 / 342	Chr 18
3	0.15	11 / 836	Chr 8
4	0.20	6 / 422	Chr 13
5	0.22	8 / 619	Chr 20
6	0.27	11 / 954	Chr 9
7	0.28	11 / 959	Chr 16
8	0.28	4 / 289	Chr 21
9	0.28	9 / 768	Chr 14
10	0.33	13 / 1211	Chr 6
11	0.39	12 / 1160	Chr 12
12	0.39	11 / 1060	Chr 5
13	0.42	8 / 769	Chr 15
14	0.46	9 / 902	Chr 4
15	0.58	21 / 2323	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−21	132 / 6970	5_Tx_Neuronal_Progenitor
2	5e−19	176 / 12298	2_TssA_Melanocytes
3	1e−15	139 / 8771	5_Tx_Melanocytes
4	1e−15	163 / 11455	2_TssA_Fibroblasts
5	3e−15	129 / 7854	5_Tx_Fibroblasts
6	2e−13	171 / 12983	2_TssA_Neuronal_Progenitor
7	2e−12	100 / 5699	6_EnhG_Melanocytes
8	1e−09	153 / 11836	3_TssF_Melanocytes
9	2e−09	146 / 11130	15_Quies_Melanocytes
10	2e−09	157 / 12393	15_Quies_Neuronal_Progenitor
11	3e−09	122 / 8613	7_Enh_Fibroblasts
12	6e−09	125 / 8990	15_Quies_Fibroblasts
13	1e−08	158 / 12741	7_Enh_Melanocytes
14	2e−04	61 / 4237	14_ZNF_Neuronal_Progenitor
15	2e−04	136 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−28	167 / 9555	TssA_Colon
2	1e−25	159 / 9054	Tx_Colon
3	1e−24	153 / 8568	TxWk_Colon
4	4e−22	150 / 8678	Quies3_Colon
5	1e−14	157 / 10999	TssWk_Colon
6	3e−13	47 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−07	104 / 7354	TssF_Colon
8	2e−07	35 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	4e−07	43 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
10	2e−05	77 / 5373	EnhWk1_Colon
11	2e−05	25 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	2e−05	130 / 10779	Enh_Colon
13	5e−03	24 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	1e−02	15 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	1e−02	8 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN

Glio

Rank	p−value	#in/all	Geneset
1	7e−07	24 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	7e−06	36 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−05	38 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	4e−05	12 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	9e−03	8 / 315	Up
6	2e−02	4 / 113	GIEZELT_GBM_WT_up_VS_mut
7	3e−02	3 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	3e−02	8 / 401	Down_b
9	4e−02	6 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
10	8e−02	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
11	1e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
12	1e−01	2 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
13	1e−01	2 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	1e−01	2 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
15	1e−01	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−26	60 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	1e−17	58 / 1797	PILON_KLF1_TARGETS_DN
3	4e−16	27 / 388	SHEN_SMARCA2_TARGETS_UP
4	8e−10	39 / 1417	PUJANA_BRCA1_PCC_NETWORK
5	2e−09	33 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
6	9e−09	21 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
7	1e−08	34 / 1241	PUJANA_ATM_PCC_NETWORK
8	2e−08	23 / 622	SCHLOSSER_SERUM_RESPONSE_DN
9	3e−08	32 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	8e−08	25 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
11	2e−07	15 / 305	JOHNSTONE_PARVB_TARGETS_2_DN
12	4e−07	18 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
13	8e−07	6 / 35	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE
14	8e−07	18 / 492	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
15	9e−07	10 / 142	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM

HM

Rank	p−value	#in/all	Geneset
1	4e−05	8 / 138	HALLMARK_FATTY_ACID_METABOLISM
2	5e−05	7 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	1e−03	7 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	1e−03	7 / 179	HALLMARK_G2M_CHECKPOINT
5	2e−03	7 / 185	HALLMARK_MTORC1_SIGNALING
6	6e−03	6 / 176	HALLMARK_ADIPOGENESIS
7	7e−03	6 / 183	HALLMARK_GLYCOLYSIS
8	8e−03	5 / 132	HALLMARK_UV_RESPONSE_DN
9	1e−02	4 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	2e−02	5 / 173	HALLMARK_E2F_TARGETS
11	5e−02	3 / 87	HALLMARK_PROTEIN_SECRETION
12	6e−02	4 / 162	HALLMARK_ALLOGRAFT_REJECTION
13	7e−02	4 / 170	HALLMARK_MYC_TARGETS_V1
14	8e−02	2 / 50	HALLMARK_TGF_BETA_SIGNALING
15	8e−02	4 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−04	8 / 211	Homuth_BMI−associated−genes_DN
2	2e−01	3 / 147	Homuth_BMI−associated−genes_UP
3	3e−01	1 / 31	DUMEAUX_Fasting enriched genes
4	3e−01	1 / 32	Marjolein_ageing−genes_DN
5	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
6	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−30	128 / 5356	HOPP_Txn_transition
2	2e−26	143 / 7275	HOPP_Txn_elongation
3	2e−16	135 / 8226	HOPP_Active_promoter
4	6e−11	115 / 7448	HOPP_Strong_enhancer
5	7e−08	113 / 8098	HOPP_Weak_promoter
6	1e−06	29 / 1169	SPANG_BCR DN
7	4e−05	92 / 6959	HOPP_Weak_enhancer
8	6e−04	83 / 6559	HOPP_Weak_txn
9	1e−03	9 / 283	TARTE_Plasmablast signature
10	2e−03	12 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
11	2e−03	12 / 493	WIRTH_lymphoma937_spot J
12	6e−03	3 / 39	CARO_OxPhos_in_DLBCL_UP
13	6e−03	3 / 40	Monti_BCR_cluster
14	2e−02	4 / 109	ROSOLOWSKI_blue total
15	3e−02	19 / 1270	SPANG_BCR UP

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	6e−07	117 / 8818	protein binding
2	2e−05	24 / 1013	poly(A) RNA binding
3	6e−04	3 / 18	TBP−class protein binding
4	7e−04	9 / 256	ubiquitin protein ligase binding
5	7e−04	3 / 19	cytokine binding
6	1e−03	14 / 580	identical protein binding
7	2e−03	3 / 28	NAD binding
8	2e−03	5 / 99	mRNA binding
9	4e−03	2 / 10	poly(A) binding
10	4e−03	3 / 35	RNA polymerase II activating transcription factor binding
11	4e−03	10 / 399	RNA binding
12	4e−03	2 / 11	nucleosome binding
13	5e−03	2 / 12	protein channel activity
14	5e−03	2 / 12	S100 protein binding
15	5e−03	7 / 227	transcription coactivator activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−09	10 / 87	hsa−miR−496
2	2e−07	13 / 221	hsa−miR−181d
3	1e−06	12 / 225	hsa−miR−181b
4	1e−06	9 / 117	hsa−miR−543
5	2e−06	9 / 121	hsa−miR−421
6	4e−06	15 / 389	hsa−miR−519a
7	8e−06	13 / 315	hsa−miR−30e
8	9e−06	14 / 366	hsa−let−7d
9	1e−05	8 / 112	hsa−miR−507
10	1e−05	10 / 190	hsa−miR−330−3p
11	1e−05	14 / 379	hsa−miR−454
12	2e−05	10 / 198	hsa−miR−181c
13	2e−05	9 / 158	hsa−miR−802
14	2e−05	11 / 250	hsa−miR−548l
15	2e−05	14 / 400	hsa−miR−519c−3p

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−13	21 / 302	Chaussabel_3,4_Protein phosphatases
2	1e−08	19 / 412	WIRTH_Immune system
3	6e−08	14 / 242	Chaussabel_3,9_Kinases
4	2e−07	11 / 153	Chaussabel_2,9_Cytosceleton
5	7e−07	23 / 759	PROTEINATLAS_epididymis
6	2e−06	29 / 1194	PROTEINATLAS_stomach
7	4e−06	21 / 724	PROTEINATLAS_lymph node
8	2e−05	26 / 1138	PROTEINATLAS_small intestine
9	5e−05	19 / 726	PROTEINATLAS_cervix, uterine
10	6e−05	22 / 933	PROTEINATLAS_adrenal gland
11	6e−05	19 / 740	PROTEINATLAS_esophagus
12	9e−05	25 / 1173	PROTEINATLAS_rectum
13	1e−04	25 / 1176	PROTEINATLAS_duodenum
14	1e−04	21 / 912	PROTEINATLAS_urinary bladder
15	1e−04	26 / 1268	PROTEINATLAS_colon

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

TF

Rank	p−value	#in/all	Geneset
1	7e−11	89 / 5067	ICGC_Taf1_targets
2	7e−07	81 / 5312	ICGC_Tcf12_targets
3	9e−07	82 / 5442	ICGC_Pmlsc71910_targets
4	9e−07	70 / 4362	ICGC_Creb1_targets
5	1e−06	71 / 4468	ICGC_Egr1_targets
6	1e−06	82 / 5466	ICGC_Nficsc81335_targets
7	1e−06	30 / 1231	KIM_MYC targets
8	2e−06	75 / 4890	ICGC_Bclaf101388_targets
9	2e−06	90 / 6322	ICGC_Tcf3_targets
10	2e−06	80 / 5383	ICGC_Sp1_targets
11	3e−06	89 / 6267	ICGC_Yy1_targets
12	4e−06	92 / 6578	ICGC_Pou2_targets
13	5e−06	42 / 2215	ICGC_GabpPcr2_targets
14	6e−06	80 / 5518	ICGC_Stat5_targets
15	7e−06	73 / 4881	ICGC_Atf2_targets

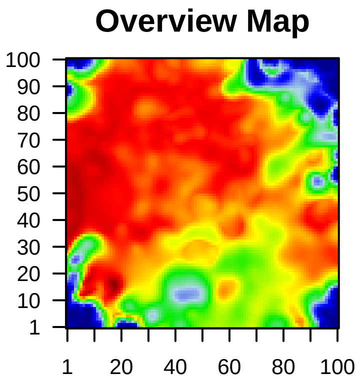
Underexpression Spots

Spot Summary: r

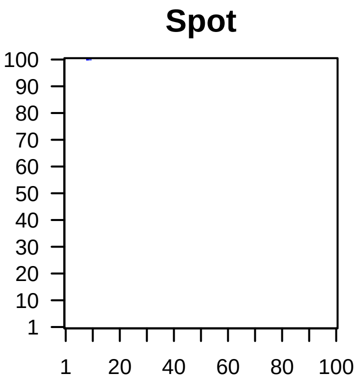
metagenes = 2
genes = 45

<r> metagenes = 1
<r> genes = 0.23
beta: r2= 6.65 / log p= −Inf

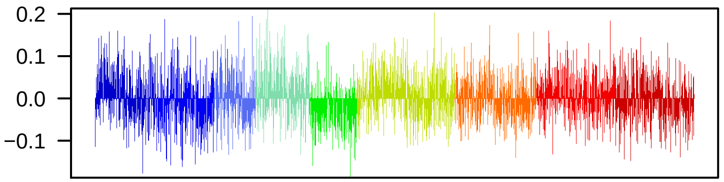
samples with spot = 96 (2.8 %)
A * : 14 (4.1 %)
A C * : 10 (3 %)
A C F * : 9 (3.8 %)
A F * : 20 (6.5 %)
C F * : 2 (0.8 %)
F * : 16 (2.9 %)
F J * : 6 (1.3 %)
J * : 11 (2.5 %)
N * : 8 (1.8 %)



Overview Map



Spot

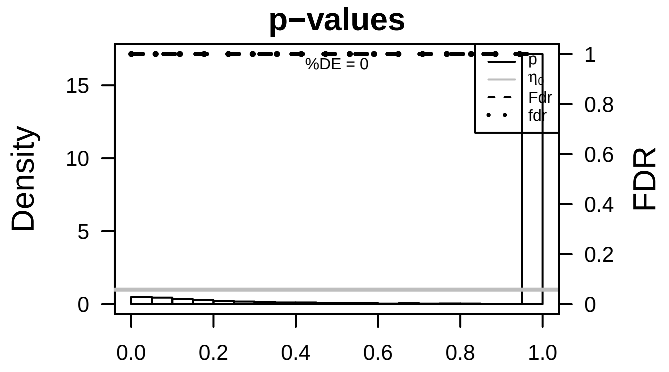


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166608	0.74	−0.67	0.28	OLIG1	oligodendrocyte transcription factor 1 [Source:HGNC Symbol
2	ILMN_167565	0.61	−0.54	0.34	PPFIBP2	PPFIA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:9
3	ILMN_173071	0.57	−0.38	0.3	ADORA3	adenosine A3 receptor [Source:HGNC Symbol;Acc:HGNC:26
4	ILMN_323393	0.57	−0.52	0.69		
5	ILMN_175974	0.57	−0.36	0.41	SLC38A10	solute carrier family 38 member 10 [Source:HGNC Symbol;A
6	ILMN_179347	0.57	−0.31	0.37	PRKCDBP	protein kinase C delta binding protein [Source:HGNC Symbol
7	ILMN_179774	0.53	−0.35	0.39		RNA, U1 small nuclear 123, pseudogene [Source:HGNC Syn
8	ILMN_181960	0.5	−0.55	0.37		
9	ILMN_237291	0.5	−0.32	0.49	P2RY2	purinergic receptor P2Y2 [Source:HGNC Symbol;Acc:HGNC:
10	ILMN_241530	0.48	−0.35	0.46	CLEC10A	C−type lectin domain family 10 member A [Source:HGNC Sy
11	ILMN_176818	0.46	−0.39	0.39	TOR3A	torsin family 3 member A [Source:HGNC Symbol;Acc:HGNC:
12	ILMN_180949	0.45	−0.53	0.6		
13	ILMN_170540	0.45	−0.32	0.48	CYP2S1	cytochrome P450 family 2 subfamily S member 1 [Source:HG
14	ILMN_171268	0.45	−0.32	0.49	FAM20C	family with sequence similarity 20 member C [Source:HGNC
15	ILMN_170561	0.45	−0.41	0.46	CFL1	cofilin 1 [Source:HGNC Symbol;Acc:HGNC:1874]
16	ILMN_324606	0.44	−0.32	0.56	CCDC151	coiled−coil domain containing 151 [Source:HGNC Symbol;Ac
17	ILMN_175620	0.44	−0.45	0.44	RPS6KA4	ribosomal protein S6 kinase A4 [Source:HGNC Symbol;Acc:H
18	ILMN_165924	0.44	−0.47	0.54	MTMR14	myotubularin related protein 14 [Source:HGNC Symbol;Acc:H
19	ILMN_205807	0.44	−0.45	0.57		
20	ILMN_177955	0.43	−0.3	0.51	GAS6	growth arrest specific 6 [Source:HGNC Symbol;Acc:HGNC:4

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	5 / 185	MF	magnesium ion binding
2	3e−04	14 / 2845	Colon	TxEnhG1_Colon
3	3e−04	2 / 15	GSEA	REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS
4	8e−04	27 / 9054	Colon	Tx_Colon
5	1e−03	2 / 27	BP	positive regulation of phagocytosis
6	1e−03	2 / 27	GSEA	WILLIAMS_ESR2_TARGETS_UP
7	2e−03	33 / 12983	Chror	2_TssA_Neuronal_Progenitor
8	2e−03	14 / 3450	Chror	4_TxTrans_Fibroblasts
9	2e−03	3 / 144	GSEA	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_DN
10	2e−03	8 / 1329	MF	ATP binding
11	3e−03	2 / 41	GSEA	APRELIKOVA_BRCA1_TARGETS
12	3e−03	2 / 42	CC	cell leading edge
13	3e−03	2 / 42	MF	manganese ion binding
14	3e−03	6 / 782	GSEA	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS
15	3e−03	17 / 4795	Chror	6_EnhG_Fibroblasts
16	3e−03	19 / 5699	Chror	6_EnhG_Melanocytes
17	3e−03	7 / 1101	CC	extracellular space
18	3e−03	6 / 820	Glio	Sturm_GBM_Meth_overexpression_E_G34_UP
19	4e−03	18 / 5373	Colon	EnhWk1_Colon
20	4e−03	2 / 50	GSEA	NADLER_OBESITY_UP
21	4e−03	3 / 178	CC	endoplasmic reticulum lumen
22	4e−03	2 / 53	Glio	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
23	4e−03	2 / 53	GSEA	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
24	4e−03	22 / 7354	Colon	TssF_Colon
25	4e−03	2 / 55	BP	cellular response to growth factor stimulus
26	4e−03	2 / 55	GSEA	ASTIER_INTEGRIN_SIGNALING
27	5e−03	4 / 374	CC	mitochondrial inner membrane
28	5e−03	3 / 187	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
29	5e−03	4 / 388	GSEA	MOOTHA_MITOCHONDRIA
30	6e−03	6 / 909	GSEA	BENPORATH_NANOG_TARGETS
31	6e−03	24 / 8568	Colon	TxWk_Colon
32	6e−03	26 / 9635	Chror	3_TssF_Fibroblasts
33	6e−03	4 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
34	6e−03	2 / 66	GSEA	LANDIS_BREAST_CANCER_PROGRESSION_DN
35	7e−03	19 / 6138	Colon	TssD2_Colon
36	7e−03	2 / 69	GSEA	KEGG_PEROXISOME
37	7e−03	1 / 4	GSEA	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_DN
38	7e−03	2 / 71	GSEA	LEE_CALORIE_RESTRICTION_NEOCORTEX_UP
39	8e−03	7 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran
40	8e−03	4 / 434	BP	protein phosphorylation



p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	0.001	2 / 27	positive regulation of phagocytosis
2	0.004	2 / 55	cellular response to growth factor stimulus
3	0.008	4 / 434	protein phosphorylation
4	0.016	2 / 106	calcium ion transmembrane transport
5	0.018	1 / 10	dendritic cell differentiation
6	0.018	1 / 10	enamel mineralization
7	0.018	1 / 10	macrophage chemotaxis
8	0.018	1 / 10	negative regulation of cell size
9	0.018	1 / 10	regulation of cilium assembly
10	0.020	1 / 11	creatine metabolic process
11	0.020	1 / 11	enzyme linked receptor protein signaling pathway
12	0.020	1 / 11	G−protein coupled purinergic nucleotide receptor signaling pathway
13	0.021	1 / 12	negative regulation of gluconeogenesis
14	0.021	1 / 12	regulation of cytokine production
15	0.021	1 / 12	regulation of dendritic spine morphogenesis

Brain

Rank	p−value	#in/all	Geneset
1	0.02	6 / 1171	Fetal_EnhP
2	0.02	11 / 3164	Mid_Frontal_Lobe_ZNF
3	0.03	13 / 4112	Mid_Frontal_Lobe_ReprPC
4	0.05	4 / 796	Overlap_fetal_midbrain_ZNF
5	0.10	8 / 2630	Fetal_TssF
6	0.10	3 / 630	Mid_Frontal_Lobe_EnhP
7	0.11	8 / 2709	Mid_Frontal_Lobe_HetRpts
8	0.13	5 / 1506	Mid_Frontal_Lobe_Quies
9	0.14	4 / 1119	Overlap_fetal_midbrain_TssA
10	0.15	21 / 9504	Overlap_fetal_midbrain_K9K27me3
11	0.15	2 / 386	Fetal_ZNF
12	0.16	14 / 5936	Overlap_fetal_midbrain_HetRpts
13	0.17	4 / 1213	Fetal_TssP
14	0.18	8 / 3046	Fetal_TssA
15	0.18	3 / 818	Mid_Frontal_Lobe_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	3 / 301	SPANG_BCL6−index2
2	0.06	1 / 36	PanCan_HK_geneset_nanostring
3	0.07	1 / 38	KUIPER_MM good survival
4	0.09	1 / 54	KUIPER_MM poor survival
5	0.10	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
6	0.19	0 / 15	LIU_PROSTATE_CANCER_DN
7	0.28	1 / 178	SPANG_LPS−index2
8	0.62	1 / 527	Lembcke_Normal vs Adenoma
9	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
10	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	1.00	0 / 12	LIU_BREAST_CANCER
13	1.00	0 / 14	LIU_COMMON_CANCER_GENES
14	1.00	0 / 13	LIU_LIVER_CANCER
15	1.00	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	0.003	2 / 42	cell leading edge
2	0.003	7 / 1101	extracellular space
3	0.004	3 / 178	endoplasmic reticulum lumen
4	0.005	4 / 374	mitochondrial inner membrane
5	0.011	2 / 88	peroxisome
6	0.020	1 / 11	actomyosin
7	0.020	1 / 11	proteasome regulatory particle, base subcomplex
8	0.021	1 / 12	proteasome regulatory particle
9	0.025	1 / 14	clathrin−coated endocytic vesicle
10	0.025	1 / 14	integral component of peroxisomal membrane
11	0.027	1 / 15	proteasome accessory complex
12	0.029	6 / 1304	mitochondrion
13	0.030	9 / 2464	extracellular exosome
14	0.030	2 / 149	lamellipodium
15	0.030	1 / 17	lamellipodium membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.04	6 / 1411	Chr 11
2	0.05	4 / 768	Chr 14
3	0.10	2 / 289	Chr 21
4	0.12	5 / 1467	Chr 19
5	0.16	3 / 769	Chr 15
6	0.18	4 / 1217	Chr 3
7	0.41	5 / 2323	Chr 1
8	0.43	3 / 1318	Chr 17
9	0.52	2 / 959	Chr 16
10	0.54	1 / 422	Chr 13
11	0.68	1 / 619	Chr 20
12	0.79	1 / 836	Chr 8
13	0.81	1 / 904	Chr 10
14	0.86	1 / 1060	Chr 5
15	0.89	1 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.002	33 / 12983	2_TssA_Neuronal_Progenitor
2	0.002	14 / 3450	4_TxTrans_Fibroblasts
3	0.003	17 / 4795	6_EnhG_Fibroblasts
4	0.003	19 / 5699	6_EnhG_Melanocytes
5	0.006	26 / 9635	3_TssF_Fibroblasts
6	0.010	13 / 3639	1_TssP_Fibroblasts
7	0.011	18 / 5956	3_TssF_Neuronal_Progenitor
8	0.014	8 / 1789	8_EnhP_Neuronal_Progenitor
9	0.019	12 / 3523	1_TssP_Melanocytes
10	0.038	22 / 8771	5_Tx_Melanocytes
11	0.044	20 / 7854	5_Tx_Fibroblasts
12	0.051	28 / 12298	2_TssA_Melanocytes
13	0.057	27 / 11836	3_TssF_Melanocytes
14	0.058	27 / 11847	7_Enh_Neuronal_Progenitor
15	0.070	7 / 2028	4_TxTrans_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	14 / 2845	TxEnhG1_Colon
2	8e−04	27 / 9054	Tx_Colon
3	4e−03	18 / 5373	EnhWk1_Colon
4	4e−03	22 / 7354	TssF_Colon
5	6e−03	24 / 8568	TxWk_Colon
6	7e−03	19 / 6138	TssD2_Colon
7	8e−03	7 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
8	9e−03	28 / 10999	TssWk_Colon
9	1e−02	5 / 789	TxEnhG2_Colon
10	2e−02	3 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
11	3e−02	10 / 2810	EnhA_Colon
12	3e−02	24 / 9555	TssA_Colon
13	3e−02	22 / 8678	Quies3_Colon
14	5e−02	6 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	5e−02	2 / 203	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Glio

Rank	p−value	#in/all	Geneset
1	0.003	6 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.004	2 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
3	0.013	7 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
4	0.021	1 / 12	Phillips MES up vs Prolif & PN
5	0.042	3 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
6	0.043	1 / 24	Martinez_Glio_hypermeth
7	0.097	2 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
8	0.101	1 / 59	Christensen_hypermethylated_in_primary_glioblastoma
9	0.105	1 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
10	0.116	1 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
11	0.144	1 / 86	laffaire_hypermeth_LGG_vs_control
12	0.146	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	0.151	1 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
14	0.159	2 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
15	0.163	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	2 / 15	REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS
2	1e−03	2 / 27	WILLIAMS_ESR2_TARGETS_UP
3	2e−03	3 / 144	RAY_TUMORIGENESIS_BY_ERBB2_CDC25A_DN
4	3e−03	2 / 41	APRELIKOVA_BRCA1_TARGETS
5	3e−03	6 / 782	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_TRANS
6	4e−03	2 / 50	NADLER_OBESITY_UP
7	4e−03	2 / 53	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
8	4e−03	2 / 55	ASTIER_INTEGRIN_SIGNALING
9	5e−03	3 / 187	WONG_MITOCHONDRIA_GENE_MODULE
10	5e−03	4 / 388	MOOTHA_MITOCHONDRIA
11	6e−03	6 / 909	BENPORATH_NANOG_TARGETS
12	6e−03	4 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
13	6e−03	2 / 66	LANDIS_BREAST_CANCER_PROGRESSION_DN
14	7e−03	2 / 69	KEGG_PEROXISOME
15	7e−03	1 / 4	OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	2 / 91	HALLMARK_PEROXISOME
2	0.16	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	0.22	1 / 138	HALLMARK_FATTY_ACID_METABOLISM
4	0.26	1 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	0.27	1 / 173	HALLMARK_E2F_TARGETS
6	0.27	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM
7	0.27	1 / 176	HALLMARK_ADIPOGENESIS
8	0.29	1 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.29	1 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.29	1 / 186	HALLMARK_MYOGENESIS
11	0.29	1 / 189	HALLMARK_HYPOXIA
12	0.29	1 / 191	HALLMARK_INFLAMMATORY_RESPONSE
13	1.00	0 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	1.00	0 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1.00	0 / 177	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 211	Homuth_BMI−associated−genes_DN
2	1.0	0 / 94	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	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 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 147	Homuth_BMI−associated−genes_UP
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.05	3 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
2	0.05	1 / 28	DAVE_Immune response 1
3	0.05	19 / 7448	HOPP_Strong_enhancer
4	0.05	3 / 464	WIRTH_lymphoma937_spot I
5	0.07	1 / 39	CARO_OxPhos_in_DLBCL_UP
6	0.08	18 / 7275	HOPP_Txn_elongation
7	0.08	14 / 5356	HOPP_Txn_transition
8	0.11	1 / 66	TARTE_Plasma cell signature
9	0.11	1 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
10	0.12	1 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
11	0.13	1 / 74	WIRTH_lymphoma937_spot IM
12	0.15	1 / 89	Subero_T−ALL_hyper_meth
13	0.15	1 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
14	0.15	8 / 2939	HOPP_Poised_promoter
15	0.16	13 / 5384	HOPP_Repressed

Melanoma

Rank	p−value	#in/all	Geneset
1	0.09	1 / 54	Hugo_melanoma−all−MET_DN
2	1.00	0 / 30	Hugo_melanoma−all−MET_UP
3	1.00	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−05	5 / 185	magnesium ion binding
2	2e−03	8 / 1329	ATP binding
3	3e−03	2 / 42	manganese ion binding
4	2e−02	3 / 315	protein serine/threonine kinase activity
5	2e−02	1 / 11	phosphatidylinositol−3,5−bisphosphate 3−phosphatase activity
6	2e−02	1 / 11	sodium channel activity
7	2e−02	1 / 12	G−protein coupled purinergic nucleotide receptor activity
8	2e−02	2 / 133	ATPase activity
9	3e−02	1 / 14	phosphatidylinositol−3−phosphatase activity
10	3e−02	1 / 15	receptor agonist activity
11	3e−02	1 / 18	TBP−class protein binding
12	3e−02	1 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
13	3e−02	2 / 160	carbohydrate binding
14	4e−02	1 / 21	steroid hydroxylase activity
15	4e−02	2 / 169	structural constituent of ribosome

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	2 / 82	hsa−miR−557
2	0.01	1 / 7	hsa−miR−339−3p
3	0.02	2 / 135	hsa−miR−488
4	0.03	2 / 140	hsa−miR−338−5p
5	0.04	2 / 175	hsa−miR−29c
6	0.05	1 / 27	hsa−miR−1292
7	0.05	2 / 195	hsa−miR−944
8	0.05	1 / 28	hsa−miR−193a−5p
9	0.05	1 / 31	hsa−miR−296−5p
10	0.06	1 / 32	hsa−miR−342−5p
11	0.06	1 / 34	hsa−miR−1231
12	0.06	1 / 36	hsa−miR−34c−3p
13	0.06	1 / 37	hsa−miR−518e
14	0.06	1 / 37	hsa−miR−1224−5p
15	0.06	1 / 37	hsa−miR−1269

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.03	1 / 17	JONGENEEL_Lung
2	0.14	1 / 84	Chaussabel_2,10_Immune related cell surface molecules
3	0.21	1 / 132	Chaussabel_1,7_MHC Ribosomal proteins
4	0.31	2 / 623	PROTEINATLAS_seminal vesicle
5	0.32	2 / 640	PROTEINATLAS_parathyroid gland
6	0.34	1 / 231	Chaussabel_2,5_Immune related molecules
7	0.35	2 / 681	PROTEINATLAS_lung
8	0.35	1 / 240	Chaussabel_3,3_Inflammation II
9	0.36	1 / 242	Chaussabel_3,2_Inflammation I
10	0.37	3 / 1194	PROTEINATLAS_stomach
11	0.39	1 / 275	Chaussabel_3,7_Spliceosome
12	0.40	2 / 759	PROTEINATLAS_epididymis
13	0.41	1 / 289	JONGENEEL_Testis
14	0.50	2 / 912	PROTEINATLAS_fallopian tube
15	0.52	2 / 959	PROTEINATLAS_nasopharynx

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	0.07	14 / 5188	ICGC_Ebfsc137065_targets
2	0.09	12 / 4468	ICGC_Egr1_targets
3	0.12	8 / 2759	ICGC_Bcl3_targets
4	0.14	15 / 6322	ICGC_Tcf3_targets
5	0.16	12 / 4890	ICGC_Bclaf101388_targets
6	0.18	4 / 1231	KIM_MYC targets
7	0.20	5 / 1723	HEBENSTREIT_high expression TF
8	0.22	11 / 4735	ICGC_Pu1_targets
9	0.24	12 / 5312	ICGC_Tcf12_targets
10	0.27	13 / 5984	ICGC_Mta3_targets
11	0.27	12 / 5466	ICGC_Nficsc81335_targets
12	0.29	4 / 1498	ICGC_Ets1_targets
13	0.32	2 / 631	ICGC_RxraPcr1_targets
14	0.33	9 / 4131	ICGC_Nfatc1_targets
15	0.34	5 / 2133	ICGC_Mef2_targets

Underexpression Spots

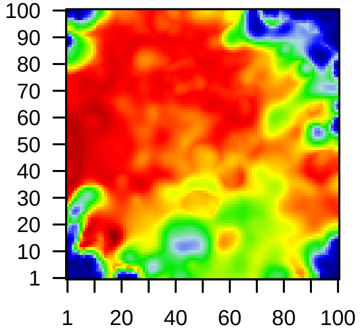
Spot Summary: s

metagenes = 17
genes = 250

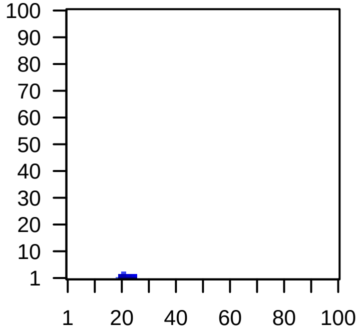
<r> metagenes = 0.92
<r> genes = 0.34
beta: r2= 34.19 / log p= −Inf

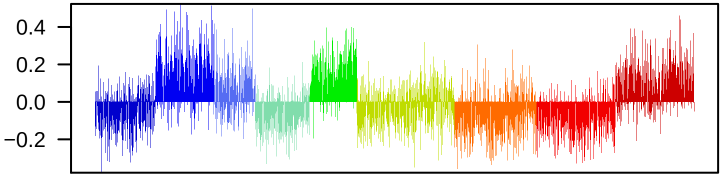
samples with spot = 699 (20.6 %)
A * : 18 (5.2 %)
A C * : 181 (55.2 %)
A C F * : 82 (34.9 %)
A F * : 4 (1.3 %)
C F * : 156 (58.9 %)
F * : 49 (8.8 %)
F J * : 20 (4.3 %)
J * : 9 (2 %)
N * : 180 (40.6 %)

Overview Map



Spot





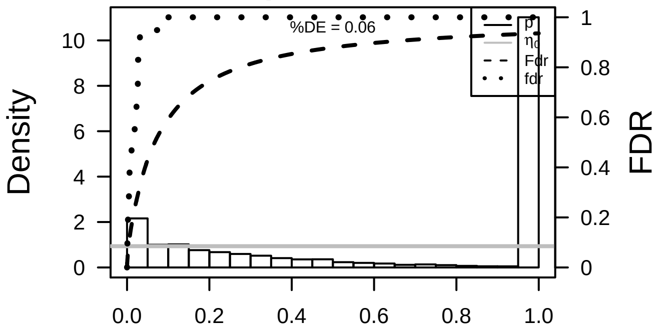
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324311	1.66	−0.52	0.27	RNF182	ring finger protein 182 [Source:HGNC Symbol;Acc:HGNC:28
2	ILMN_180823	1.58	−0.7	0.47	RBPMS2	RNA binding protein with multiple splicing 2 [Source:HGNC S
3	ILMN_172188	1.57	−1.12	0.77	ITGA2B	integrin subunit alpha 2b [Source:HGNC Symbol;Acc:HGNC:
4	ILMN_174329	1.57	−1.44	0.81	GP9	glycoprotein IX platelet [Source:HGNC Symbol;Acc:HGNC:4
5	ILMN_176728	1.52	−1.63	0.79		
6	ILMN_171896	1.46	−0.99	0.64	BNIP3L	BCL2 interacting protein 3 like [Source:HGNC Symbol;Acc:H
7	ILMN_166279	1.43	−1.26	0.62	CA2	carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137
8	ILMN_209000	1.4	−0.86	0.63	AQP10	aquaporin 10 [Source:HGNC Symbol;Acc:HGNC:16029]
9	ILMN_175764	1.37	−1.19	0.59	UBE2H	ubiquitin conjugating enzyme E2 H [Source:HGNC Symbol;A
10	ILMN_174510	1.36	−0.87	0.69	CLEC1B	C−type lectin domain family 1 member B [Source:HGNC Sym
11	ILMN_172470	1.33	−1.03	0.67	RIOK3	RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]
12	ILMN_175275	1.32	−0.85	0.61	VWF	von Willebrand factor [Source:HGNC Symbol;Acc:HGNC:127
13	ILMN_171028	1.31	−1.36	0.8	TUBB1	tubulin beta 1 class VI [Source:HGNC Symbol;Acc:HGNC:16
14	ILMN_219943	1.31	−1.09	0.63	CA2	carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137
15	ILMN_178241	1.3	−1.32	0.83	GNG11	G protein subunit gamma 11 [Source:HGNC Symbol;Acc:HG
16	ILMN_178962	1.29	−1.46	0.76	GP1BB	glycoprotein Ib platelet beta subunit [Source:HGNC Symbol;
17	ILMN_174552	1.28	−0.65	0.49	PF4V1	platelet factor 4 variant 1 [Source:HGNC Symbol;Acc:HGNC:
18	ILMN_241353	1.26	−0.84	0.62	HEMGN	hemogen [Source:HGNC Symbol;Acc:HGNC:17509]
19	ILMN_235212	1.26	−0.82	0.45	NT5C3A	5'−nucleotidase, cytosolic IIIA [Source:HGNC Symbol;Acc:H
20	ILMN_173207	1.26	−0.97	0.61	HIST2H2BE	histone cluster 2, H2be [Source:HGNC Symbol;Acc:HGNC:4

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−80	51 / 102	Refer	Chaussabel_1,2_Platelets
2	3e−52	33 / 64	GSEA	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
3	4e−37	35 / 188	GSEA	WIERENGA_STAT5A_TARGETS_DN
4	2e−15	19 / 185	HM	HALLMARK_HEME_METABOLISM
5	2e−13	17 / 181	GSEA	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATIO
6	9e−13	23 / 414	GSEA	REACTOME_HEMOSTASIS
7	9e−13	10 / 40	GSEA	GNATENKO_PLATELET_SIGNATURE
8	2e−12	21 / 352	CC	focal adhesion
9	5e−12	74 / 4018	Colon	EnhWk2_Colon
10	5e−12	23 / 451	GSEA	PILON_KLF1_TARGETS_UP
11	6e−12	11 / 64	GSEA	ROSS_AML_OF_FAB_M7_TYPE
12	8e−12	15 / 162	GSEA	JISON_SICKLE_CELL_DISEASE_UP
13	2e−11	11 / 71	GSEA	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA
14	2e−10	12 / 111	Refer	Chaussabel_2,3_Erythrocytes
15	3e−10	11 / 90	BP	platelet degranulation
16	6e−10	133 / 10779	Colon	Enh_Colon
17	2e−09	34 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
18	2e−09	147 / 12741	Chro	7_Enh_Melanocytes
19	2e−09	122 / 9635	Chro	3_TssF_Fibroblasts
20	2e−09	33 / 1216	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
21	4e−09	76 / 4822	CC	cytoplasm
22	4e−09	12 / 147	Lifesty	Homuth_BMI−associated−genes_UP
23	5e−09	7 / 30	GSEA	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
24	5e−09	18 / 387	GSEA	SWEET_LUNG_CANCER_KRAS_DN
25	9e−09	15 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
26	1e−08	6 / 20	GSEA	REACTOME_SMOOTH_MUSCLE_CONTRACTION
27	1e−08	7 / 35	GSEA	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION
28	2e−08	13 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
29	2e−08	20 / 520	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
30	2e−08	10 / 106	BP	platelet activation
31	3e−08	7 / 38	BP	platelet aggregation
32	3e−08	110 / 8613	Chro	7_Enh_Fibroblasts
33	2e−07	135 / 11836	Chro	3_TssF_Melanocytes
34	2e−07	128 / 10999	Colon	TssWk_Colon
35	2e−07	139 / 12393	Chro	15_Quies_Neuronal_Progenitor
36	3e−07	143 / 12983	Chro	2_TssA_Neuronal_Progenitor
37	5e−07	11 / 184	GSEA	KEGG_FOCAL_ADHESION
38	5e−07	6 / 36	GSEA	LEIN_ASTROCYTE_MARKERS
39	7e−07	14 / 324	GSEA	GRUETZMANN_PANCREATIC_CANCER_UP
40	7e−07	8 / 87	GSEA	HECKER_IFNB1_TARGETS

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.002	5 / 111	HORVATH_aging_genes meth DOWN
2	0.699	1 / 142	HORVATH_aging_genes meth UP
3	1.000	0 / 58	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	

Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	0 / 15	LIU_PROSTATE_CANCER_DN
2	5e−03	2 / 13	GENTLES_modul12
3	2e−02	2 / 24	PanCan_Notch_geneset_nanostring
4	2e−02	4 / 125	PanCan_CC+Apop_geneset_nanostring
5	4e−02	3 / 91	PanCan_TXmisReg_geneset_nanostring
6	6e−02	2 / 46	PanCan_TGF−B_geneset_nanostring
7	1e−01	8 / 554	Lembcke_Colonic Inflammation
8	1e−01	1 / 13	LIU_LIVER_CANCER
9	1e−01	1 / 13	GENTLES_modul18
10	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
11	1e−01	1 / 14	GENTLES_modul4
12	1e−01	1 / 14	GENTLES_modul13
13	1e−01	1 / 16	GENTLES_modul16
14	2e−01	2 / 82	PanCan_JAK−ST_geneset_nanostring
15	2e−01	3 / 178	SPANG_LPS−index2

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−09	147 / 12741	7_Enh_Melanocytes
2	2e−09	122 / 9635	3_TssF_Fibroblasts
3	3e−08	110 / 8613	7_Enh_Fibroblasts
4	2e−07	135 / 11836	3_TssF_Melanocytes
5	2e−07	139 / 12393	15_Quies_Neuronal_Progenitor
6	3e−07	143 / 12983	2_TssA_Neuronal_Progenitor
7	8e−07	133 / 11847	7_Enh_Neuronal_Progenitor
8	3e−06	68 / 4795	6_EnhG_Fibroblasts
9	3e−06	105 / 8771	5_Tx_Melanocytes
10	5e−06	134 / 12298	2_TssA_Melanocytes
11	6e−06	106 / 8990	15_Quies_Fibroblasts
12	1e−05	123 / 11130	15_Quies_Melanocytes
13	4e−05	124 / 11455	2_TssA_Fibroblasts
14	7e−05	72 / 5699	6_EnhG_Melanocytes
15	2e−04	90 / 7854	5_Tx_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−52	33 / 64	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
2	4e−37	35 / 188	WIERENGA_STAT5A_TARGETS_DN
3	2e−13	17 / 181	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
4	9e−13	23 / 414	REACTOME_HEMOSTASIS
5	9e−13	10 / 40	GNATENKO_PLATELET_SIGNATURE
6	5e−12	23 / 451	PILON_KLF1_TARGETS_UP
7	6e−12	11 / 64	ROSS_AML_OF_FAB_M7_TYPE
8	8e−12	15 / 162	JISON_SICKLE_CELL_DISEASE_UP
9	2e−11	11 / 71	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
10	2e−09	34 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	5e−09	7 / 30	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
12	5e−09	18 / 387	SWEET_LUNG_CANCER_KRAS_DN
13	9e−09	15 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
14	1e−08	6 / 20	REACTOME_SMOOTH_MUSCLE_CONTRACTION
15	1e−08	7 / 35	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	43 / 2701	HOPP_Repetitive
2	8e−05	44 / 2939	HOPP_Poised_promoter
3	4e−04	91 / 8098	HOPP_Weak_promoter
4	3e−03	73 / 6559	HOPP_Weak_txn
5	3e−03	81 / 7448	HOPP_Strong_enhancer
6	4e−03	5 / 121	SPANG_LPS 6hrs UP
7	4e−03	8 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
8	4e−03	2 / 12	WRIGHT_GCB UP
9	4e−03	8 / 306	WIRTH_lymphoma937_spot E
10	7e−03	8 / 331	WIRTH_lymphoma937_spot H
11	1e−02	18 / 1169	SPANG_BCR DN
12	1e−02	74 / 6959	HOPP_Weak_enhancer
13	1e−02	3 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
14	2e−02	6 / 244	LENZ_Stromal signature 1
15	2e−02	7 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−80	51 / 102	Chaussabel_1,2_Platelets
2	2e−10	12 / 111	Chaussabel_2,3_Erythrocytes
3	3e−06	4 / 13	WIRTH_Sec. lymphoid organs
4	8e−06	16 / 514	PROTEINATLAS_vagina
5	8e−06	25 / 1118	PROTEINATLAS_placenta
6	1e−05	21 / 850	PROTEINATLAS_skin
7	2e−05	18 / 695	PROTEINATLAS_bone marrow
8	7e−05	13 / 429	PROTEINATLAS_soft tissue
9	9e−05	22 / 1063	PROTEINATLAS_tonsil
10	1e−04	15 / 571	PROTEINATLAS_oral mucosa
11	1e−04	16 / 640	PROTEINATLAS_parathyroid gland
12	2e−04	15 / 598	PROTEINATLAS_prostate
13	2e−04	12 / 416	PROTEINATLAS_ovary
14	3e−04	23 / 1239	PROTEINATLAS_testis
15	3e−04	4 / 39	Chaussabel_2,2_Neutrophils

BP

Rank	p−value	#in/all	Geneset
1	3e−10	11 / 90	platelet degranulation
2	2e−08	10 / 106	platelet activation
3	3e−08	7 / 38	platelet aggregation
4	1e−05	4 / 18	blood coagulation, intrinsic pathway
5	1e−05	9 / 171	blood coagulation
6	1e−04	12 / 387	cell adhesion
7	1e−04	4 / 31	microtubule−based process
8	1e−04	4 / 31	response to organonitrogen compound
9	2e−04	6 / 102	muscle contraction
10	3e−04	9 / 254	cell surface receptor signaling pathway
11	5e−04	5 / 77	movement of cell or subcellular component
12	7e−04	5 / 84	cell−matrix adhesion
13	9e−04	3 / 23	negative regulation of G1/S transition of mitotic cell cycle
14	2e−03	3 / 31	lamellipodium assembly
15	3e−03	5 / 115	leukocyte migration

CC

Rank	p−value	#in/all	Geneset
1	2e−12	21 / 352	focal adhesion
2	4e−09	76 / 4822	cytoplasm
3	1e−06	44 / 2464	extracellular exosome
4	1e−06	57 / 3662	plasma membrane
5	2e−06	4 / 12	platelet alpha granule membrane
6	5e−06	13 / 330	cytoskeleton
7	5e−05	5 / 47	stress fiber
8	6e−05	45 / 2979	cytosol
9	2e−04	3 / 14	platelet alpha granule
10	3e−04	7 / 149	lamellipodium
11	8e−04	4 / 49	platelet alpha granule lumen
12	9e−04	3 / 23	cortical cytoskeleton
13	1e−03	4 / 56	autophagosome
14	1e−03	12 / 512	cell surface
15	2e−03	5 / 106	Z disc

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−12	74 / 4018	EnhWk2_Colon
2	6e−10	133 / 10779	Enh_Colon
3	2e−09	33 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	2e−07	128 / 10999	TssWk_Colon
5	9e−07	106 / 8678	Quies3_Colon
6	1e−06	113 / 9555	TssA_Colon
7	3e−06	65 / 4526	Quies1_Colon
8	2e−05	90 / 7354	TssF_Colon
9	3e−05	104 / 9054	Tx_Colon
10	4e−05	70 / 5373	EnhWk1_Colon
11	4e−05	29 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
12	4e−05	77 / 6138	TssD2_Colon
13	5e−05	99 / 8568	TxWk_Colon
14	1e−04	22 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	3e−04	13 / 489	K9acLow_Colon

HM

Rank	p−value	#in/all	Geneset
1	2e−15	19 / 185	HALLMARK_HEME_METABOLISM
2	1e−04	6 / 91	HALLMARK_ANDROGEN_RESPONSE
3	7e−04	6 / 127	HALLMARK_COAGULATION
4	7e−04	7 / 176	HALLMARK_ADIPOGENESIS
5	9e−04	7 / 183	HALLMARK_APICAL_JUNCTION
6	1e−03	7 / 186	HALLMARK_MYOGENESIS
7	1e−03	7 / 186	HALLMARK_IL2_STAT5_SIGNALING
8	4e−03	6 / 176	HALLMARK_KRAS_SIGNALING_UP
9	5e−03	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	5e−03	6 / 187	HALLMARK_COMPLEMENT
11	6e−03	6 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	9e−03	5 / 151	HALLMARK_APOPTOSIS
13	2e−02	5 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	2e−02	4 / 116	HALLMARK_SPERMATOGENESIS
15	2e−02	5 / 177	HALLMARK_MITOTIC_SPINDLE

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−05	7 / 92	hsa−miR−219−2−3p
2	8e−04	5 / 85	hsa−miR−1265
3	2e−03	5 / 105	hsa−miR−605
4	2e−03	9 / 336	hsa−miR−142−5p
5	2e−03	7 / 216	hsa−miR−548m
6	3e−03	5 / 113	hsa−miR−498
7	3e−03	5 / 119	hsa−miR−105
8	3e−03	5 / 119	hsa−miR−509−3p
9	5e−03	8 / 317	hsa−miR−559
10	8e−03	5 / 146	hsa−miR−138
11	9e−03	5 / 150	hsa−miR−633
12	9e−03	4 / 97	hsa−miR−125a−3p
13	9e−03	4 / 97	hsa−miR−526a
14	1e−02	4 / 100	hsa−miR−600
15	1e−02	4 / 101	hsa−miR−603

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	1e−05	117 / 10430	Overlap_fetal_midbrain_Quies
2	2e−05	112 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	2e−04	45 / 3164	Mid_Frontal_Lobe_ZNF
4	4e−04	106 / 9815	Overlap_fetal_midbrain_ReprPC
5	1e−03	101 / 9504	Overlap_fetal_midbrain_K9K27me3
6	9e−03	65 / 5936	Overlap_fetal_midbrain_HetRpts
7	1e−02	34 / 2700	Fetal_TxTrans
8	1e−02	18 / 1213	Fetal_TssP
9	2e−02	33 / 2709	Mid_Frontal_Lobe_HetRpts
10	2e−02	15 / 1012	Mid_Frontal_Lobe_Enh
11	6e−02	6 / 328	Fetal_Het
12	7e−02	33 / 3046	Fetal_TssA
13	8e−02	12 / 906	Fetal_HetRpts
14	8e−02	24 / 2127	Mid_Frontal_Lobe_K9K27me3
15	1e−01	42 / 4112	Mid_Frontal_Lobe_ReprPC

Chr

Rank	p−value	#in/all	Geneset
1	0.06	15 / 1160	Chr 12
2	0.08	9 / 619	Chr 20
3	0.16	5 / 342	Chr 18
4	0.17	7 / 536	Chr 22
5	0.27	15 / 1492	Chr 2
6	0.28	10 / 954	Chr 9
7	0.39	11 / 1170	Chr 7
8	0.39	21 / 2323	Chr 1
9	0.44	11 / 1217	Chr 3
10	0.47	4 / 422	Chr 13
11	0.49	8 / 902	Chr 4
12	0.49	8 / 904	Chr 10
13	0.56	8 / 959	Chr 16
14	0.57	10 / 1211	Chr 6
15	0.64	11 / 1411	Chr 11

Glio

Rank	p−value	#in/all	Geneset
1	4e−04	7 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
2	6e−03	5 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	8e−03	5 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
4	8e−03	4 / 94	Weller_LGG_A_vs_O_UP
5	2e−02	4 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
6	3e−02	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
7	3e−02	2 / 34	Shaw_down_in_1p19q
8	4e−02	2 / 37	Christensen_hypomethylated_in_ependymoma
9	4e−02	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	5e−02	7 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
11	5e−02	3 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	5e−02	3 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	7e−02	2 / 51	Gorovets_LGG_EPL_subclass
14	7e−02	2 / 52	OL vs. OPC
15	7e−02	3 / 115	Christensen_hypermethylated_in_grade3_astrocytoma

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−09	12 / 147	Homuth_BMI−associated−genes_UP
2	2e−04	3 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
4	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
5	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
12	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
13	1e+00	0 / 211	Homuth_BMI−associated−genes_DN
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	1e−06	107 / 8818	protein binding
2	1e−05	7 / 91	structural constituent of cytoskeleton
3	1e−05	10 / 213	GTPase activity
4	2e−04	6 / 98	integrin binding
5	7e−04	8 / 227	transcription coactivator activity
6	7e−04	3 / 21	G−protein beta/gamma−subunit complex binding
7	8e−04	10 / 351	GTP binding
8	3e−03	2 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
9	4e−03	3 / 39	androgen receptor binding
10	4e−03	6 / 182	signal transducer activity
11	5e−03	2 / 13	GABA receptor binding
12	5e−03	3 / 42	manganese ion binding
13	6e−03	2 / 14	5'−nucleotidase activity
14	7e−03	6 / 202	structural molecule activity
15	8e−03	7 / 268	actin binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.01	58 / 5188	ICGC_Ebfsc137065_targets
2	0.01	23 / 1669	ICGC_P300_targets
3	0.02	1 / 2	MYC_ECM cell adhesion DOWN
4	0.02	69 / 6616	ICGC_Pax5_targets
5	0.03	51 / 4735	ICGC_Pu1_targets
6	0.03	26 / 2133	ICGC_Mef2_targets
7	0.04	1 / 5	MYC_TFs
8	0.04	61 / 5961	ICGC_Pol24_targets
9	0.04	29 / 2497	ICGC_Bcl11_targets
10	0.07	60 / 5984	ICGC_Mta3_targets
11	0.07	30 / 2704	ICGC_Pbx3_targets
12	0.07	71 / 7247	ICGC_Runx3_targets
13	0.07	1 / 9	MYC_Targets DOWN
14	0.09	64 / 6552	ICGC_Pol2_targets
15	0.10	35 / 3348	ICGC_BatfPcr1_targets

Underexpression Spots

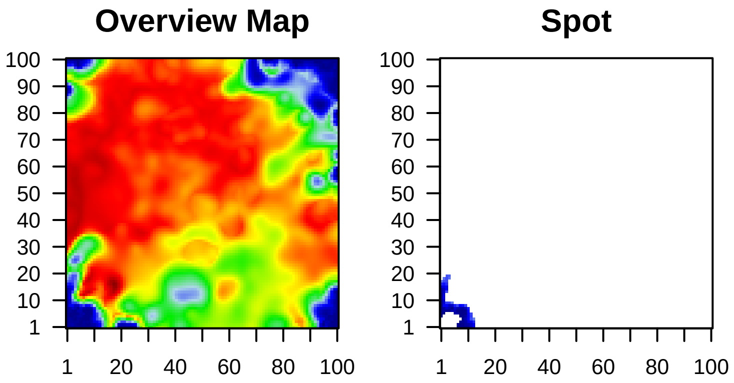
Spot Summary: t

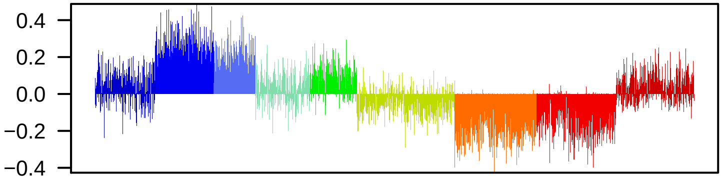
metagenes = 103
genes = 1492

<r> metagenes = 0.7

beta: r2= 86.52 / log p= −Inf

samples with spot = 762 (22.5 %)
A * : 67 (19.5 %)
A C * : 302 (92.1 %)
A C F * : 187 (79.6 %)
A F * : 48 (15.6 %)
C F * : 84 (31.7 %)
F * : 5 (0.9 %)
N * : 69 (15.6 %)



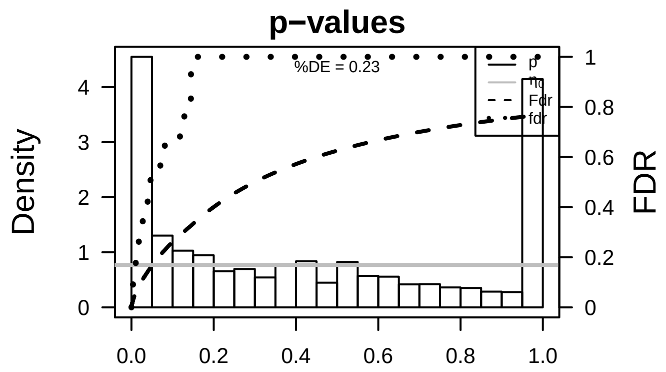


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178314	4.32	−2.71	0.14		
2	ILMN_175553	3.25	−1.79	0.22	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H
3	ILMN_177651	3.13	−1.1	0.35	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
4	ILMN_170832	2.82	−1.91	0.68	ALAS2	5'−aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:H
5	ILMN_165243	2.79	−1.83	0.59	CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:136
6	ILMN_323841	2.6	−1.51	0.1	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
7	ILMN_174983	2.5	−1.99	0.43	SMIM1	small integral membrane protein 1 (Vel blood group) [Source:
8	ILMN_176616	2.48	−2.2	0.6	SNCA	synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138]
9	ILMN_171345	2.47	−1.33	0.32	HBZ	hemoglobin subunit zeta [Source:HGNC Symbol;Acc:HGNC:
10	ILMN_328576	2.47	−2.05	0.67	SLC4A1	solute carrier family 4 member 1 (Diego blood group) [Source
11	ILMN_169651	2.44	−2.23	0.77	AHSP	alpha hemoglobin stabilizing protein [Source:HGNC Symbol;
12	ILMN_173571	2.39	−1.48	0.5	KRT1	keratin 1 [Source:HGNC Symbol;Acc:HGNC:6412]
13	ILMN_168065	2.38	−1.7	0.73	SELENBP1	selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC
14	ILMN_177409	2.28	−1.33	0.57	FECH	ferrochelatase [Source:HGNC Symbol;Acc:HGNC:3647]
15	ILMN_323518	2.25	−2.09	0.68	FAM83A−AS1	FAM83A antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC
16	ILMN_171326	2.21	−1.75	0.57	FAM46C	family with sequence similarity 46 member C [Source:HGNC
17	ILMN_181439	2.2	−1.99	0.68	EPB42	erythrocyte membrane protein band 4.2 [Source:HGNC Symb
18	ILMN_203877	2.18	−1.09	0.26	TUBB2A	tubulin beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:1
19	ILMN_181552	2.18	−2.44	0.74	HBD	hemoglobin subunit delta [Source:HGNC Symbol;Acc:HGNC:
20	ILMN_176031	2.17	−1.46	0.69	VWCE	von Willebrand factor C and EGF domains [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−66	627 / 7354	Colon	TssF_Colon
2	1e−60	77 / 150	Refer	Chaussabel_2,6_Myeloid lineage
3	2e−59	784 / 10779	Colon	Enh_Colon
4	9e−59	335 / 2845	Colon	TxEnhG1_Colon
5	1e−52	685 / 9054	Colon	Tx_Colon
6	4e−51	706 / 9555	Colon	TssA_Colon
7	4e−48	493 / 5699	Chror	6_EnhG_Melanocytes
8	8e−48	59 / 111	Refer	Chaussabel_2,3_Erythrocytes
9	2e−47	438 / 4795	Chror	6_EnhG_Fibroblasts
10	8e−47	515 / 6138	Colon	TssD2_Colon
11	8e−47	699 / 9635	Chror	3_TssF_Fibroblasts
12	7e−45	798 / 11836	Chror	3_TssF_Melanocytes
13	1e−44	347 / 3450	Chror	4_TxTrans_Fibroblasts
14	3e−44	79 / 240	Refer	Chaussabel_3,3_Inflammation II
15	2e−42	299 / 2810	Colon	EnhA_Colon
16	3e−42	812 / 12298	Chror	2_TssA_Melanocytes
17	6e−41	456 / 5373	Colon	EnhWk1_Colon
18	6e−39	624 / 8568	Colon	TxWk_Colon
19	8e−38	820 / 12741	Chror	7_Enh_Melanocytes
20	2e−37	64 / 185	HM	HALLMARK_HEME_METABOLISM
21	2e−35	229 / 2028	Chror	4_TxTrans_Melanocytes
22	1e−34	553 / 7448	Lympl	HOPP_Strong_enhancer
23	2e−33	618 / 8771	Chror	5_Tx_Melanocytes
24	1e−32	618 / 8818	MF	protein binding
25	2e−32	299 / 3164	Brain	Mid_Frontal_Lobe_ZNF
26	3e−32	745 / 11455	Chror	2_TssA_Fibroblasts
27	5e−32	723 / 10999	Colon	TssWk_Colon
28	3e−31	812 / 12983	Chror	2_TssA_Neuronal_Progenitor
29	4e−30	458 / 5956	Chror	3_TssF_Neuronal_Progenitor
30	4e−30	112 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
31	3e−29	600 / 8678	Colon	Quies3_Colon
32	5e−29	753 / 11847	Chror	7_Enh_Neuronal_Progenitor
33	3e−28	57 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
34	1e−27	49 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
35	3e−27	56 / 203	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
36	6e−27	679 / 10430	Brain	Overlap_fetal_midbrain_Quies
37	2e−26	632 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
38	2e−25	53 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
39	3e−25	114 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
40	5e−25	74 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.04	10 / 111	HORVATH_aging_genes meth DOWN
2	0.54	3 / 58	TESCHENDORFF_age_hypermethylated
3	0.69	6 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	2e−24	90 / 554	Lembcke_Colonic Inflammation
2	7e−09	40 / 301	SPANG_BCL6−index2
3	5e−07	26 / 178	SPANG_LPS−index2
4	2e−02	3 / 13	GENTLES_modul12
5	3e−02	2 / 14	LIU_COMMON_CANCER_GENES
6	6e−02	7 / 73	SHAUGHNESSY_MM high risk
7	8e−02	33 / 527	Lembcke_Normal vs Adenoma
8	1e−01	11 / 150	PanCan_MAPK_geneset_nanostring
9	1e−01	0 / 14	LIU_PROSTATE_CANCER_UP
10	1e−01	2 / 14	BEN−PORATH_UP
11	2e−01	7 / 91	PanCan_TXmisReg_geneset_nanostring
12	2e−01	9 / 125	PanCan_CC+Apop_geneset_nanostring
13	2e−01	2 / 15	WANG_ER_UP
14	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	2e−01	0 / 13	LIU_LIVER_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−48	493 / 5699	6_EnhG_Melanocytes
2	2e−47	438 / 4795	6_EnhG_Fibroblasts
3	8e−47	699 / 9635	3_TssF_Fibroblasts
4	7e−45	798 / 11836	3_TssF_Melanocytes
5	1e−44	347 / 3450	4_TxTrans_Fibroblasts
6	3e−42	812 / 12298	2_TssA_Melanocytes
7	8e−38	820 / 12741	7_Enh_Melanocytes
8	2e−35	229 / 2028	4_TxTrans_Melanocytes
9	2e−33	618 / 8771	5_Tx_Melanocytes
10	3e−32	745 / 11455	2_TssA_Fibroblasts
11	3e−31	812 / 12983	2_TssA_Neuronal_Progenitor
12	4e−30	458 / 5956	3_TssF_Neuronal_Progenitor
13	5e−29	753 / 11847	7_Enh_Neuronal_Progenitor
14	3e−21	751 / 12393	15_Quies_Neuronal_Progenitor
15	3e−20	525 / 7854	5_Tx_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−30	112 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
2	3e−28	57 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
3	1e−27	49 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
4	3e−27	56 / 203	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
5	2e−25	53 / 196	MCLACHLAN_DENTAL_CARIES_UP
6	5e−25	74 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
7	3e−23	113 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
8	3e−23	132 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
9	4e−23	74 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
10	7e−22	59 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	4e−21	44 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
12	1e−19	43 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
13	1e−19	157 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
14	1e−19	40 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
15	2e−19	54 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−34	553 / 7448	HOPP_Strong_enhancer
2	1e−18	385 / 5356	HOPP_Txn_transition
3	1e−14	471 / 7275	HOPP_Txn_elongation
4	2e−13	115 / 1169	SPANG_BCR DN
5	2e−12	47 / 306	WIRTH_lymphoma937_spot E
6	4e−12	46 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
7	9e−12	505 / 8226	HOPP_Active_promoter
8	4e−10	45 / 331	WIRTH_lymphoma937_spot H
9	1e−08	41 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	3e−08	478 / 8098	HOPP_Weak_promoter
11	2e−07	45 / 408	TARTE_Mature plasma cell signature
12	2e−06	99 / 1270	SPANG_BCR UP
13	1e−05	12 / 57	Monti_Host_response_cluster
14	2e−05	9 / 33	Subero_T−PLL_hypo_meth
15	7e−05	33 / 331	SPANG_CD40 6hrs UP

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.6	1 / 17	Thyroid carcinoma, follicular
2	0.6	1 / 18	Hodgkin lymphoma
3	0.8	1 / 29	Myelofibrosis, idiopathic
4	0.9	1 / 47	Cervical cancer, somatic
5	0.9	1 / 48	Gastric cancer
6	0.9	1 / 57	Cardiomyopathy, dilated
7	1.0	1 / 65	Hepatocellular carcinoma
8	1.0	1 / 68	Glioblastoma multiforme, somatic
9	1.0	1 / 73	Stroke, susceptibility to
10	1.0	1 / 95	Colorectal cancer
11	1.0	1 / 102	Leukemia
12	1.0	1 / 113	Ovarian cancer
13	1.0	1 / 116	Cancer
14	1.0	1 / 120	Hematological
15	1.0	1 / 123	Pancreatic cancer

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−60	77 / 150	Chaussabel_2,6_Myeloid lineage
2	8e−48	59 / 111	Chaussabel_2,3_Erythrocytes
3	3e−44	79 / 240	Chaussabel_3,3_Inflammation II
4	2e−24	40 / 113	Chaussabel_1,5_Myeloid lineage
5	7e−24	57 / 242	Chaussabel_3,2_Inflammation I
6	1e−10	15 / 39	Chaussabel_2,2_Neutrophils
7	4e−09	8 / 11	WIRTH_Prim. lymphoid organs
8	1e−08	69 / 695	PROTEINATLAS_bone marrow
9	6e−07	10 / 29	JONGENEEL_Bone Marrow
10	2e−05	6 / 13	WIRTH_Bone marrow
11	3e−05	48 / 535	PROTEINATLAS_spleen
12	7e−05	12 / 66	VAQUERIZAS_Whole blood_TF
13	5e−04	53 / 681	PROTEINATLAS_lung
14	2e−03	5 / 19	VAQUERIZAS_Bone marrow_TF
15	3e−03	33 / 412	WIRTH_Immune system

BP

Rank	p−value	#in/all	Geneset
1	4e−16	56 / 336	inflammatory response
2	5e−11	47 / 335	innate immune response
3	1e−10	32 / 178	response to lipopolysaccharide
4	5e−09	51 / 435	negative regulation of apoptotic process
5	1e−08	56 / 511	apoptotic process
6	6e−07	46 / 434	protein phosphorylation
7	6e−07	84 / 1003	signal transduction
8	8e−07	15 / 69	cellular response to mechanical stimulus
9	9e−07	9 / 24	actin filament polymerization
10	1e−06	18 / 99	defense response to bacterium
11	2e−06	10 / 32	negative regulation of MAP kinase activity
12	2e−06	31 / 254	cell surface receptor signaling pathway
13	2e−06	34 / 293	immune response
14	3e−06	26 / 195	regulation of apoptotic process
15	5e−06	6 / 11	regulation of cytokine secretion

CC

Rank	p−value	#in/all	Geneset
1	6e−22	258 / 2979	cytosol
2	3e−14	272 / 3662	plasma membrane
3	2e−13	334 / 4822	cytoplasm
4	5e−13	167 / 1979	membrane
5	3e−11	190 / 2464	extracellular exosome
6	3e−08	308 / 4828	nucleus
7	8e−08	222 / 3291	integral component of membrane
8	2e−07	29 / 202	early endosome
9	3e−07	101 / 1252	integral component of plasma membrane
10	6e−07	13 / 51	phagocytic vesicle membrane
11	8e−07	53 / 539	Golgi membrane
12	1e−06	39 / 352	focal adhesion
13	2e−06	37 / 330	cytoskeleton
14	5e−06	7 / 16	pseudopodium
15	1e−05	52 / 571	perinuclear region of cytoplasm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−66	627 / 7354	TssF_Colon
2	2e−59	784 / 10779	Enh_Colon
3	9e−59	335 / 2845	TxEnhG1_Colon
4	1e−52	685 / 9054	Tx_Colon
5	4e−51	706 / 9555	TssA_Colon
6	8e−47	515 / 6138	TssD2_Colon
7	2e−42	299 / 2810	EnhA_Colon
8	6e−41	456 / 5373	EnhWk1_Colon
9	6e−39	624 / 8568	TxWk_Colon
10	5e−32	723 / 10999	TssWk_Colon
11	3e−29	600 / 8678	Quies3_Colon
12	3e−25	114 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
13	5e−24	163 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	3e−19	138 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	2e−11	83 / 789	TxEnhG2_Colon

HM

Rank	p−value	#in/all	Geneset
1	2e−37	64 / 185	HALLMARK_HEME_METABOLISM
2	2e−11	34 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	3e−11	30 / 151	HALLMARK_APOPTOSIS
4	2e−10	33 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	7e−09	30 / 187	HALLMARK_COMPLEMENT
6	2e−06	16 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	5e−06	25 / 189	HALLMARK_HYPOXIA
8	1e−05	23 / 175	HALLMARK_XENOBIOTIC_METABOLISM
9	4e−05	22 / 176	HALLMARK_KRAS_SIGNALING_UP
10	1e−04	22 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	3e−04	21 / 185	HALLMARK_P53_PATHWAY
12	3e−04	19 / 162	HALLMARK_ALLOGRAFT_REJECTION
13	7e−04	8 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	7e−04	19 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	2e−03	10 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.7	2 / 54	Hugo_melanoma−all−MET_DN
3	0.8	1 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−07	48 / 467	hsa−miR−195
2	1e−06	49 / 489	hsa−miR−16
3	7e−06	47 / 491	hsa−miR−107
4	1e−05	43 / 441	hsa−miR−424
5	2e−05	41 / 419	hsa−miR−497
6	2e−05	46 / 493	hsa−miR−103
7	4e−05	31 / 294	hsa−miR−503
8	5e−05	46 / 516	hsa−miR−15a
9	2e−04	42 / 480	hsa−miR−15b
10	2e−04	14 / 95	hsa−miR−125a−5p
11	2e−04	13 / 84	hsa−miR−486−3p
12	2e−04	14 / 96	hsa−miR−125b
13	3e−04	25 / 239	hsa−miR−214
14	4e−04	23 / 217	hsa−miR−185
15	5e−04	19 / 168	hsa−miR−137

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
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	

Brain

Rank	p−value	#in/all	Geneset
1	2e−32	299 / 3164	Mid_Frontal_Lobe_ZNF
2	6e−27	679 / 10430	Overlap_fetal_midbrain_Quies
3	2e−26	632 / 9504	Overlap_fetal_midbrain_K9K27me3
4	2e−18	230 / 2709	Mid_Frontal_Lobe_HetRpts
5	1e−14	93 / 818	Mid_Frontal_Lobe_Het
6	3e−11	285 / 4112	Mid_Frontal_Lobe_ReprPC
7	5e−11	580 / 9815	Overlap_fetal_midbrain_ReprPC
8	4e−10	580 / 9917	Overlap_fetal_midbrain_ReprPCWk
9	1e−08	369 / 5936	Overlap_fetal_midbrain_HetRpts
10	1e−07	73 / 796	Overlap_fetal_midbrain_ZNF
11	5e−05	119 / 1728	Fetal_ReprPCWk
12	6e−05	122 / 1784	Mid_Frontal_Lobe_ReprPCWk
13	4e−04	85 / 1213	Fetal_TssP
14	4e−04	136 / 2127	Mid_Frontal_Lobe_K9K27me3
15	3e−03	160 / 2700	Fetal_TxTrans

Chr

Rank	p−value	#in/all	Geneset
1	9e−09	120 / 1467	Chr 19
2	1e−06	80 / 959	Chr 16
3	1e−02	38 / 536	Chr 22
4	5e−02	77 / 1318	Chr 17
5	1e−01	125 / 2323	Chr 1
6	4e−01	32 / 619	Chr 20
7	4e−01	42 / 836	Chr 8
8	5e−01	57 / 1170	Chr 7
9	5e−01	68 / 1411	Chr 11
10	6e−01	4 / 87	Chr Y
11	7e−01	53 / 1160	Chr 12
12	7e−01	34 / 769	Chr 15
13	8e−01	33 / 768	Chr 14
14	8e−01	65 / 1492	Chr 2
15	8e−01	11 / 289	Chr 21

Glio

Rank	p−value	#in/all	Geneset
1	7e−21	56 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	1e−08	14 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
3	2e−07	13 / 47	Donson−innate immunity−associated with LTS in HGA
4	3e−05	17 / 113	GIEZELT_GBM_WT_up_VS_mut
5	6e−05	15 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
6	1e−04	3 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
7	2e−04	14 / 94	Weller_LGG_A_vs_O_UP
8	2e−04	8 / 35	Colman_survival_associated
9	5e−04	96 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	8e−04	17 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	1e−03	14 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
12	2e−03	15 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	3e−03	27 / 315	Up
14	3e−03	8 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
15	4e−03	16 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−20	49 / 211	Homuth_BMI−associated−genes_DN
2	5e−13	32 / 147	Homuth_BMI−associated−genes_UP
3	2e−10	10 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	1e−03	5 / 18	Huan_blood−pressure_SBP−signature
5	2e−02	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	4e−02	3 / 16	Huan_blood−pressure_DBP−signature
7	5e−02	3 / 17	DUMEAUX_High bmi enriched genes
8	5e−02	2 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	2e−01	7 / 94	DUMEAUX_Smoking enriched genes
10	2e−01	1 / 5	Huan_blood−pressure_HTN−signature
11	3e−01	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	4e−01	1 / 10	DUMEAUX_Smoking literature genes up
13	4e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
14	4e−01	1 / 10	Marjolein_ageing−genes_UP
15	8e−01	1 / 32	Marjolein_ageing−genes_DN

MF

Rank	p−value	#in/all	Geneset
1	1e−32	618 / 8818	protein binding
2	5e−10	32 / 188	receptor activity
3	4e−07	37 / 311	enzyme binding
4	6e−07	37 / 315	protein serine/threonine kinase activity
5	2e−06	35 / 301	ubiquitin−protein transferase activity
6	7e−06	27 / 217	protein kinase activity
7	1e−05	22 / 160	carbohydrate binding
8	2e−05	30 / 268	actin binding
9	3e−05	6 / 14	mitogen−activated protein kinase kinase binding
10	3e−05	51 / 580	identical protein binding
11	5e−05	96 / 1329	ATP binding
12	5e−05	5 / 10	RAGE receptor binding
13	9e−05	5 / 11	oxygen transporter activity
14	1e−04	26 / 243	GTPase activator activity
15	2e−04	5 / 12	phosphotyrosine binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	7e−20	355 / 4735	ICGC_Pu1_targets
2	2e−19	490 / 7247	ICGC_Runx3_targets
3	6e−19	377 / 5188	ICGC_Ebfsc137065_targets
4	3e−17	461 / 6868	ICGC_Elf1_targets
5	4e−17	388 / 5518	ICGC_Stat5_targets
6	5e−17	413 / 5984	ICGC_Mta3_targets
7	7e−17	384 / 5466	ICGC_Nficsc81335_targets
8	1e−15	422 / 6267	ICGC_Yy1_targets
9	2e−15	323 / 4468	ICGC_Egr1_targets
10	2e−15	356 / 5067	ICGC_Taf1_targets
11	1e−14	370 / 5383	ICGC_Sp1_targets
12	1e−14	373 / 5442	ICGC_Pmlsc71910_targets
13	2e−14	313 / 4362	ICGC_Creb1_targets
14	2e−14	433 / 6578	ICGC_Pou2_targets
15	7e−14	368 / 5410	ICGC_Foxm1_targets

Underexpression Spots

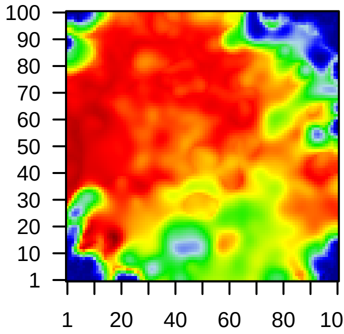
Spot Summary: u

metagenes = 4
genes = 33

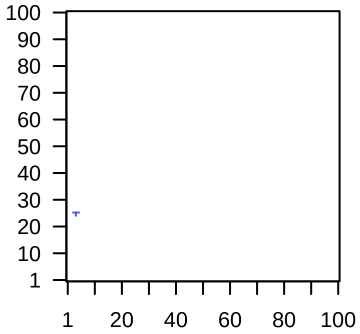
<r> metagenes = 1
<r> genes = 0.32
beta: r2= 7.98 / log p= −Inf

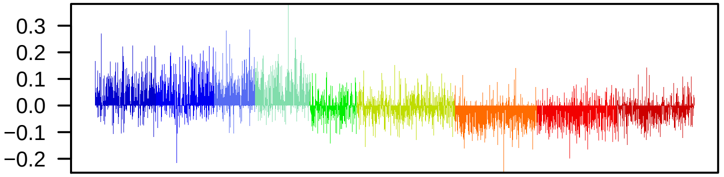
samples with spot = 195 (5.8 %)
A * : 46 (13.4 %)
A C * : 50 (15.2 %)
A C F * : 34 (14.5 %)
A F * : 50 (16.2 %)
C F * : 3 (1.1 %)
F * : 7 (1.3 %)
F J * : 2 (0.4 %)
N * : 3 (0.7 %)

Overview Map



Spot





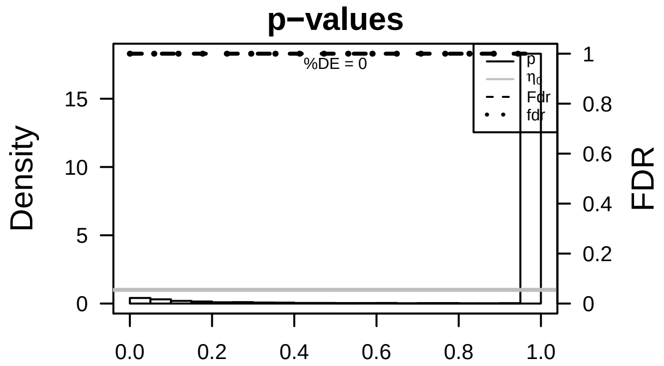
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_188649	0.8	−0.74	0.66	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGN
2	ILMN_237159	0.61	−0.48	0.48	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
3	ILMN_174194	0.57	−0.61	0.57	STX16	syntaxin 16 [Source:HGNC Symbol;Acc:HGNC:11431]
4	ILMN_180130	0.54	−0.4	0.64		
5	ILMN_169188	0.53	−0.27	0.54		
6	ILMN_181111	0.51	−0.42	0.6		
7	ILMN_167199	0.5	−0.34	0.69	PDXDC2P	pyridoxal dependent decarboxylase domain containing 2, pse
8	ILMN_183876	0.49	−0.39	0.56	LINC01451	long intergenic non−protein coding RNA 1451 [Source:HGNC
9	ILMN_176360	0.49	−0.39	0.65	DIDO1	death inducer−obliterator 1 [Source:HGNC Symbol;Acc:HGN
10	ILMN_172228	0.49	−0.29	0.39		family with sequence similarity 215 member B (non−protein c
11	ILMN_218687	0.48	−0.35	0.75	EBLN2	endogenous Bornavirus−like nucleoprotein 2 [Source:HGNC
12	ILMN_206238	0.48	−0.52	0.6	LCOR	ligand dependent nuclear receptor corepressor [Source:HGN
13	ILMN_323922	0.47	−0.38	0.74		Y RNA [Source:RFAM;Acc:RF00019]
14	ILMN_173864	0.47	−0.27	0.4		
15	ILMN_324172	0.43	−0.28	0.56	GOLGA8IP	golgin A8 family member I, pseudogene [Source:HGNC Symb
16	ILMN_182489	0.41	−0.31	0.7	MECP2	methyl−CpG binding protein 2 [Source:HGNC Symbol;Acc:H
17	ILMN_218685	0.4	−0.36	0.5	ZNF839	zinc finger protein 839 [Source:HGNC Symbol;Acc:HGNC:20
18	ILMN_185920	0.37	−0.24	0.56		
19	ILMN_182380	0.37	−0.26	0.58		
20	ILMN_189845	0.37	−0.25	0.55		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−07	7 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
2	9e−06	6 / 493	Lympl	WIRTH_lymphoma937_spot J
3	1e−04	3 / 92	miRN	hsa−miR−219−2−3p
4	7e−04	3 / 174	GSEA	WANG_CISPLATIN_RESPONSE_AND_XPC_UP
5	8e−04	2 / 41	miRN	hsa−miR−541
6	1e−03	3 / 221	Refer	Chaussabel_3,8_Enzymes
7	2e−03	2 / 58	miRN	hsa−miR−187
8	2e−03	2 / 60	GSEA	PID_ERA_GENOMIC_PATHWAY
9	2e−03	2 / 65	miRN	hsa−miR−606
10	2e−03	3 / 254	Refer	PROTEINATLAS_smooth muscle
11	2e−03	2 / 71	miRN	hsa−miR−127−5p
12	2e−03	2 / 71	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP
13	3e−03	5 / 952	GSEA	DANG_BOUND_BY_MYC
14	3e−03	2 / 78	CC	catalytic step 2 spliceosome
15	3e−03	3 / 283	miRN	hsa−miR−320a
16	3e−03	5 / 1013	MF	poly(A) RNA binding
17	4e−03	2 / 86	miRN	hsa−miR−134
18	4e−03	1 / 4	GSEA	MCGOWAN_RSP6_TARGETS_DN
19	5e−03	2 / 103	Colon	Marisa_CRC−cluster−d
20	5e−03	2 / 105	miRN	hsa−miR−361−5p
21	6e−03	2 / 108	miRN	hsa−miR−501−5p
22	6e−03	2 / 112	miRN	hsa−miR−507
23	6e−03	2 / 113	miRN	hsa−miR−217
24	6e−03	4 / 726	Refer	PROTEINATLAS_cervix, uterine
25	6e−03	2 / 117	miRN	hsa−miR−543
26	6e−03	2 / 117	GSEA	DANG_MYC_TARGETS_UP
27	7e−03	3 / 374	miRN	hsa−miR−144
28	7e−03	2 / 125	miRN	hsa−miR−508−3p
29	7e−03	2 / 125	GSEA	ONDER_CDH1_TARGETS_1_UP
30	8e−03	5 / 1239	Refer	PROTEINATLAS_testis
31	8e−03	1 / 8	TF	MYC_RNA processing binding UP
32	8e−03	2 / 134	GSEA	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
33	9e−03	2 / 140	miRN	hsa−miR−135b
34	9e−03	4 / 816	Refer	PROTEINATLAS_endometrium
35	9e−03	1 / 9	miRN	hsa−miR−615−3p
36	9e−03	1 / 9	GSEA	IIZUKA_LIVER_CANCER_EARLY_RECURRENCE
37	1e−02	2 / 143	miRN	hsa−miR−135a
38	1e−02	2 / 146	miRN	hsa−miR−548o
39	1e−02	1 / 10	BP	Golgi ribbon formation
40	1e−02	1 / 10	BP	multicellular organismal response to stress

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	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	

BP

Rank	p−value	#in/all	Geneset
1	0.01	1 / 10	Golgi ribbon formation
2	0.01	1 / 10	multicellular organismal response to stress
3	0.01	1 / 10	neuromuscular process controlling posture
4	0.01	1 / 10	neuron maturation
5	0.01	1 / 11	mitochondrial electron transport, ubiquinol to cytochrome c
6	0.01	1 / 11	phosphatidylcholine metabolic process
7	0.01	1 / 13	regulation of respiratory gaseous exchange by neurological system process
8	0.01	1 / 14	glutamine metabolic process
9	0.01	1 / 14	regulation of gene expression by genetic imprinting
10	0.02	1 / 15	formation of translation preinitiation complex
11	0.02	1 / 15	regulation of gene expression, epigenetic
12	0.02	1 / 15	ventricular system development
13	0.02	1 / 18	histone methylation
14	0.02	1 / 18	startle response
15	0.02	1 / 20	negative regulation of mRNA splicing, via spliceosome

Brain

Rank	p−value	#in/all	Geneset
1	0.1	5 / 2709	Mid_Frontal_Lobe_HetRpts
2	0.2	1 / 180	Overlap_fetal_midbrain_Het
3	0.2	2 / 796	Overlap_fetal_midbrain_ZNF
4	0.2	2 / 818	Mid_Frontal_Lobe_Het
5	0.2	5 / 3164	Mid_Frontal_Lobe_ZNF
6	0.3	3 / 1728	Fetal_ReprPCWk
7	0.3	1 / 307	Fetal_ReprPC
8	0.3	12 / 9815	Overlap_fetal_midbrain_ReprPC
9	0.3	4 / 2700	Fetal_TxTrans
10	0.4	7 / 5936	Overlap_fetal_midbrain_HetRpts
11	0.4	2 / 1436	Fetal_K9K27me3
12	0.5	1 / 630	Mid_Frontal_Lobe_EnhP
13	0.6	2 / 1784	Mid_Frontal_Lobe_ReprPCWk
14	0.6	1 / 906	Fetal_HetRpts
15	0.6	3 / 3046	Fetal_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	0 / 13	RHODES_CANCER_META_SIGNATURE
2	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
3	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	1.00	0 / 12	LIU_BREAST_CANCER
6	1.00	0 / 14	LIU_COMMON_CANCER_GENES
7	1.00	0 / 13	LIU_LIVER_CANCER
8	1.00	0 / 15	LIU_PROSTATE_CANCER_DN
9	1.00	0 / 14	LIU_PROSTATE_CANCER_UP
10	1.00	0 / 15	WANG_ER_UP
11	1.00	0 / 13	WANG_ER_DN
12	1.00	0 / 15	WOLFER_overlap genes
13	1.00	0 / 16	BEN−PORATH_DN
14	1.00	0 / 14	BEN−PORATH_UP
15	1.00	0 / 14	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	0.003	2 / 78	catalytic step 2 spliceosome
2	0.012	1 / 12	eukaryotic translation initiation factor 3 complex
3	0.015	1 / 15	vacuole
4	0.018	1 / 18	postsynapse
5	0.028	1 / 27	heterochromatin
6	0.042	1 / 41	ER to Golgi transport vesicle membrane
7	0.050	1 / 50	SNARE complex
8	0.077	1 / 77	trans−Golgi network membrane
9	0.079	1 / 79	spliceosomal complex
10	0.099	1 / 101	intracellular ribonucleoprotein complex
11	0.105	1 / 107	spindle
12	0.121	1 / 124	trans−Golgi network
13	0.307	1 / 352	focal adhesion
14	0.323	1 / 374	mitochondrial inner membrane
15	0.381	6 / 4828	nucleus

Chr

Rank	p−value	#in/all	Geneset
1	0.1	2 / 619	Chr 20
2	0.2	2 / 768	Chr 14
3	0.2	2 / 904	Chr 10
4	0.3	2 / 959	Chr 16
5	0.3	2 / 994	Chr X
6	0.3	2 / 1170	Chr 7
7	0.4	2 / 1217	Chr 3
8	0.4	1 / 536	Chr 22
9	0.6	1 / 769	Chr 15
10	0.6	1 / 836	Chr 8
11	0.6	1 / 954	Chr 9
12	0.7	1 / 1211	Chr 6
13	0.8	1 / 1318	Chr 17
14	0.8	1 / 1467	Chr 19
15	0.8	1 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.03	4 / 1206	6_EnhG_Neuronal_Progenitor
2	0.05	10 / 5699	6_EnhG_Melanocytes
3	0.10	8 / 4795	6_EnhG_Fibroblasts
4	0.13	6 / 3450	4_TxTrans_Fibroblasts
5	0.14	9 / 5956	3_TssF_Neuronal_Progenitor
6	0.15	11 / 7854	5_Tx_Fibroblasts
7	0.15	4 / 2028	4_TxTrans_Melanocytes
8	0.15	10 / 6970	5_Tx_Neuronal_Progenitor
9	0.27	11 / 8771	5_Tx_Melanocytes
10	0.39	14 / 12393	15_Quies_Neuronal_Progenitor
11	0.39	13 / 11455	2_TssA_Fibroblasts
12	0.45	5 / 4237	14_ZNF_Neuronal_Progenitor
13	0.48	1 / 630	14_ZNF_Fibroblasts
14	0.56	9 / 8613	7_Enh_Fibroblasts
15	0.61	13 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.005	2 / 103	Marisa_CRC−cluster−d
2	0.016	5 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	0.095	13 / 9054	Tx_Colon
4	0.103	11 / 7354	TssF_Colon
5	0.132	12 / 8568	TxWk_Colon
6	0.136	13 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	0.212	3 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
8	0.303	2 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	0.309	2 / 1083	ZNF_Colon
10	0.325	1 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
11	0.329	4 / 2810	EnhA_Colon
12	0.337	2 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	0.338	4 / 2845	TxEnhG1_Colon
14	0.393	11 / 9555	TssA_Colon
15	0.400	1 / 489	K9acLow_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.04	2 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	0.07	1 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.07	1 / 74	Weller_LGG_gradeII−vs−III_DOWN
4	0.09	1 / 92	Weller_LGG_A_vs_O_DOWN
5	0.14	1 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
6	0.16	4 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	0.21	2 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.28	3 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	0.28	1 / 315	Up
10	0.59	1 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
11	1.00	0 / 15	VERHAAK_CL subtype
12	1.00	0 / 15	VERHAAK_MES subtype
13	1.00	0 / 15	VERHAAK_NL subtype
14	1.00	0 / 15	VERHAAK_PN subtype
15	1.00	0 / 35	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 174	WANG_CISPLATIN_RESPONSE_AND_XPC_UP
2	2e−03	2 / 60	PID_ERA_GENOMIC_PATHWAY
3	2e−03	2 / 71	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP
4	3e−03	5 / 952	DANG_BOUND_BY_MYC
5	4e−03	1 / 4	MCGOWAN_RSP6_TARGETS_DN
6	6e−03	2 / 117	DANG_MYC_TARGETS_UP
7	7e−03	2 / 125	ONDER_CDH1_TARGETS_1_UP
8	8e−03	2 / 134	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
9	9e−03	1 / 9	IIZUKA_LIVER_CANCER_EARLY_RECURRENCE
10	1e−02	1 / 12	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_
11	1e−02	2 / 168	LEE_DIFFERENTIATING_T_LYMPHOCYTE
12	1e−02	1 / 13	MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA
13	1e−02	1 / 14	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEI
14	1e−02	1 / 14	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
15	1e−02	1 / 14	LEE_METASTASIS_AND_RNA_PROCESSING_UP

HM

Rank	p−value	#in/all	Geneset
1	0.09	1 / 87	HALLMARK_PROTEIN_SECRETION
2	0.12	1 / 127	HALLMARK_COAGULATION
3	0.16	1 / 170	HALLMARK_MYC_TARGETS_V1
4	1.00	0 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	1.00	0 / 189	HALLMARK_HYPOXIA
6	1.00	0 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	1.00	0 / 177	HALLMARK_MITOTIC_SPINDLE
8	1.00	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1.00	0 / 50	HALLMARK_TGF_BETA_SIGNALING
10	1.00	0 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	1.00	0 / 130	HALLMARK_DNA_REPAIR
12	1.00	0 / 179	HALLMARK_G2M_CHECKPOINT
13	1.00	0 / 151	HALLMARK_APOPTOSIS
14	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING
15	1.00	0 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 94	DUMEAUX_Smoking enriched genes
2	1	0 / 10	DUMEAUX_Smoking literature genes up
3	1	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	1	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
6	1	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 10	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 17	DUMEAUX_High bmi enriched genes
11	1	0 / 31	DUMEAUX_Fasting enriched genes
12	1	0 / 147	Homuth_BMI−associated−genes_UP
13	1	0 / 211	Homuth_BMI−associated−genes_DN
14	1	0 / 18	Huan_blood−pressure_SBP−signature
15	1	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−07	7 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
2	9e−06	6 / 493	WIRTH_lymphoma937_spot J
3	4e−02	12 / 7275	HOPP_Txn_elongation
4	1e−01	3 / 1169	SPANG_BCR DN
5	2e−01	8 / 5356	HOPP_Txn_transition
6	4e−01	1 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
7	4e−01	2 / 1270	SPANG_BCR UP
8	5e−01	9 / 8226	HOPP_Active_promoter
9	6e−01	8 / 8098	HOPP_Weak_promoter
10	8e−01	2 / 2701	HOPP_Repetitive
11	9e−01	5 / 6559	HOPP_Weak_txn
12	9e−01	3 / 5384	HOPP_Repressed
13	1e+00	1 / 2939	HOPP_Poised_promoter
14	1e+00	1 / 4167	HOPP_Heterochrom
15	1e+00	3 / 7448	HOPP_Strong_enhancer

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.003	5 / 1013	poly(A) RNA binding
2	0.014	1 / 14	miRNA binding
3	0.019	1 / 19	methyl−CpG binding
4	0.021	1 / 21	translation initiation factor binding
5	0.023	2 / 227	transcription coactivator activity
6	0.033	1 / 32	estrogen receptor binding
7	0.038	1 / 37	SNAP receptor activity
8	0.039	1 / 38	RNA polymerase II transcription factor activity, ligand−activated sequence−sp
9	0.040	1 / 39	translation initiation factor activity
10	0.041	1 / 40	mRNA 3'−UTR binding
11	0.050	1 / 50	steroid hormone receptor activity
12	0.056	1 / 56	ATP−dependent RNA helicase activity
13	0.062	1 / 62	syntaxin binding
14	0.063	2 / 399	RNA binding
15	0.086	1 / 87	protein N−terminus binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 92	hsa−miR−219−2−3p
2	8e−04	2 / 41	hsa−miR−541
3	2e−03	2 / 58	hsa−miR−187
4	2e−03	2 / 65	hsa−miR−606
5	2e−03	2 / 71	hsa−miR−127−5p
6	3e−03	3 / 283	hsa−miR−320a
7	4e−03	2 / 86	hsa−miR−134
8	5e−03	2 / 105	hsa−miR−361−5p
9	6e−03	2 / 108	hsa−miR−501−5p
10	6e−03	2 / 112	hsa−miR−507
11	6e−03	2 / 113	hsa−miR−217
12	6e−03	2 / 117	hsa−miR−543
13	7e−03	3 / 374	hsa−miR−144
14	7e−03	2 / 125	hsa−miR−508−3p
15	9e−03	2 / 140	hsa−miR−135b

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.001	3 / 221	Chaussabel_3,8_Enzymes
2	0.002	3 / 254	PROTEINATLAS_smooth muscle
3	0.006	4 / 726	PROTEINATLAS_cervix, uterine
4	0.008	5 / 1239	PROTEINATLAS_testis
5	0.009	4 / 816	PROTEINATLAS_endometrium
6	0.013	4 / 912	PROTEINATLAS_fallopian tube
7	0.015	3 / 514	PROTEINATLAS_vagina
8	0.017	3 / 535	PROTEINATLAS_spleen
9	0.019	4 / 1016	PROTEINATLAS_cerebral cortex
10	0.022	4 / 1063	PROTEINATLAS_tonsil
11	0.025	3 / 619	PROTEINATLAS_salivary gland
12	0.027	3 / 639	PROTEINATLAS_breast
13	0.029	3 / 650	PROTEINATLAS_hippocampus
14	0.030	1 / 29	Chaussabel_2,7_Unknown function
15	0.030	4 / 1167	PROTEINATLAS_gallbladder

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
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	

TF

Rank	p−value	#in/all	Geneset
1	0.008	1 / 8	MYC_RNA processing binding UP
2	0.029	5 / 1723	HEBENSTREIT_high expression TF
3	0.055	1 / 55	MYC_Targets UP
4	0.059	4 / 1452	ICGC_Six5_targets
5	0.089	4 / 1669	ICGC_P300_targets
6	0.139	5 / 2704	ICGC_Pbx3_targets
7	0.184	8 / 5466	ICGC_Nficsc81335_targets
8	0.216	9 / 6578	ICGC_Pou2_targets
9	0.222	9 / 6616	ICGC_Pax5_targets
10	0.254	4 / 2497	ICGC_Bcl11_targets
11	0.257	7 / 5067	ICGC_Taf1_targets
12	0.258	5 / 3348	ICGC_BatfPcr1_targets
13	0.288	6 / 4362	ICGC_Creb1_targets
14	0.300	7 / 5312	ICGC_Tcf12_targets
15	0.318	7 / 5410	ICGC_Foxm1_targets

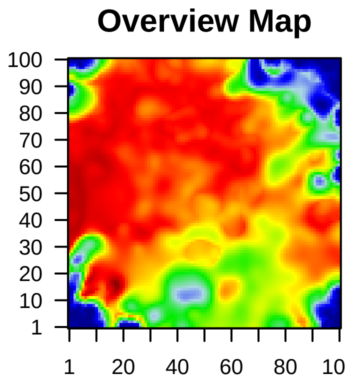
Underexpression Spots

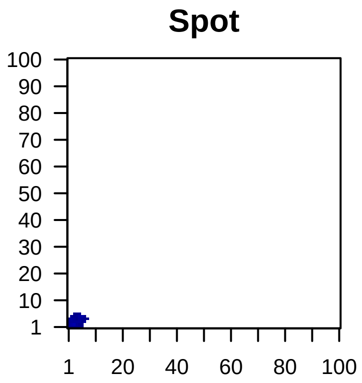
Spot Summary: v

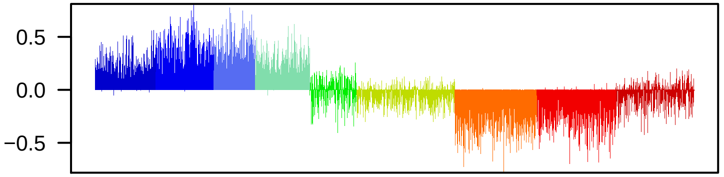
metagenes = 36
genes = 498

<r> metagenes = 0.87
<r> genes = 0.58
beta: r2= 190.6 / log p= −Inf

samples with spot = 1103 (32.6 %)
A * : 242 (70.3 %)
A C * : 306 (93.3 %)
A C F * : 232 (98.7 %)
A F * : 255 (82.8 %)
C F * : 42 (15.8 %)
F * : 7 (1.3 %)
N * : 19 (4.3 %)





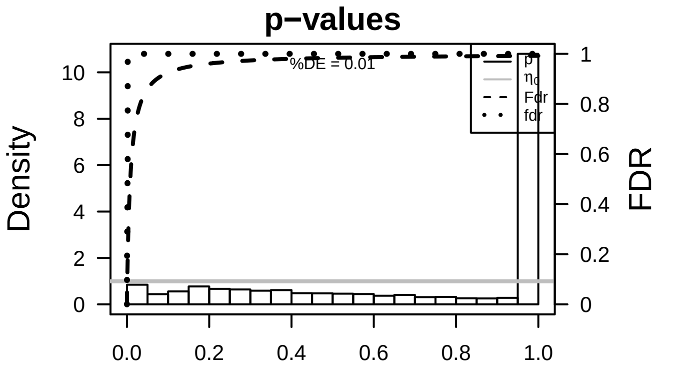


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169326	3.22	−2.11	0.38		
2	ILMN_167935	3.21	−3.04	0.35	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
3	ILMN_219321	3.07	−2.61	0.34	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
4	ILMN_216528	3.02	−1.93	0.35	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
5	ILMN_172566	2.96	−2.08	0.35	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
6	ILMN_173045	2.93	−1.93	0.25	FOLR3	folate receptor 3 [Source:HGNC Symbol;Acc:HGNC:3795]
7	ILMN_211687	2.86	−1.31	0.31	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
8	ILMN_168858	2.54	−1.91	0.5	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
9	ILMN_175334	2.49	−1.4	0.31		
10	ILMN_169222	2.41	−1.48	0.46		
11	ILMN_170663	2.3	−1.37	0.4	ELANE	elastase, neutrophil expressed [Source:HGNC Symbol;Acc:H
12	ILMN_169319	2.29	−2.04	0.51	PI3	peptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:8947
13	ILMN_180605	2.07	−0.98	0.29	CEACAM8	carcinoembryonic antigen related cell adhesion molecule 8 [S
14	ILMN_169658	2.03	−1.31	0.42		
15	ILMN_170487	1.95	−1.49	0.67	PGLYRP1	peptidoglycan recognition protein 1 [Source:HGNC Symbol;A
16	ILMN_168042	1.9	−0.91	0.31	CTSG	cathepsin G [Source:HGNC Symbol;Acc:HGNC:2532]
17	ILMN_210272	1.79	−0.83	0.33	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
18	ILMN_176673	1.6	−0.7	0.32	BPI	bactericidal/permeability−increasing protein [Source:HGNC S
19	ILMN_323194	1.5	−1.58	0.9		
20	ILMN_167769	1.49	−1.31	0.91		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−41	57 / 360	GSEA	LU_EZH2_TARGETS_DN
2	6e−09	9 / 39	Refere	Chaussabel_2,2_Neutrophils
3	4e−08	13 / 120	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
4	1e−07	16 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
5	3e−07	6 / 19	GSEA	VILIMAS_NOTCH1_TARGETS_DN
6	4e−07	77 / 2845	Colon	TxEnhG1_Colon
7	5e−07	31 / 740	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
8	6e−07	13 / 150	Refere	Chaussabel_2,6_Myeloid lineage
9	2e−06	4 / 7	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_UP
10	3e−06	120 / 5383	TF	ICGC_Sp1_targets
11	4e−06	73 / 2810	Colon	EnhA_Colon
12	4e−06	18 / 331	Lymph	WIRTH_lymphoma937_spot H
13	5e−06	15 / 240	Refere	Chaussabel_3,3_Inflammation II
14	5e−06	180 / 9054	Colon	Tx_Colon
15	9e−06	17 / 318	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−I
16	1e−05	186 / 9555	Colon	TssA_Colon
17	1e−05	27 / 708	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
18	2e−05	127 / 5984	TF	ICGC_Mta3_targets
19	2e−05	119 / 5518	TF	ICGC_Stat5_targets
20	3e−05	172 / 8771	Chron	5_Tx_Melanocytes
21	3e−05	4 / 13	BP	cellular response to hepatocyte growth factor stimulus
22	4e−05	168 / 8568	Colon	TxWk_Colon
23	4e−05	104 / 4735	TF	ICGC_Pu1_targets
24	4e−05	81 / 3450	Chron	4_TxTrans_Fibroblasts
25	5e−05	148 / 7354	Colon	TssF_Colon
26	5e−05	79 / 3348	TF	ICGC_BatfPcr1_targets
27	5e−05	15 / 293	BP	immune response
28	6e−05	116 / 5466	TF	ICGC_Nficsc81335_targets
29	6e−05	6 / 45	GSEA	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
30	6e−05	4 / 15	BP	negative regulation of growth of symbiont in host
31	7e−05	5 / 29	Refere	Chaussabel_2,7_Unknown function
32	7e−05	139 / 6868	TF	ICGC_Elf1_targets
33	8e−05	224 / 12298	Chron	2_TssA_Melanocytes
34	9e−05	105 / 4881	TF	ICGC_Atf2_targets
35	1e−04	110 / 5188	TF	ICGC_Ebfsc137065_targets
36	1e−04	126 / 6138	Colon	TssD2_Colon
37	1e−04	15 / 319	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
38	2e−04	41 / 1467	Chr	Chr 19
39	2e−04	66 / 2759	TF	ICGC_Bcl3_targets
40	2e−04	41 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon



Aging

Rank	p−value	#in/all	Geneset
1	0.09	4 / 111	HORVATH_aging_genes meth DOWN
2	0.59	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.89	1 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	1 / 14	LIU_COMMON_CANCER_GENES
2	3e−02	4 / 73	SHAUGHNESSY_MM high risk
3	1e−01	2 / 36	PanCan_HK_geneset_nanostring
4	1e−01	12 / 527	Lembcke_Normal vs Adenoma
5	1e−01	2 / 39	ZHANG_MM up
6	1e−01	12 / 554	Lembcke_Colonic Inflammation
7	2e−01	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	2e−01	1 / 12	LIU_BREAST_CANCER
9	2e−01	1 / 13	LIU_LIVER_CANCER
10	2e−01	1 / 14	LIU_PROSTATE_CANCER_UP
11	2e−01	2 / 54	KUIPER_MM poor survival
12	2e−01	1 / 15	WANG_ER_UP
13	2e−01	1 / 16	GENTLES_modul7
14	2e−01	1 / 16	GENTLES_modul14
15	3e−01	1 / 24	PanCan_Notch_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−05	172 / 8771	5_Tx_Melanocytes
2	4e−05	81 / 3450	4_TxTrans_Fibroblasts
3	8e−05	224 / 12298	2_TssA_Melanocytes
4	7e−04	206 / 11455	2_TssA_Fibroblasts
5	8e−04	135 / 6970	5_Tx_Neuronal_Progenitor
6	9e−04	149 / 7854	5_Tx_Fibroblasts
7	3e−03	208 / 11836	3_TssF_Melanocytes
8	4e−03	224 / 12983	2_TssA_Neuronal_Progenitor
9	6e−03	214 / 12393	15_Quies_Neuronal_Progenitor
10	7e−03	42 / 1846	14_ZNF_Melanocytes
11	7e−03	108 / 5699	6_EnhG_Melanocytes
12	7e−03	93 / 4795	6_EnhG_Fibroblasts
13	9e−03	18 / 630	14_ZNF_Fibroblasts
14	9e−03	170 / 9635	3_TssF_Fibroblasts
15	2e−02	43 / 2028	4_TxTrans_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−41	57 / 360	LU_EZH2_TARGETS_DN
2	4e−08	13 / 120	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
3	1e−07	16 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
4	3e−07	6 / 19	VILIMAS_NOTCH1_TARGETS_DN
5	2e−06	4 / 7	MARTINELLI_IMMATURE_NEUTROPHIL_UP
6	1e−05	27 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
7	6e−05	6 / 45	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
8	1e−04	15 / 319	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
9	2e−04	4 / 19	GAVIN_PDE3B_TARGETS
10	3e−04	17 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
11	3e−04	14 / 304	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
12	3e−04	10 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
13	3e−04	17 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
14	4e−04	1 / 14	LIU_COMMON_CANCER_GENES
15	5e−04	4 / 25	KAMIKUBO_MYELOID_CEBPA_NETWORK

Lymphnoma

Rank	p−value	#in/all	Geneset
1	4e−06	18 / 331	WIRTH_lymphoma937_spot H
2	9e−06	17 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
3	2e−04	146 / 7448	HOPP_Strong_enhancer
4	2e−03	16 / 464	WIRTH_lymphoma937_spot I
5	6e−03	103 / 5356	HOPP_Txn_transition
6	8e−03	133 / 7275	HOPP_Txn_elongation
7	1e−02	14 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
8	2e−02	146 / 8226	HOPP_Active_promoter
9	2e−02	27 / 1169	SPANG_BCR DN
10	3e−02	5 / 109	ROSOLOWSKI_blue total
11	3e−02	4 / 78	Sha_DLBCL UP
12	3e−02	5 / 115	ROSOLOWSKI_green total
13	4e−02	4 / 84	ROSOLOWSKI_green UP
14	4e−02	9 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
15	5e−02	9 / 306	WIRTH_lymphoma937_spot E

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−09	9 / 39	Chaussabel_2,2_Neutrophils
2	6e−07	13 / 150	Chaussabel_2,6_Myeloid lineage
3	5e−06	15 / 240	Chaussabel_3,3_Inflammation II
4	7e−05	5 / 29	Chaussabel_2,7_Unknown function
5	7e−04	16 / 412	WIRTH_Immune system
6	1e−03	4 / 29	JONGENEEL_Bone Marrow
7	2e−03	7 / 113	Chaussabel_1,5_Myeloid lineage
8	3e−03	3 / 19	VAQUERIZAS_Bone marrow_TF
9	3e−03	5 / 66	VAQUERIZAS_Whole blood_TF
10	4e−03	10 / 242	Chaussabel_3,2_Inflammation I
11	1e−02	2 / 11	WIRTH_Prim. lymphoid organs
12	2e−02	2 / 13	WIRTH_Bone marrow
13	4e−02	17 / 695	PROTEINATLAS_bone marrow
14	5e−02	2 / 24	Chaussabel_1,6_Signaling molecules
15	7e−02	1 / 5	VAQUERIZAS_Appendix_TF

BP

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 13	cellular response to hepatocyte growth factor stimulus
2	5e−05	15 / 293	immune response
3	6e−05	4 / 15	negative regulation of growth of symbiont in host
4	4e−04	3 / 10	mitotic recombination
5	5e−04	4 / 25	sprouting angiogenesis
6	5e−04	3 / 11	positive regulation of long−term synaptic potentiation
7	1e−03	4 / 29	mitophagy
8	1e−03	5 / 50	response to ionizing radiation
9	2e−03	5 / 57	defense response to Gram−positive bacterium
10	2e−03	4 / 37	autophagosome assembly
11	3e−03	4 / 38	chromatin silencing
12	3e−03	4 / 38	response to activity
13	3e−03	3 / 20	negative regulation of reactive oxygen species metabolic process
14	3e−03	3 / 20	positive regulation of macroautophagy
15	4e−03	6 / 96	phosphorylation

CC

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 12	specific granule
2	1e−03	6 / 76	extrinsic component of membrane
3	2e−03	3 / 16	pre−autophagosomal structure membrane
4	1e−02	2 / 10	MKS complex
5	1e−02	4 / 56	autophagosome
6	1e−02	2 / 11	uropod
7	2e−02	4 / 63	lipid particle
8	2e−02	2 / 13	A band
9	2e−02	3 / 37	cortical actin cytoskeleton
10	2e−02	5 / 101	intracellular ribonucleoprotein complex
11	3e−02	2 / 17	cell−cell contact zone
12	3e−02	4 / 80	nucleosome
13	4e−02	3 / 47	stress fiber
14	4e−02	2 / 21	autophagosome membrane
15	4e−02	2 / 21	M band

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−07	77 / 2845	TxEnhG1_Colon
2	5e−07	31 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
3	4e−06	73 / 2810	EnhA_Colon
4	5e−06	180 / 9054	Tx_Colon
5	1e−05	186 / 9555	TssA_Colon
6	4e−05	168 / 8568	TxWk_Colon
7	5e−05	148 / 7354	TssF_Colon
8	1e−04	126 / 6138	TssD2_Colon
9	2e−04	41 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	2e−04	202 / 10999	TssWk_Colon
11	5e−04	51 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	5e−04	25 / 789	TxEnhG2_Colon
13	9e−04	195 / 10779	Enh_Colon
14	1e−03	107 / 5373	EnhWk1_Colon
15	3e−03	29 / 1083	ZNF_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.02	6 / 137	HALLMARK_UV_RESPONSE_UP
2	0.02	7 / 185	HALLMARK_HEME_METABOLISM
3	0.02	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	0.05	6 / 176	HALLMARK_KRAS_SIGNALING_UP
5	0.13	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.16	5 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.16	5 / 185	HALLMARK_MTORC1_SIGNALING
8	0.16	5 / 185	HALLMARK_P53_PATHWAY
9	0.28	4 / 176	HALLMARK_ADIPOGENESIS
10	0.29	4 / 177	HALLMARK_MITOTIC_SPINDLE
11	0.34	4 / 191	HALLMARK_INFLAMMATORY_RESPONSE
12	0.36	2 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	0.36	1 / 29	HALLMARK_NOTCH_SIGNALING
14	0.40	1 / 33	HALLMARK_ANGIOGENESIS
15	0.41	3 / 151	HALLMARK_APOPTOSIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.05	3 / 54	Hugo_melanoma−all−MET_DN
2	1.00	0 / 30	Hugo_melanoma−all−MET_UP
3	1.00	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 34	hsa−miR−1178
2	0.02	4 / 67	hsa−miR−502−5p
3	0.03	3 / 42	hsa−miR−129−3p
4	0.04	3 / 47	hsa−miR−370
5	0.04	3 / 49	hsa−miR−1279
6	0.04	5 / 125	hsa−miR−508−3p
7	0.05	4 / 91	hsa−miR−425
8	0.05	6 / 176	hsa−miR−23b
9	0.06	2 / 25	hsa−miR−100
10	0.06	2 / 26	hsa−miR−663b
11	0.06	2 / 26	hsa−miR−99a
12	0.06	6 / 183	hsa−miR−23a
13	0.07	3 / 61	hsa−miR−671−5p
14	0.08	3 / 64	hsa−miR−1278
15	0.08	4 / 105	hsa−miR−605

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
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	

Brain

Rank	p−value	#in/all	Geneset
1	0.002	42 / 1728	Fetal_ReprPCWk
2	0.004	20 / 681	Overlap_fetal_midbrain_EnhP
3	0.008	22 / 818	Mid_Frontal_Lobe_Het
4	0.008	57 / 2709	Mid_Frontal_Lobe_HetRpts
5	0.021	27 / 1162	Fetal_Enh
6	0.027	164 / 9504	Overlap_fetal_midbrain_K9K27me3
7	0.046	60 / 3164	Mid_Frontal_Lobe_ZNF
8	0.050	105 / 5936	Overlap_fetal_midbrain_HetRpts
9	0.066	18 / 796	Overlap_fetal_midbrain_ZNF
10	0.072	10 / 383	Mid_Frontal_Lobe_Tx
11	0.079	35 / 1784	Mid_Frontal_Lobe_ReprPCWk
12	0.096	163 / 9815	Overlap_fetal_midbrain_ReprPC
13	0.101	8 / 307	Fetal_ReprPC
14	0.107	14 / 630	Mid_Frontal_Lobe_EnhP
15	0.114	48 / 2630	Fetal_TssF

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	41 / 1467	Chr 19
2	4e−03	33 / 1318	Chr 17
3	8e−03	29 / 1170	Chr 7
4	2e−02	20 / 769	Chr 15
5	2e−01	11 / 536	Chr 22
6	2e−01	15 / 768	Chr 14
7	3e−01	17 / 959	Chr 16
8	4e−01	37 / 2323	Chr 1
9	5e−01	17 / 1060	Chr 5
10	5e−01	10 / 619	Chr 20
11	5e−01	15 / 954	Chr 9
12	6e−01	4 / 289	Chr 21
13	7e−01	12 / 904	Chr 10
14	8e−01	4 / 342	Chr 18
15	9e−01	9 / 836	Chr 8

Glio

Rank	p−value	#in/all	Geneset
1	0.02	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
2	0.04	4 / 84	GIEZELT_GBM_STS_up_VS_LTS
3	0.05	8 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
4	0.08	5 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
5	0.10	4 / 113	GIEZELT_GBM_WT_up_VS_mut
6	0.10	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	0.12	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
8	0.14	2 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
9	0.14	27 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	0.15	3 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	0.16	1 / 11	VERHAAK_Brain
12	0.16	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
13	0.16	3 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
14	0.18	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
15	0.19	2 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	8 / 211	Homuth_BMI−associated−genes_DN
2	0.66	2 / 147	Homuth_BMI−associated−genes_UP
3	0.77	1 / 94	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 17	DUMEAUX_High bmi enriched genes
13	1.00	0 / 31	DUMEAUX_Fasting enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 20	endodeoxyribonuclease activity
2	1e−03	3 / 14	four−way junction DNA binding
3	2e−03	6 / 81	protease binding
4	2e−03	5 / 60	metallopeptidase activity
5	3e−03	6 / 94	double−stranded DNA binding
6	6e−03	3 / 25	aminopeptidase activity
7	1e−02	2 / 10	lactate transmembrane transporter activity
8	2e−02	3 / 34	phosphatidylinositol−3,4,5−trisphosphate binding
9	2e−02	2 / 13	monocarboxylic acid transmembrane transporter activity
10	2e−02	2 / 14	miRNA binding
11	2e−02	2 / 15	antioxidant activity
12	2e−02	2 / 15	transcriptional activator activity, RNA polymerase II transcription factor bindin
13	2e−02	4 / 72	single−stranded DNA binding
14	3e−02	2 / 17	metalloaminopeptidase activity
15	3e−02	2 / 18	3'−5'−exoribonuclease activity

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 / 13	BENTINK_e2f3.1
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−06	120 / 5383	ICGC_Sp1_targets
2	2e−05	127 / 5984	ICGC_Mta3_targets
3	2e−05	119 / 5518	ICGC_Stat5_targets
4	4e−05	104 / 4735	ICGC_Pu1_targets
5	5e−05	79 / 3348	ICGC_BatfPcr1_targets
6	6e−05	116 / 5466	ICGC_Nficsc81335_targets
7	7e−05	139 / 6868	ICGC_Elf1_targets
8	9e−05	105 / 4881	ICGC_Atf2_targets
9	1e−04	110 / 5188	ICGC_Ebfsc137065_targets
10	2e−04	66 / 2759	ICGC_Bcl3_targets
11	2e−04	113 / 5442	ICGC_Pmlsc71910_targets
12	2e−04	143 / 7247	ICGC_Runx3_targets
13	2e−04	94 / 4362	ICGC_Creb1_targets
14	2e−04	103 / 4890	ICGC_Bclaf101388_targets
15	3e−04	126 / 6267	ICGC_Yy1_targets