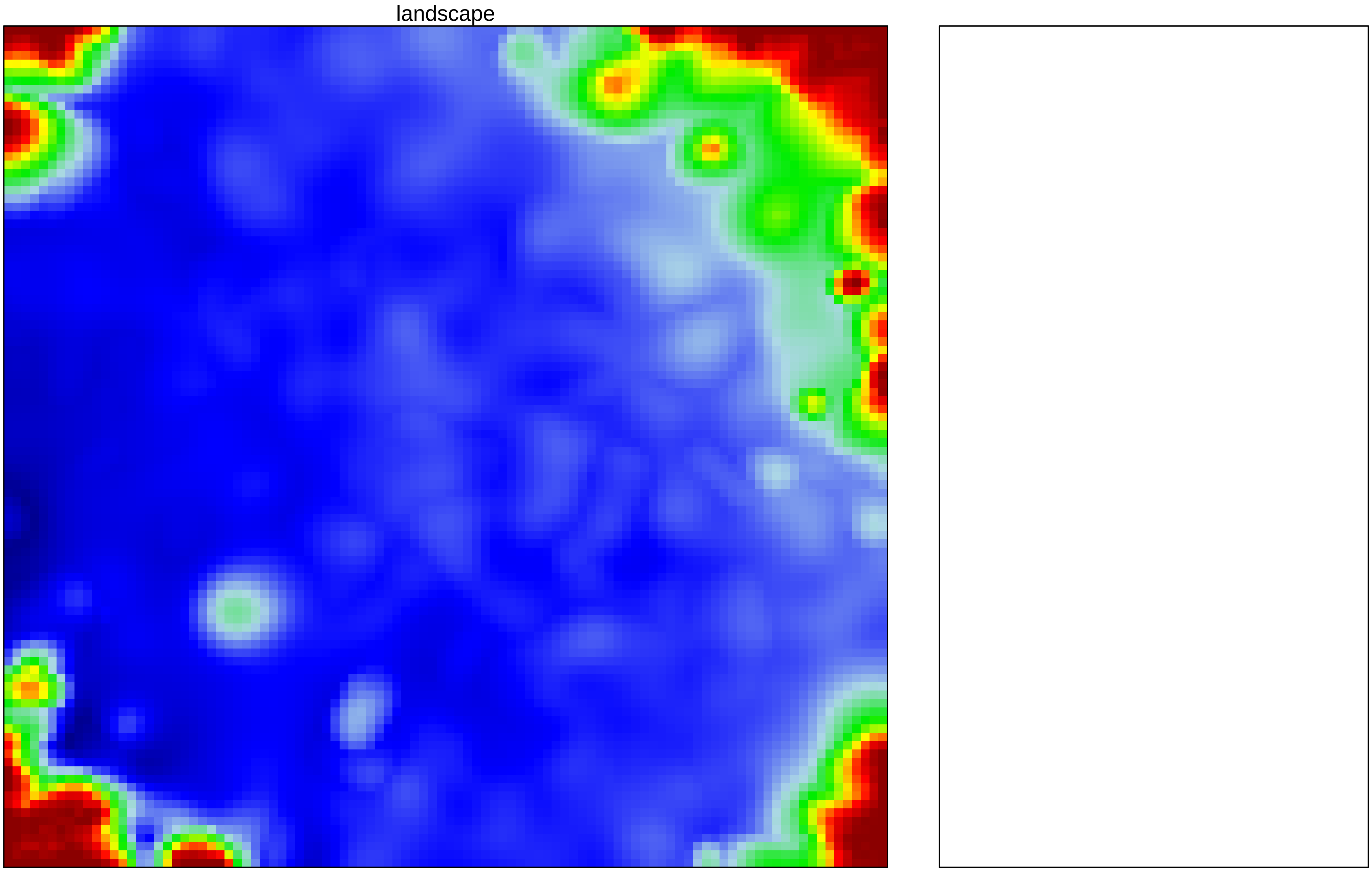
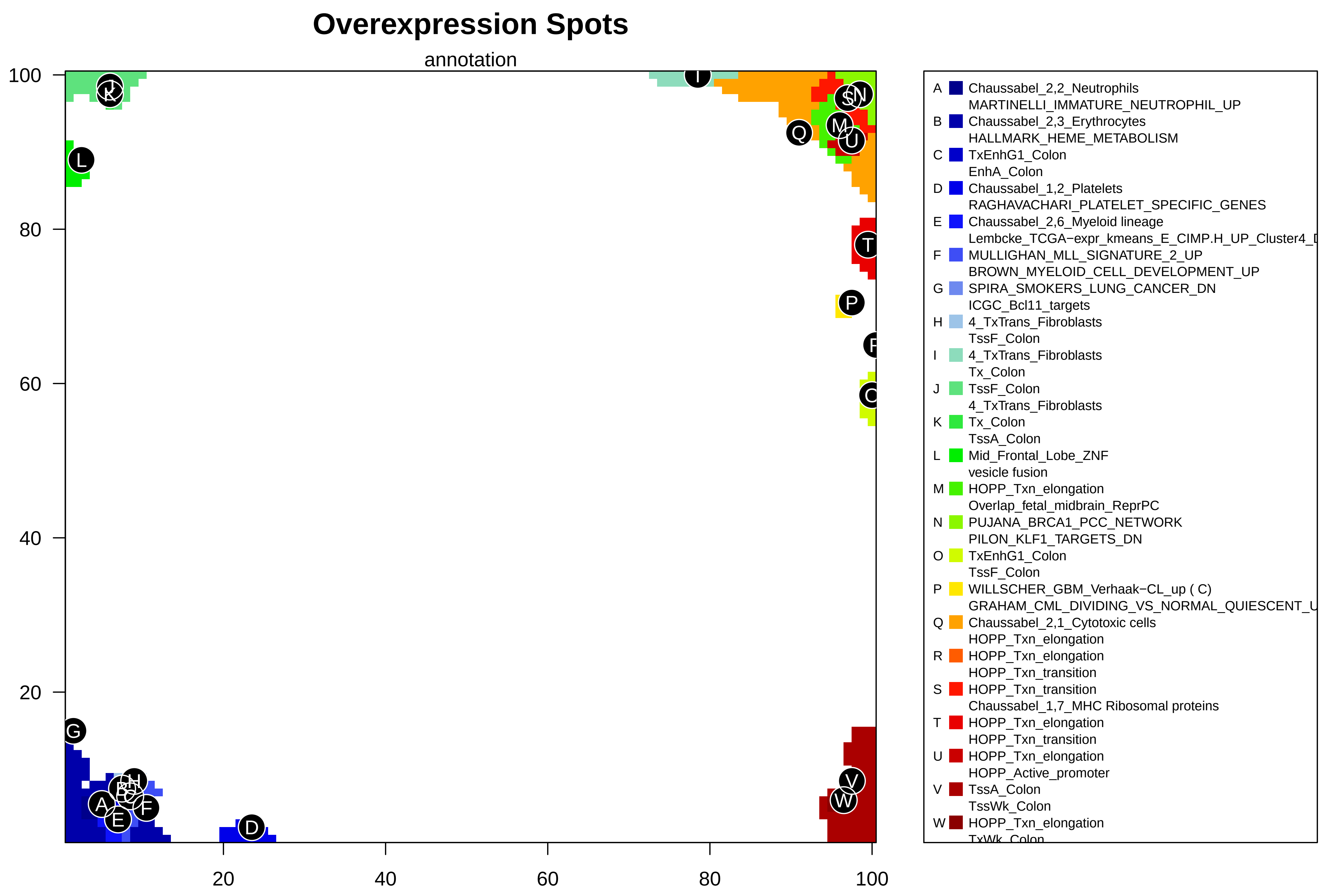
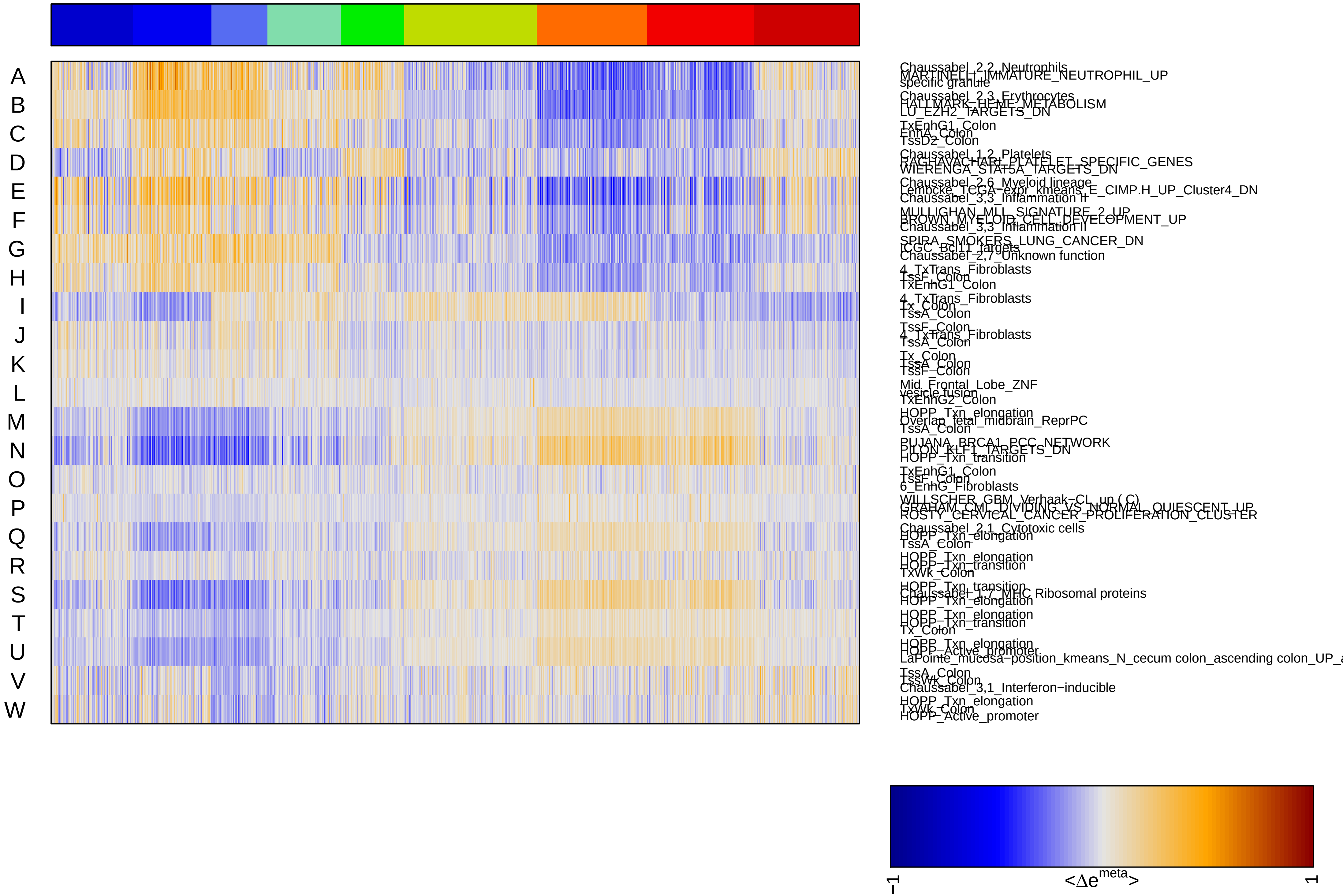
Overexpression Spots





Overexpression Spots
annotation
100
80
60
40
20
20
40
60
80
100
A Chaussabel_2,2_Neutrophils
MARTINELLI_IMMATURE_NEUTROPHIL_UP
B Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
C TxEnhG1_Colon
EnhA_Colon
D Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
E Chaussabel_2,6_Myeloid lineage
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_I
F MULLIGHAN_MLL_SIGNATURE_2_UP
BROWN_MYELOID_CELL_DEVELOPMENT_UP
G SPIRA_SMOKERS_LUNG_CANCER_DN
ICGC_Bcl11_targets
H 4_TxTrans_Fibroblasts
TssF_Colon
I 4_TxTrans_Fibroblasts
Tx_Colon
J TssF_Colon
4_TxTrans_Fibroblasts
K Tx_Colon
TssA_Colon
L Mid_Frontal_Lobe_ZNF
vesicle fusion
M HOPP_Txn_elongation
Overlap_fetal_midbrain_ReprPC
N PUJANA_BRCA1_PCC_NETWORK
PILON_KLF1_TARGETS_DN
O TxEnhG1_Colon
TssF_Colon
P WILLSCHER_GBM_Verhaak−CL_up (C)
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_U
Q Chaussabel_2,1_Cytotoxic cells
HOPP_Txn_elongation
R HOPP_Txn_elongation
HOPP_Txn_transition
S HOPP_Txn_transition
Chaussabel_1,7_MHC Ribosomal proteins
T HOPP_Txn_elongation
HOPP_Txn_transition
U HOPP_Txn_elongation
HOPP_Active_promoter
V TssA_Colon
TssWk_Colon
W HOPP_Txn_elongation
TxWk_Colon


A
B
C
D
E
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G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U
V
W
Chaussabel_2,2_Neutrophils
MARTINELLI_IMMATURE_NEUTROPHIL_UP
specific granule
Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
LU_EZH2_TARGETS_DN
TxEnhG1_Colon
EnhA_Colon
TssD2_Colon
Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
WIERENGA_STAT5A_TARGETS_DN
Chaussabel_2,6_Myeloid lineage
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
Chaussabel_3,3_Inflammation II
MULLIGHAN_MLL_SIGNATURE_2_UP
BROWN_MYELOID_CELL_DEVELOPMENT_UP
Chaussabel_3,3_Inflammation II
SPIRA_SMOKERS_LUNG_CANCER_DN
ICGC_Bcl11_Targets
Chaussabel_2,7_Unknown function
4_TxTrans_Fibroblasts
TssF_Colon
TxEnhG1_Colon
4_TxTrans_Fibroblasts
Tx_Colon
TssA_Colon
TssF_Colon
4_TxTrans_Fibroblasts
TssA_Colon
Tx_Colon
TssA_Colon
TssF_Colon
Mid_Frontal_Lobe_ZNF
vesicle fusion
TxEnhG2_Colon
HOPP_Txn_elongation
Overlap_fetal_midbrain_ReprPC
TssA_Colon
PUJANA_BRCA1_PCC_NETWORK
PILON_KLF1_TARGETS_DN
HOPP_Txn_transition
TxEnhG1_Colon
TssF_Colon
6_EnhG_Fibroblasts
WILLSCHER_GBM_Verhaak−CL_up (C)
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
Chaussabel_2,1_Cytotoxic cells
HOPP_Txn_elongation
TssA_Colon
HOPP_Txn_elongation
HOPP_Txn_transition
TxWk_Colon
HOPP_Txn_transition
Chaussabel_1,7_MHC Ribosomal proteins
HOPP_Txn_elongation
HOPP_Txn_elongation
HOPP_Txn_transition
Tx_Colon
HOPP_Txn_elongation
HOPP_Active_promoter
LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
TssA_Colon
TssWk_Colon
Chaussabel_3,1_Interferon−inducible
HOPP_Txn_elongation
TxWk_Colon
HOPP_Active_promoter
−1
<Δe^{meta}>
1

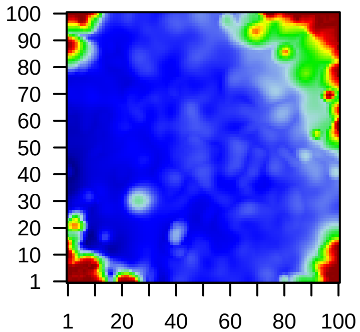
Overexpression Spots

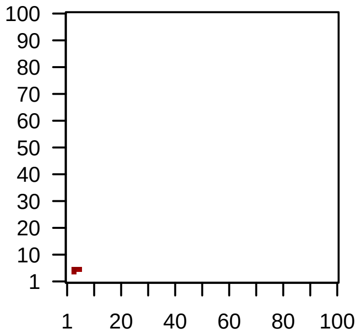
Spot Summary: A

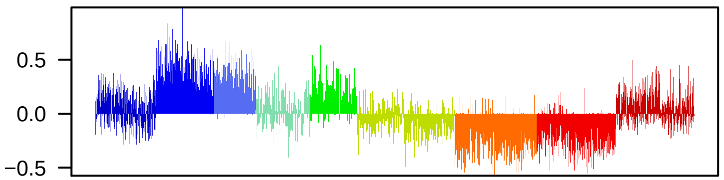
metagenes = 10
genes = 50

<r> metagenes = 0.96
<r> genes = 0.53
beta: r2= 127.83 / log p= −Inf

samples with spot = 924 (27.3 %)
- A * : 93 (27 %)
- A C * : 294 (89.6 %)
- A C F * : 183 (77.9 %)
- A F * : 63 (20.5 %)
- C F * : 137 (51.7 %)
- F * : 30 (5.4 %)
- F J * : 7 (1.5 %)
- J * : 3 (0.7 %)
- N * : 114 (25.7 %)





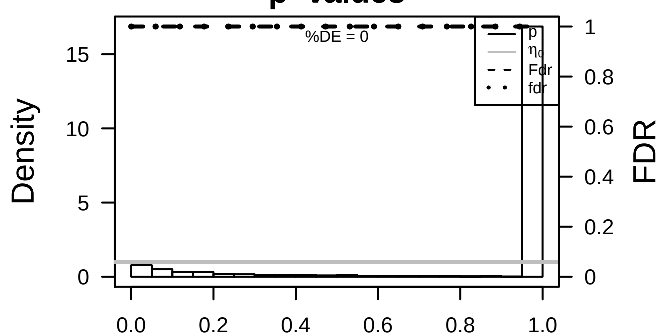


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_211687	2.86	−1.31	0.63	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
2	ILMN_168858	2.54	−1.91	0.81	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
3	ILMN_175334	2.49	−1.4	0.69		
4	ILMN_170663	2.3	−1.37	0.72	ELANE	elastase, neutrophil expressed [Source:HGNC Symbol;Acc:H
5	ILMN_180605	2.07	−0.98	0.69	CEACAM8	carcinoembryonic antigen related cell adhesion molecule 8 [S
6	ILMN_168042	1.9	−0.91	0.63	CTSG	cathepsin G [Source:HGNC Symbol;Acc:HGNC:2532]
7	ILMN_210272	1.79	−0.83	0.7	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
8	ILMN_176673	1.6	−0.7	0.69	BPI	bactericidal/permeability−increasing protein [Source:HGNC S
9	ILMN_171252	1.48	−0.61	0.65	CEACAM6	carcinoembryonic antigen related cell adhesion molecule 6 [S
10	ILMN_176846	1.32	−0.8	0.7		
11	ILMN_180482	1.26	−1.11	0.57		
12	ILMN_178792	1.15	−0.82	0.74	PNPLA2	patatin like phospholipase domain containing 2 [Source:HGN
13	ILMN_178207	1.12	−1.11	0.73	NPL	N−acetylneuraminate pyruvate lyase [Source:HGNC Symbol;
14	ILMN_171178	1.11	−1.45	0.78	NFE2	nuclear factor, erythroid 2 [Source:HGNC Symbol;Acc:HGNC
15	ILMN_166692	1.06	−0.81	0.82	MIR6084	PTEN induced putative kinase 1 [Source:HGNC Symbol;Acc:
16	ILMN_331035	1.06	−0.76	0.76		RNA, U6 small nuclear 6, pseudogene [Source:HGNC Symbo
17	ILMN_330833	1.05	−0.79	0.76		RNA, U6 small nuclear 6, pseudogene [Source:HGNC Symbo
18	ILMN_178940	1.05	−0.74	0.81	TANGO2	transport and golgi organization 2 homolog [Source:HGNC Sy
19	ILMN_239191	1.05	−1.06	0.8	SEC14L1	SEC14 like lipid binding 1 [Source:HGNC Symbol;Acc:HGNC
20	ILMN_181182	1.04	−0.76	0.84		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−13	7 / 39	Refer	Chaussabel_2,2_Neutrophils
2	4e−10	4 / 7	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_UP
3	1e−06	3 / 12	CC	specific granule
4	1e−06	4 / 45	GSEA	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
5	3e−06	3 / 15	BP	negative regulation of growth of symbiont in host
6	9e−06	3 / 22	BP	defense response to fungus
7	1e−05	17 / 2979	CC	cytosol
8	2e−05	3 / 29	Refer	JONGENEEL_Bone Marrow
9	2e−05	5 / 183	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
10	5e−05	33 / 10779	Colon	Enh_Colon
11	7e−05	4 / 120	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
12	7e−05	4 / 121	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
13	1e−04	15 / 2845	Colon	TxEnhG1_Colon
14	1e−04	8 / 818	Brain	Mid_Frontal_Lobe_Het
15	2e−04	3 / 57	BP	defense response to Gram−positive bacterium
16	3e−04	2 / 13	Refer	WIRTH_Bone marrow
17	3e−04	3 / 67	GSEA	URS_ADIPOCYTE_DIFFERENTIATION_UP
18	3e−04	3 / 70	GSEA	WATANABE_COLON_CANCER_MSI_VS_MSS_DN
19	3e−04	3 / 70	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0
20	5e−04	22 / 6138	Colon	TssD2_Colon
21	5e−04	4 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
22	6e−04	2 / 19	Refer	VAQUERIZAS_Bone marrow_TF
23	6e−04	2 / 19	GSEA	VILIMAS_NOTCH1_TARGETS_DN
24	6e−04	4 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
25	6e−04	2 / 20	BP	negative regulation of reactive oxygen species metabolic process
26	6e−04	2 / 20	GSEA	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
27	6e−04	20 / 5373	Colon	EnhWk1_Colon
28	7e−04	2 / 21	GSEA	CHEOK_RESPONSE_TO_HD_MTX_UP
29	8e−04	2 / 22	BP	lipid storage
30	8e−04	3 / 99	BP	defense response to bacterium
31	8e−04	8 / 1101	CC	extracellular space
32	9e−04	6 / 612	GSEA	MARTINEZ_RB1_TARGETS_UP
33	9e−04	2 / 24	BP	regulation of neuron apoptotic process
34	9e−04	3 / 103	GSEA	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
35	1e−03	2 / 26	GSEA	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
36	1e−03	3 / 115	BP	leukocyte migration
37	1e−03	2 / 29	BP	mitophagy
38	1e−03	20 / 5699	Chror	6_EnhG_Melanocytes
39	1e−03	3 / 119	GSEA	SMID_BREAST_CANCER_ERBB2_UP
40	1e−03	2 / 30	GSEA	GHANDHI_DIRECT_IRRADIATION_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	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	3e−06	3 / 15	negative regulation of growth of symbiont in host
2	9e−06	3 / 22	defense response to fungus
3	2e−04	3 / 57	defense response to Gram−positive bacterium
4	6e−04	2 / 20	negative regulation of reactive oxygen species metabolic process
5	8e−04	2 / 22	lipid storage
6	8e−04	3 / 99	defense response to bacterium
7	9e−04	2 / 24	regulation of neuron apoptotic process
8	1e−03	3 / 115	leukocyte migration
9	1e−03	2 / 29	mitophagy
10	2e−03	2 / 35	defense response to Gram−negative bacterium
11	2e−03	4 / 293	immune response
12	2e−03	2 / 40	response to UV
13	5e−03	2 / 56	cellular response to oxidative stress
14	7e−03	2 / 68	positive regulation of inflammatory response
15	7e−03	2 / 69	dephosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	8 / 818	Mid_Frontal_Lobe_Het
2	4e−03	13 / 3164	Mid_Frontal_Lobe_ZNF
3	6e−02	23 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−01	24 / 10430	Overlap_fetal_midbrain_Quies
5	1e−01	2 / 304	Mid_Frontal_Lobe_TssA
6	1e−01	8 / 2709	Mid_Frontal_Lobe_HetRpts
7	2e−01	3 / 796	Overlap_fetal_midbrain_ZNF
8	2e−01	1 / 110	Overlap_fetal_midbrain_Tx
9	2e−01	7 / 2630	Fetal_TssF
10	2e−01	2 / 465	Mid_Frontal_Lobe_TxTrans
11	2e−01	5 / 1728	Fetal_ReprPCWk
12	3e−01	20 / 9815	Overlap_fetal_midbrain_ReprPC
13	4e−01	3 / 1171	Fetal_EnhP
14	4e−01	12 / 5936	Overlap_fetal_midbrain_HetRpts
15	5e−01	1 / 328	Fetal_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 16	GENTLES_modul14
2	0.08	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.21	1 / 125	PanCan_CC+Apop_geneset_nanostring
4	0.27	2 / 554	Lembcke_Colonic Inflammation
5	0.43	1 / 301	SPANG_BCL6−index2
6	0.56	0 / 15	LIU_PROSTATE_CANCER_DN
7	0.63	1 / 527	Lembcke_Normal vs Adenoma
8	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
9	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
10	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_COMMON_CANCER_GENES
13	1.00	0 / 13	LIU_LIVER_CANCER
14	1.00	0 / 14	LIU_PROSTATE_CANCER_UP
15	1.00	0 / 15	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	1e−06	3 / 12	specific granule
2	1e−05	17 / 2979	cytosol
3	8e−04	8 / 1101	extracellular space
4	4e−03	2 / 50	SNARE complex
5	9e−03	2 / 75	secretory granule
6	1e−02	2 / 96	anchored component of membrane
7	2e−02	2 / 101	intracellular ribonucleoprotein complex
8	2e−02	1 / 10	mitochondrial outer membrane translocase complex
9	2e−02	1 / 10	RISC complex
10	2e−02	1 / 11	mRNA cap binding complex
11	2e−02	1 / 11	TORC2 complex
12	2e−02	1 / 11	zymogen granule membrane
13	2e−02	4 / 571	perinuclear region of cytoplasm
14	2e−02	15 / 4822	cytoplasm
15	3e−02	1 / 16	pre−autophagosomal structure membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.05	6 / 1467	Chr 19
2	0.09	4 / 904	Chr 10
3	0.09	5 / 1318	Chr 17
4	0.28	3 / 994	Chr X
5	0.32	2 / 619	Chr 20
6	0.39	3 / 1217	Chr 3
7	0.42	1 / 289	Chr 21
8	0.46	2 / 836	Chr 8
9	0.47	1 / 342	Chr 18
10	0.53	2 / 954	Chr 9
11	0.53	2 / 959	Chr 16
12	0.55	1 / 422	Chr 13
13	0.63	1 / 536	Chr 22
14	0.76	1 / 768	Chr 14
15	0.77	1 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.001	20 / 5699	6_EnhG_Melanocytes
2	0.003	14 / 3450	4_TxTrans_Fibroblasts
3	0.004	17 / 4795	6_EnhG_Fibroblasts
4	0.021	29 / 11836	3_TssF_Melanocytes
5	0.065	29 / 12741	7_Enh_Melanocytes
6	0.066	18 / 6970	5_Tx_Neuronal_Progenitor
7	0.071	5 / 1206	6_EnhG_Neuronal_Progenitor
8	0.072	12 / 4169	10_ReprPC_Fibroblasts
9	0.077	21 / 8613	7_Enh_Fibroblasts
10	0.081	27 / 11847	7_Enh_Neuronal_Progenitor
11	0.091	21 / 8771	5_Tx_Melanocytes
12	0.105	8 / 2620	1_TssP_Neuronal_Progenitor
13	0.106	9 / 3068	8_EnhP_Fibroblasts
14	0.114	15 / 5956	3_TssF_Neuronal_Progenitor
15	0.126	27 / 12298	2_TssA_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−05	33 / 10779	Enh_Colon
2	1e−04	15 / 2845	TxEnhG1_Colon
3	5e−04	22 / 6138	TssD2_Colon
4	6e−04	20 / 5373	EnhWk1_Colon
5	4e−03	12 / 2810	EnhA_Colon
6	6e−03	22 / 7354	TssF_Colon
7	7e−03	8 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
8	8e−03	26 / 9555	TssA_Colon
9	1e−02	4 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP
10	2e−02	7 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	2e−02	1 / 10	Budinska_E_Mixed_UP
12	2e−02	24 / 9054	Tx_Colon
13	2e−02	23 / 8568	TxWk_Colon
14	4e−02	22 / 8678	Quies3_Colon
15	6e−02	4 / 789	TxEnhG2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.01	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
2	0.06	1 / 32	Donson−Misc immune function−associated with LTS in HGA
3	0.06	1 / 33	Shaw_responders_down_in_oligo_glioma
4	0.08	7 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	0.09	9 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	0.13	1 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.15	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	0.16	1 / 95	Weller_LGG_1p19qDel−vs−intact_UP
9	0.17	2 / 401	Down_b
10	0.24	1 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
11	0.42	4 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
12	0.45	2 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.52	1 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
14	0.54	1 / 419	Down_a
15	0.55	1 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−10	4 / 7	MARTINELLI_IMMATURE_NEUTROPHIL_UP
2	1e−06	4 / 45	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
3	2e−05	5 / 183	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
4	7e−05	4 / 120	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
5	7e−05	4 / 121	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
6	3e−04	3 / 67	URS_ADIPOCYTE_DIFFERENTIATION_UP
7	3e−04	3 / 70	WATANABE_COLON_CANCER_MSI_VS_MSS_DN
8	3e−04	3 / 70	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0
9	5e−04	4 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
10	6e−04	2 / 19	VILIMAS_NOTCH1_TARGETS_DN
11	6e−04	4 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
12	6e−04	2 / 20	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
13	7e−04	2 / 21	CHEOK_RESPONSE_TO_HD_MTX_UP
14	9e−04	6 / 612	MARTINEZ_RB1_TARGETS_UP
15	9e−04	3 / 103	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.003	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.005	3 / 185	HALLMARK_HEME_METABOLISM
3	0.043	2 / 177	HALLMARK_MITOTIC_SPINDLE
4	0.046	2 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	0.194	1 / 116	HALLMARK_SPERMATOGENESIS
6	0.225	1 / 137	HALLMARK_UV_RESPONSE_UP
7	0.278	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM
8	0.279	1 / 176	HALLMARK_ADIPOGENESIS
9	0.281	1 / 177	HALLMARK_KRAS_SIGNALING_DN
10	0.289	1 / 183	HALLMARK_APICAL_JUNCTION
11	0.289	1 / 183	HALLMARK_GLYCOLYSIS
12	0.291	1 / 185	HALLMARK_MTORC1_SIGNALING
13	0.296	1 / 189	HALLMARK_HYPOXIA
14	1.000	0 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1.000	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 147	Homuth_BMI−associated−genes_UP
2	0.32	1 / 211	Homuth_BMI−associated−genes_DN
3	1.00	0 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	3 / 121	SPANG_LPS 6hrs UP
2	0.023	3 / 331	SPANG_CD40 6hrs UP
3	0.045	1 / 25	SPANG_BAFF 9hrs UP
4	0.117	2 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−(
5	0.125	2 / 331	WIRTH_lymphoma937_spot H
6	0.160	1 / 94	Sha_BL UP
7	0.174	1 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
8	0.177	1 / 105	WIRTH_lymphoma937_spot MM
9	0.186	17 / 7448	HOPP_Strong_enhancer
10	0.220	1 / 134	DAVE_BL−vs−DLBCL
11	0.225	1 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
12	0.226	1 / 138	WIRTH_lymphoma937_spot G
13	0.248	16 / 7275	HOPP_Txn_elongation
14	0.428	1 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−(
15	0.435	1 / 306	WIRTH_lymphoma937_spot E

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	0.002	26 / 8818	protein binding
2	0.004	2 / 52	RNA polymerase II core promoter sequence−specific DNA binding
3	0.010	2 / 81	protease binding
4	0.012	2 / 91	peptidase activity
5	0.018	1 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
6	0.018	1 / 10	glucose binding
7	0.018	1 / 10	inositol−1,4,5−trisphosphate 3−kinase activity
8	0.022	1 / 12	protein kinase B binding
9	0.024	1 / 13	glucocorticoid receptor binding
10	0.024	1 / 13	Ral GTPase binding
11	0.024	1 / 13	triglyceride lipase activity
12	0.026	1 / 14	endoribonuclease activity
13	0.026	1 / 14	miRNA binding
14	0.027	1 / 15	mitogen−activated protein kinase binding
15	0.029	2 / 143	heparin 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	0.002	3 / 129	hsa−miR−323−3p
2	0.009	2 / 75	hsa−miR−651
3	0.022	2 / 123	hsa−miR−646
4	0.029	2 / 143	hsa−miR−922
5	0.030	2 / 145	hsa−miR−143
6	0.035	2 / 160	hsa−miR−298
7	0.042	2 / 176	hsa−miR−23b
8	0.044	1 / 24	hsa−miR−602
9	0.044	1 / 24	hsa−miR−99b
10	0.045	2 / 183	hsa−miR−23a
11	0.045	1 / 25	hsa−miR−100
12	0.047	2 / 187	hsa−miR−9
13	0.047	1 / 26	hsa−miR−99a
14	0.052	2 / 199	hsa−miR−545
15	0.061	1 / 34	hsa−miR−621

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	7e−13	7 / 39	Chaussabel_2,2_Neutrophils
2	2e−05	3 / 29	JONGENEEL_Bone Marrow
3	3e−04	2 / 13	WIRTH_Bone marrow
4	6e−04	2 / 19	VAQUERIZAS_Bone marrow_TF
5	2e−03	6 / 695	PROTEINATLAS_bone marrow
6	3e−03	5 / 535	PROTEINATLAS_spleen
7	7e−03	2 / 66	VAQUERIZAS_Whole blood_TF
8	1e−02	3 / 240	Chaussabel_3,3_Inflammation II
9	2e−02	2 / 111	Chaussabel_2,3_Erythrocytes
10	2e−02	1 / 11	WIRTH_Prim. lymphoid organs
11	3e−02	1 / 14	WIRTH_B−cells
12	3e−02	1 / 15	VAQUERIZAS_Fetal liver_TF
13	3e−02	2 / 150	Chaussabel_2,6_Myeloid lineage
14	6e−02	1 / 32	VAQUERIZAS_Liver_TF
15	7e−02	1 / 39	VAQUERIZAS_Testis_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	0.008	16 / 4735	ICGC_Pu1_targets
2	0.019	7 / 1501	ICGC_Usf1_targets
3	0.048	13 / 4362	ICGC_Creb1_targets
4	0.053	6 / 1478	ICGC_Myc_targets
5	0.056	13 / 4468	ICGC_Egr1_targets
6	0.062	15 / 5466	ICGC_Nficsc81335_targets
7	0.066	15 / 5518	ICGC_Stat5_targets
8	0.087	7 / 2087	ICGC_Cebpbsc150_targets
9	0.104	10 / 3507	ICGC_Rad21_targets
10	0.126	13 / 5067	ICGC_Taf1_targets
11	0.142	5 / 1498	ICGC_Ets1_targets
12	0.155	17 / 7247	ICGC_Runx3_targets
13	0.159	15 / 6267	ICGC_Yy1_targets
14	0.165	13 / 5312	ICGC_Tcf12_targets
15	0.168	15 / 6322	ICGC_Tcf3_targets

Overexpression Spots

Spot Summary: B

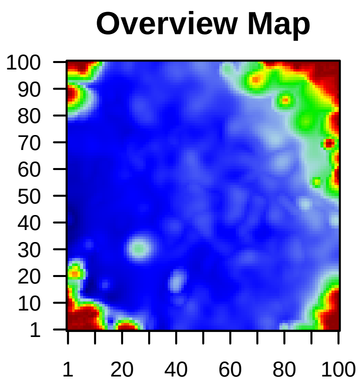
metagenes = 56
genes = 1062

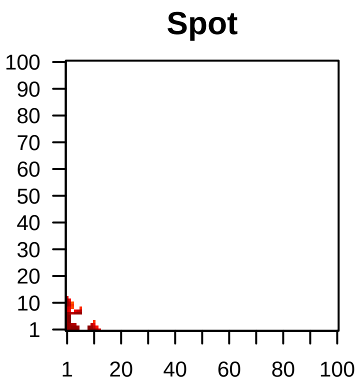
<r> metagenes = 0.74

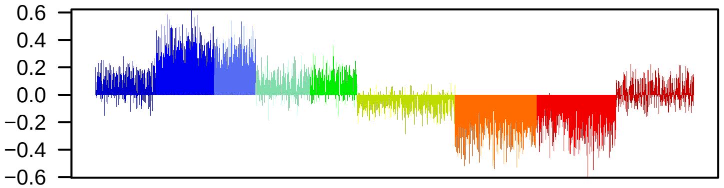
beta: r2= 163.13 / log p= −Inf

samples with spot = 858 (25.3 %)

- A * : 108 (31.4 %)
- A C * : 323 (98.5 %)
- A C F * : 227 (96.6 %)
- A F * : 74 (24 %)
- C F * : 88 (33.2 %)
- N * : 38 (8.6 %)





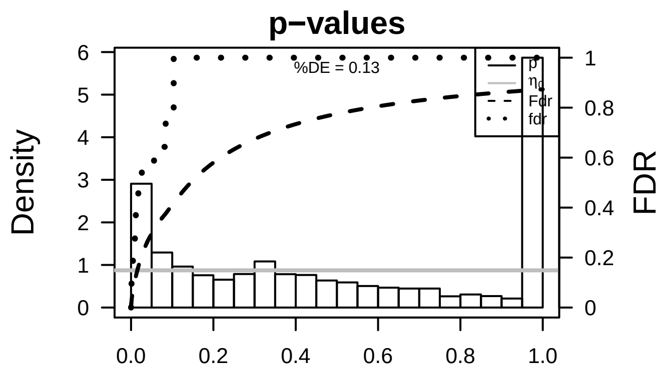


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178314	4.32	−2.71	0.13		
2	ILMN_175553	3.25	−1.79	0.2	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H(
3	ILMN_169326	3.22	−2.11	0.44		
4	ILMN_167935	3.21	−3.04	0.41	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
5	ILMN_177651	3.13	−1.1	0.35	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
6	ILMN_219321	3.07	−2.61	0.4	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
7	ILMN_216528	3.02	−1.93	0.4	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
8	ILMN_172566	2.96	−2.08	0.4	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
9	ILMN_170832	2.82	−1.91	0.69	ALAS2	5'−aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:H(
10	ILMN_165243	2.79	−1.83	0.6	CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:136
11	ILMN_323841	2.6	−1.51	0.09	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
12	ILMN_174983	2.5	−1.99	0.45	SMIM1	small integral membrane protein 1 (Vel blood group) [Source:
13	ILMN_176616	2.48	−2.2	0.61	SNCA	synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138]
14	ILMN_171345	2.47	−1.33	0.34	HBZ	hemoglobin subunit zeta [Source:HGNC Symbol;Acc:HGNC:4
15	ILMN_328576	2.47	−2.05	0.7	SLC4A1	solute carrier family 4 member 1 (Diego blood group) [Source
16	ILMN_169651	2.44	−2.23	0.8	AHSP	alpha hemoglobin stabilizing protein [Source:HGNC Symbol;A
17	ILMN_169222	2.41	−1.48	0.53		
18	ILMN_173571	2.39	−1.48	0.51	KRT1	keratin 1 [Source:HGNC Symbol;Acc:HGNC:6412]
19	ILMN_168065	2.38	−1.7	0.75	SELENBP1	selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC
20	ILMN_169319	2.29	−2.04	0.53	PI3	peptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:8947

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−58	59 / 111	Refer	Chaussabel_2,3_Erythrocytes
2	4e−42	59 / 185	HM	HALLMARK_HEME_METABOLISM
3	4e−37	73 / 360	GSEA	LU_EZH2_TARGETS_DN
4	1e−27	42 / 150	Refer	Chaussabel_2,6_Myeloid lineage
5	5e−24	44 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
6	1e−20	46 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
7	9e−19	475 / 10999	Colon	TssWk_Colon
8	2e−18	427 / 9555	Colon	TssA_Colon
9	2e−18	41 / 240	Refer	Chaussabel_3,3_Inflammation II
10	2e−17	397 / 8771	Chror	5_Tx_Melanocytes
11	4e−17	510 / 12298	Chror	2_TssA_Melanocytes
12	5e−16	401 / 9054	Colon	Tx_Colon
13	9e−15	515 / 12741	Chror	7_Enh_Melanocytes
14	3e−14	473 / 11455	Chror	2_TssA_Fibroblasts
15	5e−14	335 / 7354	Colon	TssF_Colon
16	5e−14	64 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
17	7e−14	519 / 12983	Chror	2_TssA_Neuronal_Progenitor
18	1e−13	35 / 242	Refer	Chaussabel_3,2_Inflammation I
19	2e−13	448 / 10779	Colon	Enh_Colon
20	2e−13	55 / 554	Canc	Lembcke_Colonic Inflammation
21	2e−13	289 / 6138	Colon	TssD2_Colon
22	2e−13	27 / 147	Lifest	Homuth_BMI−associated−genes_UP
23	2e−13	374 / 8568	Colon	TxWk_Colon
24	3e−13	31 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
25	6e−13	376 / 8678	Colon	Quies3_Colon
26	1e−12	28 / 169	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
27	3e−12	10 / 15	Lifest	DUMEAUX_Red blood cells in non smokers literature genes up
28	4e−12	64 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
29	8e−12	12 / 26	GSEA	VALK_AML_CLUSTER_7
30	1e−11	79 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
31	1e−11	375 / 8818	MF	protein binding
32	2e−11	83 / 1169	Lympl	SPANG_BCR DN
33	3e−11	472 / 11836	Chror	3_TssF_Melanocytes
34	4e−11	326 / 7448	Lympl	HOPP_Strong_enhancer
35	7e−11	399 / 9635	Chror	3_TssF_Fibroblasts
36	7e−11	61 / 757	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
37	7e−11	251 / 5383	TF	ICGC_Sp1_targets
38	2e−10	249 / 5373	Colon	EnhWk1_Colon
39	2e−10	64 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
40	5e−10	269 / 5984	TF	ICGC_Mta3_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 58	TESCHENDORFF_age_hypermethylated
2	0.3	5 / 111	HORVATH_aging_genes meth DOWN
3	0.7	4 / 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	2e−08	33 / 335	innate immune response
2	5e−07	6 / 11	regulation of cytokine secretion
3	2e−06	29 / 336	inflammatory response
4	2e−05	5 / 12	oxygen transport
5	3e−05	9 / 50	response to ionizing radiation
6	3e−05	16 / 151	aging
7	4e−05	31 / 435	negative regulation of apoptotic process
8	6e−05	7 / 32	MyD88−dependent toll−like receptor signaling pathway
9	7e−05	34 / 511	apoptotic process
10	1e−04	13 / 117	autophagy
11	1e−04	5 / 16	innate immune response in mucosa
12	2e−04	9 / 64	negative regulation of cysteine−type endopeptidase activity involved in apoptc
13	3e−04	7 / 40	erythrocyte differentiation
14	4e−04	11 / 99	defense response to bacterium
15	4e−04	7 / 42	regulation of protein phosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	9e−10	389 / 9504	Overlap_fetal_midbrain_K9K27me3
2	1e−08	394 / 9815	Overlap_fetal_midbrain_ReprPC
3	6e−08	410 / 10430	Overlap_fetal_midbrain_Quies
4	3e−07	253 / 5936	Overlap_fetal_midbrain_HetRpts
5	3e−06	383 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	8e−06	145 / 3164	Mid_Frontal_Lobe_ZNF
7	6e−05	48 / 818	Mid_Frontal_Lobe_Het
8	3e−04	119 / 2709	Mid_Frontal_Lobe_HetRpts
9	8e−04	80 / 1728	Fetal_ReprPCWk
10	1e−03	42 / 796	Overlap_fetal_midbrain_ZNF
11	5e−03	54 / 1162	Fetal_Enh
12	2e−02	32 / 681	Overlap_fetal_midbrain_EnhP
13	4e−02	39 / 906	Fetal_HetRpts
14	5e−02	50 / 1213	Fetal_TssP
15	6e−02	70 / 1784	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	2e−13	55 / 554	Lembcke_Colonic Inflammation
2	6e−04	9 / 73	SHAUGHNESSY_MM high risk
3	1e−03	1 / 14	LIU_COMMON_CANCER_GENES
4	2e−03	20 / 301	SPANG_BCL6−index2
5	1e−02	12 / 178	SPANG_LPS−index2
6	6e−02	24 / 527	Lembcke_Normal vs Adenoma
7	6e−02	2 / 13	GENTLES_modul12
8	7e−02	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	8e−02	2 / 15	WANG_ER_UP
10	9e−02	0 / 15	LIU_PROSTATE_CANCER_DN
11	3e−01	3 / 54	KUIPER_MM poor survival
12	3e−01	4 / 82	PanCan_JAK−ST_geneset_nanostring
13	3e−01	1 / 13	LIU_LIVER_CANCER
14	3e−01	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	3e−01	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	5e−09	152 / 2979	cytosol
2	6e−06	7 / 23	cortical cytoskeleton
3	1e−05	162 / 3662	plasma membrane
4	6e−05	200 / 4822	cytoplasm
5	3e−04	4 / 11	endolysosome membrane
6	4e−04	8 / 56	autophagosome
7	5e−04	5 / 21	autophagosome membrane
8	9e−04	16 / 202	early endosome
9	1e−03	89 / 1979	membrane
10	1e−03	191 / 4828	nucleus
11	1e−03	7 / 51	phagocytic vesicle membrane
12	2e−03	60 / 1252	integral component of plasma membrane
13	2e−03	105 / 2464	extracellular exosome
14	3e−03	30 / 539	Golgi membrane
15	4e−03	52 / 1101	extracellular space

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	71 / 1467	Chr 19
2	4e−02	49 / 1170	Chr 7
3	6e−02	40 / 959	Chr 16
4	1e−01	51 / 1318	Chr 17
5	2e−01	84 / 2323	Chr 1
6	3e−01	20 / 536	Chr 22
7	3e−01	4 / 87	Chr Y
8	4e−01	27 / 768	Chr 14
9	4e−01	27 / 769	Chr 15
10	4e−01	31 / 904	Chr 10
11	5e−01	49 / 1492	Chr 2
12	5e−01	20 / 619	Chr 20
13	6e−01	26 / 836	Chr 8
14	7e−01	8 / 289	Chr 21
15	8e−01	34 / 1160	Chr 12

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−17	397 / 8771	5_Tx_Melanocytes
2	4e−17	510 / 12298	2_TssA_Melanocytes
3	9e−15	515 / 12741	7_Enh_Melanocytes
4	3e−14	473 / 11455	2_TssA_Fibroblasts
5	7e−14	519 / 12983	2_TssA_Neuronal_Progenitor
6	3e−11	472 / 11836	3_TssF_Melanocytes
7	7e−11	399 / 9635	3_TssF_Fibroblasts
8	6e−10	466 / 11847	7_Enh_Neuronal_Progenitor
9	7e−10	334 / 7854	5_Tx_Fibroblasts
10	1e−09	257 / 5699	6_EnhG_Melanocytes
11	5e−09	479 / 12393	15_Quies_Neuronal_Progenitor
12	2e−08	260 / 5956	3_TssF_Neuronal_Progenitor
13	8e−08	349 / 8613	7_Enh_Fibroblasts
14	1e−07	215 / 4795	6_EnhG_Fibroblasts
15	1e−07	292 / 6970	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−19	475 / 10999	TssWk_Colon
2	2e−18	427 / 9555	TssA_Colon
3	5e−16	401 / 9054	Tx_Colon
4	5e−14	335 / 7354	TssF_Colon
5	2e−13	448 / 10779	Enh_Colon
6	2e−13	289 / 6138	TssD2_Colon
7	2e−13	374 / 8568	TxWk_Colon
8	6e−13	376 / 8678	Quies3_Colon
9	2e−10	249 / 5373	EnhWk1_Colon
10	1e−09	149 / 2845	TxEnhG1_Colon
11	2e−08	58 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
12	5e−07	137 / 2810	EnhA_Colon
13	6e−07	39 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP
14	4e−06	72 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	5e−06	104 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_ti

Glio

Rank	p−value	#in/all	Geneset
1	2e−07	27 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	3e−04	4 / 11	WILLSCHER_GBM_LTSwt_proteomics−G_UP
3	9e−04	10 / 94	Weller_LGG_A_vs_O_UP
4	1e−03	10 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
5	3e−03	12 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	3e−03	2 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
7	4e−03	6 / 47	Donson−innate immunity−associated with LTS in HGA
8	4e−03	5 / 33	Shaw_responders_down_in_oligo_glioma
9	9e−03	3 / 14	Christensen_hypermethylated_in_ependymoma
10	1e−02	9 / 113	GIEZELT_GBM_WT_up_VS_mut
11	1e−02	5 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
12	2e−02	4 / 34	Shaw_down_in_1p19q
13	3e−02	17 / 315	Up
14	3e−02	9 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	3e−02	10 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−37	73 / 360	LU_EZH2_TARGETS_DN
2	5e−24	44 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
3	1e−20	46 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
4	5e−14	64 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
5	3e−13	31 / 196	MCLACHLAN_DENTAL_CARIES_UP
6	1e−12	28 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
7	4e−12	64 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
8	8e−12	12 / 26	VALK_AML_CLUSTER_7
9	1e−11	79 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
10	7e−11	61 / 757	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
11	2e−10	64 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
12	7e−10	40 / 410	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
13	9e−10	32 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
14	3e−09	10 / 25	VALK_AML_CLUSTER_8
15	3e−09	16 / 78	NEMETH_INFLAMMATORY_RESPONSE_LPS_UP

HM

Rank	p−value	#in/all	Geneset
1	4e−42	59 / 185	HALLMARK_HEME_METABOLISM
2	2e−09	25 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	2e−06	18 / 151	HALLMARK_APOPTOSIS
4	3e−06	20 / 187	HALLMARK_COMPLEMENT
5	1e−05	16 / 137	HALLMARK_UV_RESPONSE_UP
6	6e−05	17 / 176	HALLMARK_KRAS_SIGNALING_UP
7	2e−04	17 / 191	HALLMARK_INFLAMMATORY_RESPONSE
8	5e−04	16 / 189	HALLMARK_HYPOXIA
9	3e−03	14 / 185	HALLMARK_P53_PATHWAY
10	5e−03	6 / 50	HALLMARK_TGF_BETA_SIGNALING
11	8e−03	13 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	8e−03	13 / 186	HALLMARK_IL2_STAT5_SIGNALING
13	1e−02	5 / 41	HALLMARK_APICAL_SURFACE
14	2e−02	7 / 87	HALLMARK_PROTEIN_SECRETION
15	3e−02	11 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−13	27 / 147	Homuth_BMI−associated−genes_UP
2	3e−12	10 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	3e−08	25 / 211	Homuth_BMI−associated−genes_DN
4	2e−03	4 / 18	Huan_blood−pressure_SBP−signature
5	2e−02	3 / 17	DUMEAUX_High bmi enriched genes
6	9e−02	2 / 16	Huan_blood−pressure_DBP−signature
7	2e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	2e−01	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	2e−01	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	3e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
11	8e−01	2 / 94	DUMEAUX_Smoking enriched genes
12	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
13	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
14	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1e+00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−11	83 / 1169	SPANG_BCR DN
2	4e−11	326 / 7448	HOPP_Strong_enhancer
3	5e−08	30 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−(
4	8e−08	30 / 306	WIRTH_lymphoma937_spot E
5	3e−07	233 / 5356	HOPP_Txn_transition
6	5e−07	30 / 331	WIRTH_lymphoma937_spot H
7	5e−07	331 / 8226	HOPP_Active_promoter
8	1e−06	296 / 7275	HOPP_Txn_elongation
9	2e−06	28 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−(
10	3e−05	315 / 8098	HOPP_Weak_promoter
11	2e−03	7 / 57	Monti_Host_response_cluster
12	3e−03	261 / 6959	HOPP_Weak_enhancer
13	3e−03	27 / 464	WIRTH_lymphoma937_spot I
14	4e−03	24 / 408	TARTE_Mature plasma cell signature
15	4e−03	4 / 21	ROSOLOWSKI_red UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	3 / 54	Hugo_melanoma−all−MET_DN
2	0.6	1 / 30	Hugo_melanoma−all−MET_UP
3	0.8	1 / 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	

MF

Rank	p−value	#in/all	Geneset
1	1e−11	375 / 8818	protein binding
2	2e−07	22 / 188	receptor activity
3	6e−06	26 / 301	ubiquitin−protein transferase activity
4	1e−05	5 / 11	oxygen transporter activity
5	3e−04	4 / 11	diacylglycerol binding
6	5e−04	9 / 72	single−stranded DNA binding
7	3e−03	32 / 580	identical protein binding
8	3e−03	4 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
9	3e−03	20 / 311	enzyme binding
10	3e−03	3 / 10	RAGE receptor binding
11	4e−03	4 / 20	endodeoxyribonuclease activity
12	4e−03	16 / 232	ligase activity
13	4e−03	17 / 256	ubiquitin protein ligase binding
14	5e−03	5 / 35	beta−tubulin binding
15	6e−03	3 / 12	lyase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 17	Thyroid carcinoma, follicular
2	0.4	1 / 18	Hodgkin lymphoma
3	0.6	1 / 29	Myelofibrosis, idiopathic
4	0.8	1 / 47	Cervical cancer, somatic
5	0.8	1 / 48	Gastric cancer
6	0.8	1 / 57	Cardiomyopathy, dilated
7	0.9	1 / 65	Hepatocellular carcinoma
8	0.9	1 / 68	Glioblastoma multiforme, somatic
9	0.9	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

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−06	37 / 491	hsa−miR−107
2	4e−06	35 / 467	hsa−miR−195
3	5e−06	36 / 489	hsa−miR−16
4	6e−06	36 / 493	hsa−miR−103
5	1e−04	23 / 294	hsa−miR−503
6	1e−04	29 / 419	hsa−miR−497
7	1e−04	30 / 441	hsa−miR−424
8	2e−04	33 / 516	hsa−miR−15a
9	3e−04	16 / 180	hsa−miR−1283
10	5e−04	30 / 480	hsa−miR−15b
11	7e−04	16 / 196	hsa−miR−206
12	1e−03	8 / 67	hsa−miR−873
13	3e−03	7 / 58	hsa−miR−187
14	3e−03	19 / 289	hsa−miR−202
15	3e−03	8 / 76	hsa−miR−592

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	2 / 15	GUSTAFSON_PI3K_DN
2	0.30	1 / 11	BENTINK_ras.4
3	0.33	1 / 12	BENTINK_ras.1
4	0.35	1 / 13	BENTINK_src.10
5	0.37	1 / 14	BENTINK_ras.6
6	1.00	0 / 14	GUSTAFSON_PI3K_UP
7	1.00	0 / 13	BENTINK_e2f3.1
8	1.00	0 / 13	BENTINK_e2f3.2
9	1.00	0 / 13	BENTINK_myc.1
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	5e−58	59 / 111	Chaussabel_2,3_Erythrocytes
2	1e−27	42 / 150	Chaussabel_2,6_Myeloid lineage
3	2e−18	41 / 240	Chaussabel_3,3_Inflammation II
4	1e−13	35 / 242	Chaussabel_3,2_Inflammation I
5	8e−10	11 / 29	JONGENEEL_Bone Marrow
6	3e−08	11 / 39	Chaussabel_2,2_Neutrophils
7	1e−05	5 / 11	WIRTH_Prim. lymphoid organs
8	2e−05	14 / 113	Chaussabel_1,5_Myeloid lineage
9	4e−05	5 / 13	WIRTH_Bone marrow
10	1e−03	38 / 695	PROTEINATLAS_bone marrow
11	2e−03	5 / 29	Chaussabel_2,7_Unknown function
12	3e−03	4 / 19	VAQUERIZAS_Bone marrow_TF
13	2e−02	22 / 412	WIRTH_Immune system
14	2e−02	3 / 17	JONGENEEL_Lung
15	6e−02	2 / 12	Chaussabel_3,5_Hemoglobin genes

Telomeres

Rank	p−value	#in/all	Geneset
1	0.06	3 / 27	Nabetani_alt len telomeres_genes_ko
2	0.35	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	

TF

Rank	p−value	#in/all	Geneset
1	7e−11	251 / 5383	ICGC_Sp1_targets
2	5e−10	269 / 5984	ICGC_Mta3_targets
3	1e−09	312 / 7247	ICGC_Runx3_targets
4	2e−09	238 / 5188	ICGC_Ebfsc137065_targets
5	2e−09	297 / 6868	ICGC_Elf1_targets
6	9e−09	284 / 6578	ICGC_Pou2_targets
7	1e−08	246 / 5518	ICGC_Stat5_targets
8	1e−08	272 / 6267	ICGC_Yy1_targets
9	2e−08	202 / 4362	ICGC_Creb1_targets
10	3e−08	240 / 5410	ICGC_Foxm1_targets
11	4e−08	280 / 6552	ICGC_Pol2_targets
12	4e−08	241 / 5466	ICGC_Nficsc81335_targets
13	5e−08	240 / 5442	ICGC_Pmlsc71910_targets
14	6e−08	219 / 4881	ICGC_Atf2_targets
15	1e−07	212 / 4735	ICGC_Pu1_targets

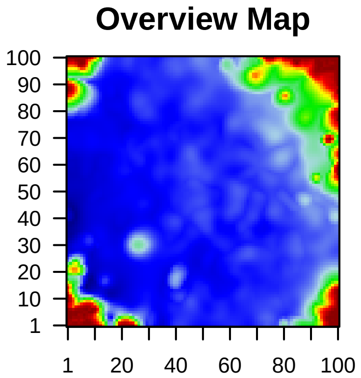
Overexpression Spots

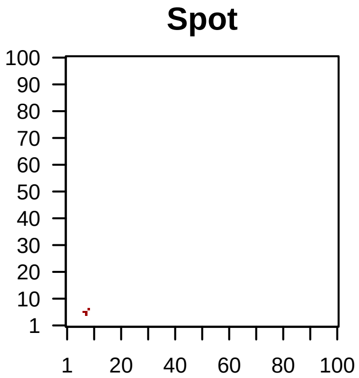
Spot Summary: C

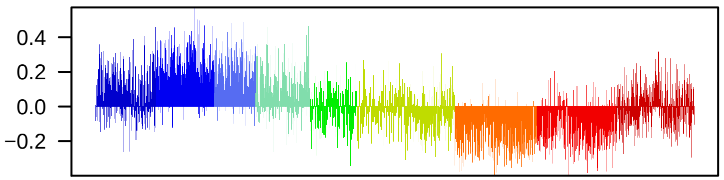
metagenes = 4
genes = 67

<r> metagenes = 0.99
<r> genes = 0.54
beta: r2= 59.61 / log p= −Inf

samples with spot = 648 (19.1 %)
- A * : 108 (31.4 %)
- A C * : 219 (66.8 %)
- A C F * : 131 (55.7 %)
- A F * : 95 (30.8 %)
- C F * : 24 (9.1 %)
- F * : 23 (4.1 %)
- F J * : 2 (0.4 %)
- J * : 5 (1.1 %)
- N * : 41 (9.3 %)





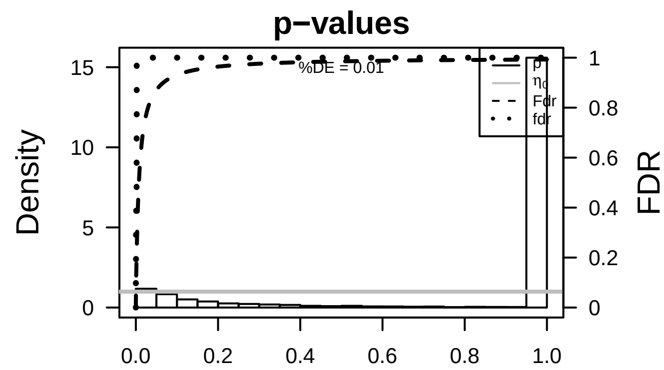


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_233613	1.01	−0.87	0.45	SULT1A2	sulfotransferase family 1A member 2 [Source:HGNC Symbol;
2	ILMN_171149	0.99	−0.72	0.83		
3	ILMN_167030	0.95	−0.79	0.77	HK3	hexokinase 3 [Source:HGNC Symbol;Acc:HGNC:4925]
4	ILMN_169524	0.94	−0.63	0.64	KLHDC8B	kelch domain containing 8B [Source:HGNC Symbol;Acc:HGN
5	ILMN_169365	0.92	−0.77	0.82	FES	FES proto−oncogene, tyrosine kinase [Source:HGNC Symbo
6	ILMN_165690	0.91	−0.82	0.57		
7	ILMN_174191	0.88	−0.86	0.7	OSCAR	osteoclast associated, immunoglobulin−like receptor [Source:
8	ILMN_219359	0.87	−0.65	0.69	UNC93B1	unc−93 homolog B1 (C. elegans) [Source:HGNC Symbol;Acc
9	ILMN_234965	0.86	−0.92	0.63	TSPO	translocator protein [Source:HGNC Symbol;Acc:HGNC:1158]
10	ILMN_166538	0.83	−0.84	0.71	SH3BP5L	SH3 binding domain protein 5 like [Source:HGNC Symbol;Ac
11	ILMN_174725	0.8	−0.6	0.88	LTB4R	leukotriene B4 receptor [Source:HGNC Symbol;Acc:HGNC:6
12	ILMN_181296	0.79	−0.53	0.79	CNPY3	canopy FGF signaling regulator 3 [Source:HGNC Symbol;Acc
13	ILMN_208231	0.79	−0.91	0.81	TOM1	target of myb1 membrane trafficking protein [Source:HGNC S
14	ILMN_166774	0.78	−0.66	0.73	ANKRD33	ankyrin repeat domain 33 [Source:HGNC Symbol;Acc:HGNC
15	ILMN_205953	0.77	−0.75	0.71	PPM1F	protein phosphatase, Mg2+/Mn2+ dependent 1F [Source:HG
16	ILMN_168996	0.76	−0.66	0.83	PLEKHO2	pleckstrin homology domain containing O2 [Source:HGNC Sy
17	ILMN_180327	0.75	−0.77	0.75	MVP	major vault protein [Source:HGNC Symbol;Acc:HGNC:7531]
18	ILMN_180104	0.75	−0.8	0.62	GSN	Gelsolin [Source:UniProtKB/Swiss−Prot;Acc:P06396]
19	ILMN_178274	0.74	−0.59	0.74	CD300LB	CD300 molecule like family member b [Source:HGNC Symbo
20	ILMN_175852	0.73	−0.56	0.69	P2RX1	purinergic receptor P2X 1 [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−15	33 / 2845	Colon	TxEnhG1_Colon
2	4e−13	30 / 2810	Colon	EnhA_Colon
3	9e−13	42 / 6138	Colon	TssD2_Colon
4	2e−11	44 / 7354	Colon	TssF_Colon
5	2e−11	52 / 10779	Colon	Enh_Colon
6	5e−10	36 / 5373	Colon	EnhWk1_Colon
7	5e−10	29 / 3450	Chror	4_TxTrans_Fibroblasts
8	5e−10	34 / 4795	Chror	6_EnhG_Fibroblasts
9	1e−08	21 / 2028	Chror	4_TxTrans_Melanocytes
10	1e−08	35 / 5699	Chror	6_EnhG_Melanocytes
11	3e−08	44 / 9054	Colon	Tx_Colon
12	6e−08	45 / 9635	Chror	3_TssF_Fibroblasts
13	9e−08	42 / 8568	Colon	TxWk_Colon
14	2e−07	8 / 240	Refer	Chaussabel_3,3_Inflammation II
15	2e−07	44 / 9555	Colon	TssA_Colon
16	3e−07	38 / 7448	Lymp	HOPP_Strong_enhancer
17	5e−07	16 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
18	7e−07	33 / 5956	Chror	3_TssF_Neuronal_Progenitor
19	1e−06	48 / 11836	Chror	3_TssF_Melanocytes
20	3e−06	44 / 10430	Brain	Overlap_fetal_midbrain_Quies
21	4e−06	11 / 789	Colon	TxEnhG2_Colon
22	5e−06	22 / 3164	Brain	Mid_Frontal_Lobe_ZNF
23	5e−06	15 / 1535	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
24	7e−06	11 / 831	GSEA	LOPEZ_MBD_TARGETS
25	1e−05	5 / 112	GSEA	SCHLOSSER_SERUM_RESPONSE_UP
26	1e−05	6 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
27	2e−05	36 / 7854	Chror	5_Tx_Fibroblasts
28	3e−05	7 / 346	GSEA	MULLIGHAN_MLL_SIGNATURE_1_UP
29	3e−05	4 / 68	GSEA	ROSS_AML_WITH_MLL_FUSIONS
30	4e−05	5 / 150	Refer	Chaussabel_2,6_Myeloid lineage
31	4e−05	5 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
32	5e−05	7 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
33	7e−05	6 / 277	GSEA	LI_INDUCED_T_TO_NATURAL_KILLER_UP
34	8e−05	7 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
35	9e−05	37 / 8771	Chror	5_Tx_Melanocytes
36	1e−04	37 / 8818	MF	protein binding
37	2e−04	3 / 41	HM	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
38	2e−04	5 / 208	CC	actin cytoskeleton
39	2e−04	36 / 8678	Colon	Quies3_Colon
40	2e−04	4 / 113	Refer	Chaussabel_1,5_Myeloid lineage



Aging

Rank	p−value	#in/all	Geneset
1	0.03	2 / 111	HORVATH_aging_genes meth DOWN
2	1.00	0 / 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	

BP

Rank	p−value	#in/all	Geneset
1	3e−04	2 / 11	negative regulation of protein tyrosine kinase activity
2	4e−04	2 / 12	barbed−end actin filament capping
3	7e−04	2 / 16	face development
4	8e−04	3 / 72	positive regulation of cell growth
5	9e−04	9 / 1003	signal transduction
6	2e−03	3 / 93	ion transport
7	2e−03	2 / 25	regulation of sensory perception of pain
8	2e−03	2 / 27	phagosome acidification
9	2e−03	2 / 29	toll−like receptor signaling pathway
10	3e−03	2 / 31	ATP hydrolysis coupled proton transport
11	3e−03	2 / 33	transferrin transport
12	3e−03	2 / 34	steroid metabolic process
13	4e−03	2 / 36	negative regulation of tumor necrosis factor production
14	4e−03	2 / 37	response to progesterone
15	4e−03	2 / 39	peptidyl−tyrosine autophosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	3e−06	44 / 10430	Overlap_fetal_midbrain_Quies
2	5e−06	22 / 3164	Mid_Frontal_Lobe_ZNF
3	3e−04	17 / 2709	Mid_Frontal_Lobe_HetRpts
4	6e−04	37 / 9504	Overlap_fetal_midbrain_K9K27me3
5	8e−04	21 / 4112	Mid_Frontal_Lobe_ReprPC
6	6e−03	12 / 2127	Mid_Frontal_Lobe_K9K27me3
7	7e−03	35 / 9917	Overlap_fetal_midbrain_ReprPCWk
8	1e−02	10 / 1784	Mid_Frontal_Lobe_ReprPCWk
9	2e−02	6 / 818	Mid_Frontal_Lobe_Het
10	5e−02	3 / 328	Fetal_Het
11	6e−02	21 / 5936	Overlap_fetal_midbrain_HetRpts
12	8e−02	11 / 2700	Fetal_TxTrans
13	8e−02	12 / 3046	Fetal_TssA
14	1e−01	10 / 2630	Fetal_TssF
15	1e−01	4 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 14	LIU_COMMON_CANCER_GENES
2	0.03	1 / 14	GENTLES_modul10
3	0.04	1 / 15	WANG_ER_UP
4	0.04	3 / 301	SPANG_BCL6−index2
5	0.11	1 / 46	PanCan_TGF−B_geneset_nanostring
6	0.15	3 / 527	Lembcke_Normal vs Adenoma
7	0.17	1 / 73	SHAUGHNESSY_MM high risk
8	0.20	0 / 14	LIU_PROSTATE_CANCER_UP
9	0.29	1 / 136	PanCan_RAS_geneset_nanostring
10	0.32	1 / 150	PanCan_MAPK_geneset_nanostring
11	0.39	1 / 193	PanCan_PI3K_geneset_nanostring
12	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
13	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
14	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 208	actin cytoskeleton
2	3e−04	6 / 352	focal adhesion
3	3e−04	16 / 2464	extracellular exosome
4	3e−04	2 / 11	vacuolar proton−transporting V−type ATPase complex
5	3e−04	14 / 1979	membrane
6	5e−04	7 / 561	intracellular membrane−bounded organelle
7	6e−04	7 / 571	perinuclear region of cytoplasm
8	1e−03	23 / 4822	cytoplasm
9	2e−03	16 / 2979	cytosol
10	4e−03	7 / 788	endoplasmic reticulum membrane
11	4e−03	5 / 422	protein complex
12	5e−03	3 / 133	microtubule organizing center
13	5e−03	4 / 273	neuron projection
14	7e−03	2 / 51	phagocytic vesicle membrane
15	8e−03	17 / 3662	plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	7 / 959	Chr 16
2	0.05	4 / 536	Chr 22
3	0.15	6 / 1411	Chr 11
4	0.17	6 / 1467	Chr 19
5	0.24	5 / 1318	Chr 17
6	0.31	3 / 769	Chr 15
7	0.52	1 / 289	Chr 21
8	0.55	6 / 2323	Chr 1
9	0.58	3 / 1170	Chr 7
10	0.59	2 / 768	Chr 14
11	0.60	3 / 1211	Chr 6
12	0.72	2 / 994	Chr X
13	0.76	2 / 1060	Chr 5
14	0.80	1 / 619	Chr 20
15	0.80	2 / 1160	Chr 12

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−10	29 / 3450	4_TxTrans_Fibroblasts
2	5e−10	34 / 4795	6_EnhG_Fibroblasts
3	1e−08	21 / 2028	4_TxTrans_Melanocytes
4	1e−08	35 / 5699	6_EnhG_Melanocytes
5	6e−08	45 / 9635	3_TssF_Fibroblasts
6	7e−07	33 / 5956	3_TssF_Neuronal_Progenitor
7	1e−06	48 / 11836	3_TssF_Melanocytes
8	2e−05	36 / 7854	5_Tx_Fibroblasts
9	9e−05	37 / 8771	5_Tx_Melanocytes
10	5e−04	43 / 11847	7_Enh_Neuronal_Progenitor
11	5e−04	45 / 12741	7_Enh_Melanocytes
12	1e−03	43 / 12298	2_TssA_Melanocytes
13	2e−03	29 / 6970	5_Tx_Neuronal_Progenitor
14	2e−03	43 / 12393	15_Quies_Neuronal_Progenitor
15	3e−03	40 / 11455	2_TssA_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−15	33 / 2845	TxEnhG1_Colon
2	4e−13	30 / 2810	EnhA_Colon
3	9e−13	42 / 6138	TssD2_Colon
4	2e−11	44 / 7354	TssF_Colon
5	2e−11	52 / 10779	Enh_Colon
6	5e−10	36 / 5373	EnhWk1_Colon
7	3e−08	44 / 9054	Tx_Colon
8	9e−08	42 / 8568	TxWk_Colon
9	2e−07	44 / 9555	TssA_Colon
10	5e−07	16 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	4e−06	11 / 789	TxEnhG2_Colon
12	2e−04	36 / 8678	Quies3_Colon
13	1e−03	6 / 489	K9acLow_Colon
14	6e−03	38 / 10999	TssWk_Colon
15	1e−02	11 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t

Glio

Rank	p−value	#in/all	Geneset
1	0.008	2 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
2	0.022	4 / 419	Down_a
3	0.023	1 / 9	Shaw_up_in_1p19qdel
4	0.023	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
5	0.025	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
6	0.035	2 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
7	0.037	1 / 15	VERHAAK_MES subtype
8	0.040	1 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
9	0.078	1 / 32	Donson−Misc immune function−associated with LTS in HGA
10	0.127	3 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
11	0.137	1 / 58	OPC
12	0.139	1 / 59	Christensen_hypermethylated_in_primary_glioblastoma
13	0.155	4 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
14	0.159	1 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
15	0.191	2 / 315	Up

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−06	15 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
2	7e−06	11 / 831	LOPEZ_MBD_TARGETS
3	1e−05	5 / 112	SCHLOSSER_SERUM_RESPONSE_UP
4	1e−05	6 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
5	3e−05	7 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
6	3e−05	4 / 68	ROSS_AML_WITH_MLL_FUSIONS
7	4e−05	5 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
8	5e−05	7 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
9	7e−05	6 / 277	LI_INDUCED_T_TO_NATURAL_KILLER_UP
10	8e−05	7 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
11	3e−04	6 / 355	BERENJENO_TRANSFORMED_BY_RHOA_DN
12	3e−04	7 / 505	WEST_ADRENOCORTICAL_TUMOR_DN
13	3e−04	4 / 129	HUANG_GATA2_TARGETS_UP
14	3e−04	2 / 11	REACTOME_TRAFFICKING_AND_PROCESSING_OF_ENDOSOMAL_TLR
15	4e−04	10 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	1e−03	4 / 177	HALLMARK_MITOTIC_SPINDLE
3	1e−03	4 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	7e−03	3 / 151	HALLMARK_APOPTOSIS
5	1e−02	3 / 183	HALLMARK_GLYCOLYSIS
6	2e−02	2 / 91	HALLMARK_PEROXISOME
7	4e−02	2 / 127	HALLMARK_COAGULATION
8	8e−02	2 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
9	8e−02	2 / 186	HALLMARK_MYOGENESIS
10	8e−02	2 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
11	1e−01	1 / 54	HALLMARK_MYC_TARGETS_V2
12	2e−01	1 / 91	HALLMARK_ANDROGEN_RESPONSE
13	2e−01	1 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	4e−01	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	4e−01	1 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 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	3e−07	38 / 7448	HOPP_Strong_enhancer
2	7e−04	2 / 15	Subero_B−ALL_hypo_meth
3	2e−03	24 / 5356	HOPP_Txn_transition
4	3e−03	2 / 33	Subero_T−PLL_hypo_meth
5	7e−03	28 / 7275	HOPP_Txn_elongation
6	9e−03	4 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
7	1e−02	4 / 331	WIRTH_lymphoma937_spot H
8	2e−02	29 / 8226	HOPP_Active_promoter
9	2e−02	1 / 9	Shaknovich_ABC_hypo_meth
10	4e−02	3 / 283	TARTE_Plasmablast signature
11	4e−02	3 / 286	ZHANG_DLBCL mutated
12	5e−02	1 / 21	Subero_MCL_hypo_meth
13	8e−02	6 / 1169	SPANG_BCR DN
14	9e−02	3 / 408	TARTE_Mature plasma cell signature
15	1e−01	1 / 45	Subero_INT_hypo_meth

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	1e−04	37 / 8818	protein binding
2	3e−04	2 / 10	glucose binding
3	5e−03	4 / 274	transcription factor binding
4	7e−03	2 / 50	steroid hormone receptor activity
5	8e−03	4 / 315	protein serine/threonine kinase activity
6	1e−02	2 / 68	drug binding
7	2e−02	3 / 204	protein domain specific binding
8	2e−02	2 / 75	kinase activity
9	2e−02	3 / 217	protein kinase activity
10	2e−02	8 / 1329	ATP binding
11	2e−02	5 / 646	protein homodimerization activity
12	2e−02	3 / 243	GTPase activator activity
13	3e−02	1 / 10	dipeptidyl−peptidase activity
14	3e−02	1 / 10	lipid phosphatase activity
15	3e−02	1 / 10	regulatory region DNA 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	0.01	2 / 71	hsa−miR−939
2	0.05	2 / 133	hsa−miR−218
3	0.05	1 / 21	hsa−miR−323−5p
4	0.05	1 / 21	hsa−miR−1282
5	0.05	2 / 146	hsa−miR−138
6	0.06	1 / 23	hsa−miR−151−5p
7	0.06	1 / 24	hsa−miR−602
8	0.06	1 / 24	hsa−miR−24−1*
9	0.06	1 / 25	hsa−miR−943
10	0.07	1 / 27	hsa−miR−558
11	0.07	2 / 166	hsa−miR−323b−5p
12	0.10	1 / 42	hsa−miR−885−3p
13	0.12	1 / 48	hsa−miR−329
14	0.12	1 / 52	hsa−miR−571
15	0.12	1 / 52	hsa−miR−362−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	1 / 11	BENTINK_ras.4
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 / 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	2e−07	8 / 240	Chaussabel_3,3_Inflammation II
2	4e−05	5 / 150	Chaussabel_2,6_Myeloid lineage
3	2e−04	4 / 113	Chaussabel_1,5_Myeloid lineage
4	1e−02	2 / 66	VAQUERIZAS_Whole blood_TF
5	3e−02	1 / 13	WIRTH_Bone marrow
6	4e−02	7 / 1268	PROTEINATLAS_colon
7	4e−02	1 / 17	VAQUERIZAS_Heart_TF
8	5e−02	4 / 535	PROTEINATLAS_spleen
9	7e−02	6 / 1138	PROTEINATLAS_small intestine
10	7e−02	4 / 619	PROTEINATLAS_salivary gland
11	1e−01	1 / 50	WIRTH_Placenta
12	1e−01	2 / 242	Chaussabel_3,2_Inflammation I
13	2e−01	4 / 960	PROTEINATLAS_cerebellum
14	2e−01	4 / 963	PROTEINATLAS_pancreas
15	2e−01	3 / 681	PROTEINATLAS_lung

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	0.04	5 / 733	ICGC_Atf3_targets
2	0.07	8 / 1723	HEBENSTREIT_high expression TF
3	0.08	7 / 1501	ICGC_Usf1_targets
4	0.09	22 / 6578	ICGC_Pou2_targets
5	0.09	16 / 4468	ICGC_Egr1_targets
6	0.09	6 / 1231	KIM_MYC targets
7	0.10	10 / 2497	ICGC_Bcl11_targets
8	0.10	13 / 3507	ICGC_Rad21_targets
9	0.13	17 / 5067	ICGC_Taf1_targets
10	0.13	16 / 4735	ICGC_Pu1_targets
11	0.13	12 / 3348	ICGC_BatfPcr1_targets
12	0.14	10 / 2704	ICGC_Pbx3_targets
13	0.14	18 / 5518	ICGC_Stat5_targets
14	0.19	22 / 7247	ICGC_Runx3_targets
15	0.21	14 / 4362	ICGC_Creb1_targets

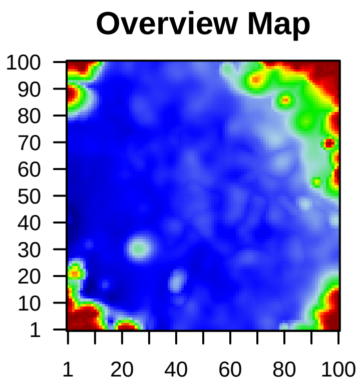
Overexpression Spots

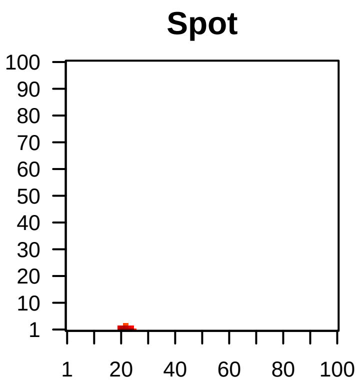
Spot Summary: D

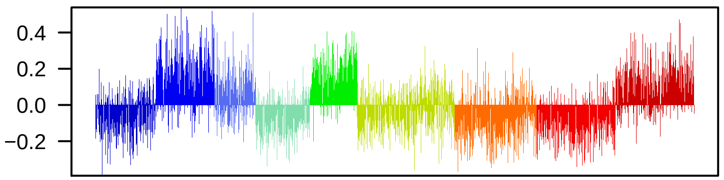
metagenes = 15
genes = 235

<r> metagenes = 0.94
<r> genes = 0.34
beta: r2= 34.79 / log p= −Inf

samples with spot = 569 (16.8 %)
A * : 10 (2.9 %)
A C * : 162 (49.4 %)
A C F * : 62 (26.4 %)
A F * : 3 (1 %)
C F * : 137 (51.7 %)
F * : 29 (5.2 %)
F J * : 15 (3.2 %)
J * : 3 (0.7 %)
N * : 148 (33.4 %)





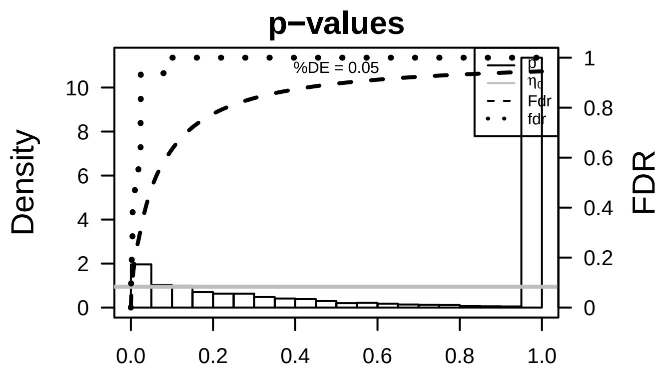


Spot Genelist

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:44
5	ILMN_176728	1.52	−1.63	0.79		
6	ILMN_171896	1.46	−0.99	0.65	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;A
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	0.63	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:HC
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	2e−79	50 / 102	Refer	Chaussabel_1,2_Platelets
2	1e−46	30 / 64	GSEA	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
3	6e−35	33 / 188	GSEA	WIERENGA_STAT5A_TARGETS_DN
4	1e−14	18 / 185	HM	HALLMARK_HEME_METABOLISM
5	2e−12	23 / 451	GSEA	PILON_KLF1_TARGETS_UP
6	2e−11	70 / 4018	Colon	EnhWk2_Colon
7	8e−11	10 / 64	GSEA	ROSS_AML_OF_FAB_M7_TYPE
8	2e−10	13 / 147	Lifest	Homuth_BMI−associated−genes_UP
9	4e−10	34 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	6e−10	13 / 162	GSEA	JISON_SICKLE_CELL_DISEASE_UP
11	9e−10	8 / 40	GSEA	GNATENKO_PLATELET_SIGNATURE
12	1e−09	19 / 414	GSEA	REACTOME_HEMOSTASIS
13	1e−09	11 / 111	Refer	Chaussabel_2,3_Erythrocytes
14	2e−09	13 / 181	GSEA	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATIO
15	3e−09	7 / 30	GSEA	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
16	4e−09	15 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
17	9e−09	31 / 1216	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
18	9e−09	13 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
19	1e−08	124 / 10779	Colon	Enh_Colon
20	1e−08	17 / 387	GSEA	SWEET_LUNG_CANCER_KRAS_DN
21	2e−08	114 / 9635	Chror	3_TssF_Fibroblasts
22	3e−08	16 / 352	CC	focal adhesion
23	5e−08	137 / 12741	Chror	7_Enh_Melanocytes
24	1e−07	8 / 71	GSEA	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA
25	2e−07	69 / 4822	CC	cytoplasm
26	2e−07	9 / 106	BP	platelet activation
27	2e−07	103 / 8613	Chror	7_Enh_Fibroblasts
28	2e−07	18 / 520	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
29	4e−07	6 / 36	GSEA	LEIN_ASTROCYTE_MARKERS
30	4e−07	5 / 20	GSEA	REACTOME_SMOOTH_MUSCLE_CONTRACTION
31	5e−07	8 / 87	GSEA	HECKER_IFNB1_TARGETS
32	5e−07	121 / 10999	Colon	TssWk_Colon
33	5e−07	6 / 38	BP	platelet aggregation
34	5e−07	6 / 38	GSEA	CHUNG_BLISTER_CYTOTOXICITY_DN
35	6e−07	8 / 90	BP	platelet degranulation
36	6e−07	102 / 8678	Colon	Quies3_Colon
37	8e−07	131 / 12393	Chror	15_Quies_Neuronal_Progenitor
38	1e−06	4 / 11	GSEA	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGEN
39	2e−06	126 / 11836	Chror	3_TssF_Melanocytes
40	2e−06	16 / 482	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.002	5 / 111	HORVATH_aging_genes meth DOWN
2	0.680	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−07	9 / 106	platelet activation
2	5e−07	6 / 38	platelet aggregation
3	6e−07	8 / 90	platelet degranulation
4	1e−05	9 / 171	blood coagulation
5	1e−05	4 / 18	blood coagulation, intrinsic pathway
6	1e−04	4 / 31	response to organonitrogen compound
7	3e−04	11 / 387	cell adhesion
8	6e−04	5 / 84	cell−matrix adhesion
9	1e−03	8 / 254	cell surface receptor signaling pathway
10	1e−03	5 / 102	muscle contraction
11	2e−03	3 / 31	lamellipodium assembly
12	2e−03	3 / 31	microtubule−based process
13	2e−03	5 / 115	leukocyte migration
14	3e−03	2 / 10	bleb assembly
15	3e−03	2 / 10	positive regulation of endothelial cell differentiation

Brain

Rank	p−value	#in/all	Geneset
1	8e−05	105 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	8e−05	109 / 10430	Overlap_fetal_midbrain_Quies
3	1e−03	99 / 9815	Overlap_fetal_midbrain_ReprPC
4	3e−03	39 / 3164	Mid_Frontal_Lobe_ZNF
5	8e−03	18 / 1213	Fetal_TssP
6	9e−03	92 / 9504	Overlap_fetal_midbrain_K9K27me3
7	1e−02	32 / 2700	Fetal_TxTrans
8	1e−02	61 / 5936	Overlap_fetal_midbrain_HetRpts
9	2e−02	31 / 2709	Mid_Frontal_Lobe_HetRpts
10	3e−02	14 / 1012	Mid_Frontal_Lobe_Enh
11	5e−02	6 / 328	Fetal_Het
12	5e−02	24 / 2127	Mid_Frontal_Lobe_K9K27me3
13	9e−02	14 / 1171	Fetal_EnhP
14	9e−02	31 / 3046	Fetal_TssA
15	1e−01	27 / 2630	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	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	5e−02	2 / 46	PanCan_TGF−B_geneset_nanostring
7	8e−02	8 / 554	Lembcke_Colonic Inflammation
8	1e−01	1 / 13	GENTLES_modul18
9	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
10	1e−01	1 / 14	GENTLES_modul4
11	1e−01	1 / 14	GENTLES_modul13
12	1e−01	2 / 82	PanCan_JAK−ST_geneset_nanostring
13	2e−01	3 / 178	SPANG_LPS−index2
14	3e−01	1 / 39	ZHANG_MM up
15	3e−01	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−08	16 / 352	focal adhesion
2	2e−07	69 / 4822	cytoplasm
3	4e−06	41 / 2464	extracellular exosome
4	3e−05	51 / 3662	plasma membrane
5	7e−05	11 / 330	cytoskeleton
6	1e−04	3 / 12	platelet alpha granule membrane
7	2e−04	3 / 14	platelet alpha granule
8	5e−04	4 / 47	stress fiber
9	6e−04	4 / 49	platelet alpha granule lumen
10	8e−04	3 / 23	cortical cytoskeleton
11	1e−03	4 / 56	autophagosome
12	1e−03	39 / 2979	cytosol
13	1e−03	6 / 149	lamellipodium
14	2e−03	3 / 31	heterotrimeric G−protein complex
15	4e−03	2 / 12	membrane−bounded vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.06	9 / 619	Chr 20
2	0.07	8 / 536	Chr 22
3	0.14	13 / 1160	Chr 12
4	0.14	5 / 342	Chr 18
5	0.30	14 / 1492	Chr 2
6	0.33	11 / 1170	Chr 7
7	0.35	9 / 954	Chr 9
8	0.39	20 / 2323	Chr 1
9	0.43	8 / 902	Chr 4
10	0.43	8 / 904	Chr 10
11	0.43	4 / 422	Chr 13
12	0.50	8 / 959	Chr 16
13	0.50	10 / 1211	Chr 6
14	0.51	10 / 1217	Chr 3
15	0.57	11 / 1411	Chr 11

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−08	114 / 9635	3_TssF_Fibroblasts
2	5e−08	137 / 12741	7_Enh_Melanocytes
3	2e−07	103 / 8613	7_Enh_Fibroblasts
4	8e−07	131 / 12393	15_Quies_Neuronal_Progenitor
5	2e−06	126 / 11836	3_TssF_Melanocytes
6	2e−06	134 / 12983	2_TssA_Neuronal_Progenitor
7	3e−06	125 / 11847	7_Enh_Neuronal_Progenitor
8	2e−05	98 / 8771	5_Tx_Melanocytes
9	3e−05	99 / 8990	15_Quies_Fibroblasts
10	6e−05	61 / 4795	6_EnhG_Fibroblasts
11	6e−05	115 / 11130	15_Quies_Melanocytes
12	7e−05	124 / 12298	2_TssA_Melanocytes
13	3e−04	115 / 11455	2_TssA_Fibroblasts
14	4e−04	66 / 5699	6_EnhG_Melanocytes
15	5e−04	11 / 416	4_TxTrans_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−11	70 / 4018	EnhWk2_Colon
2	9e−09	31 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	1e−08	124 / 10779	Enh_Colon
4	5e−07	121 / 10999	TssWk_Colon
5	6e−07	102 / 8678	Quies3_Colon
6	2e−05	68 / 5373	EnhWk1_Colon
7	2e−05	60 / 4526	Quies1_Colon
8	2e−05	104 / 9555	TssA_Colon
9	1e−04	27 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	1e−04	83 / 7354	TssF_Colon
11	1e−04	21 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	1e−04	72 / 6138	TssD2_Colon
13	2e−04	92 / 8568	TxWk_Colon
14	2e−04	96 / 9054	Tx_Colon
15	4e−04	3 / 19	Kosinski_top−crypt−short−list

Glio

Rank	p−value	#in/all	Geneset
1	3e−04	7 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
2	7e−03	4 / 94	Weller_LGG_A_vs_O_UP
3	3e−02	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
4	3e−02	2 / 34	Shaw_down_in_1p19q
5	4e−02	2 / 37	Christensen_hypomethylated_in_ependymoma
6	4e−02	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	4e−02	3 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	5e−02	3 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
9	6e−02	2 / 52	OL vs. OPC
10	7e−02	3 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	7e−02	2 / 55	Stuehler_Proteins_up_in_STS
12	8e−02	2 / 57	OL vs. MOG− OL
13	8e−02	1 / 11	VERHAAK_Brain
14	8e−02	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
15	9e−02	1 / 12	Mukasa_UP_in_Astroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−46	30 / 64	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
2	6e−35	33 / 188	WIERENGA_STAT5A_TARGETS_DN
3	2e−12	23 / 451	PILON_KLF1_TARGETS_UP
4	8e−11	10 / 64	ROSS_AML_OF_FAB_M7_TYPE
5	4e−10	34 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	6e−10	13 / 162	JISON_SICKLE_CELL_DISEASE_UP
7	9e−10	8 / 40	GNATENKO_PLATELET_SIGNATURE
8	1e−09	19 / 414	REACTOME_HEMOSTASIS
9	2e−09	13 / 181	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
10	3e−09	7 / 30	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
11	4e−09	15 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
12	9e−09	13 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
13	1e−08	17 / 387	SWEET_LUNG_CANCER_KRAS_DN
14	1e−07	8 / 71	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
15	2e−07	18 / 520	CHICAS_RB1_TARGETS_CONFLUENT

HM

Rank	p−value	#in/all	Geneset
1	1e−14	18 / 185	HALLMARK_HEME_METABOLISM
2	9e−05	6 / 91	HALLMARK_ANDROGEN_RESPONSE
3	5e−04	7 / 176	HALLMARK_ADIPOGENESIS
4	7e−04	7 / 186	HALLMARK_IL2_STAT5_SIGNALING
5	3e−03	6 / 176	HALLMARK_KRAS_SIGNALING_UP
6	4e−03	5 / 127	HALLMARK_COAGULATION
7	4e−03	6 / 183	HALLMARK_APICAL_JUNCTION
8	4e−03	6 / 186	HALLMARK_MYOGENESIS
9	4e−03	6 / 187	HALLMARK_COMPLEMENT
10	4e−03	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	4e−03	6 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	1e−02	5 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	1e−02	4 / 116	HALLMARK_SPERMATOGENESIS
14	2e−02	4 / 138	HALLMARK_FATTY_ACID_METABOLISM
15	3e−02	4 / 151	HALLMARK_APOPTOSIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−10	13 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−04	39 / 2701	HOPP_Repetitive
2	9e−04	39 / 2939	HOPP_Poised_promoter
3	2e−03	84 / 8098	HOPP_Weak_promoter
4	3e−03	5 / 121	SPANG_LPS 6hrs UP
5	3e−03	8 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−c
6	3e−03	8 / 306	WIRTH_lymphoma937_spot E
7	4e−03	2 / 12	WRIGHT_GCB UP
8	5e−03	8 / 331	WIRTH_lymphoma937_spot H
9	9e−03	75 / 7448	HOPP_Strong_enhancer
10	1e−02	67 / 6559	HOPP_Weak_txn
11	1e−02	17 / 1169	SPANG_BCR DN
12	1e−02	6 / 244	LENZ_Stromal signature 1
13	1e−02	7 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
14	2e−02	2 / 25	SPANG_BAFF 9hrs UP
15	2e−02	7 / 331	SPANG_CD40 6hrs 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	1e−05	99 / 8818	protein binding
2	6e−05	9 / 213	GTPase activity
3	5e−04	8 / 227	transcription coactivator activity
4	6e−04	3 / 21	G−protein beta/gamma−subunit complex binding
5	2e−03	9 / 351	GTP binding
6	3e−03	2 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
7	4e−03	3 / 39	androgen receptor binding
8	5e−03	3 / 42	manganese ion binding
9	5e−03	2 / 13	GABA receptor binding
10	5e−03	2 / 14	5'−nucleotidase activity
11	6e−03	4 / 91	structural constituent of cytoskeleton
12	7e−03	11 / 580	identical protein binding
13	8e−03	4 / 98	integrin binding
14	1e−02	3 / 57	collagen binding
15	1e−02	2 / 20	2 iron, 2 sulfur cluster 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	9e−06	7 / 92	hsa−miR−219−2−3p
2	1e−03	3 / 28	hsa−miR−519e*
3	2e−03	5 / 105	hsa−miR−605
4	2e−03	7 / 216	hsa−miR−548m
5	2e−03	5 / 113	hsa−miR−498
6	3e−03	4 / 76	hsa−miR−205
7	5e−03	4 / 85	hsa−miR−1265
8	6e−03	8 / 336	hsa−miR−142−5p
9	6e−03	5 / 146	hsa−miR−138
10	8e−03	4 / 97	hsa−miR−125a−3p
11	9e−03	7 / 289	hsa−miR−202
12	9e−03	4 / 101	hsa−miR−603
13	9e−03	3 / 54	hsa−miR−629
14	1e−02	3 / 55	hsa−miR−634
15	1e−02	4 / 114	hsa−miR−875−3p

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	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−79	50 / 102	Chaussabel_1,2_Platelets
2	1e−09	11 / 111	Chaussabel_2,3_Erythrocytes
3	3e−06	4 / 13	WIRTH_Sec. lymphoid organs
4	7e−05	14 / 514	PROTEINATLAS_vagina
5	9e−05	22 / 1118	PROTEINATLAS_placenta
6	2e−04	18 / 850	PROTEINATLAS_skin
7	3e−04	4 / 39	Chaussabel_2,2_Neutrophils
8	4e−04	3 / 19	VAQUERIZAS_Bone marrow_TF
9	5e−04	11 / 416	PROTEINATLAS_ovary
10	9e−04	19 / 1063	PROTEINATLAS_tonsil
11	1e−03	11 / 465	PROTEINATLAS_liver
12	1e−03	14 / 695	PROTEINATLAS_bone marrow
13	2e−03	13 / 640	PROTEINATLAS_parathyroid gland
14	2e−03	13 / 647	PROTEINATLAS_lateral ventricle
15	2e−03	20 / 1239	PROTEINATLAS_testis

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	0.02	1 / 2	MYC_ECM cell adhesion DOWN
2	0.02	54 / 5188	ICGC_Ebfsc137065_targets
3	0.03	21 / 1669	ICGC_P300_targets
4	0.04	1 / 5	MYC_TFs
5	0.04	48 / 4735	ICGC_Pu1_targets
6	0.04	64 / 6616	ICGC_Pax5_targets
7	0.07	57 / 5961	ICGC_Pol24_targets
8	0.07	1 / 9	MYC_Targets DOWN
9	0.08	67 / 7247	ICGC_Runx3_targets
10	0.08	23 / 2133	ICGC_Mef2_targets
11	0.09	19 / 1723	HEBENSTREIT_high expression TF
12	0.09	26 / 2497	ICGC_Bcl11_targets
13	0.12	55 / 5984	ICGC_Mta3_targets
14	0.13	27 / 2704	ICGC_Pbx3_targets
15	0.13	1 / 18	MYC_Metabolism UP

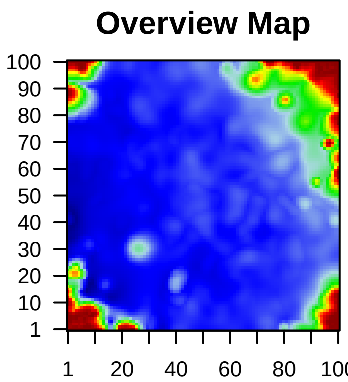
Overexpression Spots

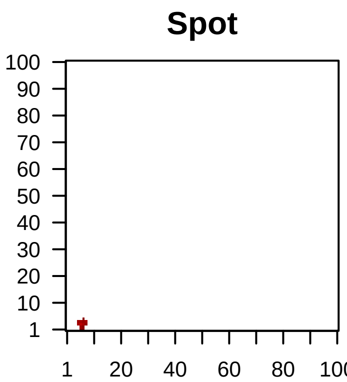
Spot Summary: E

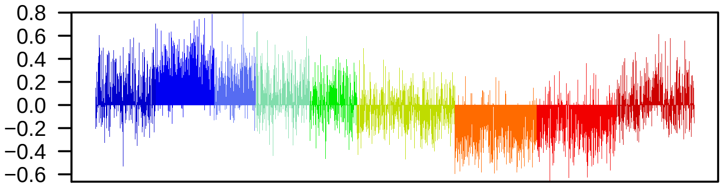
metagenes = 13
genes = 180

<r> metagenes = 0.97
<r> genes = 0.58
beta: r2= 124.21 / log p= −Inf

samples with spot = 931 (27.5 %)
A * : 145 (42.2 %)
A C * : 268 (81.7 %)
A C F * : 135 (57.4 %)
A F * : 104 (33.8 %)
C F * : 71 (26.8 %)
F * : 70 (12.6 %)
F J * : 4 (0.9 %)
J * : 15 (3.4 %)
N * : 119 (26.9 %)





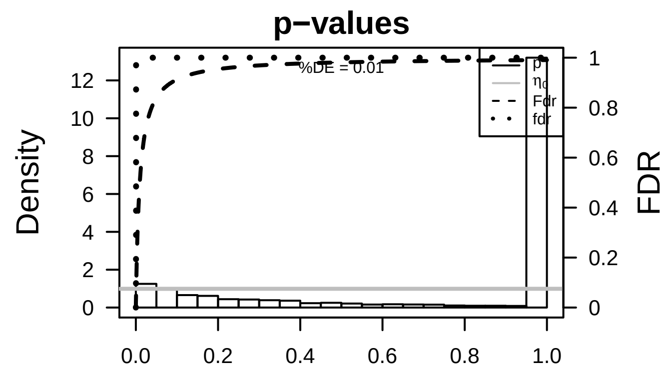


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173045	2.93	−1.93	0.34	FOLR3	folate receptor 3 [Source:HGNC Symbol;Acc:HGNC:3795]
2	ILMN_179631	2.16	−1.97	0.8	MMP9	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
3	ILMN_169658	2.03	−1.31	0.6		
4	ILMN_180121	1.96	−2.45	0.51	S100P	S100 calcium binding protein P [Source:HGNC Symbol;Acc:H
5	ILMN_170160	1.74	−2	0.75	ALPL	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
6	ILMN_174891	1.68	−1.3	0.67	S100A12	S100 calcium binding protein A12 [Source:HGNC Symbol;Acc
7	ILMN_176271	1.67	−1.13	0.74	MCEMP1	mast cell expressed membrane protein 1 [Source:HGNC Sym
8	ILMN_169454	1.63	−1.08	0.76	ANXA3	annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
9	ILMN_170893	1.62	−1.48	0.72	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
10	ILMN_173399	1.53	−1.22	0.5	DHRS9	dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:HGN
11	ILMN_171681	1.5	−1	0.6	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1 [S
12	ILMN_177213	1.48	−1.25	0.82	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGN
13	ILMN_180522	1.47	−1.18	0.89	LRG1	leucine rich alpha−2−glycoprotein 1 [Source:HGNC Symbol;A
14	ILMN_318313	1.45	−1.16	0.85		
15	ILMN_330786	1.45	−1.58	0.41	CHI3L1	chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
16	ILMN_181042	1.45	−1.5	0.93	DYSF	dysferlin [Source:HGNC Symbol;Acc:HGNC:3097]
17	ILMN_177487	1.43	−0.85	0.78	IL1RN	interleukin 1 receptor antagonist [Source:HGNC Symbol;Acc:
18	ILMN_207259	1.41	−1.12	0.8		
19	ILMN_169515	1.41	−1.17	0.86	CA4	carbonic anhydrase 4 [Source:HGNC Symbol;Acc:HGNC:137
20	ILMN_318362	1.38	−1.12	0.83		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−16	17 / 150	Refer	Chaussabel_2,6_Myeloid lineage
2	3e−12	27 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	5e−12	16 / 240	Refer	Chaussabel_3,3_Inflammation II
4	2e−11	12 / 120	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
5	3e−11	110 / 10779	Colon	Enh_Colon
6	4e−11	49 / 2810	Colon	EnhA_Colon
7	2e−09	46 / 2845	Colon	TxEnhG1_Colon
8	3e−08	9 / 107	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_DN
9	5e−08	9 / 113	Refer	Chaussabel_1,5_Myeloid lineage
10	8e−08	15 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
11	1e−07	8 / 87	GSEA	HAHTOLA_SEZARY_SYNDROM_UP
12	1e−07	17 / 554	Canc	Lembcke_Colonic Inflammation
13	2e−07	6 / 39	Refer	Chaussabel_2,2_Neutrophils
14	2e−07	12 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
15	2e−07	14 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
16	3e−07	28 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
17	4e−07	7 / 71	GSEA	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
18	6e−07	18 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
19	6e−07	9 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
20	6e−07	57 / 4735	TF	ICGC_Pu1_targets
21	7e−07	48 / 3662	CC	plasma membrane
22	1e−06	10 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
23	1e−06	4 / 13	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_DN
24	1e−06	8 / 121	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
25	1e−06	76 / 7354	Colon	TssF_Colon
26	2e−06	9 / 169	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
27	2e−06	12 / 336	BP	inflammatory response
28	3e−06	9 / 183	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
29	5e−06	9 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
30	6e−06	8 / 147	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
31	6e−06	9 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
32	9e−06	42 / 3291	CC	integral component of membrane
33	9e−06	12 / 387	BP	cell adhesion
34	1e−05	54 / 4795	Chror	6_EnhG_Fibroblasts
35	1e−05	12 / 404	GSEA	DELYS_THYROID_CANCER_UP
36	1e−05	10 / 278	Colon	Kosinski_top−crypt−long−list
37	2e−05	58 / 5373	Colon	EnhWk1_Colon
38	2e−05	73 / 7448	Lymph	HOPP_Strong_enhancer
39	2e−05	8 / 178	BP	response to lipopolysaccharide
40	2e−05	15 / 648	MF	calcium ion binding



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 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−06	12 / 336	inflammatory response
2	9e−06	12 / 387	cell adhesion
3	2e−05	8 / 178	response to lipopolysaccharide
4	4e−05	9 / 254	cell surface receptor signaling pathway
5	1e−04	6 / 115	leukocyte migration
6	1e−04	9 / 293	immune response
7	2e−04	3 / 19	positive regulation of interleukin−1 beta secretion
8	4e−04	9 / 335	innate immune response
9	5e−04	5 / 99	defense response to bacterium
10	5e−04	4 / 56	neutrophil chemotaxis
11	9e−04	4 / 65	response to glucocorticoid
12	1e−03	4 / 68	positive regulation of inflammatory response
13	2e−03	2 / 10	positive regulation of vasculogenesis
14	2e−03	2 / 10	response to muramyl dipeptide
15	2e−03	2 / 10	vacuolar acidification

Brain

Rank	p−value	#in/all	Geneset
1	9e−05	46 / 4112	Mid_Frontal_Lobe_ReprPC
2	2e−04	28 / 2127	Mid_Frontal_Lobe_K9K27me3
3	3e−04	33 / 2709	Mid_Frontal_Lobe_HetRpts
4	5e−04	24 / 1784	Mid_Frontal_Lobe_ReprPCWk
5	3e−03	29 / 2630	Fetal_TssF
6	3e−03	19 / 1476	Overlap_fetal_midbrain_TxTrans
7	4e−03	29 / 2700	Fetal_TxTrans
8	7e−03	32 / 3164	Mid_Frontal_Lobe_ZNF
9	1e−02	21 / 1893	Overlap_fetal_midbrain_TssF
10	1e−02	7 / 383	Mid_Frontal_Lobe_Tx
11	3e−02	14 / 1213	Fetal_TssP
12	3e−02	13 / 1119	Overlap_fetal_midbrain_TssA
13	6e−02	78 / 10430	Overlap_fetal_midbrain_Quies
14	1e−01	14 / 1506	Mid_Frontal_Lobe_Quies
15	1e−01	8 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	1e−07	17 / 554	Lembcke_Colonic Inflammation
2	4e−03	7 / 301	SPANG_BCL6−index2
3	2e−02	0 / 13	LIU_LIVER_CANCER
4	3e−02	2 / 39	ZHANG_MM up
5	9e−02	1 / 14	LIU_PROSTATE_CANCER_UP
6	9e−02	1 / 14	BEN−PORATH_UP
7	9e−02	1 / 14	GENTLES_modul4
8	1e−01	3 / 178	SPANG_LPS−index2
9	1e−01	2 / 91	PanCan_TXmisReg_geneset_nanostring
10	1e−01	1 / 24	PanCan_Notch_geneset_nanostring
11	2e−01	1 / 28	PanCan_HH_geneset_nanostring
12	2e−01	2 / 125	PanCan_CC+Apop_geneset_nanostring
13	2e−01	1 / 36	PanCan_HK_geneset_nanostring
14	3e−01	5 / 527	Lembcke_Normal vs Adenoma
15	3e−01	0 / 133	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	7e−07	48 / 3662	plasma membrane
2	9e−06	42 / 3291	integral component of membrane
3	6e−05	3 / 12	specific granule
4	2e−04	31 / 2464	extracellular exosome
5	2e−03	4 / 80	nucleosome
6	2e−03	16 / 1101	extracellular space
7	2e−03	2 / 11	uropod
8	3e−03	5 / 149	lamellipodium
9	3e−03	7 / 295	cell−cell adherens junction
10	3e−03	17 / 1252	integral component of plasma membrane
11	4e−03	5 / 156	cytoplasmic vesicle
12	4e−03	3 / 51	phagocytic vesicle membrane
13	5e−03	2 / 16	pre−autophagosomal structure membrane
14	5e−03	2 / 17	cell−cell contact zone
15	6e−03	4 / 109	late endosome

Chr

Rank	p−value	#in/all	Geneset
1	0.007	18 / 1467	Chr 19
2	0.015	24 / 2323	Chr 1
3	0.096	10 / 959	Chr 16
4	0.137	6 / 536	Chr 22
5	0.141	11 / 1170	Chr 7
6	0.165	11 / 1211	Chr 6
7	0.239	11 / 1318	Chr 17
8	0.376	5 / 619	Chr 20
9	0.654	2 / 342	Chr 18
10	0.704	8 / 1411	Chr 11
11	0.740	4 / 768	Chr 14
12	0.771	6 / 1160	Chr 12
13	0.797	4 / 836	Chr 8
14	0.824	5 / 1060	Chr 5
15	0.842	4 / 902	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−05	54 / 4795	6_EnhG_Fibroblasts
2	1e−04	40 / 3450	4_TxTrans_Fibroblasts
3	3e−04	36 / 3068	8_EnhP_Fibroblasts
4	5e−04	44 / 4169	10_ReprPC_Fibroblasts
5	7e−04	55 / 5699	6_EnhG_Melanocytes
6	1e−03	25 / 2028	4_TxTrans_Melanocytes
7	2e−03	95 / 11847	7_Enh_Neuronal_Progenitor
8	1e−02	77 / 9635	3_TssF_Fibroblasts
9	1e−02	33 / 3438	10_ReprPC_Melanocytes
10	1e−02	38 / 4107	9_ReprPCWk_Fibroblasts
11	3e−02	89 / 11836	3_TssF_Melanocytes
12	4e−02	94 / 12741	7_Enh_Melanocytes
13	4e−02	37 / 4304	9_ReprPCWk_Melanocytes
14	5e−02	13 / 1206	6_EnhG_Neuronal_Progenitor
15	5e−02	91 / 12393	15_Quies_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−12	27 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−11	110 / 10779	Enh_Colon
3	4e−11	49 / 2810	EnhA_Colon
4	2e−09	46 / 2845	TxEnhG1_Colon
5	3e−07	28 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
6	1e−06	76 / 7354	TssF_Colon
7	1e−05	10 / 278	Kosinski_top−crypt−long−list
8	2e−05	58 / 5373	EnhWk1_Colon
9	6e−05	16 / 789	TxEnhG2_Colon
10	6e−05	11 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
11	6e−04	79 / 9054	Tx_Colon
12	6e−04	3 / 26	Ang_CRC−CIMPH−vs−L_hypo
13	2e−03	3 / 35	Ang_CRC_Hypomethylated
14	2e−03	12 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
15	4e−03	17 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv

Glio

Rank	p−value	#in/all	Geneset
1	2e−07	12 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	5e−04	4 / 56	Christensen_hypomethylated_in_primary_glioblastoma
3	7e−04	34 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
4	1e−03	4 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
5	2e−03	19 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
6	7e−03	2 / 19	KIM deleted & downregulated in LTS
7	7e−03	3 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
8	1e−02	2 / 28	KIM prognostic signature LTS vs. STS
9	2e−02	3 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	2e−02	4 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
11	2e−02	4 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
12	2e−02	2 / 37	Christensen_hypomethylated_in_ependymoma
13	3e−02	2 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
14	4e−02	2 / 47	Donson−innate immunity−associated with LTS in HGA
15	4e−02	3 / 113	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−11	12 / 120	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
2	3e−08	9 / 107	LENAOUR_DENDRITIC_CELL_MATURATION_DN
3	8e−08	15 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
4	1e−07	8 / 87	HAHTOLA_SEZARY_SYNDROM_UP
5	2e−07	14 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
6	4e−07	7 / 71	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
7	6e−07	18 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	6e−07	9 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
9	1e−06	10 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
10	1e−06	4 / 13	MARTINELLI_IMMATURE_NEUTROPHIL_DN
11	1e−06	8 / 121	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
12	2e−06	9 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
13	3e−06	9 / 183	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
14	5e−06	9 / 192	MCLACHLAN_DENTAL_CARIES_DN
15	6e−06	8 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP

HM

Rank	p−value	#in/all	Geneset
1	0.002	4 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
2	0.008	5 / 191	HALLMARK_INFLAMMATORY_RESPONSE
3	0.028	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
4	0.033	4 / 185	HALLMARK_P53_PATHWAY
5	0.033	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.034	4 / 187	HALLMARK_COMPLEMENT
7	0.053	3 / 130	HALLMARK_DNA_REPAIR
8	0.089	3 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	0.106	2 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.107	3 / 176	HALLMARK_KRAS_SIGNALING_UP
11	0.117	3 / 183	HALLMARK_GLYCOLYSIS
12	0.131	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	0.172	1 / 29	HALLMARK_NOTCH_SIGNALING
14	0.200	2 / 127	HALLMARK_COAGULATION
15	0.235	1 / 41	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	7e−05	8 / 211	Homuth_BMI−associated−genes_DN
2	3e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	5e−01	1 / 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 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1e+00	0 / 15	DUMEAUX_Red blood cells in non 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 / 147	Homuth_BMI−associated−genes_UP
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	73 / 7448	HOPP_Strong_enhancer
2	6e−05	4 / 33	Subero_T−PLL_hypo_meth
3	2e−04	9 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−(
4	3e−04	6 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_L
5	3e−04	6 / 138	WIRTH_lymphoma937_spot G
6	3e−04	9 / 331	WIRTH_lymphoma937_spot H
7	3e−04	5 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
8	1e−03	9 / 408	TARTE_Mature plasma cell signature
9	1e−02	4 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
10	2e−02	6 / 306	WIRTH_lymphoma937_spot E
11	2e−02	3 / 84	ROSOLOWSKI_green UP
12	3e−02	7 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC·
13	3e−02	7 / 464	WIRTH_lymphoma937_spot I
14	3e−02	5 / 272	SPANG_IL21 DN
15	4e−02	2 / 46	Subero_DLBCL_hypo_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.05	2 / 54	Hugo_melanoma−all−MET_DN
3	1.00	0 / 30	Hugo_melanoma−all−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	15 / 648	calcium ion binding
2	1e−04	80 / 8818	protein binding
3	2e−04	7 / 188	receptor activity
4	2e−03	2 / 10	RAGE receptor binding
5	4e−03	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
6	7e−03	2 / 19	ionotropic glutamate receptor binding
7	7e−03	3 / 60	metallopeptidase activity
8	2e−02	3 / 81	protease binding
9	2e−02	7 / 413	protein heterodimerization activity
10	2e−02	2 / 34	phosphatidylinositol−3,4,5−trisphosphate binding
11	3e−02	3 / 99	metalloendopeptidase activity
12	3e−02	2 / 41	calcium−dependent phospholipid binding
13	4e−02	2 / 47	chromatin DNA binding
14	4e−02	2 / 47	RNA polymerase II transcription factor binding
15	4e−02	2 / 47	scaffold protein 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	0.004	3 / 47	hsa−miR−370
2	0.007	3 / 60	hsa−miR−492
3	0.017	3 / 84	hsa−miR−486−3p
4	0.018	2 / 32	hsa−miR−631
5	0.020	3 / 88	hsa−miR−423−5p
6	0.021	5 / 243	hsa−miR−26b
7	0.022	2 / 35	hsa−miR−769−5p
8	0.033	2 / 44	hsa−miR−518e*
9	0.040	2 / 49	hsa−miR−1279
10	0.048	3 / 125	hsa−miR−383
11	0.058	2 / 60	hsa−miR−514
12	0.060	2 / 61	hsa−miR−671−5p
13	0.068	4 / 235	hsa−miR−26a
14	0.071	2 / 67	hsa−miR−1246
15	0.071	2 / 67	hsa−miR−1184

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	1 / 13	BENTINK_e2f3.1
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.2
5	1.00	0 / 13	BENTINK_myc.1
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	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−16	17 / 150	Chaussabel_2,6_Myeloid lineage
2	5e−12	16 / 240	Chaussabel_3,3_Inflammation II
3	5e−08	9 / 113	Chaussabel_1,5_Myeloid lineage
4	2e−07	6 / 39	Chaussabel_2,2_Neutrophils
5	2e−04	8 / 242	Chaussabel_3,2_Inflammation I
6	6e−04	13 / 695	PROTEINATLAS_bone marrow
7	8e−04	11 / 535	PROTEINATLAS_spleen
8	2e−03	2 / 11	WIRTH_Prim. lymphoid organs
9	9e−03	3 / 66	VAQUERIZAS_Whole blood_TF
10	5e−02	6 / 412	WIRTH_Immune system
11	7e−02	2 / 64	VAQUERIZAS_Lung_TF
12	7e−02	10 / 912	PROTEINATLAS_fallopian tube
13	8e−02	1 / 12	Chaussabel_3,5_Hemoglobin genes
14	8e−02	8 / 681	PROTEINATLAS_lung
15	8e−02	6 / 465	PROTEINATLAS_liver

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	6e−07	57 / 4735	ICGC_Pu1_targets
2	1e−04	54 / 5188	ICGC_Ebfsc137065_targets
3	2e−04	39 / 3348	ICGC_BatfPcr1_targets
4	8e−04	66 / 7247	ICGC_Runx3_targets
5	1e−03	48 / 4881	ICGC_Atf2_targets
6	1e−03	56 / 5984	ICGC_Mta3_targets
7	2e−03	52 / 5466	ICGC_Nficsc81335_targets
8	2e−03	52 / 5518	ICGC_Stat5_targets
9	3e−03	28 / 2497	ICGC_Bcl11_targets
10	4e−03	50 / 5442	ICGC_Pmlsc71910_targets
11	4e−03	33 / 3194	ICGC_Irf4_targets
12	5e−03	56 / 6322	ICGC_Tcf3_targets
13	6e−03	29 / 2759	ICGC_Bcl3_targets
14	7e−03	45 / 4890	ICGC_Bclaf101388_targets
15	7e−03	57 / 6578	ICGC_Pou2_targets

Overexpression Spots

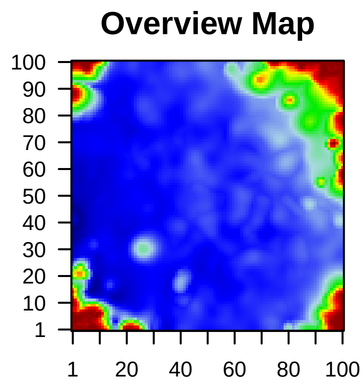
Spot Summary: F

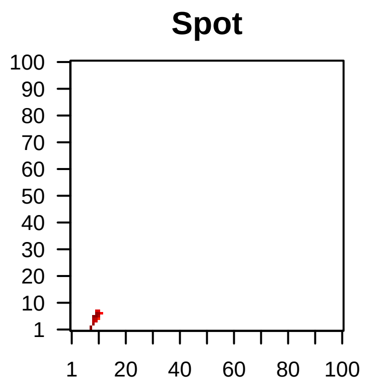
metagenes = 16
genes = 213

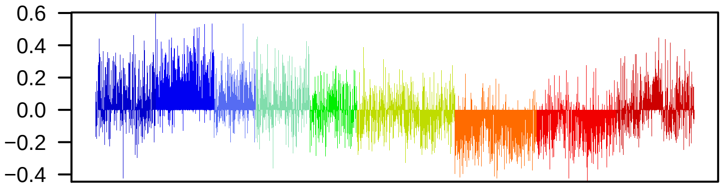
<r> metagenes = 0.96
<r> genes = 0.46
beta: r2= 67.53 / log p= −Inf

samples with spot = 668 (19.7 %)

- A * : 108 (31.4 %)
- A C * : 200 (61 %)
- A C F * : 82 (34.9 %)
- A F * : 75 (24.4 %)
- C F * : 34 (12.8 %)
- F * : 49 (8.8 %)
- F J * : 7 (1.5 %)
- J * : 14 (3.1 %)
- N * : 99 (22.3 %)





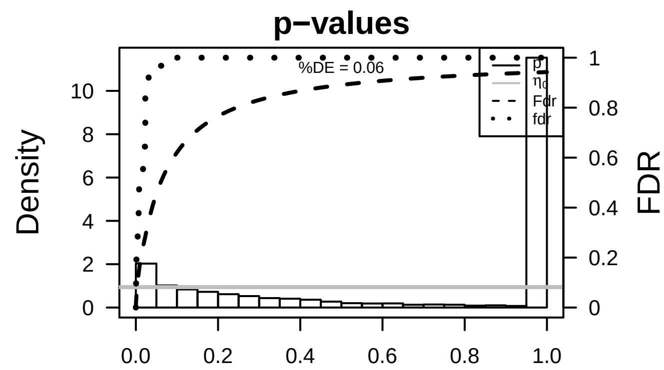


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178573	1.8	−1.22	0.6		
2	ILMN_240322	1.64	−1.03	0.24	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Syı
3	ILMN_177525	1.62	−1.53	0.68	PROK2	prokineticin 2 [Source:HGNC Symbol;Acc:HGNC:18455]
4	ILMN_177719	1.54	−1.37	0.21	CFD	complement factor D [Source:HGNC Symbol;Acc:HGNC:277
5	ILMN_166163	1.49	−2.04	0.36		
6	ILMN_181228	1.46	−0.74	0.64	ARG1	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]
7	ILMN_240650	1.44	−1.26	0.7	LOC100129518	superoxide dismutase 2, mitochondrial [Source:HGNC Symbo
8	ILMN_168458	1.42	−1.28	0.75	ACSL1	acyl−CoA synthetase long−chain family member 1 [Source:H
9	ILMN_170498	1.41	−1.25	0.41	CYP27A1	cytochrome P450 family 27 subfamily A member 1 [Source:H
10	ILMN_171299	1.4	−1.37	0.73	MGAM	maltase−glucoamylase [Source:HGNC Symbol;Acc:HGNC:7(
11	ILMN_167817	1.34	−1.43	0.76	MME	membrane metallo−endopeptidase [Source:HGNC Symbol;A
12	ILMN_173619	1.3	−1.3	0.67		
13	ILMN_235994	1.29	−1.26	0.24	CES1	carboxylesterase 1 [Source:HGNC Symbol;Acc:HGNC:1863]
14	ILMN_177550	1.24	−0.97	0.7	IL1B	interleukin 1 beta [Source:HGNC Symbol;Acc:HGNC:5992]
15	ILMN_179910	1.22	−0.92	0.75	MARC1	mitochondrial amidoxime reducing component 1 [Source:HGI
16	ILMN_171506	1.21	−1.11	0.86	AQP9	aquaporin 9 [Source:HGNC Symbol;Acc:HGNC:643]
17	ILMN_167893	1.2	−1.25	0.76	VNN2	vanin 2 [Source:HGNC Symbol;Acc:HGNC:12706]
18	ILMN_181072	1.19	−1.05	0.66	FAM129A	family with sequence similarity 129 member A [Source:HGNC
19	ILMN_171464	1.18	−1.08	0.75		
20	ILMN_213445	1.18	−1.46	0.61		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−19	28 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
2	4e−19	20 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
3	1e−18	23 / 240	Refer	Chaussabel_3,3_Inflammation II
4	2e−18	20 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
5	1e−16	35 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	6e−16	16 / 113	Refer	Chaussabel_1,5_Myeloid lineage
7	4e−15	63 / 2845	Colon	TxEnhG1_Colon
8	9e−15	127 / 9635	Chror	3_TssF_Fibroblasts
9	2e−14	135 / 10779	Colon	Enh_Colon
10	1e−13	106 / 7354	Colon	TssF_Colon
11	5e−13	17 / 203	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
12	9e−13	15 / 150	Refer	Chaussabel_2,6_Myeloid lineage
13	1e−12	118 / 9054	Colon	Tx_Colon
14	2e−12	25 / 554	Canc	Lembcke_Colonic Inflammation
15	4e−12	20 / 346	GSEA	MULLIGHAN_MLL_SIGNATURE_1_UP
16	2e−11	83 / 5373	Colon	EnhWk1_Colon
17	3e−11	77 / 4795	Chror	6_EnhG_Fibroblasts
18	4e−11	17 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
19	7e−11	62 / 3450	Chror	4_TxTrans_Fibroblasts
20	7e−11	20 / 406	GSEA	RODWELL_AGING_KIDNEY_UP
21	8e−11	20 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
22	2e−10	13 / 147	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
23	2e−10	17 / 300	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−E
24	3e−10	17 / 306	Lympl	WIRTH_lymphoma937_spot E
25	4e−10	83 / 5699	Chror	6_EnhG_Melanocytes
26	5e−10	53 / 2810	Colon	EnhA_Colon
27	6e−10	59 / 3348	TF	ICGC_BatfPcr1_targets
28	9e−10	15 / 242	Refer	Chaussabel_3,2_Inflammation I
29	1e−09	17 / 336	BP	inflammatory response
30	1e−09	107 / 8568	Colon	TxWk_Colon
31	2e−09	30 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
32	3e−09	48 / 2497	TF	ICGC_Bcl11_targets
33	3e−09	138 / 12741	Chror	7_Enh_Melanocytes
34	3e−09	76 / 5188	TF	ICGC_Ebfsc137065_targets
35	4e−09	13 / 191	HM	HALLMARK_INFLAMMATORY_RESPONSE
36	6e−09	60 / 3662	CC	plasma membrane
37	7e−09	15 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
38	9e−09	113 / 9555	Colon	TssA_Colon
39	1e−08	130 / 11836	Chror	3_TssF_Melanocytes
40	2e−08	93 / 7247	TF	ICGC_Runx3_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.06	3 / 111	HORVATH_aging_genes meth DOWN
2	0.10	3 / 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	

BP

Rank	p−value	#in/all	Geneset
1	1e−09	17 / 336	inflammatory response
2	4e−06	12 / 293	immune response
3	2e−05	6 / 69	cellular response to mechanical stimulus
4	3e−05	6 / 76	integrin−mediated signaling pathway
5	3e−05	10 / 255	viral process
6	6e−05	4 / 28	regulation of tumor necrosis factor−mediated signaling pathway
7	6e−05	4 / 28	response to axon injury
8	8e−05	5 / 56	neutrophil chemotaxis
9	8e−05	8 / 178	response to lipopolysaccharide
10	1e−04	8 / 187	regulation of cell proliferation
11	1e−04	4 / 33	triglyceride metabolic process
12	2e−04	5 / 66	Fc−gamma receptor signaling pathway involved in phagocytosis
13	2e−04	6 / 107	cellular response to lipopolysaccharide
14	2e−04	4 / 39	peptidyl−tyrosine autophosphorylation
15	3e−04	5 / 74	negative regulation of inflammatory response

Brain

Rank	p−value	#in/all	Geneset
1	6e−07	50 / 3164	Mid_Frontal_Lobe_ZNF
2	1e−06	59 / 4112	Mid_Frontal_Lobe_ReprPC
3	5e−05	40 / 2709	Mid_Frontal_Lobe_HetRpts
4	7e−05	43 / 3046	Fetal_TssA
5	2e−04	106 / 10430	Overlap_fetal_midbrain_Quies
6	3e−04	28 / 1784	Mid_Frontal_Lobe_ReprPCWk
7	1e−03	30 / 2127	Mid_Frontal_Lobe_K9K27me3
8	7e−03	18 / 1213	Fetal_TssP
9	8e−03	32 / 2630	Fetal_TssF
10	1e−02	32 / 2700	Fetal_TxTrans
11	1e−02	90 / 9504	Overlap_fetal_midbrain_K9K27me3
12	2e−02	92 / 9917	Overlap_fetal_midbrain_ReprPCWk
13	2e−02	23 / 1893	Overlap_fetal_midbrain_TssF
14	3e−02	12 / 818	Mid_Frontal_Lobe_Het
15	5e−02	11 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	25 / 554	Lembcke_Colonic Inflammation
2	8e−05	8 / 178	SPANG_LPS−index2
3	1e−04	10 / 301	SPANG_BCL6−index2
4	6e−02	8 / 527	Lembcke_Normal vs Adenoma
5	1e−01	1 / 14	BEN−PORATH_UP
6	2e−01	1 / 24	PanCan_Notch_geneset_nanostring
7	2e−01	0 / 13	LIU_LIVER_CANCER
8	3e−01	2 / 125	PanCan_CC+Apop_geneset_nanostring
9	3e−01	1 / 39	ZHANG_MM up
10	3e−01	2 / 150	PanCan_MAPK_geneset_nanostring
11	3e−01	1 / 54	KUIPER_MM poor survival
12	4e−01	1 / 73	SHAUGHNESSY_MM high risk
13	4e−01	2 / 193	PanCan_PI3K_geneset_nanostring
14	5e−01	0 / 14	LIU_PROSTATE_CANCER_UP
15	5e−01	1 / 91	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−09	60 / 3662	plasma membrane
2	1e−07	44 / 2464	extracellular exosome
3	5e−06	26 / 1252	integral component of plasma membrane
4	5e−05	6 / 83	ruffle
5	1e−04	42 / 2979	cytosol
6	1e−04	11 / 352	focal adhesion
7	1e−04	5 / 61	extrinsic component of cytoplasmic side of plasma membrane
8	2e−04	31 / 1979	membrane
9	2e−04	44 / 3291	integral component of membrane
10	4e−04	7 / 173	nuclear chromatin
11	8e−04	6 / 138	mitochondrial outer membrane
12	2e−03	6 / 170	cell−cell junction
13	3e−03	2 / 10	low−density lipoprotein particle
14	3e−03	4 / 76	ruffle membrane
15	5e−03	4 / 88	transport vesicle

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	29 / 1467	Chr 19
2	2e−02	10 / 619	Chr 20
3	1e−01	7 / 536	Chr 22
4	2e−01	14 / 1318	Chr 17
5	2e−01	14 / 1411	Chr 11
6	2e−01	10 / 959	Chr 16
7	4e−01	3 / 289	Chr 21
8	4e−01	10 / 1170	Chr 7
9	5e−01	19 / 2323	Chr 1
10	6e−01	6 / 768	Chr 14
11	6e−01	7 / 954	Chr 9
12	7e−01	8 / 1160	Chr 12
13	7e−01	6 / 904	Chr 10
14	7e−01	8 / 1211	Chr 6
15	9e−01	4 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−15	127 / 9635	3_TssF_Fibroblasts
2	3e−11	77 / 4795	6_EnhG_Fibroblasts
3	7e−11	62 / 3450	4_TxTrans_Fibroblasts
4	4e−10	83 / 5699	6_EnhG_Melanocytes
5	3e−09	138 / 12741	7_Enh_Melanocytes
6	1e−08	130 / 11836	3_TssF_Melanocytes
7	2e−08	81 / 5956	3_TssF_Neuronal_Progenitor
8	2e−07	130 / 12298	2_TssA_Melanocytes
9	1e−06	99 / 8613	7_Enh_Fibroblasts
10	9e−06	126 / 12393	15_Quies_Neuronal_Progenitor
11	1e−05	97 / 8771	5_Tx_Melanocytes
12	2e−05	121 / 11847	7_Enh_Neuronal_Progenitor
13	2e−05	34 / 2028	4_TxTrans_Melanocytes
14	8e−05	113 / 11130	15_Quies_Melanocytes
15	5e−04	124 / 12983	2_TssA_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−16	35 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−15	63 / 2845	TxEnhG1_Colon
3	2e−14	135 / 10779	Enh_Colon
4	1e−13	106 / 7354	TssF_Colon
5	1e−12	118 / 9054	Tx_Colon
6	2e−11	83 / 5373	EnhWk1_Colon
7	5e−10	53 / 2810	EnhA_Colon
8	1e−09	107 / 8568	TxWk_Colon
9	9e−09	113 / 9555	TssA_Colon
10	4e−08	82 / 6138	TssD2_Colon
11	7e−08	30 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	1e−07	103 / 8678	Quies3_Colon
13	1e−05	28 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	2e−05	12 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
15	4e−05	113 / 10999	TssWk_Colon

Glio

Rank	p−value	#in/all	Geneset
1	4e−11	17 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	3e−05	5 / 47	Donson−innate immunity−associated with LTS in HGA
3	9e−04	5 / 94	Weller_LGG_A_vs_O_UP
4	2e−03	5 / 113	GIEZELT_GBM_WT_up_VS_mut
5	2e−03	5 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
6	4e−03	21 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
7	5e−03	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
8	6e−03	5 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	7e−03	5 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
10	7e−03	4 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
11	7e−03	4 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	8e−03	3 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
13	8e−03	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
14	1e−02	4 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	2e−02	34 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−19	28 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
2	4e−19	20 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
3	2e−18	20 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
4	5e−13	17 / 203	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
5	4e−12	20 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
6	7e−11	20 / 406	RODWELL_AGING_KIDNEY_UP
7	8e−11	20 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
8	2e−10	13 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
9	2e−09	30 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
10	7e−09	15 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	5e−08	12 / 196	MCLACHLAN_DENTAL_CARIES_UP
12	7e−08	6 / 28	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
13	1e−07	33 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
14	1e−07	21 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
15	1e−07	12 / 214	GAL_LEUKEMIC_STEM_CELL_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−09	13 / 191	HALLMARK_INFLAMMATORY_RESPONSE
2	2e−07	11 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	3e−07	8 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	2e−05	6 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	2e−04	7 / 151	HALLMARK_APOPTOSIS
6	4e−04	7 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	5e−04	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
8	5e−04	7 / 176	HALLMARK_KRAS_SIGNALING_UP
9	8e−04	5 / 91	HALLMARK_PEROXISOME
10	2e−03	6 / 162	HALLMARK_ALLOGRAFT_REJECTION
11	9e−03	4 / 103	HALLMARK_BILE_ACID_METABOLISM
12	2e−02	5 / 185	HALLMARK_P53_PATHWAY
13	2e−02	5 / 186	HALLMARK_IL2_STAT5_SIGNALING
14	2e−02	5 / 189	HALLMARK_HYPOXIA
15	3e−02	3 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−07	12 / 211	Homuth_BMI−associated−genes_DN
2	4e−02	1 / 5	Huan_blood−pressure_HTN−signature
3	6e−02	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
4	8e−02	1 / 10	DUMEAUX_Smoking literature genes up
5	1e−01	1 / 16	Huan_blood−pressure_DBP−signature
6	2e−01	2 / 94	DUMEAUX_Smoking enriched genes
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 / 147	Homuth_BMI−associated−genes_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−10	17 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−(
2	3e−10	17 / 306	WIRTH_lymphoma937_spot E
3	2e−07	92 / 7448	HOPP_Strong_enhancer
4	6e−06	6 / 57	Monti_Host_response_cluster
5	1e−05	11 / 272	SPANG_IL21 DN
6	8e−05	9 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
7	3e−04	21 / 1169	SPANG_BCR DN
8	4e−04	5 / 78	Sha_DLBCL UP
9	4e−04	11 / 408	TARTE_Mature plasma cell signature
10	1e−03	2 / 7	Care_GCB UP
11	2e−03	20 / 1270	SPANG_BCR UP
12	3e−03	2 / 10	BENTINK_mBL DOWN
13	3e−03	10 / 455	SPANG_CD40 6hrs DN
14	4e−03	5 / 134	DAVE_BL−vs−DLBCL
15	4e−03	4 / 84	ROSOLOWSKI_green 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	2e−06	100 / 8818	protein binding
2	4e−04	4 / 45	non−membrane spanning protein tyrosine kinase activity
3	7e−04	3 / 22	tumor necrosis factor−activated receptor activity
4	2e−03	6 / 160	carbohydrate binding
5	3e−03	5 / 120	protein tyrosine kinase activity
6	4e−03	2 / 12	S100 protein binding
7	4e−03	2 / 13	oxidoreductase activity, acting on paired donors, with incorporation or reductio
8	4e−03	2 / 13	tropomyosin binding
9	5e−03	12 / 646	protein homodimerization activity
10	6e−03	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
11	6e−03	2 / 15	low−density lipoprotein particle binding
12	7e−03	3 / 49	pyridoxal phosphate binding
13	7e−03	2 / 16	GTP−Rho binding
14	8e−03	3 / 52	RNA polymerase II core promoter sequence−specific DNA binding
15	8e−03	19 / 1329	ATP 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	0.002	6 / 157	hsa−miR−31
2	0.002	3 / 33	hsa−miR−615−5p
3	0.004	3 / 41	hsa−miR−532−3p
4	0.004	2 / 13	hsa−miR−1234
5	0.011	5 / 168	hsa−miR−137
6	0.011	5 / 170	hsa−miR−580
7	0.011	3 / 59	hsa−miR−665
8	0.019	7 / 342	hsa−let−7e
9	0.020	2 / 28	hsa−miR−597
10	0.021	4 / 134	hsa−miR−198
11	0.023	3 / 78	hsa−miR−30a*
12	0.027	3 / 82	hsa−miR−557
13	0.029	3 / 85	hsa−miR−149
14	0.030	8 / 463	hsa−miR−301a
15	0.032	3 / 88	hsa−miR−188−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.005	2 / 14	GUSTAFSON_PI3K_UP
2	0.083	1 / 11	BENTINK_ras.4
3	0.097	1 / 13	BENTINK_e2f3.1
4	1.000	0 / 15	GUSTAFSON_PI3K_DN
5	1.000	0 / 13	BENTINK_e2f3.2
6	1.000	0 / 13	BENTINK_myc.1
7	1.000	0 / 12	BENTINK_ras.1
8	1.000	0 / 14	BENTINK_ras.6
9	1.000	0 / 13	BENTINK_src.10
10	1.000	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−18	23 / 240	Chaussabel_3,3_Inflammation II
2	6e−16	16 / 113	Chaussabel_1,5_Myeloid lineage
3	9e−13	15 / 150	Chaussabel_2,6_Myeloid lineage
4	9e−10	15 / 242	Chaussabel_3,2_Inflammation I
5	9e−07	7 / 66	VAQUERIZAS_Whole blood_TF
6	3e−04	15 / 681	PROTEINATLAS_lung
7	1e−03	14 / 695	PROTEINATLAS_bone marrow
8	3e−03	2 / 11	WIRTH_Prim. lymphoid organs
9	3e−03	2 / 11	JONGENEEL_Spleen
10	3e−03	11 / 535	PROTEINATLAS_spleen
11	7e−03	2 / 16	VAQUERIZAS_Ovary_TF
12	1e−02	3 / 64	VAQUERIZAS_Lung_TF
13	4e−02	2 / 39	Chaussabel_2,2_Neutrophils
14	4e−02	3 / 96	Chaussabel_3,1_Interferon−inducible
15	8e−02	1 / 10	VAQUERIZAS_Skeletal muscle_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	6e−10	59 / 3348	ICGC_BatfPcr1_targets
2	3e−09	48 / 2497	ICGC_Bcl11_targets
3	3e−09	76 / 5188	ICGC_Ebfsc137065_targets
4	2e−08	93 / 7247	ICGC_Runx3_targets
5	4e−08	69 / 4735	ICGC_Pu1_targets
6	2e−07	87 / 6868	ICGC_Elf1_targets
7	1e−06	72 / 5466	ICGC_Nficsc81335_targets
8	3e−06	78 / 6267	ICGC_Yy1_targets
9	4e−06	75 / 5984	ICGC_Mta3_targets
10	7e−06	59 / 4362	ICGC_Creb1_targets
11	2e−05	59 / 4468	ICGC_Egr1_targets
12	2e−05	78 / 6578	ICGC_Pou2_targets
13	2e−05	35 / 2133	ICGC_Mef2_targets
14	2e−05	78 / 6616	ICGC_Pax5_targets
15	3e−05	49 / 3507	ICGC_Rad21_targets

Overexpression Spots

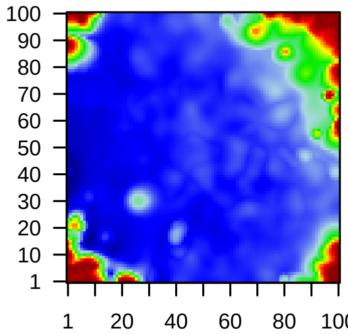
Spot Summary: G

metagenes = 2
genes = 100

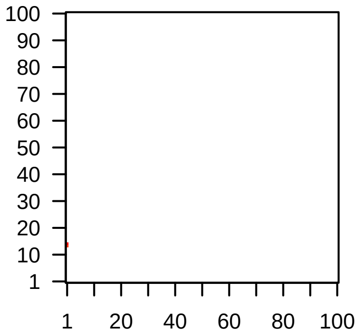
<r> metagenes = 1
<r> genes = 0.63
beta: r2= 46.07 / log p= −Inf

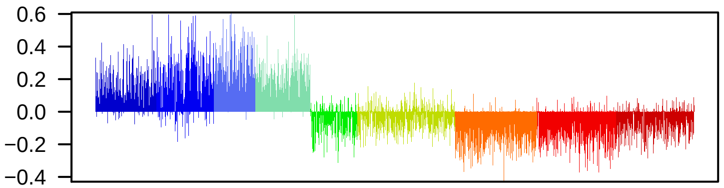
samples with spot = 629 (18.6 %)
- A * : 130 (37.8 %)
- A C * : 154 (47 %)
- A C F * : 166 (70.6 %)
- A F * : 174 (56.5 %)
- F * : 5 (0.9 %)

Overview Map



Spot





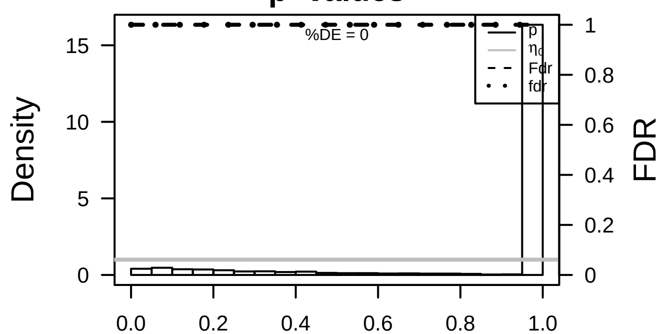
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_323060	1.23	−1.06	0.47	NBPF20	neuroblastoma breakpoint family member 20 [Source:HGNC
2	ILMN_211549	1.17	−1.21	0.37		
3	ILMN_320036	1.15	−0.81	0.52	NBPF26	neuroblastoma breakpoint family member 9 [Source:HGNC S
4	ILMN_226204	1	−0.66	0.63	PARP10	poly(ADP−ribose) polymerase family member 10 [Source:HG
5	ILMN_169737	1	−1.03	0.35		
6	ILMN_180104	0.94	−1.06	0.54	LOC105369247	sialophorin [Source:HGNC Symbol;Acc:HGNC:11249]
7	ILMN_171019	0.93	−0.54	0.86	SMG1	SMG1, nonsense mediated mRNA decay associated PI3K rel
8	ILMN_226244	0.91	−0.68	0.71	PDE7A	phosphodiesterase 7A [Source:HGNC Symbol;Acc:HGNC:87
9	ILMN_209566	0.89	−0.72	0.76	TMEM156	transmembrane protein 156 [Source:HGNC Symbol;Acc:HGN
10	ILMN_325378	0.89	−0.54	0.75		
11	ILMN_222490	0.88	−0.71	0.84	SMIM14	small integral membrane protein 14 [Source:HGNC Symbol;A
12	ILMN_218922	0.84	−0.66	0.67	KLHL8	kelch like family member 8 [Source:HGNC Symbol;Acc:HGNC
13	ILMN_210348	0.83	−0.52	0.88	ZNF320	zinc finger protein 320 [Source:HGNC Symbol;Acc:HGNC:13
14	ILMN_179078	0.82	−0.68	0.58	MED16	mediator complex subunit 16 [Source:HGNC Symbol;Acc:HG
15	ILMN_169779	0.81	−0.58	0.89	SYNJ2BP	synaptojanin 2 binding protein [Source:HGNC Symbol;Acc:HG
16	ILMN_218023	0.81	−0.65	0.91	DOPEY2	dopey family member 2 [Source:HGNC Symbol;Acc:HGNC:1
17	ILMN_212341	0.8	−0.53	0.83	BMP8B	bone morphogenetic protein 8b [Source:HGNC Symbol;Acc:H
18	ILMN_324538	0.8	−0.5	0.92	ZNF860	zinc finger protein 860 [Source:HGNC Symbol;Acc:HGNC:34
19	ILMN_239627	0.79	−0.69	0.74	MIR4680	programmed cell death 4 (neoplastic transformation inhibitor)
20	ILMN_235224	0.78	−0.5	0.9	RASSF6	Ras association domain family member 6 [Source:HGNC Syn

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−05	3 / 18	GSEA	SPIRA_SMOKERS_LUNG_CANCER_DN
2	4e−05	22 / 2497	TF	ICGC_Bcl11_targets
3	1e−04	3 / 29	Refer	Chaussabel_2,7_Unknown function
4	3e−04	10 / 740	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
5	3e−04	4 / 91	GSEA	ZWANG_EGF_INTERVAL_UP
6	5e−04	3 / 45	miRN	hsa−miR−524−3p
7	1e−03	3 / 56	GSEA	RIZKI_TUMOR_INVASIVENESS_2D_DN
8	1e−03	29 / 4735	TF	ICGC_Pu1_targets
9	1e−03	7 / 472	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B
10	2e−03	1 / 14	Canc	LIU_COMMON_CANCER_GENES
11	2e−03	7 / 493	Lymph	WIRTH_lymphoma937_spot J
12	2e−03	2 / 18	BP	replication fork processing
13	2e−03	2 / 18	GSEA	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP
14	2e−03	15 / 1846	Chror	14_ZNF_Melanocytes
15	2e−03	8 / 641	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
16	2e−03	17 / 2255	TF	ICGC_SrfV0416101_targets
17	2e−03	9 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
18	2e−03	3 / 71	GSEA	MORI_PRE_BI_LYMPHOCYTE_DN
19	2e−03	16 / 2087	TF	ICGC_Cebpbsc150_targets
20	3e−03	10 / 1003	Refer	PROTEINATLAS_appendix
21	3e−03	5 / 273	GSEA	HORIUCHI_WTAP_TARGETS_DN
22	3e−03	6 / 398	Refer	PROTEINATLAS_skeletal muscle
23	3e−03	2 / 23	BP	mitochondrial translation
24	4e−03	6 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
25	4e−03	28 / 4881	TF	ICGC_Atf2_targets
26	5e−03	2 / 30	miRN	hsa−miR−626
27	5e−03	3 / 99	GSEA	KAYO_AGING_MUSCLE_DN
28	5e−03	4 / 197	GSEA	LEE_RECENT_THYMIC_EMIGRANT
29	5e−03	21 / 3348	TF	ICGC_BatfPcr1_targets
30	5e−03	3 / 100	GSEA	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP
31	6e−03	4 / 206	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
32	6e−03	12 / 1501	TF	ICGC_Usf1_targets
33	6e−03	5 / 331	Lymph	SPANG_CD40 6hrs UP
34	6e−03	3 / 107	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_UP
35	7e−03	5 / 343	GSEA	BASAKI_YBX1_TARGETS_DN
36	8e−03	2 / 37	BP	negative regulation of I−kappaB kinase/NF−kappaB signaling
37	8e−03	2 / 37	miRN	hsa−miR−518e
38	8e−03	6 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
39	8e−03	5 / 354	GSEA	REACTOME_METABOLISM_OF_PROTEINS
40	8e−03	2 / 39	GSEA	OLSSON_E2F3_TARGETS_DN

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	0.002	2 / 18	replication fork processing
2	0.003	2 / 23	mitochondrial translation
3	0.008	2 / 37	negative regulation of I−kappaB kinase/NF−kappaB signaling
4	0.009	2 / 40	response to UV
5	0.011	3 / 130	DNA replication
6	0.012	2 / 48	cellular defense response
7	0.016	2 / 55	negative regulation of ERK1 and ERK2 cascade
8	0.016	2 / 55	response to stimulus
9	0.020	2 / 62	negative regulation of NF−kappaB transcription factor activity
10	0.023	2 / 66	double−strand break repair via homologous recombination
11	0.027	3 / 184	translation
12	0.029	4 / 330	protein ubiquitination
13	0.032	3 / 195	regulation of apoptotic process
14	0.035	1 / 10	cellular response to X−ray
15	0.035	1 / 10	lysine catabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.02	44 / 9815	Overlap_fetal_midbrain_ReprPC
2	0.06	41 / 9504	Overlap_fetal_midbrain_K9K27me3
3	0.08	10 / 1728	Fetal_ReprPCWk
4	0.09	16 / 3164	Mid_Frontal_Lobe_ZNF
5	0.09	5 / 681	Overlap_fetal_midbrain_EnhP
6	0.13	26 / 5936	Overlap_fetal_midbrain_HetRpts
7	0.15	5 / 796	Overlap_fetal_midbrain_ZNF
8	0.24	12 / 2709	Mid_Frontal_Lobe_HetRpts
9	0.26	6 / 1213	Fetal_TssP
10	0.27	40 / 10430	Overlap_fetal_midbrain_Quies
11	0.30	2 / 307	Fetal_ReprPC
12	0.33	11 / 2654	Fetal_Quies
13	0.34	9 / 2127	Mid_Frontal_Lobe_K9K27me3
14	0.36	5 / 1115	Overlap_fetal_midbrain_EnhG
15	0.37	37 / 9917	Overlap_fetal_midbrain_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	1 / 14	LIU_COMMON_CANCER_GENES
2	0.031	1 / 9	GENTLES_modul5
3	0.046	5 / 554	Lembcke_Colonic Inflammation
4	0.168	0 / 13	RHODES_CANCER_META_SIGNATURE
5	0.174	1 / 54	KUIPER_MM poor survival
6	0.183	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
7	0.276	1 / 91	PanCan_TXmisReg_geneset_nanostring
8	0.358	1 / 125	PanCan_CC+Apop_geneset_nanostring
9	0.657	1 / 301	SPANG_BCL6−index2
10	0.848	1 / 527	Lembcke_Normal vs Adenoma
11	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.000	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.000	0 / 12	LIU_BREAST_CANCER
14	1.000	0 / 13	LIU_LIVER_CANCER
15	1.000	0 / 15	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	0.03	1 / 10	90S preribosome
2	0.03	1 / 10	sperm midpiece
3	0.04	1 / 11	uropod
4	0.04	2 / 90	chromatin
5	0.04	1 / 12	clathrin adaptor complex
6	0.05	1 / 14	Cul4−RING E3 ubiquitin ligase complex
7	0.06	1 / 16	pre−autophagosomal structure membrane
8	0.06	1 / 16	sperm principal piece
9	0.07	1 / 20	integral component of mitochondrial outer membrane
10	0.07	1 / 20	mitochondrial small ribosomal subunit
11	0.07	1 / 20	sperm flagellum
12	0.07	23 / 4828	nucleus
13	0.08	3 / 287	mitochondrial matrix
14	0.08	1 / 24	mitochondrial ribosome
15	0.09	11 / 1979	membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.03	10 / 1467	Chr 19
2	0.05	6 / 769	Chr 15
3	0.08	9 / 1492	Chr 2
4	0.10	6 / 902	Chr 4
5	0.14	5 / 768	Chr 14
6	0.17	6 / 1060	Chr 5
7	0.25	5 / 959	Chr 16
8	0.44	2 / 422	Chr 13
9	0.57	2 / 536	Chr 22
10	0.62	3 / 904	Chr 10
11	0.64	1 / 289	Chr 21
12	0.74	4 / 1411	Chr 11
13	0.78	3 / 1160	Chr 12
14	0.80	2 / 836	Chr 8
15	0.84	6 / 2323	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.002	15 / 1846	14_ZNF_Melanocytes
2	0.009	42 / 8771	5_Tx_Melanocytes
3	0.009	56 / 12741	7_Enh_Melanocytes
4	0.010	35 / 6970	5_Tx_Neuronal_Progenitor
5	0.036	52 / 12298	2_TssA_Melanocytes
6	0.061	21 / 4237	14_ZNF_Neuronal_Progenitor
7	0.063	39 / 8990	15_Quies_Fibroblasts
8	0.068	49 / 11836	3_TssF_Melanocytes
9	0.072	5 / 630	14_ZNF_Fibroblasts
10	0.090	47 / 11455	2_TssA_Fibroblasts
11	0.103	52 / 12983	2_TssA_Neuronal_Progenitor
12	0.109	40 / 9635	3_TssF_Fibroblasts
13	0.113	12 / 2315	13_HetRpts_Melanocytes
14	0.133	33 / 7854	5_Tx_Fibroblasts
15	0.133	7 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	10 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
2	1e−02	9 / 1083	ZNF_Colon
3	2e−02	49 / 10999	TssWk_Colon
4	2e−02	1 / 6	TCGA_Mutated−in−CRC_mismatch−repair−genes
5	2e−02	1 / 6	Boland_CRC−MMR−system
6	3e−02	10 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
7	4e−02	3 / 203	Pentrack_CRC_TCGA_corr_U_msi−h_UP
8	4e−02	39 / 8678	Quies3_Colon
9	4e−02	1 / 13	KIM_MSI−in−CRC
10	5e−02	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	5e−02	1 / 15	TCGA_Mutated−in−CRC_hypermutated
12	5e−02	1 / 15	Budinska_B_Lower crypt−like_DOWN
13	5e−02	2 / 104	Marisa_CRC−cluster−h
14	6e−02	1 / 17	TCGA−CRC_less−agressive−disease−markers
15	6e−02	5 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN

Glio

Rank	p−value	#in/all	Geneset
1	0.04	2 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
2	0.08	3 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
3	0.09	1 / 26	Gorovets_LGG_NB_subclass
4	0.14	1 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
5	0.17	1 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
6	0.17	1 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
7	0.21	1 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	0.22	1 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
9	0.23	1 / 74	Weller_LGG_gradeII−vs−III_DOWN
10	0.23	7 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
11	0.24	2 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
12	0.26	1 / 84	GIEZELT_GBM_STS_up_VS_LTS
13	0.27	1 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
14	0.29	1 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
15	0.32	1 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	3 / 18	SPIRA_SMOKERS_LUNG_CANCER_DN
2	3e−04	4 / 91	ZWANG_EGF_INTERVAL_UP
3	1e−03	3 / 56	RIZKI_TUMOR_INVASIVENESS_2D_DN
4	2e−03	1 / 14	LIU_COMMON_CANCER_GENES
5	2e−03	2 / 18	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP
6	2e−03	8 / 641	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	2e−03	9 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
8	2e−03	3 / 71	MORI_PRE_BI_LYMPHOCYTE_DN
9	3e−03	5 / 273	HORIUCHI_WTAP_TARGETS_DN
10	4e−03	6 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
11	5e−03	3 / 99	KAYO_AGING_MUSCLE_DN
12	5e−03	4 / 197	LEE_RECENT_THYMIC_EMIGRANT
13	5e−03	3 / 100	MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_UP
14	6e−03	4 / 206	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
15	6e−03	3 / 107	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_UP

HM

Rank	p−value	#in/all	Geneset
1	0.1	2 / 151	HALLMARK_APOPTOSIS
2	0.1	2 / 173	HALLMARK_E2F_TARGETS
3	0.1	2 / 176	HALLMARK_ADIPOGENESIS
4	0.1	2 / 176	HALLMARK_KRAS_SIGNALING_UP
5	0.1	2 / 185	HALLMARK_HEME_METABOLISM
6	0.2	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	0.3	1 / 91	HALLMARK_PEROXISOME
8	0.3	1 / 103	HALLMARK_BILE_ACID_METABOLISM
9	0.5	1 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	0.5	1 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
11	1.0	0 / 189	HALLMARK_HYPOXIA
12	1.0	0 / 177	HALLMARK_MITOTIC_SPINDLE
13	1.0	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	1.0	0 / 50	HALLMARK_TGF_BETA_SIGNALING
15	1.0	0 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 32	Marjolein_ageing−genes_DN
2	0.5	1 / 211	Homuth_BMI−associated−genes_DN
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 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 147	Homuth_BMI−associated−genes_UP
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	7 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
2	0.002	7 / 493	WIRTH_lymphoma937_spot J
3	0.006	5 / 331	SPANG_CD40 6hrs UP
4	0.009	37 / 7448	HOPP_Strong_enhancer
5	0.014	10 / 1270	SPANG_BCR UP
6	0.015	28 / 5356	HOPP_Txn_transition
7	0.033	34 / 7275	HOPP_Txn_elongation
8	0.057	2 / 109	ROSOLOWSKI_blue total
9	0.068	1 / 20	DAVE_NFkB BL DN
10	0.069	36 / 8226	HOPP_Active_promoter
11	0.075	4 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC·
12	0.077	4 / 455	SPANG_CD40 6hrs DN
13	0.082	4 / 464	WIRTH_lymphoma937_spot I
14	0.132	1 / 40	ROSOLOWSKI_blue DOWN
15	0.141	1 / 43	Monti_OxPhos_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	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	0.01	2 / 42	manganese ion binding
2	0.01	2 / 49	protein serine/threonine phosphatase activity
3	0.02	3 / 169	structural constituent of ribosome
4	0.03	2 / 72	single−stranded DNA binding
5	0.03	3 / 188	receptor activity
6	0.04	1 / 12	C−C chemokine receptor activity
7	0.04	2 / 94	double−stranded DNA binding
8	0.04	1 / 13	monocarboxylic acid transmembrane transporter activity
9	0.05	1 / 14	vitamin D receptor binding
10	0.05	1 / 15	3',5'−cyclic−AMP phosphodiesterase activity
11	0.05	1 / 15	3'−5' exonuclease activity
12	0.05	1 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
13	0.06	1 / 16	K63−linked polyubiquitin binding
14	0.06	1 / 17	polypeptide N−acetylgalactosaminyltransferase activity
15	0.06	1 / 18	DNA 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	5e−04	3 / 45	hsa−miR−524−3p
2	5e−03	2 / 30	hsa−miR−626
3	8e−03	2 / 37	hsa−miR−518e
4	2e−02	2 / 64	hsa−miR−1278
5	3e−02	2 / 72	hsa−miR−890
6	4e−02	2 / 88	hsa−miR−608
7	6e−02	2 / 113	hsa−miR−217
8	7e−02	1 / 19	hsa−miR−563
9	7e−02	2 / 123	hsa−miR−646
10	7e−02	2 / 126	hsa−miR−223
11	8e−02	1 / 24	hsa−miR−24−1*
12	8e−02	2 / 134	hsa−miR−200a
13	8e−02	2 / 135	hsa−miR−488
14	8e−02	1 / 25	hsa−miR−432*
15	9e−02	2 / 146	hsa−miR−548o

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	1 / 14	BENTINK_ras.6
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 / 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	1e−04	3 / 29	Chaussabel_2,7_Unknown function
2	3e−03	10 / 1003	PROTEINATLAS_appendix
3	3e−03	6 / 398	PROTEINATLAS_skeletal muscle
4	1e−02	4 / 254	PROTEINATLAS_smooth muscle
5	2e−02	8 / 929	PROTEINATLAS_bronchus
6	2e−02	9 / 1167	PROTEINATLAS_gallbladder
7	2e−02	9 / 1194	PROTEINATLAS_stomach
8	3e−02	6 / 639	PROTEINATLAS_breast
9	4e−02	6 / 695	PROTEINATLAS_bone marrow
10	4e−02	8 / 1118	PROTEINATLAS_placenta
11	5e−02	6 / 759	PROTEINATLAS_epididymis
12	5e−02	8 / 1173	PROTEINATLAS_rectum
13	6e−02	8 / 1176	PROTEINATLAS_duodenum
14	7e−02	2 / 119	Chaussabel_2,11_Replication
15	7e−02	1 / 22	Chaussabel_1,1_Plasma Cells

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	4e−05	22 / 2497	ICGC_Bcl11_targets
2	1e−03	29 / 4735	ICGC_Pu1_targets
3	2e−03	17 / 2255	ICGC_SrfV0416101_targets
4	2e−03	16 / 2087	ICGC_Cebpbsc150_targets
5	4e−03	28 / 4881	ICGC_Atf2_targets
6	5e−03	21 / 3348	ICGC_BatfPcr1_targets
7	6e−03	12 / 1501	ICGC_Usf1_targets
8	1e−02	28 / 5188	ICGC_Ebfsc137065_targets
9	1e−02	29 / 5466	ICGC_Nficsc81335_targets
10	1e−02	19 / 3194	ICGC_Irf4_targets
11	1e−02	23 / 4131	ICGC_Nfatc1_targets
12	2e−02	28 / 5383	ICGC_Sp1_targets
13	2e−02	32 / 6578	ICGC_Pou2_targets
14	3e−02	23 / 4362	ICGC_Creb1_targets
15	3e−02	25 / 4890	ICGC_Bclaf101388_targets

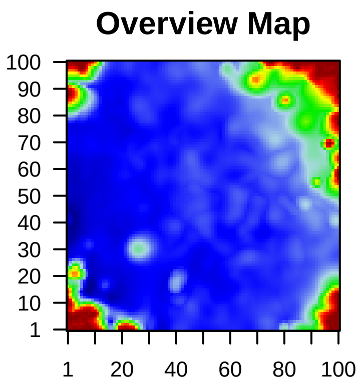
Overexpression Spots

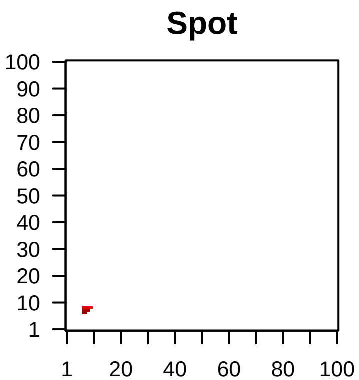
Spot Summary: H

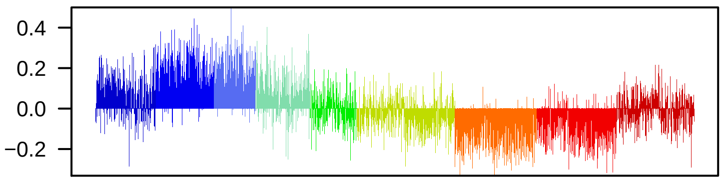
metagenes = 9
genes = 79

<r> metagenes = 0.99
<r> genes = 0.48
beta: r2= 42.87 / log p= −Inf

samples with spot = 510 (15.1 %)
A * : 81 (23.5 %)
A C * : 187 (57 %)
A C F * : 134 (57 %)
A F * : 75 (24.4 %)
C F * : 14 (5.3 %)
F * : 7 (1.3 %)
N * : 12 (2.7 %)





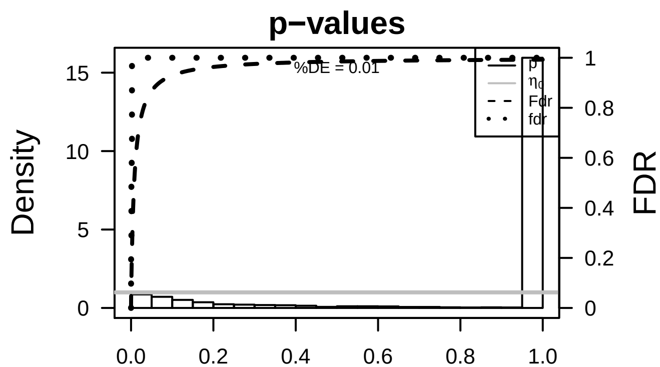


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173081	1.11	−0.88	0.43	GPR162	G protein−coupled receptor 162 [Source:HGNC Symbol;Acc:I
2	ILMN_173470	1.03	−1.41	0.43	CHST13	carbohydrate sulfotransferase 13 [Source:HGNC Symbol;Acc
3	ILMN_176689	1.03	−0.47	0.5	ZDHHC19	zinc finger DHHC−type containing 19 [Source:HGNC Symbol
4	ILMN_171156	0.98	−0.83	0.54	TIMP1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc
5	ILMN_180797	0.85	−0.63	0.77	MICAL1	microtubule associated monooxygenase, calponin and LIM do
6	ILMN_237263	0.82	−0.61	0.63	TRAPPC5	trafficking protein particle complex 5 [Source:HGNC Symbol;A
7	ILMN_169093	0.81	−0.54	0.66	TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:HGNC:
8	ILMN_170331	0.81	−0.63	0.75	INAFM1	InaF motif containing 1 [Source:HGNC Symbol;Acc:HGNC:27
9	ILMN_215751	0.79	−0.71	0.6		
10	ILMN_170332	0.78	−0.64	0.83	PSTPIP1	proline−serine−threonine phosphatase interacting protein 1 [S
11	ILMN_178473	0.77	−0.98	0.75	S1PR4	sphingosine−1−phosphate receptor 4 [Source:HGNC Symbol
12	ILMN_178828	0.77	−0.86	0.56	COTL1	coactosin like F−actin binding protein 1 [Source:HGNC Symb
13	ILMN_171075	0.75	−1.07	0.56	NAPRT	nicotinate phosphoribosyltransferase [Source:HGNC Symbol;
14	ILMN_165138	0.75	−0.64	0.56	MFN2	mitofusin 2 [Source:HGNC Symbol;Acc:HGNC:16877]
15	ILMN_204751	0.75	−0.69	0.68	COX19	COX19, cytochrome c oxidase assembly factor [Source:HGN
16	ILMN_178005	0.72	−0.61	0.88		
17	ILMN_165582	0.71	−0.54	0.55		
18	ILMN_225557	0.71	−0.64	0.63	RAB37	RAB37, member RAS oncogene family [Source:HGNC Symb
19	ILMN_169535	0.7	−0.55	0.7	RNF166	ring finger protein 166 [Source:HGNC Symbol;Acc:HGNC:28
20	ILMN_172822	0.7	−0.67	0.77	OGFR	opioid growth factor receptor [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−17	39 / 3450	Chror	4_TxTrans_Fibroblasts
2	1e−16	52 / 7354	Colon	TssF_Colon
3	2e−16	35 / 2845	Colon	TxEnhG1_Colon
4	1e−14	46 / 6138	Colon	TssD2_Colon
5	8e−14	32 / 2810	Colon	EnhA_Colon
6	5e−13	27 / 2028	Chror	4_TxTrans_Melanocytes
7	1e−12	39 / 4795	Chror	6_EnhG_Fibroblasts
8	1e−11	41 / 5699	Chror	6_EnhG_Melanocytes
9	1e−11	55 / 10779	Colon	Enh_Colon
10	2e−11	52 / 9555	Colon	TssA_Colon
11	2e−11	57 / 11836	Chror	3_TssF_Melanocytes
12	3e−11	46 / 7448	Lymp	HOPP_Strong_enhancer
13	5e−11	39 / 5373	Colon	EnhWk1_Colon
14	7e−11	50 / 9054	Colon	Tx_Colon
15	2e−09	28 / 3164	Brain	Mid_Frontal_Lobe_ZNF
16	5e−09	49 / 9635	Chror	3_TssF_Fibroblasts
17	7e−09	55 / 12298	Chror	2_TssA_Melanocytes
18	2e−08	50 / 10430	Brain	Overlap_fetal_midbrain_Quies
19	3e−08	45 / 8568	Colon	TxWk_Colon
20	6e−08	47 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
21	1e−07	34 / 5356	Lymp	HOPP_Txn_transition
22	1e−07	10 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
23	4e−07	54 / 12983	Chror	2_TssA_Neuronal_Progenitor
24	1e−06	12 / 789	Colon	TxEnhG2_Colon
25	2e−06	6 / 133	BP	endocytosis
26	2e−06	38 / 7275	Lymp	HOPP_Txn_elongation
27	3e−06	6 / 149	CC	lamellipodium
28	3e−06	49 / 11455	Chror	2_TssA_Fibroblasts
29	6e−06	29 / 4822	CC	cytoplasm
30	7e−06	14 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
31	8e−06	7 / 268	MF	actin binding
32	1e−05	51 / 12741	Chror	7_Enh_Melanocytes
33	2e−05	32 / 5956	Chror	3_TssF_Neuronal_Progenitor
34	2e−05	21 / 2979	CC	cytosol
35	3e−05	40 / 8771	Chror	5_Tx_Melanocytes
36	3e−05	7 / 330	CC	cytoskeleton
37	3e−05	25 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
38	3e−05	40 / 8818	MF	protein binding
39	5e−05	8 / 484	GSEA	ACEVEDO_LIVER_CANCER_DN
40	7e−05	4 / 80	GSEA	BASSO_CD40_SIGNALING_UP



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−06	6 / 133	endocytosis
2	3e−04	3 / 47	response to stress
3	3e−04	2 / 10	protein localization to pre−autophagosomal structure
4	4e−04	2 / 11	G−protein coupled receptor internalization
5	4e−04	2 / 11	synaptic vesicle transport
6	5e−04	2 / 12	stress fiber assembly
7	7e−04	3 / 64	negative regulation of cysteine−type endopeptidase activity involved in apoptc
8	7e−04	2 / 15	positive regulation of lamellipodium assembly
9	1e−03	2 / 20	G2 DNA damage checkpoint
10	2e−03	2 / 24	actin filament polymerization
11	2e−03	2 / 24	focal adhesion assembly
12	2e−03	5 / 335	protein transport
13	2e−03	2 / 26	phototransduction
14	2e−03	2 / 26	positive regulation of cytokine production
15	2e−03	2 / 27	positive regulation of phagocytosis

Brain

Rank	p−value	#in/all	Geneset
1	2e−09	28 / 3164	Mid_Frontal_Lobe_ZNF
2	2e−08	50 / 10430	Overlap_fetal_midbrain_Quies
3	6e−08	47 / 9504	Overlap_fetal_midbrain_K9K27me3
4	3e−05	25 / 4112	Mid_Frontal_Lobe_ReprPC
5	2e−03	8 / 818	Mid_Frontal_Lobe_Het
6	1e−02	14 / 2709	Mid_Frontal_Lobe_HetRpts
7	1e−02	36 / 9917	Overlap_fetal_midbrain_ReprPCWk
8	2e−02	24 / 5936	Overlap_fetal_midbrain_HetRpts
9	2e−02	6 / 796	Overlap_fetal_midbrain_ZNF
10	1e−01	5 / 906	Fetal_HetRpts
11	1e−01	32 / 9815	Overlap_fetal_midbrain_ReprPC
12	2e−01	8 / 2127	Mid_Frontal_Lobe_K9K27me3
13	3e−01	10 / 3046	Fetal_TssA
14	3e−01	6 / 1728	Fetal_ReprPCWk
15	4e−01	1 / 180	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	4 / 178	SPANG_LPS−index2
2	0.765	1 / 527	Lembcke_Normal vs Adenoma
3	0.782	1 / 554	Lembcke_Colonic Inflammation
4	1.000	0 / 13	RHODES_CANCER_META_SIGNATURE
5	1.000	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
6	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	1.000	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	1.000	0 / 12	LIU_BREAST_CANCER
9	1.000	0 / 14	LIU_COMMON_CANCER_GENES
10	1.000	0 / 13	LIU_LIVER_CANCER
11	1.000	0 / 15	LIU_PROSTATE_CANCER_DN
12	1.000	0 / 14	LIU_PROSTATE_CANCER_UP
13	1.000	0 / 15	WANG_ER_UP
14	1.000	0 / 13	WANG_ER_DN
15	1.000	0 / 15	WOLFER_overlap genes

CC

Rank	p−value	#in/all	Geneset
1	3e−06	6 / 149	lamellipodium
2	6e−06	29 / 4822	cytoplasm
3	2e−05	21 / 2979	cytosol
4	3e−05	7 / 330	cytoskeleton
5	1e−04	8 / 539	Golgi membrane
6	4e−04	3 / 54	clathrin−coated pit
7	7e−04	16 / 2464	extracellular exosome
8	8e−04	2 / 16	pseudopodium
9	1e−03	4 / 171	postsynaptic density
10	3e−03	3 / 109	growth cone
11	6e−03	3 / 136	cytoplasmic, membrane−bounded vesicle
12	7e−03	2 / 47	stress fiber
13	8e−03	2 / 49	platelet alpha granule lumen
14	1e−02	4 / 310	dendrite
15	1e−02	2 / 67	filopodium

Chr

Rank	p−value	#in/all	Geneset
1	0.004	8 / 959	Chr 16
2	0.017	9 / 1467	Chr 19
3	0.097	6 / 1170	Chr 7
4	0.234	5 / 1217	Chr 3
5	0.286	5 / 1318	Chr 17
6	0.336	5 / 1411	Chr 11
7	0.429	2 / 536	Chr 22
8	0.446	3 / 904	Chr 10
9	0.503	2 / 619	Chr 20
10	0.612	6 / 2323	Chr 1
11	0.615	3 / 1160	Chr 12
12	0.622	2 / 769	Chr 15
13	0.667	2 / 836	Chr 8
14	0.929	1 / 954	Chr 9
15	0.937	1 / 994	Chr X

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−17	39 / 3450	4_TxTrans_Fibroblasts
2	5e−13	27 / 2028	4_TxTrans_Melanocytes
3	1e−12	39 / 4795	6_EnhG_Fibroblasts
4	1e−11	41 / 5699	6_EnhG_Melanocytes
5	2e−11	57 / 11836	3_TssF_Melanocytes
6	5e−09	49 / 9635	3_TssF_Fibroblasts
7	7e−09	55 / 12298	2_TssA_Melanocytes
8	4e−07	54 / 12983	2_TssA_Neuronal_Progenitor
9	3e−06	49 / 11455	2_TssA_Fibroblasts
10	1e−05	51 / 12741	7_Enh_Melanocytes
11	2e−05	32 / 5956	3_TssF_Neuronal_Progenitor
12	3e−05	40 / 8771	5_Tx_Melanocytes
13	1e−04	36 / 7854	5_Tx_Fibroblasts
14	3e−04	46 / 11847	7_Enh_Neuronal_Progenitor
15	4e−04	11 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−16	52 / 7354	TssF_Colon
2	2e−16	35 / 2845	TxEnhG1_Colon
3	1e−14	46 / 6138	TssD2_Colon
4	8e−14	32 / 2810	EnhA_Colon
5	1e−11	55 / 10779	Enh_Colon
6	2e−11	52 / 9555	TssA_Colon
7	5e−11	39 / 5373	EnhWk1_Colon
8	7e−11	50 / 9054	Tx_Colon
9	3e−08	45 / 8568	TxWk_Colon
10	1e−06	12 / 789	TxEnhG2_Colon
11	7e−06	14 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	9e−05	45 / 10999	TssWk_Colon
13	5e−04	12 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	1e−03	36 / 8678	Quies3_Colon
15	2e−03	7 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Glio

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	1e−02	4 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	2e−02	6 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	3e−02	1 / 12	Phillips MES up vs Prolif & PN
5	4e−02	3 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
6	5e−02	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
7	5e−02	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
8	5e−02	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
9	5e−02	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
10	5e−02	1 / 19	KIM deleted & downregulated in LTS
11	7e−02	1 / 28	KIM prognostic signature LTS vs. STS
12	8e−02	1 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
13	8e−02	1 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
14	9e−02	1 / 35	Colman_survival_associated
15	9e−02	3 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−07	10 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
2	5e−05	8 / 484	ACEVEDO_LIVER_CANCER_DN
3	7e−05	4 / 80	BASSO_CD40_SIGNALING_UP
4	3e−04	6 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
5	4e−04	5 / 232	RICKMAN_METASTASIS_DN
6	5e−04	5 / 242	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
7	6e−04	6 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
8	7e−04	3 / 64	AMIT_EGF_RESPONSE_120_HELA
9	7e−04	8 / 723	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
10	7e−04	2 / 15	LIU_IL13_MEMORY_MODEL_UP
11	8e−04	3 / 66	PID_VEGFR1_2_PATHWAY
12	8e−04	4 / 153	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
13	8e−04	2 / 16	BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN
14	1e−03	5 / 284	HELLER_HDAC_TARGETS_UP
15	1e−03	4 / 166	DARWICHE_SKIN_TUMOR_PROMOTER_DN

HM

Rank	p−value	#in/all	Geneset
1	0.08	2 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.08	1 / 29	HALLMARK_NOTCH_SIGNALING
3	0.08	2 / 175	HALLMARK_XENOBIOTIC_METABOLISM
4	0.09	1 / 33	HALLMARK_ANGIOGENESIS
5	0.09	2 / 183	HALLMARK_APICAL_JUNCTION
6	0.09	2 / 191	HALLMARK_INFLAMMATORY_RESPONSE
7	0.21	1 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.22	1 / 91	HALLMARK_ANDROGEN_RESPONSE
9	0.27	1 / 116	HALLMARK_SPERMATOGENESIS
10	0.29	1 / 127	HALLMARK_COAGULATION
11	0.31	1 / 137	HALLMARK_UV_RESPONSE_UP
12	0.34	1 / 151	HALLMARK_APOPTOSIS
13	0.36	1 / 162	HALLMARK_ALLOGRAFT_REJECTION
14	0.37	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	0.38	1 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 211	Homuth_BMI−associated−genes_DN
2	0.3	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 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−11	46 / 7448	HOPP_Strong_enhancer
2	1e−07	34 / 5356	HOPP_Txn_transition
3	2e−06	38 / 7275	HOPP_Txn_elongation
4	9e−03	32 / 8226	HOPP_Active_promoter
5	3e−02	4 / 455	SPANG_CD40 6hrs DN
6	4e−02	1 / 14	Subero_T−ALL_hypo_meth
7	5e−02	1 / 19	DAVE_BL Inter
8	6e−02	3 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−(
9	6e−02	3 / 331	WIRTH_lymphoma937_spot H
10	7e−02	1 / 28	DAVE_Immune response 1
11	8e−02	1 / 31	Care_Extended T−cell
12	9e−02	1 / 33	Subero_T−PLL_hypo_meth
13	1e−01	3 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC·
14	1e−01	3 / 464	WIRTH_lymphoma937_spot I
15	2e−01	1 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_(

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	8e−06	7 / 268	actin binding
2	3e−05	40 / 8818	protein binding
3	3e−04	4 / 115	actin filament binding
4	6e−04	2 / 14	mitogen−activated protein kinase kinase binding
5	2e−03	5 / 311	enzyme binding
6	2e−03	2 / 22	calmodulin−dependent protein kinase activity
7	3e−03	3 / 107	SH3 domain binding
8	5e−03	3 / 127	lipid binding
9	2e−02	4 / 351	GTP binding
10	2e−02	2 / 72	protein binding, bridging
11	2e−02	3 / 213	GTPase activity
12	2e−02	3 / 213	protein complex binding
13	2e−02	3 / 217	protein kinase activity
14	3e−02	1 / 10	inositol−1,4,5−trisphosphate 3−kinase activity
15	3e−02	1 / 12	actin−dependent ATPase 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	0.006	3 / 133	hsa−miR−485−5p
2	0.014	2 / 66	hsa−miR−637
3	0.016	2 / 72	hsa−miR−935
4	0.017	2 / 74	hsa−miR−877
5	0.022	2 / 84	hsa−miR−486−3p
6	0.024	2 / 88	hsa−miR−423−5p
7	0.028	2 / 96	hsa−miR−125b
8	0.036	2 / 110	hsa−miR−190b
9	0.042	2 / 120	hsa−miR−493
10	0.048	1 / 18	hsa−miR−564
11	0.048	2 / 129	hsa−miR−320d
12	0.058	2 / 143	hsa−miR−320c
13	0.058	1 / 22	hsa−miR−663
14	0.063	1 / 24	hsa−miR−602
15	0.063	1 / 24	hsa−miR−632

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	5e−04	5 / 240	Chaussabel_3,3_Inflammation II
2	2e−03	10 / 1268	PROTEINATLAS_colon
3	8e−03	3 / 150	Chaussabel_2,6_Myeloid lineage
4	9e−03	5 / 465	PROTEINATLAS_liver
5	1e−02	8 / 1173	PROTEINATLAS_rectum
6	1e−02	8 / 1176	PROTEINATLAS_duodenum
7	2e−02	5 / 598	PROTEINATLAS_prostate
8	3e−02	4 / 412	WIRTH_Immune system
9	3e−02	7 / 1138	PROTEINATLAS_small intestine
10	4e−02	7 / 1194	PROTEINATLAS_stomach
11	6e−02	5 / 782	PROTEINATLAS_thyroid gland
12	6e−02	1 / 24	VAQUERIZAS_Spinal cord_TF
13	8e−02	6 / 1118	PROTEINATLAS_placenta
14	1e−01	4 / 640	PROTEINATLAS_parathyroid gland
15	1e−01	6 / 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	0.02	10 / 1723	HEBENSTREIT_high expression TF
2	0.02	20 / 4735	ICGC_Pu1_targets
3	0.02	19 / 4468	ICGC_Egr1_targets
4	0.03	13 / 2759	ICGC_Bcl3_targets
5	0.04	23 / 5984	ICGC_Mta3_targets
6	0.05	20 / 5188	ICGC_Ebfsc137065_targets
7	0.05	21 / 5518	ICGC_Stat5_targets
8	0.06	26 / 7247	ICGC_Runx3_targets
9	0.07	20 / 5312	ICGC_Tcf12_targets
10	0.08	19 / 5067	ICGC_Taf1_targets
11	0.08	10 / 2255	ICGC_SrfV0416101_targets
12	0.09	24 / 6868	ICGC_Elf1_targets
13	0.09	23 / 6552	ICGC_Pol2_targets
14	0.10	22 / 6267	ICGC_Yy1_targets
15	0.11	22 / 6322	ICGC_Tcf3_targets

Overexpression Spots

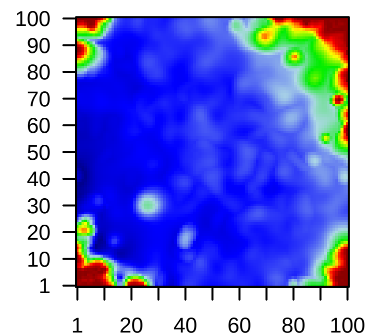
Spot Summary: I

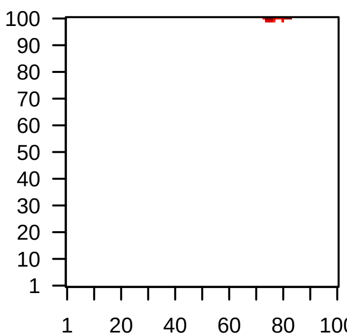
metagenes = 16
genes = 203

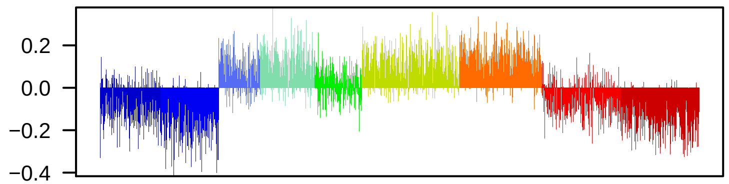
<r> metagenes = 0.81
<r> genes = 0.32
beta: r2= 20.46 / log p= −Inf

samples with spot = 504 (14.9 %)

- A * : 1 (0.3 %)
- A C F * : 51 (21.7 %)
- A F * : 97 (31.5 %)
- C F * : 11 (4.2 %)
- F * : 161 (29 %)
- F J * : 181 (39.1 %)
- J * : 2 (0.4 %)





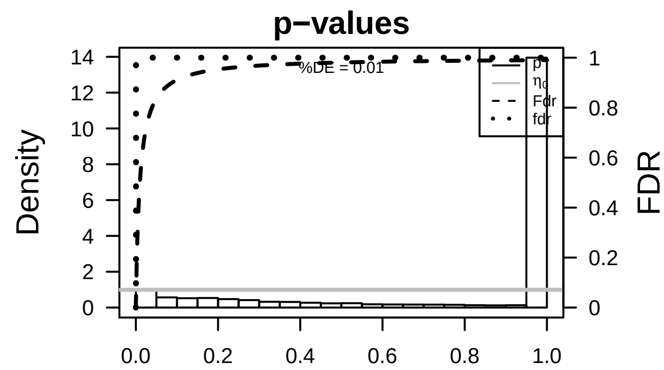


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_175063	2.47	−2.69	0.76		
2	ILMN_218086	2.33	−2.64	0.75		ribosomal protein S26 pseudogene 11 [Source:HGNC Symbo
3	ILMN_172664	2.23	−2.64	0.75		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
4	ILMN_324883	2.2	−2.25	0.77		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
5	ILMN_231070	2.2	−2.41	0.77		
6	ILMN_320919	2.15	−2.18	0.75	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
7	ILMN_167852	2.13	−2.24	0.75		
8	ILMN_220902	2.12	−2.29	0.75	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
9	ILMN_169558	2.09	−2.34	0.76	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_329699	2.07	−2.21	0.77		
11	ILMN_329001	2.01	−1.81	0.76		ribosomal protein S26 pseudogene 2 [Source:HGNC Symbol;
12	ILMN_167769	2.01	−2.28	0.78		ribosomal protein S26 pseudogene 35 [Source:HGNC Symbo
13	ILMN_328515	1.94	−2.25	0.78	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
14	ILMN_324228	1.92	−2.21	0.77	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
15	ILMN_325449	1.92	−1.96	0.76		ribosomal protein S26 pseudogene 55 [Source:HGNC Symbo
16	ILMN_329995	1.62	−2.05	0.73	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
17	ILMN_173799	1.42	−0.99	0.76		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
18	ILMN_329151	1.39	−1.4	0.76		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
19	ILMN_165795	1.29	−0.97	0.77		
20	ILMN_323667	1.29	−0.96	0.76		ribosomal protein S26 pseudogene 13 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−15	70 / 3450	Chror	4_TxTrans_Fibroblasts
2	2e−12	118 / 9054	Colon	Tx_Colon
3	7e−12	121 / 9555	Colon	TssA_Colon
4	8e−12	37 / 1304	CC	mitochondrion
5	2e−11	83 / 5356	Lympl	HOPP_Txn_transition
6	9e−11	118 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
7	1e−10	55 / 2845	Colon	TxEnhG1_Colon
8	2e−10	84 / 5699	Chror	6_EnhG_Melanocytes
9	2e−10	99 / 7354	Colon	TssF_Colon
10	3e−09	19 / 450	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
11	3e−08	133 / 12298	Chror	2_TssA_Melanocytes
12	3e−08	25 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
13	4e−08	24 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
14	5e−08	34 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
15	5e−08	16 / 374	CC	mitochondrial inner membrane
16	5e−08	129 / 11836	Chror	3_TssF_Melanocytes
17	7e−08	8 / 69	BP	mitochondrial translational elongation
18	1e−07	125 / 11455	Chror	2_TssA_Fibroblasts
19	1e−07	28 / 1167	Refer	PROTEINATLAS_gallbladder
20	1e−07	91 / 7275	Lympl	HOPP_Txn_elongation
21	2e−07	112 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
22	2e−07	68 / 4795	Chror	6_EnhG_Fibroblasts
23	4e−07	24 / 933	Refer	PROTEINATLAS_adrenal gland
24	4e−07	10 / 154	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
25	4e−07	25 / 1013	MF	poly(A) RNA binding
26	6e−07	6 / 39	GSEA	CHEN_HOXA5_TARGETS_9HR_DN
27	1e−06	11 / 217	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
28	1e−06	7 / 71	BP	mitochondrial translational termination
29	1e−06	99 / 8568	Colon	TxWk_Colon
30	2e−06	14 / 371	GSEA	MOOTHA_HUMAN_MITODB_6_2002
31	2e−06	26 / 1176	Refer	PROTEINATLAS_duodenum
32	3e−06	14 / 388	GSEA	MOOTHA_MITOCHONDRIA
33	3e−06	5 / 29	CC	mitochondrial large ribosomal subunit
34	3e−06	36 / 2028	Chror	4_TxTrans_Melanocytes
35	6e−06	14 / 416	Chror	4_TxTrans_Neuronal_Progenitor
36	6e−06	9 / 163	BP	rRNA processing
37	7e−06	22 / 959	Refer	PROTEINATLAS_nasopharynx
38	7e−06	9 / 167	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
39	8e−06	22 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
40	8e−06	9 / 169	MF	structural constituent of ribosome



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	7e−08	8 / 69	mitochondrial translational elongation
2	1e−06	7 / 71	mitochondrial translational termination
3	6e−06	9 / 163	rRNA processing
4	1e−04	4 / 32	mitochondrial electron transport, NADH to ubiquinone
5	5e−04	4 / 46	mitochondrial respiratory chain complex I assembly
6	7e−04	7 / 184	translation
7	3e−03	2 / 10	microvillus assembly
8	3e−03	2 / 10	negative regulation of intrinsic apoptotic signaling pathway in response to DN/
9	3e−03	3 / 36	cellular response to UV
10	3e−03	6 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
11	3e−03	2 / 11	positive regulation of transcription from RNA polymerase II promoter in respor
12	4e−03	2 / 12	maturation of LSU−rRNA
13	4e−03	2 / 12	PERK−mediated unfolded protein response
14	5e−03	2 / 13	alternative mRNA splicing, via spliceosome
15	5e−03	2 / 13	cerebellar Purkinje cell layer development

Brain

Rank	p−value	#in/all	Geneset
1	9e−11	118 / 9504	Overlap_fetal_midbrain_K9K27me3
2	2e−07	112 / 9815	Overlap_fetal_midbrain_ReprPC
3	5e−05	45 / 3164	Mid_Frontal_Lobe_ZNF
4	6e−05	18 / 796	Overlap_fetal_midbrain_ZNF
5	8e−05	108 / 10430	Overlap_fetal_midbrain_Quies
6	3e−04	17 / 818	Mid_Frontal_Lobe_Het
7	2e−02	60 / 5936	Overlap_fetal_midbrain_HetRpts
8	3e−02	21 / 1728	Fetal_ReprPCWk
9	5e−02	6 / 328	Fetal_Het
10	1e−01	11 / 906	Fetal_HetRpts
11	4e−01	4 / 386	Fetal_ZNF
12	4e−01	2 / 180	Overlap_fetal_midbrain_Het
13	6e−01	1 / 110	Overlap_fetal_midbrain_Tx
14	8e−01	18 / 2654	Fetal_Quies
15	9e−01	17 / 2709	Mid_Frontal_Lobe_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	6 / 301	SPANG_BCL6−index2
2	0.07	1 / 9	GENTLES_modul5
3	0.10	1 / 14	GENTLES_modul10
4	0.11	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.11	2 / 73	SHAUGHNESSY_MM high risk
6	0.17	3 / 178	SPANG_LPS−index2
7	0.26	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.26	1 / 38	KUIPER_MM good survival
9	0.27	1 / 39	ZHANG_MM up
10	0.31	1 / 46	PanCan_DNARepair_geneset_nanostring
11	0.34	0 / 13	RHODES_CANCER_META_SIGNATURE
12	0.49	0 / 14	LIU_PROSTATE_CANCER_UP
13	0.60	4 / 527	Lembcke_Normal vs Adenoma
14	0.60	1 / 117	PanCan_Driver_Gene_geneset_nanostring
15	0.63	1 / 125	PanCan_CC+Apop_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	8e−12	37 / 1304	mitochondrion
2	5e−08	16 / 374	mitochondrial inner membrane
3	3e−06	5 / 29	mitochondrial large ribosomal subunit
4	1e−04	4 / 33	mitochondrial respiratory chain complex I
5	1e−03	3 / 25	preribosome, large subunit precursor
6	1e−03	34 / 2535	nucleoplasm
7	2e−03	14 / 721	nucleolus
8	3e−03	3 / 36	condensed nuclear chromosome
9	4e−03	2 / 12	small ribosomal subunit
10	5e−03	53 / 4828	nucleus
11	6e−03	31 / 2464	extracellular exosome
12	7e−03	2 / 16	proteasome core complex
13	8e−03	3 / 51	proteasome complex
14	9e−03	2 / 18	telomerase holoenzyme complex
15	1e−02	2 / 20	mitochondrial small ribosomal subunit

Chr

Rank	p−value	#in/all	Geneset
1	0.08	12 / 954	Chr 9
2	0.08	12 / 959	Chr 16
3	0.08	14 / 1170	Chr 7
4	0.22	7 / 619	Chr 20
5	0.25	6 / 536	Chr 22
6	0.28	4 / 342	Chr 18
7	0.32	13 / 1411	Chr 11
8	0.35	12 / 1318	Chr 17
9	0.37	13 / 1467	Chr 19
10	0.43	4 / 422	Chr 13
11	0.43	10 / 1160	Chr 12
12	0.46	9 / 1060	Chr 5
13	0.57	6 / 769	Chr 15
14	0.65	6 / 836	Chr 8
15	0.74	8 / 1211	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−15	70 / 3450	4_TxTrans_Fibroblasts
2	2e−10	84 / 5699	6_EnhG_Melanocytes
3	3e−08	133 / 12298	2_TssA_Melanocytes
4	5e−08	129 / 11836	3_TssF_Melanocytes
5	1e−07	125 / 11455	2_TssA_Fibroblasts
6	2e−07	68 / 4795	6_EnhG_Fibroblasts
7	3e−06	36 / 2028	4_TxTrans_Melanocytes
8	6e−06	14 / 416	4_TxTrans_Neuronal_Progenitor
9	8e−06	131 / 12983	2_TssA_Neuronal_Progenitor
10	6e−04	98 / 9635	3_TssF_Fibroblasts
11	1e−03	75 / 6970	5_Tx_Neuronal_Progenitor
12	7e−03	18 / 1206	6_EnhG_Neuronal_Progenitor
13	1e−02	61 / 5956	3_TssF_Neuronal_Progenitor
14	2e−02	76 / 7854	5_Tx_Fibroblasts
15	3e−02	82 / 8771	5_Tx_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	118 / 9054	Tx_Colon
2	7e−12	121 / 9555	TssA_Colon
3	1e−10	55 / 2845	TxEnhG1_Colon
4	2e−10	99 / 7354	TssF_Colon
5	4e−08	24 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	5e−08	34 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	1e−06	99 / 8568	TxWk_Colon
8	8e−06	22 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
9	1e−05	75 / 6138	TssD2_Colon
10	4e−04	108 / 10779	Enh_Colon
11	1e−03	21 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	4e−03	105 / 10999	TssWk_Colon
13	1e−02	84 / 8678	Quies3_Colon
14	1e−02	56 / 5373	EnhWk1_Colon
15	2e−02	5 / 203	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Glio

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 55	Stuehler_Proteins_up_in_STS
2	3e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
3	4e−02	6 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	1e−01	5 / 315	Up
5	1e−01	2 / 84	GIEZELT_GBM_STS_up_VS_LTS
6	2e−01	2 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
7	2e−01	1 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
8	2e−01	9 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
9	2e−01	2 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	2e−01	1 / 32	Donson−Misc immune function−associated with LTS in HGA
11	2e−01	1 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
12	3e−01	1 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
13	3e−01	16 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
14	3e−01	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	3e−01	2 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−09	19 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
2	3e−08	25 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	4e−07	10 / 154	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
4	6e−07	6 / 39	CHEN_HOXA5_TARGETS_9HR_DN
5	1e−06	11 / 217	PENG_RAPAMYCIN_RESPONSE_DN
6	2e−06	14 / 371	MOOTHA_HUMAN_MITODB_6_2002
7	3e−06	14 / 388	MOOTHA_MITOCHONDRIA
8	1e−05	13 / 389	GARY_CD5_TARGETS_DN
9	2e−05	11 / 282	PENG_GLUTAMINE_DEPRIVATION_DN
10	2e−05	17 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
11	4e−05	5 / 49	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
12	5e−05	26 / 1417	PUJANA_BRCA1_PCC_NETWORK
13	6e−05	14 / 515	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
14	6e−05	18 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
15	7e−05	8 / 171	BURTON_ADIPOGENESIS_6

HM

Rank	p−value	#in/all	Geneset
1	7e−06	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	3e−03	6 / 176	HALLMARK_ADIPOGENESIS
3	9e−03	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	2e−02	4 / 130	HALLMARK_DNA_REPAIR
5	5e−02	4 / 179	HALLMARK_G2M_CHECKPOINT
6	6e−02	4 / 185	HALLMARK_MTORC1_SIGNALING
7	7e−02	2 / 54	HALLMARK_MYC_TARGETS_V2
8	1e−01	3 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	2e−01	3 / 170	HALLMARK_MYC_TARGETS_V1
10	2e−01	3 / 173	HALLMARK_E2F_TARGETS
11	2e−01	3 / 183	HALLMARK_GLYCOLYSIS
12	3e−01	2 / 137	HALLMARK_UV_RESPONSE_UP
13	3e−01	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	4e−01	2 / 185	HALLMARK_P53_PATHWAY
15	4e−01	2 / 189	HALLMARK_HYPOXIA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	5 / 211	Homuth_BMI−associated−genes_DN
2	0.32	2 / 147	Homuth_BMI−associated−genes_UP
3	1.00	0 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−11	83 / 5356	HOPP_Txn_transition
2	1e−07	91 / 7275	HOPP_Txn_elongation
3	2e−04	89 / 8226	HOPP_Active_promoter
4	2e−04	4 / 39	CARO_OxPhos_in_DLBCL_UP
5	1e−03	15 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	1e−03	4 / 60	SPANG_BAFF 9hrs DN
7	1e−03	15 / 777	WIRTH_lymphoma937_spot D
8	2e−03	7 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
9	2e−03	7 / 232	WIRTH_lymphoma937_spot B
10	9e−03	2 / 18	Aukema_BCL2 UP_BCL6 DN
11	1e−02	9 / 455	SPANG_CD40 6hrs DN
12	1e−02	4 / 115	ROSOLOWSKI_green total
13	2e−02	78 / 8098	HOPP_Weak_promoter
14	2e−02	6 / 283	TARTE_Plasmablast signature
15	5e−02	2 / 43	Monti_OxPhos_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	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	4e−07	25 / 1013	poly(A) RNA binding
2	8e−06	9 / 169	structural constituent of ribosome
3	1e−04	4 / 32	NADH dehydrogenase (ubiquinone) activity
4	1e−03	4 / 59	damaged DNA binding
5	3e−03	88 / 8818	protein binding
6	4e−03	2 / 12	exonuclease activity
7	5e−03	2 / 14	telomerase RNA binding
8	6e−03	3 / 46	ligand−dependent nuclear receptor transcription coactivator activity
9	9e−03	2 / 18	threonine−type endopeptidase activity
10	1e−02	2 / 21	cytokine receptor activity
11	1e−02	2 / 22	protein kinase activator activity
12	1e−02	3 / 62	p53 binding
13	1e−02	3 / 62	syntaxin binding
14	2e−02	5 / 185	magnesium ion binding
15	2e−02	2 / 29	rRNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	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	0.4	1 / 73	Stroke, susceptibility to
14	0.5	1 / 76	Muscular
15	0.5	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 85	hsa−miR−510
2	6e−04	11 / 425	hsa−let−7b
3	1e−03	6 / 144	hsa−miR−140−5p
4	1e−03	4 / 58	hsa−miR−379
5	2e−03	4 / 71	hsa−miR−939
6	6e−03	3 / 46	hsa−miR−658
7	6e−03	3 / 46	hsa−miR−575
8	6e−03	8 / 342	hsa−let−7e
9	8e−03	3 / 52	hsa−miR−940
10	1e−02	8 / 382	hsa−let−7c
11	1e−02	7 / 316	hsa−let−7f
12	2e−02	3 / 66	hsa−miR−550
13	2e−02	5 / 191	hsa−miR−222
14	2e−02	3 / 71	hsa−miR−1266
15	2e−02	7 / 343	hsa−let−7a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	1 / 12	BENTINK_ras.1
2	0.10	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	1e−07	28 / 1167	PROTEINATLAS_gallbladder
2	4e−07	24 / 933	PROTEINATLAS_adrenal gland
3	2e−06	26 / 1176	PROTEINATLAS_duodenum
4	7e−06	22 / 959	PROTEINATLAS_nasopharynx
5	2e−05	15 / 535	PROTEINATLAS_spleen
6	2e−05	24 / 1194	PROTEINATLAS_stomach
7	3e−05	19 / 816	PROTEINATLAS_endometrium
8	3e−05	18 / 759	PROTEINATLAS_epididymis
9	3e−05	16 / 619	PROTEINATLAS_salivary gland
10	3e−05	22 / 1063	PROTEINATLAS_tonsil
11	4e−05	14 / 490	PROTEINATLAS_heart muscle
12	4e−05	16 / 623	PROTEINATLAS_seminal vesicle
13	4e−05	7 / 119	Chaussabel_2,4_Ribosomal proteins
14	5e−05	21 / 1003	PROTEINATLAS_appendix
15	6e−05	24 / 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−05	26 / 1452	ICGC_Six5_targets
2	1e−04	23 / 1231	KIM_MYC targets
3	3e−04	25 / 1498	ICGC_Ets1_targets
4	4e−04	60 / 5067	ICGC_Taf1_targets
5	9e−04	52 / 4345	ICGC_Zeb1_targets
6	2e−03	30 / 2215	ICGC_GabpPcr2_targets
7	3e−03	22 / 1478	ICGC_Myc_targets
8	3e−03	69 / 6552	ICGC_Pol2_targets
9	5e−03	63 / 5961	ICGC_Pol24_targets
10	5e−03	59 / 5518	ICGC_Stat5_targets
11	6e−03	58 / 5442	ICGC_Pmlsc71910_targets
12	8e−03	57 / 5383	ICGC_Sp1_targets
13	9e−03	3 / 55	MYC_Targets UP
14	1e−02	69 / 6868	ICGC_Elf1_targets
15	1e−02	61 / 5984	ICGC_Mta3_targets

Overexpression Spots

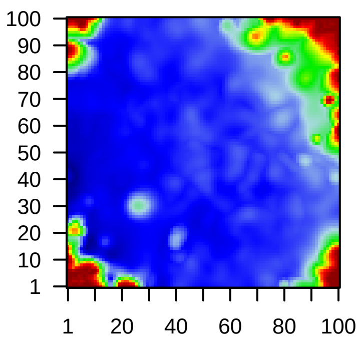
Spot Summary: J

metagenes = 30
genes = 622

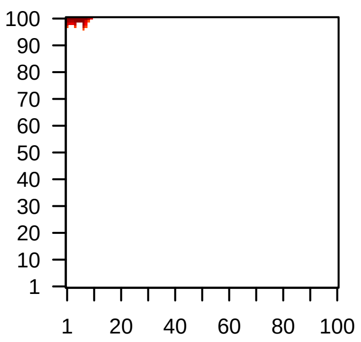
<r> metagenes = 0.91
<r> genes = 0.33
beta: r2= 21.97 / log p= −Inf

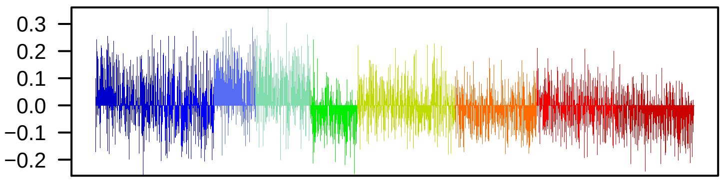
samples with spot = 247 (7.3 %)
- A * : 54 (15.7 %)
- A C * : 31 (9.5 %)
- A C F * : 56 (23.8 %)
- A F * : 60 (19.5 %)
- C F * : 2 (0.8 %)
- F * : 24 (4.3 %)
- F J * : 7 (1.5 %)
- J * : 11 (2.5 %)
- N * : 2 (0.5 %)

Overview Map



Spot





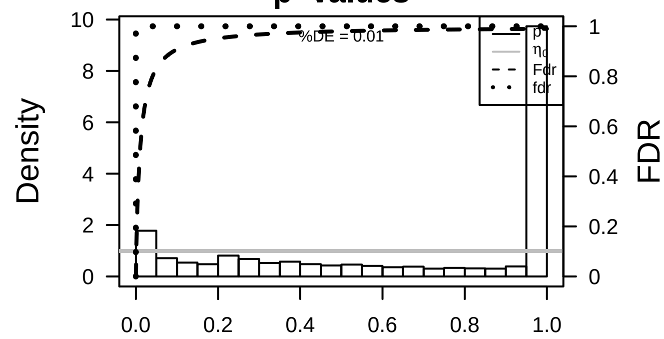
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_220158	1.9	−1.61	0.21		
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	0.24		
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	0.44	RRP7A	ribosomal RNA processing 7 homolog A [Source:HGNC Sym
11	ILMN_178404	0.93	−0.68	0.39		
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	0.49		
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	0.52	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	0.46	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	3e−96	399 / 7354	Colon	TssF_Colon
2	6e−83	265 / 3450	Chror	4_TxTrans_Fibroblasts
3	2e−71	418 / 9555	Colon	TssA_Colon
4	4e−70	293 / 4795	Chror	6_EnhG_Fibroblasts
5	1e−68	318 / 5699	Chror	6_EnhG_Melanocytes
6	1e−63	396 / 9054	Colon	Tx_Colon
7	5e−63	452 / 11836	Chror	3_TssF_Melanocytes
8	2e−57	453 / 12298	Chror	2_TssA_Melanocytes
9	4e−54	203 / 2845	Colon	TxEnhG1_Colon
10	1e−49	300 / 6138	Colon	TssD2_Colon
11	2e−47	408 / 10779	Colon	Enh_Colon
12	2e−47	451 / 12983	Chror	2_TssA_Neuronal_Progenitor
13	3e−47	161 / 2028	Chror	4_TxTrans_Melanocytes
14	2e−45	201 / 3164	Brain	Mid_Frontal_Lobe_ZNF
15	1e−44	378 / 9635	Chror	3_TssF_Fibroblasts
16	2e−43	373 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
17	2e−43	351 / 8568	Colon	TxWk_Colon
18	7e−43	414 / 11455	Chror	2_TssA_Fibroblasts
19	9e−40	179 / 2810	Colon	EnhA_Colon
20	9e−39	275 / 5956	Chror	3_TssF_Neuronal_Progenitor
21	2e−33	248 / 5373	Colon	EnhWk1_Colon
22	1e−24	354 / 10430	Brain	Overlap_fetal_midbrain_Quies
23	9e−24	291 / 7854	Chror	5_Tx_Fibroblasts
24	1e−23	217 / 5067	TF	ICGC_Taf1_targets
25	3e−23	312 / 8771	Chror	5_Tx_Melanocytes
26	1e−22	102 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
27	1e−20	61 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
28	2e−20	243 / 6322	TF	ICGC_Tcf3_targets
29	2e−20	257 / 6868	TF	ICGC_Elf1_targets
30	4e−20	216 / 5356	Lympl	HOPP_Txn_transition
31	1e−19	218 / 5466	TF	ICGC_Nficsc81335_targets
32	1e−19	219 / 5518	TF	ICGC_Stat5_targets
33	5e−19	85 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
34	2e−18	65 / 818	Brain	Mid_Frontal_Lobe_Het
35	4e−18	213 / 5442	TF	ICGC_Pmlsc71910_targets
36	5e−18	182 / 4345	TF	ICGC_Zeb1_targets
37	9e−18	242 / 6578	TF	ICGC_Pou2_targets
38	1e−17	175 / 4131	TF	ICGC_Nfatc1_targets
39	2e−17	251 / 6970	Chror	5_Tx_Neuronal_Progenitor
40	5e−17	257 / 7247	TF	ICGC_Runx3_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	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	

BP

Rank	p−value	#in/all	Geneset
1	5e−07	8 / 32	mitochondrial electron transport, NADH to ubiquinone
2	8e−07	9 / 46	mitochondrial respiratory chain complex I assembly
3	3e−06	14 / 137	ER to Golgi vesicle−mediated transport
4	3e−05	9 / 69	mitochondrial translational elongation
5	3e−05	9 / 71	mitochondrial translational termination
6	9e−05	7 / 47	proton transport
7	1e−04	9 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
8	1e−04	5 / 23	mitochondrial translation
9	2e−04	7 / 52	IRE1−mediated unfolded protein response
10	2e−04	14 / 196	mRNA splicing, via spliceosome
11	3e−04	4 / 15	apoptotic cell clearance
12	6e−04	25 / 530	biological_process
13	8e−04	6 / 48	negative regulation of protein binding
14	1e−03	4 / 20	positive regulation of protein dephosphorylation
15	1e−03	5 / 35	activation of JUN kinase activity

Brain

Rank	p−value	#in/all	Geneset
1	2e−45	201 / 3164	Mid_Frontal_Lobe_ZNF
2	2e−43	373 / 9504	Overlap_fetal_midbrain_K9K27me3
3	1e−24	354 / 10430	Overlap_fetal_midbrain_Quies
4	2e−18	65 / 818	Mid_Frontal_Lobe_Het
5	4e−16	128 / 2709	Mid_Frontal_Lobe_HetRpts
6	4e−15	313 / 9815	Overlap_fetal_midbrain_ReprPC
7	3e−13	89 / 1728	Fetal_ReprPCWk
8	9e−10	150 / 4112	Mid_Frontal_Lobe_ReprPC
9	1e−04	173 / 5936	Overlap_fetal_midbrain_HetRpts
10	2e−03	32 / 796	Overlap_fetal_midbrain_ZNF
11	1e−02	32 / 906	Fetal_HetRpts
12	2e−02	63 / 2127	Mid_Frontal_Lobe_K9K27me3
13	2e−02	9 / 180	Overlap_fetal_midbrain_Het
14	5e−02	73 / 2654	Fetal_Quies
15	1e−01	13 / 386	Fetal_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	15 / 301	SPANG_BCL6−index2
2	0.005	22 / 527	Lembcke_Normal vs Adenoma
3	0.034	2 / 13	GENTLES_modul2
4	0.040	2 / 14	LIU_PROSTATE_CANCER_UP
5	0.051	2 / 16	GENTLES_modul7
6	0.053	8 / 178	SPANG_LPS−index2
7	0.059	1 / 14	LIU_COMMON_CANCER_GENES
8	0.126	3 / 54	KUIPER_MM poor survival
9	0.188	1 / 9	GENTLES_modul3
10	0.188	1 / 9	GENTLES_modul5
11	0.199	2 / 36	PanCan_HK_geneset_nanostring
12	0.260	1 / 13	GENTLES_modul12
13	0.277	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
14	0.277	1 / 14	GENTLES_modul1
15	0.277	1 / 14	GENTLES_modul10

CC

Rank	p−value	#in/all	Geneset
1	8e−15	117 / 2464	extracellular exosome
2	1e−13	75 / 1304	mitochondrion
3	9e−12	34 / 374	mitochondrial inner membrane
4	2e−10	90 / 1979	membrane
5	2e−10	120 / 2979	cytosol
6	4e−08	9 / 33	mitochondrial respiratory chain complex I
7	1e−06	156 / 4822	cytoplasm
8	8e−06	18 / 234	lysosomal membrane
9	9e−06	91 / 2535	nucleoplasm
10	1e−05	38 / 775	endoplasmic reticulum
11	1e−05	20 / 287	mitochondrial matrix
12	2e−05	12 / 119	vesicle
13	4e−05	8 / 57	endoplasmic reticulum−Golgi intermediate compartment
14	6e−05	14 / 178	endoplasmic reticulum lumen
15	3e−04	34 / 788	endoplasmic reticulum membrane

Chr

Rank	p−value	#in/all	Geneset
1	7e−12	77 / 1467	Chr 19
2	5e−06	45 / 959	Chr 16
3	3e−04	26 / 536	Chr 22
4	8e−04	51 / 1411	Chr 11
5	5e−03	45 / 1318	Chr 17
6	5e−02	21 / 619	Chr 20
7	5e−02	30 / 954	Chr 9
8	6e−01	51 / 2323	Chr 1
9	8e−01	5 / 289	Chr 21
10	9e−01	22 / 1170	Chr 7
11	9e−01	22 / 1217	Chr 3
12	9e−01	13 / 768	Chr 14
13	1e+00	14 / 904	Chr 10
14	1e+00	11 / 769	Chr 15
15	1e+00	19 / 1211	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−83	265 / 3450	4_TxTrans_Fibroblasts
2	4e−70	293 / 4795	6_EnhG_Fibroblasts
3	1e−68	318 / 5699	6_EnhG_Melanocytes
4	5e−63	452 / 11836	3_TssF_Melanocytes
5	2e−57	453 / 12298	2_TssA_Melanocytes
6	2e−47	451 / 12983	2_TssA_Neuronal_Progenitor
7	3e−47	161 / 2028	4_TxTrans_Melanocytes
8	1e−44	378 / 9635	3_TssF_Fibroblasts
9	7e−43	414 / 11455	2_TssA_Fibroblasts
10	9e−39	275 / 5956	3_TssF_Neuronal_Progenitor
11	9e−24	291 / 7854	5_Tx_Fibroblasts
12	3e−23	312 / 8771	5_Tx_Melanocytes
13	2e−17	251 / 6970	5_Tx_Neuronal_Progenitor
14	8e−13	351 / 11847	7_Enh_Neuronal_Progenitor
15	5e−11	364 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−96	399 / 7354	TssF_Colon
2	2e−71	418 / 9555	TssA_Colon
3	1e−63	396 / 9054	Tx_Colon
4	4e−54	203 / 2845	TxEnhG1_Colon
5	1e−49	300 / 6138	TssD2_Colon
6	2e−47	408 / 10779	Enh_Colon
7	2e−43	351 / 8568	TxWk_Colon
8	9e−40	179 / 2810	EnhA_Colon
9	2e−33	248 / 5373	EnhWk1_Colon
10	1e−22	102 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	5e−19	85 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	2e−14	57 / 789	TxEnhG2_Colon
13	2e−09	265 / 8678	Quies3_Colon
14	3e−09	318 / 10999	TssWk_Colon
15	1e−06	81 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tr

Glio

Rank	p−value	#in/all	Geneset
1	3e−08	15 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	4e−08	10 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
3	3e−06	15 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	7e−05	37 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	3e−04	63 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	9e−04	6 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	3e−03	16 / 315	Up
8	4e−03	6 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	4e−03	65 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
10	3e−02	6 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
11	3e−02	8 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
12	4e−02	3 / 32	Donson−Misc immune function−associated with LTS in HGA
13	4e−02	4 / 55	Stuehler_Proteins_up_in_STS
14	4e−02	11 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
15	5e−02	6 / 113	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−20	61 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
2	1e−16	65 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	2e−15	56 / 723	GRADE_COLON_CANCER_UP
4	3e−15	60 / 831	LOPEZ_MBD_TARGETS
5	6e−14	41 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
6	6e−14	41 / 451	ENK_UV_RESPONSE_KERATINOCYTE_UP
7	2e−13	47 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
8	5e−13	17 / 73	LI_DCP2_BOUND_MRNA
9	1e−12	54 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
10	1e−12	46 / 607	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
11	1e−12	28 / 237	LU_EZH2_TARGETS_UP
12	5e−12	33 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
13	2e−11	35 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
14	2e−11	31 / 325	DAIRKEE_TERT_TARGETS_UP
15	3e−11	43 / 593	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−06	16 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	2e−06	14 / 130	HALLMARK_DNA_REPAIR
3	7e−03	10 / 176	HALLMARK_ADIPOGENESIS
4	8e−03	5 / 54	HALLMARK_MYC_TARGETS_V2
5	2e−02	6 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	3e−02	9 / 183	HALLMARK_GLYCOLYSIS
7	3e−02	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	6e−02	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
9	7e−02	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	1e−01	6 / 138	HALLMARK_FATTY_ACID_METABOLISM
11	2e−01	6 / 170	HALLMARK_MYC_TARGETS_V1
12	2e−01	6 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	2e−01	5 / 137	HALLMARK_UV_RESPONSE_UP
14	2e−01	6 / 175	HALLMARK_XENOBIOTIC_METABOLISM
15	2e−01	6 / 177	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	10 / 147	Homuth_BMI−associated−genes_UP
2	0.169	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
3	0.206	1 / 10	Marjolein_ageing−genes_UP
4	0.210	7 / 211	Homuth_BMI−associated−genes_DN
5	0.512	1 / 31	DUMEAUX_Fasting enriched genes
6	1.000	0 / 94	DUMEAUX_Smoking enriched genes
7	1.000	0 / 10	DUMEAUX_Smoking literature genes up
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.000	0 / 6	DUMEAUX_Hormon therapy in non 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 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−20	216 / 5356	HOPP_Txn_transition
2	9e−15	274 / 8226	HOPP_Active_promoter
3	4e−13	245 / 7275	HOPP_Txn_elongation
4	1e−09	236 / 7448	HOPP_Strong_enhancer
5	4e−07	240 / 8098	HOPP_Weak_promoter
6	9e−06	38 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	2e−05	21 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−c
8	3e−05	21 / 331	WIRTH_lymphoma937_spot H
9	5e−05	36 / 777	WIRTH_lymphoma937_spot D
10	1e−04	8 / 66	TARTE_Plasma cell signature
11	2e−04	6 / 39	CARO_OxPhos_in_DLBCL_UP
12	1e−02	3 / 21	ROSOLOWSKI_red UP
13	3e−02	3 / 28	DAVE_Immune response 1
14	3e−02	6 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
15	3e−02	6 / 105	WIRTH_lymphoma937_spot MM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 30	Hugo_melanoma−all−MET_UP
2	0.7	1 / 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	

MF

Rank	p−value	#in/all	Geneset
1	2e−16	294 / 8818	protein binding
2	8e−06	46 / 1013	poly(A) RNA binding
3	8e−05	6 / 32	NADH dehydrogenase (ubiquinone) activity
4	4e−04	50 / 1329	ATP binding
5	1e−03	10 / 133	ATPase activity
6	1e−03	27 / 627	molecular_function
7	1e−03	4 / 22	polyubiquitin binding
8	2e−03	4 / 23	proton−transporting ATPase activity, rotational mechanism
9	2e−03	4 / 24	fatty−acyl−CoA binding
10	2e−03	4 / 24	transmembrane transporter activity
11	4e−03	11 / 185	magnesium ion binding
12	5e−03	5 / 49	protein serine/threonine phosphatase activity
13	5e−03	4 / 31	ADP binding
14	6e−03	10 / 169	structural constituent of ribosome
15	8e−03	13 / 265	cadherin binding involved in cell−cell adhesion

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 18	Non−Hodgkin lymphoma, somatic
2	0.4	1 / 20	Parkinson disease
3	0.5	1 / 28	Immunological
4	0.5	1 / 29	Neuroblastoma
5	0.6	1 / 40	Medulloblastoma
6	0.7	1 / 47	Cervical cancer, somatic
7	0.7	1 / 48	Gastric cancer
8	0.7	1 / 48	Multiple myeloma
9	0.7	1 / 56	Myopathy, nemaline, 3
10	0.8	1 / 63	Gastrointestinal
11	0.8	1 / 65	Hepatocellular carcinoma
12	0.8	1 / 68	Glioblastoma multiforme, somatic
13	0.8	1 / 73	Stroke, susceptibility to
14	0.8	1 / 76	Muscular
15	0.9	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	3 / 18	hsa−miR−542−5p
2	0.010	2 / 7	hsa−miR−339−3p
3	0.031	3 / 30	hsa−miR−371−3p
4	0.040	2 / 14	hsa−miR−574−3p
5	0.051	5 / 88	hsa−miR−608
6	0.052	3 / 37	hsa−miR−518e
7	0.052	3 / 37	hsa−miR−1224−5p
8	0.053	4 / 62	hsa−miR−324−3p
9	0.059	3 / 39	hsa−miR−517*
10	0.068	11 / 288	hsa−miR−34a
11	0.075	3 / 43	hsa−miR−661
12	0.088	3 / 46	hsa−miR−874
13	0.092	3 / 47	hsa−miR−370
14	0.096	2 / 23	hsa−miR−668
15	0.097	3 / 48	hsa−miR−329

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 12	BENTINK_ras.1
2	0.03	2 / 13	BENTINK_myc.1
3	0.22	1 / 11	BENTINK_ras.4
4	0.29	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	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−11	28 / 275	Chaussabel_3,7_Spliceosome
2	3e−08	51 / 963	PROTEINATLAS_pancreas
3	3e−08	39 / 640	PROTEINATLAS_parathyroid gland
4	3e−08	61 / 1268	PROTEINATLAS_colon
5	6e−08	40 / 681	PROTEINATLAS_lung
6	1e−07	57 / 1194	PROTEINATLAS_stomach
7	1e−07	56 / 1167	PROTEINATLAS_gallbladder
8	2e−07	56 / 1176	PROTEINATLAS_duodenum
9	4e−07	41 / 759	PROTEINATLAS_epididymis
10	5e−07	51 / 1063	PROTEINATLAS_tonsil
11	9e−07	54 / 1173	PROTEINATLAS_rectum
12	1e−06	52 / 1118	PROTEINATLAS_placenta
13	2e−06	45 / 933	PROTEINATLAS_adrenal gland
14	4e−06	54 / 1239	PROTEINATLAS_testis
15	7e−06	49 / 1097	PROTEINATLAS_kidney

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−23	217 / 5067	ICGC_Taf1_targets
2	2e−20	243 / 6322	ICGC_Tcf3_targets
3	2e−20	257 / 6868	ICGC_Elf1_targets
4	1e−19	218 / 5466	ICGC_Nficsc81335_targets
5	1e−19	219 / 5518	ICGC_Stat5_targets
6	4e−18	213 / 5442	ICGC_Pmlsc71910_targets
7	5e−18	182 / 4345	ICGC_Zeb1_targets
8	9e−18	242 / 6578	ICGC_Pou2_targets
9	1e−17	175 / 4131	ICGC_Nfatc1_targets
10	5e−17	257 / 7247	ICGC_Runx3_targets
11	6e−17	208 / 5383	ICGC_Sp1_targets
12	7e−17	114 / 2215	ICGC_GabpPcr2_targets
13	1e−16	205 / 5312	ICGC_Tcf12_targets
14	1e−15	176 / 4362	ICGC_Creb1_targets
15	2e−15	190 / 4881	ICGC_Atf2_targets

Overexpression Spots

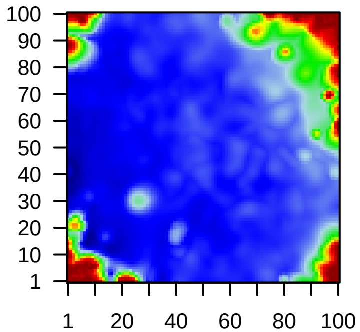
Spot Summary: K

metagenes = 5
genes = 74

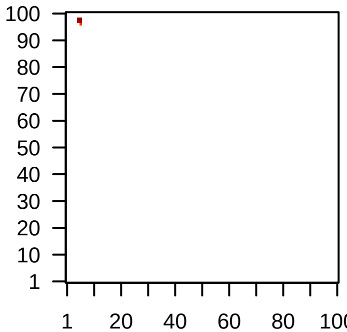
<r> metagenes = 0.99
<r> genes = 0.35
beta: r2= 11.94 / log p= −Inf

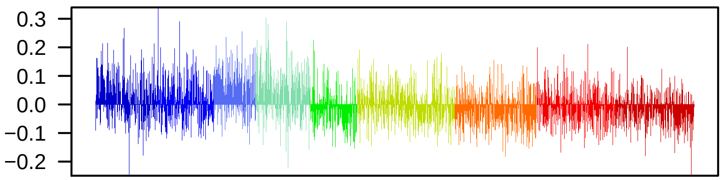
samples with spot = 121 (3.6 %)
- A * : 24 (7 %)
- A C * : 15 (4.6 %)
- A C F * : 26 (11.1 %)
- A F * : 30 (9.7 %)
- C F * : 3 (1.1 %)
- F * : 13 (2.3 %)
- F J * : 5 (1.1 %)
- J * : 4 (0.9 %)
- N * : 1 (0.2 %)

Overview Map



Spot





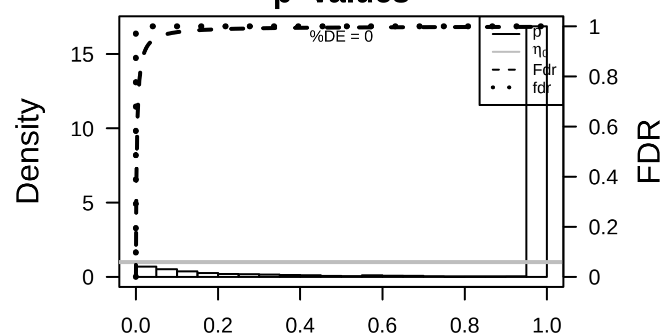
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_182151	1.46	−1.14	0.34		
2	ILMN_213367	0.68	−0.67	0.46	SGSH	N−sulfoglucosamine sulfohydrolase [Source:HGNC Symbol;A
3	ILMN_212574	0.67	−0.6	0.56	CORO1A	coronin 1A [Source:HGNC Symbol;Acc:HGNC:2252]
4	ILMN_179472	0.67	−0.57	0.44	RNF167	ring finger protein 167 [Source:HGNC Symbol;Acc:HGNC:24!
5	ILMN_172570	0.65	−0.36	0.41	MOV10	Mov10 RISC complex RNA helicase [Source:HGNC Symbol;/
6	ILMN_324695	0.64	−0.39	0.45	CMTR1	cap methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:2
7	ILMN_175175	0.63	−0.49	0.57	IDH2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial [Source
8	ILMN_181132	0.6	−0.45	0.74	DPP7	dipeptidyl peptidase 7 [Source:HGNC Symbol;Acc:HGNC:14!
9	ILMN_234413	0.59	−0.69	0.6		
10	ILMN_172835	0.57	−0.68	0.58		
11	ILMN_177511	0.54	−0.52	0.5	SND1	staphylococcal nuclease and tudor domain containing 1 [Sour
12	ILMN_181516	0.54	−0.4	0.48		
13	ILMN_177186	0.5	−0.37	0.5	TXNDC11	thioredoxin domain containing 11 [Source:HGNC Symbol;Acc
14	ILMN_168444	0.5	−0.35	0.65	SPAG7	sperm associated antigen 7 [Source:HGNC Symbol;Acc:HGN
15	ILMN_176368	0.48	−0.42	0.62	C17orf49	chromosome 17 open reading frame 49 [Source:HGNC Symt
16	ILMN_213363	0.48	−0.5	0.58	CTDNEP1	CTD nuclear envelope phosphatase 1 [Source:HGNC Symbo
17	ILMN_180465	0.48	−0.3	0.62	COX14	COX14, cytochrome c oxidase assembly factor [Source:HGN
18	ILMN_240810	0.48	−0.46	0.48	TFIP11	tuftelin interacting protein 11 [Source:HGNC Symbol;Acc:HG
19	ILMN_173934	0.47	−0.35	0.6		
20	ILMN_166909	0.47	−0.34	0.7	ZNF672	zinc finger protein 672 [Source:HGNC Symbol;Acc:HGNC:26

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	9e−17	57 / 9054	Colon	Tx_Colon
2	2e−15	57 / 9555	Colon	TssA_Colon
3	3e−15	51 / 7354	Colon	TssF_Colon
4	2e−14	45 / 5699	Chror	6_EnhG_Melanocytes
5	6e−14	61 / 12298	Chror	2_TssA_Melanocytes
6	1e−13	55 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
7	1e−12	59 / 11836	Chror	3_TssF_Melanocytes
8	1e−12	31 / 2845	Colon	TxEnhG1_Colon
9	6e−12	33 / 3450	Chror	4_TxTrans_Fibroblasts
10	4e−11	25 / 2028	Chror	4_TxTrans_Melanocytes
11	5e−11	55 / 10779	Colon	Enh_Colon
12	1e−09	58 / 12983	Chror	2_TssA_Neuronal_Progenitor
13	1e−09	40 / 6138	Colon	TssD2_Colon
14	5e−08	37 / 5956	Chror	3_TssF_Neuronal_Progenitor
15	6e−08	45 / 8568	Colon	TxWk_Colon
16	9e−08	26 / 3164	Brain	Mid_Frontal_Lobe_ZNF
17	2e−07	32 / 4795	Chror	6_EnhG_Fibroblasts
18	2e−07	34 / 5356	Lympl	HOPP_Txn_transition
19	3e−07	13 / 818	Brain	Mid_Frontal_Lobe_Het
20	5e−07	51 / 11455	Chror	2_TssA_Fibroblasts
21	1e−06	6 / 123	GSEA	KIM_ALL_DISORDERS_DURATION_CORR_DN
22	3e−06	30 / 4822	CC	cytoplasm
23	3e−06	13 / 1013	MF	poly(A) RNA binding
24	9e−06	40 / 8226	Lympl	HOPP_Active_promoter
25	9e−06	11 / 789	Colon	TxEnhG2_Colon
26	1e−05	46 / 10430	Brain	Overlap_fetal_midbrain_Quies
27	2e−05	44 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
28	3e−05	43 / 9635	Chror	3_TssF_Fibroblasts
29	3e−05	8 / 450	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
30	3e−05	14 / 1452	TF	ICGC_Six5_targets
31	7e−05	9 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
32	9e−05	35 / 7275	Lympl	HOPP_Txn_elongation
33	1e−04	19 / 2810	Colon	EnhA_Colon
34	2e−04	39 / 8818	MF	protein binding
35	2e−04	12 / 1304	CC	mitochondrion
36	2e−04	28 / 5373	Colon	EnhWk1_Colon
37	3e−04	13 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
38	3e−04	11 / 1167	Refer	PROTEINATLAS_gallbladder
39	4e−04	4 / 123	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
40	4e−04	4 / 126	GSEA	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	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	0.001	2 / 20	negative regulation of mRNA splicing, via spliceosome
2	0.003	3 / 103	activation of MAPK activity
3	0.003	6 / 530	biological_process
4	0.009	2 / 51	positive regulation of type I interferon production
5	0.009	3 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
6	0.009	2 / 52	IRE1−mediated unfolded protein response
7	0.016	2 / 69	mitochondrial translational elongation
8	0.016	2 / 71	mitochondrial translational termination
9	0.023	8 / 1272	regulation of transcription, DNA−templated
10	0.027	1 / 10	ESCRT III complex disassembly
11	0.027	1 / 10	leukocyte chemotaxis
12	0.027	1 / 10	mitochondrial respiratory chain complex IV assembly
13	0.027	1 / 10	poly(A)+ mRNA export from nucleus
14	0.027	1 / 10	positive regulation of protein sumoylation
15	0.027	1 / 10	regulation of release of sequestered calcium ion into cytosol

Brain

Rank	p−value	#in/all	Geneset
1	1e−13	55 / 9504	Overlap_fetal_midbrain_K9K27me3
2	9e−08	26 / 3164	Mid_Frontal_Lobe_ZNF
3	3e−07	13 / 818	Mid_Frontal_Lobe_Het
4	1e−05	46 / 10430	Overlap_fetal_midbrain_Quies
5	2e−05	44 / 9815	Overlap_fetal_midbrain_ReprPC
6	2e−03	12 / 1728	Fetal_ReprPCWk
7	6e−03	7 / 796	Overlap_fetal_midbrain_ZNF
8	1e−02	25 / 5936	Overlap_fetal_midbrain_HetRpts
9	1e−02	7 / 906	Fetal_HetRpts
10	6e−02	3 / 328	Fetal_Het
11	9e−02	3 / 386	Fetal_ZNF
12	1e−01	11 / 2709	Mid_Frontal_Lobe_HetRpts
13	1e−01	15 / 4112	Mid_Frontal_Lobe_ReprPC
14	2e−01	10 / 2654	Fetal_Quies
15	3e−01	3 / 681	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	1 / 36	PanCan_HK_geneset_nanostring
2	0.21	0 / 14	LIU_PROSTATE_CANCER_UP
3	0.28	1 / 117	PanCan_Driver_Gene_geneset_nanostring
4	0.31	1 / 136	PanCan_RAS_geneset_nanostring
5	0.43	2 / 527	Lembcke_Normal vs Adenoma
6	0.79	1 / 554	Lembcke_Colonic Inflammation
7	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
8	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
9	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_COMMON_CANCER_GENES
13	1.00	0 / 13	LIU_LIVER_CANCER
14	1.00	0 / 15	LIU_PROSTATE_CANCER_DN
15	1.00	0 / 15	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	3e−06	30 / 4822	cytoplasm
2	2e−04	12 / 1304	mitochondrion
3	4e−03	5 / 374	mitochondrial inner membrane
4	8e−03	22 / 4828	nucleus
5	8e−03	4 / 287	mitochondrial matrix
6	2e−02	2 / 74	mitochondrial membrane
7	2e−02	3 / 207	lysosome
8	2e−02	2 / 78	catalytic step 2 spliceosome
9	2e−02	2 / 79	spliceosomal complex
10	2e−02	3 / 221	endosome
11	2e−02	2 / 88	peroxisome
12	3e−02	1 / 10	ESCRT III complex
13	3e−02	1 / 10	mitochondrial outer membrane translocase complex
14	3e−02	1 / 10	RISC complex
15	3e−02	1 / 11	endoplasmic reticulum exit site

Chr

Rank	p−value	#in/all	Geneset
1	9e−04	11 / 1318	Chr 17
2	1e−01	5 / 959	Chr 16
3	1e−01	5 / 994	Chr X
4	2e−01	3 / 536	Chr 22
5	2e−01	6 / 1492	Chr 2
6	3e−01	4 / 1060	Chr 5
7	4e−01	4 / 1211	Chr 6
8	6e−01	4 / 1411	Chr 11
9	6e−01	4 / 1467	Chr 19
10	6e−01	6 / 2323	Chr 1
11	6e−01	2 / 768	Chr 14
12	6e−01	3 / 1170	Chr 7
13	7e−01	2 / 954	Chr 9
14	8e−01	2 / 1160	Chr 12
15	9e−01	1 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−14	45 / 5699	6_EnhG_Melanocytes
2	6e−14	61 / 12298	2_TssA_Melanocytes
3	1e−12	59 / 11836	3_TssF_Melanocytes
4	6e−12	33 / 3450	4_TxTrans_Fibroblasts
5	4e−11	25 / 2028	4_TxTrans_Melanocytes
6	1e−09	58 / 12983	2_TssA_Neuronal_Progenitor
7	5e−08	37 / 5956	3_TssF_Neuronal_Progenitor
8	2e−07	32 / 4795	6_EnhG_Fibroblasts
9	5e−07	51 / 11455	2_TssA_Fibroblasts
10	3e−05	43 / 9635	3_TssF_Fibroblasts
11	1e−03	45 / 11847	7_Enh_Neuronal_Progenitor
12	3e−03	30 / 6970	5_Tx_Neuronal_Progenitor
13	4e−03	46 / 12741	7_Enh_Melanocytes
14	4e−03	35 / 8771	5_Tx_Melanocytes
15	6e−03	9 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−17	57 / 9054	Tx_Colon
2	2e−15	57 / 9555	TssA_Colon
3	3e−15	51 / 7354	TssF_Colon
4	1e−12	31 / 2845	TxEnhG1_Colon
5	5e−11	55 / 10779	Enh_Colon
6	1e−09	40 / 6138	TssD2_Colon
7	6e−08	45 / 8568	TxWk_Colon
8	9e−06	11 / 789	TxEnhG2_Colon
9	1e−04	19 / 2810	EnhA_Colon
10	2e−04	28 / 5373	EnhWk1_Colon
11	3e−04	13 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
12	6e−04	12 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	2e−03	42 / 10999	TssWk_Colon
14	8e−03	9 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	2e−02	7 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN

Glio

Rank	p−value	#in/all	Geneset
1	0.01	2 / 55	Stuehler_Proteins_up_in_STS
2	0.02	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
3	0.04	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	0.05	9 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	0.06	3 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	0.11	9 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	0.11	1 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
8	0.13	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
9	0.13	1 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	0.19	4 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
11	0.24	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	0.26	1 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
13	0.34	1 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
14	0.35	1 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	0.55	1 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−06	6 / 123	KIM_ALL_DISORDERS_DURATION_CORR_DN
2	3e−05	8 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
3	7e−05	9 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
4	4e−04	4 / 123	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
5	4e−04	4 / 126	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
6	5e−04	5 / 237	LU_EZH2_TARGETS_UP
7	6e−04	4 / 141	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
8	1e−03	7 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
9	2e−03	5 / 322	YANG_BCL3_TARGETS_UP
10	2e−03	5 / 325	DAIRKEE_TERT_TARGETS_UP
11	2e−03	4 / 197	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN
12	4e−03	7 / 723	GRADE_COLON_CANCER_UP
13	4e−03	3 / 117	CHUNG_BLISTER_CYTOTOXICITY_UP
14	4e−03	5 / 388	MOOTHA_MITOCHONDRIA
15	5e−03	2 / 40	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S

HM

Rank	p−value	#in/all	Geneset
1	0.001	4 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.023	2 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.033	2 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.139	1 / 54	HALLMARK_MYC_TARGETS_V2
5	0.222	1 / 91	HALLMARK_PEROXISOME
6	0.248	1 / 103	HALLMARK_BILE_ACID_METABOLISM
7	0.302	1 / 130	HALLMARK_DNA_REPAIR
8	0.317	1 / 138	HALLMARK_FATTY_ACID_METABOLISM
9	0.342	1 / 151	HALLMARK_APOPTOSIS
10	0.379	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	0.386	1 / 176	HALLMARK_ADIPOGENESIS
12	0.387	1 / 177	HALLMARK_MITOTIC_SPINDLE
13	0.398	1 / 183	HALLMARK_APICAL_JUNCTION
14	0.401	1 / 185	HALLMARK_MTORC1_SIGNALING
15	0.401	1 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	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	2e−07	34 / 5356	HOPP_Txn_transition
2	9e−06	40 / 8226	HOPP_Active_promoter
3	9e−05	35 / 7275	HOPP_Txn_elongation
4	6e−04	11 / 1270	SPANG_BCR UP
5	2e−03	34 / 8098	HOPP_Weak_promoter
6	2e−03	32 / 7448	HOPP_Strong_enhancer
7	8e−03	4 / 283	TARTE_Plasmablast signature
8	4e−02	4 / 455	SPANG_CD40 6hrs DN
9	1e−01	1 / 39	CARO_OxPhos_in_DLBCL_UP
10	2e−01	21 / 6559	HOPP_Weak_txn
11	2e−01	1 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U
12	3e−01	1 / 105	WIRTH_lymphoma937_spot MM
13	3e−01	1 / 115	ROSOLOWSKI_green total
14	3e−01	1 / 134	DAVE_BL−vs−DLBCL
15	4e−01	2 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c

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	3e−06	13 / 1013	poly(A) RNA binding
2	2e−04	39 / 8818	protein binding
3	7e−04	4 / 145	nucleic acid binding
4	5e−03	6 / 580	identical protein binding
5	7e−03	2 / 45	cytoskeletal protein binding
6	8e−03	4 / 283	nucleotide binding
7	1e−02	2 / 54	serine−type peptidase activity
8	3e−02	1 / 10	cullin family protein binding
9	3e−02	1 / 10	dipeptidyl−peptidase activity
10	3e−02	1 / 10	leucine zipper domain binding
11	3e−02	1 / 10	protein serine/threonine phosphatase inhibitor activity
12	3e−02	1 / 10	tau protein binding
13	3e−02	1 / 10	transmembrane receptor protein tyrosine kinase adaptor activity
14	3e−02	1 / 11	sugar:proton symporter activity
15	3e−02	1 / 12	nuclease 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	0.002	3 / 97	hsa−miR−125a−3p
2	0.023	2 / 84	hsa−miR−486−3p
3	0.024	2 / 86	hsa−miR−339−5p
4	0.074	1 / 28	hsa−miR−519e*
5	0.100	1 / 38	hsa−miR−1277
6	0.102	1 / 39	hsa−miR−517*
7	0.102	1 / 39	hsa−miR−525−3p
8	0.138	3 / 467	hsa−miR−195
9	0.141	1 / 55	hsa−miR−634
10	0.146	3 / 480	hsa−miR−15b
11	0.152	3 / 489	hsa−miR−16
12	0.160	1 / 63	hsa−miR−518c*
13	0.170	3 / 516	hsa−miR−15a
14	0.178	1 / 71	hsa−miR−939
15	0.178	1 / 71	hsa−miR−127−5p

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	3e−04	11 / 1167	PROTEINATLAS_gallbladder
2	6e−04	10 / 1063	PROTEINATLAS_tonsil
3	1e−03	8 / 759	PROTEINATLAS_epididymis
4	1e−03	9 / 963	PROTEINATLAS_pancreas
5	1e−03	10 / 1194	PROTEINATLAS_stomach
6	2e−03	8 / 850	PROTEINATLAS_skin
7	3e−03	9 / 1118	PROTEINATLAS_placenta
8	6e−03	6 / 598	PROTEINATLAS_prostate
9	7e−03	7 / 816	PROTEINATLAS_endometrium
10	7e−03	6 / 623	PROTEINATLAS_seminal vesicle
11	8e−03	9 / 1268	PROTEINATLAS_colon
12	1e−02	8 / 1097	PROTEINATLAS_kidney
13	1e−02	6 / 695	PROTEINATLAS_bone marrow
14	1e−02	8 / 1138	PROTEINATLAS_small intestine
15	1e−02	8 / 1173	PROTEINATLAS_rectum

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	3e−05	14 / 1452	ICGC_Six5_targets
2	5e−04	26 / 5067	ICGC_Taf1_targets
3	7e−04	13 / 1723	HEBENSTREIT_high expression TF
4	8e−04	27 / 5518	ICGC_Stat5_targets
5	2e−03	24 / 4890	ICGC_Bclaf101388_targets
6	3e−03	21 / 4131	ICGC_Nfatc1_targets
7	4e−03	25 / 5442	ICGC_Pmlsc71910_targets
8	4e−03	25 / 5466	ICGC_Nficsc81335_targets
9	5e−03	17 / 3194	ICGC_Irf4_targets
10	5e−03	21 / 4362	ICGC_Creb1_targets
11	6e−03	9 / 1231	KIM_MYC targets
12	7e−03	21 / 4468	ICGC_Egr1_targets
13	7e−03	24 / 5383	ICGC_Sp1_targets
14	1e−02	12 / 2087	ICGC_Cebpbsc150_targets
15	1e−02	28 / 6868	ICGC_Elf1_targets

Overexpression Spots

Spot Summary: L

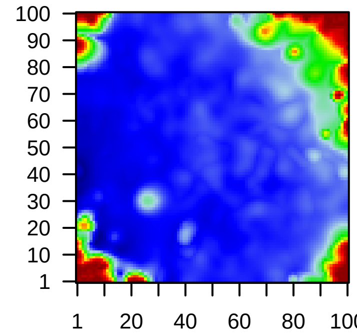
metagenes = 15
genes = 328

<r> metagenes = 0.99
<r> genes = 0.27
beta: r2= 7.03 / log p= −Inf

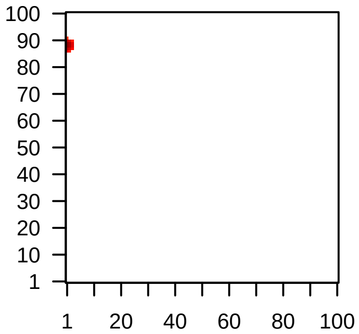
samples with spot = 111 (3.3 %)

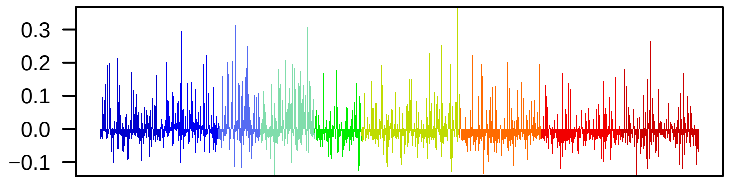
A * : 14 (4.1 %)
A C * : 13 (4 %)
A C F * : 20 (8.5 %)
A F * : 18 (5.8 %)
C F * : 5 (1.9 %)
F * : 14 (2.5 %)
F J * : 13 (2.8 %)
J * : 6 (1.3 %)
N * : 8 (1.8 %)

Overview Map



Spot





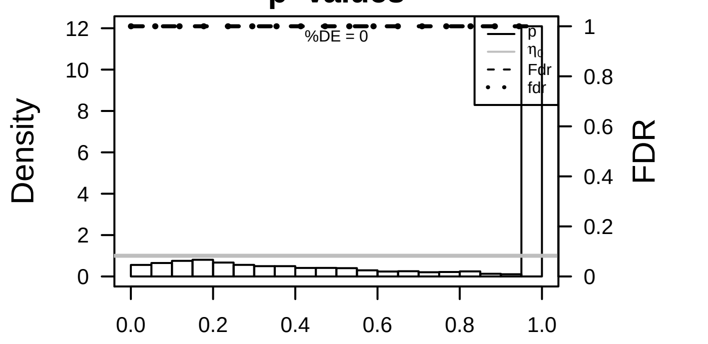
Spot Genelist

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 [Sc
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	0.7	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
9	ILMN_170981	0.63	−0.45	0.29	SLC35A5	solute carrier family 35 member A5 [Source:HGNC Symbol;A
10	ILMN_180048	0.61	−0.38	0.36	CT47B1	cancer/testis antigen family 47, member B1 [Source:HGNC S
11	ILMN_224967	0.57	−0.36	0.66	LSR	lipolysis stimulated lipoprotein receptor [Source:HGNC Symb
12	ILMN_328824	0.57	−0.43	0.53		
13	ILMN_183964	0.56	−0.31	0.64	LINC00323	long intergenic non−protein coding RNA 323 [Source:HGNC S
14	ILMN_176111	0.56	−0.35	0.66	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
15	ILMN_178092	0.56	−0.32	0.68	SLC43A1	solute carrier family 43 member 1 [Source:HGNC Symbol;Acc
16	ILMN_190200	0.55	−0.35	0.43		
17	ILMN_165712	0.55	−0.34	0.39	PTPRU	protein tyrosine phosphatase, receptor type U [Source:HGNC
18	ILMN_324766	0.55	−0.36	0.7		
19	ILMN_323756	0.54	−0.32	0.45	PP14571	uncharacterized LOC100130449 [Source:EntrezGene;Acc:10
20	ILMN_181169	0.54	−0.31	0.6	FDXR	ferredoxin reductase [Source:HGNC Symbol;Acc:HGNC:3642

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−05	52 / 3164	Brain	Mid_Frontal_Lobe_ZNF
2	7e−05	5 / 46	BP	vesicle fusion
3	2e−04	19 / 789	Colon	TxEnhG2_Colon
4	2e−04	3 / 13	GSEA	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
5	3e−04	44 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
6	4e−04	128 / 10779	Colon	Enh_Colon
7	4e−04	94 / 7354	Colon	TssF_Colon
8	5e−04	2 / 4	GSEA	COURTOIS_SENESCENCE_TRIGGERS
9	6e−04	3 / 18	BP	B cell homeostasis
10	8e−04	7 / 156	BP	negative regulation of gene expression
11	8e−04	53 / 3639	Chror	1_TssP_Fibroblasts
12	9e−04	18 / 818	Brain	Mid_Frontal_Lobe_Het
13	1e−03	3 / 21	GSEA	PID_HEDGEHOG_2PATHWAY
14	1e−03	10 / 336	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
15	2e−03	4 / 55	BP	cellular response to growth factor stimulus
16	2e−03	12 / 471	GSEA	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
17	2e−03	13 / 539	CC	Golgi membrane
18	2e−03	3 / 27	BP	positive regulation of release of cytochrome c from mitochondria
19	2e−03	3 / 27	miRN	hsa−miR−1292
20	2e−03	3 / 27	GSEA	MATZUK_MALE_REPRODUCTION_SERTOLI
21	2e−03	3 / 28	BP	cellular response to nerve growth factor stimulus
22	2e−03	3 / 28	GSEA	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
23	2e−03	3 / 28	GSEA	JAZAG_TGFB1_SIGNALING_DN
24	2e−03	4 / 59	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
25	2e−03	8 / 244	GSEA	ROZANOV_MMP14_TARGETS_UP
26	2e−03	2 / 8	GSEA	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
27	3e−03	11 / 425	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
28	3e−03	56 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
29	3e−03	5 / 101	GSEA	WANG_HCP_PROSTATE_CANCER
30	3e−03	3 / 30	GSEA	YANG_BREAST_CANCER_ESR1_LASER_UP
31	3e−03	3 / 32	miRN	hsa−miR−1229
32	4e−03	18 / 933	Refer	PROTEINATLAS_adrenal gland
33	4e−03	16 / 788	CC	endoplasmic reticulum membrane
34	4e−03	2 / 10	BP	negative regulation of cell size
35	4e−03	2 / 10	BP	negative regulation of interleukin−10 production
36	4e−03	8 / 265	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
37	4e−03	72 / 5699	Chror	6_EnhG_Melanocytes
38	4e−03	8 / 268	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
39	5e−03	2 / 11	BP	cytoplasmic sequestering of transcription factor
40	5e−03	2 / 11	BP	male sex determination

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 142	HORVATH_aging_genes meth UP
2	0.4	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.7	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	

BP

Rank	p−value	#in/all	Geneset
1	7e−05	5 / 46	vesicle fusion
2	6e−04	3 / 18	B cell homeostasis
3	8e−04	7 / 156	negative regulation of gene expression
4	2e−03	4 / 55	cellular response to growth factor stimulus
5	2e−03	3 / 27	positive regulation of release of cytochrome c from mitochondria
6	2e−03	3 / 28	cellular response to nerve growth factor stimulus
7	4e−03	2 / 10	negative regulation of cell size
8	4e−03	2 / 10	negative regulation of interleukin−10 production
9	5e−03	2 / 11	cytoplasmic sequestering of transcription factor
10	5e−03	2 / 11	male sex determination
11	5e−03	3 / 37	positive regulation of nitric oxide biosynthetic process
12	6e−03	2 / 12	trophoblast giant cell differentiation
13	6e−03	3 / 38	positive regulation of cysteine−type endopeptidase activity involved in apoptot
14	7e−03	2 / 13	positive regulation of monocyte chemotaxis
15	7e−03	2 / 13	striated muscle cell differentiation

Brain

Rank	p−value	#in/all	Geneset
1	5e−05	52 / 3164	Mid_Frontal_Lobe_ZNF
2	3e−04	44 / 2709	Mid_Frontal_Lobe_HetRpts
3	9e−04	18 / 818	Mid_Frontal_Lobe_Het
4	3e−03	56 / 4112	Mid_Frontal_Lobe_ReprPC
5	2e−02	106 / 9504	Overlap_fetal_midbrain_K9K27me3
6	3e−02	7 / 304	Mid_Frontal_Lobe_TssA
7	4e−02	20 / 1360	Mid_Frontal_Lobe_TssP
8	8e−02	23 / 1784	Mid_Frontal_Lobe_ReprPCWk
9	9e−02	24 / 1893	Overlap_fetal_midbrain_TssF
10	1e−01	15 / 1119	Overlap_fetal_midbrain_TssA
11	2e−01	7 / 465	Mid_Frontal_Lobe_TxTrans
12	2e−01	12 / 924	Mid_Frontal_Lobe_TssF
13	2e−01	18 / 1506	Mid_Frontal_Lobe_Quies
14	2e−01	106 / 10430	Overlap_fetal_midbrain_Quies
15	2e−01	17 / 1476	Overlap_fetal_midbrain_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	3 / 125	PanCan_CC+Apop_geneset_nanostring
2	0.1	1 / 16	GENTLES_modul11
3	0.2	3 / 150	PanCan_MAPK_geneset_nanostring
4	0.2	2 / 82	PanCan_JAK−ST_geneset_nanostring
5	0.2	0 / 14	LIU_PROSTATE_CANCER_UP
6	0.2	2 / 91	PanCan_TXmisReg_geneset_nanostring
7	0.4	1 / 46	PanCan_DNARepair_geneset_nanostring
8	0.4	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	0.4	2 / 136	PanCan_RAS_geneset_nanostring
10	0.4	0 / 13	RHODES_CANCER_META_SIGNATURE
11	0.5	3 / 301	SPANG_BCL6−index2
12	0.6	2 / 193	PanCan_PI3K_geneset_nanostring
13	0.6	5 / 527	Lembcke_Normal vs Adenoma
14	0.6	0 / 15	LIU_PROSTATE_CANCER_DN
15	0.7	1 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.002	13 / 539	Golgi membrane
2	0.004	16 / 788	endoplasmic reticulum membrane
3	0.012	6 / 200	nuclear membrane
4	0.016	3 / 55	synaptic vesicle membrane
5	0.017	14 / 775	endoplasmic reticulum
6	0.019	3 / 59	presynaptic membrane
7	0.024	3 / 65	caveola
8	0.027	2 / 27	intrinsic component of plasma membrane
9	0.027	2 / 27	presynaptic active zone
10	0.027	4 / 119	vesicle
11	0.037	2 / 32	dendritic shaft
12	0.056	2 / 40	SCF ubiquitin ligase complex
13	0.061	5 / 221	endosome
14	0.069	3 / 99	recycling endosome
15	0.076	4 / 167	external side of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.05	3 / 87	Chr Y
2	0.15	15 / 1170	Chr 7
3	0.15	13 / 994	Chr X
4	0.16	18 / 1467	Chr 19
5	0.26	14 / 1211	Chr 6
6	0.27	15 / 1318	Chr 17
7	0.31	11 / 959	Chr 16
8	0.37	24 / 2323	Chr 1
9	0.43	12 / 1160	Chr 12
10	0.45	8 / 768	Chr 14
11	0.52	3 / 289	Chr 21
12	0.60	7 / 769	Chr 15
13	0.63	8 / 902	Chr 4
14	0.63	8 / 904	Chr 10
15	0.63	3 / 342	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−04	53 / 3639	1_TssP_Fibroblasts
2	4e−03	72 / 5699	6_EnhG_Melanocytes
3	6e−03	43 / 3068	8_EnhP_Fibroblasts
4	6e−03	31 / 2028	4_TxTrans_Melanocytes
5	8e−03	73 / 5956	3_TssF_Neuronal_Progenitor
6	2e−02	19 / 1206	6_EnhG_Neuronal_Progenitor
7	3e−02	35 / 2660	8_EnhP_Melanocytes
8	4e−02	126 / 11836	3_TssF_Melanocytes
9	4e−02	126 / 11847	7_Enh_Neuronal_Progenitor
10	6e−02	24 / 1789	8_EnhP_Neuronal_Progenitor
11	6e−02	49 / 4169	10_ReprPC_Fibroblasts
12	7e−02	55 / 4795	6_EnhG_Fibroblasts
13	7e−02	41 / 3438	10_ReprPC_Melanocytes
14	9e−02	134 / 12983	2_TssA_Neuronal_Progenitor
15	1e−01	49 / 4304	9_ReprPCWk_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	19 / 789	TxEnhG2_Colon
2	4e−04	128 / 10779	Enh_Colon
3	4e−04	94 / 7354	TssF_Colon
4	7e−03	24 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
5	1e−02	39 / 2810	EnhA_Colon
6	1e−02	3 / 47	Marisa_CRC−cluster−f
7	1e−02	39 / 2845	TxEnhG1_Colon
8	2e−02	38 / 2894	TssP_Colon
9	3e−02	18 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
10	3e−02	71 / 6138	TssD2_Colon
11	4e−02	26 / 1895	EnhP_Colon
12	6e−02	17 / 1186	HetRpts_Colon
13	8e−02	12 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	9e−02	6 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
15	1e−01	37 / 3173	ReprPC_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.02	7 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
2	0.04	4 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	0.05	3 / 86	laffaire_hypermeth_LGG_vs_control
4	0.06	1 / 6	laffaire_hypometh_LGG_vs_control
5	0.08	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	0.09	3 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.09	2 / 53	mature astrocytes
8	0.11	1 / 12	Mukasa_UP_in_Astroglioma
9	0.12	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
10	0.13	1 / 15	VERHAAK_PN subtype
11	0.15	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
12	0.15	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
13	0.15	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
14	0.16	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	0.16	3 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 13	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
2	5e−04	2 / 4	COURTOIS_SENESCENCE_TRIGGERS
3	1e−03	3 / 21	PID_HEDGEHOG_2PATHWAY
4	1e−03	10 / 336	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
5	2e−03	12 / 471	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
6	2e−03	3 / 27	MATZUK_MALE_REPRODUCTION_SERTOLI
7	2e−03	3 / 28	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS
8	2e−03	3 / 28	JAZAG_TGFB1_SIGNALING_DN
9	2e−03	4 / 59	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
10	2e−03	8 / 244	ROZANOV_MMP14_TARGETS_UP
11	2e−03	2 / 8	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
12	3e−03	11 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
13	3e−03	5 / 101	WANG_HCP_PROSTATE_CANCER
14	3e−03	3 / 30	YANG_BREAST_CANCER_ESR1_LASER_UP
15	4e−03	8 / 265	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP

HM

Rank	p−value	#in/all	Geneset
1	0.008	4 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
2	0.033	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.065	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
4	0.101	4 / 185	HALLMARK_P53_PATHWAY
5	0.142	3 / 137	HALLMARK_UV_RESPONSE_UP
6	0.253	3 / 183	HALLMARK_APICAL_JUNCTION
7	0.258	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	0.258	3 / 185	HALLMARK_HEME_METABOLISM
9	0.268	3 / 189	HALLMARK_HYPOXIA
10	0.271	1 / 33	HALLMARK_ANGIOGENESIS
11	0.303	2 / 116	HALLMARK_SPERMATOGENESIS
12	0.358	2 / 132	HALLMARK_UV_RESPONSE_DN
13	0.379	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	0.501	2 / 176	HALLMARK_KRAS_SIGNALING_UP
15	0.504	2 / 177	HALLMARK_KRAS_SIGNALING_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 94	DUMEAUX_Smoking enriched genes
2	0.4	2 / 147	Homuth_BMI−associated−genes_UP
3	0.6	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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.06	5 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
2	0.07	8 / 455	SPANG_CD40 6hrs DN
3	0.07	5 / 232	WIRTH_lymphoma937_spot B
4	0.09	60 / 5384	HOPP_Repressed
5	0.13	1 / 15	Subero_B−ALL_hypo_meth
6	0.14	3 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_L
7	0.14	2 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
8	0.14	3 / 138	WIRTH_lymphoma937_spot G
9	0.16	7 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
10	0.19	7 / 493	WIRTH_lymphoma937_spot J
11	0.19	6 / 408	TARTE_Mature plasma cell signature
12	0.20	1 / 23	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
13	0.20	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
14	0.21	1 / 25	SPANG_BAFF 9hrs UP
15	0.23	2 / 94	Sha_BL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.08	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	0.40	1 / 54	Hugo_melanoma−all−MET_DN
3	1.00	0 / 30	Hugo_melanoma−all−MET_UP
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	

MF

Rank	p−value	#in/all	Geneset
1	0.006	2 / 12	insulin−like growth factor I binding
2	0.006	3 / 39	clathrin binding
3	0.011	101 / 8818	protein binding
4	0.012	2 / 18	peroxidase activity
5	0.013	3 / 52	SNARE binding
6	0.017	2 / 21	insulin−like growth factor binding
7	0.021	3 / 62	syntaxin binding
8	0.022	2 / 24	steroid binding
9	0.023	2 / 25	protein phosphatase 2A binding
10	0.025	5 / 172	RNA polymerase II transcription factor activity, sequence−specific DNA bindir
11	0.029	2 / 28	transmembrane receptor protein tyrosine kinase activity
12	0.033	2 / 30	cysteine−type peptidase activity
13	0.038	3 / 78	phospholipid binding
14	0.046	2 / 36	protein complex scaffold
15	0.048	2 / 37	SNAP receptor activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 30	Systemic lupus erythematosus (SLE)
2	0.5	1 / 73	Stroke, susceptibility to
3	0.5	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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 27	hsa−miR−1292
2	0.003	3 / 32	hsa−miR−1229
3	0.006	2 / 12	hsa−miR−652
4	0.008	4 / 83	hsa−miR−630
5	0.009	6 / 188	hsa−miR−548d−3p
6	0.021	5 / 166	hsa−miR−183
7	0.029	3 / 70	hsa−miR−548b−3p
8	0.034	4 / 128	hsa−miR−335
9	0.046	3 / 84	hsa−miR−486−3p
10	0.048	3 / 85	hsa−miR−220c
11	0.052	3 / 88	hsa−miR−608
12	0.053	2 / 39	hsa−miR−635
13	0.053	2 / 39	hsa−miR−484
14	0.054	4 / 149	hsa−miR−142−3p
15	0.055	4 / 150	hsa−miR−633

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	0.004	18 / 933	PROTEINATLAS_adrenal gland
2	0.011	19 / 1118	PROTEINATLAS_placenta
3	0.014	16 / 912	PROTEINATLAS_fallopian tube
4	0.017	19 / 1173	PROTEINATLAS_rectum
5	0.031	16 / 1003	PROTEINATLAS_appendix
6	0.033	2 / 30	VAQUERIZAS_Smooth muscle_TF
7	0.054	17 / 1167	PROTEINATLAS_gallbladder
8	0.054	14 / 912	PROTEINATLAS_urinary bladder
9	0.057	17 / 1176	PROTEINATLAS_duodenum
10	0.059	18 / 1268	PROTEINATLAS_colon
11	0.060	12 / 759	PROTEINATLAS_epididymis
12	0.060	16 / 1097	PROTEINATLAS_kidney
13	0.070	5 / 231	Chaussabel_2,5_Immune related molecules
14	0.074	1 / 8	JONGENEEL_Fetal Brain
15	0.077	14 / 963	PROTEINATLAS_pancreas

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	0.02	29 / 2087	ICGC_Cebpbsc150_targets
2	0.05	1 / 5	MYC_TFs
3	0.08	22 / 1669	ICGC_P300_targets
4	0.10	19 / 1452	ICGC_Six5_targets
5	0.11	32 / 2704	ICGC_Pbx3_targets
6	0.12	37 / 3194	ICGC_Irf4_targets
7	0.12	57 / 5188	ICGC_Ebfsc137065_targets
8	0.13	16 / 1231	KIM_MYC targets
9	0.16	10 / 733	ICGC_Atf3_targets
10	0.17	39 / 3507	ICGC_Rad21_targets
11	0.23	17 / 1466	ICGC_NrsfPcr1_targets
12	0.28	49 / 4735	ICGC_Pu1_targets
13	0.30	45 / 4362	ICGC_Creb1_targets
14	0.31	24 / 2255	ICGC_SrfV0416101_targets
15	0.31	29 / 2759	ICGC_Bcl3_targets

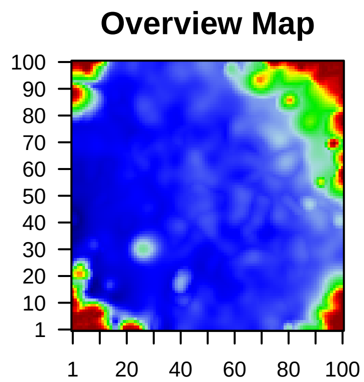
Overexpression Spots

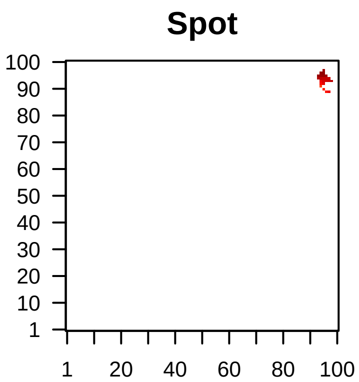
Spot Summary: M

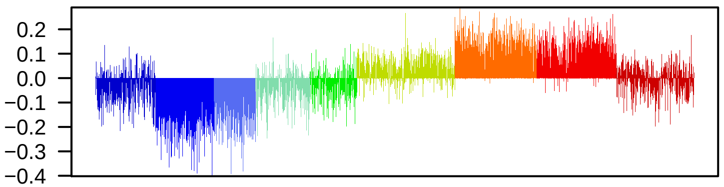
metagenes = 23
genes = 350

<r> metagenes = 0.97
<r> genes = 0.5
beta: r2= 40.5 / log p= −Inf

samples with spot = 377 (11.1 %)
- A * : 1 (0.3 %)
- A F * : 1 (0.3 %)
- C F * : 1 (0.4 %)
- F * : 9 (1.6 %)
- F J * : 207 (44.7 %)
- J * : 157 (35.1 %)
- N * : 1 (0.2 %)





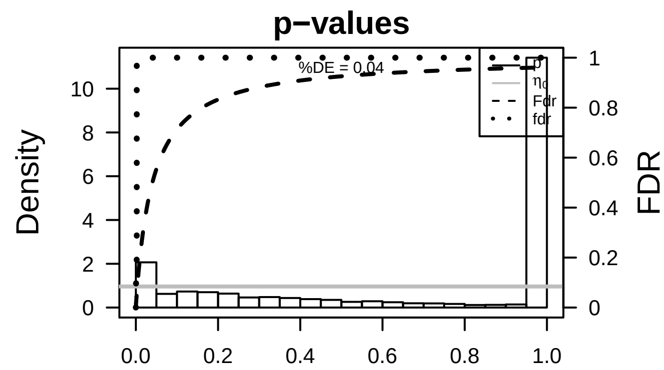


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_174314	1.89	−2.07	0.14	ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Sym
2	ILMN_176126	1.09	−0.7	0.54	COBLL1	cordon−bleu WH2 repeat protein like 1 [Source:HGNC Symbo
3	ILMN_168842	1.05	−1.38	0.3	FCER1A	Fc fragment of IgE receptor Ia [Source:HGNC Symbol;Acc:HG
4	ILMN_170168	0.98	−0.74	0.65		
5	ILMN_325126	0.89	−0.8	0.44	SRP14	signal recognition particle 14 [Source:HGNC Symbol;Acc:HG
6	ILMN_178517	0.87	−0.58	0.54	SWAP70	SWAP switching B−cell complex 70kDa subunit [Source:HGN
7	ILMN_175995	0.87	−0.7	0.46	MIR1244−1	prothymosin, alpha [Source:HGNC Symbol;Acc:HGNC:9623]
8	ILMN_320871	0.83	−0.75	0.69		
9	ILMN_175424	0.79	−0.69	0.39		
10	ILMN_168279	0.77	−0.65	0.72	STAMBPL1	STAM binding protein like 1 [Source:HGNC Symbol;Acc:HGN
11	ILMN_169342	0.77	−0.67	0.54		
12	ILMN_179865	0.76	−0.64	0.66	MCM6	minichromosome maintenance complex component 6 [Source
13	ILMN_323188	0.76	−0.65	0.51		
14	ILMN_230211	0.76	−0.6	0.62	CCDC50	coiled−coil domain containing 50 [Source:HGNC Symbol;Acc
15	ILMN_237351	0.73	−0.71	0.66	HSP90AA1	heat shock protein 90 alpha family class A member 1 [Source
16	ILMN_177159	0.73	−0.66	0.77	RRM1	ribonucleotide reductase catalytic subunit M1 [Source:HGNC
17	ILMN_169417	0.72	−0.62	0.76	PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:I
18	ILMN_213186	0.72	−0.54	0.5	SOCS2	suppressor of cytokine signaling 2 [Source:HGNC Symbol;Ac
19	ILMN_224355	0.72	−0.54	0.55	LOC105373378	zinc finger protein 275 [Source:HGNC Symbol;Acc:HGNC:13
20	ILMN_324799	0.71	−0.46	0.59	STAP1	signal transducing adaptor family member 1 [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	8e−44	214 / 7275	Lympl	HOPP_Txn_elongation
2	3e−43	247 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
3	2e−40	240 / 9555	Colon	TssA_Colon
4	1e−36	266 / 12298	Chror	2_TssA_Melanocytes
5	1e−36	217 / 8226	Lympl	HOPP_Active_promoter
6	5e−36	172 / 5356	Lympl	HOPP_Txn_transition
7	3e−35	255 / 11455	Chror	2_TssA_Fibroblasts
8	8e−34	220 / 8771	Chror	5_Tx_Melanocytes
9	4e−33	177 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
10	8e−32	214 / 8568	Colon	TxWk_Colon
11	5e−30	242 / 10999	Colon	TssWk_Colon
12	9e−30	223 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
13	9e−30	212 / 8678	Colon	Quies3_Colon
14	1e−29	217 / 9054	Colon	Tx_Colon
15	2e−29	187 / 6970	Chror	5_Tx_Neuronal_Progenitor
16	9e−29	262 / 12983	Chror	2_TssA_Neuronal_Progenitor
17	6e−27	54 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
18	1e−25	75 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
19	1e−24	83 / 1797	GSEA	PILON_KLF1_TARGETS_DN
20	1e−24	191 / 7854	Chror	5_Tx_Fibroblasts
21	3e−24	66 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
22	3e−23	192 / 8098	Lympl	HOPP_Weak_promoter
23	5e−22	73 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
24	5e−21	236 / 11836	Chror	3_TssF_Melanocytes
25	8e−21	49 / 737	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
26	1e−20	140 / 5067	TF	ICGC_Taf1_targets
27	2e−19	209 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
28	2e−19	62 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
29	2e−18	49 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
30	2e−17	235 / 12393	Chror	15_Quies_Neuronal_Progenitor
31	5e−17	210 / 10430	Brain	Overlap_fetal_midbrain_Quies
32	3e−16	56 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
33	3e−16	189 / 8990	Chror	15_Quies_Fibroblasts
34	1e−15	136 / 5518	TF	ICGC_Stat5_targets
35	1e−14	133 / 5466	TF	ICGC_Nficsc81335_targets
36	1e−14	62 / 1601	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
37	5e−14	131 / 5442	TF	ICGC_Pmlsc71910_targets
38	7e−14	49 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
39	2e−13	41 / 811	GSEA	LEE_BMP2_TARGETS_DN
40	2e−13	147 / 6578	TF	ICGC_Pou2_targets



Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 142	HORVATH_aging_genes meth UP
2	0.8	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	

BP

Rank	p−value	#in/all	Geneset
1	1e−05	12 / 196	mRNA splicing, via spliceosome
2	6e−04	3 / 13	nucleotide biosynthetic process
3	6e−04	3 / 13	positive regulation of mRNA splicing, via spliceosome
4	6e−04	11 / 254	cell−cell adhesion
5	8e−04	4 / 32	tRNA aminoacylation for protein translation
6	1e−03	6 / 86	mRNA export from nucleus
7	1e−03	6 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
8	1e−03	3 / 17	mitochondrial ATP synthesis coupled proton transport
9	2e−03	3 / 18	cytoplasmic translation
10	2e−03	3 / 18	histone methylation
11	2e−03	4 / 39	mitotic nuclear envelope disassembly
12	2e−03	5 / 69	mitochondrial translational elongation
13	2e−03	10 / 255	viral process
14	2e−03	5 / 71	mitochondrial translational termination
15	3e−03	3 / 21	nuclear−transcribed mRNA poly(A) tail shortening

Brain

Rank	p−value	#in/all	Geneset
1	3e−43	247 / 9815	Overlap_fetal_midbrain_ReprPC
2	4e−33	177 / 5936	Overlap_fetal_midbrain_HetRpts
3	9e−30	223 / 9504	Overlap_fetal_midbrain_K9K27me3
4	2e−19	209 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	5e−17	210 / 10430	Overlap_fetal_midbrain_Quies
6	2e−04	15 / 386	Fetal_ZNF
7	2e−03	23 / 906	Fetal_HetRpts
8	1e−02	19 / 796	Overlap_fetal_midbrain_ZNF
9	2e−02	24 / 1171	Fetal_EnhP
10	3e−02	9 / 328	Fetal_Het
11	6e−02	22 / 1162	Fetal_Enh
12	1e−01	13 / 681	Overlap_fetal_midbrain_EnhP
13	2e−01	23 / 1436	Fetal_K9K27me3
14	2e−01	47 / 3164	Mid_Frontal_Lobe_ZNF
15	4e−01	14 / 937	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	4 / 39	ZHANG_MM up
2	0.005	0 / 13	RHODES_CANCER_META_SIGNATURE
3	0.014	2 / 14	GENTLES_modul10
4	0.018	2 / 16	GENTLES_modul11
5	0.018	2 / 16	GENTLES_modul16
6	0.040	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
7	0.106	1 / 14	LIU_PROSTATE_CANCER_UP
8	0.113	1 / 9	GENTLES_modul5
9	0.148	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	0.148	1 / 12	LIU_BREAST_CANCER
11	0.159	1 / 13	GENTLES_modul6
12	0.170	1 / 14	LIU_COMMON_CANCER_GENES
13	0.170	1 / 14	GENTLES_modul1
14	0.181	1 / 15	LIU_PROSTATE_CANCER_DN
15	0.192	1 / 16	GENTLES_modul7

CC

Rank	p−value	#in/all	Geneset
1	2e−08	67 / 2535	nucleoplasm
2	3e−08	43 / 1304	mitochondrion
3	1e−07	103 / 4828	nucleus
4	1e−07	29 / 721	nucleolus
5	9e−06	8 / 78	catalytic step 2 spliceosome
6	1e−05	17 / 374	mitochondrial inner membrane
7	2e−05	5 / 25	preribosome, large subunit precursor
8	8e−05	92 / 4822	cytoplasm
9	3e−04	10 / 200	nuclear membrane
10	7e−04	8 / 144	nuclear envelope
11	1e−03	3 / 16	Ada2/Gcn5/Ada3 transcription activator complex
12	1e−03	5 / 60	nuclear pore
13	2e−03	42 / 1979	membrane
14	2e−03	3 / 19	mitochondrial proton−transporting ATP synthase complex
15	2e−03	11 / 295	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	0.002	28 / 1160	Chr 12
2	0.005	10 / 289	Chr 21
3	0.111	18 / 994	Chr X
4	0.144	16 / 902	Chr 4
5	0.169	7 / 342	Chr 18
6	0.178	36 / 2323	Chr 1
7	0.187	20 / 1217	Chr 3
8	0.197	8 / 422	Chr 13
9	0.328	22 / 1492	Chr 2
10	0.535	12 / 904	Chr 10
11	0.540	14 / 1060	Chr 5
12	0.549	11 / 836	Chr 8
13	0.596	18 / 1411	Chr 11
14	0.687	14 / 1170	Chr 7
15	0.689	9 / 768	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−36	266 / 12298	2_TssA_Melanocytes
2	3e−35	255 / 11455	2_TssA_Fibroblasts
3	8e−34	220 / 8771	5_Tx_Melanocytes
4	2e−29	187 / 6970	5_Tx_Neuronal_Progenitor
5	9e−29	262 / 12983	2_TssA_Neuronal_Progenitor
6	1e−24	191 / 7854	5_Tx_Fibroblasts
7	5e−21	236 / 11836	3_TssF_Melanocytes
8	2e−17	235 / 12393	15_Quies_Neuronal_Progenitor
9	3e−16	189 / 8990	15_Quies_Fibroblasts
10	7e−12	226 / 12741	7_Enh_Melanocytes
11	7e−11	203 / 11130	15_Quies_Melanocytes
12	5e−07	156 / 8613	7_Enh_Fibroblasts
13	2e−06	168 / 9635	3_TssF_Fibroblasts
14	8e−05	105 / 5699	6_EnhG_Melanocytes
15	4e−04	42 / 1846	14_ZNF_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−40	240 / 9555	TssA_Colon
2	8e−32	214 / 8568	TxWk_Colon
3	5e−30	242 / 10999	TssWk_Colon
4	9e−30	212 / 8678	Quies3_Colon
5	1e−29	217 / 9054	Tx_Colon
6	5e−22	73 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	6e−10	39 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
8	2e−08	33 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	5e−08	142 / 7354	TssF_Colon
10	5e−05	81 / 4034	TssD1_Colon
11	6e−05	38 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
12	2e−04	47 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_ti
13	4e−04	172 / 10779	Enh_Colon
14	3e−03	28 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
15	1e−02	24 / 1083	ZNF_Colon

Glio

Rank	p−value	#in/all	Geneset
1	1e−11	60 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	2e−11	65 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−05	15 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	3e−04	24 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	3e−03	11 / 315	Up
6	2e−02	2 / 15	VERHAAK_MES subtype
7	4e−02	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
8	9e−02	9 / 401	Down_b
9	1e−01	3 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	1e−01	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
11	1e−01	3 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
12	2e−01	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	2e−01	2 / 55	Stuehler_Proteins_up_in_STS
14	2e−01	2 / 55	developing astrocytes
15	2e−01	1 / 14	Christensen_hypermethylated_in_ependymoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−27	54 / 669	PUJANA_CHEK2_PCC_NETWORK
2	1e−25	75 / 1417	PUJANA_BRCA1_PCC_NETWORK
3	1e−24	83 / 1797	PILON_KLF1_TARGETS_DN
4	3e−24	66 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	8e−21	49 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
6	2e−19	62 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	2e−18	49 / 841	ACEVEDO_LIVER_CANCER_UP
8	3e−16	56 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	1e−14	62 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
10	7e−14	49 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
11	2e−13	41 / 811	LEE_BMP2_TARGETS_DN
12	2e−12	50 / 1241	PUJANA_ATM_PCC_NETWORK
13	2e−12	27 / 388	SHEN_SMARCA2_TARGETS_UP
14	2e−11	30 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
15	4e−11	23 / 316	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN

HM

Rank	p−value	#in/all	Geneset
1	6e−08	14 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−04	10 / 185	HALLMARK_MTORC1_SIGNALING
3	4e−04	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	2e−03	8 / 173	HALLMARK_E2F_TARGETS
5	3e−03	8 / 179	HALLMARK_G2M_CHECKPOINT
6	6e−03	4 / 54	HALLMARK_MYC_TARGETS_V2
7	3e−02	6 / 176	HALLMARK_ADIPOGENESIS
8	4e−02	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
9	4e−02	6 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	5e−02	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	8e−02	5 / 176	HALLMARK_KRAS_SIGNALING_UP
12	9e−02	4 / 130	HALLMARK_DNA_REPAIR
13	1e−01	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	1e−01	3 / 91	HALLMARK_PEROXISOME
15	4e−01	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−04	8 / 147	Homuth_BMI−associated−genes_UP
2	6e−02	2 / 31	DUMEAUX_Fasting enriched genes
3	2e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
4	2e−01	1 / 17	DUMEAUX_High bmi enriched genes
5	3e−01	1 / 32	Marjolein_ageing−genes_DN
6	7e−01	1 / 94	DUMEAUX_Smoking enriched genes
7	8e−01	2 / 211	Homuth_BMI−associated−genes_DN
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 / 10	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−44	214 / 7275	HOPP_Txn_elongation
2	1e−36	217 / 8226	HOPP_Active_promoter
3	5e−36	172 / 5356	HOPP_Txn_transition
4	3e−23	192 / 8098	HOPP_Weak_promoter
5	2e−09	148 / 7448	HOPP_Strong_enhancer
6	4e−08	31 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	6e−07	29 / 777	WIRTH_lymphoma937_spot D
8	5e−06	123 / 6559	HOPP_Weak_txn
9	9e−06	11 / 158	WIRTH_lymphoma937_spot C
10	9e−06	11 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
11	2e−05	126 / 6959	HOPP_Weak_enhancer
12	4e−05	33 / 1169	SPANG_BCR DN
13	1e−04	13 / 283	TARTE_Plasmablast signature
14	4e−04	8 / 134	DAVE_BL−vs−DLBCL
15	2e−03	6 / 94	Sha_BL 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	1e−12	45 / 1013	poly(A) RNA binding
2	2e−08	164 / 8818	protein binding
3	3e−05	14 / 283	nucleotide binding
4	3e−04	15 / 399	RNA binding
5	3e−04	7 / 99	mRNA binding
6	9e−04	11 / 265	cadherin binding involved in cell−cell adhesion
7	1e−03	34 / 1475	DNA binding
8	1e−03	3 / 17	structural constituent of nuclear pore
9	2e−03	3 / 19	nucleocytoplasmic transporter activity
10	4e−03	4 / 48	SH3/SH2 adaptor activity
11	4e−03	3 / 24	transmembrane transporter activity
12	7e−03	2 / 10	GDP−dissociation inhibitor activity
13	7e−03	2 / 10	poly(A) binding
14	7e−03	2 / 10	transmembrane receptor protein tyrosine kinase adaptor activity
15	8e−03	5 / 94	double−stranded DNA 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	7e−07	13 / 176	hsa−miR−199b−3p
2	2e−06	22 / 516	hsa−miR−15a
3	4e−06	20 / 463	hsa−miR−301a
4	7e−06	16 / 321	hsa−miR−590−3p
5	9e−06	20 / 489	hsa−miR−16
6	1e−05	19 / 455	hsa−miR−130a
7	1e−05	17 / 379	hsa−miR−454
8	1e−05	13 / 233	hsa−miR−1252
9	2e−05	17 / 394	hsa−miR−301b
10	3e−05	12 / 215	hsa−miR−199a−3p
11	3e−05	14 / 288	hsa−miR−34a
12	3e−05	19 / 493	hsa−miR−103
13	5e−05	15 / 336	hsa−miR−142−5p
14	5e−05	17 / 419	hsa−miR−497
15	6e−05	18 / 467	hsa−miR−195

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 12	BENTINK_src.2
2	0.15	1 / 12	BENTINK_ras.1
3	0.17	1 / 14	BENTINK_ras.6
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 11	BENTINK_ras.4
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	2e−10	39 / 933	PROTEINATLAS_adrenal gland
2	5e−10	40 / 1003	PROTEINATLAS_appendix
3	1e−09	30 / 619	PROTEINATLAS_salivary gland
4	9e−09	39 / 1063	PROTEINATLAS_tonsil
5	6e−08	34 / 912	PROTEINATLAS_urinary bladder
6	6e−08	41 / 1239	PROTEINATLAS_testis
7	1e−07	39 / 1173	PROTEINATLAS_rectum
8	1e−07	39 / 1176	PROTEINATLAS_duodenum
9	1e−07	27 / 639	PROTEINATLAS_breast
10	1e−07	27 / 640	PROTEINATLAS_parathyroid gland
11	1e−07	29 / 724	PROTEINATLAS_lymph node
12	1e−07	29 / 726	PROTEINATLAS_cervix, uterine
13	2e−07	38 / 1138	PROTEINATLAS_small intestine
14	2e−07	29 / 740	PROTEINATLAS_esophagus
15	5e−07	36 / 1097	PROTEINATLAS_kidney

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	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	1e−20	140 / 5067	ICGC_Taf1_targets
2	1e−15	136 / 5518	ICGC_Stat5_targets
3	1e−14	133 / 5466	ICGC_Nficsc81335_targets
4	5e−14	131 / 5442	ICGC_Pmlsc71910_targets
5	2e−13	147 / 6578	ICGC_Pou2_targets
6	8e−13	119 / 4890	ICGC_Bclaf101388_targets
7	1e−12	110 / 4362	ICGC_Creb1_targets
8	4e−12	139 / 6267	ICGC_Yy1_targets
9	4e−12	117 / 4881	ICGC_Atf2_targets
10	3e−11	123 / 5410	ICGC_Foxm1_targets
11	5e−11	65 / 2087	ICGC_Cebpbsc150_targets
12	5e−11	131 / 5961	ICGC_Pol24_targets
13	6e−11	150 / 7247	ICGC_Runx3_targets
14	1e−10	121 / 5383	ICGC_Sp1_targets
15	2e−10	130 / 5984	ICGC_Mta3_targets

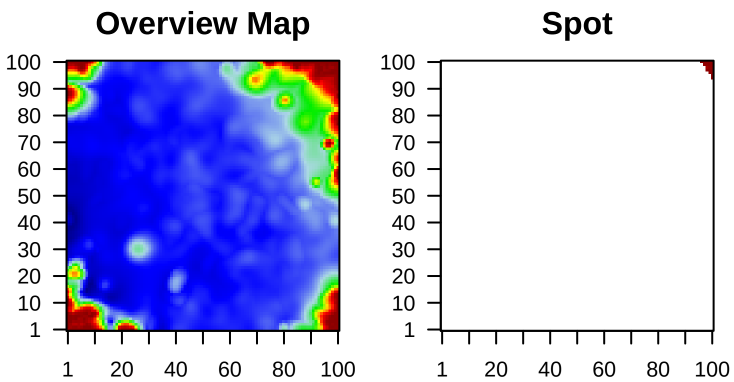
Overexpression Spots

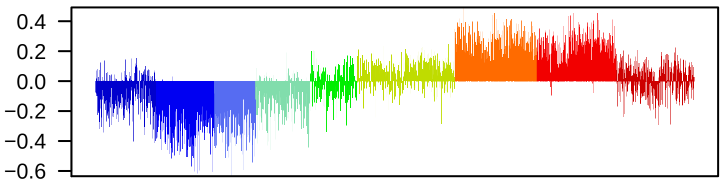
Spot Summary: N

metagenes = 19
genes = 443

<r> metagenes = 0.96
<r> genes = 0.57
beta: r2= 90.74 / log p= −Inf

samples with spot = 838 (24.7 %)
- A * : 4 (1.2 %)
- A F * : 1 (0.3 %)
- C F * : 10 (3.8 %)
- F * : 92 (16.6 %)
- F J * : 398 (86 %)
- J * : 297 (66.4 %)
- N * : 36 (8.1 %)



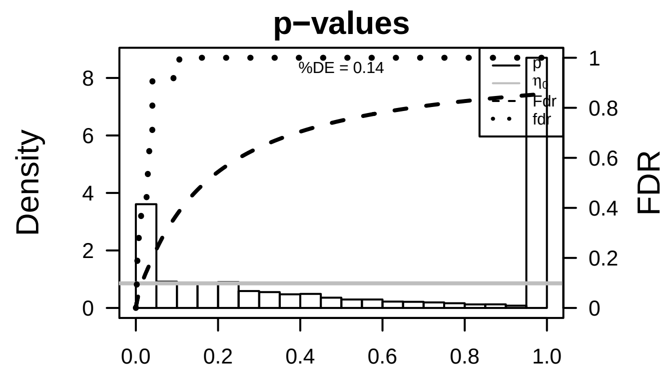


Spot Genelist

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	0.28		
3	ILMN_173950	2.08	−1.34	0.31		
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_171073	1.39	−1.44	0.47	GZMK	granzyme K [Source:HGNC Symbol;Acc:HGNC:4711]
8	ILMN_170496	1.38	−1.61	0.65		
9	ILMN_166708	1.34	−1.65	0.74	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
10	ILMN_234257	1.32	−1.58	0.59	IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
11	ILMN_238175	1.25	−1.46	0.37	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
12	ILMN_207965	1.24	−1.4	0.59	KLRB1	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
13	ILMN_206765	1.22	−1.32	0.77	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
14	ILMN_176037	1.22	−0.81	0.52	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
15	ILMN_187303	1.2	−1.66	0.83		
16	ILMN_328411	1.18	−0.87	0.78		nucleophosmin 1 pseudogene 25 [Source:HGNC Symbol;Acc
17	ILMN_172413	1.15	−1.15	0.78	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
18	ILMN_167918	1.15	−1.53	0.74	LEF1	lymphoid enhancer binding factor 1 [Source:HGNC Symbol;A
19	ILMN_236546	1.13	−0.95	0.8	XBP1	X−box binding protein 1 [Source:HGNC Symbol;Acc:HGNC:1
20	ILMN_171594	1.13	−1.24	0.87		heterogeneous nuclear ribonucleoprotein A1 pseudogene 12

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−41	104 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
2	2e−37	111 / 1797	GSEA	PILON_KLF1_TARGETS_DN
3	3e−37	197 / 5356	Lympl	HOPP_Txn_transition
4	7e−36	231 / 7275	Lympl	HOPP_Txn_elongation
5	2e−34	90 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	2e−30	84 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
7	7e−29	61 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
8	5e−26	229 / 8226	Lympl	HOPP_Active_promoter
9	6e−23	66 / 1013	MF	poly(A) RNA binding
10	4e−22	51 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
11	2e−21	178 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
12	3e−20	42 / 455	GSEA	ZHENG_BOUND_BY_FOXP3
13	5e−20	242 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
14	1e−19	43 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
15	3e−19	236 / 9555	Colon	TssA_Colon
16	3e−19	34 / 302	Refer	Chaussabel_3,4_Protein phosphatases
17	2e−18	75 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
18	2e−18	62 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
19	9e−18	49 / 724	Refer	PROTEINATLAS_lymph node
20	2e−17	22 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
21	3e−17	207 / 8098	Lympl	HOPP_Weak_promoter
22	3e−17	223 / 9054	Colon	Tx_Colon
23	3e−17	25 / 170	HM	HALLMARK_MYC_TARGETS_V1
24	4e−17	64 / 1239	Refer	PROTEINATLAS_testis
25	6e−17	214 / 8568	Colon	TxWk_Colon
26	8e−17	33 / 338	miRN	hsa−miR−548d−5p
27	8e−17	33 / 338	miRN	hsa−miR−548b−5p
28	1e−16	252 / 10999	Colon	TssWk_Colon
29	1e−15	183 / 6970	Chror	5_Tx_Neuronal_Progenitor
30	2e−15	49 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
31	6e−15	212 / 8771	Chror	5_Tx_Melanocytes
32	6e−15	32 / 368	GSEA	OSMAN_BLADDER_CANCER_UP
33	8e−15	30 / 323	miRN	hsa−miR−548a−5p
34	1e−14	34 / 429	miRN	hsa−miR−548n
35	1e−14	29 / 307	miRN	hsa−miR−548c−5p
36	3e−14	29 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
37	4e−14	21 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
38	4e−14	36 / 500	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
39	4e−14	208 / 8678	Colon	Quies3_Colon
40	6e−14	47 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 111	HORVATH_aging_genes meth DOWN
2	0.6	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	4e−07	11 / 96	translational initiation
2	2e−05	20 / 435	negative regulation of apoptotic process
3	3e−05	4 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
4	3e−05	10 / 126	T cell receptor signaling pathway
5	6e−05	6 / 44	gene expression
6	7e−05	5 / 28	regulation of translational initiation
7	7e−05	12 / 196	mRNA splicing, via spliceosome
8	7e−05	4 / 15	formation of translation preinitiation complex
9	2e−04	13 / 255	viral process
10	3e−04	4 / 21	nuclear−transcribed mRNA poly(A) tail shortening
11	4e−04	3 / 10	cellular response to X−ray
12	5e−04	8 / 115	leukocyte migration
13	5e−04	9 / 145	mRNA processing
14	6e−04	5 / 43	T cell activation
15	6e−04	7 / 91	sister chromatid cohesion

Brain

Rank	p−value	#in/all	Geneset
1	2e−21	178 / 5936	Overlap_fetal_midbrain_HetRpts
2	5e−20	242 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−10	210 / 9504	Overlap_fetal_midbrain_K9K27me3
4	3e−09	213 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	1e−05	206 / 10430	Overlap_fetal_midbrain_Quies
6	1e−05	19 / 386	Fetal_ZNF
7	8e−05	28 / 796	Overlap_fetal_midbrain_ZNF
8	1e−04	11 / 180	Overlap_fetal_midbrain_Het
9	8e−04	14 / 328	Fetal_Het
10	3e−03	31 / 1162	Fetal_Enh
11	1e−02	24 / 937	Fetal_EnhG
12	2e−02	28 / 1171	Fetal_EnhP
13	9e−02	20 / 906	Fetal_HetRpts
14	3e−01	22 / 1213	Fetal_TssP
15	5e−01	50 / 3164	Mid_Frontal_Lobe_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	1 / 13	RHODES_CANCER_META_SIGNATURE
2	0.002	3 / 16	GENTLES_modul11
3	0.002	6 / 82	PanCan_JAK−ST_geneset_nanostring
4	0.003	12 / 301	SPANG_BCL6−index2
5	0.004	7 / 125	PanCan_CC+Apop_geneset_nanostring
6	0.008	17 / 554	Lembcke_Colonic Inflammation
7	0.011	6 / 117	PanCan_Driver_Gene_geneset_nanostring
8	0.017	2 / 13	GENTLES_modul12
9	0.017	2 / 13	GENTLES_modul18
10	0.020	2 / 14	GENTLES_modul1
11	0.023	2 / 15	WANG_ER_UP
12	0.023	2 / 15	WOLFER_overlap genes
13	0.024	7 / 178	SPANG_LPS−index2
14	0.026	2 / 16	GENTLES_modul7
15	0.026	2 / 16	GENTLES_modul14

CC

Rank	p−value	#in/all	Geneset
1	5e−12	133 / 4822	cytoplasm
2	7e−12	73 / 1979	membrane
3	2e−10	82 / 2535	nucleoplasm
4	7e−10	90 / 2979	cytosol
5	2e−09	125 / 4828	nucleus
6	5e−09	35 / 721	nucleolus
7	7e−08	12 / 101	intracellular ribonucleoprotein complex
8	3e−05	65 / 2464	extracellular exosome
9	9e−05	8 / 90	chromatin
10	2e−04	16 / 352	focal adhesion
11	5e−04	5 / 41	ER to Golgi transport vesicle membrane
12	5e−04	7 / 88	melanosome
13	6e−04	3 / 11	CCR4−NOT complex
14	8e−04	3 / 12	eukaryotic translation initiation factor 3 complex
15	9e−04	13 / 295	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	6e−04	28 / 904	Chr 10
2	2e−02	11 / 342	Chr 18
3	3e−02	28 / 1217	Chr 3
4	8e−02	23 / 1060	Chr 5
5	8e−02	20 / 902	Chr 4
6	1e−01	24 / 1160	Chr 12
7	2e−01	23 / 1211	Chr 6
8	3e−01	40 / 2323	Chr 1
9	3e−01	18 / 994	Chr X
10	3e−01	14 / 768	Chr 14
11	4e−01	20 / 1170	Chr 7
12	5e−01	5 / 289	Chr 21
13	5e−01	24 / 1492	Chr 2
14	5e−01	7 / 422	Chr 13
15	7e−01	12 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−15	183 / 6970	5_Tx_Neuronal_Progenitor
2	6e−15	212 / 8771	5_Tx_Melanocytes
3	5e−13	191 / 7854	5_Tx_Fibroblasts
4	6e−12	246 / 11455	2_TssA_Fibroblasts
5	3e−09	250 / 12298	2_TssA_Melanocytes
6	4e−09	197 / 8990	15_Quies_Fibroblasts
7	1e−08	258 / 12983	2_TssA_Neuronal_Progenitor
8	4e−07	133 / 5699	6_EnhG_Melanocytes
9	7e−05	213 / 11130	15_Quies_Melanocytes
10	8e−05	172 / 8613	7_Enh_Fibroblasts
11	1e−04	231 / 12393	15_Quies_Neuronal_Progenitor
12	1e−03	231 / 12741	7_Enh_Melanocytes
13	2e−03	216 / 11836	3_TssF_Melanocytes
14	3e−03	32 / 1206	6_EnhG_Neuronal_Progenitor
15	3e−02	171 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−19	236 / 9555	TssA_Colon
2	2e−18	75 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
3	3e−17	223 / 9054	Tx_Colon
4	6e−17	214 / 8568	TxWk_Colon
5	1e−16	252 / 10999	TssWk_Colon
6	2e−15	49 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	4e−14	208 / 8678	Quies3_Colon
8	7e−12	54 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	2e−11	74 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_ti
10	5e−06	98 / 4034	TssD1_Colon
11	1e−05	34 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	2e−04	42 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	4e−04	3 / 10	KIM_MSI−in−EC
14	1e−03	111 / 5373	EnhWk1_Colon
15	5e−03	23 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN

Glio

Rank	p−value	#in/all	Geneset
1	2e−07	20 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−06	55 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−06	18 / 315	Up
4	4e−05	56 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−03	7 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	1e−03	3 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
7	2e−03	6 / 84	GIEZELT_GBM_WT_down_VS_mut
8	4e−03	5 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	4e−02	20 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
10	4e−02	6 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	4e−02	3 / 48	Vishal_subnetwork signature of survival in GBM
12	6e−02	4 / 92	Weller_LGG_A_vs_O_DOWN
13	9e−02	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
14	1e−01	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
15	1e−01	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−41	104 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	2e−37	111 / 1797	PILON_KLF1_TARGETS_DN
3	2e−34	90 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	2e−30	84 / 1241	PUJANA_ATM_PCC_NETWORK
5	7e−29	61 / 669	PUJANA_CHEK2_PCC_NETWORK
6	4e−22	51 / 622	SCHLOSSER_SERUM_RESPONSE_DN
7	3e−20	42 / 455	ZHENG_BOUND_BY_FOXP3
8	1e−19	43 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
9	2e−18	62 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
10	6e−15	32 / 368	OSMAN_BLADDER_CANCER_UP
11	3e−14	29 / 317	HSIAO_HOUSEKEEPING_GENES
12	4e−14	21 / 151	JISON_SICKLE_CELL_DISEASE_DN
13	4e−14	36 / 500	KIM_ALL_DISORDERS_CALB1_CORR_UP
14	6e−14	47 / 841	ACEVEDO_LIVER_CANCER_UP
15	2e−13	31 / 388	SHEN_SMARCA2_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−17	25 / 170	HALLMARK_MYC_TARGETS_V1
2	1e−05	12 / 162	HALLMARK_ALLOGRAFT_REJECTION
3	2e−05	12 / 173	HALLMARK_E2F_TARGETS
4	4e−05	12 / 185	HALLMARK_MTORC1_SIGNALING
5	4e−05	12 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	8e−04	10 / 187	HALLMARK_COMPLEMENT
7	3e−03	9 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
8	3e−03	9 / 186	HALLMARK_IL2_STAT5_SIGNALING
9	6e−03	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
10	1e−02	5 / 87	HALLMARK_PROTEIN_SECRETION
11	2e−02	7 / 176	HALLMARK_KRAS_SIGNALING_UP
12	2e−02	6 / 138	HALLMARK_FATTY_ACID_METABOLISM
13	2e−02	7 / 179	HALLMARK_G2M_CHECKPOINT
14	3e−02	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
15	3e−02	7 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−04	5 / 32	Marjolein_ageing−genes_DN
2	7e−03	9 / 211	Homuth_BMI−associated−genes_DN
3	8e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	7e−01	2 / 147	Homuth_BMI−associated−genes_UP
5	8e−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	3e−37	197 / 5356	HOPP_Txn_transition
2	7e−36	231 / 7275	HOPP_Txn_elongation
3	5e−26	229 / 8226	HOPP_Active_promoter
4	3e−17	207 / 8098	HOPP_Weak_promoter
5	5e−13	184 / 7448	HOPP_Strong_enhancer
6	1e−08	46 / 1169	SPANG_BCR DN
7	3e−07	13 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
8	4e−07	13 / 141	WIRTH_lymphoma937_spot F
9	1e−06	5 / 13	Care_Polarized immune response
10	7e−05	5 / 28	DAVE_Immune response 1
11	2e−04	136 / 6559	HOPP_Weak_txn
12	5e−04	140 / 6959	HOPP_Weak_enhancer
13	6e−04	5 / 43	Monti_OxPhos_cluster
14	6e−04	13 / 283	TARTE_Plasmablast signature
15	1e−03	11 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.5	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	6e−23	66 / 1013	poly(A) RNA binding
2	1e−12	206 / 8818	protein binding
3	5e−07	22 / 399	RNA binding
4	3e−05	6 / 39	translation initiation factor activity
5	2e−04	39 / 1329	ATP binding
6	2e−04	16 / 355	chromatin binding
7	3e−04	13 / 265	cadherin binding involved in cell−cell adhesion
8	6e−04	13 / 283	nucleotide binding
9	1e−03	5 / 48	SH3/SH2 adaptor activity
10	1e−03	4 / 30	coreceptor activity
11	1e−03	5 / 52	calcium−dependent protein binding
12	2e−03	12 / 274	transcription factor binding
13	2e−03	5 / 54	double−stranded RNA binding
14	2e−03	5 / 56	ATP−dependent RNA helicase activity
15	2e−03	6 / 82	unfolded protein 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	8e−17	33 / 338	hsa−miR−548d−5p
2	8e−17	33 / 338	hsa−miR−548b−5p
3	8e−15	30 / 323	hsa−miR−548a−5p
4	1e−14	34 / 429	hsa−miR−548n
5	1e−14	29 / 307	hsa−miR−548c−5p
6	2e−13	28 / 317	hsa−miR−559
7	3e−13	27 / 295	hsa−miR−561
8	5e−13	24 / 235	hsa−miR−26a
9	9e−13	26 / 287	hsa−miR−548j
10	2e−12	25 / 272	hsa−miR−577
11	2e−12	24 / 249	hsa−miR−524−5p
12	2e−12	20 / 166	hsa−miR−452
13	5e−12	25 / 283	hsa−miR−320a
14	5e−12	20 / 173	hsa−miR−607
15	8e−12	20 / 178	hsa−miR−582−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 12	BENTINK_src.2
2	0.02	2 / 14	BENTINK_ras.6
3	0.19	1 / 13	BENTINK_e2f3.2
4	0.19	1 / 13	BENTINK_myc.1
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 13	BENTINK_e2f3.1
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 11	BENTINK_ras.4
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	3e−19	34 / 302	Chaussabel_3,4_Protein phosphatases
2	9e−18	49 / 724	PROTEINATLAS_lymph node
3	2e−17	22 / 119	Chaussabel_2,4_Ribosomal proteins
4	4e−17	64 / 1239	PROTEINATLAS_testis
5	9e−14	38 / 571	PROTEINATLAS_oral mucosa
6	1e−13	43 / 726	PROTEINATLAS_cervix, uterine
7	4e−13	45 / 816	PROTEINATLAS_endometrium
8	5e−13	52 / 1063	PROTEINATLAS_tonsil
9	5e−13	41 / 695	PROTEINATLAS_bone marrow
10	5e−13	43 / 759	PROTEINATLAS_epididymis
11	1e−12	38 / 623	PROTEINATLAS_seminal vesicle
12	1e−12	54 / 1167	PROTEINATLAS_gallbladder
13	5e−12	30 / 412	WIRTH_Immune system
14	7e−12	47 / 959	PROTEINATLAS_nasopharynx
15	8e−12	47 / 963	PROTEINATLAS_pancreas

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	4e−07	44 / 1231	KIM_MYC targets
2	3e−06	118 / 5067	ICGC_Taf1_targets
3	2e−05	58 / 2087	ICGC_Cebpbsc150_targets
4	2e−05	45 / 1478	ICGC_Myc_targets
5	4e−05	129 / 5961	ICGC_Pol24_targets
6	5e−05	49 / 1723	HEBENSTREIT_high expression TF
7	7e−05	68 / 2704	ICGC_Pbx3_targets
8	2e−04	42 / 1498	ICGC_Ets1_targets
9	2e−04	106 / 4890	ICGC_Bclaf101388_targets
10	4e−04	105 / 4881	ICGC_Atf2_targets
11	4e−04	134 / 6578	ICGC_Pou2_targets
12	5e−04	97 / 4468	ICGC_Egr1_targets
13	5e−04	56 / 2255	ICGC_Srfv0416101_targets
14	5e−04	95 / 4362	ICGC_Creb1_targets
15	5e−04	55 / 2215	ICGC_GabpPcr2_targets

Overexpression Spots

Spot Summary: O

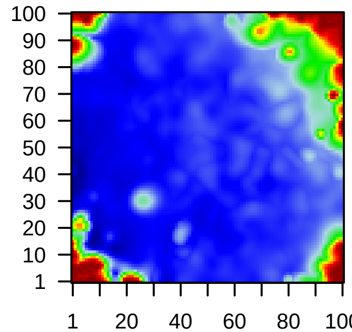
\# metagenes = 12
\# genes = 130

<r> metagenes = 0.9
<r> genes = 0.2
beta: r2= 5.04 / log p= −Inf

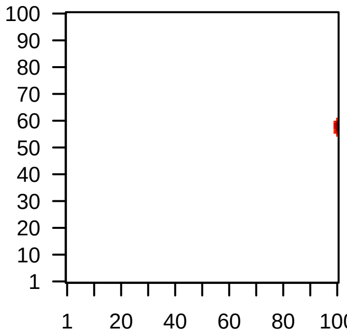
\# samples with spot = 98 (2.9 %)

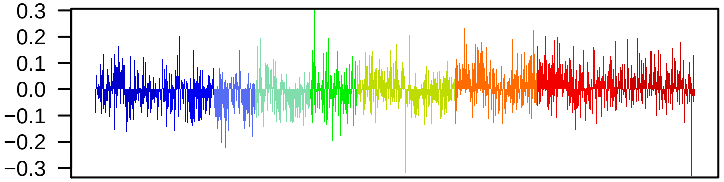
- A * : 5 (1.5 %)
- A C * : 3 (0.9 %)
- A C F * : 4 (1.7 %)
- A F * : 4 (1.3 %)
- C F * : 9 (3.4 %)
- F * : 12 (2.2 %)
- F J * : 29 (6.3 %)
- J * : 19 (4.3 %)
- N * : 13 (2.9 %)

Overview Map



Spot





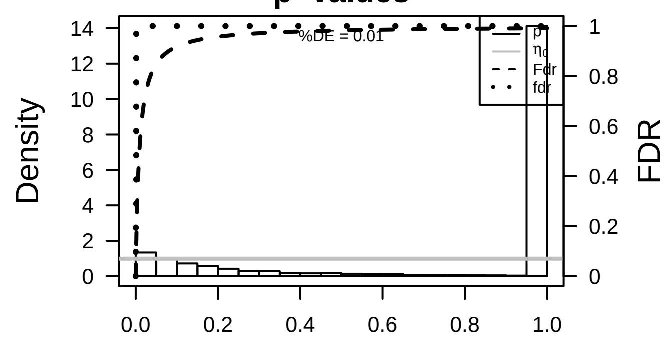
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_215969	2.92	−1.39	0.32		
2	ILMN_216575	2.67	−3.76	0.4		
3	ILMN_179153	2.13	−0.79	0.32		
4	ILMN_324215	1.9	−0.58	0.26		
5	ILMN_166607	1.73	−2.16	0.41		
6	ILMN_210557	1.53	−0.75	0.13	CCL3L3	C−C motif chemokine ligand 3 like 3 [Source:HGNC Symbol;A
7	ILMN_324371	1.44	−1.23	0.39		
8	ILMN_165667	0.98	−0.73	0.35	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:H
10	ILMN_166092	0.92	−0.81	0.61	LOC554223	major histocompatibility complex, class I, V (pseudogene) [Sc
11	ILMN_173324	0.91	−0.52	0.46		
12	ILMN_176286	0.88	−0.93	0.31	HLA−F	major histocompatibility complex, class I, F [Source:HGNC Sy
13	ILMN_169180	0.83	−0.57	0.4		
14	ILMN_167888	0.83	−0.55	0.43	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:H
16	ILMN_237582	0.79	−0.86	0.48	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
17	ILMN_208259	0.79	−0.51	0.44	KIR3DL3	killer cell immunoglobulin like receptor, three Ig domains and
18	ILMN_172728	0.69	−0.63	0.39	CD4	CD4 molecule [Source:HGNC Symbol;Acc:HGNC:1678]
19	ILMN_178951	0.67	−0.67	0.42	STIP1	stress induced phosphoprotein 1 [Source:HGNC Symbol;Acc
20	ILMN_232467	0.64	−0.67	0.58	USF2	upstream transcription factor 2, c−fos interacting [Source:HGI

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−14	40 / 2845	Colon	TxEnhG1_Colon
2	4e−13	63 / 7354	Colon	TssF_Colon
3	5e−12	49 / 4795	Chror	6_EnhG_Fibroblasts
4	2e−11	31 / 2028	Chror	4_TxTrans_Melanocytes
5	5e−11	52 / 5699	Chror	6_EnhG_Melanocytes
6	2e−10	39 / 3450	Chror	4_TxTrans_Fibroblasts
7	2e−10	37 / 3164	Brain	Mid_Frontal_Lobe_ZNF
8	7e−10	67 / 9555	Colon	TssA_Colon
9	7e−10	65 / 9054	Colon	Tx_Colon
10	4e−09	51 / 6138	Colon	TssD2_Colon
11	2e−08	46 / 5356	Lympl	HOPP_Txn_transition
12	2e−08	21 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
13	4e−08	74 / 12298	Chror	2_TssA_Melanocytes
14	7e−08	68 / 10779	Colon	Enh_Colon
15	2e−07	30 / 2810	Colon	EnhA_Colon
16	6e−07	70 / 11836	Chror	3_TssF_Melanocytes
17	7e−07	11 / 412	Refer	WIRTH_Immune system
18	9e−07	57 / 8568	Colon	TxWk_Colon
19	2e−06	4 / 22	BP	antigen processing and presentation of peptide antigen via MHC class I
20	2e−06	18 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
21	3e−06	17 / 1169	Lympl	SPANG_BCR DN
22	4e−06	12 / 594	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UI
23	6e−06	59 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
24	6e−06	4 / 30	miRN	hsa−miR−371−3p
25	6e−06	52 / 7854	Chror	5_Tx_Fibroblasts
26	8e−06	19 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
27	1e−05	66 / 11455	Chror	2_TssA_Fibroblasts
28	1e−05	40 / 5373	Colon	EnhWk1_Colon
29	2e−05	6 / 136	GSEA	ELVIDGE_HYPOXIA_DN
30	2e−05	7 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
31	2e−05	21 / 1979	CC	membrane
32	3e−05	4 / 44	Glio	WILLSCHER_GBM_Verhaak−PNwt_up
33	4e−05	54 / 8771	Chror	5_Tx_Melanocytes
34	4e−05	7 / 232	GSEA	RICKMAN_METASTASIS_DN
35	4e−05	4 / 49	CC	transcriptional repressor complex
36	5e−05	5 / 100	miRN	hsa−miR−150
37	7e−05	12 / 789	Colon	TxEnhG2_Colon
38	7e−05	3 / 20	MF	peptide antigen binding
39	8e−05	3 / 21	MF	14−3−3 protein binding
40	8e−05	3 / 21	CC	integral component of lumenal side of endoplasmic reticulum membrane

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	2e−06	4 / 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	2 / 16	nucleosome disassembly
5	2e−03	2 / 18	positive regulation of proteolysis
6	3e−03	3 / 73	liver development
7	3e−03	2 / 21	ATP−dependent chromatin remodeling
8	3e−03	2 / 21	nuclear−transcribed mRNA poly(A) tail shortening
9	3e−03	2 / 22	positive regulation of T cell activation
10	4e−03	3 / 78	response to nutrient
11	4e−03	2 / 24	cellular response to interleukin−4
12	4e−03	2 / 24	oligosaccharide metabolic process
13	4e−03	2 / 25	protein import into nucleus, translocation
14	5e−03	3 / 86	response to organic substance
15	5e−03	2 / 27	glycogen metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−10	37 / 3164	Mid_Frontal_Lobe_ZNF
2	6e−06	59 / 9504	Overlap_fetal_midbrain_K9K27me3
3	2e−04	59 / 10430	Overlap_fetal_midbrain_Quies
4	3e−04	39 / 5936	Overlap_fetal_midbrain_HetRpts
5	3e−03	15 / 1728	Fetal_ReprPCWk
6	4e−03	27 / 4112	Mid_Frontal_Lobe_ReprPC
7	5e−03	9 / 818	Mid_Frontal_Lobe_Het
8	4e−02	17 / 2709	Mid_Frontal_Lobe_HetRpts
9	5e−02	16 / 2630	Fetal_TssF
10	5e−02	47 / 9815	Overlap_fetal_midbrain_ReprPC
11	1e−01	6 / 796	Overlap_fetal_midbrain_ZNF
12	1e−01	6 / 906	Fetal_HetRpts
13	2e−01	10 / 1784	Mid_Frontal_Lobe_ReprPCWk
14	2e−01	11 / 2127	Mid_Frontal_Lobe_K9K27me3
15	3e−01	42 / 9917	Overlap_fetal_midbrain_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	2 / 13	GENTLES_modul18
2	0.022	3 / 150	PanCan_MAPK_geneset_nanostring
3	0.034	3 / 178	SPANG_LPS−index2
4	0.050	1 / 13	GENTLES_modul2
5	0.069	5 / 554	Lembcke_Colonic Inflammation
6	0.088	2 / 125	PanCan_CC+Apop_geneset_nanostring
7	0.101	2 / 136	PanCan_RAS_geneset_nanostring
8	0.117	3 / 301	SPANG_BCL6−index2
9	0.119	0 / 13	LIU_LIVER_CANCER
10	0.170	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.178	2 / 193	PanCan_PI3K_geneset_nanostring
12	0.278	1 / 82	PanCan_JAK−ST_geneset_nanostring
13	0.304	1 / 91	PanCan_TXmisReg_geneset_nanostring
14	0.372	1 / 117	PanCan_Driver_Gene_geneset_nanostring
15	0.392	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−05	21 / 1979	membrane
2	4e−05	4 / 49	transcriptional repressor complex
3	8e−05	3 / 21	integral component of lumenal side of endoplasmic reticulum membrane
4	3e−04	8 / 422	protein complex
5	3e−04	22 / 2535	nucleoplasm
6	8e−04	2 / 11	transcription factor TFTC complex
7	1e−03	10 / 775	endoplasmic reticulum
8	1e−03	2 / 12	BAF−type complex
9	1e−03	3 / 51	phagocytic vesicle membrane
10	1e−03	23 / 2979	cytosol
11	1e−03	2 / 13	SWI/SNF complex
12	1e−03	20 / 2464	extracellular exosome
13	5e−03	30 / 4828	nucleus
14	6e−03	7 / 539	Golgi membrane
15	6e−03	2 / 30	immunological synapse

Chr

Rank	p−value	#in/all	Geneset
1	0.01	12 / 1411	Chr 11
2	0.05	2 / 87	Chr Y
3	0.05	9 / 1211	Chr 6
4	0.13	9 / 1467	Chr 19
5	0.16	4 / 536	Chr 22
6	0.31	6 / 1160	Chr 12
7	0.33	5 / 954	Chr 9
8	0.42	4 / 836	Chr 8
9	0.48	4 / 904	Chr 10
10	0.53	4 / 959	Chr 16
11	0.53	5 / 1217	Chr 3
12	0.59	3 / 768	Chr 14
13	0.60	5 / 1318	Chr 17
14	0.68	1 / 289	Chr 21
15	0.83	7 / 2323	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−12	49 / 4795	6_EnhG_Fibroblasts
2	2e−11	31 / 2028	4_TxTrans_Melanocytes
3	5e−11	52 / 5699	6_EnhG_Melanocytes
4	2e−10	39 / 3450	4_TxTrans_Fibroblasts
5	4e−08	74 / 12298	2_TssA_Melanocytes
6	6e−07	70 / 11836	3_TssF_Melanocytes
7	6e−06	52 / 7854	5_Tx_Fibroblasts
8	1e−05	66 / 11455	2_TssA_Fibroblasts
9	4e−05	54 / 8771	5_Tx_Melanocytes
10	1e−04	45 / 6970	5_Tx_Neuronal_Progenitor
11	1e−04	56 / 9635	3_TssF_Fibroblasts
12	1e−04	40 / 5956	3_TssF_Neuronal_Progenitor
13	3e−04	14 / 1206	6_EnhG_Neuronal_Progenitor
14	6e−04	67 / 12983	2_TssA_Neuronal_Progenitor
15	3e−03	64 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−14	40 / 2845	TxEnhG1_Colon
2	4e−13	63 / 7354	TssF_Colon
3	7e−10	67 / 9555	TssA_Colon
4	7e−10	65 / 9054	Tx_Colon
5	4e−09	51 / 6138	TssD2_Colon
6	2e−08	21 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
7	7e−08	68 / 10779	Enh_Colon
8	2e−07	30 / 2810	EnhA_Colon
9	9e−07	57 / 8568	TxWk_Colon
10	8e−06	19 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	1e−05	40 / 5373	EnhWk1_Colon
12	7e−05	12 / 789	TxEnhG2_Colon
13	4e−04	19 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e−03	9 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	6e−03	56 / 10999	TssWk_Colon

Glio

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	1e−03	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
3	4e−03	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	8e−03	5 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	3e−02	14 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	3e−02	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
7	4e−02	1 / 9	Colman_survival_robust
8	4e−02	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
9	4e−02	7 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
10	5e−02	10 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
11	6e−02	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
12	6e−02	1 / 15	Mukasa_UP_in_GBM
13	6e−02	1 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
14	9e−02	3 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
15	1e−01	1 / 32	Donson−Misc immune function−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	18 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	4e−06	12 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
3	2e−05	6 / 136	ELVIDGE_HYPOXIA_DN
4	2e−05	7 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
5	4e−05	7 / 232	RICKMAN_METASTASIS_DN
6	1e−04	17 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
7	1e−04	12 / 831	LOPEZ_MBD_TARGETS
8	1e−04	6 / 190	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
9	2e−04	4 / 72	PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP
10	2e−04	8 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
11	2e−04	11 / 774	REACTOME_IMMUNE_SYSTEM
12	4e−04	2 / 8	RUNNE_GENDER_EFFECT_UP
13	7e−04	4 / 100	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR
14	7e−04	3 / 44	CHIBA_RESPONSE_TO_TSA
15	8e−04	3 / 45	PID_HES_HEY_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.007	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
2	0.017	2 / 50	HALLMARK_TGF_BETA_SIGNALING
3	0.037	3 / 185	HALLMARK_MTORC1_SIGNALING
4	0.040	3 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	0.063	2 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	0.109	1 / 29	HALLMARK_NOTCH_SIGNALING
7	0.121	2 / 151	HALLMARK_APOPTOSIS
8	0.135	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	0.142	2 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.147	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.153	2 / 175	HALLMARK_XENOBIOTIC_METABOLISM
12	0.158	2 / 179	HALLMARK_G2M_CHECKPOINT
13	0.164	2 / 183	HALLMARK_GLYCOLYSIS
14	0.167	2 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	0.167	2 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	4 / 211	Homuth_BMI−associated−genes_DN
2	0.02	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
3	0.02	3 / 147	Homuth_BMI−associated−genes_UP
4	0.04	1 / 10	DUMEAUX_Women normal BMI literature genes up
5	1.00	0 / 94	DUMEAUX_Smoking enriched genes
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−08	46 / 5356	HOPP_Txn_transition
2	3e−06	17 / 1169	SPANG_BCR DN
3	1e−04	47 / 7448	HOPP_Strong_enhancer
4	1e−04	46 / 7275	HOPP_Txn_elongation
5	2e−04	2 / 5	DAVE_MHCCII BL DN
6	3e−04	49 / 8226	HOPP_Active_promoter
7	9e−03	6 / 455	SPANG_CD40 6hrs DN
8	2e−02	3 / 134	DAVE_BL−vs−DLBCL
9	2e−02	2 / 60	SPANG_BAFF 9hrs DN
10	3e−02	7 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
11	3e−02	41 / 8098	HOPP_Weak_promoter
12	3e−02	7 / 777	WIRTH_lymphoma937_spot D
13	4e−02	2 / 75	SPANG_LPS 6hrs DN
14	4e−02	4 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
15	4e−02	2 / 78	Sha_DLBCL 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	7e−05	3 / 20	peptide antigen binding
2	8e−05	3 / 21	14−3−3 protein binding
3	1e−04	53 / 8818	protein binding
4	7e−04	2 / 10	dipeptidyl−peptidase activity
5	1e−03	9 / 646	protein homodimerization activity
6	1e−03	6 / 311	enzyme binding
7	2e−03	3 / 59	RNA polymerase II distal enhancer sequence−specific DNA binding
8	2e−03	2 / 17	ligand−dependent nuclear receptor binding
9	3e−03	3 / 70	chaperone binding
10	4e−03	2 / 25	protein phosphatase 2A binding
11	5e−03	5 / 274	transcription factor binding
12	5e−03	2 / 26	nucleosomal DNA binding
13	5e−03	2 / 26	retinoic acid receptor binding
14	6e−03	2 / 29	repressing transcription factor binding
15	7e−03	2 / 31	ADP 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	6e−06	4 / 30	hsa−miR−371−3p
2	5e−05	5 / 100	hsa−miR−150
3	1e−04	4 / 61	hsa−miR−296−3p
4	3e−04	5 / 144	hsa−miR−491−5p
5	4e−04	4 / 88	hsa−miR−423−5p
6	1e−03	6 / 288	hsa−miR−34a
7	1e−03	6 / 299	hsa−miR−548c−3p
8	2e−03	3 / 58	hsa−miR−193a−3p
9	3e−03	4 / 148	hsa−miR−409−3p
10	4e−03	2 / 23	hsa−miR−1227
11	5e−03	3 / 85	hsa−miR−149
12	5e−03	3 / 88	hsa−miR−188−3p
13	6e−03	3 / 91	hsa−miR−10b
14	6e−03	5 / 294	hsa−miR−503
15	7e−03	3 / 98	hsa−miR−653

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	7e−07	11 / 412	WIRTH_Immune system
2	1e−04	11 / 724	PROTEINATLAS_lymph node
3	1e−03	12 / 1063	PROTEINATLAS_tonsil
4	2e−03	9 / 681	PROTEINATLAS_lung
5	2e−03	11 / 1003	PROTEINATLAS_appendix
6	3e−03	10 / 912	PROTEINATLAS_urinary bladder
7	4e−03	9 / 782	PROTEINATLAS_thyroid gland
8	5e−03	11 / 1118	PROTEINATLAS_placenta
9	5e−03	7 / 535	PROTEINATLAS_spleen
10	1e−02	11 / 1268	PROTEINATLAS_colon
11	1e−02	9 / 960	PROTEINATLAS_cerebellum
12	2e−02	10 / 1167	PROTEINATLAS_gallbladder
13	2e−02	10 / 1173	PROTEINATLAS_rectum
14	2e−02	9 / 1016	PROTEINATLAS_cerebral cortex
15	2e−02	10 / 1194	PROTEINATLAS_stomach

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	3e−04	35 / 5067	ICGC_Taf1_targets
2	4e−04	33 / 4735	ICGC_Pu1_targets
3	7e−04	31 / 4468	ICGC_Egr1_targets
4	8e−04	15 / 1498	ICGC_Ets1_targets
5	8e−04	15 / 1501	ICGC_Usf1_targets
6	1e−03	13 / 1231	KIM_MYC targets
7	1e−03	35 / 5442	ICGC_Pmlsc71910_targets
8	2e−03	34 / 5312	ICGC_Tcf12_targets
9	2e−03	33 / 5188	ICGC_Ebfsc137065_targets
10	2e−03	29 / 4345	ICGC_Zeb1_targets
11	2e−03	29 / 4362	ICGC_Creb1_targets
12	2e−03	38 / 6322	ICGC_Tcf3_targets
13	3e−03	18 / 2255	ICGC_SrfV0416101_targets
14	3e−03	34 / 5518	ICGC_Stat5_targets
15	3e−03	40 / 6868	ICGC_Elf1_targets

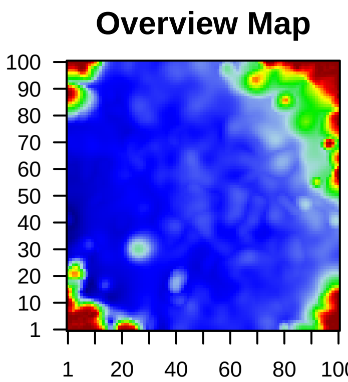
Overexpression Spots

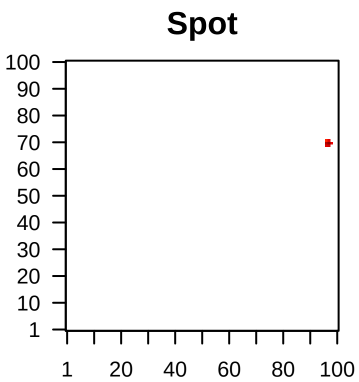
Spot Summary: P

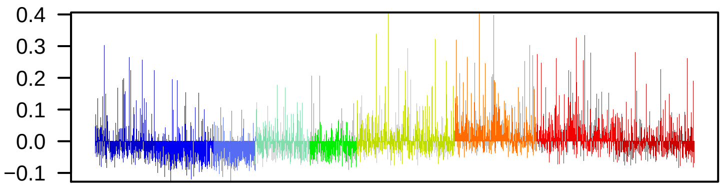
metagenes = 7
genes = 97

<r> metagenes = 0.99
<r> genes = 0.29
beta: r2= 3.51 / log p= −Inf

samples with spot = 93 (2.7 %)
A * : 14 (4.1 %)
A C * : 4 (1.2 %)
A F * : 2 (0.6 %)
C F * : 2 (0.8 %)
F * : 17 (3.1 %)
F J * : 26 (5.6 %)
J * : 21 (4.7 %)
N * : 7 (1.6 %)





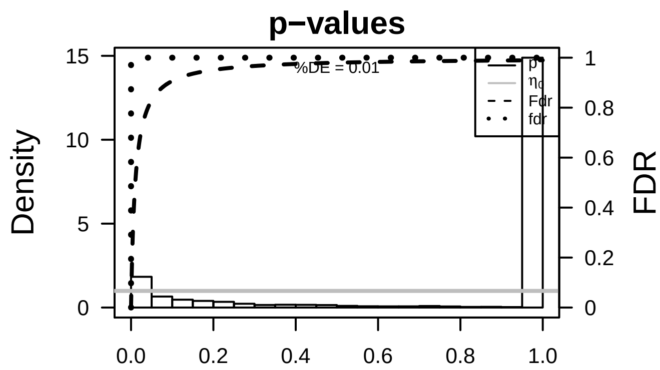


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_208306	1.69	−0.7	0.57		immunoglobulin lambda like polypeptide 3, pseudogene [Sour
2	ILMN_180460	1.38	−0.59	0.62		
3	ILMN_240396	1.27	−0.58	0.81		
4	ILMN_167422	1.18	−0.67	0.63		
5	ILMN_176801	1.09	−0.44	0.78	TNFRSF17	TNF receptor superfamily member 17 [Source:HGNC Symbol
6	ILMN_170744	0.93	−0.49	0.62	CDK12	cyclin dependent kinase 12 [Source:HGNC Symbol;Acc:HGN
7	ILMN_166339	0.85	−0.34	0.84	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723
8	ILMN_167885	0.84	−0.34	0.39		immunoglobulin lambda variable 8−61 [Source:HGNC Symbo
9	ILMN_171375	0.82	−0.58	0.33	UBE2J1	ubiquitin conjugating enzyme E2 J1 [Source:HGNC Symbol;A
10	ILMN_223378	0.8	−0.38	0.71	CD38	CD38 molecule [Source:HGNC Symbol;Acc:HGNC:1667]
11	ILMN_180675	0.75	−0.33	0.75	GLDC	glycine decarboxylase [Source:HGNC Symbol;Acc:HGNC:43
12	ILMN_173718	0.7	−0.44	0.62	CDCA7	cell division cycle associated 7 [Source:HGNC Symbol;Acc:H
13	ILMN_171906	0.68	−0.47	0.12	KCTD10	potassium channel tetramerization domain containing 10 [Sou
14	ILMN_167148	0.66	−0.49	0.29	GALM	galactose mutarotase [Source:HGNC Symbol;Acc:HGNC:240
15	ILMN_323269	0.66	−0.54	0.36		dihydrofolate reductase pseudogene 2 [Source:HGNC Symbo
16	ILMN_180604	0.64	−0.39	0.69	TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
17	ILMN_170069	0.63	−0.49	0.44	SLC44A1	solute carrier family 44 member 1 [Source:HGNC Symbol;Acc
18	ILMN_172672	0.62	−0.37	0.69	NUSAP1	nucleolar and spindle associated protein 1 [Source:HGNC Sy
19	ILMN_169589	0.57	−0.25	0.43		
20	ILMN_165601	0.54	−0.36	0.25	RGS1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	6e−69	39 / 132	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	2e−60	37 / 162	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
3	5e−56	33 / 124	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	4e−51	28 / 80	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
5	7e−51	43 / 518	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	2e−50	35 / 228	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	3e−49	5 / 12	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	1e−45	37 / 381	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
9	6e−45	29 / 145	GSEA	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
10	2e−42	33 / 295	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
11	2e−42	36 / 418	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	8e−42	25 / 96	GSEA	LEE_EARLY_T_LYMPHOCYTE_UP
13	6e−41	25 / 103	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
14	2e−39	27 / 162	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
15	5e−39	23 / 84	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
16	1e−38	40 / 772	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
17	1e−38	40 / 777	Lymp	WIRTH_lymphoma937_spot D
18	1e−35	19 / 49	GSEA	KANG_DOXORUBICIN_RESISTANCE_UP
19	7e−35	43 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
20	1e−34	28 / 273	GSEA	HORIUCHI_WTAP_TARGETS_DN
21	4e−34	24 / 155	GSEA	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
22	4e−34	27 / 249	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
23	1e−33	27 / 258	GSEA	BASAKI_YBX1_TARGETS_UP
24	2e−33	22 / 115	GSEA	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
25	5e−33	41 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
26	2e−32	26 / 249	GSEA	ZHANG_TLX_TARGETS_60HR_DN
27	6e−32	22 / 133	GSEA	CHANG_CYCLING_GENES
28	6e−32	27 / 298	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
29	8e−32	27 / 301	GSEA	GOLDRATH_ANTIGEN_RESPONSE
30	9e−31	18 / 64	GSEA	CROONQUIST_NRAS_SIGNALING_DN
31	5e−30	36 / 926	GSEA	NUYTTEN_EZH2_TARGETS_DN
32	9e−30	32 / 641	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
33	2e−29	16 / 44	GSEA	ZHAN_MULTIPLE_MYELOMA_PR_UP
34	2e−29	31 / 589	GSEA	BENPORATH_CYCLING_GENES
35	2e−29	30 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
36	2e−29	31 / 593	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
37	3e−29	21 / 145	GSEA	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
38	2e−27	17 / 74	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
39	3e−27	21 / 179	HM	HALLMARK_G2M_CHECKPOINT
40	5e−27	21 / 182	GSEA	FUJII_YBX1_TARGETS_DN



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	6e−14	15 / 300	cell division
2	4e−13	13 / 219	mitotic nuclear division
3	3e−10	9 / 122	G2/M transition of mitotic cell cycle
4	9e−10	8 / 94	G1/S transition of mitotic cell cycle
5	5e−09	5 / 20	regulation of transcription involved in G1/S transition of mitotic cell cycle
6	3e−07	4 / 18	mitotic sister chromatid segregation
7	1e−06	5 / 56	chromosome segregation
8	2e−06	4 / 27	mitotic spindle assembly
9	2e−06	4 / 27	mitotic spindle organization
10	8e−06	3 / 12	mitotic G2 DNA damage checkpoint
11	1e−05	3 / 13	mitotic chromosome condensation
12	1e−05	3 / 13	spindle organization
13	1e−05	5 / 91	sister chromatid cohesion
14	2e−05	8 / 343	cell proliferation
15	7e−05	5 / 130	DNA replication

Brain

Rank	p−value	#in/all	Geneset
1	5e−05	50 / 9815	Overlap_fetal_midbrain_ReprPC
2	3e−04	20 / 2654	Fetal_Quies
3	1e−02	8 / 906	Fetal_HetRpts
4	1e−02	42 / 9504	Overlap_fetal_midbrain_K9K27me3
5	1e−02	12 / 1728	Fetal_ReprPCWk
6	9e−02	11 / 2127	Mid_Frontal_Lobe_K9K27me3
7	1e−01	8 / 1436	Fetal_K9K27me3
8	1e−01	9 / 1784	Mid_Frontal_Lobe_ReprPCWk
9	2e−01	5 / 1012	Mid_Frontal_Lobe_Enh
10	3e−01	1 / 110	Overlap_fetal_midbrain_Tx
11	3e−01	5 / 1171	Fetal_EnhP
12	5e−01	3 / 819	Overlap_fetal_midbrain_TssP
13	6e−01	3 / 924	Mid_Frontal_Lobe_TssF
14	6e−01	1 / 307	Fetal_ReprPC
15	7e−01	33 / 10430	Overlap_fetal_midbrain_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	3e−49	5 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	2e−22	25 / 527	Lembcke_Normal vs Adenoma
3	4e−17	4 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	1e−10	8 / 73	SHAUGHNESSY_MM high risk
5	1e−08	4 / 9	GENTLES_modul3
6	2e−07	5 / 38	KUIPER_MM good survival
7	3e−05	1 / 13	RHODES_CANCER_META_SIGNATURE
8	1e−03	2 / 14	BEN−PORATH_UP
9	8e−03	3 / 125	PanCan_CC+Apop_geneset_nanostring
10	1e−02	6 / 554	Lembcke_Colonic Inflammation
11	1e−02	2 / 54	KUIPER_MM poor survival
12	5e−02	1 / 16	GENTLES_modul7
13	1e−01	1 / 46	PanCan_DNARepair_geneset_nanostring
14	3e−01	1 / 117	PanCan_Driver_Gene_geneset_nanostring
15	4e−01	0 / 15	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	1e−10	30 / 2535	nucleoplasm
2	5e−09	8 / 116	midbody
3	5e−08	11 / 379	centrosome
4	1e−07	5 / 36	spindle microtubule
5	5e−07	27 / 2979	cytosol
6	5e−07	6 / 90	spindle pole
7	9e−07	5 / 53	chromosome, centromeric region
8	1e−06	35 / 4828	nucleus
9	2e−06	6 / 107	spindle
10	5e−06	5 / 75	condensed chromosome kinetochore
11	1e−05	5 / 89	centriole
12	3e−05	32 / 4822	cytoplasm
13	9e−05	4 / 70	kinetochore
14	2e−04	4 / 90	chromatin
15	3e−04	3 / 37	mitotic spindle

Chr

Rank	p−value	#in/all	Geneset
1	0.04	6 / 769	Chr 15
2	0.18	5 / 904	Chr 10
3	0.26	3 / 536	Chr 22
4	0.27	6 / 1318	Chr 17
5	0.30	4 / 836	Chr 8
6	0.31	2 / 342	Chr 18
7	0.35	4 / 902	Chr 4
8	0.37	5 / 1211	Chr 6
9	0.55	4 / 1170	Chr 7
10	0.58	4 / 1217	Chr 3
11	0.61	2 / 619	Chr 20
12	0.62	3 / 954	Chr 9
13	0.62	3 / 959	Chr 16
14	0.66	7 / 2323	Chr 1
15	0.69	3 / 1060	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−07	60 / 11455	2_TssA_Fibroblasts
2	7e−07	44 / 6970	5_Tx_Neuronal_Progenitor
3	2e−06	61 / 12298	2_TssA_Melanocytes
4	5e−06	62 / 12983	2_TssA_Neuronal_Progenitor
5	7e−05	49 / 9635	3_TssF_Fibroblasts
6	8e−05	56 / 11836	3_TssF_Melanocytes
7	2e−04	45 / 8771	5_Tx_Melanocytes
8	4e−04	56 / 12393	15_Quies_Neuronal_Progenitor
9	1e−03	56 / 12741	7_Enh_Melanocytes
10	2e−03	39 / 7854	5_Tx_Fibroblasts
11	2e−03	50 / 11130	15_Quies_Melanocytes
12	1e−02	40 / 8990	15_Quies_Fibroblasts
13	1e−01	19 / 4237	14_ZNF_Neuronal_Progenitor
14	1e−01	25 / 5956	3_TssF_Neuronal_Progenitor
15	1e−01	24 / 5699	6_EnhG_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−18	16 / 193	Kosinski_lower−crypt−long−list
2	2e−06	57 / 10999	TssWk_Colon
3	3e−06	4 / 31	Kosinski_lower−crypt−short−list
4	1e−04	27 / 4034	TssD1_Colon
5	2e−03	2 / 19	Boland_CRC−MSI−A6−A10
6	3e−03	12 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colc
7	6e−03	8 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	7e−03	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
9	7e−03	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
10	1e−02	30 / 6138	TssD2_Colon
11	1e−02	9 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
12	2e−02	41 / 9555	TssA_Colon
13	3e−02	1 / 10	Marisa_CRC−C1
14	4e−02	37 / 8678	Quies3_Colon
15	4e−02	7 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN

Glio

Rank	p−value	#in/all	Geneset
1	6e−69	39 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−17	12 / 74	Weller_LGG_gradeII−vs−III_DOWN
3	3e−17	11 / 55	developing astrocytes
4	2e−06	5 / 65	cultured astroglia vs. in vivo astrocytes
5	8e−06	20 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	6e−03	2 / 34	Shaw_down_in_1p19q
7	1e−02	12 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
8	2e−02	1 / 5	Phillips Prolif up vs PN & MES
9	8e−02	1 / 25	Barbus_GBM_STS_vs._LTS
10	1e−01	1 / 35	Colman_survival_associated
11	1e−01	1 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
12	1e−01	5 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
13	1e−01	3 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
14	2e−01	1 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	2e−01	1 / 51	Gorovets_LGG_PG_subclass

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−60	37 / 162	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
2	5e−56	33 / 124	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	4e−51	28 / 80	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
4	7e−51	43 / 518	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	2e−50	35 / 228	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	3e−49	5 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	1e−45	37 / 381	VECCHI_GASTRIC_CANCER_EARLY_UP
8	6e−45	29 / 145	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
9	2e−42	33 / 295	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
10	2e−42	36 / 418	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	8e−42	25 / 96	LEE_EARLY_T_LYMPHOCYTE_UP
12	6e−41	25 / 103	WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	2e−39	27 / 162	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
14	5e−39	23 / 84	CROONQUIST_IL6_DEPRIVATION_DN
15	1e−35	19 / 49	KANG_DOXORUBICIN_RESISTANCE_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−27	21 / 179	HALLMARK_G2M_CHECKPOINT
2	1e−20	17 / 173	HALLMARK_E2F_TARGETS
3	2e−14	13 / 177	HALLMARK_MITOTIC_SPINDLE
4	2e−06	6 / 116	HALLMARK_SPERMATOGENESIS
5	3e−06	7 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
6	3e−04	5 / 170	HALLMARK_MYC_TARGETS_V1
7	1e−02	3 / 151	HALLMARK_APOPTOSIS
8	1e−02	2 / 54	HALLMARK_MYC_TARGETS_V2
9	2e−02	2 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	2e−02	3 / 183	HALLMARK_GLYCOLYSIS
11	2e−02	3 / 185	HALLMARK_MTORC1_SIGNALING
12	3e−02	2 / 87	HALLMARK_PROTEIN_SECRETION
13	7e−02	2 / 130	HALLMARK_DNA_REPAIR
14	1e−01	2 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
15	2e−01	1 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 94	DUMEAUX_Smoking enriched genes
2	0.4	1 / 147	Homuth_BMI−associated−genes_UP
3	0.5	1 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−38	40 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
2	1e−38	40 / 777	WIRTH_lymphoma937_spot D
3	2e−21	20 / 283	TARTE_Plasmablast signature
4	7e−11	52 / 7275	HOPP_Txn_elongation
5	3e−09	8 / 109	ROSOLOWSKI_blue total
6	9e−09	41 / 5356	HOPP_Txn_transition
7	4e−07	49 / 8226	HOPP_Active_promoter
8	7e−07	6 / 94	Sha_BL UP
9	4e−05	42 / 7448	HOPP_Strong_enhancer
10	7e−05	4 / 66	TARTE_Plasma cell signature
11	3e−04	42 / 8098	HOPP_Weak_promoter
12	1e−03	4 / 134	DAVE_BL−vs−DLBCL
13	3e−03	11 / 1270	SPANG_BCR UP
14	3e−03	3 / 88	WIRTH_lymphoma937_spot A
15	4e−03	3 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce

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	1e−06	17 / 1329	ATP binding
2	8e−05	6 / 217	protein kinase activity
3	9e−05	46 / 8818	protein binding
4	1e−04	3 / 29	cyclin−dependent protein serine/threonine kinase activity
5	6e−04	6 / 315	protein serine/threonine kinase activity
6	1e−03	2 / 14	RNA polymerase II carboxy−terminal domain kinase activity
7	1e−03	6 / 350	protein kinase binding
8	1e−03	6 / 355	chromatin binding
9	2e−03	3 / 68	drug binding
10	2e−03	2 / 18	protein disulfide isomerase activity
11	2e−03	2 / 19	cyclin binding
12	3e−03	7 / 580	identical protein binding
13	3e−03	4 / 185	microtubule binding
14	4e−03	3 / 92	histone deacetylase binding
15	4e−03	5 / 311	enzyme 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−04	5 / 166	hsa−miR−323b−5p
2	4e−03	2 / 28	hsa−miR−519e*
3	5e−03	3 / 101	hsa−miR−210
4	8e−03	2 / 41	hsa−miR−518f*
5	8e−03	3 / 125	hsa−miR−508−3p
6	9e−03	2 / 44	hsa−miR−518e*
7	2e−02	3 / 164	hsa−miR−495
8	2e−02	3 / 166	hsa−miR−7
9	2e−02	2 / 62	hsa−miR−324−3p
10	2e−02	2 / 73	hsa−miR−1261
11	3e−02	3 / 193	hsa−miR−448
12	3e−02	2 / 76	hsa−miR−205
13	3e−02	2 / 79	hsa−miR−1321
14	4e−02	2 / 93	hsa−miR−378
15	4e−02	2 / 97	hsa−miR−125a−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	9e−09	5 / 22	Chaussabel_1,1_Plasma Cells
2	6e−04	9 / 724	PROTEINATLAS_lymph node
3	7e−04	11 / 1063	PROTEINATLAS_tonsil
4	2e−03	8 / 695	PROTEINATLAS_bone marrow
5	8e−03	10 / 1239	PROTEINATLAS_testis
6	1e−02	6 / 571	PROTEINATLAS_oral mucosa
7	2e−02	7 / 816	PROTEINATLAS_endometrium
8	2e−02	9 / 1268	PROTEINATLAS_colon
9	4e−02	1 / 13	WIRTH_Thymus
10	6e−02	6 / 850	PROTEINATLAS_skin
11	8e−02	5 / 681	PROTEINATLAS_lung
12	8e−02	7 / 1118	PROTEINATLAS_placenta
13	9e−02	7 / 1176	PROTEINATLAS_duodenum
14	1e−01	5 / 740	PROTEINATLAS_esophagus
15	1e−01	7 / 1194	PROTEINATLAS_stomach

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	2e−04	31 / 5067	ICGC_Taf1_targets
2	2e−04	28 / 4362	ICGC_Creb1_targets
3	8e−04	31 / 5466	ICGC_Nficsc81335_targets
4	1e−03	16 / 2087	ICGC_Cebpbsc150_targets
5	2e−03	11 / 1231	KIM_MYC targets
6	3e−03	29 / 5383	ICGC_Sp1_targets
7	3e−03	27 / 4881	ICGC_Atf2_targets
8	3e−03	29 / 5410	ICGC_Foxm1_targets
9	4e−03	29 / 5442	ICGC_Pmlsc71910_targets
10	4e−03	31 / 5984	ICGC_Mta3_targets
11	4e−03	29 / 5518	ICGC_Stat5_targets
12	1e−02	34 / 7247	ICGC_Runx3_targets
13	1e−02	25 / 4890	ICGC_Bclaf101388_targets
14	1e−02	29 / 5961	ICGC_Pol24_targets
15	1e−02	2 / 55	MYC_Targets UP

Overexpression Spots

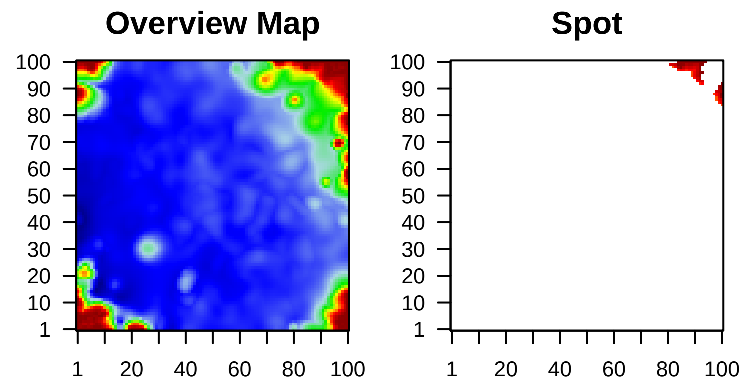
Spot Summary: Q

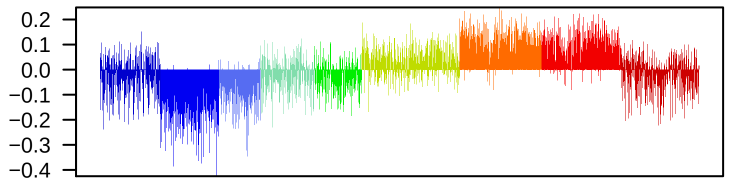
metagenes = 82
genes = 1194

<r> metagenes = 0.71

beta: r2= 43.73 / log p= −Inf

samples with spot = 237 (7 %)
A * : 1 (0.3 %)
F * : 14 (2.5 %)
F J * : 129 (27.9 %)
J * : 93 (20.8 %)



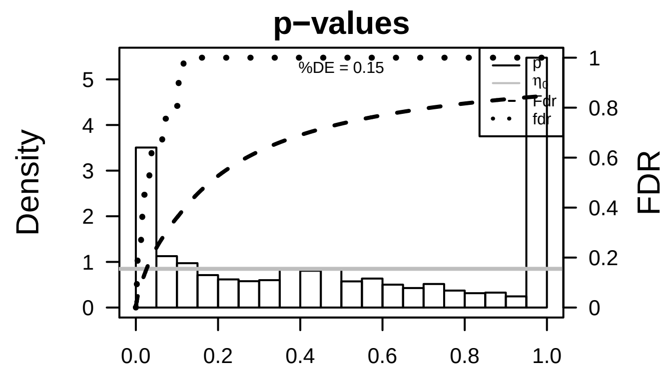


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169749	5.33	−1.74	0.05	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	ILMN_171516	4.62	−2.25	0.06		
3	ILMN_171673	3.14	−1.47	0.09	MYOM2	myomesin 2 [Source:HGNC Symbol;Acc:HGNC:7614]
4	ILMN_206606	2.72	−3.26	0.09	HLA−DRB6	major histocompatibility complex, class II, DR beta 6 (pseudo
5	ILMN_239376	2.36	−2.48	0.25	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
6	ILMN_179817	2.09	−1.22	0.07	CHURC1	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
7	ILMN_178681	2.01	−1.2	0.17	LOC105379645	killer cell immunoglobulin like receptor, two Ig domains and lo
8	ILMN_173123	1.91	−2.04	0.28	GZMH	granzyme H [Source:HGNC Symbol;Acc:HGNC:4710]
9	ILMN_177365	1.78	−1.17	0.34	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
10	ILMN_169107	1.77	−1.46	0.44	FCRLA	Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]
11	ILMN_240485	1.7	−1.35	0.3	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:103
12	ILMN_173487	1.64	−1.96	0.49	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
13	ILMN_173975	1.64	−1.34	0.25		
14	ILMN_179069	1.63	−1.97	0.36		
15	ILMN_176848	1.63	−1.62	0.55	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
16	ILMN_178270	1.6	−1.28	0.28		
17	ILMN_170877	1.59	−1.49	0.32	GNLY	granulysin [Source:HGNC Symbol;Acc:HGNC:4414]
18	ILMN_165379	1.59	−1.31	0.25		
19	ILMN_166446	1.59	−1.05	0.08		
20	ILMN_166723	1.58	−1.63	0.27	KIR2DL3	killer cell immunoglobulin like receptor, two Ig domains and lo

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−60	58 / 84	Refer	Chaussabel_2,1_Cytotoxic cells
2	3e−50	528 / 7275	Lympl	HOPP_Txn_elongation
3	9e−46	620 / 9555	Colon	TssA_Colon
4	3e−45	560 / 8226	Lympl	HOPP_Active_promoter
5	5e−45	421 / 5356	Lympl	HOPP_Txn_transition
6	2e−36	574 / 9054	Colon	Tx_Colon
7	3e−35	528 / 8098	Lympl	HOPP_Weak_promoter
8	4e−34	546 / 8568	Colon	TxWk_Colon
9	8e−33	547 / 8678	Colon	Quies3_Colon
10	3e−32	595 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	1e−29	656 / 11455	Chror	2_TssA_Fibroblasts
12	9e−29	687 / 12298	Chror	2_TssA_Melanocytes
13	1e−28	634 / 10999	Colon	TssWk_Colon
14	3e−28	537 / 8771	Chror	5_Tx_Melanocytes
15	2e−26	449 / 6970	Chror	5_Tx_Neuronal_Progenitor
16	5e−26	562 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
17	6e−26	61 / 288	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
18	2e−25	40 / 119	Refer	Chaussabel_2,8_T−cells
19	2e−25	487 / 7854	Chror	5_Tx_Fibroblasts
20	1e−23	524 / 8818	MF	protein binding
21	2e−23	153 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
22	3e−22	386 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
23	4e−22	693 / 12983	Chror	2_TssA_Neuronal_Progenitor
24	1e−21	67 / 412	Refer	WIRTH_Immune system
25	2e−21	454 / 7448	Lympl	HOPP_Strong_enhancer
26	4e−21	98 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
27	6e−21	129 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
28	2e−18	133 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
29	3e−18	632 / 11836	Chror	3_TssF_Melanocytes
30	6e−17	59 / 402	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
31	7e−17	152 / 1797	GSEA	PILON_KLF1_TARGETS_DN
32	2e−16	161 / 1979	CC	membrane
33	3e−16	102 / 1013	MF	poly(A) RNA binding
34	4e−16	90 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
35	6e−16	65 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
36	8e−16	428 / 7354	Colon	TssF_Colon
37	9e−16	104 / 1063	Refer	PROTEINATLAS_tonsil
38	1e−15	144 / 1723	TF	HEBENSTREIT_high expression TF
39	3e−15	657 / 12741	Chror	7_Enh_Melanocytes
40	3e−15	105 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.02	10 / 111	HORVATH_aging_genes meth DOWN
2	0.56	6 / 142	HORVATH_aging_genes meth UP
3	0.92	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	

BP

Rank	p−value	#in/all	Geneset
1	9e−12	24 / 105	regulation of immune response
2	5e−09	16 / 63	T cell costimulation
3	1e−08	36 / 293	immune response
4	1e−08	22 / 126	T cell receptor signaling pathway
5	3e−07	25 / 184	translation
6	4e−07	23 / 163	rRNA processing
7	4e−07	14 / 65	SRP−dependent cotranslational protein targeting to membrane
8	6e−07	16 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
9	1e−06	29 / 255	viral process
10	7e−06	14 / 81	viral transcription
11	1e−05	15 / 96	translational initiation
12	2e−05	11 / 56	positive regulation of T cell proliferation
13	2e−05	8 / 29	B cell receptor signaling pathway
14	2e−05	7 / 22	positive regulation of T cell activation
15	3e−05	13 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c

Brain

Rank	p−value	#in/all	Geneset
1	3e−32	595 / 9815	Overlap_fetal_midbrain_ReprPC
2	5e−26	562 / 9504	Overlap_fetal_midbrain_K9K27me3
3	3e−22	386 / 5936	Overlap_fetal_midbrain_HetRpts
4	8e−15	559 / 10430	Overlap_fetal_midbrain_Quies
5	6e−14	533 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	1e−05	181 / 3164	Mid_Frontal_Lobe_ZNF
7	2e−04	32 / 386	Fetal_ZNF
8	4e−04	54 / 796	Overlap_fetal_midbrain_ZNF
9	7e−04	59 / 906	Fetal_HetRpts
10	1e−02	15 / 180	Overlap_fetal_midbrain_Het
11	1e−02	54 / 937	Fetal_EnhG
12	4e−02	62 / 1171	Fetal_EnhP
13	2e−01	18 / 328	Fetal_Het
14	2e−01	80 / 1728	Fetal_ReprPCWk
15	3e−01	53 / 1162	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	41 / 554	Lembcke_Colonic Inflammation
2	1e−03	7 / 39	ZHANG_MM up
3	2e−03	4 / 13	GENTLES_modul18
4	2e−03	24 / 301	SPANG_BCL6−index2
5	3e−03	4 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	6e−03	3 / 13	RHODES_CANCER_META_SIGNATURE
7	2e−02	3 / 13	GENTLES_modul6
8	2e−02	3 / 14	GENTLES_modul1
9	3e−02	10 / 117	PanCan_Driver_Gene_geneset_nanostring
10	3e−02	3 / 16	GENTLES_modul7
11	3e−02	3 / 16	GENTLES_modul11
12	8e−02	4 / 38	KUIPER_MM good survival
13	8e−02	12 / 178	SPANG_LPS−index2
14	8e−02	5 / 54	KUIPER_MM poor survival
15	9e−02	1 / 14	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−16	161 / 1979	membrane
2	2e−14	182 / 2464	extracellular exosome
3	2e−11	199 / 2979	cytosol
4	3e−10	9 / 13	MHC class II protein complex
5	6e−10	103 / 1304	mitochondrion
6	2e−09	280 / 4822	cytoplasm
7	1e−07	62 / 721	nucleolus
8	1e−07	271 / 4828	nucleus
9	5e−07	157 / 2535	nucleoplasm
10	7e−07	28 / 234	lysosomal membrane
11	1e−06	8 / 21	integral component of lumenal side of endoplasmic reticulum membrane
12	1e−06	15 / 81	late endosome membrane
13	3e−06	7 / 17	T cell receptor complex
14	8e−06	24 / 207	lysosome
15	8e−06	21 / 167	external side of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.004	55 / 902	Chr 4
2	0.027	58 / 1060	Chr 5
3	0.029	65 / 1211	Chr 6
4	0.036	26 / 422	Chr 13
5	0.046	61 / 1160	Chr 12
6	0.073	62 / 1217	Chr 3
7	0.317	103 / 2323	Chr 1
8	0.383	28 / 619	Chr 20
9	0.471	39 / 904	Chr 10
10	0.576	62 / 1492	Chr 2
11	0.588	22 / 536	Chr 22
12	0.608	48 / 1170	Chr 7
13	0.618	34 / 836	Chr 8
14	0.709	39 / 994	Chr X
15	0.816	28 / 768	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−29	656 / 11455	2_TssA_Fibroblasts
2	9e−29	687 / 12298	2_TssA_Melanocytes
3	3e−28	537 / 8771	5_Tx_Melanocytes
4	2e−26	449 / 6970	5_Tx_Neuronal_Progenitor
5	2e−25	487 / 7854	5_Tx_Fibroblasts
6	4e−22	693 / 12983	2_TssA_Neuronal_Progenitor
7	3e−18	632 / 11836	3_TssF_Melanocytes
8	3e−15	657 / 12741	7_Enh_Melanocytes
9	4e−15	348 / 5699	6_EnhG_Melanocytes
10	9e−14	636 / 12393	15_Quies_Neuronal_Progenitor
11	3e−11	463 / 8613	7_Enh_Fibroblasts
12	4e−11	479 / 8990	15_Quies_Fibroblasts
13	3e−09	560 / 11130	15_Quies_Melanocytes
14	3e−07	484 / 9635	3_TssF_Fibroblasts
15	2e−05	256 / 4795	6_EnhG_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−46	620 / 9555	TssA_Colon
2	2e−36	574 / 9054	Tx_Colon
3	4e−34	546 / 8568	TxWk_Colon
4	8e−33	547 / 8678	Quies3_Colon
5	1e−28	634 / 10999	TssWk_Colon
6	2e−23	153 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	4e−21	98 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	8e−16	428 / 7354	TssF_Colon
9	1e−13	84 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	2e−11	117 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	1e−10	85 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	2e−09	547 / 10779	Enh_Colon
13	2e−09	306 / 5373	EnhWk1_Colon
14	3e−09	143 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
15	3e−08	84 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

Glio

Rank	p−value	#in/all	Geneset
1	5e−06	114 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	4e−05	8 / 32	Donson−Misc immune function−associated with LTS in HGA
3	8e−05	29 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	1e−04	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
5	4e−04	17 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	6e−04	116 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	1e−03	31 / 401	Down_b
8	2e−03	8 / 55	Stuehler_Proteins_up_in_STS
9	2e−03	3 / 7	Donson−adaptive−immunity−associated with LTS in HGA
10	3e−03	4 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
11	5e−03	7 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
12	6e−03	50 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
13	3e−02	3 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
14	4e−02	2 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
15	5e−02	11 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−26	61 / 288	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
2	6e−21	129 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
3	2e−18	133 / 1417	PUJANA_BRCA1_PCC_NETWORK
4	6e−17	59 / 402	SMID_BREAST_CANCER_NORMAL_LIKE_UP
5	7e−17	152 / 1797	PILON_KLF1_TARGETS_DN
6	4e−16	90 / 841	ACEVEDO_LIVER_CANCER_UP
7	6e−16	65 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
8	3e−15	105 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
9	7e−15	38 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
10	6e−14	47 / 317	HSIAO_HOUSEKEEPING_GENES
11	1e−13	56 / 436	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
12	2e−12	15 / 34	HAHTOLA_SEZARY_SYNDROM_DN
13	3e−12	69 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
14	4e−12	58 / 500	KIM_ALL_DISORDERS_CALB1_CORR_UP
15	2e−11	68 / 666	BENPORATH_MYC_MAX_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	3e−11	30 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−10	28 / 162	HALLMARK_ALLOGRAFT_REJECTION
3	8e−06	21 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	7e−05	13 / 87	HALLMARK_PROTEIN_SECRETION
5	4e−04	19 / 186	HALLMARK_IL2_STAT5_SIGNALING
6	1e−03	17 / 177	HALLMARK_MITOTIC_SPINDLE
7	1e−03	14 / 132	HALLMARK_UV_RESPONSE_DN
8	2e−03	15 / 151	HALLMARK_APOPTOSIS
9	4e−03	11 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
10	5e−03	16 / 185	HALLMARK_MTORC1_SIGNALING
11	7e−03	7 / 54	HALLMARK_MYC_TARGETS_V2
12	2e−02	14 / 173	HALLMARK_E2F_TARGETS
13	2e−02	14 / 176	HALLMARK_ADIPOGENESIS
14	2e−02	6 / 50	HALLMARK_TGF_BETA_SIGNALING
15	2e−02	9 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−14	10 / 10	Marjolein_ageing−genes_UP
2	6e−13	15 / 32	Marjolein_ageing−genes_DN
3	8e−05	5 / 10	DUMEAUX_Women normal BMI literature genes up
4	7e−05	6 / 18	Huan_blood−pressure_SBP−signature
5	3e−04	3 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	4e−04	5 / 16	Huan_blood−pressure_DBP−signature
7	4e−03	14 / 147	Homuth_BMI−associated−genes_UP
8	5e−03	4 / 17	DUMEAUX_High bmi enriched genes
9	2e−01	1 / 5	Huan_blood−pressure_HTN−signature
10	4e−01	1 / 10	DUMEAUX_Smoking literature genes up
11	5e−01	9 / 211	Homuth_BMI−associated−genes_DN
12	8e−01	3 / 94	DUMEAUX_Smoking enriched genes
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	3e−50	528 / 7275	HOPP_Txn_elongation
2	3e−45	560 / 8226	HOPP_Active_promoter
3	5e−45	421 / 5356	HOPP_Txn_transition
4	3e−35	528 / 8098	HOPP_Weak_promoter
5	2e−21	454 / 7448	HOPP_Strong_enhancer
6	1e−14	386 / 6559	HOPP_Weak_txn
7	5e−14	402 / 6959	HOPP_Weak_enhancer
8	7e−10	95 / 1169	SPANG_BCR DN
9	2e−07	36 / 331	WIRTH_lymphoma937_spot H
10	3e−07	92 / 1270	SPANG_BCR UP
11	2e−06	20 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
12	2e−06	42 / 455	SPANG_CD40 6hrs DN
13	2e−06	20 / 141	WIRTH_lymphoma937_spot F
14	2e−06	33 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
15	3e−06	32 / 306	WIRTH_lymphoma937_spot E

Melanoma

Rank	p−value	#in/all	Geneset
1	0.7	1 / 27	Hugo_melanoma−all−LEF1_UP
2	0.8	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.9	1 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 30	Hugo_melanoma−all−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	1e−23	524 / 8818	protein binding
2	3e−16	102 / 1013	poly(A) RNA binding
3	8e−07	23 / 169	structural constituent of ribosome
4	1e−05	6 / 14	MHC class II protein complex binding
5	4e−05	35 / 399	RNA binding
6	2e−04	24 / 256	ubiquitin protein ligase binding
7	4e−04	24 / 265	cadherin binding involved in cell−cell adhesion
8	1e−03	41 / 580	identical protein binding
9	1e−03	17 / 174	transmembrane signaling receptor activity
10	1e−03	5 / 20	peptide antigen binding
11	2e−03	20 / 227	transcription coactivator activity
12	2e−03	4 / 14	telomerase RNA binding
13	3e−03	4 / 15	MHC class I protein binding
14	4e−03	7 / 48	SH3/SH2 adaptor activity
15	5e−03	4 / 17	phosphatidylinositol 3−kinase 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−07	34 / 299	hsa−miR−548c−3p
2	1e−06	24 / 184	hsa−miR−129−5p
3	3e−06	15 / 87	hsa−miR−299−3p
4	7e−06	21 / 166	hsa−miR−323b−5p
5	8e−06	23 / 193	hsa−miR−513a−3p
6	1e−05	16 / 106	hsa−miR−22
7	1e−05	35 / 374	hsa−miR−144
8	1e−05	31 / 317	hsa−miR−559
9	2e−05	29 / 291	hsa−miR−186
10	2e−05	15 / 100	hsa−miR−376a
11	3e−05	10 / 48	hsa−miR−1291
12	3e−05	44 / 540	hsa−miR−17
13	3e−05	22 / 196	hsa−miR−206
14	4e−05	27 / 272	hsa−miR−101
15	4e−05	19 / 158	hsa−miR−200b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	3 / 13	BENTINK_e2f3.1
2	0.12	2 / 14	BENTINK_ras.6
3	0.38	1 / 11	BENTINK_ras.4
4	0.40	1 / 12	BENTINK_ras.1
5	0.43	1 / 13	BENTINK_myc.1
6	0.45	1 / 14	GUSTAFSON_PI3K_UP
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	BENTINK_e2f3.2
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	5e−60	58 / 84	Chaussabel_2,1_Cytotoxic cells
2	2e−25	40 / 119	Chaussabel_2,8_T−cells
3	1e−21	67 / 412	WIRTH_Immune system
4	9e−16	104 / 1063	PROTEINATLAS_tonsil
5	4e−15	80 / 724	PROTEINATLAS_lymph node
6	6e−13	27 / 119	Chaussabel_2,4_Ribosomal proteins
7	9e−13	100 / 1118	PROTEINATLAS_placenta
8	8e−12	27 / 132	Chaussabel_1,7_MHC Ribosomal proteins
9	5e−11	58 / 535	PROTEINATLAS_spleen
10	9e−11	76 / 816	PROTEINATLAS_endometrium
11	1e−09	75 / 850	PROTEINATLAS_skin
12	1e−09	85 / 1016	PROTEINATLAS_cerebral cortex
13	2e−09	15 / 51	Chaussabel_1,3_B−cells
14	3e−09	89 / 1097	PROTEINATLAS_kidney
15	5e−09	80 / 960	PROTEINATLAS_cerebellum

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	

TF

Rank	p−value	#in/all	Geneset
1	1e−15	144 / 1723	HEBENSTREIT_high expression TF
2	3e−15	318 / 5067	ICGC_Taf1_targets
3	2e−13	330 / 5466	ICGC_Nficsc81335_targets
4	8e−13	299 / 4881	ICGC_Atf2_targets
5	2e−12	377 / 6578	ICGC_Pou2_targets
6	4e−12	105 / 1231	KIM_MYC targets
7	5e−12	326 / 5518	ICGC_Stat5_targets
8	2e−11	345 / 5984	ICGC_Mta3_targets
9	3e−11	267 / 4362	ICGC_Creb1_targets
10	2e−10	315 / 5442	ICGC_Pmlsc71910_targets
11	2e−10	288 / 4890	ICGC_Bclaf101388_targets
12	3e−10	114 / 1478	ICGC_Myc_targets
13	3e−10	280 / 4735	ICGC_Pu1_targets
14	4e−10	147 / 2087	ICGC_Cebpbsc150_targets
15	4e−10	267 / 4468	ICGC_Egr1_targets

Overexpression Spots

Spot Summary: R

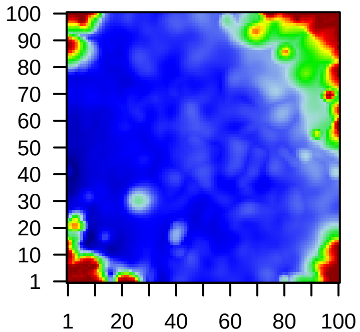
metagenes = 2
genes = 140

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

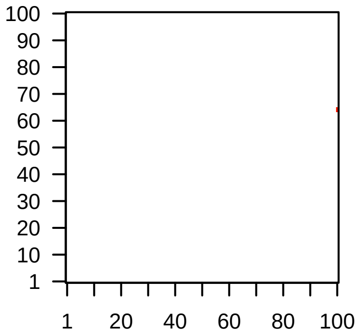
samples with spot = 164 (4.8 %)

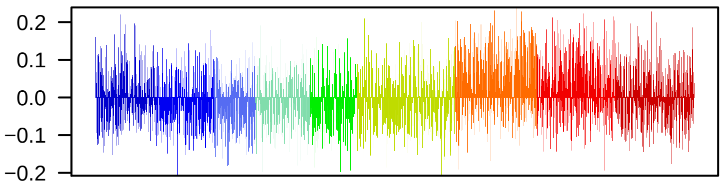
- A * : 12 (3.5 %)
- A C * : 4 (1.2 %)
- A C F * : 1 (0.4 %)
- A F * : 4 (1.3 %)
- C F * : 5 (1.9 %)
- F * : 13 (2.3 %)
- F J * : 68 (14.7 %)
- J * : 43 (9.6 %)
- N * : 14 (3.2 %)

Overview Map



Spot





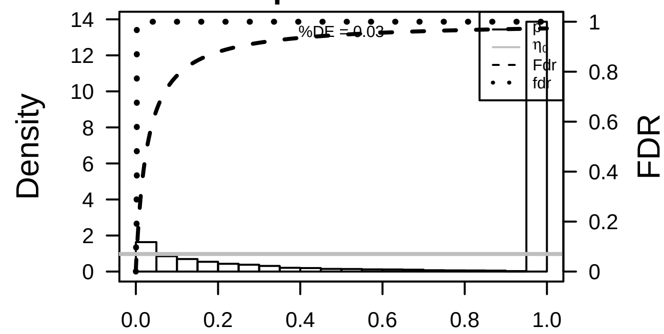
Spot Genelist

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 Symb
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	Lympl	HOPP_Txn_elongation
2	6e−29	84 / 5356	Lympl	HOPP_Txn_transition
3	9e−23	95 / 8568	Colon	TxWk_Colon
4	2e−22	91 / 7854	Chror	5_Tx_Fibroblasts
5	1e−21	96 / 9054	Colon	Tx_Colon
6	2e−19	92 / 8771	Chror	5_Tx_Melanocytes
7	9e−18	87 / 8226	Lympl	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	Chror	2_TssA_Melanocytes
12	4e−15	70 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
13	5e−14	103 / 12983	Chror	2_TssA_Neuronal_Progenitor
14	1e−13	74 / 6970	Chror	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	Chror	3_TssF_Melanocytes
18	4e−12	94 / 11455	Chror	2_TssA_Fibroblasts
19	7e−12	34 / 1797	GSEA	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	Lympl	HOPP_Weak_promoter
26	1e−09	59 / 5699	Chror	6_EnhG_Melanocytes
27	2e−09	28 / 1535	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
28	3e−09	77 / 8990	Chror	15_Quies_Fibroblasts
29	3e−09	75 / 8613	Chror	7_Enh_Fibroblasts
30	5e−09	68 / 7448	Lympl	HOPP_Strong_enhancer
31	1e−08	92 / 12393	Chror	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	Chror	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	Chror	7_Enh_Melanocytes

p−values



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−c
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

Overexpression Spots

Spot Summary: S

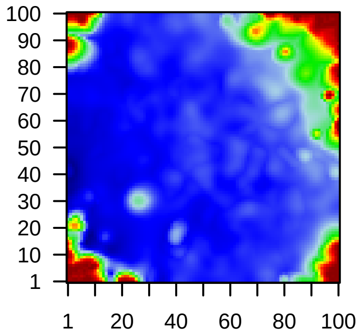
metagenes = 23
genes = 399

<r> metagenes = 0.91
<r> genes = 0.51
beta: r2= 71.06 / log p= −Inf

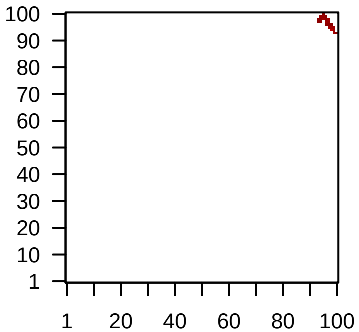
samples with spot = 623 (18.4 %)

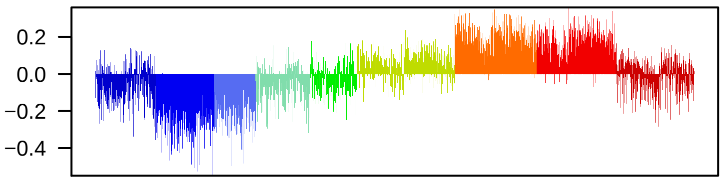
- A * : 1 (0.3 %)
- A F * : 3 (1 %)
- C F * : 3 (1.1 %)
- F * : 52 (9.4 %)
- F J * : 314 (67.8 %)
- J * : 242 (54.1 %)
- N * : 8 (1.8 %)

Overview Map



Spot





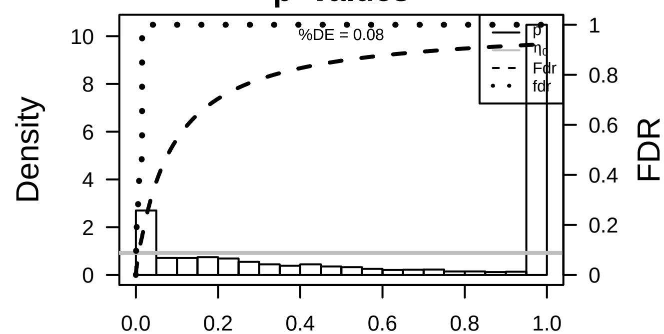
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324037	2.04	−1.35	0.37		immunoglobulin kappa variable 1D−17 [Source:HGNC Symbo
2	ILMN_169921	1.89	−1.18	0.3		
3	ILMN_178810	1.79	−0.92	0.37		BLOC1S5−TXNDC5 readthrough (NMD candidate) [Source:H
4	ILMN_177245	1.73	−2.05	0.38	RPS23	ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10
5	ILMN_168027	1.73	−0.94	0.33		immunoglobulin kappa variable 1−33 [Source:HGNC Symbol;
6	ILMN_175259	1.47	−1.51	0.34		
7	ILMN_169022	1.38	−0.68	0.42	CNTNAP2	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
8	ILMN_177554	1.28	−1.27	0.79	FCMR	Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGN
9	ILMN_172541	1.2	−1.21	0.69	NELL2	neural EGFL like 2 [Source:HGNC Symbol;Acc:HGNC:7751]
10	ILMN_188665	1.18	−1.35	0.72		
11	ILMN_330772	1.18	−1.05	0.53	CXXC5	CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26
12	ILMN_166949	1.17	−0.76	0.58	OSBPL10	oxysterol binding protein like 10 [Source:HGNC Symbol;Acc:H
13	ILMN_216683	1.17	−1.25	0.69	RPS4X	ribosomal protein S4, X−linked [Source:HGNC Symbol;Acc:H
14	ILMN_179492	1.16	−0.86	0.54	MIR5195	microRNA 5195 [Source:HGNC Symbol;Acc:HGNC:43526]
15	ILMN_165571	1.13	−1.29	0.8		
16	ILMN_209334	1.09	−0.92	0.64	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254
17	ILMN_205846	1.06	−0.88	0.74	BACH2	BTB domain and CNC homolog 2 [Source:HGNC Symbol;Acc
18	ILMN_221313	1.05	−1.51	0.8		
19	ILMN_166659	1.05	−0.8	0.56	IRF8	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:HG
20	ILMN_177618	0.98	−0.93	0.73	BIRC3	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−28	166 / 5356	Lympl	HOPP_Txn_transition
2	1e−27	30 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
3	1e−25	194 / 7275	Lympl	HOPP_Txn_elongation
4	3e−23	204 / 8226	Lympl	HOPP_Active_promoter
5	8e−23	62 / 1013	MF	poly(A) RNA binding
6	1e−22	222 / 9555	Colon	TssA_Colon
7	2e−22	73 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
8	3e−20	210 / 9054	Colon	Tx_Colon
9	6e−20	202 / 8568	Colon	TxWk_Colon
10	3e−19	64 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	5e−19	71 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
12	5e−19	218 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
13	6e−19	158 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
14	7e−19	51 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	1e−17	57 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
16	2e−16	37 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
17	4e−16	51 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
18	2e−15	29 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
19	3e−15	41 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
20	4e−15	21 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
21	8e−15	31 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
22	8e−15	165 / 6970	Chror	5_Tx_Neuronal_Progenitor
23	1e−14	25 / 242	Refer	Chaussabel_3,9_Kinases
24	2e−14	13 / 44	GSEA	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
25	3e−14	240 / 12298	Chror	2_TssA_Melanocytes
26	3e−14	191 / 8771	Chror	5_Tx_Melanocytes
27	3e−14	14 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
28	4e−14	55 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
29	4e−14	21 / 170	HM	HALLMARK_MYC_TARGETS_V1
30	5e−14	68 / 1797	GSEA	PILON_KLF1_TARGETS_DN
31	6e−14	17 / 101	GSEA	REACTOME_TRANSLATION
32	7e−14	180 / 8098	Lympl	HOPP_Weak_promoter
33	1e−13	47 / 963	Refer	PROTEINATLAS_pancreas
34	2e−13	227 / 11455	Chror	2_TssA_Fibroblasts
35	2e−13	34 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
36	3e−13	187 / 8678	Colon	Quies3_Colon
37	3e−13	14 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
38	4e−13	52 / 1194	Refer	PROTEINATLAS_stomach
39	5e−13	15 / 81	BP	viral transcription
40	7e−13	198 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	2 / 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	3e−13	14 / 65	SRP−dependent cotranslational protein targeting to membrane
2	5e−13	15 / 81	viral transcription
3	1e−12	15 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
4	6e−12	15 / 96	translational initiation
5	2e−10	17 / 163	rRNA processing
6	9e−09	16 / 184	translation
7	7e−07	12 / 139	RNA splicing
8	2e−05	14 / 254	cell−cell adhesion
9	7e−05	12 / 219	mitotic nuclear division
10	3e−04	7 / 90	regulation of mRNA stability
11	3e−04	4 / 24	RNA splicing, via transesterification reactions
12	5e−04	6 / 70	regulation of cellular response to heat
13	5e−04	16 / 435	negative regulation of apoptotic process
14	6e−04	3 / 12	maturation of SSU−rRNA
15	6e−04	5 / 49	response to hydrogen peroxide

Brain

Rank	p−value	#in/all	Geneset
1	5e−19	218 / 9815	Overlap_fetal_midbrain_ReprPC
2	6e−19	158 / 5936	Overlap_fetal_midbrain_HetRpts
3	7e−13	198 / 9504	Overlap_fetal_midbrain_K9K27me3
4	2e−11	39 / 796	Overlap_fetal_midbrain_ZNF
5	6e−08	188 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	6e−06	187 / 10430	Overlap_fetal_midbrain_Quies
7	3e−04	10 / 180	Overlap_fetal_midbrain_Het
8	8e−04	13 / 328	Fetal_Het
9	2e−02	11 / 386	Fetal_ZNF
10	3e−02	21 / 937	Fetal_EnhG
11	4e−02	24 / 1171	Fetal_EnhP
12	7e−02	23 / 1162	Fetal_Enh
13	2e−01	21 / 1213	Fetal_TssP
14	2e−01	16 / 906	Fetal_HetRpts
15	3e−01	6 / 307	Fetal_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	6e−07	2 / 13	RHODES_CANCER_META_SIGNATURE
2	7e−04	3 / 13	GENTLES_modul12
3	1e−03	3 / 15	WOLFER_overlap genes
4	1e−03	3 / 16	GENTLES_modul16
5	4e−03	5 / 73	SHAUGHNESSY_MM high risk
6	4e−03	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	1e−02	1 / 14	LIU_COMMON_CANCER_GENES
8	1e−02	2 / 13	WANG_ER_DN
9	1e−02	2 / 13	GENTLES_modul6
10	2e−02	3 / 39	ZHANG_MM up
11	2e−02	2 / 16	GENTLES_modul11
12	3e−02	9 / 301	SPANG_BCL6−index2
13	4e−02	6 / 178	SPANG_LPS−index2
14	8e−02	1 / 6	ZHANG_MGUS up
15	8e−02	4 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−10	76 / 2535	nucleoplasm
2	1e−09	115 / 4822	cytoplasm
3	1e−08	32 / 721	nucleolus
4	1e−08	9 / 46	ribosome
5	4e−08	110 / 4828	nucleus
6	2e−07	8 / 45	cytosolic large ribosomal subunit
7	1e−06	73 / 2979	cytosol
8	2e−06	10 / 101	intracellular ribonucleoprotein complex
9	2e−06	54 / 1979	membrane
10	2e−06	6 / 28	cytosolic small ribosomal subunit
11	9e−05	14 / 295	cell−cell adherens junction
12	2e−04	12 / 248	extracellular matrix
13	5e−04	14 / 352	focal adhesion
14	7e−04	54 / 2464	extracellular exosome
15	9e−04	33 / 1304	mitochondrion

Chr

Rank	p−value	#in/all	Geneset
1	0.02	26 / 1217	Chr 3
2	0.03	23 / 1060	Chr 5
3	0.03	30 / 1492	Chr 2
4	0.04	11 / 422	Chr 13
5	0.08	16 / 769	Chr 15
6	0.09	17 / 836	Chr 8
7	0.11	8 / 342	Chr 18
8	0.20	14 / 768	Chr 14
9	0.27	20 / 1211	Chr 6
10	0.29	19 / 1160	Chr 12
11	0.29	15 / 902	Chr 4
12	0.30	36 / 2323	Chr 1
13	0.54	14 / 994	Chr X
14	0.58	4 / 289	Chr 21
15	0.84	15 / 1318	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−15	165 / 6970	5_Tx_Neuronal_Progenitor
2	3e−14	240 / 12298	2_TssA_Melanocytes
3	3e−14	191 / 8771	5_Tx_Melanocytes
4	2e−13	227 / 11455	2_TssA_Fibroblasts
5	1e−11	170 / 7854	5_Tx_Fibroblasts
6	1e−10	239 / 12983	2_TssA_Neuronal_Progenitor
7	4e−10	182 / 8990	15_Quies_Fibroblasts
8	2e−09	129 / 5699	6_EnhG_Melanocytes
9	5e−06	207 / 11836	3_TssF_Melanocytes
10	1e−04	17 / 416	4_TxTrans_Neuronal_Progenitor
11	2e−04	207 / 12393	15_Quies_Neuronal_Progenitor
12	2e−04	153 / 8613	7_Enh_Fibroblasts
13	2e−04	33 / 1206	6_EnhG_Neuronal_Progenitor
14	3e−04	85 / 4237	14_ZNF_Neuronal_Progenitor
15	5e−04	187 / 11130	15_Quies_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−22	222 / 9555	TssA_Colon
2	3e−20	210 / 9054	Tx_Colon
3	6e−20	202 / 8568	TxWk_Colon
4	5e−19	71 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	7e−19	51 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	4e−16	51 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
7	3e−13	187 / 8678	Quies3_Colon
8	8e−11	213 / 10999	TssWk_Colon
9	1e−10	48 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
10	8e−07	57 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
11	6e−06	142 / 7354	TssF_Colon
12	1e−05	88 / 4034	TssD1_Colon
13	1e−04	31 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	4e−04	3 / 11	Juehling−MSI−enriched−in−7
15	4e−04	10 / 193	Kosinski_lower−crypt−long−list

Glio

Rank	p−value	#in/all	Geneset
1	5e−06	54 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−05	47 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−04	14 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	4e−02	9 / 315	Up
5	4e−02	18 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	7e−02	3 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	8e−02	2 / 33	Shaw_responders_down_in_oligo_glioma
8	9e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
9	1e−01	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
10	1e−01	9 / 401	Down_b
11	1e−01	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
12	2e−01	1 / 12	Mukasa_UP_in_Astroglioma
13	2e−01	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
14	2e−01	3 / 100	GIEZELT_GBM_STS_down_VS_LTS
15	2e−01	1 / 13	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−22	73 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	3e−19	64 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
3	1e−17	57 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
4	2e−16	37 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
5	2e−15	29 / 317	HSIAO_HOUSEKEEPING_GENES
6	3e−15	41 / 669	PUJANA_CHEK2_PCC_NETWORK
7	4e−15	21 / 151	JISON_SICKLE_CELL_DISEASE_DN
8	8e−15	31 / 388	SHEN_SMARCA2_TARGETS_UP
9	2e−14	13 / 44	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
10	3e−14	14 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
11	4e−14	55 / 1241	PUJANA_ATM_PCC_NETWORK
12	5e−14	68 / 1797	PILON_KLF1_TARGETS_DN
13	6e−14	17 / 101	REACTOME_TRANSLATION
14	2e−13	34 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
15	2e−12	30 / 445	ENK_UV_RESPONSE_KERATINOCYTE_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−14	21 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−05	9 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	3e−05	11 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	5e−03	4 / 50	HALLMARK_TGF_BETA_SIGNALING
5	2e−02	7 / 185	HALLMARK_MTORC1_SIGNALING
6	2e−02	7 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	2e−02	7 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
8	4e−02	6 / 179	HALLMARK_G2M_CHECKPOINT
9	5e−02	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
10	8e−02	5 / 162	HALLMARK_ALLOGRAFT_REJECTION
11	8e−02	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
12	1e−01	5 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	1e−01	5 / 189	HALLMARK_HYPOXIA
14	2e−01	2 / 54	HALLMARK_MYC_TARGETS_V2
15	2e−01	4 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	5e−05	12 / 211	Homuth_BMI−associated−genes_DN
2	3e−04	9 / 147	Homuth_BMI−associated−genes_UP
3	1e−03	4 / 32	Marjolein_ageing−genes_DN
4	7e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	7e−02	2 / 31	DUMEAUX_Fasting enriched genes
6	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
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	7e−28	166 / 5356	HOPP_Txn_transition
2	1e−25	194 / 7275	HOPP_Txn_elongation
3	3e−23	204 / 8226	HOPP_Active_promoter
4	7e−14	180 / 8098	HOPP_Weak_promoter
5	2e−08	153 / 7448	HOPP_Strong_enhancer
6	2e−06	138 / 6959	HOPP_Weak_enhancer
7	6e−05	125 / 6559	HOPP_Weak_txn
8	4e−04	17 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
9	7e−04	17 / 493	WIRTH_lymphoma937_spot J
10	2e−03	6 / 88	ROSOLOWSKI_red total
11	3e−03	3 / 20	DAVE_NFkB BL DN
12	9e−03	27 / 1169	SPANG_BCR DN
13	1e−02	2 / 12	WRIGHT_GCB UP
14	1e−02	3 / 35	TARTE_B−cell signature
15	2e−02	3 / 40	Monti_BCR_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.3	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	8e−23	62 / 1013	poly(A) RNA binding
2	3e−11	183 / 8818	protein binding
3	2e−08	15 / 169	structural constituent of ribosome
4	3e−05	14 / 265	cadherin binding involved in cell−cell adhesion
5	6e−05	17 / 399	RNA binding
6	4e−04	5 / 45	tRNA binding
7	1e−03	6 / 82	unfolded protein binding
8	2e−03	3 / 17	translation elongation factor activity
9	2e−03	4 / 40	mRNA 3'−UTR binding
10	2e−03	11 / 283	nucleotide binding
11	4e−03	3 / 22	transferase activity
12	4e−03	12 / 351	GTP binding
13	6e−03	10 / 274	transcription factor binding
14	8e−03	3 / 29	rRNA binding
15	1e−02	2 / 11	NADPH 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	3e−11	33 / 602	hsa−miR−20a
2	2e−10	18 / 187	hsa−miR−586
3	3e−10	22 / 295	hsa−miR−561
4	4e−10	16 / 150	hsa−miR−633
5	1e−09	22 / 321	hsa−miR−590−3p
6	2e−09	21 / 299	hsa−miR−548c−3p
7	3e−09	26 / 463	hsa−miR−301a
8	1e−08	14 / 141	hsa−miR−522
9	2e−08	22 / 374	hsa−miR−144
10	2e−08	14 / 146	hsa−miR−518a−5p
11	3e−08	14 / 149	hsa−miR−527
12	8e−08	18 / 274	hsa−miR−1244
13	8e−08	11 / 93	hsa−miR−1206
14	9e−08	25 / 513	hsa−miR−106b
15	1e−07	13 / 140	hsa−miR−338−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_src.2
2	0.2	1 / 13	BENTINK_e2f3.2
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_myc.1
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	1e−27	30 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	1e−14	25 / 242	Chaussabel_3,9_Kinases
3	1e−13	47 / 963	PROTEINATLAS_pancreas
4	4e−13	52 / 1194	PROTEINATLAS_stomach
5	1e−12	48 / 1063	PROTEINATLAS_tonsil
6	4e−10	22 / 302	Chaussabel_3,4_Protein phosphatases
7	8e−10	39 / 912	PROTEINATLAS_urinary bladder
8	4e−09	33 / 726	PROTEINATLAS_cervix, uterine
9	1e−08	13 / 119	Chaussabel_2,4_Ribosomal proteins
10	2e−08	35 / 850	PROTEINATLAS_skin
11	2e−08	34 / 816	PROTEINATLAS_endometrium
12	3e−08	42 / 1167	PROTEINATLAS_gallbladder
13	4e−08	29 / 639	PROTEINATLAS_breast
14	5e−08	43 / 1239	PROTEINATLAS_testis
15	1e−07	43 / 1268	PROTEINATLAS_colon

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	5e−12	51 / 1231	KIM_MYC targets
2	3e−05	41 / 1478	ICGC_Myc_targets
3	2e−04	43 / 1723	HEBENSTREIT_high expression TF
4	3e−03	90 / 4881	ICGC_Atf2_targets
5	4e−03	18 / 631	ICGC_RxraPcr1_targets
6	4e−03	34 / 1498	ICGC_Ets1_targets
7	6e−03	91 / 5067	ICGC_Taf1_targets
8	1e−02	2 / 12	MYC_Protein synthesis degradation UP
9	3e−02	84 / 4890	ICGC_Bclaf101388_targets
10	3e−02	92 / 5466	ICGC_Nficsc81335_targets
11	4e−02	3 / 55	MYC_Targets UP
12	5e−02	98 / 5961	ICGC_Pol24_targets
13	5e−02	70 / 4131	ICGC_Nfatc1_targets
14	6e−02	41 / 2255	ICGC_SrfV0416101_targets
15	6e−02	38 / 2087	ICGC_Cebpbsc150_targets

Overexpression Spots

Spot Summary: T

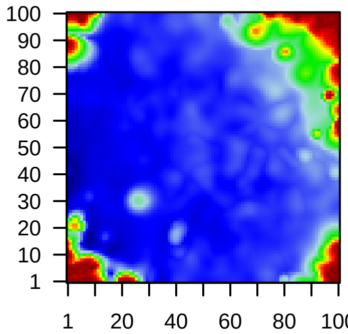
metagenes = 20
genes = 360

<r> metagenes = 0.98
<r> genes = 0.4
beta: r2= 14.19 / log p= −Inf

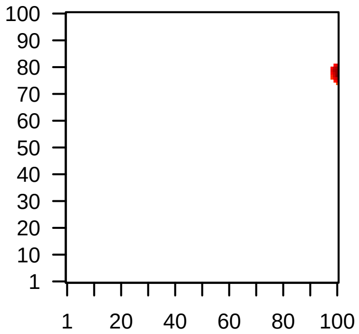
samples with spot = 75 (2.2 %)

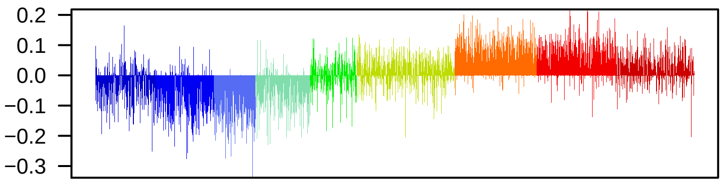
- A * : 1 (0.3 %)
- F * : 1 (0.2 %)
- F J * : 41 (8.9 %)
- J * : 28 (6.3 %)
- N * : 4 (0.9 %)

Overview Map



Spot





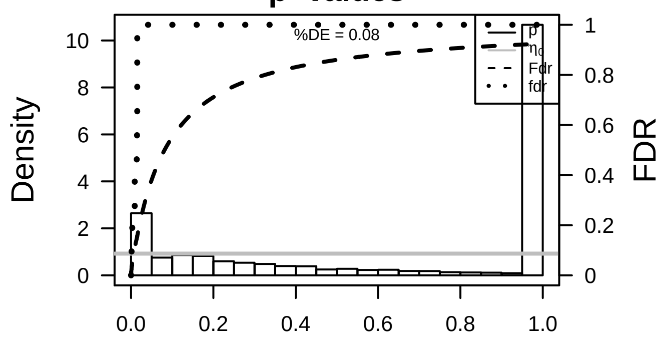
Spot Genelist

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	0.46	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	0.67	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
6	ILMN_232088	0.78	−0.79	0.47	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	0.32	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	0.56		
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	0.48	CUL4A	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
14	ILMN_170684	0.66	−0.72	0.63	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	0.74	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
17	ILMN_237416	0.64	−0.6	0.71		
18	ILMN_177602	0.64	−0.65	0.7	EIF4H	eukaryotic translation initiation factor 4H [Source:HGNC Syml
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−43	201 / 7275	Lympl	HOPP_Txn_elongation
2	1e−40	169 / 5356	Lympl	HOPP_Txn_transition
3	3e−38	216 / 9054	Colon	Tx_Colon
4	4e−38	210 / 8568	Colon	TxWk_Colon
5	2e−35	218 / 9555	Colon	TssA_Colon
6	2e−31	164 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
7	6e−30	199 / 8678	Colon	Quies3_Colon
8	1e−29	176 / 6970	Chror	5_Tx_Neuronal_Progenitor
9	5e−29	72 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	6e−29	211 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	9e−26	193 / 8771	Chror	5_Tx_Melanocytes
12	1e−25	186 / 8226	Lympl	HOPP_Active_promoter
13	3e−25	232 / 12298	Chror	2_TssA_Melanocytes
14	4e−25	180 / 7854	Chror	5_Tx_Fibroblasts
15	2e−23	220 / 11455	Chror	2_TssA_Fibroblasts
16	6e−22	75 / 1797	GSEA	PILON_KLF1_TARGETS_DN
17	2e−19	86 / 2535	CC	nucleoplasm
18	3e−19	207 / 10999	Colon	TssWk_Colon
19	6e−19	228 / 12983	Chror	2_TssA_Neuronal_Progenitor
20	1e−18	137 / 5699	Chror	6_EnhG_Melanocytes
21	2e−18	27 / 242	Refer	Chaussabel_3,9_Kinases
22	4e−17	190 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
23	1e−16	31 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
24	7e−16	182 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
25	1e−15	155 / 7448	Lympl	HOPP_Strong_enhancer
26	6e−15	26 / 302	Refer	Chaussabel_3,4_Protein phosphatases
27	2e−14	172 / 8990	Chror	15_Quies_Fibroblasts
28	7e−14	117 / 5067	TF	ICGC_Taf1_targets
29	1e−13	56 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
30	1e−13	196 / 11130	Chror	15_Quies_Melanocytes
31	4e−13	203 / 11836	Chror	3_TssF_Melanocytes
32	5e−13	209 / 12393	Chror	15_Quies_Neuronal_Progenitor
33	1e−12	156 / 8098	Lympl	HOPP_Weak_promoter
34	2e−12	185 / 10430	Brain	Overlap_fetal_midbrain_Quies
35	2e−12	211 / 12741	Chror	7_Enh_Melanocytes
36	5e−12	161 / 8613	Chror	7_Enh_Fibroblasts
37	9e−12	163 / 8818	MF	protein binding
38	3e−11	49 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
39	3e−11	35 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
40	2e−10	30 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.8	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	1e−05	5 / 25	tricarboxylic acid cycle
2	1e−05	11 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
3	7e−05	14 / 335	protein transport
4	3e−04	8 / 137	ER to Golgi vesicle−mediated transport
5	3e−04	6 / 75	exocytosis
6	4e−04	3 / 12	response to arsenic−containing substance
7	4e−04	4 / 29	telomere maintenance
8	4e−04	4 / 29	tRNA export from nucleus
9	5e−04	7 / 115	regulation of signal transduction by p53 class mediator
10	6e−04	4 / 32	protein K63−linked ubiquitination
11	6e−04	6 / 86	mRNA export from nucleus
12	8e−04	6 / 90	regulation of mRNA stability
13	9e−04	5 / 62	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
14	1e−03	3 / 17	nucleotide−excision repair, DNA incision, 3'−to lesion
15	1e−03	3 / 17	nucleotide−excision repair, preincision complex stabilization

Brain

Rank	p−value	#in/all	Geneset
1	2e−31	164 / 5936	Overlap_fetal_midbrain_HetRpts
2	6e−29	211 / 9815	Overlap_fetal_midbrain_ReprPC
3	4e−17	190 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	7e−16	182 / 9504	Overlap_fetal_midbrain_K9K27me3
5	2e−12	185 / 10430	Overlap_fetal_midbrain_Quies
6	4e−05	63 / 3164	Mid_Frontal_Lobe_ZNF
7	3e−04	22 / 796	Overlap_fetal_midbrain_ZNF
8	5e−03	25 / 1171	Fetal_EnhP
9	7e−03	7 / 180	Overlap_fetal_midbrain_Het
10	3e−02	26 / 1436	Fetal_K9K27me3
11	4e−02	14 / 681	Overlap_fetal_midbrain_EnhP
12	5e−02	9 / 386	Fetal_ZNF
13	1e−01	7 / 328	Fetal_Het
14	1e−01	19 / 1162	Fetal_Enh
15	1e−01	15 / 906	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	0 / 13	RHODES_CANCER_META_SIGNATURE
2	3e−03	6 / 117	PanCan_Driver_Gene_geneset_nanostring
3	1e−02	2 / 15	WOLFER_overlap genes
4	2e−02	6 / 178	SPANG_LPS−index2
5	3e−02	0 / 12	LIU_BREAST_CANCER
6	7e−02	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	7e−02	4 / 125	PanCan_CC+Apop_geneset_nanostring
8	7e−02	2 / 36	PanCan_HK_geneset_nanostring
9	1e−01	1 / 9	GENTLES_modul3
10	1e−01	2 / 46	PanCan_DNARepair_geneset_nanostring
11	1e−01	10 / 554	Lembcke_Colonic Inflammation
12	1e−01	1 / 13	GENTLES_modul2
13	1e−01	1 / 13	GENTLES_modul6
14	2e−01	1 / 14	GENTLES_modul1
15	2e−01	1 / 14	GENTLES_modul4

CC

Rank	p−value	#in/all	Geneset
1	2e−19	86 / 2535	nucleoplasm
2	2e−09	56 / 1979	membrane
3	3e−07	95 / 4822	cytoplasm
4	1e−06	93 / 4828	nucleus
5	3e−05	23 / 721	nucleolus
6	4e−05	19 / 539	Golgi membrane
7	5e−05	60 / 2979	cytosol
8	3e−04	3 / 11	proteasome regulatory particle, base subcomplex
9	8e−04	5 / 60	nuclear pore
10	2e−03	8 / 179	nuclear speck
11	3e−03	4 / 49	cytoplasmic microtubule
12	3e−03	4 / 49	transcriptional repressor complex
13	3e−03	4 / 51	proteasome complex
14	4e−03	5 / 88	melanosome
15	5e−03	3 / 28	Golgi stack

Chr

Rank	p−value	#in/all	Geneset
1	0.004	26 / 1217	Chr 3
2	0.058	8 / 342	Chr 18
3	0.086	14 / 768	Chr 14
4	0.218	13 / 836	Chr 8
5	0.227	12 / 769	Chr 15
6	0.246	17 / 1160	Chr 12
7	0.277	14 / 959	Chr 16
8	0.339	9 / 619	Chr 20
9	0.400	16 / 1211	Chr 6
10	0.406	6 / 422	Chr 13
11	0.412	14 / 1060	Chr 5
12	0.418	12 / 904	Chr 10
13	0.467	4 / 289	Chr 21
14	0.492	12 / 954	Chr 9
15	0.537	11 / 902	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−29	176 / 6970	5_Tx_Neuronal_Progenitor
2	9e−26	193 / 8771	5_Tx_Melanocytes
3	3e−25	232 / 12298	2_TssA_Melanocytes
4	4e−25	180 / 7854	5_Tx_Fibroblasts
5	2e−23	220 / 11455	2_TssA_Fibroblasts
6	6e−19	228 / 12983	2_TssA_Neuronal_Progenitor
7	1e−18	137 / 5699	6_EnhG_Melanocytes
8	2e−14	172 / 8990	15_Quies_Fibroblasts
9	1e−13	196 / 11130	15_Quies_Melanocytes
10	4e−13	203 / 11836	3_TssF_Melanocytes
11	5e−13	209 / 12393	15_Quies_Neuronal_Progenitor
12	2e−12	211 / 12741	7_Enh_Melanocytes
13	5e−12	161 / 8613	7_Enh_Fibroblasts
14	1e−06	84 / 4237	14_ZNF_Neuronal_Progenitor
15	3e−06	182 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−38	216 / 9054	Tx_Colon
2	4e−38	210 / 8568	TxWk_Colon
3	2e−35	218 / 9555	TssA_Colon
4	6e−30	199 / 8678	Quies3_Colon
5	3e−19	207 / 10999	TssWk_Colon
6	1e−13	56 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−09	137 / 7354	TssF_Colon
8	9e−09	56 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	7e−08	43 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	1e−07	35 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	1e−07	174 / 10779	Enh_Colon
12	3e−06	99 / 5373	EnhWk1_Colon
13	5e−05	36 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	6e−04	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
15	2e−03	28 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv

Glio

Rank	p−value	#in/all	Geneset
1	2e−09	20 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	3e−06	27 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	1e−05	43 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−05	47 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	2e−03	5 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	2e−02	9 / 315	Up
7	3e−02	10 / 401	Down_b
8	5e−02	4 / 113	GIEZELT_GBM_WT_up_VS_mut
9	1e−01	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	1e−01	6 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
11	1e−01	3 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	1e−01	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	1e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
14	2e−01	2 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
15	2e−01	2 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−29	72 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	6e−22	75 / 1797	PILON_KLF1_TARGETS_DN
3	1e−16	31 / 388	SHEN_SMARCA2_TARGETS_UP
4	3e−11	49 / 1417	PUJANA_BRCA1_PCC_NETWORK
5	3e−11	35 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
6	2e−10	30 / 622	SCHLOSSER_SERUM_RESPONSE_DN
7	2e−10	44 / 1241	PUJANA_ATM_PCC_NETWORK
8	2e−10	42 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	5e−10	26 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
10	1e−09	12 / 92	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER
11	1e−08	23 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
12	4e−08	46 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
13	6e−08	36 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
14	3e−07	16 / 277	GABRIELY_MIR21_TARGETS
15	5e−07	20 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−05	8 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	3e−04	8 / 138	HALLMARK_FATTY_ACID_METABOLISM
3	1e−03	8 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	1e−03	8 / 173	HALLMARK_E2F_TARGETS
5	2e−03	8 / 179	HALLMARK_G2M_CHECKPOINT
6	2e−03	8 / 185	HALLMARK_MTORC1_SIGNALING
7	6e−03	7 / 176	HALLMARK_ADIPOGENESIS
8	2e−02	4 / 87	HALLMARK_PROTEIN_SECRETION
9	2e−02	5 / 132	HALLMARK_UV_RESPONSE_DN
10	2e−02	6 / 183	HALLMARK_GLYCOLYSIS
11	3e−02	4 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	6e−02	5 / 170	HALLMARK_MYC_TARGETS_V1
13	7e−02	4 / 130	HALLMARK_DNA_REPAIR
14	1e−01	3 / 91	HALLMARK_PEROXISOME
15	1e−01	2 / 50	HALLMARK_TGF_BETA_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.001	9 / 211	Homuth_BMI−associated−genes_DN
2	0.265	3 / 147	Homuth_BMI−associated−genes_UP
3	0.315	1 / 31	DUMEAUX_Fasting enriched genes
4	0.324	1 / 32	Marjolein_ageing−genes_DN
5	0.684	1 / 94	DUMEAUX_Smoking enriched genes
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 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 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−43	201 / 7275	HOPP_Txn_elongation
2	1e−40	169 / 5356	HOPP_Txn_transition
3	1e−25	186 / 8226	HOPP_Active_promoter
4	1e−15	155 / 7448	HOPP_Strong_enhancer
5	1e−12	156 / 8098	HOPP_Weak_promoter
6	3e−08	38 / 1169	SPANG_BCR DN
7	4e−06	115 / 6559	HOPP_Weak_txn
8	1e−05	118 / 6959	HOPP_Weak_enhancer
9	6e−04	21 / 777	WIRTH_lymphoma937_spot D
10	8e−04	29 / 1270	SPANG_BCR UP
11	1e−03	15 / 493	WIRTH_lymphoma937_spot J
12	2e−03	14 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
13	3e−03	10 / 283	TARTE_Plasmablast signature
14	3e−03	19 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
15	1e−02	3 / 39	CARO_OxPhos_in_DLBCL_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	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	9e−12	163 / 8818	protein binding
2	8e−07	32 / 1013	poly(A) RNA binding
3	3e−04	11 / 256	ubiquitin protein ligase binding
4	8e−04	4 / 35	RNA polymerase II activating transcription factor binding
5	1e−03	3 / 18	TBP−class protein binding
6	1e−03	13 / 399	RNA binding
7	1e−03	3 / 19	cytokine binding
8	2e−03	6 / 105	histone binding
9	2e−03	9 / 227	transcription coactivator activity
10	2e−03	3 / 21	protein phosphatase type 2A regulator activity
11	2e−03	16 / 580	identical protein binding
12	3e−03	3 / 25	ATP−dependent DNA helicase activity
13	4e−03	3 / 26	Ran GTPase binding
14	5e−03	3 / 28	NAD binding
15	5e−03	3 / 28	tumor necrosis factor 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−09	16 / 190	hsa−miR−330−3p
2	3e−08	12 / 121	hsa−miR−421
3	1e−07	10 / 87	hsa−miR−496
4	2e−07	11 / 117	hsa−miR−543
5	4e−07	17 / 315	hsa−miR−30e
6	6e−07	14 / 221	hsa−miR−181d
7	9e−07	13 / 196	hsa−miR−206
8	1e−06	10 / 112	hsa−miR−507
9	1e−06	14 / 235	hsa−miR−26a
10	1e−06	18 / 389	hsa−miR−519a
11	2e−06	14 / 243	hsa−miR−26b
12	3e−06	17 / 366	hsa−let−7d
13	4e−06	11 / 158	hsa−miR−802
14	4e−06	13 / 225	hsa−miR−181b
15	4e−06	15 / 299	hsa−miR−548c−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	2e−18	27 / 242	Chaussabel_3,9_Kinases
2	6e−15	26 / 302	Chaussabel_3,4_Protein phosphatases
3	6e−10	15 / 153	Chaussabel_2,9_Cytosceleton
4	2e−08	30 / 759	PROTEINATLAS_epididymis
5	4e−08	21 / 412	WIRTH_Immune system
6	2e−07	37 / 1194	PROTEINATLAS_stomach
7	3e−07	36 / 1173	PROTEINATLAS_rectum
8	4e−07	27 / 740	PROTEINATLAS_esophagus
9	1e−06	35 / 1176	PROTEINATLAS_duodenum
10	2e−06	36 / 1268	PROTEINATLAS_colon
11	2e−06	30 / 960	PROTEINATLAS_cerebellum
12	3e−06	25 / 724	PROTEINATLAS_lymph node
13	3e−06	33 / 1138	PROTEINATLAS_small intestine
14	4e−06	29 / 933	PROTEINATLAS_adrenal gland
15	5e−06	20 / 514	PROTEINATLAS_vagina

Telomeres

Rank	p−value	#in/all	Geneset
1	0.04	2 / 27	Nabetani_alt len telomeres_genes_ko
2	0.15	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	

TF

Rank	p−value	#in/all	Geneset
1	7e−14	117 / 5067	ICGC_Taf1_targets
2	9e−10	112 / 5466	ICGC_Nficsc81335_targets
3	3e−09	110 / 5442	ICGC_Pmlsc71910_targets
4	5e−09	90 / 4131	ICGC_Nfatc1_targets
5	1e−08	100 / 4881	ICGC_Atf2_targets
6	1e−08	100 / 4890	ICGC_Bclaf101388_targets
7	3e−08	108 / 5518	ICGC_Stat5_targets
8	3e−08	105 / 5312	ICGC_Tcf12_targets
9	3e−08	106 / 5383	ICGC_Sp1_targets
10	4e−08	91 / 4362	ICGC_Creb1_targets
11	4e−08	118 / 6267	ICGC_Yy1_targets
12	4e−08	39 / 1231	KIM_MYC targets
13	4e−08	114 / 5984	ICGC_Mta3_targets
14	5e−08	122 / 6578	ICGC_Pou2_targets
15	6e−08	92 / 4468	ICGC_Egr1_targets

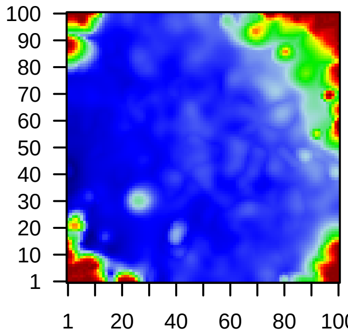
Overexpression Spots

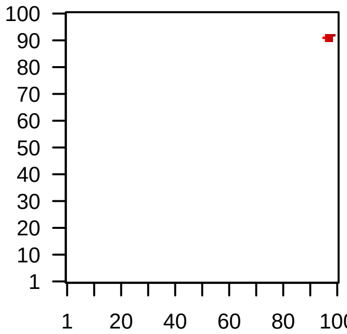
Spot Summary: U

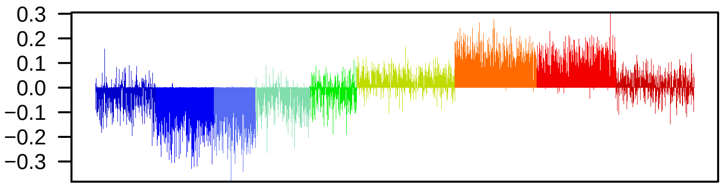
metagenes = 11
genes = 162

<r> metagenes = 0.99
<r> genes = 0.5
beta: r2= 33.01 / log p= −Inf

samples with spot = 279 (8.2 %)
- A * : 1 (0.3 %)
- F * : 1 (0.2 %)
- F J * : 152 (32.8 %)
- J * : 124 (27.7 %)
- N * : 1 (0.2 %)





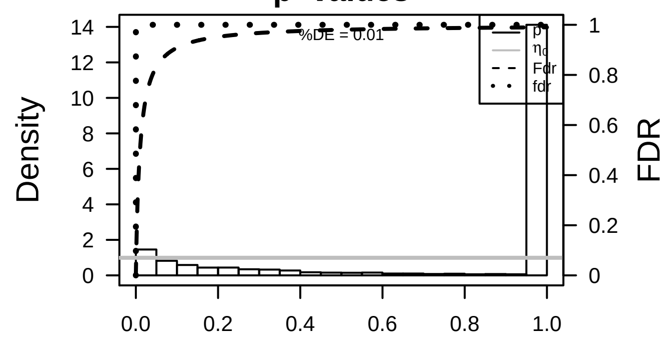


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_172676	0.86	−0.89	0.61	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:H
2	ILMN_166464	0.84	−0.6	0.37	MED4	mediator complex subunit 4 [Source:HGNC Symbol;Acc:HGN
3	ILMN_175109	0.71	−0.52	0.71	CREB3L2	cAMP responsive element binding protein 3 like 2 [Source:HG
4	ILMN_172081	0.7	−0.57	0.75	SPCS2	signal peptidase complex subunit 2 [Source:HGNC Symbol;A
5	ILMN_177963	0.69	−0.53	0.68	PSMD6	proteasome 26S subunit, non−ATPase 6 [Source:HGNC Sym
6	ILMN_180185	0.68	−0.46	0.66	SEC61B	Sec61 translocon beta subunit [Source:HGNC Symbol;Acc:H
7	ILMN_180384	0.67	−0.52	0.55	EIF1	eukaryotic translation initiation factor 1 [Source:HGNC Symbo
8	ILMN_178038	0.64	−0.59	0.67		signal peptidase complex subunit 2 homolog (S. cerevisiae) p
9	ILMN_230554	0.63	−0.5	0.64		
10	ILMN_236639	0.63	−0.62	0.65		
11	ILMN_236571	0.63	−0.6	0.58	SEPT2	septin 2 [Source:HGNC Symbol;Acc:HGNC:7729]
12	ILMN_176878	0.63	−0.57	0.84	PSMC2	proteasome 26S subunit, ATPase 2 [Source:HGNC Symbol;A
13	ILMN_166751	0.62	−0.43	0.7	RRAS2	related RAS viral (r−ras) oncogene homolog 2 [Source:HGNC
14	ILMN_205616	0.62	−0.53	0.67	OSTC	oligosaccharyltransferase complex non−catalytic subunit [Sou
15	ILMN_167955	0.61	−0.49	0.68	TIMM23	translocase of inner mitochondrial membrane 23 [Source:HG
16	ILMN_238755	0.6	−0.61	0.68	PSMA3	proteasome subunit alpha 3 [Source:HGNC Symbol;Acc:HGN
17	ILMN_240864	0.59	−0.54	0.73		signal peptidase complex subunit 2 homolog (S. cerevisiae) p
18	ILMN_173061	0.59	−0.66	0.6	DBNDD2	dysbindin domain containing 2 [Source:HGNC Symbol;Acc:H
19	ILMN_328084	0.59	−0.44	0.6		
20	ILMN_174759	0.59	−0.57	0.5	PPP1R11	protein phosphatase 1 regulatory inhibitor subunit 11 [Source

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	9e−29	104 / 7275	Lympl	HOPP_Txn_elongation
2	9e−25	105 / 8226	Lympl	HOPP_Active_promoter
3	3e−24	49 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
4	9e−24	111 / 9555	Colon	TssA_Colon
5	5e−23	84 / 5356	Lympl	HOPP_Txn_transition
6	1e−19	119 / 12298	Chror	2_TssA_Melanocytes
7	2e−19	115 / 11455	Chror	2_TssA_Fibroblasts
8	9e−19	106 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
9	3e−17	98 / 8771	Chror	5_Tx_Melanocytes
10	4e−17	94 / 8098	Lympl	HOPP_Weak_promoter
11	9e−17	99 / 9054	Colon	Tx_Colon
12	2e−16	118 / 12983	Chror	2_TssA_Neuronal_Progenitor
13	2e−16	101 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
14	3e−16	91 / 7854	Chror	5_Tx_Fibroblasts
15	5e−16	95 / 8568	Colon	TxWk_Colon
16	1e−15	95 / 8678	Colon	Quies3_Colon
17	2e−15	77 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
18	4e−15	111 / 11836	Chror	3_TssF_Melanocytes
19	1e−14	83 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	1e−11	110 / 12741	Chror	7_Enh_Melanocytes
21	2e−11	95 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
22	1e−10	29 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	2e−10	99 / 10999	Colon	TssWk_Colon
24	4e−10	87 / 8990	Chror	15_Quies_Fibroblasts
25	1e−09	94 / 10430	Brain	Overlap_fetal_midbrain_Quies
26	2e−09	35 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
27	4e−09	97 / 11130	Chror	15_Quies_Melanocytes
28	6e−09	32 / 1797	GSEA	PILON_KLF1_TARGETS_DN
29	6e−09	26 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
30	1e−08	24 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
31	2e−08	33 / 1979	CC	membrane
32	2e−08	31 / 1777	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
33	4e−08	19 / 737	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
34	2e−07	11 / 242	Refer	Chaussabel_3,9_Kinases
35	2e−07	19 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
36	2e−07	71 / 7354	Colon	TssF_Colon
37	2e−07	23 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
38	3e−07	71 / 7448	Lympl	HOPP_Strong_enhancer
39	4e−07	25 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
40	4e−07	99 / 12393	Chror	15_Quies_Neuronal_Progenitor



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−05	9 / 255	viral process
2	4e−04	4 / 62	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
3	6e−04	4 / 67	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
4	2e−03	3 / 43	regulation of cellular amino acid metabolic process
5	2e−03	4 / 93	osteoblast differentiation
6	2e−03	2 / 13	retrograde protein transport, ER to cytosol
7	3e−03	3 / 48	antigen processing and presentation of exogenous peptide antigen via MHC c
8	3e−03	4 / 102	protein sumoylation
9	3e−03	2 / 15	anion transport
10	3e−03	3 / 52	ER−associated ubiquitin−dependent protein catabolic process
11	4e−03	4 / 113	Fc−epsilon receptor signaling pathway
12	4e−03	2 / 17	oocyte maturation
13	4e−03	2 / 17	regulation of neuron death
14	4e−03	3 / 57	NIK/NF−kappaB signaling
15	5e−03	5 / 189	intracellular protein transport

Brain

Rank	p−value	#in/all	Geneset
1	9e−19	106 / 9815	Overlap_fetal_midbrain_ReprPC
2	2e−16	101 / 9504	Overlap_fetal_midbrain_K9K27me3
3	2e−15	77 / 5936	Overlap_fetal_midbrain_HetRpts
4	2e−11	95 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	1e−09	94 / 10430	Overlap_fetal_midbrain_Quies
6	4e−02	9 / 796	Overlap_fetal_midbrain_ZNF
7	9e−02	11 / 1213	Fetal_TssP
8	1e−01	10 / 1162	Fetal_Enh
9	2e−01	6 / 630	Mid_Frontal_Lobe_EnhP
10	2e−01	4 / 386	Fetal_ZNF
11	2e−01	11 / 1436	Fetal_K9K27me3
12	2e−01	9 / 1171	Fetal_EnhP
13	3e−01	3 / 328	Fetal_Het
14	3e−01	7 / 937	Fetal_EnhG
15	4e−01	7 / 1012	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	0 / 13	RHODES_CANCER_META_SIGNATURE
2	0.04	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
3	0.07	2 / 73	SHAUGHNESSY_MM high risk
4	0.07	1 / 12	LIU_BREAST_CANCER
5	0.08	1 / 14	GENTLES_modul1
6	0.08	1 / 15	WOLFER_overlap genes
7	0.09	1 / 16	GENTLES_modul7
8	0.16	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	0.19	1 / 36	PanCan_HK_geneset_nanostring
10	0.20	1 / 39	ZHANG_MM up
11	0.21	2 / 150	PanCan_MAPK_geneset_nanostring
12	0.23	1 / 46	PanCan_DNARepair_geneset_nanostring
13	0.27	2 / 178	SPANG_LPS−index2
14	0.31	0 / 14	LIU_COMMON_CANCER_GENES
15	0.35	1 / 76	PanCan_Wnt_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−08	33 / 1979	membrane
2	1e−06	8 / 134	myelin sheath
3	2e−05	3 / 10	COPI−coated vesicle
4	5e−05	34 / 2979	cytosol
5	5e−05	20 / 1304	mitochondrion
6	1e−04	6 / 138	mitochondrial outer membrane
7	1e−04	14 / 775	endoplasmic reticulum
8	2e−04	4 / 51	proteasome complex
9	3e−04	9 / 374	mitochondrial inner membrane
10	5e−04	28 / 2535	nucleoplasm
11	5e−04	13 / 777	Golgi apparatus
12	6e−04	13 / 788	endoplasmic reticulum membrane
13	2e−03	2 / 12	COPI vesicle coat
14	2e−03	42 / 4822	cytoplasm
15	3e−03	2 / 15	proteasome accessory complex

Chr

Rank	p−value	#in/all	Geneset
1	0.04	10 / 904	Chr 10
2	0.04	12 / 1170	Chr 7
3	0.15	8 / 902	Chr 4
4	0.15	9 / 1060	Chr 5
5	0.26	9 / 1211	Chr 6
6	0.35	10 / 1492	Chr 2
7	0.44	3 / 422	Chr 13
8	0.46	14 / 2323	Chr 1
9	0.47	4 / 619	Chr 20
10	0.49	2 / 289	Chr 21
11	0.50	7 / 1160	Chr 12
12	0.59	2 / 342	Chr 18
13	0.63	7 / 1318	Chr 17
14	0.64	4 / 768	Chr 14
15	0.68	5 / 994	Chr X

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−19	119 / 12298	2_TssA_Melanocytes
2	2e−19	115 / 11455	2_TssA_Fibroblasts
3	3e−17	98 / 8771	5_Tx_Melanocytes
4	2e−16	118 / 12983	2_TssA_Neuronal_Progenitor
5	3e−16	91 / 7854	5_Tx_Fibroblasts
6	4e−15	111 / 11836	3_TssF_Melanocytes
7	1e−14	83 / 6970	5_Tx_Neuronal_Progenitor
8	1e−11	110 / 12741	7_Enh_Melanocytes
9	4e−10	87 / 8990	15_Quies_Fibroblasts
10	4e−09	97 / 11130	15_Quies_Melanocytes
11	4e−07	99 / 12393	15_Quies_Neuronal_Progenitor
12	5e−05	78 / 9635	3_TssF_Fibroblasts
13	9e−05	71 / 8613	7_Enh_Fibroblasts
14	1e−04	52 / 5699	6_EnhG_Melanocytes
15	2e−03	38 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−24	49 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	9e−24	111 / 9555	TssA_Colon
3	9e−17	99 / 9054	Tx_Colon
4	5e−16	95 / 8568	TxWk_Colon
5	1e−15	95 / 8678	Quies3_Colon
6	2e−10	99 / 10999	TssWk_Colon
7	2e−07	71 / 7354	TssF_Colon
8	3e−04	25 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	5e−04	81 / 10779	Enh_Colon
10	8e−03	13 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	1e−02	14 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	2e−02	15 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	2e−02	10 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
14	2e−02	46 / 6138	TssD2_Colon
15	3e−02	4 / 203	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Glio

Rank	p−value	#in/all	Geneset
1	2e−09	35 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−08	31 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	7e−07	6 / 55	Stuehler_Proteins_up_in_STS
4	2e−03	7 / 315	Up
5	5e−02	2 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	6e−02	2 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	6e−02	3 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	1e−01	8 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
9	1e−01	5 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
10	1e−01	1 / 19	KIM deleted & downregulated in LTS
11	1e−01	4 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
12	1e−01	2 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	1e−01	1 / 25	Barbus_GBM_STS_vs._LTS
14	1e−01	1 / 28	KIM prognostic signature LTS vs. STS
15	2e−01	4 / 401	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−10	29 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	6e−09	32 / 1797	PILON_KLF1_TARGETS_DN
3	6e−09	26 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	1e−08	24 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
5	4e−08	19 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
6	2e−07	19 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
7	2e−07	23 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	4e−07	25 / 1417	PUJANA_BRCA1_PCC_NETWORK
9	4e−07	13 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
10	1e−06	6 / 61	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10
11	2e−06	18 / 841	ACEVEDO_LIVER_CANCER_UP
12	2e−06	12 / 388	SHEN_SMARCA2_TARGETS_UP
13	3e−06	12 / 389	GARY_CD5_TARGETS_DN
14	3e−06	13 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
15	3e−06	5 / 40	NAKAMURA_CANCER_MICROENVIRONMENT_DN

HM

Rank	p−value	#in/all	Geneset
1	6e−06	8 / 170	HALLMARK_MYC_TARGETS_V1
2	5e−05	7 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	4e−03	5 / 185	HALLMARK_MTORC1_SIGNALING
4	4e−03	4 / 116	HALLMARK_SPERMATOGENESIS
5	1e−02	3 / 87	HALLMARK_PROTEIN_SECRETION
6	2e−02	3 / 91	HALLMARK_PEROXISOME
7	2e−02	4 / 176	HALLMARK_ADIPOGENESIS
8	2e−02	3 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	4e−02	3 / 137	HALLMARK_UV_RESPONSE_UP
10	5e−02	3 / 138	HALLMARK_FATTY_ACID_METABOLISM
11	8e−02	3 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	9e−02	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
13	1e−01	2 / 103	HALLMARK_BILE_ACID_METABOLISM
14	3e−01	2 / 173	HALLMARK_E2F_TARGETS
15	3e−01	2 / 179	HALLMARK_G2M_CHECKPOINT

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 147	Homuth_BMI−associated−genes_UP
2	0.3	2 / 211	Homuth_BMI−associated−genes_DN
3	0.4	1 / 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 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−29	104 / 7275	HOPP_Txn_elongation
2	9e−25	105 / 8226	HOPP_Active_promoter
3	5e−23	84 / 5356	HOPP_Txn_transition
4	4e−17	94 / 8098	HOPP_Weak_promoter
5	3e−07	71 / 7448	HOPP_Strong_enhancer
6	1e−06	66 / 6959	HOPP_Weak_enhancer
7	2e−06	17 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
8	2e−06	17 / 777	WIRTH_lymphoma937_spot D
9	5e−06	62 / 6559	HOPP_Weak_txn
10	9e−06	6 / 84	ROSOLOWSKI_green UP
11	5e−05	6 / 115	ROSOLOWSKI_green total
12	6e−04	4 / 66	TARTE_Plasma cell signature
13	1e−03	7 / 283	TARTE_Plasmablast signature
14	2e−03	3 / 43	Monti_OxPhos_cluster
15	5e−03	8 / 455	SPANG_CD40 6hrs DN

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	2e−06	77 / 8818	protein binding
2	2e−05	18 / 1013	poly(A) RNA binding
3	1e−03	2 / 10	proteasome binding
4	2e−03	8 / 399	RNA binding
5	3e−03	2 / 14	small GTPase binding
6	5e−03	2 / 18	TBP−class protein binding
7	5e−03	2 / 19	1−acylglycerol−3−phosphate O−acyltransferase activity
8	6e−03	6 / 283	nucleotide binding
9	8e−03	2 / 24	translation factor activity, RNA binding
10	1e−02	2 / 30	RNA polymerase II transcription cofactor activity
11	2e−02	3 / 91	peptidase activity
12	2e−02	5 / 265	cadherin binding involved in cell−cell adhesion
13	2e−02	2 / 39	translation initiation factor activity
14	2e−02	2 / 42	symporter activity
15	3e−02	2 / 45	protein kinase C 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−06	13 / 425	hsa−let−7b
2	4e−06	9 / 212	hsa−miR−196a
3	5e−06	13 / 491	hsa−miR−107
4	5e−06	13 / 493	hsa−miR−103
5	7e−06	12 / 429	hsa−miR−548n
6	1e−05	11 / 382	hsa−let−7c
7	3e−05	12 / 489	hsa−miR−16
8	3e−05	5 / 61	hsa−miR−627
9	3e−05	5 / 62	hsa−miR−324−5p
10	4e−05	8 / 216	hsa−miR−548m
11	4e−05	12 / 516	hsa−miR−15a
12	5e−05	9 / 295	hsa−miR−561
13	6e−05	5 / 72	hsa−miR−890
14	7e−05	11 / 463	hsa−miR−301a
15	8e−05	11 / 467	hsa−miR−195

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.07	1 / 13	BENTINK_e2f3.2
2	0.07	1 / 13	BENTINK_myc.1
3	0.08	1 / 14	BENTINK_ras.6
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
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	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−07	11 / 242	Chaussabel_3,9_Kinases
2	2e−06	10 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
3	2e−03	7 / 302	Chaussabel_3,4_Protein phosphatases
4	2e−03	5 / 153	Chaussabel_2,9_Cytosceleton
5	2e−03	14 / 1016	PROTEINATLAS_cerebral cortex
6	4e−03	10 / 647	PROTEINATLAS_lateral ventricle
7	4e−03	10 / 650	PROTEINATLAS_hippocampus
8	5e−03	15 / 1239	PROTEINATLAS_testis
9	5e−03	6 / 275	Chaussabel_3,7_Spliceosome
10	8e−03	4 / 139	Chaussabel_1,8_Metabolism Biosynthesis
11	1e−02	7 / 412	WIRTH_Immune system
12	1e−02	7 / 416	PROTEINATLAS_ovary
13	2e−02	11 / 960	PROTEINATLAS_cerebellum
14	2e−02	9 / 724	PROTEINATLAS_lymph node
15	2e−02	12 / 1097	PROTEINATLAS_kidney

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	2e−06	53 / 5067	ICGC_Taf1_targets
2	1e−05	25 / 1723	HEBENSTREIT_high expression TF
3	2e−05	20 / 1231	KIM_MYC targets
4	3e−05	22 / 1452	ICGC_Six5_targets
5	1e−04	51 / 5518	ICGC_Stat5_targets
6	1e−04	21 / 1498	ICGC_Ets1_targets
7	2e−04	50 / 5442	ICGC_Pmlsc71910_targets
8	2e−04	50 / 5466	ICGC_Nficsc81335_targets
9	2e−04	46 / 4890	ICGC_Bclaf101388_targets
10	5e−04	48 / 5383	ICGC_Sp1_targets
11	6e−04	41 / 4362	ICGC_Creb1_targets
12	7e−04	47 / 5312	ICGC_Tcf12_targets
13	8e−04	19 / 1478	ICGC_Myc_targets
14	1e−03	56 / 6868	ICGC_Elf1_targets
15	2e−03	54 / 6578	ICGC_Pou2_targets

Overexpression Spots

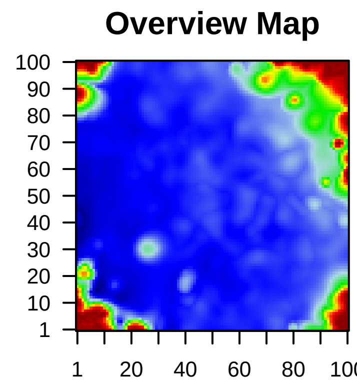
Spot Summary: V

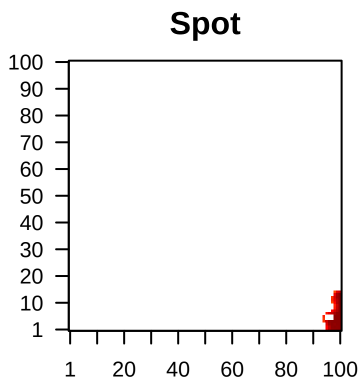
metagenes = 67
genes = 930

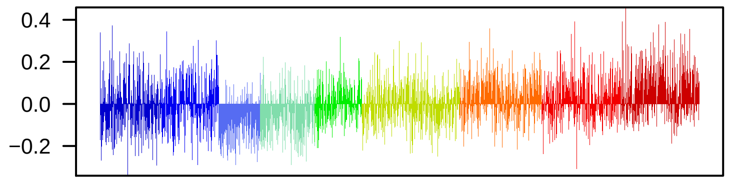
<r> metagenes = 0.71
<r> genes = 0.22
beta: r2= 41.29 / log p= −Inf

samples with spot = 347 (10.2 %)

- A * : 34 (9.9 %)
- A C * : 42 (12.8 %)
- A C F * : 1 (0.4 %)
- A F * : 9 (2.9 %)
- C F * : 16 (6 %)
- F * : 34 (6.1 %)
- F J * : 58 (12.5 %)
- J * : 54 (12.1 %)
- N * : 99 (22.3 %)





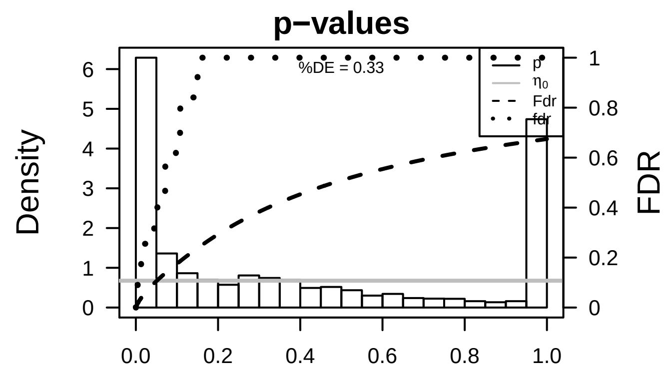


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_170769	2.95	−1.6	0.43	IFIT1	interferon induced protein with tetratricopeptide repeats 1 [So
2	ILMN_205878	2.77	−0.73	0.17	IFI27	interferon alpha inducible protein 27 [Source:HGNC Symbol;A
3	ILMN_180575	2.64	−2.03	0.32	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC S
4	ILMN_172391	2.52	−1.06	0.44	IFI44L	interferon induced protein 44 like [Source:HGNC Symbol;Acc
5	ILMN_170178	2.51	−1.31	0.39	IFIT3	interferon induced protein with tetratricopeptide repeats 3 [So
6	ILMN_165787	2.46	−0.83	0.44	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:I
7	ILMN_181520	2.38	−5.09	0.24		
8	ILMN_205401	2.34	−1	0.21	ISG15	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:HG
9	ILMN_172974	2.3	−1.14	0.38	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase
10	ILMN_238854	2.22	−1.39	0.43	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
11	ILMN_174539	2.13	−1.15	0.48	OAS3	2'−5'−oligoadenylate synthetase 3 [Source:HGNC Symbol;Ac
12	ILMN_166235	2.12	−1.32	0.36	MX1	MX dynamin like GTPase 1 [Source:HGNC Symbol;Acc:HGN
13	ILMN_176006	2.1	−1.07	0.42	IFI44	interferon induced protein 44 [Source:HGNC Symbol;Acc:HG
14	ILMN_324640	2.08	−1.52	0.32	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
15	ILMN_166314	1.94	−1.51	0.13	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Syi
16	ILMN_168738	1.93	−1.08	0.33	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	0.21	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	0.37	OASL	2'−5'−oligoadenylate synthetase like [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−71	533 / 9555	Colon	TssA_Colon
2	9e−70	572 / 10999	Colon	TssWk_Colon
3	9e−68	61 / 96	Refer	Chaussabel_3,1_Interferon−inducible
4	3e−66	142 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
5	4e−65	453 / 7448	Lympl	HOPP_Strong_enhancer
6	9e−64	504 / 9054	Colon	Tx_Colon
7	9e−61	101 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
8	2e−59	70 / 172	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	3e−57	480 / 8678	Colon	Quies3_Colon
10	7e−55	472 / 8568	Colon	TxWk_Colon
11	3e−54	139 / 960	GSEA	NUYTTEN_EZH2_TARGETS_UP
12	5e−54	459 / 8226	Lympl	HOPP_Active_promoter
13	2e−52	50 / 87	GSEA	HECKER_IFNB1_TARGETS
14	9e−52	422 / 7275	Lympl	HOPP_Txn_elongation
15	2e−51	49 / 85	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
16	1e−50	186 / 1797	GSEA	PILON_KLF1_TARGETS_DN
17	2e−49	346 / 5356	Lympl	HOPP_Txn_transition
18	5e−45	541 / 11455	Chror	2_TssA_Fibroblasts
19	2e−44	459 / 8818	MF	protein binding
20	4e−42	48 / 113	Refer	Chaussabel_1,5_Myeloid lineage
21	1e−41	545 / 11836	Chror	3_TssF_Melanocytes
22	1e−41	28 / 29	GSEA	MOSERLE_IFNA_RESPONSE
23	1e−41	37 / 58	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
24	2e−41	230 / 2979	CC	cytosol
25	4e−40	63 / 240	Refer	Chaussabel_3,3_Inflammation II
26	1e−39	69 / 301	Canc	SPANG_BCL6−index2
27	2e−39	53 / 161	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
28	2e−38	551 / 12298	Chror	2_TssA_Melanocytes
29	3e−38	563 / 12741	Chror	7_Enh_Melanocytes
30	3e−38	68 / 306	Lympl	WIRTH_lymphoma937_spot E
31	8e−38	67 / 300	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−E
32	9e−38	40 / 84	Refer	Chaussabel_2,10_Immune related cell surface molecules
33	9e−38	420 / 8098	Lympl	HOPP_Weak_promoter
34	9e−37	440 / 8771	Chror	5_Tx_Melanocytes
35	9e−36	102 / 774	GSEA	REACTOME_IMMUNE_SYSTEM
36	2e−34	29 / 42	GSEA	DAUER_STAT3_TARGETS_DN
37	1e−33	61 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
38	2e−33	495 / 10779	Colon	Enh_Colon
39	2e−33	401 / 7854	Chror	5_Tx_Fibroblasts
40	1e−32	59 / 272	Lympl	SPANG_IL21 DN



Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 111	HORVATH_aging_genes meth DOWN
2	0.9	2 / 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−26	27 / 57	type I interferon signaling pathway
2	1e−23	38 / 153	defense response to virus
3	1e−23	32 / 102	response to virus
4	1e−18	48 / 335	innate immune response
5	1e−13	15 / 37	negative regulation of viral genome replication
6	2e−12	17 / 60	interferon−gamma−mediated signaling pathway
7	2e−09	34 / 336	inflammatory response
8	1e−08	42 / 511	apoptotic process
9	1e−08	10 / 30	negative regulation of type I interferon production
10	4e−08	37 / 434	protein phosphorylation
11	4e−08	37 / 435	negative regulation of apoptotic process
12	9e−08	20 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
13	2e−07	6 / 10	response to interferon−alpha
14	3e−07	17 / 123	adaptive immune response
15	9e−07	9 / 35	antigen processing and presentation

Brain

Rank	p−value	#in/all	Geneset
1	1e−31	461 / 9815	Overlap_fetal_midbrain_ReprPC
2	5e−24	443 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	3e−23	306 / 5936	Overlap_fetal_midbrain_HetRpts
4	5e−23	456 / 10430	Overlap_fetal_midbrain_Quies
5	2e−16	405 / 9504	Overlap_fetal_midbrain_K9K27me3
6	6e−12	84 / 1213	Fetal_TssP
7	2e−05	138 / 3164	Mid_Frontal_Lobe_ZNF
8	3e−04	23 / 328	Fetal_Het
9	6e−04	15 / 180	Overlap_fetal_midbrain_Het
10	7e−04	42 / 796	Overlap_fetal_midbrain_ZNF
11	1e−03	112 / 2709	Mid_Frontal_Lobe_HetRpts
12	1e−03	91 / 2127	Mid_Frontal_Lobe_K9K27me3
13	2e−03	123 / 3046	Fetal_TssA
14	2e−03	77 / 1784	Mid_Frontal_Lobe_ReprPCWk
15	5e−03	53 / 1171	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	1e−39	69 / 301	SPANG_BCL6−index2
2	4e−27	44 / 178	SPANG_LPS−index2
3	2e−19	64 / 554	Lembcke_Colonic Inflammation
4	6e−04	12 / 125	PanCan_CC+Apop_geneset_nanostring
5	1e−03	4 / 16	GENTLES_modul14
6	4e−03	10 / 117	PanCan_Driver_Gene_geneset_nanostring
7	4e−03	8 / 82	PanCan_JAK−ST_geneset_nanostring
8	7e−03	3 / 13	GENTLES_modul12
9	8e−03	7 / 73	SHAUGHNESSY_MM high risk
10	1e−02	2 / 6	ZHANG_MGUS up
11	1e−02	5 / 46	PanCan_TGF−B_geneset_nanostring
12	2e−02	7 / 91	PanCan_TXmisReg_geneset_nanostring
13	3e−02	6 / 76	PanCan_Wnt_geneset_nanostring
14	6e−02	1 / 15	LIU_PROSTATE_CANCER_DN
15	9e−02	4 / 54	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	2e−41	230 / 2979	cytosol
2	2e−31	186 / 2464	extracellular exosome
3	2e−27	276 / 4822	cytoplasm
4	9e−14	123 / 1979	membrane
5	4e−10	27 / 207	lysosome
6	6e−10	48 / 571	perinuclear region of cytoplasm
7	9e−09	45 / 561	intracellular membrane−bounded organelle
8	1e−08	172 / 3662	plasma membrane
9	2e−08	22 / 172	endosome membrane
10	4e−08	54 / 777	Golgi apparatus
11	5e−08	211 / 4828	nucleus
12	6e−08	14 / 74	lysosomal lumen
13	8e−08	126 / 2535	nucleoplasm
14	2e−07	28 / 295	cell−cell adherens junction
15	3e−07	14 / 83	ruffle

Chr

Rank	p−value	#in/all	Geneset
1	0.02	40 / 902	Chr 4
2	0.03	60 / 1492	Chr 2
3	0.04	49 / 1217	Chr 3
4	0.14	43 / 1160	Chr 12
5	0.14	36 / 954	Chr 9
6	0.17	44 / 1211	Chr 6
7	0.19	14 / 342	Chr 18
8	0.21	38 / 1060	Chr 5
9	0.29	27 / 769	Chr 15
10	0.30	11 / 289	Chr 21
11	0.41	43 / 1318	Chr 17
12	0.45	25 / 768	Chr 14
13	0.55	28 / 904	Chr 10
14	0.56	13 / 422	Chr 13
15	0.65	70 / 2323	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−45	541 / 11455	2_TssA_Fibroblasts
2	1e−41	545 / 11836	3_TssF_Melanocytes
3	2e−38	551 / 12298	2_TssA_Melanocytes
4	3e−38	563 / 12741	7_Enh_Melanocytes
5	9e−37	440 / 8771	5_Tx_Melanocytes
6	2e−33	401 / 7854	5_Tx_Fibroblasts
7	2e−30	419 / 8613	7_Enh_Fibroblasts
8	2e−30	431 / 8990	15_Quies_Fibroblasts
9	9e−27	442 / 9635	3_TssF_Fibroblasts
10	6e−26	305 / 5699	6_EnhG_Melanocytes
11	1e−25	485 / 11130	15_Quies_Melanocytes
12	3e−21	527 / 12983	2_TssA_Neuronal_Progenitor
13	1e−15	318 / 6970	5_Tx_Neuronal_Progenitor
14	5e−15	489 / 12393	15_Quies_Neuronal_Progenitor
15	2e−11	458 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−71	533 / 9555	TssA_Colon
2	9e−70	572 / 10999	TssWk_Colon
3	3e−66	142 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	9e−64	504 / 9054	Tx_Colon
5	3e−57	480 / 8678	Quies3_Colon
6	7e−55	472 / 8568	TxWk_Colon
7	2e−33	495 / 10779	Enh_Colon
8	2e−32	64 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
9	4e−30	112 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	5e−29	61 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
11	4e−24	288 / 5373	EnhWk1_Colon
12	3e−23	356 / 7354	TssF_Colon
13	2e−17	100 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	1e−12	101 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	7e−12	153 / 2845	TxEnhG1_Colon

Glio

Rank	p−value	#in/all	Geneset
1	3e−31	57 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−15	42 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	1e−14	41 / 315	Up
4	2e−08	12 / 47	Donson−innate immunity−associated with LTS in HGA
5	5e−06	8 / 32	Donson−Misc immune function−associated with LTS in HGA
6	9e−06	13 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
7	1e−05	17 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	1e−05	98 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
9	3e−05	5 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
10	6e−04	80 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
11	7e−04	10 / 94	Weller_LGG_A_vs_O_UP
12	1e−03	13 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	2e−03	12 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	3e−03	10 / 113	GIEZELT_GBM_WT_up_VS_mut
15	4e−03	7 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−61	101 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
2	3e−54	139 / 960	NUYTTEN_EZH2_TARGETS_UP
3	2e−52	50 / 87	HECKER_IFNB1_TARGETS
4	1e−50	186 / 1797	PILON_KLF1_TARGETS_DN
5	1e−41	28 / 29	MOSERLE_IFNA_RESPONSE
6	1e−41	37 / 58	BROWNE_INTERFERON_RESPONSIVE_GENES
7	2e−39	53 / 161	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
8	9e−36	102 / 774	REACTOME_IMMUNE_SYSTEM
9	2e−34	29 / 42	DAUER_STAT3_TARGETS_DN
10	1e−33	61 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	2e−32	57 / 253	WALLACE_PROSTATE_CANCER_RACE_UP
12	4e−32	116 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
13	7e−32	34 / 73	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
14	6e−31	76 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
15	9e−29	82 / 622	SCHLOSSER_SERUM_RESPONSE_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−59	70 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	2e−51	49 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	6e−12	28 / 187	HALLMARK_COMPLEMENT
4	3e−10	26 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	8e−10	25 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	2e−09	22 / 151	HALLMARK_APOPTOSIS
7	2e−08	23 / 185	HALLMARK_MTORC1_SIGNALING
8	8e−07	19 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	1e−06	13 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	2e−06	20 / 185	HALLMARK_P53_PATHWAY
11	8e−06	19 / 189	HALLMARK_HYPOXIA
12	1e−05	18 / 176	HALLMARK_KRAS_SIGNALING_UP
13	2e−05	12 / 87	HALLMARK_PROTEIN_SECRETION
14	2e−05	18 / 186	HALLMARK_IL2_STAT5_SIGNALING
15	1e−04	14 / 138	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−11	29 / 211	Homuth_BMI−associated−genes_DN
2	2e−06	5 / 8	DUMEAUX_Monocytes in smokers literature genes up
3	1e−05	6 / 18	Huan_blood−pressure_SBP−signature
4	1e−04	5 / 16	Huan_blood−pressure_DBP−signature
5	2e−04	4 / 10	DUMEAUX_Smoking literature genes up
6	3e−04	3 / 5	Huan_blood−pressure_HTN−signature
7	1e−01	2 / 17	DUMEAUX_High bmi enriched genes
8	1e−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	4 / 94	DUMEAUX_Smoking enriched genes
11	4e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	5e−01	5 / 147	Homuth_BMI−associated−genes_UP
13	6e−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

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−65	453 / 7448	HOPP_Strong_enhancer
2	5e−54	459 / 8226	HOPP_Active_promoter
3	9e−52	422 / 7275	HOPP_Txn_elongation
4	2e−49	346 / 5356	HOPP_Txn_transition
5	3e−38	68 / 306	WIRTH_lymphoma937_spot E
6	8e−38	67 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−c
7	9e−38	420 / 8098	HOPP_Weak_promoter
8	1e−32	59 / 272	SPANG_IL21 DN
9	4e−23	342 / 6959	HOPP_Weak_enhancer
10	3e−19	316 / 6559	HOPP_Weak_txn
11	6e−15	89 / 1169	SPANG_BCR DN
12	9e−13	17 / 57	Monti_Host_response_cluster
13	1e−12	39 / 331	SPANG_CD40 6hrs UP
14	4e−10	42 / 455	SPANG_CD40 6hrs DN
15	2e−09	16 / 78	Sha_DLBCL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.04	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.58	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.61	1 / 30	Hugo_melanoma−all−MET_UP
4	1.00	0 / 54	Hugo_melanoma−all−MET_DN
5	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
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−44	459 / 8818	protein binding
2	2e−08	28 / 265	cadherin binding involved in cell−cell adhesion
3	5e−08	30 / 311	enzyme binding
4	2e−07	43 / 580	identical protein binding
5	7e−07	11 / 54	double−stranded RNA binding
6	1e−06	22 / 213	GTPase activity
7	2e−06	73 / 1329	ATP binding
8	3e−06	43 / 646	protein homodimerization activity
9	4e−06	59 / 1013	poly(A) RNA binding
10	4e−06	22 / 232	ligase activity
11	5e−06	21 / 217	protein kinase activity
12	2e−05	25 / 315	protein serine/threonine kinase activity
13	2e−05	19 / 204	protein domain specific binding
14	3e−05	24 / 301	ubiquitin−protein transferase activity
15	5e−05	26 / 350	protein kinase 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−16	62 / 602	hsa−miR−20a
2	2e−16	57 / 520	hsa−miR−106a
3	3e−16	59 / 561	hsa−miR−20b
4	9e−16	44 / 336	hsa−miR−142−5p
5	1e−15	49 / 416	hsa−miR−372
6	2e−15	57 / 546	hsa−miR−93
7	4e−15	37 / 250	hsa−miR−548l
8	5e−15	49 / 429	hsa−miR−548n
9	6e−15	39 / 281	hsa−miR−570
10	1e−14	50 / 455	hsa−miR−130a
11	5e−14	54 / 540	hsa−miR−17
12	9e−14	52 / 513	hsa−miR−106b
13	3e−13	46 / 428	hsa−miR−519d
14	3e−13	35 / 259	hsa−miR−548p
15	4e−13	51 / 516	hsa−miR−15a

Pathw Act

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 11	BENTINK_ras.4
2	5e−02	2 / 12	BENTINK_ras.1
3	6e−02	2 / 13	BENTINK_src.10
4	3e−01	1 / 13	BENTINK_e2f3.1
5	4e−01	1 / 14	GUSTAFSON_PI3K_UP
6	4e−01	1 / 14	BENTINK_ras.6
7	4e−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	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−68	61 / 96	Chaussabel_3,1_Interferon−inducible
2	4e−42	48 / 113	Chaussabel_1,5_Myeloid lineage
3	4e−40	63 / 240	Chaussabel_3,3_Inflammation II
4	9e−38	40 / 84	Chaussabel_2,10_Immune related cell surface molecules
5	8e−20	55 / 412	WIRTH_Immune system
6	5e−18	32 / 150	Chaussabel_2,6_Myeloid lineage
7	4e−14	35 / 242	Chaussabel_3,2_Inflammation I
8	2e−12	59 / 681	PROTEINATLAS_lung
9	2e−12	26 / 153	Chaussabel_2,9_Cytosceleton
10	7e−10	46 / 535	PROTEINATLAS_spleen
11	1e−09	15 / 66	VAQUERIZAS_Whole blood_TF
12	1e−08	53 / 724	PROTEINATLAS_lymph node
13	1e−07	49 / 695	PROTEINATLAS_bone marrow
14	1e−06	27 / 302	Chaussabel_3,4_Protein phosphatases
15	5e−06	63 / 1118	PROTEINATLAS_placenta

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	2 / 27	Nabetani_alt len telomeres_genes_ko
2	0.3	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	

TF

Rank	p−value	#in/all	Geneset
1	4e−17	243 / 4735	ICGC_Pu1_targets
2	1e−15	250 / 5067	ICGC_Taf1_targets
3	7e−15	262 / 5466	ICGC_Nficsc81335_targets
4	3e−13	126 / 2087	ICGC_Cebpbsc150_targets
5	5e−13	234 / 4881	ICGC_Atf2_targets
6	7e−13	127 / 2133	ICGC_Mef2_targets
7	3e−12	314 / 7247	ICGC_Runx3_targets
8	3e−12	140 / 2497	ICGC_Bcl11_targets
9	4e−12	231 / 4890	ICGC_Bclaf101388_targets
10	9e−12	252 / 5518	ICGC_Stat5_targets
11	3e−11	247 / 5442	ICGC_Pmlsc71910_targets
12	4e−11	242 / 5312	ICGC_Tcf12_targets
13	6e−11	104 / 1723	HEBENSTREIT_high expression TF
14	1e−10	264 / 5984	ICGC_Mta3_targets
15	1e−10	263 / 5961	ICGC_Pol24_targets

Overexpression Spots

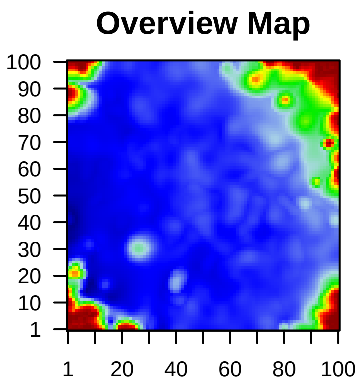
Spot Summary: W

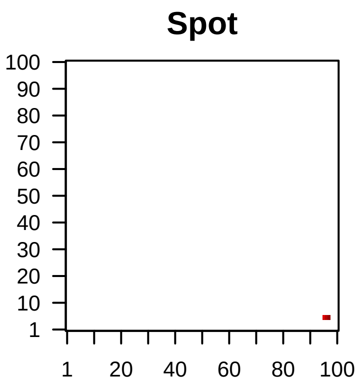
metagenes = 6
genes = 69

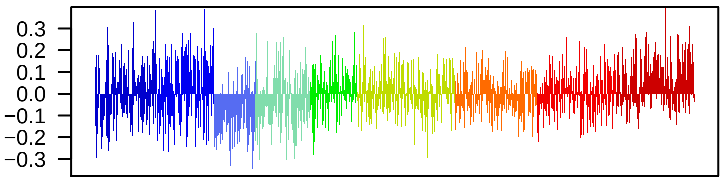
<r> metagenes = 0.99
<r> genes = 0.43
beta: r2= 29.48 / log p= −Inf

samples with spot = 358 (10.6 %)

- A * : 45 (13.1 %)
- A C * : 75 (22.9 %)
- A C F * : 4 (1.7 %)
- A F * : 21 (6.8 %)
- C F * : 26 (9.8 %)
- F * : 38 (6.8 %)
- F J * : 23 (5 %)
- J * : 30 (6.7 %)
- N * : 96 (21.7 %)





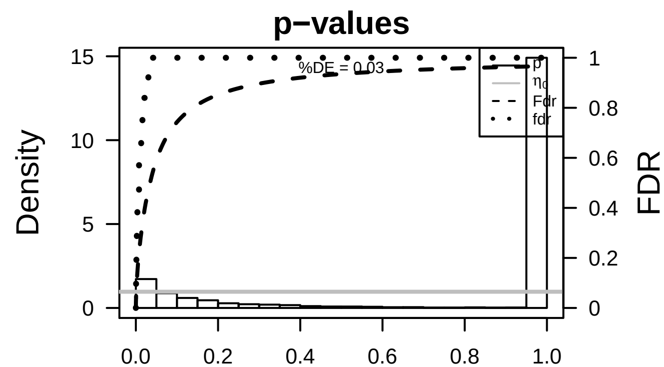


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_237640	0.81	−0.96	0.42	TSC22D3	TSC22 domain family member 3 [Source:HGNC Symbol;Acc:
2	ILMN_178245	0.79	−0.67	0.55	OSBPL8	oxysterol binding protein like 8 [Source:HGNC Symbol;Acc:H
3	ILMN_170224	0.78	−0.58	0.65	CCNDBP1	cyclin D1 binding protein 1 [Source:HGNC Symbol;Acc:HGN
4	ILMN_237978	0.77	−0.64	0.57	HIF1A	hypoxia inducible factor 1 alpha subunit [Source:HGNC Symb
5	ILMN_167595	0.69	−0.66	0.69	LYST	lysosomal trafficking regulator [Source:HGNC Symbol;Acc:H
6	ILMN_230774	0.69	−0.63	0.71	CD46	CD46 molecule [Source:HGNC Symbol;Acc:HGNC:6953]
7	ILMN_207646	0.68	−0.59	0.67		
8	ILMN_169600	0.66	−0.63	0.54	MIR197	G protein subunit alpha i3 [Source:HGNC Symbol;Acc:HGNC
9	ILMN_241380	0.65	−0.6	0.53	CD53	CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]
10	ILMN_212237	0.64	−0.63	0.75	FAM49B	family with sequence similarity 49 member B [Source:HGNC
11	ILMN_173958	0.63	−0.64	0.42	FEZ2	fasciculation and elongation protein zeta 2 [Source:HGNC Sy
12	ILMN_222073	0.63	−0.47	0.61	TMCO3	transmembrane and coiled−coil domains 3 [Source:HGNC Sy
13	ILMN_175558	0.61	−0.56	0.68	DIP2B	disco interacting protein 2 homolog B [Source:HGNC Symbol
14	ILMN_179854	0.61	−0.6	0.71	STK17B	serine/threonine kinase 17b [Source:HGNC Symbol;Acc:HGN
15	ILMN_218196	0.6	−0.6	0.75	CBL	Cbl proto−oncogene [Source:HGNC Symbol;Acc:HGNC:1541
16	ILMN_232992	0.6	−0.53	0.51	ABCG1	ATP binding cassette subfamily G member 1 [Source:HGNC
17	ILMN_178576	0.6	−0.5	0.73	TM9SF2	transmembrane 9 superfamily member 2 [Source:HGNC Sym
18	ILMN_176839	0.6	−0.55	0.71	ARPC5	actin related protein 2/3 complex subunit 5 [Source:HGNC Sy
19	ILMN_215932	0.6	−0.49	0.68	SLK	STE20 like kinase [Source:HGNC Symbol;Acc:HGNC:11088]
20	ILMN_166430	0.6	−0.49	0.69	HTATIP2	HIV−1 Tat interactive protein 2 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−14	48 / 7275	Lymp	HOPP_Txn_elongation
2	2e−13	50 / 8568	Colon	TxWk_Colon
3	2e−13	49 / 8226	Lymp	HOPP_Active_promoter
4	2e−13	51 / 9054	Colon	Tx_Colon
5	7e−13	13 / 301	Canc	SPANG_BCL6−index2
6	2e−12	52 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
7	2e−12	49 / 8678	Colon	Quies3_Colon
8	3e−12	54 / 10999	Colon	TssWk_Colon
9	4e−12	49 / 8771	Chror	5_Tx_Melanocytes
10	1e−11	46 / 7854	Chror	5_Tx_Fibroblasts
11	7e−11	48 / 8990	Chror	15_Quies_Fibroblasts
12	1e−10	10 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
13	4e−10	52 / 11130	Chror	15_Quies_Melanocytes
14	4e−10	49 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
15	5e−10	55 / 12741	Chror	7_Enh_Melanocytes
16	7e−10	54 / 12298	Chror	2_TssA_Melanocytes
17	1e−09	17 / 1069	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
18	1e−09	52 / 11455	Chror	2_TssA_Fibroblasts
19	2e−09	42 / 7448	Lymp	HOPP_Strong_enhancer
20	2e−09	15 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
21	4e−09	37 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
22	5e−09	47 / 9555	Colon	TssA_Colon
23	5e−09	49 / 10430	Brain	Overlap_fetal_midbrain_Quies
24	4e−08	11 / 482	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
25	5e−08	43 / 8613	Chror	7_Enh_Fibroblasts
26	6e−08	53 / 12983	Chror	2_TssA_Neuronal_Progenitor
27	9e−08	22 / 2464	CC	extracellular exosome
28	1e−07	11 / 532	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
29	1e−07	41 / 8098	Lymp	HOPP_Weak_promoter
30	1e−07	28 / 4034	Colon	TssD1_Colon
31	2e−07	50 / 11836	Chror	3_TssF_Melanocytes
32	3e−07	8 / 250	miRN	hsa−miR−548l
33	4e−07	18 / 1797	GSEA	PILON_KLF1_TARGETS_DN
34	5e−07	14 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
35	5e−07	10 / 492	GSEA	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
36	5e−07	12 / 770	GSEA	CUI_TCF21_TARGETS_2_DN
37	8e−07	8 / 292	miRN	hsa−miR−18b
38	1e−06	31 / 5356	Lymp	HOPP_Txn_transition
39	1e−06	43 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
40	3e−06	8 / 352	CC	focal adhesion



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	3e−04	7 / 511	apoptotic process
2	5e−04	2 / 13	striated muscle cell differentiation
3	5e−04	5 / 254	cell−cell adhesion
4	7e−04	2 / 15	cellular response to platelet−derived growth factor stimulus
5	1e−03	2 / 21	bone resorption
6	2e−03	2 / 25	glycogen biosynthetic process
7	2e−03	2 / 27	phagosome acidification
8	2e−03	2 / 28	cytoplasmic microtubule organization
9	3e−03	2 / 34	toxin transport
10	4e−03	2 / 35	activation of JUN kinase activity
11	4e−03	8 / 1003	signal transduction
12	5e−03	3 / 131	cell cycle arrest
13	5e−03	3 / 134	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
14	6e−03	2 / 43	cytokinesis
15	6e−03	2 / 44	activation of MAPKK activity

Brain

Rank	p−value	#in/all	Geneset
1	2e−12	52 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	4e−10	49 / 9815	Overlap_fetal_midbrain_ReprPC
3	4e−09	37 / 5936	Overlap_fetal_midbrain_HetRpts
4	5e−09	49 / 10430	Overlap_fetal_midbrain_Quies
5	1e−06	43 / 9504	Overlap_fetal_midbrain_K9K27me3
6	3e−03	9 / 1171	Fetal_EnhP
7	5e−02	3 / 328	Fetal_Het
8	8e−02	5 / 906	Fetal_HetRpts
9	1e−01	10 / 2630	Fetal_TssF
10	1e−01	4 / 796	Overlap_fetal_midbrain_ZNF
11	2e−01	4 / 818	Mid_Frontal_Lobe_Het
12	2e−01	5 / 1162	Fetal_Enh
13	2e−01	5 / 1213	Fetal_TssP
14	2e−01	4 / 937	Fetal_EnhG
15	3e−01	10 / 3164	Mid_Frontal_Lobe_ZNF

Cancer

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

CC

Rank	p−value	#in/all	Geneset
1	9e−08	22 / 2464	extracellular exosome
2	3e−06	8 / 352	focal adhesion
3	6e−06	28 / 4822	cytoplasm
4	1e−04	6 / 295	cell−cell adherens junction
5	2e−04	4 / 107	spindle
6	2e−04	3 / 42	cell leading edge
7	3e−04	3 / 51	phagocytic vesicle membrane
8	5e−04	4 / 139	microtubule cytoskeleton
9	5e−04	4 / 144	nuclear envelope
10	8e−04	8 / 777	Golgi apparatus
11	9e−04	8 / 788	endoplasmic reticulum membrane
12	1e−03	4 / 172	endosome membrane
13	1e−03	17 / 2979	cytosol
14	1e−03	3 / 86	cell projection
15	2e−03	4 / 208	actin cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.08	5 / 902	Chr 4
2	0.09	7 / 1492	Chr 2
3	0.14	4 / 768	Chr 14
4	0.30	2 / 422	Chr 13
5	0.32	3 / 769	Chr 15
6	0.37	3 / 836	Chr 8
7	0.39	7 / 2323	Chr 1
8	0.40	2 / 536	Chr 22
9	0.48	3 / 994	Chr X
10	0.53	1 / 289	Chr 21
11	0.58	3 / 1160	Chr 12
12	0.59	3 / 1170	Chr 7
13	0.59	1 / 342	Chr 18
14	0.67	3 / 1318	Chr 17
15	0.68	2 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−12	49 / 8771	5_Tx_Melanocytes
2	1e−11	46 / 7854	5_Tx_Fibroblasts
3	7e−11	48 / 8990	15_Quies_Fibroblasts
4	4e−10	52 / 11130	15_Quies_Melanocytes
5	5e−10	55 / 12741	7_Enh_Melanocytes
6	7e−10	54 / 12298	2_TssA_Melanocytes
7	1e−09	52 / 11455	2_TssA_Fibroblasts
8	5e−08	43 / 8613	7_Enh_Fibroblasts
9	6e−08	53 / 12983	2_TssA_Neuronal_Progenitor
10	2e−07	50 / 11836	3_TssF_Melanocytes
11	4e−06	49 / 12393	15_Quies_Neuronal_Progenitor
12	1e−05	47 / 11847	7_Enh_Neuronal_Progenitor
13	2e−04	23 / 4237	14_ZNF_Neuronal_Progenitor
14	4e−04	27 / 5699	6_EnhG_Melanocytes
15	9e−04	30 / 6970	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−13	50 / 8568	TxWk_Colon
2	2e−13	51 / 9054	Tx_Colon
3	2e−12	49 / 8678	Quies3_Colon
4	3e−12	54 / 10999	TssWk_Colon
5	1e−09	17 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	5e−09	47 / 9555	TssA_Colon
7	1e−07	28 / 4034	TssD1_Colon
8	4e−04	26 / 5373	EnhWk1_Colon
9	2e−03	11 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	3e−03	39 / 10779	Enh_Colon
11	6e−03	8 / 1083	ZNF_Colon
12	1e−02	9 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	2e−02	11 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	2e−02	17 / 4018	EnhWk2_Colon
15	3e−02	8 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_

Glio

Rank	p−value	#in/all	Geneset
1	0.001	8 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.001	5 / 315	Up
3	0.009	4 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.012	2 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
5	0.024	2 / 92	Weller_LGG_A_vs_O_DOWN
6	0.032	3 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
7	0.038	1 / 15	VERHAAK_NL subtype
8	0.078	9 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
9	0.172	2 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
10	0.202	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
11	0.208	1 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.224	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	0.254	1 / 113	GIEZELT_GBM_WT_up_VS_mut
14	0.303	5 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
15	0.309	6 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−10	10 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
2	2e−09	15 / 841	ACEVEDO_LIVER_CANCER_UP
3	4e−08	11 / 482	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
4	1e−07	11 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
5	4e−07	18 / 1797	PILON_KLF1_TARGETS_DN
6	5e−07	14 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
7	5e−07	10 / 492	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
8	5e−07	12 / 770	CUI_TCF21_TARGETS_2_DN
9	4e−06	4 / 41	IKEDA_MIR133_TARGETS_UP
10	9e−06	8 / 406	RODWELL_AGING_KIDNEY_UP
11	3e−05	4 / 66	PID_CDC42_PATHWAY
12	3e−05	10 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
13	3e−05	8 / 483	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
14	3e−05	10 / 794	NUYTTEN_NIPP1_TARGETS_DN
15	4e−05	5 / 151	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP

HM

Rank	p−value	#in/all	Geneset
1	0.01	3 / 177	HALLMARK_MITOTIC_SPINDLE
2	0.01	3 / 189	HALLMARK_HYPOXIA
3	0.02	2 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	0.08	2 / 176	HALLMARK_ADIPOGENESIS
5	0.08	2 / 183	HALLMARK_APICAL_JUNCTION
6	0.08	2 / 186	HALLMARK_IL2_STAT5_SIGNALING
7	0.08	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
8	0.08	2 / 187	HALLMARK_COMPLEMENT
9	0.09	2 / 191	HALLMARK_INFLAMMATORY_RESPONSE
10	0.16	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	0.21	1 / 91	HALLMARK_ANDROGEN_RESPONSE
12	0.32	1 / 151	HALLMARK_APOPTOSIS
13	0.34	1 / 162	HALLMARK_ALLOGRAFT_REJECTION
14	0.35	1 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
15	0.36	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	3 / 211	Homuth_BMI−associated−genes_DN
2	0.03	1 / 10	DUMEAUX_Women normal BMI literature genes up
3	0.04	1 / 16	Huan_blood−pressure_DBP−signature
4	0.04	1 / 17	DUMEAUX_High bmi enriched genes
5	0.05	1 / 18	Huan_blood−pressure_SBP−signature
6	1.00	0 / 94	DUMEAUX_Smoking enriched genes
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 31	DUMEAUX_Fasting enriched genes
15	1.00	0 / 147	Homuth_BMI−associated−genes_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−14	48 / 7275	HOPP_Txn_elongation
2	2e−13	49 / 8226	HOPP_Active_promoter
3	2e−09	42 / 7448	HOPP_Strong_enhancer
4	1e−07	41 / 8098	HOPP_Weak_promoter
5	1e−06	31 / 5356	HOPP_Txn_transition
6	1e−04	31 / 6559	HOPP_Weak_txn
7	9e−04	30 / 6959	HOPP_Weak_enhancer
8	1e−02	8 / 1169	SPANG_BCR DN
9	2e−02	2 / 78	Sha_DLBCL UP
10	2e−02	2 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
11	3e−02	1 / 10	BENTINK_mBL DOWN
12	3e−02	3 / 272	SPANG_IL21 DN
13	4e−02	3 / 286	ZHANG_DLBCL mutated
14	5e−02	2 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
15	5e−02	3 / 331	SPANG_CD40 6hrs UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	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−05	39 / 8818	protein binding
2	6e−05	6 / 265	cadherin binding involved in cell−cell adhesion
3	3e−04	3 / 48	receptor signaling protein serine/threonine kinase activity
4	4e−04	2 / 12	phospholipid transporter activity
5	3e−03	2 / 31	ADP binding
6	3e−03	3 / 115	actin filament binding
7	4e−03	2 / 38	cholesterol binding
8	4e−03	2 / 38	Rac GTPase binding
9	8e−03	2 / 51	GDP binding
10	2e−02	3 / 204	protein domain specific binding
11	2e−02	3 / 213	GTPase activity
12	2e−02	2 / 83	oxidoreductase activity
13	3e−02	1 / 10	phosphatidylcholine 1−acylhydrolase activity
14	3e−02	2 / 98	transcriptional activator activity, RNA polymerase II transcription regulatory re
15	3e−02	1 / 11	ion transmembrane 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	3e−07	8 / 250	hsa−miR−548l
2	8e−07	8 / 292	hsa−miR−18b
3	3e−06	6 / 158	hsa−miR−802
4	1e−05	9 / 546	hsa−miR−93
5	2e−05	7 / 317	hsa−miR−18a
6	2e−05	4 / 61	hsa−miR−627
7	4e−05	5 / 145	hsa−miR−143
8	7e−05	5 / 164	hsa−miR−96
9	7e−05	7 / 400	hsa−miR−519c−3p
10	9e−05	5 / 176	hsa−miR−199b−3p
11	9e−05	8 / 561	hsa−miR−20b
12	1e−04	6 / 303	hsa−miR−548i
13	2e−04	8 / 602	hsa−miR−20a
14	2e−04	4 / 110	hsa−miR−1271
15	2e−04	5 / 216	hsa−miR−182

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	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	6e−05	9 / 681	PROTEINATLAS_lung
2	8e−05	12 / 1268	PROTEINATLAS_colon
3	1e−04	11 / 1118	PROTEINATLAS_placenta
4	2e−04	11 / 1194	PROTEINATLAS_stomach
5	2e−04	10 / 1003	PROTEINATLAS_appendix
6	7e−04	6 / 412	WIRTH_Immune system
7	8e−04	10 / 1173	PROTEINATLAS_rectum
8	9e−04	8 / 782	PROTEINATLAS_thyroid gland
9	1e−03	9 / 1016	PROTEINATLAS_cerebral cortex
10	3e−03	6 / 535	PROTEINATLAS_spleen
11	3e−03	2 / 31	VAQUERIZAS_Fetal lung_TF
12	4e−03	4 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
13	4e−03	9 / 1239	PROTEINATLAS_testis
14	5e−03	7 / 816	PROTEINATLAS_endometrium
15	6e−03	8 / 1063	PROTEINATLAS_tonsil

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	2e−05	14 / 1501	ICGC_Usf1_targets
2	2e−04	26 / 5067	ICGC_Taf1_targets
3	2e−04	27 / 5466	ICGC_Nficsc81335_targets
4	2e−04	25 / 4890	ICGC_Bclaf101388_targets
5	4e−04	24 / 4735	ICGC_Pu1_targets
6	5e−04	26 / 5442	ICGC_Pmlsc71910_targets
7	5e−04	19 / 3348	ICGC_BatfPcr1_targets
8	1e−03	22 / 4468	ICGC_Egr1_targets
9	1e−03	12 / 1723	HEBENSTREIT_high expression TF
10	2e−03	29 / 6868	ICGC_Elf1_targets
11	2e−03	30 / 7247	ICGC_Runx3_targets
12	2e−03	27 / 6267	ICGC_Yy1_targets
13	2e−03	21 / 4345	ICGC_Zeb1_targets
14	2e−03	26 / 5961	ICGC_Pol24_targets
15	3e−03	13 / 2133	ICGC_Mef2_targets