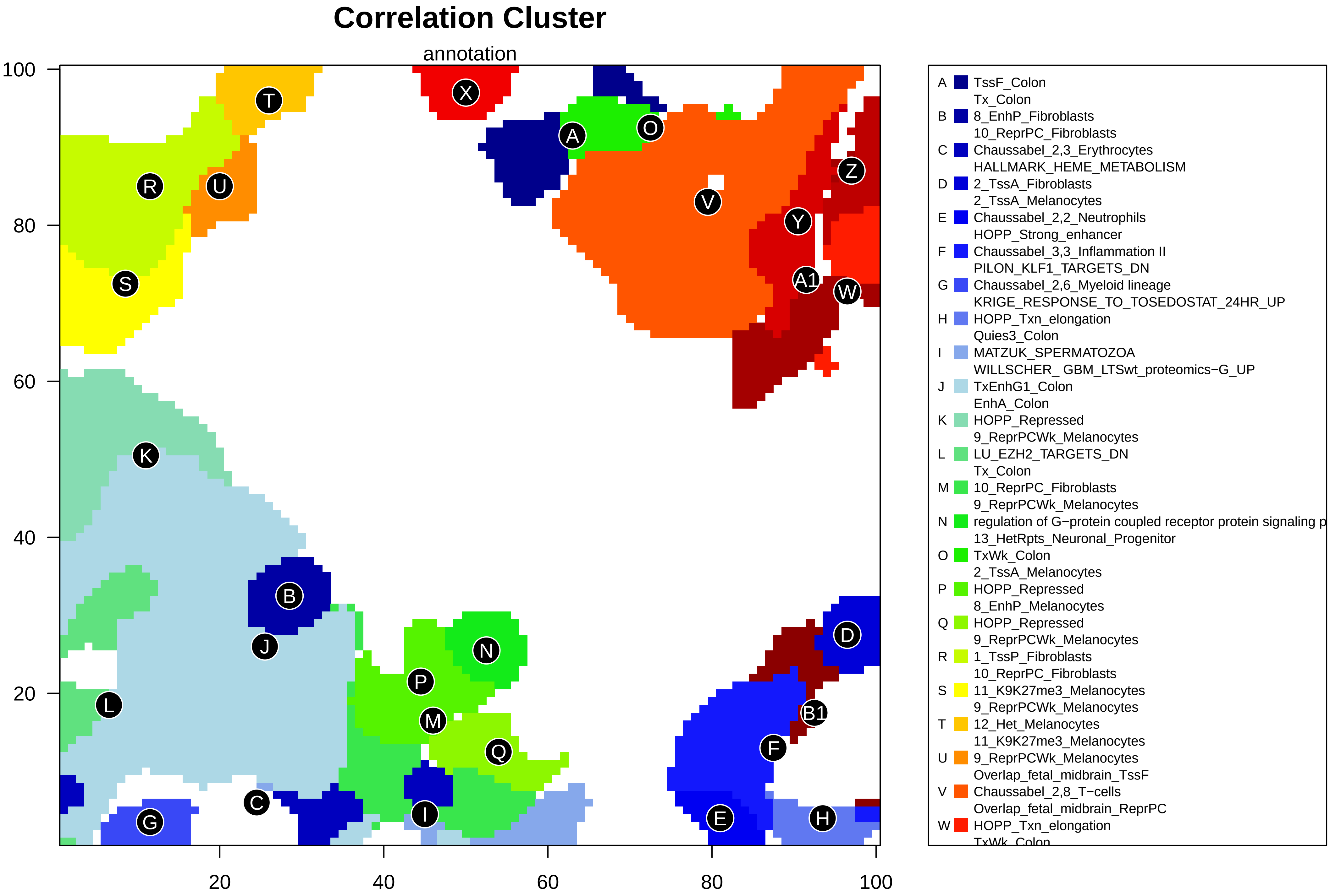
Correlation Cluster
annotation
100
80
60
40
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20
40
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100
X
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Z
Y
A1
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P
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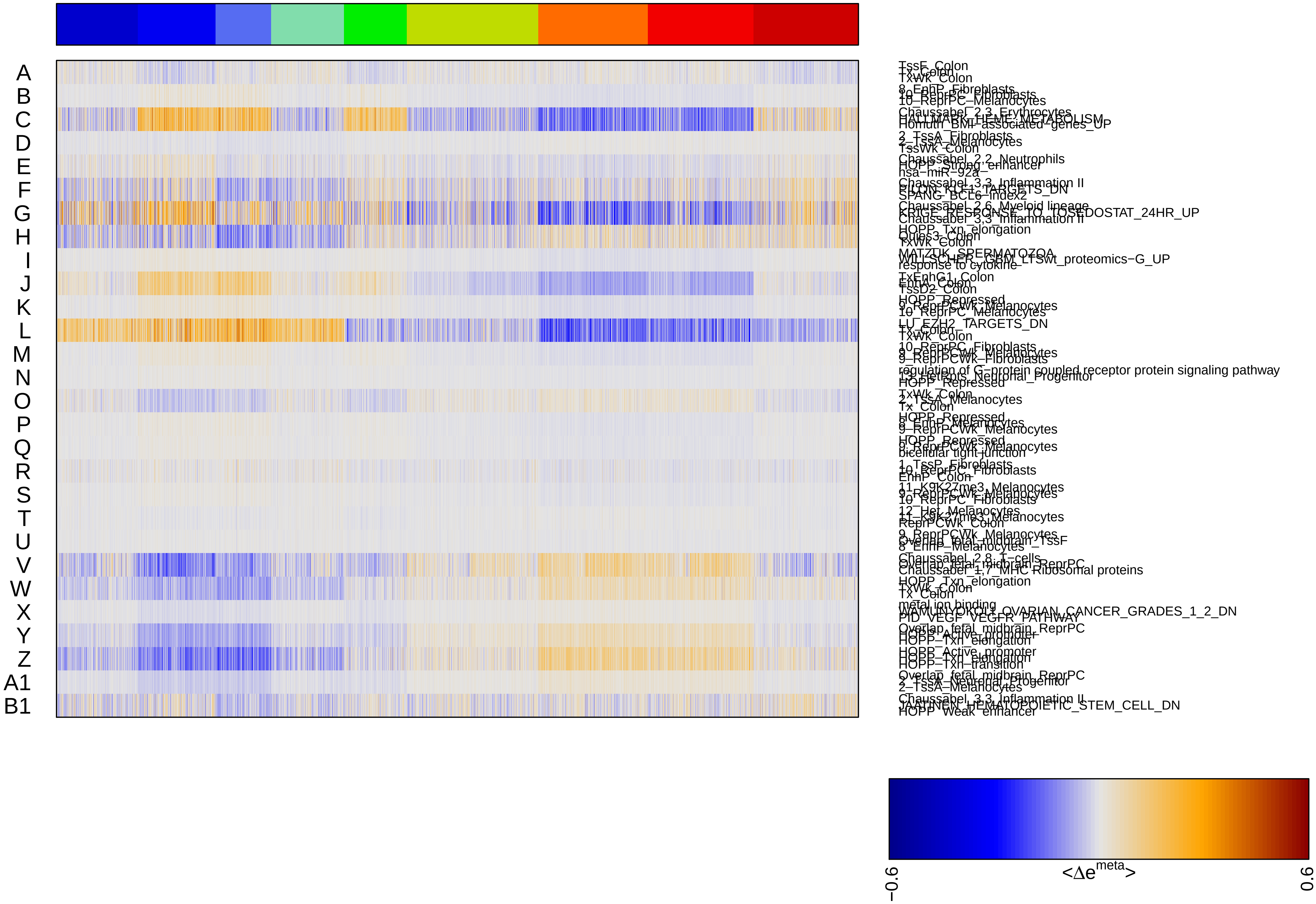
D
B1
F
E
H
A TsssF_Colon
Tx_Colon
B 8_EnhP_Fibroblasts
10_ReprPC_Fibroblasts
C Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
D 2_TssA_Fibroblasts
2_TssA_Melanocytes
E Chaussabel_2,2_Neutrophils
HOPP_Strong_enhancer
F Chaussabel_3,3_Inflammation II
PILON_KLF1_TARGETS_DN
G Chaussabel_2,6_Myeloid lineage
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
H HOPP_Txn_elongation
Quies3_Colon
I MATZUK_SPERMATOZOA
WILLSCHER_ GBM_LTSwt_proteomics−G_UP
J TxEnhG1_Colon
EnhA_Colon
K HOPP_Repressed
9_ReprPCWk_Melanocytes
L LU_EZH2_TARGETS_DN
Tx_Colon
M 10_ReprPC_Fibroblasts
9_ReprPCWk_Melanocytes
N regulation of G−protein coupled receptor protein signaling p
13_HetRpts_Neuronal_Progenitor
O TxWk_Colon
2_TssA_Melanocytes
P HOPP_Repressed
8_EnhP_Melanocytes
Q HOPP_Repressed
9_ReprPCWk_Melanocytes
R 1_TssP_Fibroblasts
10_ReprPC_Fibroblasts
S 11_K9K27me3_Melanocytes
9_ReprPCWk_Melanocytes
T 12_Het_Melanocytes
11_K9K27me3_Melanocytes
U 9_ReprPCWk_Melanocytes
Overlap_fetal_midbrain_TssF
V Chaussabel_2,8_T−cells
Overlap_fetal_midbrain_ReprPC
W HOPP_Txn_elongation
TxWk_Colon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X
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Z
A1
B1
TssF_Colon
Tx_Colon
TxWk_Colon
8_EnhP_Fibroblasts
10_ReprPC_Fibroblasts
10_ReprPC_Melanocytes
Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
Homuth_BMI−associated−genes_UP
2_TssA_Fibroblasts
2_TssA_Melanocytes
TssWk_Colon
Chaussabel_2,2_Neutrophils
HOPP_Strong_enhancer
hsa−miR−92a
Chaussabel_3,3_Inflammation II
PILON_KLF1_TARGETS_DN
SPANG_BCL6_index2
Chaussabel_2,6_Myeloid lineage
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
Chaussabel_3,3_Inflammation II
HOPP_Txn_elongation
Quies3_Colon
TxWk_Colon
MATZUK_SPERMATOZOA
WILLSCHER_GBM_LTSwt_proteomics−G_UP
response to cytokine
TxEnhG1_Colon
EnhA_Colon
TssD2_Colon
HOPP_Repressed
9_ReprPCWk_Melanocytes
10_ReprPC_Melanocytes
LU_EZH2_TARGETS_DN
Tx_Colon
TxWk_Colon
10_ReprPC_Fibroblasts
9_ReprPCWk_Melanocytes
9_ReprPCWk_Fibroblasts
regulation of G−protein coupled receptor protein signaling pathway
13_HetRpts_Neuronal_Progenitor
HOPP_Repressed
TxWk_Colon
2_TssA_Melanocytes
Tx_Colon
HOPP_Repressed
8_EnhP_Melanocytes
9_ReprPCWk_Melanocytes
HOPP_Repressed
9_ReprPCWk_Melanocytes
bicellular tight junction
1_TssP_Fibroblasts
10_ReprPC_Fibroblasts
EnhP_Colon
11_K9K27me3_Melanocytes
9_ReprPCWk_Melanocytes
10_ReprPC_Fibroblasts
12_Het_Melanocytes
11_K9K27me3_Melanocytes
ReprPCWk_Colon
9_ReprPCWk_Melanocytes
Overlap_fetal_midbrain_TssF
8_EnhP_Melanocytes
Chaussabel_2,8_T−cells
Overlap_fetal_midbrain_ReprPC
Chaussabel_1,7_MHC Ribosomal proteins
HOPP_Txn_elongation
TxWk_Colon
Tx_Colon
metal ion binding
WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN
PID_VEGF_VEGFR_PATHWAY
Overlap_fetal_midbrain_ReprPC
HOPP_Active_promoter
HOPP_Txn_elongation
HOPP_Active_promoter
HOPP_Txn_elongation
HOPP_Txn_transition
Overlap_fetal_midbrain_ReprPC
2_TssA_Neuronal_Progenitor
2_TssA_Melanocytes
Chaussabel_3,3_Inflammation II
JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
HOPP_Weak_enhancer
−0.6
<Δe^meta>
0.6

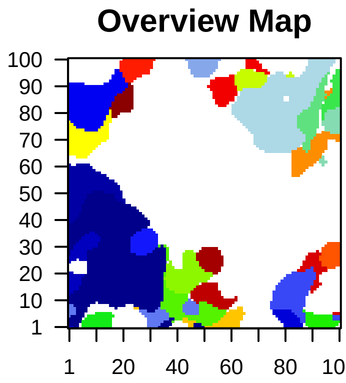
Correlation Cluster

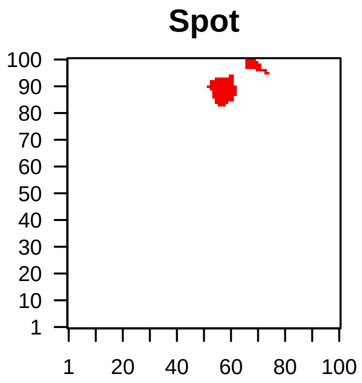
Spot Summary: A

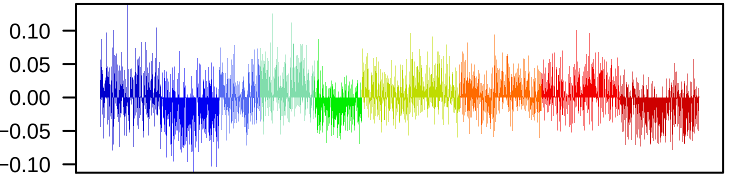
metagenes = 116
genes = 320

<r> metagenes = 0.92
<r> genes = 0.12
beta: r2= 2.76 / log p= −Inf

samples with spot = 65 (1.9 %)
A * : 14 (4.1 %)
A C * : 1 (0.3 %)
A C F * : 6 (2.6 %)
A F * : 17 (5.5 %)
C F * : 1 (0.4 %)
F * : 12 (2.2 %)
F J * : 6 (1.3 %)
J * : 8 (1.8 %)





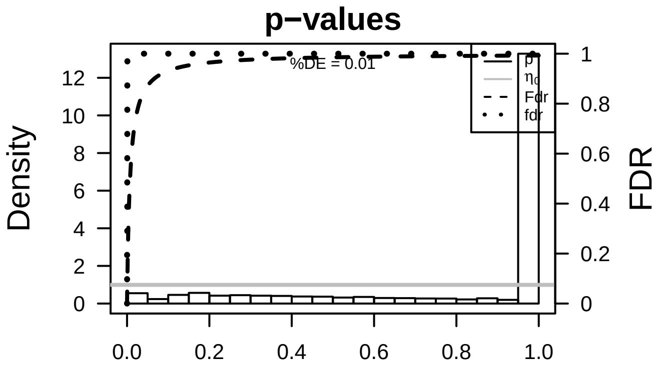


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_234304	0.75	−0.36	0.32	ABCB9	ATP binding cassette subfamily B member 9 [Source:HGNC
2	ILMN_173820	0.69	−0.54	0.3	CISH	cytokine inducible SH2 containing protein [Source:HGNC Sy
3	ILMN_166733	0.66	−0.74	0.18		
4	ILMN_185990	0.61	−0.37	0.41	TRAPPC2L	trafficking protein particle complex 2 like [Source:HGNC Sym
5	ILMN_206932	0.6	−0.4	0.24		
6	ILMN_323532	0.6	−0.39	0.29		Small nucleolar RNA SNORA71 [Source:RFAM;Acc:RF0005
7	ILMN_206156	0.55	−0.4	0.36	PLCH2	phospholipase C eta 2 [Source:HGNC Symbol;Acc:HGNC:29
8	ILMN_172317	0.52	−0.41	0.65	ANAPC5	anaphase promoting complex subunit 5 [Source:HGNC Symb
9	ILMN_220505	0.52	−0.41	0.36		
10	ILMN_180314	0.51	−0.38	0.42	MIR6751	synoviolin 1 [Source:HGNC Symbol;Acc:HGNC:20738]
11	ILMN_241112	0.5	−0.38	0.2	YBEY	ybeY metallopeptidase (putative) [Source:HGNC Symbol;Acc
12	ILMN_179047	0.5	−0.34	0.39	SLC25A28	solute carrier family 25 member 28 [Source:HGNC Symbol;A
13	ILMN_234304	0.49	−0.25	0.3	ABCB9	ATP binding cassette subfamily B member 9 [Source:HGNC
14	ILMN_184692	0.49	−0.42	0.29	STK32C	serine/threonine kinase 32C [Source:HGNC Symbol;Acc:HG
15	ILMN_169129	0.49	−0.33	0.38	MIR4793	cadherin EGF LAG seven−pass G−type receptor 3 [Source:H
16	ILMN_165747	0.47	−0.39	0.55	IL11RA	interleukin 11 receptor subunit alpha [Source:HGNC Symbol;
17	ILMN_318753	0.47	−0.28	0.4	FAM30A	family with sequence similarity 30, member A [Source:HGNC
18	ILMN_240385	0.46	−0.46	0.49	CYTH1	cytohesin 1 [Source:HGNC Symbol;Acc:HGNC:9501]
19	ILMN_173298	0.45	−0.29	0.29	ZBTB32	zinc finger and BTB domain containing 32 [Source:HGNC Sy
20	ILMN_241484	0.45	−0.35	0.61	TBRG4	transforming growth factor beta regulator 4 [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−21	161 / 7354	Colon	TssF_Colon
2	1e−17	175 / 9054	Colon	Tx_Colon
3	1e−17	169 / 8568	Colon	TxWk_Colon
4	8e−17	179 / 9555	Colon	TssA_Colon
5	1e−16	135 / 6138	Colon	TssD2_Colon
6	2e−16	179 / 9635	Chror	3_TssF_Fibroblasts
7	3e−16	215 / 12983	Chror	2_TssA_Neuronal_Progenitor
8	9e−15	200 / 11836	Chror	3_TssF_Melanocytes
9	6e−14	203 / 12298	Chror	2_TssA_Melanocytes
10	1e−13	171 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−13	162 / 8771	Chror	5_Tx_Melanocytes
12	1e−13	193 / 11455	Chror	2_TssA_Fibroblasts
13	3e−13	108 / 4795	Chror	6_EnhG_Fibroblasts
14	2e−12	136 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	3e−12	147 / 7854	Chror	5_Tx_Fibroblasts
16	8e−12	181 / 10779	Colon	Enh_Colon
17	2e−10	117 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
18	5e−10	172 / 10430	Brain	Overlap_fetal_midbrain_Quies
19	1e−09	150 / 8678	Colon	Quies3_Colon
20	2e−09	111 / 5699	Chror	6_EnhG_Melanocytes
21	5e−09	105 / 5373	Colon	EnhWk1_Colon
22	5e−09	191 / 12393	Chror	15_Quies_Neuronal_Progenitor
23	5e−09	125 / 6868	TF	ICGC_Elf1_targets
24	8e−09	161 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
25	1e−08	112 / 5956	Chror	3_TssF_Neuronal_Progenitor
26	1e−08	106 / 5518	TF	ICGC_Stat5_targets
27	2e−08	99 / 5067	TF	ICGC_Taf1_targets
28	2e−08	89 / 4362	TF	ICGC_Creb1_targets
29	3e−08	140 / 8226	Lympl	HOPP_Active_promoter
30	3e−08	75 / 3450	Chror	4_TxTrans_Fibroblasts
31	2e−07	54 / 2255	TF	ICGC_SrfV0416101_targets
32	3e−07	53 / 2215	TF	ICGC_GabpPcr2_targets
33	3e−07	85 / 4345	TF	ICGC_Zeb1_targets
34	6e−07	40 / 1478	TF	ICGC_Myc_targets
35	6e−07	123 / 7247	TF	ICGC_Runx3_targets
36	1e−06	85 / 4468	TF	ICGC_Egr1_targets
37	1e−06	66 / 3164	Brain	Mid_Frontal_Lobe_ZNF
38	2e−06	90 / 4881	TF	ICGC_Atf2_targets
39	2e−06	176 / 11847	Chror	7_Enh_Neuronal_Progenitor
40	3e−06	97 / 5466	TF	ICGC_Nficsc81335_targets



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	4e−04	35 / 1643	transcription, DNA−templated
2	4e−04	4 / 31	chromatin organization
3	8e−04	3 / 16	protein O−linked mannosylation
4	2e−03	4 / 44	interstrand cross−link repair
5	2e−03	27 / 1272	regulation of transcription, DNA−templated
6	3e−03	3 / 24	tRNA modification
7	6e−03	3 / 31	protein O−linked glycosylation
8	7e−03	2 / 11	arachidonic acid secretion
9	7e−03	2 / 11	endocardial cushion development
10	8e−03	2 / 12	cytoplasmic mRNA processing body assembly
11	8e−03	2 / 12	neural retina development
12	8e−03	2 / 12	positive regulation of kinase activity
13	1e−02	3 / 38	histone H3 acetylation
14	1e−02	2 / 14	cardiac septum development
15	1e−02	4 / 75	chromatin remodeling

Brain

Rank	p−value	#in/all	Geneset
1	1e−13	171 / 9504	Overlap_fetal_midbrain_K9K27me3
2	2e−10	117 / 5936	Overlap_fetal_midbrain_HetRpts
3	5e−10	172 / 10430	Overlap_fetal_midbrain_Quies
4	8e−09	161 / 9815	Overlap_fetal_midbrain_ReprPC
5	1e−06	66 / 3164	Mid_Frontal_Lobe_ZNF
6	5e−04	21 / 796	Overlap_fetal_midbrain_ZNF
7	5e−04	143 / 9917	Overlap_fetal_midbrain_ReprPCWk
8	5e−04	12 / 328	Fetal_Het
9	1e−03	35 / 1728	Fetal_ReprPCWk
10	9e−03	45 / 2709	Mid_Frontal_Lobe_HetRpts
11	3e−02	18 / 937	Fetal_EnhG
12	3e−02	14 / 681	Overlap_fetal_midbrain_EnhP
13	3e−02	16 / 818	Mid_Frontal_Lobe_Het
14	6e−02	5 / 180	Overlap_fetal_midbrain_Het
15	7e−02	12 / 630	Mid_Frontal_Lobe_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	12 / 527	Lembcke_Normal vs Adenoma
2	0.02	2 / 20	PanCan_ChromMod_geneset_nanostring
3	0.02	1 / 2	GENTLES_modul8
4	0.07	2 / 36	PanCan_HK_geneset_nanostring
5	0.10	2 / 46	PanCan_DNARepair_geneset_nanostring
6	0.13	2 / 54	KUIPER_MM poor survival
7	0.14	1 / 13	LIU_LIVER_CANCER
8	0.15	1 / 14	GENTLES_modul10
9	0.16	1 / 15	WOLFER_overlap genes
10	0.25	1 / 24	PanCan_Notch_geneset_nanostring
11	0.27	0 / 14	LIU_PROSTATE_CANCER_UP
12	0.28	1 / 28	PanCan_HH_geneset_nanostring
13	0.36	1 / 38	KUIPER_MM good survival
14	0.42	1 / 46	PanCan_TGF−B_geneset_nanostring
15	0.46	0 / 13	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	6e−04	79 / 4828	nucleus
2	3e−03	45 / 2535	nucleoplasm
3	3e−03	27 / 1304	mitochondrion
4	1e−02	2 / 14	integral component of nuclear inner membrane
5	2e−02	2 / 20	anaphase−promoting complex
6	3e−02	2 / 23	vesicle membrane
7	3e−02	2 / 24	mitochondrial ribosome
8	4e−02	3 / 67	cytoplasmic mRNA processing body
9	5e−02	3 / 69	primary cilium
10	8e−02	3 / 85	ciliary basal body
11	8e−02	4 / 138	mitochondrial outer membrane
12	8e−02	4 / 139	microtubule cytoskeleton
13	1e−01	2 / 45	brush border membrane
14	1e−01	1 / 10	chromocenter
15	1e−01	1 / 10	npBAF complex

Chr

Rank	p−value	#in/all	Geneset
1	0.01	13 / 536	Chr 22
2	0.02	8 / 289	Chr 21
3	0.04	25 / 1467	Chr 19
4	0.15	15 / 959	Chr 16
5	0.19	12 / 768	Chr 14
6	0.19	12 / 769	Chr 15
7	0.29	19 / 1411	Chr 11
8	0.30	9 / 619	Chr 20
9	0.32	13 / 954	Chr 9
10	0.37	12 / 904	Chr 10
11	0.38	15 / 1160	Chr 12
12	0.50	14 / 1170	Chr 7
13	0.56	14 / 1217	Chr 3
14	0.61	10 / 902	Chr 4
15	0.73	10 / 994	Chr X

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−16	179 / 9635	3_TssF_Fibroblasts
2	3e−16	215 / 12983	2_TssA_Neuronal_Progenitor
3	9e−15	200 / 11836	3_TssF_Melanocytes
4	6e−14	203 / 12298	2_TssA_Melanocytes
5	1e−13	162 / 8771	5_Tx_Melanocytes
6	1e−13	193 / 11455	2_TssA_Fibroblasts
7	3e−13	108 / 4795	6_EnhG_Fibroblasts
8	2e−12	136 / 6970	5_Tx_Neuronal_Progenitor
9	3e−12	147 / 7854	5_Tx_Fibroblasts
10	2e−09	111 / 5699	6_EnhG_Melanocytes
11	5e−09	191 / 12393	15_Quies_Neuronal_Progenitor
12	1e−08	112 / 5956	3_TssF_Neuronal_Progenitor
13	3e−08	75 / 3450	4_TxTrans_Fibroblasts
14	2e−06	176 / 11847	7_Enh_Neuronal_Progenitor
15	7e−06	184 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−21	161 / 7354	TssF_Colon
2	1e−17	175 / 9054	Tx_Colon
3	1e−17	169 / 8568	TxWk_Colon
4	8e−17	179 / 9555	TssA_Colon
5	1e−16	135 / 6138	TssD2_Colon
6	8e−12	181 / 10779	Enh_Colon
7	1e−09	150 / 8678	Quies3_Colon
8	5e−09	105 / 5373	EnhWk1_Colon
9	4e−06	31 / 1083	ZNF_Colon
10	1e−05	58 / 2845	TxEnhG1_Colon
11	2e−04	43 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	4e−04	156 / 10999	TssWk_Colon
13	9e−04	137 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
14	3e−03	49 / 2810	EnhA_Colon
15	4e−03	29 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

Glio

Rank	p−value	#in/all	Geneset
1	1e−04	39 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	4e−04	41 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	9e−03	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
4	3e−02	4 / 100	GIEZELT_GBM_STS_down_VS_LTS
5	3e−02	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
6	6e−02	2 / 35	WIRTH_PN subtype
7	7e−02	1 / 6	laffaire_hypometh_LGG_vs_control
8	9e−02	3 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
9	9e−02	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
10	1e−01	3 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
11	1e−01	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
12	2e−01	2 / 59	Christensen_hypermethylated_in_primary_glioblastoma
13	2e−01	3 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
14	2e−01	1 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
15	2e−01	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	14 / 336	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
2	1e−04	12 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
3	4e−04	9 / 188	SANSOM_APC_TARGETS_REQUIRE_MYC
4	4e−04	7 / 114	FIGUEROA_AML_METHYLATION_CLUSTER_1_UP
5	8e−04	22 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
6	1e−03	10 / 262	MANALO_HYPOXIA_DN
7	1e−03	16 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
8	2e−03	8 / 193	LINSLEY_MIR16_TARGETS
9	3e−03	19 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
10	3e−03	2 / 7	REACTOME_REGULATION_OF_THE_FANCONI_ANEMIA_PATHWAY
11	4e−03	7 / 167	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
12	4e−03	6 / 126	FIGUEROA_AML_METHYLATION_CLUSTER_6_UP
13	4e−03	3 / 27	MAYBURD_RESPONSE_TO_L663536_UP
14	5e−03	7 / 179	KASLER_HDAC7_TARGETS_1_UP
15	6e−03	3 / 31	BREDEMEYER_RAG_SIGNALING_VIA_ATM_NOT_VIA_NFKB_DN

HM

Rank	p−value	#in/all	Geneset
1	0.009	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
2	0.078	4 / 138	HALLMARK_FATTY_ACID_METABOLISM
3	0.131	2 / 54	HALLMARK_MYC_TARGETS_V2
4	0.144	4 / 173	HALLMARK_E2F_TARGETS
5	0.289	1 / 29	HALLMARK_NOTCH_SIGNALING
6	0.338	3 / 176	HALLMARK_KRAS_SIGNALING_UP
7	0.370	3 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
8	0.370	3 / 186	HALLMARK_MYOGENESIS
9	0.370	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	0.375	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.437	2 / 127	HALLMARK_COAGULATION
12	0.566	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
13	0.632	1 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
14	0.632	2 / 183	HALLMARK_APICAL_JUNCTION
15	0.638	2 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	2 / 31	DUMEAUX_Fasting enriched genes
2	0.30	2 / 94	DUMEAUX_Smoking enriched genes
3	0.92	1 / 211	Homuth_BMI−associated−genes_DN
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 17	DUMEAUX_High bmi enriched genes
13	1.00	0 / 147	Homuth_BMI−associated−genes_UP
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−08	140 / 8226	HOPP_Active_promoter
2	1e−05	118 / 7275	HOPP_Txn_elongation
3	8e−05	90 / 5356	HOPP_Txn_transition
4	5e−04	121 / 8098	HOPP_Weak_promoter
5	1e−03	2 / 5	MASCQUE_mBL UP
6	1e−03	14 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
7	4e−03	26 / 1270	SPANG_BCR UP
8	5e−03	18 / 777	WIRTH_lymphoma937_spot D
9	5e−03	13 / 493	WIRTH_lymphoma937_spot J
10	1e−02	9 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
11	2e−02	9 / 331	WIRTH_lymphoma937_spot H
12	2e−02	7 / 232	WIRTH_lymphoma937_spot B
13	2e−02	16 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
14	4e−02	6 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
15	5e−02	100 / 7448	HOPP_Strong_enhancer

Melanoma

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

MF

Rank	p−value	#in/all	Geneset
1	0.002	34 / 1717	metal ion binding
2	0.004	4 / 54	flavin adenine dinucleotide binding
3	0.005	5 / 94	double−stranded DNA binding
4	0.006	2 / 10	DNA polymerase binding
5	0.007	2 / 11	N−acetyltransferase activity
6	0.008	2 / 12	pseudouridine synthase activity
7	0.015	3 / 44	methylated histone binding
8	0.016	2 / 17	retinol dehydrogenase activity
9	0.020	2 / 19	oxidoreductase activity, acting on paired donors, with incorporation or reducti
10	0.022	2 / 20	L−ascorbic acid binding
11	0.030	3 / 58	core promoter binding
12	0.033	3 / 60	microtubule motor activity
13	0.037	2 / 26	Ran GTPase binding
14	0.042	2 / 28	DNA−dependent ATPase activity
15	0.045	3 / 68	drug binding

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.006	4 / 63	hsa−miR−518c*
2	0.022	4 / 91	hsa−miR−425
3	0.027	2 / 22	hsa−miR−1288
4	0.049	3 / 70	hsa−miR−193b
5	0.054	4 / 121	hsa−miR−421
6	0.060	4 / 126	hsa−miR−223
7	0.068	1 / 6	hsa−miR−1281
8	0.076	2 / 39	hsa−miR−517*
9	0.083	2 / 41	hsa−miR−423−3p
10	0.083	2 / 41	hsa−miR−516a−3p
11	0.090	2 / 43	hsa−miR−661
12	0.097	2 / 45	hsa−miR−766
13	0.101	2 / 46	hsa−miR−658
14	0.105	3 / 97	hsa−miR−526a
15	0.108	2 / 48	hsa−miR−346

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	BENTINK_ras.4
2	0.1	1 / 13	BENTINK_src.10
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 13	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 14	BENTINK_ras.6
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−04	10 / 221	Chaussabel_3,8_Enzymes
2	4e−02	2 / 29	Chaussabel_2,7_Unknown function
3	8e−02	12 / 647	PROTEINATLAS_lateral ventricle
4	1e−01	4 / 148	VAQUERIZAS_General_TF
5	1e−01	9 / 490	PROTEINATLAS_heart muscle
6	1e−01	1 / 13	WIRTH_Thymus
7	1e−01	3 / 113	Chaussabel_1,4_Replication
8	2e−01	1 / 14	WIRTH_Thyroid gland
9	2e−01	3 / 119	Chaussabel_2,4_Ribosomal proteins
10	2e−01	3 / 119	Chaussabel_2,8_T−cells
11	2e−01	1 / 17	VAQUERIZAS_Heart_TF
12	2e−01	3 / 132	WIRTH_Muscle
13	2e−01	3 / 139	Chaussabel_1,8_Metabolism Biosynthesis
14	2e−01	10 / 650	PROTEINATLAS_hippocampus
15	2e−01	7 / 429	PROTEINATLAS_soft tissue

Telomeres

Rank	p−value	#in/all	Geneset
1	0.004	3 / 27	Nabetani_alt len telomeres_genes_ko
2	1.000	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	5e−09	125 / 6868	ICGC_Elf1_targets
2	1e−08	106 / 5518	ICGC_Stat5_targets
3	2e−08	99 / 5067	ICGC_Taf1_targets
4	2e−08	89 / 4362	ICGC_Creb1_targets
5	2e−07	54 / 2255	ICGC_SrfV0416101_targets
6	3e−07	53 / 2215	ICGC_GabpPcr2_targets
7	3e−07	85 / 4345	ICGC_Zeb1_targets
8	6e−07	40 / 1478	ICGC_Myc_targets
9	6e−07	123 / 7247	ICGC_Runx3_targets
10	1e−06	85 / 4468	ICGC_Egr1_targets
11	2e−06	90 / 4881	ICGC_Atf2_targets
12	3e−06	97 / 5466	ICGC_Nficsc81335_targets
13	5e−06	111 / 6578	ICGC_Pou2_targets
14	5e−06	78 / 4131	ICGC_Nfatc1_targets
15	7e−06	107 / 6322	ICGC_Tcf3_targets

Correlation Cluster

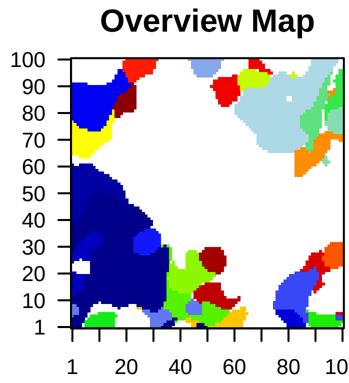
Spot Summary: B

metagenes = 81
genes = 359

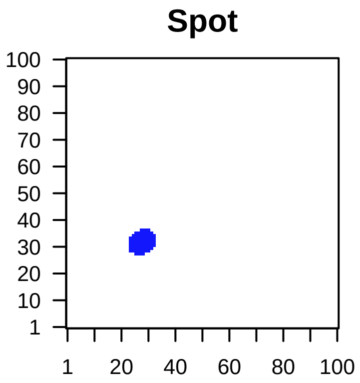
<r> metagenes = 0.96
<r> genes = 0.08
beta: r2= 0.66 / log p= −Inf

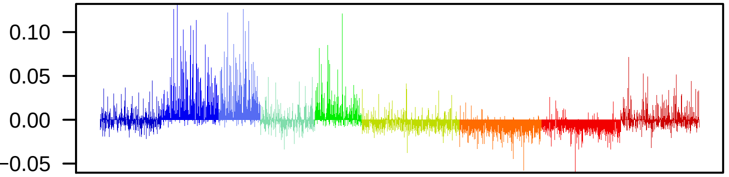
samples with spot = 39 (1.2 %)
A C * : 19 (5.8 %)
A C F * : 13 (5.5 %)
C F * : 6 (2.3 %)
N * : 1 (0.2 %)

Overview Map



Spot





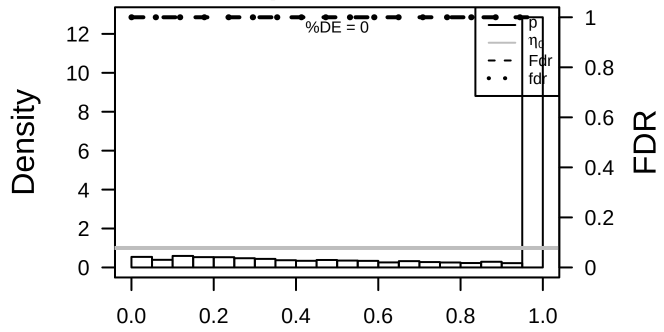
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324031	0.43	−0.23	0.56	SCX	scleraxis bHLH transcription factor [Source:HGNC Symbol;Ac
2	ILMN_169884	0.41	−0.23	0.19	SLC8A2	solute carrier family 8 member A2 [Source:HGNC Symbol;Ac
3	ILMN_176126	0.41	−0.3	0.54	MPI	mannose phosphate isomerase [Source:HGNC Symbol;Acc:H
4	ILMN_170878	0.39	−0.33	0.41	MFAP3	microfibrillar associated protein 3 [Source:HGNC Symbol;Acc
5	ILMN_172379	0.38	−0.29	0.51	PALB2	partner and localizer of BRCA2 [Source:HGNC Symbol;Acc:H
6	ILMN_171944	0.37	−0.24	0.55	DCLK2	doublecortin like kinase 2 [Source:HGNC Symbol;Acc:HGNC
7	ILMN_171582	0.36	−0.24	0.55	FBXO16	F−box protein 16 [Source:HGNC Symbol;Acc:HGNC:13618]
8	ILMN_180525	0.36	−0.23	0.47		cell division cycle 14C, pseudogene [Source:HGNC Symbol;A
9	ILMN_167495	0.35	−0.23	0.59	SCP2	sterol carrier protein 2 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_179226	0.35	−0.24	0.18	TRIM4	tripartite motif containing 4 [Source:HGNC Symbol;Acc:HGN
11	ILMN_212956	0.35	−0.23	0.51	LDLRAD3	low density lipoprotein receptor class A domain containing 3 [
12	ILMN_175976	0.34	−0.19	0.56	CTXN1	cortexin 1 [Source:HGNC Symbol;Acc:HGNC:31108]
13	ILMN_176615	0.34	−0.27	0.21		
14	ILMN_240575	0.34	−0.24	0.51	VAMP1	vesicle associated membrane protein 1 [Source:HGNC Symb
15	ILMN_180579	0.34	−0.22	0.42	TRIO	trio Rho guanine nucleotide exchange factor [Source:HGNC S
16	ILMN_171695	0.34	−0.2	0.53	C1QL1	complement C1q like 1 [Source:HGNC Symbol;Acc:HGNC:24
17	ILMN_181439	0.34	−0.21	0.46		
18	ILMN_172207	0.33	−0.21	0.56	APOC3	apolipoprotein C3 [Source:HGNC Symbol;Acc:HGNC:610]
19	ILMN_324559	0.32	−0.19	0.45	MIR1247	DIO3 opposite strand/antisense RNA (head to head) [Source:
20	ILMN_165785	0.32	−0.21	0.54	ACTL6B	actin like 6B [Source:HGNC Symbol;Acc:HGNC:160]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−13	81 / 3068	Chror	8_EnhP_Fibroblasts
2	3e−11	94 / 4169	Chror	10_ReprPC_Fibroblasts
3	7e−11	82 / 3438	Chror	10_ReprPC_Melanocytes
4	5e−10	90 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	1e−09	75 / 3173	Colon	ReprPC_Colon
6	7e−09	66 / 2740	Colon	ReprPCWk_Colon
7	5e−07	99 / 5384	Lympl	HOPP_Repressed
8	2e−06	46 / 1895	Colon	EnhP_Colon
9	2e−06	58 / 2660	Chror	8_EnhP_Melanocytes
10	4e−06	81 / 4304	Chror	9_ReprPCWk_Melanocytes
11	6e−06	60 / 2894	Colon	TssP_Colon
12	2e−05	41 / 1753	TF	HEBENSTREIT_low expression TF
13	2e−05	69 / 3639	Chror	1_TssP_Fibroblasts
14	2e−05	36 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
15	3e−05	41 / 1789	Chror	8_EnhP_Neuronal_Progenitor
16	5e−05	48 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
17	1e−04	14 / 364	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
18	1e−04	13 / 325	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
19	2e−04	64 / 3523	Chror	1_TssP_Melanocytes
20	2e−04	21 / 746	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
21	3e−04	27 / 1119	Brain	Overlap_fetal_midbrain_TssA
22	4e−04	65 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
23	4e−04	39 / 1893	Brain	Overlap_fetal_midbrain_TssF
24	5e−04	4 / 32	CC	photoreceptor connecting cilium
25	5e−04	3 / 14	MF	glycine binding
26	5e−04	3 / 14	BP	regulation of short−term neuronal synaptic plasticity
27	6e−04	15 / 478	Refer	WIRTH_Nervous System
28	6e−04	23 / 924	Brain	Mid_Frontal_Lobe_TssF
29	6e−04	16 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
30	7e−04	4 / 35	CC	photoreceptor inner segment
31	9e−04	53 / 2939	Lympl	HOPP_Poised_promoter
32	1e−03	12 / 366	Colon	K9K27me3_Colon
33	2e−03	14 / 476	MF	sequence−specific DNA binding
34	2e−03	53 / 3046	Brain	Fetal_TssA
35	2e−03	47 / 2620	Chror	1_TssP_Neuronal_Progenitor
36	2e−03	4 / 46	BP	skeletal muscle tissue development
37	2e−03	23 / 1021	GSEA	BENPORATH_ES_WITH_H3K27ME3
38	2e−03	5 / 79	BP	neuropeptide signaling pathway
39	2e−03	5 / 79	BP	regulation of membrane potential
40	3e−03	28 / 1360	Brain	Mid_Frontal_Lobe_TssP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.03	5 / 142	HORVATH_aging_genes meth UP
2	0.03	3 / 58	TESCHENDORFF_age_hypermethylated
3	0.73	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 14	regulation of short−term neuronal synaptic plasticity
2	2e−03	4 / 46	skeletal muscle tissue development
3	2e−03	5 / 79	neuropeptide signaling pathway
4	2e−03	5 / 79	regulation of membrane potential
5	6e−03	3 / 31	pituitary gland development
6	6e−03	14 / 550	positive regulation of transcription, DNA−templated
7	6e−03	2 / 10	multicellular organismal response to stress
8	6e−03	2 / 10	neuromuscular process controlling posture
9	6e−03	2 / 10	positive regulation of myelination
10	6e−03	2 / 10	regulation of dendrite development
11	6e−03	7 / 185	visual perception
12	7e−03	2 / 11	positive regulation of astrocyte differentiation
13	8e−03	2 / 12	sensory perception of light stimulus
14	9e−03	9 / 297	nervous system development
15	9e−03	4 / 69	dephosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	2e−05	36 / 1476	Overlap_fetal_midbrain_TxTrans
2	3e−04	27 / 1119	Overlap_fetal_midbrain_TssA
3	4e−04	39 / 1893	Overlap_fetal_midbrain_TssF
4	6e−04	23 / 924	Mid_Frontal_Lobe_TssF
5	2e−03	53 / 3046	Fetal_TssA
6	3e−03	28 / 1360	Mid_Frontal_Lobe_TssP
7	9e−03	14 / 578	Fetal_Tx
8	9e−03	64 / 4112	Mid_Frontal_Lobe_ReprPC
9	3e−02	16 / 819	Overlap_fetal_midbrain_TssP
10	5e−02	10 / 465	Mid_Frontal_Lobe_TxTrans
11	7e−02	7 / 304	Mid_Frontal_Lobe_TssA
12	8e−02	8 / 383	Mid_Frontal_Lobe_Tx
13	9e−02	7 / 328	Fetal_Het
14	1e−01	3 / 110	Overlap_fetal_midbrain_Tx
15	2e−01	37 / 2709	Mid_Frontal_Lobe_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	3 / 76	PanCan_Wnt_geneset_nanostring
2	0.10	4 / 150	PanCan_MAPK_geneset_nanostring
3	0.13	1 / 12	LIU_BREAST_CANCER
4	0.15	1 / 14	GENTLES_modul1
5	0.16	1 / 15	WANG_ER_UP
6	0.17	1 / 16	GENTLES_modul16
7	0.21	3 / 136	PanCan_RAS_geneset_nanostring
8	0.25	1 / 24	PanCan_Notch_geneset_nanostring
9	0.27	0 / 14	LIU_PROSTATE_CANCER_UP
10	0.28	1 / 28	PanCan_HH_geneset_nanostring
11	0.31	0 / 13	LIU_LIVER_CANCER
12	0.42	1 / 46	PanCan_TGF−B_geneset_nanostring
13	0.53	0 / 14	LIU_COMMON_CANCER_GENES
14	0.59	0 / 15	LIU_PROSTATE_CANCER_DN
15	0.62	1 / 82	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 32	photoreceptor connecting cilium
2	7e−04	4 / 35	photoreceptor inner segment
3	4e−03	14 / 524	intracellular
4	4e−03	5 / 88	keratin filament
5	4e−03	3 / 27	heterochromatin
6	1e−02	2 / 14	Cul4−RING E3 ubiquitin ligase complex
7	1e−02	11 / 423	cell junction
8	1e−02	52 / 3291	integral component of membrane
9	1e−02	2 / 16	photoreceptor disc membrane
10	2e−02	7 / 220	synapse
11	2e−02	2 / 21	excitatory synapse
12	3e−02	2 / 22	I band
13	3e−02	6 / 196	postsynaptic membrane
14	3e−02	8 / 310	dendrite
15	3e−02	7 / 256	apical plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	23 / 1170	Chr 7
2	0.02	12 / 536	Chr 22
3	0.10	16 / 959	Chr 16
4	0.11	15 / 904	Chr 10
5	0.17	14 / 902	Chr 4
6	0.20	21 / 1467	Chr 19
7	0.25	5 / 289	Chr 21
8	0.30	19 / 1411	Chr 11
9	0.38	17 / 1318	Chr 17
10	0.62	11 / 994	Chr X
11	0.67	13 / 1217	Chr 3
12	0.68	8 / 769	Chr 15
13	0.71	12 / 1160	Chr 12
14	0.77	3 / 342	Chr 18
15	0.77	8 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−13	81 / 3068	8_EnhP_Fibroblasts
2	3e−11	94 / 4169	10_ReprPC_Fibroblasts
3	7e−11	82 / 3438	10_ReprPC_Melanocytes
4	5e−10	90 / 4107	9_ReprPCWk_Fibroblasts
5	2e−06	58 / 2660	8_EnhP_Melanocytes
6	4e−06	81 / 4304	9_ReprPCWk_Melanocytes
7	2e−05	69 / 3639	1_TssP_Fibroblasts
8	3e−05	41 / 1789	8_EnhP_Neuronal_Progenitor
9	5e−05	48 / 2297	10_ReprPC_Neuronal_Progenitor
10	2e−04	64 / 3523	1_TssP_Melanocytes
11	4e−04	65 / 3691	9_ReprPCWk_Neuronal_Progenitor
12	2e−03	47 / 2620	1_TssP_Neuronal_Progenitor
13	3e−02	40 / 2516	11_K9K27me3_Melanocytes
14	8e−02	151 / 11847	7_Enh_Neuronal_Progenitor
15	1e−01	34 / 2315	13_HetRpts_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−09	75 / 3173	ReprPC_Colon
2	7e−09	66 / 2740	ReprPCWk_Colon
3	2e−06	46 / 1895	EnhP_Colon
4	6e−06	60 / 2894	TssP_Colon
5	1e−03	12 / 366	K9K27me3_Colon
6	5e−03	12 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	5e−03	16 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	9e−03	9 / 299	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
9	1e−02	16 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
10	1e−02	14 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	2e−02	61 / 4018	EnhWk2_Colon
12	2e−02	5 / 129	Marisa_CRC−cluster−b
13	2e−02	143 / 10779	Enh_Colon
14	3e−02	11 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
15	3e−02	16 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

Glio

Rank	p−value	#in/all	Geneset
1	0.01	48 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.02	4 / 84	Weller_LGG_gradeII−vs−III_UP
3	0.03	17 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	0.03	2 / 22	Shinawi_with_increased_methylation_in_STS
5	0.03	2 / 25	Barbus_GBM_STS_vs._LTS
6	0.08	3 / 84	GIEZELT_GBM_STS_up_VS_LTS
7	0.09	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
8	0.09	2 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
9	0.10	3 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
10	0.10	4 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
11	0.10	1 / 9	oligodendrocytes_glio
12	0.11	3 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	0.12	9 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
14	0.12	8 / 419	Down_a
15	0.12	3 / 104	WIRTH_Normal Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	14 / 364	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	1e−04	13 / 325	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
3	2e−04	21 / 746	MARTENS_TRETINOIN_RESPONSE_UP
4	6e−04	16 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
5	2e−03	23 / 1021	BENPORATH_ES_WITH_H3K27ME3
6	3e−03	8 / 204	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
7	4e−03	21 / 956	BENPORATH_SUZ12_TARGETS
8	5e−03	2 / 9	REACTOME_GLYCOPROTEIN_HORMONES
9	5e−03	4 / 58	MIKKELSEN_ES_HCP_WITH_H3_UNMETHYLATED
10	5e−03	21 / 962	BENPORATH_EED_TARGETS
11	5e−03	15 / 598	BENPORATH_PRC2_TARGETS
12	5e−03	6 / 134	LEE_NEURAL_CREST_STEM_CELL_UP
13	5e−03	3 / 30	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
14	5e−03	11 / 379	ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
15	6e−03	9 / 278	IVANOVA_HEMATOPOIESIS_STEM_CELL_LONG_TERM

HM

Rank	p−value	#in/all	Geneset
1	0.009	3 / 37	HALLMARK_PANCREAS_BETA_CELLS
2	0.048	4 / 116	HALLMARK_SPERMATOGENESIS
3	0.068	5 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	0.155	4 / 177	HALLMARK_MITOTIC_SPINDLE
5	0.168	4 / 183	HALLMARK_GLYCOLYSIS
6	0.175	4 / 186	HALLMARK_MYOGENESIS
7	0.217	3 / 137	HALLMARK_UV_RESPONSE_UP
8	0.290	1 / 29	HALLMARK_NOTCH_SIGNALING
9	0.340	2 / 103	HALLMARK_BILE_ACID_METABOLISM
10	0.343	3 / 177	HALLMARK_KRAS_SIGNALING_DN
11	0.369	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.376	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	0.657	2 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.658	1 / 91	HALLMARK_ANDROGEN_RESPONSE
15	0.658	1 / 91	HALLMARK_PEROXISOME

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	2 / 94	DUMEAUX_Smoking enriched genes
2	0.3	1 / 31	DUMEAUX_Fasting enriched genes
3	0.8	1 / 147	Homuth_BMI−associated−genes_UP
4	0.9	1 / 211	Homuth_BMI−associated−genes_DN
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−07	99 / 5384	HOPP_Repressed
2	9e−04	53 / 2939	HOPP_Poised_promoter
3	1e−02	4 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_C
4	1e−02	4 / 74	WIRTH_lymphoma937_spot IM
5	4e−02	10 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
6	5e−02	3 / 70	LEE_Developmental_regulators
7	1e−01	9 / 464	WIRTH_lymphoma937_spot I
8	1e−01	1 / 12	DAVE_BL_DN
9	1e−01	1 / 13	Care_Polarized immune response
10	2e−01	7 / 408	TARTE_Mature plasma cell signature
11	2e−01	1 / 21	ROSOLOWSKI_red UP
12	3e−01	2 / 88	ROSOLOWSKI_red total
13	3e−01	1 / 28	DAVE_Immune response 1
14	3e−01	35 / 2701	HOPP_Repetitive
15	3e−01	2 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_U

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.13	2 / 54	Hugo_melanoma−all−MET_DN
3	0.30	1 / 30	Hugo_melanoma−all−MET_UP
4	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 14	glycine binding
2	2e−03	14 / 476	sequence−specific DNA binding
3	5e−03	3 / 29	beta−amyloid binding
4	8e−03	3 / 35	kinesin binding
5	2e−02	3 / 47	chromatin DNA binding
6	2e−02	2 / 21	acetylcholine−activated cation−selective channel activity
7	2e−02	2 / 21	acetylcholine receptor activity
8	3e−02	4 / 99	transcriptional repressor activity, RNA polymerase II core promoter proximal r
9	3e−02	2 / 25	protein phosphatase inhibitor activity
10	3e−02	2 / 25	spectrin binding
11	4e−02	2 / 26	phospholipase A2 activity
12	4e−02	6 / 218	transcriptional activator activity, RNA polymerase II core promoter proximal re
13	5e−02	2 / 31	protein tyrosine/serine/threonine phosphatase activity
14	5e−02	5 / 172	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
15	5e−02	2 / 32	delayed rectifier potassium channel activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.01	3 / 41	Melanoma, cutaneous malignant, 2
2	0.18	1 / 17	Thyroid carcinoma, follicular
3	0.19	1 / 18	Non−Hodgkin lymphoma, somatic
4	0.28	1 / 28	Immunological
5	0.38	1 / 40	Medulloblastoma
6	0.43	1 / 48	Multiple myeloma
7	0.50	2 / 142	Lung cancer
8	0.54	1 / 65	Hepatocellular carcinoma
9	0.55	1 / 68	Glioblastoma multiforme, somatic
10	0.58	1 / 73	Stroke, susceptibility to
11	0.67	1 / 95	Colorectal cancer
12	0.70	1 / 102	Leukemia
13	0.74	1 / 113	Ovarian cancer
14	0.75	1 / 116	Cancer
15	0.76	1 / 120	Hematological

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	3 / 25	hsa−miR−943
2	0.005	5 / 93	hsa−miR−216a
3	0.008	7 / 193	hsa−miR−448
4	0.009	4 / 70	hsa−miR−548b−3p
5	0.030	4 / 100	hsa−miR−147
6	0.031	5 / 149	hsa−miR−142−3p
7	0.032	2 / 24	hsa−miR−99b
8	0.038	3 / 63	hsa−miR−1243
9	0.040	5 / 159	hsa−miR−520h
10	0.041	3 / 65	hsa−miR−606
11	0.041	6 / 215	hsa−miR−199a−3p
12	0.046	3 / 68	hsa−miR−649
13	0.053	4 / 120	hsa−miR−664
14	0.058	3 / 75	hsa−miR−651
15	0.060	3 / 76	hsa−miR−592

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	6e−04	15 / 478	WIRTH_Nervous System
2	4e−03	2 / 8	VAQUERIZAS_Tongue_TF
3	7e−03	4 / 64	VAQUERIZAS_Lung_TF
4	1e−02	3 / 40	VAQUERIZAS_Thyroid_TF
5	1e−02	2 / 16	VAQUERIZAS_Fetal thyroid_TF
6	2e−02	3 / 48	WIRTH_Pancreas
7	2e−02	3 / 49	JONGENEEL_Retina
8	3e−02	2 / 25	VAQUERIZAS_Adrenal cortex_TF
9	1e−01	1 / 10	VAQUERIZAS_Skeletal muscle_TF
10	1e−01	3 / 107	WIRTH_Liver
11	1e−01	1 / 12	VAQUERIZAS_Skin_TF
12	1e−01	1 / 13	WIRTH_Thymus
13	1e−01	1 / 13	JONGENEEL_Thyroid
14	2e−01	5 / 242	Chaussabel_3,9_Kinases
15	2e−01	1 / 16	VAQUERIZAS_Ovary_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	2e−05	41 / 1753	HEBENSTREIT_low expression TF
2	2e−02	16 / 747	ICGC_NrsfPcr2_targets
3	6e−02	24 / 1466	ICGC_NrsfPcr1_targets
4	6e−01	59 / 5188	ICGC_Ebfsc137065_targets
5	7e−01	16 / 1478	ICGC_Myc_targets
6	7e−01	18 / 1669	ICGC_P300_targets
7	7e−01	30 / 2759	ICGC_Bcl3_targets
8	7e−01	77 / 6868	ICGC_Elf1_targets
9	7e−01	38 / 3507	ICGC_Rad21_targets
10	8e−01	6 / 631	ICGC_RxraPcr1_targets
11	8e−01	48 / 4468	ICGC_Egr1_targets
12	8e−01	51 / 4735	ICGC_Pu1_targets
13	9e−01	11 / 1231	KIM_MYC targets
14	9e−01	6 / 733	ICGC_Atf3_targets
15	9e−01	20 / 2133	ICGC_Mef2_targets

Correlation Cluster

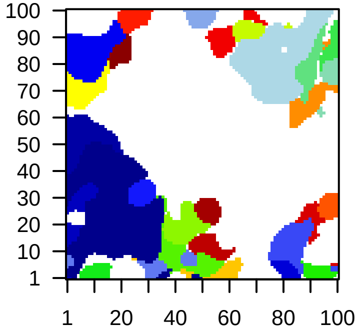
Spot Summary: C

metagenes = 90
genes = 772

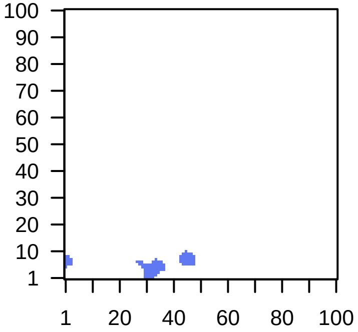
<r> metagenes = 0.93
<r> genes = 0.28
beta: r2= 42.05 / log p= −Inf

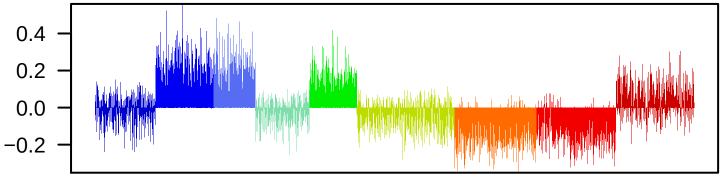
samples with spot = 1047 (30.9 %)
A * : 50 (14.5 %)
A C * : 310 (94.5 %)
A C F * : 225 (95.7 %)
A F * : 22 (7.1 %)
C F * : 240 (90.6 %)
F * : 24 (4.3 %)
F J * : 1 (0.2 %)
J * : 4 (0.9 %)
N * : 171 (38.6 %)

Overview Map



Spot





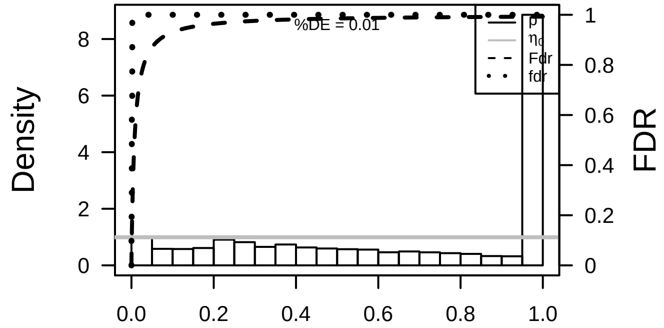
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_177651	3.13	−1.1	0.44	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
2	ILMN_170832	2.82	−1.91	0.84	ALAS2	5'−aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:H
3	ILMN_165243	2.79	−1.83	0.82	CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:13
4	ILMN_174983	2.5	−1.99	0.5	SMIM1	small integral membrane protein 1 (Vel blood group) [Source:
5	ILMN_176616	2.48	−2.2	0.85	SNCA	synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138]
6	ILMN_171345	2.47	−1.33	0.39	HBZ	hemoglobin subunit zeta [Source:HGNC Symbol;Acc:HGNC:
7	ILMN_328576	2.47	−2.05	0.9	SLC4A1	solute carrier family 4 member 1 (Diego blood group) [Source
8	ILMN_169651	2.44	−2.23	0.92	AHSP	alpha hemoglobin stabilizing protein [Source:HGNC Symbol;
9	ILMN_173571	2.39	−1.48	0.66	KRT1	keratin 1 [Source:HGNC Symbol;Acc:HGNC:6412]
10	ILMN_168065	2.38	−1.7	0.94	SELENBP1	selenium binding protein 1 [Source:HGNC Symbol;Acc:HGN
11	ILMN_177409	2.28	−1.33	0.77	FECH	ferrochelatase [Source:HGNC Symbol;Acc:HGNC:3647]
12	ILMN_323518	2.25	−2.09	0.85	FAM83A−AS1	FAM83A antisense RNA 1 [Source:HGNC Symbol;Acc:HGN
13	ILMN_171326	2.21	−1.75	0.83	FAM46C	family with sequence similarity 46 member C [Source:HGNC
14	ILMN_181439	2.2	−1.99	0.93	EPB42	erythrocyte membrane protein band 4.2 [Source:HGNC Sym
15	ILMN_203877	2.18	−1.09	0.35	TUBB2A	tubulin beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:1
16	ILMN_181552	2.18	−2.44	0.93	HBD	hemoglobin subunit delta [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_176031	2.17	−1.46	0.8	VWCE	von Willebrand factor C and EGF domains [Source:HGNC Sy
18	ILMN_209145	2.09	−2.18	0.83		
19	ILMN_169518	2.09	−1.42	0.88	GYPE	glycophorin E (MNS blood group) [Source:HGNC Symbol;Ac
20	ILMN_179245	2.08	−1.49	0.65	TMEM158	transmembrane protein 158 (gene/pseudogene) [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−66	58 / 111	Refer	Chaussabel_2,3_Erythrocytes
2	2e−45	54 / 185	HM	HALLMARK_HEME_METABOLISM
3	2e−14	24 / 147	Lifest	Homuth_BMI−associated−genes_UP
4	4e−14	31 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
5	4e−14	12 / 25	GSEA	VALK_AML_CLUSTER_8
6	6e−14	10 / 15	Lifest	DUMEAUX_Red blood cells in non smokers literature genes up
7	8e−14	12 / 26	GSEA	VALK_AML_CLUSTER_7
8	2e−11	24 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
9	4e−11	308 / 10779	Colon	Enh_Colon
10	4e−10	34 / 451	GSEA	PILON_KLF1_TARGETS_UP
11	4e−08	6 / 11	MF	oxygen transporter activity
12	9e−08	6 / 12	BP	oxygen transport
13	1e−07	9 / 39	Refer	Chaussabel_2,2_Neutrophils
14	2e−07	19 / 210	GSEA	CHYLA_CBFA2T3_TARGETS_DN
15	3e−07	152 / 4795	Chror	6_EnhG_Fibroblasts
16	4e−07	136 / 4169	Chror	10_ReprPC_Fibroblasts
17	4e−07	7 / 23	CC	cortical cytoskeleton
18	4e−07	122 / 3639	Chror	1_TssP_Fibroblasts
19	5e−07	98 / 2740	Colon	ReprPCWk_Colon
20	1e−06	5 / 10	GSEA	BIOCARTA_AHSP_PATHWAY
21	1e−06	99 / 2845	Colon	TxEnhG1_Colon
22	2e−06	107 / 3173	Colon	ReprPC_Colon
23	3e−06	99 / 2894	Colon	TssP_Colon
24	1e−05	101 / 3068	Chror	8_EnhP_Fibroblasts
25	2e−05	10 / 87	GSEA	HAHTOLA_SEZARY_SYNDROM_UP
26	2e−05	124 / 4018	Colon	EnhWk2_Colon
27	3e−05	304 / 11847	Chror	7_Enh_Neuronal_Progenitor
28	3e−05	126 / 4107	Chror	9_ReprPCWk_Fibroblasts
29	3e−05	6 / 29	BP	mitophagy
30	3e−05	6 / 29	Refer	JONGENEEL_Bone Marrow
31	4e−05	125 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
32	5e−05	26 / 505	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
33	6e−05	5 / 20	GSEA	VANDESLUIS_NORMAL_EMBRYOS_DN
34	7e−05	4 / 11	Refer	WIRTH_Prim. lymphoid organs
35	7e−05	107 / 3438	Chror	10_ReprPC_Melanocytes
36	8e−05	107 / 3450	Chror	4_TxTrans_Fibroblasts
37	9e−05	128 / 4304	Chror	9_ReprPCWk_Melanocytes
38	1e−04	161 / 5699	Chror	6_EnhG_Melanocytes
39	1e−04	30 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
40	1e−04	251 / 9635	Chror	3_TssF_Fibroblasts

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	4 / 142	HORVATH_aging_genes meth UP
2	0.4	3 / 111	HORVATH_aging_genes meth DOWN
3	0.7	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−08	6 / 12	oxygen transport
2	3e−05	6 / 29	mitophagy
3	2e−04	6 / 40	erythrocyte differentiation
4	3e−04	4 / 16	erythrocyte development
5	8e−04	4 / 20	heme biosynthetic process
6	1e−03	3 / 10	negative regulation of inclusion body assembly
7	2e−03	3 / 12	axoneme assembly
8	2e−03	3 / 12	regulation of proteasomal protein catabolic process
9	2e−03	4 / 25	protein targeting to plasma membrane
10	3e−03	7 / 89	negative regulation of protein kinase activity
11	3e−03	4 / 29	iron ion homeostasis
12	4e−03	3 / 15	cardiac muscle hypertrophy in response to stress
13	4e−03	11 / 197	in utero embryonic development
14	5e−03	3 / 16	negative regulation of lipid catabolic process
15	6e−03	3 / 17	regulation of long−term neuronal synaptic plasticity

Brain

Rank	p−value	#in/all	Geneset
1	4e−05	125 / 4112	Mid_Frontal_Lobe_ReprPC
2	3e−04	266 / 10430	Overlap_fetal_midbrain_Quies
3	5e−04	96 / 3164	Mid_Frontal_Lobe_ZNF
4	1e−03	82 / 2709	Mid_Frontal_Lobe_HetRpts
5	4e−03	30 / 818	Mid_Frontal_Lobe_Het
6	8e−03	63 / 2127	Mid_Frontal_Lobe_K9K27me3
7	1e−02	43 / 1360	Mid_Frontal_Lobe_TssP
8	1e−02	52 / 1728	Fetal_ReprPCWk
9	2e−02	75 / 2700	Fetal_TxTrans
10	3e−02	228 / 9504	Overlap_fetal_midbrain_K9K27me3
11	5e−02	33 / 1119	Overlap_fetal_midbrain_TssA
12	5e−02	235 / 9917	Overlap_fetal_midbrain_ReprPCWk
13	6e−02	79 / 3046	Fetal_TssA
14	7e−02	51 / 1893	Overlap_fetal_midbrain_TssF
15	1e−01	14 / 465	Mid_Frontal_Lobe_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	0 / 14	LIU_PROSTATE_CANCER_UP
2	0.05	0 / 14	LIU_COMMON_CANCER_GENES
3	0.21	3 / 73	SHAUGHNESSY_MM high risk
4	0.23	15 / 554	Lembcke_Colonic Inflammation
5	0.25	1 / 13	RHODES_CANCER_META_SIGNATURE
6	0.25	1 / 13	GENTLES_modul2
7	0.25	1 / 13	GENTLES_modul12
8	0.25	4 / 117	PanCan_Driver_Gene_geneset_nanostring
9	0.27	1 / 14	GENTLES_modul1
10	0.27	3 / 82	PanCan_JAK−ST_geneset_nanostring
11	0.27	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.28	1 / 15	WANG_ER_UP
13	0.28	1 / 15	GENTLES_modul17
14	0.30	1 / 16	GENTLES_modul11
15	0.30	1 / 16	GENTLES_modul16

CC

Rank	p−value	#in/all	Geneset
1	4e−07	7 / 23	cortical cytoskeleton
2	3e−04	92 / 2979	cytosol
3	1e−03	3 / 11	TORC2 complex
4	4e−03	7 / 93	blood microparticle
5	6e−03	3 / 17	cell−cell contact zone
6	7e−03	13 / 273	neuron projection
7	8e−03	7 / 104	endomembrane system
8	1e−02	90 / 3291	integral component of membrane
9	2e−02	11 / 249	axon
10	2e−02	3 / 28	voltage−gated calcium channel complex
11	2e−02	2 / 11	actomyosin
12	2e−02	2 / 11	inhibitory synapse
13	3e−02	5 / 76	extrinsic component of membrane
14	3e−02	8 / 162	basolateral plasma membrane
15	3e−02	13 / 330	cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.05	38 / 1318	Chr 17
2	0.08	39 / 1411	Chr 11
3	0.13	16 / 536	Chr 22
4	0.13	11 / 342	Chr 18
5	0.16	38 / 1467	Chr 19
6	0.21	25 / 959	Chr 16
7	0.23	56 / 2323	Chr 1
8	0.27	30 / 1217	Chr 3
9	0.28	16 / 619	Chr 20
10	0.33	28 / 1170	Chr 7
11	0.37	20 / 836	Chr 8
12	0.61	6 / 289	Chr 21
13	0.61	16 / 768	Chr 14
14	0.71	30 / 1492	Chr 2
15	0.71	15 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−07	152 / 4795	6_EnhG_Fibroblasts
2	4e−07	136 / 4169	10_ReprPC_Fibroblasts
3	4e−07	122 / 3639	1_TssP_Fibroblasts
4	1e−05	101 / 3068	8_EnhP_Fibroblasts
5	3e−05	304 / 11847	7_Enh_Neuronal_Progenitor
6	3e−05	126 / 4107	9_ReprPCWk_Fibroblasts
7	7e−05	107 / 3438	10_ReprPC_Melanocytes
8	8e−05	107 / 3450	4_TxTrans_Fibroblasts
9	9e−05	128 / 4304	9_ReprPCWk_Melanocytes
10	1e−04	161 / 5699	6_EnhG_Melanocytes
11	1e−04	251 / 9635	3_TssF_Fibroblasts
12	5e−04	83 / 2660	8_EnhP_Melanocytes
13	7e−04	319 / 12983	2_TssA_Neuronal_Progenitor
14	8e−04	294 / 11836	3_TssF_Melanocytes
15	9e−04	313 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−11	308 / 10779	Enh_Colon
2	5e−07	98 / 2740	ReprPCWk_Colon
3	1e−06	99 / 2845	TxEnhG1_Colon
4	2e−06	107 / 3173	ReprPC_Colon
5	3e−06	99 / 2894	TssP_Colon
6	2e−05	124 / 4018	EnhWk2_Colon
7	5e−05	26 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP
8	2e−04	89 / 2810	EnhA_Colon
9	2e−04	170 / 6138	TssD2_Colon
10	6e−04	149 / 5373	EnhWk1_Colon
11	1e−03	193 / 7354	TssF_Colon
12	6e−03	25 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	8e−03	25 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	8e−03	57 / 1895	EnhP_Colon
15	2e−02	221 / 9054	Tx_Colon

Glio

Rank	p−value	#in/all	Geneset
1	6e−04	50 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
2	6e−03	7 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
3	1e−02	83 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
4	2e−02	18 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	3e−02	15 / 401	Down_b
6	4e−02	5 / 84	Weller_LGG_gradeII−vs−III_UP
7	4e−02	3 / 35	Colman_survival_associated
8	7e−02	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
9	7e−02	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
10	8e−02	5 / 104	WIRTH_Normal Brain
11	9e−02	5 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
12	1e−01	10 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
13	1e−01	4 / 86	laffaire_hypermeth_LGG_vs_control
14	1e−01	13 / 419	Down_a
15	1e−01	4 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−14	31 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
2	4e−14	12 / 25	VALK_AML_CLUSTER_8
3	8e−14	12 / 26	VALK_AML_CLUSTER_7
4	2e−11	24 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	4e−10	34 / 451	PILON_KLF1_TARGETS_UP
6	2e−07	19 / 210	CHYLA_CBFA2T3_TARGETS_DN
7	1e−06	5 / 10	BIOCARTA_AHSP_PATHWAY
8	2e−05	10 / 87	HAHTOLA_SEZARY_SYNDROM_UP
9	6e−05	5 / 20	VANDESLUIS_NORMAL_EMBRYOS_DN
10	1e−04	30 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
11	2e−04	8 / 75	LEE_AGING_CEREBELLUM_DN
12	2e−04	10 / 117	MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3
13	3e−04	4 / 15	STEINER_ERYTHROCYTE_MEMBRANE_GENES
14	3e−04	8 / 78	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
15	4e−04	12 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−45	54 / 185	HALLMARK_HEME_METABOLISM
2	2e−02	9 / 189	HALLMARK_HYPOXIA
3	4e−02	8 / 175	HALLMARK_XENOBIOTIC_METABOLISM
4	4e−02	6 / 116	HALLMARK_SPERMATOGENESIS
5	8e−02	5 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	9e−02	7 / 176	HALLMARK_KRAS_SIGNALING_UP
7	2e−01	6 / 176	HALLMARK_ADIPOGENESIS
8	2e−01	6 / 177	HALLMARK_KRAS_SIGNALING_DN
9	2e−01	6 / 183	HALLMARK_APICAL_JUNCTION
10	2e−01	6 / 186	HALLMARK_MYOGENESIS
11	2e−01	2 / 41	HALLMARK_APICAL_SURFACE
12	2e−01	5 / 151	HALLMARK_APOPTOSIS
13	3e−01	4 / 127	HALLMARK_COAGULATION
14	4e−01	4 / 137	HALLMARK_UV_RESPONSE_UP
15	4e−01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	146 / 5384	HOPP_Repressed
2	0.003	86 / 2939	HOPP_Poised_promoter
3	0.012	2 / 8	YAMANE_AICDA_targets_nonrecruited
4	0.053	9 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
5	0.069	9 / 232	WIRTH_lymphoma937_spot B
6	0.091	5 / 109	ROSOLOWSKI_blue total
7	0.118	14 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
8	0.140	14 / 464	WIRTH_lymphoma937_spot I
9	0.160	10 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	0.184	12 / 408	TARTE_Mature plasma cell signature
11	0.189	10 / 331	WIRTH_lymphoma937_spot H
12	0.197	3 / 70	LEE_Developmental_regulators
13	0.208	3 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
14	0.216	1 / 11	DAVE_BL UP
15	0.219	3 / 74	WIRTH_lymphoma937_spot IM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	3 / 30	Hugo_melanoma−all−MET_UP
2	0.07	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.16	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
4	0.33	2 / 54	Hugo_melanoma−all−MET_DN
5	0.45	1 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	4e−08	6 / 11	oxygen transporter activity
2	2e−04	6 / 38	oxygen binding
3	2e−04	10 / 112	heme binding
4	3e−04	10 / 121	iron ion binding
5	2e−03	13 / 232	ligase activity
6	3e−03	15 / 301	ubiquitin−protein transferase activity
7	5e−03	221 / 8818	protein binding
8	6e−03	3 / 17	promoter−specific chromatin binding
9	9e−03	3 / 20	2 iron, 2 sulfur cluster binding
10	9e−03	3 / 20	Wnt−activated receptor activity
11	2e−02	2 / 10	GDP−dissociation inhibitor activity
12	2e−02	2 / 10	peptide hormone receptor binding
13	2e−02	2 / 10	proteasome binding
14	2e−02	4 / 48	protein kinase inhibitor activity
15	2e−02	3 / 28	protein serine/threonine/tyrosine kinase activity

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	0.5	2 / 73	Stroke, susceptibility to
5	0.6	1 / 47	Cervical cancer, somatic
6	0.7	1 / 48	Gastric cancer
7	0.7	1 / 57	Cardiomyopathy, dilated
8	0.7	2 / 116	Cancer
9	0.8	1 / 65	Hepatocellular carcinoma
10	0.8	1 / 68	Glioblastoma multiforme, somatic
11	0.9	1 / 95	Colorectal cancer
12	0.9	1 / 102	Leukemia
13	0.9	1 / 113	Ovarian cancer
14	0.9	1 / 120	Hematological
15	0.9	1 / 123	Pancreatic cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	8 / 113	hsa−miR−498
2	0.006	9 / 149	hsa−miR−142−3p
3	0.007	7 / 103	hsa−miR−146b−5p
4	0.009	7 / 106	hsa−miR−146a
5	0.011	6 / 85	hsa−miR−149
6	0.013	5 / 64	hsa−miR−1278
7	0.014	8 / 144	hsa−miR−24
8	0.016	6 / 93	hsa−miR−216a
9	0.018	5 / 70	hsa−miR−342−3p
10	0.022	6 / 100	hsa−miR−516b
11	0.022	6 / 100	hsa−miR−150
12	0.027	5 / 77	hsa−miR−422a
13	0.027	4 / 52	hsa−miR−508−5p
14	0.027	2 / 12	hsa−miR−639
15	0.031	6 / 108	hsa−miR−501−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.1
2	0.2	1 / 13	BENTINK_e2f3.2
3	0.3	1 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
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	1e−66	58 / 111	Chaussabel_2,3_Erythrocytes
2	1e−07	9 / 39	Chaussabel_2,2_Neutrophils
3	3e−05	6 / 29	JONGENEEL_Bone Marrow
4	7e−05	4 / 11	WIRTH_Prim. lymphoid organs
5	3e−03	3 / 13	WIRTH_Bone marrow
6	9e−03	19 / 478	WIRTH_Nervous System
7	1e−02	3 / 23	JONGENEEL_Heart
8	3e−02	2 / 12	VAQUERIZAS_Kidney_TF
9	4e−02	2 / 14	WIRTH_Telencephalon
10	6e−02	2 / 19	VAQUERIZAS_Bone marrow_TF
11	1e−01	3 / 53	JONGENEEL_Kidney
12	2e−01	1 / 8	VAQUERIZAS_Tongue_TF
13	2e−01	1 / 8	JONGENEEL_Fetal Brain
14	2e−01	4 / 102	Chaussabel_1,2_Platelets
15	2e−01	1 / 10	VAQUERIZAS_Skeletal muscle_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−04	185 / 6868	ICGC_Elf1_targets
2	7e−04	127 / 4468	ICGC_Egr1_targets
3	9e−04	162 / 5984	ICGC_Mta3_targets
4	2e−03	29 / 733	ICGC_Atf3_targets
5	2e−03	168 / 6322	ICGC_Tcf3_targets
6	2e−03	189 / 7247	ICGC_Runx3_targets
7	2e−03	145 / 5383	ICGC_Sp1_targets
8	3e−03	140 / 5188	ICGC_Ebfsc137065_targets
9	6e−03	78 / 2704	ICGC_Pbx3_targets
10	7e−03	162 / 6267	ICGC_Yy1_targets
11	7e−03	79 / 2759	ICGC_Bcl3_targets
12	1e−02	124 / 4735	ICGC_Pu1_targets
13	1e−02	142 / 5518	ICGC_Stat5_targets
14	1e−02	167 / 6616	ICGC_Pax5_targets
15	2e−02	137 / 5312	ICGC_Tcf12_targets

Correlation Cluster

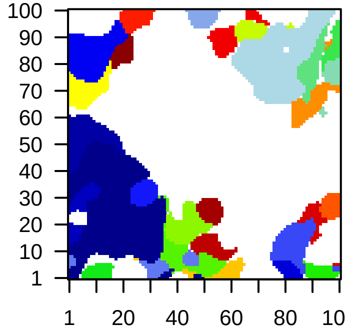
Spot Summary: D

metagenes = 65
genes = 163

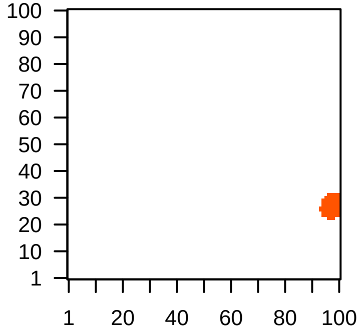
<r> metagenes = 0.93
<r> genes = 0.05
beta: r2= 0.37 / log p= −Inf

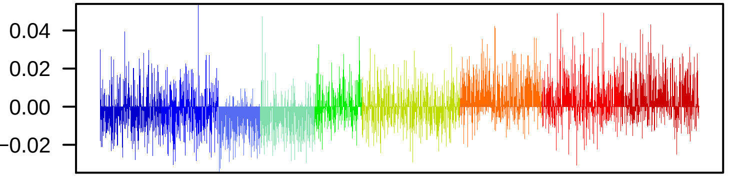
samples with spot = 0 (0 %)

Overview Map



Spot





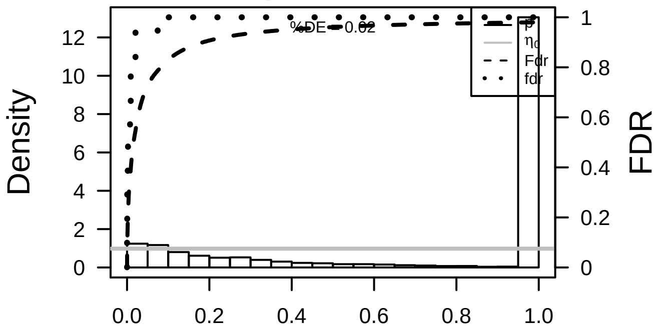
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173454	0.38	−0.21	0.26	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
2	ILMN_219344	0.37	−0.22	0.18	TRIM16L	tripartite motif containing 16−like [Source:HGNC Symbol;Acc:
3	ILMN_218621	0.36	−0.23	0.2	GOLIM4	golgi integral membrane protein 4 [Source:HGNC Symbol;Acc
4	ILMN_169410	0.35	−0.22	0.22	PRIM2	primase (DNA) subunit 2 [Source:HGNC Symbol;Acc:HGNC:
5	ILMN_330089	0.29	−0.19	0.2	LOC729652	
6	ILMN_170191	0.28	−0.19	0.17	CD274	CD274 molecule [Source:HGNC Symbol;Acc:HGNC:17635]
7	ILMN_172532	0.27	−0.15	0.19		
8	ILMN_177837	0.26	−0.21	0.26		
9	ILMN_177687	0.26	−0.2	0.35	HMGN2	high mobility group nucleosomal binding domain 2 [Source:H
10	ILMN_169186	0.26	−0.2	0.1	RABIF	RAB interacting factor [Source:HGNC Symbol;Acc:HGNC:97
11	ILMN_166533	0.26	−0.2	0.17		iduronate 2−sulfatase pseudogene 1 [Source:HGNC Symbol;
12	ILMN_324439	0.26	−0.17	0.35		
13	ILMN_330480	0.25	−0.17	0.32	ANKRD36BP1	ankyrin repeat domain 36B pseudogene 1 [Source:HGNC Sy
14	ILMN_180495	0.24	−0.18	0.13	ZFY	zinc finger protein, Y−linked [Source:HGNC Symbol;Acc:HGN
15	ILMN_168330	0.24	−0.2	0.27	BAX	BCL2 associated X, apoptosis regulator [Source:HGNC Symb
16	ILMN_214103	0.24	−0.18	0.18		
17	ILMN_167489	0.24	−0.19	0.25	RNF213	ring finger protein 213 [Source:HGNC Symbol;Acc:HGNC:14
18	ILMN_238696	0.23	−0.17	0.23		
19	ILMN_168013	0.23	−0.19	0.17	MAFF	MAF bZIP transcription factor F [Source:HGNC Symbol;Acc:H
20	ILMN_328119	0.23	−0.16	0.21		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−10	97 / 11455	Chror	2_TssA_Fibroblasts
2	8e−08	97 / 12298	Chror	2_TssA_Melanocytes
3	3e−07	89 / 10999	Colon	TssWk_Colon
4	5e−07	82 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
5	7e−07	85 / 10430	Brain	Overlap_fetal_midbrain_Quies
6	9e−07	98 / 12983	Chror	2_TssA_Neuronal_Progenitor
7	1e−06	92 / 11836	Chror	3_TssF_Melanocytes
8	1e−06	75 / 8771	Chror	5_Tx_Melanocytes
9	2e−06	67 / 7448	Lympl	HOPP_Strong_enhancer
10	2e−06	79 / 9555	Colon	TssA_Colon
11	2e−06	11 / 331	Lympl	SPANG_CD40 6hrs UP
12	3e−06	9 / 211	Lifest	Homuth_BMI−associated−genes_DN
13	5e−06	68 / 7854	Chror	5_Tx_Fibroblasts
14	7e−06	16 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	8e−06	64 / 7275	Lympl	HOPP_Txn_elongation
16	9e−06	74 / 8990	Chror	15_Quies_Fibroblasts
17	1e−05	23 / 1535	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
18	1e−05	69 / 8226	Lympl	HOPP_Active_promoter
19	2e−05	16 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
20	2e−05	68 / 8098	Lympl	HOPP_Weak_promoter
21	2e−05	25 / 1846	Chror	14_ZNF_Melanocytes
22	3e−05	58 / 6559	Lympl	HOPP_Weak_txn
23	3e−05	51 / 5466	TF	ICGC_Nficsc81335_targets
24	3e−05	14 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
25	3e−05	76 / 9635	Chror	3_TssF_Fibroblasts
26	4e−05	60 / 6959	Lympl	HOPP_Weak_enhancer
27	6e−05	7 / 176	HM	HALLMARK_ADIPOGENESIS
28	6e−05	11 / 471	GSEA	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
29	7e−05	18 / 1169	Lympl	SPANG_BCR DN
30	1e−04	76 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
31	1e−04	6 / 138	GSEA	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR
32	1e−04	8 / 272	Lympl	SPANG_IL21 DN
33	2e−04	7 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
34	2e−04	48 / 5356	Lympl	HOPP_Txn_transition
35	2e−04	82 / 11130	Chror	15_Quies_Melanocytes
36	2e−04	4 / 51	CC	peroxisomal membrane
37	2e−04	68 / 8678	Colon	Quies3_Colon
38	2e−04	3 / 21	GSEA	BREUHAHN_GROWTH_FACTOR_SIGNALING_IN_LIVER_CANCER
39	2e−04	33 / 3194	TF	ICGC_Irf4_targets
40	2e−04	10 / 454	GSEA	SENESE_HDAC3_TARGETS_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	2 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 27	negative regulation of autophagy
2	1e−03	2 / 10	microvillus assembly
3	1e−03	3 / 40	response to UV
4	2e−03	2 / 11	hyaluronan metabolic process
5	2e−03	2 / 13	activation of cysteine−type endopeptidase activity involved in apoptotic signali
6	4e−03	3 / 56	negative regulation of transforming growth factor beta receptor signaling pathw
7	4e−03	3 / 58	regulation of inflammatory response
8	5e−03	2 / 19	response to osmotic stress
9	6e−03	2 / 22	negative regulation of peptidyl−serine phosphorylation
10	7e−03	2 / 23	inactivation of MAPK activity
11	7e−03	2 / 23	nucleotide−binding oligomerization domain containing signaling pathway
12	8e−03	3 / 74	cellular response to organic cyclic compound
13	9e−03	3 / 76	post−embryonic development
14	1e−02	3 / 80	wound healing
15	1e−02	2 / 31	germ cell development

Brain

Rank	p−value	#in/all	Geneset
1	5e−07	82 / 9815	Overlap_fetal_midbrain_ReprPC
2	7e−07	85 / 10430	Overlap_fetal_midbrain_Quies
3	1e−04	76 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	1e−03	16 / 1213	Fetal_TssP
5	2e−03	69 / 9504	Overlap_fetal_midbrain_K9K27me3
6	6e−03	46 / 5936	Overlap_fetal_midbrain_HetRpts
7	2e−02	23 / 2630	Fetal_TssF
8	2e−02	12 / 1115	Overlap_fetal_midbrain_EnhG
9	3e−02	25 / 3046	Fetal_TssA
10	3e−02	8 / 681	Overlap_fetal_midbrain_EnhP
11	6e−02	11 / 1162	Fetal_Enh
12	6e−02	12 / 1329	Overlap_fetal_midbrain_Enh
13	7e−02	21 / 2709	Mid_Frontal_Lobe_HetRpts
14	1e−01	9 / 1012	Mid_Frontal_Lobe_Enh
15	1e−01	8 / 924	Mid_Frontal_Lobe_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	3 / 117	PanCan_Driver_Gene_geneset_nanostring
2	0.03	3 / 125	PanCan_CC+Apop_geneset_nanostring
3	0.05	3 / 150	PanCan_MAPK_geneset_nanostring
4	0.07	1 / 13	GENTLES_modul12
5	0.07	1 / 14	LIU_PROSTATE_CANCER_UP
6	0.08	2 / 82	PanCan_JAK−ST_geneset_nanostring
7	0.09	6 / 554	Lembcke_Colonic Inflammation
8	0.09	2 / 91	PanCan_TXmisReg_geneset_nanostring
9	0.09	3 / 193	PanCan_PI3K_geneset_nanostring
10	0.10	0 / 15	LIU_PROSTATE_CANCER_DN
11	0.10	1 / 20	PanCan_ChromMod_geneset_nanostring
12	0.17	2 / 136	PanCan_RAS_geneset_nanostring
13	0.22	1 / 46	PanCan_TGF−B_geneset_nanostring
14	0.23	3 / 301	SPANG_BCL6−index2
15	0.26	1 / 54	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 51	peroxisomal membrane
2	6e−04	27 / 2535	nucleoplasm
3	1e−03	22 / 1979	membrane
4	6e−03	39 / 4828	nucleus
5	7e−03	4 / 138	mitochondrial outer membrane
6	2e−02	4 / 173	nuclear chromatin
7	2e−02	4 / 200	nuclear membrane
8	3e−02	3 / 121	receptor complex
9	3e−02	2 / 49	lateral plasma membrane
10	3e−02	2 / 50	endocytic vesicle
11	4e−02	2 / 55	cell periphery
12	4e−02	2 / 55	synaptic vesicle membrane
13	4e−02	3 / 136	cytoplasmic, membrane−bounded vesicle
14	4e−02	2 / 60	nuclear pore
15	5e−02	4 / 256	apical plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.07	11 / 1217	Chr 3
2	0.13	10 / 1211	Chr 6
3	0.17	5 / 536	Chr 22
4	0.20	11 / 1492	Chr 2
5	0.27	7 / 954	Chr 9
6	0.29	10 / 1467	Chr 19
7	0.30	15 / 2323	Chr 1
8	0.31	7 / 994	Chr X
9	0.38	1 / 87	Chr Y
10	0.49	5 / 836	Chr 8
11	0.68	2 / 422	Chr 13
12	0.70	5 / 1060	Chr 5
13	0.74	4 / 902	Chr 4
14	0.74	6 / 1318	Chr 17
15	0.78	5 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−10	97 / 11455	2_TssA_Fibroblasts
2	8e−08	97 / 12298	2_TssA_Melanocytes
3	9e−07	98 / 12983	2_TssA_Neuronal_Progenitor
4	1e−06	92 / 11836	3_TssF_Melanocytes
5	1e−06	75 / 8771	5_Tx_Melanocytes
6	5e−06	68 / 7854	5_Tx_Fibroblasts
7	9e−06	74 / 8990	15_Quies_Fibroblasts
8	2e−05	25 / 1846	14_ZNF_Melanocytes
9	3e−05	76 / 9635	3_TssF_Fibroblasts
10	2e−04	82 / 11130	15_Quies_Melanocytes
11	2e−04	90 / 12741	7_Enh_Melanocytes
12	3e−04	88 / 12393	15_Quies_Neuronal_Progenitor
13	4e−04	49 / 5699	6_EnhG_Melanocytes
14	1e−03	65 / 8613	7_Enh_Fibroblasts
15	1e−03	55 / 6970	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−07	89 / 10999	TssWk_Colon
2	2e−06	79 / 9555	TssA_Colon
3	2e−04	68 / 8678	Quies3_Colon
4	2e−04	70 / 9054	Tx_Colon
5	5e−04	66 / 8568	TxWk_Colon
6	1e−03	70 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	1e−03	57 / 7354	TssF_Colon
8	2e−03	36 / 4034	TssD1_Colon
9	2e−03	44 / 5373	EnhWk1_Colon
10	3e−03	17 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	3e−03	2 / 15	TCGA_Mutated−in−CRC_hypermutated
12	4e−03	75 / 10779	Enh_Colon
13	6e−03	13 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	7e−03	16 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	1e−02	36 / 4526	Quies1_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.002	20 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.029	2 / 48	Vishal_subnetwork signature of survival in GBM
3	0.038	1 / 7	Donson−adaptive−immunity−associated with LTS in HGA
4	0.050	3 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
5	0.057	17 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	0.078	2 / 84	GIEZELT_GBM_WT_down_VS_mut
7	0.080	1 / 15	VERHAAK_MES subtype
8	0.080	1 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
9	0.085	1 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
10	0.097	4 / 315	Up
11	0.153	2 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
12	0.185	1 / 37	Christensen_hypomethylated_in_ependymoma
13	0.201	4 / 419	Down_a
14	0.212	1 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
15	0.229	1 / 47	Donson−innate immunity−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−06	16 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	1e−05	23 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
3	2e−05	16 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
4	3e−05	14 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
5	6e−05	11 / 471	ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
6	1e−04	6 / 138	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_36HR
7	2e−04	7 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
8	2e−04	3 / 21	BREUHAHN_GROWTH_FACTOR_SIGNALING_IN_LIVER_CANCER
9	2e−04	10 / 454	SENESE_HDAC3_TARGETS_UP
10	3e−04	3 / 24	LEE_DOUBLE_POLAR_THYMOCYTE
11	3e−04	13 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
12	3e−04	13 / 770	CUI_TCF21_TARGETS_2_DN
13	4e−04	8 / 315	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
14	4e−04	16 / 1104	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
15	4e−04	3 / 26	BIOCARTA_ERK_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	6e−05	7 / 176	HALLMARK_ADIPOGENESIS
2	2e−02	4 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	2e−02	4 / 187	HALLMARK_COMPLEMENT
4	2e−02	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	2e−02	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
6	3e−02	3 / 127	HALLMARK_COAGULATION
7	5e−02	3 / 151	HALLMARK_APOPTOSIS
8	8e−02	3 / 179	HALLMARK_G2M_CHECKPOINT
9	8e−02	2 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	8e−02	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	9e−02	2 / 91	HALLMARK_ANDROGEN_RESPONSE
12	2e−01	2 / 132	HALLMARK_UV_RESPONSE_DN
13	2e−01	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	2e−01	2 / 173	HALLMARK_E2F_TARGETS
15	3e−01	2 / 176	HALLMARK_KRAS_SIGNALING_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−06	9 / 211	Homuth_BMI−associated−genes_DN
2	9e−02	1 / 17	DUMEAUX_High bmi enriched genes
3	4e−01	1 / 94	DUMEAUX_Smoking enriched genes
4	6e−01	1 / 147	Homuth_BMI−associated−genes_UP
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−06	67 / 7448	HOPP_Strong_enhancer
2	2e−06	11 / 331	SPANG_CD40 6hrs UP
3	8e−06	64 / 7275	HOPP_Txn_elongation
4	1e−05	69 / 8226	HOPP_Active_promoter
5	2e−05	68 / 8098	HOPP_Weak_promoter
6	3e−05	58 / 6559	HOPP_Weak_txn
7	4e−05	60 / 6959	HOPP_Weak_enhancer
8	7e−05	18 / 1169	SPANG_BCR DN
9	1e−04	8 / 272	SPANG_IL21 DN
10	2e−04	48 / 5356	HOPP_Txn_transition
11	2e−03	2 / 11	Subero_MM_hypo_meth
12	5e−03	6 / 286	ZHANG_DLBCL mutated
13	1e−02	2 / 31	Care_Extended T−cell
14	1e−02	3 / 88	WIRTH_lymphoma937_spot A
15	1e−02	3 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP

Melanoma

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

MF

Rank	p−value	#in/all	Geneset
1	0.004	64 / 8818	protein binding
2	0.006	15 / 1329	ATP binding
3	0.008	2 / 24	fatty−acyl−CoA binding
4	0.009	3 / 77	PDZ domain binding
5	0.013	6 / 350	protein kinase binding
6	0.016	7 / 476	sequence−specific DNA binding
7	0.021	3 / 107	SH3 domain binding
8	0.022	2 / 42	SMAD binding
9	0.027	6 / 413	protein heterodimerization activity
10	0.028	2 / 47	scaffold protein binding
11	0.030	2 / 49	cysteine−type endopeptidase activity
12	0.031	2 / 50	chloride channel activity
13	0.033	3 / 127	lipid binding
14	0.043	2 / 60	metallopeptidase activity
15	0.054	9 / 877	transcription factor activity, sequence−specific DNA binding

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 63	hsa−miR−659
2	4e−04	3 / 27	hsa−miR−1292
3	6e−04	5 / 123	hsa−miR−646
4	7e−04	6 / 194	hsa−miR−568
5	8e−04	4 / 75	hsa−miR−375
6	1e−03	7 / 299	hsa−miR−548c−3p
7	1e−03	9 / 480	hsa−miR−15b
8	2e−03	9 / 516	hsa−miR−15a
9	2e−03	4 / 100	hsa−miR−150
10	2e−03	3 / 48	hsa−miR−1291
11	3e−03	8 / 441	hsa−miR−424
12	4e−03	3 / 57	hsa−miR−1260
13	5e−03	3 / 61	hsa−miR−296−3p
14	6e−03	5 / 204	hsa−miR−432
15	7e−03	2 / 23	hsa−miR−517a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 12	BENTINK_ras.1
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	6 / 240	Chaussabel_3,3_Inflammation II
2	0.004	4 / 119	Chaussabel_2,11_Replication
3	0.005	10 / 695	PROTEINATLAS_bone marrow
4	0.009	9 / 639	PROTEINATLAS_breast
5	0.010	4 / 150	Chaussabel_2,6_Myeloid lineage
6	0.011	10 / 782	PROTEINATLAS_thyroid gland
7	0.012	5 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
8	0.013	2 / 31	VAQUERIZAS_Fetal lung_TF
9	0.015	7 / 465	PROTEINATLAS_liver
10	0.016	2 / 35	VAQUERIZAS_Prostate_TF
11	0.018	8 / 598	PROTEINATLAS_prostate
12	0.019	9 / 726	PROTEINATLAS_cervix, uterine
13	0.023	13 / 1268	PROTEINATLAS_colon
14	0.029	12 / 1176	PROTEINATLAS_duodenum
15	0.032	12 / 1194	PROTEINATLAS_stomach

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	3e−05	51 / 5466	ICGC_Nficsc81335_targets
2	2e−04	33 / 3194	ICGC_Irf4_targets
3	3e−04	43 / 4735	ICGC_Pu1_targets
4	1e−03	23 / 2133	ICGC_Mef2_targets
5	2e−03	45 / 5410	ICGC_Foxm1_targets
6	2e−03	45 / 5442	ICGC_Pmlsc71910_targets
7	2e−03	38 / 4362	ICGC_Creb1_targets
8	2e−03	31 / 3348	ICGC_BatfPcr1_targets
9	3e−03	55 / 7247	ICGC_Runx3_targets
10	4e−03	17 / 1501	ICGC_Usf1_targets
11	4e−03	40 / 4881	ICGC_Atf2_targets
12	5e−03	41 / 5067	ICGC_Taf1_targets
13	6e−03	50 / 6578	ICGC_Pou2_targets
14	6e−03	22 / 2255	ICGC_SrfV0416101_targets
15	6e−03	50 / 6616	ICGC_Pax5_targets

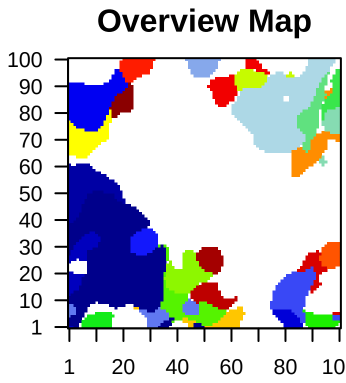
Correlation Cluster

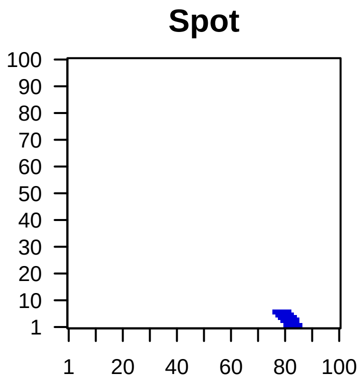
Spot Summary: E

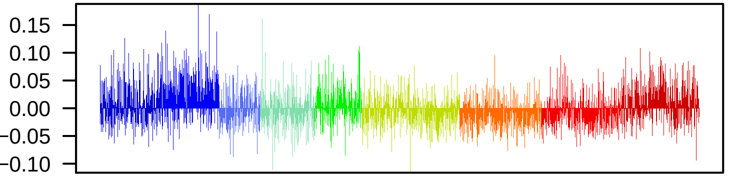
metagenes = 52
genes = 156

<r> metagenes = 0.93
<r> genes = 0.14
beta: r2= 2.07 / log p= −Inf

samples with spot = 131 (3.9 %)
- A * : 23 (6.7 %)
- A C * : 47 (14.3 %)
- A C F * : 3 (1.3 %)
- A F * : 7 (2.3 %)
- C F * : 10 (3.8 %)
- F * : 3 (0.5 %)
- F J * : 1 (0.2 %)
- J * : 7 (1.6 %)
- N * : 30 (6.8 %)


Overview Map


Spot

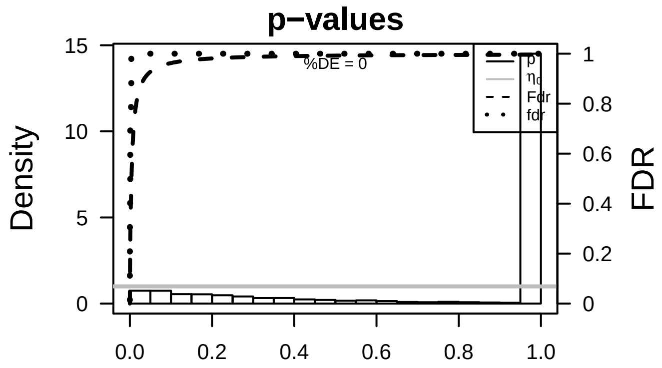


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_206041	1.52	−1.23	0.13	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
2	ILMN_167604	0.78	−0.4	0.14	ALOX15	arachidonate 15−lipoxygenase [Source:HGNC Symbol;Acc:H
3	ILMN_172303	0.75	−0.29	0.36	OLR1	oxidized low density lipoprotein receptor 1 [Source:HGNC Sy
4	ILMN_223469	0.68	−0.26	0.21	BEX1	brain expressed X−linked 1 [Source:HGNC Symbol;Acc:HGN
5	ILMN_236859	0.66	−0.56	0.21	SMG7	SMG7, nonsense mediated mRNA decay factor [Source:HGN
6	ILMN_167133	0.63	−0.32	0.19	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
7	ILMN_324763	0.61	−0.26	0.39		
8	ILMN_231307	0.59	−0.46	0.6	NLRP1	NLR family pyrin domain containing 1 [Source:HGNC Symbol
9	ILMN_175162	0.54	−0.29	0.36	MS4A3	membrane spanning 4−domains A3 [Source:HGNC Symbol;
10	ILMN_173602	0.53	−0.23	0.33	MMP8	matrix metallopeptidase 8 [Source:HGNC Symbol;Acc:HGNC
11	ILMN_176343	0.51	−0.43	0.47	SETX	senataxin [Source:HGNC Symbol;Acc:HGNC:445]
12	ILMN_175608	0.51	−0.74	0.54	INTS3	integrator complex subunit 3 [Source:HGNC Symbol;Acc:HG
13	ILMN_172611	0.51	−0.38	0.16	SLC45A3	solute carrier family 45 member 3 [Source:HGNC Symbol;Ac
14	ILMN_168066	0.49	−0.28	0.46	SASS6	SAS−6 centriolar assembly protein [Source:HGNC Symbol;A
15	ILMN_169922	0.48	−0.54	0.56	UBR4	ubiquitin protein ligase E3 component n−recognin 4 [Source:
16	ILMN_176570	0.47	−0.41	0.54		
17	ILMN_173448	0.47	−0.37	0.25	BSDC1	BSD domain containing 1 [Source:HGNC Symbol;Acc:HGNC
18	ILMN_225963	0.47	−0.41	0.45		
19	ILMN_168396	0.46	−0.35	0.41		
20	ILMN_239752	0.45	−0.3	0.67	KDM6B	lysine demethylase 6B [Source:HGNC Symbol;Acc:HGNC:29

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−13	9 / 39	Refer	Chaussabel_2,2_Neutrophils
2	2e−06	59 / 7448	Lymp	HOPP_Strong_enhancer
3	6e−06	9 / 272	miRN	hsa−miR−92a
4	7e−06	46 / 5356	Lymp	HOPP_Txn_transition
5	7e−06	64 / 8771	Chror	5_Tx_Melanocytes
6	7e−06	10 / 358	GSEA	CHYLA_CBFA2T3_TARGETS_UP
7	1e−05	65 / 9054	Colon	Tx_Colon
8	1e−05	42 / 4795	Chror	6_EnhG_Fibroblasts
9	2e−05	55 / 7275	Lymp	HOPP_Txn_elongation
10	2e−05	9 / 328	miRN	hsa−miR−32
11	4e−05	61 / 8568	Colon	TxWk_Colon
12	5e−05	5 / 85	miRN	hsa−miR−220c
13	6e−05	72 / 10999	Colon	TssWk_Colon
14	9e−05	3 / 19	MF	1−acylglycerol−3−phosphate O−acyltransferase activity
15	1e−04	17 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tra
16	1e−04	61 / 8818	MF	protein binding
17	1e−04	14 / 924	GSEA	MARSON_BOUND_BY_FOXP3_STIMULATED
18	2e−04	27 / 2845	Colon	TxEnhG1_Colon
19	2e−04	20 / 1797	GSEA	PILON_KLF1_TARGETS_DN
20	2e−04	3 / 26	GSEA	CHEN_LUNG_CANCER_SURVIVAL
21	2e−04	7 / 263	miRN	hsa−miR−92b
22	3e−04	7 / 271	miRN	hsa−miR−363
23	3e−04	7 / 277	GSEA	GABRIELY_MIR21_TARGETS
24	3e−04	5 / 128	BP	actin cytoskeleton organization
25	4e−04	43 / 5699	Chror	6_EnhG_Melanocytes
26	4e−04	6 / 204	miRN	hsa−miR−432
27	5e−04	26 / 2810	Colon	EnhA_Colon
28	5e−04	54 / 7854	Chror	5_Tx_Fibroblasts
29	5e−04	7 / 298	miRN	hsa−miR−25
30	5e−04	4 / 79	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP
31	6e−04	62 / 9555	Colon	TssA_Colon
32	7e−04	4 / 84	GSEA	HOEBEKE_LYMPHOID_STEM_CELL_UP
33	8e−04	7 / 318	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−
34	8e−04	20 / 1979	CC	membrane
35	9e−04	8 / 425	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
36	9e−04	7 / 328	miRN	hsa−miR−367
37	9e−04	3 / 41	GSEA	IKEDA_MIR133_TARGETS_UP
38	1e−03	6 / 240	Refer	Chaussabel_3,3_Inflammation II
39	1e−03	2 / 10	GSEA	BIOCARTA_GLYCOLYSIS_PATHWAY
40	1e−03	76 / 12741	Chror	7_Enh_Melanocytes


p−values

Aging

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

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	8 / 554	Lembcke_Colonic Inflammation
2	0.012	2 / 36	PanCan_HK_geneset_nanostring
3	0.014	5 / 301	SPANG_BCL6−index2
4	0.064	1 / 14	GENTLES_modul13
5	0.073	1 / 16	BEN−PORATH_DN
6	0.140	0 / 13	LIU_LIVER_CANCER
7	0.199	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.204	2 / 178	SPANG_LPS−index2
9	0.424	1 / 117	PanCan_Driver_Gene_geneset_nanostring
10	0.711	2 / 527	Lembcke_Normal vs Adenoma
11	0.877	0 / 15	LIU_PROSTATE_CANCER_DN
12	1.000	0 / 13	RHODES_CANCER_META_SIGNATURE
13	1.000	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
14	1.000	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.000	0 / 12	LIU_BREAST_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−06	64 / 8771	5_Tx_Melanocytes
2	1e−05	42 / 4795	6_EnhG_Fibroblasts
3	4e−04	43 / 5699	6_EnhG_Melanocytes
4	5e−04	54 / 7854	5_Tx_Fibroblasts
5	1e−03	76 / 12741	7_Enh_Melanocytes
6	2e−03	71 / 11836	3_TssF_Melanocytes
7	2e−03	73 / 12298	2_TssA_Melanocytes
8	6e−03	18 / 2028	4_TxTrans_Melanocytes
9	9e−03	58 / 9635	3_TssF_Fibroblasts
10	1e−02	68 / 11847	7_Enh_Neuronal_Progenitor
11	2e−02	25 / 3450	4_TxTrans_Fibroblasts
12	3e−02	15 / 1846	14_ZNF_Melanocytes
13	3e−02	64 / 11455	2_TssA_Fibroblasts
14	3e−02	71 / 12983	2_TssA_Neuronal_Progenitor
15	3e−02	42 / 6970	5_Tx_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−06	10 / 358	CHYLA_CBFA2T3_TARGETS_UP
2	1e−04	14 / 924	MARSON_BOUND_BY_FOXP3_STIMULATED
3	2e−04	20 / 1797	PILON_KLF1_TARGETS_DN
4	2e−04	3 / 26	CHEN_LUNG_CANCER_SURVIVAL
5	3e−04	7 / 277	GABRIELY_MIR21_TARGETS
6	5e−04	4 / 79	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP
7	7e−04	4 / 84	HOEBEKE_LYMPHOID_STEM_CELL_UP
8	9e−04	8 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
9	9e−04	3 / 41	IKEDA_MIR133_TARGETS_UP
10	1e−03	2 / 10	BIOCARTA_GLYCOLYSIS_PATHWAY
11	2e−03	4 / 107	LENAOUR_DENDRITIC_CELL_MATURATION_DN
12	2e−03	8 / 471	ONKEN_UVEAL_MELANOMA_DN
13	2e−03	3 / 51	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
14	2e−03	2 / 14	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
15	2e−03	5 / 197	AMUNDSON_RESPONSE_TO_ARSENITE

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−06	59 / 7448	HOPP_Strong_enhancer
2	7e−06	46 / 5356	HOPP_Txn_transition
3	2e−05	55 / 7275	HOPP_Txn_elongation
4	8e−04	7 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
5	5e−03	6 / 331	WIRTH_lymphoma937_spot H
6	7e−03	51 / 8098	HOPP_Weak_promoter
7	9e−03	51 / 8226	HOPP_Active_promoter
8	3e−02	6 / 493	WIRTH_lymphoma937_spot J
9	6e−02	5 / 455	SPANG_CD40 6hrs DN
10	7e−02	4 / 331	SPANG_CD40 6hrs UP
11	7e−02	5 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
12	8e−02	38 / 6559	HOPP_Weak_txn
13	8e−02	2 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
14	9e−02	2 / 105	WIRTH_lymphoma937_spot MM
15	1e−01	9 / 1169	SPANG_BCR DN

miRNA Disease

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−13	9 / 39	Chaussabel_2,2_Neutrophils
2	1e−03	6 / 240	Chaussabel_3,3_Inflammation II
3	5e−03	9 / 695	PROTEINATLAS_bone marrow
4	8e−03	2 / 29	JONGENEEL_Bone Marrow
5	3e−02	4 / 242	Chaussabel_3,2_Inflammation I
6	3e−02	3 / 139	Chaussabel_1,8_Metabolism Biosynthesis
7	3e−02	7 / 640	PROTEINATLAS_parathyroid gland
8	3e−02	3 / 148	VAQUERIZAS_General_TF
9	4e−02	1 / 8	VAQUERIZAS_Tongue_TF
10	4e−02	9 / 963	PROTEINATLAS_pancreas
11	4e−02	6 / 535	PROTEINATLAS_spleen
12	4e−02	5 / 412	WIRTH_Immune system
13	5e−02	8 / 850	PROTEINATLAS_skin
14	5e−02	1 / 11	JONGENEEL_Spleen
15	5e−02	1 / 12	VAQUERIZAS_Skin_TF

BP

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 128	actin cytoskeleton organization
2	3e−03	2 / 17	positive regulation of myoblast differentiation
3	3e−03	3 / 64	negative regulation of cysteine−type endopeptidase activity involved in apoptc
4	4e−03	2 / 21	positive regulation of focal adhesion assembly
5	6e−03	2 / 25	canonical glycolysis
6	6e−03	3 / 80	peptidyl−tyrosine dephosphorylation
7	8e−03	2 / 28	mitotic cell cycle checkpoint
8	8e−03	2 / 29	phospholipid biosynthetic process
9	8e−03	2 / 29	positive chemotaxis
10	8e−03	2 / 29	T cell homeostasis
11	9e−03	10 / 889	positive regulation of transcription from RNA polymerase II promoter
12	1e−02	2 / 32	neuron apoptotic process
13	2e−02	2 / 41	gluconeogenesis
14	2e−02	4 / 208	cellular response to DNA damage stimulus
15	2e−02	3 / 115	leukocyte migration

CC

Rank	p−value	#in/all	Geneset
1	8e−04	20 / 1979	membrane
2	1e−03	2 / 12	specific granule
3	2e−03	36 / 4822	cytoplasm
4	2e−03	3 / 56	autophagosome
5	3e−03	3 / 58	actin filament
6	7e−03	21 / 2535	nucleoplasm
7	9e−03	2 / 30	immunological synapse
8	1e−02	2 / 37	phagocytic vesicle
9	2e−02	24 / 3291	integral component of membrane
10	2e−02	22 / 2979	cytosol
11	2e−02	2 / 47	stress fiber
12	3e−02	2 / 59	endoplasmic reticulum−Golgi intermediate compartment membrane
13	4e−02	2 / 63	lipid particle
14	4e−02	18 / 2464	extracellular exosome
15	5e−02	3 / 170	cell−cell junction

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−05	65 / 9054	Tx_Colon
2	4e−05	61 / 8568	TxWk_Colon
3	6e−05	72 / 10999	TssWk_Colon
4	1e−04	17 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
5	2e−04	27 / 2845	TxEnhG1_Colon
6	5e−04	26 / 2810	EnhA_Colon
7	6e−04	62 / 9555	TssA_Colon
8	1e−03	16 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	2e−03	49 / 7354	TssF_Colon
10	4e−03	55 / 8678	Quies3_Colon
11	4e−03	2 / 19	Boland_CRC−MSI−A6−A10
12	6e−03	64 / 10779	Enh_Colon
13	8e−03	18 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e−02	11 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	2e−02	35 / 5373	EnhWk1_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.003	4 / 127	HALLMARK_COAGULATION
2	0.051	3 / 177	HALLMARK_MITOTIC_SPINDLE
3	0.055	3 / 183	HALLMARK_GLYCOLYSIS
4	0.057	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	0.057	3 / 185	HALLMARK_MTORC1_SIGNALING
6	0.058	3 / 187	HALLMARK_COMPLEMENT
7	0.060	3 / 189	HALLMARK_HYPOXIA
8	0.103	2 / 116	HALLMARK_SPERMATOGENESIS
9	0.144	1 / 33	HALLMARK_ANGIOGENESIS
10	0.172	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.200	2 / 176	HALLMARK_ADIPOGENESIS
12	0.226	2 / 191	HALLMARK_INFLAMMATORY_RESPONSE
13	0.349	1 / 91	HALLMARK_PEROXISOME
14	0.385	1 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	0.478	1 / 138	HALLMARK_FATTY_ACID_METABOLISM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.007	2 / 27	Hugo_melanoma−all−LEF1_UP
2	0.037	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.041	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
4	1.000	0 / 30	Hugo_melanoma−all−MET_UP
5	1.000	0 / 54	Hugo_melanoma−all−MET_DN
6	1.000	0 / 43	Hugo_melanoma−BRAFmut−MET_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	6e−06	9 / 272	hsa−miR−92a
2	2e−05	9 / 328	hsa−miR−32
3	5e−05	5 / 85	hsa−miR−220c
4	2e−04	7 / 263	hsa−miR−92b
5	3e−04	7 / 271	hsa−miR−363
6	4e−04	6 / 204	hsa−miR−432
7	5e−04	7 / 298	hsa−miR−25
8	9e−04	7 / 328	hsa−miR−367
9	2e−03	3 / 49	hsa−miR−1279
10	2e−03	7 / 366	hsa−miR−519b−3p
11	2e−03	7 / 389	hsa−miR−519a
12	3e−03	4 / 122	hsa−miR−212
13	3e−03	7 / 400	hsa−miR−519c−3p
14	5e−03	3 / 71	hsa−miR−939
15	5e−03	3 / 72	hsa−miR−489

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	0.001	27 / 3164	Mid_Frontal_Lobe_ZNF
2	0.006	58 / 9504	Overlap_fetal_midbrain_K9K27me3
3	0.019	38 / 5936	Overlap_fetal_midbrain_HetRpts
4	0.021	60 / 10430	Overlap_fetal_midbrain_Quies
5	0.034	8 / 796	Overlap_fetal_midbrain_ZNF
6	0.051	55 / 9815	Overlap_fetal_midbrain_ReprPC
7	0.090	7 / 818	Mid_Frontal_Lobe_Het
8	0.130	17 / 2709	Mid_Frontal_Lobe_HetRpts
9	0.168	52 / 9917	Overlap_fetal_midbrain_ReprPCWk
10	0.168	16 / 2630	Fetal_TssF
11	0.175	5 / 630	Mid_Frontal_Lobe_EnhP
12	0.187	11 / 1728	Fetal_ReprPCWk
13	0.272	3 / 386	Fetal_ZNF
14	0.277	6 / 937	Fetal_EnhG
15	0.283	15 / 2700	Fetal_TxTrans

Chr

Rank	p−value	#in/all	Geneset
1	0.02	12 / 1318	Chr 17
2	0.04	17 / 2323	Chr 1
3	0.23	7 / 1060	Chr 5
4	0.30	6 / 959	Chr 16
5	0.31	7 / 1170	Chr 7
6	0.34	1 / 87	Chr Y
7	0.42	5 / 904	Chr 10
8	0.46	6 / 1160	Chr 12
9	0.47	5 / 954	Chr 9
10	0.48	2 / 342	Chr 18
11	0.51	6 / 1211	Chr 6
12	0.59	2 / 422	Chr 13
13	0.66	6 / 1411	Chr 11
14	0.68	5 / 1217	Chr 3
15	0.69	4 / 994	Chr X

Glio

Rank	p−value	#in/all	Geneset
1	0.005	10 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.007	4 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
3	0.019	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
4	0.037	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
5	0.050	2 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	0.072	2 / 94	Weller_LGG_A_vs_O_UP
7	0.075	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
8	0.094	2 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	0.111	1 / 25	Barbus_GBM_STS_vs._LTS
10	0.128	10 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
11	0.131	3 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
12	0.152	1 / 35	WIRTH_PN subtype
13	0.196	4 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
14	0.217	1 / 52	OL vs. OPC
15	0.221	1 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	3 / 211	Homuth_BMI−associated−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 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	9e−05	3 / 19	1−acylglycerol−3−phosphate O−acyltransferase activity
2	1e−04	61 / 8818	protein binding
3	2e−03	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
4	2e−03	2 / 15	mitogen−activated protein kinase binding
5	4e−03	2 / 20	peptide antigen binding
6	5e−03	2 / 22	histone demethylase activity
7	6e−03	8 / 580	identical protein binding
8	7e−03	2 / 26	actin monomer binding
9	8e−03	2 / 28	transmembrane receptor protein tyrosine kinase activity
10	1e−02	5 / 301	ubiquitin−protein transferase activity
11	2e−02	4 / 218	transcriptional activator activity, RNA polymerase II core promoter proximal re
12	5e−02	1 / 10	glucose binding
13	5e−02	1 / 10	lactate transmembrane transporter activity
14	5e−02	1 / 10	leucine zipper domain binding
15	5e−02	1 / 10	transmembrane receptor protein tyrosine kinase adaptor activity

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.01	33 / 4890	ICGC_Bclaf101388_targets
2	0.02	17 / 2087	ICGC_Cebpbsc150_targets
3	0.02	13 / 1498	ICGC_Ets1_targets
4	0.03	31 / 4735	ICGC_Pu1_targets
5	0.04	34 / 5442	ICGC_Pmlsc71910_targets
6	0.04	27 / 4131	ICGC_Nfatc1_targets
7	0.05	16 / 2215	ICGC_GabpPcr2_targets
8	0.06	28 / 4468	ICGC_Egr1_targets
9	0.06	16 / 2255	ICGC_SrfV0416101_targets
10	0.06	33 / 5466	ICGC_Nficsc81335_targets
11	0.08	35 / 5961	ICGC_Pol24_targets
12	0.09	11 / 1478	ICGC_Myc_targets
13	0.10	36 / 6267	ICGC_Yy1_targets
14	0.10	29 / 4881	ICGC_Atf2_targets
15	0.10	32 / 5518	ICGC_Stat5_targets

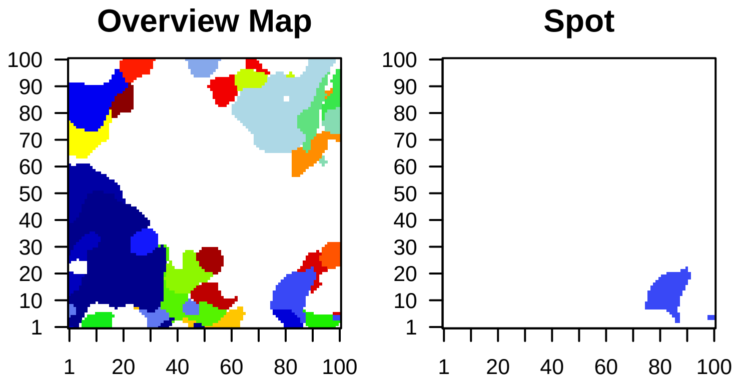
Correlation Cluster

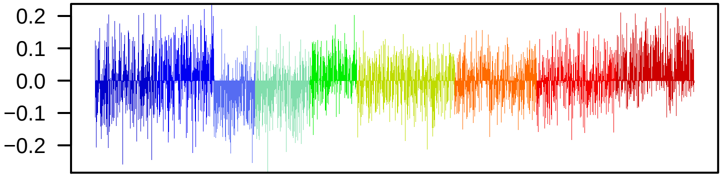
Spot Summary: F

metagenes = 196
genes = 238

<r> metagenes = 0.92
<r> genes = 0.17
beta: r2= 12.28 / log p= −Inf

samples with spot = 656 (19.4 %)
- A * : 62 (18 %)
- A C * : 95 (29 %)
- A C F * : 9 (3.8 %)
- A F * : 21 (6.8 %)
- C F * : 75 (28.3 %)
- F * : 85 (15.3 %)
- F J * : 65 (14 %)
- J * : 67 (15 %)
- N * : 177 (40 %)



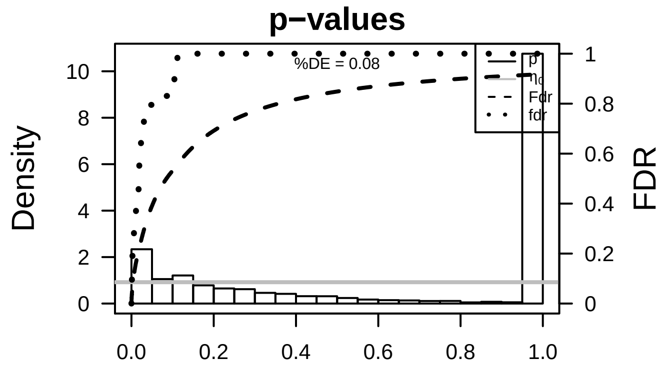


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_218437	1.61	−1.4	0.43	CXCL8	C−X−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
2	ILMN_176605	1.31	−1.01	0.49	ABCA1	ATP binding cassette subfamily A member 1 [Source:HGNC
3	ILMN_175886	1.2	−1.23	0.77	VNN2	vanin 2 [Source:HGNC Symbol;Acc:HGNC:12706]
4	ILMN_172442	1.14	−1.08	0.65	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
5	ILMN_180704	1.08	−0.95	0.65	MARCKS	myristoylated alanine rich protein kinase C substrate [Source:
6	ILMN_175981	0.99	−1.14	0.75	SORL1	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
7	ILMN_171230	0.99	−0.91	0.62	CYBRD1	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:HGNC
8	ILMN_208769	0.97	−0.83	0.58	CYBRD1	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:HGNC
9	ILMN_236359	0.96	−1.31	0.87	SDCBP	syndecan binding protein [Source:HGNC Symbol;Acc:HGNC:
10	ILMN_236358	0.95	−1.19	0.92	SDCBP	syndecan binding protein [Source:HGNC Symbol;Acc:HGNC:
11	ILMN_177948	0.92	−0.88	0.78	FAM126B	family with sequence similarity 126 member B [Source:HGNC
12	ILMN_170504	0.91	−0.83	0.82	TLR8	toll like receptor 8 [Source:HGNC Symbol;Acc:HGNC:15632]
13	ILMN_222514	0.91	−0.87	0.68	EIF4E3	eukaryotic translation initiation factor 4E family member 3 [So
14	ILMN_168359	0.89	−0.81	0.77	ACSL4	acyl−CoA synthetase long−chain family member 4 [Source:H
15	ILMN_171679	0.89	−0.99	0.7	CD302	CD302 molecule [Source:HGNC Symbol;Acc:HGNC:30843]
16	ILMN_171969	0.87	−0.81	0.61	NFKBIZ	NFKB inhibitor zeta [Source:HGNC Symbol;Acc:HGNC:2980
17	ILMN_217094	0.87	−0.84	0.81	SNX10	sorting nexin 10 [Source:HGNC Symbol;Acc:HGNC:14974]
18	ILMN_179268	0.87	−0.98	0.7	HIST1H2AC	histone cluster 1, H2ac [Source:HGNC Symbol;Acc:HGNC:47
19	ILMN_211762	0.84	−0.7	0.79	PLXNC1	plexin C1 [Source:HGNC Symbol;Acc:HGNC:9106]
20	ILMN_170248	0.83	−1.04	0.63	SGK1	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−12	18 / 240	Refer	Chaussabel_3,3_Inflammation II
2	3e−11	45 / 1797	GSEA	PILON_KLF1_TARGETS_DN
3	8e−10	17 / 301	Cance	SPANG_BCL6−index2
4	1e−09	14 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
5	2e−09	134 / 10999	Colon	TssWk_Colon
6	8e−09	93 / 6559	Lymp	HOPP_Weak_txn
7	9e−09	20 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
8	2e−08	10 / 102	Refer	Chaussabel_1,2_Platelets
9	2e−08	18 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
10	3e−08	121 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
11	4e−08	112 / 8818	MF	protein binding
12	5e−08	113 / 8990	Chro	15_Quies_Fibroblasts
13	8e−08	26 / 924	GSEA	MARSON_BOUND_BY_FOXP3_STIMULATED
14	9e−08	12 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
15	1e−07	19 / 532	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
16	2e−07	13 / 242	Refer	Chaussabel_3,2_Inflammation I
17	2e−07	28 / 1104	GSEA	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
18	2e−07	23 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
19	3e−07	109 / 8771	Chro	5_Tx_Melanocytes
20	3e−07	30 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
21	4e−07	21 / 684	GSEA	GOZGIT_ESR1_TARGETS_DN
22	4e−07	92 / 6959	Lymp	HOPP_Weak_enhancer
23	4e−07	21 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
24	5e−07	8 / 82	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
25	5e−07	14 / 315	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
26	6e−07	28 / 1169	Lymp	SPANG_BCR DN
27	9e−07	106 / 8613	Chro	7_Enh_Fibroblasts
28	1e−06	114 / 9555	Colon	TssA_Colon
29	1e−06	22 / 794	GSEA	NUYTTEN_NIPP1_TARGETS_DN
30	1e−06	95 / 7448	Lymp	HOPP_Strong_enhancer
31	1e−06	16 / 445	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_DN
32	2e−06	16 / 455	GSEA	ZHENG_BOUND_BY_FOXP3
33	2e−06	32 / 1535	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
34	2e−06	80 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
35	3e−06	13 / 315	Glio	Up
36	3e−06	13 / 317	miRN	hsa−miR−559
37	3e−06	4 / 13	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_DN
38	4e−06	16 / 482	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
39	4e−06	97 / 7854	Chro	5_Tx_Fibroblasts
40	4e−06	7 / 77	GSEA	MORI_MATURE_B_LYMPHOCYTE_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 58	TESCHENDORFF_age_hypermethylated
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−05	3 / 11	positive regulation of long−term synaptic potentiation
2	1e−04	10 / 280	response to drug
3	2e−04	3 / 14	apoptotic DNA fragmentation
4	4e−04	4 / 42	negative regulation of neuron death
5	5e−04	3 / 19	cell fate determination
6	5e−04	3 / 19	positive regulation of protein autophosphorylation
7	7e−04	4 / 47	phagocytosis
8	1e−03	5 / 94	response to estradiol
9	1e−03	3 / 27	vesicle organization
10	2e−03	3 / 28	cellular response to nerve growth factor stimulus
11	2e−03	3 / 29	cellular response to fibroblast growth factor stimulus
12	2e−03	3 / 29	iron ion homeostasis
13	2e−03	4 / 62	cellular response to interleukin−1
14	2e−03	3 / 32	positive regulation of epithelial to mesenchymal transition
15	3e−03	3 / 33	cell maturation

Brain

Rank	p−value	#in/all	Geneset
1	3e−08	121 / 9815	Overlap_fetal_midbrain_ReprPC
2	2e−06	80 / 5936	Overlap_fetal_midbrain_HetRpts
3	4e−06	115 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	6e−04	111 / 10430	Overlap_fetal_midbrain_Quies
5	1e−03	102 / 9504	Overlap_fetal_midbrain_K9K27me3
6	1e−03	21 / 1213	Fetal_TssP
7	1e−02	15 / 906	Fetal_HetRpts
8	2e−02	13 / 796	Overlap_fetal_midbrain_ZNF
9	3e−02	18 / 1329	Overlap_fetal_midbrain_Enh
10	5e−02	34 / 3046	Fetal_TssA
11	9e−02	9 / 630	Mid_Frontal_Lobe_EnhP
12	1e−01	5 / 328	Fetal_Het
13	1e−01	12 / 1012	Mid_Frontal_Lobe_Enh
14	2e−01	32 / 3164	Mid_Frontal_Lobe_ZNF
15	2e−01	13 / 1171	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	8e−10	17 / 301	SPANG_BCL6−index2
2	2e−05	9 / 178	SPANG_LPS−index2
3	3e−04	14 / 554	Lembcke_Colonic Inflammation
4	3e−02	3 / 76	PanCan_Wnt_geneset_nanostring
5	1e−01	1 / 12	LIU_BREAST_CANCER
6	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
7	1e−01	1 / 13	WANG_ER_DN
8	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
9	1e−01	1 / 14	BEN−PORATH_UP
10	1e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	1e−01	1 / 16	GENTLES_modul14
12	2e−01	1 / 20	PanCan_ChromMod_geneset_nanostring
13	2e−01	2 / 91	PanCan_TXmisReg_geneset_nanostring
14	2e−01	1 / 28	PanCan_HH_geneset_nanostring
15	3e−01	2 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−05	35 / 1979	membrane
2	4e−05	40 / 2464	extracellular exosome
3	7e−05	52 / 3662	plasma membrane
4	1e−04	44 / 2979	cytosol
5	3e−04	8 / 194	membrane raft
6	3e−04	17 / 775	endoplasmic reticulum
7	7e−04	7 / 172	endosome membrane
8	7e−04	7 / 173	nuclear chromatin
9	7e−04	60 / 4822	cytoplasm
10	1e−03	6 / 138	mitochondrial outer membrane
11	1e−03	5 / 96	anchored component of membrane
12	2e−03	8 / 273	neuron projection
13	3e−03	19 / 1101	extracellular space
14	3e−03	12 / 571	perinuclear region of cytoplasm
15	4e−03	8 / 295	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	0.01	15 / 902	Chr 4
2	0.03	13 / 836	Chr 8
3	0.19	16 / 1492	Chr 2
4	0.22	13 / 1211	Chr 6
5	0.23	13 / 1217	Chr 3
6	0.28	11 / 1060	Chr 5
7	0.30	6 / 536	Chr 22
8	0.32	13 / 1318	Chr 17
9	0.32	8 / 768	Chr 14
10	0.33	10 / 994	Chr X
11	0.44	3 / 289	Chr 21
12	0.47	7 / 769	Chr 15
13	0.48	4 / 422	Chr 13
14	0.56	8 / 954	Chr 9
15	0.64	7 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−08	113 / 8990	15_Quies_Fibroblasts
2	3e−07	109 / 8771	5_Tx_Melanocytes
3	9e−07	106 / 8613	7_Enh_Fibroblasts
4	4e−06	97 / 7854	5_Tx_Fibroblasts
5	5e−06	125 / 11130	15_Quies_Melanocytes
6	8e−06	127 / 11455	2_TssA_Fibroblasts
7	3e−05	132 / 12298	2_TssA_Melanocytes
8	4e−05	137 / 12983	2_TssA_Neuronal_Progenitor
9	2e−04	71 / 5699	6_EnhG_Melanocytes
10	2e−04	132 / 12741	7_Enh_Melanocytes
11	4e−04	105 / 9635	3_TssF_Fibroblasts
12	1e−03	126 / 12393	15_Quies_Neuronal_Progenitor
13	2e−03	120 / 11836	3_TssF_Melanocytes
14	3e−03	77 / 6970	5_Tx_Neuronal_Progenitor
15	6e−03	118 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−09	134 / 10999	TssWk_Colon
2	1e−06	114 / 9555	TssA_Colon
3	8e−06	64 / 4526	Quies1_Colon
4	1e−05	27 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
5	6e−05	100 / 8678	Quies3_Colon
6	1e−04	22 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	1e−04	11 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	2e−04	18 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
9	2e−04	54 / 4034	TssD1_Colon
10	3e−04	96 / 8568	TxWk_Colon
11	4e−04	100 / 9054	Tx_Colon
12	1e−03	24 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	2e−03	9 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
14	1e−02	18 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
15	1e−02	10 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP

Glio

Rank	p−value	#in/all	Geneset
1	3e−06	13 / 315	Up
2	2e−05	11 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
3	4e−04	10 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	8e−03	3 / 48	Vishal_subnetwork signature of survival in GBM
5	1e−02	5 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	1e−02	2 / 19	KIM deleted & downregulated in LTS
7	1e−02	3 / 57	OL vs. MOG− OL
8	2e−02	2 / 28	KIM prognostic signature LTS vs. STS
9	3e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
10	4e−02	3 / 92	Weller_LGG_A_vs_O_DOWN
11	5e−02	3 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
12	5e−02	1 / 6	Martinez_Glio_hypometh
13	5e−02	3 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
14	7e−02	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
15	7e−02	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−11	45 / 1797	PILON_KLF1_TARGETS_DN
2	1e−09	14 / 196	MCLACHLAN_DENTAL_CARIES_UP
3	9e−09	20 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
4	2e−08	18 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
5	8e−08	26 / 924	MARSON_BOUND_BY_FOXP3_STIMULATED
6	9e−08	12 / 192	MCLACHLAN_DENTAL_CARIES_DN
7	1e−07	19 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
8	2e−07	28 / 1104	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
9	2e−07	23 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	3e−07	30 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	4e−07	21 / 684	GOZGIT_ESR1_TARGETS_DN
12	4e−07	21 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
13	5e−07	8 / 82	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
14	5e−07	14 / 315	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
15	1e−06	22 / 794	NUYTTEN_NIPP1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−04	6 / 91	HALLMARK_ANDROGEN_RESPONSE
2	9e−04	5 / 87	HALLMARK_PROTEIN_SECRETION
3	1e−03	7 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	1e−03	7 / 186	HALLMARK_IL2_STAT5_SIGNALING
5	1e−03	7 / 187	HALLMARK_COMPLEMENT
6	3e−03	6 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	4e−03	6 / 176	HALLMARK_KRAS_SIGNALING_UP
8	2e−02	4 / 127	HALLMARK_COAGULATION
9	2e−02	5 / 191	HALLMARK_INFLAMMATORY_RESPONSE
10	4e−02	4 / 151	HALLMARK_APOPTOSIS
11	4e−02	3 / 91	HALLMARK_PEROXISOME
12	6e−02	3 / 103	HALLMARK_BILE_ACID_METABOLISM
13	6e−02	4 / 176	HALLMARK_ADIPOGENESIS
14	7e−02	4 / 185	HALLMARK_HEME_METABOLISM
15	7e−02	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−04	8 / 211	Homuth_BMI−associated−genes_DN
2	8e−02	1 / 10	DUMEAUX_Women normal BMI literature genes up
3	1e−01	1 / 16	Huan_blood−pressure_DBP−signature
4	1e−01	1 / 17	DUMEAUX_High bmi enriched genes
5	1e−01	1 / 18	Huan_blood−pressure_SBP−signature
6	7e−01	1 / 147	Homuth_BMI−associated−genes_UP
7	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
15	1e+00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−09	93 / 6559	HOPP_Weak_txn
2	4e−07	92 / 6959	HOPP_Weak_enhancer
3	6e−07	28 / 1169	SPANG_BCR DN
4	1e−06	95 / 7448	HOPP_Strong_enhancer
5	6e−05	95 / 8098	HOPP_Weak_promoter
6	6e−05	96 / 8226	HOPP_Active_promoter
7	1e−04	86 / 7275	HOPP_Txn_elongation
8	5e−04	12 / 455	SPANG_CD40 6hrs DN
9	8e−04	65 / 5356	HOPP_Txn_transition
10	2e−03	8 / 272	SPANG_IL21 DN
11	2e−03	5 / 109	ROSOLOWSKI_blue total
12	4e−03	4 / 78	Sha_DLBCL UP
13	1e−02	2 / 19	DAVE_BL Inter
14	1e−02	3 / 57	LENZ_Stromal signature 2
15	1e−02	6 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.05	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.20	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.22	1 / 30	Hugo_melanoma−all−MET_UP
4	0.37	1 / 54	Hugo_melanoma−all−MET_DN
5	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	4e−08	112 / 8818	protein binding
2	5e−05	13 / 413	protein heterodimerization activity
3	6e−05	9 / 204	protein domain specific binding
4	4e−04	3 / 17	1−phosphatidylinositol binding
5	2e−03	3 / 28	Hsp90 protein binding
6	2e−03	8 / 265	cadherin binding involved in cell−cell adhesion
7	2e−03	5 / 108	ion channel binding
8	3e−03	2 / 10	translation repressor activity, nucleic acid binding
9	3e−03	3 / 36	frizzled binding
10	5e−03	2 / 13	long−chain fatty acid−CoA ligase activity
11	5e−03	2 / 13	transcription factor activity, RNA polymerase II transcription factor binding
12	5e−03	6 / 188	receptor activity
13	7e−03	2 / 15	apolipoprotein binding
14	7e−03	2 / 15	protein phosphatase 1 binding
15	9e−03	2 / 17	syntaxin−1 binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	Psoriasis, susceptibility to
2	0.1	1 / 14	Autism, susceptibility to
3	0.2	1 / 27	Duchenne muscular dystrophy
4	0.2	1 / 28	Miyoshi myopathy
5	0.2	2 / 113	Ovarian cancer
6	0.3	1 / 40	Medulloblastoma
7	0.3	1 / 40	Muscular dystrophy
8	0.3	1 / 48	Alzheimer disease, susceptibility to
9	0.4	1 / 56	Myopathy, nemaline, 3
10	0.4	1 / 57	Cardiomyopathy, dilated
11	0.5	1 / 73	Stroke, susceptibility to
12	0.5	1 / 76	Muscular
13	0.6	1 / 116	Cancer
14	0.6	1 / 120	Hematological
15	0.6	1 / 123	Pancreatic cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−06	13 / 317	hsa−miR−559
2	6e−06	11 / 237	hsa−miR−152
3	8e−06	16 / 513	hsa−miR−106b
4	1e−05	14 / 416	hsa−miR−372
5	1e−05	9 / 169	hsa−miR−190
6	2e−05	17 / 602	hsa−miR−20a
7	2e−05	16 / 540	hsa−miR−17
8	2e−05	10 / 216	hsa−miR−548m
9	2e−05	6 / 64	hsa−miR−1278
10	2e−05	16 / 546	hsa−miR−93
11	2e−05	11 / 270	hsa−miR−548h
12	2e−05	16 / 561	hsa−miR−20b
13	3e−05	12 / 332	hsa−miR−302d
14	3e−05	10 / 234	hsa−miR−27a
15	3e−05	12 / 338	hsa−miR−548d−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_src.10
2	0.1	1 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 14	BENTINK_ras.6
10	1.0	0 / 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−12	18 / 240	Chaussabel_3,3_Inflammation II
2	2e−08	10 / 102	Chaussabel_1,2_Platelets
3	2e−07	13 / 242	Chaussabel_3,2_Inflammation I
4	5e−06	9 / 150	Chaussabel_2,6_Myeloid lineage
5	2e−04	22 / 1118	PROTEINATLAS_placenta
6	2e−04	12 / 412	WIRTH_Immune system
7	2e−04	16 / 681	PROTEINATLAS_lung
8	4e−04	6 / 113	Chaussabel_1,5_Myeloid lineage
9	8e−04	22 / 1239	PROTEINATLAS_testis
10	9e−04	15 / 695	PROTEINATLAS_bone marrow
11	1e−03	16 / 782	PROTEINATLAS_thyroid gland
12	2e−03	6 / 153	Chaussabel_2,9_Cytosceleton
13	3e−03	5 / 119	Chaussabel_2,11_Replication
14	3e−03	13 / 647	PROTEINATLAS_lateral ventricle
15	6e−03	17 / 1016	PROTEINATLAS_cerebral cortex

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	Alternative lengthening of telomeres
2	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−04	35 / 2133	ICGC_Mef2_targets
2	6e−04	44 / 3194	ICGC_Irf4_targets
3	1e−03	65 / 5466	ICGC_Nficsc81335_targets
4	2e−03	81 / 7247	ICGC_Runx3_targets
5	2e−03	57 / 4735	ICGC_Pu1_targets
6	3e−03	30 / 2087	ICGC_Cebpbsc150_targets
7	3e−03	58 / 4881	ICGC_Atf2_targets
8	3e−03	23 / 1466	ICGC_NrsfPcr1_targets
9	8e−03	52 / 4468	ICGC_Egr1_targets
10	8e−03	41 / 3348	ICGC_BatfPcr1_targets
11	1e−02	58 / 5188	ICGC_Ebfsc137065_targets
12	1e−02	34 / 2759	ICGC_Bcl3_targets
13	2e−02	21 / 1498	ICGC_Ets1_targets
14	2e−02	58 / 5312	ICGC_Tcf12_targets
15	2e−02	33 / 2704	ICGC_Pbx3_targets

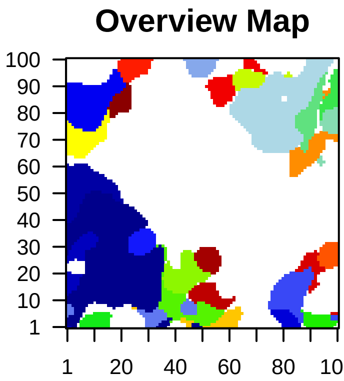
Correlation Cluster

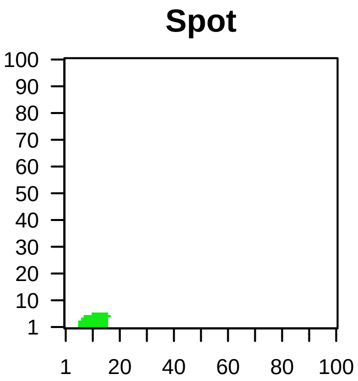
Spot Summary: G

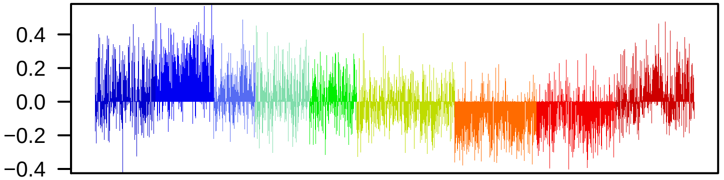
metagenes = 59
genes = 915

<r> metagenes = 0.96
<r> genes = 0.44
beta: r2= 65.32 / log p= −Inf

samples with spot = 1066 (31.5 %)
A * : 148 (43 %)
A C * : 253 (77.1 %)
A C F * : 101 (43 %)
A F * : 110 (35.7 %)
C F * : 89 (33.6 %)
F * : 117 (21.1 %)
F J * : 22 (4.8 %)
J * : 43 (9.6 %)
N * : 183 (41.3 %)


Overview Map


Spot

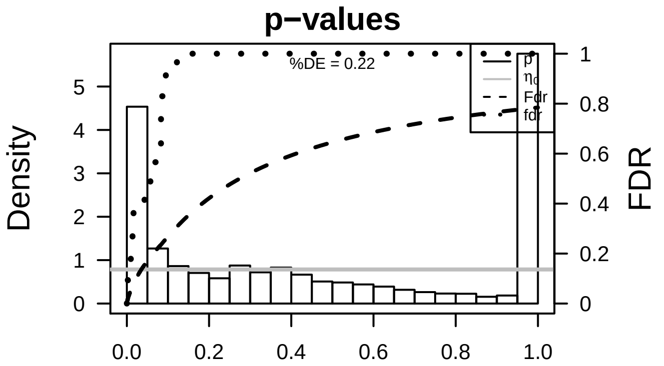


Spot Genelist

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	0.78	MMP9	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
3	ILMN_169658	2.03	−1.31	0.57		
4	ILMN_180121	1.96	−2.45	0.5	S100P	S100 calcium binding protein P [Source:HGNC Symbol;Acc:
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 Sym
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	0.72	MCEMP1	mast cell expressed membrane protein 1 [Source:HGNC Sy
9	ILMN_240322	1.64	−1.03	0.21	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Sy
10	ILMN_169454	1.63	−1.08	0.79	ANXA3	annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
11	ILMN_170893	1.62	−1.48	0.74	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
12	ILMN_177525	1.62	−1.53	0.75	PROK2	prokineticin 2 [Source:HGNC Symbol;Acc:HGNC:18455]
13	ILMN_172176	1.57	−1.48	0.46	IL18RAP	interleukin 18 receptor accessory protein [Source:HGNC Sy
14	ILMN_173399	1.53	−1.22	0.52	DHRS9	dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:HG
15	ILMN_172111	1.53	−2.22	0.2		
16	ILMN_171681	1.5	−1	0.62	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1 [S
17	ILMN_166163	1.49	−2.04	0.34		
18	ILMN_177213	1.48	−1.25	0.83	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HG
19	ILMN_180522	1.47	−1.18	0.82	LRG1	leucine rich alpha−2−glycoprotein 1 [Source:HGNC Symbol;
20	ILMN_181228	1.46	−0.74	0.69	ARG1	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−62	68 / 150	Refer	Chaussabel_2,6_Myeloid lineage
2	4e−42	103 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
3	5e−42	64 / 240	Refer	Chaussabel_3,3_Inflammation II
4	4e−41	110 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
5	1e−35	55 / 211	Lifesty	Homuth_BMI−associated−genes_DN
6	7e−34	490 / 10999	Colon	TssWk_Colon
7	3e−33	82 / 554	Canc	Lembcke_Colonic Inflammation
8	6e−33	429 / 9054	Colon	Tx_Colon
9	5e−32	50 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
10	8e−32	374 / 7448	Lymp	HOPP_Strong_enhancer
11	1e−31	478 / 10779	Colon	Enh_Colon
12	1e−29	56 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
13	1e−29	436 / 9555	Colon	TssA_Colon
14	1e−28	48 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
15	2e−28	51 / 242	Refer	Chaussabel_3,2_Inflammation I
16	2e−28	94 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
17	3e−28	405 / 8678	Colon	Quies3_Colon
18	9e−28	190 / 2810	Colon	EnhA_Colon
19	9e−28	41 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
20	2e−27	399 / 8568	Colon	TxWk_Colon
21	1e−26	288 / 5373	Colon	EnhWk1_Colon
22	3e−26	51 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
23	4e−26	41 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
24	3e−25	45 / 212	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
25	3e−25	43 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
26	8e−25	352 / 7354	Colon	TssF_Colon
27	6e−24	514 / 12741	Chro	7_Enh_Melanocytes
28	1e−23	390 / 8613	Chro	7_Enh_Fibroblasts
29	1e−23	57 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
30	8e−23	58 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
31	9e−23	213 / 3662	CC	plasma membrane
32	2e−22	179 / 2845	Colon	TxEnhG1_Colon
33	3e−22	52 / 336	BP	inflammatory response
34	5e−22	97 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
35	5e−22	417 / 9635	Chro	3_TssF_Fibroblasts
36	1e−21	461 / 11130	Chro	15_Quies_Melanocytes
37	2e−21	53 / 366	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
38	3e−21	40 / 205	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
39	1e−20	34 / 147	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
40	1e−20	129 / 1797	GSEA	PILON_KLF1_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 111	HORVATH_aging_genes meth DOWN
2	0.1	7 / 142	HORVATH_aging_genes meth UP
3	0.3	3 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−22	52 / 336	inflammatory response
2	9e−15	39 / 293	immune response
3	2e−14	30 / 178	response to lipopolysaccharide
4	3e−12	38 / 335	innate immune response
5	8e−11	70 / 1003	signal transduction
6	9e−10	15 / 66	Fc−gamma receptor signaling pathway involved in phagocytosis
7	9e−09	13 / 56	neutrophil chemotaxis
8	2e−08	14 / 69	cellular response to mechanical stimulus
9	2e−08	41 / 511	apoptotic process
10	5e−08	16 / 99	defense response to bacterium
11	6e−08	36 / 434	protein phosphorylation
12	7e−08	31 / 342	intracellular signal transduction
13	3e−07	25 / 254	cell surface receptor signaling pathway
14	3e−07	9 / 32	negative regulation of MAP kinase activity
15	3e−07	6 / 11	regulation of cytokine secretion

Brain

Rank	p−value	#in/all	Geneset
1	1e−14	400 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	4e−14	414 / 10430	Overlap_fetal_midbrain_Quies
3	5e−11	80 / 1213	Fetal_TssP
4	2e−09	136 / 2709	Mid_Frontal_Lobe_HetRpts
5	8e−08	242 / 5936	Overlap_fetal_midbrain_HetRpts
6	3e−07	353 / 9504	Overlap_fetal_midbrain_K9K27me3
7	3e−07	124 / 2630	Fetal_TssF
8	5e−07	176 / 4112	Mid_Frontal_Lobe_ReprPC
9	7e−07	142 / 3164	Mid_Frontal_Lobe_ZNF
10	2e−06	136 / 3046	Fetal_TssA
11	2e−06	123 / 2700	Fetal_TxTrans
12	5e−05	45 / 796	Overlap_fetal_midbrain_ZNF
13	3e−04	343 / 9815	Overlap_fetal_midbrain_ReprPC
14	7e−04	42 / 818	Mid_Frontal_Lobe_Het
15	1e−03	89 / 2127	Mid_Frontal_Lobe_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	3e−33	82 / 554	Lembcke_Colonic Inflammation
2	5e−11	34 / 301	SPANG_BCL6−index2
3	2e−08	22 / 178	SPANG_LPS−index2
4	2e−03	12 / 150	PanCan_MAPK_geneset_nanostring
5	1e−02	12 / 193	PanCan_PI3K_geneset_nanostring
6	2e−02	6 / 73	SHAUGHNESSY_MM high risk
7	4e−02	6 / 82	PanCan_JAK−ST_geneset_nanostring
8	6e−02	8 / 136	PanCan_RAS_geneset_nanostring
9	6e−02	2 / 13	GENTLES_modul12
10	6e−02	2 / 13	GENTLES_modul18
11	7e−02	2 / 14	BEN−PORATH_UP
12	8e−02	1 / 15	LIU_PROSTATE_CANCER_DN
13	2e−01	6 / 125	PanCan_CC+Apop_geneset_nanostring
14	3e−01	0 / 13	LIU_LIVER_CANCER
15	3e−01	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−23	213 / 3662	plasma membrane
2	5e−13	138 / 2464	extracellular exosome
3	2e−12	156 / 2979	cytosol
4	1e−09	78 / 1252	integral component of plasma membrane
5	8e−09	209 / 4822	cytoplasm
6	7e−08	102 / 1979	membrane
7	2e−06	144 / 3291	integral component of membrane
8	2e−05	9 / 51	phagocytic vesicle membrane
9	2e−05	16 / 156	cytoplasmic vesicle
10	4e−05	9 / 56	autophagosome
11	8e−05	5 / 16	pseudopodium
12	1e−04	187 / 4828	nucleus
13	1e−04	33 / 539	Golgi membrane
14	2e−04	55 / 1101	extracellular space
15	2e−04	24 / 352	focal adhesion

Chr

Rank	p−value	#in/all	Geneset
1	0.03	57 / 1467	Chr 19
2	0.05	84 / 2323	Chr 1
3	0.06	26 / 619	Chr 20
4	0.07	44 / 1160	Chr 12
5	0.12	34 / 904	Chr 10
6	0.16	43 / 1211	Chr 6
7	0.19	34 / 959	Chr 16
8	0.31	26 / 768	Chr 14
9	0.38	10 / 289	Chr 21
10	0.45	41 / 1318	Chr 17
11	0.56	25 / 836	Chr 8
12	0.56	16 / 536	Chr 22
13	0.58	36 / 1217	Chr 3
14	0.63	34 / 1170	Chr 7
15	0.79	20 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−24	514 / 12741	7_Enh_Melanocytes
2	1e−23	390 / 8613	7_Enh_Fibroblasts
3	5e−22	417 / 9635	3_TssF_Fibroblasts
4	1e−21	461 / 11130	15_Quies_Melanocytes
5	8e−20	476 / 11836	3_TssF_Melanocytes
6	8e−20	492 / 12393	15_Quies_Neuronal_Progenitor
7	1e−19	382 / 8771	5_Tx_Melanocytes
8	6e−18	242 / 4795	6_EnhG_Fibroblasts
9	7e−18	483 / 12298	2_TssA_Melanocytes
10	3e−17	272 / 5699	6_EnhG_Melanocytes
11	2e−16	465 / 11847	7_Enh_Neuronal_Progenitor
12	5e−16	452 / 11455	2_TssA_Fibroblasts
13	5e−15	373 / 8990	15_Quies_Fibroblasts
14	4e−14	333 / 7854	5_Tx_Fibroblasts
15	1e−11	479 / 12983	2_TssA_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−41	110 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	7e−34	490 / 10999	TssWk_Colon
3	6e−33	429 / 9054	Tx_Colon
4	1e−31	478 / 10779	Enh_Colon
5	1e−29	436 / 9555	TssA_Colon
6	3e−28	405 / 8678	Quies3_Colon
7	9e−28	190 / 2810	EnhA_Colon
8	2e−27	399 / 8568	TxWk_Colon
9	1e−26	288 / 5373	EnhWk1_Colon
10	8e−25	352 / 7354	TssF_Colon
11	2e−22	179 / 2845	TxEnhG1_Colon
12	6e−17	286 / 6138	TssD2_Colon
13	4e−15	93 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	2e−14	100 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	4e−14	37 / 278	Kosinski_top−crypt−long−list

Glio

Rank	p−value	#in/all	Geneset
1	3e−26	51 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−08	16 / 94	Weller_LGG_A_vs_O_UP
3	3e−06	74 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
4	7e−06	13 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
5	1e−05	9 / 47	Donson−innate immunity−associated with LTS in HGA
6	1e−05	15 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	3e−05	3 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
8	4e−05	24 / 315	Up
9	4e−05	15 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	2e−04	12 / 113	GIEZELT_GBM_WT_up_VS_mut
11	3e−04	14 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
12	2e−03	7 / 57	OL vs. MOG− OL
13	2e−03	7 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
14	3e−03	10 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
15	3e−03	5 / 33	Shaw_responders_down_in_oligo_glioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−42	103 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
2	5e−32	50 / 196	MCLACHLAN_DENTAL_CARIES_UP
3	1e−29	56 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
4	1e−28	48 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
5	2e−28	94 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
6	9e−28	41 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
7	4e−26	41 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
8	3e−25	45 / 212	RUTELLA_RESPONSE_TO_HGF_DN
9	3e−25	43 / 192	MCLACHLAN_DENTAL_CARIES_DN
10	1e−23	57 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
11	8e−23	58 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
12	5e−22	97 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
13	2e−21	53 / 366	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
14	3e−21	40 / 205	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
15	1e−20	34 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP

HM

Rank	p−value	#in/all	Geneset
1	4e−19	36 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	1e−13	30 / 191	HALLMARK_INFLAMMATORY_RESPONSE
3	2e−11	27 / 187	HALLMARK_COMPLEMENT
4	3e−10	17 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	9e−06	17 / 162	HALLMARK_ALLOGRAFT_REJECTION
6	2e−05	18 / 186	HALLMARK_IL2_STAT5_SIGNALING
7	2e−05	18 / 189	HALLMARK_HYPOXIA
8	3e−05	17 / 176	HALLMARK_KRAS_SIGNALING_UP
9	5e−05	17 / 185	HALLMARK_P53_PATHWAY
10	6e−05	15 / 151	HALLMARK_APOPTOSIS
11	2e−04	15 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	7e−04	10 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	9e−04	14 / 175	HALLMARK_XENOBIOTIC_METABOLISM
14	1e−03	8 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	8e−03	5 / 41	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−35	55 / 211	Homuth_BMI−associated−genes_DN
2	2e−04	5 / 18	Huan_blood−pressure_SBP−signature
3	9e−03	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	1e−02	3 / 16	Huan_blood−pressure_DBP−signature
5	2e−02	2 / 8	DUMEAUX_Monocytes in smokers literature genes up
6	1e−01	1 / 5	Huan_blood−pressure_HTN−signature
7	2e−01	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	3e−01	1 / 10	DUMEAUX_Smoking literature genes up
9	3e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
10	4e−01	1 / 17	DUMEAUX_High bmi enriched genes
11	8e−01	2 / 94	DUMEAUX_Smoking enriched genes
12	9e−01	2 / 147	Homuth_BMI−associated−genes_UP
13	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
14	1e+00	0 / 7	DUMEAUX_Estrogen related 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	8e−32	374 / 7448	HOPP_Strong_enhancer
2	1e−17	93 / 1169	SPANG_BCR DN
3	1e−13	38 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
4	2e−13	38 / 306	WIRTH_lymphoma937_spot E
5	4e−13	341 / 8226	HOPP_Active_promoter
6	9e−12	37 / 331	WIRTH_lymphoma937_spot H
7	1e−11	36 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
8	1e−10	300 / 7275	HOPP_Txn_elongation
9	3e−10	234 / 5356	HOPP_Txn_transition
10	4e−10	324 / 8098	HOPP_Weak_promoter
11	3e−07	26 / 272	SPANG_IL21 DN
12	4e−07	29 / 331	SPANG_CD40 6hrs UP
13	1e−06	11 / 57	Monti_Host_response_cluster
14	1e−06	256 / 6559	HOPP_Weak_txn
15	8e−06	264 / 6959	HOPP_Weak_enhancer

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	3 / 54	Hugo_melanoma−all−MET_DN
2	0.4	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.6	1 / 27	Hugo_melanoma−all−LEF1_UP
4	1.0	0 / 30	Hugo_melanoma−all−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−19	383 / 8818	protein binding
2	2e−11	27 / 188	receptor activity
3	6e−06	5 / 10	RAGE receptor binding
4	1e−05	20 / 217	protein kinase activity
5	2e−05	5 / 12	phosphotyrosine binding
6	2e−05	9 / 52	RNA polymerase II core promoter sequence−specific DNA binding
7	1e−04	23 / 315	protein serine/threonine kinase activity
8	2e−04	8 / 52	calcium−dependent protein binding
9	2e−04	19 / 243	GTPase activator activity
10	2e−04	27 / 413	protein heterodimerization activity
11	2e−04	5 / 19	G−protein alpha−subunit binding
12	2e−04	22 / 311	enzyme binding
13	5e−04	15 / 182	signal transducer activity
14	8e−04	61 / 1329	ATP binding
15	2e−03	4 / 19	1−acylglycerol−3−phosphate O−acyltransferase activity

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−06	36 / 513	hsa−miR−106b
2	3e−06	35 / 493	hsa−miR−103
3	3e−06	40 / 602	hsa−miR−20a
4	4e−06	38 / 561	hsa−miR−20b
5	4e−06	36 / 520	hsa−miR−106a
6	1e−05	36 / 540	hsa−miR−17
7	1e−05	30 / 416	hsa−miR−372
8	1e−05	36 / 546	hsa−miR−93
9	2e−05	33 / 491	hsa−miR−107
10	3e−05	12 / 95	hsa−miR−125a−5p
11	4e−05	31 / 467	hsa−miR−195
12	6e−05	6 / 24	hsa−miR−632
13	1e−04	27 / 400	hsa−miR−519c−3p
14	1e−04	28 / 428	hsa−miR−519d
15	1e−04	12 / 110	hsa−miR−1271

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 11	BENTINK_ras.4
2	0.05	2 / 12	BENTINK_ras.1
3	0.33	1 / 13	BENTINK_e2f3.1
4	0.33	1 / 13	BENTINK_src.10
5	0.35	1 / 14	GUSTAFSON_PI3K_UP
6	0.35	1 / 14	BENTINK_ras.6
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	BENTINK_e2f3.2
9	1.00	0 / 13	BENTINK_myc.1
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−62	68 / 150	Chaussabel_2,6_Myeloid lineage
2	5e−42	64 / 240	Chaussabel_3,3_Inflammation II
3	2e−28	51 / 242	Chaussabel_3,2_Inflammation I
4	4e−19	29 / 113	Chaussabel_1,5_Myeloid lineage
5	2e−09	52 / 695	PROTEINATLAS_bone marrow
6	6e−07	12 / 66	VAQUERIZAS_Whole blood_TF
7	1e−06	38 / 535	PROTEINATLAS_spleen
8	1e−05	30 / 412	WIRTH_Immune system
9	2e−05	10 / 64	VAQUERIZAS_Lung_TF
10	2e−04	7 / 39	Chaussabel_2,2_Neutrophils
11	2e−04	4 / 11	WIRTH_Prim. lymphoid organs
12	2e−04	38 / 681	PROTEINATLAS_lung
13	1e−03	9 / 84	Chaussabel_2,10_Immune related cell surface molecules
14	1e−03	4 / 16	VAQUERIZAS_Ovary_TF
15	5e−03	3 / 12	Chaussabel_3,5_Hemoglobin genes

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	2e−17	186 / 3348	ICGC_BatfPcr1_targets
2	2e−16	235 / 4735	ICGC_Pu1_targets
3	7e−13	139 / 2497	ICGC_Bcl11_targets
4	1e−11	234 / 5188	ICGC_Ebfsc137065_targets
5	2e−11	302 / 7247	ICGC_Runx3_targets
6	5e−11	241 / 5466	ICGC_Nficsc81335_targets
7	6e−10	238 / 5518	ICGC_Stat5_targets
8	8e−10	222 / 5067	ICGC_Taf1_targets
9	9e−10	253 / 5984	ICGC_Mta3_targets
10	2e−09	214 / 4881	ICGC_Atf2_targets
11	2e−09	233 / 5442	ICGC_Pmlsc71910_targets
12	3e−09	113 / 2133	ICGC_Mef2_targets
13	3e−09	260 / 6267	ICGC_Yy1_targets
14	3e−09	231 / 5410	ICGC_Foxm1_targets
15	4e−09	279 / 6868	ICGC_Elf1_targets

Correlation Cluster

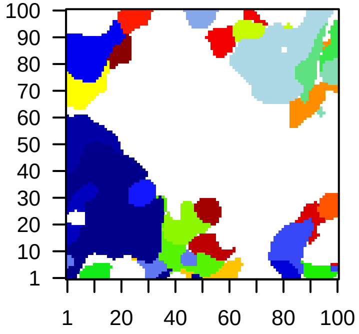
Spot Summary: H

metagenes = 59
genes = 535

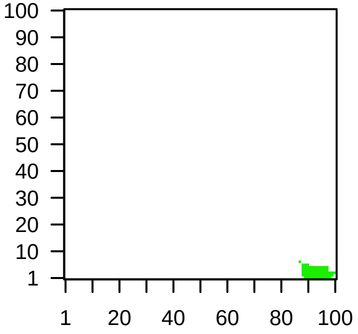
<r> metagenes = 0.94
<r> genes = 0.33
beta: r2= 21.18 / log p= −Inf

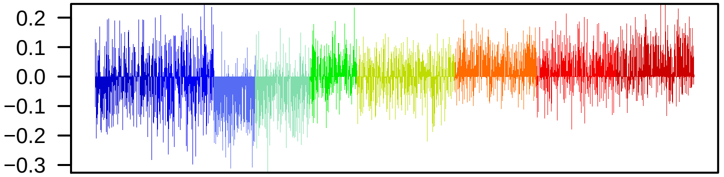
samples with spot = 753 (22.2 %)
A * : 54 (15.7 %)
A C * : 63 (19.2 %)
A C F * : 3 (1.3 %)
A F * : 18 (5.8 %)
C F * : 65 (24.5 %)
F * : 90 (16.2 %)
F J * : 155 (33.5 %)
J * : 125 (28 %)
N * : 180 (40.6 %)

Overview Map



Spot





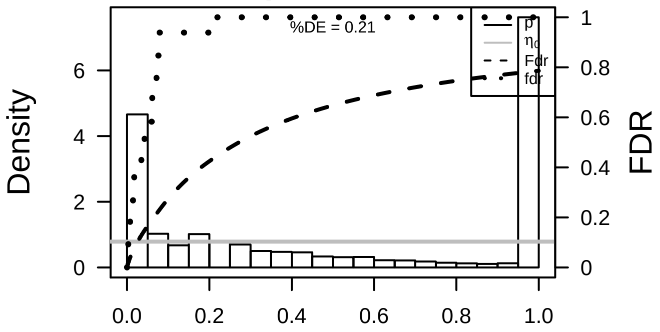
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_238959	1.51	−2.92	0.19	PRKAR1A	protein kinase cAMP−dependent type I regulatory subunit alp
2	ILMN_175311	1.45	−1.67	0.74	NAMPT	nicotinamide phosphoribosyltransferase [Source:HGNC Symb
3	ILMN_177844	1.16	−0.92	0.26	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3
4	ILMN_166673	1.1	−0.73	0.38	CXCL8	C−X−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
5	ILMN_183046	1.01	−0.99	0.17	XYLT1	xylosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:1551
6	ILMN_174018	0.95	−0.81	0.63	SNX3	sorting nexin 3 [Source:HGNC Symbol;Acc:HGNC:11174]
7	ILMN_176966	0.89	−0.99	0.28	RAB5C	RAB5C, member RAS oncogene family [Source:HGNC Symb
8	ILMN_176896	0.88	−0.95	0.82		
9	ILMN_239571	0.87	−0.96	0.44	ARRB2	arrestin beta 2 [Source:HGNC Symbol;Acc:HGNC:712]
10	ILMN_168870	0.83	−1.13	0.45	PJA2	praja ring finger ubiquitin ligase 2 [Source:HGNC Symbol;Acc
11	ILMN_232085	0.82	−0.7	0.68	UBE2D3	ubiquitin conjugating enzyme E2 D3 [Source:HGNC Symbol;A
12	ILMN_168869	0.81	−0.8	0.67	ZEB2	zinc finger E−box binding homeobox 2 [Source:HGNC Symbo
13	ILMN_227695	0.81	−0.72	0.6	TSC22D3	TSC22 domain family member 3 [Source:HGNC Symbol;Acc:
14	ILMN_233336	0.8	−0.66	0.5	MIR6869	FK506 binding protein 1A [Source:HGNC Symbol;Acc:HGNC
15	ILMN_220475	0.8	−0.69	0.61	TMX4	thioredoxin related transmembrane protein 4 [Source:HGNC
16	ILMN_178846	0.8	−0.75	0.39	ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HG
17	ILMN_222992	0.79	−0.77	0.64	KIAA1551	KIAA1551 [Source:HGNC Symbol;Acc:HGNC:25559]
18	ILMN_178245	0.79	−0.67	0.44	OSBPL8	oxysterol binding protein like 8 [Source:HGNC Symbol;Acc:H
19	ILMN_329840	0.79	−0.72	0.49		supervillin pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:
20	ILMN_171410	0.79	−0.89	0.61	TP53INP1	tumor protein p53 inducible nuclear protein 1 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	344 / 7275	Lympl	HOPP_Txn_elongation
2	4e−82	351 / 8678	Colon	Quies3_Colon
3	2e−78	345 / 8568	Colon	TxWk_Colon
4	1e−76	290 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
5	2e−76	351 / 9054	Colon	Tx_Colon
6	2e−75	345 / 8771	Chror	5_Tx_Melanocytes
7	4e−74	361 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
8	1e−73	333 / 8226	Lympl	HOPP_Active_promoter
9	9e−72	354 / 9555	Colon	TssA_Colon
10	4e−71	323 / 7854	Chror	5_Tx_Fibroblasts
11	1e−69	374 / 10999	Colon	TssWk_Colon
12	1e−67	265 / 5356	Lympl	HOPP_Txn_transition
13	2e−64	351 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
14	4e−64	335 / 8990	Chror	15_Quies_Fibroblasts
15	3e−61	371 / 11455	Chror	2_TssA_Fibroblasts
16	1e−59	381 / 12298	Chror	2_TssA_Melanocytes
17	3e−56	295 / 7448	Lympl	HOPP_Strong_enhancer
18	2e−55	348 / 10430	Brain	Overlap_fetal_midbrain_Quies
19	4e−54	282 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	7e−52	381 / 12983	Chror	2_TssA_Neuronal_Progenitor
21	1e−48	93 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
22	4e−48	349 / 11130	Chror	15_Quies_Melanocytes
23	9e−48	295 / 8098	Lympl	HOPP_Weak_promoter
24	1e−46	371 / 12741	Chror	7_Enh_Melanocytes
25	5e−41	358 / 12393	Chror	15_Quies_Neuronal_Progenitor
26	1e−40	349 / 11836	Chror	3_TssF_Melanocytes
27	2e−40	125 / 1797	GSEA	PILON_KLF1_TARGETS_DN
28	4e−39	307 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
29	7e−39	294 / 8818	MF	protein binding
30	3e−38	289 / 8613	Chror	7_Enh_Fibroblasts
31	1e−37	80 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
32	2e−36	225 / 5699	Chror	6_EnhG_Melanocytes
33	3e−31	234 / 6559	Lympl	HOPP_Weak_txn
34	6e−30	91 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
35	1e−29	55 / 442	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
36	1e−27	50 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
37	6e−27	61 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
38	1e−26	67 / 770	GSEA	CUI_TCF21_TARGETS_2_DN
39	3e−26	232 / 6959	Lympl	HOPP_Weak_enhancer
40	6e−25	55 / 546	miRN	hsa−miR−93

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.05	5 / 111	HORVATH_aging_genes meth DOWN
2	0.93	1 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	1e−08	23 / 301	SPANG_BCL6−index2
2	1e−06	15 / 178	SPANG_LPS−index2
3	2e−06	12 / 117	PanCan_Driver_Gene_geneset_nanostring
4	8e−06	5 / 16	GENTLES_modul14
5	1e−04	10 / 125	PanCan_CC+Apop_geneset_nanostring
6	8e−04	7 / 82	PanCan_JAK−ST_geneset_nanostring
7	2e−03	3 / 13	GENTLES_modul12
8	4e−03	8 / 136	PanCan_RAS_geneset_nanostring
9	7e−03	8 / 150	PanCan_MAPK_geneset_nanostring
10	1e−02	18 / 554	Lembcke_Colonic Inflammation
11	3e−02	8 / 193	PanCan_PI3K_geneset_nanostring
12	5e−02	4 / 76	PanCan_Wnt_geneset_nanostring
13	5e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
14	1e−01	1 / 6	ZHANG_MGUS up
15	2e−01	2 / 39	ZHANG_MM up

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−75	345 / 8771	5_Tx_Melanocytes
2	4e−71	323 / 7854	5_Tx_Fibroblasts
3	4e−64	335 / 8990	15_Quies_Fibroblasts
4	3e−61	371 / 11455	2_TssA_Fibroblasts
5	1e−59	381 / 12298	2_TssA_Melanocytes
6	4e−54	282 / 6970	5_Tx_Neuronal_Progenitor
7	7e−52	381 / 12983	2_TssA_Neuronal_Progenitor
8	4e−48	349 / 11130	15_Quies_Melanocytes
9	1e−46	371 / 12741	7_Enh_Melanocytes
10	5e−41	358 / 12393	15_Quies_Neuronal_Progenitor
11	1e−40	349 / 11836	3_TssF_Melanocytes
12	3e−38	289 / 8613	7_Enh_Fibroblasts
13	2e−36	225 / 5699	6_EnhG_Melanocytes
14	1e−22	163 / 4237	14_ZNF_Neuronal_Progenitor
15	1e−17	264 / 9635	3_TssF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−48	93 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	2e−40	125 / 1797	PILON_KLF1_TARGETS_DN
3	1e−37	80 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
4	6e−30	91 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	1e−29	55 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
6	1e−27	50 / 388	SHEN_SMARCA2_TARGETS_UP
7	6e−27	61 / 622	SCHLOSSER_SERUM_RESPONSE_DN
8	1e−26	67 / 770	CUI_TCF21_TARGETS_2_DN
9	2e−23	51 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
10	6e−22	90 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
11	2e−19	36 / 291	DAZARD_RESPONSE_TO_UV_NHEK_DN
12	5e−19	47 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
13	8e−19	73 / 1241	PUJANA_ATM_PCC_NETWORK
14	1e−17	43 / 482	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
15	8e−17	65 / 1104	MARSON_BOUND_BY_FOXP3_UNSTIMULATED

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	344 / 7275	HOPP_Txn_elongation
2	1e−73	333 / 8226	HOPP_Active_promoter
3	1e−67	265 / 5356	HOPP_Txn_transition
4	3e−56	295 / 7448	HOPP_Strong_enhancer
5	9e−48	295 / 8098	HOPP_Weak_promoter
6	3e−31	234 / 6559	HOPP_Weak_txn
7	3e−26	232 / 6959	HOPP_Weak_enhancer
8	9e−17	67 / 1169	SPANG_BCR DN
9	2e−12	36 / 493	WIRTH_lymphoma937_spot J
10	3e−12	35 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
11	5e−11	97 / 2701	HOPP_Repetitive
12	8e−07	19 / 272	SPANG_IL21 DN
13	8e−06	19 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
14	9e−06	46 / 1270	SPANG_BCR UP
15	5e−05	18 / 331	WIRTH_lymphoma937_spot H

miRNA Disease

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−20	28 / 153	Chaussabel_2,9_Cytosceleton
2	6e−20	37 / 302	Chaussabel_3,4_Protein phosphatases
3	2e−15	37 / 412	WIRTH_Immune system
4	5e−13	26 / 242	Chaussabel_3,2_Inflammation I
5	1e−10	23 / 242	Chaussabel_3,9_Kinases
6	3e−08	50 / 1173	PROTEINATLAS_rectum
7	3e−08	49 / 1138	PROTEINATLAS_small intestine
8	4e−08	20 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
9	4e−08	14 / 119	Chaussabel_2,11_Replication
10	5e−08	48 / 1118	PROTEINATLAS_placenta
11	5e−08	50 / 1194	PROTEINATLAS_stomach
12	5e−08	52 / 1268	PROTEINATLAS_colon
13	2e−07	37 / 782	PROTEINATLAS_thyroid gland
14	3e−07	43 / 1003	PROTEINATLAS_appendix
15	5e−07	41 / 960	PROTEINATLAS_cerebellum

BP

Rank	p−value	#in/all	Geneset
1	3e−13	35 / 434	protein phosphorylation
2	1e−08	28 / 435	negative regulation of apoptotic process
3	3e−07	17 / 207	small GTPase mediated signal transduction
4	6e−07	20 / 293	positive regulation of gene expression
5	1e−06	27 / 511	apoptotic process
6	2e−06	12 / 119	peptidyl−serine phosphorylation
7	4e−06	7 / 36	peptidyl−threonine phosphorylation
8	4e−06	11 / 106	platelet activation
9	5e−06	7 / 38	signal transduction by protein phosphorylation
10	1e−05	6 / 28	cellular response to nerve growth factor stimulus
11	1e−05	26 / 550	positive regulation of transcription, DNA−templated
12	2e−05	19 / 342	intracellular signal transduction
13	2e−05	11 / 127	regulation of cell shape
14	3e−05	8 / 66	vascular endothelial growth factor receptor signaling pathway
15	3e−05	13 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process

CC

Rank	p−value	#in/all	Geneset
1	1e−22	177 / 4822	cytoplasm
2	1e−21	129 / 2979	cytosol
3	2e−16	162 / 4828	nucleus
4	6e−16	105 / 2535	nucleoplasm
5	3e−08	83 / 2464	extracellular exosome
6	2e−07	30 / 561	intracellular membrane−bounded organelle
7	8e−07	67 / 1979	membrane
8	6e−06	14 / 179	nuclear speck
9	8e−06	27 / 571	perinuclear region of cytoplasm
10	3e−05	32 / 788	endoplasmic reticulum membrane
11	5e−05	6 / 37	phagocytic vesicle
12	6e−05	14 / 221	endosome
13	9e−05	12 / 172	endosome membrane
14	1e−04	30 / 777	Golgi apparatus
15	1e−04	16 / 295	cell−cell adherens junction

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−82	351 / 8678	Quies3_Colon
2	2e−78	345 / 8568	TxWk_Colon
3	2e−76	351 / 9054	Tx_Colon
4	9e−72	354 / 9555	TssA_Colon
5	1e−69	374 / 10999	TssWk_Colon
6	1e−23	91 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	3e−23	74 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
8	1e−19	290 / 10779	Enh_Colon
9	2e−17	177 / 5373	EnhWk1_Colon
10	6e−16	75 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	6e−14	137 / 4034	TssD1_Colon
12	6e−11	199 / 7354	TssF_Colon
13	2e−10	56 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	9e−10	60 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
15	2e−09	77 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t

HM

Rank	p−value	#in/all	Geneset
1	2e−04	12 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	5e−04	10 / 151	HALLMARK_APOPTOSIS
3	8e−04	9 / 132	HALLMARK_UV_RESPONSE_DN
4	8e−04	11 / 189	HALLMARK_HYPOXIA
5	2e−03	5 / 50	HALLMARK_TGF_BETA_SIGNALING
6	2e−03	10 / 185	HALLMARK_HEME_METABOLISM
7	4e−03	8 / 137	HALLMARK_UV_RESPONSE_UP
8	7e−03	6 / 91	HALLMARK_ANDROGEN_RESPONSE
9	8e−03	9 / 187	HALLMARK_COMPLEMENT
10	9e−03	6 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	1e−02	8 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	2e−02	8 / 177	HALLMARK_MITOTIC_SPINDLE
13	2e−02	5 / 87	HALLMARK_PROTEIN_SECRETION
14	4e−02	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	5e−02	7 / 179	HALLMARK_G2M_CHECKPOINT

Melanoma

Rank	p−value	#in/all	Geneset
1	0.008	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.394	1 / 27	Hugo_melanoma−all−LEF1_UP
3	1.000	0 / 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	

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−25	55 / 546	hsa−miR−93
2	6e−24	42 / 315	hsa−miR−30e
3	8e−24	38 / 250	hsa−miR−548l
4	2e−23	48 / 438	hsa−miR−19a
5	9e−23	47 / 433	hsa−miR−19b
6	2e−22	48 / 463	hsa−miR−301a
7	3e−21	45 / 429	hsa−miR−548n
8	6e−21	40 / 336	hsa−miR−142−5p
9	3e−20	45 / 455	hsa−miR−130a
10	1e−19	35 / 272	hsa−miR−30d
11	3e−19	40 / 374	hsa−miR−144
12	4e−19	50 / 602	hsa−miR−20a
13	7e−19	48 / 561	hsa−miR−20b
14	8e−19	43 / 449	hsa−miR−130b
15	1e−18	37 / 328	hsa−miR−367

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	1e−76	290 / 5936	Overlap_fetal_midbrain_HetRpts
2	4e−74	361 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−64	351 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	2e−55	348 / 10430	Overlap_fetal_midbrain_Quies
5	4e−39	307 / 9504	Overlap_fetal_midbrain_K9K27me3
6	2e−07	48 / 1171	Fetal_EnhP
7	9e−07	46 / 1162	Fetal_Enh
8	7e−06	91 / 3164	Mid_Frontal_Lobe_ZNF
9	2e−04	30 / 796	Overlap_fetal_midbrain_ZNF
10	3e−04	45 / 1436	Fetal_K9K27me3
11	2e−03	10 / 180	Overlap_fetal_midbrain_Het
12	8e−03	22 / 681	Overlap_fetal_midbrain_EnhP
13	8e−03	13 / 328	Fetal_Het
14	1e−02	27 / 937	Fetal_EnhG
15	2e−02	19 / 630	Mid_Frontal_Lobe_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	0.001	44 / 1492	Chr 2
2	0.027	32 / 1217	Chr 3
3	0.047	24 / 904	Chr 10
4	0.053	11 / 342	Chr 18
5	0.061	30 / 1211	Chr 6
6	0.110	22 / 902	Chr 4
7	0.122	25 / 1060	Chr 5
8	0.173	26 / 1160	Chr 12
9	0.252	17 / 769	Chr 15
10	0.370	17 / 836	Chr 8
11	0.383	26 / 1318	Chr 17
12	0.488	22 / 1170	Chr 7
13	0.570	42 / 2323	Chr 1
14	0.616	5 / 289	Chr 21
15	0.658	13 / 768	Chr 14

Glio

Rank	p−value	#in/all	Geneset
1	5e−21	39 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−18	97 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−14	81 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−10	26 / 315	Up
5	8e−10	43 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	7e−04	10 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	1e−03	13 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
8	7e−03	5 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	1e−02	3 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
10	3e−02	2 / 15	VERHAAK_NL subtype
11	3e−02	2 / 15	VERHAAK_PN subtype
12	3e−02	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
13	4e−02	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
14	5e−02	4 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
15	7e−02	4 / 84	GIEZELT_GBM_WT_down_VS_mut

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−15	27 / 211	Homuth_BMI−associated−genes_DN
2	3e−04	4 / 18	Huan_blood−pressure_SBP−signature
3	5e−02	6 / 147	Homuth_BMI−associated−genes_UP
4	9e−02	1 / 5	Huan_blood−pressure_HTN−signature
5	2e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
6	2e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
7	3e−01	1 / 16	Huan_blood−pressure_DBP−signature
8	4e−01	1 / 31	DUMEAUX_Fasting enriched genes
9	8e−01	1 / 94	DUMEAUX_Smoking enriched genes
10	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
11	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
13	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
14	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	7e−39	294 / 8818	protein binding
2	1e−12	29 / 315	protein serine/threonine kinase activity
3	6e−09	56 / 1329	ATP binding
4	2e−08	19 / 213	GTPase activity
5	3e−08	10 / 51	GDP binding
6	1e−07	18 / 217	protein kinase activity
7	1e−06	43 / 1065	zinc ion binding
8	2e−06	8 / 48	receptor signaling protein serine/threonine kinase activity
9	4e−06	19 / 301	ubiquitin−protein transferase activity
10	9e−06	20 / 351	GTP binding
11	2e−05	13 / 173	ubiquitin protein ligase activity
12	3e−05	15 / 232	ligase activity
13	4e−05	16 / 265	cadherin binding involved in cell−cell adhesion
14	9e−05	48 / 1475	DNA binding
15	1e−04	53 / 1717	metal ion binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.001	3 / 12	BENTINK_ras.1
2	0.023	2 / 13	BENTINK_src.10
3	0.200	1 / 12	BENTINK_src.2
4	0.229	1 / 14	BENTINK_ras.6
5	1.000	0 / 14	GUSTAFSON_PI3K_UP
6	1.000	0 / 15	GUSTAFSON_PI3K_DN
7	1.000	0 / 13	BENTINK_e2f3.1
8	1.000	0 / 13	BENTINK_e2f3.2
9	1.000	0 / 13	BENTINK_myc.1
10	1.000	0 / 11	BENTINK_ras.4
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−21	179 / 5067	ICGC_Taf1_targets
2	4e−17	178 / 5466	ICGC_Nficsc81335_targets
3	8e−17	96 / 2133	ICGC_Mef2_targets
4	1e−16	164 / 4890	ICGC_Bclaf101388_targets
5	2e−16	163 / 4881	ICGC_Atf2_targets
6	4e−16	153 / 4468	ICGC_Egr1_targets
7	5e−16	93 / 2087	ICGC_Cebpbsc150_targets
8	2e−15	173 / 5442	ICGC_Pmlsc71910_targets
9	3e−15	174 / 5518	ICGC_Stat5_targets
10	8e−15	147 / 4362	ICGC_Creb1_targets
11	3e−14	140 / 4131	ICGC_Nfatc1_targets
12	3e−13	119 / 3348	ICGC_BatfPcr1_targets
13	3e−13	184 / 6267	ICGC_Yy1_targets
14	5e−13	177 / 5961	ICGC_Pol24_targets
15	6e−13	165 / 5410	ICGC_Foxm1_targets

Correlation Cluster

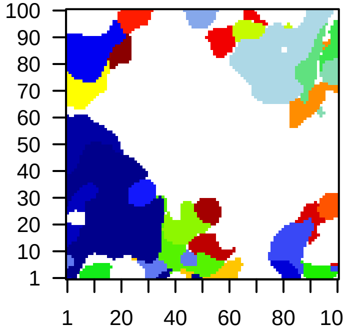
Spot Summary: I

metagenes = 73
genes = 92

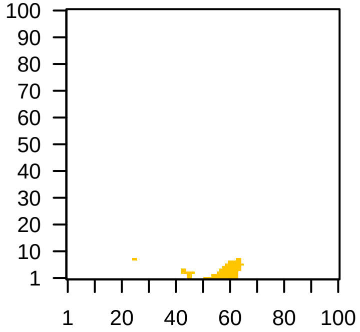
<r> metagenes = 0.94
<r> genes = 0.05
beta: r2= 0.41 / log p= −Inf

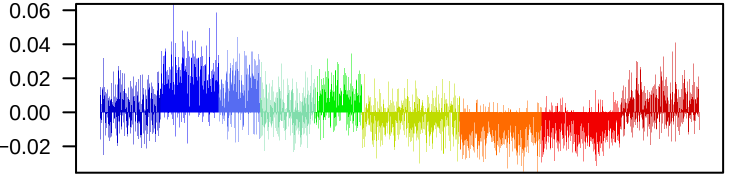
samples with spot = 1 (0 %)
A C * : 1 (0.3 %)

Overview Map



Spot





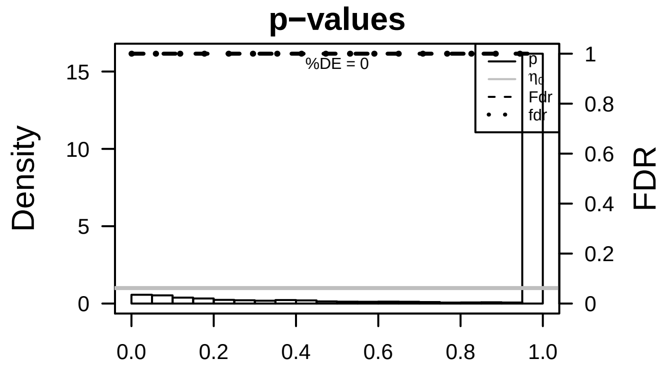
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_181019	0.69	−0.38	0.21	PLA2G4C	phospholipase A2 group IVC [Source:HGNC Symbol;Acc:HG
2	ILMN_320963	0.56	−0.4	0.23		ribosomal protein L23a pseudogene 49 [Source:HGNC Symb
3	ILMN_177556	0.36	−0.21	0.2	CRISP2	cysteine rich secretory protein 2 [Source:HGNC Symbol;Acc:
4	ILMN_177407	0.31	−0.25	0.21	CD177	CD177 molecule [Source:HGNC Symbol;Acc:HGNC:30072]
5	ILMN_326605	0.3	−0.27	0.37	PSMA3−AS1	PSMA3 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
6	ILMN_175583	0.29	−0.24	0.24	FEN1	flap structure−specific endonuclease 1 [Source:HGNC Symbo
7	ILMN_235838	0.28	−0.29	0.38	ZFYVE1	zinc finger FYVE−type containing 1 [Source:HGNC Symbol;A
8	ILMN_185656	0.27	−0.23	0.44		JARID2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
9	ILMN_173840	0.27	−0.17	0.26	FOXC1	forkhead box C1 [Source:HGNC Symbol;Acc:HGNC:3800]
10	ILMN_165868	0.26	−0.17	0.18		HYDIN2, axonemal central pair apparatus protein (pseudoger
11	ILMN_177747	0.26	−0.17	0.2		
12	ILMN_330174	0.25	−0.19	0.31	SPNS2	sphingolipid transporter 2 [Source:HGNC Symbol;Acc:HGNC
13	ILMN_330215	0.25	−0.18	0.26		
14	ILMN_178936	0.25	−0.17	0.17	PKD2L1	polycystin 2 like 1, transient receptor potential cation channel
15	ILMN_166402	0.24	−0.16	0.29		
16	ILMN_168513	0.24	−0.15	0.24		
17	ILMN_173523	0.24	−0.17	0.2	ZSWIM4	zinc finger SWIM−type containing 4 [Source:HGNC Symbol;A
18	ILMN_179956	0.24	−0.17	0.27	LIMS1	LIM zinc finger domain containing 1 [Source:HGNC Symbol;A
19	ILMN_169241	0.24	−0.2	0.25	NMNAT1	nicotinamide nucleotide adenylyltransferase 1 [Source:HGNC
20	ILMN_180089	0.23	−0.15	0.24	ARG2	arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	4 / 96	GSEA	MATZUK_SPERMATOZOA
2	4e−04	2 / 11	Glio	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
3	6e−04	3 / 59	BP	response to cytokine
4	8e−04	2 / 15	GSEA	PID_LPA4_PATHWAY
5	9e−04	2 / 16	BP	neural crest cell development
6	1e−03	2 / 17	BP	activation of protein kinase A activity
7	1e−03	2 / 17	Refer	VAQUERIZAS_Salivary gland_TF
8	1e−03	2 / 17	GSEA	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
9	1e−03	2 / 18	GSEA	TOMIDA_METASTASIS_DN
10	1e−03	2 / 19	BP	hindbrain development
11	1e−03	2 / 20	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_M
12	2e−03	2 / 21	CC	calcium channel complex
13	2e−03	2 / 23	BP	negative regulation of mitotic cell cycle
14	2e−03	2 / 24	Refer	VAQUERIZAS_Trachea_TF
15	2e−03	3 / 91	CC	perikaryon
16	3e−03	2 / 28	GSEA	REACTOME_CA_DEPENDENT_EVENTS
17	3e−03	2 / 30	BP	renal water homeostasis
18	3e−03	2 / 30	GSEA	REACTOME_DAG_AND_IP3_SIGNALING
19	4e−03	2 / 31	GSEA	PID_INTEGRIN_A4B1_PATHWAY
20	4e−03	2 / 31	GSEA	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION
21	4e−03	2 / 31	GSEA	DOANE_BREAST_CANCER_CLASSES_DN
22	4e−03	3 / 110	miRN	hsa−miR−190b
23	5e−03	2 / 37	BP	cellular response to glucagon stimulus
24	6e−03	2 / 39	BP	RNA phosphodiester bond hydrolysis, endonucleolytic
25	6e−03	2 / 40	GSEA	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION
26	6e−03	2 / 40	GSEA	REACTOME_PLC_BETA_MEDIATED_EVENTS
27	6e−03	2 / 40	GSEA	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON
28	6e−03	17 / 3173	Colon	ReprPC_Colon
29	6e−03	2 / 42	BP	ureteric bud development
30	6e−03	2 / 42	GSEA	REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUA
31	7e−03	21 / 4304	Chror	9_ReprPCWk_Melanocytes
32	7e−03	2 / 43	BP	somitogenesis
33	7e−03	2 / 43	GSEA	KEGG_TASTE_TRANSDUCTION
34	7e−03	4 / 265	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
35	7e−03	2 / 45	MF	cytoskeletal protein binding
36	7e−03	3 / 139	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_to
37	8e−03	3 / 141	Lympl	WIRTH_lymphoma937_spot F
38	8e−03	2 / 48	GSEA	REACTOME_AQUAPORIN_MEDIATED_TRANSPORT
39	8e−03	2 / 48	GSEA	GRABARCZYK_BCL11B_TARGETS_DN
40	8e−03	20 / 4107	Chror	9_ReprPCWk_Fibroblasts

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	2 / 58	TESCHENDORFF_age_hypermethylated
2	1.00	0 / 111	HORVATH_aging_genes meth DOWN
3	1.00	0 / 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	6e−04	3 / 59	response to cytokine
2	9e−04	2 / 16	neural crest cell development
3	1e−03	2 / 17	activation of protein kinase A activity
4	1e−03	2 / 19	hindbrain development
5	2e−03	2 / 23	negative regulation of mitotic cell cycle
6	3e−03	2 / 30	renal water homeostasis
7	5e−03	2 / 37	cellular response to glucagon stimulus
8	6e−03	2 / 39	RNA phosphodiester bond hydrolysis, endonucleolytic
9	6e−03	2 / 42	ureteric bud development
10	7e−03	2 / 43	somitogenesis
11	9e−03	2 / 49	heart morphogenesis
12	9e−03	3 / 151	aging
13	9e−03	2 / 51	cellular response to transforming growth factor beta stimulus
14	1e−02	2 / 56	blood vessel development
15	1e−02	2 / 57	camera−type eye development

Brain

Rank	p−value	#in/all	Geneset
1	0.08	5 / 819	Overlap_fetal_midbrain_TssP
2	0.09	13 / 3046	Fetal_TssA
3	0.09	9 / 1893	Overlap_fetal_midbrain_TssF
4	0.09	7 / 1360	Mid_Frontal_Lobe_TssP
5	0.14	11 / 2700	Fetal_TxTrans
6	0.18	15 / 4112	Mid_Frontal_Lobe_ReprPC
7	0.21	5 / 1115	Overlap_fetal_midbrain_EnhG
8	0.22	2 / 307	Fetal_ReprPC
9	0.22	10 / 2654	Fetal_Quies
10	0.23	3 / 578	Fetal_Tx
11	0.24	5 / 1171	Fetal_EnhP
12	0.24	2 / 328	Fetal_Het
13	0.24	6 / 1476	Overlap_fetal_midbrain_TxTrans
14	0.30	2 / 383	Mid_Frontal_Lobe_Tx
15	0.32	4 / 1012	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	1 / 13	WANG_ER_DN
2	0.04	0 / 15	LIU_PROSTATE_CANCER_DN
3	0.04	1 / 14	GENTLES_modul13
4	0.06	2 / 136	PanCan_RAS_geneset_nanostring
5	0.06	4 / 527	Lembcke_Normal vs Adenoma
6	0.07	2 / 150	PanCan_MAPK_geneset_nanostring
7	0.08	1 / 28	PanCan_HH_geneset_nanostring
8	0.12	1 / 46	PanCan_DNARepair_geneset_nanostring
9	0.19	1 / 73	SHAUGHNESSY_MM high risk
10	0.19	1 / 76	PanCan_Wnt_geneset_nanostring
11	0.30	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	0.30	1 / 125	PanCan_CC+Apop_geneset_nanostring
13	0.40	1 / 178	SPANG_LPS−index2
14	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
15	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.002	2 / 21	calcium channel complex
2	0.002	3 / 91	perikaryon
3	0.009	2 / 49	axon terminus
4	0.012	2 / 58	actin filament
5	0.013	2 / 60	motile cilium
6	0.014	2 / 64	axoneme
7	0.028	1 / 10	plasma membrane raft
8	0.036	1 / 13	mitochondrial envelope
9	0.039	2 / 109	growth cone
10	0.041	3 / 268	microtubule
11	0.050	1 / 18	phagocytic cup
12	0.052	10 / 1979	membrane
13	0.053	1 / 19	nuclear heterochromatin
14	0.055	1 / 20	integral component of mitochondrial outer membrane
15	0.055	1 / 20	pre−autophagosomal structure

Chr

Rank	p−value	#in/all	Geneset
1	0.07	5 / 768	Chr 14
2	0.11	5 / 904	Chr 10
3	0.17	6 / 1318	Chr 17
4	0.41	5 / 1467	Chr 19
5	0.43	3 / 836	Chr 8
6	0.45	4 / 1211	Chr 6
7	0.46	4 / 1217	Chr 3
8	0.48	3 / 902	Chr 4
9	0.51	3 / 954	Chr 9
10	0.53	2 / 619	Chr 20
11	0.59	3 / 1060	Chr 5
12	0.62	1 / 342	Chr 18
13	0.65	3 / 1160	Chr 12
14	0.65	2 / 769	Chr 15
15	0.70	1 / 422	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.007	21 / 4304	9_ReprPCWk_Melanocytes
2	0.008	20 / 4107	9_ReprPCWk_Fibroblasts
3	0.012	13 / 2297	10_ReprPC_Neuronal_Progenitor
4	0.022	33 / 8613	7_Enh_Fibroblasts
5	0.029	16 / 3438	10_ReprPC_Melanocytes
6	0.047	14 / 3068	8_EnhP_Fibroblasts
7	0.072	17 / 4169	10_ReprPC_Fibroblasts
8	0.092	15 / 3691	9_ReprPCWk_Neuronal_Progenitor
9	0.097	11 / 2516	11_K9K27me3_Melanocytes
10	0.118	10 / 2315	13_HetRpts_Melanocytes
11	0.120	11 / 2620	1_TssP_Neuronal_Progenitor
12	0.143	14 / 3639	1_TssP_Fibroblasts
13	0.216	8 / 2028	4_TxTrans_Melanocytes
14	0.219	10 / 2660	8_EnhP_Melanocytes
15	0.244	7 / 1789	8_EnhP_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.006	17 / 3173	ReprPC_Colon
2	0.009	15 / 2740	ReprPCWk_Colon
3	0.020	4 / 366	K9K27me3_Colon
4	0.031	14 / 2894	TssP_Colon
5	0.035	2 / 104	Marisa_CRC−cluster−h
6	0.038	22 / 5373	EnhWk1_Colon
7	0.059	5 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
8	0.077	5 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
9	0.079	1 / 29	Marisa_CRC−cluster−c
10	0.119	4 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
11	0.134	32 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	0.144	4 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	0.168	8 / 1895	EnhP_Colon
14	0.188	1 / 73	Ang_CRC−CIMPH−vs−L_hyper
15	0.199	1 / 78	Ang_CRC_Hypermethylated

Glio

Rank	p−value	#in/all	Geneset
1	4e−04	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
2	3e−02	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
3	7e−02	1 / 24	Martinez_Glio_hypermeth
4	9e−02	1 / 35	Colman_survival_associated
5	1e−01	1 / 47	Donson−innate immunity−associated with LTS in HGA
6	1e−01	1 / 51	Gorovets_LGG_PG_subclass
7	1e−01	1 / 52	OL vs. OPC
8	1e−01	1 / 53	mature astrocytes
9	1e−01	1 / 55	Stuehler_Proteins_up_in_STS
10	1e−01	1 / 55	developing astrocytes
11	2e−01	1 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	2e−01	2 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
13	2e−01	1 / 84	GIEZELT_GBM_WT_down_VS_mut
14	2e−01	1 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
15	2e−01	1 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 96	MATZUK_SPERMATOZOA
2	8e−04	2 / 15	PID_LPA4_PATHWAY
3	1e−03	2 / 17	REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB
4	1e−03	2 / 18	TOMIDA_METASTASIS_DN
5	1e−03	2 / 20	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MON
6	3e−03	2 / 28	REACTOME_CA_DEPENDENT_EVENTS
7	3e−03	2 / 30	REACTOME_DAG_AND_IP3_SIGNALING
8	4e−03	2 / 31	PID_INTEGRIN_A4B1_PATHWAY
9	4e−03	2 / 31	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION
10	4e−03	2 / 31	DOANE_BREAST_CANCER_CLASSES_DN
11	6e−03	2 / 40	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION
12	6e−03	2 / 40	REACTOME_PLC_BETA_MEDIATED_EVENTS
13	6e−03	2 / 40	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_I
14	6e−03	2 / 42	REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_AQUAPO
15	7e−03	2 / 43	KEGG_TASTE_TRANSDUCTION

HM

Rank	p−value	#in/all	Geneset
1	0.05	2 / 130	HALLMARK_DNA_REPAIR
2	0.06	2 / 137	HALLMARK_UV_RESPONSE_UP
3	0.28	1 / 116	HALLMARK_SPERMATOGENESIS
4	0.31	1 / 132	HALLMARK_UV_RESPONSE_DN
5	0.35	1 / 151	HALLMARK_APOPTOSIS
6	0.37	1 / 162	HALLMARK_ALLOGRAFT_REJECTION
7	0.38	1 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	0.39	1 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	0.39	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM
10	0.40	1 / 176	HALLMARK_ADIPOGENESIS
11	0.40	1 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.40	1 / 177	HALLMARK_MITOTIC_SPINDLE
13	0.41	1 / 183	HALLMARK_APICAL_JUNCTION
14	0.41	1 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	0.41	1 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 147	Homuth_BMI−associated−genes_UP
2	1.0	0 / 94	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 211	Homuth_BMI−associated−genes_DN
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.007	3 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
2	0.008	3 / 141	WIRTH_lymphoma937_spot F
3	0.011	24 / 5384	HOPP_Repressed
4	0.068	13 / 2939	HOPP_Poised_promoter
5	0.110	3 / 408	TARTE_Mature plasma cell signature
6	0.128	1 / 48	Subero_B−ALL_hyper_meth
7	0.150	1 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
8	0.153	2 / 244	LENZ_Stromal signature 1
9	0.157	1 / 60	Subero_mBL_hyper_meth
10	0.174	1 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
11	0.181	1 / 70	LEE_Developmental_regulators
12	0.181	1 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
13	0.190	1 / 74	Subero_FL_hyper_meth
14	0.210	2 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
15	0.216	2 / 306	WIRTH_lymphoma937_spot E

Melanoma

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

MF

Rank	p−value	#in/all	Geneset
1	0.007	2 / 45	cytoskeletal protein binding
2	0.028	1 / 10	phosphatidylcholine 1−acylhydrolase activity
3	0.029	2 / 94	double−stranded DNA binding
4	0.031	1 / 11	adenylate cyclase activity
5	0.031	1 / 11	glucose transmembrane transporter activity
6	0.031	1 / 11	sodium channel activity
7	0.031	1 / 11	sugar:proton symporter activity
8	0.034	1 / 12	calcium activated cation channel activity
9	0.034	1 / 12	exonuclease activity
10	0.039	1 / 14	endoribonuclease activity
11	0.039	1 / 14	metalloendopeptidase inhibitor activity
12	0.042	1 / 15	aldehyde dehydrogenase (NAD) activity
13	0.042	1 / 15	calcium−activated potassium channel activity
14	0.042	1 / 15	magnesium ion transmembrane transporter activity
15	0.042	1 / 15	protein kinase A regulatory subunit binding

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	3 / 110	hsa−miR−190b
2	0.009	3 / 149	hsa−miR−655
3	0.012	3 / 169	hsa−miR−190
4	0.015	2 / 65	hsa−miR−643
5	0.016	2 / 67	hsa−miR−1262
6	0.017	2 / 71	hsa−miR−578
7	0.028	1 / 10	hsa−miR−887
8	0.029	2 / 94	hsa−miR−133b
9	0.029	2 / 94	hsa−miR−133a
10	0.033	2 / 100	hsa−miR−600
11	0.033	2 / 100	hsa−miR−516b
12	0.042	2 / 114	hsa−miR−875−3p
13	0.045	2 / 119	hsa−miR−380
14	0.046	2 / 120	hsa−miR−1248
15	0.047	2 / 121	hsa−miR−515−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	1 / 14	GUSTAFSON_PI3K_UP
2	1.00	0 / 15	GUSTAFSON_PI3K_DN
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	0.001	2 / 17	VAQUERIZAS_Salivary gland_TF
2	0.002	2 / 24	VAQUERIZAS_Trachea_TF
3	0.031	4 / 416	PROTEINATLAS_ovary
4	0.045	1 / 16	VAQUERIZAS_Fetal thyroid_TF
5	0.082	1 / 30	VAQUERIZAS_Smooth muscle_TF
6	0.084	1 / 31	VAQUERIZAS_Fetal lung_TF
7	0.095	1 / 35	VAQUERIZAS_Prostate_TF
8	0.105	1 / 39	Chaussabel_2,2_Neutrophils
9	0.108	1 / 40	VAQUERIZAS_Thyroid_TF
10	0.113	1 / 42	VAQUERIZAS_Fetal brain_TF
11	0.115	1 / 43	VAQUERIZAS_Placenta_TF
12	0.129	2 / 220	WIRTH_Testis
13	0.130	1 / 49	VAQUERIZAS_Uterus_TF
14	0.130	1 / 49	JONGENEEL_Retina
15	0.133	1 / 50	WIRTH_Placenta

Telomeres

Rank	p−value	#in/all	Geneset
1	0.07	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.1	9 / 2133	ICGC_Mef2_targets
2	0.2	7 / 1753	HEBENSTREIT_low expression TF
3	0.4	3 / 747	ICGC_NrsfPcr2_targets
4	0.5	4 / 1231	KIM_MYC targets
5	0.5	15 / 5188	ICGC_Ebfsc137065_targets
6	0.5	2 / 631	ICGC_RxraPcr1_targets
7	0.6	7 / 2497	ICGC_Bcl11_targets
8	0.6	4 / 1466	ICGC_NrsfPcr1_targets
9	0.7	7 / 2704	ICGC_Pbx3_targets
10	0.7	8 / 3194	ICGC_Irf4_targets
11	0.8	8 / 3348	ICGC_BatfPcr1_targets
12	0.8	3 / 1501	ICGC_Usf1_targets
13	0.8	13 / 5466	ICGC_Nficsc81335_targets
14	0.8	6 / 2759	ICGC_Bcl3_targets
15	0.8	11 / 4735	ICGC_Pu1_targets

Correlation Cluster

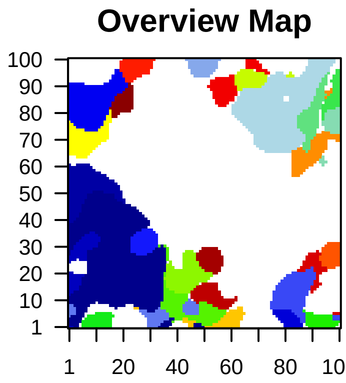
Spot Summary: J

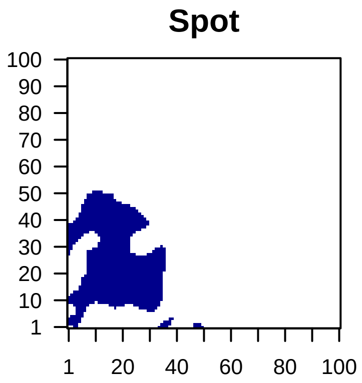
metagenes = 1105
genes = 1442

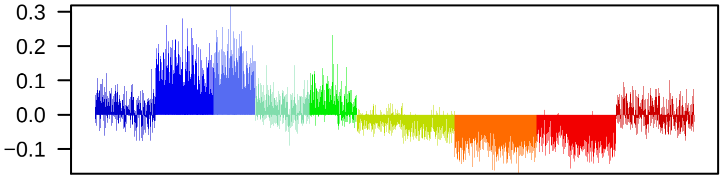
<r> metagenes = 0.92

beta: r2= 17.83 / log p= −Inf

samples with spot = 594 (17.5 %)
A * : 30 (8.7 %)
A C * : 264 (80.5 %)
A C F * : 205 (87.2 %)
A F * : 24 (7.8 %)
C F * : 55 (20.8 %)
N * : 16 (3.6 %)





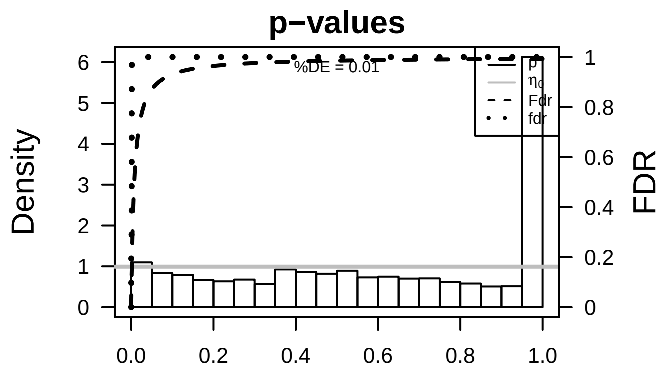


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178314	4.32	−2.71	0.24		
2	ILMN_175553	3.25	−1.79	0.31	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:HG
3	ILMN_169326	3.22	−2.11	0.54		
4	ILMN_167935	3.21	−3.04	0.5	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
5	ILMN_219321	3.07	−2.61	0.48	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
6	ILMN_216528	3.02	−1.93	0.48	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
7	ILMN_172566	2.96	−2.08	0.48	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
8	ILMN_211687	2.86	−1.31	0.41	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
9	ILMN_323841	2.6	−1.51	0.21	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
10	ILMN_168858	2.54	−1.91	0.6	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
11	ILMN_175334	2.49	−1.4	0.44		
12	ILMN_169222	2.41	−1.48	0.6		
13	ILMN_170663	2.3	−1.37	0.54	ELANE	elastase, neutrophil expressed [Source:HGNC Symbol;Acc:H
14	ILMN_180605	2.07	−0.98	0.42	CEACAM8	carcinoembryonic antigen related cell adhesion molecule 8 [S
15	ILMN_219133	1.92	−1.09	0.24	RPS4Y2	ribosomal protein S4, Y−linked 2 [Source:HGNC Symbol;Acc:
16	ILMN_168042	1.9	−0.91	0.43	CTSG	cathepsin G [Source:HGNC Symbol;Acc:HGNC:2532]
17	ILMN_210272	1.79	−0.83	0.46	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
18	ILMN_165487	1.7	−1.92	0.28	CLC	Charcot−Leyden crystal galectin [Source:HGNC Symbol;Acc:
19	ILMN_176673	1.6	−0.7	0.46	BPI	bactericidal/permeability−increasing protein [Source:HGNC S
20	ILMN_168569	1.57	−0.79	0.24	KDM5D	lysine demethylase 5D [Source:HGNC Symbol;Acc:HGNC:11

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−17	215 / 2845	Colon	TxEnhG1_Colon
2	8e−13	197 / 2810	Colon	EnhA_Colon
3	2e−12	361 / 6138	Colon	TssD2_Colon
4	6e−12	227 / 3450	Chror	4_TxTrans_Fibroblasts
5	2e−11	412 / 7354	Colon	TssF_Colon
6	1e−10	331 / 5699	Chror	6_EnhG_Melanocytes
7	2e−10	287 / 4795	Chror	6_EnhG_Fibroblasts
8	3e−09	142 / 2028	Chror	4_TxTrans_Melanocytes
9	3e−09	201 / 3164	Brain	Mid_Frontal_Lobe_ZNF
10	3e−09	551 / 10779	Colon	Enh_Colon
11	2e−08	174 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
12	3e−08	303 / 5373	Colon	EnhWk1_Colon
13	4e−08	6 / 7	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_UP
14	6e−08	69 / 818	Brain	Mid_Frontal_Lobe_Het
15	1e−07	327 / 5956	Chror	3_TssF_Neuronal_Progenitor
16	4e−07	117 / 1728	Brain	Fetal_ReprPCWk
17	5e−07	11 / 39	Refer	Chaussabel_2,2_Neutrophils
18	5e−07	462 / 9054	Colon	Tx_Colon
19	1e−06	599 / 12298	Chror	2_TssA_Melanocytes
20	4e−06	576 / 11836	Chror	3_TssF_Melanocytes
21	5e−06	20 / 147	Lifesty	Homuth_BMI−associated−genes_UP
22	7e−06	622 / 12983	Chror	2_TssA_Neuronal_Progenitor
23	8e−06	75 / 1043	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
24	1e−05	26 / 237	GSEA	LU_EZH2_TARGETS_UP
25	1e−05	7 / 20	GSEA	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
26	1e−05	555 / 11455	Chror	2_TssA_Fibroblasts
27	2e−05	227 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
28	2e−05	476 / 9635	Chror	3_TssF_Fibroblasts
29	2e−05	7 / 21	GSEA	REACTOME_REGULATORY_RNA_PATHWAYS
30	2e−05	55 / 713	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
31	2e−05	6 / 15	GSEA	LIU_IL13_MEMORY_MODEL_UP
32	2e−05	570 / 11847	Chror	7_Enh_Neuronal_Progenitor
33	3e−05	11 / 58	GSEA	ZHANG_GATA6_TARGETS_DN
34	4e−05	95 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
35	4e−05	45 / 558	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
36	5e−05	507 / 10430	Brain	Overlap_fetal_midbrain_Quies
37	5e−05	21 / 185	HM	HALLMARK_HEME_METABOLISM
38	8e−05	57 / 789	Colon	TxEnhG2_Colon
39	9e−05	5 / 12	CC	specific granule
40	9e−05	5 / 12	miRN	hsa−miR−652



Aging

Rank	p−value	#in/all	Geneset
1	0.3	8 / 142	HORVATH_aging_genes meth UP
2	0.5	5 / 111	HORVATH_aging_genes meth DOWN
3	0.9	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	8 / 40	establishment of protein localization to plasma membrane
2	3e−04	6 / 23	antibacterial humoral response
3	4e−04	5 / 16	megakaryocyte development
4	5e−04	12 / 92	anatomical structure morphogenesis
5	6e−04	4 / 10	protein localization to pre−autophagosomal structure
6	1e−03	5 / 19	clathrin−mediated endocytosis
7	1e−03	4 / 12	stress fiber assembly
8	2e−03	5 / 22	defense response to fungus
9	3e−03	5 / 24	neuromuscular synaptic transmission
10	3e−03	4 / 15	negative regulation of growth of symbiont in host
11	3e−03	4 / 15	positive regulation of lamellipodium assembly
12	4e−03	12 / 117	autophagy
13	6e−03	6 / 39	androgen receptor signaling pathway
14	7e−03	3 / 10	hemidesmosome assembly
15	7e−03	3 / 10	protein lipidation

Brain

Rank	p−value	#in/all	Geneset
1	3e−09	201 / 3164	Mid_Frontal_Lobe_ZNF
2	2e−08	174 / 2709	Mid_Frontal_Lobe_HetRpts
3	6e−08	69 / 818	Mid_Frontal_Lobe_Het
4	4e−07	117 / 1728	Fetal_ReprPCWk
5	2e−05	227 / 4112	Mid_Frontal_Lobe_ReprPC
6	5e−05	507 / 10430	Overlap_fetal_midbrain_Quies
7	1e−04	463 / 9504	Overlap_fetal_midbrain_K9K27me3
8	6e−04	54 / 796	Overlap_fetal_midbrain_ZNF
9	3e−02	93 / 1784	Mid_Frontal_Lobe_ReprPCWk
10	7e−02	105 / 2127	Mid_Frontal_Lobe_K9K27me3
11	1e−01	73 / 1476	Overlap_fetal_midbrain_TxTrans
12	2e−01	30 / 578	Fetal_Tx
13	2e−01	40 / 819	Overlap_fetal_midbrain_TssP
14	2e−01	53 / 1119	Overlap_fetal_midbrain_TssA
15	3e−01	44 / 924	Mid_Frontal_Lobe_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	2 / 15	LIU_PROSTATE_CANCER_DN
2	0.07	30 / 527	Lembcke_Normal vs Adenoma
3	0.09	2 / 12	LIU_BREAST_CANCER
4	0.12	2 / 14	GENTLES_modul1
5	0.15	2 / 16	BEN−PORATH_DN
6	0.15	2 / 16	GENTLES_modul14
7	0.19	6 / 91	PanCan_TXmisReg_geneset_nanostring
8	0.20	5 / 73	SHAUGHNESSY_MM high risk
9	0.21	2 / 20	PanCan_ChromMod_geneset_nanostring
10	0.23	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
11	0.29	0 / 14	LIU_COMMON_CANCER_GENES
12	0.31	8 / 150	PanCan_MAPK_geneset_nanostring
13	0.31	10 / 193	PanCan_PI3K_geneset_nanostring
14	0.33	1 / 9	GENTLES_modul5
15	0.39	6 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	9e−05	5 / 12	specific granule
2	8e−04	12 / 96	anchored component of membrane
3	3e−03	39 / 571	perinuclear region of cytoplasm
4	4e−03	4 / 16	acetylcholine−gated channel complex
5	7e−03	12 / 124	trans−Golgi network
6	7e−03	7 / 53	photoreceptor outer segment
7	1e−02	3 / 11	endolysosome membrane
8	1e−02	3 / 12	AP−2 adaptor complex
9	1e−02	8 / 75	secretory granule
10	2e−02	3 / 13	Golgi−associated vesicle
11	2e−02	150 / 2979	cytosol
12	2e−02	6 / 50	SNARE complex
13	2e−02	5 / 38	cis−Golgi network
14	2e−02	7 / 67	cytoplasmic mRNA processing body
15	2e−02	3 / 15	ESC/E(Z) complex

Chr

Rank	p−value	#in/all	Geneset
1	8e−04	88 / 1467	Chr 19
2	5e−03	58 / 959	Chr 16
3	1e−01	111 / 2323	Chr 1
4	2e−01	28 / 536	Chr 22
5	2e−01	6 / 87	Chr Y
6	2e−01	57 / 1170	Chr 7
7	3e−01	30 / 619	Chr 20
8	3e−01	61 / 1318	Chr 17
9	3e−01	42 / 904	Chr 10
10	3e−01	64 / 1411	Chr 11
11	4e−01	35 / 768	Chr 14
12	5e−01	43 / 994	Chr X
13	6e−01	40 / 954	Chr 9
14	7e−01	47 / 1160	Chr 12
15	7e−01	33 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−12	227 / 3450	4_TxTrans_Fibroblasts
2	1e−10	331 / 5699	6_EnhG_Melanocytes
3	2e−10	287 / 4795	6_EnhG_Fibroblasts
4	3e−09	142 / 2028	4_TxTrans_Melanocytes
5	1e−07	327 / 5956	3_TssF_Neuronal_Progenitor
6	1e−06	599 / 12298	2_TssA_Melanocytes
7	4e−06	576 / 11836	3_TssF_Melanocytes
8	7e−06	622 / 12983	2_TssA_Neuronal_Progenitor
9	1e−05	555 / 11455	2_TssA_Fibroblasts
10	2e−05	476 / 9635	3_TssF_Fibroblasts
11	2e−05	570 / 11847	7_Enh_Neuronal_Progenitor
12	2e−04	600 / 12741	7_Enh_Melanocytes
13	3e−04	427 / 8771	5_Tx_Melanocytes
14	8e−04	75 / 1206	6_EnhG_Neuronal_Progenitor
15	8e−03	568 / 12393	15_Quies_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−17	215 / 2845	TxEnhG1_Colon
2	8e−13	197 / 2810	EnhA_Colon
3	2e−12	361 / 6138	TssD2_Colon
4	2e−11	412 / 7354	TssF_Colon
5	3e−09	551 / 10779	Enh_Colon
6	3e−08	303 / 5373	EnhWk1_Colon
7	5e−07	462 / 9054	Tx_Colon
8	2e−05	55 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	4e−05	95 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	8e−05	57 / 789	TxEnhG2_Colon
11	1e−04	423 / 8568	TxWk_Colon
12	2e−04	463 / 9555	TssA_Colon
13	1e−03	117 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	7e−03	3 / 10	TCGA−CRC_agressive−disease−markers
15	2e−02	504 / 10999	TssWk_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.01	3 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
2	0.01	6 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
3	0.02	10 / 113	GIEZELT_GBM_WT_up_VS_mut
4	0.02	27 / 419	Down_a
5	0.03	25 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
6	0.03	8 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
7	0.04	3 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
8	0.04	25 / 401	Down_b
9	0.05	11 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	0.06	9 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
11	0.07	7 / 84	GIEZELT_GBM_STS_up_VS_LTS
12	0.08	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
13	0.10	8 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
14	0.10	2 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
15	0.11	7 / 95	Weller_LGG_1p19qDel−vs−intact_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−08	6 / 7	MARTINELLI_IMMATURE_NEUTROPHIL_UP
2	8e−06	75 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
3	1e−05	26 / 237	LU_EZH2_TARGETS_UP
4	1e−05	7 / 20	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
5	2e−05	7 / 21	REACTOME_REGULATORY_RNA_PATHWAYS
6	2e−05	6 / 15	LIU_IL13_MEMORY_MODEL_UP
7	3e−05	11 / 58	ZHANG_GATA6_TARGETS_DN
8	4e−05	45 / 558	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
9	2e−04	32 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
10	3e−04	45 / 612	MARTINEZ_RB1_TARGETS_UP
11	4e−04	22 / 232	RICKMAN_METASTASIS_DN
12	5e−04	41 / 552	MARTINEZ_TP53_TARGETS_UP
13	5e−04	41 / 553	MARTINEZ_RB1_AND_TP53_TARGETS_UP
14	5e−04	19 / 190	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
15	6e−04	4 / 10	REACTOME_GAP_JUNCTION_DEGRADATION

HM

Rank	p−value	#in/all	Geneset
1	5e−05	21 / 185	HALLMARK_HEME_METABOLISM
2	2e−03	7 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	2e−03	17 / 183	HALLMARK_APICAL_JUNCTION
4	3e−02	9 / 103	HALLMARK_BILE_ACID_METABOLISM
5	7e−02	10 / 137	HALLMARK_UV_RESPONSE_UP
6	8e−02	12 / 176	HALLMARK_ADIPOGENESIS
7	9e−02	7 / 91	HALLMARK_PEROXISOME
8	1e−01	12 / 189	HALLMARK_HYPOXIA
9	1e−01	9 / 138	HALLMARK_FATTY_ACID_METABOLISM
10	1e−01	11 / 177	HALLMARK_MITOTIC_SPINDLE
11	2e−01	11 / 183	HALLMARK_GLYCOLYSIS
12	2e−01	4 / 50	HALLMARK_TGF_BETA_SIGNALING
13	2e−01	6 / 87	HALLMARK_PROTEIN_SECRETION
14	2e−01	11 / 185	HALLMARK_P53_PATHWAY
15	2e−01	6 / 91	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	5e−06	20 / 147	Homuth_BMI−associated−genes_UP
2	4e−01	1 / 10	Marjolein_ageing−genes_UP
3	5e−01	1 / 16	Huan_blood−pressure_DBP−signature
4	5e−01	1 / 17	DUMEAUX_High bmi enriched genes
5	6e−01	4 / 94	DUMEAUX_Smoking enriched genes
6	7e−01	8 / 211	Homuth_BMI−associated−genes_DN
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1e+00	0 / 7	DUMEAUX_Estrogen related in non 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 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−04	369 / 7448	HOPP_Strong_enhancer
2	9e−03	24 / 331	WIRTH_lymphoma937_spot H
3	1e−02	23 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
4	1e−02	4 / 21	ROSOLOWSKI_red UP
5	1e−02	30 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
6	2e−02	30 / 464	WIRTH_lymphoma937_spot I
7	5e−02	251 / 5356	HOPP_Txn_transition
8	7e−02	5 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
9	8e−02	2 / 11	Subero_MM_hypo_meth
10	8e−02	26 / 455	SPANG_CD40 6hrs DN
11	1e−01	2 / 13	Subero_B−CLL_hypo_meth
12	1e−01	4 / 45	Subero_INT_hypo_meth
13	1e−01	4 / 46	Subero_DLBCL_hypo_meth
14	2e−01	6 / 88	ROSOLOWSKI_red total
15	2e−01	5 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.04	2 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
2	0.41	3 / 54	Hugo_melanoma−all−MET_DN
3	0.55	2 / 43	Hugo_melanoma−BRAFmut−MET_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 / 27	Hugo_melanoma−all−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	5e−04	7 / 34	histone−lysine N−methyltransferase activity
2	6e−03	416 / 8818	protein binding
3	8e−03	4 / 19	acetylcholine binding
4	1e−02	4 / 21	acetylcholine−activated cation−selective channel activity
5	1e−02	4 / 21	acetylcholine receptor activity
6	1e−02	4 / 22	calmodulin−dependent protein kinase activity
7	1e−02	4 / 22	polyubiquitin binding
8	2e−02	36 / 580	identical protein binding
9	2e−02	3 / 14	mitogen−activated protein kinase kinase binding
10	2e−02	4 / 25	enzyme inhibitor activity
11	3e−02	3 / 16	enzyme regulator activity
12	3e−02	3 / 16	K63−linked polyubiquitin binding
13	3e−02	3 / 16	RNA polymerase III activity
14	3e−02	4 / 28	SH2 domain binding
15	3e−02	10 / 120	protein tyrosine kinase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.08	1 / 2	Burkitt lymphoma
2	0.12	1 / 3	Down syndrome, risk of
3	0.30	1 / 8	Cardiomyopathy, idiopathic dilated
4	0.34	3 / 48	Gastric cancer
5	0.34	2 / 28	Immunological
6	0.35	1 / 10	Cardiovascular
7	0.46	1 / 14	Autism, susceptibility to
8	0.48	1 / 15	Supravalvar aortic stenosis
9	0.51	3 / 63	Gastrointestinal
10	0.52	1 / 17	Bladder cancer
11	0.55	1 / 18	Non−Hodgkin lymphoma, somatic
12	0.56	3 / 68	Glioblastoma multiforme, somatic
13	0.58	1 / 20	Parkinson disease
14	0.59	5 / 120	Hematological
15	0.61	5 / 123	Pancreatic cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−05	5 / 12	hsa−miR−652
2	8e−04	5 / 18	hsa−miR−564
3	9e−04	8 / 48	hsa−miR−329
4	1e−03	16 / 160	hsa−miR−298
5	3e−03	17 / 188	hsa−miR−548d−3p
6	6e−03	7 / 52	hsa−miR−362−3p
7	7e−03	9 / 79	hsa−miR−942
8	8e−03	7 / 54	hsa−miR−629
9	8e−03	7 / 54	hsa−miR−1302
10	1e−02	6 / 43	hsa−miR−412
11	1e−02	22 / 299	hsa−miR−548c−3p
12	1e−02	10 / 105	hsa−miR−361−5p
13	2e−02	4 / 24	hsa−miR−1228
14	2e−02	20 / 281	hsa−miR−570
15	2e−02	7 / 64	hsa−miR−1275

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.4	1 / 12	BENTINK_ras.1
2	0.4	1 / 13	BENTINK_e2f3.2
3	0.5	1 / 14	BENTINK_ras.6
4	0.5	1 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 14	GUSTAFSON_PI3K_UP
6	1.0	0 / 13	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 11	BENTINK_ras.4
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	5e−07	11 / 39	Chaussabel_2,2_Neutrophils
2	1e−04	5 / 13	WIRTH_Bone marrow
3	2e−04	7 / 29	JONGENEEL_Bone Marrow
4	3e−03	4 / 15	VAQUERIZAS_Fetal liver_TF
5	8e−03	4 / 19	VAQUERIZAS_Bone marrow_TF
6	9e−03	4 / 20	JONGENEEL_Thymus
7	1e−02	5 / 32	VAQUERIZAS_Liver_TF
8	2e−02	5 / 39	VAQUERIZAS_Testis_TF
9	3e−02	12 / 150	Chaussabel_2,6_Myeloid lineage
10	3e−02	5 / 41	VAQUERIZAS_Thymus_TF
11	4e−02	5 / 43	VAQUERIZAS_Placenta_TF
12	5e−02	11 / 148	VAQUERIZAS_General_TF
13	8e−02	2 / 11	WIRTH_Prim. lymphoid organs
14	1e−01	2 / 13	WIRTH_Thymus
15	1e−01	2 / 14	WIRTH_B−cells

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	2 / 13	Alternative lengthening of telomeres
2	0.3	2 / 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	0.006	291 / 5984	ICGC_Mta3_targets
2	0.006	46 / 733	ICGC_Atf3_targets
3	0.009	221 / 4468	ICGC_Egr1_targets
4	0.011	261 / 5383	ICGC_Sp1_targets
5	0.013	313 / 6578	ICGC_Pou2_targets
6	0.014	251 / 5188	ICGC_Ebfsc137065_targets
7	0.016	256 / 5312	ICGC_Tcf12_targets
8	0.017	140 / 2759	ICGC_Bcl3_targets
9	0.028	262 / 5518	ICGC_Stat5_targets
10	0.029	257 / 5410	ICGC_Foxm1_targets
11	0.030	297 / 6322	ICGC_Tcf3_targets
12	0.033	337 / 7247	ICGC_Runx3_targets
13	0.036	306 / 6552	ICGC_Pol2_targets
14	0.047	231 / 4890	ICGC_Bclaf101388_targets
15	0.047	318 / 6868	ICGC_Elf1_targets

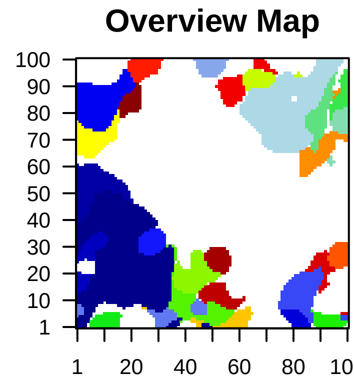
Correlation Cluster

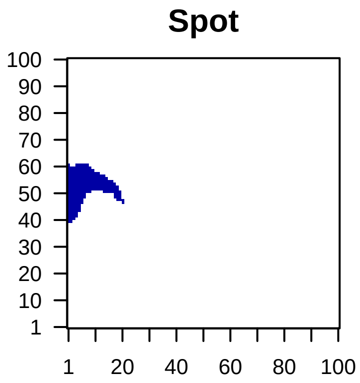
Spot Summary: K

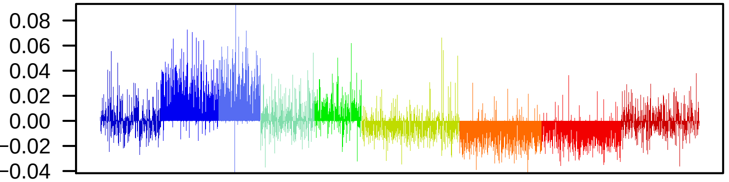
metagenes = 219
genes = 606

<r> metagenes = 0.93
<r> genes = 0.06
beta: r2= 0.77 / log p= −Inf

samples with spot = 10 (0.3 %)
A C * : 6 (1.8 %)
A C F * : 3 (1.3 %)
F * : 1 (0.2 %)





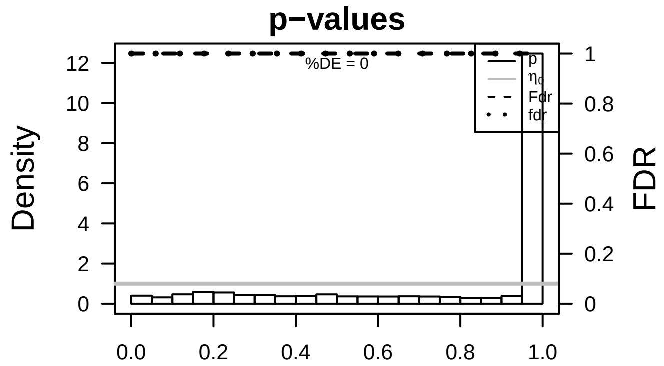


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178470	0.44	−0.27	0.28	MIR452	gamma−aminobutyric acid type A receptor epsilon subunit [S
2	ILMN_165780	0.39	−0.24	0.29	CFH	complement factor H [Source:HGNC Symbol;Acc:HGNC:488
3	ILMN_180492	0.39	−0.27	0.39	OXTR	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]
4	ILMN_167875	0.38	−0.26	0.44	PFDN2	prefoldin subunit 2 [Source:HGNC Symbol;Acc:HGNC:8867]
5	ILMN_169097	0.37	−0.21	0.49		
6	ILMN_177633	0.37	−0.27	0.47	UXS1	UDP−glucuronate decarboxylase 1 [Source:HGNC Symbol;A
7	ILMN_187880	0.36	−0.22	0.54		
8	ILMN_166264	0.36	−0.31	0.2		metallothionein 1 pseudogene 3 [Source:HGNC Symbol;Acc:
9	ILMN_324794	0.36	−0.27	0.37	GOLGA7B	golgin A7 family member B [Source:HGNC Symbol;Acc:HGN
10	ILMN_167769	0.35	−0.23	0.48		
11	ILMN_189591	0.35	−0.29	0.57		
12	ILMN_318212	0.35	−0.25	0.5		
13	ILMN_172168	0.35	−0.25	0.46		
14	ILMN_320086	0.34	−0.24	0.22	GSE1	Gse1 coiled−coil protein [Source:HGNC Symbol;Acc:HGNC:2
15	ILMN_168085	0.34	−0.33	0.14		
16	ILMN_328896	0.34	−0.2	0.45	LINC01451	long intergenic non−protein coding RNA 1451 [Source:HGNC
17	ILMN_212874	0.34	−0.28	0.21	RDH11	retinol dehydrogenase 11 (all−trans/9−cis/11−cis) [Source:HG
18	ILMN_170164	0.34	−0.26	0.46	PCDHGB6	protocadherin gamma subfamily B, 6 [Source:HGNC Symbol;
19	ILMN_324467	0.34	−0.26	0.46	SNORA5B	small nucleolar RNA, H/ACA box 5B [Source:HGNC Symbol;
20	ILMN_174325	0.34	−0.24	0.24		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−06	111 / 5384	Lympl	HOPP_Repressed
2	1e−05	93 / 4304	Chror	9_ReprPCWk_Melanocytes
3	1e−05	78 / 3438	Chror	10_ReprPC_Melanocytes
4	2e−05	90 / 4169	Chror	10_ReprPC_Fibroblasts
5	2e−05	81 / 3639	Chror	1_TssP_Fibroblasts
6	3e−05	70 / 3068	Chror	8_EnhP_Fibroblasts
7	7e−05	7 / 72	GSEA	RODRIGUES_THYROID_CARCINOMA_DN
8	1e−04	60 / 2620	Chror	1_TssP_Neuronal_Progenitor
9	3e−04	74 / 3523	Chror	1_TssP_Melanocytes
10	3e−04	4 / 23	BP	vesicle docking involved in exocytosis
11	5e−04	56 / 2516	Chror	11_K9K27me3_Melanocytes
12	6e−04	7 / 100	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
13	6e−04	58 / 2660	Chror	8_EnhP_Melanocytes
14	8e−04	66 / 3173	Colon	ReprPC_Colon
15	9e−04	44 / 1895	Colon	EnhP_Colon
16	9e−04	51 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
17	1e−03	74 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
18	1e−03	3 / 15	GSEA	MURAKAMI_UV_RESPONSE_1HR_UP
19	2e−03	3 / 18	BP	positive regulation of dendritic spine development
20	2e−03	4 / 40	GSEA	ULE_SPLICING_VIA_NOVA2
21	3e−03	3 / 21	BP	cholesterol transport
22	3e−03	3 / 21	GSEA	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP
23	3e−03	55 / 2682	Chror	12_Het_Neuronal_Progenitor
24	4e−03	54 / 2630	Brain	Fetal_TssF
25	4e−03	78 / 4107	Chror	9_ReprPCWk_Fibroblasts
26	4e−03	59 / 2939	Lympl	HOPP_Poised_promoter
27	4e−03	16 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
28	5e−03	33 / 1448	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
29	5e−03	4 / 49	CC	lateral plasma membrane
30	5e−03	3 / 25	BP	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion
31	5e−03	3 / 25	GSEA	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP
32	5e−03	27 / 1119	Brain	Overlap_fetal_midbrain_TssA
33	6e−03	3 / 27	BP	positive regulation of extrinsic apoptotic signaling pathway
34	6e−03	3 / 27	GSEA	NAKAYAMA_FGF2_TARGETS
35	7e−03	5 / 83	CC	voltage−gated potassium channel complex
36	7e−03	63 / 3272	Chror	13_HetRpts_Neuronal_Progenitor
37	7e−03	14 / 465	Brain	Mid_Frontal_Lobe_TxTrans
38	7e−03	8 / 196	CC	postsynaptic membrane
39	7e−03	3 / 28	BP	telencephalon development
40	7e−03	9 / 238	GSEA	JAEGER_METASTASIS_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 58	TESCHENDORFF_age_hypermethylated
2	0.9	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 9	GENTLES_modul3
2	0.1	4 / 136	PanCan_RAS_geneset_nanostring
3	0.2	1 / 13	WANG_ER_DN
4	0.2	2 / 54	KUIPER_MM poor survival
5	0.2	0 / 15	LIU_PROSTATE_CANCER_DN
6	0.2	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.2	1 / 20	PanCan_ChromMod_geneset_nanostring
8	0.3	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	0.3	0 / 12	LIU_BREAST_CANCER
10	0.4	3 / 150	PanCan_MAPK_geneset_nanostring
11	0.4	1 / 39	ZHANG_MM up
12	0.5	8 / 527	Lembcke_Normal vs Adenoma
13	0.5	1 / 46	PanCan_DNARepair_geneset_nanostring
14	0.5	8 / 554	Lembcke_Colonic Inflammation
15	0.6	0 / 14	LIU_COMMON_CANCER_GENES

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−05	93 / 4304	9_ReprPCWk_Melanocytes
2	1e−05	78 / 3438	10_ReprPC_Melanocytes
3	2e−05	90 / 4169	10_ReprPC_Fibroblasts
4	2e−05	81 / 3639	1_TssP_Fibroblasts
5	3e−05	70 / 3068	8_EnhP_Fibroblasts
6	1e−04	60 / 2620	1_TssP_Neuronal_Progenitor
7	3e−04	74 / 3523	1_TssP_Melanocytes
8	5e−04	56 / 2516	11_K9K27me3_Melanocytes
9	6e−04	58 / 2660	8_EnhP_Melanocytes
10	9e−04	51 / 2297	10_ReprPC_Neuronal_Progenitor
11	1e−03	74 / 3691	9_ReprPCWk_Neuronal_Progenitor
12	3e−03	55 / 2682	12_Het_Neuronal_Progenitor
13	4e−03	78 / 4107	9_ReprPCWk_Fibroblasts
14	7e−03	63 / 3272	13_HetRpts_Neuronal_Progenitor
15	3e−02	35 / 1789	8_EnhP_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−05	7 / 72	RODRIGUES_THYROID_CARCINOMA_DN
2	6e−04	7 / 100	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
3	1e−03	3 / 15	MURAKAMI_UV_RESPONSE_1HR_UP
4	2e−03	4 / 40	ULE_SPLICING_VIA_NOVA2
5	3e−03	3 / 21	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP
6	4e−03	16 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
7	5e−03	33 / 1448	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
8	5e−03	3 / 25	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP
9	6e−03	3 / 27	NAKAYAMA_FGF2_TARGETS
10	7e−03	9 / 238	JAEGER_METASTASIS_DN
11	8e−03	5 / 86	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_
12	8e−03	2 / 10	REACTOME_REGULATION_OF_COMPLEMENT_CASCADE
13	9e−03	7 / 164	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_TRANS
14	1e−02	3 / 31	NABA_PROTEOGLYCANS
15	1e−02	2 / 11	BIOCARTA_ACE2_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−06	111 / 5384	HOPP_Repressed
2	4e−03	59 / 2939	HOPP_Poised_promoter
3	8e−03	77 / 4167	HOPP_Heterochrom
4	9e−03	5 / 89	Subero_T−ALL_hyper_meth
5	8e−02	3 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
6	9e−02	4 / 118	Subero_INT_hyper_meth
7	9e−02	3 / 74	Subero_FL_hyper_meth
8	1e−01	4 / 134	Subero_DLBCL_hyper_meth
9	1e−01	4 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
10	1e−01	1 / 10	BENTINK_mBL DOWN
11	1e−01	4 / 138	WIRTH_lymphoma937_spot G
12	1e−01	2 / 48	Subero_B−ALL_hyper_meth
13	2e−01	1 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
14	2e−01	44 / 2701	HOPP_Repetitive
15	2e−01	5 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 4	Nasopharyngeal carcinoma
2	0.22	3 / 113	Ovarian cancer
3	0.23	1 / 18	Hodgkin lymphoma
4	0.23	1 / 18	Non−Hodgkin lymphoma, somatic
5	0.25	3 / 123	Pancreatic cancer
6	0.27	3 / 127	Melanoma and neural system tumor syndrome
7	0.27	3 / 127	Squamous cell carcinoma, head and neck
8	0.33	3 / 142	Lung cancer
9	0.33	1 / 28	Miyoshi myopathy
10	0.33	1 / 28	Immunological
11	0.43	2 / 102	Leukemia
12	0.49	1 / 47	Cervical cancer, somatic
13	0.49	2 / 116	Cancer
14	0.51	2 / 120	Hematological
15	0.53	2 / 124	Prostate cancer

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.02	2 / 17	JONGENEEL_Pancreas
2	0.03	3 / 48	WIRTH_Pancreas
3	0.04	5 / 134	WIRTH_Mucosa
4	0.05	7 / 231	Chaussabel_2,5_Immune related molecules
5	0.08	1 / 6	JONGENEEL_SpinalCord
6	0.09	3 / 76	WIRTH_Homeostasis
7	0.11	1 / 8	JONGENEEL_Fetal Brain
8	0.12	2 / 42	VAQUERIZAS_Fetal brain_TF
9	0.13	1 / 10	JONGENEEL_Pituitary Gland
10	0.15	1 / 11	WIRTH_Tonsil
11	0.17	1 / 13	JONGENEEL_Thyroid
12	0.17	2 / 53	JONGENEEL_Kidney
13	0.29	1 / 24	VAQUERIZAS_Pituitary_TF
14	0.39	5 / 289	JONGENEEL_Testis
15	0.43	1 / 39	VAQUERIZAS_Testis_TF

BP

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 23	vesicle docking involved in exocytosis
2	2e−03	3 / 18	positive regulation of dendritic spine development
3	3e−03	3 / 21	cholesterol transport
4	5e−03	3 / 25	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion m
5	6e−03	3 / 27	positive regulation of extrinsic apoptotic signaling pathway
6	7e−03	3 / 28	telencephalon development
7	8e−03	3 / 29	neuromuscular junction development
8	9e−03	4 / 57	positive regulation of synapse assembly
9	1e−02	2 / 11	gene silencing by miRNA
10	1e−02	2 / 11	negative regulation of protein tyrosine kinase activity
11	1e−02	4 / 60	positive regulation of epithelial cell proliferation
12	1e−02	2 / 12	central nervous system neuron development
13	1e−02	2 / 12	positive regulation of synaptic transmission, GABAergic
14	1e−02	2 / 12	regulation of smooth muscle contraction
15	1e−02	2 / 13	sterol biosynthetic process

CC

Rank	p−value	#in/all	Geneset
1	0.005	4 / 49	lateral plasma membrane
2	0.007	5 / 83	voltage−gated potassium channel complex
3	0.007	8 / 196	postsynaptic membrane
4	0.011	9 / 256	apical plasma membrane
5	0.015	3 / 37	T−tubule
6	0.018	14 / 524	intracellular
7	0.019	3 / 40	cytoplasmic side of plasma membrane
8	0.024	2 / 17	neuronal cell body membrane
9	0.035	6 / 170	cell−cell junction
10	0.040	3 / 53	brush border
11	0.047	3 / 57	terminal bouton
12	0.065	3 / 65	caveola
13	0.076	2 / 32	dendritic shaft
14	0.082	5 / 162	basolateral plasma membrane
15	0.085	24 / 1252	integral component of plasma membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−04	66 / 3173	ReprPC_Colon
2	9e−04	44 / 1895	EnhP_Colon
3	8e−03	54 / 2740	ReprPCWk_Colon
4	1e−02	55 / 2894	TssP_Colon
5	2e−02	27 / 1224	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
6	2e−02	13 / 484	Quies2_Colon
7	4e−02	10 / 366	K9K27me3_Colon
8	5e−02	15 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
9	6e−02	10 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	1e−01	74 / 4526	Quies1_Colon
11	1e−01	1 / 10	TCGA−CRC_agressive−disease−markers
12	1e−01	12 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
13	2e−01	1 / 15	Budinska_B_Lower crypt−like_DOWN
14	2e−01	14 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
15	2e−01	1 / 20	Budinska_B_Lower crypt−like_UP

HM

Rank	p−value	#in/all	Geneset
1	0.01	6 / 132	HALLMARK_UV_RESPONSE_DN
2	0.02	7 / 191	HALLMARK_INFLAMMATORY_RESPONSE
3	0.12	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	0.27	3 / 127	HALLMARK_COAGULATION
5	0.36	3 / 151	HALLMARK_APOPTOSIS
6	0.45	3 / 173	HALLMARK_E2F_TARGETS
7	0.46	3 / 176	HALLMARK_KRAS_SIGNALING_UP
8	0.48	3 / 183	HALLMARK_APICAL_JUNCTION
9	0.48	3 / 183	HALLMARK_GLYCOLYSIS
10	0.49	3 / 185	HALLMARK_MTORC1_SIGNALING
11	0.49	3 / 185	HALLMARK_P53_PATHWAY
12	0.49	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
13	0.50	3 / 189	HALLMARK_HYPOXIA
14	0.51	1 / 50	HALLMARK_TGF_BETA_SIGNALING
15	0.51	3 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Melanoma

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	hsa−miR−551a
2	0.06	2 / 28	hsa−miR−591
3	0.08	3 / 72	hsa−miR−361−3p
4	0.09	2 / 35	hsa−miR−770−5p
5	0.11	2 / 39	hsa−miR−501−3p
6	0.11	2 / 40	hsa−miR−518b
7	0.11	2 / 40	hsa−miR−885−5p
8	0.14	3 / 92	hsa−miR−219−2−3p
9	0.15	1 / 11	hsa−miR−369−5p
10	0.16	2 / 50	hsa−miR−1224−3p
11	0.18	1 / 14	hsa−miR−551b
12	0.19	4 / 157	hsa−miR−31
13	0.20	2 / 59	hsa−miR−526b*
14	0.21	4 / 166	hsa−miR−7
15	0.22	1 / 17	hsa−miR−302a*

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	0.004	54 / 2630	Fetal_TssF
2	0.005	27 / 1119	Overlap_fetal_midbrain_TssA
3	0.007	14 / 465	Mid_Frontal_Lobe_TxTrans
4	0.011	75 / 4112	Mid_Frontal_Lobe_ReprPC
5	0.012	39 / 1893	Overlap_fetal_midbrain_TssF
6	0.013	10 / 307	Fetal_ReprPC
7	0.019	29 / 1360	Mid_Frontal_Lobe_TssP
8	0.026	19 / 819	Overlap_fetal_midbrain_TssP
9	0.031	30 / 1476	Overlap_fetal_midbrain_TxTrans
10	0.036	55 / 3046	Fetal_TssA
11	0.064	24 / 1213	Fetal_TssP
12	0.070	8 / 304	Mid_Frontal_Lobe_TssA
13	0.072	18 / 869	Mid_Frontal_Lobe_EnhG
14	0.072	4 / 110	Overlap_fetal_midbrain_Tx
15	0.082	47 / 2700	Fetal_TxTrans

Chr

Rank	p−value	#in/all	Geneset
1	0.06	8 / 289	Chr 21
2	0.09	18 / 902	Chr 4
3	0.25	17 / 994	Chr X
4	0.27	24 / 1467	Chr 19
5	0.28	16 / 954	Chr 9
6	0.30	13 / 768	Chr 14
7	0.36	19 / 1211	Chr 6
8	0.38	10 / 619	Chr 20
9	0.44	16 / 1060	Chr 5
10	0.48	17 / 1160	Chr 12
11	0.53	33 / 2323	Chr 1
12	0.54	5 / 342	Chr 18
13	0.55	21 / 1492	Chr 2
14	0.56	17 / 1217	Chr 3
15	0.64	7 / 536	Chr 22

Glio

Rank	p−value	#in/all	Geneset
1	0.009	13 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
2	0.011	5 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
3	0.013	3 / 35	WIRTH_PN subtype
4	0.019	6 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	0.023	9 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
6	0.029	2 / 19	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
7	0.038	3 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
8	0.089	11 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	0.094	3 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.108	1 / 8	Shaw_responders_up_in_oligo_glioma
11	0.109	26 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
12	0.121	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
13	0.133	3 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	0.141	5 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
15	0.153	3 / 95	Weller_LGG_1p19qDel−vs−intact_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.19	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.39	2 / 94	DUMEAUX_Smoking enriched genes
4	0.62	2 / 147	Homuth_BMI−associated−genes_UP
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Monocytes in 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 / 211	Homuth_BMI−associated−genes_DN
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.01	4 / 59	cell adhesion molecule binding
2	0.01	2 / 12	neurexin family protein binding
3	0.01	2 / 13	NAD+ binding
4	0.02	2 / 14	nitric−oxide synthase binding
5	0.02	3 / 38	cholesterol binding
6	0.02	2 / 15	calcium−activated potassium channel activity
7	0.02	2 / 17	transferase activity, transferring acyl groups
8	0.02	4 / 77	PDZ domain binding
9	0.03	2 / 20	hyaluronic acid binding
10	0.04	2 / 21	cytokine receptor activity
11	0.05	2 / 25	protein−cysteine S−palmitoyltransferase activity
12	0.05	2 / 26	retinoic acid receptor binding
13	0.06	2 / 27	peptide hormone binding
14	0.07	2 / 30	NADP binding
15	0.07	4 / 108	ion channel binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.1	31 / 1753	HEBENSTREIT_low expression TF
2	0.2	57 / 3507	ICGC_Rad21_targets
3	0.2	14 / 747	ICGC_NrsfPcr2_targets
4	0.4	76 / 5188	ICGC_Ebfsc137065_targets
5	0.4	10 / 631	ICGC_RxraPcr1_targets
6	0.5	46 / 3194	ICGC_Irf4_targets
7	0.5	36 / 2497	ICGC_Bcl11_targets
8	0.6	30 / 2133	ICGC_Mef2_targets
9	0.6	47 / 3348	ICGC_BatfPcr1_targets
10	0.6	88 / 6267	ICGC_Yy1_targets
11	0.6	10 / 721	ICGC_SrfPcr2_targets
12	0.7	87 / 6322	ICGC_Tcf3_targets
13	0.7	22 / 1669	ICGC_P300_targets
14	0.7	19 / 1466	ICGC_NrsfPcr1_targets
15	0.7	19 / 1478	ICGC_Myc_targets

Correlation Cluster

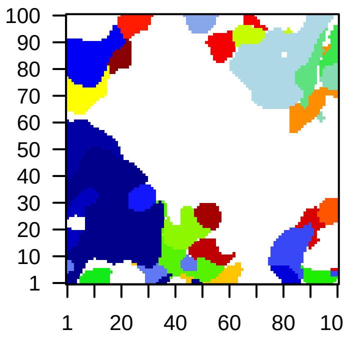
Spot Summary: L

metagenes = 108
genes = 837

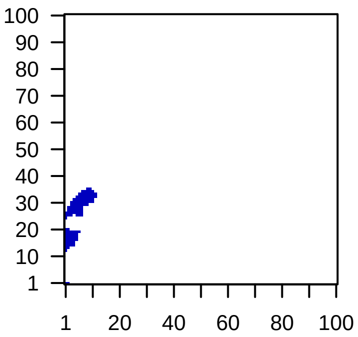
<r> metagenes = 0.95
<r> genes = 0.42
beta: r2= 58.98 / log p= −Inf

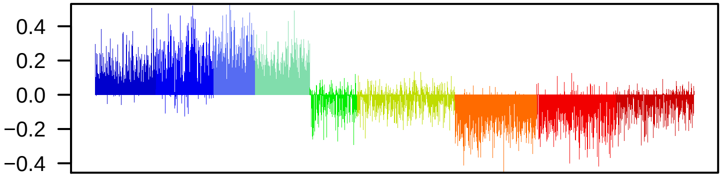
samples with spot = 1088 (32.1 %)
A * : 267 (77.6 %)
A C * : 252 (76.8 %)
A C F * : 230 (97.9 %)
A F * : 283 (91.9 %)
C F * : 10 (3.8 %)
F * : 34 (6.1 %)
J * : 7 (1.6 %)
N * : 5 (1.1 %)

Overview Map



Spot





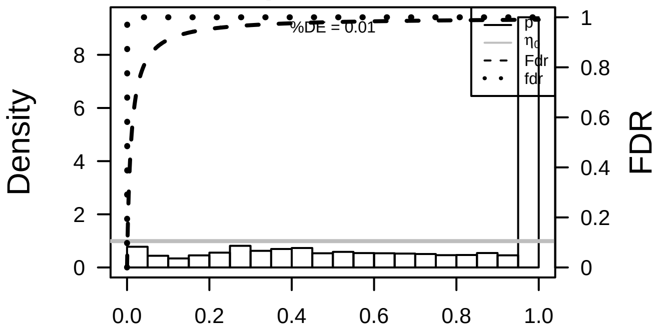
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_323194	1.5	−1.58	0.94		
2	ILMN_167769	1.49	−1.31	0.96		
3	ILMN_323717	1.48	−1.61	0.95	FAM175A	family with sequence similarity 175 member A [Source:HGNC
4	ILMN_323740	1.46	−1.46	0.95		
5	ILMN_318148	1.44	−1.46	0.92	LOC102723623	golgin A6 family−like 1 [Source:HGNC Symbol;Acc:HGNC:37
6	ILMN_327479	1.42	−1.12	0.96	ACTG1P17	actin gamma 1 pseudogene 17 [Source:HGNC Symbol;Acc:H
7	ILMN_172134	1.41	−1.5	0.95		
8	ILMN_218811	1.41	−1.53	0.93	ARL16	ADP ribosylation factor like GTPase 16 [Source:HGNC Symb
9	ILMN_228601	1.4	−1.5	0.93	CATSPER2	cation channel sperm associated 2 [Source:HGNC Symbol;A
10	ILMN_187241	1.4	−1.22	0.88		
11	ILMN_329421	1.39	−1.29	0.97		
12	ILMN_212355	1.38	−1.32	0.95		
13	ILMN_205455	1.38	−1.41	0.96	DTWD2	DTW domain containing 2 [Source:HGNC Symbol;Acc:HGNC
14	ILMN_329841	1.38	−1.2	0.96		
15	ILMN_212251	1.37	−1.45	0.9	CCBE1	collagen and calcium binding EGF domains 1 [Source:HGNC
16	ILMN_215029	1.37	−1.43	0.9	FKBP14	FK506 binding protein 14 [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_207354	1.35	−1.37	0.95	SERF2	small EDRK−rich factor 2 [Source:HGNC Symbol;Acc:HGNC:
18	ILMN_321318	1.35	−1.43	0.95		
19	ILMN_215046	1.35	−1.28	0.84	TMEM267	transmembrane protein 267 [Source:HGNC Symbol;Acc:HGN
20	ILMN_207579	1.34	−1.33	0.93	NLRP8	NLR family pyrin domain containing 8 [Source:HGNC Symbol

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−26	56 / 360	GSEA	LU_EZH2_TARGETS_DN
2	1e−24	367 / 9054	Colon	Tx_Colon
3	1e−19	339 / 8568	Colon	TxWk_Colon
4	3e−18	340 / 8771	Chror	5_Tx_Melanocytes
5	4e−17	296 / 7354	Colon	TssF_Colon
6	4e−17	151 / 2845	Colon	TxEnhG1_Colon
7	5e−17	310 / 7854	Chror	5_Tx_Fibroblasts
8	5e−17	172 / 3450	Chror	4_TxTrans_Fibroblasts
9	2e−16	356 / 9555	Colon	TssA_Colon
10	3e−16	243 / 5699	Chror	6_EnhG_Melanocytes
11	5e−16	427 / 12298	Chror	2_TssA_Melanocytes
12	6e−15	286 / 7275	Lympl	HOPP_Txn_elongation
13	2e−14	209 / 4795	Chror	6_EnhG_Fibroblasts
14	2e−14	275 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	2e−13	406 / 11836	Chror	3_TssF_Melanocytes
16	5e−13	240 / 5956	Chror	3_TssF_Neuronal_Progenitor
17	7e−13	150 / 3164	Brain	Mid_Frontal_Lobe_ZNF
18	2e−12	243 / 6138	Colon	TssD2_Colon
19	3e−12	339 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
20	4e−12	391 / 11455	Chror	2_TssA_Fibroblasts
21	5e−12	430 / 12983	Chror	2_TssA_Neuronal_Progenitor
22	8e−12	217 / 5356	Lympl	HOPP_Txn_transition
23	3e−11	105 / 2028	Chror	4_TxTrans_Melanocytes
24	1e−10	336 / 9635	Chror	3_TssF_Fibroblasts
25	5e−10	338 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
26	6e−10	179 / 4362	TF	ICGC_Creb1_targets
27	8e−10	210 / 5383	TF	ICGC_Sp1_targets
28	1e−09	80 / 1467	Chr	Chr 19
29	1e−09	213 / 5518	TF	ICGC_Stat5_targets
30	2e−09	225 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
31	2e−09	38 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B
32	5e−09	197 / 5067	TF	ICGC_Taf1_targets
33	1e−08	166 / 4131	TF	ICGC_Nfatc1_targets
34	2e−08	37 / 493	Lympl	WIRTH_lymphoma937_spot J
35	3e−08	188 / 4881	TF	ICGC_Atf2_targets
36	4e−08	263 / 7448	Lympl	HOPP_Strong_enhancer
37	4e−08	246 / 6868	TF	ICGC_Elf1_targets
38	6e−08	284 / 8226	Lympl	HOPP_Active_promoter
39	7e−08	203 / 5442	TF	ICGC_Pmlsc71910_targets
40	1e−07	203 / 5466	TF	ICGC_Nficsc81335_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	3 / 111	HORVATH_aging_genes meth DOWN
2	0.8	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	

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	2 / 14	LIU_COMMON_CANCER_GENES
2	0.007	3 / 15	WANG_ER_UP
3	0.071	3 / 36	PanCan_HK_geneset_nanostring
4	0.196	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
5	0.217	1 / 9	GENTLES_modul5
6	0.297	1 / 13	LIU_LIVER_CANCER
7	0.297	1 / 13	WANG_ER_DN
8	0.316	1 / 14	GENTLES_modul10
9	0.335	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	0.350	2 / 46	PanCan_DNARepair_geneset_nanostring
11	0.377	3 / 82	PanCan_JAK−ST_geneset_nanostring
12	0.408	0 / 13	RHODES_CANCER_META_SIGNATURE
13	0.419	1 / 20	PanCan_ChromMod_geneset_nanostring
14	0.426	2 / 54	KUIPER_MM poor survival
15	0.431	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−18	340 / 8771	5_Tx_Melanocytes
2	5e−17	310 / 7854	5_Tx_Fibroblasts
3	5e−17	172 / 3450	4_TxTrans_Fibroblasts
4	3e−16	243 / 5699	6_EnhG_Melanocytes
5	5e−16	427 / 12298	2_TssA_Melanocytes
6	2e−14	209 / 4795	6_EnhG_Fibroblasts
7	2e−14	275 / 6970	5_Tx_Neuronal_Progenitor
8	2e−13	406 / 11836	3_TssF_Melanocytes
9	5e−13	240 / 5956	3_TssF_Neuronal_Progenitor
10	4e−12	391 / 11455	2_TssA_Fibroblasts
11	5e−12	430 / 12983	2_TssA_Neuronal_Progenitor
12	3e−11	105 / 2028	4_TxTrans_Melanocytes
13	1e−10	336 / 9635	3_TssF_Fibroblasts
14	1e−06	84 / 1846	14_ZNF_Melanocytes
15	1e−06	399 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−26	56 / 360	LU_EZH2_TARGETS_DN
2	5e−06	6 / 18	SPIRA_SMOKERS_LUNG_CANCER_DN
3	2e−05	10 / 73	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP
4	8e−05	20 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
5	9e−05	37 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
6	1e−04	4 / 11	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
7	2e−04	65 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
8	3e−04	16 / 221	WANG_CLIM2_TARGETS_UP
9	3e−04	15 / 200	KAUFFMANN_DNA_REPAIR_GENES
10	5e−04	20 / 325	DAIRKEE_TERT_TARGETS_UP
11	1e−03	4 / 19	HEDENFALK_BREAST_CANCER_BRACX_DN
12	2e−03	2 / 14	LIU_COMMON_CANCER_GENES
13	2e−03	13 / 189	CHANG_CORE_SERUM_RESPONSE_DN
14	2e−03	20 / 361	ODONNELL_TFRC_TARGETS_UP
15	2e−03	21 / 387	LIM_MAMMARY_STEM_CELL_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−15	286 / 7275	HOPP_Txn_elongation
2	8e−12	217 / 5356	HOPP_Txn_transition
3	2e−09	38 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
4	2e−08	37 / 493	WIRTH_lymphoma937_spot J
5	4e−08	263 / 7448	HOPP_Strong_enhancer
6	6e−08	284 / 8226	HOPP_Active_promoter
7	4e−04	257 / 8098	HOPP_Weak_promoter
8	3e−03	23 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
9	4e−03	23 / 464	WIRTH_lymphoma937_spot I
10	4e−03	47 / 1169	SPANG_BCR DN
11	4e−03	18 / 331	WIRTH_lymphoma937_spot H
12	1e−02	3 / 19	DAVE_BL Inter
13	2e−02	200 / 6559	HOPP_Weak_txn
14	2e−02	16 / 331	SPANG_CD40 6hrs UP
15	3e−02	15 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	Immunoglobulin A deficiency
2	0.37	1 / 17	Thyroid carcinoma, follicular
3	0.39	1 / 18	Non−Hodgkin lymphoma, somatic
4	0.45	1 / 22	Pigmented adrenocortical disease, primary isolated
5	0.55	1 / 29	Myelofibrosis, idiopathic
6	0.73	1 / 48	Multiple myeloma
7	0.82	1 / 63	Gastrointestinal
8	0.83	1 / 65	Hepatocellular carcinoma
9	0.92	1 / 95	Colorectal cancer
10	0.94	1 / 102	Leukemia
11	0.95	1 / 113	Ovarian cancer
12	0.96	1 / 116	Cancer
13	0.96	1 / 120	Hematological
14	0.96	1 / 123	Pancreatic cancer
15	0.97	1 / 124	Prostate cancer

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−06	7 / 29	Chaussabel_2,7_Unknown function
2	1e−04	17 / 221	Chaussabel_3,8_Enzymes
3	8e−03	15 / 275	Chaussabel_3,7_Spliceosome
4	1e−02	19 / 398	PROTEINATLAS_skeletal muscle
5	2e−02	13 / 254	PROTEINATLAS_smooth muscle
6	3e−02	3 / 24	Chaussabel_1,6_Signaling molecules
7	3e−02	35 / 929	PROTEINATLAS_bronchus
8	3e−02	18 / 412	WIRTH_Immune system
9	4e−02	29 / 759	PROTEINATLAS_epididymis
10	4e−02	6 / 96	Chaussabel_3,1_Interferon−inducible
11	5e−02	2 / 14	WIRTH_B−cells
12	8e−02	26 / 726	PROTEINATLAS_cervix, uterine
13	9e−02	3 / 39	VAQUERIZAS_Testis_TF
14	9e−02	23 / 639	PROTEINATLAS_breast
15	1e−01	7 / 148	VAQUERIZAS_General_TF

BP

Rank	p−value	#in/all	Geneset
1	2e−05	60 / 1272	regulation of transcription, DNA−templated
2	6e−05	7 / 38	response to activity
3	1e−04	7 / 42	histone deacetylation
4	2e−04	15 / 187	DNA repair
5	2e−04	8 / 62	nucleic acid phosphodiester bond hydrolysis
6	4e−04	7 / 50	response to ionizing radiation
7	4e−04	67 / 1643	transcription, DNA−templated
8	6e−04	5 / 26	meiotic nuclear division
9	2e−03	7 / 66	cholesterol metabolic process
10	2e−03	7 / 66	double−strand break repair via homologous recombination
11	2e−03	3 / 10	mitotic recombination
12	3e−03	3 / 11	sleep
13	3e−03	23 / 457	regulation of transcription from RNA polymerase II promoter
14	4e−03	3 / 12	positive regulation of insulin receptor signaling pathway
15	4e−03	3 / 12	regulation of protein catabolic process

CC

Rank	p−value	#in/all	Geneset
1	6e−06	104 / 2535	nucleoplasm
2	6e−04	163 / 4828	nucleus
3	6e−03	3 / 14	Cul4−RING E3 ubiquitin ligase complex
4	1e−02	3 / 18	NuRD complex
5	1e−02	3 / 18	telomerase holoenzyme complex
6	2e−02	151 / 4822	cytoplasm
7	2e−02	3 / 23	filamentous actin
8	3e−02	2 / 10	sperm midpiece
9	4e−02	2 / 12	clathrin adaptor complex
10	5e−02	2 / 13	Golgi−associated vesicle
11	5e−02	2 / 13	HOPS complex
12	5e−02	10 / 202	early endosome
13	5e−02	4 / 51	proteasome complex
14	5e−02	4 / 53	clathrin−coated vesicle
15	6e−02	6 / 104	endomembrane system

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−24	367 / 9054	Tx_Colon
2	1e−19	339 / 8568	TxWk_Colon
3	4e−17	296 / 7354	TssF_Colon
4	4e−17	151 / 2845	TxEnhG1_Colon
5	2e−16	356 / 9555	TssA_Colon
6	2e−12	243 / 6138	TssD2_Colon
7	1e−07	46 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
8	2e−07	119 / 2810	EnhA_Colon
9	5e−07	355 / 10999	TssWk_Colon
10	1e−06	71 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	1e−06	347 / 10779	Enh_Colon
12	2e−06	289 / 8678	Quies3_Colon
13	2e−06	56 / 1083	ZNF_Colon
14	2e−05	188 / 5373	EnhWk1_Colon
15	1e−04	63 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	0.2	4 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.2	7 / 176	HALLMARK_ADIPOGENESIS
4	0.3	5 / 130	HALLMARK_DNA_REPAIR
5	0.3	5 / 137	HALLMARK_UV_RESPONSE_UP
6	0.3	6 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.3	6 / 176	HALLMARK_KRAS_SIGNALING_UP
8	0.4	6 / 185	HALLMARK_P53_PATHWAY
9	0.4	5 / 151	HALLMARK_APOPTOSIS
10	0.4	5 / 162	HALLMARK_ALLOGRAFT_REJECTION
11	0.4	3 / 91	HALLMARK_ANDROGEN_RESPONSE
12	0.4	3 / 91	HALLMARK_PEROXISOME
13	0.5	3 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.5	3 / 103	HALLMARK_BILE_ACID_METABOLISM
15	0.6	5 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Melanoma

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	7 / 66	hsa−miR−550
2	0.005	6 / 60	hsa−miR−514
3	0.007	5 / 45	hsa−miR−524−3p
4	0.017	11 / 196	hsa−miR−206
5	0.028	19 / 438	hsa−miR−19a
6	0.028	5 / 64	hsa−miR−1278
7	0.030	4 / 44	hsa−miR−518e*
8	0.038	3 / 28	hsa−miR−519e*
9	0.040	2 / 12	hsa−miR−652
10	0.042	3 / 29	hsa−miR−1293
11	0.045	18 / 433	hsa−miR−19b
12	0.052	6 / 100	hsa−miR−613
13	0.053	7 / 126	hsa−miR−223
14	0.054	9 / 180	hsa−miR−1
15	0.054	6 / 101	hsa−miR−574−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	Alternative lengthening of telomeres
2	0.5	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	7e−13	150 / 3164	Mid_Frontal_Lobe_ZNF
2	3e−12	339 / 9504	Overlap_fetal_midbrain_K9K27me3
3	5e−10	338 / 9815	Overlap_fetal_midbrain_ReprPC
4	2e−09	225 / 5936	Overlap_fetal_midbrain_HetRpts
5	7e−06	77 / 1728	Fetal_ReprPCWk
6	2e−05	43 / 818	Mid_Frontal_Lobe_Het
7	4e−05	328 / 10430	Overlap_fetal_midbrain_Quies
8	2e−04	102 / 2709	Mid_Frontal_Lobe_HetRpts
9	4e−04	34 / 681	Overlap_fetal_midbrain_EnhP
10	5e−04	38 / 796	Overlap_fetal_midbrain_ZNF
11	4e−03	93 / 2654	Fetal_Quies
12	4e−03	38 / 906	Fetal_HetRpts
13	7e−03	296 / 9917	Overlap_fetal_midbrain_ReprPCWk
14	2e−02	16 / 328	Fetal_Het
15	6e−02	40 / 1162	Fetal_Enh

Chr

Rank	p−value	#in/all	Geneset
1	1e−09	80 / 1467	Chr 19
2	3e−02	47 / 1318	Chr 17
3	4e−02	35 / 959	Chr 16
4	9e−02	27 / 768	Chr 14
5	1e−01	26 / 769	Chr 15
6	3e−01	34 / 1170	Chr 7
7	4e−01	16 / 536	Chr 22
8	4e−01	27 / 954	Chr 9
9	5e−01	23 / 836	Chr 8
10	5e−01	8 / 289	Chr 21
11	6e−01	61 / 2323	Chr 1
12	6e−01	31 / 1217	Chr 3
13	7e−01	38 / 1492	Chr 2
14	7e−01	22 / 902	Chr 4
15	9e−01	31 / 1411	Chr 11

Glio

Rank	p−value	#in/all	Geneset
1	0.001	6 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	0.010	6 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.034	6 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
4	0.060	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
5	0.066	3 / 35	Colman_survival_associated
6	0.067	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
7	0.083	13 / 315	Up
8	0.084	5 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
9	0.108	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
10	0.129	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	0.135	5 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
12	0.144	2 / 25	Barbus_GBM_STS_vs._LTS
13	0.153	2 / 26	Gorovets_LGG_NB_subclass
14	0.188	4 / 84	GIEZELT_GBM_STS_up_VS_LTS
15	0.201	61 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	3 / 31	DUMEAUX_Fasting enriched genes
2	0.06	10 / 211	Homuth_BMI−associated−genes_DN
3	0.46	3 / 94	DUMEAUX_Smoking enriched genes
4	0.58	1 / 32	Marjolein_ageing−genes_DN
5	0.76	3 / 147	Homuth_BMI−associated−genes_UP
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 17	DUMEAUX_High bmi enriched genes
15	1.00	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−05	75 / 1717	metal ion binding
2	2e−04	5 / 20	endodeoxyribonuclease activity
3	4e−04	6 / 36	histone deacetylase activity
4	7e−04	275 / 8818	protein binding
5	9e−04	55 / 1329	ATP binding
6	9e−04	9 / 94	double−stranded DNA binding
7	2e−03	18 / 315	protein serine/threonine kinase activity
8	4e−03	3 / 13	SUMO transferase activity
9	5e−03	56 / 1475	DNA binding
10	6e−03	3 / 14	four−way junction DNA binding
11	7e−03	3 / 15	protein kinase C activity
12	8e−03	36 / 877	transcription factor activity, sequence−specific DNA binding
13	1e−02	4 / 33	endonuclease activity
14	1e−02	3 / 18	telomeric DNA binding
15	1e−02	6 / 72	single−stranded DNA binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	6e−10	179 / 4362	ICGC_Creb1_targets
2	8e−10	210 / 5383	ICGC_Sp1_targets
3	1e−09	213 / 5518	ICGC_Stat5_targets
4	5e−09	197 / 5067	ICGC_Taf1_targets
5	1e−08	166 / 4131	ICGC_Nfatc1_targets
6	3e−08	188 / 4881	ICGC_Atf2_targets
7	4e−08	246 / 6868	ICGC_Elf1_targets
8	7e−08	203 / 5442	ICGC_Pmlsc71910_targets
9	1e−07	203 / 5466	ICGC_Nficsc81335_targets
10	2e−07	116 / 2704	ICGC_Pbx3_targets
11	2e−07	225 / 6267	ICGC_Yy1_targets
12	2e−07	99 / 2215	ICGC_GabpPcr2_targets
13	3e−07	167 / 4345	ICGC_Zeb1_targets
14	3e−07	216 / 5984	ICGC_Mta3_targets
15	5e−07	198 / 5410	ICGC_Foxm1_targets

Correlation Cluster

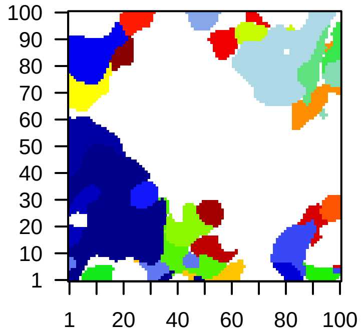
Spot Summary: M

metagenes = 165
genes = 747

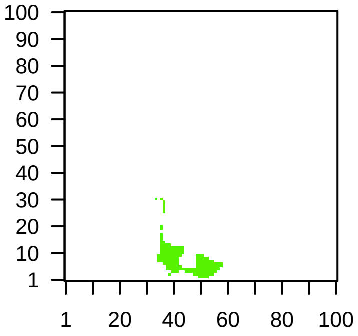
<r> metagenes = 0.92
<r> genes = 0.07
beta: r2= 0.72 / log p= −Inf

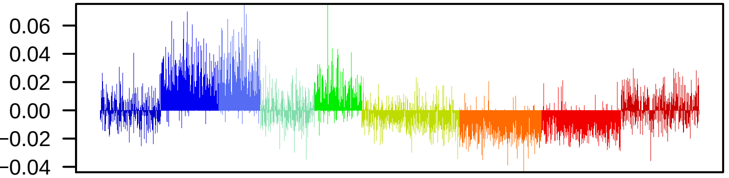
samples with spot = 6 (0.2 %)
A C * : 2 (0.6 %)
A C F * : 3 (1.3 %)
C F * : 1 (0.4 %)

Overview Map



Spot





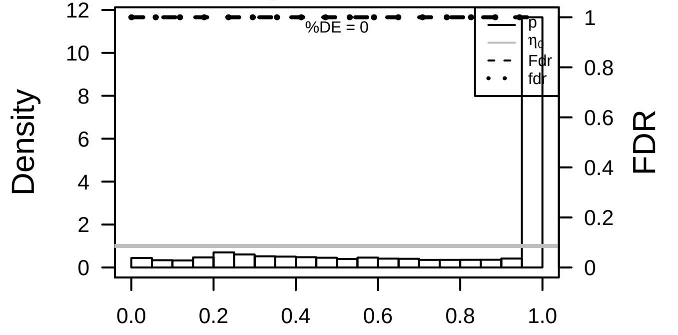
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_212539	1.08	−0.27	0.1	ADGRG7	adhesion G protein−coupled receptor G7 [Source:HGNC Syn
2	ILMN_180807	0.62	−0.27	0.08	ADGRG7	adhesion G protein−coupled receptor G7 [Source:HGNC Syn
3	ILMN_321489	0.55	−0.42	0.3		
4	ILMN_169156	0.43	−0.23	0.11		
5	ILMN_175106	0.41	−0.25	0.2	LOC105369277	chromosome 16 open reading frame 54 [Source:HGNC Symb
6	ILMN_165272	0.4	−0.31	0.29	C14orf2	chromosome 14 open reading frame 2 [Source:HGNC Symbo
7	ILMN_172519	0.37	−0.21	0.14	IGFBP2	insulin like growth factor binding protein 2 [Source:HGNC Syn
8	ILMN_174941	0.37	−0.39	0.18	PKP4	plakophilin 4 [Source:HGNC Symbol;Acc:HGNC:9026]
9	ILMN_169347	0.36	−0.21	0.23	KLHL35	kelch like family member 35 [Source:HGNC Symbol;Acc:HGN
10	ILMN_318514	0.34	−0.2	0.24		CD177 molecule pseudogene 1 [Source:HGNC Symbol;Acc:I
11	ILMN_170311	0.33	−0.18	0.25	PIK3CD−AS1	PIK3CD antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC
12	ILMN_168749	0.32	−0.28	0.23	SLC37A1	solute carrier family 37 member 1 [Source:HGNC Symbol;Acc
13	ILMN_167329	0.31	−0.18	0.28	ZNF80	zinc finger protein 80 [Source:HGNC Symbol;Acc:HGNC:131
14	ILMN_325125	0.3	−0.2	0.17		
15	ILMN_168050	0.3	−0.27	0.26	GTF2IRD2	GTF2I repeat domain containing 2 [Source:HGNC Symbol;Ac
16	ILMN_180095	0.3	−0.2	0.2	PSMD11	proteasome 26S subunit, non−ATPase 11 [Source:HGNC Syn
17	ILMN_165989	0.3	−0.21	0.37	SLC25A26	solute carrier family 25 member 26 [Source:HGNC Symbol;Ac
18	ILMN_185799	0.29	−0.19	0.26		
19	ILMN_323317	0.29	−0.28	0.3		
20	ILMN_184616	0.29	−0.22	0.33		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−08	124 / 4169	Chror	10_ReprPC_Fibroblasts
2	3e−08	126 / 4304	Chror	9_ReprPCWk_Melanocytes
3	1e−07	119 / 4107	Chror	9_ReprPCWk_Fibroblasts
4	2e−07	146 / 5384	Lympl	HOPP_Repressed
5	1e−06	88 / 2894	Colon	TssP_Colon
6	1e−06	89 / 2939	Lympl	HOPP_Poised_promoter
7	2e−06	102 / 3523	Chror	1_TssP_Melanocytes
8	8e−06	89 / 3068	Chror	8_EnhP_Fibroblasts
9	1e−05	79 / 2660	Chror	8_EnhP_Melanocytes
10	2e−05	17 / 279	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
11	4e−05	8 / 70	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
12	1e−04	92 / 3438	Chror	10_ReprPC_Melanocytes
13	1e−04	25 / 594	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
14	1e−04	31 / 819	Brain	Overlap_fetal_midbrain_TssP
15	2e−04	85 / 3173	Colon	ReprPC_Colon
16	2e−04	43 / 1324	Chror	13_HetRpts_Fibroblasts
17	4e−04	24 / 599	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
18	4e−04	94 / 3639	Chror	1_TssP_Fibroblasts
19	5e−04	38 / 1163	Chror	12_Het_Fibroblasts
20	7e−04	8 / 104	Colon	Marisa_CRC−cluster−h
21	9e−04	68 / 2516	Chror	11_K9K27me3_Melanocytes
22	9e−04	54 / 1893	Brain	Overlap_fetal_midbrain_TssF
23	1e−03	44 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
24	1e−03	72 / 2740	Colon	ReprPCWk_Colon
25	2e−03	4 / 29	BP	regulation of lipid metabolic process
26	2e−03	3 / 14	GSEA	REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPOF
27	2e−03	76 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
28	2e−03	8 / 125	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
29	2e−03	77 / 3046	Brain	Fetal_TssA
30	3e−03	52 / 1895	Colon	EnhP_Colon
31	3e−03	100 / 4167	Lympl	HOPP_Heterochrom
32	3e−03	8 / 130	GSEA	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN
33	3e−03	5 / 53	Glio	WILLSCHER_GBM_Verhaak−PNmut_down (G)
34	3e−03	12 / 256	CC	apical plasma membrane
35	3e−03	25 / 746	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
36	4e−03	67 / 2620	Chror	1_TssP_Neuronal_Progenitor
37	4e−03	60 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
38	4e−03	29 / 924	Brain	Mid_Frontal_Lobe_TssF
39	4e−03	3 / 18	MF	DNA helicase activity
40	4e−03	3 / 18	BP	startle response

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 111	HORVATH_aging_genes meth DOWN
2	0.9	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	4 / 29	regulation of lipid metabolic process
2	0.004	3 / 18	startle response
3	0.005	4 / 37	DNA duplex unwinding
4	0.006	4 / 39	bicarbonate transport
5	0.008	4 / 43	visual learning
6	0.009	4 / 45	positive regulation of signal transduction
7	0.010	4 / 46	keratinization
8	0.012	4 / 48	cellular response to interferon−gamma
9	0.012	3 / 26	reciprocal meiotic recombination
10	0.013	3 / 27	neurotransmitter transport
11	0.014	2 / 10	positive regulation of fatty acid biosynthetic process
12	0.014	2 / 10	proteasome assembly
13	0.017	2 / 11	embryonic skeletal joint morphogenesis
14	0.017	2 / 11	glycoprotein metabolic process
15	0.017	2 / 11	organic anion transport

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	31 / 819	Overlap_fetal_midbrain_TssP
2	9e−04	54 / 1893	Overlap_fetal_midbrain_TssF
3	1e−03	44 / 1476	Overlap_fetal_midbrain_TxTrans
4	2e−03	77 / 3046	Fetal_TssA
5	4e−03	29 / 924	Mid_Frontal_Lobe_TssF
6	6e−03	48 / 1784	Mid_Frontal_Lobe_ReprPCWk
7	7e−03	38 / 1360	Mid_Frontal_Lobe_TssP
8	1e−02	32 / 1119	Overlap_fetal_midbrain_TssA
9	1e−02	16 / 465	Mid_Frontal_Lobe_TxTrans
10	2e−02	6 / 110	Overlap_fetal_midbrain_Tx
11	7e−02	59 / 2630	Fetal_TssF
12	9e−02	48 / 2127	Mid_Frontal_Lobe_K9K27me3
13	1e−01	35 / 1506	Mid_Frontal_Lobe_Quies
14	1e−01	9 / 307	Fetal_ReprPC
15	1e−01	15 / 578	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	2 / 15	GENTLES_modul17
2	0.09	2 / 28	PanCan_HH_geneset_nanostring
3	0.17	3 / 76	PanCan_Wnt_geneset_nanostring
4	0.21	2 / 46	PanCan_DNARepair_geneset_nanostring
5	0.22	1 / 13	RHODES_CANCER_META_SIGNATURE
6	0.22	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.23	1 / 14	LIU_COMMON_CANCER_GENES
8	0.23	1 / 14	GENTLES_modul13
9	0.24	1 / 15	LIU_PROSTATE_CANCER_DN
10	0.26	1 / 16	BEN−PORATH_DN
11	0.36	1 / 24	PanCan_Notch_geneset_nanostring
12	0.39	2 / 73	SHAUGHNESSY_MM high risk
13	0.45	0 / 13	LIU_LIVER_CANCER
14	0.65	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	0.69	3 / 193	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.003	12 / 256	apical plasma membrane
2	0.015	5 / 78	Golgi lumen
3	0.017	2 / 11	zymogen granule membrane
4	0.019	4 / 55	synaptic vesicle membrane
5	0.020	2 / 12	membrane−bounded vesicle
6	0.022	30 / 1101	extracellular space
7	0.026	83 / 3662	plasma membrane
8	0.028	3 / 36	sarcoplasmic reticulum
9	0.031	7 / 162	basolateral plasma membrane
10	0.040	3 / 41	cornified envelope
11	0.043	2 / 18	spindle midzone
12	0.052	13 / 423	cell junction
13	0.052	2 / 20	high−density lipoprotein particle
14	0.052	2 / 20	synaptonemal complex
15	0.053	3 / 46	kinesin complex

Chr

Rank	p−value	#in/all	Geneset
1	0.03	32 / 1217	Chr 3
2	0.05	25 / 959	Chr 16
3	0.08	23 / 902	Chr 4
4	0.16	23 / 994	Chr X
5	0.22	3 / 87	Chr Y
6	0.26	14 / 619	Chr 20
7	0.30	29 / 1411	Chr 11
8	0.45	7 / 342	Chr 18
9	0.45	44 / 2323	Chr 1
10	0.47	25 / 1318	Chr 17
11	0.49	28 / 1492	Chr 2
12	0.50	18 / 954	Chr 9
13	0.52	8 / 422	Chr 13
14	0.66	20 / 1160	Chr 12
15	0.66	9 / 536	Chr 22

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−08	124 / 4169	10_ReprPC_Fibroblasts
2	3e−08	126 / 4304	9_ReprPCWk_Melanocytes
3	1e−07	119 / 4107	9_ReprPCWk_Fibroblasts
4	2e−06	102 / 3523	1_TssP_Melanocytes
5	8e−06	89 / 3068	8_EnhP_Fibroblasts
6	1e−05	79 / 2660	8_EnhP_Melanocytes
7	1e−04	92 / 3438	10_ReprPC_Melanocytes
8	2e−04	43 / 1324	13_HetRpts_Fibroblasts
9	4e−04	94 / 3639	1_TssP_Fibroblasts
10	5e−04	38 / 1163	12_Het_Fibroblasts
11	9e−04	68 / 2516	11_K9K27me3_Melanocytes
12	4e−03	67 / 2620	1_TssP_Neuronal_Progenitor
13	4e−03	60 / 2297	10_ReprPC_Neuronal_Progenitor
14	5e−03	34 / 1154	11_K9K27me3_Neuronal_Progenitor
15	6e−03	88 / 3691	9_ReprPCWk_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−06	88 / 2894	TssP_Colon
2	1e−04	25 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	2e−04	85 / 3173	ReprPC_Colon
4	4e−04	24 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	7e−04	8 / 104	Marisa_CRC−cluster−h
6	1e−03	72 / 2740	ReprPCWk_Colon
7	3e−03	52 / 1895	EnhP_Colon
8	1e−02	2 / 10	KIM_MSI−in−EC
9	7e−02	34 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
10	7e−02	18 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
11	8e−02	38 / 1623	Het_Colon
12	8e−02	11 / 366	K9K27me3_Colon
13	9e−02	5 / 129	Marisa_CRC−cluster−b
14	9e−02	19 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
15	1e−01	12 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_

Glio

Rank	p−value	#in/all	Geneset
1	0.002	76 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.003	5 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
3	0.011	2 / 9	Colman_survival_robust
4	0.015	4 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
5	0.020	5 / 84	Weller_LGG_gradeII−vs−III_UP
6	0.026	3 / 35	WIRTH_PN subtype
7	0.026	3 / 35	Colman_survival_associated
8	0.030	2 / 15	Mukasa_UP_in_GBM
9	0.047	2 / 19	KIM deleted & downregulated in LTS
10	0.060	6 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
11	0.083	2 / 26	Gorovets_LGG_NB_subclass
12	0.094	2 / 28	KIM prognostic signature LTS vs. STS
13	0.099	4 / 95	Weller_LGG_1p19qDel−vs−intact_UP
14	0.099	21 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
15	0.118	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	17 / 279	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
2	4e−05	8 / 70	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
3	2e−03	3 / 14	REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTI
4	2e−03	8 / 125	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
5	3e−03	8 / 130	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN
6	3e−03	25 / 746	MARTENS_TRETINOIN_RESPONSE_UP
7	5e−03	5 / 59	MASSARWEH_RESPONSE_TO_ESTRADIOL
8	6e−03	4 / 39	CHEN_HOXA5_TARGETS_9HR_DN
9	6e−03	4 / 40	ULE_SPLICING_VIA_NOVA2
10	7e−03	6 / 92	KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3
11	7e−03	7 / 121	POOLA_INVASIVE_BREAST_CANCER_DN
12	8e−03	5 / 67	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_DN
13	9e−03	2 / 8	NAISHIRO_CTNNB1_TARGETS_WITH_LEF1_MOTIF
14	9e−03	3 / 24	REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS
15	9e−03	3 / 24	BYSTRYKH_HEMATOPOIESIS_STEM_CELL_SCP2_QTL_TRANS

HM

Rank	p−value	#in/all	Geneset
1	0.006	9 / 177	HALLMARK_KRAS_SIGNALING_DN
2	0.042	6 / 137	HALLMARK_UV_RESPONSE_UP
3	0.058	7 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	0.124	6 / 183	HALLMARK_APICAL_JUNCTION
5	0.131	6 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.143	6 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	0.167	4 / 116	HALLMARK_SPERMATOGENESIS
8	0.257	5 / 185	HALLMARK_P53_PATHWAY
9	0.261	5 / 186	HALLMARK_MYOGENESIS
10	0.263	2 / 54	HALLMARK_MYC_TARGETS_V2
11	0.417	3 / 127	HALLMARK_COAGULATION
12	0.418	1 / 29	HALLMARK_NOTCH_SIGNALING
13	0.446	4 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	0.470	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
15	0.503	2 / 91	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	3 / 147	Homuth_BMI−associated−genes_UP
2	0.5	2 / 94	DUMEAUX_Smoking enriched genes
3	0.9	2 / 211	Homuth_BMI−associated−genes_DN
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−07	146 / 5384	HOPP_Repressed
2	1e−06	89 / 2939	HOPP_Poised_promoter
3	3e−03	100 / 4167	HOPP_Heterochrom
4	1e−02	10 / 232	WIRTH_lymphoma937_spot B
5	2e−02	4 / 57	LENZ_Stromal signature 2
6	2e−02	9 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
7	3e−02	63 / 2701	HOPP_Repetitive
8	8e−02	12 / 408	TARTE_Mature plasma cell signature
9	1e−01	5 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
10	1e−01	5 / 138	WIRTH_lymphoma937_spot G
11	2e−01	7 / 244	LENZ_Stromal signature 1
12	2e−01	4 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
13	3e−01	7 / 286	ZHANG_DLBCL mutated
14	3e−01	1 / 19	DAVE_Immune response 2
15	3e−01	2 / 60	SPANG_BAFF 9hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 30	Hugo_melanoma−all−MET_UP
2	0.6	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.004	3 / 18	DNA helicase activity
2	0.005	3 / 19	sodium−independent organic anion transmembrane transporter activity
3	0.009	4 / 45	cytoskeletal protein binding
4	0.011	5 / 72	protein binding, bridging
5	0.012	4 / 48	SH3/SH2 adaptor activity
6	0.015	3 / 28	DNA−dependent ATPase activity
7	0.019	3 / 31	E−box binding
8	0.027	2 / 14	neurotransmitter:sodium symporter activity
9	0.027	2 / 14	organic anion transmembrane transporter activity
10	0.039	2 / 17	ATP−dependent microtubule motor activity, plus−end−directed
11	0.044	4 / 72	single−stranded DNA binding
12	0.052	2 / 20	anion:anion antiporter activity
13	0.057	2 / 21	protein phosphatase type 2A regulator activity
14	0.059	4 / 79	hormone activity
15	0.070	4 / 84	hydrolase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.04	1 / 2	Burkitt lymphoma
2	0.05	1 / 3	Pituitary adenoma
3	0.06	3 / 48	Multiple myeloma
4	0.06	2 / 22	Pigmented adrenocortical disease, primary isolated
5	0.06	5 / 116	Cancer
6	0.09	1 / 5	Rhabdomyosarcoma
7	0.10	2 / 29	Neuroblastoma
8	0.17	1 / 10	Dermatitis, atopic
9	0.26	3 / 95	Colorectal cancer
10	0.28	2 / 56	Myopathy, nemaline, 3
11	0.28	2 / 57	Cardiomyopathy, dilated
12	0.29	1 / 18	Hodgkin lymphoma
13	0.29	3 / 102	Leukemia
14	0.31	1 / 20	Parkinson disease
15	0.32	2 / 63	Gastrointestinal

miRNA target

Rank	p−value	#in/all	Geneset
1	0.07	4 / 83	hsa−miR−630
2	0.11	1 / 6	hsa−miR−937
3	0.11	2 / 31	hsa−miR−617
4	0.12	4 / 101	hsa−miR−210
5	0.14	2 / 36	hsa−miR−127−3p
6	0.17	3 / 76	hsa−miR−1827
7	0.18	2 / 41	hsa−miR−192
8	0.22	2 / 47	hsa−miR−553
9	0.22	3 / 87	hsa−miR−595
10	0.23	1 / 14	hsa−miR−551b
11	0.23	1 / 14	hsa−miR−638
12	0.24	2 / 51	hsa−miR−628−5p
13	0.26	1 / 16	hsa−miR−551a
14	0.26	1 / 16	hsa−miR−598
15	0.30	2 / 60	hsa−miR−650

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.04	10 / 289	JONGENEEL_Testis
2	0.05	2 / 20	JONGENEEL_Thymus
3	0.06	3 / 50	WIRTH_Placenta
4	0.11	1 / 6	WIRTH_Pituitary gland
5	0.11	7 / 220	WIRTH_Testis
6	0.12	1 / 7	JONGENEEL_Mammary Gland
7	0.14	4 / 107	WIRTH_Liver
8	0.19	1 / 11	WIRTH_Tonsil
9	0.20	1 / 12	Chaussabel_3,5_Hemoglobin genes
10	0.22	1 / 13	WIRTH_Sec. lymphoid organs
11	0.23	2 / 49	JONGENEEL_Retina
12	0.23	1 / 14	WIRTH_Thalamus
13	0.23	1 / 14	WIRTH_Thyroid gland
14	0.23	1 / 14	JONGENEEL_Peripheral Blood Lymphocytes
15	0.24	4 / 134	WIRTH_Mucosa

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	45 / 1753	HEBENSTREIT_low expression TF
2	0.16	53 / 2497	ICGC_Bcl11_targets
3	0.18	72 / 3507	ICGC_Rad21_targets
4	0.19	32 / 1466	ICGC_NrsfPcr1_targets
5	0.22	17 / 747	ICGC_NrsfPcr2_targets
6	0.23	1 / 14	NOWICK_TF
7	0.24	56 / 2759	ICGC_Bcl3_targets
8	0.35	30 / 1501	ICGC_Usf1_targets
9	0.38	15 / 733	ICGC_Atf3_targets
10	0.38	13 / 631	ICGC_RxraPcr1_targets
11	0.40	64 / 3348	ICGC_BatfPcr1_targets
12	0.44	32 / 1669	ICGC_P300_targets
13	0.46	14 / 721	ICGC_SrfPcr2_targets
14	0.48	40 / 2133	ICGC_Mef2_targets
15	0.57	41 / 2255	ICGC_SrfV0416101_targets

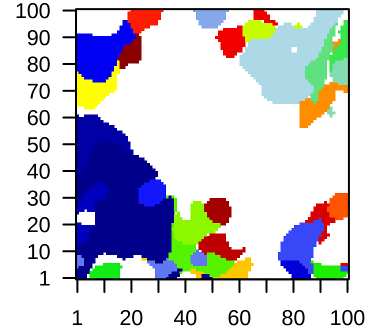
Correlation Cluster

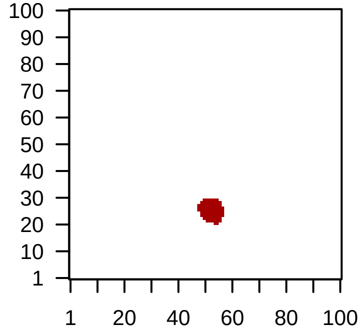
Spot Summary: N

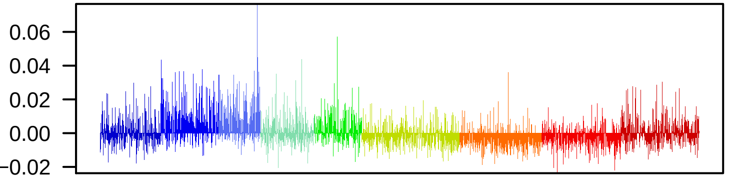
metagenes = 76
genes = 918

<r> metagenes = 0.93
<r> genes = 0.03
beta: r2= 0.23 / log p= −Inf

samples with spot = 1 (0 %)
A C F * : 1 (0.4 %)


Overview Map


Spot

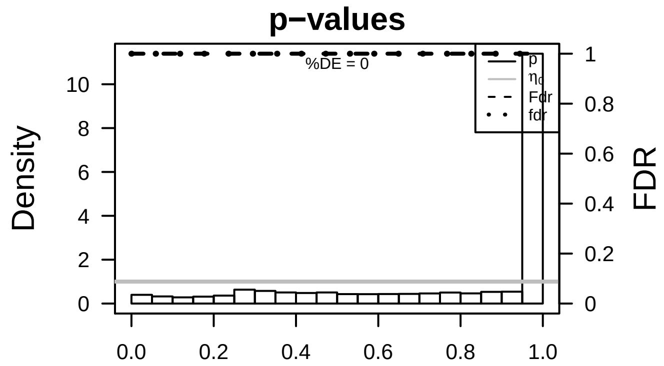


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_231025	0.28	−0.2	0.18		
2	ILMN_212483	0.26	−0.17	0.26	TRAT1	T cell receptor associated transmembrane adaptor 1 [Source:
3	ILMN_326522	0.26	−0.2	0.2		
4	ILMN_170641	0.26	−0.19	0.21	HUS1B	HUS1 checkpoint clamp component B [Source:HGNC Symbo
5	ILMN_211586	0.25	−0.16	0.18	ESPNL	espin−like [Source:HGNC Symbol;Acc:HGNC:27937]
6	ILMN_168925	0.25	−0.2	0.11	ATL1	atlastin GTPase 1 [Source:HGNC Symbol;Acc:HGNC:11231]
7	ILMN_169987	0.25	−0.16	0.23	RAB27A	RAB27A, member RAS oncogene family [Source:HGNC Sym
8	ILMN_171142	0.24	−0.17	0.16	PLEKHN1	pleckstrin homology domain containing N1 [Source:HGNC Sy
9	ILMN_187067	0.24	−0.17	0.26		
10	ILMN_189644	0.24	−0.18	0.15		
11	ILMN_178251	0.24	−0.17	0.23	TRMT10B	tRNA methyltransferase 10B [Source:HGNC Symbol;Acc:HGI
12	ILMN_191639	0.24	−0.17	0.16		
13	ILMN_188326	0.24	−0.17	0.17	MBNL1−AS1	MBNL1 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
14	ILMN_204735	0.24	−0.18	0.23		long intergenic non−protein coding RNA 467 [Source:HGNC
15	ILMN_218377	0.24	−0.19	0.12	CCDC121	coiled−coil domain containing 121 [Source:HGNC Symbol;Ac
16	ILMN_206472	0.24	−0.15	0.18	METTL7B	methyltransferase like 7B [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_184674	0.23	−0.16	0.24		
18	ILMN_187715	0.23	−0.2	0.16		
19	ILMN_175589	0.23	−0.15	0.35		
20	ILMN_173976	0.23	−0.16	0.15	OR13C4	olfactory receptor family 13 subfamily C member 4 [Source:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−06	8 / 40	BP	regulation of G−protein coupled receptor protein signaling pathway
2	7e−05	119 / 3272	Chror	13_HetRpts_Neuronal_Progenitor
3	9e−05	180 / 5384	Lympl	HOPP_Repressed
4	4e−04	7 / 52	Lympl	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
5	6e−04	144 / 4304	Chror	9_ReprPCWk_Melanocytes
6	7e−04	8 / 74	GSEA	ODONNELL_METASTASIS_UP
7	1e−03	5 / 30	BP	positive regulation of multicellular organism growth
8	1e−03	67 / 1753	TF	HEBENSTREIT_low expression TF
9	1e−03	48 / 1163	Chror	12_Het_Fibroblasts
10	1e−03	6 / 47	CC	adherens junction
11	1e−03	10 / 122	BP	sensory perception of sound
12	1e−03	46 / 1115	Brain	Overlap_fetal_midbrain_EnhG
13	2e−03	4 / 20	BP	modulation of synaptic transmission
14	2e−03	11 / 147	BP	homophilic cell adhesion via plasma membrane adhesion molecules
15	2e−03	5 / 34	BP	excretion
16	2e−03	3 / 10	BP	auditory receptor cell stereocilium organization
17	2e−03	52 / 1324	Chror	13_HetRpts_Fibroblasts
18	2e−03	52 / 1329	Brain	Overlap_fetal_midbrain_Enh
19	2e−03	82 / 2315	Chror	13_HetRpts_Melanocytes
20	3e−03	5 / 37	BP	synapse organization
21	3e−03	92 / 2660	Chror	8_EnhP_Melanocytes
22	3e−03	4 / 24	Lympl	Subero_mBL_hypo_meth
23	4e−03	23 / 478	Refer	WIRTH_Nervous System
24	4e−03	5 / 41	BP	blood circulation
25	4e−03	5 / 41	GSEA	MANTOVANI_NFKB_TARGETS_UP
26	4e−03	31 / 720	GSEA	REACTOME_GPCR_DOWNSTREAM_SIGNALING
27	5e−03	132 / 4107	Chror	9_ReprPCWk_Fibroblasts
28	5e−03	45 / 1154	Chror	11_K9K27me3_Neuronal_Progenitor
29	5e−03	4 / 27	BP	adult behavior
30	5e−03	3 / 14	BP	aorta morphogenesis
31	5e−03	3 / 14	BP	behavioral response to cocaine
32	5e−03	3 / 14	GSEA	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
33	6e−03	5 / 45	Lympl	Subero_INT_hypo_meth
34	6e−03	2 / 5	GSEA	CASTELLANO_HRAS_TARGETS_UP
35	6e−03	71 / 2031	Chror	12_Het_Melanocytes
36	7e−03	104 / 3173	Colon	ReprPC_Colon
37	7e−03	85 / 2516	Chror	11_K9K27me3_Melanocytes
38	8e−03	3 / 16	BP	estrous cycle
39	8e−03	3 / 16	BP	positive regulation of calcium−mediated signaling
40	8e−03	4 / 31	GSEA	STAEGE_EWING_FAMILY_TUMOR


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 58	TESCHENDORFF_age_hypermethylated
2	0.6	3 / 111	HORVATH_aging_genes meth DOWN
3	0.7	3 / 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	7e−06	8 / 40	regulation of G−protein coupled receptor protein signaling pathway
2	1e−03	5 / 30	positive regulation of multicellular organism growth
3	1e−03	10 / 122	sensory perception of sound
4	2e−03	4 / 20	modulation of synaptic transmission
5	2e−03	11 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
6	2e−03	5 / 34	excretion
7	2e−03	3 / 10	auditory receptor cell stereocilium organization
8	3e−03	5 / 37	synapse organization
9	4e−03	5 / 41	blood circulation
10	5e−03	4 / 27	adult behavior
11	5e−03	3 / 14	aorta morphogenesis
12	5e−03	3 / 14	behavioral response to cocaine
13	8e−03	3 / 16	estrous cycle
14	8e−03	3 / 16	positive regulation of calcium−mediated signaling
15	1e−02	6 / 71	neural tube closure

Brain

Rank	p−value	#in/all	Geneset
1	0.001	46 / 1115	Overlap_fetal_midbrain_EnhG
2	0.002	52 / 1329	Overlap_fetal_midbrain_Enh
3	0.026	63 / 1893	Overlap_fetal_midbrain_TssF
4	0.036	19 / 465	Mid_Frontal_Lobe_TxTrans
5	0.038	30 / 819	Overlap_fetal_midbrain_TssP
6	0.045	50 / 1506	Mid_Frontal_Lobe_Quies
7	0.062	32 / 924	Mid_Frontal_Lobe_TssF
8	0.065	48 / 1476	Overlap_fetal_midbrain_TxTrans
9	0.077	34 / 1012	Mid_Frontal_Lobe_Enh
10	0.101	39 / 1213	Fetal_TssP
11	0.106	90 / 3046	Fetal_TssA
12	0.107	43 / 1360	Mid_Frontal_Lobe_TssP
13	0.143	79 / 2700	Fetal_TxTrans
14	0.177	19 / 578	Fetal_Tx
15	0.195	27 / 869	Mid_Frontal_Lobe_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	2 / 13	GENTLES_modul18
2	0.05	2 / 14	GENTLES_modul13
3	0.06	2 / 15	GENTLES_modul17
4	0.12	3 / 46	PanCan_TGF−B_geneset_nanostring
5	0.21	1 / 9	GENTLES_modul3
6	0.23	5 / 125	PanCan_CC+Apop_geneset_nanostring
7	0.29	1 / 13	WANG_ER_DN
8	0.29	1 / 13	GENTLES_modul12
9	0.31	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
10	0.32	3 / 76	PanCan_Wnt_geneset_nanostring
11	0.33	1 / 15	WOLFER_overlap genes
12	0.36	4 / 117	PanCan_Driver_Gene_geneset_nanostring
13	0.42	3 / 91	PanCan_TXmisReg_geneset_nanostring
14	0.47	4 / 136	PanCan_RAS_geneset_nanostring
15	0.51	14 / 527	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	0.001	6 / 47	adherens junction
2	0.018	5 / 59	presynaptic membrane
3	0.027	4 / 44	chloride channel complex
4	0.031	6 / 91	perikaryon
5	0.032	2 / 11	inhibitory synapse
6	0.032	2 / 11	stereocilium bundle
7	0.044	2 / 13	dendrite membrane
8	0.046	3 / 31	sarcoplasmic reticulum membrane
9	0.050	3 / 32	photoreceptor connecting cilium
10	0.050	2 / 14	integral component of nuclear inner membrane
11	0.057	2 / 15	dendrite cytoplasm
12	0.071	9 / 196	postsynaptic membrane
13	0.072	11 / 256	apical plasma membrane
14	0.079	2 / 18	postsynapse
15	0.079	8 / 171	postsynaptic density

Chr

Rank	p−value	#in/all	Geneset
1	0.07	46 / 1411	Chr 11
2	0.07	27 / 769	Chr 15
3	0.08	5 / 87	Chr Y
4	0.09	38 / 1170	Chr 7
5	0.10	39 / 1211	Chr 6
6	0.19	28 / 904	Chr 10
7	0.21	14 / 422	Chr 13
8	0.22	29 / 954	Chr 9
9	0.23	36 / 1217	Chr 3
10	0.25	27 / 902	Chr 4
11	0.26	25 / 836	Chr 8
12	0.34	9 / 289	Chr 21
13	0.35	18 / 619	Chr 20
14	0.38	41 / 1492	Chr 2
15	0.40	10 / 342	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−05	119 / 3272	13_HetRpts_Neuronal_Progenitor
2	6e−04	144 / 4304	9_ReprPCWk_Melanocytes
3	1e−03	48 / 1163	12_Het_Fibroblasts
4	2e−03	52 / 1324	13_HetRpts_Fibroblasts
5	2e−03	82 / 2315	13_HetRpts_Melanocytes
6	3e−03	92 / 2660	8_EnhP_Melanocytes
7	5e−03	132 / 4107	9_ReprPCWk_Fibroblasts
8	5e−03	45 / 1154	11_K9K27me3_Neuronal_Progenitor
9	6e−03	71 / 2031	12_Het_Melanocytes
10	7e−03	85 / 2516	11_K9K27me3_Melanocytes
11	1e−02	109 / 3438	10_ReprPC_Melanocytes
12	2e−02	61 / 1789	8_EnhP_Neuronal_Progenitor
13	2e−02	97 / 3068	8_EnhP_Fibroblasts
14	3e−02	112 / 3639	1_TssP_Fibroblasts
15	3e−02	126 / 4169	10_ReprPC_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	104 / 3173	ReprPC_Colon
2	0.012	90 / 2740	ReprPCWk_Colon
3	0.016	21 / 484	Quies2_Colon
4	0.027	6 / 88	Pentrack_CRC_TCGA_corr_S_normal_DN
5	0.031	16 / 366	K9K27me3_Colon
6	0.039	16 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
7	0.042	25 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	0.052	7 / 129	Marisa_CRC−cluster−b
9	0.076	1 / 3	Budinska_E_Mixed_DOWN
10	0.085	59 / 1895	EnhP_Colon
11	0.089	5 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
12	0.102	86 / 2894	TssP_Colon
13	0.138	115 / 4018	EnhWk2_Colon
14	0.145	15 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
15	0.153	3 / 52	Marisa_CRC−cluster−e

Glio

Rank	p−value	#in/all	Geneset
1	0.02	5 / 56	Christensen_hypomethylated_in_primary_glioblastoma
2	0.02	95 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
3	0.03	9 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
4	0.03	5 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
5	0.05	2 / 14	astrocytes_glio
6	0.06	2 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
7	0.06	30 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
8	0.07	9 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	0.07	3 / 37	Christensen_hypomethylated_in_ependymoma
10	0.07	2 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
11	0.07	2 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
12	0.07	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
13	0.07	4 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
14	0.08	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
15	0.08	2 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−04	8 / 74	ODONNELL_METASTASIS_UP
2	4e−03	5 / 41	MANTOVANI_NFKB_TARGETS_UP
3	4e−03	31 / 720	REACTOME_GPCR_DOWNSTREAM_SIGNALING
4	5e−03	3 / 14	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
5	6e−03	2 / 5	CASTELLANO_HRAS_TARGETS_UP
6	8e−03	4 / 31	STAEGE_EWING_FAMILY_TUMOR
7	9e−03	3 / 17	BIOCARTA_ARF_PATHWAY
8	1e−02	11 / 189	PLASARI_TGFB1_TARGETS_10HR_UP
9	1e−02	10 / 164	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
10	1e−02	4 / 35	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN
11	1e−02	30 / 746	MARTENS_TRETINOIN_RESPONSE_UP
12	1e−02	4 / 36	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
13	2e−02	7 / 100	TAVAZOIE_METASTASIS
14	2e−02	32 / 822	REACTOME_SIGNALING_BY_GPCR
15	2e−02	10 / 174	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP

HM

Rank	p−value	#in/all	Geneset
1	0.09	8 / 177	HALLMARK_KRAS_SIGNALING_DN
2	0.23	7 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	0.26	5 / 132	HALLMARK_UV_RESPONSE_DN
4	0.29	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
5	0.36	4 / 116	HALLMARK_SPERMATOGENESIS
6	0.42	4 / 127	HALLMARK_COAGULATION
7	0.46	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	0.50	3 / 103	HALLMARK_BILE_ACID_METABOLISM
9	0.59	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
10	0.66	4 / 173	HALLMARK_E2F_TARGETS
11	0.67	4 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.69	4 / 179	HALLMARK_G2M_CHECKPOINT
13	0.70	3 / 137	HALLMARK_UV_RESPONSE_UP
14	0.70	4 / 183	HALLMARK_APICAL_JUNCTION
15	0.71	4 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 5	Huan_blood−pressure_HTN−signature
2	0.2	1 / 10	DUMEAUX_Women normal BMI literature genes up
3	0.3	1 / 16	Huan_blood−pressure_DBP−signature
4	0.4	1 / 18	Huan_blood−pressure_SBP−signature
5	0.4	3 / 94	DUMEAUX_Smoking enriched genes
6	0.6	1 / 32	Marjolein_ageing−genes_DN
7	0.9	2 / 147	Homuth_BMI−associated−genes_UP
8	0.9	3 / 211	Homuth_BMI−associated−genes_DN
9	1.0	0 / 10	DUMEAUX_Smoking literature genes up
10	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
15	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−05	180 / 5384	HOPP_Repressed
2	4e−04	7 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
3	3e−03	4 / 24	Subero_mBL_hypo_meth
4	6e−03	5 / 45	Subero_INT_hypo_meth
5	2e−02	8 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
6	3e−02	93 / 2939	HOPP_Poised_promoter
7	8e−02	2 / 18	Aukema_BCL2 UP_BCL6 DN
8	1e−01	2 / 21	Subero_MCL_hypo_meth
9	1e−01	3 / 46	Subero_DLBCL_hypo_meth
10	1e−01	1 / 5	WRIGHT_custom ABC−DLBCL UP
11	2e−01	1 / 10	Care_ABC UP
12	3e−01	1 / 12	WRIGHT_GCB UP
13	3e−01	1 / 13	Care_Polarized immune response
14	3e−01	5 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
15	3e−01	1 / 14	BENTINK_mBL UP

Melanoma

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

MF

Rank	p−value	#in/all	Geneset
1	0.009	3 / 17	thiol−dependent ubiquitinyl hydrolase activity
2	0.009	5 / 50	chloride channel activity
3	0.012	3 / 19	G−protein alpha−subunit binding
4	0.012	3 / 19	neuropeptide binding
5	0.020	6 / 82	odorant binding
6	0.025	16 / 357	olfactory receptor activity
7	0.026	3 / 25	cation channel activity
8	0.026	2 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
9	0.026	2 / 10	peptide hormone receptor binding
10	0.026	2 / 10	peptidoglycan binding
11	0.032	2 / 11	chloride ion binding
12	0.037	2 / 12	neurexin family protein binding
13	0.044	2 / 13	thioesterase binding
14	0.050	3 / 32	carboxylic ester hydrolase activity
15	0.050	2 / 14	3',5'−cyclic−GMP phosphodiesterase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	Immunoglobulin A deficiency
2	0.23	1 / 10	Cardiovascular
3	0.23	1 / 10	Dermatitis, atopic
4	0.23	4 / 95	Colorectal cancer
5	0.28	2 / 40	Muscular dystrophy
6	0.29	2 / 41	Melanoma, cutaneous malignant, 2
7	0.36	2 / 48	Alzheimer disease, susceptibility to
8	0.36	2 / 48	Multiple myeloma
9	0.36	1 / 17	Thyroid carcinoma, follicular
10	0.36	1 / 17	Gastroesphageal reflux
11	0.38	1 / 18	Non−Hodgkin lymphoma, somatic
12	0.43	2 / 56	Myopathy, nemaline, 3
13	0.44	2 / 57	Cardiomyopathy, dilated
14	0.44	1 / 22	Pigmented adrenocortical disease, primary isolated
15	0.45	1 / 23	Esophageal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.09	3 / 40	hsa−miR−518b
2	0.12	4 / 72	hsa−miR−518c
3	0.14	4 / 76	hsa−miR−1304
4	0.15	1 / 6	hsa−miR−886−5p
5	0.17	3 / 54	hsa−miR−518f
6	0.19	1 / 8	hsa−miR−886−3p
7	0.23	2 / 35	hsa−miR−892b
8	0.23	1 / 10	hsa−miR−933
9	0.24	5 / 127	hsa−miR−1272
10	0.25	4 / 97	hsa−miR−125a−3p
11	0.25	1 / 11	hsa−miR−487b
12	0.26	6 / 164	hsa−miR−495
13	0.27	1 / 12	hsa−miR−652
14	0.29	1 / 13	hsa−miR−147b
15	0.31	1 / 14	hsa−miR−191*

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.004	23 / 478	WIRTH_Nervous System
2	0.009	15 / 289	JONGENEEL_Testis
3	0.121	9 / 220	WIRTH_Testis
4	0.150	9 / 231	Chaussabel_2,5_Immune related molecules
5	0.271	1 / 12	WIRTH_Globus pallidus
6	0.290	1 / 13	WIRTH_Thymus
7	0.290	1 / 13	JONGENEEL_Thyroid
8	0.309	1 / 14	WIRTH_Thalamus
9	0.309	1 / 14	WIRTH_Cerebellum
10	0.317	3 / 76	WIRTH_Homeostasis
11	0.341	5 / 148	VAQUERIZAS_General_TF
12	0.356	2 / 48	WIRTH_Pancreas
13	0.361	1 / 17	JONGENEEL_Pancreas
14	0.365	2 / 49	JONGENEEL_Retina
15	0.394	1 / 19	JONGENEEL_Small Intestine

Telomeres

Rank	p−value	#in/all	Geneset
1	0.5	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.001	67 / 1753	HEBENSTREIT_low expression TF
2	0.051	1 / 2	MYC_Cell cycle DOWN
3	0.211	1 / 9	MYC_Targets DOWN
4	0.479	20 / 747	ICGC_NrsfPcr2_targets
5	0.661	88 / 3507	ICGC_Rad21_targets
6	0.780	39 / 1669	ICGC_P300_targets
7	0.844	15 / 721	ICGC_SrfPcr2_targets
8	0.871	32 / 1466	ICGC_NrsfPcr1_targets
9	0.971	68 / 3194	ICGC_Irf4_targets
10	0.983	50 / 2497	ICGC_Bcl11_targets
11	0.986	27 / 1501	ICGC_Usf1_targets
12	0.993	10 / 733	ICGC_Atf3_targets
13	0.995	99 / 4735	ICGC_Pu1_targets
14	0.997	50 / 2704	ICGC_Pbx3_targets
15	0.998	51 / 2759	ICGC_Bcl3_targets

Correlation Cluster

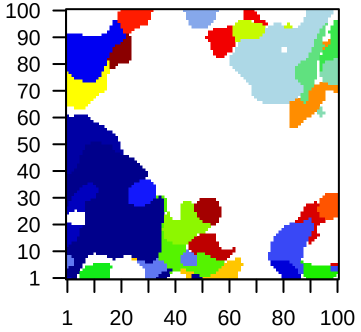
Spot Summary: O

metagenes = 77
genes = 422

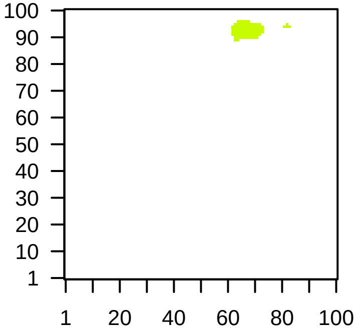
<r> metagenes = 0.95
<r> genes = 0.19
beta: r2= 3.44 / log p= −Inf

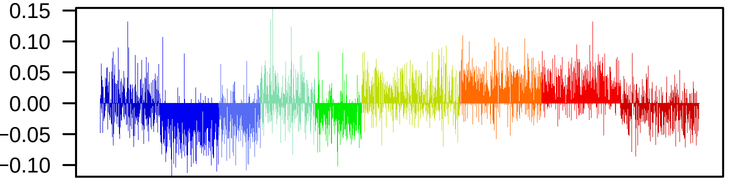
samples with spot = 100 (3 %)
A * : 13 (3.8 %)
A C * : 2 (0.6 %)
A C F * : 2 (0.9 %)
A F * : 8 (2.6 %)
C F * : 2 (0.8 %)
F * : 14 (2.5 %)
F J * : 29 (6.3 %)
J * : 29 (6.5 %)
N * : 1 (0.2 %)

Overview Map



Spot





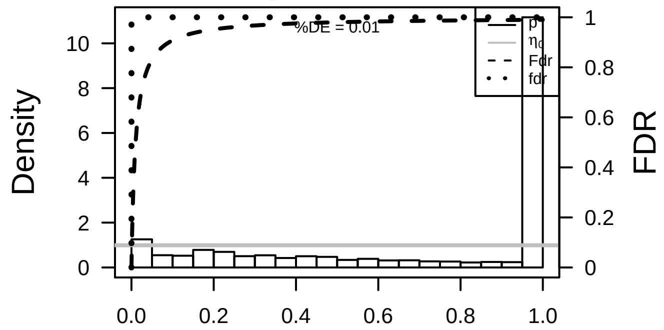
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166126	1.62	−1.38	0.21		
2	ILMN_179985	0.75	−0.61	0.26	NOMO3	NODAL modulator 3 [Source:HGNC Symbol;Acc:HGNC:2524
3	ILMN_173005	0.63	−0.55	0.12		
4	ILMN_323822	0.6	−0.43	0.22		
5	ILMN_178023	0.54	−0.38	0.67	PMM1	phosphomannomutase 1 [Source:HGNC Symbol;Acc:HGNC:
6	ILMN_166479	0.54	−0.43	0.35	GRHPR	glyoxylate and hydroxypyruvate reductase [Source:HGNC Sy
7	ILMN_180046	0.53	−0.43	0.49		
8	ILMN_168370	0.52	−0.53	0.39	TNFSF12	tumor necrosis factor superfamily member 12 [Source:HGNC
9	ILMN_168934	0.52	−0.45	0.62	NUBP1	nucleotide binding protein 1 [Source:HGNC Symbol;Acc:HGN
10	ILMN_176423	0.51	−0.43	0.52	GNPTG	N−acetylglucosamine−1−phosphate transferase gamma subu
11	ILMN_178918	0.51	−0.38	0.4		
12	ILMN_208641	0.5	−0.36	0.57		
13	ILMN_329369	0.49	−0.3	0.16		MAFF interacting protein (pseudogene) [Source:HGNC Symb
14	ILMN_323826	0.49	−0.41	0.44	NDUFA6	NADH:ubiquinone oxidoreductase subunit A6 [Source:HGNC
15	ILMN_168150	0.48	−0.31	0.58	MCM2	minichromosome maintenance complex component 2 [Source
16	ILMN_166846	0.47	−0.36	0.42	KIAA0922	KIAA0922 [Source:HGNC Symbol;Acc:HGNC:29146]
17	ILMN_240324	0.46	−0.66	0.38	CMTM7	CKLF like MARVEL transmembrane domain containing 7 [So
18	ILMN_174932	0.46	−0.33	0.48	MAPK13	mitogen−activated protein kinase 13 [Source:HGNC Symbol;
19	ILMN_324790	0.45	−0.35	0.45	RNF114	ring finger protein 114 [Source:HGNC Symbol;Acc:HGNC:13
20	ILMN_234944	0.45	−0.39	0.32	NUDT2	nudix hydrolase 2 [Source:HGNC Symbol;Acc:HGNC:8049]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset
1	1e−43	254 / 8568	Colon TxWk_Colon
2	4e−43	303 / 12298	Chror 2_TssA_Melanocytes
3	1e−42	260 / 9054	Colon Tx_Colon
4	1e−42	267 / 9555	Colon TssA_Colon
5	4e−41	231 / 7354	Colon TssF_Colon
6	4e−38	286 / 11455	Chror 2_TssA_Fibroblasts
7	9e−38	259 / 9504	Brain Overlap_fetal_midbrain_K9K27me3
8	2e−35	287 / 11836	Chror 3_TssF_Melanocytes
9	5e−35	300 / 12983	Chror 2_TssA_Neuronal_Progenitor
10	2e−32	170 / 4795	Chror 6_EnhG_Fibroblasts
11	2e−30	184 / 5699	Chror 6_EnhG_Melanocytes
12	3e−29	219 / 7854	Chror 5_Tx_Fibroblasts
13	2e−28	232 / 8771	Chror 5_Tx_Melanocytes
14	2e−27	243 / 9635	Chror 3_TssF_Fibroblasts
15	3e−26	184 / 6138	Colon TssD2_Colon
16	5e−25	129 / 3450	Chror 4_TxTrans_Fibroblasts
17	2e−24	249 / 10430	Brain Overlap_fetal_midbrain_Quies
18	7e−24	176 / 5956	Chror 3_TssF_Neuronal_Progenitor
19	2e−23	193 / 6970	Chror 5_Tx_Neuronal_Progenitor
20	2e−22	196 / 7275	Lympl HOPP_Txn_elongation
21	2e−22	236 / 9815	Brain Overlap_fetal_midbrain_ReprPC
22	5e−22	249 / 10779	Colon Enh_Colon
23	6e−22	110 / 2845	Colon TxEnhG1_Colon
24	8e−22	210 / 8226	Lympl HOPP_Active_promoter
25	8e−21	215 / 8678	Colon Quies3_Colon
26	2e−20	158 / 5373	Colon EnhWk1_Colon
27	2e−19	166 / 5936	Brain Overlap_fetal_midbrain_HetRpts
28	2e−18	148 / 5067	TF ICGC_Taf1_targets
29	2e−17	108 / 3164	Brain Mid_Frontal_Lobe_ZNF
30	5e−17	265 / 12741	Chror 7_Enh_Melanocytes
31	2e−16	259 / 12393	Chror 15_Quies_Neuronal_Progenitor
32	8e−16	147 / 5356	Lympl HOPP_Txn_transition
33	3e−15	127 / 4362	TF ICGC_Creb1_targets
34	8e−15	128 / 4468	TF ICGC_Egr1_targets
35	5e−14	93 / 2810	Colon EnhA_Colon
36	1e−13	75 / 2028	Chror 4_TxTrans_Melanocytes
37	3e−13	142 / 5466	TF ICGC_Nficsc81335_targets
38	7e−13	175 / 7448	Lympl HOPP_Strong_enhancer
39	7e−13	242 / 11847	Chror 7_Enh_Neuronal_Progenitor
40	8e−13	142 / 5518	TF ICGC_Stat5_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.8	1 / 111	HORVATH_aging_genes meth DOWN
2	0.9	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	5e−08	8 / 36	PanCan_HK_geneset_nanostring
2	6e−03	16 / 527	Lembcke_Normal vs Adenoma
3	4e−02	5 / 125	PanCan_CC+Apop_geneset_nanostring
4	5e−02	3 / 54	KUIPER_MM poor survival
5	7e−02	1 / 14	LIU_COMMON_CANCER_GENES
6	1e−01	1 / 9	GENTLES_modul5
7	2e−01	4 / 150	PanCan_MAPK_geneset_nanostring
8	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	2e−01	1 / 15	WANG_ER_UP
10	2e−01	1 / 15	WOLFER_overlap genes
11	2e−01	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
12	3e−01	6 / 301	SPANG_BCL6−index2
13	3e−01	2 / 76	PanCan_Wnt_geneset_nanostring
14	3e−01	1 / 28	PanCan_HH_geneset_nanostring
15	4e−01	0 / 13	LIU_LIVER_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−43	303 / 12298	2_TssA_Melanocytes
2	4e−38	286 / 11455	2_TssA_Fibroblasts
3	2e−35	287 / 11836	3_TssF_Melanocytes
4	5e−35	300 / 12983	2_TssA_Neuronal_Progenitor
5	2e−32	170 / 4795	6_EnhG_Fibroblasts
6	2e−30	184 / 5699	6_EnhG_Melanocytes
7	3e−29	219 / 7854	5_Tx_Fibroblasts
8	2e−28	232 / 8771	5_Tx_Melanocytes
9	2e−27	243 / 9635	3_TssF_Fibroblasts
10	5e−25	129 / 3450	4_TxTrans_Fibroblasts
11	7e−24	176 / 5956	3_TssF_Neuronal_Progenitor
12	2e−23	193 / 6970	5_Tx_Neuronal_Progenitor
13	5e−17	265 / 12741	7_Enh_Melanocytes
14	2e−16	259 / 12393	15_Quies_Neuronal_Progenitor
15	1e−13	75 / 2028	4_TxTrans_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−09	28 / 509	PARENT_MTOR_SIGNALING_UP
2	4e−09	40 / 952	DANG_BOUND_BY_MYC
3	3e−08	31 / 666	BENPORATH_MYC_MAX_TARGETS
4	1e−07	24 / 459	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
5	1e−06	31 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
6	4e−06	19 / 371	MOOTHA_HUMAN_MITODB_6_2002
7	4e−06	32 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
8	7e−06	47 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
9	1e−05	21 / 478	STEIN_ESRRA_TARGETS
10	1e−05	26 / 684	KRIEG_HYPOXIA_NOT_VIA_KDM3A
11	2e−05	9 / 101	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
12	3e−05	12 / 190	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
13	3e−05	4 / 13	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
14	3e−05	23 / 593	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
15	4e−05	12 / 193	SANSOM_APC_MYC_TARGETS

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−22	196 / 7275	HOPP_Txn_elongation
2	8e−22	210 / 8226	HOPP_Active_promoter
3	8e−16	147 / 5356	HOPP_Txn_transition
4	7e−13	175 / 7448	HOPP_Strong_enhancer
5	2e−11	181 / 8098	HOPP_Weak_promoter
6	5e−10	37 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	6e−10	37 / 777	WIRTH_lymphoma937_spot D
8	3e−06	41 / 1270	SPANG_BCR UP
9	1e−04	130 / 6559	HOPP_Weak_txn
10	3e−03	10 / 232	WIRTH_lymphoma937_spot B
11	6e−03	9 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
12	2e−02	123 / 6959	HOPP_Weak_enhancer
13	2e−02	27 / 1169	SPANG_BCR DN
14	4e−02	12 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
15	5e−02	12 / 464	WIRTH_lymphoma937_spot I

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 4	Carcinoid tumors, intestinal
2	0.51	1 / 48	Alzheimer disease, susceptibility to
3	0.61	1 / 63	Gastrointestinal
4	0.82	1 / 113	Ovarian cancer
5	0.85	1 / 127	Melanoma and neural system tumor syndrome
6	0.91	1 / 156	Breast cancer
7	1.00	0 / 7	Thyroid carcinoma, papillary
8	1.00	0 / 123	Pancreatic cancer
9	1.00	0 / 68	Glioblastoma multiforme, somatic
10	1.00	0 / 3	Pituitary adenoma
11	1.00	0 / 116	Cancer
12	1.00	0 / 95	Colorectal cancer
13	1.00	0 / 2	Adenomas, multiple colorectal
14	1.00	0 / 124	Prostate cancer
15	1.00	0 / 7	Schizophrenia, susceptibility to

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−05	32 / 929	PROTEINATLAS_bronchus
2	1e−04	34 / 1138	PROTEINATLAS_small intestine
3	3e−04	30 / 1003	PROTEINATLAS_appendix
4	4e−04	33 / 1173	PROTEINATLAS_rectum
5	5e−04	33 / 1194	PROTEINATLAS_stomach
6	7e−04	32 / 1167	PROTEINATLAS_gallbladder
7	8e−04	16 / 429	PROTEINATLAS_soft tissue
8	8e−04	32 / 1176	PROTEINATLAS_duodenum
9	9e−04	12 / 275	Chaussabel_3,7_Spliceosome
10	1e−03	33 / 1268	PROTEINATLAS_colon
11	2e−03	20 / 639	PROTEINATLAS_breast
12	2e−03	29 / 1097	PROTEINATLAS_kidney
13	3e−03	28 / 1063	PROTEINATLAS_tonsil
14	4e−03	25 / 933	PROTEINATLAS_adrenal gland
15	7e−03	30 / 1239	PROTEINATLAS_testis

BP

Rank	p−value	#in/all	Geneset
1	2e−04	20 / 530	biological_process
2	2e−04	8 / 104	tumor necrosis factor−mediated signaling pathway
3	4e−04	4 / 24	protein targeting to membrane
4	1e−03	3 / 14	apoptotic DNA fragmentation
5	1e−03	3 / 15	protein localization to organelle
6	2e−03	3 / 16	iron−sulfur cluster assembly
7	2e−03	5 / 59	protein localization
8	2e−03	3 / 17	acyl−CoA metabolic process
9	2e−03	3 / 18	carbohydrate phosphorylation
10	2e−03	5 / 62	transcription−coupled nucleotide−excision repair
11	3e−03	4 / 39	RNA phosphodiester bond hydrolysis, endonucleolytic
12	3e−03	3 / 19	RNA catabolic process
13	3e−03	6 / 94	gene silencing by RNA
14	4e−03	4 / 43	regulation of cellular amino acid metabolic process
15	4e−03	5 / 71	spermatid development

CC

Rank	p−value	#in/all	Geneset
1	6e−08	46 / 1304	mitochondrion
2	1e−07	80 / 2979	cytosol
3	7e−05	62 / 2535	nucleoplasm
4	5e−04	98 / 4828	nucleus
5	6e−04	15 / 374	mitochondrial inner membrane
6	9e−04	15 / 392	cellular_component
7	1e−03	18 / 539	Golgi membrane
8	2e−03	6 / 89	centriole
9	4e−03	11 / 287	mitochondrial matrix
10	4e−03	7 / 135	cilium
11	6e−03	5 / 77	trans−Golgi network membrane
12	7e−03	4 / 51	proteasome complex
13	9e−03	5 / 85	integral component of endoplasmic reticulum membrane
14	9e−03	2 / 10	CD40 receptor complex
15	9e−03	2 / 10	Gemini of coiled bodies

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−43	254 / 8568	TxWk_Colon
2	1e−42	260 / 9054	Tx_Colon
3	1e−42	267 / 9555	TssA_Colon
4	4e−41	231 / 7354	TssF_Colon
5	3e−26	184 / 6138	TssD2_Colon
6	5e−22	249 / 10779	Enh_Colon
7	6e−22	110 / 2845	TxEnhG1_Colon
8	8e−21	215 / 8678	Quies3_Colon
9	2e−20	158 / 5373	EnhWk1_Colon
10	5e−14	93 / 2810	EnhA_Colon
11	1e−10	223 / 10999	TssWk_Colon
12	1e−06	59 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	2e−05	32 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
14	2e−03	33 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	3e−03	37 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

HM

Rank	p−value	#in/all	Geneset
1	0.001	9 / 177	HALLMARK_MITOTIC_SPINDLE
2	0.002	9 / 185	HALLMARK_MTORC1_SIGNALING
3	0.003	7 / 130	HALLMARK_DNA_REPAIR
4	0.005	7 / 138	HALLMARK_FATTY_ACID_METABOLISM
5	0.009	4 / 54	HALLMARK_MYC_TARGETS_V2
6	0.019	5 / 103	HALLMARK_BILE_ACID_METABOLISM
7	0.022	7 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
8	0.046	6 / 173	HALLMARK_E2F_TARGETS
9	0.048	4 / 91	HALLMARK_PEROXISOME
10	0.048	6 / 175	HALLMARK_XENOBIOTIC_METABOLISM
11	0.053	6 / 179	HALLMARK_G2M_CHECKPOINT
12	0.124	5 / 176	HALLMARK_ADIPOGENESIS
13	0.125	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	0.155	3 / 91	HALLMARK_ANDROGEN_RESPONSE
15	0.177	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Melanoma

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	5 / 61	hsa−miR−671−5p
2	0.008	4 / 52	hsa−miR−940
3	0.011	6 / 124	hsa−miR−515−3p
4	0.018	3 / 37	hsa−miR−518e
5	0.020	3 / 39	hsa−miR−484
6	0.022	4 / 71	hsa−miR−939
7	0.023	6 / 147	hsa−miR−506
8	0.028	3 / 44	hsa−miR−411
9	0.032	6 / 158	hsa−miR−802
10	0.033	3 / 47	hsa−miR−553
11	0.042	10 / 355	hsa−let−7i
12	0.045	6 / 172	hsa−miR−548k
13	0.049	9 / 316	hsa−let−7f
14	0.049	2 / 24	hsa−miR−609
15	0.049	2 / 24	hsa−miR−24−1*

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	

Brain

Rank	p−value	#in/all	Geneset
1	9e−38	259 / 9504	Overlap_fetal_midbrain_K9K27me3
2	2e−24	249 / 10430	Overlap_fetal_midbrain_Quies
3	2e−22	236 / 9815	Overlap_fetal_midbrain_ReprPC
4	2e−19	166 / 5936	Overlap_fetal_midbrain_HetRpts
5	2e−17	108 / 3164	Mid_Frontal_Lobe_ZNF
6	4e−07	194 / 9917	Overlap_fetal_midbrain_ReprPCWk
7	2e−06	31 / 818	Mid_Frontal_Lobe_Het
8	1e−04	64 / 2709	Mid_Frontal_Lobe_HetRpts
9	2e−04	45 / 1728	Fetal_ReprPCWk
10	1e−03	24 / 796	Overlap_fetal_midbrain_ZNF
11	1e−02	23 / 906	Fetal_HetRpts
12	5e−02	15 / 630	Mid_Frontal_Lobe_EnhP
13	8e−02	72 / 4112	Mid_Frontal_Lobe_ReprPC
14	2e−01	8 / 386	Fetal_ZNF
15	3e−01	20 / 1171	Fetal_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	6e−05	21 / 536	Chr 22
2	6e−04	28 / 959	Chr 16
3	3e−02	31 / 1467	Chr 19
4	3e−01	21 / 1217	Chr 3
5	3e−01	24 / 1411	Chr 11
6	3e−01	25 / 1492	Chr 2
7	3e−01	11 / 619	Chr 20
8	4e−01	16 / 954	Chr 9
9	4e−01	5 / 289	Chr 21
10	5e−01	20 / 1318	Chr 17
11	6e−01	17 / 1170	Chr 7
12	7e−01	16 / 1160	Chr 12
13	7e−01	11 / 836	Chr 8
14	7e−01	32 / 2323	Chr 1
15	7e−01	1 / 87	Chr Y

Glio

Rank	p−value	#in/all	Geneset
1	7e−06	30 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	1e−05	55 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−04	47 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−02	10 / 315	Up
5	3e−02	3 / 48	Vishal_subnetwork signature of survival in GBM
6	4e−02	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	4e−02	3 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
8	6e−02	4 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	8e−02	28 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	1e−01	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
11	2e−01	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
12	2e−01	3 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
13	2e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
14	2e−01	1 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
15	2e−01	2 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 17	DUMEAUX_High bmi enriched genes
2	0.14	1 / 10	DUMEAUX_Smoking literature genes up
3	0.17	3 / 94	DUMEAUX_Smoking enriched genes
4	0.37	1 / 31	DUMEAUX_Fasting enriched genes
5	0.39	4 / 211	Homuth_BMI−associated−genes_DN
6	0.65	2 / 147	Homuth_BMI−associated−genes_UP
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	1e−06	175 / 8818	protein binding
2	1e−04	38 / 1329	ATP binding
3	2e−04	22 / 627	molecular_function
4	7e−04	3 / 12	phosphatidic acid binding
5	8e−04	4 / 28	tumor necrosis factor receptor binding
6	2e−03	3 / 18	DNA helicase activity
7	2e−03	13 / 350	protein kinase binding
8	3e−03	12 / 311	enzyme binding
9	3e−03	28 / 1065	zinc ion binding
10	5e−03	4 / 45	tRNA binding
11	6e−03	3 / 25	protein−cysteine S−palmitoyltransferase activity
12	7e−03	12 / 351	GTP binding
13	7e−03	13 / 399	RNA binding
14	9e−03	2 / 10	glutathione binding
15	9e−03	2 / 10	ribonuclease P activity

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	2e−18	148 / 5067	ICGC_Taf1_targets
2	3e−15	127 / 4362	ICGC_Creb1_targets
3	8e−15	128 / 4468	ICGC_Egr1_targets
4	3e−13	142 / 5466	ICGC_Nficsc81335_targets
5	8e−13	142 / 5518	ICGC_Stat5_targets
6	8e−13	156 / 6322	ICGC_Tcf3_targets
7	9e−13	165 / 6868	ICGC_Elf1_targets
8	2e−11	156 / 6578	ICGC_Pou2_targets
9	5e−11	166 / 7247	ICGC_Runx3_targets
10	7e−11	135 / 5442	ICGC_Pmlsc71910_targets
11	2e−10	124 / 4890	ICGC_Bclaf101388_targets
12	2e−10	110 / 4131	ICGC_Nfatc1_targets
13	4e−10	142 / 5984	ICGC_Mta3_targets
14	7e−10	146 / 6267	ICGC_Yy1_targets
15	1e−09	130 / 5383	ICGC_Sp1_targets

Correlation Cluster

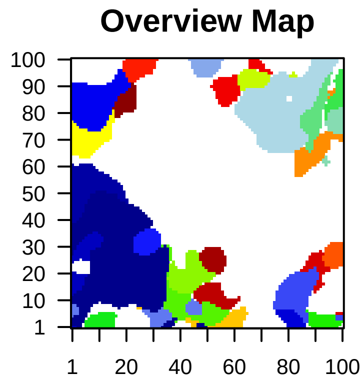
Spot Summary: P

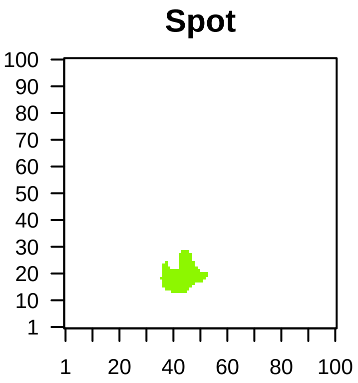
metagenes = 161
genes = 1177

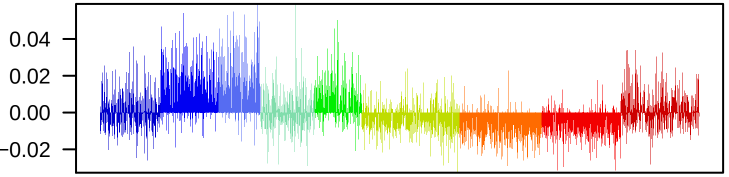
<r> metagenes = 0.91

beta: r2= 0.44 / log p= −Inf

samples with spot = 0 (0 %)





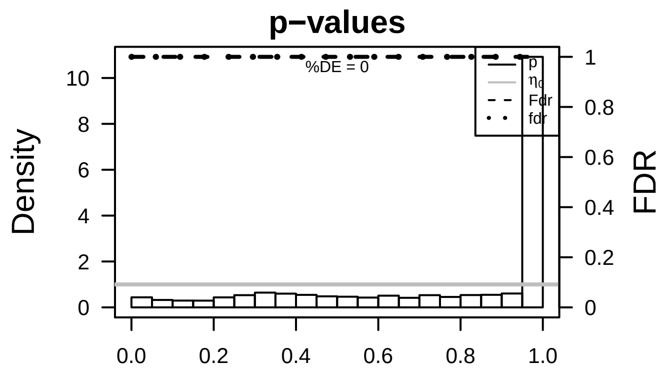


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_180882	0.47	−0.2	0.1	NEBL	nebulette [Source:HGNC Symbol;Acc:HGNC:16932]
2	ILMN_184313	0.43	−0.19	0.22		
3	ILMN_233658	0.38	−0.2	0.16		
4	ILMN_166114	0.34	−0.18	0.17		
5	ILMN_181203	0.33	−0.18	0.19	PALM	paralemmin [Source:HGNC Symbol;Acc:HGNC:8594]
6	ILMN_324054	0.33	−0.28	0.32		
7	ILMN_175604	0.3	−0.23	0.13	NT5DC3	5'−nucleotidase domain containing 3 [Source:HGNC Symbol;
8	ILMN_190919	0.3	−0.2	0.27		
9	ILMN_209958	0.3	−0.22	0.5	CCDC28B	coiled−coil domain containing 28B [Source:HGNC Symbol;Ac
10	ILMN_177061	0.3	−0.18	0.27	MERTK	MER proto−oncogene, tyrosine kinase [Source:HGNC Symbo
11	ILMN_214916	0.29	−0.19	0.15	SFRP1	secreted frizzled related protein 1 [Source:HGNC Symbol;Acc
12	ILMN_167475	0.29	−0.2	0.3	LPCAT4	lysophosphatidylcholine acyltransferase 4 [Source:HGNC Syr
13	ILMN_178838	0.28	−0.18	0.41	UGGT2	UDP−glucose glycoprotein glucosyltransferase 2 [Source:HG
14	ILMN_179530	0.28	−0.19	0.35	ARHGEF37	Rho guanine nucleotide exchange factor 37 [Source:HGNC S
15	ILMN_172594	0.27	−0.19	0.22	IRF6	interferon regulatory factor 6 [Source:HGNC Symbol;Acc:HGI
16	ILMN_208286	0.27	−0.21	0.37	PLLP	plasmolipin [Source:HGNC Symbol;Acc:HGNC:18553]
17	ILMN_323538	0.27	−0.17	0.46		
18	ILMN_175393	0.27	−0.19	0.27	CDO1	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:HGI
19	ILMN_166573	0.26	−0.18	0.35		
20	ILMN_176780	0.26	−0.19	0.2	SAMD10	sterile alpha motif domain containing 10 [Source:HGNC Syml

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−07	206 / 5384	Lympl	HOPP_Repressed
2	4e−07	116 / 2660	Chror	8_EnhP_Melanocytes
3	4e−06	165 / 4304	Chror	9_ReprPCWk_Melanocytes
4	8e−06	70 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
5	3e−05	154 / 4107	Chror	9_ReprPCWk_Fibroblasts
6	5e−05	132 / 3438	Chror	10_ReprPC_Melanocytes
7	9e−05	133 / 3523	Chror	1_TssP_Melanocytes
8	1e−04	136 / 3639	Chror	1_TssP_Fibroblasts
9	3e−04	23 / 366	Colon	K9K27me3_Colon
10	5e−04	90 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
11	5e−04	134 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
12	5e−04	97 / 2516	Chror	11_K9K27me3_Melanocytes
13	5e−04	29 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
14	6e−04	100 / 2620	Chror	1_TssP_Neuronal_Progenitor
15	6e−04	148 / 4169	Chror	10_ReprPC_Fibroblasts
16	7e−04	51 / 1154	Chror	11_K9K27me3_Neuronal_Progenitor
17	7e−04	108 / 2894	Colon	TssP_Colon
18	8e−04	39 / 819	Brain	Overlap_fetal_midbrain_TssP
19	1e−03	7 / 58	Aging	TESCHENDORFF_age_hypermethylated
20	1e−03	26 / 484	Colon	Quies2_Colon
21	1e−03	112 / 3068	Chror	8_EnhP_Fibroblasts
22	1e−03	19 / 315	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
23	1e−03	8 / 78	GSEA	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
24	2e−03	3 / 9	GSEA	SCHLESINGER_METHYLATED_IN_COLON_CANCER
25	2e−03	3 / 9	GSEA	CHESLER_BRAIN_D6MIT150_QTL_TRANS
26	2e−03	4 / 19	BP	flavonoid biosynthetic process
27	2e−03	48 / 1119	Brain	Overlap_fetal_midbrain_TssA
28	2e−03	87 / 2315	Chror	13_HetRpts_Melanocytes
29	2e−03	18 / 306	GSEA	NABA_SECRETED_FACTORS
30	2e−03	4 / 21	BP	flavonoid glucuronidation
31	2e−03	4 / 21	GSEA	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
32	2e−03	142 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
33	3e−03	42 / 962	GSEA	BENPORATH_EED_TARGETS
34	3e−03	5 / 35	GSEA	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN
35	3e−03	11 / 147	BP	homophilic cell adhesion via plasma membrane adhesion molecules
36	3e−03	113 / 3173	Colon	ReprPC_Colon
37	3e−03	8 / 87	Lympl	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
38	3e−03	3 / 11	BP	activation of transmembrane receptor protein tyrosine kinase activity
39	3e−03	107 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
40	3e−03	5 / 37	GSEA	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM



Aging

Rank	p−value	#in/all	Geneset
1	0.001	7 / 58	TESCHENDORFF_age_hypermethylated
2	0.757	3 / 142	HORVATH_aging_genes meth UP
3	0.956	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	2 / 13	LIU_LIVER_CANCER
2	0.06	5 / 76	PanCan_Wnt_geneset_nanostring
3	0.07	2 / 16	GENTLES_modul14
4	0.14	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.25	0 / 15	LIU_PROSTATE_CANCER_DN
6	0.28	2 / 38	KUIPER_MM good survival
7	0.31	1 / 13	RHODES_CANCER_META_SIGNATURE
8	0.33	1 / 14	LIU_PROSTATE_CANCER_UP
9	0.33	1 / 14	GENTLES_modul1
10	0.33	1 / 14	GENTLES_modul13
11	0.40	3 / 82	PanCan_JAK−ST_geneset_nanostring
12	0.41	4 / 117	PanCan_Driver_Gene_geneset_nanostring
13	0.46	0 / 12	LIU_BREAST_CANCER
14	0.53	0 / 14	LIU_COMMON_CANCER_GENES
15	0.55	1 / 28	PanCan_HH_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−07	116 / 2660	8_EnhP_Melanocytes
2	4e−06	165 / 4304	9_ReprPCWk_Melanocytes
3	3e−05	154 / 4107	9_ReprPCWk_Fibroblasts
4	5e−05	132 / 3438	10_ReprPC_Melanocytes
5	9e−05	133 / 3523	1_TssP_Melanocytes
6	1e−04	136 / 3639	1_TssP_Fibroblasts
7	5e−04	90 / 2297	10_ReprPC_Neuronal_Progenitor
8	5e−04	134 / 3691	9_ReprPCWk_Neuronal_Progenitor
9	5e−04	97 / 2516	11_K9K27me3_Melanocytes
10	6e−04	100 / 2620	1_TssP_Neuronal_Progenitor
11	6e−04	148 / 4169	10_ReprPC_Fibroblasts
12	7e−04	51 / 1154	11_K9K27me3_Neuronal_Progenitor
13	1e−03	112 / 3068	8_EnhP_Fibroblasts
14	2e−03	87 / 2315	13_HetRpts_Melanocytes
15	2e−02	72 / 2031	12_Het_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	29 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
2	1e−03	19 / 315	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
3	1e−03	8 / 78	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
4	2e−03	3 / 9	SCHLESINGER_METHYLATED_IN_COLON_CANCER
5	2e−03	3 / 9	CHESLER_BRAIN_D6MIT150_QTL_TRANS
6	2e−03	18 / 306	NABA_SECRETED_FACTORS
7	2e−03	4 / 21	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
8	3e−03	42 / 962	BENPORATH_EED_TARGETS
9	3e−03	5 / 35	CEBALLOS_TARGETS_OF_TP53_AND_MYC_DN
10	3e−03	5 / 37	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM
11	5e−03	4 / 25	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS
12	5e−03	3 / 13	PID_ERBB_NETWORK_PATHWAY
13	5e−03	7 / 76	RICKMAN_HEAD_AND_NECK_CANCER_E
14	7e−03	12 / 190	AFFAR_YY1_TARGETS_UP
15	8e−03	13 / 216	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−07	206 / 5384	HOPP_Repressed
2	3e−03	8 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
3	2e−02	4 / 36	Subero_MM_hyper_meth
4	2e−02	5 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
5	3e−02	5 / 60	Subero_mBL_hyper_meth
6	4e−02	2 / 12	WRIGHT_GCB UP
7	5e−02	96 / 2939	HOPP_Poised_promoter
8	5e−02	132 / 4167	HOPP_Heterochrom
9	7e−02	4 / 57	LENZ_Stromal signature 2
10	8e−02	1 / 3	WRIGHT_custom GCB−DLBCL UP
11	9e−02	7 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
12	9e−02	7 / 138	WIRTH_lymphoma937_spot G
13	1e−01	5 / 88	ROSOLOWSKI_red total
14	1e−01	5 / 89	Subero_T−ALL_hyper_meth
15	1e−01	4 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	3 / 40	Muscular dystrophy
2	0.2	2 / 27	Duchenne muscular dystrophy
3	0.2	1 / 7	Thyroid carcinoma, papillary
4	0.2	2 / 28	Miyoshi myopathy
5	0.2	1 / 8	Cardiomyopathy, idiopathic dilated
6	0.2	2 / 30	Systemic lupus erythematosus (SLE)
7	0.2	3 / 56	Myopathy, nemaline, 3
8	0.3	3 / 68	Glioblastoma multiforme, somatic
9	0.3	2 / 40	Medulloblastoma
10	0.3	2 / 41	Melanoma, cutaneous malignant, 2
11	0.3	1 / 15	Supravalvar aortic stenosis
12	0.4	2 / 47	Cervical cancer, somatic
13	0.4	1 / 17	Thyroid carcinoma, follicular
14	0.4	1 / 17	Gastroesphageal reflux
15	0.4	2 / 48	Alzheimer disease, susceptibility to

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.01	3 / 17	VAQUERIZAS_Heart_TF
2	0.01	3 / 17	JONGENEEL_Lung
3	0.03	8 / 134	WIRTH_Mucosa
4	0.04	11 / 220	WIRTH_Testis
5	0.06	13 / 289	JONGENEEL_Testis
6	0.11	10 / 231	Chaussabel_2,5_Immune related molecules
7	0.11	2 / 21	JONGENEEL_Monocytes
8	0.11	2 / 21	JONGENEEL_Salivary Gland
9	0.12	18 / 478	WIRTH_Nervous System
10	0.19	2 / 29	Chaussabel_2,7_Unknown function
11	0.25	1 / 10	JONGENEEL_Pituitary Gland
12	0.27	1 / 11	WIRTH_Tonsil
13	0.29	1 / 12	WIRTH_Globus pallidus
14	0.30	5 / 132	WIRTH_Muscle
15	0.31	1 / 13	WIRTH_Sec. lymphoid organs

BP

Rank	p−value	#in/all	Geneset
1	0.002	4 / 19	flavonoid biosynthetic process
2	0.002	4 / 21	flavonoid glucuronidation
3	0.003	11 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
4	0.003	3 / 11	activation of transmembrane receptor protein tyrosine kinase activity
5	0.006	5 / 42	ureteric bud development
6	0.006	3 / 14	cellular glucuronidation
7	0.009	3 / 16	response to vitamin A
8	0.010	4 / 31	germ cell development
9	0.011	3 / 17	cobalamin metabolic process
10	0.011	3 / 17	male genitalia development
11	0.011	5 / 49	negative regulation of Wnt signaling pathway
12	0.013	4 / 33	limb development
13	0.013	4 / 33	regulation of heart contraction
14	0.013	6 / 70	xenobiotic metabolic process
15	0.013	17 / 337	spermatogenesis

CC

Rank	p−value	#in/all	Geneset
1	0.02	6 / 77	organelle membrane
2	0.02	47 / 1249	extracellular region
3	0.03	2 / 10	fascia adherens
4	0.03	41 / 1101	extracellular space
5	0.04	6 / 88	keratin filament
6	0.04	2 / 11	endoplasmic reticulum exit site
7	0.06	2 / 14	basal lamina
8	0.06	2 / 14	clathrin−coated endocytic vesicle
9	0.06	5 / 75	secretory granule
10	0.07	6 / 104	bicellular tight junction
11	0.07	4 / 57	endoplasmic reticulum−Golgi intermediate compartment
12	0.07	6 / 106	Z disc
13	0.10	2 / 19	connexon complex
14	0.11	2 / 20	cytoplasmic ribonucleoprotein granule
15	0.11	2 / 20	multivesicular body

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	23 / 366	K9K27me3_Colon
2	7e−04	108 / 2894	TssP_Colon
3	1e−03	26 / 484	Quies2_Colon
4	3e−03	113 / 3173	ReprPC_Colon
5	6e−03	71 / 1895	EnhP_Colon
6	9e−03	96 / 2740	ReprPCWk_Colon
7	4e−02	6 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
8	4e−02	24 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	5e−02	3 / 31	Kosinski_lower−crypt−short−list
10	1e−01	1 / 4	Budinska_C_CIMP−H−like_DOWN
11	1e−01	280 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	1e−01	24 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	1e−01	138 / 4526	Quies1_Colon
14	1e−01	26 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
15	2e−01	17 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

HM

Rank	p−value	#in/all	Geneset
1	0.2	8 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	0.3	7 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.3	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
4	0.3	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.4	6 / 177	HALLMARK_KRAS_SIGNALING_DN
6	0.4	4 / 116	HALLMARK_SPERMATOGENESIS
7	0.4	6 / 186	HALLMARK_MYOGENESIS
8	0.5	3 / 91	HALLMARK_ANDROGEN_RESPONSE
9	0.5	4 / 137	HALLMARK_UV_RESPONSE_UP
10	0.6	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
11	0.6	4 / 151	HALLMARK_APOPTOSIS
12	0.6	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
13	0.7	2 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	0.7	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	0.7	4 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 30	Hugo_melanoma−all−MET_UP
2	0.4	2 / 54	Hugo_melanoma−all−MET_DN
3	0.7	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	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.06	5 / 75	hsa−miR−375
2	0.09	4 / 62	hsa−miR−485−3p
3	0.11	2 / 21	hsa−miR−1282
4	0.13	3 / 45	hsa−miR−524−3p
5	0.13	2 / 23	hsa−miR−151−5p
6	0.16	4 / 76	hsa−miR−205
7	0.16	4 / 76	hsa−miR−1827
8	0.18	1 / 7	hsa−miR−566
9	0.18	2 / 28	hsa−miR−519e*
10	0.19	4 / 82	hsa−miR−542−3p
11	0.22	4 / 87	hsa−miR−362−5p
12	0.22	3 / 59	hsa−miR−219−1−3p
13	0.25	1 / 10	hsa−miR−887
14	0.25	2 / 35	hsa−miR−197
15	0.27	7 / 188	hsa−miR−382

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	8e−06	70 / 1476	Overlap_fetal_midbrain_TxTrans
2	8e−04	39 / 819	Overlap_fetal_midbrain_TssP
3	2e−03	48 / 1119	Overlap_fetal_midbrain_TssA
4	2e−03	142 / 4112	Mid_Frontal_Lobe_ReprPC
5	6e−03	39 / 924	Mid_Frontal_Lobe_TssF
6	1e−02	46 / 1162	Fetal_Enh
7	1e−02	69 / 1893	Overlap_fetal_midbrain_TssF
8	1e−02	52 / 1360	Mid_Frontal_Lobe_TssP
9	3e−02	101 / 3046	Fetal_TssA
10	4e−02	90 / 2700	Fetal_TxTrans
11	4e−02	17 / 383	Mid_Frontal_Lobe_Tx
12	5e−02	47 / 1329	Overlap_fetal_midbrain_Enh
13	1e−01	38 / 1115	Overlap_fetal_midbrain_EnhG
14	1e−01	30 / 869	Mid_Frontal_Lobe_EnhG
15	1e−01	47 / 1436	Fetal_K9K27me3

Chr

Rank	p−value	#in/all	Geneset
1	0.01	7 / 87	Chr Y
2	0.03	19 / 422	Chr 13
3	0.04	34 / 902	Chr 4
4	0.06	31 / 836	Chr 8
5	0.16	13 / 342	Chr 18
6	0.18	38 / 1170	Chr 7
7	0.18	11 / 289	Chr 21
8	0.23	29 / 904	Chr 10
9	0.25	46 / 1492	Chr 2
10	0.30	24 / 768	Chr 14
11	0.34	42 / 1411	Chr 11
12	0.41	31 / 1060	Chr 5
13	0.46	33 / 1160	Chr 12
14	0.50	34 / 1211	Chr 6
15	0.58	26 / 959	Chr 16

Glio

Rank	p−value	#in/all	Geneset
1	0.003	107 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.015	2 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
3	0.022	3 / 22	Shinawi_with_increased_methylation_in_STS
4	0.024	52 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	0.027	5 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
6	0.031	19 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
7	0.034	3 / 26	Gorovets_LGG_NB_subclass
8	0.038	33 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
9	0.041	7 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.059	4 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
11	0.063	2 / 15	VERHAAK_PN_Brain
12	0.063	2 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
13	0.072	3 / 35	Colman_survival_associated
14	0.080	7 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	0.090	9 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	3 / 32	Marjolein_ageing−genes_DN
2	0.26	4 / 94	DUMEAUX_Smoking enriched genes
3	0.38	1 / 17	DUMEAUX_High bmi enriched genes
4	0.78	3 / 147	Homuth_BMI−associated−genes_UP
5	1.00	1 / 211	Homuth_BMI−associated−genes_DN
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 31	DUMEAUX_Fasting enriched genes
15	1.00	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.007	4 / 28	glucuronosyltransferase activity
2	0.008	3 / 15	retinoic acid binding
3	0.020	9 / 145	growth factor activity
4	0.022	17 / 357	olfactory receptor activity
5	0.024	5 / 59	cell adhesion molecule binding
6	0.030	2 / 10	co−receptor binding
7	0.030	2 / 10	regulatory region DNA binding
8	0.030	2 / 10	translation repressor activity, nucleic acid binding
9	0.031	3 / 25	chemorepellent activity
10	0.040	5 / 68	drug binding
11	0.041	4 / 47	RNA polymerase II transcription factor binding
12	0.041	4 / 47	scaffold protein binding
13	0.042	2 / 12	cytokine receptor binding
14	0.049	2 / 13	filamin binding
15	0.049	2 / 13	L−amino acid transmembrane transporter activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	2 / 15	GUSTAFSON_PI3K_DN
2	0.33	1 / 14	BENTINK_ras.6
3	1.00	0 / 14	GUSTAFSON_PI3K_UP
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	60 / 1753	HEBENSTREIT_low expression TF
2	0.22	21 / 631	ICGC_RxraPcr1_targets
3	0.66	94 / 3507	ICGC_Rad21_targets
4	0.80	37 / 1501	ICGC_Usf1_targets
5	0.88	34 / 1466	ICGC_NrsfPcr1_targets
6	0.90	15 / 721	ICGC_SrfPcr2_targets
7	0.92	38 / 1669	ICGC_P300_targets
8	0.93	15 / 747	ICGC_NrsfPcr2_targets
9	0.97	13 / 733	ICGC_Atf3_targets
10	0.97	45 / 2087	ICGC_Cebpbsc150_targets
11	0.97	46 / 2133	ICGC_Mef2_targets
12	0.99	53 / 2497	ICGC_Bcl11_targets
13	0.99	70 / 3194	ICGC_Irf4_targets
14	0.99	99 / 4345	ICGC_Zeb1_targets
15	0.99	27 / 1478	ICGC_Myc_targets

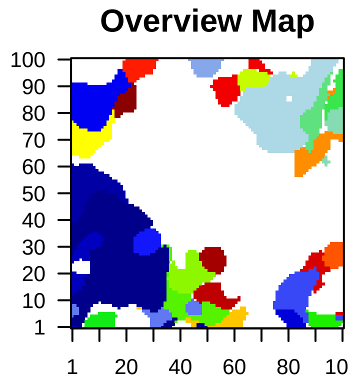
Correlation Cluster

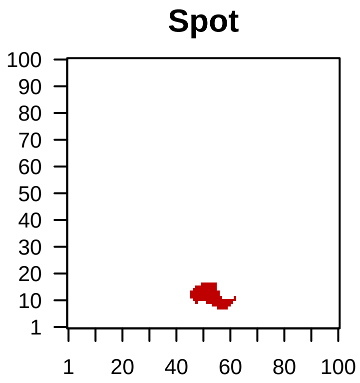
Spot Summary: Q

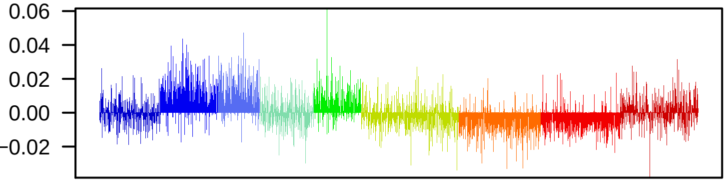
metagenes = 96
genes = 854

<r> metagenes = 0.92
<r> genes = 0.04
beta: r2= 0.31 / log p= −Inf

samples with spot = 0 (0 %)





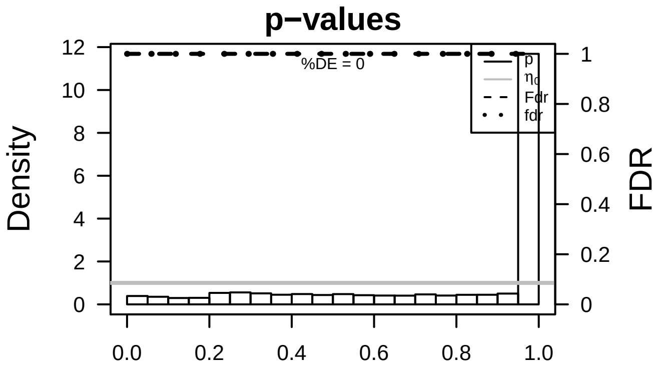


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178963	0.59	−0.29	0.24	FMOD	fibromodulin [Source:HGNC Symbol;Acc:HGNC:3774]
2	ILMN_241552	0.42	−0.3	0.14		
3	ILMN_165165	0.41	−0.19	0.21	ADAM33	ADAM metallopeptidase domain 33 [Source:HGNC Symbol;A
4	ILMN_167829	0.33	−0.34	0.18	HMG20A	high mobility group 20A [Source:HGNC Symbol;Acc:HGNC:5
5	ILMN_170217	0.28	−0.23	0.17	MIR6132	suppression of tumorigenicity 7 [Source:HGNC Symbol;Acc:H
6	ILMN_174286	0.28	−0.27	0.21		
7	ILMN_180600	0.28	−0.18	0.1	SPEF2	sperm flagellar 2 [Source:HGNC Symbol;Acc:HGNC:26293]
8	ILMN_186218	0.28	−0.21	0.12	C11orf95	chromosome 11 open reading frame 95 [Source:HGNC Symb
9	ILMN_175904	0.27	−0.19	0.13		
10	ILMN_172888	0.27	−0.2	0.21	PAK4	p21 (RAC1) activated kinase 4 [Source:HGNC Symbol;Acc:H
11	ILMN_168786	0.27	−0.19	0.15	LSS	lanosterol synthase (2,3−oxidosqualene−lanosterol cyclase) [
12	ILMN_234122	0.27	−0.19	0.13	CD34	CD34 molecule [Source:HGNC Symbol;Acc:HGNC:1662]
13	ILMN_177665	0.26	−0.18	0.14		
14	ILMN_323939	0.26	−0.16	0.22		
15	ILMN_179592	0.25	−0.24	0.16		paraspeckle component 1 pseudogene 1 [Source:HGNC Sym
16	ILMN_165604	0.25	−0.18	0.21	CELF6	CUGBP, Elav−like family member 6 [Source:HGNC Symbol;A
17	ILMN_320305	0.25	−0.19	0.24	WDR86−AS1	WDR86 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC
18	ILMN_170003	0.25	−0.16	0.27	PRAME	preferentially expressed antigen in melanoma [Source:HGNC
19	ILMN_186323	0.25	−0.17	0.16		long intergenic non−protein coding RNA 382 [Source:HGNC S
20	ILMN_324544	0.25	−0.14	0.26		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−05	162 / 5384	Lympl	HOPP_Repressed
2	1e−04	129 / 4304	Chror	9_ReprPCWk_Melanocytes
3	5e−04	9 / 104	CC	bicellular tight junction
4	6e−04	104 / 3438	Chror	10_ReprPC_Melanocytes
5	6e−04	75 / 2315	Chror	13_HetRpts_Melanocytes
6	1e−03	3 / 10	GSEA	WEBER_METHYLATED_ICP_IN_SPERM_DN
7	1e−03	7 / 73	miRN	Stroke, susceptibility to
8	2e−03	4 / 23	BP	dopaminergic neuron differentiation
9	2e−03	5 / 39	BP	learning or memory
10	2e−03	97 / 3272	Chror	13_HetRpts_Neuronal_Progenitor
11	2e−03	34 / 902	Chr	Chr 4
12	3e−03	11 / 182	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_DN
13	3e−03	3 / 13	BP	dendritic spine development
14	3e−03	3 / 13	GSEA	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_F
15	3e−03	64 / 2031	Chror	12_Het_Melanocytes
16	3e−03	4 / 28	BP	regulation of signal transduction
17	4e−03	76 / 2516	Chror	11_K9K27me3_Melanocytes
18	4e−03	8 / 113	miRN	Ovarian cancer
19	4e−03	6 / 68	miRN	Glioblastoma multiforme, somatic
20	4e−03	3 / 15	BP	sympathetic nervous system development
21	4e−03	3 / 15	GSEA	WEBER_METHYLATED_ICP_IN_FIBROBLAST
22	4e−03	40 / 1163	Chror	12_Het_Fibroblasts
23	5e−03	11 / 196	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
24	5e−03	59 / 1893	Brain	Overlap_fetal_midbrain_TssF
25	6e−03	5 / 52	GSEA	REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE
26	6e−03	3 / 17	miRN	Bladder cancer
27	7e−03	9 / 150	Cance	PanCan_MAPK_geneset_nanostring
28	7e−03	8 / 124	GSEA	MIKKELSEN_ES_LCP_WITH_H3K4ME3
29	7e−03	115 / 4167	Lympl	HOPP_Heterochrom
30	7e−03	3 / 18	GSEA	MCCABE_HOXC6_TARGETS_DN
31	7e−03	4 / 35	GSEA	FRASOR_RESPONSE_TO_ESTRADIOL_UP
32	8e−03	23 / 594	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
33	8e−03	103 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
34	8e−03	6 / 79	GSEA	WONG_ENDMETRIUM_CANCER_DN
35	8e−03	9 / 156	BP	axon guidance
36	8e−03	9 / 156	miRN	Breast cancer
37	9e−03	7 / 105	BP	kidney development
38	9e−03	3 / 20	BP	calcium−independent cell−cell adhesion via plasma membrane cell−adhesi
39	9e−03	3 / 20	GSEA	VALK_AML_WITH_EVI1
40	1e−02	79 / 2740	Colon	ReprPCWk_Colon



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 58	TESCHENDORFF_age_hypermethylated
2	0.8	2 / 142	HORVATH_aging_genes meth UP
3	0.9	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	4 / 23	dopaminergic neuron differentiation
2	0.002	5 / 39	learning or memory
3	0.003	3 / 13	dendritic spine development
4	0.003	4 / 28	regulation of signal transduction
5	0.004	3 / 15	sympathetic nervous system development
6	0.008	9 / 156	axon guidance
7	0.009	7 / 105	kidney development
8	0.009	3 / 20	calcium−independent cell−cell adhesion via plasma membrane cell−adhesion
9	0.011	6 / 84	cell−matrix adhesion
10	0.012	3 / 22	antigen processing and presentation of peptide antigen via MHC class I
11	0.012	6 / 86	transmembrane receptor protein tyrosine kinase signaling pathway
12	0.014	4 / 42	branching involved in ureteric bud morphogenesis
13	0.014	4 / 42	ureteric bud development
14	0.017	8 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
15	0.019	4 / 46	skeletal muscle tissue development

Brain

Rank	p−value	#in/all	Geneset
1	0.005	59 / 1893	Overlap_fetal_midbrain_TssF
2	0.017	28 / 819	Overlap_fetal_midbrain_TssP
3	0.017	18 / 465	Mid_Frontal_Lobe_TxTrans
4	0.041	12 / 304	Mid_Frontal_Lobe_TssA
5	0.049	14 / 383	Mid_Frontal_Lobe_Tx
6	0.052	27 / 869	Mid_Frontal_Lobe_EnhG
7	0.069	38 / 1329	Overlap_fetal_midbrain_Enh
8	0.086	32 / 1115	Overlap_fetal_midbrain_EnhG
9	0.089	38 / 1360	Mid_Frontal_Lobe_TssP
10	0.115	40 / 1476	Overlap_fetal_midbrain_TxTrans
11	0.150	17 / 578	Fetal_Tx
12	0.155	76 / 3046	Fetal_TssA
13	0.213	6 / 180	Overlap_fetal_midbrain_Het
14	0.224	66 / 2700	Fetal_TxTrans
15	0.246	24 / 924	Mid_Frontal_Lobe_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	9 / 150	PanCan_MAPK_geneset_nanostring
2	0.043	2 / 15	GENTLES_modul17
3	0.053	5 / 91	PanCan_TXmisReg_geneset_nanostring
4	0.084	6 / 136	PanCan_RAS_geneset_nanostring
5	0.125	0 / 14	LIU_PROSTATE_CANCER_UP
6	0.239	3 / 76	PanCan_Wnt_geneset_nanostring
7	0.270	1 / 14	GENTLES_modul4
8	0.287	1 / 15	LIU_PROSTATE_CANCER_DN
9	0.302	1 / 16	BEN−PORATH_DN
10	0.302	1 / 16	GENTLES_modul11
11	0.363	1 / 20	PanCan_ChromMod_geneset_nanostring
12	0.392	13 / 527	Lembcke_Normal vs Adenoma
13	0.430	5 / 193	PanCan_PI3K_geneset_nanostring
14	0.468	1 / 28	PanCan_HH_geneset_nanostring
15	0.485	3 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	5e−04	9 / 104	bicellular tight junction
2	2e−02	2 / 10	sperm midpiece
3	3e−02	8 / 162	basolateral plasma membrane
4	3e−02	3 / 32	histone deacetylase complex
5	4e−02	97 / 3662	plasma membrane
6	5e−02	12 / 311	neuronal cell body
7	5e−02	2 / 16	photoreceptor disc membrane
8	5e−02	5 / 91	perikaryon
9	5e−02	6 / 121	receptor complex
10	8e−02	6 / 135	cilium
11	9e−02	3 / 47	adherens junction
12	9e−02	2 / 23	nonmotile primary cilium
13	1e−01	2 / 24	ciliary base
14	1e−01	4 / 82	apical part of cell
15	1e−01	16 / 512	cell surface

Chr

Rank	p−value	#in/all	Geneset
1	0.002	34 / 902	Chr 4
2	0.038	31 / 994	Chr X
3	0.150	13 / 422	Chr 13
4	0.217	15 / 536	Chr 22
5	0.269	20 / 769	Chr 15
6	0.282	56 / 2323	Chr 1
7	0.493	8 / 342	Chr 18
8	0.495	24 / 1060	Chr 5
9	0.514	26 / 1160	Chr 12
10	0.532	26 / 1170	Chr 7
11	0.580	2 / 87	Chr Y
12	0.604	26 / 1211	Chr 6
13	0.613	32 / 1492	Chr 2
14	0.683	17 / 836	Chr 8
15	0.700	27 / 1318	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−04	129 / 4304	9_ReprPCWk_Melanocytes
2	6e−04	104 / 3438	10_ReprPC_Melanocytes
3	6e−04	75 / 2315	13_HetRpts_Melanocytes
4	2e−03	97 / 3272	13_HetRpts_Neuronal_Progenitor
5	3e−03	64 / 2031	12_Het_Melanocytes
6	4e−03	76 / 2516	11_K9K27me3_Melanocytes
7	4e−03	40 / 1163	12_Het_Fibroblasts
8	8e−03	103 / 3691	9_ReprPCWk_Neuronal_Progenitor
9	1e−02	98 / 3523	1_TssP_Melanocytes
10	1e−02	42 / 1324	13_HetRpts_Fibroblasts
11	2e−02	25 / 717	11_K9K27me3_Fibroblasts
12	2e−02	111 / 4169	10_ReprPC_Fibroblasts
13	2e−02	75 / 2682	12_Het_Neuronal_Progenitor
14	3e−02	73 / 2660	8_EnhP_Melanocytes
15	4e−02	64 / 2297	10_ReprPC_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.008	23 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	0.010	79 / 2740	ReprPCWk_Colon
3	0.013	2 / 8	Budinska_C_CIMP−H−like_UP
4	0.022	87 / 3173	ReprPC_Colon
5	0.030	5 / 78	Ang_CRC_Hypermethylated
6	0.042	78 / 2894	TssP_Colon
7	0.044	17 / 484	Quies2_Colon
8	0.055	46 / 1623	Het_Colon
9	0.063	115 / 4526	Quies1_Colon
10	0.065	1 / 3	Budinska_E_Mixed_DOWN
11	0.066	40 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
12	0.069	6 / 129	Marisa_CRC−cluster−b
13	0.078	35 / 1224	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
14	0.080	4 / 73	Ang_CRC−CIMPH−vs−L_hyper
15	0.091	51 / 1895	EnhP_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.02	6 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
2	0.06	5 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
3	0.07	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
4	0.07	78 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
5	0.09	2 / 22	Shinawi_with_increased_methylation_in_STS
6	0.11	3 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
7	0.11	3 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
8	0.12	3 / 55	developing astrocytes
9	0.13	15 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
10	0.14	3 / 58	OPC
11	0.15	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
12	0.16	1 / 8	Shaw_responders_up_in_oligo_glioma
13	0.17	6 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
14	0.18	23 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
15	0.18	5 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	3 / 10	WEBER_METHYLATED_ICP_IN_SPERM_DN
2	0.003	11 / 182	CAIRO_HEPATOBLASTOMA_CLASSES_DN
3	0.003	3 / 13	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEI
4	0.004	3 / 15	WEBER_METHYLATED_ICP_IN_FIBROBLAST
5	0.005	11 / 196	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
6	0.006	5 / 52	REACTOME_PHOSPHOLIPASE_C_MEDIATED_CASCADE
7	0.007	8 / 124	MIKKELSEN_ES_LCP_WITH_H3K4ME3
8	0.007	3 / 18	MCCABE_HOXC6_TARGETS_DN
9	0.007	4 / 35	FRASOR_RESPONSE_TO_ESTRADIOL_UP
10	0.008	6 / 79	WONG_ENDMETRIUM_CANCER_DN
11	0.009	3 / 20	VALK_AML_WITH_EVI1
12	0.010	5 / 59	MASSARWEH_RESPONSE_TO_ESTRADIOL
13	0.012	12 / 253	NABA_CORE_MATRISOME
14	0.012	3 / 22	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION
15	0.014	26 / 735	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN

HM

Rank	p−value	#in/all	Geneset
1	0.06	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
2	0.23	6 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.26	4 / 116	HALLMARK_SPERMATOGENESIS
4	0.34	4 / 132	HALLMARK_UV_RESPONSE_DN
5	0.35	5 / 175	HALLMARK_XENOBIOTIC_METABOLISM
6	0.37	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	0.39	5 / 183	HALLMARK_APICAL_JUNCTION
8	0.40	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.42	5 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	0.48	1 / 29	HALLMARK_NOTCH_SIGNALING
11	0.52	1 / 33	HALLMARK_ANGIOGENESIS
12	0.54	3 / 127	HALLMARK_COAGULATION
13	0.58	4 / 183	HALLMARK_GLYCOLYSIS
14	0.59	3 / 137	HALLMARK_UV_RESPONSE_UP
15	0.60	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.6	2 / 94	DUMEAUX_Smoking enriched genes
2	1.0	2 / 211	Homuth_BMI−associated−genes_DN
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 147	Homuth_BMI−associated−genes_UP
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−05	162 / 5384	HOPP_Repressed
2	7e−03	115 / 4167	HOPP_Heterochrom
3	6e−02	78 / 2939	HOPP_Poised_promoter
4	8e−02	6 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
5	2e−01	5 / 134	Subero_DLBCL_hyper_meth
6	2e−01	12 / 408	TARTE_Mature plasma cell signature
7	2e−01	3 / 70	LEE_Developmental_regulators
8	2e−01	3 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
9	2e−01	1 / 11	DAVE_BL UP
10	3e−01	1 / 16	WRIGHT_ABC UP
11	3e−01	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
12	3e−01	1 / 18	Aukema_BCL2 UP_BCL6 DN
13	4e−01	2 / 57	LENZ_Stromal signature 2
14	4e−01	1 / 21	Subero_MCL_hyper_meth
15	4e−01	2 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	2 / 54	Hugo_melanoma−all−MET_DN
2	0.5	1 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.01	7 / 108	Ras guanyl−nucleotide exchange factor activity
2	0.01	3 / 21	fibroblast growth factor receptor binding
3	0.01	3 / 23	core promoter proximal region sequence−specific DNA binding
4	0.02	3 / 25	RNA polymerase II transcription corepressor activity
5	0.02	4 / 48	peptide binding
6	0.02	3 / 28	transmembrane receptor protein tyrosine kinase activity
7	0.02	2 / 11	NAD−dependent histone deacetylase activity (H3−K14 specific)
8	0.02	2 / 11	nucleotidyltransferase activity
9	0.04	5 / 82	odorant binding
10	0.04	4 / 59	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
11	0.04	7 / 145	growth factor activity
12	0.05	2 / 16	cGMP binding
13	0.05	6 / 120	protein tyrosine kinase activity
14	0.05	2 / 17	metalloaminopeptidase activity
15	0.05	2 / 17	myosin V binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.001	7 / 73	Stroke, susceptibility to
2	0.004	8 / 113	Ovarian cancer
3	0.004	6 / 68	Glioblastoma multiforme, somatic
4	0.006	3 / 17	Bladder cancer
5	0.008	9 / 156	Breast cancer
6	0.013	4 / 41	Melanoma, cutaneous malignant, 2
7	0.021	7 / 124	Prostate cancer
8	0.024	7 / 127	Melanoma and neural system tumor syndrome
9	0.027	5 / 76	Muscular
10	0.036	4 / 56	Myopathy, nemaline, 3
11	0.044	1 / 2	Hepatic adenoma
12	0.045	6 / 116	Cancer
13	0.052	6 / 120	Hematological
14	0.057	6 / 123	Pancreatic cancer
15	0.061	5 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.09	5 / 105	hsa−miR−605
2	0.12	4 / 85	hsa−miR−220c
3	0.13	1 / 6	hsa−miR−886−5p
4	0.15	3 / 61	hsa−miR−671−5p
5	0.18	2 / 35	hsa−miR−892b
6	0.20	1 / 10	hsa−miR−887
7	0.20	3 / 70	hsa−miR−548b−3p
8	0.21	2 / 38	hsa−miR−1277
9	0.22	3 / 72	hsa−miR−518c
10	0.22	2 / 40	hsa−miR−518b
11	0.24	4 / 113	hsa−miR−376c
12	0.25	1 / 13	hsa−miR−1234
13	0.26	2 / 44	hsa−miR−518e*
14	0.27	1 / 14	hsa−miR−191*
15	0.27	1 / 14	hsa−miR−638

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 14	BENTINK_ras.6
2	0.3	1 / 15	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 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	0.03	5 / 76	WIRTH_Homeostasis
2	0.03	6 / 107	WIRTH_Liver
3	0.07	2 / 19	JONGENEEL_Small Intestine
4	0.12	8 / 220	WIRTH_Testis
5	0.17	5 / 132	WIRTH_Muscle
6	0.24	1 / 12	VAQUERIZAS_Skin_TF
7	0.25	2 / 43	VAQUERIZAS_Placenta_TF
8	0.27	1 / 14	WIRTH_Telencephalon
9	0.27	1 / 14	WIRTH_Cerebellum
10	0.27	1 / 14	JONGENEEL_Peripheral Blood Lymphocytes
11	0.30	2 / 49	JONGENEEL_Retina
12	0.30	1 / 16	VAQUERIZAS_Ovary_TF
13	0.32	1 / 17	VAQUERIZAS_Salivary gland_TF
14	0.33	1 / 18	JONGENEEL_Trachea
15	0.34	4 / 132	Chaussabel_1,7_MHC Ribosomal proteins

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.02	52 / 1753	HEBENSTREIT_low expression TF
2	0.24	1 / 12	MYC_Protein synthesis degradation UP
3	0.33	1 / 18	MYC_Metabolism UP
4	0.35	2 / 55	MYC_Targets UP
5	0.43	15 / 631	ICGC_RxraPcr1_targets
6	0.64	15 / 721	ICGC_SrfPcr2_targets
7	0.73	44 / 2133	ICGC_Mef2_targets
8	0.83	71 / 3507	ICGC_Rad21_targets
9	0.85	13 / 747	ICGC_NrsfPcr2_targets
10	0.89	62 / 3194	ICGC_Irf4_targets
11	0.91	26 / 1466	ICGC_NrsfPcr1_targets
12	0.91	30 / 1669	ICGC_P300_targets
13	0.93	46 / 2497	ICGC_Bcl11_targets
14	0.96	61 / 3348	ICGC_BatfPcr1_targets
15	0.97	24 / 1498	ICGC_Ets1_targets

Correlation Cluster

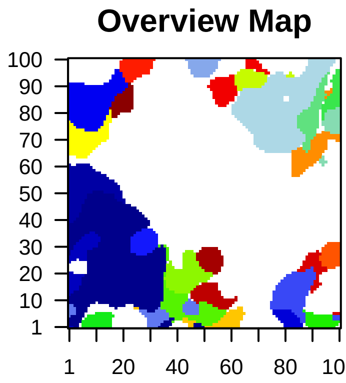
Spot Summary: R

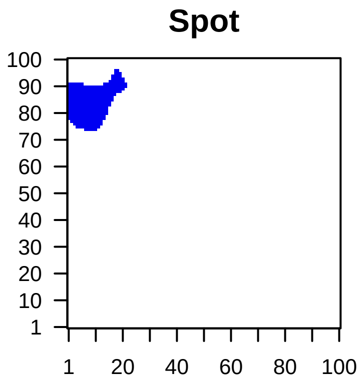
metagenes = 292
genes = 1945

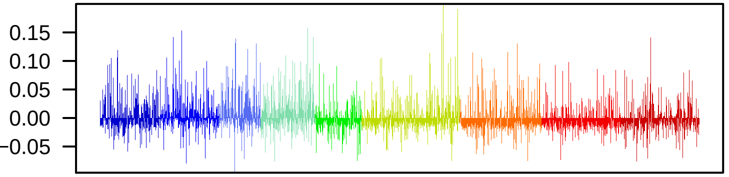
<r> metagenes = 0.93

beta: r2= 2.24 / log p= −Inf

samples with spot = 110 (3.2 %)
A * : 12 (3.5 %)
A C * : 13 (4 %)
A C F * : 14 (6 %)
A F * : 20 (6.5 %)
C F * : 4 (1.5 %)
F * : 15 (2.7 %)
F J * : 17 (3.7 %)
J * : 6 (1.3 %)
N * : 9 (2 %)





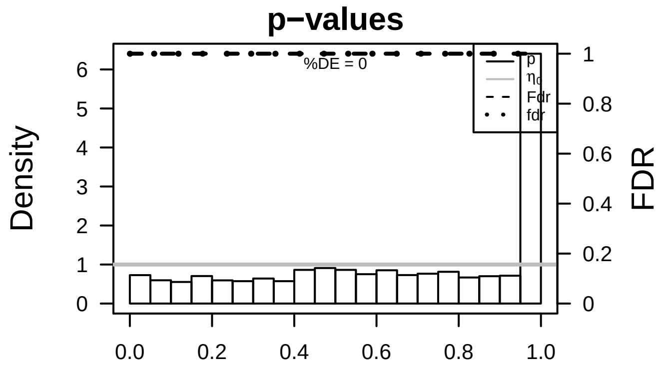


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166406	0.86	−0.57	0.45	ERGIC1	endoplasmic reticulum−golgi intermediate compartment 1 [Sc
2	ILMN_324781	0.75	−0.41	0.31		RAS p21 protein activator 4CD, pseudogene [Source:HGNC S
3	ILMN_168507	0.72	−0.49	0.28	TELO2	telomere maintenance 2 [Source:HGNC Symbol;Acc:HGNC:2
4	ILMN_326869	0.72	−0.54	0.25		
5	ILMN_330822	0.69	−0.43	0.34	MIR1282	microRNA 1282 [Source:HGNC Symbol;Acc:HGNC:35360]
6	ILMN_324665	0.68	−0.42	0.33		
7	ILMN_186927	0.68	−0.4	0.31		
8	ILMN_165761	0.65	−0.35	0.68	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
9	ILMN_170981	0.63	−0.45	0.3	SLC35A5	solute carrier family 35 member A5 [Source:HGNC Symbol;A
10	ILMN_134394	0.62	−0.4	0.31		
11	ILMN_180048	0.61	−0.38	0.36	CT47B1	cancer/testis antigen family 47, member B1 [Source:HGNC S
12	ILMN_224967	0.57	−0.36	0.64	LSR	lipolysis stimulated lipoprotein receptor [Source:HGNC Symb
13	ILMN_328824	0.57	−0.43	0.52		
14	ILMN_183964	0.56	−0.31	0.62	LINC00323	long intergenic non−protein coding RNA 323 [Source:HGNC S
15	ILMN_176111	0.56	−0.35	0.64	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
16	ILMN_178092	0.56	−0.32	0.66	SLC43A1	solute carrier family 43 member 1 [Source:HGNC Symbol;Acc
17	ILMN_190200	0.55	−0.35	0.43		
18	ILMN_165712	0.55	−0.34	0.39	PTPRU	protein tyrosine phosphatase, receptor type U [Source:HGNC
19	ILMN_324766	0.55	−0.36	0.67		
20	ILMN_170872	0.55	−0.44	0.13		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−17	293 / 3639	Chror	1_TssP_Fibroblasts
2	3e−13	307 / 4169	Chror	10_ReprPC_Fibroblasts
3	4e−13	167 / 1895	Colon	EnhP_Colon
4	1e−12	239 / 3068	Chror	8_EnhP_Fibroblasts
5	1e−12	245 / 3173	Colon	ReprPC_Colon
6	2e−11	161 / 1893	Brain	Overlap_fetal_midbrain_TssF
7	2e−11	223 / 2894	Colon	TssP_Colon
8	4e−11	208 / 2660	Chror	8_EnhP_Melanocytes
9	9e−11	253 / 3438	Chror	10_ReprPC_Melanocytes
10	2e−10	210 / 2740	Colon	ReprPCWk_Colon
11	6e−10	360 / 5384	Lympl	HOPP_Repressed
12	1e−09	287 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
13	5e−09	283 / 4107	Chror	9_ReprPCWk_Fibroblasts
14	1e−08	292 / 4304	Chror	9_ReprPCWk_Melanocytes
15	2e−08	247 / 3523	Chror	1_TssP_Melanocytes
16	9e−08	113 / 1360	Brain	Mid_Frontal_Lobe_TssP
17	1e−06	178 / 2516	Chror	11_K9K27me3_Melanocytes
18	2e−06	165 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
19	2e−06	115 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
20	2e−06	183 / 2620	Chror	1_TssP_Neuronal_Progenitor
21	2e−05	129 / 1789	Chror	8_EnhP_Neuronal_Progenitor
22	2e−05	88 / 1119	Brain	Overlap_fetal_midbrain_TssA
23	4e−05	194 / 2939	Lympl	HOPP_Poised_promoter
24	4e−05	200 / 3046	Brain	Fetal_TssA
25	5e−05	61 / 717	Chror	11_K9K27me3_Fibroblasts
26	5e−05	235 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
27	7e−05	543 / 9530	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
28	8e−05	62 / 746	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
29	1e−04	178 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
30	1e−04	66 / 819	Brain	Overlap_fetal_midbrain_TssP
31	1e−04	8 / 32	miRN	hsa−miR−1229
32	2e−04	104 / 1448	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
33	2e−04	9 / 43	GSEA	MCCLUNG_DELTA_FOSB_TARGETS_2WK
34	3e−04	174 / 2700	Brain	Fetal_TxTrans
35	6e−04	140 / 2127	Brain	Mid_Frontal_Lobe_K9K27me3
36	7e−04	41 / 478	Refer	WIRTH_Nervous System
37	1e−03	88 / 1252	CC	integral component of plasma membrane
38	1e−03	44 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
39	1e−03	3 / 5	GSEA	LU_TUMOR_ENDOTHELIAL_MARKERS_DN
40	1e−03	15 / 122	BP	sensory perception of sound



Aging

Rank	p−value	#in/all	Geneset
1	0.2	5 / 58	TESCHENDORFF_age_hypermethylated
2	0.6	7 / 142	HORVATH_aging_genes meth UP
3	0.7	5 / 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	0.001	15 / 122	sensory perception of sound
2	0.001	13 / 99	axonogenesis
3	0.002	6 / 26	chromatin modification
4	0.002	4 / 11	hyaluronan metabolic process
5	0.002	5 / 19	histone H3 deacetylation
6	0.002	4 / 12	biosynthetic process
7	0.002	4 / 12	response to lead ion
8	0.003	37 / 457	regulation of transcription from RNA polymerase II promoter
9	0.004	4 / 14	positive regulation of glycogen biosynthetic process
10	0.005	9 / 64	memory
11	0.006	10 / 79	regulation of membrane potential
12	0.007	9 / 68	forebrain development
13	0.007	4 / 16	positive regulation of dendrite extension
14	0.009	5 / 26	glycosaminoglycan metabolic process
15	0.009	5 / 26	positive regulation of establishment of protein localization to plasma membran

Brain

Rank	p−value	#in/all	Geneset
1	2e−11	161 / 1893	Overlap_fetal_midbrain_TssF
2	1e−09	287 / 4112	Mid_Frontal_Lobe_ReprPC
3	9e−08	113 / 1360	Mid_Frontal_Lobe_TssP
4	2e−06	115 / 1476	Overlap_fetal_midbrain_TxTrans
5	2e−05	88 / 1119	Overlap_fetal_midbrain_TssA
6	4e−05	200 / 3046	Fetal_TssA
7	1e−04	178 / 2709	Mid_Frontal_Lobe_HetRpts
8	1e−04	66 / 819	Overlap_fetal_midbrain_TssP
9	3e−04	174 / 2700	Fetal_TxTrans
10	6e−04	140 / 2127	Mid_Frontal_Lobe_K9K27me3
11	2e−03	28 / 304	Mid_Frontal_Lobe_TssA
12	8e−03	188 / 3164	Mid_Frontal_Lobe_ZNF
13	3e−02	33 / 465	Mid_Frontal_Lobe_TxTrans
14	5e−02	52 / 818	Mid_Frontal_Lobe_Het
15	6e−02	22 / 307	Fetal_ReprPC

Cancer

Rank	p−value	#in/all	Geneset
1	0.09	1 / 15	LIU_PROSTATE_CANCER_DN
2	0.10	2 / 12	LIU_BREAST_CANCER
3	0.14	11 / 150	PanCan_MAPK_geneset_nanostring
4	0.14	2 / 13	GENTLES_modul2
5	0.17	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.17	7 / 91	PanCan_TXmisReg_geneset_nanostring
7	0.22	1 / 13	LIU_LIVER_CANCER
8	0.37	1 / 9	GENTLES_modul3
9	0.41	3 / 46	PanCan_DNARepair_geneset_nanostring
10	0.44	0 / 14	LIU_PROSTATE_CANCER_UP
11	0.44	7 / 125	PanCan_CC+Apop_geneset_nanostring
12	0.46	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	0.49	1 / 13	GENTLES_modul6
14	0.49	1 / 13	GENTLES_modul12
15	0.49	27 / 527	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	0.001	88 / 1252	integral component of plasma membrane
2	0.002	24 / 249	axon
3	0.009	4 / 17	pericentriolar material
4	0.009	8 / 59	presynaptic membrane
5	0.010	5 / 27	presynaptic active zone
6	0.019	10 / 93	ubiquitin ligase complex
7	0.020	7 / 55	synaptic vesicle membrane
8	0.020	3 / 12	paranode region of axon
9	0.021	5 / 32	histone deacetylase complex
10	0.026	24 / 311	neuronal cell body
11	0.031	3 / 14	axolemma
12	0.033	5 / 36	condensed nuclear chromosome
13	0.036	6 / 49	axon terminus
14	0.037	9 / 90	chromatin
15	0.042	8 / 78	Golgi lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.04	61 / 959	Chr 16
2	0.06	87 / 1467	Chr 19
3	0.10	69 / 1170	Chr 7
4	0.10	77 / 1318	Chr 17
5	0.10	86 / 1492	Chr 2
6	0.14	19 / 289	Chr 21
7	0.23	25 / 422	Chr 13
8	0.37	29 / 536	Chr 22
9	0.45	5 / 87	Chr Y
10	0.52	117 / 2323	Chr 1
11	0.52	48 / 954	Chr 9
12	0.53	50 / 994	Chr X
13	0.57	38 / 769	Chr 15
14	0.67	43 / 904	Chr 10
15	0.70	55 / 1160	Chr 12

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−17	293 / 3639	1_TssP_Fibroblasts
2	3e−13	307 / 4169	10_ReprPC_Fibroblasts
3	1e−12	239 / 3068	8_EnhP_Fibroblasts
4	4e−11	208 / 2660	8_EnhP_Melanocytes
5	9e−11	253 / 3438	10_ReprPC_Melanocytes
6	5e−09	283 / 4107	9_ReprPCWk_Fibroblasts
7	1e−08	292 / 4304	9_ReprPCWk_Melanocytes
8	2e−08	247 / 3523	1_TssP_Melanocytes
9	1e−06	178 / 2516	11_K9K27me3_Melanocytes
10	2e−06	165 / 2297	10_ReprPC_Neuronal_Progenitor
11	2e−06	183 / 2620	1_TssP_Neuronal_Progenitor
12	2e−05	129 / 1789	8_EnhP_Neuronal_Progenitor
13	5e−05	61 / 717	11_K9K27me3_Fibroblasts
14	5e−05	235 / 3691	9_ReprPCWk_Neuronal_Progenitor
15	1e−02	333 / 5956	3_TssF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−13	167 / 1895	EnhP_Colon
2	1e−12	245 / 3173	ReprPC_Colon
3	2e−11	223 / 2894	TssP_Colon
4	2e−10	210 / 2740	ReprPCWk_Colon
5	7e−05	543 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
6	3e−03	31 / 366	K9K27me3_Colon
7	5e−03	586 / 10779	Enh_Colon
8	7e−03	44 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	1e−02	36 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
10	1e−02	7 / 52	Marisa_CRC−cluster−e
11	2e−02	164 / 2810	EnhA_Colon
12	3e−02	254 / 4526	Quies1_Colon
13	4e−02	47 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	5e−02	17 / 217	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	6e−02	50 / 789	TxEnhG2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.003	183 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.004	14 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
3	0.006	3 / 8	Shaw_responders_up_in_oligo_glioma
4	0.022	6 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
5	0.055	7 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
6	0.068	8 / 86	laffaire_hypermeth_LGG_vs_control
7	0.077	13 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
8	0.079	8 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
9	0.097	20 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
10	0.103	2 / 11	VERHAAK_Brain
11	0.120	2 / 12	Phillips MES up vs Prolif & PN
12	0.120	5 / 52	OL vs. OPC
13	0.120	5 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
14	0.127	5 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
15	0.128	11 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−05	62 / 746	MARTENS_TRETINOIN_RESPONSE_UP
2	2e−04	104 / 1448	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
3	2e−04	9 / 43	MCCLUNG_DELTA_FOSB_TARGETS_2WK
4	1e−03	44 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
5	1e−03	3 / 5	LU_TUMOR_ENDOTHELIAL_MARKERS_DN
6	2e−03	21 / 204	COLDREN_GEFITINIB_RESISTANCE_DN
7	2e−03	21 / 207	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
8	2e−03	10 / 68	KIM_GLIS2_TARGETS_UP
9	2e−03	66 / 916	NABA_MATRISOME
10	2e−03	72 / 1021	BENPORATH_ES_WITH_H3K27ME3
11	3e−03	34 / 405	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
12	3e−03	19 / 188	SANSOM_APC_TARGETS_REQUIRE_MYC
13	3e−03	4 / 13	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
14	4e−03	8 / 51	LAU_APOPTOSIS_CDKN2A_UP
15	4e−03	6 / 31	PID_SYNDECAN_4_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.02	16 / 177	HALLMARK_KRAS_SIGNALING_DN
2	0.05	5 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	0.09	11 / 137	HALLMARK_UV_RESPONSE_UP
4	0.09	14 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.13	13 / 183	HALLMARK_APICAL_JUNCTION
6	0.15	4 / 41	HALLMARK_APICAL_SURFACE
7	0.16	13 / 189	HALLMARK_HYPOXIA
8	0.22	7 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	0.23	12 / 186	HALLMARK_MYOGENESIS
10	0.26	11 / 173	HALLMARK_E2F_TARGETS
11	0.29	11 / 179	HALLMARK_G2M_CHECKPOINT
12	0.30	10 / 162	HALLMARK_ALLOGRAFT_REJECTION
13	0.31	6 / 91	HALLMARK_ANDROGEN_RESPONSE
14	0.33	11 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	0.35	8 / 132	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	8 / 94	DUMEAUX_Smoking enriched genes
2	0.5	2 / 31	DUMEAUX_Fasting enriched genes
3	0.6	1 / 16	Huan_blood−pressure_DBP−signature
4	0.6	1 / 18	Huan_blood−pressure_SBP−signature
5	0.9	5 / 147	Homuth_BMI−associated−genes_UP
6	1.0	6 / 211	Homuth_BMI−associated−genes_DN
7	1.0	0 / 10	DUMEAUX_Smoking literature genes up
8	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1.0	0 / 17	DUMEAUX_High bmi enriched genes

Lympnoma

Rank	p−value	#in/all	Geneset
1	6e−10	360 / 5384	HOPP_Repressed
2	4e−05	194 / 2939	HOPP_Poised_promoter
3	4e−03	15 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
4	4e−03	15 / 138	WIRTH_lymphoma937_spot G
5	1e−01	15 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
6	1e−01	7 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
7	2e−01	6 / 75	SPANG_LPS 6hrs DN
8	2e−01	15 / 232	WIRTH_lymphoma937_spot B
9	2e−01	145 / 2701	HOPP_Repetitive
10	2e−01	20 / 331	SPANG_CD40 6hrs UP
11	2e−01	2 / 19	DAVE_c−myc BL UP
12	3e−01	14 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
13	3e−01	17 / 286	ZHANG_DLBCL mutated
14	3e−01	5 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	3e−01	2 / 21	Subero_MCL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	2 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	0.29	4 / 54	Hugo_melanoma−all−MET_DN
3	0.75	1 / 27	Hugo_melanoma−all−LEF1_UP
4	0.79	1 / 30	Hugo_melanoma−all−MET_UP
5	0.89	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.001	9 / 54	serine−type peptidase activity
2	0.003	18 / 173	ubiquitin protein ligase activity
3	0.007	13 / 120	protein tyrosine kinase activity
4	0.009	4 / 17	G−protein coupled peptide receptor activity
5	0.011	7 / 49	transcription regulatory region sequence−specific DNA binding
6	0.012	3 / 10	sodium−dependent phosphate transmembrane transporter activity
7	0.014	6 / 40	mRNA 3'−UTR binding
8	0.015	7 / 52	SNARE binding
9	0.016	3 / 11	NAD−dependent histone deacetylase activity (H3−K14 specific)
10	0.016	3 / 11	oxalate transmembrane transporter activity
11	0.016	3 / 11	sulfate transmembrane transporter activity
12	0.016	3 / 11	ubiquitin−ubiquitin ligase activity
13	0.016	4 / 20	anion:anion antiporter activity
14	0.019	4 / 21	insulin−like growth factor binding
15	0.020	3 / 12	hormone binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 2	Adenomas, multiple colorectal
2	0.3	1 / 6	Thrombocytopenic purpurea, autoimmune
3	0.3	1 / 7	Thyroid carcinoma, papillary
4	0.4	1 / 9	Systemic lupus erythematosus, susceptibility
5	0.5	2 / 30	Systemic lupus erythematosus (SLE)
6	0.5	1 / 15	Supravalvar aortic stenosis
7	0.5	3 / 56	Myopathy, nemaline, 3
8	0.6	1 / 17	Thyroid carcinoma, follicular
9	0.6	1 / 18	Hodgkin lymphoma
10	0.6	2 / 41	Melanoma, cutaneous malignant, 2
11	0.7	3 / 68	Glioblastoma multiforme, somatic
12	0.7	2 / 47	Cervical cancer, somatic
13	0.7	1 / 23	Esophageal cancer
14	0.7	2 / 48	Multiple myeloma
15	0.7	3 / 73	Stroke, susceptibility to

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	8 / 32	hsa−miR−1229
2	1e−02	11 / 100	hsa−miR−590−5p
3	2e−02	20 / 235	hsa−miR−26a
4	2e−02	7 / 54	hsa−miR−504
5	2e−02	19 / 225	hsa−miR−181b
6	2e−02	3 / 12	hsa−miR−652
7	2e−02	20 / 243	hsa−miR−26b
8	2e−02	5 / 33	hsa−miR−1296
9	2e−02	8 / 70	hsa−miR−548b−3p
10	3e−02	16 / 190	hsa−miR−330−3p
11	3e−02	9 / 88	hsa−miR−608
12	4e−02	5 / 39	hsa−miR−484
13	5e−02	17 / 217	hsa−miR−185
14	5e−02	6 / 53	hsa−miR−431
15	5e−02	15 / 188	hsa−miR−548d−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	2 / 15	GUSTAFSON_PI3K_DN
2	0.5	1 / 13	BENTINK_e2f3.1
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
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	7e−04	41 / 478	WIRTH_Nervous System
2	3e−02	4 / 25	VAQUERIZAS_Adrenal cortex_TF
3	4e−02	8 / 76	WIRTH_Homeostasis
4	4e−02	12 / 134	WIRTH_Mucosa
5	4e−02	10 / 107	WIRTH_Liver
6	4e−02	5 / 39	VAQUERIZAS_Testis_TF
7	8e−02	4 / 32	JONGENEEL_Placenta
8	9e−02	3 / 21	JONGENEEL_Salivary Gland
9	9e−02	2 / 10	JONGENEEL_Colon
10	9e−02	2 / 10	JONGENEEL_Pituitary Gland
11	1e−01	5 / 50	WIRTH_Placenta
12	1e−01	16 / 231	Chaussabel_2,5_Immune related molecules
13	2e−01	2 / 15	VAQUERIZAS_Fetal liver_TF
14	2e−01	4 / 44	VAQUERIZAS_Whole brain_TF
15	2e−01	3 / 30	VAQUERIZAS_Smooth muscle_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.02	3 / 13	Alternative lengthening of telomeres
2	0.40	2 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	2 / 5	MYC_TFs
2	0.04	104 / 1753	HEBENSTREIT_low expression TF
3	0.05	48 / 747	ICGC_NrsfPcr2_targets
4	0.10	1 / 2	MYC_ECM cell adhesion DOWN
5	0.28	184 / 3507	ICGC_Rad21_targets
6	0.37	1 / 9	MYC_Targets DOWN
7	0.43	128 / 2497	ICGC_Bcl11_targets
8	0.46	1 / 12	MYC_Protein synthesis degradation UP
9	0.48	140 / 2759	ICGC_Bcl3_targets
10	0.50	76 / 1501	ICGC_Usf1_targets
11	0.55	36 / 721	ICGC_SrfPcr2_targets
12	0.59	36 / 733	ICGC_Atf3_targets
13	0.61	1 / 18	MYC_Metabolism UP
14	0.61	72 / 1466	ICGC_NrsfPcr1_targets
15	0.63	133 / 2704	ICGC_Pbx3_targets

Correlation Cluster

Spot Summary: S

metagenes = 143
genes = 273

<r> metagenes = 0.93
<r> genes = 0.04
beta: r2= 0.38 / log p= −Inf

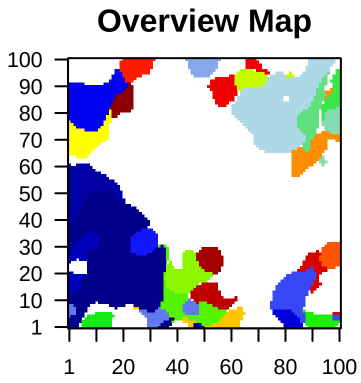
samples with spot = 3 (0.1 %)
F * : 3 (0.5 %)

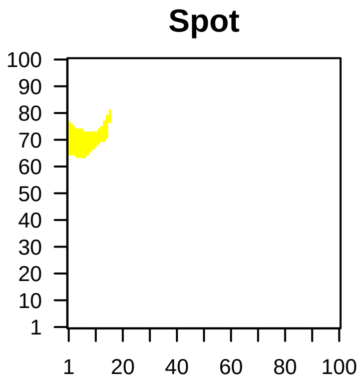
Spot Genelist

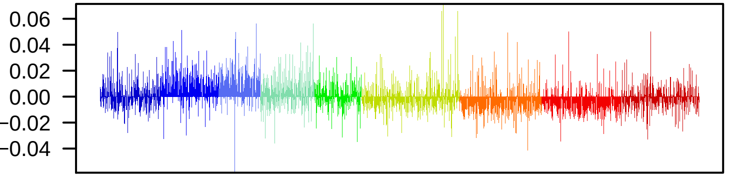
Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_219415	0.41	−0.21	0.21	ADAM29	ADAM metallopeptidase domain 29 [Source:HGNC Symbol;A
2	ILMN_172449	0.37	−0.3	0.29	ABI2	abl interactor 2 [Source:HGNC Symbol;Acc:HGNC:24011]
3	ILMN_330795	0.31	−0.21	0.18	L3MBTL4	l(3)mbt−like 4 (Drosophila) [Source:HGNC Symbol;Acc:HGN
4	ILMN_324575	0.29	−0.23	0.24		
5	ILMN_186191	0.29	−0.22	0.23		
6	ILMN_167558	0.28	−0.2	0.25	HTRA4	HtrA serine peptidase 4 [Source:HGNC Symbol;Acc:HGNC:2
7	ILMN_166509	0.28	−0.18	0.21	TTC34	tetratricopeptide repeat domain 34 [Source:HGNC Symbol;Ac
8	ILMN_191704	0.28	−0.2	0.19		
9	ILMN_172289	0.28	−0.2	0.22	CHST10	carbohydrate sulfotransferase 10 [Source:HGNC Symbol;Acc
10	ILMN_189594	0.28	−0.21	0.24		
11	ILMN_134387	0.28	−0.2	0.17		
12	ILMN_227914	0.27	−0.2	0.25	JADE3	jade family PHD finger 3 [Source:HGNC Symbol;Acc:HGNC:2
13	ILMN_173884	0.27	−0.2	0.27	SLC9A2	solute carrier family 9 member A2 [Source:HGNC Symbol;Ac
14	ILMN_183218	0.27	−0.24	0.25		
15	ILMN_165575	0.27	−0.19	0.24	LINC01296	double homeobox A pseudogene 8 [Source:EntrezGene;Acc:
16	ILMN_328311	0.27	−0.21	0.2		
17	ILMN_321928	0.27	−0.21	0.21		
18	ILMN_326159	0.27	−0.18	0.21	LOC100128770	
19	ILMN_176429	0.27	−0.2	0.15		
20	ILMN_176567	0.27	−0.21	0.17	ALS2CR12	amyotrophic lateral sclerosis 2 chromosome region candidate

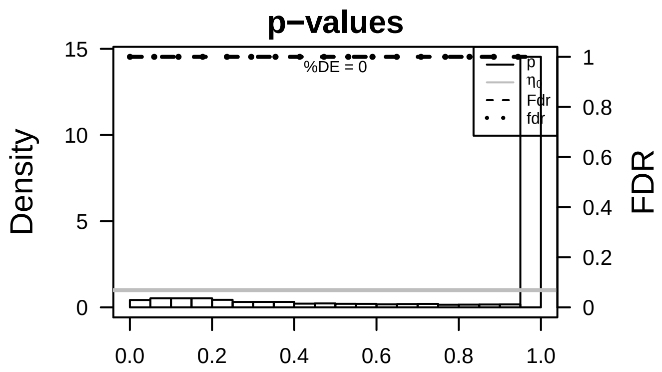
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−09	43 / 2516	Chror	11_K9K27me3_Melanocytes
2	1e−07	57 / 4304	Chror	9_ReprPCWk_Melanocytes
3	2e−07	55 / 4169	Chror	10_ReprPC_Fibroblasts
4	9e−07	53 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	1e−05	44 / 3438	Chror	10_ReprPC_Melanocytes
6	2e−05	60 / 5384	Lympl	HOPP_Repressed
7	5e−05	39 / 3046	Brain	Fetal_TssA
8	6e−05	44 / 3639	Chror	1_TssP_Fibroblasts
9	8e−05	35 / 2660	Chror	8_EnhP_Melanocytes
10	1e−04	15 / 717	Chror	11_K9K27me3_Fibroblasts
11	2e−04	34 / 2700	Brain	Fetal_TxTrans
12	3e−04	37 / 3068	Chror	8_EnhP_Fibroblasts
13	4e−04	26 / 1893	Brain	Overlap_fetal_midbrain_TssF
14	6e−04	7 / 210	GSEA	NABA_ECM_REGULATORS
15	6e−04	13 / 663	GSEA	NABA_MATRISOME_ASSOCIATED
16	7e−04	2 / 6	GSEA	TCGA_GLIOBLASTOMA_MUTATED
17	7e−04	24 / 1753	TF	HEBENSTREIT_low expression TF
18	8e−04	5 / 107	Refer	WIRTH_Liver
19	8e−04	15 / 869	Brain	Mid_Frontal_Lobe_EnhG
20	1e−03	26 / 2031	Chror	12_Het_Melanocytes
21	1e−03	44 / 4167	Lympl	HOPP_Heterochrom
22	1e−03	9 / 383	BP	proteolysis
23	1e−03	31 / 2630	Brain	Fetal_TssF
24	1e−03	16 / 1012	Brain	Mid_Frontal_Lobe_Enh
25	2e−03	9 / 398	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
26	2e−03	2 / 10	GSEA	PID_ALK2_PATHWAY
27	2e−03	46 / 4526	Colon	Quies1_Colon
28	2e−03	6 / 193	Glio	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
29	2e−03	6 / 193	GSEA	CAIRO_LIVER_DEVELOPMENT_DN
30	2e−03	2 / 11	BP	enteric nervous system development
31	2e−03	39 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
32	3e−03	4 / 84	Glio	GIEZELT_GBM_STS_up_VS_LTS
33	3e−03	30 / 2620	Chror	1_TssP_Neuronal_Progenitor
34	3e−03	3 / 41	BP	ovarian follicle development
35	3e−03	2 / 12	GSEA	BIOCARTA_FIBRINOLYSIS_PATHWAY
36	3e−03	3 / 44	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
37	4e−03	37 / 3523	Chror	1_TssP_Melanocytes
38	4e−03	3 / 46	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
39	4e−03	14 / 916	GSEA	NABA_MATRISOME
40	4e−03	34 / 3173	Colon	ReprPC_Colon









Aging

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

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 16	BEN−PORATH_DN
2	0.1	1 / 16	GENTLES_modul16
3	0.1	2 / 91	PanCan_TXmisReg_geneset_nanostring
4	0.2	1 / 24	PanCan_Notch_geneset_nanostring
5	0.2	0 / 15	LIU_PROSTATE_CANCER_DN
6	0.2	2 / 117	PanCan_Driver_Gene_geneset_nanostring
7	0.2	1 / 39	ZHANG_MM up
8	0.2	2 / 136	PanCan_RAS_geneset_nanostring
9	0.3	0 / 13	RHODES_CANCER_META_SIGNATURE
10	0.3	1 / 54	KUIPER_MM poor survival
11	0.4	0 / 14	LIU_COMMON_CANCER_GENES
12	0.4	2 / 193	PanCan_PI3K_geneset_nanostring
13	0.4	1 / 82	PanCan_JAK−ST_geneset_nanostring
14	0.5	4 / 527	Lembcke_Normal vs Adenoma
15	0.6	1 / 125	PanCan_CC+Apop_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−09	43 / 2516	11_K9K27me3_Melanocytes
2	1e−07	57 / 4304	9_ReprPCWk_Melanocytes
3	2e−07	55 / 4169	10_ReprPC_Fibroblasts
4	9e−07	53 / 4107	9_ReprPCWk_Fibroblasts
5	1e−05	44 / 3438	10_ReprPC_Melanocytes
6	6e−05	44 / 3639	1_TssP_Fibroblasts
7	8e−05	35 / 2660	8_EnhP_Melanocytes
8	1e−04	15 / 717	11_K9K27me3_Fibroblasts
9	3e−04	37 / 3068	8_EnhP_Fibroblasts
10	1e−03	26 / 2031	12_Het_Melanocytes
11	2e−03	39 / 3691	9_ReprPCWk_Neuronal_Progenitor
12	3e−03	30 / 2620	1_TssP_Neuronal_Progenitor
13	4e−03	37 / 3523	1_TssP_Melanocytes
14	7e−03	26 / 2315	13_HetRpts_Melanocytes
15	3e−02	14 / 1163	12_Het_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−04	7 / 210	NABA_ECM_REGULATORS
2	6e−04	13 / 663	NABA_MATRISOME_ASSOCIATED
3	7e−04	2 / 6	TCGA_GLIOBLASTOMA_MUTATED
4	2e−03	9 / 398	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
5	2e−03	2 / 10	PID_ALK2_PATHWAY
6	2e−03	6 / 193	CAIRO_LIVER_DEVELOPMENT_DN
7	3e−03	2 / 12	BIOCARTA_FIBRINOLYSIS_PATHWAY
8	3e−03	3 / 44	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
9	4e−03	3 / 46	BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
10	4e−03	14 / 916	NABA_MATRISOME
11	4e−03	3 / 49	BORLAK_LIVER_CANCER_EGF_UP
12	4e−03	2 / 15	HE_PTEN_TARGETS_UP
13	5e−03	12 / 746	MARTENS_TRETINOIN_RESPONSE_UP
14	5e−03	2 / 16	LEIN_LOCALIZED_TO_DISTAL_AND_PROXIMAL_DENDRITES
15	5e−03	5 / 166	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	60 / 5384	HOPP_Repressed
2	1e−03	44 / 4167	HOPP_Heterochrom
3	8e−03	31 / 2939	HOPP_Poised_promoter
4	1e−02	4 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
5	1e−02	4 / 138	WIRTH_lymphoma937_spot G
6	1e−01	1 / 19	DAVE_Immune response 2
7	1e−01	4 / 286	ZHANG_DLBCL mutated
8	2e−01	3 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
9	2e−01	2 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
10	4e−01	4 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
11	4e−01	1 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
12	4e−01	20 / 2701	HOPP_Repetitive
13	4e−01	1 / 70	LEE_Developmental_regulators
14	4e−01	1 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	4e−01	4 / 464	WIRTH_lymphoma937_spot I

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 76	Muscular
2	0.5	1 / 116	Cancer
3	0.6	1 / 127	Melanoma and neural system tumor syndrome
4	0.7	1 / 156	Breast cancer
5	1.0	0 / 7	Thyroid carcinoma, papillary
6	1.0	0 / 123	Pancreatic cancer
7	1.0	0 / 68	Glioblastoma multiforme, somatic
8	1.0	0 / 63	Gastrointestinal
9	1.0	0 / 3	Pituitary adenoma
10	1.0	0 / 95	Colorectal cancer
11	1.0	0 / 2	Adenomas, multiple colorectal
12	1.0	0 / 124	Prostate cancer
13	1.0	0 / 48	Alzheimer disease, susceptibility to
14	1.0	0 / 7	Schizophrenia, susceptibility to
15	1.0	0 / 20	Parkinson disease

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−04	5 / 107	WIRTH_Liver
2	2e−02	8 / 478	WIRTH_Nervous System
3	2e−02	2 / 32	VAQUERIZAS_Liver_TF
4	3e−02	2 / 43	VAQUERIZAS_Placenta_TF
5	4e−02	2 / 49	JONGENEEL_Retina
6	5e−02	5 / 289	JONGENEEL_Testis
7	6e−02	4 / 220	WIRTH_Testis
8	7e−02	1 / 10	JONGENEEL_Pituitary Gland
9	7e−02	4 / 231	Chaussabel_2,5_Immune related molecules
10	8e−02	1 / 12	VAQUERIZAS_Kidney_TF
11	9e−02	2 / 76	WIRTH_Homeostasis
12	1e−01	1 / 16	VAQUERIZAS_Pancreas_TF
13	1e−01	1 / 17	VAQUERIZAS_Adrenal gland_TF
14	1e−01	1 / 17	JONGENEEL_Lung
15	2e−01	1 / 24	VAQUERIZAS_Pituitary_TF

BP

Rank	p−value	#in/all	Geneset
1	0.001	9 / 383	proteolysis
2	0.002	2 / 11	enteric nervous system development
3	0.003	3 / 41	ovarian follicle development
4	0.004	3 / 47	negative regulation of cell differentiation
5	0.006	3 / 56	negative regulation of transforming growth factor beta receptor signaling pathw
6	0.008	2 / 20	negative regulation of retinoic acid receptor signaling pathway
7	0.009	2 / 21	fibrinolysis
8	0.009	4 / 121	organ morphogenesis
9	0.010	2 / 22	liver regeneration
10	0.010	2 / 23	phosphatidylinositol 3−kinase signaling
11	0.010	2 / 23	positive regulation of exocytosis
12	0.012	2 / 25	pancreas development
13	0.013	2 / 26	adipose tissue development
14	0.014	3 / 75	regulation of phosphatidylinositol 3−kinase signaling
15	0.015	2 / 28	cellular response to epidermal growth factor stimulus

CC

Rank	p−value	#in/all	Geneset
1	0.03	3 / 93	blood microparticle
2	0.04	2 / 45	extracellular vesicle
3	0.04	2 / 49	platelet alpha granule lumen
4	0.05	2 / 50	endocytic vesicle
5	0.05	2 / 52	microvillus
6	0.05	5 / 295	cell−cell adherens junction
7	0.07	1 / 10	Gemini of coiled bodies
8	0.07	1 / 10	ionotropic glutamate receptor complex
9	0.07	1 / 11	phosphatidylinositol 3−kinase complex
10	0.07	1 / 11	SMN complex
11	0.07	1 / 11	TORC2 complex
12	0.08	2 / 67	filopodium
13	0.08	1 / 12	eukaryotic translation initiation factor 3 complex
14	0.08	1 / 13	intrinsic component of the cytoplasmic side of the plasma membrane
15	0.08	1 / 13	mitochondrial envelope

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	46 / 4526	Quies1_Colon
2	0.004	34 / 3173	ReprPC_Colon
3	0.004	2 / 15	TCGA_Mutated−in−CRC_hypermutated
4	0.005	81 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
5	0.005	30 / 2740	ReprPCWk_Colon
6	0.005	16 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
7	0.006	31 / 2894	TssP_Colon
8	0.007	2 / 19	Vilar_hypermutated−in−CRC
9	0.008	10 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	0.015	15 / 1186	HetRpts_Colon
11	0.020	1 / 3	Juehling_HNPCC−mutated−in−6−to−8
12	0.027	1 / 4	Budinska_C_CIMP−H−like_DOWN
13	0.041	5 / 278	Kosinski_top−crypt−long−list
14	0.043	6 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	0.053	1 / 8	Marisa_CRC−C2

HM

Rank	p−value	#in/all	Geneset
1	0.01	4 / 127	HALLMARK_COAGULATION
2	0.07	3 / 138	HALLMARK_FATTY_ACID_METABOLISM
3	0.12	3 / 177	HALLMARK_KRAS_SIGNALING_DN
4	0.13	3 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.18	1 / 29	HALLMARK_NOTCH_SIGNALING
6	0.20	1 / 33	HALLMARK_ANGIOGENESIS
7	0.24	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	0.29	1 / 50	HALLMARK_TGF_BETA_SIGNALING
9	0.36	2 / 187	HALLMARK_COMPLEMENT
10	0.46	1 / 91	HALLMARK_ANDROGEN_RESPONSE
11	0.46	1 / 91	HALLMARK_PEROXISOME
12	0.50	1 / 103	HALLMARK_BILE_ACID_METABOLISM
13	0.59	1 / 130	HALLMARK_DNA_REPAIR
14	0.59	1 / 132	HALLMARK_UV_RESPONSE_DN
15	0.61	1 / 137	HALLMARK_UV_RESPONSE_UP

Melanoma

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	2 / 24	hsa−miR−99b
2	0.04	5 / 271	hsa−miR−363
3	0.04	2 / 48	hsa−miR−610
4	0.05	3 / 123	hsa−miR−646
5	0.10	4 / 263	hsa−miR−92b
6	0.11	4 / 272	hsa−miR−92a
7	0.13	1 / 20	hsa−miR−516a−5p
8	0.14	3 / 190	hsa−miR−128
9	0.14	3 / 191	hsa−miR−222
10	0.14	4 / 298	hsa−miR−25
11	0.15	3 / 198	hsa−miR−221
12	0.16	1 / 25	hsa−miR−432*
13	0.16	2 / 104	hsa−miR−33b
14	0.16	1 / 26	hsa−miR−675
15	0.18	2 / 113	hsa−miR−154

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	5e−05	39 / 3046	Fetal_TssA
2	2e−04	34 / 2700	Fetal_TxTrans
3	4e−04	26 / 1893	Overlap_fetal_midbrain_TssF
4	8e−04	15 / 869	Mid_Frontal_Lobe_EnhG
5	1e−03	31 / 2630	Fetal_TssF
6	1e−03	16 / 1012	Mid_Frontal_Lobe_Enh
7	1e−02	13 / 924	Mid_Frontal_Lobe_TssF
8	1e−02	17 / 1360	Mid_Frontal_Lobe_TssP
9	2e−02	14 / 1115	Overlap_fetal_midbrain_EnhG
10	4e−02	37 / 4112	Mid_Frontal_Lobe_ReprPC
11	4e−02	3 / 110	Overlap_fetal_midbrain_Tx
12	4e−02	7 / 465	Mid_Frontal_Lobe_TxTrans
13	6e−02	5 / 307	Fetal_ReprPC
14	1e−01	7 / 578	Fetal_Tx
15	1e−01	5 / 383	Mid_Frontal_Lobe_Tx

Chr

Rank	p−value	#in/all	Geneset
1	0.07	22 / 2323	Chr 1
2	0.20	4 / 342	Chr 18
3	0.20	9 / 959	Chr 16
4	0.21	13 / 1492	Chr 2
5	0.24	6 / 619	Chr 20
6	0.31	3 / 289	Chr 21
7	0.32	8 / 954	Chr 9
8	0.43	8 / 1060	Chr 5
9	0.44	9 / 1217	Chr 3
10	0.45	1 / 87	Chr Y
11	0.50	6 / 836	Chr 8
12	0.58	6 / 904	Chr 10
13	0.60	5 / 768	Chr 14
14	0.60	5 / 769	Chr 15
15	0.67	6 / 994	Chr X

Glio

Rank	p−value	#in/all	Geneset
1	0.002	6 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
2	0.003	4 / 84	GIEZELT_GBM_STS_up_VS_LTS
3	0.005	13 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
4	0.018	7 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
5	0.020	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
6	0.024	7 / 419	Down_a
7	0.045	28 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
8	0.053	2 / 55	Stuehler_Proteins_up_in_STS
9	0.072	1 / 11	VERHAAK_Brain
10	0.091	3 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	0.131	2 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
12	0.135	2 / 95	Weller_LGG_1p19qDel−vs−intact_UP
13	0.201	1 / 33	Shaw_responders_down_in_oligo_glioma
14	0.264	2 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
15	0.287	4 / 401	Down_b

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	1 / 94	DUMEAUX_Smoking enriched genes
2	0.8	1 / 211	Homuth_BMI−associated−genes_DN
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 147	Homuth_BMI−associated−genes_UP
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 16	enzyme regulator activity
2	0.006	2 / 17	phosphatidylinositol 3−kinase binding
3	0.007	3 / 59	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
4	0.011	3 / 67	protein phosphatase binding
5	0.013	2 / 26	retinoic acid receptor binding
6	0.015	2 / 28	NAD binding
7	0.027	2 / 38	RNA polymerase II transcription factor activity, ligand−activated sequence−sp
8	0.029	3 / 98	transcriptional activator activity, RNA polymerase II transcription regulatory re
9	0.036	3 / 107	SH3 domain binding
10	0.040	3 / 112	heme binding
11	0.045	2 / 50	steroid hormone receptor activity
12	0.049	4 / 202	structural molecule activity
13	0.055	2 / 56	endopeptidase activity
14	0.060	2 / 59	cell adhesion molecule binding
15	0.062	2 / 60	metallopeptidase activity

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	7e−04	24 / 1753	HEBENSTREIT_low expression TF
2	3e−02	10 / 747	ICGC_NrsfPcr2_targets
3	4e−02	32 / 3507	ICGC_Rad21_targets
4	4e−01	6 / 733	ICGC_Atf3_targets
5	6e−01	10 / 1501	ICGC_Usf1_targets
6	6e−01	22 / 3348	ICGC_BatfPcr1_targets
7	7e−01	9 / 1466	ICGC_NrsfPcr1_targets
8	7e−01	40 / 6267	ICGC_Yy1_targets
9	7e−01	17 / 2759	ICGC_Bcl3_targets
10	7e−01	4 / 721	ICGC_SrfPcr2_targets
11	7e−01	33 / 5312	ICGC_Tcf12_targets
12	8e−01	39 / 6322	ICGC_Tcf3_targets
13	8e−01	45 / 7247	ICGC_Runx3_targets
14	8e−01	42 / 6868	ICGC_Elf1_targets
15	8e−01	14 / 2497	ICGC_Bcl11_targets

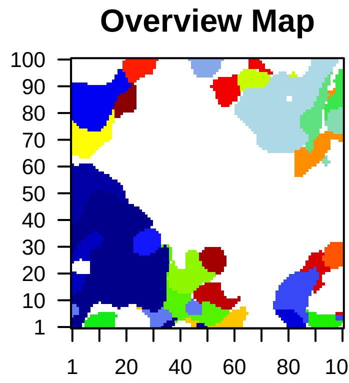
Correlation Cluster

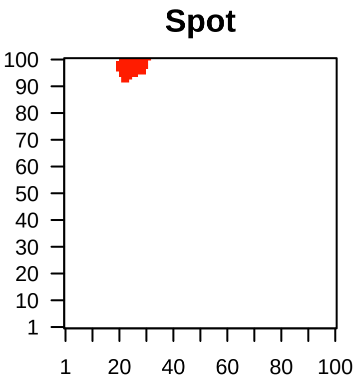
Spot Summary: T

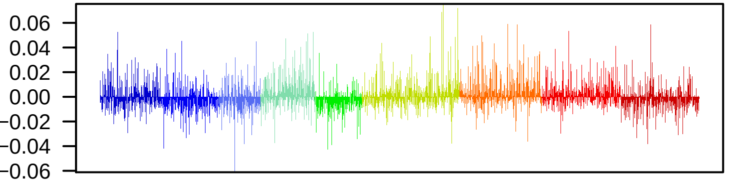
metagenes = 83
genes = 503

<r> metagenes = 0.95
<r> genes = 0.04
beta: r2= 0.34 / log p= −Inf

samples with spot = 3 (0.1 %)
F * : 3 (0.5 %)


Overview Map


Spot

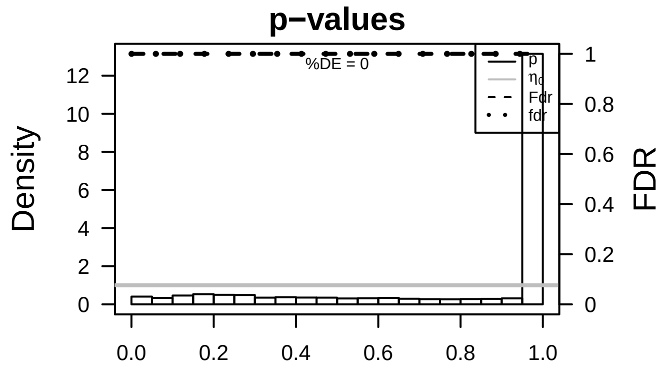


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_330104	0.38	−0.33	0.15	FLVCR1−AS1	FLVCR1 antisense RNA 1 (head to head) [Source:HGNC Syr
2	ILMN_179077	0.33	−0.22	0.2	PNMA2	paraneoplastic Ma antigen 2 [Source:HGNC Symbol;Acc:HGI
3	ILMN_240217	0.32	−0.19	0.16		
4	ILMN_216182	0.3	−0.19	0.17		
5	ILMN_321955	0.3	−0.21	0.19		
6	ILMN_180959	0.28	−0.17	0.19	C12orf40	chromosome 12 open reading frame 40 [Source:HGNC Symb
7	ILMN_169427	0.28	−0.19	0.22		
8	ILMN_223160	0.28	−0.22	0.22	CTAGE15	CTAGE family member 15 [Source:HGNC Symbol;Acc:HGNC
9	ILMN_213824	0.27	−0.21	0.24	PRSS45	protease, serine 45 [Source:HGNC Symbol;Acc:HGNC:3071
10	ILMN_327713	0.27	−0.2	0.17		ribosomal protein L9 pseudogene 18 [Source:HGNC Symbol;
11	ILMN_324908	0.27	−0.26	0.22		
12	ILMN_329937	0.27	−0.2	0.14		
13	ILMN_191464	0.27	−0.23	0.18		
14	ILMN_184821	0.27	−0.17	0.16		
15	ILMN_208418	0.27	−0.17	0.2	RPL10	ribosomal protein L10 [Source:HGNC Symbol;Acc:HGNC:10
16	ILMN_328453	0.26	−0.19	0.2		
17	ILMN_183933	0.26	−0.22	0.23	SUCLG2−AS1	SUCLG2 antisense RNA 1 (head to head) [Source:HGNC Sy
18	ILMN_184676	0.26	−0.21	0.21		
19	ILMN_177770	0.26	−0.21	0.14	OR4C12	olfactory receptor family 4 subfamily C member 12 [Source:H
20	ILMN_318304	0.26	−0.22	0.24	C11orf86	chromosome 11 open reading frame 86 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−07	54 / 2031	Chror	12_Het_Melanocytes
2	6e−07	62 / 2516	Chror	11_K9K27me3_Melanocytes
3	2e−06	64 / 2740	Colon	ReprPCWk_Colon
4	5e−06	85 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	5e−06	88 / 4304	Chror	9_ReprPCWk_Melanocytes
6	6e−06	104 / 5384	Lympl	HOPP_Repressed
7	1e−05	73 / 3438	Chror	10_ReprPC_Melanocytes
8	3e−05	83 / 4169	Chror	10_ReprPC_Fibroblasts
9	3e−05	59 / 2660	Chror	8_EnhP_Melanocytes
10	4e−05	53 / 2315	Chror	13_HetRpts_Melanocytes
11	4e−05	67 / 3173	Colon	ReprPC_Colon
12	8e−05	8 / 106	CC	Z disc
13	1e−04	34 / 1324	Chror	13_HetRpts_Fibroblasts
14	2e−04	71 / 3639	Chror	1_TssP_Fibroblasts
15	3e−04	30 / 1163	Chror	12_Het_Fibroblasts
16	4e−04	13 / 323	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
17	5e−04	58 / 2894	Colon	TssP_Colon
18	8e−04	54 / 2682	Chror	12_Het_Neuronal_Progenitor
19	1e−03	81 / 4526	Colon	Quies1_Colon
20	1e−03	6 / 92	GSEA	BURTON_ADIPOGENESIS_3
21	1e−03	4 / 37	GSEA	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP
22	1e−03	4 / 37	GSEA	VALK_AML_WITH_FLT3_ITD
23	2e−03	3 / 19	CC	costamere
24	2e−03	3 / 19	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN
25	2e−03	6 / 99	MF	metalloendopeptidase activity
26	2e−03	9 / 217	BP	chemical synaptic transmission
27	3e−03	67 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
28	3e−03	4 / 45	BP	cardiac muscle contraction
29	3e−03	3 / 23	MF	endopeptidase inhibitor activity
30	3e−03	2 / 7	GSEA	OXFORD_RALB_TARGETS_UP
31	4e−03	3 / 24	BP	complement activation
32	4e−03	73 / 4167	Lympl	HOPP_Heterochrom
33	4e−03	4 / 50	Refer	WIRTH_Placenta
34	4e−03	3 / 25	GSEA	VALK_AML_CLUSTER_2
35	5e−03	36 / 1753	TF	HEBENSTREIT_low expression TF
36	5e−03	8 / 199	GSEA	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP
37	5e−03	27 / 1213	Brain	Fetal_TssP
38	5e−03	13 / 436	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
39	5e−03	55 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
40	5e−03	3 / 27	BP	mitotic cytokinesis


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 111	HORVATH_aging_genes meth DOWN
2	0.5	1 / 58	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	1 / 15	LIU_PROSTATE_CANCER_DN
2	0.111	1 / 9	GENTLES_modul3
3	0.111	1 / 9	GENTLES_modul5
4	0.146	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	0.146	1 / 12	LIU_BREAST_CANCER
6	0.157	1 / 13	GENTLES_modul2
7	0.168	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
8	0.168	1 / 14	BEN−PORATH_UP
9	0.179	1 / 15	WANG_ER_UP
10	0.311	3 / 150	PanCan_MAPK_geneset_nanostring
11	0.454	1 / 46	PanCan_TGF−B_geneset_nanostring
12	0.508	1 / 54	KUIPER_MM poor survival
13	0.587	7 / 554	Lembcke_Colonic Inflammation
14	0.617	1 / 73	SHAUGHNESSY_MM high risk
15	0.677	2 / 178	SPANG_LPS−index2

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−07	54 / 2031	12_Het_Melanocytes
2	6e−07	62 / 2516	11_K9K27me3_Melanocytes
3	5e−06	85 / 4107	9_ReprPCWk_Fibroblasts
4	5e−06	88 / 4304	9_ReprPCWk_Melanocytes
5	1e−05	73 / 3438	10_ReprPC_Melanocytes
6	3e−05	83 / 4169	10_ReprPC_Fibroblasts
7	3e−05	59 / 2660	8_EnhP_Melanocytes
8	4e−05	53 / 2315	13_HetRpts_Melanocytes
9	1e−04	34 / 1324	13_HetRpts_Fibroblasts
10	2e−04	71 / 3639	1_TssP_Fibroblasts
11	3e−04	30 / 1163	12_Het_Fibroblasts
12	8e−04	54 / 2682	12_Het_Neuronal_Progenitor
13	3e−03	67 / 3691	9_ReprPCWk_Neuronal_Progenitor
14	6e−03	56 / 3068	8_EnhP_Fibroblasts
15	1e−02	61 / 3523	1_TssP_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	13 / 323	VECCHI_GASTRIC_CANCER_EARLY_DN
2	1e−03	6 / 92	BURTON_ADIPOGENESIS_3
3	1e−03	4 / 37	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP
4	1e−03	4 / 37	VALK_AML_WITH_FLT3_ITD
5	2e−03	3 / 19	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN
6	3e−03	2 / 7	OXFORD_RALB_TARGETS_UP
7	4e−03	3 / 25	VALK_AML_CLUSTER_2
8	5e−03	8 / 199	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP
9	5e−03	13 / 436	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
10	6e−03	1 / 15	LIU_PROSTATE_CANCER_DN
11	6e−03	2 / 9	KIM_ALL_DISORDERS_DURATION_CORR_UP
12	6e−03	9 / 253	SABATES_COLORECTAL_ADENOMA_DN
13	8e−03	9 / 265	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_UP
14	9e−03	3 / 33	TERAO_AOX4_TARGETS_SKIN_UP
15	1e−02	3 / 34	PID_AURORA_B_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−06	104 / 5384	HOPP_Repressed
2	4e−03	73 / 4167	HOPP_Heterochrom
3	6e−03	54 / 2939	HOPP_Poised_promoter
4	3e−02	5 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
5	4e−02	46 / 2701	HOPP_Repetitive
6	1e−01	4 / 138	WIRTH_lymphoma937_spot G
7	2e−01	3 / 109	ROSOLOWSKI_blue total
8	2e−01	6 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
9	2e−01	1 / 21	ROSOLOWSKI_red UP
10	3e−01	8 / 464	WIRTH_lymphoma937_spot I
11	3e−01	6 / 331	WIRTH_lymphoma937_spot H
12	3e−01	7 / 408	TARTE_Mature plasma cell signature
13	3e−01	5 / 286	ZHANG_DLBCL mutated
14	4e−01	7 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
15	4e−01	2 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.09	1 / 7	Multiple sclerosis, susceptibility to
2	0.12	1 / 10	Dermatitis, atopic
3	0.16	1 / 13	Psoriasis, susceptibility to
4	0.21	1 / 18	Hodgkin lymphoma
5	0.23	1 / 20	Parkinson disease
6	0.31	1 / 28	Immunological
7	0.32	1 / 29	Neuroblastoma
8	0.32	1 / 29	Myelofibrosis, idiopathic
9	0.41	1 / 40	Medulloblastoma
10	0.46	1 / 47	Cervical cancer, somatic
11	0.57	1 / 65	Hepatocellular carcinoma
12	0.62	1 / 73	Stroke, susceptibility to
13	0.63	1 / 76	Muscular
14	0.71	1 / 95	Colorectal cancer
15	0.74	1 / 102	Leukemia

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.004	4 / 50	WIRTH_Placenta
2	0.077	3 / 76	WIRTH_Homeostasis
3	0.097	10 / 478	WIRTH_Nervous System
4	0.100	1 / 8	JONGENEEL_Fetal Brain
5	0.135	1 / 11	WIRTH_Tonsil
6	0.157	1 / 13	WIRTH_Thymus
7	0.168	1 / 14	WIRTH_Telencephalon
8	0.185	5 / 231	Chaussabel_2,5_Immune related molecules
9	0.221	1 / 19	JONGENEEL_Small Intestine
10	0.343	1 / 32	JONGENEEL_Placenta
11	0.382	4 / 240	Chaussabel_3,3_Inflammation II
12	0.408	2 / 107	WIRTH_Liver
13	0.435	2 / 113	Chaussabel_1,4_Replication
14	0.468	1 / 48	WIRTH_Pancreas
15	0.475	1 / 49	JONGENEEL_Retina

BP

Rank	p−value	#in/all	Geneset
1	0.002	9 / 217	chemical synaptic transmission
2	0.003	4 / 45	cardiac muscle contraction
3	0.004	3 / 24	complement activation
4	0.005	3 / 27	mitotic cytokinesis
5	0.006	5 / 89	locomotory behavior
6	0.008	3 / 32	cation transport
7	0.008	3 / 32	cellular response to heat
8	0.008	3 / 32	regulation of heart rate
9	0.009	2 / 11	positive regulation of G−protein coupled receptor protein signaling pathway
10	0.010	3 / 34	excretion
11	0.010	2 / 12	L−amino acid transport
12	0.010	2 / 12	regulation of cardiac muscle cell contraction
13	0.010	2 / 12	urea cycle
14	0.012	2 / 13	negative regulation of axon extension
15	0.012	2 / 13	negative regulation of tumor necrosis factor−mediated signaling pathway

CC

Rank	p−value	#in/all	Geneset
1	8e−05	8 / 106	Z disc
2	2e−03	3 / 19	costamere
3	6e−03	3 / 28	voltage−gated calcium channel complex
4	8e−03	64 / 3662	plasma membrane
5	1e−02	3 / 36	myofibril
6	2e−02	4 / 76	extrinsic component of membrane
7	2e−02	23 / 1101	extracellular space
8	2e−02	3 / 44	chloride channel complex
9	2e−02	13 / 524	intracellular
10	2e−02	4 / 84	sarcolemma
11	2e−02	8 / 267	proteinaceous extracellular matrix
12	3e−02	2 / 19	connexon complex
13	3e−02	3 / 53	brush border
14	3e−02	4 / 93	intermediate filament
15	4e−02	4 / 96	anchored component of membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	64 / 2740	ReprPCWk_Colon
2	4e−05	67 / 3173	ReprPC_Colon
3	5e−04	58 / 2894	TssP_Colon
4	1e−03	81 / 4526	Quies1_Colon
5	2e−02	10 / 366	K9K27me3_Colon
6	3e−02	4 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
7	3e−02	30 / 1623	Het_Colon
8	4e−02	34 / 1895	EnhP_Colon
9	4e−02	23 / 1186	HetRpts_Colon
10	5e−02	64 / 4018	EnhWk2_Colon
11	5e−02	139 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	5e−02	13 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	8e−02	21 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	9e−02	4 / 129	Marisa_CRC−cluster−b
15	9e−02	12 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	0.04	6 / 186	HALLMARK_MYOGENESIS
2	0.08	4 / 127	HALLMARK_COAGULATION
3	0.09	4 / 132	HALLMARK_UV_RESPONSE_DN
4	0.10	5 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.10	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
6	0.20	4 / 176	HALLMARK_KRAS_SIGNALING_UP
7	0.21	4 / 179	HALLMARK_G2M_CHECKPOINT
8	0.23	2 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.36	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
10	0.39	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
11	0.39	3 / 173	HALLMARK_E2F_TARGETS
12	0.40	3 / 176	HALLMARK_ADIPOGENESIS
13	0.41	3 / 177	HALLMARK_MITOTIC_SPINDLE
14	0.43	3 / 183	HALLMARK_GLYCOLYSIS
15	0.45	2 / 116	HALLMARK_SPERMATOGENESIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.05	2 / 27	Hugo_melanoma−all−LEF1_UP
2	0.10	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.33	1 / 30	Hugo_melanoma−all−MET_UP
4	0.43	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.00	0 / 54	Hugo_melanoma−all−MET_DN
6	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.06	2 / 30	hsa−miR−626
2	0.13	2 / 47	hsa−miR−553
3	0.13	5 / 202	hsa−miR−148b
4	0.13	2 / 48	hsa−miR−610
5	0.14	2 / 50	hsa−miR−337−3p
6	0.14	3 / 100	hsa−miR−21
7	0.14	4 / 154	hsa−miR−139−5p
8	0.15	3 / 102	hsa−miR−1284
9	0.15	4 / 157	hsa−miR−31
10	0.16	1 / 13	hsa−miR−744
11	0.16	3 / 106	hsa−miR−22
12	0.17	2 / 58	hsa−miR−455−5p
13	0.19	2 / 61	hsa−miR−627
14	0.20	4 / 175	hsa−miR−548e
15	0.20	3 / 117	hsa−miR−543

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	0.005	27 / 1213	Fetal_TssP
2	0.006	25 / 1115	Overlap_fetal_midbrain_EnhG
3	0.007	50 / 2700	Fetal_TxTrans
4	0.007	55 / 3046	Fetal_TssA
5	0.043	25 / 1329	Overlap_fetal_midbrain_Enh
6	0.048	27 / 1476	Overlap_fetal_midbrain_TxTrans
7	0.054	33 / 1893	Overlap_fetal_midbrain_TssF
8	0.071	43 / 2630	Fetal_TssF
9	0.130	8 / 383	Mid_Frontal_Lobe_Tx
10	0.154	16 / 924	Mid_Frontal_Lobe_TssF
11	0.166	15 / 869	Mid_Frontal_Lobe_EnhG
12	0.173	17 / 1012	Mid_Frontal_Lobe_Enh
13	0.242	21 / 1360	Mid_Frontal_Lobe_TssP
14	0.276	58 / 4112	Mid_Frontal_Lobe_ReprPC
15	0.364	5 / 304	Mid_Frontal_Lobe_TssA

Chr

Rank	p−value	#in/all	Geneset
1	0.02	11 / 422	Chr 13
2	0.05	17 / 836	Chr 8
3	0.08	22 / 1217	Chr 3
4	0.22	22 / 1411	Chr 11
5	0.22	17 / 1060	Chr 5
6	0.26	34 / 2323	Chr 1
7	0.31	2 / 87	Chr Y
8	0.33	5 / 289	Chr 21
9	0.36	17 / 1170	Chr 7
10	0.36	19 / 1318	Chr 17
11	0.36	14 / 954	Chr 9
12	0.42	9 / 619	Chr 20
13	0.42	14 / 994	Chr X
14	0.48	20 / 1492	Chr 2
15	0.55	7 / 536	Chr 22

Glio

Rank	p−value	#in/all	Geneset
1	0.005	55 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.025	5 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
3	0.032	3 / 53	mature astrocytes
4	0.035	3 / 55	developing astrocytes
5	0.036	4 / 95	Weller_LGG_1p19qDel−vs−intact_UP
6	0.038	3 / 57	OL vs. MOG− OL
7	0.040	3 / 58	in vivo astrocytes vs. cultured astroglia
8	0.047	4 / 104	WIRTH_Normal Brain
9	0.084	16 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
10	0.100	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
11	0.100	1 / 8	Shaw_responders_up_in_oligo_glioma
12	0.144	8 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
13	0.146	1 / 12	Mukasa_UP_in_Astroglioma
14	0.147	2 / 52	OL vs. OPC
15	0.152	4 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	2 / 94	DUMEAUX_Smoking enriched genes
2	0.9	1 / 147	Homuth_BMI−associated−genes_UP
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 211	Homuth_BMI−associated−genes_DN
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.002	6 / 99	metalloendopeptidase activity
2	0.003	3 / 23	endopeptidase inhibitor activity
3	0.006	3 / 29	cysteine−type endopeptidase inhibitor activity
4	0.007	3 / 30	antigen binding
5	0.007	2 / 10	vinculin binding
6	0.012	2 / 13	L−amino acid transmembrane transporter activity
7	0.012	3 / 37	structural constituent of muscle
8	0.014	2 / 14	nitric−oxide synthase binding
9	0.015	3 / 40	receptor tyrosine kinase binding
10	0.020	2 / 17	inorganic anion exchanger activity
11	0.025	2 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
12	0.027	3 / 50	chloride channel activity
13	0.030	2 / 21	14−3−3 protein binding
14	0.036	2 / 23	alpha−tubulin binding
15	0.045	2 / 26	Ran GTPase binding

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.005	36 / 1753	HEBENSTREIT_low expression TF
2	0.168	1 / 14	NOWICK_TF
3	0.382	48 / 3507	ICGC_Rad21_targets
4	0.512	10 / 747	ICGC_NrsfPcr2_targets
5	0.637	84 / 6616	ICGC_Pax5_targets
6	0.727	8 / 721	ICGC_SrfPcr2_targets
7	0.834	6 / 631	ICGC_RxraPcr1_targets
8	0.873	27 / 2497	ICGC_Bcl11_targets
9	0.885	62 / 5383	ICGC_Sp1_targets
10	0.891	29 / 2704	ICGC_Pbx3_targets
11	0.894	62 / 5410	ICGC_Foxm1_targets
12	0.900	59 / 5188	ICGC_Ebfsc137065_targets
13	0.919	6 / 733	ICGC_Atf3_targets
14	0.925	16 / 1669	ICGC_P300_targets
15	0.949	13 / 1466	ICGC_NrsfPcr1_targets

Correlation Cluster

Spot Summary: U

metagenes = 67
genes = 181

<r> metagenes = 0.93
<r> genes = 0.03
beta: r2= 0.21 / log p= −Inf

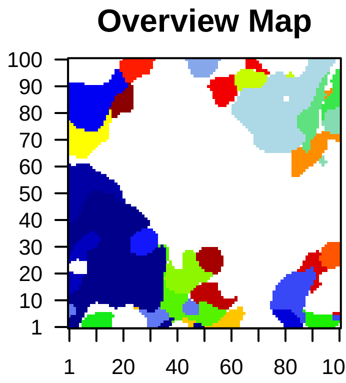
samples with spot = 0 (0 %)

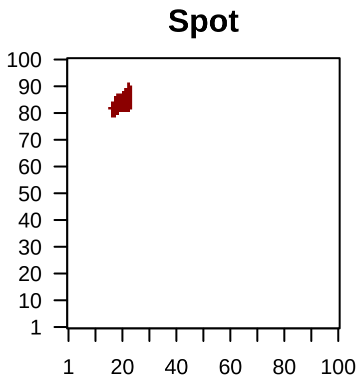
Spot Genelist

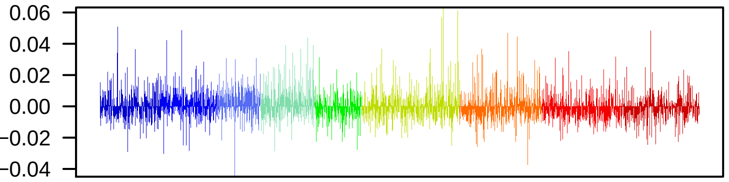
Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_187298	0.27	−0.18	0.18		
2	ILMN_180753	0.26	−0.3	0.2		
3	ILMN_177696	0.25	−0.15	0.18		
4	ILMN_189172	0.24	−0.19	0.13		
5	ILMN_175268	0.24	−0.16	0.22	WDR78	WD repeat domain 78 [Source:HGNC Symbol;Acc:HGNC:26
6	ILMN_227753	0.23	−0.17	0.17	MUTYH	mutY DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:75
7	ILMN_176564	0.23	−0.19	0.17	MAZ	MYC associated zinc finger protein [Source:HGNC Symbol;A
8	ILMN_182604	0.23	−0.19	0.16		
9	ILMN_179693	0.23	−0.17	0.19	CHAT	choline O−acetyltransferase [Source:HGNC Symbol;Acc:HGN
10	ILMN_175536	0.23	−0.19	0.16	RAB3A	RAB3A, member RAS oncogene family [Source:HGNC Symb
11	ILMN_177400	0.23	−0.16	0.15	ZIC1	Zic family member 1 [Source:HGNC Symbol;Acc:HGNC:1287
12	ILMN_188536	0.23	−0.16	0.18		
13	ILMN_322557	0.23	−0.2	0.15		long intergenic non−protein coding RNA 1438 [Source:HGNC
14	ILMN_184795	0.22	−0.17	0.15		
15	ILMN_323728	0.22	−0.19	0.22		
16	ILMN_218526	0.22	−0.17	0.17		
17	ILMN_180709	0.22	−0.17	0.18	LOC401472	
18	ILMN_326232	0.22	−0.14	0.2	PATE4	prostate and testis expressed 4 [Source:HGNC Symbol;Acc:H
19	ILMN_180290	0.22	−0.17	0.24	CBWD1	COBW domain containing 1 [Source:HGNC Symbol;Acc:HGN
20	ILMN_326937	0.22	−0.16	0.21		

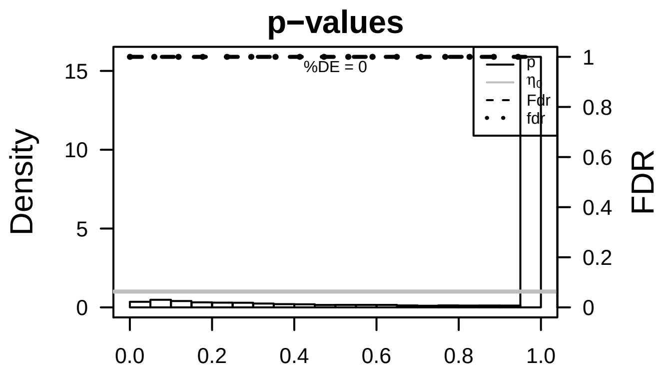
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	41 / 4304	Chro	9_ReprPCWk_Melanocytes
2	2e−05	24 / 1893	Brain	Overlap_fetal_midbrain_TssF
3	4e−05	29 / 2660	Chro	8_EnhP_Melanocytes
4	6e−05	5 / 82	MF	odorant binding
5	1e−04	27 / 2516	Chro	11_K9K27me3_Melanocytes
6	1e−04	2 / 4	GSE	TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP
7	2e−04	16 / 1119	Brain	Overlap_fetal_midbrain_TssA
8	2e−04	2 / 5	GSE	TESAR_ALK_TARGETS_HUMAN_ES_5D_UP
9	4e−04	2 / 6	GSE	TESAR_ALK_TARGETS_EPISC_4D_UP
10	6e−04	43 / 5384	Lymp	HOPP_Repressed
11	7e−04	31 / 3438	Chro	10_ReprPC_Melanocytes
12	1e−03	11 / 720	GSE	REACTOME_GPCR_DOWNSTREAM_SIGNALING
13	1e−03	2 / 10	MF	high voltage−gated calcium channel activity
14	1e−03	2 / 10	GSE	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CY
15	1e−03	17 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
16	1e−03	25 / 2620	Chro	1_TssP_Neuronal_Progenitor
17	1e−03	3 / 42	BP	cellular response to hormone stimulus
18	1e−03	2 / 11	BP	response to peptide
19	1e−03	2 / 11	GSE	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
20	1e−03	3 / 44	GSE	ZHAN_MULTIPLE_MYELOMA_PR_UP
21	1e−03	4 / 96	GSE	LEE_EARLY_T_LYMPHOCYTE_UP
22	2e−03	34 / 4107	Chro	9_ReprPCWk_Fibroblasts
23	2e−03	31 / 3639	Chro	1_TssP_Fibroblasts
24	2e−03	3 / 48	BP	neurotransmitter secretion
25	2e−03	4 / 103	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
26	2e−03	2 / 13	miRN	hsa−miR−1234
27	2e−03	7 / 347	GSE	KEGG_OLFACTORY_TRANSDUCTION
28	2e−03	4 / 106	BP	calcium ion transmembrane transport
29	2e−03	14 / 1163	Chro	12_Het_Fibroblasts
30	2e−03	30 / 3523	Chro	1_TssP_Melanocytes
31	2e−03	25 / 2740	Colon	ReprPCWk_Colon
32	2e−03	7 / 357	BP	detection of chemical stimulus involved in sensory perception of smell
33	2e−03	7 / 357	MF	olfactory receptor activity
34	2e−03	27 / 3068	Chro	8_EnhP_Fibroblasts
35	2e−03	11 / 803	BP	G−protein coupled receptor signaling pathway
36	3e−03	2 / 16	BP	calcium ion import
37	3e−03	19 / 1895	Colon	EnhP_Colon
38	3e−03	11 / 822	GSE	REACTOME_SIGNALING_BY_GPCR
39	3e−03	2 / 17	BP	synaptic vesicle exocytosis
40	3e−03	6 / 287	GSE	REACTOME_OLFACTORY_SIGNALING_PATHWAY









Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.07	1 / 14	GENTLES_modul4
2	0.17	1 / 38	KUIPER_MM good survival
3	0.17	2 / 150	PanCan_MAPK_geneset_nanostring
4	0.21	1 / 46	PanCan_DNARepair_geneset_nanostring
5	0.25	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
6	0.27	4 / 527	Lembcke_Normal vs Adenoma
7	0.37	1 / 91	PanCan_TXmisReg_geneset_nanostring
8	0.45	1 / 117	PanCan_Driver_Gene_geneset_nanostring
9	0.47	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	0.89	0 / 15	LIU_PROSTATE_CANCER_DN
11	0.94	1 / 554	Lembcke_Colonic Inflammation
12	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
13	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1.00	0 / 12	LIU_BREAST_CANCER
15	1.00	0 / 14	LIU_COMMON_CANCER_GENES

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−05	41 / 4304	9_ReprPCWk_Melanocytes
2	4e−05	29 / 2660	8_EnhP_Melanocytes
3	1e−04	27 / 2516	11_K9K27me3_Melanocytes
4	7e−04	31 / 3438	10_ReprPC_Melanocytes
5	1e−03	25 / 2620	1_TssP_Neuronal_Progenitor
6	2e−03	34 / 4107	9_ReprPCWk_Fibroblasts
7	2e−03	31 / 3639	1_TssP_Fibroblasts
8	2e−03	14 / 1163	12_Het_Fibroblasts
9	2e−03	30 / 3523	1_TssP_Melanocytes
10	2e−03	27 / 3068	8_EnhP_Fibroblasts
11	3e−03	10 / 717	11_K9K27me3_Fibroblasts
12	4e−03	18 / 1789	8_EnhP_Neuronal_Progenitor
13	5e−03	13 / 1154	11_K9K27me3_Neuronal_Progenitor
14	1e−02	20 / 2297	10_ReprPC_Neuronal_Progenitor
15	1e−02	18 / 2031	12_Het_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	2 / 4	TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP
2	2e−04	2 / 5	TESAR_ALK_TARGETS_HUMAN_ES_5D_UP
3	4e−04	2 / 6	TESAR_ALK_TARGETS_EPISC_4D_UP
4	1e−03	11 / 720	REACTOME_GPCR_DOWNSTREAM_SIGNALING
5	1e−03	2 / 10	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLI
6	1e−03	2 / 11	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
7	1e−03	3 / 44	ZHAN_MULTIPLE_MYELOMA_PR_UP
8	1e−03	4 / 96	LEE_EARLY_T_LYMPHOCYTE_UP
9	2e−03	4 / 103	WHITEFORD_PEDIATRIC_CANCER_MARKERS
10	2e−03	7 / 347	KEGG_OLFACTORY_TRANSDUCTION
11	3e−03	11 / 822	REACTOME_SIGNALING_BY_GPCR
12	3e−03	6 / 287	REACTOME_OLFACTORY_SIGNALING_PATHWAY
13	5e−03	4 / 133	CHANG_CYCLING_GENES
14	5e−03	4 / 135	RODWELL_AGING_KIDNEY_DN
15	7e−03	2 / 25	SU_PLACENTA

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−04	43 / 5384	HOPP_Repressed
2	1e−02	24 / 2939	HOPP_Poised_promoter
3	1e−01	1 / 21	Subero_MCL_hyper_meth
4	1e−01	2 / 118	Subero_INT_hyper_meth
5	1e−01	2 / 134	Subero_DLBCL_hyper_meth
6	2e−01	4 / 408	TARTE_Mature plasma cell signature
7	2e−01	2 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
8	2e−01	2 / 138	WIRTH_lymphoma937_spot G
9	2e−01	3 / 283	TARTE_Plasmablast signature
10	3e−01	1 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
11	3e−01	1 / 60	Subero_mBL_hyper_meth
12	3e−01	16 / 2701	HOPP_Repetitive
13	3e−01	1 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	3e−01	1 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	3e−01	2 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 30	Systemic lupus erythematosus (SLE)
2	0.3	1 / 68	Glioblastoma multiforme, somatic
3	0.5	1 / 127	Melanoma and neural system tumor syndrome
4	0.5	1 / 156	Breast cancer
5	1.0	0 / 7	Thyroid carcinoma, papillary
6	1.0	0 / 123	Pancreatic cancer
7	1.0	0 / 63	Gastrointestinal
8	1.0	0 / 3	Pituitary adenoma
9	1.0	0 / 116	Cancer
10	1.0	0 / 95	Colorectal cancer
11	1.0	0 / 2	Adenomas, multiple colorectal
12	1.0	0 / 124	Prostate cancer
13	1.0	0 / 48	Alzheimer disease, susceptibility to
14	1.0	0 / 7	Schizophrenia, susceptibility to
15	1.0	0 / 20	Parkinson disease

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.03	3 / 134	WIRTH_Mucosa
2	0.09	1 / 19	JONGENEEL_Small Intestine
3	0.10	1 / 21	JONGENEEL_Adrenal Gland
4	0.11	1 / 23	JONGENEEL_Heart
5	0.11	1 / 24	VAQUERIZAS_Spinal cord_TF
6	0.11	1 / 24	JONGENEEL_Prostate
7	0.14	1 / 29	JONGENEEL_Bone Marrow
8	0.15	1 / 32	JONGENEEL_Placenta
9	0.17	2 / 148	VAQUERIZAS_General_TF
10	0.19	1 / 42	VAQUERIZAS_Fetal brain_TF
11	0.20	1 / 43	VAQUERIZAS_Placenta_TF
12	0.20	1 / 44	VAQUERIZAS_Whole brain_TF
13	0.22	4 / 478	WIRTH_Nervous System
14	0.24	1 / 53	JONGENEEL_Kidney
15	0.30	2 / 220	WIRTH_Testis

BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 42	cellular response to hormone stimulus
2	0.001	2 / 11	response to peptide
3	0.002	3 / 48	neurotransmitter secretion
4	0.002	4 / 106	calcium ion transmembrane transport
5	0.002	7 / 357	detection of chemical stimulus involved in sensory perception of smell
6	0.002	11 / 803	G−protein coupled receptor signaling pathway
7	0.003	2 / 16	calcium ion import
8	0.003	2 / 17	synaptic vesicle exocytosis
9	0.004	4 / 125	central nervous system development
10	0.005	2 / 22	cellular response to peptide hormone stimulus
11	0.007	3 / 76	post−embryonic development
12	0.007	2 / 25	response to tumor necrosis factor
13	0.008	2 / 26	protein K11−linked ubiquitination
14	0.009	2 / 29	regulation of heart rate by cardiac conduction
15	0.011	2 / 32	cellular response to heat

CC

Rank	p−value	#in/all	Geneset
1	0.009	2 / 28	voltage−gated calcium channel complex
2	0.023	2 / 47	presynapse
3	0.052	2 / 73	acrosomal vesicle
4	0.059	1 / 12	interstitial matrix
5	0.066	2 / 83	synaptic vesicle
6	0.078	1 / 16	inclusion body
7	0.087	1 / 18	anchored component of external side of plasma membrane
8	0.088	3 / 208	actin cytoskeleton
9	0.096	1 / 20	anaphase−promoting complex
10	0.096	1 / 20	extrinsic component of plasma membrane
11	0.098	22 / 3291	integral component of membrane
12	0.101	3 / 221	endosome
13	0.102	24 / 3662	plasma membrane
14	0.105	1 / 22	histone methyltransferase complex
15	0.117	5 / 512	cell surface

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.002	25 / 2740	ReprPCWk_Colon
2	0.003	19 / 1895	EnhP_Colon
3	0.004	27 / 3173	ReprPC_Colon
4	0.009	24 / 2894	TssP_Colon
5	0.011	6 / 366	K9K27me3_Colon
6	0.082	1 / 17	TCGA−CRC_less−agressive−disease−markers
7	0.097	3 / 217	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
8	0.123	1 / 26	Ang_CRC−CIMPH−vs−L_hypo
9	0.135	9 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
10	0.151	6 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	0.162	1 / 35	Ang_CRC_Hypomethylated
12	0.167	4 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	0.192	3 / 299	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	0.248	8 / 1186	HetRpts_Colon
15	0.255	5 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	0.2	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
2	0.2	1 / 41	HALLMARK_APICAL_SURFACE
3	0.2	2 / 173	HALLMARK_E2F_TARGETS
4	0.2	2 / 179	HALLMARK_G2M_CHECKPOINT
5	0.2	2 / 183	HALLMARK_GLYCOLYSIS
6	0.4	1 / 116	HALLMARK_SPERMATOGENESIS
7	0.6	1 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	0.6	1 / 175	HALLMARK_XENOBIOTIC_METABOLISM
9	0.6	1 / 177	HALLMARK_MITOTIC_SPINDLE
10	0.6	1 / 177	HALLMARK_KRAS_SIGNALING_DN
11	0.6	1 / 185	HALLMARK_HEME_METABOLISM
12	0.6	1 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.6	1 / 186	HALLMARK_MYOGENESIS
14	0.6	1 / 187	HALLMARK_COMPLEMENT
15	0.6	1 / 189	HALLMARK_HYPOXIA

Melanoma

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

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	2 / 13	hsa−miR−1234
2	0.011	2 / 31	hsa−miR−296−5p
3	0.012	2 / 33	hsa−miR−1296
4	0.024	3 / 122	hsa−miR−520a−5p
5	0.030	1 / 6	hsa−miR−937
6	0.039	2 / 62	hsa−miR−140−3p
7	0.040	2 / 63	hsa−miR−1267
8	0.042	4 / 259	hsa−miR−548p
9	0.049	1 / 10	hsa−miR−720
10	0.051	2 / 72	hsa−miR−708
11	0.054	1 / 11	hsa−miR−604
12	0.074	4 / 314	hsa−miR−340
13	0.091	2 / 100	hsa−miR−147
14	0.091	2 / 100	hsa−miR−525−5p
15	0.095	2 / 103	hsa−miR−224

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	2e−05	24 / 1893	Overlap_fetal_midbrain_TssF
2	2e−04	16 / 1119	Overlap_fetal_midbrain_TssA
3	1e−03	17 / 1476	Overlap_fetal_midbrain_TxTrans
4	1e−02	8 / 630	Mid_Frontal_Lobe_EnhP
5	2e−02	9 / 819	Overlap_fetal_midbrain_TssP
6	3e−02	6 / 465	Mid_Frontal_Lobe_TxTrans
7	7e−02	9 / 1012	Mid_Frontal_Lobe_Enh
8	1e−01	7 / 869	Mid_Frontal_Lobe_EnhG
9	2e−01	9 / 1360	Mid_Frontal_Lobe_TssP
10	3e−01	16 / 2654	Fetal_Quies
11	3e−01	11 / 1784	Mid_Frontal_Lobe_ReprPCWk
12	3e−01	6 / 924	Mid_Frontal_Lobe_TssF
13	3e−01	23 / 4112	Mid_Frontal_Lobe_ReprPC
14	3e−01	7 / 1115	Overlap_fetal_midbrain_EnhG
15	4e−01	8 / 1329	Overlap_fetal_midbrain_Enh

Chr

Rank	p−value	#in/all	Geneset
1	0.06	8 / 836	Chr 8
2	0.17	8 / 1060	Chr 5
3	0.17	10 / 1411	Chr 11
4	0.19	15 / 2323	Chr 1
5	0.24	7 / 994	Chr X
6	0.25	3 / 342	Chr 18
7	0.28	4 / 536	Chr 22
8	0.34	5 / 768	Chr 14
9	0.41	7 / 1211	Chr 6
10	0.54	4 / 769	Chr 15
11	0.58	6 / 1217	Chr 3
12	0.61	7 / 1467	Chr 19
13	0.63	2 / 422	Chr 13
14	0.67	4 / 902	Chr 4
15	0.70	5 / 1160	Chr 12

Glio

Rank	p−value	#in/all	Geneset
1	0.006	3 / 74	Weller_LGG_gradeII−vs−III_DOWN
2	0.018	3 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.024	23 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
4	0.029	3 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
5	0.029	2 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
6	0.068	1 / 14	astrocytes_glio
7	0.073	1 / 15	VERHAAK_NL subtype
8	0.074	3 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	0.076	2 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
10	0.076	2 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
11	0.085	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
12	0.092	2 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	0.105	1 / 22	Shinawi_with_increased_methylation_in_STS
14	0.114	1 / 24	Martinez_Glio_hypermeth
15	0.114	2 / 115	Christensen_hypermethylated_in_grade3_astrocytoma

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	2 / 94	DUMEAUX_Smoking enriched genes
2	0.66	1 / 211	Homuth_BMI−associated−genes_DN
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 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	6e−05	5 / 82	odorant binding
2	1e−03	2 / 10	high voltage−gated calcium channel activity
3	2e−03	7 / 357	olfactory receptor activity
4	4e−03	3 / 64	calcium channel activity
5	5e−03	2 / 21	R−SMAD binding
6	5e−03	2 / 22	tumor necrosis factor−activated receptor activity
7	7e−03	2 / 25	fibronectin binding
8	1e−02	8 / 588	G−protein coupled receptor activity
9	2e−02	2 / 40	voltage−gated calcium channel activity
10	2e−02	5 / 301	ubiquitin−protein transferase activity
11	2e−02	2 / 45	protein kinase C binding
12	2e−02	2 / 48	peptide binding
13	2e−02	4 / 218	transcriptional activator activity, RNA polymerase II core promoter proximal re
14	3e−02	2 / 52	RNA polymerase II core promoter sequence−specific DNA binding
15	5e−02	1 / 10	adenyl−nucleotide exchange factor activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 13	BENTINK_e2f3.2
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_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	

TF

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	MYC_TFs
2	0.06	1 / 12	MYC_Protein synthesis degradation UP
3	0.10	13 / 1753	HEBENSTREIT_low expression TF
4	0.18	6 / 747	ICGC_NrsfPcr2_targets
5	0.24	1 / 55	MYC_Targets UP
6	0.31	20 / 3507	ICGC_Rad21_targets
7	0.33	9 / 1478	ICGC_Myc_targets
8	0.46	8 / 1466	ICGC_NrsfPcr1_targets
9	0.48	11 / 2087	ICGC_Cebpbsc150_targets
10	0.61	12 / 2497	ICGC_Bcl11_targets
11	0.71	3 / 721	ICGC_SrfPcr2_targets
12	0.71	20 / 4345	ICGC_Zeb1_targets
13	0.72	3 / 733	ICGC_Atf3_targets
14	0.75	6 / 1452	ICGC_Six5_targets
15	0.75	5 / 1231	KIM_MYC targets

Correlation Cluster

Spot Summary: V

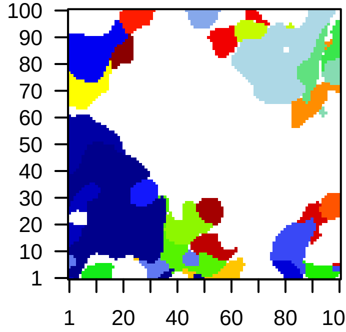
metagenes = 684
genes = 2352

<r> metagenes = 0.92

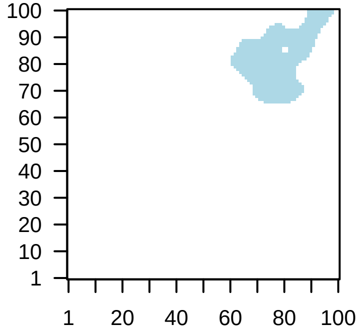
beta: r2= 24.36 / log p= −Inf

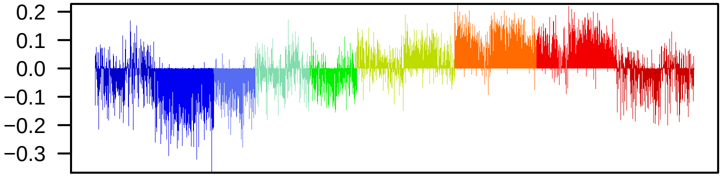
samples with spot = 812 (24 %)
A * : 33 (9.6 %)
A F * : 30 (9.7 %)
C F * : 7 (2.6 %)
F * : 151 (27.2 %)
F J * : 314 (67.8 %)
J * : 255 (57 %)
N * : 22 (5 %)

Overview Map



Spot





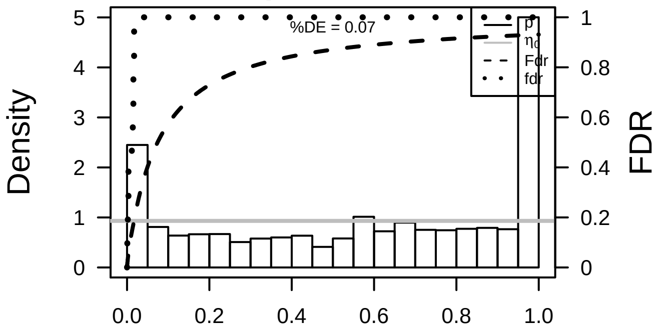
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_239376	2.36	−2.48	0.3	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
2	ILMN_165219	2.24	−1.63	0.26		
3	ILMN_173950	2.08	−1.34	0.29		
4	ILMN_324037	2.04	−1.35	0.35		immunoglobulin kappa variable 1D−17 [Source:HGNC Symbo
5	ILMN_169921	1.89	−1.18	0.28		
6	ILMN_174314	1.89	−2.07	0.13	ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Syn
7	ILMN_178810	1.79	−0.92	0.36		BLOC1S5−TXNDC5 readthrough (NMD candidate) [Source:
8	ILMN_177365	1.78	−1.17	0.51	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:H
9	ILMN_169107	1.77	−1.46	0.5	FCRLA	Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]
10	ILMN_177245	1.73	−2.05	0.4	RPS23	ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10
11	ILMN_168027	1.73	−0.94	0.34		immunoglobulin kappa variable 1−33 [Source:HGNC Symbol;
12	ILMN_240485	1.7	−1.35	0.32	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10
13	ILMN_180840	1.68	−1.68	0.34	HLA−DQA1	major histocompatibility complex, class II, DQ alpha 1 [Sourc
14	ILMN_173487	1.64	−1.96	0.55	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
15	ILMN_178270	1.6	−1.28	0.36		
16	ILMN_165379	1.59	−1.31	0.27		
17	ILMN_233792	1.41	−1.24	0.6	CXCR5	C−X−C motif chemokine receptor 5 [Source:HGNC Symbol;A
18	ILMN_165303	1.4	−1.48	0.4		
19	ILMN_171073	1.39	−1.44	0.49	GZMK	granzyme K [Source:HGNC Symbol;Acc:HGNC:4711]
20	ILMN_170014	1.38	−1.08	0.44	VPREB3	pre−B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−66	85 / 119	Refer	Chaussabel_2,8_T−cells
2	1e−54	1091 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
3	5e−48	75 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
4	2e−47	1261 / 12298	Chror	2_TssA_Melanocytes
5	1e−46	1045 / 9555	Colon	TssA_Colon
6	2e−46	215 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
7	4e−46	196 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	6e−46	933 / 8226	Lympl	HOPP_Active_promoter
9	1e−45	1191 / 11455	Chror	2_TssA_Fibroblasts
10	4e−39	64 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
11	9e−39	977 / 9054	Colon	Tx_Colon
12	3e−38	935 / 8568	Colon	TxWk_Colon
13	4e−38	1281 / 12983	Chror	2_TssA_Neuronal_Progenitor
14	5e−38	825 / 7275	Lympl	HOPP_Txn_elongation
15	8e−35	999 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
16	2e−34	786 / 6970	Chror	5_Tx_Neuronal_Progenitor
17	3e−34	694 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
18	5e−34	936 / 8771	Chror	5_Tx_Melanocytes
19	8e−33	637 / 5356	Lympl	HOPP_Txn_transition
20	2e−32	243 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
21	3e−32	1108 / 10999	Colon	TssWk_Colon
22	1e−31	67 / 163	BP	rRNA processing
23	8e−31	127 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
24	2e−30	39 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
25	1e−29	863 / 8098	Lympl	HOPP_Weak_promoter
26	1e−28	838 / 7854	Chror	5_Tx_Fibroblasts
27	2e−28	906 / 8678	Colon	Quies3_Colon
28	4e−28	40 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
29	7e−28	41 / 69	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
30	1e−27	210 / 1231	TF	KIM_MYC targets
31	1e−27	44 / 81	BP	viral transcription
32	3e−27	28 / 32	Lifesty	Marjolein_ageing−genes_DN
33	7e−27	37 / 58	GSEA	KEGG_RIBOSOME
34	1e−26	182 / 1013	MF	poly(A) RNA binding
35	1e−26	47 / 96	BP	translational initiation
36	1e−26	59 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
37	3e−26	41 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
38	8e−26	44 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
39	3e−25	154 / 811	GSEA	LEE_BMP2_TARGETS_DN
40	1e−24	38 / 68	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	13 / 142	HORVATH_aging_genes meth UP
2	0.4	10 / 111	HORVATH_aging_genes meth DOWN
3	1.0	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−31	67 / 163	rRNA processing
2	4e−28	40 / 65	SRP−dependent cotranslational protein targeting to membrane
3	1e−27	44 / 81	viral transcription
4	1e−26	47 / 96	translational initiation
5	8e−26	44 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
6	5e−20	57 / 184	translation
7	6e−14	214 / 1643	transcription, DNA−templated
8	5e−09	158 / 1272	regulation of transcription, DNA−templated
9	2e−08	9 / 12	maturation of LSU−rRNA
10	3e−06	8 / 14	positive regulation of telomerase RNA localization to Cajal body
11	6e−06	8 / 15	ribosomal large subunit assembly
12	1e−05	10 / 26	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
13	2e−05	11 / 32	tRNA aminoacylation for protein translation
14	3e−05	8 / 18	ribosomal large subunit biogenesis
15	4e−05	21 / 102	protein sumoylation

Brain

Rank	p−value	#in/all	Geneset
1	1e−54	1091 / 9815	Overlap_fetal_midbrain_ReprPC
2	8e−35	999 / 9504	Overlap_fetal_midbrain_K9K27me3
3	3e−34	694 / 5936	Overlap_fetal_midbrain_HetRpts
4	1e−19	966 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	3e−13	970 / 10430	Overlap_fetal_midbrain_Quies
6	3e−08	95 / 681	Overlap_fetal_midbrain_EnhP
7	6e−08	106 / 796	Overlap_fetal_midbrain_ZNF
8	1e−05	80 / 630	Mid_Frontal_Lobe_EnhP
9	3e−05	308 / 3164	Mid_Frontal_Lobe_ZNF
10	2e−04	29 / 180	Overlap_fetal_midbrain_Het
11	2e−04	101 / 906	Fetal_HetRpts
12	2e−03	47 / 386	Fetal_ZNF
13	7e−03	242 / 2654	Fetal_Quies
14	2e−02	37 / 328	Fetal_Het
15	4e−02	109 / 1171	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	7e−06	4 / 13	RHODES_CANCER_META_SIGNATURE
2	4e−05	7 / 14	GENTLES_modul1
3	1e−04	11 / 39	ZHANG_MM up
4	1e−03	6 / 16	GENTLES_modul11
5	2e−03	5 / 13	GENTLES_modul6
6	5e−03	5 / 15	WOLFER_overlap genes
7	6e−03	5 / 16	GENTLES_modul7
8	2e−02	4 / 13	GENTLES_modul18
9	3e−02	7 / 38	KUIPER_MM good survival
10	3e−02	3 / 14	LIU_COMMON_CANCER_GENES
11	3e−02	54 / 527	Lembcke_Normal vs Adenoma
12	3e−02	4 / 16	GENTLES_modul16
13	3e−02	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
14	7e−02	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	8e−02	2 / 6	ZHANG_MGUS up

CC

Rank	p−value	#in/all	Geneset
1	7e−20	131 / 721	nucleolus
2	1e−17	26 / 45	cytosolic large ribosomal subunit
3	2e−17	315 / 2535	nucleoplasm
4	5e−15	183 / 1304	mitochondrion
5	5e−15	514 / 4828	nucleus
6	3e−09	64 / 374	mitochondrial inner membrane
7	5e−09	14 / 28	cytosolic small ribosomal subunit
8	3e−08	17 / 46	ribosome
9	5e−07	8 / 12	small ribosomal subunit
10	1e−06	47 / 287	mitochondrial matrix
11	2e−06	459 / 4822	cytoplasm
12	3e−06	299 / 2979	cytosol
13	1e−04	7 / 16	small nuclear ribonucleoprotein complex
14	1e−04	8 / 21	U4/U6 x U5 tri−snRNP complex
15	3e−04	9 / 29	small−subunit processome

Chr

Rank	p−value	#in/all	Geneset
1	0.03	95 / 994	Chr X
2	0.03	44 / 422	Chr 13
3	0.13	102 / 1160	Chr 12
4	0.15	106 / 1217	Chr 3
5	0.18	79 / 904	Chr 10
6	0.19	127 / 1492	Chr 2
7	0.22	103 / 1211	Chr 6
8	0.35	96 / 1170	Chr 7
9	0.37	29 / 342	Chr 18
10	0.38	119 / 1467	Chr 19
11	0.44	62 / 768	Chr 14
12	0.48	76 / 954	Chr 9
13	0.49	84 / 1060	Chr 5
14	0.55	75 / 959	Chr 16
15	0.55	60 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−47	1261 / 12298	2_TssA_Melanocytes
2	1e−45	1191 / 11455	2_TssA_Fibroblasts
3	4e−38	1281 / 12983	2_TssA_Neuronal_Progenitor
4	2e−34	786 / 6970	5_Tx_Neuronal_Progenitor
5	5e−34	936 / 8771	5_Tx_Melanocytes
6	1e−28	838 / 7854	5_Tx_Fibroblasts
7	2e−22	1131 / 11836	3_TssF_Melanocytes
8	9e−15	1133 / 12393	15_Quies_Neuronal_Progenitor
9	5e−11	839 / 8990	15_Quies_Fibroblasts
10	9e−11	221 / 1846	14_ZNF_Melanocytes
11	2e−09	998 / 11130	15_Quies_Melanocytes
12	3e−09	429 / 4237	14_ZNF_Neuronal_Progenitor
13	9e−09	551 / 5699	6_EnhG_Melanocytes
14	4e−07	1105 / 12741	7_Enh_Melanocytes
15	2e−06	854 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−46	1045 / 9555	TssA_Colon
2	2e−46	215 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	4e−46	196 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	9e−39	977 / 9054	Tx_Colon
5	3e−38	935 / 8568	TxWk_Colon
6	3e−32	1108 / 10999	TssWk_Colon
7	2e−28	906 / 8678	Quies3_Colon
8	3e−17	743 / 7354	TssF_Colon
9	3e−13	154 / 1083	ZNF_Colon
10	5e−11	193 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	9e−11	421 / 4034	TssD1_Colon
12	4e−09	235 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	4e−09	41 / 193	Kosinski_lower−crypt−long−list
14	7e−09	146 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	9e−09	176 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

Glio

Rank	p−value	#in/all	Geneset
1	4e−08	202 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	5e−07	221 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−02	45 / 401	Down_b
4	2e−02	81 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	4e−02	11 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	4e−02	5 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
7	1e−01	7 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
8	1e−01	2 / 7	Donson−adaptive−immunity−associated with LTS in HGA
9	1e−01	3 / 15	VERHAAK_CL subtype
10	1e−01	3 / 15	VERHAAK_NL subtype
11	1e−01	3 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
12	1e−01	2 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
13	1e−01	4 / 26	Gorovets_LGG_NB_subclass
14	2e−01	2 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
15	2e−01	11 / 100	GIEZELT_GBM_STS_down_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−32	243 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	8e−31	127 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
3	2e−30	39 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
4	7e−28	41 / 69	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
5	7e−27	37 / 58	KEGG_RIBOSOME
6	1e−26	59 / 151	JISON_SICKLE_CELL_DISEASE_DN
7	3e−26	41 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
8	3e−25	154 / 811	LEE_BMP2_TARGETS_DN
9	1e−24	38 / 68	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
10	2e−24	65 / 196	REACTOME_METABOLISM_OF_RNA
11	2e−24	46 / 101	REACTOME_TRANSLATION
12	6e−24	39 / 74	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
13	9e−24	133 / 669	PUJANA_CHEK2_PCC_NETWORK
14	6e−23	44 / 99	REACTOME_INFLUENZA_LIFE_CYCLE
15	5e−22	156 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−21	56 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−06	16 / 54	HALLMARK_MYC_TARGETS_V2
3	4e−06	23 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	2e−03	25 / 173	HALLMARK_E2F_TARGETS
5	3e−03	20 / 130	HALLMARK_DNA_REPAIR
6	1e−02	22 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
7	3e−02	20 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	9e−02	6 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1e−01	20 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	1e−01	19 / 179	HALLMARK_G2M_CHECKPOINT
11	1e−01	19 / 185	HALLMARK_MTORC1_SIGNALING
12	1e−01	19 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	2e−01	14 / 132	HALLMARK_UV_RESPONSE_DN
14	3e−01	9 / 91	HALLMARK_PEROXISOME
15	3e−01	16 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−27	28 / 32	Marjolein_ageing−genes_DN
2	1e−05	28 / 147	Homuth_BMI−associated−genes_UP
3	1e−01	3 / 17	DUMEAUX_High bmi enriched genes
4	4e−01	3 / 31	DUMEAUX_Fasting enriched genes
5	6e−01	1 / 10	DUMEAUX_Smoking literature genes up
6	6e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
7	6e−01	16 / 211	Homuth_BMI−associated−genes_DN
8	7e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
9	7e−01	1 / 16	Huan_blood−pressure_DBP−signature
10	8e−01	6 / 94	DUMEAUX_Smoking enriched genes
11	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
13	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
14	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−46	933 / 8226	HOPP_Active_promoter
2	5e−38	825 / 7275	HOPP_Txn_elongation
3	8e−33	637 / 5356	HOPP_Txn_transition
4	1e−29	863 / 8098	HOPP_Weak_promoter
5	3e−18	134 / 777	WIRTH_lymphoma937_spot D
6	3e−17	131 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	1e−12	724 / 7448	HOPP_Strong_enhancer
8	1e−12	39 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
9	2e−12	39 / 141	WIRTH_lymphoma937_spot F
10	6e−12	169 / 1270	SPANG_BCR UP
11	6e−08	34 / 158	WIRTH_lymphoma937_spot C
12	7e−08	34 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
13	2e−07	613 / 6559	HOPP_Weak_txn
14	5e−07	71 / 493	WIRTH_lymphoma937_spot J
15	6e−07	641 / 6959	HOPP_Weak_enhancer

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
3	0.7	2 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−26	182 / 1013	poly(A) RNA binding
2	3e−21	56 / 169	structural constituent of ribosome
3	7e−11	71 / 399	RNA binding
4	2e−08	805 / 8818	protein binding
5	5e−08	173 / 1475	DNA binding
6	8e−08	195 / 1717	metal ion binding
7	6e−06	11 / 29	rRNA binding
8	1e−04	6 / 12	pseudouridine synthase activity
9	4e−04	6 / 14	telomerase RNA binding
10	5e−04	5 / 10	adenyl−nucleotide exchange factor activity
11	6e−04	96 / 877	transcription factor activity, sequence−specific DNA binding
12	1e−03	11 / 48	methyltransferase activity
13	2e−03	6 / 18	snoRNA binding
14	2e−03	5 / 13	enhancer binding
15	3e−03	9 / 39	translation initiation factor activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 6	Thrombocytopenic purpurea, autoimmune
2	0.4	1 / 7	Multiple sclerosis, susceptibility to
3	0.5	1 / 9	Systemic lupus erythematosus, susceptibility
4	1.0	1 / 40	Medulloblastoma
5	1.0	1 / 63	Gastrointestinal
6	1.0	1 / 68	Glioblastoma multiforme, somatic
7	1.0	1 / 102	Leukemia
8	1.0	1 / 113	Ovarian cancer
9	1.0	1 / 120	Hematological
10	1.0	1 / 123	Pancreatic cancer
11	1.0	1 / 124	Prostate cancer
12	1.0	1 / 127	Melanoma and neural system tumor syndrome
13	1.0	1 / 127	Squamous cell carcinoma, head and neck
14	1.0	1 / 142	Lung cancer
15	1.0	1 / 156	Breast cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	14 / 60	hsa−miR−1200
2	3e−04	15 / 70	hsa−miR−193b
3	4e−04	38 / 272	hsa−miR−101
4	6e−04	28 / 184	hsa−miR−129−5p
5	6e−04	16 / 82	hsa−miR−188−5p
6	1e−03	14 / 71	hsa−miR−578
7	1e−03	58 / 493	hsa−miR−103
8	2e−03	12 / 58	hsa−miR−193a−3p
9	2e−03	38 / 293	hsa−miR−34c−5p
10	2e−03	17 / 100	hsa−miR−525−5p
11	2e−03	38 / 299	hsa−miR−548c−3p
12	3e−03	14 / 77	hsa−miR−569
13	3e−03	25 / 176	hsa−miR−199b−3p
14	3e−03	10 / 47	hsa−miR−623
15	3e−03	19 / 122	hsa−miR−520a−5p

Pathw Act

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−66	85 / 119	Chaussabel_2,8_T−cells
2	5e−48	75 / 132	Chaussabel_1,7_MHC Ribosomal proteins
3	4e−39	64 / 119	Chaussabel_2,4_Ribosomal proteins
4	8e−13	23 / 51	Chaussabel_1,3_B−cells
5	3e−10	71 / 412	WIRTH_Immune system
6	1e−08	136 / 1063	PROTEINATLAS_tonsil
7	1e−08	101 / 724	PROTEINATLAS_lymph node
8	1e−08	139 / 1097	PROTEINATLAS_kidney
9	2e−08	50 / 275	Chaussabel_3,7_Spliceosome
10	5e−08	90 / 639	PROTEINATLAS_breast
11	9e−08	143 / 1173	PROTEINATLAS_rectum
12	1e−07	126 / 1003	PROTEINATLAS_appendix
13	2e−07	116 / 912	PROTEINATLAS_urinary bladder
14	2e−07	41 / 221	Chaussabel_3,8_Enzymes
15	2e−07	143 / 1194	PROTEINATLAS_stomach

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	3 / 27	Nabetani_alt len telomeres_genes_ko
2	0.7	1 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−27	210 / 1231	KIM_MYC targets
2	1e−20	219 / 1478	ICGC_Myc_targets
3	7e−20	559 / 5067	ICGC_Taf1_targets
4	5e−15	570 / 5466	ICGC_Nficsc81335_targets
5	2e−13	565 / 5518	ICGC_Stat5_targets
6	4e−12	551 / 5442	ICGC_Pmlsc71910_targets
7	7e−12	187 / 1452	ICGC_Six5_targets
8	8e−12	646 / 6578	ICGC_Pou2_targets
9	1e−11	501 / 4890	ICGC_Bclaf101388_targets
10	4e−11	497 / 4881	ICGC_Atf2_targets
11	1e−10	636 / 6552	ICGC_Pol2_targets
12	2e−10	255 / 2215	ICGC_GabpPcr2_targets
13	2e−10	447 / 4362	ICGC_Creb1_targets
14	2e−10	586 / 5984	ICGC_Mta3_targets
15	3e−10	609 / 6267	ICGC_Yy1_targets

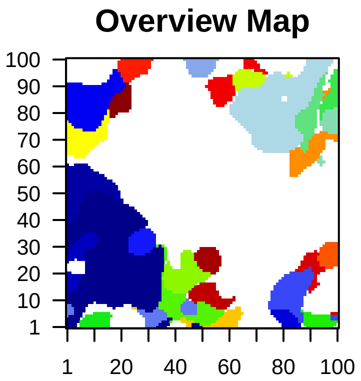
Correlation Cluster

Spot Summary: W

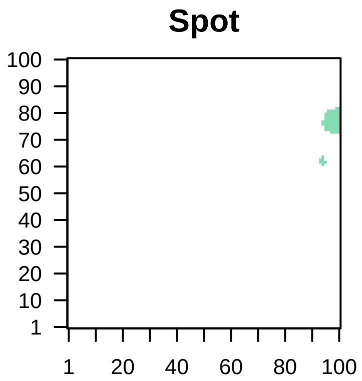
metagenes = 62
genes = 823

<r> metagenes = 0.95
<r> genes = 0.31
beta: r2= 9.52 / log p= −Inf

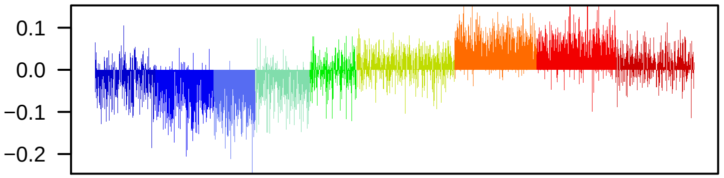
samples with spot = 413 (12.2 %)
A * : 2 (0.6 %)
A F * : 2 (0.6 %)
C F * : 7 (2.6 %)
F * : 25 (4.5 %)
F J * : 189 (40.8 %)
J * : 155 (34.7 %)
N * : 33 (7.4 %)



Overview Map



Spot

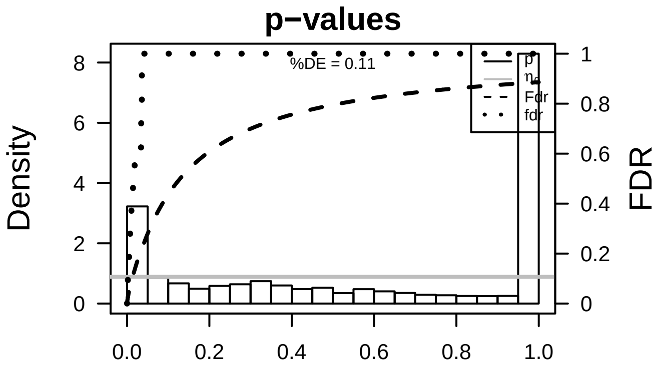


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_176146	0.96	−0.79	0.51	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
2	ILMN_166860	0.89	−0.76	0.41		
3	ILMN_178617	0.85	−0.97	0.44	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
4	ILMN_165798	0.82	−0.55	0.52	TERF2IP	TERF2 interacting protein [Source:HGNC Symbol;Acc:HGNC
5	ILMN_174216	0.79	−0.89	0.64	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
6	ILMN_232088	0.78	−0.79	0.49	CXCR4	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
7	ILMN_178181	0.76	−0.72	0.34	PAPSS1	3'−phosphoadenosine 5'−phosphosulfate synthase 1 [Source
8	ILMN_228556	0.76	−0.7	0.41		
9	ILMN_177801	0.75	−0.6	0.32	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit [So
10	ILMN_235945	0.72	−0.67	0.36	ERGIC3	ERGIC and golgi 3 [Source:HGNC Symbol;Acc:HGNC:15927
11	ILMN_173185	0.71	−0.59	0.57		
12	ILMN_177279	0.7	−0.49	0.58	ARPP19	cAMP regulated phosphoprotein 19 [Source:HGNC Symbol;A
13	ILMN_165611	0.68	−0.67	0.4	MYLIP	myosin regulatory light chain interacting protein [Source:HGN
14	ILMN_324439	0.68	−0.68	0.57		
15	ILMN_169579	0.67	−0.52	0.48	CUL4A	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
16	ILMN_170684	0.66	−0.72	0.59	PGAM4	phosphoglycerate mutase family member 4 [Source:HGNC S
17	ILMN_225118	0.65	−0.74	0.73	ERP29	endoplasmic reticulum protein 29 [Source:HGNC Symbol;Acc
18	ILMN_165588	0.64	−0.59	0.7	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
19	ILMN_237416	0.64	−0.6	0.7		
20	ILMN_177602	0.64	−0.65	0.69	EIF4H	eukaryotic translation initiation factor 4H [Source:HGNC Syml

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−93	445 / 7275	Lympl	HOPP_Txn_elongation
2	6e−86	472 / 8568	Colon	TxWk_Colon
3	2e−84	483 / 9054	Colon	Tx_Colon
4	2e−80	384 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
5	2e−79	489 / 9555	Colon	TssA_Colon
6	9e−77	492 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
7	8e−70	454 / 8771	Chror	5_Tx_Melanocytes
8	1e−68	426 / 7854	Chror	5_Tx_Fibroblasts
9	3e−68	449 / 8678	Colon	Quies3_Colon
10	5e−68	538 / 12298	Chror	2_TssA_Melanocytes
11	2e−67	435 / 8226	Lympl	HOPP_Active_promoter
12	3e−67	344 / 5356	Lympl	HOPP_Txn_transition
13	3e−61	509 / 11455	Chror	2_TssA_Fibroblasts
14	4e−61	387 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	4e−53	531 / 12983	Chror	2_TssA_Neuronal_Progenitor
16	2e−51	443 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
17	1e−48	477 / 10999	Colon	TssWk_Colon
18	6e−43	438 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
19	3e−39	405 / 8990	Chror	15_Quies_Fibroblasts
20	2e−36	438 / 10430	Brain	Overlap_fetal_midbrain_Quies
21	5e−36	473 / 11836	Chror	3_TssF_Melanocytes
22	2e−35	122 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	3e−34	483 / 12393	Chror	15_Quies_Neuronal_Progenitor
24	1e−32	143 / 1797	GSEA	PILON_KLF1_TARGETS_DN
25	5e−32	363 / 8098	Lympl	HOPP_Weak_promoter
26	3e−31	287 / 5699	Chror	6_EnhG_Melanocytes
27	6e−31	484 / 12741	Chror	7_Enh_Melanocytes
28	1e−28	260 / 5067	TF	ICGC_Taf1_targets
29	4e−28	85 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
30	1e−27	48 / 242	Refer	Chaussabel_3,9_Kinases
31	1e−26	163 / 2535	CC	nucleoplasm
32	1e−26	433 / 11130	Chror	15_Quies_Melanocytes
33	1e−24	359 / 8613	Chror	7_Enh_Fibroblasts
34	6e−24	116 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
35	4e−23	54 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
36	3e−22	318 / 7448	Lympl	HOPP_Strong_enhancer
37	6e−22	357 / 8818	MF	protein binding
38	2e−21	46 / 302	Refer	Chaussabel_3,4_Protein phosphatases
39	3e−21	113 / 1601	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
40	3e−20	103 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	3 / 111	HORVATH_aging_genes meth DOWN
2	0.7	3 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−07	67 / 1272	regulation of transcription, DNA−templated
2	1e−06	7 / 22	regulation of protein phosphatase type 2A activity
3	4e−06	12 / 86	mRNA export from nucleus
4	4e−06	76 / 1643	transcription, DNA−templated
5	8e−06	8 / 39	mitotic nuclear envelope disassembly
6	1e−05	7 / 29	tRNA export from nucleus
7	2e−05	12 / 102	protein sumoylation
8	2e−05	20 / 255	viral process
9	5e−05	23 / 335	protein transport
10	7e−05	12 / 115	regulation of signal transduction by p53 class mediator
11	8e−05	23 / 346	transcription from RNA polymerase II promoter
12	1e−04	4 / 10	microtubule organizing center organization
13	1e−04	6 / 29	regulation of glucose transport
14	2e−04	12 / 130	DNA replication
15	4e−04	26 / 457	regulation of transcription from RNA polymerase II promoter

Brain

Rank	p−value	#in/all	Geneset
1	2e−80	384 / 5936	Overlap_fetal_midbrain_HetRpts
2	9e−77	492 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−51	443 / 9504	Overlap_fetal_midbrain_K9K27me3
4	6e−43	438 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	2e−36	438 / 10430	Overlap_fetal_midbrain_Quies
6	2e−08	136 / 3164	Mid_Frontal_Lobe_ZNF
7	4e−08	65 / 1171	Fetal_EnhP
8	5e−06	40 / 681	Overlap_fetal_midbrain_EnhP
9	2e−05	43 / 796	Overlap_fetal_midbrain_ZNF
10	1e−03	22 / 386	Fetal_ZNF
11	7e−03	46 / 1162	Fetal_Enh
12	9e−03	17 / 328	Fetal_Het
13	2e−02	37 / 937	Fetal_EnhG
14	3e−02	10 / 180	Overlap_fetal_midbrain_Het
15	1e−01	47 / 1436	Fetal_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	0 / 13	RHODES_CANCER_META_SIGNATURE
2	0.005	9 / 117	PanCan_Driver_Gene_geneset_nanostring
3	0.016	4 / 36	PanCan_HK_geneset_nanostring
4	0.054	2 / 14	GENTLES_modul4
5	0.055	9 / 178	SPANG_LPS−index2
6	0.061	2 / 15	WOLFER_overlap genes
7	0.069	2 / 16	GENTLES_modul14
8	0.096	0 / 14	LIU_COMMON_CANCER_GENES
9	0.119	1 / 12	LIU_BREAST_CANCER
10	0.129	3 / 46	PanCan_DNARepair_geneset_nanostring
11	0.135	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.152	4 / 76	PanCan_Wnt_geneset_nanostring
13	0.220	1 / 9	GENTLES_modul3
14	0.220	1 / 9	GENTLES_modul5
15	0.224	6 / 150	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−26	163 / 2535	nucleoplasm
2	3e−19	227 / 4828	nucleus
3	3e−10	197 / 4822	cytoplasm
4	4e−10	101 / 1979	membrane
5	4e−09	49 / 721	nucleolus
6	2e−08	130 / 2979	cytosol
7	2e−06	18 / 179	nuclear speck
8	5e−06	10 / 60	nuclear pore
9	5e−06	35 / 561	intracellular membrane−bounded organelle
10	2e−05	42 / 777	Golgi apparatus
11	4e−05	14 / 144	nuclear envelope
12	5e−05	60 / 1304	mitochondrion
13	8e−05	7 / 39	chromosome, telomeric region
14	1e−04	10 / 88	peroxisome
15	6e−04	4 / 15	nuclear periphery

Chr

Rank	p−value	#in/all	Geneset
1	0.01	47 / 1217	Chr 3
2	0.04	42 / 1170	Chr 7
3	0.05	15 / 342	Chr 18
4	0.05	29 / 769	Chr 15
5	0.07	28 / 768	Chr 14
6	0.16	47 / 1492	Chr 2
7	0.18	15 / 422	Chr 13
8	0.18	34 / 1060	Chr 5
9	0.28	35 / 1160	Chr 12
10	0.38	35 / 1211	Chr 6
11	0.42	18 / 619	Chr 20
12	0.52	26 / 954	Chr 9
13	0.61	25 / 959	Chr 16
14	0.65	23 / 902	Chr 4
15	0.66	23 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−70	454 / 8771	5_Tx_Melanocytes
2	1e−68	426 / 7854	5_Tx_Fibroblasts
3	5e−68	538 / 12298	2_TssA_Melanocytes
4	3e−61	509 / 11455	2_TssA_Fibroblasts
5	4e−61	387 / 6970	5_Tx_Neuronal_Progenitor
6	4e−53	531 / 12983	2_TssA_Neuronal_Progenitor
7	3e−39	405 / 8990	15_Quies_Fibroblasts
8	5e−36	473 / 11836	3_TssF_Melanocytes
9	3e−34	483 / 12393	15_Quies_Neuronal_Progenitor
10	3e−31	287 / 5699	6_EnhG_Melanocytes
11	6e−31	484 / 12741	7_Enh_Melanocytes
12	1e−26	433 / 11130	15_Quies_Melanocytes
13	1e−24	359 / 8613	7_Enh_Fibroblasts
14	4e−19	207 / 4237	14_ZNF_Neuronal_Progenitor
15	1e−14	356 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−86	472 / 8568	TxWk_Colon
2	2e−84	483 / 9054	Tx_Colon
3	2e−79	489 / 9555	TssA_Colon
4	3e−68	449 / 8678	Quies3_Colon
5	1e−48	477 / 10999	TssWk_Colon
6	6e−24	116 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	7e−19	305 / 7354	TssF_Colon
8	2e−15	95 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	5e−11	217 / 5373	EnhWk1_Colon
10	3e−10	370 / 10779	Enh_Colon
11	6e−10	104 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	7e−09	63 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	5e−08	76 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	7e−06	55 / 1083	ZNF_Colon
15	7e−06	58 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_

Glio

Rank	p−value	#in/all	Geneset
1	7e−20	45 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	5e−15	117 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−14	65 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	4e−13	102 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	3e−03	7 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	1e−02	16 / 315	Up
7	4e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
8	5e−02	6 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	7e−02	8 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	2e−01	3 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	2e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
12	2e−01	14 / 401	Down_b
13	2e−01	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
14	3e−01	3 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	3e−01	1 / 11	KIM amplified & overexpressed in LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−35	122 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	1e−32	143 / 1797	PILON_KLF1_TARGETS_DN
3	4e−28	85 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
4	4e−23	54 / 388	SHEN_SMARCA2_TARGETS_UP
5	3e−21	113 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
6	3e−20	103 / 1417	PUJANA_BRCA1_PCC_NETWORK
7	2e−18	88 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	1e−15	47 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
9	2e−13	45 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
10	2e−13	75 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
11	6e−13	80 / 1241	PUJANA_ATM_PCC_NETWORK
12	1e−12	53 / 649	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
13	3e−12	49 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
14	5e−12	19 / 92	DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER
15	1e−11	52 / 666	BENPORATH_MYC_MAX_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	2e−05	12 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	2e−03	12 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	5e−03	10 / 138	HALLMARK_FATTY_ACID_METABOLISM
4	5e−03	12 / 185	HALLMARK_MTORC1_SIGNALING
5	7e−03	11 / 170	HALLMARK_MYC_TARGETS_V1
6	8e−03	11 / 173	HALLMARK_E2F_TARGETS
7	9e−03	9 / 130	HALLMARK_DNA_REPAIR
8	1e−02	11 / 179	HALLMARK_G2M_CHECKPOINT
9	1e−02	9 / 132	HALLMARK_UV_RESPONSE_DN
10	2e−02	7 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	2e−02	7 / 103	HALLMARK_BILE_ACID_METABOLISM
12	3e−02	6 / 87	HALLMARK_PROTEIN_SECRETION
13	5e−02	9 / 176	HALLMARK_ADIPOGENESIS
14	7e−02	9 / 185	HALLMARK_P53_PATHWAY
15	1e−01	5 / 91	HALLMARK_PEROXISOME

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.005	13 / 211	Homuth_BMI−associated−genes_DN
2	0.206	2 / 31	DUMEAUX_Fasting enriched genes
3	0.211	6 / 147	Homuth_BMI−associated−genes_UP
4	0.241	1 / 10	DUMEAUX_Smoking literature genes up
5	0.586	1 / 32	Marjolein_ageing−genes_DN
6	0.925	1 / 94	DUMEAUX_Smoking enriched genes
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−93	445 / 7275	HOPP_Txn_elongation
2	2e−67	435 / 8226	HOPP_Active_promoter
3	3e−67	344 / 5356	HOPP_Txn_transition
4	5e−32	363 / 8098	HOPP_Weak_promoter
5	3e−22	318 / 7448	HOPP_Strong_enhancer
6	1e−14	267 / 6559	HOPP_Weak_txn
7	8e−14	276 / 6959	HOPP_Weak_enhancer
8	2e−13	78 / 1169	SPANG_BCR DN
9	8e−11	76 / 1270	SPANG_BCR UP
10	3e−09	38 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
11	3e−09	39 / 493	WIRTH_lymphoma937_spot J
12	1e−07	48 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
13	1e−07	48 / 777	WIRTH_lymphoma937_spot D
14	3e−05	21 / 283	TARTE_Plasmablast signature
15	2e−04	11 / 109	ROSOLOWSKI_blue total

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 27	Hugo_melanoma−all−LEF1_UP
2	0.3	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	6e−22	357 / 8818	protein binding
2	5e−11	66 / 1013	poly(A) RNA binding
3	1e−07	75 / 1475	DNA binding
4	9e−07	7 / 21	protein phosphatase type 2A regulator activity
5	3e−06	8 / 34	histone−lysine N−methyltransferase activity
6	6e−06	20 / 232	ligase activity
7	8e−06	21 / 256	ubiquitin protein ligase binding
8	9e−06	23 / 301	ubiquitin−protein transferase activity
9	3e−05	52 / 1065	zinc ion binding
10	8e−05	15 / 173	ubiquitin protein ligase activity
11	1e−04	4 / 10	poly(A) binding
12	1e−04	20 / 283	nucleotide binding
13	2e−04	17 / 227	transcription coactivator activity
14	3e−04	24 / 399	RNA binding
15	3e−04	42 / 877	transcription factor activity, sequence−specific DNA binding

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−12	40 / 400	hsa−miR−519c−3p
2	2e−12	38 / 366	hsa−miR−519b−3p
3	2e−12	27 / 190	hsa−miR−330−3p
4	1e−11	38 / 389	hsa−miR−519a
5	2e−09	21 / 157	hsa−miR−141
6	3e−09	29 / 295	hsa−miR−561
7	9e−09	35 / 429	hsa−miR−548n
8	9e−09	22 / 187	hsa−miR−586
9	1e−08	39 / 520	hsa−miR−106a
10	3e−08	38 / 513	hsa−miR−106b
11	3e−08	37 / 493	hsa−miR−103
12	3e−08	17 / 121	hsa−miR−421
13	4e−08	23 / 221	hsa−miR−181d
14	5e−08	19 / 155	hsa−miR−450b−5p
15	6e−08	23 / 225	hsa−miR−181b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 12	BENTINK_src.2
2	0.26	1 / 11	BENTINK_ras.4
3	0.30	1 / 13	BENTINK_myc.1
4	0.32	1 / 14	GUSTAFSON_PI3K_UP
5	0.34	1 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−27	48 / 242	Chaussabel_3,9_Kinases
2	2e−21	46 / 302	Chaussabel_3,4_Protein phosphatases
3	4e−12	23 / 139	Chaussabel_1,8_Metabolism Biosynthesis
4	4e−11	55 / 759	PROTEINATLAS_epididymis
5	1e−10	72 / 1176	PROTEINATLAS_duodenum
6	2e−10	53 / 740	PROTEINATLAS_esophagus
7	2e−10	72 / 1194	PROTEINATLAS_stomach
8	2e−10	71 / 1173	PROTEINATLAS_rectum
9	3e−10	62 / 959	PROTEINATLAS_nasopharynx
10	1e−09	56 / 850	PROTEINATLAS_skin
11	1e−09	27 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
12	1e−09	73 / 1268	PROTEINATLAS_colon
13	2e−09	58 / 912	PROTEINATLAS_urinary bladder
14	3e−09	35 / 412	WIRTH_Immune system
15	1e−08	66 / 1167	PROTEINATLAS_gallbladder

Telomeres

Rank	p−value	#in/all	Geneset
1	0.005	3 / 13	Alternative lengthening of telomeres
2	0.036	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	

TF

Rank	p−value	#in/all	Geneset
1	1e−28	260 / 5067	ICGC_Taf1_targets
2	3e−19	247 / 5442	ICGC_Pmlsc71910_targets
3	2e−18	209 / 4362	ICGC_Creb1_targets
4	6e−18	244 / 5466	ICGC_Nficsc81335_targets
5	1e−17	130 / 2215	ICGC_GabpPcr2_targets
6	2e−17	224 / 4890	ICGC_Bclaf101388_targets
7	1e−16	265 / 6267	ICGC_Yy1_targets
8	1e−15	253 / 5984	ICGC_Mta3_targets
9	1e−15	218 / 4881	ICGC_Atf2_targets
10	1e−15	238 / 5518	ICGC_Stat5_targets
11	9e−15	231 / 5383	ICGC_Sp1_targets
12	1e−14	197 / 4345	ICGC_Zeb1_targets
13	2e−14	228 / 5312	ICGC_Tcf12_targets
14	3e−14	200 / 4468	ICGC_Egr1_targets
15	6e−14	91 / 1452	ICGC_Six5_targets

Correlation Cluster

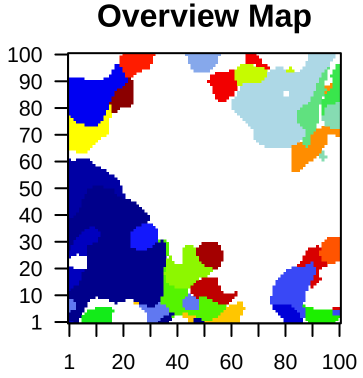
Spot Summary: X

metagenes = 69
genes = 172

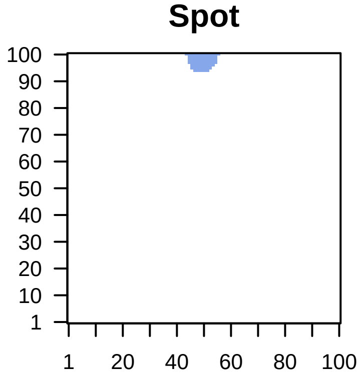
<r> metagenes = 0.95
<r> genes = 0.05
beta: r2= 0.41 / log p= −Inf

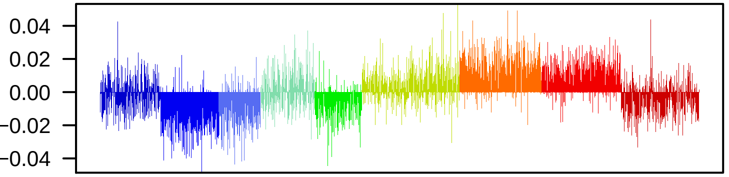
samples with spot = 0 (0 %)

Overview Map



Spot





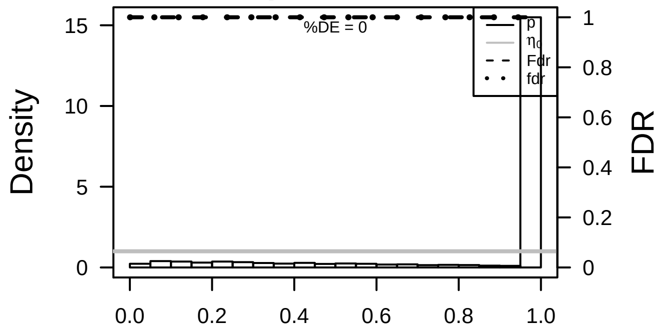
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_167181	0.84	−0.38	0.13	UTS2	urotensin 2 [Source:HGNC Symbol;Acc:HGNC:12636]
2	ILMN_323087	0.57	−0.29	0.16		phosphodiesterase 4D interacting protein pseudogene 1 [Sou
3	ILMN_186309	0.36	−0.19	0.2		T cell receptor delta variable 3 [Source:HGNC Symbol;Acc:H
4	ILMN_174888	0.33	−0.28	0.26	TOB2	transducer of ERBB2, 2 [Source:HGNC Symbol;Acc:HGNC:1
5	ILMN_165872	0.31	−0.25	0.27	ZBTB25	zinc finger and BTB domain containing 25 [Source:HGNC Sy
6	ILMN_221287	0.3	−0.19	0.17	ESM1	endothelial cell specific molecule 1 [Source:HGNC Symbol;A
7	ILMN_171117	0.3	−0.19	0.35	CREB3L4	cAMP responsive element binding protein 3 like 4 [Source:HG
8	ILMN_171949	0.3	−0.2	0.19	EPHX4	epoxide hydrolase 4 [Source:HGNC Symbol;Acc:HGNC:2375
9	ILMN_324806	0.29	−0.28	0.26		
10	ILMN_191509	0.29	−0.22	0.25		
11	ILMN_179765	0.28	−0.21	0.37	ASCC3	activating signal cointegrator 1 complex subunit 3 [Source:HG
12	ILMN_176630	0.28	−0.21	0.44	MIR658	ankyrin repeat domain 54 [Source:HGNC Symbol;Acc:HGNC
13	ILMN_323387	0.27	−0.31	0.29	ATXN1L	ataxin 1 like [Source:HGNC Symbol;Acc:HGNC:33279]
14	ILMN_177146	0.27	−0.18	0.37	RPL36	ribosomal protein L36 [Source:HGNC Symbol;Acc:HGNC:136
15	ILMN_178141	0.27	−0.29	0.38		
16	ILMN_177185	0.27	−0.22	0.38	ZNF575	zinc finger protein 575 [Source:HGNC Symbol;Acc:HGNC:27
17	ILMN_330862	0.27	−0.2	0.19	MIR1471	microRNA 1471 [Source:HGNC Symbol;Acc:HGNC:35380]
18	ILMN_174958	0.26	−0.22	0.35	ZNF777	zinc finger protein 777 [Source:HGNC Symbol;Acc:HGNC:22
19	ILMN_177438	0.26	−0.21	0.31	ZHX3	zinc fingers and homeoboxes 3 [Source:HGNC Symbol;Acc:H
20	ILMN_181196	0.26	−0.23	0.26		protein geranylgeranyltransferase type I subunit beta pseudo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−04	22 / 1717	MF	metal ion binding
2	4e−04	4 / 61	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN
3	1e−03	2 / 9	GSEA	PID_VEGF_VEGFR_PATHWAY
4	1e−03	2 / 9	GSEA	REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS
5	1e−03	3 / 38	GSEA	KRASNOSELSKAYA_ILF3_TARGETS_DN
6	2e−03	2 / 11	MF	actinin binding
7	2e−03	2 / 11	BP	positive regulation of nitric−oxide synthase biosynthetic process
8	4e−03	3 / 53	GSEA	LEE_LIVER_CANCER_E2F1_UP
9	4e−03	2 / 16	GSEA	TERAMOTO_OPN_TARGETS_CLUSTER_7
10	4e−03	2 / 17	BP	calcium−mediated signaling using intracellular calcium source
11	4e−03	3 / 57	Lymph	LENZ_Stromal signature 2
12	5e−03	41 / 4828	CC	nucleus
13	6e−03	10 / 681	Brain	Overlap_fetal_midbrain_EnhP
14	6e−03	18 / 1643	BP	transcription, DNA−templated
15	6e−03	2 / 21	GSEA	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON
16	8e−03	2 / 23	GSEA	ALONSO_METASTASIS_DN
17	8e−03	3 / 70	GSEA	MCBRYAN_PUBERTAL_BREAST_6_7WK_DN
18	8e−03	4 / 136	GSEA	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20
19	9e−03	2 / 25	BP	response to testosterone
20	1e−02	69 / 9555	Colon	TssA_Colon
21	1e−02	2 / 26	GSEA	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP
22	1e−02	2 / 26	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN
23	1e−02	2 / 26	GSEA	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY
24	1e−02	7 / 414	GSEA	KIM_WT1_TARGETS_DN
25	1e−02	6 / 318	GSEA	COLINA_TARGETS_OF_4EBP1_AND_4EBP2
26	1e−02	16 / 1475	MF	DNA binding
27	1e−02	6 / 323	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
28	1e−02	2 / 28	MF	glucuronosyltransferase activity
29	1e−02	69 / 9635	Chrom	3_TssF_Fibroblasts
30	1e−02	5 / 236	GSEA	XU_GH1_AUTOCRINE_TARGETS_UP
31	1e−02	2 / 29	MF	cyclin−dependent protein serine/threonine kinase activity
32	1e−02	2 / 29	BP	regulation of protein kinase activity
33	1e−02	3 / 84	MF	hydrolase activity
34	1e−02	4 / 156	GSEA	DARWICHE_PAPILLOMA_RISK_HIGH_DN
35	1e−02	2 / 30	GSEA	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
36	1e−02	4 / 158	GSEA	DARWICHE_SQUAMOUS_CELL_CARCINOMA_DN
37	1e−02	2 / 31	BP	protein O−linked glycosylation
38	1e−02	2 / 31	GSEA	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN
39	1e−02	2 / 32	CC	dendritic shaft
40	1e−02	2 / 32	BP	muscle filament sliding

p−values



Aging

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

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	2 / 54	KUIPER_MM poor survival
2	0.08	1 / 15	LIU_PROSTATE_CANCER_DN
3	0.17	0 / 13	LIU_LIVER_CANCER
4	0.20	1 / 39	ZHANG_MM up
5	0.22	5 / 554	Lembcke_Colonic Inflammation
6	0.31	2 / 193	PanCan_PI3K_geneset_nanostring
7	0.34	1 / 73	SHAUGHNESSY_MM high risk
8	0.36	1 / 76	PanCan_Wnt_geneset_nanostring
9	0.52	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	0.58	1 / 150	PanCan_MAPK_geneset_nanostring
11	0.59	3 / 527	Lembcke_Normal vs Adenoma
12	0.83	1 / 301	SPANG_BCL6−index2
13	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
14	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.01	69 / 9635	3_TssF_Fibroblasts
2	0.02	79 / 11455	2_TssA_Fibroblasts
3	0.03	8 / 630	14_ZNF_Fibroblasts
4	0.03	86 / 12983	2_TssA_Neuronal_Progenitor
5	0.04	17 / 1846	14_ZNF_Melanocytes
6	0.04	44 / 5956	3_TssF_Neuronal_Progenitor
7	0.07	80 / 12298	2_TssA_Melanocytes
8	0.08	59 / 8771	5_Tx_Melanocytes
9	0.11	76 / 11836	3_TssF_Melanocytes
10	0.11	79 / 12393	15_Quies_Neuronal_Progenitor
11	0.12	59 / 8990	15_Quies_Fibroblasts
12	0.15	80 / 12741	7_Enh_Melanocytes
13	0.15	33 / 4795	6_EnhG_Fibroblasts
14	0.20	19 / 2682	12_Het_Neuronal_Progenitor
15	0.23	69 / 11130	15_Quies_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 61	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN
2	1e−03	2 / 9	PID_VEGF_VEGFR_PATHWAY
3	1e−03	2 / 9	REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS
4	1e−03	3 / 38	KRASNOSELSKAYA_ILF3_TARGETS_DN
5	4e−03	3 / 53	LEE_LIVER_CANCER_E2F1_UP
6	4e−03	2 / 16	TERAMOTO_OPN_TARGETS_CLUSTER_7
7	6e−03	2 / 21	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON
8	8e−03	2 / 23	ALONSO_METASTASIS_DN
9	8e−03	3 / 70	MCBRYAN_PUBERTAL_BREAST_6_7WK_DN
10	8e−03	4 / 136	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20M
11	1e−02	2 / 26	BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_UP
12	1e−02	2 / 26	BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN
13	1e−02	2 / 26	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY
14	1e−02	7 / 414	KIM_WT1_TARGETS_DN
15	1e−02	6 / 318	COLINA_TARGETS_OF_4EBP1_AND_4EBP2

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.004	3 / 57	LENZ_Stromal signature 2
2	0.078	1 / 14	BENTINK_mBL UP
3	0.117	11 / 1270	SPANG_BCR UP
4	0.135	3 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
5	0.138	5 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
6	0.151	3 / 232	WIRTH_lymphoma937_spot B
7	0.157	5 / 493	WIRTH_lymphoma937_spot J
8	0.188	1 / 36	Subero_MM_hyper_meth
9	0.207	1 / 40	Monti_BCR_cluster
10	0.229	3 / 286	ZHANG_DLBCL mutated
11	0.234	1 / 46	Subero_DLBCL_hypo_meth
12	0.243	1 / 48	Subero_B−ALL_hyper_meth
13	0.294	1 / 60	Subero_mBL_hyper_meth
14	0.322	1 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
15	0.333	1 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 23	Esophageal cancer
2	0.2	1 / 30	Systemic lupus erythematosus (SLE)
3	0.5	1 / 116	Cancer
4	1.0	0 / 7	Thyroid carcinoma, papillary
5	1.0	0 / 123	Pancreatic cancer
6	1.0	0 / 68	Glioblastoma multiforme, somatic
7	1.0	0 / 63	Gastrointestinal
8	1.0	0 / 3	Pituitary adenoma
9	1.0	0 / 95	Colorectal cancer
10	1.0	0 / 2	Adenomas, multiple colorectal
11	1.0	0 / 124	Prostate cancer
12	1.0	0 / 48	Alzheimer disease, susceptibility to
13	1.0	0 / 7	Schizophrenia, susceptibility to
14	1.0	0 / 20	Parkinson disease
15	1.0	0 / 65	Hepatocellular carcinoma

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.03	3 / 119	Chaussabel_2,8_T−cells
2	0.07	1 / 13	JONGENEEL_Uterus
3	0.08	4 / 275	Chaussabel_3,7_Spliceosome
4	0.08	1 / 14	JONGENEEL_Peripheral Blood Lymphocytes
5	0.10	1 / 18	JONGENEEL_Trachea
6	0.11	1 / 20	JONGENEEL_Thymus
7	0.11	1 / 21	JONGENEEL_Adrenal Gland
8	0.13	3 / 220	WIRTH_Testis
9	0.15	2 / 119	Chaussabel_2,4_Ribosomal proteins
10	0.18	2 / 132	WIRTH_Muscle
11	0.20	4 / 398	PROTEINATLAS_skeletal muscle
12	0.20	1 / 39	VAQUERIZAS_Testis_TF
13	0.32	5 / 647	PROTEINATLAS_lateral ventricle
14	0.36	1 / 76	WIRTH_Homeostasis
15	0.41	2 / 242	Chaussabel_3,9_Kinases

BP

Rank	p−value	#in/all	Geneset
1	0.002	2 / 11	positive regulation of nitric−oxide synthase biosynthetic process
2	0.004	2 / 17	calcium−mediated signaling using intracellular calcium source
3	0.006	18 / 1643	transcription, DNA−templated
4	0.009	2 / 25	response to testosterone
5	0.012	2 / 29	regulation of protein kinase activity
6	0.014	2 / 31	protein O−linked glycosylation
7	0.015	2 / 32	muscle filament sliding
8	0.017	2 / 35	regulation of synaptic plasticity
9	0.021	3 / 102	muscle contraction
10	0.021	4 / 182	extracellular matrix organization
11	0.028	2 / 45	cardiac muscle contraction
12	0.037	4 / 217	chemical synaptic transmission
13	0.046	2 / 59	regulation of protein stability
14	0.048	3 / 141	skeletal system development
15	0.056	2 / 66	microtubule−based movement

CC

Rank	p−value	#in/all	Geneset
1	0.005	41 / 4828	nucleus
2	0.015	2 / 32	dendritic shaft
3	0.017	3 / 94	dendritic spine
4	0.020	2 / 38	ciliary tip
5	0.024	3 / 106	Z disc
6	0.028	2 / 45	cytosolic large ribosomal subunit
7	0.035	2 / 51	phagocytic vesicle membrane
8	0.039	4 / 220	synapse
9	0.056	1 / 10	dense core granule
10	0.062	1 / 11	cytoplasmic dynein complex
11	0.067	1 / 12	interstitial matrix
12	0.067	1 / 12	membrane−bounded vesicle
13	0.067	1 / 12	muscle myosin complex
14	0.068	2 / 74	cell body
15	0.077	3 / 171	postsynaptic density

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	69 / 9555	TssA_Colon
2	0.02	13 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	0.02	12 / 1083	ZNF_Colon
4	0.04	1 / 7	Budinska_A_Surface crypt−like_UP
5	0.04	74 / 10999	TssWk_Colon
6	0.05	60 / 8678	Quies3_Colon
7	0.05	1 / 9	Marisa_CRC−C3
8	0.11	1 / 20	Juehling_HNPCC−mutated−in−4
9	0.15	10 / 1186	HetRpts_Colon
10	0.18	7 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
11	0.19	8 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
12	0.20	2 / 142	Marisa_CRC−cluster−a
13	0.22	47 / 7354	TssF_Colon
14	0.23	11 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	0.26	6 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv

HM

Rank	p−value	#in/all	Geneset
1	0.04	3 / 132	HALLMARK_UV_RESPONSE_DN
2	0.14	2 / 116	HALLMARK_SPERMATOGENESIS
3	0.17	1 / 33	HALLMARK_ANGIOGENESIS
4	0.19	2 / 137	HALLMARK_UV_RESPONSE_UP
5	0.27	1 / 54	HALLMARK_MYC_TARGETS_V2
6	0.27	2 / 176	HALLMARK_ADIPOGENESIS
7	0.29	2 / 185	HALLMARK_P53_PATHWAY
8	0.38	1 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	0.39	1 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.53	1 / 130	HALLMARK_DNA_REPAIR
11	0.63	1 / 173	HALLMARK_E2F_TARGETS
12	0.64	1 / 176	HALLMARK_KRAS_SIGNALING_UP
13	0.65	1 / 179	HALLMARK_G2M_CHECKPOINT
14	0.65	1 / 183	HALLMARK_APICAL_JUNCTION
15	0.65	1 / 183	HALLMARK_GLYCOLYSIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 54	Hugo_melanoma−all−MET_DN
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	2 / 32	hsa−miR−1229
2	0.04	3 / 125	hsa−miR−383
3	0.06	1 / 11	hsa−miR−1180
4	0.06	2 / 72	hsa−miR−876−3p
5	0.07	1 / 13	hsa−miR−147b
6	0.07	4 / 272	hsa−miR−101
7	0.09	2 / 87	hsa−miR−496
8	0.09	2 / 89	hsa−miR−10a
9	0.12	2 / 105	hsa−miR−526b
10	0.14	2 / 113	hsa−miR−376c
11	0.15	1 / 28	hsa−miR−597
12	0.15	2 / 119	hsa−miR−380
13	0.15	3 / 233	hsa−miR−1252
14	0.15	2 / 121	hsa−miR−515−5p
15	0.16	2 / 123	hsa−miR−646

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	0.006	10 / 681	Overlap_fetal_midbrain_EnhP
2	0.042	67 / 9815	Overlap_fetal_midbrain_ReprPC
3	0.064	64 / 9504	Overlap_fetal_midbrain_K9K27me3
4	0.077	21 / 2630	Fetal_TssF
5	0.230	8 / 1012	Mid_Frontal_Lobe_Enh
6	0.295	12 / 1728	Fetal_ReprPCWk
7	0.322	37 / 5936	Overlap_fetal_midbrain_HetRpts
8	0.343	60 / 9917	Overlap_fetal_midbrain_ReprPCWk
9	0.359	9 / 1329	Overlap_fetal_midbrain_Enh
10	0.370	10 / 1506	Mid_Frontal_Lobe_Quies
11	0.401	8 / 1213	Fetal_TssP
12	0.425	6 / 906	Fetal_HetRpts
13	0.448	9 / 1436	Fetal_K9K27me3
14	0.494	4 / 630	Mid_Frontal_Lobe_EnhP
15	0.500	16 / 2709	Mid_Frontal_Lobe_HetRpts

Chr

Rank	p−value	#in/all	Geneset
1	0.02	15 / 1467	Chr 19
2	0.04	7 / 536	Chr 22
3	0.14	10 / 1170	Chr 7
4	0.22	8 / 994	Chr X
5	0.24	11 / 1492	Chr 2
6	0.27	8 / 1060	Chr 5
7	0.28	6 / 768	Chr 14
8	0.32	7 / 959	Chr 16
9	0.36	15 / 2323	Chr 1
10	0.42	6 / 904	Chr 10
11	0.50	2 / 289	Chr 21
12	0.59	2 / 342	Chr 18
13	0.60	5 / 902	Chr 4
14	0.70	3 / 619	Chr 20
15	0.70	2 / 422	Chr 13

Glio

Rank	p−value	#in/all	Geneset
1	0.06	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
2	0.14	1 / 26	Gorovets_LGG_NB_subclass
3	0.17	1 / 32	Donson−Misc immune function−associated with LTS in HGA
4	0.21	2 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	0.23	3 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
6	0.26	1 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
7	0.27	1 / 55	developing astrocytes
8	0.28	1 / 57	OL vs. MOG− OL
9	0.31	4 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
10	0.31	1 / 65	cultured astroglia vs. in vivo astrocytes
11	0.34	6 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
12	0.40	1 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
13	0.41	1 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
14	0.42	1 / 94	Weller_LGG_A_vs_O_UP
15	0.43	1 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN

Lifestyle

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

MF

Rank	p−value	#in/all	Geneset
1	3e−04	22 / 1717	metal ion binding
2	2e−03	2 / 11	actinin binding
3	1e−02	16 / 1475	DNA binding
4	1e−02	2 / 28	glucuronosyltransferase activity
5	1e−02	2 / 29	cyclin−dependent protein serine/threonine kinase activity
6	1e−02	3 / 84	hydrolase activity
7	2e−02	2 / 37	structural constituent of muscle
8	2e−02	2 / 42	SMAD binding
9	3e−02	8 / 646	protein homodimerization activity
10	5e−02	2 / 60	microtubule motor activity
11	6e−02	1 / 11	nucleotidyltransferase activity
12	7e−02	1 / 12	cAMP response element binding
13	7e−02	3 / 169	structural constituent of ribosome
14	8e−02	2 / 79	hormone activity
15	8e−02	1 / 14	G−protein coupled serotonin receptor activity

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.1	1 / 18	MYC_Metabolism UP
2	0.1	12 / 1478	ICGC_Myc_targets
3	0.2	13 / 1723	HEBENSTREIT_high expression TF
4	0.2	44 / 6868	ICGC_Elf1_targets
5	0.2	11 / 1501	ICGC_Usf1_targets
6	0.3	1 / 55	MYC_Targets UP
7	0.3	10 / 1452	ICGC_Six5_targets
8	0.4	16 / 2497	ICGC_Bcl11_targets
9	0.4	33 / 5383	ICGC_Sp1_targets
10	0.4	40 / 6578	ICGC_Pou2_targets
11	0.4	14 / 2215	ICGC_GabpPcr2_targets
12	0.4	38 / 6322	ICGC_Tcf3_targets
13	0.4	17 / 2759	ICGC_Bcl3_targets
14	0.5	26 / 4362	ICGC_Creb1_targets
15	0.5	32 / 5466	ICGC_Nficsc81335_targets

Correlation Cluster

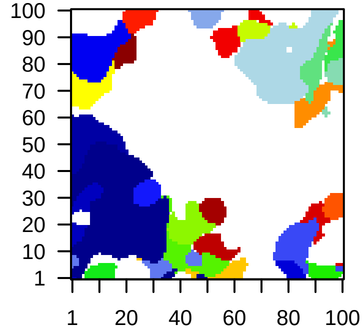
Spot Summary: Y

metagenes = 125
genes = 830

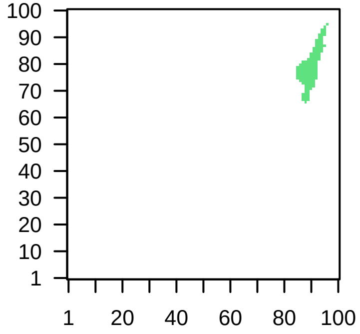
<r> metagenes = 0.95
<r> genes = 0.27
beta: r2= 9.17 / log p= −Inf

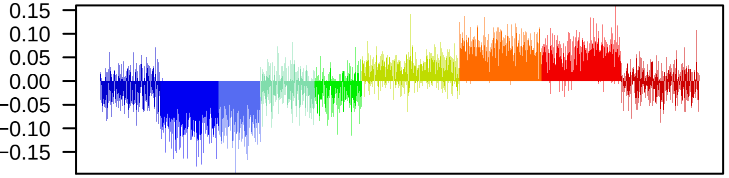
samples with spot = 343 (10.1 %)
A * : 1 (0.3 %)
A F * : 2 (0.6 %)
C F * : 1 (0.4 %)
F * : 15 (2.7 %)
F J * : 193 (41.7 %)
J * : 128 (28.6 %)
N * : 3 (0.7 %)

Overview Map



Spot





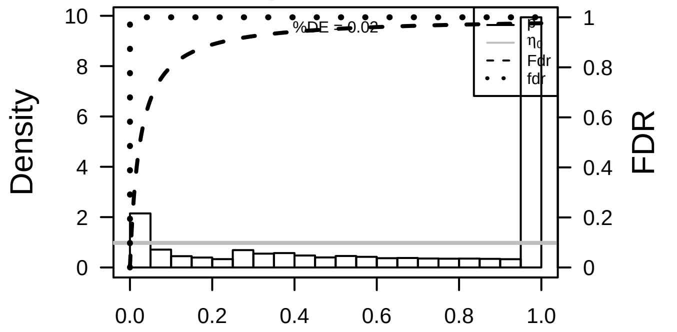
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_229476	1.15	−0.77	0.28	AMY1A	amylase, alpha 1A (salivary) [Source:HGNC Symbol;Acc:HGI
2	ILMN_168842	1.05	−1.38	0.29	FCER1A	Fc fragment of IgE receptor Ia [Source:HGNC Symbol;Acc:H(
3	ILMN_175424	0.79	−0.69	0.39		
4	ILMN_175316	0.77	−0.9	0.16	IPO8	importin 8 [Source:HGNC Symbol;Acc:HGNC:9853]
5	ILMN_169342	0.77	−0.67	0.61		
6	ILMN_169417	0.72	−0.62	0.78	PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:I
7	ILMN_235202	0.71	−0.97	0.08	DSTYK	dual serine/threonine and tyrosine protein kinase [Source:HG
8	ILMN_236702	0.69	−0.59	0.71	SEC61G	Sec61 translocon gamma subunit [Source:HGNC Symbol;Acc
9	ILMN_213613	0.68	−0.71	0.61	MIR7705	poly(A) binding protein cytoplasmic 1 [Source:HGNC Symbol;
10	ILMN_326660	0.65	−0.47	0.56		fatty acid binding protein 5 pseudogene 2 [Source:HGNC Syn
11	ILMN_240021	0.65	−0.5	0.35	SRI	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
12	ILMN_180948	0.64	−0.47	0.67	SPCS2	signal peptidase complex subunit 2 [Source:HGNC Symbol;A
13	ILMN_229907	0.64	−0.61	0.23	LUC7L3	LUC7 like 3 pre−mRNA splicing factor [Source:HGNC Symbo
14	ILMN_236639	0.63	−0.62	0.62		
15	ILMN_168356	0.63	−0.56	0.74		small nuclear ribonucleoprotein polypeptide G pseudogene 5
16	ILMN_172028	0.62	−0.56	0.73	ESD	esterase D [Source:HGNC Symbol;Acc:HGNC:3465]
17	ILMN_330066	0.62	−0.82	0.64	SLC35E2B	solute carrier family 35 member E2B [Source:HGNC Symbol;
18	ILMN_165546	0.62	−0.42	0.58	TSPAN3	tetraspanin 3 [Source:HGNC Symbol;Acc:HGNC:17752]
19	ILMN_322858	0.61	−0.68	0.5	SLC35E2B	solute carrier family 35 member E2B [Source:HGNC Symbol;
20	ILMN_176766	0.61	−0.63	0.47	CERS6	ceramide synthase 6 [Source:HGNC Symbol;Acc:HGNC:238

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−90	537 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
2	4e−76	471 / 8226	Lympl	HOPP_Active_promoter
3	3e−74	438 / 7275	Lympl	HOPP_Txn_elongation
4	1e−71	553 / 11455	Chror	2_TssA_Fibroblasts
5	2e−69	570 / 12298	Chror	2_TssA_Melanocytes
6	5e−60	461 / 8771	Chror	5_Tx_Melanocytes
7	4e−59	367 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
8	7e−58	569 / 12983	Chror	2_TssA_Neuronal_Progenitor
9	1e−54	423 / 7854	Chror	5_Tx_Fibroblasts
10	2e−53	472 / 9555	Colon	TssA_Colon
11	4e−49	420 / 8098	Lympl	HOPP_Weak_promoter
12	2e−46	429 / 8568	Colon	TxWk_Colon
13	1e−45	431 / 8678	Colon	Quies3_Colon
14	2e−43	451 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
15	2e−42	491 / 10999	Colon	TssWk_Colon
16	4e−42	435 / 9054	Colon	Tx_Colon
17	2e−40	366 / 6970	Chror	5_Tx_Neuronal_Progenitor
18	2e−39	427 / 8990	Chror	15_Quies_Fibroblasts
19	1e−33	441 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
20	2e−32	492 / 11836	Chror	3_TssF_Melanocytes
21	3e−29	111 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
22	2e−28	113 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
23	4e−28	462 / 11130	Chror	15_Quies_Melanocytes
24	8e−28	281 / 5356	Lympl	HOPP_Txn_transition
25	3e−26	318 / 6559	Lympl	HOPP_Weak_txn
26	1e−24	134 / 1797	GSEA	PILON_KLF1_TARGETS_DN
27	2e−23	82 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
28	8e−23	141 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
29	5e−21	422 / 10430	Brain	Overlap_fetal_midbrain_Quies
30	1e−19	312 / 6959	Lympl	HOPP_Weak_enhancer
31	2e−19	472 / 12393	Chror	15_Quies_Neuronal_Progenitor
32	1e−18	110 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
33	1e−18	104 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
34	1e−18	123 / 1846	Chror	14_ZNF_Melanocytes
35	1e−18	120 / 1777	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
36	2e−18	245 / 5067	TF	ICGC_Taf1_targets
37	7e−18	68 / 716	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
38	1e−17	95 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
39	2e−17	48 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
40	3e−17	72 / 811	GSEA	LEE_BMP2_TARGETS_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	4 / 111	HORVATH_aging_genes meth DOWN
2	0.6	4 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	3 / 13	GENTLES_modul6
2	0.007	3 / 14	GENTLES_modul4
3	0.010	5 / 46	PanCan_DNARepair_geneset_nanostring
4	0.017	1 / 13	RHODES_CANCER_META_SIGNATURE
5	0.026	4 / 39	ZHANG_MM up
6	0.057	1 / 2	GENTLES_modul8
7	0.071	4 / 54	KUIPER_MM poor survival
8	0.077	2 / 16	GENTLES_modul7
9	0.086	3 / 36	PanCan_HK_geneset_nanostring
10	0.090	21 / 527	Lembcke_Normal vs Adenoma
11	0.162	4 / 73	SHAUGHNESSY_MM high risk
12	0.229	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
13	0.284	0 / 14	LIU_COMMON_CANCER_GENES
14	0.297	5 / 125	PanCan_CC+Apop_geneset_nanostring
15	0.318	1 / 13	GENTLES_modul12

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−71	553 / 11455	2_TssA_Fibroblasts
2	2e−69	570 / 12298	2_TssA_Melanocytes
3	5e−60	461 / 8771	5_Tx_Melanocytes
4	7e−58	569 / 12983	2_TssA_Neuronal_Progenitor
5	1e−54	423 / 7854	5_Tx_Fibroblasts
6	2e−40	366 / 6970	5_Tx_Neuronal_Progenitor
7	2e−39	427 / 8990	15_Quies_Fibroblasts
8	2e−32	492 / 11836	3_TssF_Melanocytes
9	4e−28	462 / 11130	15_Quies_Melanocytes
10	2e−19	472 / 12393	15_Quies_Neuronal_Progenitor
11	1e−18	123 / 1846	14_ZNF_Melanocytes
12	1e−15	469 / 12741	7_Enh_Melanocytes
13	2e−12	338 / 8613	7_Enh_Fibroblasts
14	9e−11	190 / 4237	14_ZNF_Neuronal_Progenitor
15	4e−07	343 / 9635	3_TssF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−29	111 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	2e−28	113 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	1e−24	134 / 1797	PILON_KLF1_TARGETS_DN
4	2e−23	82 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
5	1e−18	104 / 1417	PUJANA_BRCA1_PCC_NETWORK
6	7e−18	68 / 716	WEI_MYCN_TARGETS_WITH_E_BOX
7	1e−17	95 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
8	2e−17	48 / 388	SHEN_SMARCA2_TARGETS_UP
9	3e−17	72 / 811	LEE_BMP2_TARGETS_DN
10	5e−17	64 / 669	PUJANA_CHEK2_PCC_NETWORK
11	1e−14	81 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
12	1e−14	44 / 389	GARY_CD5_TARGETS_DN
13	1e−14	55 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
14	4e−13	42 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
15	7e−13	65 / 841	ACEVEDO_LIVER_CANCER_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−76	471 / 8226	HOPP_Active_promoter
2	3e−74	438 / 7275	HOPP_Txn_elongation
3	4e−49	420 / 8098	HOPP_Weak_promoter
4	8e−28	281 / 5356	HOPP_Txn_transition
5	3e−26	318 / 6559	HOPP_Weak_txn
6	1e−19	312 / 6959	HOPP_Weak_enhancer
7	1e−15	67 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
8	6e−15	66 / 777	WIRTH_lymphoma937_spot D
9	9e−12	82 / 1270	SPANG_BCR UP
10	1e−09	22 / 158	WIRTH_lymphoma937_spot C
11	1e−09	22 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line
12	5e−05	58 / 1169	SPANG_BCR DN
13	2e−04	7 / 43	Monti_OxPhos_cluster
14	2e−04	20 / 283	TARTE_Plasmablast signature
15	2e−03	9 / 94	Sha_BL UP

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	8e−13	36 / 302	Chaussabel_3,4_Protein phosphatases
2	9e−13	32 / 242	Chaussabel_3,9_Kinases
3	6e−10	30 / 275	Chaussabel_3,7_Spliceosome
4	3e−09	61 / 933	PROTEINATLAS_adrenal gland
5	5e−08	68 / 1176	PROTEINATLAS_duodenum
6	1e−07	67 / 1173	PROTEINATLAS_rectum
7	3e−07	24 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
8	4e−07	65 / 1167	PROTEINATLAS_gallbladder
9	7e−07	67 / 1239	PROTEINATLAS_testis
10	8e−07	42 / 639	PROTEINATLAS_breast
11	9e−07	41 / 619	PROTEINATLAS_salivary gland
12	1e−06	57 / 1003	PROTEINATLAS_appendix
13	2e−06	59 / 1063	PROTEINATLAS_tonsil
14	2e−06	64 / 1194	PROTEINATLAS_stomach
15	2e−06	41 / 640	PROTEINATLAS_parathyroid gland

BP

Rank	p−value	#in/all	Geneset
1	3e−12	28 / 196	mRNA splicing, via spliceosome
2	2e−08	73 / 1272	regulation of transcription, DNA−templated
3	3e−08	87 / 1643	transcription, DNA−templated
4	3e−06	16 / 139	RNA splicing
5	3e−05	8 / 43	mRNA 3'−end processing
6	3e−05	8 / 44	RNA export from nucleus
7	4e−05	6 / 23	tRNA methylation
8	6e−05	6 / 25	mRNA polyadenylation
9	1e−04	8 / 53	termination of RNA polymerase II transcription
10	2e−04	9 / 69	mitochondrial translational elongation
11	2e−04	9 / 71	mitochondrial translational termination
12	4e−04	8 / 62	transcription−coupled nucleotide−excision repair
13	5e−04	5 / 24	RNA splicing, via transesterification reactions
14	6e−04	4 / 14	isotype switching
15	9e−04	9 / 86	mRNA export from nucleus

CC

Rank	p−value	#in/all	Geneset
1	9e−17	147 / 2535	nucleoplasm
2	4e−15	226 / 4828	nucleus
3	2e−09	77 / 1304	mitochondrion
4	4e−08	49 / 721	nucleolus
5	8e−07	192 / 4822	cytoplasm
6	2e−06	12 / 78	catalytic step 2 spliceosome
7	3e−06	12 / 79	spliceosomal complex
8	2e−05	27 / 374	mitochondrial inner membrane
9	2e−04	15 / 179	nuclear speck
10	8e−04	23 / 379	centrosome
11	1e−03	5 / 29	mitochondrial large ribosomal subunit
12	2e−03	4 / 18	transcriptionally active chromatin
13	3e−03	3 / 10	Gemini of coiled bodies
14	3e−03	3 / 11	SMN complex
15	6e−03	9 / 115	nuclear chromosome, telomeric region

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−53	472 / 9555	TssA_Colon
2	2e−46	429 / 8568	TxWk_Colon
3	1e−45	431 / 8678	Quies3_Colon
4	2e−42	491 / 10999	TssWk_Colon
5	4e−42	435 / 9054	Tx_Colon
6	1e−18	110 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	5e−17	204 / 4034	TssD1_Colon
8	4e−14	79 / 1083	ZNF_Colon
9	7e−14	73 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
10	9e−11	60 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	4e−09	284 / 7354	TssF_Colon
12	4e−08	103 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	1e−06	81 / 1623	Het_Colon
14	1e−06	75 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	1e−06	64 / 1186	HetRpts_Colon

HM

Rank	p−value	#in/all	Geneset
1	1e−05	17 / 170	HALLMARK_MYC_TARGETS_V1
2	4e−04	14 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	2e−03	13 / 173	HALLMARK_E2F_TARGETS
4	5e−03	10 / 130	HALLMARK_DNA_REPAIR
5	7e−03	9 / 116	HALLMARK_SPERMATOGENESIS
6	4e−02	10 / 185	HALLMARK_MTORC1_SIGNALING
7	7e−02	9 / 176	HALLMARK_ADIPOGENESIS
8	8e−02	9 / 179	HALLMARK_G2M_CHECKPOINT
9	9e−02	9 / 185	HALLMARK_P53_PATHWAY
10	1e−01	7 / 138	HALLMARK_FATTY_ACID_METABOLISM
11	2e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
12	2e−01	3 / 54	HALLMARK_MYC_TARGETS_V2
13	3e−01	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	4e−01	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	4e−01	5 / 137	HALLMARK_UV_RESPONSE_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.6	1 / 30	Hugo_melanoma−all−MET_UP
3	0.8	1 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−08	38 / 463	hsa−miR−301a
2	2e−08	27 / 263	hsa−miR−449a
3	2e−08	34 / 394	hsa−miR−301b
4	2e−08	33 / 379	hsa−miR−454
5	5e−08	36 / 449	hsa−miR−130b
6	7e−08	18 / 134	hsa−miR−656
7	2e−07	38 / 516	hsa−miR−15a
8	4e−07	35 / 467	hsa−miR−195
9	6e−07	23 / 240	hsa−miR−122
10	7e−07	35 / 480	hsa−miR−15b
11	8e−07	33 / 441	hsa−miR−424
12	9e−07	19 / 176	hsa−miR−199b−3p
13	1e−06	35 / 489	hsa−miR−16
14	1e−06	30 / 389	hsa−miR−519a
15	2e−06	33 / 455	hsa−miR−130a

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	

Brain

Rank	p−value	#in/all	Geneset
1	2e−90	537 / 9815	Overlap_fetal_midbrain_ReprPC
2	4e−59	367 / 5936	Overlap_fetal_midbrain_HetRpts
3	2e−43	451 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−33	441 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	5e−21	422 / 10430	Overlap_fetal_midbrain_Quies
6	6e−09	49 / 681	Overlap_fetal_midbrain_EnhP
7	4e−06	62 / 1171	Fetal_EnhP
8	2e−04	46 / 906	Fetal_HetRpts
9	4e−04	64 / 1436	Fetal_K9K27me3
10	1e−02	97 / 2654	Fetal_Quies
11	1e−02	53 / 1329	Overlap_fetal_midbrain_Enh
12	2e−02	44 / 1115	Overlap_fetal_midbrain_EnhG
13	3e−02	27 / 630	Mid_Frontal_Lobe_EnhP
14	3e−02	45 / 1162	Fetal_Enh
15	5e−02	36 / 937	Fetal_EnhG

Chr

Rank	p−value	#in/all	Geneset
1	5e−05	28 / 422	Chr 13
2	7e−03	60 / 1492	Chr 2
3	7e−03	45 / 1060	Chr 5
4	3e−02	34 / 836	Chr 8
5	3e−02	36 / 902	Chr 4
6	1e−01	32 / 904	Chr 10
7	2e−01	41 / 1211	Chr 6
8	3e−01	10 / 289	Chr 21
9	4e−01	35 / 1160	Chr 12
10	5e−01	10 / 342	Chr 18
11	6e−01	28 / 994	Chr X
12	6e−01	21 / 768	Chr 14
13	7e−01	32 / 1170	Chr 7
14	7e−01	25 / 954	Chr 9
15	7e−01	39 / 1467	Chr 19

Glio

Rank	p−value	#in/all	Geneset
1	8e−23	141 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−18	120 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	4e−06	48 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	2e−03	3 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
5	7e−02	5 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	8e−02	14 / 315	Up
7	1e−01	5 / 84	GIEZELT_GBM_WT_down_VS_mut
8	1e−01	13 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	1e−01	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	2e−01	3 / 48	Vishal_subnetwork signature of survival in GBM
11	2e−01	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
12	3e−01	1 / 12	Phillips PN up vs MES & Prolif
13	3e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
14	3e−01	6 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	3e−01	4 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	5 / 31	DUMEAUX_Fasting enriched genes
2	0.394	1 / 17	DUMEAUX_High bmi enriched genes
3	0.864	4 / 211	Homuth_BMI−associated−genes_DN
4	0.929	2 / 147	Homuth_BMI−associated−genes_UP
5	0.938	1 / 94	DUMEAUX_Smoking enriched genes
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−11	70 / 1013	poly(A) RNA binding
2	1e−07	321 / 8818	protein binding
3	2e−07	87 / 1717	metal ion binding
4	6e−06	13 / 99	mRNA binding
5	6e−06	29 / 399	RNA binding
6	1e−05	23 / 283	nucleotide binding
7	3e−05	70 / 1475	DNA binding
8	8e−05	9 / 63	protein transporter activity
9	6e−04	4 / 14	four−way junction DNA binding
10	1e−03	6 / 41	peptidyl−prolyl cis−trans isomerase activity
11	2e−03	41 / 877	transcription factor activity, sequence−specific DNA binding
12	3e−03	3 / 10	poly(A) binding
13	3e−03	3 / 11	phospholipase activity
14	5e−03	7 / 72	single−stranded DNA binding
15	6e−03	6 / 56	ATP−dependent RNA helicase activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.007	3 / 14	BENTINK_ras.6
2	0.046	2 / 12	BENTINK_src.2
3	1.000	0 / 14	GUSTAFSON_PI3K_UP
4	1.000	0 / 15	GUSTAFSON_PI3K_DN
5	1.000	0 / 13	BENTINK_e2f3.1
6	1.000	0 / 13	BENTINK_e2f3.2
7	1.000	0 / 13	BENTINK_myc.1
8	1.000	0 / 12	BENTINK_ras.1
9	1.000	0 / 11	BENTINK_ras.4
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−18	245 / 5067	ICGC_Taf1_targets
2	1e−12	238 / 5442	ICGC_Pmlsc71910_targets
3	3e−12	218 / 4890	ICGC_Bclaf101388_targets
4	8e−12	101 / 1723	HEBENSTREIT_high expression TF
5	4e−11	88 / 1452	ICGC_Six5_targets
6	8e−11	212 / 4881	ICGC_Atf2_targets
7	1e−10	117 / 2215	ICGC_GabpPcr2_targets
8	5e−10	254 / 6267	ICGC_Yy1_targets
9	1e−09	228 / 5518	ICGC_Stat5_targets
10	1e−09	226 / 5466	ICGC_Nficsc81335_targets
11	2e−09	223 / 5383	ICGC_Sp1_targets
12	2e−09	261 / 6578	ICGC_Pou2_targets
13	9e−09	186 / 4362	ICGC_Creb1_targets
14	1e−08	83 / 1498	ICGC_Ets1_targets
15	3e−08	71 / 1231	KIM_MYC targets

Correlation Cluster

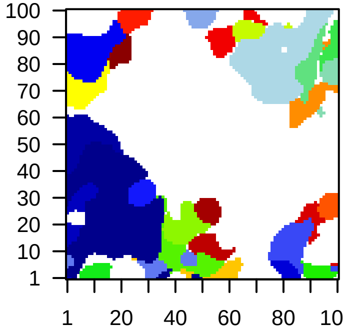
Spot Summary: Z

metagenes = 64
genes = 938

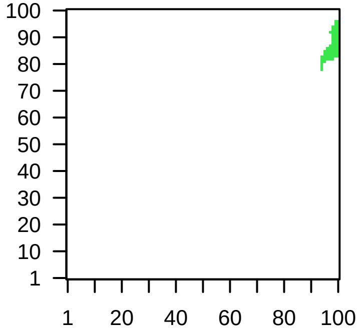
<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 28.39 / log p= −Inf

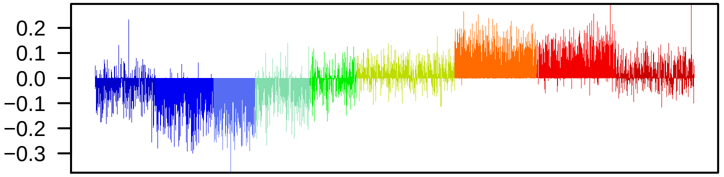
samples with spot = 865 (25.5 %)
A * : 9 (2.6 %)
A F * : 6 (1.9 %)
C F * : 22 (8.3 %)
F * : 87 (15.7 %)
F J * : 367 (79.3 %)
J * : 291 (65.1 %)
N * : 83 (18.7 %)

Overview Map



Spot





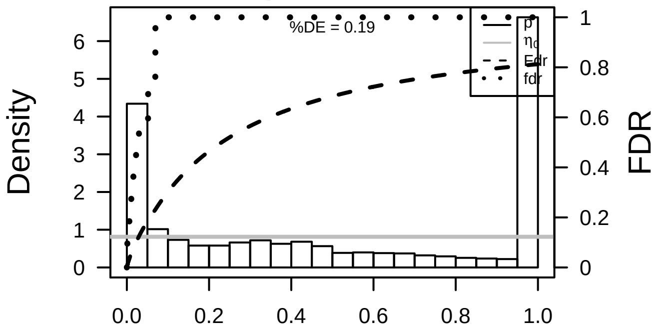
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169749	5.33	−1.74	0.06	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	ILMN_171516	4.62	−2.25	0.07		
3	ILMN_179817	2.09	−1.22	0.16	CHURC1	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
4	ILMN_181589	1.69	−2.79	0.16		
5	ILMN_175259	1.47	−1.51	0.39		
6	ILMN_321438	1.33	−1.23	0.23		
7	ILMN_224608	1.32	−1.59	0.12	CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis
8	ILMN_238175	1.25	−1.46	0.39	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
9	ILMN_171726	1.21	−1.06	0.35		
10	ILMN_170123	1.12	−0.93	0.41	SH2D1B	SH2 domain containing 1B [Source:HGNC Symbol;Acc:HGN
11	ILMN_207328	1.1	−0.98	0.58	MTSS1	metastasis suppressor 1 [Source:HGNC Symbol;Acc:HGNC:
12	ILMN_172042	1.05	−0.98	0.4	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
13	ILMN_177221	1.05	−1	0.59	HLA−DPA1	major histocompatibility complex, class II, DP alpha 1 [Source
14	ILMN_322868	1.04	−0.87	0.52	HLA−DRB1	major histocompatibility complex, class II, DR beta 1 [Source:
15	ILMN_176641	1.03	−0.96	0.75	AP1S2	adaptor related protein complex 1 sigma 2 subunit [Source:H
16	ILMN_231390	1.03	−0.92	0.31	PAM	peptidylglycine alpha−amidating monooxygenase [Source:HG
17	ILMN_174907	0.99	−0.68	0.44	HLA−DPB1	major histocompatibility complex, class II, DP beta 1 [Source:
18	ILMN_219840	0.97	−1.14	0.22		
19	ILMN_173656	0.96	−1.09	0.48	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
20	ILMN_171806	0.96	−0.89	0.59	LIPA	lipase A, lysosomal acid type [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	642 / 8226	Lympl	HOPP_Active_promoter
2	1e−99	612 / 7275	Lympl	HOPP_Txn_elongation
3	1e−99	468 / 5356	Lympl	HOPP_Txn_transition
4	1e−99	612 / 8678	Colon	Quies3_Colon
5	1e−99	661 / 9555	Colon	TssA_Colon
6	1e−99	672 / 10999	Colon	TssWk_Colon
7	1e−99	632 / 9054	Colon	Tx_Colon
8	1e−99	621 / 8568	Colon	TxWk_Colon
9	1e−99	680 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
10	1e−99	517 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
11	1e−99	723 / 12983	Chror	2_TssA_Neuronal_Progenitor
12	1e−99	522 / 6970	Chror	5_Tx_Neuronal_Progenitor
13	1e−99	715 / 12298	Chror	2_TssA_Melanocytes
14	1e−99	639 / 8771	Chror	5_Tx_Melanocytes
15	1e−99	591 / 8990	Chror	15_Quies_Fibroblasts
16	1e−99	701 / 11455	Chror	2_TssA_Fibroblasts
17	1e−99	586 / 7854	Chror	5_Tx_Fibroblasts
18	4e−96	555 / 8098	Lympl	HOPP_Weak_promoter
19	9e−89	592 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
20	3e−87	603 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
21	1e−76	670 / 12741	Chror	7_Enh_Melanocytes
22	7e−74	192 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
23	8e−71	615 / 11130	Chror	15_Quies_Melanocytes
24	5e−70	592 / 10430	Brain	Overlap_fetal_midbrain_Quies
25	2e−69	206 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
26	1e−67	220 / 1797	GSEA	PILON_KLF1_TARGETS_DN
27	7e−66	644 / 12393	Chror	15_Quies_Neuronal_Progenitor
28	1e−64	626 / 11836	Chror	3_TssF_Melanocytes
29	2e−55	96 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
30	2e−52	101 / 465	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
31	7e−51	495 / 8613	Chror	7_Enh_Fibroblasts
32	9e−48	99 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
33	5e−47	494 / 8818	MF	protein binding
34	1e−45	441 / 7448	Lympl	HOPP_Strong_enhancer
35	3e−45	124 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
36	1e−44	405 / 6559	Lympl	HOPP_Weak_txn
37	2e−41	73 / 302	Refer	Chaussabel_3,4_Protein phosphatases
38	1e−39	409 / 6959	Lympl	HOPP_Weak_enhancer
39	1e−38	112 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
40	2e−37	97 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.03	8 / 111	HORVATH_aging_genes meth DOWN
2	0.96	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	

Cancer

Rank	p−value	#in/all	Geneset
1	8e−09	24 / 178	SPANG_LPS−index2
2	4e−06	27 / 301	SPANG_BCL6−index2
3	6e−04	12 / 117	PanCan_Driver_Gene_geneset_nanostring
4	8e−03	3 / 13	RHODES_CANCER_META_SIGNATURE
5	1e−02	6 / 54	KUIPER_MM poor survival
6	1e−02	3 / 15	WOLFER_overlap genes
7	2e−02	3 / 16	GENTLES_modul14
8	4e−02	4 / 39	ZHANG_MM up
9	6e−02	2 / 12	LIU_BREAST_CANCER
10	7e−02	2 / 13	GENTLES_modul6
11	7e−02	2 / 13	GENTLES_modul12
12	1e−01	5 / 76	PanCan_Wnt_geneset_nanostring
13	2e−01	3 / 46	PanCan_TGF−B_geneset_nanostring
14	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	2e−01	4 / 73	SHAUGHNESSY_MM high risk

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−99	723 / 12983	2_TssA_Neuronal_Progenitor
2	1e−99	522 / 6970	5_Tx_Neuronal_Progenitor
3	1e−99	715 / 12298	2_TssA_Melanocytes
4	1e−99	639 / 8771	5_Tx_Melanocytes
5	1e−99	591 / 8990	15_Quies_Fibroblasts
6	1e−99	701 / 11455	2_TssA_Fibroblasts
7	1e−99	586 / 7854	5_Tx_Fibroblasts
8	1e−76	670 / 12741	7_Enh_Melanocytes
9	8e−71	615 / 11130	15_Quies_Melanocytes
10	7e−66	644 / 12393	15_Quies_Neuronal_Progenitor
11	1e−64	626 / 11836	3_TssF_Melanocytes
12	7e−51	495 / 8613	7_Enh_Fibroblasts
13	2e−33	344 / 5699	6_EnhG_Melanocytes
14	5e−29	272 / 4237	14_ZNF_Neuronal_Progenitor
15	3e−15	128 / 1846	14_ZNF_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−74	192 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	1e−67	220 / 1797	PILON_KLF1_TARGETS_DN
3	2e−55	96 / 388	SHEN_SMARCA2_TARGETS_UP
4	2e−52	101 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
5	9e−48	99 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
6	3e−45	124 / 841	ACEVEDO_LIVER_CANCER_UP
7	1e−38	112 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
8	2e−37	97 / 622	SCHLOSSER_SERUM_RESPONSE_DN
9	1e−36	108 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	3e−36	129 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
11	3e−35	73 / 368	OSMAN_BLADDER_CANCER_UP
12	2e−32	142 / 1417	PUJANA_BRCA1_PCC_NETWORK
13	5e−27	76 / 527	HAMAI_APOPTOSIS_VIA_TRAIL_UP
14	9e−27	76 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
15	2e−26	69 / 445	ENK_UV_RESPONSE_KERATINOCYTE_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	642 / 8226	HOPP_Active_promoter
2	1e−99	612 / 7275	HOPP_Txn_elongation
3	1e−99	468 / 5356	HOPP_Txn_transition
4	4e−96	555 / 8098	HOPP_Weak_promoter
5	1e−45	441 / 7448	HOPP_Strong_enhancer
6	1e−44	405 / 6559	HOPP_Weak_txn
7	1e−39	409 / 6959	HOPP_Weak_enhancer
8	4e−15	94 / 1169	SPANG_BCR DN
9	1e−08	41 / 455	SPANG_CD40 6hrs DN
10	2e−07	139 / 2701	HOPP_Repetitive
11	4e−06	74 / 1270	SPANG_BCR UP
12	5e−06	13 / 84	ROSOLOWSKI_green UP
13	1e−05	35 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
14	1e−05	36 / 493	WIRTH_lymphoma937_spot J
15	3e−05	14 / 115	ROSOLOWSKI_green total

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−41	73 / 302	Chaussabel_3,4_Protein phosphatases
2	3e−25	50 / 242	Chaussabel_3,9_Kinases
3	1e−21	105 / 1118	PROTEINATLAS_placenta
4	9e−17	32 / 153	Chaussabel_2,9_Cytosceleton
5	3e−16	91 / 1063	PROTEINATLAS_tonsil
6	1e−15	39 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
7	1e−14	93 / 1173	PROTEINATLAS_rectum
8	3e−14	81 / 959	PROTEINATLAS_nasopharynx
9	6e−14	95 / 1239	PROTEINATLAS_testis
10	1e−13	80 / 963	PROTEINATLAS_pancreas
11	2e−13	27 / 139	Chaussabel_1,8_Metabolism Biosynthesis
12	3e−13	71 / 816	PROTEINATLAS_endometrium
13	4e−13	77 / 933	PROTEINATLAS_adrenal gland
14	5e−13	89 / 1167	PROTEINATLAS_gallbladder
15	6e−13	94 / 1268	PROTEINATLAS_colon

BP

Rank	p−value	#in/all	Geneset
1	5e−08	28 / 255	viral process
2	1e−07	23 / 189	intracellular protein transport
3	2e−07	18 / 126	T cell receptor signaling pathway
4	9e−07	18 / 137	ER to Golgi vesicle−mediated transport
5	9e−07	21 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
6	3e−06	13 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
7	4e−06	29 / 335	protein transport
8	2e−05	34 / 457	regulation of transcription from RNA polymerase II promoter
9	2e−05	10 / 57	COPII vesicle coating
10	2e−05	27 / 330	protein ubiquitination
11	3e−05	5 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
12	4e−05	13 / 101	vesicle−mediated transport
13	6e−05	22 / 254	cell−cell adhesion
14	1e−04	5 / 15	regulation of DNA replication
15	1e−04	15 / 145	mRNA processing

CC

Rank	p−value	#in/all	Geneset
1	1e−22	200 / 2979	cytosol
2	1e−20	273 / 4822	cytoplasm
3	2e−20	273 / 4828	nucleus
4	2e−17	140 / 1979	membrane
5	4e−17	165 / 2535	nucleoplasm
6	2e−13	151 / 2464	extracellular exosome
7	1e−10	50 / 539	Golgi membrane
8	1e−09	61 / 777	Golgi apparatus
9	7e−09	28 / 234	lysosomal membrane
10	1e−08	59 / 788	endoplasmic reticulum membrane
11	7e−08	7 / 13	MHC class II protein complex
12	8e−08	11 / 41	ER to Golgi transport vesicle membrane
13	2e−07	8 / 21	integral component of lumenal side of endoplasmic reticulum membrane
14	6e−07	51 / 721	nucleolus
15	1e−06	17 / 124	trans−Golgi network

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	612 / 8678	Quies3_Colon
2	1e−99	661 / 9555	TssA_Colon
3	1e−99	672 / 10999	TssWk_Colon
4	1e−99	632 / 9054	Tx_Colon
5	1e−99	621 / 8568	TxWk_Colon
6	2e−69	206 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−25	254 / 4034	TssD1_Colon
8	3e−24	107 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	4e−16	141 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
10	1e−14	349 / 7354	TssF_Colon
11	8e−14	106 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
12	9e−14	466 / 10779	Enh_Colon
13	1e−13	93 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	2e−12	93 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	8e−09	250 / 5373	EnhWk1_Colon

HM

Rank	p−value	#in/all	Geneset
1	8e−12	20 / 87	HALLMARK_PROTEIN_SECRETION
2	3e−09	24 / 170	HALLMARK_MYC_TARGETS_V1
3	2e−05	18 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	6e−05	18 / 185	HALLMARK_MTORC1_SIGNALING
5	4e−04	11 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	1e−03	15 / 177	HALLMARK_MITOTIC_SPINDLE
7	1e−03	15 / 179	HALLMARK_G2M_CHECKPOINT
8	2e−03	14 / 173	HALLMARK_E2F_TARGETS
9	7e−03	6 / 50	HALLMARK_TGF_BETA_SIGNALING
10	1e−02	13 / 183	HALLMARK_GLYCOLYSIS
11	1e−02	10 / 132	HALLMARK_UV_RESPONSE_DN
12	2e−02	12 / 176	HALLMARK_ADIPOGENESIS
13	2e−02	10 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	3e−02	12 / 187	HALLMARK_COMPLEMENT
15	3e−02	10 / 151	HALLMARK_APOPTOSIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.6	1 / 27	Hugo_melanoma−all−LEF1_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−34	77 / 429	hsa−miR−548n
2	5e−30	75 / 463	hsa−miR−301a
3	2e−28	59 / 299	hsa−miR−548c−3p
4	3e−28	67 / 394	hsa−miR−301b
5	8e−28	71 / 449	hsa−miR−130b
6	2e−27	71 / 455	hsa−miR−130a
7	7e−27	73 / 491	hsa−miR−107
8	3e−26	63 / 374	hsa−miR−144
9	5e−26	72 / 493	hsa−miR−103
10	2e−25	66 / 425	hsa−let−7b
11	4e−25	57 / 321	hsa−miR−590−3p
12	9e−24	55 / 317	hsa−miR−559
13	2e−23	60 / 382	hsa−let−7c
14	2e−23	55 / 321	hsa−miR−302a
15	4e−23	56 / 338	hsa−miR−548d−5p

Telomeres

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

Brain

Rank	p−value	#in/all	Geneset
1	1e−99	680 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−99	517 / 5936	Overlap_fetal_midbrain_HetRpts
3	9e−89	592 / 9504	Overlap_fetal_midbrain_K9K27me3
4	3e−87	603 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	5e−70	592 / 10430	Overlap_fetal_midbrain_Quies
6	5e−10	70 / 937	Fetal_EnhG
7	2e−08	77 / 1171	Fetal_EnhP
8	4e−08	36 / 386	Fetal_ZNF
9	9e−08	32 / 328	Fetal_Het
10	3e−07	73 / 1162	Fetal_Enh
11	1e−06	54 / 796	Overlap_fetal_midbrain_ZNF
12	4e−05	77 / 1436	Fetal_K9K27me3
13	5e−04	40 / 681	Overlap_fetal_midbrain_EnhP
14	3e−03	35 / 630	Mid_Frontal_Lobe_EnhP
15	7e−03	45 / 906	Fetal_HetRpts

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	63 / 1060	Chr 5
2	1e−04	30 / 422	Chr 13
3	2e−03	42 / 768	Chr 14
4	3e−03	22 / 342	Chr 18
5	5e−03	58 / 1217	Chr 3
6	6e−03	45 / 902	Chr 4
7	7e−02	15 / 289	Chr 21
8	8e−02	36 / 836	Chr 8
9	1e−01	47 / 1160	Chr 12
10	1e−01	37 / 904	Chr 10
11	1e−01	48 / 1211	Chr 6
12	2e−01	57 / 1492	Chr 2
13	5e−01	78 / 2323	Chr 1
14	6e−01	33 / 994	Chr X
15	6e−01	38 / 1170	Chr 7

Glio

Rank	p−value	#in/all	Geneset
1	8e−37	185 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−36	170 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−22	53 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	4e−14	73 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	5e−11	37 / 315	Up
6	9e−05	16 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	5e−04	10 / 84	GIEZELT_GBM_WT_down_VS_mut
8	1e−03	26 / 401	Down_b
9	1e−03	4 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	1e−03	7 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	1e−03	6 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
12	2e−03	10 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	5e−03	6 / 48	Vishal_subnetwork signature of survival in GBM
14	6e−03	7 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	2e−02	4 / 32	Donson−Misc immune function−associated with LTS in HGA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	15 / 211	Homuth_BMI−associated−genes_DN
2	0.015	3 / 16	Huan_blood−pressure_DBP−signature
3	0.158	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	0.443	1 / 17	DUMEAUX_High bmi enriched genes
5	0.462	1 / 18	Huan_blood−pressure_SBP−signature
6	0.994	1 / 147	Homuth_BMI−associated−genes_UP
7	1.000	0 / 94	DUMEAUX_Smoking enriched genes
8	1.000	0 / 10	DUMEAUX_Smoking literature genes up
9	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1.000	0 / 31	DUMEAUX_Fasting enriched genes

MF

Rank	p−value	#in/all	Geneset
1	5e−47	494 / 8818	protein binding
2	3e−23	102 / 1013	poly(A) RNA binding
3	5e−07	29 / 301	ubiquitin−protein transferase activity
4	1e−06	26 / 265	cadherin binding involved in cell−cell adhesion
5	2e−05	18 / 173	ubiquitin protein ligase activity
6	4e−05	39 / 580	identical protein binding
7	5e−05	10 / 63	phosphatidylinositol binding
8	5e−05	10 / 63	protein transporter activity
9	5e−05	9 / 52	calcium−dependent protein binding
10	7e−05	5 / 14	MHC class II protein complex binding
11	1e−04	29 / 399	RNA binding
12	2e−04	4 / 10	poly(A)−specific ribonuclease activity
13	3e−04	58 / 1065	zinc ion binding
14	3e−04	5 / 18	TBP−class protein binding
15	3e−04	7 / 40	receptor tyrosine kinase binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	3 / 14	BENTINK_ras.6
2	0.07	2 / 13	BENTINK_e2f3.2
3	0.31	1 / 11	BENTINK_ras.4
4	0.34	1 / 12	BENTINK_src.2
5	0.36	1 / 13	BENTINK_e2f3.1
6	0.38	1 / 14	GUSTAFSON_PI3K_UP
7	0.40	1 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 12	BENTINK_ras.1
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−30	309 / 5067	ICGC_Taf1_targets
2	2e−23	284 / 4881	ICGC_Atf2_targets
3	2e−22	139 / 1723	HEBENSTREIT_high expression TF
4	3e−22	259 / 4362	ICGC_Creb1_targets
5	3e−20	300 / 5518	ICGC_Stat5_targets
6	5e−20	274 / 4890	ICGC_Bclaf101388_targets
7	1e−19	256 / 4468	ICGC_Egr1_targets
8	2e−19	294 / 5442	ICGC_Pmlsc71910_targets
9	2e−18	292 / 5466	ICGC_Nficsc81335_targets
10	1e−17	103 / 1231	KIM_MYC targets
11	4e−17	285 / 5410	ICGC_Foxm1_targets
12	3e−16	142 / 2087	ICGC_Cebpbsc150_targets
13	3e−16	315 / 6267	ICGC_Yy1_targets
14	1e−15	229 / 4131	ICGC_Nfatc1_targets
15	1e−15	276 / 5312	ICGC_Tcf12_targets

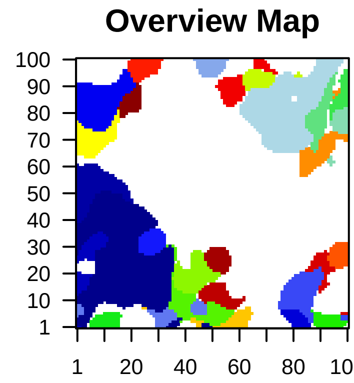
Correlation Cluster

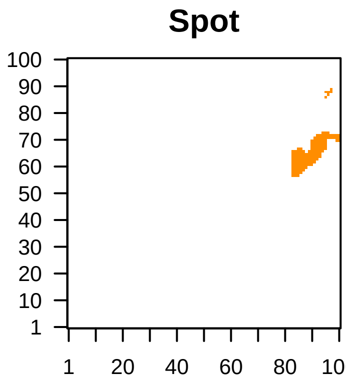
Spot Summary: A1

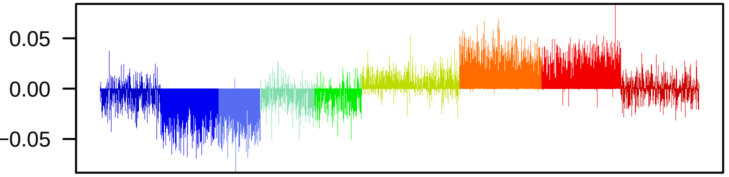
metagenes = 134
genes = 827

<r> metagenes = 0.92
<r> genes = 0.11
beta: r2= 1.85 / log p= −Inf

samples with spot = 3 (0.1 %)
F J * : 2 (0.4 %)
J * : 1 (0.2 %)





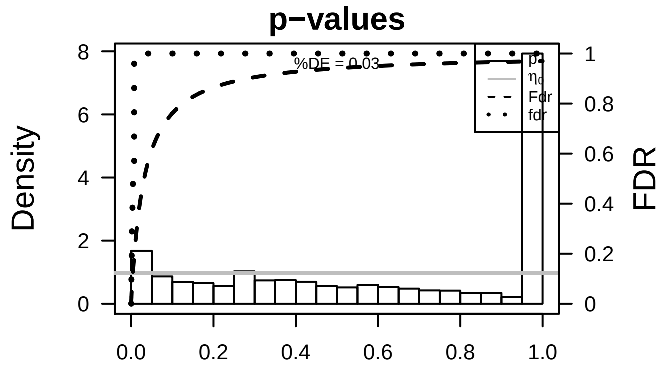


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173219	0.79	−0.26	0.14	UTS2	urotensin 2 [Source:HGNC Symbol;Acc:HGNC:12636]
2	ILMN_172429	0.78	−0.57	0.27	KDELR2	KDEL endoplasmic reticulum protein retention receptor 2 [Sou
3	ILMN_178460	0.75	−0.58	0.18		
4	ILMN_207543	0.69	−0.47	0.56		protein disulfide isomerase family A member 3 pseudogene 1
5	ILMN_171906	0.68	−0.47	0.18	KCTD10	potassium channel tetramerization domain containing 10 [Sou
6	ILMN_180026	0.64	−0.56	0.46	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
7	ILMN_181512	0.6	−0.63	0.38	CHCHD2	coiled−coil−helix−coiled−coil−helix domain containing 2 [Sour
8	ILMN_171813	0.57	−0.72	0.46	UQCRHL	ubiquinol−cytochrome c reductase hinge protein like [Source:
9	ILMN_170816	0.57	−0.55	0.55	EIF3A	eukaryotic translation initiation factor 3 subunit A [Source:HG
10	ILMN_219168	0.56	−0.66	0.31	CHCHD2	coiled−coil−helix−coiled−coil−helix domain containing 2 [Sour
11	ILMN_172085	0.55	−0.56	0.34	ABRACL	ABRA C−terminal like [Source:HGNC Symbol;Acc:HGNC:21
12	ILMN_168035	0.55	−0.44	0.6	NSF	N−ethylmaleimide sensitive factor, vesicle fusing ATPase [Sou
13	ILMN_177331	0.55	−0.42	0.17	MIR1307	up−regulated during skeletal muscle growth 5 homolog (mous
14	ILMN_175592	0.54	−0.51	0.35		
15	ILMN_165601	0.54	−0.36	0.35	RGS1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
16	ILMN_174246	0.54	−0.43	0.61	UAP1	UDP−N−acetylglucosamine pyrophosphorylase 1 [Source:HG
17	ILMN_173118	0.52	−0.39	0.64	TEX2	testis expressed 2 [Source:HGNC Symbol;Acc:HGNC:30884]
18	ILMN_172784	0.51	−0.33	0.45	SLC35B1	solute carrier family 35 member B1 [Source:HGNC Symbol;A
19	ILMN_222018	0.51	−0.39	0.73	GFPT1	glutamine−−fructose−6−phosphate transaminase 1 [Source:H
20	ILMN_231801	0.51	−0.45	0.61	PSMA3	proteasome subunit alpha 3 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−56	488 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
2	2e−53	566 / 12983	Chror	2_TssA_Neuronal_Progenitor
3	1e−52	548 / 12298	Chror	2_TssA_Melanocytes
4	3e−51	448 / 8771	Chror	5_Tx_Melanocytes
5	1e−48	426 / 8226	Lympl	HOPP_Active_promoter
6	2e−46	410 / 7854	Chror	5_Tx_Fibroblasts
7	2e−45	513 / 11455	Chror	2_TssA_Fibroblasts
8	6e−45	442 / 8990	Chror	15_Quies_Fibroblasts
9	4e−42	494 / 10999	Colon	TssWk_Colon
10	8e−42	497 / 11130	Chror	15_Quies_Melanocytes
11	1e−37	443 / 9555	Colon	TssA_Colon
12	1e−34	447 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
13	4e−33	388 / 8098	Lympl	HOPP_Weak_promoter
14	4e−33	406 / 8678	Colon	Quies3_Colon
15	3e−31	357 / 7275	Lympl	HOPP_Txn_elongation
16	1e−29	343 / 6970	Chror	5_Tx_Neuronal_Progenitor
17	1e−29	308 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
18	3e−29	503 / 12393	Chror	15_Quies_Neuronal_Progenitor
19	1e−28	391 / 8568	Colon	TxWk_Colon
20	2e−25	411 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
21	2e−25	478 / 11836	Chror	3_TssF_Melanocytes
22	2e−24	500 / 12741	Chror	7_Enh_Melanocytes
23	7e−24	393 / 9054	Colon	Tx_Colon
24	7e−23	142 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
25	6e−21	97 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
26	1e−18	298 / 6559	Lympl	HOPP_Weak_txn
27	2e−18	417 / 10430	Brain	Overlap_fetal_midbrain_Quies
28	4e−18	216 / 4237	Chror	14_ZNF_Neuronal_Progenitor
29	5e−16	302 / 6959	Lympl	HOPP_Weak_enhancer
30	7e−16	68 / 777	Lympl	WIRTH_lymphoma937_spot D
31	3e−15	351 / 8613	Chror	7_Enh_Fibroblasts
32	6e−15	199 / 4034	Colon	TssD1_Colon
33	6e−15	66 / 772	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
34	4e−14	86 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
35	3e−13	229 / 5067	TF	ICGC_Taf1_targets
36	1e−12	109 / 1846	Chror	14_ZNF_Melanocytes
37	3e−12	105 / 1777	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
38	3e−12	62 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
39	2e−11	214 / 4828	CC	nucleus
40	8e−11	80 / 1270	Lympl	SPANG_BCR UP



Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 111	HORVATH_aging_genes meth DOWN
2	0.1	7 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−07	84 / 1643	transcription, DNA−templated
2	9e−06	65 / 1272	regulation of transcription, DNA−templated
3	3e−05	5 / 14	dolichol−linked oligosaccharide biosynthetic process
4	2e−04	12 / 117	cilium assembly
5	2e−04	4 / 11	mRNA cleavage
6	4e−04	4 / 13	intraciliary transport
7	8e−04	5 / 26	chromatin modification
8	1e−03	19 / 300	cell division
9	3e−03	3 / 10	positive regulation of interferon−gamma biosynthetic process
10	3e−03	10 / 119	mitophagy in response to mitochondrial depolarization
11	3e−03	4 / 22	intra−Golgi vesicle−mediated transport
12	4e−03	4 / 23	tRNA methylation
13	5e−03	14 / 219	mitotic nuclear division
14	6e−03	9 / 112	positive regulation of defense response to virus by host
15	6e−03	10 / 134	transcription initiation from RNA polymerase II promoter

Brain

Rank	p−value	#in/all	Geneset
1	3e−56	488 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−34	447 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	1e−29	308 / 5936	Overlap_fetal_midbrain_HetRpts
4	2e−25	411 / 9504	Overlap_fetal_midbrain_K9K27me3
5	2e−18	417 / 10430	Overlap_fetal_midbrain_Quies
6	2e−06	43 / 681	Overlap_fetal_midbrain_EnhP
7	3e−06	63 / 1171	Fetal_EnhP
8	6e−05	68 / 1436	Fetal_K9K27me3
9	1e−04	57 / 1162	Fetal_Enh
10	5e−04	46 / 937	Fetal_EnhG
11	8e−04	44 / 906	Fetal_HetRpts
12	1e−03	23 / 386	Fetal_ZNF
13	6e−03	55 / 1329	Overlap_fetal_midbrain_Enh
14	3e−02	44 / 1115	Overlap_fetal_midbrain_EnhG
15	9e−02	91 / 2709	Mid_Frontal_Lobe_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	9e−05	32 / 527	Lembcke_Normal vs Adenoma
2	3e−02	4 / 39	ZHANG_MM up
3	6e−02	7 / 117	PanCan_Driver_Gene_geneset_nanostring
4	6e−02	5 / 73	SHAUGHNESSY_MM high risk
5	7e−02	2 / 15	LIU_PROSTATE_CANCER_DN
6	7e−02	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	7e−02	7 / 125	PanCan_CC+Apop_geneset_nanostring
8	9e−02	5 / 82	PanCan_JAK−ST_geneset_nanostring
9	2e−01	0 / 13	RHODES_CANCER_META_SIGNATURE
10	2e−01	2 / 28	PanCan_HH_geneset_nanostring
11	2e−01	3 / 54	KUIPER_MM poor survival
12	2e−01	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
13	2e−01	1 / 14	LIU_PROSTATE_CANCER_UP
14	3e−01	1 / 12	LIU_BREAST_CANCER
15	3e−01	2 / 38	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	2e−11	214 / 4828	nucleus
2	6e−06	112 / 2535	nucleoplasm
3	1e−04	121 / 2979	cytosol
4	2e−04	61 / 1304	mitochondrion
5	5e−04	5 / 23	precatalytic spliceosome
6	6e−04	31 / 561	intracellular membrane−bounded organelle
7	1e−03	36 / 721	nucleolus
8	2e−03	7 / 59	Cul3−RING ubiquitin ligase complex
9	2e−03	5 / 32	mediator complex
10	3e−03	7 / 64	axoneme
11	6e−03	3 / 13	HOPS complex
12	6e−03	36 / 788	endoplasmic reticulum membrane
13	6e−03	8 / 93	ubiquitin ligase complex
14	7e−03	3 / 14	integral component of peroxisomal membrane
15	9e−03	20 / 379	centrosome

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	44 / 902	Chr 4
2	5e−02	31 / 769	Chr 15
3	1e−01	17 / 422	Chr 13
4	1e−01	77 / 2323	Chr 1
5	1e−01	42 / 1211	Chr 6
6	2e−01	39 / 1160	Chr 12
7	2e−01	26 / 768	Chr 14
8	3e−01	12 / 342	Chr 18
9	3e−01	29 / 904	Chr 10
10	3e−01	10 / 289	Chr 21
11	5e−01	28 / 954	Chr 9
12	5e−01	31 / 1060	Chr 5
13	6e−01	35 / 1217	Chr 3
14	6e−01	24 / 836	Chr 8
15	6e−01	33 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−53	566 / 12983	2_TssA_Neuronal_Progenitor
2	1e−52	548 / 12298	2_TssA_Melanocytes
3	3e−51	448 / 8771	5_Tx_Melanocytes
4	2e−46	410 / 7854	5_Tx_Fibroblasts
5	2e−45	513 / 11455	2_TssA_Fibroblasts
6	6e−45	442 / 8990	15_Quies_Fibroblasts
7	8e−42	497 / 11130	15_Quies_Melanocytes
8	1e−29	343 / 6970	5_Tx_Neuronal_Progenitor
9	3e−29	503 / 12393	15_Quies_Neuronal_Progenitor
10	2e−25	478 / 11836	3_TssF_Melanocytes
11	2e−24	500 / 12741	7_Enh_Melanocytes
12	4e−18	216 / 4237	14_ZNF_Neuronal_Progenitor
13	3e−15	351 / 8613	7_Enh_Fibroblasts
14	1e−12	109 / 1846	14_ZNF_Melanocytes
15	6e−10	360 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−42	494 / 10999	TssWk_Colon
2	1e−37	443 / 9555	TssA_Colon
3	4e−33	406 / 8678	Quies3_Colon
4	1e−28	391 / 8568	TxWk_Colon
5	7e−24	393 / 9054	Tx_Colon
6	6e−15	199 / 4034	TssD1_Colon
7	4e−08	190 / 4526	Quies1_Colon
8	2e−07	278 / 7354	TssF_Colon
9	3e−07	75 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
10	4e−06	59 / 1083	ZNF_Colon
11	2e−05	332 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	2e−05	93 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	2e−04	73 / 1623	Het_Colon
14	4e−04	41 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
15	9e−04	54 / 1186	HetRpts_Colon

Glio

Rank	p−value	#in/all	Geneset
1	7e−23	142 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	3e−12	105 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	7e−08	53 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	5e−04	12 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
5	3e−03	19 / 315	Up
6	7e−03	7 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	4e−02	4 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
8	5e−02	4 / 47	Donson−innate immunity−associated with LTS in HGA
9	7e−02	5 / 74	Weller_LGG_gradeII−vs−III_DOWN
10	8e−02	14 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	9e−02	8 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	9e−02	8 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	1e−01	2 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
14	1e−01	49 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
15	1e−01	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−21	97 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	4e−14	86 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	3e−12	62 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
4	4e−10	58 / 811	LEE_BMP2_TARGETS_DN
5	6e−10	46 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
6	1e−09	46 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
7	3e−08	86 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
8	5e−08	58 / 926	NUYTTEN_EZH2_TARGETS_DN
9	5e−08	53 / 812	GEORGES_TARGETS_OF_MIR192_AND_MIR215
10	2e−07	44 / 641	MARSON_BOUND_BY_E2F4_UNSTIMULATED
11	2e−07	28 / 316	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
12	2e−07	47 / 716	WEI_MYCN_TARGETS_WITH_E_BOX
13	2e−07	44 / 649	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
14	6e−07	24 / 255	FORTSCHEGGER_PHF8_TARGETS_UP
15	2e−06	30 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.002	13 / 173	HALLMARK_E2F_TARGETS
2	0.002	11 / 138	HALLMARK_FATTY_ACID_METABOLISM
3	0.006	12 / 176	HALLMARK_ADIPOGENESIS
4	0.014	7 / 87	HALLMARK_PROTEIN_SECRETION
5	0.017	11 / 179	HALLMARK_G2M_CHECKPOINT
6	0.021	11 / 185	HALLMARK_MTORC1_SIGNALING
7	0.051	6 / 91	HALLMARK_ANDROGEN_RESPONSE
8	0.051	6 / 91	HALLMARK_PEROXISOME
9	0.058	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.082	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	0.097	9 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.118	3 / 41	HALLMARK_APICAL_SURFACE
13	0.191	6 / 132	HALLMARK_UV_RESPONSE_DN
14	0.198	7 / 162	HALLMARK_ALLOGRAFT_REJECTION
15	0.232	7 / 170	HALLMARK_MYC_TARGETS_V1

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	6 / 94	DUMEAUX_Smoking enriched genes
2	0.16	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.40	1 / 17	DUMEAUX_High bmi enriched genes
4	0.43	5 / 147	Homuth_BMI−associated−genes_UP
5	0.74	5 / 211	Homuth_BMI−associated−genes_DN
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 31	DUMEAUX_Fasting enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−48	426 / 8226	HOPP_Active_promoter
2	4e−33	388 / 8098	HOPP_Weak_promoter
3	3e−31	357 / 7275	HOPP_Txn_elongation
4	1e−18	298 / 6559	HOPP_Weak_txn
5	5e−16	302 / 6959	HOPP_Weak_enhancer
6	7e−16	68 / 777	WIRTH_lymphoma937_spot D
7	6e−15	66 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
8	8e−11	80 / 1270	SPANG_BCR UP
9	2e−09	224 / 5356	HOPP_Txn_transition
10	3e−06	274 / 7448	HOPP_Strong_enhancer
11	9e−05	18 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
12	2e−04	18 / 232	WIRTH_lymphoma937_spot B
13	3e−03	51 / 1169	SPANG_BCR DN
14	5e−03	17 / 290	SPANG_IL21 UP
15	7e−03	7 / 77	Aukema_BCL2 DN_BCL6 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.6	1 / 27	Hugo_melanoma−all−LEF1_UP
2	0.8	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	8e−09	330 / 8818	protein binding
2	5e−08	90 / 1717	metal ion binding
3	4e−04	66 / 1475	DNA binding
4	2e−03	5 / 30	RNA polymerase II transcription cofactor activity
5	7e−03	5 / 41	scavenger receptor activity
6	9e−03	4 / 28	ubiquitin conjugating enzyme binding
7	9e−03	3 / 15	protein−lysine N−methyltransferase activity
8	1e−02	10 / 145	nucleic acid binding
9	1e−02	3 / 16	palmitoyltransferase activity
10	1e−02	3 / 18	snoRNA binding
11	2e−02	3 / 20	2 iron, 2 sulfur cluster binding
12	2e−02	3 / 21	cytokine receptor activity
13	3e−02	3 / 22	cytochrome−c oxidase activity
14	3e−02	36 / 877	transcription factor activity, sequence−specific DNA binding
15	3e−02	19 / 399	RNA binding

miRNA Disease

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

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	18 / 193	hsa−miR−513a−3p
2	6e−05	26 / 379	hsa−miR−454
3	9e−05	26 / 389	hsa−miR−519a
4	1e−04	35 / 602	hsa−miR−20a
5	1e−04	26 / 394	hsa−miR−301b
6	2e−04	27 / 425	hsa−let−7b
7	3e−04	28 / 463	hsa−miR−301a
8	3e−04	19 / 263	hsa−miR−449a
9	3e−04	25 / 400	hsa−miR−519c−3p
10	3e−04	20 / 288	hsa−miR−34a
11	4e−04	30 / 520	hsa−miR−106a
12	4e−04	26 / 429	hsa−miR−548n
13	5e−04	13 / 149	hsa−miR−142−3p
14	5e−04	16 / 210	hsa−miR−29b
15	5e−04	23 / 366	hsa−miR−519b−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	2 / 12	BENTINK_ras.1
2	0.05	2 / 13	BENTINK_e2f3.2
3	0.30	1 / 12	BENTINK_src.2
4	0.32	1 / 13	BENTINK_e2f3.1
5	0.32	1 / 13	BENTINK_myc.1
6	0.34	1 / 14	GUSTAFSON_PI3K_UP
7	0.34	1 / 14	BENTINK_ras.6
8	1.00	0 / 15	GUSTAFSON_PI3K_DN
9	1.00	0 / 11	BENTINK_ras.4
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−07	24 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
2	1e−04	12 / 113	Chaussabel_1,4_Replication
3	2e−03	38 / 782	PROTEINATLAS_thyroid gland
4	2e−03	39 / 816	PROTEINATLAS_endometrium
5	4e−03	18 / 302	Chaussabel_3,4_Protein phosphatases
6	6e−03	42 / 959	PROTEINATLAS_nasopharynx
7	7e−03	42 / 963	PROTEINATLAS_pancreas
8	1e−02	39 / 912	PROTEINATLAS_fallopian tube
9	2e−02	20 / 416	PROTEINATLAS_ovary
10	3e−02	46 / 1167	PROTEINATLAS_gallbladder
11	3e−02	38 / 933	PROTEINATLAS_adrenal gland
12	3e−02	13 / 242	Chaussabel_3,9_Kinases
13	3e−02	48 / 1239	PROTEINATLAS_testis
14	3e−02	9 / 148	VAQUERIZAS_General_TF
15	4e−02	12 / 231	Chaussabel_2,5_Immune related molecules

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	3e−13	229 / 5067	ICGC_Taf1_targets
2	8e−10	228 / 5442	ICGC_Pmlsc71910_targets
3	1e−09	191 / 4362	ICGC_Creb1_targets
4	1e−08	111 / 2215	ICGC_GabpPcr2_targets
5	2e−08	203 / 4881	ICGC_Atf2_targets
6	4e−08	247 / 6267	ICGC_Yy1_targets
7	6e−08	277 / 7247	ICGC_Runx3_targets
8	1e−07	264 / 6868	ICGC_Elf1_targets
9	1e−07	219 / 5466	ICGC_Nficsc81335_targets
10	1e−07	235 / 5984	ICGC_Mta3_targets
11	2e−07	199 / 4890	ICGC_Bclaf101388_targets
12	2e−07	108 / 2255	ICGC_SrfV0416101_targets
13	2e−07	219 / 5518	ICGC_Stat5_targets
14	3e−07	180 / 4345	ICGC_Zeb1_targets
15	3e−07	215 / 5410	ICGC_Foxm1_targets

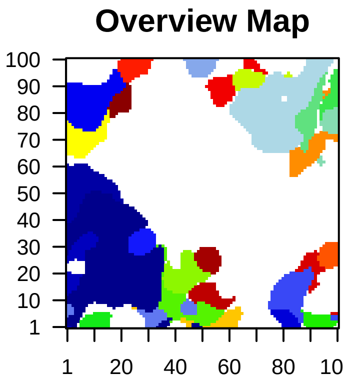
Correlation Cluster

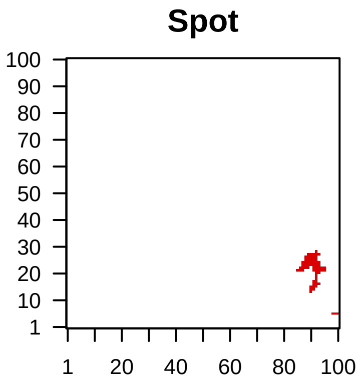
Spot Summary: B1

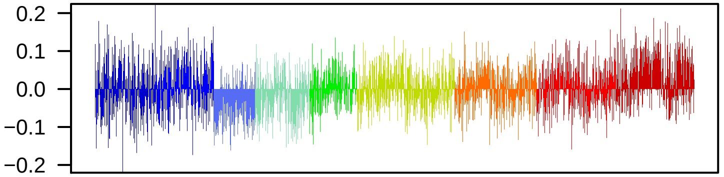
metagenes = 65
genes = 131

<r> metagenes = 0.92
<r> genes = 0.11
beta: r2= 7.99 / log p= −Inf

samples with spot = 451 (13.3 %)
- A * : 50 (14.5 %)
- A C * : 62 (18.9 %)
- A C F * : 4 (1.7 %)
- A F * : 22 (7.1 %)
- C F * : 22 (8.3 %)
- F * : 55 (9.9 %)
- F J * : 43 (9.3 %)
- J * : 60 (13.4 %)
- N * : 133 (30 %)





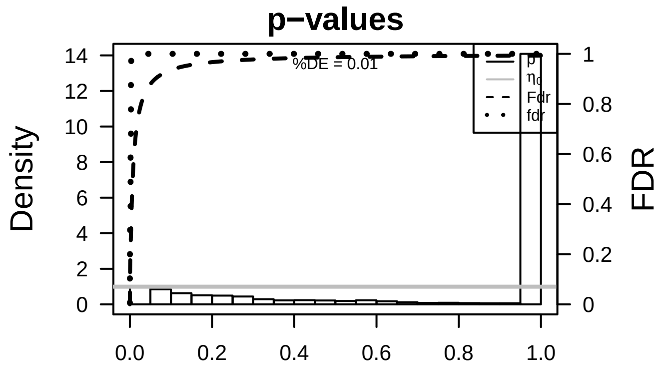


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_209565	1.43	−0.84	0.3	AFMID	arylformamidase [Source:HGNC Symbol;Acc:HGNC:20910]
2	ILMN_169333	1.29	−1.28	0.64	CYP1B1	cytochrome P450 family 1 subfamily B member 1 [Source:HG
3	ILMN_172077	1.2	−0.92	0.76	STX11	syntaxin 11 [Source:HGNC Symbol;Acc:HGNC:11429]
4	ILMN_170728	1.06	−0.97	0.8	PLBD1	phospholipase B domain containing 1 [Source:HGNC Symbo
5	ILMN_191367	1.04	−0.95	0.67	MIR6502	interleukin 1 receptor associated kinase 3 [Source:HGNC Sy
6	ILMN_180125	1.01	−0.7	0.54		
7	ILMN_167212	1	−0.82	0.67	FAM198B	family with sequence similarity 198 member B [Source:HGNC
8	ILMN_174233	1	−0.98	0.64	KCTD12	potassium channel tetramerization domain containing 12 [Sou
9	ILMN_167962	0.92	−0.8	0.58		
10	ILMN_170473	0.9	−0.89	0.66	CD93	CD93 molecule [Source:HGNC Symbol;Acc:HGNC:15855]
11	ILMN_223086	0.89	−0.68	0.64	GYG1	glycogenin 1 [Source:HGNC Symbol;Acc:HGNC:4699]
12	ILMN_175893	0.88	−0.83	0.67	SLC31A2	solute carrier family 31 member 2 [Source:HGNC Symbol;Ac
13	ILMN_166906	0.87	−0.75	0.58	CCR2	C−C motif chemokine receptor 2 [Source:HGNC Symbol;Acc:
14	ILMN_177954	0.86	−0.66	0.66	HPSE	heparanase [Source:HGNC Symbol;Acc:HGNC:5164]
15	ILMN_239602	0.85	−0.87	0.58	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:H
16	ILMN_175331	0.83	−0.7	0.77	PLXDC2	plexin domain containing 2 [Source:HGNC Symbol;Acc:HGN
17	ILMN_323642	0.82	−0.77	0.74	TMEM170B	transmembrane protein 170B [Source:HGNC Symbol;Acc:HG
18	ILMN_167519	0.82	−0.87	0.43	GAPT	GRB2−binding adaptor protein, transmembrane [Source:HGN
19	ILMN_179571	0.82	−0.82	0.7	DPYD	dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Ac
20	ILMN_174100	0.81	−0.77	0.54	ANXA5	annexin A5 [Source:HGNC Symbol;Acc:HGNC:543]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−08	11 / 240	Refer	Chaussabel_3,3_Inflammation II
2	7e−07	9 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
3	2e−06	58 / 6959	Lymph	HOPP_Weak_enhancer
4	3e−06	7 / 129	GSEA	HUANG_GATA2_TARGETS_UP
5	6e−06	9 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
6	9e−06	15 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
7	9e−06	7 / 151	GSEA	DURAND_STROMA_NS_UP
8	2e−05	9 / 300	Lymph	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−
9	2e−05	9 / 301	Canc	SPANG_BCL6−index2
10	2e−05	9 / 306	Lymph	WIRTH_lymphoma937_spot E
11	2e−05	9 / 315	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
12	3e−05	10 / 413	MF	protein heterodimerization activity
13	4e−05	7 / 187	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	4e−05	5 / 79	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP
15	4e−05	6 / 131	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
16	7e−05	5 / 87	Lymph	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
17	7e−05	6 / 142	Colon	Marisa_CRC−cluster−a
18	7e−05	74 / 10999	Colon	TssWk_Colon
19	9e−05	7 / 214	GSEA	GAL_LEUKEMIC_STEM_CELL_DN
20	9e−05	4 / 48	GSEA	ROSS_AML_WITH_CBFB_MYH11_FUSION
21	9e−05	6 / 150	Refer	Chaussabel_2,6_Myeloid lineage
22	9e−05	6 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
23	1e−04	21 / 1797	GSEA	PILON_KLF1_TARGETS_DN
24	2e−04	6 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
25	2e−04	7 / 236	GSEA	BILD_HRAS_ONCOGENIC_SIGNATURE
26	2e−04	7 / 238	GSEA	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
27	2e−04	5 / 113	Refer	Chaussabel_1,5_Myeloid lineage
28	3e−04	4 / 63	miRN	hsa−miR−618
29	3e−04	3 / 26	BP	positive regulation of vascular endothelial growth factor production
30	3e−04	4 / 64	miRN	hsa−miR−1278
31	3e−04	4 / 64	GSEA	REACTOME_MEIOTIC_SYNAPSIS
32	3e−04	7 / 268	GSEA	WANG_SMARCE1_TARGETS_UP
33	3e−04	7 / 268	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
34	4e−04	8 / 358	GSEA	CHYLA_CBFA2T3_TARGETS_UP
35	4e−04	3 / 29	GSEA	VALK_AML_CLUSTER_5
36	4e−04	8 / 366	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
37	4e−04	8 / 368	GSEA	OSMAN_BLADDER_CANCER_UP
38	5e−04	2 / 7	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_2_DN
39	5e−04	4 / 75	GSEA	BASSO_HAIRY_CELL_LEUKEMIA_DN
40	6e−04	7 / 293	miRN	hsa−miR−34c−5p



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 26	positive regulation of vascular endothelial growth factor production
2	6e−04	4 / 80	wound healing
3	1e−03	3 / 40	protein peptidyl−prolyl isomerization
4	1e−03	2 / 10	regulation of neuron migration
5	1e−03	4 / 93	nucleosome assembly
6	1e−03	2 / 11	G−protein coupled purinergic nucleotide receptor signaling pathway
7	1e−03	2 / 12	positive regulation of leukocyte migration
8	2e−03	2 / 15	response to growth factor
9	3e−03	6 / 293	immune response
10	3e−03	4 / 125	cytokine−mediated signaling pathway
11	3e−03	2 / 18	B cell homeostasis
12	3e−03	2 / 18	signal transduction involved in regulation of gene expression
13	3e−03	3 / 62	negative regulation of NF−kappaB transcription factor activity
14	4e−03	2 / 19	synaptonemal complex assembly
15	4e−03	2 / 19	telomere capping

Brain

Rank	p−value	#in/all	Geneset
1	0.001	65 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	0.002	16 / 1436	Fetal_K9K27me3
3	0.002	14 / 1213	Fetal_TssP
4	0.004	13 / 1162	Fetal_Enh
5	0.016	10 / 937	Fetal_EnhG
6	0.020	11 / 1115	Overlap_fetal_midbrain_EnhG
7	0.058	9 / 1012	Mid_Frontal_Lobe_Enh
8	0.059	11 / 1329	Overlap_fetal_midbrain_Enh
9	0.062	8 / 869	Mid_Frontal_Lobe_EnhG
10	0.070	56 / 9815	Overlap_fetal_midbrain_ReprPC
11	0.075	8 / 906	Fetal_HetRpts
12	0.076	4 / 328	Fetal_Het
13	0.085	18 / 2630	Fetal_TssF
14	0.100	58 / 10430	Overlap_fetal_midbrain_Quies
15	0.105	7 / 819	Overlap_fetal_midbrain_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 301	SPANG_BCL6−index2
2	6e−03	8 / 554	Lembcke_Colonic Inflammation
3	6e−03	0 / 15	LIU_PROSTATE_CANCER_DN
4	2e−02	3 / 125	PanCan_CC+Apop_geneset_nanostring
5	6e−02	3 / 178	SPANG_LPS−index2
6	1e−01	5 / 527	Lembcke_Normal vs Adenoma
7	2e−01	1 / 46	PanCan_TGF−B_geneset_nanostring
8	3e−01	1 / 73	SHAUGHNESSY_MM high risk
9	4e−01	1 / 91	PanCan_TXmisReg_geneset_nanostring
10	4e−01	1 / 117	PanCan_Driver_Gene_geneset_nanostring
11	5e−01	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	5e−01	1 / 150	PanCan_MAPK_geneset_nanostring
13	6e−01	1 / 193	PanCan_PI3K_geneset_nanostring
14	1e+00	0 / 13	RHODES_CANCER_META_SIGNATURE
15	1e+00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	0.002	9 / 561	intracellular membrane−bounded organelle
2	0.004	2 / 20	synaptonemal complex
3	0.006	2 / 24	integrin complex
4	0.007	3 / 80	nucleosome
5	0.012	2 / 34	nuclear nucleosome
6	0.015	20 / 2464	extracellular exosome
7	0.021	2 / 46	nuclear chromosome
8	0.023	4 / 221	endosome
9	0.024	2 / 49	axon terminus
10	0.029	3 / 136	cytoplasmic, membrane−bounded vesicle
11	0.029	22 / 2979	cytosol
12	0.044	23 / 3291	integral component of membrane
13	0.048	1 / 10	protein phosphatase type 1 complex
14	0.048	1 / 10	semaphorin receptor complex
15	0.051	2 / 74	lysosomal lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.005	12 / 1060	Chr 5
2	0.034	11 / 1211	Chr 6
3	0.073	10 / 1217	Chr 3
4	0.152	7 / 904	Chr 10
5	0.184	5 / 619	Chr 20
6	0.210	8 / 1170	Chr 7
7	0.411	2 / 289	Chr 21
8	0.441	8 / 1492	Chr 2
9	0.448	5 / 902	Chr 4
10	0.584	4 / 836	Chr 8
11	0.584	11 / 2323	Chr 1
12	0.611	2 / 422	Chr 13
13	0.671	5 / 1160	Chr 12
14	0.687	4 / 954	Chr 9
15	0.814	1 / 342	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.001	60 / 8990	15_Quies_Fibroblasts
2	0.002	28 / 3272	13_HetRpts_Neuronal_Progenitor
3	0.003	69 / 11130	15_Quies_Melanocytes
4	0.018	21 / 2682	12_Het_Neuronal_Progenitor
5	0.020	53 / 8613	7_Enh_Fibroblasts
6	0.021	67 / 11455	2_TssA_Fibroblasts
7	0.028	12 / 1324	13_HetRpts_Fibroblasts
8	0.031	18 / 2315	13_HetRpts_Melanocytes
9	0.034	15 / 1846	14_ZNF_Melanocytes
10	0.035	72 / 12741	7_Enh_Melanocytes
11	0.068	15 / 2031	12_Het_Melanocytes
12	0.069	66 / 11847	7_Enh_Neuronal_Progenitor
13	0.081	71 / 12983	2_TssA_Neuronal_Progenitor
14	0.103	54 / 9635	3_TssF_Fibroblasts
15	0.170	25 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−06	15 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	7e−05	6 / 142	Marisa_CRC−cluster−a
3	7e−05	74 / 10999	TssWk_Colon
4	1e−03	2 / 10	Marisa_CRC−C1
5	3e−03	15 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
6	5e−03	15 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
7	5e−03	6 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
8	1e−02	7 / 489	K9acLow_Colon
9	2e−02	12 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
10	2e−02	29 / 4018	EnhWk2_Colon
11	3e−02	3 / 129	Marisa_CRC−cluster−b
12	3e−02	57 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
13	3e−02	6 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	4e−02	52 / 8678	Quies3_Colon
15	4e−02	1 / 8	Marisa_CRC−C2

Glio

Rank	p−value	#in/all	Geneset
1	6e−06	9 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	4e−03	15 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	2e−02	5 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	5e−02	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
5	9e−02	1 / 19	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
6	9e−02	1 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
7	1e−01	2 / 113	GIEZELT_GBM_WT_up_VS_mut
8	1e−01	2 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
9	1e−01	1 / 24	Martinez_Glio_hypermeth
10	1e−01	2 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	1e−01	1 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
12	1e−01	1 / 26	Gorovets_LGG_NB_subclass
13	1e−01	2 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	1e−01	1 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
15	2e−01	2 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−07	9 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
2	3e−06	7 / 129	HUANG_GATA2_TARGETS_UP
3	9e−06	7 / 151	DURAND_STROMA_NS_UP
4	2e−05	9 / 315	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	4e−05	7 / 187	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	4e−05	5 / 79	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP
7	4e−05	6 / 131	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
8	9e−05	7 / 214	GAL_LEUKEMIC_STEM_CELL_DN
9	9e−05	4 / 48	ROSS_AML_WITH_CBFB_MYH11_FUSION
10	9e−05	6 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
11	1e−04	21 / 1797	PILON_KLF1_TARGETS_DN
12	2e−04	6 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
13	2e−04	7 / 236	BILD_HRAS_ONCOGENIC_SIGNATURE
14	2e−04	7 / 238	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
15	3e−04	4 / 64	REACTOME_MEIOTIC_SYNAPSIS

HM

Rank	p−value	#in/all	Geneset
1	0.003	4 / 127	HALLMARK_COAGULATION
2	0.013	4 / 187	HALLMARK_COMPLEMENT
3	0.067	3 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	0.167	2 / 151	HALLMARK_APOPTOSIS
5	0.181	1 / 41	HALLMARK_APICAL_SURFACE
6	0.186	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
7	0.204	2 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	0.211	2 / 176	HALLMARK_KRAS_SIGNALING_UP
9	0.217	1 / 50	HALLMARK_TGF_BETA_SIGNALING
10	0.224	2 / 183	HALLMARK_APICAL_JUNCTION
11	0.229	2 / 186	HALLMARK_IL2_STAT5_SIGNALING
12	0.286	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	0.377	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.488	1 / 137	HALLMARK_UV_RESPONSE_UP
15	0.580	1 / 177	HALLMARK_MITOTIC_SPINDLE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	Huan_blood−pressure_HTN−signature
2	0.05	1 / 10	DUMEAUX_Smoking literature genes up
3	0.08	1 / 16	Huan_blood−pressure_DBP−signature
4	0.08	1 / 18	Huan_blood−pressure_SBP−signature
5	0.37	1 / 94	DUMEAUX_Smoking enriched genes
6	0.64	1 / 211	Homuth_BMI−associated−genes_DN
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 17	DUMEAUX_High bmi enriched genes
15	1.00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−06	58 / 6959	HOPP_Weak_enhancer
2	2e−05	9 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
3	2e−05	9 / 306	WIRTH_lymphoma937_spot E
4	7e−05	5 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
5	2e−03	47 / 6559	HOPP_Weak_txn
6	3e−03	4 / 118	Subero_INT_hyper_meth
7	3e−03	3 / 57	LENZ_Stromal signature 2
8	3e−03	54 / 8098	HOPP_Weak_promoter
9	4e−03	4 / 134	Subero_DLBCL_hyper_meth
10	5e−03	23 / 2701	HOPP_Repetitive
11	6e−03	6 / 331	SPANG_CD40 6hrs UP
12	8e−03	3 / 84	ROSOLOWSKI_green UP
13	9e−03	3 / 88	ROSOLOWSKI_red total
14	1e−02	2 / 36	Subero_MM_hyper_meth
15	2e−02	3 / 115	ROSOLOWSKI_green total

Melanoma

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

MF

Rank	p−value	#in/all	Geneset
1	3e−05	10 / 413	protein heterodimerization activity
2	1e−03	3 / 41	peptidyl−prolyl cis−trans isomerase activity
3	1e−03	2 / 12	G−protein coupled purinergic nucleotide receptor activity
4	4e−03	2 / 19	FK506 binding
5	1e−02	2 / 31	phosphatidylinositol−3−phosphate binding
6	1e−02	4 / 182	signal transducer activity
7	1e−02	2 / 35	monooxygenase activity
8	1e−02	55 / 8818	protein binding
9	1e−02	8 / 646	protein homodimerization activity
10	1e−02	2 / 38	oxygen binding
11	2e−02	2 / 40	transforming growth factor beta receptor binding
12	2e−02	2 / 42	SMAD binding
13	2e−02	2 / 43	phosphatase binding
14	2e−02	3 / 121	iron ion binding
15	2e−02	2 / 47	phosphoprotein phosphatase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 113	Ovarian cancer
2	0.4	1 / 120	Hematological
3	0.5	1 / 123	Pancreatic cancer
4	0.5	1 / 124	Prostate cancer
5	0.5	1 / 127	Squamous cell carcinoma, head and neck
6	0.5	1 / 142	Lung cancer
7	0.5	1 / 156	Breast cancer
8	1.0	0 / 7	Thyroid carcinoma, papillary
9	1.0	0 / 68	Glioblastoma multiforme, somatic
10	1.0	0 / 63	Gastrointestinal
11	1.0	0 / 3	Pituitary adenoma
12	1.0	0 / 116	Cancer
13	1.0	0 / 95	Colorectal cancer
14	1.0	0 / 2	Adenomas, multiple colorectal
15	1.0	0 / 48	Alzheimer disease, susceptibility to

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 63	hsa−miR−618
2	3e−04	4 / 64	hsa−miR−1278
3	6e−04	7 / 293	hsa−miR−34c−5p
4	2e−03	3 / 49	hsa−miR−549
5	2e−03	6 / 272	hsa−miR−101
6	3e−03	6 / 281	hsa−miR−570
7	4e−03	3 / 63	hsa−miR−1267
8	4e−03	2 / 19	hsa−miR−563
9	5e−03	7 / 429	hsa−miR−548n
10	5e−03	7 / 433	hsa−miR−19b
11	5e−03	3 / 73	hsa−miR−1261
12	6e−03	7 / 438	hsa−miR−19a
13	6e−03	5 / 237	hsa−miR−152
14	9e−03	3 / 86	hsa−miR−339−5p
15	9e−03	5 / 263	hsa−miR−449a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.05	1 / 11	BENTINK_ras.4
2	0.07	1 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−08	11 / 240	Chaussabel_3,3_Inflammation II
2	9e−05	6 / 150	Chaussabel_2,6_Myeloid lineage
3	2e−04	5 / 113	Chaussabel_1,5_Myeloid lineage
4	8e−04	4 / 84	Chaussabel_2,10_Immune related cell surface molecules
5	3e−02	4 / 242	Chaussabel_3,2_Inflammation I
6	6e−02	9 / 1016	PROTEINATLAS_cerebral cortex
7	6e−02	1 / 13	JONGENEEL_Uterus
8	7e−02	1 / 14	WIRTH_Telencephalon
9	9e−02	2 / 102	Chaussabel_1,2_Platelets
10	1e−01	1 / 21	JONGENEEL_Monocytes
11	1e−01	1 / 24	VAQUERIZAS_Spinal cord_TF
12	1e−01	4 / 412	WIRTH_Immune system
13	2e−01	2 / 153	Chaussabel_2,9_Cytosceleton
14	2e−01	7 / 960	PROTEINATLAS_cerebellum
15	2e−01	5 / 647	PROTEINATLAS_lateral ventricle

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.02	13 / 1452	ICGC_Six5_targets
2	0.03	24 / 3348	ICGC_BatfPcr1_targets
3	0.08	13 / 1723	HEBENSTREIT_high expression TF
4	0.10	11 / 1466	ICGC_NrsfPcr1_targets
5	0.11	11 / 1498	ICGC_Ets1_targets
6	0.14	6 / 721	ICGC_SrfPcr2_targets
7	0.15	31 / 5312	ICGC_Tcf12_targets
8	0.17	31 / 5410	ICGC_Foxm1_targets
9	0.19	28 / 4881	ICGC_Atf2_targets
10	0.21	19 / 3194	ICGC_Irf4_targets
11	0.22	33 / 5961	ICGC_Pol24_targets
12	0.23	15 / 2497	ICGC_Bcl11_targets
13	0.23	11 / 1753	HEBENSTREIT_low expression TF
14	0.25	28 / 5067	ICGC_Taf1_targets
15	0.25	20 / 3507	ICGC_Rad21_targets