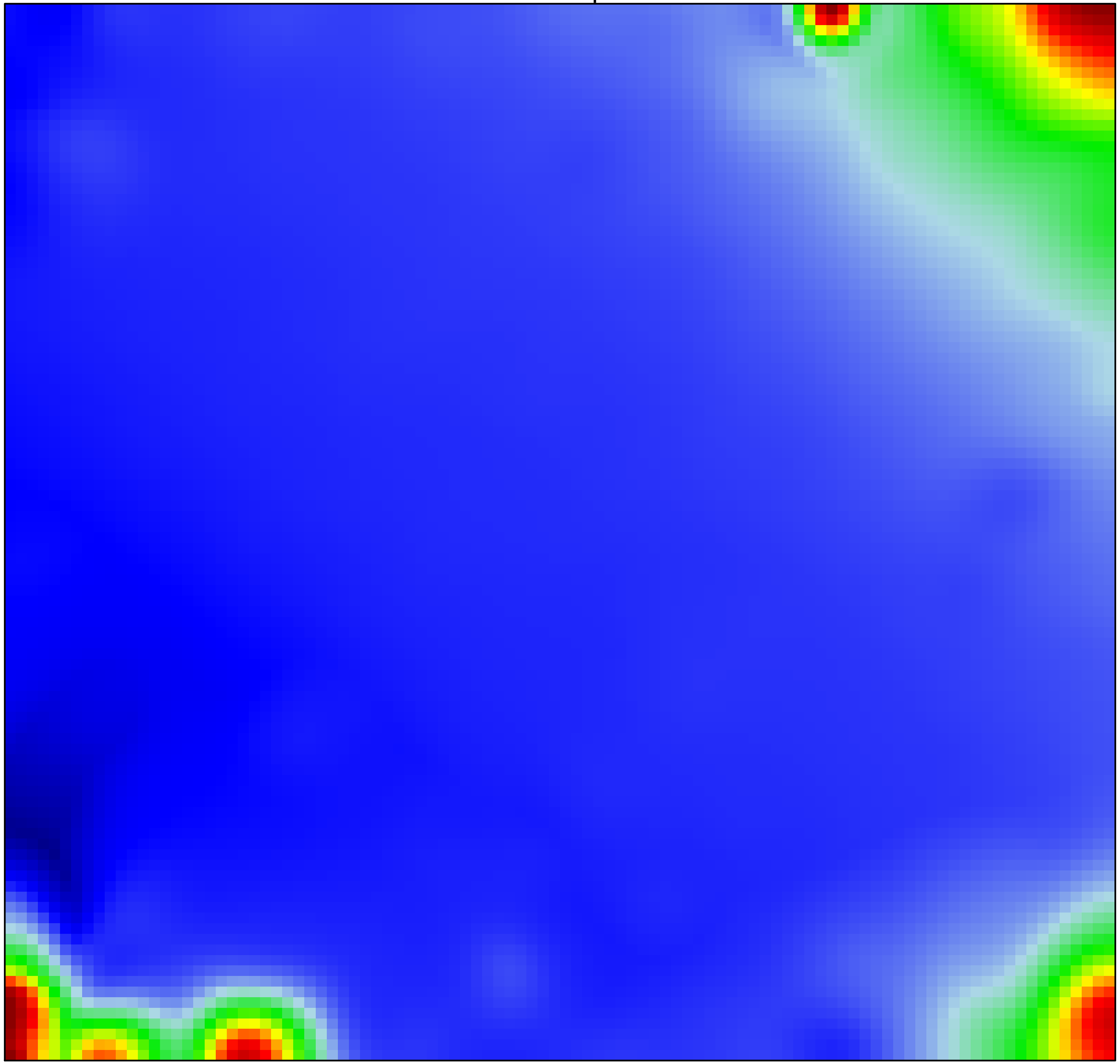
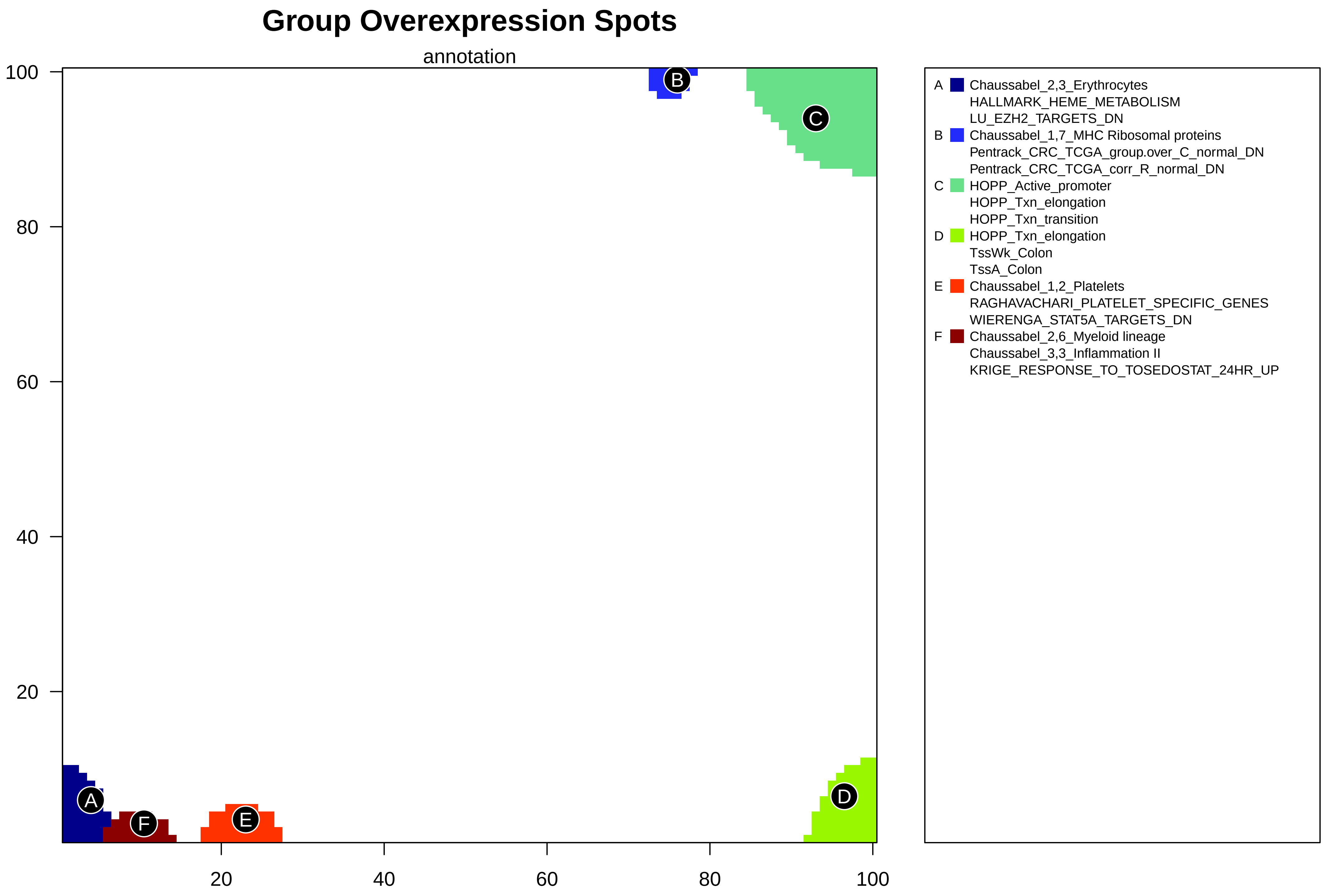
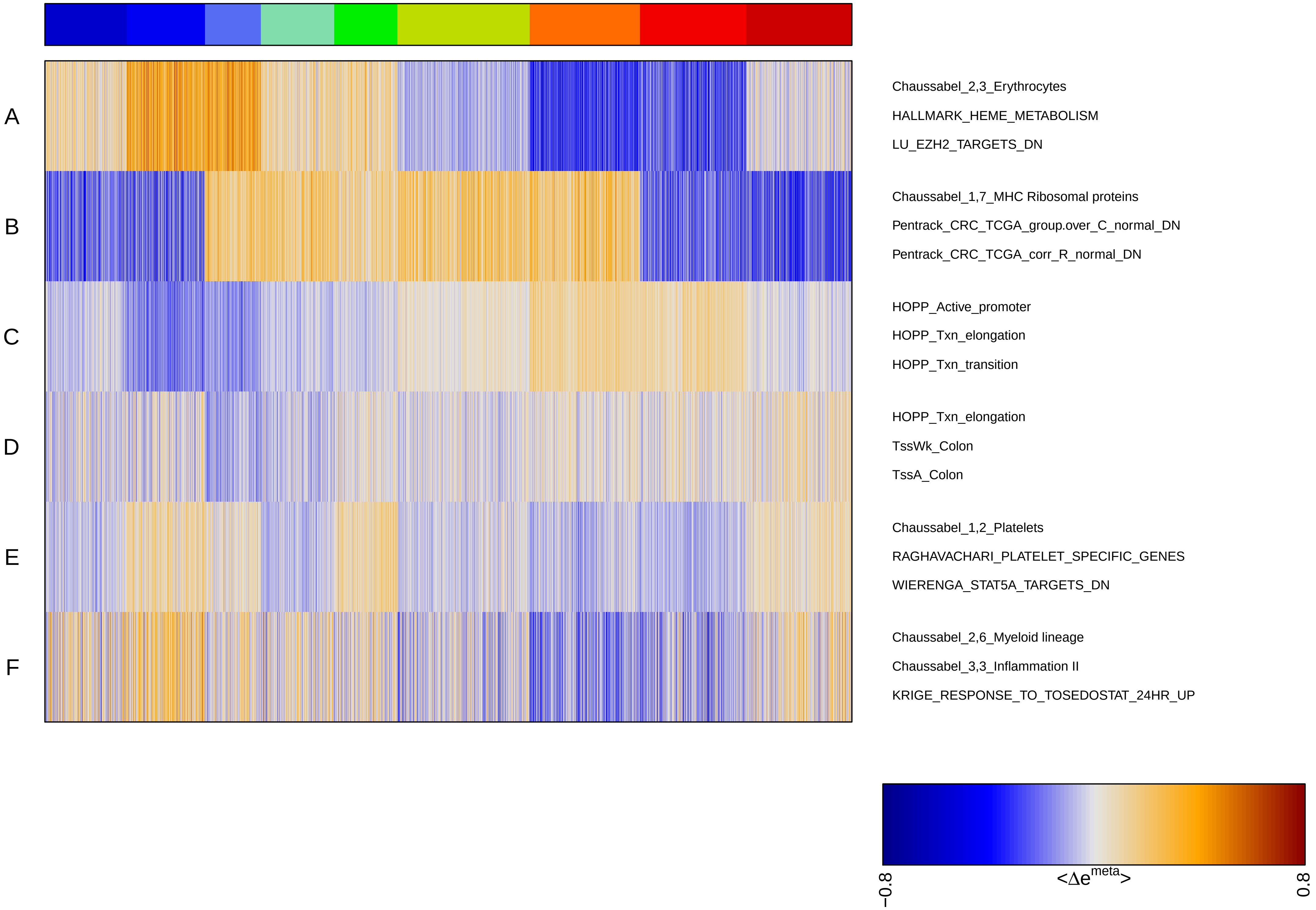
Group Overexpression Spots

landscape




Group Overexpression Spots
annotation
100
80
60
40
20
20
40
60
80
100
A
B
C
D
E
F
A Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
LU_EZH2_TARGETS_DN
B Chaussabel_1,7_MHC Ribosomal proteins
Pentrack_CRC_TCGA_group.over_C_normal_DN
Pentrack_CRC_TCGA_corr_R_normal_DN
C HOPP_Active_promoter
HOPP_Txn_elongation
HOPP_Txn_transition
D HOPP_Txn_elongation
TssWk_Colon
TssA_Colon
E Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
WIERENGA_STAT5A_TARGETS_DN
F Chaussabel_2,6_Myeloid lineage
Chaussabel_3,3_Inflammation II
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP


A
B
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Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
LU_EZH2_TARGETS_DN
Chaussabel_1,7_MHC Ribosomal proteins
Pentrack_CRC_TCGA_group.over_C_normal_DN
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Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
WIERENGA_STAT5A_TARGETS_DN
Chaussabel_2,6_Myeloid lineage
Chaussabel_3,3_Inflammation II
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
−0.8
<Δe^meta>
0.8

Group Overexpression Sp

Spot Summary: A

\# metagenes = 46
\# genes = 735

<r> metagenes = 0.88
<r> genes = 0.49
beta: r2= 208.91 / log p= −Inf

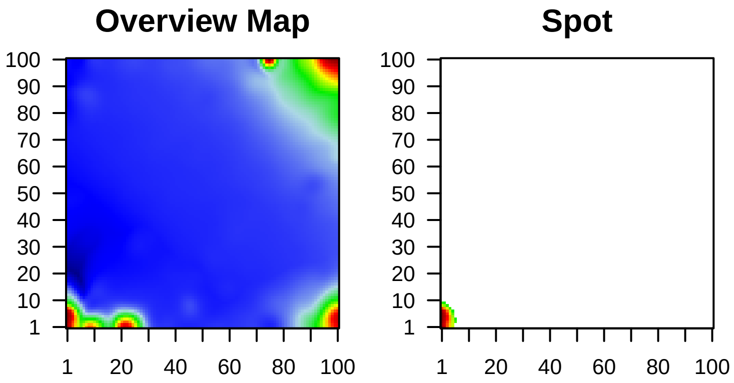
\# samples with spot = 816 (24.1 %)
- A * : 81 (23.5 %)
- A C * : 319 (97.3 %)
- A C F * : 235 (100 %)
- A F * : 76 (24.7 %)
- C F * : 78 (29.4 %)
- N * : 27 (6.1 %)

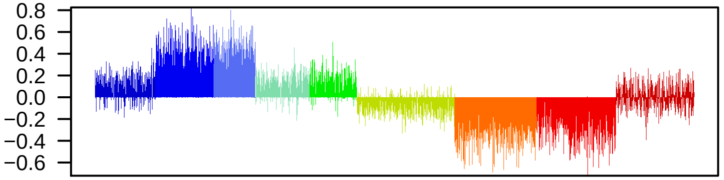
Spot Genelist

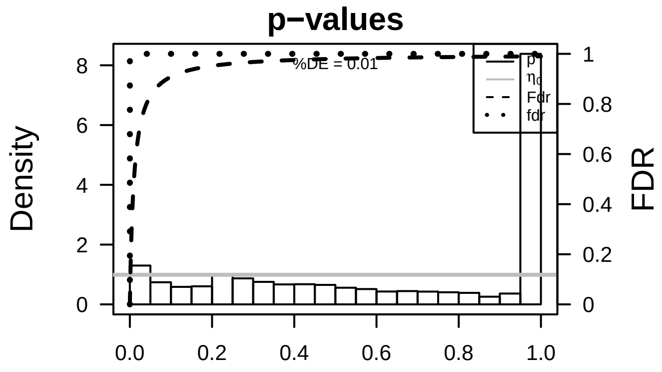
Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178314	4.32	−2.71	0.13		
2	ILMN_175553	3.25	−1.79	0.2	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H
3	ILMN_169326	3.22	−2.11	0.47		
4	ILMN_167935	3.21	−3.04	0.43	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
5	ILMN_177651	3.13	−1.1	0.36	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
6	ILMN_219321	3.07	−2.61	0.41	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
7	ILMN_216528	3.02	−1.93	0.41	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
8	ILMN_172566	2.96	−2.08	0.41	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
9	ILMN_211687	2.86	−1.31	0.36	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
10	ILMN_170832	2.82	−1.91	0.72	ALAS2	5'−aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:H
11	ILMN_165243	2.79	−1.83	0.61	CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:136
12	ILMN_168858	2.54	−1.91	0.54	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
13	ILMN_174983	2.5	−1.99	0.46	SMIM1	small integral membrane protein 1 (Vel blood group) [Source:
14	ILMN_175334	2.49	−1.4	0.37		
15	ILMN_176616	2.48	−2.2	0.63	SNCA	synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138]
16	ILMN_171345	2.47	−1.33	0.35	HBZ	hemoglobin subunit zeta [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_328576	2.47	−2.05	0.72	SLC4A1	solute carrier family 4 member 1 (Diego blood group) [Source
18	ILMN_169651	2.44	−2.23	0.84	AHSP	alpha hemoglobin stabilizing protein [Source:HGNC Symbol;
19	ILMN_169222	2.41	−1.48	0.54		
20	ILMN_173571	2.39	−1.48	0.52	KRT1	keratin 1 [Source:HGNC Symbol;Acc:HGNC:6412]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−72	62 / 111	Refer	Chaussabel_2,3_Erythrocytes
2	4e−52	60 / 185	HM	HALLMARK_HEME_METABOLISM
3	8e−36	62 / 360	GSEA	LU_EZH2_TARGETS_DN
4	4e−18	17 / 39	Refer	Chaussabel_2,2_Neutrophils
5	6e−16	26 / 147	Lifesty	Homuth_BMI−associated−genes_UP
6	7e−16	34 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
7	1e−13	10 / 15	Lifesty	DUMEAUX_Red blood cells in non smokers literature genes up
8	1e−13	12 / 26	GSEA	VALK_AML_CLUSTER_7
9	7e−13	12 / 29	Refer	JONGENEEL_Bone Marrow
10	1e−12	247 / 7354	Colon	TssF_Colon
11	1e−12	26 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
12	2e−11	359 / 12298	Chror	2_TssA_Melanocytes
13	2e−11	296 / 9555	Colon	TssA_Colon
14	9e−11	10 / 25	GSEA	VALK_AML_CLUSTER_8
15	2e−10	208 / 6138	Colon	TssD2_Colon
16	6e−10	368 / 12983	Chror	2_TssA_Neuronal_Progenitor
17	7e−10	278 / 9054	Colon	Tx_Colon
18	9e−10	115 / 2845	Colon	TxEnhG1_Colon
19	2e−09	269 / 8771	Chror	5_Tx_Melanocytes
20	6e−09	182 / 5383	TF	ICGC_Sp1_targets
21	7e−09	314 / 10779	Colon	Enh_Colon
22	1e−08	19 / 169	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
23	2e−08	327 / 11455	Chror	2_TssA_Fibroblasts
24	3e−08	316 / 10999	Colon	TssWk_Colon
25	3e−08	335 / 11836	Chror	3_TssF_Melanocytes
26	4e−08	194 / 5984	TF	ICGC_Mta3_targets
27	5e−08	216 / 6868	TF	ICGC_Elf1_targets
28	6e−08	126 / 3450	Chror	4_TxTrans_Fibroblasts
29	6e−08	6 / 11	Refer	WIRTH_Prim. lymphoid organs
30	8e−08	31 / 451	GSEA	PILON_KLF1_TARGETS_UP
31	1e−07	282 / 9635	Chror	3_TssF_Fibroblasts
32	1e−07	256 / 8568	Colon	TxWk_Colon
33	1e−07	5 / 7	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_UP
34	2e−07	52 / 1043	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
35	2e−07	277 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
36	3e−07	183 / 5699	Chror	6_EnhG_Melanocytes
37	6e−07	7 / 23	CC	cortical cytoskeleton
38	7e−07	168 / 5188	TF	ICGC_Ebfsc137065_targets
39	7e−07	220 / 7247	TF	ICGC_Runx3_targets
40	8e−07	81 / 2028	Chror	4_TxTrans_Melanocytes







Aging

Rank	p−value	#in/all	Geneset
1	0.3	4 / 111	HORVATH_aging_genes meth DOWN
2	0.7	1 / 58	TESCHENDORFF_age_hypermethylated
3	1.0	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−06	5 / 12	oxygen transport
2	1e−05	26 / 435	negative regulation of apoptotic process
3	2e−05	5 / 15	negative regulation of growth of symbiont in host
4	3e−05	7 / 40	erythrocyte differentiation
5	4e−05	6 / 29	mitophagy
6	1e−04	8 / 64	negative regulation of cysteine−type endopeptidase activity involved in apoptc
7	1e−04	7 / 50	response to ionizing radiation
8	2e−04	4 / 13	cellular response to hepatocyte growth factor stimulus
9	4e−04	4 / 16	mitochondrion morphogenesis
10	8e−04	4 / 19	regulation of cell size
11	1e−03	4 / 20	heme biosynthetic process
12	1e−03	4 / 20	positive regulation of macroautophagy
13	1e−03	3 / 10	mitotic recombination
14	1e−03	4 / 22	defense response to fungus
15	2e−03	3 / 11	positive regulation of long−term synaptic potentiation

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	277 / 9504	Overlap_fetal_midbrain_K9K27me3
2	3e−06	293 / 10430	Overlap_fetal_midbrain_Quies
3	2e−05	39 / 818	Mid_Frontal_Lobe_Het
4	2e−05	67 / 1728	Fetal_ReprPCWk
5	2e−05	107 / 3164	Mid_Frontal_Lobe_ZNF
6	1e−04	269 / 9815	Overlap_fetal_midbrain_ReprPC
7	3e−04	173 / 5936	Overlap_fetal_midbrain_HetRpts
8	4e−04	89 / 2709	Mid_Frontal_Lobe_HetRpts
9	3e−03	31 / 796	Overlap_fetal_midbrain_ZNF
10	3e−02	251 / 9917	Overlap_fetal_midbrain_ReprPCWk
11	5e−02	52 / 1784	Mid_Frontal_Lobe_ReprPCWk
12	5e−02	110 / 4112	Mid_Frontal_Lobe_ReprPC
13	7e−02	22 / 681	Overlap_fetal_midbrain_EnhP
14	9e−02	34 / 1162	Fetal_Enh
15	1e−01	27 / 906	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	1 / 14	LIU_COMMON_CANCER_GENES
2	3e−02	5 / 73	SHAUGHNESSY_MM high risk
3	4e−02	19 / 527	Lembcke_Normal vs Adenoma
4	5e−02	2 / 15	WANG_ER_UP
5	6e−02	19 / 554	Lembcke_Colonic Inflammation
6	9e−02	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	1e−01	3 / 54	KUIPER_MM poor survival
8	2e−01	2 / 36	PanCan_HK_geneset_nanostring
9	2e−01	1 / 12	LIU_BREAST_CANCER
10	3e−01	1 / 13	RHODES_CANCER_META_SIGNATURE
11	3e−01	1 / 13	LIU_LIVER_CANCER
12	3e−01	1 / 13	GENTLES_modul2
13	3e−01	1 / 13	GENTLES_modul12
14	3e−01	1 / 14	GENTLES_modul1
15	3e−01	2 / 46	PanCan_DNARepair_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−07	7 / 23	cortical cytoskeleton
2	2e−04	98 / 2979	cytosol
3	1e−03	5 / 34	polysome
4	2e−03	3 / 11	TORC2 complex
5	2e−03	3 / 12	specific granule
6	3e−03	8 / 104	endomembrane system
7	3e−03	138 / 4828	nucleus
8	4e−03	137 / 4822	cytoplasm
9	1e−02	3 / 21	M band
10	1e−02	3 / 22	nuclear euchromatin
11	2e−02	13 / 287	mitochondrial matrix
12	2e−02	6 / 93	blood microparticle
13	2e−02	2 / 10	MKS complex
14	2e−02	10 / 208	actin cytoskeleton
15	3e−02	2 / 11	endolysosome membrane

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	60 / 1467	Chr 19
2	1e−02	39 / 1170	Chr 7
3	1e−02	43 / 1318	Chr 17
4	7e−02	18 / 536	Chr 22
5	8e−02	24 / 769	Chr 15
6	2e−01	61 / 2323	Chr 1
7	2e−01	27 / 959	Chr 16
8	2e−01	21 / 768	Chr 14
9	5e−01	15 / 619	Chr 20
10	7e−01	17 / 836	Chr 8
11	8e−01	19 / 954	Chr 9
12	8e−01	6 / 342	Chr 18
13	8e−01	17 / 904	Chr 10
14	9e−01	29 / 1492	Chr 2
15	9e−01	23 / 1217	Chr 3

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−11	359 / 12298	2_TssA_Melanocytes
2	6e−10	368 / 12983	2_TssA_Neuronal_Progenitor
3	2e−09	269 / 8771	5_Tx_Melanocytes
4	2e−08	327 / 11455	2_TssA_Fibroblasts
5	3e−08	335 / 11836	3_TssF_Melanocytes
6	6e−08	126 / 3450	4_TxTrans_Fibroblasts
7	1e−07	282 / 9635	3_TssF_Fibroblasts
8	3e−07	183 / 5699	6_EnhG_Melanocytes
9	8e−07	81 / 2028	4_TxTrans_Melanocytes
10	1e−06	157 / 4795	6_EnhG_Fibroblasts
11	2e−06	347 / 12741	7_Enh_Melanocytes
12	3e−06	210 / 6970	5_Tx_Neuronal_Progenitor
13	4e−06	184 / 5956	3_TssF_Neuronal_Progenitor
14	2e−05	227 / 7854	5_Tx_Fibroblasts
15	3e−05	320 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−12	247 / 7354	TssF_Colon
2	2e−11	296 / 9555	TssA_Colon
3	2e−10	208 / 6138	TssD2_Colon
4	7e−10	278 / 9054	Tx_Colon
5	9e−10	115 / 2845	TxEnhG1_Colon
6	7e−09	314 / 10779	Enh_Colon
7	3e−08	316 / 10999	TssWk_Colon
8	1e−07	256 / 8568	TxWk_Colon
9	2e−06	253 / 8678	Quies3_Colon
10	2e−05	98 / 2810	EnhA_Colon
11	2e−05	59 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	4e−05	164 / 5373	EnhWk1_Colon
13	6e−05	35 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
14	3e−04	72 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
15	2e−03	23 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP

Glio

Rank	p−value	#in/all	Geneset
1	0.002	3 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
2	0.013	6 / 84	GIEZELT_GBM_STS_up_VS_LTS
3	0.033	53 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.046	2 / 15	VERHAAK_MES subtype
5	0.046	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
6	0.047	15 / 401	Down_b
7	0.058	2 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
8	0.058	2 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
9	0.058	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
10	0.064	2 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
11	0.072	4 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
12	0.077	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
13	0.077	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	0.081	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
15	0.108	14 / 419	Down_a

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−36	62 / 360	LU_EZH2_TARGETS_DN
2	7e−16	34 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
3	1e−13	12 / 26	VALK_AML_CLUSTER_7
4	1e−12	26 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	9e−11	10 / 25	VALK_AML_CLUSTER_8
6	1e−08	19 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
7	8e−08	31 / 451	PILON_KLF1_TARGETS_UP
8	1e−07	5 / 7	MARTINELLI_IMMATURE_NEUTROPHIL_UP
9	2e−07	52 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
10	1e−06	6 / 17	WELCH_GATA1_TARGETS
11	3e−06	6 / 19	VILIMAS_NOTCH1_TARGETS_DN
12	4e−06	37 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
13	5e−06	11 / 87	HAHTOLA_SEZARY_SYNDROM_UP
14	8e−06	17 / 210	CHYLA_CBFA2T3_TARGETS_DN
15	2e−05	5 / 15	STEINER_ERYTHROCYTE_MEMBRANE_GENES

HM

Rank	p−value	#in/all	Geneset
1	4e−52	60 / 185	HALLMARK_HEME_METABOLISM
2	3e−04	11 / 137	HALLMARK_UV_RESPONSE_UP
3	2e−02	9 / 176	HALLMARK_KRAS_SIGNALING_UP
4	2e−02	8 / 151	HALLMARK_APOPTOSIS
5	3e−02	9 / 189	HALLMARK_HYPOXIA
6	5e−02	8 / 176	HALLMARK_ADIPOGENESIS
7	7e−02	8 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	7e−02	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	7e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	9e−02	5 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	1e−01	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
12	1e−01	7 / 185	HALLMARK_MTORC1_SIGNALING
13	1e−01	7 / 186	HALLMARK_IL2_STAT5_SIGNALING
14	2e−01	4 / 103	HALLMARK_BILE_ACID_METABOLISM
15	2e−01	2 / 41	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	6e−16	26 / 147	Homuth_BMI−associated−genes_UP
2	1e−13	10 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	6e−02	2 / 17	DUMEAUX_High bmi enriched genes
4	2e−01	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
5	3e−01	1 / 18	Huan_blood−pressure_SBP−signature
6	4e−01	6 / 211	Homuth_BMI−associated−genes_DN
7	6e−01	2 / 94	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−07	24 / 331	WIRTH_lymphoma937_spot H
2	2e−06	23 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
3	2e−04	211 / 7448	HOPP_Strong_enhancer
4	2e−04	159 / 5356	HOPP_Txn_transition
5	5e−04	23 / 464	WIRTH_lymphoma937_spot I
6	7e−04	203 / 7275	HOPP_Txn_elongation
7	2e−03	21 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
8	3e−03	42 / 1169	SPANG_BCR DN
9	7e−03	20 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
10	1e−02	215 / 8226	HOPP_Active_promoter
11	2e−02	19 / 493	WIRTH_lymphoma937_spot J
12	4e−02	6 / 109	ROSOLOWSKI_blue total
13	5e−02	12 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
14	5e−02	12 / 306	WIRTH_lymphoma937_spot E
15	7e−02	9 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	2 / 54	Hugo_melanoma−all−MET_DN
2	0.5	1 / 30	Hugo_melanoma−all−MET_UP
3	0.6	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	3e−06	5 / 11	oxygen transporter activity
2	6e−05	247 / 8818	protein binding
3	8e−04	4 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
4	1e−03	4 / 20	endodeoxyribonuclease activity
5	1e−03	7 / 72	single−stranded DNA binding
6	1e−03	4 / 22	polyubiquitin binding
7	2e−03	5 / 38	oxygen binding
8	4e−03	3 / 14	four−way junction DNA binding
9	4e−03	8 / 112	heme binding
10	5e−03	15 / 301	ubiquitin−protein transferase activity
11	5e−03	24 / 580	identical protein binding
12	6e−03	7 / 94	double−stranded DNA binding
13	8e−03	4 / 35	4 iron, 4 sulfur cluster binding
14	1e−02	5 / 58	core promoter binding
15	1e−02	6 / 81	protease binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 17	Thyroid carcinoma, follicular
2	0.3	1 / 18	Hodgkin lymphoma
3	0.5	1 / 29	Myelofibrosis, idiopathic
4	0.7	1 / 47	Cervical cancer, somatic
5	0.7	1 / 48	Gastric cancer
6	0.7	1 / 57	Cardiomyopathy, dilated
7	0.8	1 / 65	Hepatocellular carcinoma
8	0.8	1 / 68	Glioblastoma multiforme, somatic
9	0.8	1 / 73	Stroke, susceptibility to
10	0.9	1 / 95	Colorectal cancer
11	0.9	1 / 102	Leukemia
12	0.9	1 / 113	Ovarian cancer
13	0.9	1 / 116	Cancer
14	0.9	1 / 120	Hematological
15	0.9	1 / 123	Pancreatic cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	7 / 96	hsa−miR−125b
2	0.008	4 / 34	hsa−miR−1178
3	0.008	10 / 176	hsa−miR−23b
4	0.010	10 / 183	hsa−miR−23a
5	0.015	5 / 63	hsa−miR−371−5p
6	0.019	6 / 91	hsa−miR−425
7	0.020	19 / 489	hsa−miR−16
8	0.023	6 / 95	hsa−miR−125a−5p
9	0.024	11 / 239	hsa−miR−214
10	0.024	5 / 71	hsa−miR−628−3p
11	0.024	18 / 467	hsa−miR−195
12	0.025	2 / 11	hsa−miR−604
13	0.026	7 / 125	hsa−miR−508−3p
14	0.028	4 / 50	hsa−miR−337−3p
15	0.031	5 / 76	hsa−miR−620

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	2 / 15	GUSTAFSON_PI3K_DN
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 13	BENTINK_e2f3.1
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	3e−72	62 / 111	Chaussabel_2,3_Erythrocytes
2	4e−18	17 / 39	Chaussabel_2,2_Neutrophils
3	7e−13	12 / 29	JONGENEEL_Bone Marrow
4	6e−08	6 / 11	WIRTH_Prim. lymphoid organs
5	7e−06	5 / 13	WIRTH_Bone marrow
6	2e−04	12 / 150	Chaussabel_2,6_Myeloid lineage
7	5e−04	5 / 29	Chaussabel_2,7_Unknown function
8	8e−04	4 / 19	VAQUERIZAS_Bone marrow_TF
9	2e−02	25 / 695	PROTEINATLAS_bone marrow
10	4e−02	2 / 14	WIRTH_B−cells
11	5e−02	2 / 15	VAQUERIZAS_Fetal liver_TF
12	5e−02	10 / 240	Chaussabel_3,3_Inflammation II
13	6e−02	3 / 39	VAQUERIZAS_Testis_TF
14	9e−02	5 / 102	Chaussabel_1,2_Platelets
15	1e−01	14 / 412	WIRTH_Immune system

Telomeres

Rank	p−value	#in/all	Geneset
1	0.02	3 / 27	Nabetani_alt len telomeres_genes_ko
2	0.26	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	6e−09	182 / 5383	ICGC_Sp1_targets
2	4e−08	194 / 5984	ICGC_Mta3_targets
3	5e−08	216 / 6868	ICGC_Elf1_targets
4	7e−07	168 / 5188	ICGC_Ebfsc137065_targets
5	7e−07	220 / 7247	ICGC_Runx3_targets
6	8e−07	146 / 4362	ICGC_Creb1_targets
7	9e−07	195 / 6267	ICGC_Yy1_targets
8	1e−06	148 / 4468	ICGC_Egr1_targets
9	1e−06	202 / 6578	ICGC_Pou2_targets
10	2e−06	173 / 5466	ICGC_Nficsc81335_targets
11	3e−06	157 / 4890	ICGC_Bclaf101388_targets
12	4e−06	173 / 5518	ICGC_Stat5_targets
13	6e−06	169 / 5410	ICGC_Foxm1_targets
14	7e−06	155 / 4881	ICGC_Atf2_targets
15	9e−06	197 / 6552	ICGC_Pol2_targets

Group Overexpression Sp

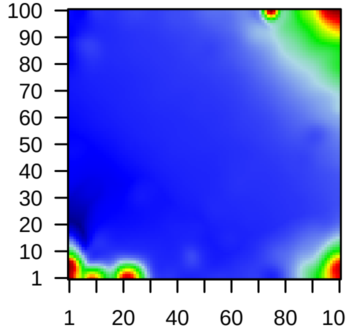
Spot Summary: B

metagenes = 19
genes = 79

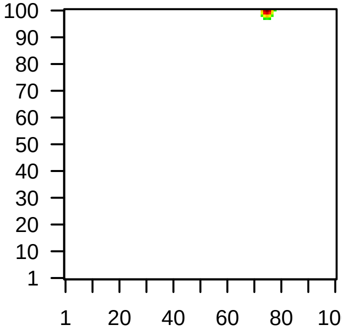
<r> metagenes = 0.97
<r> genes = 0.34
beta: r2= 27.07 / log p= −Inf

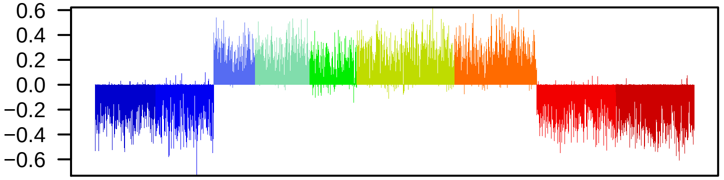
samples with spot = 948 (28 %)
A C F * : 118 (50.2 %)
A F * : 170 (55.2 %)
C F * : 92 (34.7 %)
F * : 303 (54.6 %)
F J * : 265 (57.2 %)

Overview Map



Spot





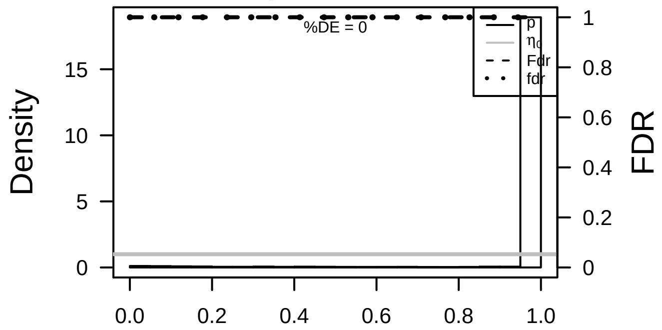
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_175063	2.47	−2.69	0.92		
2	ILMN_218086	2.33	−2.64	0.91		ribosomal protein S26 pseudogene 11 [Source:HGNC Symbo
3	ILMN_172664	2.23	−2.64	0.91		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
4	ILMN_324883	2.2	−2.25	0.93		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
5	ILMN_231070	2.2	−2.41	0.92		
6	ILMN_320919	2.15	−2.18	0.92	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
7	ILMN_167852	2.13	−2.24	0.92		
8	ILMN_220902	2.12	−2.29	0.92	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
9	ILMN_169558	2.09	−2.34	0.91	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_329699	2.07	−2.21	0.94		
11	ILMN_329001	2.01	−1.81	0.91		ribosomal protein S26 pseudogene 2 [Source:HGNC Symbol
12	ILMN_167769	2.01	−2.28	0.94		ribosomal protein S26 pseudogene 35 [Source:HGNC Symbo
13	ILMN_328515	1.94	−2.25	0.94	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
14	ILMN_324228	1.92	−2.21	0.94	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
15	ILMN_325449	1.92	−1.96	0.92		ribosomal protein S26 pseudogene 55 [Source:HGNC Symbo
16	ILMN_329995	1.62	−2.05	0.9	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
17	ILMN_173799	1.42	−0.99	0.9		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
18	ILMN_329151	1.39	−1.4	0.93		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
19	ILMN_165795	1.29	−0.97	0.92		
20	ILMN_323667	1.29	−0.96	0.9		ribosomal protein S26 pseudogene 13 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−10	9 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
2	2e−05	11 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	9e−05	11 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
4	5e−04	2 / 12	CC	small ribosomal subunit
5	6e−04	3 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	6e−04	3 / 58	GSEA	KEGG_RIBOSOME
7	9e−04	3 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
8	1e−03	3 / 68	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
9	1e−03	3 / 69	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
10	1e−03	3 / 74	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
11	1e−03	3 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
12	2e−03	3 / 81	BP	viral transcription
13	2e−03	3 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	3e−03	3 / 96	BP	translational initiation
15	3e−03	2 / 28	CC	cytosolic small ribosomal subunit
16	3e−03	2 / 28	GSEA	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
17	3e−03	3 / 99	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
18	3e−03	3 / 101	GSEA	REACTOME_TRANSLATION
19	4e−03	3 / 110	GSEA	PECE_MAMMARY_STEM_CELL_UP
20	5e−03	2 / 35	GSEA	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_
21	1e−02	3 / 155	GSEA	REACTOME_METABOLISM_OF_MRNA
22	1e−02	2 / 56	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
23	1e−02	3 / 163	BP	rRNA processing
24	1e−02	2 / 58	GSEA	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2
25	1e−02	3 / 169	MF	structural constituent of ribosome
26	2e−02	3 / 184	BP	translation
27	2e−02	1 / 6	GSEA	MCBRYAN_TERMINAL_END_BUD_DN
28	2e−02	1 / 6	GSEA	MIKKELSEN_ES_LCP_WITH_H3K4ME3_AND_H3K27ME3
29	2e−02	3 / 196	GSEA	REACTOME_METABOLISM_OF_RNA
30	2e−02	1 / 7	GSEA	FARDIN_HYPOXIA_9
31	3e−02	1 / 9	GSEA	MIKKELSEN_IPS_LCP_WITH_H3K27ME3
32	3e−02	9 / 1492	Chr	Chr 2
33	3e−02	1 / 10	BP	fructose metabolic process
34	3e−02	1 / 10	MF	inositol−1,4,5−trisphosphate 3−kinase activity
35	3e−02	1 / 10	GSEA	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP
36	3e−02	1 / 11	BP	glycoprotein metabolic process
37	3e−02	1 / 11	BP	intra−S DNA damage checkpoint
38	3e−02	1 / 11	GSEA	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
39	3e−02	1 / 12	BP	synaptic vesicle fusion to presynaptic active zone membrane
40	4e−02	1 / 13	BP	proteoglycan biosynthetic process

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	9e−04	3 / 65	SRP−dependent cotranslational protein targeting to membrane
2	2e−03	3 / 81	viral transcription
3	2e−03	3 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
4	3e−03	3 / 96	translational initiation
5	1e−02	3 / 163	rRNA processing
6	2e−02	3 / 184	translation
7	3e−02	1 / 10	fructose metabolic process
8	3e−02	1 / 11	glycoprotein metabolic process
9	3e−02	1 / 11	intra−S DNA damage checkpoint
10	3e−02	1 / 12	synaptic vesicle fusion to presynaptic active zone membrane
11	4e−02	1 / 13	proteoglycan biosynthetic process
12	4e−02	1 / 14	glutamine metabolic process
13	4e−02	1 / 14	ribosomal small subunit biogenesis
14	4e−02	1 / 15	translational elongation
15	5e−02	1 / 17	sulfur compound metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.4	3 / 818	Mid_Frontal_Lobe_Het
2	0.6	1 / 328	Fetal_Het
3	0.7	1 / 386	Fetal_ZNF
4	0.8	1 / 578	Fetal_Tx
5	0.9	4 / 2127	Mid_Frontal_Lobe_K9K27me3
6	0.9	5 / 2654	Fetal_Quies
7	0.9	1 / 796	Overlap_fetal_midbrain_ZNF
8	0.9	1 / 906	Fetal_HetRpts
9	0.9	1 / 1012	Mid_Frontal_Lobe_Enh
10	1.0	4 / 2630	Fetal_TssF
11	1.0	2 / 1728	Fetal_ReprPCWk
12	1.0	1 / 1213	Fetal_TssP
13	1.0	1 / 1436	Fetal_K9K27me3
14	1.0	3 / 2709	Mid_Frontal_Lobe_HetRpts
15	1.0	1 / 1506	Mid_Frontal_Lobe_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	1 / 13	WANG_ER_DN
2	0.05	1 / 16	GENTLES_modul7
3	0.10	1 / 38	KUIPER_MM good survival
4	0.19	1 / 73	SHAUGHNESSY_MM high risk
5	0.40	1 / 178	SPANG_LPS−index2
6	0.79	1 / 527	Lembcke_Normal vs Adenoma
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 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	5e−04	2 / 12	small ribosomal subunit
2	3e−03	2 / 28	cytosolic small ribosomal subunit
3	7e−02	1 / 25	preribosome, large subunit precursor
4	1e−01	1 / 45	cytosolic large ribosomal subunit
5	1e−01	1 / 46	intermediate filament cytoskeleton
6	1e−01	1 / 50	SNARE complex
7	2e−01	1 / 68	Golgi cisterna membrane
8	2e−01	1 / 83	synaptic vesicle
9	3e−01	1 / 107	spindle
10	3e−01	1 / 133	microtubule organizing center
11	3e−01	1 / 134	myelin sheath
12	4e−01	1 / 173	nuclear chromatin
13	5e−01	2 / 561	intracellular membrane−bounded organelle
14	6e−01	1 / 295	cell−cell adherens junction
15	6e−01	1 / 330	cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.03	9 / 1492	Chr 2
2	0.07	5 / 769	Chr 15
3	0.12	6 / 1170	Chr 7
4	0.12	3 / 422	Chr 13
5	0.18	6 / 1318	Chr 17
6	0.22	9 / 2323	Chr 1
7	0.43	4 / 1160	Chr 12
8	0.44	3 / 836	Chr 8
9	0.49	3 / 902	Chr 4
10	0.53	3 / 959	Chr 16
11	0.63	1 / 342	Chr 18
12	0.69	3 / 1217	Chr 3
13	0.74	2 / 904	Chr 10
14	0.77	2 / 954	Chr 9
15	0.87	2 / 1211	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.3	5 / 1206	6_EnhG_Neuronal_Progenitor
2	0.3	2 / 416	4_TxTrans_Neuronal_Progenitor
3	0.8	4 / 2028	4_TxTrans_Melanocytes
4	0.9	1 / 717	11_K9K27me3_Fibroblasts
5	1.0	5 / 3450	4_TxTrans_Fibroblasts
6	1.0	4 / 3068	8_EnhP_Fibroblasts
7	1.0	2 / 2315	13_HetRpts_Melanocytes
8	1.0	2 / 2660	8_EnhP_Melanocytes
9	1.0	3 / 3272	13_HetRpts_Neuronal_Progenitor
10	1.0	2 / 2682	12_Het_Neuronal_Progenitor
11	1.0	1 / 2031	12_Het_Melanocytes
12	1.0	4 / 4107	9_ReprPCWk_Fibroblasts
13	1.0	3 / 3639	1_TssP_Fibroblasts
14	1.0	7 / 5956	3_TssF_Neuronal_Progenitor
15	1.0	6 / 5699	6_EnhG_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	11 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	9e−05	11 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	2e−01	1 / 88	Pentrack_CRC_TCGA_corr_S_normal_DN
4	5e−01	1 / 217	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
5	6e−01	1 / 278	Kosinski_top−crypt−long−list
6	7e−01	1 / 366	K9K27me3_Colon
7	8e−01	4 / 1895	EnhP_Colon
8	8e−01	2 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	8e−01	1 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	9e−01	1 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	9e−01	1 / 789	TxEnhG2_Colon
12	9e−01	2 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	9e−01	3 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e+00	1 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	1e+00	1 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_

Glio

Rank	p−value	#in/all	Geneset
1	0.04	1 / 14	astrocytes_glio
2	0.17	1 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
3	0.22	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
4	0.60	1 / 315	Up
5	0.69	1 / 401	Down_b
6	0.69	2 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	0.99	1 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
8	1.00	1 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
9	1.00	0 / 15	VERHAAK_CL subtype
10	1.00	0 / 15	VERHAAK_MES subtype
11	1.00	0 / 15	VERHAAK_NL subtype
12	1.00	0 / 15	VERHAAK_PN subtype
13	1.00	0 / 35	WIRTH_PN subtype
14	1.00	0 / 104	WIRTH_Normal Brain
15	1.00	0 / 11	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
2	6e−04	3 / 58	KEGG_RIBOSOME
3	1e−03	3 / 68	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
4	1e−03	3 / 69	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
5	1e−03	3 / 74	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
6	1e−03	3 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
7	3e−03	2 / 28	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSE
8	3e−03	3 / 99	REACTOME_INFLUENZA_LIFE_CYCLE
9	3e−03	3 / 101	REACTOME_TRANSLATION
10	4e−03	3 / 110	PECE_MAMMARY_STEM_CELL_UP
11	5e−03	2 / 35	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_C
12	1e−02	3 / 155	REACTOME_METABOLISM_OF_MRNA
13	1e−02	2 / 56	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
14	1e−02	2 / 58	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2
15	2e−02	1 / 6	MCBRYAN_TERMINAL_END_BUD_DN

HM

Rank	p−value	#in/all	Geneset
1	0.2	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
2	0.4	1 / 173	HALLMARK_E2F_TARGETS
3	0.4	1 / 185	HALLMARK_MTORC1_SIGNALING
4	0.4	1 / 185	HALLMARK_P53_PATHWAY
5	0.4	1 / 189	HALLMARK_HYPOXIA
6	1.0	0 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	1.0	0 / 177	HALLMARK_MITOTIC_SPINDLE
8	1.0	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1.0	0 / 50	HALLMARK_TGF_BETA_SIGNALING
10	1.0	0 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	1.0	0 / 130	HALLMARK_DNA_REPAIR
12	1.0	0 / 179	HALLMARK_G2M_CHECKPOINT
13	1.0	0 / 151	HALLMARK_APOPTOSIS
14	1.0	0 / 29	HALLMARK_NOTCH_SIGNALING
15	1.0	0 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	1 / 32	Marjolein_ageing−genes_DN
2	1.00	0 / 94	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 17	DUMEAUX_High bmi enriched genes
12	1.00	0 / 31	DUMEAUX_Fasting enriched genes
13	1.00	0 / 147	Homuth_BMI−associated−genes_UP
14	1.00	0 / 211	Homuth_BMI−associated−genes_DN
15	1.00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.07	1 / 25	SPANG_BAFF 9hrs UP
2	0.13	16 / 4167	HOPP_Heterochrom
3	0.25	2 / 331	SPANG_CD40 6hrs UP
4	0.37	1 / 158	WIRTH_lymphoma937_spot C
5	0.37	1 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
6	0.47	1 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
7	0.49	1 / 232	WIRTH_lymphoma937_spot B
8	0.55	1 / 272	SPANG_IL21 DN
9	0.66	2 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
10	0.66	2 / 777	WIRTH_lymphoma937_spot D
11	0.70	1 / 408	TARTE_Mature plasma cell signature
12	0.98	1 / 1270	SPANG_BCR UP
13	0.99	3 / 2701	HOPP_Repetitive
14	0.99	11 / 6559	HOPP_Weak_txn
15	1.00	6 / 5356	HOPP_Txn_transition

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	0.01	3 / 169	structural constituent of ribosome
2	0.03	1 / 10	inositol−1,4,5−trisphosphate 3−kinase activity
3	0.06	1 / 22	protein kinase activator activity
4	0.08	1 / 28	NAD binding
5	0.10	1 / 37	SNAP receptor activity
6	0.12	1 / 45	cytoskeletal protein binding
7	0.14	1 / 52	SNARE binding
8	0.20	1 / 77	electron carrier activity
9	0.25	1 / 99	mRNA binding
10	0.45	1 / 204	protein domain specific binding
11	0.54	1 / 265	cadherin binding involved in cell−cell adhesion
12	0.64	1 / 350	protein kinase binding
13	0.80	2 / 1013	poly(A) RNA binding
14	0.98	1 / 1329	ATP binding
15	1.00	7 / 8818	protein binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 20	Parkinson disease
2	0.06	1 / 22	Pigmented adrenocortical disease, primary isolated
3	0.08	1 / 27	Duchenne muscular dystrophy
4	0.08	1 / 28	Miyoshi myopathy
5	0.08	1 / 29	Myelofibrosis, idiopathic
6	0.11	1 / 40	Muscular dystrophy
7	0.13	1 / 47	Cervical cancer, somatic
8	0.13	1 / 48	Multiple myeloma
9	0.15	1 / 56	Myopathy, nemaline, 3
10	0.15	1 / 57	Cardiomyopathy, dilated
11	0.17	1 / 65	Hepatocellular carcinoma
12	0.18	1 / 68	Glioblastoma multiforme, somatic
13	0.19	1 / 73	Stroke, susceptibility to
14	0.20	1 / 76	Muscular
15	0.24	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	1 / 85	hsa−miR−510
2	0.2	1 / 87	hsa−miR−299−3p
3	0.2	1 / 98	hsa−miR−653
4	0.3	1 / 100	hsa−miR−613
5	0.3	1 / 135	hsa−miR−576−3p
6	0.3	1 / 148	hsa−miR−409−3p
7	0.4	1 / 152	hsa−miR−583
8	0.4	1 / 180	hsa−miR−1
9	0.4	1 / 196	hsa−miR−206
10	0.5	1 / 274	hsa−miR−1244
11	0.6	1 / 287	hsa−miR−548j
12	0.6	1 / 289	hsa−miR−202
13	0.6	1 / 303	hsa−miR−548i
14	0.6	1 / 317	hsa−miR−559
15	1.0	0 / 419	hsa−miR−497

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	2e−10	9 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	5e−02	2 / 119	Chaussabel_2,4_Ribosomal proteins
3	4e−01	2 / 478	WIRTH_Nervous System
4	7e−01	1 / 416	PROTEINATLAS_ovary
5	7e−01	1 / 465	PROTEINATLAS_liver
6	8e−01	1 / 514	PROTEINATLAS_vagina
7	8e−01	1 / 598	PROTEINATLAS_prostate
8	8e−01	1 / 619	PROTEINATLAS_salivary gland
9	8e−01	1 / 623	PROTEINATLAS_seminal vesicle
10	8e−01	1 / 639	PROTEINATLAS_breast
11	8e−01	1 / 647	PROTEINATLAS_lateral ventricle
12	9e−01	1 / 650	PROTEINATLAS_hippocampus
13	9e−01	1 / 724	PROTEINATLAS_lymph node
14	9e−01	1 / 726	PROTEINATLAS_cervix, uterine
15	9e−01	1 / 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	0.5	4 / 1231	KIM_MYC targets
2	0.6	2 / 721	ICGC_SrfPcr2_targets
3	0.6	2 / 733	ICGC_Atf3_targets
4	0.8	15 / 5961	ICGC_Pol24_targets
5	0.8	1 / 631	ICGC_RxraPcr1_targets
6	0.9	5 / 2497	ICGC_Bcl11_targets
7	0.9	3 / 1669	ICGC_P300_targets
8	0.9	1 / 747	ICGC_NrsfPcr2_targets
9	0.9	4 / 2255	ICGC_SrfV0416101_targets
10	0.9	2 / 1452	ICGC_Six5_targets
11	0.9	14 / 6552	ICGC_Pol2_targets
12	1.0	4 / 2704	ICGC_Pbx3_targets
13	1.0	13 / 6578	ICGC_Pou2_targets
14	1.0	13 / 6616	ICGC_Pax5_targets
15	1.0	12 / 6322	ICGC_Tcf3_targets

Group Overexpression Sp

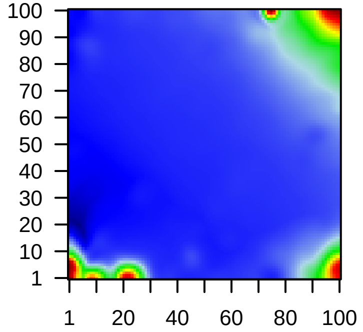
Spot Summary: C

metagenes = 168
genes = 2558

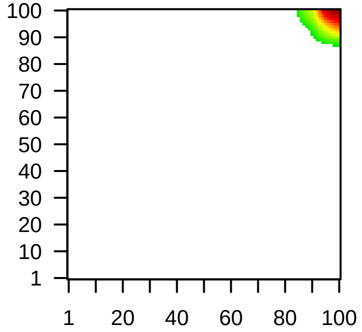
<r> metagenes = 0.84

beta: r2= 52.3 / log p= −Inf

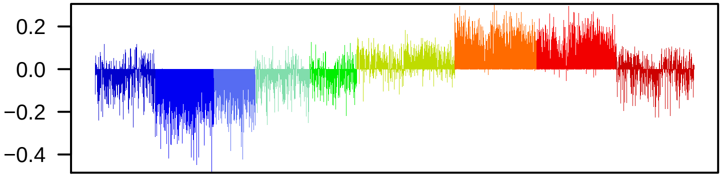
samples with spot = 170 (5 %)
F * : 1 (0.2 %)
F J * : 98 (21.2 %)
J * : 71 (15.9 %)



Overview Map



Spot

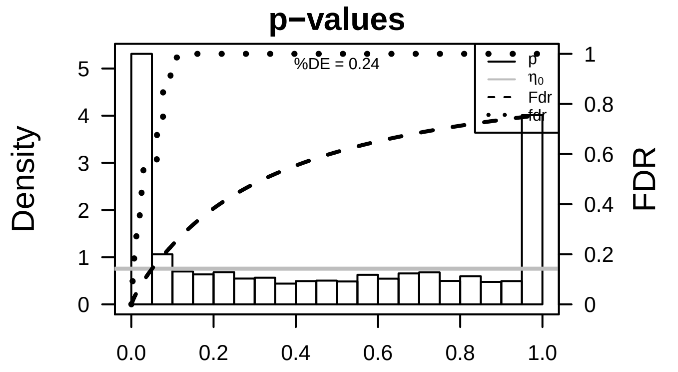


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169749	5.33	−1.74	0.04	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	ILMN_171516	4.62	−2.25	0.05		
3	ILMN_206606	2.72	−3.26	0.08	HLA−DRB6	major histocompatibility complex, class II, DR beta 6 (pseudo
4	ILMN_210544	2.45	−1.45	0.3	JCHAIN	joining chain of multimeric IgA and IgM [Source:HGNC Symb
5	ILMN_239376	2.36	−2.48	0.26	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
6	ILMN_165219	2.24	−1.63	0.26		
7	ILMN_173950	2.08	−1.34	0.29		
8	ILMN_324037	2.04	−1.35	0.35		immunoglobulin kappa variable 1D−17 [Source:HGNC Symbo
9	ILMN_173123	1.91	−2.04	0.13	GZMH	granzyme H [Source:HGNC Symbol;Acc:HGNC:4710]
10	ILMN_324966	1.89	−1.85	0.35		
11	ILMN_169921	1.89	−1.18	0.28		
12	ILMN_174314	1.89	−2.07	0.13	ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Syn
13	ILMN_178810	1.79	−0.92	0.36		BLOC1S5−TXNDC5 readthrough (NMD candidate) [Source:H
14	ILMN_177365	1.78	−1.17	0.37	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
15	ILMN_169107	1.77	−1.46	0.43	FCRLA	Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]
16	ILMN_177245	1.73	−2.05	0.37	RPS23	ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10
17	ILMN_168027	1.73	−0.94	0.31		immunoglobulin kappa variable 1−33 [Source:HGNC Symbol;
18	ILMN_240485	1.7	−1.35	0.29	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10
19	ILMN_181589	1.69	−2.79	0.14		
20	ILMN_180840	1.68	−1.68	0.38	HLA−DQA1	major histocompatibility complex, class II, DQ alpha 1 [Source

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	1254 / 8226	Lympl	HOPP_Active_promoter
2	1e−99	1208 / 7275	Lympl	HOPP_Txn_elongation
3	1e−99	1003 / 5356	Lympl	HOPP_Txn_transition
4	1e−99	1139 / 8098	Lympl	HOPP_Weak_promoter
5	1e−99	1362 / 9555	Colon	TssA_Colon
6	1e−99	1270 / 9054	Colon	Tx_Colon
7	1e−99	1221 / 8568	Colon	TxWk_Colon
8	1e−99	1349 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
9	1e−99	931 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
10	1e−99	405 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
11	3e−99	1427 / 11455	Chror	2_TssA_Fibroblasts
12	1e−98	1196 / 8771	Chror	5_Tx_Melanocytes
13	2e−98	1187 / 8678	Colon	Quies3_Colon
14	4e−96	1487 / 12298	Chror	2_TssA_Melanocytes
15	4e−92	389 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
16	3e−91	1010 / 6970	Chror	5_Tx_Neuronal_Progenitor
17	3e−89	1239 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
18	2e−86	1360 / 10999	Colon	TssWk_Colon
19	2e−84	412 / 1797	GSEA	PILON_KLF1_TARGETS_DN
20	6e−83	232 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
21	2e−81	1070 / 7854	Chror	5_Tx_Fibroblasts
22	8e−80	327 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	8e−79	286 / 1013	MF	poly(A) RNA binding
24	9e−76	1493 / 12983	Chror	2_TssA_Neuronal_Progenitor
25	6e−64	276 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
26	8e−62	231 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
27	6e−61	99 / 170	HM	HALLMARK_MYC_TARGETS_V1
28	4e−57	285 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
29	2e−54	221 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
30	3e−53	1339 / 11836	Chror	3_TssF_Melanocytes
31	2e−52	251 / 1063	Refer	PROTEINATLAS_tonsil
32	5e−52	1075 / 8818	MF	protein binding
33	6e−52	949 / 7448	Lympl	HOPP_Strong_enhancer
34	6e−51	197 / 724	Refer	PROTEINATLAS_lymph node
35	6e−51	199 / 737	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
36	2e−47	120 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
37	8e−47	263 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
38	3e−46	1153 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
39	4e−45	156 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
40	1e−44	1192 / 10430	Brain	Overlap_fetal_midbrain_Quies



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.003	19 / 111	HORVATH_aging_genes meth DOWN
2	0.682	11 / 142	HORVATH_aging_genes meth UP
3	0.965	2 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	9e−15	6 / 13	RHODES_CANCER_META_SIGNATURE
2	6e−09	17 / 39	ZHANG_MM up
3	1e−07	10 / 16	GENTLES_modul11
4	2e−06	9 / 16	GENTLES_modul7
5	1e−05	49 / 301	SPANG_BCL6−index2
6	4e−05	7 / 13	GENTLES_modul6
7	7e−05	7 / 14	GENTLES_modul1
8	4e−04	6 / 13	GENTLES_modul18
9	1e−03	6 / 15	WOLFER_overlap genes
10	3e−03	2 / 14	RHODES_UNDIFFERENTIATED_CANCER
11	3e−03	5 / 13	GENTLES_modul12
12	4e−03	9 / 38	KUIPER_MM good survival
13	7e−03	5 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	9e−03	4 / 12	LIU_BREAST_CANCER
15	9e−03	5 / 16	GENTLES_modul16

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−99	1427 / 11455	2_TssA_Fibroblasts
2	1e−98	1196 / 8771	5_Tx_Melanocytes
3	4e−96	1487 / 12298	2_TssA_Melanocytes
4	3e−91	1010 / 6970	5_Tx_Neuronal_Progenitor
5	2e−81	1070 / 7854	5_Tx_Fibroblasts
6	9e−76	1493 / 12983	2_TssA_Neuronal_Progenitor
7	3e−53	1339 / 11836	3_TssF_Melanocytes
8	2e−39	1047 / 8990	15_Quies_Fibroblasts
9	1e−36	730 / 5699	6_EnhG_Melanocytes
10	3e−36	1327 / 12393	15_Quies_Neuronal_Progenitor
11	8e−30	1330 / 12741	7_Enh_Melanocytes
12	5e−27	1183 / 11130	15_Quies_Melanocytes
13	1e−20	932 / 8613	7_Enh_Fibroblasts
14	1e−18	1012 / 9635	3_TssF_Fibroblasts
15	2e−10	470 / 4237	14_ZNF_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	405 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	2e−84	412 / 1797	PILON_KLF1_TARGETS_DN
3	6e−83	232 / 669	PUJANA_CHEK2_PCC_NETWORK
4	8e−80	327 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	6e−64	276 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
6	4e−57	285 / 1241	PUJANA_ATM_PCC_NETWORK
7	2e−54	221 / 841	ACEVEDO_LIVER_CANCER_UP
8	6e−51	199 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
9	2e−47	120 / 317	HSIAO_HOUSEKEEPING_GENES
10	8e−47	263 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	4e−45	156 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
12	2e−44	250 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	3e−44	116 / 316	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
14	2e−43	198 / 811	LEE_BMP2_TARGETS_DN
15	3e−39	142 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	1254 / 8226	HOPP_Active_promoter
2	1e−99	1208 / 7275	HOPP_Txn_elongation
3	1e−99	1003 / 5356	HOPP_Txn_transition
4	1e−99	1139 / 8098	HOPP_Weak_promoter
5	6e−52	949 / 7448	HOPP_Strong_enhancer
6	2e−30	826 / 6959	HOPP_Weak_enhancer
7	2e−29	785 / 6559	HOPP_Weak_txn
8	1e−22	202 / 1169	SPANG_BCR DN
9	4e−14	66 / 283	TARTE_Plasmablast signature
10	5e−13	127 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
11	2e−12	126 / 777	WIRTH_lymphoma937_spot D
12	4e−12	181 / 1270	SPANG_BCR UP
13	4e−12	32 / 94	Sha_BL UP
14	4e−12	40 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
15	6e−12	40 / 141	WIRTH_lymphoma937_spot F

miRNA Disease

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−52	251 / 1063	PROTEINATLAS_tonsil
2	6e−51	197 / 724	PROTEINATLAS_lymph node
3	5e−43	73 / 132	Chaussabel_1,7_MHC Ribosomal proteins
4	3e−41	130 / 412	WIRTH_Immune system
5	3e−40	67 / 119	Chaussabel_2,4_Ribosomal proteins
6	3e−40	252 / 1239	PROTEINATLAS_testis
7	3e−39	208 / 933	PROTEINATLAS_adrenal gland
8	8e−38	215 / 1003	PROTEINATLAS_appendix
9	7e−37	64 / 119	Chaussabel_2,8_T−cells
10	1e−35	236 / 1194	PROTEINATLAS_stomach
11	4e−35	197 / 912	PROTEINATLAS_urinary bladder
12	2e−34	182 / 816	PROTEINATLAS_endometrium
13	7e−34	100 / 302	Chaussabel_3,4_Protein phosphatases
14	1e−33	228 / 1167	PROTEINATLAS_gallbladder
15	7e−33	220 / 1118	PROTEINATLAS_placenta

BP

Rank	p−value	#in/all	Geneset
1	4e−25	47 / 96	translational initiation
2	8e−24	42 / 81	viral transcription
3	4e−23	37 / 65	SRP−dependent cotranslational protein targeting to membrane
4	1e−22	59 / 163	rRNA processing
5	3e−21	41 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
6	3e−18	69 / 255	viral process
7	6e−17	55 / 184	translation
8	1e−15	55 / 196	mRNA splicing, via spliceosome
9	1e−13	40 / 126	T cell receptor signaling pathway
10	3e−12	58 / 254	cell−cell adhesion
11	2e−11	39 / 139	RNA splicing
12	1e−09	16 / 32	tRNA aminoacylation for protein translation
13	1e−09	27 / 86	mRNA export from nucleus
14	3e−08	11 / 18	cytoplasmic translation
15	4e−08	9 / 12	maturation of LSU−rRNA

CC

Rank	p−value	#in/all	Geneset
1	1e−38	406 / 2535	nucleoplasm
2	2e−32	325 / 1979	membrane
3	8e−32	435 / 2979	cytosol
4	2e−30	161 / 721	nucleolus
5	4e−29	616 / 4828	nucleus
6	3e−25	225 / 1304	mitochondrion
7	3e−25	600 / 4822	cytoplasm
8	2e−20	341 / 2464	extracellular exosome
9	5e−16	83 / 374	mitochondrial inner membrane
10	2e−11	21 / 45	cytosolic large ribosomal subunit
11	3e−11	62 / 295	cell−cell adherens junction
12	3e−11	21 / 46	ribosome
13	3e−11	32 / 101	intracellular ribonucleoprotein complex
14	1e−10	27 / 78	catalytic step 2 spliceosome
15	4e−10	36 / 134	myelin sheath

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	1362 / 9555	TssA_Colon
2	1e−99	1270 / 9054	Tx_Colon
3	1e−99	1221 / 8568	TxWk_Colon
4	2e−98	1187 / 8678	Quies3_Colon
5	4e−92	389 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
6	2e−86	1360 / 10999	TssWk_Colon
7	8e−62	231 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	1e−41	217 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
9	2e−35	883 / 7354	TssF_Colon
10	1e−26	319 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
11	6e−24	211 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	9e−20	499 / 4034	TssD1_Colon
13	1e−18	225 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	3e−14	1085 / 10779	Enh_Colon
15	1e−13	597 / 5373	EnhWk1_Colon

HM

Rank	p−value	#in/all	Geneset
1	6e−61	99 / 170	HALLMARK_MYC_TARGETS_V1
2	6e−17	52 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	4e−13	35 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	7e−12	47 / 185	HALLMARK_MTORC1_SIGNALING
5	1e−10	43 / 173	HALLMARK_E2F_TARGETS
6	8e−09	38 / 162	HALLMARK_ALLOGRAFT_REJECTION
7	7e−06	16 / 54	HALLMARK_MYC_TARGETS_V2
8	8e−06	35 / 186	HALLMARK_IL2_STAT5_SIGNALING
9	5e−05	32 / 179	HALLMARK_G2M_CHECKPOINT
10	9e−05	31 / 176	HALLMARK_ADIPOGENESIS
11	1e−04	25 / 130	HALLMARK_DNA_REPAIR
12	1e−04	19 / 87	HALLMARK_PROTEIN_SECRETION
13	3e−04	25 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	5e−03	27 / 187	HALLMARK_COMPLEMENT
15	1e−02	20 / 137	HALLMARK_UV_RESPONSE_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.6	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	0.7	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.9	1 / 27	Hugo_melanoma−all−LEF1_UP
4	0.9	1 / 30	Hugo_melanoma−all−MET_UP
5	1.0	0 / 54	Hugo_melanoma−all−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	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−21	81 / 295	hsa−miR−561
2	4e−21	110 / 493	hsa−miR−103
3	1e−20	109 / 491	hsa−miR−107
4	1e−20	80 / 299	hsa−miR−548c−3p
5	5e−20	85 / 338	hsa−miR−548d−5p
6	5e−20	85 / 338	hsa−miR−548b−5p
7	3e−19	81 / 321	hsa−miR−590−3p
8	3e−18	58 / 190	hsa−miR−330−3p
9	4e−18	77 / 307	hsa−miR−548c−5p
10	4e−18	95 / 429	hsa−miR−548n
11	7e−18	78 / 317	hsa−miR−559
12	8e−17	77 / 323	hsa−miR−548a−5p
13	9e−17	97 / 463	hsa−miR−301a
14	4e−16	68 / 272	hsa−miR−577
15	6e−16	90 / 425	hsa−let−7b

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	2 / 13	Alternative lengthening of telomeres
2	0.4	3 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−99	1349 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−99	931 / 5936	Overlap_fetal_midbrain_HetRpts
3	3e−89	1239 / 9504	Overlap_fetal_midbrain_K9K27me3
4	3e−46	1153 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	1e−44	1192 / 10430	Overlap_fetal_midbrain_Quies
6	1e−18	145 / 796	Overlap_fetal_midbrain_ZNF
7	2e−09	42 / 180	Overlap_fetal_midbrain_Het
8	2e−08	67 / 386	Fetal_ZNF
9	6e−07	121 / 906	Fetal_HetRpts
10	3e−06	54 / 328	Fetal_Het
11	2e−05	141 / 1171	Fetal_EnhP
12	3e−04	323 / 3164	Mid_Frontal_Lobe_ZNF
13	7e−03	102 / 937	Fetal_EnhG
14	3e−02	118 / 1162	Fetal_Enh
15	3e−01	62 / 681	Overlap_fetal_midbrain_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	132 / 1160	Chr 12
2	5e−04	122 / 1060	Chr 5
3	1e−03	55 / 422	Chr 13
4	2e−03	103 / 902	Chr 4
5	1e−02	127 / 1211	Chr 6
6	1e−02	127 / 1217	Chr 3
7	4e−02	147 / 1492	Chr 2
8	2e−01	86 / 904	Chr 10
9	3e−01	207 / 2323	Chr 1
10	4e−01	31 / 342	Chr 18
11	4e−01	26 / 289	Chr 21
12	4e−01	102 / 1170	Chr 7
13	5e−01	86 / 994	Chr X
14	6e−01	71 / 836	Chr 8
15	6e−01	64 / 768	Chr 14

Glio

Rank	p−value	#in/all	Geneset
1	1e−26	285 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	5e−23	304 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−12	68 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	8e−09	59 / 315	Up
5	4e−07	18 / 55	Stuehler_Proteins_up_in_STS
6	5e−07	112 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	8e−05	5 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
8	2e−04	28 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
9	2e−04	56 / 401	Down_b
10	5e−03	8 / 32	Donson−Misc immune function−associated with LTS in HGA
11	5e−03	4 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
12	9e−03	12 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
13	2e−02	6 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
14	2e−02	3 / 7	Donson−adaptive−immunity−associated with LTS in HGA
15	2e−02	9 / 48	Vishal_subnetwork signature of survival in GBM

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−19	24 / 32	Marjolein_ageing−genes_DN
2	7e−08	34 / 147	Homuth_BMI−associated−genes_UP
3	1e−07	8 / 10	Marjolein_ageing−genes_UP
4	1e−03	32 / 211	Homuth_BMI−associated−genes_DN
5	1e−03	6 / 16	Huan_blood−pressure_DBP−signature
6	2e−03	6 / 17	DUMEAUX_High bmi enriched genes
7	7e−03	4 / 10	DUMEAUX_Women normal BMI literature genes up
8	2e−02	5 / 18	Huan_blood−pressure_SBP−signature
9	1e−01	5 / 31	DUMEAUX_Fasting enriched genes
10	4e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	4e−01	1 / 5	Huan_blood−pressure_HTN−signature
12	4e−01	2 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	6e−01	1 / 10	DUMEAUX_Smoking literature genes up
14	7e−01	7 / 94	DUMEAUX_Smoking enriched genes
15	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes

MF

Rank	p−value	#in/all	Geneset
1	8e−79	286 / 1013	poly(A) RNA binding
2	5e−52	1075 / 8818	protein binding
3	4e−18	54 / 169	structural constituent of ribosome
4	3e−17	89 / 399	RNA binding
5	2e−13	62 / 265	cadherin binding involved in cell−cell adhesion
6	3e−09	56 / 283	nucleotide binding
7	3e−07	15 / 39	translation initiation factor activity
8	1e−06	22 / 82	unfolded protein binding
9	4e−06	161 / 1329	ATP binding
10	5e−06	8 / 14	MHC class II protein complex binding
11	2e−05	80 / 580	identical protein binding
12	2e−05	43 / 256	ubiquitin protein ligase binding
13	7e−05	52 / 351	GTP binding
14	9e−05	12 / 40	receptor tyrosine kinase binding
15	9e−05	8 / 19	nucleocytoplasmic transporter activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.002	5 / 12	BENTINK_src.2
2	0.003	5 / 13	BENTINK_myc.1
3	0.027	4 / 14	BENTINK_ras.6
4	0.094	3 / 13	BENTINK_e2f3.1
5	0.275	2 / 12	BENTINK_ras.1
6	0.308	2 / 13	BENTINK_e2f3.2
7	0.373	2 / 15	GUSTAFSON_PI3K_DN
8	0.627	1 / 11	BENTINK_ras.4
9	0.715	1 / 14	GUSTAFSON_PI3K_UP
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−44	259 / 1231	KIM_MYC targets
2	1e−43	691 / 5067	ICGC_Taf1_targets
3	2e−33	267 / 1478	ICGC_Myc_targets
4	3e−31	687 / 5466	ICGC_Nficsc81335_targets
5	2e−30	289 / 1723	HEBENSTREIT_high expression TF
6	9e−29	620 / 4881	ICGC_Atf2_targets
7	1e−27	678 / 5518	ICGC_Stat5_targets
8	2e−27	670 / 5442	ICGC_Pmlsc71910_targets
9	8e−26	557 / 4362	ICGC_Creb1_targets
10	2e−25	608 / 4890	ICGC_Bclaf101388_targets
11	1e−23	761 / 6578	ICGC_Pou2_targets
12	2e−23	310 / 2087	ICGC_Cebpbsc150_targets
13	1e−22	646 / 5410	ICGC_Foxm1_targets
14	4e−22	634 / 5312	ICGC_Tcf12_targets
15	3e−21	237 / 1498	ICGC_Ets1_targets

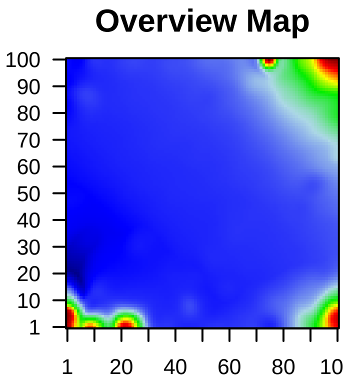
Group Overexpression Sp

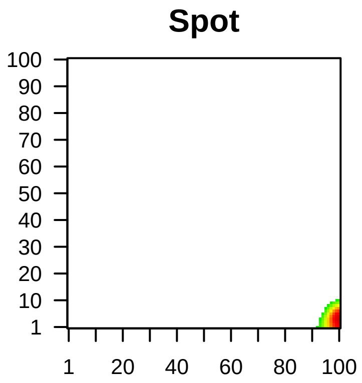
Spot Summary: D

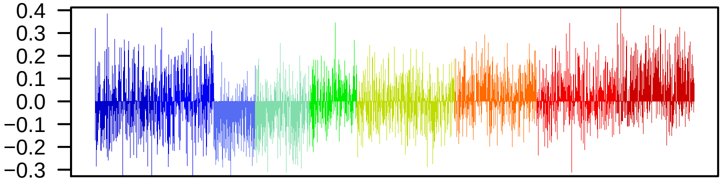
metagenes = 70
genes = 935

<r> metagenes = 0.81
<r> genes = 0.27
beta: r2= 40.61 / log p= −Inf

samples with spot = 173 (5.1 %)
A * : 19 (5.5 %)
A C * : 24 (7.3 %)
A F * : 3 (1 %)
C F * : 8 (3 %)
F * : 15 (2.7 %)
F J * : 18 (3.9 %)
J * : 23 (5.1 %)
N * : 63 (14.2 %)





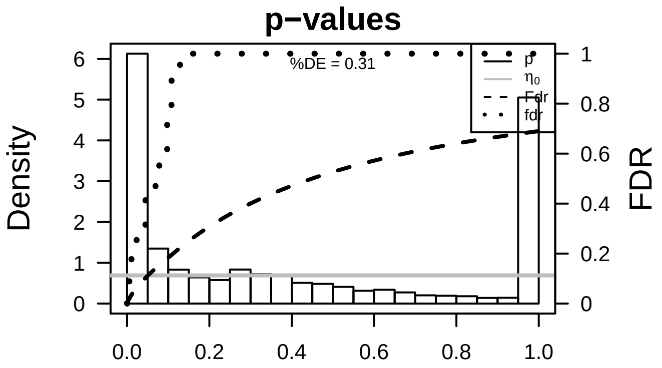


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_170769	2.95	−1.6	0.39	IFIT1	interferon induced protein with tetratricopeptide repeats 1 [So
2	ILMN_205878	2.77	−0.73	0.13	IFI27	interferon alpha inducible protein 27 [Source:HGNC Symbol;
3	ILMN_180575	2.64	−2.03	0.26	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC
4	ILMN_172391	2.52	−1.06	0.37	IFI44L	interferon induced protein 44 like [Source:HGNC Symbol;Acc
5	ILMN_170178	2.51	−1.31	0.34	IFIT3	interferon induced protein with tetratricopeptide repeats 3 [So
6	ILMN_165787	2.46	−0.83	0.39	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:
7	ILMN_181520	2.38	−5.09	0.23		
8	ILMN_205401	2.34	−1	0.13	ISG15	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:HG
9	ILMN_172974	2.3	−1.14	0.32	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase
10	ILMN_238854	2.22	−1.39	0.35	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
11	ILMN_174539	2.13	−1.15	0.4	OAS3	2'−5'−oligoadenylate synthetase 3 [Source:HGNC Symbol;Ac
12	ILMN_166235	2.12	−1.32	0.3	MX1	MX dynamin like GTPase 1 [Source:HGNC Symbol;Acc:HGN
13	ILMN_176006	2.1	−1.07	0.35	IFI44	interferon induced protein 44 [Source:HGNC Symbol;Acc:HG
14	ILMN_324640	2.08	−1.52	0.34	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HG
15	ILMN_166314	1.94	−1.51	0.11	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Sy
16	ILMN_168738	1.93	−1.08	0.26	IFI6	interferon alpha inducible protein 6 [Source:HGNC Symbol;A
17	ILMN_173942	1.91	−1.24	0.6	IFIT2	interferon induced protein with tetratricopeptide repeats 2 [So
18	ILMN_172311	1.86	−0.84	0.22	AMFR	autocrine motility factor receptor [Source:HGNC Symbol;Acc:
19	ILMN_324306	1.85	−2.53	0.25	SIGLEC14	sialic acid binding Ig like lectin 14 [Source:HGNC Symbol;Acc
20	ILMN_167481	1.79	−0.91	0.32	OASL	2'−5'−oligoadenylate synthetase like [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−88	485 / 7275	Lymp	HOPP_Txn_elongation
2	2e−85	595 / 10999	Colon	TssWk_Colon
3	1e−82	550 / 9555	Colon	TssA_Colon
4	7e−81	532 / 9054	Colon	Tx_Colon
5	6e−80	504 / 8226	Lymp	HOPP_Active_promoter
6	8e−79	476 / 7448	Lymp	HOPP_Strong_enhancer
7	1e−73	505 / 8568	Colon	TxWk_Colon
8	4e−72	387 / 5356	Lymp	HOPP_Txn_transition
9	5e−72	506 / 8678	Colon	Quies3_Colon
10	6e−68	211 / 1797	GSE	PILON_KLF1_TARGETS_DN
11	5e−66	60 / 96	Refer	Chaussabel_3,1_Interferon−inducible
12	9e−61	570 / 11455	Chror	2_TssA_Fibroblasts
13	1e−56	586 / 12298	Chror	2_TssA_Melanocytes
14	1e−55	513 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
15	1e−55	480 / 8771	Chror	5_Tx_Melanocytes
16	6e−55	140 / 960	GSE	NUYTTEN_EZH2_TARGETS_UP
17	1e−54	456 / 8098	Lymp	HOPP_Weak_promoter
18	3e−52	475 / 8818	MF	protein binding
19	9e−52	442 / 7854	Chror	5_Tx_Fibroblasts
20	2e−51	49 / 85	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
21	2e−51	64 / 172	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
22	2e−49	90 / 416	GSE	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
23	1e−48	559 / 11836	Chror	3_TssF_Melanocytes
24	2e−47	471 / 8990	Chror	15_Quies_Fibroblasts
25	5e−47	76 / 301	Canc	SPANG_BCL6−index2
26	3e−46	579 / 12741	Chror	7_Enh_Melanocytes
27	9e−46	361 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
28	2e−44	45 / 87	GSE	HECKER_IFNB1_TARGETS
29	4e−43	233 / 2979	CC	cytosol
30	9e−42	488 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
31	1e−41	28 / 29	GSE	MOSERLE_IFNA_RESPONSE
32	7e−40	127 / 1069	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
33	4e−39	109 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
34	1e−38	518 / 11130	Chror	15_Quies_Melanocytes
35	4e−38	35 / 58	GSE	BROWNE_INTERFERON_RESPONSIVE_GENES
36	3e−37	436 / 8613	Chror	7_Enh_Fibroblasts
37	1e−36	83 / 498	GSE	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
38	1e−36	63 / 272	Lymp	SPANG_IL21 DN
39	1e−36	298 / 4822	CC	cytoplasm
40	3e−36	92 / 622	GSE	SCHLOSSER_SERUM_RESPONSE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.06	7 / 111	HORVATH_aging_genes meth DOWN
2	0.94	2 / 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	2e−24	26 / 57	type I interferon signaling pathway
2	1e−22	37 / 153	defense response to virus
3	3e−21	30 / 102	response to virus
4	5e−15	16 / 37	negative regulation of viral genome replication
5	4e−13	40 / 335	innate immune response
6	1e−12	50 / 511	apoptotic process
7	2e−12	17 / 60	interferon−gamma−mediated signaling pathway
8	8e−12	44 / 435	negative regulation of apoptotic process
9	2e−11	25 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
10	3e−11	43 / 434	protein phosphorylation
11	2e−07	6 / 10	response to interferon−alpha
12	2e−07	10 / 38	positive regulation of autophagy
13	2e−07	9 / 30	negative regulation of type I interferon production
14	3e−07	17 / 122	positive regulation of NF−kappaB transcription factor activity
15	4e−07	13 / 74	cellular response to organic cyclic compound

Brain

Rank	p−value	#in/all	Geneset
1	1e−55	513 / 9815	Overlap_fetal_midbrain_ReprPC
2	9e−46	361 / 5936	Overlap_fetal_midbrain_HetRpts
3	9e−42	488 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	2e−34	487 / 10430	Overlap_fetal_midbrain_Quies
5	8e−27	438 / 9504	Overlap_fetal_midbrain_K9K27me3
6	3e−08	74 / 1213	Fetal_TssP
7	3e−06	66 / 1171	Fetal_EnhP
8	2e−05	139 / 3164	Mid_Frontal_Lobe_ZNF
9	4e−05	25 / 328	Fetal_Het
10	4e−04	43 / 796	Overlap_fetal_midbrain_ZNF
11	6e−04	15 / 180	Overlap_fetal_midbrain_Het
12	2e−03	55 / 1162	Fetal_Enh
13	3e−03	33 / 630	Mid_Frontal_Lobe_EnhP
14	2e−02	83 / 2127	Mid_Frontal_Lobe_K9K27me3
15	3e−02	58 / 1436	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	5e−47	76 / 301	SPANG_BCL6−index2
2	3e−28	45 / 178	SPANG_LPS−index2
3	5e−13	53 / 554	Lembcke_Colonic Inflammation
4	6e−06	6 / 16	GENTLES_modul14
5	4e−05	14 / 125	PanCan_CC+Apop_geneset_nanostring
6	3e−04	12 / 117	PanCan_Driver_Gene_geneset_nanostring
7	1e−03	9 / 82	PanCan_JAK−ST_geneset_nanostring
8	7e−03	6 / 54	KUIPER_MM poor survival
9	7e−03	3 / 13	GENTLES_modul12
10	8e−03	8 / 91	PanCan_TXmisReg_geneset_nanostring
11	1e−02	2 / 6	ZHANG_MGUS up
12	1e−02	5 / 46	PanCan_TGF−B_geneset_nanostring
13	3e−02	6 / 73	SHAUGHNESSY_MM high risk
14	5e−02	9 / 150	PanCan_MAPK_geneset_nanostring
15	7e−02	2 / 14	GENTLES_modul4

CC

Rank	p−value	#in/all	Geneset
1	4e−43	233 / 2979	cytosol
2	1e−36	298 / 4822	cytoplasm
3	3e−20	161 / 2464	extracellular exosome
4	1e−17	133 / 1979	membrane
5	3e−13	233 / 4828	nucleus
6	6e−13	144 / 2535	nucleoplasm
7	1e−10	60 / 777	Golgi apparatus
8	2e−10	25 / 172	endosome membrane
9	2e−09	35 / 352	focal adhesion
10	2e−09	25 / 194	membrane raft
11	9e−09	45 / 561	intracellular membrane−bounded organelle
12	2e−08	45 / 571	perinuclear region of cytoplasm
13	4e−08	24 / 208	actin cytoskeleton
14	2e−07	28 / 295	cell−cell adherens junction
15	4e−07	52 / 788	endoplasmic reticulum membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.004	65 / 1492	Chr 2
2	0.011	41 / 902	Chr 4
3	0.042	47 / 1160	Chr 12
4	0.042	49 / 1217	Chr 3
5	0.055	48 / 1211	Chr 6
6	0.119	15 / 342	Chr 18
7	0.266	37 / 1060	Chr 5
8	0.295	11 / 289	Chr 21
9	0.342	15 / 422	Chr 13
10	0.368	26 / 769	Chr 15
11	0.449	74 / 2323	Chr 1
12	0.530	24 / 768	Chr 14
13	0.539	26 / 836	Chr 8
14	0.547	28 / 904	Chr 10
15	0.657	18 / 619	Chr 20

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−61	570 / 11455	2_TssA_Fibroblasts
2	1e−56	586 / 12298	2_TssA_Melanocytes
3	1e−55	480 / 8771	5_Tx_Melanocytes
4	9e−52	442 / 7854	5_Tx_Fibroblasts
5	1e−48	559 / 11836	3_TssF_Melanocytes
6	2e−47	471 / 8990	15_Quies_Fibroblasts
7	3e−46	579 / 12741	7_Enh_Melanocytes
8	1e−38	518 / 11130	15_Quies_Melanocytes
9	3e−37	436 / 8613	7_Enh_Fibroblasts
10	1e−35	564 / 12983	2_TssA_Neuronal_Progenitor
11	2e−35	329 / 5699	6_EnhG_Melanocytes
12	2e−27	355 / 6970	5_Tx_Neuronal_Progenitor
13	1e−25	439 / 9635	3_TssF_Fibroblasts
14	3e−24	519 / 12393	15_Quies_Neuronal_Progenitor
15	7e−13	464 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−85	595 / 10999	TssWk_Colon
2	1e−82	550 / 9555	TssA_Colon
3	7e−81	532 / 9054	Tx_Colon
4	1e−73	505 / 8568	TxWk_Colon
5	5e−72	506 / 8678	Quies3_Colon
6	7e−40	127 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	4e−39	109 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	3e−30	487 / 10779	Enh_Colon
9	8e−24	54 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	4e−20	276 / 5373	EnhWk1_Colon
11	2e−18	48 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
12	6e−18	101 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	9e−16	212 / 4034	TssD1_Colon
14	2e−15	330 / 7354	TssF_Colon
15	1e−14	106 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

Glio

Rank	p−value	#in/all	Geneset
1	1e−20	49 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	8e−20	48 / 315	Up
3	1e−19	44 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
4	5e−09	111 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−07	55 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	2e−07	95 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	1e−05	9 / 47	Donson−innate immunity−associated with LTS in HGA
8	3e−05	5 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
9	5e−04	14 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
10	3e−03	5 / 32	Donson−Misc immune function−associated with LTS in HGA
11	3e−03	9 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
12	4e−03	12 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	4e−03	7 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	6e−03	2 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
15	9e−03	9 / 113	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−68	211 / 1797	PILON_KLF1_TARGETS_DN
2	6e−55	140 / 960	NUYTTEN_EZH2_TARGETS_UP
3	2e−49	90 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
4	2e−44	45 / 87	HECKER_IFNB1_TARGETS
5	1e−41	28 / 29	MOSERLE_IFNA_RESPONSE
6	4e−38	35 / 58	BROWNE_INTERFERON_RESPONSIVE_GENES
7	1e−36	83 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
8	3e−36	92 / 622	SCHLOSSER_SERUM_RESPONSE_DN
9	9e−35	49 / 161	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
10	2e−34	29 / 42	DAUER_STAT3_TARGETS_DN
11	1e−32	61 / 293	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
12	5e−32	80 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
13	3e−31	100 / 841	ACEVEDO_LIVER_CANCER_UP
14	8e−31	95 / 774	REACTOME_IMMUNE_SYSTEM
15	2e−30	95 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−51	49 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	2e−51	64 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	8e−10	25 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	5e−09	24 / 187	HALLMARK_COMPLEMENT
5	1e−08	21 / 151	HALLMARK_APOPTOSIS
6	3e−08	23 / 191	HALLMARK_INFLAMMATORY_RESPONSE
7	2e−07	14 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
8	1e−05	17 / 162	HALLMARK_ALLOGRAFT_REJECTION
9	2e−05	18 / 185	HALLMARK_MTORC1_SIGNALING
10	7e−05	17 / 183	HALLMARK_APICAL_JUNCTION
11	8e−05	17 / 186	HALLMARK_IL2_STAT5_SIGNALING
12	3e−04	16 / 189	HALLMARK_HYPOXIA
13	4e−04	10 / 87	HALLMARK_PROTEIN_SECRETION
14	4e−04	15 / 176	HALLMARK_KRAS_SIGNALING_UP
15	2e−03	14 / 185	HALLMARK_HEME_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−15	34 / 211	Homuth_BMI−associated−genes_DN
2	7e−07	7 / 18	Huan_blood−pressure_SBP−signature
3	6e−05	4 / 8	DUMEAUX_Monocytes in smokers literature genes up
4	1e−04	5 / 16	Huan_blood−pressure_DBP−signature
5	3e−04	3 / 5	Huan_blood−pressure_HTN−signature
6	3e−03	3 / 10	DUMEAUX_Smoking literature genes up
7	1e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	3e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
9	4e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	4e−01	1 / 17	DUMEAUX_High bmi enriched genes
11	6e−01	1 / 31	DUMEAUX_Fasting enriched genes
12	7e−01	4 / 147	Homuth_BMI−associated−genes_UP
13	8e−01	2 / 94	DUMEAUX_Smoking 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	1e−88	485 / 7275	HOPP_Txn_elongation
2	6e−80	504 / 8226	HOPP_Active_promoter
3	8e−79	476 / 7448	HOPP_Strong_enhancer
4	4e−72	387 / 5356	HOPP_Txn_transition
5	1e−54	456 / 8098	HOPP_Weak_promoter
6	1e−36	63 / 272	SPANG_IL21 DN
7	2e−29	360 / 6959	HOPP_Weak_enhancer
8	9e−29	344 / 6559	HOPP_Weak_txn
9	5e−18	45 / 306	WIRTH_lymphoma937_spot E
10	1e−17	95 / 1169	SPANG_BCR DN
11	1e−17	44 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
12	9e−11	36 / 331	SPANG_CD40 6hrs UP
13	2e−10	17 / 78	Sha_DLBCL UP
14	5e−10	34 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
15	1e−09	34 / 331	WIRTH_lymphoma937_spot H

Melanoma

Rank	p−value	#in/all	Geneset
1	0.002	6 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.576	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.614	1 / 30	Hugo_melanoma−all−MET_UP
4	1.000	0 / 54	Hugo_melanoma−all−MET_DN
5	1.000	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.000	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−52	475 / 8818	protein binding
2	3e−09	82 / 1329	ATP binding
3	5e−09	32 / 315	protein serine/threonine kinase activity
4	1e−08	25 / 213	GTPase activity
5	2e−08	28 / 265	cadherin binding involved in cell−cell adhesion
6	8e−08	25 / 232	ligase activity
7	9e−08	24 / 217	protein kinase activity
8	2e−07	63 / 1013	poly(A) RNA binding
9	6e−07	28 / 311	enzyme binding
10	7e−07	11 / 54	double−stranded RNA binding
11	1e−06	27 / 301	ubiquitin−protein transferase activity
12	1e−06	20 / 182	signal transducer activity
13	2e−06	21 / 204	protein domain specific binding
14	2e−06	10 / 48	receptor signaling protein serine/threonine kinase activity
15	3e−06	40 / 580	identical 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	1e−24	71 / 546	hsa−miR−93
2	5e−24	62 / 429	hsa−miR−548n
3	2e−22	69 / 561	hsa−miR−20b
4	2e−22	59 / 416	hsa−miR−372
5	4e−22	71 / 602	hsa−miR−20a
6	1e−21	65 / 520	hsa−miR−106a
7	1e−21	45 / 250	hsa−miR−548l
8	3e−21	64 / 513	hsa−miR−106b
9	3e−21	60 / 455	hsa−miR−130a
10	4e−20	59 / 463	hsa−miR−301a
11	2e−19	45 / 281	hsa−miR−570
12	2e−19	63 / 540	hsa−miR−17
13	2e−19	49 / 336	hsa−miR−142−5p
14	5e−19	55 / 428	hsa−miR−519d
15	9e−19	56 / 449	hsa−miR−130b

Pathw Act

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 13	BENTINK_src.10
2	4e−03	3 / 11	BENTINK_ras.4
3	5e−02	2 / 12	BENTINK_ras.1
4	3e−01	1 / 13	BENTINK_e2f3.1
5	4e−01	1 / 14	GUSTAFSON_PI3K_UP
6	4e−01	1 / 15	GUSTAFSON_PI3K_DN
7	1e+00	0 / 13	BENTINK_e2f3.2
8	1e+00	0 / 13	BENTINK_myc.1
9	1e+00	0 / 14	BENTINK_ras.6
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	5e−66	60 / 96	Chaussabel_3,1_Interferon−inducible
2	3e−28	66 / 412	WIRTH_Immune system
3	5e−26	49 / 240	Chaussabel_3,3_Inflammation II
4	3e−17	39 / 242	Chaussabel_3,2_Inflammation I
5	8e−17	31 / 153	Chaussabel_2,9_Cytosceleton
6	1e−15	26 / 113	Chaussabel_1,5_Myeloid lineage
7	2e−13	27 / 150	Chaussabel_2,6_Myeloid lineage
8	1e−11	17 / 66	VAQUERIZAS_Whole blood_TF
9	3e−11	35 / 302	Chaussabel_3,4_Protein phosphatases
10	9e−11	18 / 84	Chaussabel_2,10_Immune related cell surface molecules
11	1e−10	55 / 681	PROTEINATLAS_lung
12	2e−10	47 / 535	PROTEINATLAS_spleen
13	3e−09	75 / 1173	PROTEINATLAS_rectum
14	4e−09	54 / 724	PROTEINATLAS_lymph node
15	4e−09	79 / 1268	PROTEINATLAS_colon

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	2e−20	266 / 5067	ICGC_Taf1_targets
2	2e−17	121 / 1723	HEBENSTREIT_high expression TF
3	3e−17	249 / 4881	ICGC_Atf2_targets
4	1e−16	268 / 5466	ICGC_Nficsc81335_targets
5	2e−15	243 / 4890	ICGC_Bclaf101388_targets
6	2e−15	237 / 4735	ICGC_Pu1_targets
7	1e−14	130 / 2087	ICGC_Cebpbsc150_targets
8	3e−14	131 / 2133	ICGC_Mef2_targets
9	2e−13	259 / 5518	ICGC_Stat5_targets
10	2e−13	256 / 5442	ICGC_Pmlsc71910_targets
11	9e−13	218 / 4468	ICGC_Egr1_targets
12	4e−12	203 / 4131	ICGC_Nfatc1_targets
13	5e−12	167 / 3194	ICGC_Irf4_targets
14	6e−12	279 / 6267	ICGC_Yy1_targets
15	1e−11	248 / 5410	ICGC_Foxm1_targets

Group Overexpression Sp

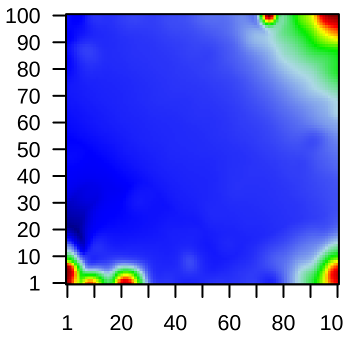
Spot Summary: E

metagenes = 40
genes = 357

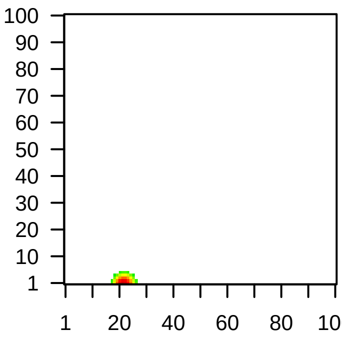
<r> metagenes = 0.9
<r> genes = 0.31
beta: r2= 28.61 / log p= −Inf

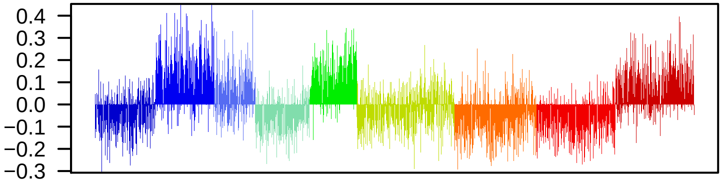
samples with spot = 221 (6.5 %)
A C * : 81 (24.7 %)
A C F * : 24 (10.2 %)
C F * : 58 (21.9 %)
F * : 3 (0.5 %)
F J * : 3 (0.6 %)
N * : 52 (11.7 %)

Overview Map



Spot





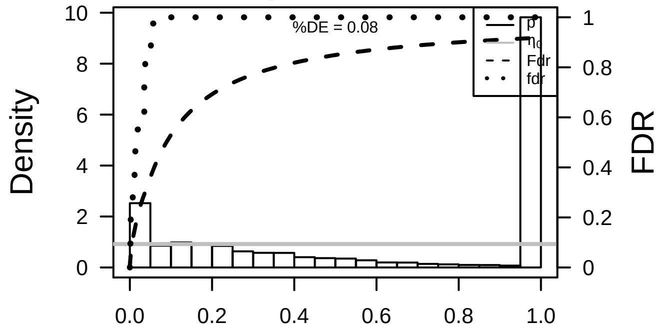
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324311	1.66	−0.52	0.27	RNF182	ring finger protein 182 [Source:HGNC Symbol;Acc:HGNC:28
2	ILMN_180823	1.58	−0.7	0.47	RBPMS2	RNA binding protein with multiple splicing 2 [Source:HGNC S
3	ILMN_172188	1.57	−1.12	0.78	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	0.64	BNIP3L	BCL2 interacting protein 3 like [Source:HGNC Symbol;Acc:H
7	ILMN_166279	1.43	−1.26	0.61	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	0.58	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	0.66	RIOK3	RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]
12	ILMN_175275	1.32	−0.85	0.62	VWF	von Willebrand factor [Source:HGNC Symbol;Acc:HGNC:127
13	ILMN_171028	1.31	−1.36	0.79	TUBB1	tubulin beta 1 class VI [Source:HGNC Symbol;Acc:HGNC:16
14	ILMN_219943	1.31	−1.09	0.62	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	0.77	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	0.62	HEMGN	hemogen [Source:HGNC Symbol;Acc:HGNC:17509]
19	ILMN_235212	1.26	−0.82	0.44	NT5C3A	5'−nucleotidase, cytosolic IIIA [Source:HGNC Symbol;Acc:HG
20	ILMN_173207	1.26	−0.97	0.61	HIST2H2BE	histone cluster 2, H2be [Source:HGNC Symbol;Acc:HGNC:47

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−95	62 / 102	Refer	Chaussabel_1,2_Platelets
2	2e−55	37 / 64	GSEA	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
3	4e−43	43 / 188	GSEA	WIERENGA_STAT5A_TARGETS_DN
4	1e−20	26 / 185	HM	HALLMARK_HEME_METABOLISM
5	2e−14	14 / 64	GSEA	ROSS_AML_OF_FAB_M7_TYPE
6	5e−14	20 / 181	GSEA	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATIO
7	7e−14	19 / 162	GSEA	JISON_SICKLE_CELL_DISEASE_UP
8	1e−13	28 / 414	GSEA	REACTOME_HEMOSTASIS
9	8e−13	96 / 4018	Colon	EnhWk2_Colon
10	8e−13	25 / 352	CC	focal adhesion
11	1e−12	171 / 9635	Chror	3_TssF_Fibroblasts
12	2e−12	17 / 147	Lifesty	Homuth_BMI−associated−genes_UP
13	2e−12	13 / 71	GSEA	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA
14	4e−12	183 / 10779	Colon	Enh_Colon
15	5e−12	157 / 8613	Chror	7_Enh_Fibroblasts
16	5e−12	27 / 451	GSEA	PILON_KLF1_TARGETS_UP
17	6e−12	25 / 387	GSEA	SWEET_LUNG_CANCER_KRAS_DN
18	8e−12	21 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
19	2e−11	193 / 11836	Chror	3_TssF_Melanocytes
20	3e−11	10 / 40	GSEA	GNATENKO_PLATELET_SIGNATURE
21	5e−11	13 / 90	BP	platelet degranulation
22	1e−10	44 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	1e−10	201 / 12741	Chror	7_Enh_Melanocytes
24	3e−10	8 / 25	GSEA	VALK_AML_CLUSTER_8
25	3e−10	42 / 1216	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
26	4e−10	101 / 4822	CC	cytoplasm
27	5e−10	9 / 38	GSEA	CHUNG_BLISTER_CYTOTOXICITY_DN
28	5e−10	152 / 8678	Colon	Quies3_Colon
29	6e−10	189 / 11847	Chror	7_Enh_Neuronal_Progenitor
30	6e−10	195 / 12393	Chror	15_Quies_Neuronal_Progenitor
31	7e−10	13 / 111	Refer	Chaussabel_2,3_Erythrocytes
32	7e−10	100 / 4795	Chror	6_EnhG_Fibroblasts
33	3e−09	25 / 520	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
34	5e−09	62 / 2464	CC	extracellular exosome
35	9e−09	198 / 12983	Chror	2_TssA_Neuronal_Progenitor
36	1e−08	8 / 38	BP	platelet aggregation
37	2e−08	158 / 9555	Colon	TssA_Colon
38	2e−08	151 / 8990	Chror	15_Quies_Fibroblasts
39	2e−08	15 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
40	2e−08	148 / 8771	Chror	5_Tx_Melanocytes

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	5 / 111	HORVATH_aging_genes meth DOWN
2	0.50	2 / 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	5e−11	13 / 90	platelet degranulation
2	1e−08	8 / 38	platelet aggregation
3	5e−07	10 / 106	platelet activation
4	9e−07	12 / 171	blood coagulation
5	3e−05	5 / 31	microtubule−based process
6	5e−05	4 / 18	blood coagulation, intrinsic pathway
7	2e−04	14 / 387	cell adhesion
8	3e−04	3 / 12	response to arsenic−containing substance
9	5e−04	4 / 31	lamellipodium assembly
10	5e−04	4 / 31	response to organonitrogen compound
11	5e−04	3 / 14	glutamate metabolic process
12	8e−04	3 / 16	megakaryocyte development
13	9e−04	10 / 254	cell surface receptor signaling pathway
14	1e−03	3 / 17	calcium−mediated signaling using intracellular calcium source
15	1e−03	3 / 18	T cell proliferation

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	165 / 10430	Overlap_fetal_midbrain_Quies
2	3e−07	158 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	1e−05	147 / 9504	Overlap_fetal_midbrain_K9K27me3
4	2e−05	149 / 9815	Overlap_fetal_midbrain_ReprPC
5	5e−05	61 / 3164	Mid_Frontal_Lobe_ZNF
6	1e−03	93 / 5936	Overlap_fetal_midbrain_HetRpts
7	5e−03	25 / 1213	Fetal_TssP
8	6e−03	10 / 328	Fetal_Het
9	7e−03	46 / 2709	Mid_Frontal_Lobe_HetRpts
10	9e−03	21 / 1012	Mid_Frontal_Lobe_Enh
11	2e−02	44 / 2700	Fetal_TxTrans
12	4e−02	41 / 2630	Fetal_TssF
13	4e−02	17 / 906	Fetal_HetRpts
14	4e−02	46 / 3046	Fetal_TssA
15	5e−02	16 / 869	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	8e−05	0 / 15	LIU_PROSTATE_CANCER_DN
2	4e−03	5 / 91	PanCan_TXmisReg_geneset_nanostring
3	1e−02	2 / 13	GENTLES_modul12
4	1e−02	2 / 14	GENTLES_modul13
5	3e−02	2 / 24	PanCan_Notch_geneset_nanostring
6	6e−02	4 / 125	PanCan_CC+Apop_geneset_nanostring
7	7e−02	3 / 82	PanCan_JAK−ST_geneset_nanostring
8	1e−01	2 / 46	PanCan_TGF−B_geneset_nanostring
9	1e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1e−01	10 / 554	Lembcke_Colonic Inflammation
11	1e−01	1 / 13	LIU_LIVER_CANCER
12	1e−01	1 / 13	WANG_ER_DN
13	1e−01	1 / 13	GENTLES_modul18
14	2e−01	1 / 14	LIU_PROSTATE_CANCER_UP
15	2e−01	1 / 14	GENTLES_modul4

CC

Rank	p−value	#in/all	Geneset
1	8e−13	25 / 352	focal adhesion
2	4e−10	101 / 4822	cytoplasm
3	5e−09	62 / 2464	extracellular exosome
4	4e−07	17 / 330	cytoskeleton
5	9e−06	4 / 12	platelet alpha granule membrane
6	2e−05	60 / 2979	cytosol
7	2e−05	6 / 49	platelet alpha granule lumen
8	6e−05	68 / 3662	plasma membrane
9	2e−04	5 / 47	stress fiber
10	4e−04	8 / 149	lamellipodium
11	5e−04	5 / 56	autophagosome
12	5e−04	3 / 14	platelet alpha granule
13	7e−04	4 / 34	nuclear nucleosome
14	1e−03	7 / 138	mitochondrial outer membrane
15	2e−03	6 / 106	Z disc

Chr

Rank	p−value	#in/all	Geneset
1	0.1	10 / 536	Chr 22
2	0.1	11 / 619	Chr 20
3	0.1	18 / 1160	Chr 12
4	0.2	6 / 342	Chr 18
5	0.2	21 / 1492	Chr 2
6	0.3	31 / 2323	Chr 1
7	0.3	13 / 902	Chr 4
8	0.3	13 / 904	Chr 10
9	0.4	16 / 1211	Chr 6
10	0.4	6 / 422	Chr 13
11	0.4	12 / 954	Chr 9
12	0.5	12 / 959	Chr 16
13	0.5	15 / 1217	Chr 3
14	0.5	12 / 994	Chr X
15	0.6	13 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−12	171 / 9635	3_TssF_Fibroblasts
2	5e−12	157 / 8613	7_Enh_Fibroblasts
3	2e−11	193 / 11836	3_TssF_Melanocytes
4	1e−10	201 / 12741	7_Enh_Melanocytes
5	6e−10	189 / 11847	7_Enh_Neuronal_Progenitor
6	6e−10	195 / 12393	15_Quies_Neuronal_Progenitor
7	7e−10	100 / 4795	6_EnhG_Fibroblasts
8	9e−09	198 / 12983	2_TssA_Neuronal_Progenitor
9	2e−08	151 / 8990	15_Quies_Fibroblasts
10	2e−08	148 / 8771	5_Tx_Melanocytes
11	2e−07	186 / 12298	2_TssA_Melanocytes
12	3e−07	172 / 11130	15_Quies_Melanocytes
13	4e−07	132 / 7854	5_Tx_Fibroblasts
14	5e−07	175 / 11455	2_TssA_Fibroblasts
15	2e−05	98 / 5699	6_EnhG_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−13	96 / 4018	EnhWk2_Colon
2	4e−12	183 / 10779	Enh_Colon
3	3e−10	42 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	5e−10	152 / 8678	Quies3_Colon
5	2e−08	158 / 9555	TssA_Colon
6	8e−08	102 / 5373	EnhWk1_Colon
7	1e−07	172 / 10999	TssWk_Colon
8	2e−07	89 / 4526	Quies1_Colon
9	2e−07	127 / 7354	TssF_Colon
10	7e−07	109 / 6138	TssD2_Colon
11	1e−06	145 / 9054	Tx_Colon
12	4e−06	137 / 8568	TxWk_Colon
13	1e−05	30 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	3e−05	13 / 278	Kosinski_top−crypt−long−list
15	7e−05	36 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

Glio

Rank	p−value	#in/all	Geneset
1	1e−04	9 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
2	3e−03	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
3	4e−03	4 / 55	Stuehler_Proteins_up_in_STS
4	5e−03	5 / 94	Weller_LGG_A_vs_O_UP
5	5e−03	6 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	8e−03	2 / 12	Phillips MES up vs Prolif & PN
7	1e−02	2 / 14	astrocytes_glio
8	1e−02	5 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	1e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	2e−02	3 / 52	OL vs. OPC
11	3e−02	4 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	3e−02	3 / 57	OL vs. MOG− OL
13	3e−02	5 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	3e−02	16 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
15	5e−02	24 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−55	37 / 64	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
2	4e−43	43 / 188	WIERENGA_STAT5A_TARGETS_DN
3	2e−14	14 / 64	ROSS_AML_OF_FAB_M7_TYPE
4	5e−14	20 / 181	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
5	7e−14	19 / 162	JISON_SICKLE_CELL_DISEASE_UP
6	1e−13	28 / 414	REACTOME_HEMOSTASIS
7	2e−12	13 / 71	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
8	5e−12	27 / 451	PILON_KLF1_TARGETS_UP
9	6e−12	25 / 387	SWEET_LUNG_CANCER_KRAS_DN
10	8e−12	21 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
11	3e−11	10 / 40	GNATENKO_PLATELET_SIGNATURE
12	1e−10	44 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	3e−10	8 / 25	VALK_AML_CLUSTER_8
14	5e−10	9 / 38	CHUNG_BLISTER_CYTOTOXICITY_DN
15	3e−09	25 / 520	CHICAS_RB1_TARGETS_CONFLUENT

HM

Rank	p−value	#in/all	Geneset
1	1e−20	26 / 185	HALLMARK_HEME_METABOLISM
2	9e−05	10 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	1e−04	7 / 91	HALLMARK_ANDROGEN_RESPONSE
4	4e−04	8 / 151	HALLMARK_APOPTOSIS
5	8e−04	7 / 127	HALLMARK_COAGULATION
6	1e−03	8 / 176	HALLMARK_ADIPOGENESIS
7	1e−03	4 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	1e−03	8 / 183	HALLMARK_APICAL_JUNCTION
9	2e−03	8 / 186	HALLMARK_MYOGENESIS
10	2e−03	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	5e−03	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
12	5e−03	6 / 132	HALLMARK_UV_RESPONSE_DN
13	6e−03	6 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	6e−03	7 / 185	HALLMARK_MTORC1_SIGNALING
15	7e−03	7 / 187	HALLMARK_COMPLEMENT

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−12	17 / 147	Homuth_BMI−associated−genes_UP
2	7e−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	4e−05	58 / 2939	HOPP_Poised_promoter
2	7e−04	113 / 7448	HOPP_Strong_enhancer
3	7e−04	50 / 2701	HOPP_Repetitive
4	1e−03	120 / 8098	HOPP_Weak_promoter
5	1e−03	7 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
6	1e−03	7 / 141	WIRTH_lymphoma937_spot F
7	2e−03	11 / 331	WIRTH_lymphoma937_spot H
8	3e−03	119 / 8226	HOPP_Active_promoter
9	3e−03	10 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−(
10	3e−03	6 / 121	SPANG_LPS 6hrs UP
11	3e−03	98 / 6559	HOPP_Weak_txn
12	4e−03	10 / 306	WIRTH_lymphoma937_spot E
13	5e−03	10 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−(
14	5e−03	102 / 6959	HOPP_Weak_enhancer
15	7e−03	9 / 283	TARTE_Plasmablast signature

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−07	143 / 8818	protein binding
2	2e−06	18 / 413	protein heterodimerization activity
3	1e−05	8 / 91	structural constituent of cytoskeleton
4	5e−05	11 / 213	GTPase activity
5	8e−05	4 / 20	2 iron, 2 sulfur cluster binding
6	2e−04	7 / 98	integrin binding
7	3e−04	13 / 351	GTP binding
8	1e−03	10 / 268	actin binding
9	1e−03	4 / 42	manganese ion binding
10	2e−03	17 / 646	protein homodimerization activity
11	2e−03	3 / 21	ferrous iron binding
12	2e−03	3 / 21	G−protein beta/gamma−subunit complex binding
13	3e−03	3 / 25	spectrin binding
14	4e−03	9 / 265	cadherin binding involved in cell−cell adhesion
15	6e−03	8 / 227	transcription coactivator activity

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 92	hsa−miR−219−2−3p
2	4e−04	7 / 113	hsa−miR−498
3	1e−03	9 / 216	hsa−miR−548m
4	2e−03	10 / 288	hsa−miR−34a
5	3e−03	6 / 119	hsa−miR−509−3p
6	3e−03	3 / 25	hsa−miR−941
7	3e−03	5 / 85	hsa−miR−1265
8	4e−03	7 / 166	hsa−miR−183
9	4e−03	3 / 28	hsa−miR−519e*
10	7e−03	5 / 100	hsa−miR−600
11	7e−03	10 / 336	hsa−miR−142−5p
12	7e−03	5 / 101	hsa−miR−603
13	8e−03	3 / 35	hsa−miR−770−5p
14	8e−03	5 / 105	hsa−miR−605
15	9e−03	6 / 150	hsa−miR−633

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_e2f3.1
2	0.2	1 / 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	3e−95	62 / 102	Chaussabel_1,2_Platelets
2	7e−10	13 / 111	Chaussabel_2,3_Erythrocytes
3	2e−07	22 / 514	PROTEINATLAS_vagina
4	9e−07	19 / 429	PROTEINATLAS_soft tissue
5	2e−06	18 / 416	PROTEINATLAS_ovary
6	9e−06	31 / 1118	PROTEINATLAS_placenta
7	9e−06	21 / 598	PROTEINATLAS_prostate
8	1e−05	4 / 13	WIRTH_Sec. lymphoid organs
9	2e−05	21 / 619	PROTEINATLAS_salivary gland
10	3e−05	25 / 850	PROTEINATLAS_skin
11	3e−05	22 / 695	PROTEINATLAS_bone marrow
12	3e−05	26 / 912	PROTEINATLAS_urinary bladder
13	5e−05	20 / 623	PROTEINATLAS_seminal vesicle
14	6e−05	4 / 19	VAQUERIZAS_Bone marrow_TF
15	8e−05	20 / 640	PROTEINATLAS_parathyroid gland

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	0.002	33 / 1669	ICGC_P300_targets
2	0.004	80 / 5188	ICGC_Ebfsc137065_targets
3	0.004	74 / 4735	ICGC_Pu1_targets
4	0.006	46 / 2704	ICGC_Pbx3_targets
5	0.006	38 / 2133	ICGC_Mef2_targets
6	0.015	66 / 4362	ICGC_Creb1_targets
7	0.017	86 / 5961	ICGC_Pol24_targets
8	0.019	2 / 18	MYC_Metabolism UP
9	0.023	1 / 2	MYC_ECM cell adhesion DOWN
10	0.025	93 / 6616	ICGC_Pax5_targets
11	0.027	40 / 2497	ICGC_Bcl11_targets
12	0.031	100 / 7247	ICGC_Runx3_targets
13	0.032	29 / 1723	HEBENSTREIT_high expression TF
14	0.033	43 / 2759	ICGC_Bcl3_targets
15	0.034	65 / 4468	ICGC_Egr1_targets

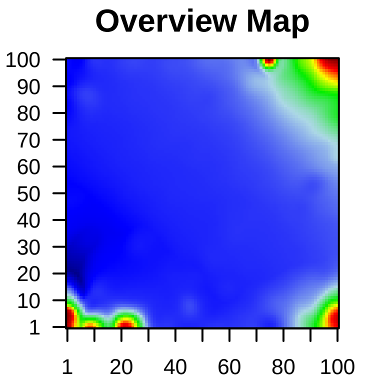
Group Overexpression Spo

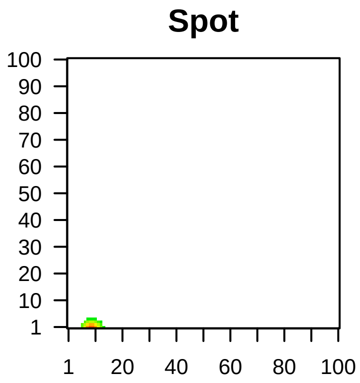
Spot Summary: F

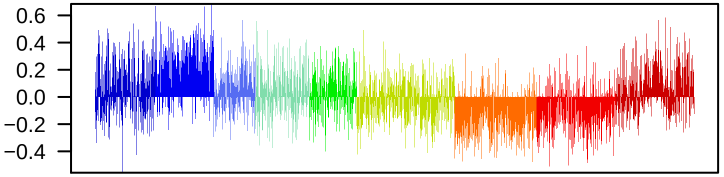
metagenes = 28
genes = 572

<r> metagenes = 0.97
<r> genes = 0.5
beta: r2= 90.07 / log p= −Inf

samples with spot = 560 (16.5 %)
A * : 83 (24.1 %)
A C * : 170 (51.8 %)
A C F * : 42 (17.9 %)
A F * : 57 (18.5 %)
C F * : 41 (15.5 %)
F * : 41 (7.4 %)
F J * : 8 (1.7 %)
J * : 14 (3.1 %)
N * : 104 (23.5 %)


Overview Map


Spot

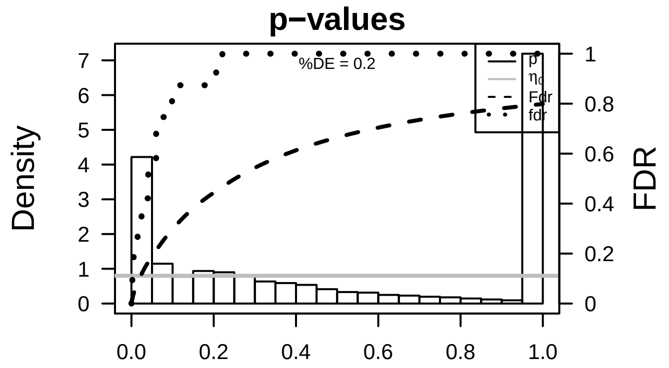


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173045	2.93	−1.93	0.31	FOLR3	folate receptor 3 [Source:HGNC Symbol;Acc:HGNC:3795]
2	ILMN_179631	2.16	−1.97	0.77	MMP9	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
3	ILMN_169658	2.03	−1.31	0.56		
4	ILMN_180121	1.96	−2.45	0.5	S100P	S100 calcium binding protein P [Source:HGNC Symbol;Acc:H
5	ILMN_178573	1.8	−1.22	0.64		
6	ILMN_170160	1.74	−2	0.72	ALPL	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
7	ILMN_174891	1.68	−1.3	0.69	S100A12	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac
8	ILMN_176271	1.67	−1.13	0.71	MCEMP1	mast cell expressed membrane protein 1 [Source:HGNC Sym
9	ILMN_169454	1.63	−1.08	0.8	ANXA3	annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
10	ILMN_170893	1.62	−1.48	0.75	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
11	ILMN_177525	1.62	−1.53	0.77	PROK2	prokineticin 2 [Source:HGNC Symbol;Acc:HGNC:18455]
12	ILMN_172176	1.57	−1.48	0.46	IL18RAP	interleukin 18 receptor accessory protein [Source:HGNC Sym
13	ILMN_173399	1.53	−1.22	0.51	DHRS9	dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:HGN
14	ILMN_172111	1.53	−2.22	0.2		
15	ILMN_171681	1.5	−1	0.62	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1 [S
16	ILMN_166163	1.49	−2.04	0.34		
17	ILMN_177213	1.48	−1.25	0.82	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGN
18	ILMN_180522	1.47	−1.18	0.8	LRG1	leucine rich alpha−2−glycoprotein 1 [Source:HGNC Symbol;A
19	ILMN_181228	1.46	−0.74	0.69	ARG1	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]
20	ILMN_318313	1.45	−1.16	0.75		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−59	57 / 150	Refer	Chaussabel_2,6_Myeloid lineage
2	5e−42	54 / 240	Refer	Chaussabel_3,3_Inflammation II
3	1e−38	79 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
4	2e−35	81 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
5	2e−33	66 / 554	Cance	Lembcke_Colonic Inflammation
6	4e−33	43 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
7	1e−28	74 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
8	5e−28	42 / 242	Refer	Chaussabel_3,2_Inflammation I
9	7e−28	36 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
10	7e−27	34 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
11	5e−26	38 / 211	Lifest	Homuth_BMI−associated−genes_DN
12	2e−25	36 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
13	3e−25	42 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
14	3e−24	40 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
15	2e−23	154 / 3662	CC	plasma membrane
16	1e−22	310 / 10999	Colon	TssWk_Colon
17	2e−22	34 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
18	1e−21	34 / 212	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
19	2e−21	41 / 336	BP	inflammatory response
20	3e−21	29 / 147	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
21	8e−21	42 / 366	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
22	4e−20	32 / 205	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
23	4e−20	71 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
24	1e−19	25 / 114	GSEA	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
25	6e−19	31 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
26	1e−18	296 / 10779	Colon	Enh_Colon
27	1e−18	32 / 230	GSEA	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
28	2e−18	20 / 71	GSEA	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
29	3e−18	30 / 203	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
30	3e−18	229 / 7448	Lympl	HOPP_Strong_enhancer
31	5e−18	23 / 107	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_DN
32	2e−17	28 / 183	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
33	2e−17	23 / 113	Refer	Chaussabel_1,5_Myeloid lineage
34	2e−17	28 / 185	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
35	8e−17	38 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
36	1e−16	88 / 1797	GSEA	PILON_KLF1_TARGETS_DN
37	1e−16	39 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
38	3e−16	27 / 188	MF	receptor activity
39	5e−16	251 / 8818	MF	protein binding
40	7e−16	26 / 178	BP	response to lipopolysaccharide


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.05	6 / 142	HORVATH_aging_genes meth UP
2	0.10	3 / 58	TESCHENDORFF_age_hypermethylated
3	0.35	3 / 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	2e−21	41 / 336	inflammatory response
2	7e−16	26 / 178	response to lipopolysaccharide
3	2e−15	34 / 335	innate immune response
4	2e−11	27 / 293	immune response
5	6e−10	15 / 99	defense response to bacterium
6	2e−08	6 / 11	regulation of cytokine secretion
7	2e−08	21 / 254	cell surface receptor signaling pathway
8	9e−08	10 / 56	neutrophil chemotaxis
9	3e−07	44 / 1003	signal transduction
10	7e−07	28 / 511	apoptotic process
11	2e−06	7 / 32	MyD88−dependent toll−like receptor signaling pathway
12	2e−06	7 / 32	negative regulation of MAP kinase activity
13	3e−06	12 / 118	chemotaxis
14	4e−06	12 / 122	positive regulation of NF−kappaB transcription factor activity
15	4e−06	9 / 66	Fc−gamma receptor signaling pathway involved in phagocytosis

Brain

Rank	p−value	#in/all	Geneset
1	8e−10	56 / 1213	Fetal_TssP
2	1e−08	247 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	1e−06	86 / 2700	Fetal_TxTrans
4	1e−05	90 / 3046	Fetal_TssA
5	3e−05	79 / 2630	Fetal_TssF
6	1e−04	237 / 10430	Overlap_fetal_midbrain_Quies
7	3e−04	145 / 5936	Overlap_fetal_midbrain_HetRpts
8	9e−04	84 / 3164	Mid_Frontal_Lobe_ZNF
9	1e−03	219 / 9815	Overlap_fetal_midbrain_ReprPC
10	1e−03	55 / 1893	Overlap_fetal_midbrain_TssF
11	1e−03	28 / 796	Overlap_fetal_midbrain_ZNF
12	1e−03	212 / 9504	Overlap_fetal_midbrain_K9K27me3
13	2e−03	102 / 4112	Mid_Frontal_Lobe_ReprPC
14	3e−03	71 / 2709	Mid_Frontal_Lobe_HetRpts
15	1e−02	33 / 1162	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	2e−33	66 / 554	Lembcke_Colonic Inflammation
2	5e−12	28 / 301	SPANG_BCL6−index2
3	8e−06	14 / 178	SPANG_LPS−index2
4	8e−03	8 / 150	PanCan_MAPK_geneset_nanostring
5	1e−02	5 / 73	SHAUGHNESSY_MM high risk
6	3e−02	2 / 14	BEN−PORATH_UP
7	4e−02	0 / 15	LIU_PROSTATE_CANCER_DN
8	8e−02	7 / 193	PanCan_PI3K_geneset_nanostring
9	9e−02	5 / 125	PanCan_CC+Apop_geneset_nanostring
10	1e−01	5 / 136	PanCan_RAS_geneset_nanostring
11	2e−01	2 / 39	ZHANG_MM up
12	2e−01	1 / 13	GENTLES_modul12
13	2e−01	1 / 13	GENTLES_modul18
14	2e−01	0 / 14	LIU_PROSTATE_CANCER_UP
15	2e−01	1 / 14	GENTLES_modul4

CC

Rank	p−value	#in/all	Geneset
1	2e−23	154 / 3662	plasma membrane
2	5e−12	96 / 2464	extracellular exosome
3	1e−11	61 / 1252	integral component of plasma membrane
4	1e−08	99 / 2979	cytosol
5	8e−08	104 / 3291	integral component of membrane
6	6e−07	69 / 1979	membrane
7	5e−06	8 / 51	phagocytic vesicle membrane
8	1e−05	129 / 4822	cytoplasm
9	2e−05	42 / 1101	extracellular space
10	5e−05	19 / 352	focal adhesion
11	9e−05	7 / 56	autophagosome
12	1e−04	24 / 539	Golgi membrane
13	1e−04	13 / 202	early endosome
14	2e−04	4 / 16	pseudopodium
15	2e−04	11 / 156	cytoplasmic vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.003	63 / 2323	Chr 1
2	0.039	32 / 1211	Chr 6
3	0.085	17 / 619	Chr 20
4	0.100	35 / 1467	Chr 19
5	0.203	21 / 904	Chr 10
6	0.313	7 / 289	Chr 21
7	0.442	11 / 536	Chr 22
8	0.450	23 / 1160	Chr 12
9	0.452	18 / 902	Chr 4
10	0.467	23 / 1170	Chr 7
11	0.527	16 / 836	Chr 8
12	0.708	26 / 1492	Chr 2
13	0.740	16 / 959	Chr 16
14	0.767	22 / 1318	Chr 17
15	0.795	12 / 768	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−15	323 / 12741	7_Enh_Melanocytes
2	2e−15	245 / 8613	7_Enh_Fibroblasts
3	3e−14	290 / 11130	15_Quies_Melanocytes
4	3e−12	255 / 9635	3_TssF_Fibroblasts
5	1e−10	291 / 11847	7_Enh_Neuronal_Progenitor
6	2e−09	297 / 12393	15_Quies_Neuronal_Progenitor
7	2e−09	295 / 12298	2_TssA_Melanocytes
8	2e−09	232 / 8990	15_Quies_Fibroblasts
9	3e−09	286 / 11836	3_TssF_Melanocytes
10	3e−09	227 / 8771	5_Tx_Melanocytes
11	5e−09	278 / 11455	2_TssA_Fibroblasts
12	7e−08	158 / 5699	6_EnhG_Melanocytes
13	9e−08	138 / 4795	6_EnhG_Fibroblasts
14	1e−06	296 / 12983	2_TssA_Neuronal_Progenitor
15	2e−06	196 / 7854	5_Tx_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−35	81 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	1e−22	310 / 10999	TssWk_Colon
3	1e−18	296 / 10779	Enh_Colon
4	8e−15	252 / 9054	Tx_Colon
5	5e−14	172 / 5373	EnhWk1_Colon
6	1e−13	29 / 278	Kosinski_top−crypt−long−list
7	2e−13	109 / 2810	EnhA_Colon
8	2e−13	240 / 8678	Quies3_Colon
9	2e−12	254 / 9555	TssA_Colon
10	3e−12	234 / 8568	TxWk_Colon
11	2e−11	133 / 4018	EnhWk2_Colon
12	2e−09	199 / 7354	TssF_Colon
13	1e−08	31 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP
14	1e−08	49 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	1e−08	55 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv

Glio

Rank	p−value	#in/all	Geneset
1	3e−24	40 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−07	9 / 47	Donson−innate immunity−associated with LTS in HGA
3	2e−06	11 / 94	Weller_LGG_A_vs_O_UP
4	2e−06	11 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
5	6e−05	10 / 113	GIEZELT_GBM_WT_up_VS_mut
6	2e−04	7 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
7	3e−04	10 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	4e−04	16 / 315	Up
9	5e−04	10 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	5e−04	45 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
11	6e−04	10 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
12	1e−03	2 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
13	3e−03	77 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	3e−03	4 / 33	Shaw_responders_down_in_oligo_glioma
15	4e−03	4 / 34	Shaw_down_in_1p19q

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−38	79 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
2	4e−33	43 / 196	MCLACHLAN_DENTAL_CARIES_UP
3	1e−28	74 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
4	7e−28	36 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
5	7e−27	34 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
6	2e−25	36 / 192	MCLACHLAN_DENTAL_CARIES_DN
7	3e−25	42 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
8	2e−22	34 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
9	1e−21	34 / 212	RUTELLA_RESPONSE_TO_HGF_DN
10	3e−21	29 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
11	8e−21	42 / 366	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
12	4e−20	32 / 205	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
13	4e−20	71 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
14	1e−19	25 / 114	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
15	6e−19	31 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−17	28 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	3e−13	24 / 191	HALLMARK_INFLAMMATORY_RESPONSE
3	5e−10	20 / 187	HALLMARK_COMPLEMENT
4	5e−08	12 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	1e−06	15 / 176	HALLMARK_KRAS_SIGNALING_UP
6	3e−05	12 / 151	HALLMARK_APOPTOSIS
7	7e−05	12 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	1e−04	12 / 175	HALLMARK_XENOBIOTIC_METABOLISM
9	2e−04	12 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	3e−04	7 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	9e−04	11 / 185	HALLMARK_P53_PATHWAY
12	3e−03	7 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	3e−03	10 / 183	HALLMARK_GLYCOLYSIS
14	3e−03	10 / 189	HALLMARK_HYPOXIA
15	8e−03	4 / 41	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	5e−26	38 / 211	Homuth_BMI−associated−genes_DN
2	3e−04	4 / 18	Huan_blood−pressure_SBP−signature
3	3e−03	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	9e−03	2 / 8	DUMEAUX_Monocytes in smokers literature genes up
5	4e−02	2 / 16	Huan_blood−pressure_DBP−signature
6	9e−02	1 / 5	Huan_blood−pressure_HTN−signature
7	2e−01	1 / 10	DUMEAUX_Smoking literature genes up
8	2e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
9	3e−01	1 / 17	DUMEAUX_High bmi enriched genes
10	5e−01	2 / 94	DUMEAUX_Smoking enriched genes
11	9e−01	1 / 147	Homuth_BMI−associated−genes_UP
12	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
13	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
14	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−18	229 / 7448	HOPP_Strong_enhancer
2	2e−14	31 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
3	4e−14	31 / 306	WIRTH_lymphoma937_spot E
4	8e−14	63 / 1169	SPANG_BCR DN
5	2e−08	210 / 8098	HOPP_Weak_promoter
6	5e−08	211 / 8226	HOPP_Active_promoter
7	3e−07	25 / 408	TARTE_Mature plasma cell signature
8	1e−06	179 / 6959	HOPP_Weak_enhancer
9	2e−06	21 / 331	SPANG_CD40 6hrs UP
10	4e−06	4 / 7	Care_GCB UP
11	7e−06	167 / 6559	HOPP_Weak_txn
12	2e−05	9 / 77	Aukema_BCL2 DN_BCL6 UP
13	2e−05	9 / 78	Sha_DLBCL UP
14	2e−05	19 / 331	WIRTH_lymphoma937_spot H
15	3e−05	139 / 5356	HOPP_Txn_transition

Melanoma

Rank	p−value	#in/all	Geneset
1	0.08	3 / 54	Hugo_melanoma−all−MET_DN
2	0.20	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.40	1 / 27	Hugo_melanoma−all−LEF1_UP
4	1.00	0 / 30	Hugo_melanoma−all−MET_UP
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	3e−16	27 / 188	receptor activity
2	5e−16	251 / 8818	protein binding
3	6e−07	5 / 10	RAGE receptor binding
4	8e−05	14 / 217	protein kinase activity
5	1e−04	20 / 413	protein heterodimerization activity
6	3e−04	11 / 160	carbohydrate binding
7	3e−04	26 / 648	calcium ion binding
8	3e−04	16 / 311	enzyme binding
9	4e−04	4 / 19	1−acylglycerol−3−phosphate O−acyltransferase activity
10	8e−04	11 / 182	signal transducer activity
11	1e−03	15 / 315	protein serine/threonine kinase activity
12	1e−03	3 / 12	phosphotyrosine binding
13	2e−03	24 / 646	protein homodimerization activity
14	2e−03	5 / 45	non−membrane spanning protein tyrosine kinase activity
15	2e−03	10 / 174	transmembrane signaling receptor activity

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−06	26 / 467	hsa−miR−195
2	3e−06	26 / 493	hsa−miR−103
3	9e−06	25 / 489	hsa−miR−16
4	9e−06	25 / 491	hsa−miR−107
5	5e−05	17 / 294	hsa−miR−503
6	8e−05	5 / 24	hsa−miR−632
7	1e−04	21 / 441	hsa−miR−424
8	2e−04	17 / 328	hsa−miR−367
9	3e−04	9 / 111	hsa−miR−297
10	3e−04	6 / 49	hsa−miR−556−3p
11	4e−04	22 / 516	hsa−miR−15a
12	5e−04	19 / 419	hsa−miR−497
13	5e−04	7 / 74	hsa−miR−1290
14	6e−04	14 / 263	hsa−miR−92b
15	6e−04	7 / 76	hsa−miR−592

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−59	57 / 150	Chaussabel_2,6_Myeloid lineage
2	5e−42	54 / 240	Chaussabel_3,3_Inflammation II
3	5e−28	42 / 242	Chaussabel_3,2_Inflammation I
4	2e−17	23 / 113	Chaussabel_1,5_Myeloid lineage
5	2e−07	35 / 695	PROTEINATLAS_bone marrow
6	4e−05	25 / 535	PROTEINATLAS_spleen
7	9e−05	6 / 39	Chaussabel_2,2_Neutrophils
8	3e−04	7 / 66	VAQUERIZAS_Whole blood_TF
9	1e−03	3 / 11	WIRTH_Prim. lymphoid organs
10	1e−03	3 / 12	Chaussabel_3,5_Hemoglobin genes
11	1e−03	6 / 64	VAQUERIZAS_Lung_TF
12	6e−03	16 / 412	WIRTH_Immune system
13	7e−03	3 / 21	JONGENEEL_Monocytes
14	2e−02	3 / 31	VAQUERIZAS_Fetal lung_TF
15	2e−02	21 / 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	6e−13	121 / 3348	ICGC_BatfPcr1_targets
2	7e−12	151 / 4735	ICGC_Pu1_targets
3	3e−10	92 / 2497	ICGC_Bcl11_targets
4	6e−09	151 / 5188	ICGC_Ebfsc137065_targets
5	1e−08	194 / 7247	ICGC_Runx3_targets
6	2e−07	100 / 3194	ICGC_Irf4_targets
7	3e−07	74 / 2133	ICGC_Mef2_targets
8	4e−07	150 / 5466	ICGC_Nficsc81335_targets
9	1e−06	135 / 4881	ICGC_Atf2_targets
10	1e−06	87 / 2759	ICGC_Bcl3_targets
11	2e−06	104 / 3507	ICGC_Rad21_targets
12	3e−06	147 / 5518	ICGC_Stat5_targets
13	3e−06	169 / 6578	ICGC_Pou2_targets
14	5e−06	156 / 5984	ICGC_Mta3_targets
15	7e−06	143 / 5410	ICGC_Foxm1_targets