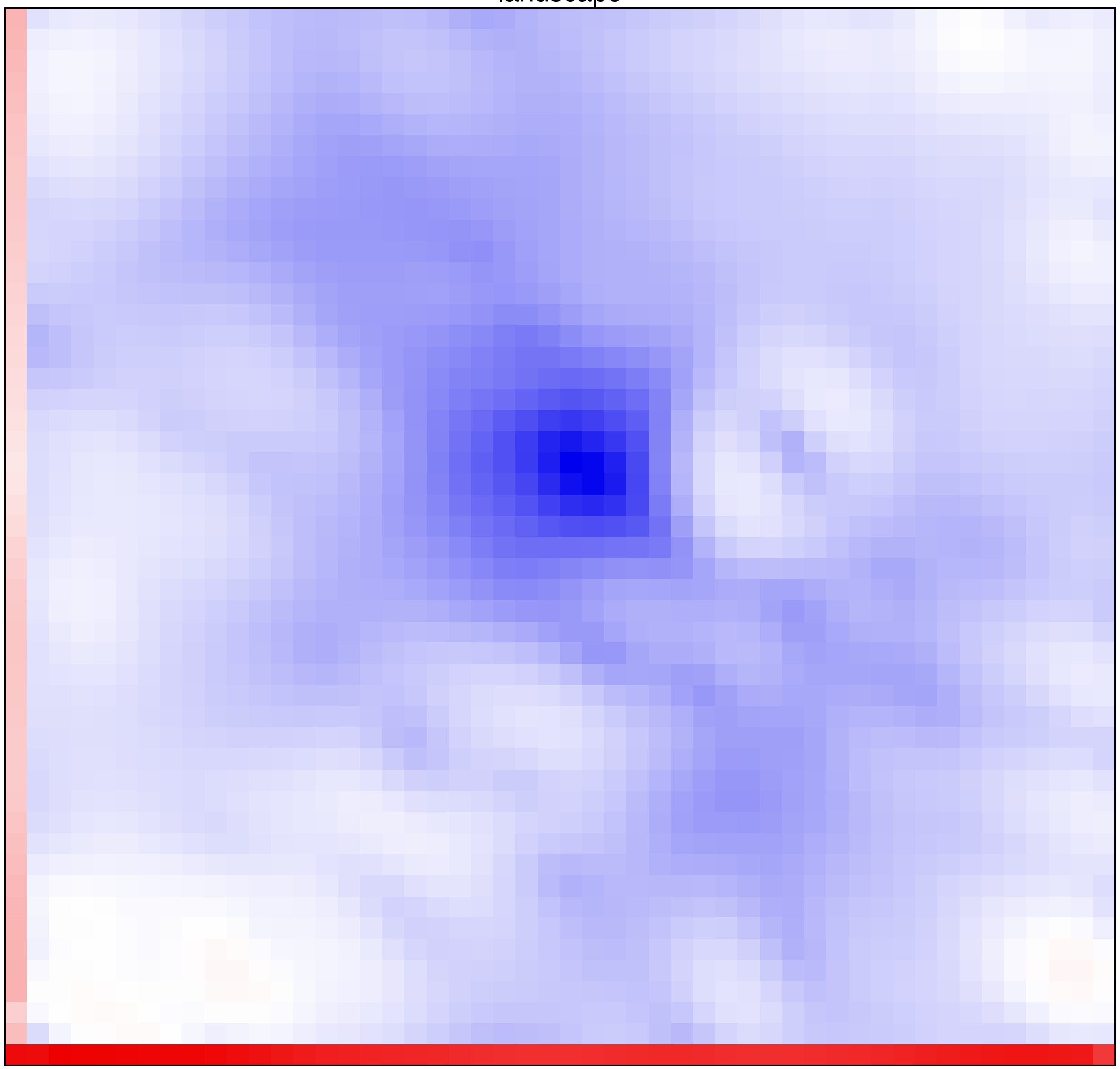
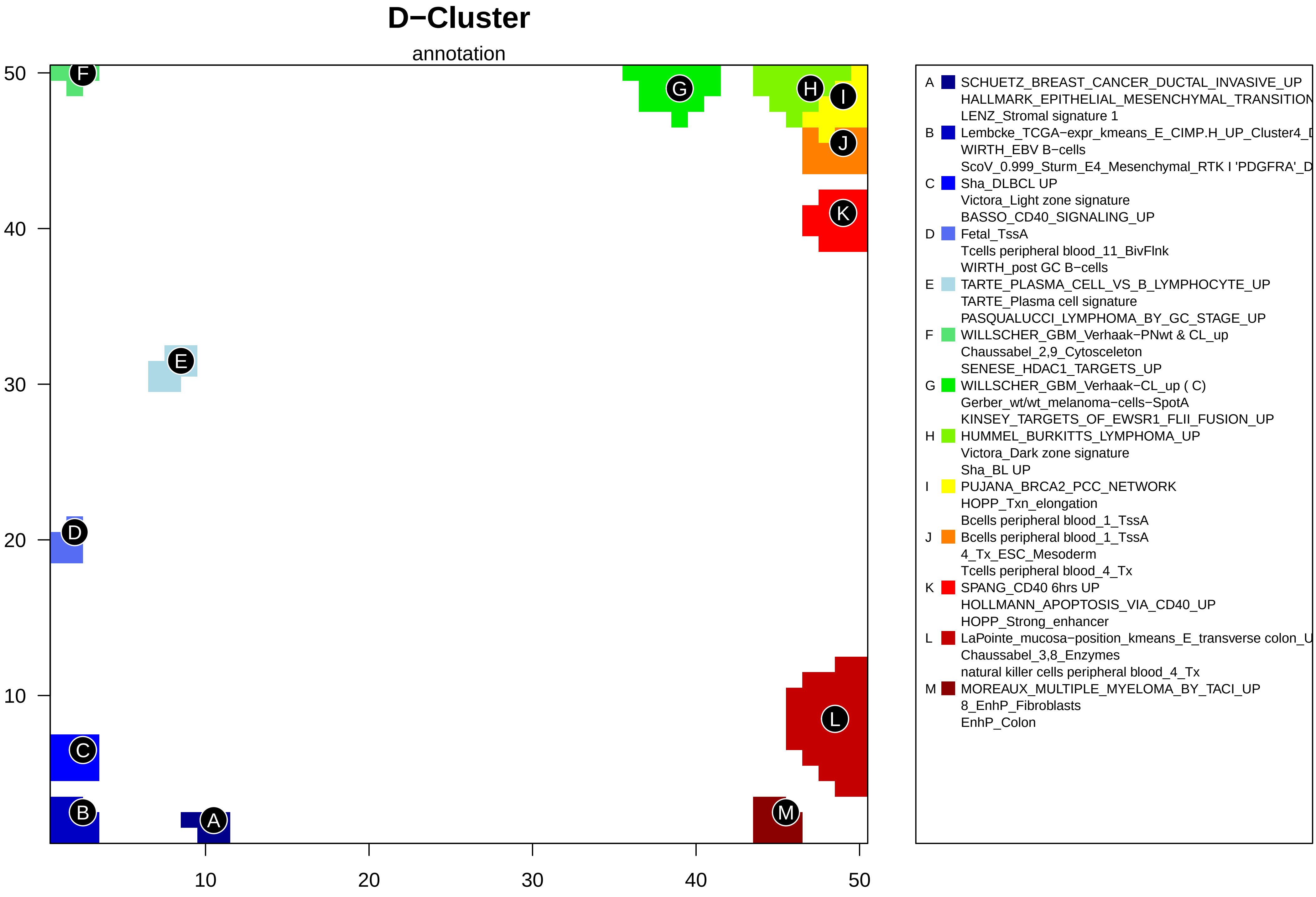
D−Cluster



landscape


D−Cluster
annotation
50
40
30
20
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A
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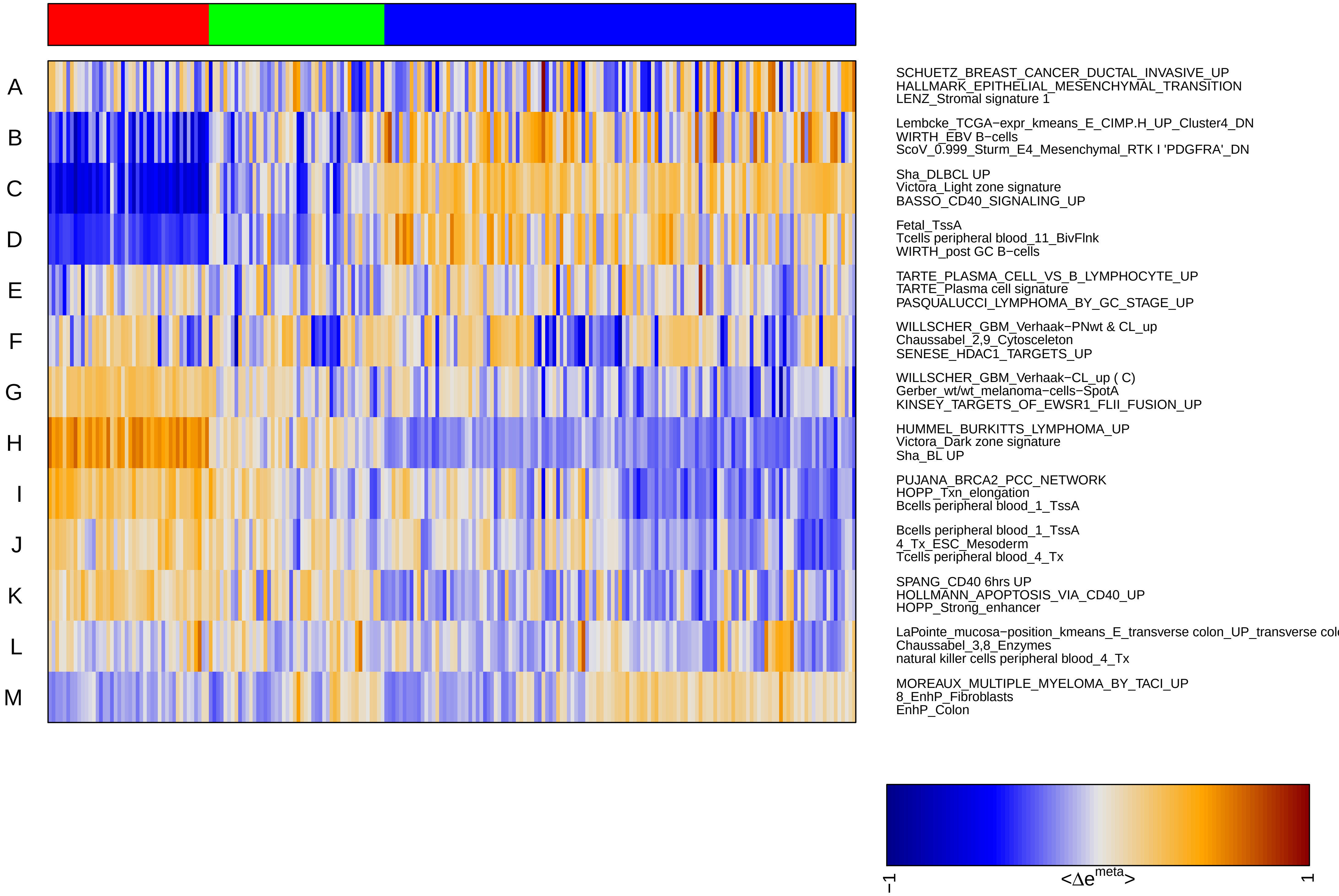
L
M
A SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
LENZ_Stromal signature 1
B Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_I
WIRTH_EBV B−cells
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_D
C Sha_DLBCL UP
Victora_Light zone signature
BASSO_CD40_SIGNALING_UP
D Fetal_TssA
Tcells peripheral blood_11_BivFlnk
WIRTH_post GC B−cells
E TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
TARTE_Plasma cell signature
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
F WILLSCHER_GBM_Verhaak−PNwt & CL_up
Chaussabel_2,9_Cytosceleton
SENESE_HDAC1_TARGETS_UP
G WILLSCHER_GBM_Verhaak−CL_up (C)
Gerber_wt/wt_melanoma−cells−SpotA
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
H HUMMEL_BURKITTS_LYMPHOMA_UP
Victora_Dark zone signature
Sha_BL UP
I PUJANA_BRCA2_PCC_NETWORK
HOPP_Txn_elongation
Bcells peripheral blood_1_TssA
J Bcells peripheral blood_1_TssA
4_Tx_ESC_Mesoderm
Tcells peripheral blood_4_Tx
K SPANG_CD40 6hrs UP
HOLLMANN_APOPTOSIS_VIA_CD40_UP
HOPP_Strong_enhancer
L LaPointe_mucosa−position_kmeans_E_transverse colon_U
Chaussabel_3,8_Enzymes
natural killer cells peripheral blood_4_Tx
M MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
8_EnhP_Fibroblasts
EnhP_Colon


A
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SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
LENZ_Stromal signature 1
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
WIRTH_EBV B−cells
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
Sha_DLBCL UP
Victora_Light zone signature
BASSO_CD40_SIGNALING_UP
Fetal_TssA
Tcells peripheral blood_11_BivFlnk
WIRTH_post GC B−cells
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
TARTE_Plasma cell signature
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
WILLSCHER_GBM_Verhaak−PNwt & CL_up
Chaussabel_2,9_Cytosceleton
SENESE_HDAC1_TARGETS_UP
WILLSCHER_GBM_Verhaak−CL_up (C)
Gerber_wt/wt_melanoma−cells−SpotA
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
HUMMEL_BURKITTS_LYMPHOMA_UP
Victora_Dark zone signature
Sha_BL UP
PUJANA_BRCA2_PCC_NETWORK
HOPP_Txn_elongation
Bcells peripheral blood_1_TssA
Bcells peripheral blood_1_TssA
4_Tx_ESC_Mesoderm
Tcells peripheral blood_4_Tx
SPANG_CD40 6hrs UP
HOLLMANN_APOPTOSIS_VIA_CD40_UP
HOPP_Strong_enhancer
LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse col
Chaussabel_3,8_Enzymes
natural killer cells peripheral blood_4_Tx
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
8_EnhP_Fibroblasts
EnhP_Colon
−1
<Δe^meta>
1

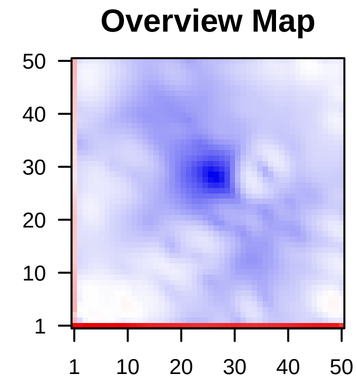
D−Cluster

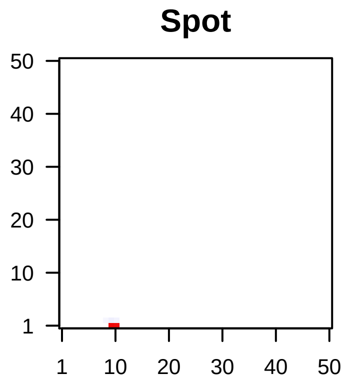
Spot Summary: A

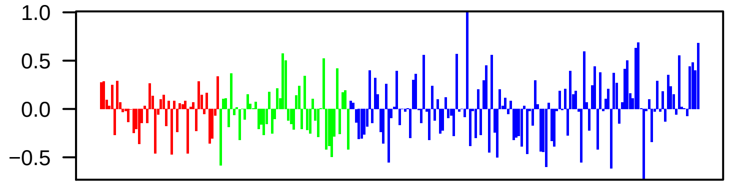
metagenes = 5
genes = 80

<r> metagenes = 0.99
<r> genes = 0.44
beta: r2= 14.45 / log p= −Inf

samples with spot = 42 (19 %)
mBL : 6 (13.6 %)
intermediate : 6 (12.5 %)
non−mBL : 30 (23.3 %)


Overview Map


Spot

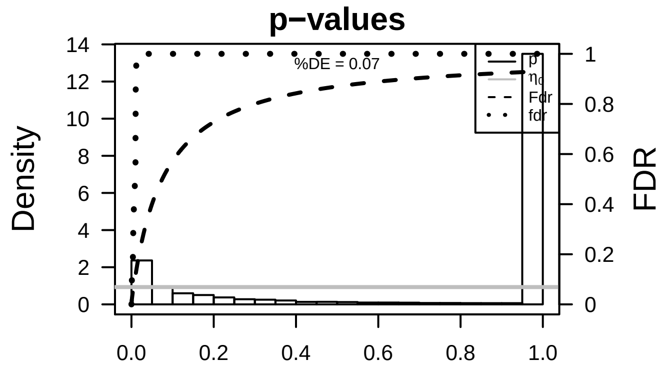


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202718_at	2.31	−1.6	0.57	IGFBP2	insulin like growth factor binding protein 2 [Source:HGNC Sy
2	209621_s_at	1.92	−1.24	0.52	PDLIM3	PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:HGNC:2
3	201325_s_at	1.82	−1.23	0.72	EMP1	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:H
4	212488_at	1.77	−1.28	0.79	COL5A1	collagen type V alpha 1 chain [Source:HGNC Symbol;Acc:H
5	204051_s_at	1.71	−1.02	0.4	SFRP4	secreted frizzled related protein 4 [Source:HGNC Symbol;Ac
6	209189_at	1.69	−1.6	0.44	FOS	Fos proto−oncogene, AP−1 transcription factor subunit [Sour
7	217430_x_at	1.69	−1.01	0.75	COL1A1	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HG
8	213869_x_at	1.67	−1.02	0.67	THY1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:HGN
9	212489_at	1.59	−1.39	0.81	COL5A1	collagen type V alpha 1 chain [Source:HGNC Symbol;Acc:H
10	203325_s_at	1.57	−1.2	0.77	COL5A1	collagen type V alpha 1 chain [Source:HGNC Symbol;Acc:H
11	205713_s_at	1.55	−1	0.4	COMP	cartilage oligomeric matrix protein [Source:HGNC Symbol;Ac
12	215446_s_at	1.55	−0.98	0.72	LOX	lysyl oxidase [Source:HGNC Symbol;Acc:HGNC:6664]
13	203886_s_at	1.54	−1.37	0.65	FBLN2	fibulin 2 [Source:HGNC Symbol;Acc:HGNC:3601]
14	213004_at	1.54	−0.78	0.72	ANGPTL2	angiopoietin like 2 [Source:HGNC Symbol;Acc:HGNC:490]
15	212154_at	1.49	−1.07	0.58	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
16	208850_s_at	1.49	−1.28	0.73	THY1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:HGN
17	217369_at	1.47	−1.05	0.68		
18	201324_at	1.47	−1.08	0.76	EMP1	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:H
19	202310_s_at	1.45	−2.36	0.89	COL1A1	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HG
20	210809_s_at	1.41	−2.02	0.77	POSTN	periostin [Source:HGNC Symbol;Acc:HGNC:16953]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−43	37 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	3e−37	29 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	3e−34	28 / 214	Lymp	LENZ_Stromal signature 1
4	8e−32	26 / 197	GSEA	NABA_CORE_MATRISOME
5	1e−27	24 / 212	CC	extracellular matrix
6	2e−27	23 / 183	BP	extracellular matrix organization
7	2e−27	21 / 132	Colon	Marisa_CRC−cluster−a
8	2e−26	17 / 63	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
9	1e−25	24 / 253	CC	proteinaceous extracellular matrix
10	6e−24	32 / 747	GSEA	NABA_MATRISOME
11	7e−24	27 / 443	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
12	1e−23	35 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
13	6e−23	20 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	9e−22	18 / 138	GSEA	IGLESIAS_E2F_TARGETS_UP
15	1e−21	14 / 53	MF	extracellular matrix structural constituent
16	5e−21	24 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
17	5e−21	15 / 77	GSEA	KEGG_ECM_RECEPTOR_INTERACTION
18	1e−20	27 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
19	4e−20	17 / 138	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
20	1e−19	16 / 117	GSEA	ZHU_CMV_ALL_DN
21	3e−19	11 / 29	GSEA	ROZANOV_MMP14_TARGETS_SUBSET
22	4e−19	22 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
23	5e−19	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
24	5e−19	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
25	5e−19	13 / 59	GSEA	PID_INTEGRIN1_PATHWAY
26	6e−19	32 / 1090	CC	extracellular space
27	2e−18	14 / 86	GSEA	ZHU_CMV_24_HR_DN
28	2e−18	13 / 66	CC	basement membrane
29	2e−17	13 / 78	Mela	Tirosh_CAF−cell specific genes
30	3e−17	12 / 58	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
31	4e−17	18 / 249	GSEA	ONDER_CDH1_TARGETS_2_UP
32	4e−17	12 / 60	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
33	1e−16	10 / 31	GSEA	NABA_BASEMENT_MEMBRANES
34	1e−16	10 / 32	GSEA	NABA_COLLAGENS
35	6e−16	17 / 241	CC	endoplasmic reticulum lumen
36	7e−16	34 / 1611	CC	extracellular region
37	1e−15	16 / 207	GSEA	ROZANOV_MMP14_TARGETS_UP
38	1e−15	11 / 56	GSEA	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
39	1e−15	14 / 136	GSEA	NABA_ECM_GLYCOPROTEINS
40	2e−15	17 / 262	GSEA	PASINI_SUZ12_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.4	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−27	23 / 183	extracellular matrix organization
2	1e−13	10 / 58	collagen catabolic process
3	8e−11	17 / 500	cell adhesion
4	7e−08	7 / 78	wound healing
5	9e−08	6 / 48	blood vessel development
6	1e−07	4 / 11	protein heterotrimerization
7	2e−07	8 / 130	skeletal system development
8	5e−07	6 / 64	response to mechanical stimulus
9	6e−07	5 / 35	collagen fibril organization
10	1e−06	5 / 42	cellular response to amino acid stimulus
11	2e−06	8 / 185	cellular protein metabolic process
12	5e−06	4 / 25	endodermal cell differentiation
13	8e−06	7 / 157	positive regulation of cell migration
14	9e−06	8 / 223	angiogenesis
15	1e−05	7 / 169	cell migration

Cancer

Rank	p−value	#in/all	Geneset
1	5e−19	0 / 14	LIU_PROSTATE_CANCER_DN
2	4e−09	15 / 480	Lembcke_Colonic Inflammation
3	3e−05	7 / 187	PanCan_PI3K_geneset_nanostring
4	3e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
5	7e−02	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
6	7e−02	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	7e−02	1 / 16	GENTLES_modul16
8	8e−02	1 / 18	PanCan_Notch_geneset_nanostring
9	2e−01	2 / 147	PanCan_MAPK_geneset_nanostring
10	2e−01	1 / 47	PanCan_TGF−B_geneset_nanostring
11	3e−01	1 / 72	PanCan_Wnt_geneset_nanostring
12	3e−01	0 / 11	LIU_PROSTATE_CANCER_UP
13	4e−01	1 / 96	PanCan_TXmisReg_geneset_nanostring
14	5e−01	1 / 134	PanCan_RAS_geneset_nanostring
15	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	1e−27	24 / 212	extracellular matrix
2	1e−25	24 / 253	proteinaceous extracellular matrix
3	6e−19	32 / 1090	extracellular space
4	2e−18	13 / 66	basement membrane
5	6e−16	17 / 241	endoplasmic reticulum lumen
6	7e−16	34 / 1611	extracellular region
7	7e−15	11 / 65	collagen trimer
8	7e−11	33 / 2239	extracellular exosome
9	5e−05	10 / 462	cell surface
10	7e−05	4 / 47	extracellular vesicle
11	2e−04	8 / 345	focal adhesion
12	2e−04	3 / 25	filamentous actin
13	7e−04	4 / 85	lysosomal lumen
14	1e−03	2 / 12	platelet alpha granule membrane
15	2e−03	2 / 14	basal lamina

Chr

Rank	p−value	#in/all	Geneset
1	0.006	8 / 585	Chr 7
2	0.028	3 / 139	Chr 21
3	0.105	3 / 242	Chr 13
4	0.188	4 / 480	Chr 4
5	0.262	4 / 554	Chr 5
6	0.352	5 / 832	Chr 2
7	0.407	4 / 689	Chr 3
8	0.409	3 / 492	Chr 9
9	0.419	4 / 700	Chr 12
10	0.466	2 / 333	Chr 22
11	0.539	2 / 382	Chr 15
12	0.613	2 / 437	Chr 8
13	0.697	3 / 756	Chr 11
14	0.714	3 / 776	Chr 17
15	0.735	2 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−19	44 / 2405	Bcells peripheral blood_13_ReprPC
2	3e−19	46 / 2765	Tregulatory cells peripheral blood_13_ReprPC
3	1e−18	51 / 3724	Tcells peripheral blood_12_EnhBiv
4	7e−18	43 / 2515	natural killer cells peripheral blood_13_ReprPC
5	8e−18	47 / 3150	monocytes peripheral blood_13_ReprPC
6	1e−17	50 / 3734	Tcells peripheral blood_13_ReprPC
7	2e−17	41 / 2300	Thelper cells peripheral blood_13_ReprPC
8	3e−17	43 / 2602	natural killer cells peripheral blood_12_EnhBiv
9	9e−17	45 / 3001	Bcells peripheral blood_14_ReprPCWk
10	1e−16	50 / 3918	Tcells peripheral blood_14_ReprPCWk
11	2e−16	35 / 1660	T CD8+ naive cells peripheral blood_12_EnhBiv
12	3e−16	39 / 2194	Thelper cells peripheral blood_12_EnhBiv
13	3e−15	45 / 3272	monocytes peripheral blood_14_ReprPCWk
14	5e−15	43 / 2984	natural killer cells peripheral blood_14_ReprPCWk
15	3e−14	33 / 1694	Thelper cells peripheral blood_11_BivFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−27	21 / 132	Marisa_CRC−cluster−a
2	1e−23	35 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	8e−09	12 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	1e−07	11 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	1e−04	8 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
6	1e−04	5 / 103	Marisa_CRC−cluster−b
7	2e−04	8 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
8	4e−04	4 / 72	Ang_CRC−CIMPH−vs−L_hyper
9	5e−04	4 / 77	Ang_CRC_Hypermethylated
10	6e−04	2 / 8	Marisa_CRC−C3
11	4e−03	8 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
12	4e−03	5 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	9e−03	1 / 2	Budinska_A_Surface crypt−like_DOWN
14	1e−02	5 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	2e−02	1 / 5	Kaneda_CIMP−group1

Glioma

Rank	p−value	#in/all	Geneset
1	6e−15	16 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−13	11 / 85	ScoV_0.999_Sturm_E2_IDH_DN
3	1e−07	7 / 82	laffaire_hypermeth_LGG_vs_control
4	2e−07	8 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
5	3e−07	8 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	4e−07	10 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
7	9e−07	7 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
8	1e−06	7 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	7e−06	6 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
10	1e−05	5 / 64	cultured astroglia vs. in vivo astrocytes
11	1e−04	3 / 21	KIM deleted & downregulated in LTS
12	3e−04	4 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
13	4e−04	3 / 30	KIM prognostic signature LTS vs. STS
14	6e−04	3 / 35	Colman_survival_associated
15	9e−04	3 / 41	Gorovets_LGG_PG_subclass

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−43	37 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	8e−32	26 / 197	NABA_CORE_MATRISOME
3	2e−26	17 / 63	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
4	6e−24	32 / 747	NABA_MATRISOME
5	7e−24	27 / 443	CHICAS_RB1_TARGETS_CONFLUENT
6	6e−23	20 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	9e−22	18 / 138	IGLESIAS_E2F_TARGETS_UP
8	5e−21	24 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
9	5e−21	15 / 77	KEGG_ECM_RECEPTOR_INTERACTION
10	1e−20	27 / 589	WONG_ADULT_TISSUE_STEM_MODULE
11	4e−20	17 / 138	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
12	1e−19	16 / 117	ZHU_CMV_ALL_DN
13	3e−19	11 / 29	ROZANOV_MMP14_TARGETS_SUBSET
14	4e−19	22 / 366	LIM_MAMMARY_STEM_CELL_UP
15	5e−19	0 / 14	LIU_PROSTATE_CANCER_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−37	29 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	3e−06	8 / 188	HALLMARK_HYPOXIA
3	4e−06	7 / 141	HALLMARK_UV_RESPONSE_DN
4	2e−05	4 / 34	HALLMARK_ANGIOGENESIS
5	3e−05	7 / 194	HALLMARK_MYOGENESIS
6	4e−04	5 / 130	HALLMARK_COAGULATION
7	5e−03	4 / 150	HALLMARK_APOPTOSIS
8	9e−03	4 / 174	HALLMARK_ADIPOGENESIS
9	3e−02	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	3e−02	3 / 149	HALLMARK_UV_RESPONSE_UP
11	5e−02	3 / 182	HALLMARK_GLYCOLYSIS
12	6e−02	3 / 191	HALLMARK_P53_PATHWAY
13	6e−02	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
14	1e−01	1 / 29	HALLMARK_NOTCH_SIGNALING
15	1e−01	1 / 34	HALLMARK_APICAL_SURFACE

Immunome

Rank	p−value	#in/all	Geneset
1	0.004	2 / 21	Angelova_immune−metagene−central_memory_CD4
2	0.103	1 / 23	Angelova_immune−metagene−Th2
3	0.111	1 / 25	Angelova_immune−metagene−DC
4	0.164	1 / 38	Angelova_immune−metagene−mast−cells
5	0.180	1 / 42	Angelova_immune−metagene−TGD
6	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
8	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
9	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
10	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
11	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
12	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
13	1.000	0 / 14	Angelova_immune−metagene−eosinophil
14	1.000	0 / 19	Angelova_immune−metagene−iDC
15	1.000	0 / 13	Angelova_immune−metagene−immature_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	1 / 14	Huan_blood−pressure_SBP−signature
2	0.14	1 / 32	Marjolein_ageing−genes_DN
3	0.63	1 / 210	Homuth_BMI−associated−genes_DN
4	1.00	0 / 62	DUMEAUX_Smoking enriched genes
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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 22	DUMEAUX_High bmi enriched genes
14	1.00	0 / 22	DUMEAUX_Fasting enriched genes
15	1.00	0 / 150	Homuth_BMI−associated−genes_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−34	28 / 214	LENZ_Stromal signature 1
2	3e−13	12 / 121	ROSOLOWSKI_green total
3	2e−10	30 / 1894	HOPP_Poised_promoter
4	2e−09	37 / 3168	HOPP_Repressed
5	7e−08	8 / 118	Subero_INT_hyper_meth
6	2e−07	6 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
7	3e−06	7 / 132	Subero_DLBCL_hyper_meth
8	3e−06	6 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
9	2e−05	5 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
10	1e−04	4 / 53	LENZ_Stromal signature 2
11	9e−04	4 / 91	Subero_T−ALL_hyper_meth
12	2e−03	7 / 378	TARTE_Mature plasma cell signature
13	2e−03	3 / 56	Subero_mBL_hyper_meth
14	4e−03	3 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
15	4e−03	3 / 70	Subero_FL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−17	13 / 78	Tirosh_CAF−cell specific genes
2	3e−06	12 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	7e−04	3 / 37	Hugo_melanoma−all−MET_DN
4	5e−03	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma
5	7e−03	3 / 85	Tirosh_AXL−signature
6	2e−02	2 / 41	Tirosh_top50 correlated genes PC3
7	5e−02	3 / 171	Landsberg_dedifferentiation_up
8	9e−02	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	1e−01	3 / 236	Gerber_wt/wt_group3−specific
10	2e−01	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	2e−01	2 / 204	Landsberg_dedifferentiation_down
12	3e−01	1 / 81	Tirosh_Genes in the MITF program
13	6e−01	1 / 189	Tirosh_genes preferentially expressed by Tregs
14	1e+00	0 / 17	Hugo_melanoma−all−MET_UP
15	1e+00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	1e−21	14 / 53	extracellular matrix structural constituent
2	1e−14	7 / 11	platelet−derived growth factor binding
3	1e−09	6 / 24	extracellular matrix binding
4	1e−08	15 / 517	calcium ion binding
5	2e−06	4 / 19	fibronectin binding
6	1e−05	6 / 106	integrin binding
7	2e−05	3 / 12	insulin−like growth factor I binding
8	2e−05	3 / 12	proteoglycan binding
9	3e−05	6 / 126	heparin binding
10	7e−05	5 / 93	protease binding
11	1e−04	3 / 20	insulin−like growth factor binding
12	1e−04	51 / 7864	protein binding
13	7e−04	3 / 37	growth factor binding
14	2e−03	2 / 13	metalloendopeptidase inhibitor activity
15	2e−03	3 / 52	collagen binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−05	6 / 129	hsa−miR−29a
2	4e−05	6 / 135	hsa−miR−29c
3	1e−04	6 / 166	hsa−miR−29b
4	3e−03	5 / 216	hsa−miR−524−5p
5	5e−03	5 / 235	hsa−let−7f
6	5e−03	4 / 151	hsa−miR−1283
7	6e−03	3 / 78	hsa−miR−219−2−3p
8	7e−03	5 / 257	hsa−let−7i
9	8e−03	5 / 262	hsa−miR−32
10	1e−02	5 / 278	hsa−let−7d
11	1e−02	3 / 103	hsa−miR−576−3p
12	2e−02	2 / 45	hsa−miR−487a
13	2e−02	2 / 47	hsa−miR−1279
14	2e−02	2 / 49	hsa−miR−550
15	3e−02	3 / 135	hsa−miR−548g

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.4	1 / 122	Terre_IMS_influenza_meta_signature
2	0.5	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.6	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	1.0	0 / 68	Burnham_sep_vs_con_UP
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
8	1.0	0 / 48	Burnham_viral_DN
9	1.0	0 / 57	Burnham_viral_UP
10	1.0	0 / 57	Burnham_day1_vs_5_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 54	Burnham_timecourse
13	1.0	0 / 18	Scicluna_UP
14	1.0	0 / 41	Scicluna_DN
15	1.0	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−04	4 / 81	Chaussabel_1,2_Platelets
2	3e−03	7 / 399	PROTEINATLAS_soft tissue
3	3e−03	3 / 62	VAQUERIZAS_Lung_TF
4	5e−03	5 / 233	PROTEINATLAS_smooth muscle
5	5e−03	2 / 22	VAQUERIZAS_Trachea_TF
6	9e−03	2 / 30	VAQUERIZAS_Smooth muscle_TF
7	9e−03	2 / 30	VAQUERIZAS_Fetal lung_TF
8	1e−02	2 / 36	VAQUERIZAS_Prostate_TF
9	2e−02	2 / 41	VAQUERIZAS_Thyroid_TF
10	2e−02	4 / 209	Chaussabel_2,5_Immune related molecules
11	2e−02	2 / 49	VAQUERIZAS_Uterus_TF
12	3e−02	8 / 776	PROTEINATLAS_skin
13	5e−02	1 / 12	WIRTH_Globus pallidus
14	5e−02	1 / 12	VAQUERIZAS_Kidney_TF
15	6e−02	1 / 13	WIRTH_Sec. lymphoid organs

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	7e−04	14 / 1148	HEBENSTREIT_low expression TF
2	2e−02	18 / 2321	ICGC_Rad21_targets
3	3e−01	17 / 3213	ICGC_Pu1_targets
4	4e−01	17 / 3435	ICGC_Ebfsc137065_targets
5	5e−01	11 / 2254	ICGC_BatfPcr1_targets
6	5e−01	5 / 1032	ICGC_Usf1_targets
7	5e−01	5 / 1041	ICGC_P300_targets
8	6e−01	10 / 2150	ICGC_Irf4_targets
9	6e−01	22 / 4851	ICGC_Runx3_targets
10	7e−01	16 / 3703	ICGC_Foxm1_targets
11	7e−01	8 / 1941	ICGC_Bcl3_targets
12	7e−01	2 / 522	ICGC_SrfPcr2_targets
13	7e−01	6 / 1508	ICGC_Mef2_targets
14	8e−01	18 / 4264	ICGC_Pax5_targets
15	8e−01	14 / 3451	ICGC_Atf2_targets

D−Cluster

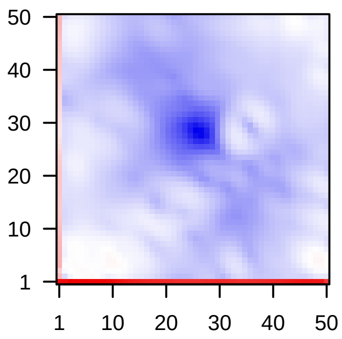
Spot Summary: B

metagenes = 8
genes = 211

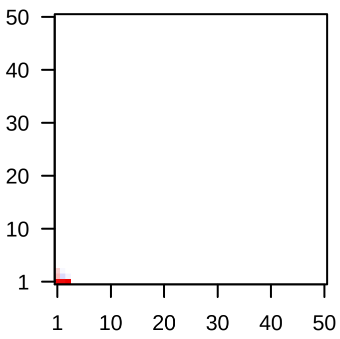
<r> metagenes = 0.99
<r> genes = 0.46
beta: r2= 26.09 / log p= −Inf

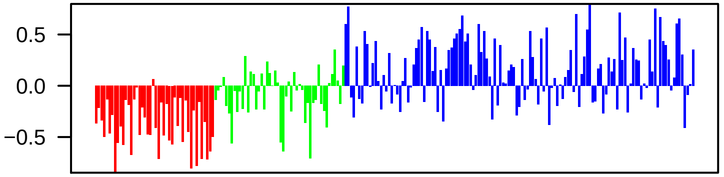
samples with spot = 54 (24.4 %)
intermediate : 2 (4.2 %)
non−mBL : 52 (40.3 %)

Overview Map



Spot





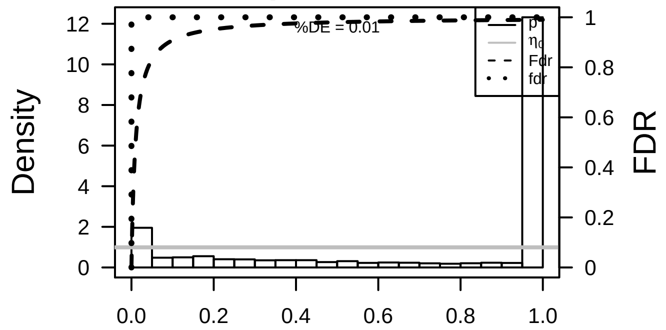
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	211644_x_at	2.59	−1.77	0.34		immunoglobulin kappa variable 3−20 [Source:HGNC Symbol;
2	214551_s_at	2.53	−1.11	0.7	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
3	208451_s_at	2.38	−1.57	0.63	C4A	complement C4A (Rodgers blood group) [Source:HGNC Sym
4	203535_at	2.34	−1.86	0.6	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
5	217022_s_at	2.33	−2.54	0.45		immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
6	205819_at	2.09	−0.95	0.55	MARCO	macrophage receptor with collagenous structure [Source:HGI
7	202833_s_at	2.04	−2.04	0.8	SERPINA1	serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC
8	212062_at	1.97	−1.07	0.51	ATP9A	ATPase phospholipid transporting 9A (putative) [Source:HGN
9	202917_s_at	1.96	−1.75	0.63	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:
10	214049_x_at	1.96	−1.08	0.66	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
11	210116_at	1.95	−1.66	0.65	SH2D1A	SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGN
12	207979_s_at	1.93	−1.42	0.57	CD8B	CD8b molecule [Source:HGNC Symbol;Acc:HGNC:1707]
13	204787_at	1.89	−1.35	0.55	VSIG4	V−set and immunoglobulin domain containing 4 [Source:HGN
14	204006_s_at	1.87	−1.43	0.58	FCGR3A	Fc fragment of IgG receptor IIIa [Source:HGNC Symbol;Acc:
15	205403_at	1.87	−1.01	0.51	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGN
16	206974_at	1.84	−1.08	0.76	CXCR6	C−X−C motif chemokine receptor 6 [Source:HGNC Symbol;A
17	206486_at	1.79	−1.26	0.68	LAG3	lymphocyte activating 3 [Source:HGNC Symbol;Acc:HGNC:6
18	206461_x_at	1.76	−2.22	0.64	MT1H	metallothionein 1H [Source:HGNC Symbol;Acc:HGNC:7400]
19	211469_s_at	1.74	−1.28	0.79	CXCR6	C−X−C motif chemokine receptor 6 [Source:HGNC Symbol;A
20	211210_x_at	1.72	−1.42	0.57	SH2D1A	SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−86	95 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−78	54 / 102	Refer	WIRTH_EBV B−cells
3	4e−50	63 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
4	1e−31	27 / 83	Melar	TCGA_melanoma_immune_high
5	2e−28	41 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
6	2e−28	37 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
7	2e−27	36 / 265	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
8	6e−27	23 / 71	Melar	Tirosh_Macrophage specific genes−melanoma
9	3e−25	21 / 62	Lympl	Monti_Host_response_cluster
10	3e−25	21 / 62	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
11	1e−24	30 / 194	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
12	5e−24	28 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	5e−24	40 / 431	BP	immune system process
14	3e−23	41 / 480	Canc	Lembcke_Colonic Inflammation
15	4e−23	22 / 87	GSEA	BOSCO_TH1_CYTOTOXIC_MODULE
16	5e−23	22 / 88	GSEA	WIELAND_UP_BY_HBV_INFECTION
17	9e−23	21 / 78	Melar	Tirosh_expression higher in CAFs than in T−cells
18	9e−23	21 / 78	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
19	2e−22	16 / 33	Melar	Tirosh_T−cell specific genes−melanoma
20	5e−22	27 / 176	HM	HALLMARK_ALLOGRAFT_REJECTION
21	1e−21	34 / 336	BP	immune response
22	1e−21	29 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
23	4e−21	37 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
24	1e−20	35 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
25	2e−20	31 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
26	3e−20	17 / 52	GSEA	SANA_RESPONSE_TO_IFNG_UP
27	4e−20	32 / 323	BP	inflammatory response
28	5e−20	28 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
29	1e−19	17 / 56	Pneu	Burnham_sep_vs_con_DN
30	1e−18	28 / 261	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
31	2e−18	26 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
32	5e−18	17 / 68	Refer	Chaussabel_2,1_Cytotoxic cells
33	2e−17	36 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
34	1e−16	16 / 67	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
35	4e−16	27 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
36	7e−16	18 / 105	GSEA	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
37	1e−15	13 / 40	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
38	5e−15	26 / 299	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
39	6e−15	16 / 85	GSEA	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP
40	7e−15	15 / 71	GSEA	SANA_TNF_SIGNALING_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.7	1 / 92	HORVATH_aging_genes meth DOWN
3	0.7	1 / 107	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	

CC

Rank	p−value	#in/all	Geneset
1	8e−13	55 / 1611	extracellular region
2	9e−11	41 / 1090	extracellular space
3	7e−10	7 / 17	T cell receptor complex
4	8e−10	16 / 179	external side of plasma membrane
5	3e−09	39 / 1128	integral component of plasma membrane
6	3e−08	73 / 3270	integral component of membrane
7	1e−06	6 / 29	immunological synapse
8	4e−06	8 / 74	secretory granule membrane
9	1e−05	65 / 3210	plasma membrane
10	2e−05	93 / 5339	membrane
11	1e−03	16 / 537	perinuclear region of cytoplasm
12	2e−03	7 / 146	cell−cell junction
13	3e−03	6 / 116	blood microparticle
14	5e−03	13 / 462	cell surface
15	7e−03	2 / 10	amyloid−beta complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−86	95 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−20	31 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	3e−13	24 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	7e−07	8 / 60	Marisa_CRC−cluster−g
5	9e−07	7 / 43	Marisa_CRC−cluster−f
6	4e−06	15 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
7	1e−04	15 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	5e−04	3 / 13	Budinska_B_Lower crypt−like_DOWN
9	8e−04	3 / 15	TCGA−CRC_less−agressive−disease−markers
10	9e−04	4 / 35	Ang_CRC_Hypomethylated
11	2e−03	35 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	3e−03	2 / 7	Budinska_C_CIMP−H−like_UP
13	4e−03	5 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	5e−03	2 / 9	Marisa_CRC−C2
15	6e−03	6 / 132	Marisa_CRC−cluster−a

HM

Rank	p−value	#in/all	Geneset
1	5e−24	28 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	5e−22	27 / 176	HALLMARK_ALLOGRAFT_REJECTION
3	2e−14	21 / 187	HALLMARK_INFLAMMATORY_RESPONSE
4	2e−09	11 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	4e−07	13 / 178	HALLMARK_COMPLEMENT
6	1e−06	9 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	9e−06	11 / 170	HALLMARK_IL2_STAT5_SIGNALING
8	3e−05	11 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	3e−03	7 / 150	HALLMARK_APOPTOSIS
10	3e−03	8 / 194	HALLMARK_KRAS_SIGNALING_UP
11	2e−01	3 / 130	HALLMARK_COAGULATION
12	2e−01	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
13	3e−01	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
14	3e−01	3 / 149	HALLMARK_UV_RESPONSE_UP
15	3e−01	2 / 97	HALLMARK_BILE_ACID_METABOLISM

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−25	21 / 62	Monti_Host_response_cluster
2	3e−14	9 / 15	Care_Polarized immune response
3	1e−13	11 / 33	Care_Extended T−cell
4	1e−06	9 / 85	Sha_DLBCL UP
5	2e−06	5 / 18	DAVE_Immune response 2
6	3e−06	13 / 213	SPANG_IL21 DN
7	1e−05	6 / 41	ROSOLOWSKI_blue DOWN
8	2e−05	16 / 378	TARTE_Mature plasma cell signature
9	1e−03	6 / 97	ROSOLOWSKI_red total
10	4e−03	3 / 26	DAVE_Immune response 1
11	7e−03	6 / 135	DAVE_BL−vs−DLBCL
12	9e−03	5 / 102	ROSOLOWSKI_blue total
13	3e−02	2 / 22	DAVE_NFkB BL DN
14	3e−02	9 / 353	SPANG_CD40 6hrs DN
15	3e−02	3 / 57	SPANG_LPS 6hrs DN

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 18	hsa−miR−1228
2	0.02	2 / 18	hsa−miR−591
3	0.02	3 / 50	hsa−miR−384
4	0.10	2 / 44	hsa−miR−629
5	0.11	2 / 45	hsa−miR−891b
6	0.16	3 / 109	hsa−miR−485−5p
7	0.17	1 / 15	hsa−miR−598
8	0.19	1 / 17	hsa−miR−323−5p
9	0.20	1 / 18	hsa−miR−668
10	0.21	1 / 19	hsa−miR−596
11	0.22	3 / 128	hsa−miR−583
12	0.22	2 / 71	hsa−miR−188−3p
13	0.23	2 / 72	hsa−miR−149
14	0.23	2 / 72	hsa−miR−339−5p
15	0.24	2 / 74	hsa−miR−496

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	

BP

Rank	p−value	#in/all	Geneset
1	5e−24	40 / 431	immune system process
2	1e−21	34 / 336	immune response
3	4e−20	32 / 323	inflammatory response
4	4e−14	17 / 113	regulation of immune response
5	1e−13	22 / 232	cell surface receptor signaling pathway
6	5e−13	17 / 131	chemotaxis
7	1e−12	18 / 161	adaptive immune response
8	4e−12	25 / 367	innate immune response
9	1e−11	12 / 63	chemokine−mediated signaling pathway
10	2e−09	44 / 1361	signal transduction
11	2e−08	8 / 39	T cell activation
12	3e−08	14 / 169	response to lipopolysaccharide
13	3e−08	13 / 146	defense response to virus
14	7e−08	11 / 104	response to virus
15	1e−07	8 / 49	positive regulation of T cell proliferation

Chr

Rank	p−value	#in/all	Geneset
1	0.07	23 / 1325	Chr 1
2	0.16	10 / 554	Chr 5
3	0.31	6 / 369	Chr 20
4	0.38	11 / 776	Chr 17
5	0.39	6 / 403	Chr 14
6	0.39	7 / 480	Chr 4
7	0.40	3 / 184	Chr 18
8	0.45	8 / 585	Chr 7
9	0.51	9 / 700	Chr 12
10	0.53	7 / 548	Chr 16
11	0.60	10 / 832	Chr 2
12	0.60	4 / 333	Chr 22
13	0.64	8 / 689	Chr 3
14	0.72	9 / 833	Chr 19
15	0.74	8 / 756	Chr 11

Glioma

Rank	p−value	#in/all	Geneset
1	4e−50	63 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	2e−28	37 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	5e−20	28 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
4	3e−11	13 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
5	1e−09	19 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
6	4e−09	9 / 45	Donson−innate immunity−associated with LTS in HGA
7	9e−09	17 / 242	ScoV_0.5_Sturm_C1_IDH_DN
8	1e−08	6 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
9	2e−07	45 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
10	8e−07	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
11	2e−06	14 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
12	1e−05	4 / 12	Donson−immune cell intra signaling−associated with LTS in HGA
13	3e−05	7 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
14	7e−05	8 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
15	3e−04	4 / 27	Donson−Misc immune function−associated with LTS in HGA

Immunome

Rank	p−value	#in/all	Geneset
1	3e−11	12 / 67	Angelova_immune−metagene−T−cells
2	4e−09	8 / 32	Angelova_immune−metagene−effector_memory_CD8
3	3e−05	5 / 29	Angelova_immune−metagene−Th1
4	4e−05	3 / 6	Immunity_immune−checkpoint−inhibitors
5	2e−04	5 / 42	Angelova_immune−metagene−TGD
6	2e−04	5 / 45	Angelova_immune−metagene−MDSC
7	2e−03	3 / 19	Angelova_immune−metagene−iDC
8	3e−03	3 / 23	Angelova_immune−metagene−Treg
9	7e−03	2 / 10	Angelova_CRC_immonoinhibitors
10	1e−02	2 / 13	Angelova_immune−metagene−activated_B−cells
11	4e−02	2 / 25	Angelova_immune−metagene−DC
12	6e−02	1 / 5	Angelova_immune−metagene−NKT
13	8e−02	1 / 7	Angelova_immune−metagene−cytotoxic_cells
14	1e−01	1 / 10	Angelova_immune−metagene−neutrophils
15	2e−01	1 / 15	Angelova_immune−metagene−NK

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−31	27 / 83	TCGA_melanoma_immune_high
2	6e−27	23 / 71	Tirosh_Macrophage specific genes−melanoma
3	9e−23	21 / 78	Tirosh_expression higher in CAFs than in T−cells
4	2e−22	16 / 33	Tirosh_T−cell specific genes−melanoma
5	4e−10	16 / 171	Landsberg_dedifferentiation_up
6	9e−09	12 / 107	Tirosh_Exhaustion program in Mel75
7	1e−07	14 / 189	Tirosh_genes preferentially expressed by Tregs
8	2e−05	3 / 5	Joensson_Melanoma Proliferative subtype
9	3e−03	3 / 24	Tirosh_exhuastion−associated genes consitent across tumors
10	8e−03	8 / 230	Gerber_wt/wt_melanoma−cells−SpotC
11	3e−02	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
12	4e−02	2 / 24	Gerami_melanoma−metastatic−risk_DN
13	4e−02	6 / 204	Landsberg_dedifferentiation_down
14	7e−02	1 / 6	Joensson_Melanoma high immune response subtype
15	8e−02	2 / 38	Hugo_melanoma−BRAFmut−MET_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	1e−19	17 / 56	Burnham_sep_vs_con_DN
2	1e−14	13 / 48	Burnham_cap_fp_vs_con_DN
3	3e−10	14 / 122	Terre_IMS_influenza_meta_signature
4	1e−08	9 / 52	Burnham_day1_vs_5_DN
5	6e−06	6 / 37	Sweeney_viral_up
6	7e−06	7 / 57	Burnham_viral_UP
7	3e−04	5 / 48	Burnham_viral_DN
8	2e−02	2 / 18	Scicluna_UP
9	5e−02	3 / 68	Burnham_sep_vs_con_UP
10	6e−02	3 / 71	Burnham_cap_fp_vs_con_UP
11	9e−02	4 / 135	Terre_MSV_multiple_respiratory_viruses_up
12	9e−02	2 / 41	Scicluna_DN
13	2e−01	2 / 57	Burnham_day1_vs_5_UP
14	3e−01	1 / 33	Sweeney_viral_dn
15	5e−01	1 / 54	Burnham_timecourse

TF

Rank	p−value	#in/all	Geneset
1	0.003	24 / 1041	ICGC_P300_targets
2	0.024	37 / 2150	ICGC_Irf4_targets
3	0.027	59 / 3778	ICGC_Pol24_targets
4	0.032	51 / 3213	ICGC_Pu1_targets
5	0.046	53 / 3435	ICGC_Ebfsc137065_targets
6	0.055	26 / 1508	ICGC_Mef2_targets
7	0.079	27 / 1636	ICGC_Bcl11_targets
8	0.096	35 / 2254	ICGC_BatfPcr1_targets
9	0.100	59 / 4072	ICGC_Mta3_targets
10	0.173	29 / 1941	ICGC_Bcl3_targets
11	0.214	66 / 4851	ICGC_Runx3_targets
12	0.222	52 / 3769	ICGC_Pmlsc71910_targets
13	0.299	32 / 2321	ICGC_Rad21_targets
14	0.302	51 / 3804	ICGC_Stat5_targets
15	0.317	21 / 1494	ICGC_Cebpbsc150_targets

Cancer

Rank	p−value	#in/all	Geneset
1	3e−23	41 / 480	Lembcke_Colonic Inflammation
2	1e−14	21 / 186	SPANG_LPS−index2
3	7e−11	7 / 13	GENTLES_modul18
4	2e−08	19 / 317	SPANG_BCL6−index2
5	7e−03	2 / 10	BENTINK_ras.4
6	7e−03	5 / 96	PanCan_TXmisReg_geneset_nanostring
7	9e−03	2 / 12	HLA2_signature
8	1e−02	2 / 15	WANG_ER_UP
9	8e−02	3 / 80	PanCan_JAK−ST_geneset_nanostring
10	1e−01	1 / 9	WANG_ER_DN
11	1e−01	4 / 147	PanCan_MAPK_geneset_nanostring
12	2e−01	1 / 13	GENTLES_modul11
13	2e−01	1 / 14	BENTINK_src.10
14	2e−01	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	3e−01	0 / 16	LIU_LIVER_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−09	28 / 626	natural killer cells peripheral blood_3_TxFlnk
2	4e−09	23 / 432	monocytes peripheral blood_3_TxFlnk
3	4e−06	29 / 932	Tcells peripheral blood_3_TxFlnk
4	8e−06	55 / 2507	Mid_Frontal_Lobe_ReprPC
5	6e−05	29 / 1072	Mid_Frontal_Lobe_ReprPCWk
6	9e−05	15 / 383	K9acLow_Colon
7	1e−04	12 / 258	T CD8+ naive cells peripheral blood_3_TxFlnk
8	3e−04	37 / 1676	Fetal_TxTrans
9	4e−04	19 / 642	Thelper cells peripheral blood_3_TxFlnk
10	5e−04	23 / 867	Mid_Frontal_Lobe_Quies
11	4e−03	56 / 3223	monocytes peripheral blood_6_EnhG
12	7e−03	32 / 1639	Fetal_TssF
13	1e−02	13 / 497	Mid_Frontal_Lobe_TssF
14	3e−02	32 / 1833	12_EnhBiv_ESC_Endoderm
15	4e−02	49 / 3110	14_ReprPCWk_ESC_Endoderm

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−28	41 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
2	2e−27	36 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
3	3e−25	21 / 62	BROWNE_INTERFERON_RESPONSIVE_GENES
4	1e−24	30 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	4e−23	22 / 87	BOSCO_TH1_CYTOTOXIC_MODULE
6	5e−23	22 / 88	WIELAND_UP_BY_HBV_INFECTION
7	9e−23	21 / 78	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
8	1e−21	29 / 223	MCLACHLAN_DENTAL_CARIES_UP
9	4e−21	37 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	1e−20	35 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
11	3e−20	17 / 52	SANA_RESPONSE_TO_IFNG_UP
12	1e−18	28 / 261	POOLA_INVASIVE_BREAST_CANCER_UP
13	2e−18	26 / 219	MCLACHLAN_DENTAL_CARIES_DN
14	2e−17	36 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
15	1e−16	16 / 67	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 12	DUMEAUX_Women normal BMI literature genes up
2	2e−05	4 / 14	Huan_blood−pressure_SBP−signature
3	5e−04	2 / 3	Huan_blood−pressure_HTN−signature
4	2e−03	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	2e−03	3 / 22	DUMEAUX_High bmi enriched genes
6	4e−03	2 / 8	Marjolein_ageing−genes_UP
7	5e−03	2 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1e−02	2 / 13	Huan_blood−pressure_DBP−signature
9	1e−01	1 / 10	DUMEAUX_Smoking literature genes up
10	3e−01	1 / 32	Marjolein_ageing−genes_DN
11	6e−01	2 / 150	Homuth_BMI−associated−genes_UP
12	7e−01	2 / 210	Homuth_BMI−associated−genes_DN
13	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
14	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
15	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	3e−08	14 / 173	cytokine activity
2	5e−07	7 / 39	chemokine activity
3	1e−06	21 / 500	signal transducer activity
4	4e−06	5 / 20	chemokine receptor activity
5	5e−06	12 / 191	transmembrane signaling receptor activity
6	3e−05	5 / 29	coreceptor activity
7	5e−05	4 / 17	MHC class I protein binding
8	5e−05	21 / 644	protein homodimerization activity
9	7e−04	8 / 154	serine−type endopeptidase activity
10	1e−03	3 / 16	CCR chemokine receptor binding
11	1e−03	12 / 337	G−protein coupled receptor activity
12	1e−03	9 / 205	receptor activity
13	2e−03	3 / 19	lipopolysaccharide binding
14	3e−03	4 / 50	amyloid−beta binding
15	6e−03	3 / 30	protein tyrosine/serine/threonine phosphatase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−78	54 / 102	WIRTH_EBV B−cells
2	5e−18	17 / 68	Chaussabel_2,1_Cytotoxic cells
3	2e−13	14 / 72	Chaussabel_3,1_Interferon−inducible
4	3e−13	26 / 355	WIRTH_Immune system
5	2e−11	14 / 99	Chaussabel_1,5_Myeloid lineage
6	1e−07	11 / 109	Chaussabel_2,6_Myeloid lineage
7	2e−04	17 / 496	PROTEINATLAS_spleen
8	8e−04	5 / 59	Chaussabel_2,10_Immune related cell surface molecules
9	8e−03	5 / 100	Chaussabel_2,8_T−cells
10	1e−02	2 / 13	WIRTH_Lymphocytes
11	1e−02	7 / 198	Chaussabel_3,3_Inflammation II
12	2e−02	2 / 18	JONGENEEL_Monocytes
13	2e−02	15 / 678	PROTEINATLAS_lymph node
14	3e−02	6 / 182	WIRTH_post GC B−cells
15	4e−02	19 / 989	PROTEINATLAS_tonsil

D−Cluster

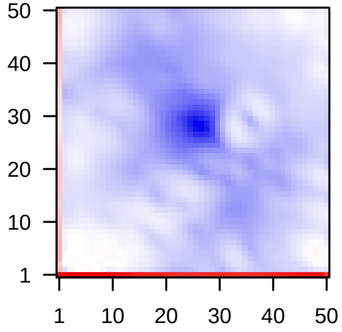
Spot Summary: C

metagenes = 9
genes = 162

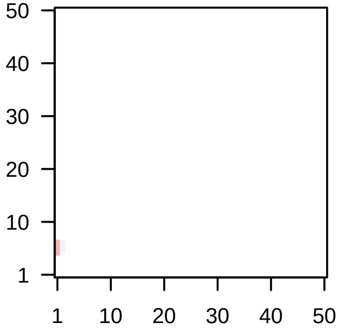
<r> metagenes = 0.99
<r> genes = 0.45
beta: r2= 21.65 / log p= −Inf

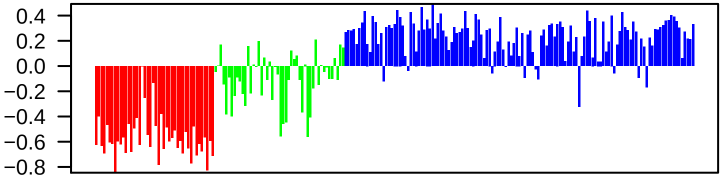
samples with spot = 70 (31.7 %)
non−mBL : 70 (54.3 %)

Overview Map



Spot





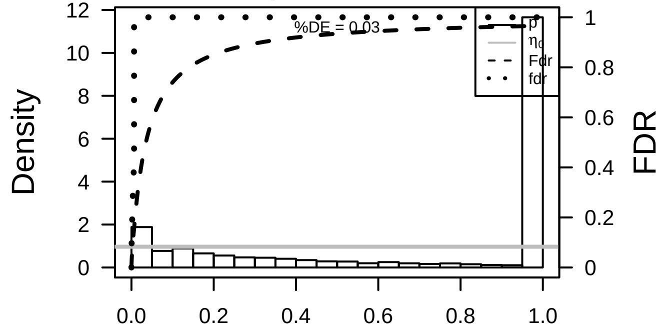
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	216615_s_at	2.49	−1.56	0.44	HTR3A	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
2	207245_at	2.21	−1.2	0.48	UGT2B17	UDP glucuronosyltransferase family 2 member B17 [Source:H
3	202274_at	1.93	−2	0.55	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
4	210437_at	1.88	−1.26	0.43	MAGEA9B	MAGE family member A9B [Source:HGNC Symbol;Acc:HGN
5	210916_s_at	1.78	−1.66	0.84	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;
6	219799_s_at	1.78	−1.76	0.65	DHRS9	dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:HGN
7	207113_s_at	1.77	−1.49	0.66	TNF	tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:118
8	204489_s_at	1.76	−2.02	0.85	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;
9	203404_at	1.73	−1.41	0.48	ARMCX2	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
10	206337_at	1.72	−2.11	0.7	CCR7	C−C motif chemokine receptor 7 [Source:HGNC Symbol;Acc:
11	203562_at	1.7	−1.4	0.62	FEZ1	fasciculation and elongation protein zeta 1 [Source:HGNC Sy
12	222043_at	1.7	−1.38	0.56	CLU	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
13	203835_at	1.7	−1.1	0.46	LRRC32	leucine rich repeat containing 32 [Source:HGNC Symbol;Acc:
14	217966_s_at	1.67	−0.98	0.53	FAM129A	family with sequence similarity 129 member A [Source:HGNC
15	219424_at	1.67	−2.01	0.84	EBI3	Epstein−Barr virus induced 3 [Source:HGNC Symbol;Acc:HG
16	220358_at	1.64	−1.04	0.64	BATF3	basic leucine zipper ATF−like transcription factor 3 [Source:H
17	203642_s_at	1.63	−1.51	0.58	COBLL1	cordon−bleu WH2 repeat protein like 1 [Source:HGNC Symb
18	206975_at	1.59	−1.2	0.61	LTA	lymphotoxin alpha [Source:HGNC Symbol;Acc:HGNC:6709]
19	823_at	1.58	−0.88	0.58	CX3CL1	C−X3−C motif chemokine ligand 1 [Source:HGNC Symbol;Ac
20	201464_x_at	1.54	−1.66	0.6	JUN	Jun proto−oncogene, AP−1 transcription factor subunit [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−42	31 / 85	Lympl	Sha_DLBCL UP
2	2e−24	26 / 173	Lympl	Victora_Light zone signature
3	2e−22	20 / 90	GSEA	BASSO_CD40_SIGNALING_UP
4	2e−21	22 / 135	Lympl	DAVE_BL−vs−DLBCL
5	1e−20	11 / 14	GSEA	HUMMEL_BURKITTS_LYMPHOMA_DN
6	9e−20	28 / 317	Canc	SPANG_BCL6−index2
7	1e−19	23 / 186	Canc	SPANG_LPS−index2
8	3e−18	23 / 213	Lympl	SPANG_IL21 DN
9	9e−17	9 / 12	Lympl	BENTINK_mBL DOWN
10	2e−14	24 / 353	Lympl	SPANG_CD40 6hrs DN
11	4e−12	18 / 229	GSEA	QI_PLASMACYTOMA_UP
12	1e−11	88 / 5404	Lympl	HOPP_Strong_enhancer
13	1e−11	8 / 22	Lympl	DAVE_NFkB BL DN
14	2e−11	23 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
15	8e−11	10 / 55	GSEA	DIRMEIER_LMP1_RESPONSE_EARLY
16	8e−11	10 / 55	GSEA	DIRMEIER_LMP1_RESPONSE_LATE_UP
17	1e−10	23 / 480	Canc	Lembcke_Colonic Inflammation
18	3e−10	15 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	1e−09	24 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	6e−09	15 / 238	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
21	7e−09	4 / 4	Lympl	MASCQUE_mBL DOWN
22	8e−09	17 / 321	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38
23	2e−08	8 / 50	GSEA	LINDSTEDT_DENDRITIC_CELL_MATURATION_B
24	3e−08	15 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
25	5e−08	8 / 57	Lympl	SPANG_LPS 6hrs DN
26	1e−07	9 / 85	Lympl	Aukema_BCL2 DN_BCL6 UP
27	1e−07	9 / 85	HM	HALLMARK_IL6_JAK_STAT3_SIGNALING
28	1e−07	8 / 63	GSEA	BOYLAN_MULTIPLE_MYELOMA_D_DN
29	1e−07	9 / 88	Lympl	ROSOLOWSKI_green UP
30	1e−07	12 / 182	Refer	WIRTH_post GC B−cells
31	2e−07	17 / 400	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
32	2e−07	26 / 902	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
33	2e−07	26 / 906	Lympl	SPANG_BCR DN
34	4e−07	15 / 327	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
35	6e−07	11 / 170	HM	HALLMARK_IL2_STAT5_SIGNALING
36	7e−07	8 / 79	GSEA	LU_IL4_SIGNALING
37	8e−07	14 / 299	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
38	9e−07	16 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
39	1e−06	7 / 57	GSEA	AMIT_SERUM_RESPONSE_60_MCF10A
40	1e−06	17 / 453	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 92	HORVATH_aging_genes meth DOWN
2	0.4	1 / 47	TESCHENDORFF_age_hypermethylated
3	0.6	1 / 107	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	5e−05	14 / 431	immune system process
2	1e−04	15 / 520	positive regulation of transcription, DNA−templated
3	1e−04	10 / 250	regulation of apoptotic process
4	2e−04	4 / 30	negative regulation of extrinsic apoptotic signaling pathway via death domain
5	2e−04	4 / 30	regulation of tumor necrosis factor−mediated signaling pathway
6	2e−04	7 / 127	positive regulation of NF−kappaB transcription factor activity
7	2e−04	15 / 553	apoptotic process
8	2e−04	13 / 434	negative regulation of apoptotic process
9	2e−04	11 / 323	inflammatory response
10	3e−04	11 / 336	immune response
11	3e−04	3 / 15	regulation of extrinsic apoptotic signaling pathway via death domain receptors
12	4e−04	3 / 16	defense response to protozoan
13	6e−04	4 / 42	positive regulation of cell adhesion
14	7e−04	7 / 156	positive regulation of ERK1 and ERK2 cascade
15	1e−03	3 / 21	positive regulation of apoptotic signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	9e−20	28 / 317	SPANG_BCL6−index2
2	1e−19	23 / 186	SPANG_LPS−index2
3	1e−10	23 / 480	Lembcke_Colonic Inflammation
4	9e−05	3 / 10	BENTINK_ras.4
5	3e−03	1 / 14	LIU_PROSTATE_CANCER_DN
6	3e−03	6 / 147	PanCan_MAPK_geneset_nanostring
7	2e−02	1 / 16	LIU_LIVER_CANCER
8	4e−02	3 / 80	PanCan_JAK−ST_geneset_nanostring
9	6e−02	3 / 96	PanCan_TXmisReg_geneset_nanostring
10	7e−02	2 / 45	KUIPER_MM poor survival
11	9e−02	7 / 409	Lembcke_Normal vs Adenoma
12	1e−01	1 / 13	GENTLES_modul11
13	1e−01	3 / 130	PanCan_CC+Apop_geneset_nanostring
14	1e−01	1 / 14	GUSTAFSON_PI3K_UP
15	1e−01	1 / 14	BENTINK_src.10

CC

Rank	p−value	#in/all	Geneset
1	5e−06	53 / 3210	plasma membrane
2	3e−05	15 / 462	cell surface
3	1e−03	7 / 179	external side of plasma membrane
4	3e−03	5 / 104	trans−Golgi network
5	4e−03	50 / 3805	cytosol
6	5e−03	12 / 537	perinuclear region of cytoplasm
7	5e−03	4 / 74	secretory granule membrane
8	5e−03	2 / 12	apical dendrite
9	1e−02	63 / 5339	membrane
10	1e−02	2 / 18	phagocytic cup
11	1e−02	2 / 18	vacuole
12	2e−02	7 / 277	neuron projection
13	2e−02	7 / 281	lysosome
14	2e−02	56 / 4701	cytoplasm
15	3e−02	11 / 604	intracellular membrane−bounded organelle

Chr

Rank	p−value	#in/all	Geneset
1	0.01	14 / 756	Chr 11
2	0.05	13 / 832	Chr 2
3	0.09	8 / 490	Chr 10
4	0.15	8 / 556	Chr X
5	0.31	9 / 776	Chr 17
6	0.44	7 / 669	Chr 6
7	0.46	4 / 369	Chr 20
8	0.47	7 / 689	Chr 3
9	0.47	6 / 585	Chr 7
10	0.48	13 / 1325	Chr 1
11	0.70	3 / 382	Chr 15
12	0.73	1 / 139	Chr 21
13	0.76	4 / 548	Chr 16
14	0.77	4 / 554	Chr 5
15	0.79	5 / 700	Chr 12

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−07	105 / 8406	Bcells peripheral blood_2_TssAFlnk
2	3e−07	37 / 1676	Fetal_TxTrans
3	6e−07	16 / 383	K9acLow_Colon
4	6e−07	47 / 2507	Mid_Frontal_Lobe_ReprPC
5	3e−06	30 / 1308	Mid_Frontal_Lobe_K9K27me3
6	5e−06	59 / 3767	Bcells peripheral blood_6_EnhG
7	6e−06	100 / 8200	monocytes peripheral blood_2_TssAFlnk
8	8e−06	37 / 1911	Mid_Frontal_Lobe_HetRpts
9	2e−05	96 / 7833	Bcells peripheral blood_1_TssA
10	2e−05	95 / 7751	natural killer cells peripheral blood_1_TssA
11	2e−05	100 / 8370	natural killer cells peripheral blood_2_TssAFlnk
12	2e−05	33 / 1684	1_TssP_Neuronal_Progenitor
13	2e−05	89 / 7078	7_Enh_ESC_Mesoderm
14	3e−05	36 / 1930	Fetal_TssA
15	3e−05	107 / 9298	Bcells peripheral blood_7_Enh

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−09	24 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	1e−04	22 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	4e−04	10 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	2e−03	17 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
5	4e−03	10 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
6	7e−03	8 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
7	7e−03	4 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
8	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
9	2e−02	5 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
10	3e−02	10 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	5e−02	1 / 5	Kaneda_CIMP−group1
12	5e−02	1 / 5	Hewish_dMMR−secondary−mutations_Apoptosis
13	5e−02	2 / 38	Marisa_CRC−cluster−e
14	6e−02	1 / 7	Boland_CRC−MSI−TGC
15	7e−02	1 / 8	Marisa_CRC−C3

Glioma

Rank	p−value	#in/all	Geneset
1	2e−11	23 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	3e−08	15 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	3e−05	5 / 38	OL vs. OPC
4	2e−04	10 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
5	3e−04	9 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
6	5e−04	9 / 242	ScoV_0.5_Sturm_C1_IDH_DN
7	8e−04	20 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
8	2e−03	8 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
9	4e−03	5 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
10	6e−03	2 / 13	Mukasa_UP_in_Astroglioma
11	7e−03	4 / 82	laffaire_hypermeth_LGG_vs_control
12	8e−03	3 / 43	Patel_stemness signatures
13	8e−03	2 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
14	1e−02	5 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	1e−02	5 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−22	20 / 90	BASSO_CD40_SIGNALING_UP
2	1e−20	11 / 14	HUMMEL_BURKITTS_LYMPHOMA_DN
3	4e−12	18 / 229	QI_PLASMACYTOMA_UP
4	8e−11	10 / 55	DIRMEIER_LMP1_RESPONSE_EARLY
5	8e−11	10 / 55	DIRMEIER_LMP1_RESPONSE_LATE_UP
6	6e−09	15 / 238	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
7	8e−09	17 / 321	PHONG_TNF_RESPONSE_NOT_VIA_P38
8	2e−08	8 / 50	LINDSTEDT_DENDRITIC_CELL_MATURATION_B
9	1e−07	8 / 63	BOYLAN_MULTIPLE_MYELOMA_D_DN
10	2e−07	17 / 400	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
11	2e−07	26 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
12	4e−07	15 / 327	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
13	7e−07	8 / 79	LU_IL4_SIGNALING
14	8e−07	14 / 299	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
15	9e−07	16 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−10	15 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	1e−07	9 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	6e−07	11 / 170	HALLMARK_IL2_STAT5_SIGNALING
4	1e−06	11 / 187	HALLMARK_INFLAMMATORY_RESPONSE
5	4e−06	10 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	3e−04	8 / 178	HALLMARK_COMPLEMENT
7	5e−04	7 / 150	HALLMARK_APOPTOSIS
8	6e−03	6 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	9e−03	6 / 188	HALLMARK_HYPOXIA
10	9e−03	6 / 191	HALLMARK_P53_PATHWAY
11	2e−02	5 / 174	HALLMARK_APICAL_JUNCTION
12	3e−02	4 / 130	HALLMARK_COAGULATION
13	1e−01	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	1e−01	4 / 193	HALLMARK_HEME_METABOLISM
15	1e−01	4 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome

Rank	p−value	#in/all	Geneset
1	9e−05	3 / 10	Angelova_immune−metagene−TFH
2	5e−04	3 / 17	Angelova_immune−metagene−central_memory_CD8
3	8e−04	4 / 45	Angelova_immune−metagene−MDSC
4	2e−03	2 / 7	Angelova_immune−metagene−cytotoxic_cells
5	7e−03	3 / 42	Angelova_immune−metagene−TGD
6	1e−02	2 / 18	Angelova_CRC_immunostimulators
7	2e−02	2 / 21	Angelova_immune−metagene−central_memory_CD4
8	3e−02	3 / 67	Angelova_immune−metagene−T−cells
9	3e−02	2 / 29	Angelova_immune−metagene−Th1
10	6e−02	1 / 7	Angelova_CRC_MSI−neoantigens
11	1e−01	1 / 13	Angelova_immune−metagene−activated_B−cells
12	1e−01	1 / 13	Angelova_CRC_MSS^−neoantigens
13	2e−01	1 / 23	Angelova_immune−metagene−Treg
14	3e−01	1 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	2 / 32	Marjolein_ageing−genes_DN
2	0.12	1 / 14	Huan_blood−pressure_SBP−signature
3	0.14	4 / 210	Homuth_BMI−associated−genes_DN
4	0.19	1 / 22	DUMEAUX_High bmi enriched genes
5	0.41	2 / 150	Homuth_BMI−associated−genes_UP
6	1.00	0 / 62	DUMEAUX_Smoking enriched genes
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1.00	0 / 22	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−42	31 / 85	Sha_DLBCL UP
2	2e−24	26 / 173	Victora_Light zone signature
3	2e−21	22 / 135	DAVE_BL−vs−DLBCL
4	3e−18	23 / 213	SPANG_IL21 DN
5	9e−17	9 / 12	BENTINK_mBL DOWN
6	2e−14	24 / 353	SPANG_CD40 6hrs DN
7	1e−11	88 / 5404	HOPP_Strong_enhancer
8	1e−11	8 / 22	DAVE_NFkB BL DN
9	7e−09	4 / 4	MASCQUE_mBL DOWN
10	5e−08	8 / 57	SPANG_LPS 6hrs DN
11	1e−07	9 / 85	Aukema_BCL2 DN_BCL6 UP
12	1e−07	9 / 88	ROSOLOWSKI_green UP
13	2e−07	26 / 906	SPANG_BCR DN
14	2e−06	9 / 121	ROSOLOWSKI_green total
15	7e−05	10 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.008	4 / 85	Tirosh_AXL−signature
2	0.009	6 / 189	Tirosh_genes preferentially expressed by Tregs
3	0.013	6 / 204	Landsberg_dedifferentiation_down
4	0.033	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma
5	0.037	3 / 78	Tirosh_expression higher in CAFs than in T−cells
6	0.046	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
7	0.080	3 / 107	Tirosh_Exhaustion program in Mel75
8	0.083	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
9	0.096	8 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	0.097	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	0.140	1 / 16	Hugo_melanoma−all−LEF1_UP
12	0.144	2 / 71	Tirosh_Macrophage specific genes−melanoma
13	0.203	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
14	0.261	4 / 276	Gerber_wt/wt_melanoma−cells−SpotB
15	0.295	1 / 37	Hugo_melanoma−all−MET_DN

MF

Rank	p−value	#in/all	Geneset
1	2e−05	96 / 7864	protein binding
2	2e−04	4 / 30	tumor necrosis factor receptor binding
3	6e−04	4 / 41	protein kinase C binding
4	1e−03	3 / 24	MAP kinase kinase kinase activity
5	2e−03	5 / 93	protease binding
6	3e−03	7 / 206	transcription regulatory region DNA binding
7	5e−03	3 / 38	cytokine receptor activity
8	6e−03	2 / 13	K63−linked polyubiquitin modification−dependent protein binding
9	7e−03	2 / 14	S100 protein binding
10	1e−02	2 / 17	transcriptional activator activity, RNA polymerase II transcription factor bindin
11	1e−02	3 / 50	amyloid−beta binding
12	1e−02	3 / 50	cysteine−type endopeptidase activity
13	1e−02	7 / 268	transcription factor binding
14	1e−02	2 / 19	tumor necrosis factor−activated receptor activity
15	1e−02	15 / 851	identical protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	2 / 9	hsa−miR−604
2	0.003	4 / 64	hsa−miR−890
3	0.005	6 / 165	hsa−miR−448
4	0.013	2 / 19	hsa−miR−554
5	0.018	2 / 22	hsa−miR−24−1*
6	0.018	3 / 59	hsa−miR−499−3p
7	0.024	6 / 237	hsa−miR−302c
8	0.029	3 / 71	hsa−miR−188−3p
9	0.037	4 / 134	hsa−miR−31
10	0.045	2 / 36	hsa−miR−129−3p
11	0.059	2 / 42	hsa−miR−1224−3p
12	0.060	6 / 295	hsa−miR−373
13	0.062	5 / 226	hsa−miR−302b
14	0.069	2 / 46	hsa−miR−1260
15	0.072	2 / 47	hsa−miR−665

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.01	2 / 18	Scicluna_UP
2	0.06	2 / 41	Scicluna_DN
3	0.09	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	0.13	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
5	0.36	1 / 48	Burnham_cap_fp_vs_con_DN
6	0.39	1 / 52	Burnham_day1_vs_5_DN
7	0.47	1 / 68	Burnham_sep_vs_con_UP
8	0.69	1 / 122	Terre_IMS_influenza_meta_signature
9	1.00	0 / 56	Burnham_sep_vs_con_DN
10	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
11	1.00	0 / 48	Burnham_viral_DN
12	1.00	0 / 57	Burnham_viral_UP
13	1.00	0 / 57	Burnham_day1_vs_5_UP
14	1.00	0 / 54	Burnham_timecourse
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−07	12 / 182	WIRTH_post GC B−cells
2	1e−06	15 / 355	WIRTH_Immune system
3	7e−06	11 / 219	WIRTH_GC B−cells
4	7e−04	8 / 204	Chaussabel_3,2_Inflammation I
5	7e−03	11 / 496	PROTEINATLAS_spleen
6	1e−02	6 / 198	Chaussabel_3,3_Inflammation II
7	1e−02	4 / 99	Chaussabel_1,5_Myeloid lineage
8	2e−02	16 / 989	PROTEINATLAS_tonsil
9	4e−02	3 / 81	Chaussabel_1,2_Platelets
10	4e−02	14 / 905	PROTEINATLAS_appendix
11	5e−02	11 / 678	PROTEINATLAS_lymph node
12	6e−02	1 / 6	JONGENEEL_Uterus
13	6e−02	2 / 42	Chaussabel_1,3_B−cells
14	6e−02	1 / 7	VAQUERIZAS_Tongue_TF
15	7e−02	2 / 45	VAQUERIZAS_Placenta_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	3e−05	36 / 1941	ICGC_Bcl3_targets
2	6e−05	39 / 2254	ICGC_BatfPcr1_targets
3	3e−04	28 / 1508	ICGC_Mef2_targets
4	3e−04	50 / 3435	ICGC_Ebfsc137065_targets
5	5e−04	37 / 2321	ICGC_Rad21_targets
6	1e−03	42 / 2899	ICGC_Nfatc1_targets
7	2e−03	62 / 4851	ICGC_Runx3_targets
8	2e−03	51 / 3796	ICGC_Nficsc81335_targets
9	2e−03	47 / 3420	ICGC_Bclaf101388_targets
10	2e−03	27 / 1636	ICGC_Bcl11_targets
11	4e−03	58 / 4602	ICGC_Elf1_targets
12	5e−03	53 / 4131	ICGC_Tcf3_targets
13	5e−03	49 / 3769	ICGC_Pmlsc71910_targets
14	6e−03	52 / 4072	ICGC_Mta3_targets
15	6e−03	24 / 1494	ICGC_Cebpbsc150_targets

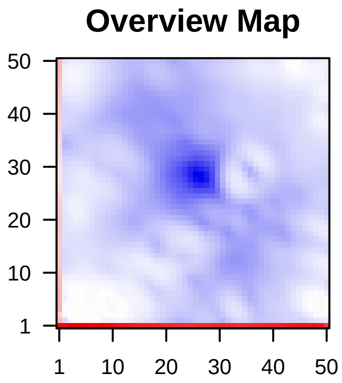
D−Cluster

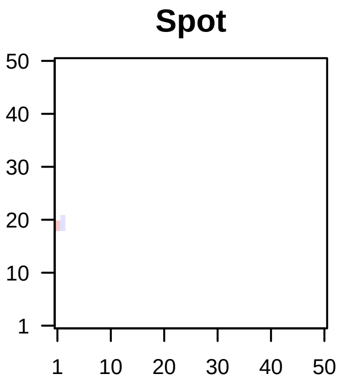
Spot Summary: D

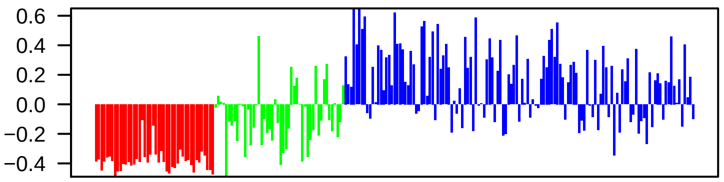
metagenes = 5
genes = 70

<r> metagenes = 0.99
<r> genes = 0.31
beta: r2= 9.57 / log p= −Inf

samples with spot = 52 (23.5 %)
intermediate : 3 (6.2 %)
non−mBL : 49 (38 %)


Overview Map


Spot

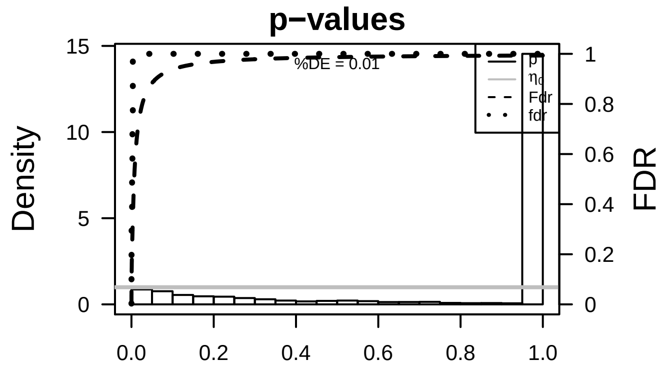


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	201839_s_at	2.49	−1.02	0.34	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
2	219836_at	2.38	−1.24	0.61	ZBED2	zinc finger BED−type containing 2 [Source:HGNC Symbol;Ac
3	217523_at	2.2	−1.4	0.72	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;
4	219255_x_at	2.16	−1.57	0.47	IL17RB	interleukin 17 receptor B [Source:HGNC Symbol;Acc:HGNC:
5	204724_s_at	2.01	−1.6	0.38	COL9A3	collagen type IX alpha 3 chain [Source:HGNC Symbol;Acc:H
6	202986_at	1.95	−0.86	0.63	ARNT2	aryl hydrocarbon receptor nuclear translocator 2 [Source:HG
7	205987_at	1.93	−1.33	0.37	CD1C	CD1c molecule [Source:HGNC Symbol;Acc:HGNC:1636]
8	33197_at	1.89	−0.9	0.53	MYO7A	myosin VIIA [Source:HGNC Symbol;Acc:HGNC:7606]
9	219959_at	1.84	−0.95	0.59	MOCOS	molybdenum cofactor sulfurase [Source:HGNC Symbol;Acc:
10	205542_at	1.83	−1.05	0.47	STEAP1	STEAP family member 1 [Source:HGNC Symbol;Acc:HGNC:
11	210753_s_at	1.81	−1.19	0.63	EPHB1	EPH receptor B1 [Source:HGNC Symbol;Acc:HGNC:3392]
12	222281_s_at	1.76	−1.97	0.73		
13	206698_at	1.73	−1.34	0.64	XK	X−linked Kx blood group [Source:HGNC Symbol;Acc:HGNC:
14	220565_at	1.72	−1.38	0.66	CCR10	C−C motif chemokine receptor 10 [Source:HGNC Symbol;Ac
15	206756_at	1.69	−0.96	0.45	CHST7	carbohydrate sulfotransferase 7 [Source:HGNC Symbol;Acc:
16	209094_at	1.63	−1.37	0.49	DDAH1	dimethylarginine dimethylaminohydrolase 1 [Source:HGNC S
17	201750_s_at	1.6	−1.11	0.68	ECE1	endothelin converting enzyme 1 [Source:HGNC Symbol;Acc:
18	207433_at	1.6	−0.83	0.68	IL10	interleukin 10 [Source:HGNC Symbol;Acc:HGNC:5962]
19	208189_s_at	1.54	−0.68	0.41	MYO7A	myosin VIIA [Source:HGNC Symbol;Acc:HGNC:7606]
20	211269_s_at	1.51	−1.3	0.46	IL2RA	interleukin 2 receptor subunit alpha [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−06	8 / 182	Refer	WIRTH_post GC B−cells
2	3e−06	10 / 317	Canc	SPANG_BCL6−index2
3	3e−06	6 / 85	Lymp	Aukema_BCL2 DN_BCL6 UP
4	2e−05	3 / 12	BP	leukocyte chemotaxis
5	2e−05	3 / 12	GSE	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
6	6e−05	5 / 85	Lymp	Sha_DLBCL UP
7	6e−05	42 / 5404	Lymp	HOPP_Strong_enhancer
8	6e−05	5 / 87	GSE	BOSCO_TH1_CYTOTOXIC_MODULE
9	7e−05	7 / 213	Lymp	SPANG_IL21 DN
10	8e−05	3 / 18	Lymp	WRIGHT_ABC UP
11	9e−05	4 / 49	GSE	GAURNIER_PSMD4_TARGETS
12	2e−04	7 / 249	GSE	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
13	2e−04	6 / 175	GSE	OKUMURA_INFLAMMATORY_RESPONSE_LPS
14	2e−04	4 / 63	GSE	BOYLAN_MULTIPLE_MYELOMA_D_DN
15	3e−04	4 / 67	Immu	Angelova_immune−metagene−T−cells
16	5e−04	4 / 77	GSE	KEGG_HEMATOPOIETIC_CELL_LINEAGE
17	8e−04	4 / 85	HM	HALLMARK_IL6_JAK_STAT3_SIGNALING
18	8e−04	11 / 741	GSE	PEREZ_TP53_TARGETS
19	8e−04	7 / 318	GSE	MEISSNER_NPC_HCP_WITH_H3K4ME2
20	9e−04	7 / 321	GSE	PHONG_TNF_RESPONSE_NOT_VIA_P38
21	1e−03	2 / 10	BP	N−acetylglucosamine metabolic process
22	1e−03	9 / 539	Colon	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
23	1e−03	8 / 434	BP	negative regulation of apoptotic process
24	1e−03	2 / 11	BP	negative regulation of nitric oxide biosynthetic process
25	1e−03	5 / 168	BP	regulation of gene expression
26	1e−03	3 / 46	GSE	WORSCHECH_TUMOR_REJECTION_UP
27	1e−03	7 / 348	GSE	MARTENS_BOUND_BY_PML_RARA_FUSION
28	1e−03	2 / 12	BP	positive regulation of heterotypic cell−cell adhesion
29	1e−03	2 / 12	Lymp	BENTINK_mBL DOWN
30	1e−03	8 / 453	GSE	ONDER_CDH1_TARGETS_2_DN
31	1e−03	5 / 173	Lymp	Victora_Light zone signature
32	2e−03	5 / 176	HM	HALLMARK_ALLOGRAFT_REJECTION
33	2e−03	2 / 13	Canc	BENTINK_e2f3.1
34	2e−03	2 / 13	GSE	LIU_IL13_PRIMING_MODEL
35	2e−03	6 / 271	GSE	ENK_UV_RESPONSE_EPIDERMIS_UP
36	2e−03	2 / 14	Gliom	Donson−chemokines/cytokines−associated with LTS in HGA
37	2e−03	2 / 14	GSE	HUMMEL_BURKITTS_LYMPHOMA_DN
38	2e−03	5 / 186	Canc	SPANG_LPS−index2
39	2e−03	4 / 113	GSE	LEE_NEURAL_CREST_STEM_CELL_DN
40	2e−03	3 / 54	BP	phagocytosis


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.4	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−05	3 / 12	leukocyte chemotaxis
2	1e−03	2 / 10	N−acetylglucosamine metabolic process
3	1e−03	8 / 434	negative regulation of apoptotic process
4	1e−03	2 / 11	negative regulation of nitric oxide biosynthetic process
5	1e−03	5 / 168	regulation of gene expression
6	1e−03	2 / 12	positive regulation of heterotypic cell−cell adhesion
7	2e−03	3 / 54	phagocytosis
8	3e−03	2 / 16	defense response to protozoan
9	3e−03	2 / 16	positive regulation of T cell differentiation
10	3e−03	8 / 520	positive regulation of transcription, DNA−templated
11	4e−03	3 / 64	negative regulation of inflammatory response
12	5e−03	2 / 21	negative regulation of interleukin−6 production
13	6e−03	6 / 336	biological_process
14	6e−03	6 / 336	immune response
15	6e−03	2 / 24	negative regulation of mitotic cell cycle

Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	10 / 317	SPANG_BCL6−index2
2	2e−03	2 / 13	BENTINK_e2f3.1
3	2e−03	5 / 186	SPANG_LPS−index2
4	7e−03	3 / 80	PanCan_JAK−ST_geneset_nanostring
5	8e−03	7 / 480	Lembcke_Colonic Inflammation
6	7e−02	1 / 14	LIU_COMMON_CANCER_GENES
7	2e−01	1 / 45	KUIPER_MM poor survival
8	2e−01	2 / 187	PanCan_PI3K_geneset_nanostring
9	3e−01	0 / 11	LIU_PROSTATE_CANCER_UP
10	4e−01	1 / 96	PanCan_TXmisReg_geneset_nanostring
11	5e−01	0 / 14	LIU_PROSTATE_CANCER_DN
12	6e−01	2 / 409	Lembcke_Normal vs Adenoma
13	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	0.003	2 / 18	phagocytic cup
2	0.007	7 / 462	cell surface
3	0.007	12 / 1128	integral component of plasma membrane
4	0.008	25 / 3270	integral component of membrane
5	0.010	7 / 494	endosome
6	0.023	2 / 48	ficolin−1−rich granule membrane
7	0.023	2 / 48	microvillus
8	0.026	4 / 231	apical plasma membrane
9	0.050	2 / 74	secretory granule membrane
10	0.052	1 / 11	exocyst
11	0.052	1 / 11	paranode region of axon
12	0.061	1 / 13	integral component of nuclear inner membrane
13	0.061	1 / 13	specific granule
14	0.063	3 / 188	endosome membrane
15	0.066	1 / 14	filopodium tip

Chr

Rank	p−value	#in/all	Geneset
1	0.04	5 / 382	Chr 15
2	0.05	11 / 1325	Chr 1
3	0.16	6 / 756	Chr 11
4	0.24	5 / 689	Chr 3
5	0.28	4 / 556	Chr X
6	0.32	4 / 585	Chr 7
7	0.48	2 / 333	Chr 22
8	0.50	3 / 548	Chr 16
9	0.52	4 / 776	Chr 17
10	0.54	2 / 369	Chr 20
11	0.58	4 / 832	Chr 2
12	0.59	1 / 184	Chr 18
13	0.68	2 / 480	Chr 4
14	0.69	2 / 490	Chr 10
15	0.78	3 / 833	Chr 19

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−07	26 / 1930	Fetal_TssA
2	6e−07	31 / 2724	Tcells peripheral blood_11_BivFlnk
3	3e−06	22 / 1611	natural killer cells peripheral blood_11_BivFlnk
4	6e−06	11 / 432	monocytes peripheral blood_3_TxFlnk
5	2e−05	31 / 3150	monocytes peripheral blood_13_ReprPC
6	2e−05	27 / 2507	Mid_Frontal_Lobe_ReprPC
7	2e−05	27 / 2531	10_TssBiv_ESC_Endoderm
8	2e−05	13 / 693	Bcells peripheral blood_3_TxFlnk
9	3e−05	24 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
10	4e−05	12 / 626	natural killer cells peripheral blood_3_TxFlnk
11	8e−05	20 / 1676	Fetal_TxTrans
12	1e−04	29 / 3110	14_ReprPCWk_ESC_Endoderm
13	1e−04	17 / 1308	Mid_Frontal_Lobe_K9K27me3
14	1e−04	24 / 2327	14_ReprPCWk_ESC_Mesoderm
15	1e−04	28 / 2972	13_ReprPC_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	9 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
2	0.007	8 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	0.051	3 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
4	0.051	4 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	0.051	8 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
6	0.053	10 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
7	0.084	5 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
8	0.134	7 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	0.140	1 / 31	Kosinski_lower−crypt−short−list
10	0.174	3 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
11	0.176	4 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
12	0.200	3 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	0.412	2 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	0.429	3 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
15	0.464	9 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	2 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
2	0.010	5 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	0.014	1 / 3	laffaire_hypometh_LGG_vs_control
4	0.016	6 / 423	Down_a
5	0.021	6 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
6	0.024	2 / 49	OPC
7	0.024	2 / 50	Christensen_hypomethylated_in_primary_glioblastoma
8	0.033	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
9	0.033	1 / 7	oligodendrocytes_glio
10	0.035	2 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
11	0.041	4 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
12	0.046	9 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
13	0.060	2 / 82	laffaire_hypermeth_LGG_vs_control
14	0.061	1 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
15	0.061	1 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	3 / 12	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
2	6e−05	5 / 87	BOSCO_TH1_CYTOTOXIC_MODULE
3	9e−05	4 / 49	GAURNIER_PSMD4_TARGETS
4	2e−04	7 / 249	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
5	2e−04	6 / 175	OKUMURA_INFLAMMATORY_RESPONSE_LPS
6	2e−04	4 / 63	BOYLAN_MULTIPLE_MYELOMA_D_DN
7	5e−04	4 / 77	KEGG_HEMATOPOIETIC_CELL_LINEAGE
8	8e−04	11 / 741	PEREZ_TP53_TARGETS
9	8e−04	7 / 318	MEISSNER_NPC_HCP_WITH_H3K4ME2
10	9e−04	7 / 321	PHONG_TNF_RESPONSE_NOT_VIA_P38
11	1e−03	3 / 46	WORSCHECH_TUMOR_REJECTION_UP
12	1e−03	7 / 348	MARTENS_BOUND_BY_PML_RARA_FUSION
13	1e−03	8 / 453	ONDER_CDH1_TARGETS_2_DN
14	2e−03	2 / 13	LIU_IL13_PRIMING_MODEL
15	2e−03	6 / 271	ENK_UV_RESPONSE_EPIDERMIS_UP

HM

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
2	2e−03	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
3	1e−02	4 / 193	HALLMARK_HEME_METABOLISM
4	5e−02	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
5	5e−02	2 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	6e−02	3 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	7e−02	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
8	7e−02	3 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	2e−01	2 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	2e−01	2 / 194	HALLMARK_KRAS_SIGNALING_UP
11	2e−01	2 / 195	HALLMARK_G2M_CHECKPOINT
12	2e−01	1 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	4e−01	1 / 122	HALLMARK_SPERMATOGENESIS
14	5e−01	1 / 141	HALLMARK_UV_RESPONSE_DN
15	5e−01	1 / 149	HALLMARK_UV_RESPONSE_UP

Immunome

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 67	Angelova_immune−metagene−T−cells
2	9e−03	2 / 29	Angelova_immune−metagene−Th1
3	5e−02	1 / 10	Angelova_CRC_immonoinhibitors
4	5e−02	1 / 11	Angelova_immune−metagene−macrophages
5	7e−02	1 / 16	Angelova_immune−metagene−Th17
6	2e−01	1 / 45	Angelova_immune−metagene−MDSC
7	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
8	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
9	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
10	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
12	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1e+00	0 / 25	Angelova_immune−metagene−DC
14	1e+00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1e+00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 22	DUMEAUX_High bmi enriched genes
2	1.0	0 / 62	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 22	DUMEAUX_Fasting enriched genes
12	1.0	0 / 150	Homuth_BMI−associated−genes_UP
13	1.0	0 / 210	Homuth_BMI−associated−genes_DN
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−06	6 / 85	Aukema_BCL2 DN_BCL6 UP
2	6e−05	5 / 85	Sha_DLBCL UP
3	6e−05	42 / 5404	HOPP_Strong_enhancer
4	7e−05	7 / 213	SPANG_IL21 DN
5	8e−05	3 / 18	WRIGHT_ABC UP
6	1e−03	2 / 12	BENTINK_mBL DOWN
7	1e−03	5 / 173	Victora_Light zone signature
8	2e−03	2 / 15	Subero_T−ALL_hypo_meth
9	4e−03	11 / 906	SPANG_BCR DN
10	4e−03	4 / 135	DAVE_BL−vs−DLBCL
11	5e−03	5 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
12	7e−03	6 / 353	SPANG_CD40 6hrs DN
13	2e−02	16 / 1894	HOPP_Poised_promoter
14	2e−02	1 / 4	MASCQUE_mBL DOWN
15	4e−02	28 / 4261	HOPP_Txn_transition

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
2	0.07	1 / 16	Hugo_melanoma−all−LEF1_UP
3	0.10	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.11	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
5	0.11	1 / 24	Tirosh_B−cell specific genes−melanoma
6	0.17	1 / 39	Tirosh_top50 correlated genes PC4
7	0.17	1 / 39	Tirosh_melanoma specific genes
8	0.18	1 / 41	Tirosh_top50 correlated genes PC3
9	0.20	1 / 46	Tirosh_top50 correlated genes PC5
10	0.20	2 / 171	Landsberg_dedifferentiation_up
11	0.23	2 / 189	Tirosh_genes preferentially expressed by Tregs
12	0.26	2 / 204	Landsberg_dedifferentiation_down
13	0.27	1 / 64	Harbst_melanoma_lowgrade_up
14	0.27	1 / 65	Harbst_melanoma_highgrade_up
15	0.31	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	0.003	4 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
2	0.010	4 / 173	cytokine activity
3	0.011	3 / 96	SH3 domain binding
4	0.012	4 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
5	0.015	2 / 38	cytokine receptor activity
6	0.021	2 / 46	SH3/SH2 adaptor activity
7	0.022	3 / 123	transporter activity
8	0.031	3 / 141	growth factor activity
9	0.036	2 / 62	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
10	0.042	5 / 393	molecular_function
11	0.042	2 / 67	drug binding
12	0.044	2 / 69	ATPase binding
13	0.047	1 / 10	lipopeptide binding
14	0.047	1 / 10	monocarboxylic acid transmembrane transporter activity
15	0.050	2 / 74	protein binding, bridging

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 55	hsa−miR−140−3p
2	0.007	2 / 26	hsa−miR−1292
3	0.010	3 / 92	hsa−miR−500
4	0.012	2 / 35	hsa−miR−331−5p
5	0.015	2 / 38	hsa−miR−658
6	0.019	2 / 44	hsa−miR−552
7	0.021	2 / 46	hsa−miR−296−3p
8	0.024	2 / 50	hsa−miR−219−5p
9	0.029	1 / 6	hsa−miR−523
10	0.033	2 / 59	hsa−miR−643
11	0.036	2 / 62	hsa−miR−578
12	0.036	2 / 62	hsa−miR−205
13	0.043	1 / 9	hsa−miR−887
14	0.043	1 / 9	hsa−miR−604
15	0.054	2 / 77	hsa−miR−362−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.2	1 / 41	Scicluna_DN
3	0.2	1 / 52	Burnham_day1_vs_5_DN
4	0.2	1 / 54	Burnham_timecourse
5	0.2	1 / 57	Burnham_viral_UP
6	0.4	1 / 122	Terre_IMS_influenza_meta_signature
7	1.0	0 / 68	Burnham_sep_vs_con_UP
8	1.0	0 / 56	Burnham_sep_vs_con_DN
9	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
10	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
11	1.0	0 / 48	Burnham_viral_DN
12	1.0	0 / 57	Burnham_day1_vs_5_UP
13	1.0	0 / 18	Scicluna_UP
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−06	8 / 182	WIRTH_post GC B−cells
2	2e−02	2 / 42	Chaussabel_1,3_B−cells
3	3e−02	5 / 352	WIRTH_Nervous System
4	3e−02	5 / 355	WIRTH_Immune system
5	6e−02	1 / 12	VAQUERIZAS_Kidney_TF
6	7e−02	1 / 15	WIRTH_Telencephalon
7	7e−02	1 / 16	VAQUERIZAS_Fetal liver_TF
8	7e−02	1 / 16	VAQUERIZAS_Salivary gland_TF
9	8e−02	3 / 204	Chaussabel_3,2_Inflammation I
10	9e−02	3 / 218	WIRTH_pre+post GC B−cells
11	1e−01	1 / 21	VAQUERIZAS_Tonsil_TF
12	1e−01	1 / 22	VAQUERIZAS_Trachea_TF
13	1e−01	1 / 24	VAQUERIZAS_Spinal cord_TF
14	1e−01	1 / 30	VAQUERIZAS_Smooth muscle_TF
15	1e−01	1 / 30	VAQUERIZAS_Fetal lung_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.06	9 / 1041	ICGC_P300_targets
2	0.07	16 / 2254	ICGC_BatfPcr1_targets
3	0.09	12 / 1636	ICGC_Bcl11_targets
4	0.22	12 / 1941	ICGC_Bcl3_targets
5	0.23	9 / 1387	HEBENSTREIT_high expression TF
6	0.25	4 / 522	ICGC_SrfPcr2_targets
7	0.31	9 / 1508	ICGC_Mef2_targets
8	0.44	8 / 1494	ICGC_Cebpbsc150_targets
9	0.49	15 / 2994	ICGC_Zeb1_targets
10	0.56	14 / 2899	ICGC_Nfatc1_targets
11	0.58	11 / 2321	ICGC_Rad21_targets
12	0.63	16 / 3451	ICGC_Atf2_targets
13	0.64	20 / 4319	ICGC_Pou2_targets
14	0.65	17 / 3703	ICGC_Foxm1_targets
15	0.68	14 / 3121	ICGC_Egr1_targets

D−Cluster

Spot Summary: E

\# metagenes = 7
\# genes = 49

<r> metagenes = 0.99
<r> genes = 0.23
beta: r2= 2.08 / log p= −Inf

\# samples with spot = 20 (9 %)
mBL : 2 (4.5 %)
intermediate : 5 (10.4 %)
non−mBL : 13 (10.1 %)

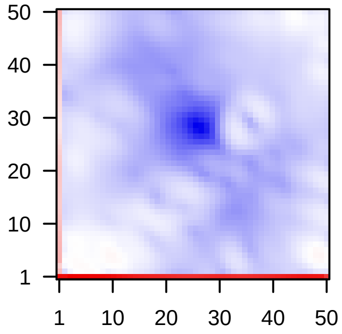
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	217414_x_at	2.09	−2.18	0.8	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
2	217232_x_at	1.87	−1.68	0.76	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
3	209458_x_at	1.77	−1.81	0.8	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
4	211699_x_at	1.76	−1.79	0.81	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
5	209116_x_at	1.75	−1.74	0.77	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
6	204018_x_at	1.74	−1.94	0.8	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
7	39248_at	1.74	−1.59	0.34	AQP3	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:H
8	211696_x_at	1.67	−1.34	0.75	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
9	211745_x_at	1.66	−1.57	0.8	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
10	214414_x_at	1.47	−1.7	0.79	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
11	219911_s_at	1.32	−2.03	0.23	SLCO4A1	solute carrier organic anion transporter family member 4A1 [S
12	213447_at	1.29	−1.37	0.17		small nucleolar RNA host gene 14 [Source:HGNC Symbol;Ac
13	218681_s_at	1.27	−1.26	0.43	SDF2L1	stromal cell derived factor 2 like 1 [Source:HGNC Symbol;Ac
14	207542_s_at	1.25	−0.94	0.34	AQP1	aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Ac
15	219118_at	1.23	−0.75	0.55	FKBP11	FK506 binding protein 11 [Source:HGNC Symbol;Acc:HGNC:
16	219117_s_at	1.23	−0.99	0.52	FKBP11	FK506 binding protein 11 [Source:HGNC Symbol;Acc:HGNC:
17	221529_s_at	1.2	−1.15	0.4	PLVAP	plasmalemma vesicle associated protein [Source:HGNC Sym
18	202053_s_at	1.12	−1.77	0.31	ALDH3A2	aldehyde dehydrogenase 3 family member A2 [Source:HGNC
19	210006_at	1.11	−0.98	0.33	ABHD14A	abhydrolase domain containing 14A [Source:HGNC Symbol;
20	200998_s_at	1.09	−1.26	0.42	CKAP4	cytoskeleton associated protein 4 [Source:HGNC Symbol;Ac

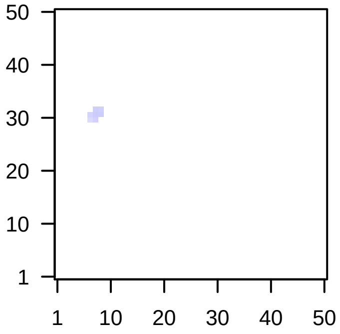
Geneset Overrepresentation

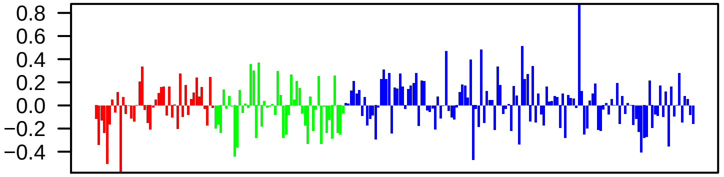
Rank	p−value	#in/all	Geneset	
1	9e−13	9 / 75	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
2	1e−12	9 / 77	Lymp	TARTE_Plasma cell signature
3	3e−11	11 / 216	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
4	2e−10	18 / 1035	CC	endoplasmic reticulum
5	2e−09	13 / 518	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
6	6e−09	14 / 683	CC	endoplasmic reticulum membrane
7	1e−07	5 / 41	GSEA	MORI_PLASMA_CELL_UP
8	1e−05	23 / 3270	CC	integral component of membrane
9	2e−05	4 / 54	BP	IRE1−mediated unfolded protein response
10	5e−05	4 / 68	GSEA	REACTOME_UNFOLDED_PROTEIN_RESPONSE
11	6e−05	4 / 71	GSEA	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
12	1e−04	7 / 384	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
13	1e−04	3 / 34	BP	bicarbonate transport
14	2e−04	24 / 4131	TF	ICGC_Tcf3_targets
15	2e−04	3 / 37	GSEA	KEGG_N_GLYCAN_BIOSYNTHESIS
16	2e−04	4 / 95	MF	isomerase activity
17	2e−04	2 / 8	GSEA	RODRIGUES_THYROID_CARCINOMA_UP
18	3e−04	3 / 41	GSEA	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S
19	3e−04	3 / 42	BP	chaperone−mediated protein folding
20	3e−04	4 / 110	GSEA	REACTOME_DIABETES_PATHWAYS
21	4e−04	24 / 4319	TF	ICGC_Pou2_targets
22	4e−04	2 / 10	MF	water channel activity
23	4e−04	2 / 10	GSEA	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
24	4e−04	6 / 325	GSEA	REACTOME_METABOLISM_OF_PROTEINS
25	4e−04	4 / 119	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
26	5e−04	2 / 11	BP	oxygen transport
27	5e−04	2 / 11	Refer	JONGENEEL_Peripheral Blood Lymphocytes
28	5e−04	2 / 11	Refer	Chaussabel_3,5_Hemoglobin genes
29	5e−04	27 / 5339	CC	membrane
30	5e−04	3 / 53	CC	rough endoplasmic reticulum
31	6e−04	2 / 12	GSEA	BIOCARTA_AHSP_PATHWAY
32	7e−04	2 / 13	CC	endocytic vesicle lumen
33	7e−04	2 / 13	GSEA	REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CA
34	7e−04	2 / 13	GSEA	REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1
35	7e−04	2 / 13	GSEA	REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_T
36	8e−04	4 / 137	GSEA	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
37	8e−04	5 / 241	CC	endoplasmic reticulum lumen
38	8e−04	2 / 14	BP	water transport
39	8e−04	19 / 3121	TF	ICGC_Egr1_targets
40	8e−04	4 / 140	BP	protein folding

Overview Map

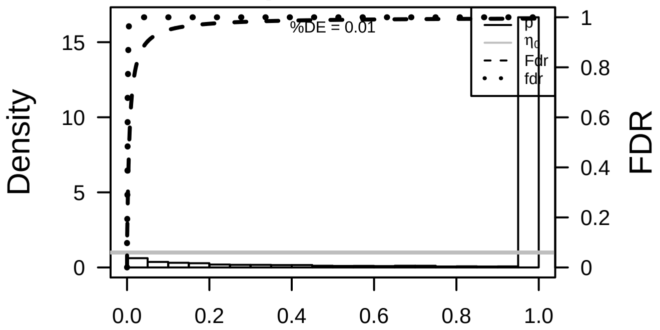


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	1 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 54	IRE1−mediated unfolded protein response
2	1e−04	3 / 34	bicarbonate transport
3	3e−04	3 / 42	chaperone−mediated protein folding
4	5e−04	2 / 11	oxygen transport
5	8e−04	2 / 14	water transport
6	8e−04	4 / 140	protein folding
7	9e−04	2 / 15	hydrogen peroxide catabolic process
8	1e−03	3 / 71	response to endoplasmic reticulum stress
9	3e−03	2 / 29	odontogenesis
10	4e−03	2 / 30	renal water homeostasis
11	4e−03	2 / 32	protein peptidyl−prolyl isomerization
12	4e−03	2 / 33	protein N−linked glycosylation via asparagine
13	6e−03	3 / 125	protein glycosylation
14	7e−03	2 / 43	positive regulation of cell death
15	9e−03	2 / 48	response to hydrogen peroxide

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	0 / 11	LIU_PROSTATE_CANCER_UP
2	0.04	1 / 14	GENTLES_modul13
3	0.04	1 / 15	WANG_ER_UP
4	0.05	1 / 16	GENTLES_modul6
5	0.16	0 / 15	RHODES_CANCER_META_SIGNATURE
6	0.31	0 / 14	LIU_PROSTATE_CANCER_DN
7	0.43	2 / 480	Lembcke_Colonic Inflammation
8	0.43	1 / 186	SPANG_LPS−index2
9	0.72	1 / 409	Lembcke_Normal vs Adenoma
10	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.00	0 / 12	LIU_BREAST_CANCER
14	1.00	0 / 14	LIU_COMMON_CANCER_GENES
15	1.00	0 / 16	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−10	18 / 1035	endoplasmic reticulum
2	6e−09	14 / 683	endoplasmic reticulum membrane
3	1e−05	23 / 3270	integral component of membrane
4	5e−04	27 / 5339	membrane
5	5e−04	3 / 53	rough endoplasmic reticulum
6	7e−04	2 / 13	endocytic vesicle lumen
7	8e−04	5 / 241	endoplasmic reticulum lumen
8	3e−03	3 / 96	melanosome
9	2e−02	5 / 537	perinuclear region of cytoplasm
10	2e−02	2 / 77	cell
11	2e−02	2 / 77	specific granule membrane
12	2e−02	2 / 79	integral component of endoplasmic reticulum membrane
13	3e−02	1 / 10	PRC1 complex
14	4e−02	1 / 13	exosome (RNase complex)
15	5e−02	2 / 116	blood microparticle

Chr

Rank	p−value	#in/all	Geneset
1	0.003	5 / 333	Chr 22
2	0.004	7 / 689	Chr 3
3	0.230	3 / 548	Chr 16
4	0.244	4 / 833	Chr 19
5	0.308	2 / 369	Chr 20
6	0.323	2 / 382	Chr 15
7	0.331	3 / 669	Chr 6
8	0.357	3 / 700	Chr 12
9	0.404	3 / 756	Chr 11
10	0.442	2 / 492	Chr 9
11	0.535	2 / 585	Chr 7
12	0.820	1 / 554	Chr 5
13	0.912	1 / 776	Chr 17
14	0.921	2 / 1325	Chr 1
15	1.000	0 / 490	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−05	30 / 5620	TssF_Colon
2	1e−04	23 / 3803	6_EnhG_Fibroblasts
3	4e−04	16 / 2203	EnhA_Colon
4	4e−04	18 / 2704	4_TxTrans_Fibroblasts
5	5e−04	21 / 3524	Tregulatory cells peripheral blood_6_EnhG
6	6e−04	32 / 7165	Tx_Colon
7	6e−04	31 / 6798	TxWk_Colon
8	1e−03	24 / 4672	TssD2_Colon
9	1e−03	15 / 2204	3_TxFlnk_ESC_Mesoderm
10	2e−03	34 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
11	2e−03	36 / 9146	3_TssF_Skeletal_Muscle
12	2e−03	16 / 2563	Mid_Frontal_Lobe_ZNF
13	2e−03	21 / 3938	Thelper cells peripheral blood_6_EnhG
14	2e−03	33 / 7957	Tcells peripheral blood_2_TssAFlnk
15	3e−03	35 / 8816	Thelper cells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	2 / 60	Marisa_CRC−cluster−g
2	0.04	7 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
3	0.05	8 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	0.10	2 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
5	0.14	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
6	0.24	3 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	0.39	1 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
8	0.40	2 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
9	0.43	6 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
10	0.43	1 / 184	Kosinski_lower−crypt−long−list
11	0.43	2 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	0.48	4 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	0.48	2 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	0.54	2 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
15	0.54	1 / 255	Kosinski_top−crypt−long−list

Glioma

Rank	p−value	#in/all	Geneset
1	0.03	1 / 9	Colman_survival_robust
2	0.03	2 / 85	ScoV_0.999_Sturm_E2_IDH_DN
3	0.04	1 / 15	Mukasa_UP_in_GBM
4	0.10	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
5	0.10	1 / 35	Gorovets_LGG_EPL_subclass
6	0.10	1 / 35	Colman_survival_associated
7	0.19	1 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
8	0.21	2 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	0.21	1 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
10	0.23	1 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
11	0.26	1 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
12	0.26	2 / 330	Up
13	0.26	1 / 101	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	0.39	5 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
15	0.39	2 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−13	9 / 75	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
2	3e−11	11 / 216	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
3	2e−09	13 / 518	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
4	1e−07	5 / 41	MORI_PLASMA_CELL_UP
5	5e−05	4 / 68	REACTOME_UNFOLDED_PROTEIN_RESPONSE
6	6e−05	4 / 71	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
7	1e−04	7 / 384	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
8	2e−04	3 / 37	KEGG_N_GLYCAN_BIOSYNTHESIS
9	2e−04	2 / 8	RODRIGUES_THYROID_CARCINOMA_UP
10	3e−04	3 / 41	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S
11	3e−04	4 / 110	REACTOME_DIABETES_PATHWAYS
12	4e−04	2 / 10	REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
13	4e−04	6 / 325	REACTOME_METABOLISM_OF_PROTEINS
14	4e−04	4 / 119	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
15	6e−04	2 / 12	BIOCARTA_AHSP_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.004	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	0.061	2 / 133	HALLMARK_DNA_REPAIR
3	0.075	2 / 149	HALLMARK_UV_RESPONSE_UP
4	0.094	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
5	0.112	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
6	0.115	2 / 192	HALLMARK_MTORC1_SIGNALING
7	0.116	2 / 193	HALLMARK_HEME_METABOLISM
8	0.117	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.346	1 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	0.441	1 / 190	HALLMARK_MYC_TARGETS_V1
11	0.442	1 / 191	HALLMARK_P53_PATHWAY
12	0.446	1 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
13	0.447	1 / 194	HALLMARK_MYOGENESIS
14	0.447	1 / 194	HALLMARK_KRAS_SIGNALING_UP
15	0.451	1 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 18	Angelova_immune−metagene−pDC
2	0.18	1 / 67	Angelova_immune−metagene−T−cells
3	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

Rank	p−value	#in/all	Geneset
1	1	0 / 62	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
7	1	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1	0 / 12	DUMEAUX_Women normal BMI literature genes up
10	1	0 / 22	DUMEAUX_High bmi enriched genes
11	1	0 / 22	DUMEAUX_Fasting enriched genes
12	1	0 / 150	Homuth_BMI−associated−genes_UP
13	1	0 / 210	Homuth_BMI−associated−genes_DN
14	1	0 / 14	Huan_blood−pressure_SBP−signature
15	1	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−12	9 / 77	TARTE_Plasma cell signature
2	3e−02	2 / 85	Aukema_BCL2 DN_BCL6 UP
3	4e−02	2 / 102	ROSOLOWSKI_blue total
4	5e−02	22 / 5404	HOPP_Strong_enhancer
5	7e−02	6 / 955	SPANG_BCR UP
6	1e−01	17 / 4261	HOPP_Txn_transition
7	1e−01	1 / 45	SPANG_BAFF 9hrs DN
8	1e−01	1 / 53	LENZ_Stromal signature 2
9	2e−01	1 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
10	2e−01	1 / 57	SPANG_LPS 6hrs DN
11	2e−01	20 / 5529	HOPP_Txn_elongation
12	2e−01	20 / 5682	HOPP_Weak_promoter
13	3e−01	4 / 906	SPANG_BCR DN
14	3e−01	20 / 5908	HOPP_Active_promoter
15	3e−01	2 / 378	TARTE_Mature plasma cell signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	1 / 24	Gerami_melanoma−metastatic−risk_DN
2	0.11	2 / 189	Tirosh_genes preferentially expressed by Tregs
3	0.16	2 / 236	Gerber_wt/wt_group3−specific
4	0.20	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
5	0.21	1 / 78	Tirosh_CAF−cell specific genes
6	0.21	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
7	0.22	1 / 83	TCGA_melanoma_immune_high
8	0.43	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
9	0.45	2 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	1.00	0 / 17	Hugo_melanoma−all−MET_UP
11	1.00	0 / 37	Hugo_melanoma−all−MET_DN
12	1.00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	1.00	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1.00	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 95	isomerase activity
2	4e−04	2 / 10	water channel activity
3	1e−03	2 / 16	protein disulfide isomerase activity
4	2e−03	2 / 23	channel activity
5	2e−03	2 / 23	peroxidase activity
6	4e−03	2 / 30	oxygen binding
7	4e−03	2 / 32	peptidyl−prolyl cis−trans isomerase activity
8	4e−02	1 / 12	aldehyde dehydrogenase (NAD) activity
9	4e−02	1 / 12	calcium−transporting ATPase activity
10	4e−02	1 / 12	misfolded protein binding
11	4e−02	2 / 103	heme binding
12	4e−02	1 / 14	FK506 binding
13	5e−02	2 / 113	iron ion binding
14	5e−02	1 / 16	3'−5'−exoribonuclease activity
15	5e−02	1 / 16	AU−rich element binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	2 / 26	hsa−miR−1226
2	0.011	3 / 155	hsa−miR−129−5p
3	0.014	2 / 60	hsa−miR−548b−3p
4	0.015	2 / 62	hsa−miR−578
5	0.032	2 / 93	hsa−miR−605
6	0.045	2 / 112	hsa−miR−218
7	0.060	2 / 132	hsa−miR−298
8	0.079	1 / 27	hsa−miR−589
9	0.082	1 / 28	hsa−miR−296−5p
10	0.104	1 / 36	hsa−miR−412
11	0.117	1 / 41	hsa−miR−302b*
12	0.123	3 / 404	hsa−miR−103
13	0.123	3 / 405	hsa−miR−107
14	0.128	2 / 205	hsa−miR−548p
15	0.128	1 / 45	hsa−miR−379

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	1 / 37	Sweeney_viral_up
2	0.2	1 / 68	Burnham_sep_vs_con_UP
3	0.2	1 / 71	Burnham_cap_fp_vs_con_UP
4	0.4	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 48	Burnham_viral_DN
8	1.0	0 / 57	Burnham_viral_UP
9	1.0	0 / 57	Burnham_day1_vs_5_UP
10	1.0	0 / 52	Burnham_day1_vs_5_DN
11	1.0	0 / 54	Burnham_timecourse
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 33	Sweeney_viral_dn
15	1.0	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−04	2 / 11	JONGENEEL_Peripheral Blood Lymphocytes
2	5e−04	2 / 11	Chaussabel_3,5_Hemoglobin genes
3	1e−03	3 / 68	Chaussabel_2,1_Cytotoxic cells
4	1e−02	8 / 1022	PROTEINATLAS_placenta
5	2e−02	7 / 893	PROTEINATLAS_pancreas
6	6e−02	5 / 708	PROTEINATLAS_thyroid gland
7	9e−02	1 / 30	JONGENEEL_Bone Marrow
8	9e−02	1 / 32	Chaussabel_1,1_Plasma Cells
9	1e−01	6 / 1076	PROTEINATLAS_stomach
10	1e−01	2 / 204	Chaussabel_3,2_Inflammation I
11	1e−01	4 / 645	PROTEINATLAS_bone marrow
12	2e−01	4 / 770	PROTEINATLAS_endometrium
13	2e−01	4 / 819	PROTEINATLAS_bronchus
14	2e−01	1 / 89	Chaussabel_2,3_Erythrocytes
15	3e−01	1 / 100	Chaussabel_2,8_T−cells

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	2e−04	24 / 4131	ICGC_Tcf3_targets
2	4e−04	24 / 4319	ICGC_Pou2_targets
3	8e−04	19 / 3121	ICGC_Egr1_targets
4	9e−04	19 / 3150	ICGC_Creb1_targets
5	1e−03	24 / 4602	ICGC_Elf1_targets
6	1e−03	21 / 3796	ICGC_Nficsc81335_targets
7	2e−03	24 / 4851	ICGC_Runx3_targets
8	4e−03	20 / 3804	ICGC_Stat5_targets
9	4e−03	19 / 3564	ICGC_Taf1_targets
10	7e−03	10 / 1387	HEBENSTREIT_high expression TF
11	8e−03	16 / 2899	ICGC_Nfatc1_targets
12	9e−03	13 / 2150	ICGC_Irf4_targets
13	9e−03	17 / 3213	ICGC_Pu1_targets
14	1e−02	16 / 2994	ICGC_Zeb1_targets
15	2e−02	17 / 3451	ICGC_Atf2_targets

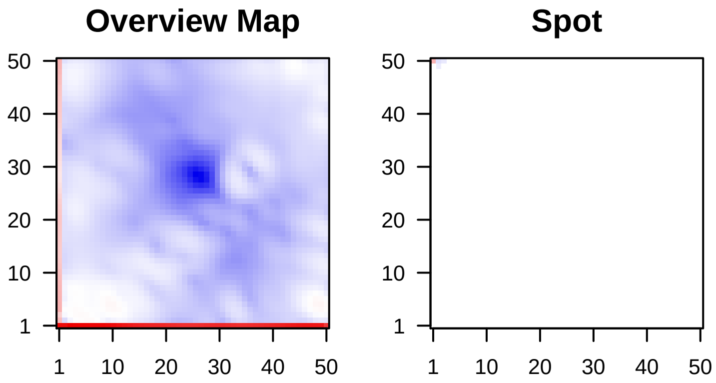
D−Cluster

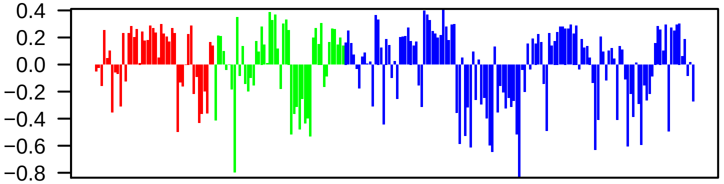
Spot Summary: F

metagenes = 4
genes = 141

<r> metagenes = 1
<r> genes = 0.48
beta: r2= 14.81 / log p= −Inf

samples with spot = 39 (17.6 %)
mBL : 7 (15.9 %)
intermediate : 11 (22.9 %)
non−mBL : 21 (16.3 %)



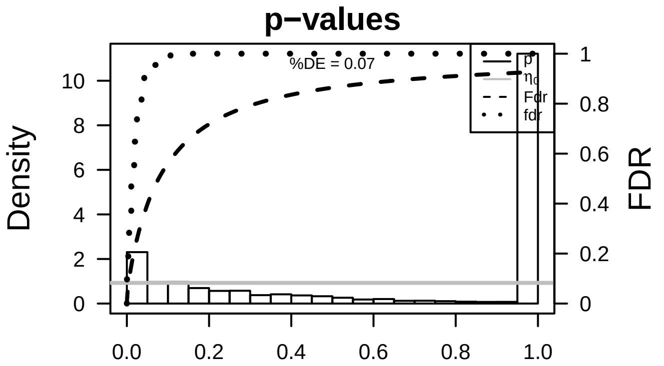


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207686_s_at	1.62	−1.44	0.66	CASP8	caspase 8 [Source:HGNC Symbol;Acc:HGNC:1509]
2	211708_s_at	1.43	−1.2	0.57	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
3	214971_s_at	1.4	−1.95	0.74	ST6GAL1	ST6 beta−galactoside alpha−2,6−sialyltransferase 1 [Source:
4	204429_s_at	1.31	−2.03	0.45	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
5	209629_s_at	1.29	−1.56	0.66	NXT2	nuclear transport factor 2 like export factor 2 [Source:HGNC
6	203676_at	1.21	−1.22	0.75	GNS	glucosamine (N−acetyl)−6−sulfatase [Source:HGNC Symbol;
7	203472_s_at	1.21	−0.99	0.6	SLCO2B1	solute carrier organic anion transporter family member 2B1 [S
8	206925_at	1.2	−1.29	0.56	ST8SIA4	ST8 alpha−N−acetyl−neuraminide alpha−2,8−sialyltransferas
9	219558_at	1.19	−1.83	0.81	ATP13A3	ATPase 13A3 [Source:HGNC Symbol;Acc:HGNC:24113]
10	201942_s_at	1.19	−0.92	0.65	CPD	carboxypeptidase D [Source:HGNC Symbol;Acc:HGNC:2301
11	216100_s_at	1.17	−1.67	0.66	TOR1AIP1	torsin 1A interacting protein 1 [Source:HGNC Symbol;Acc:HG
12	214390_s_at	1.13	−1.23	0.53	BCAT1	branched chain amino acid transaminase 1 [Source:HGNC S
13	202226_s_at	1.1	−1.78	0.59	CRK	CRK proto−oncogene, adaptor protein [Source:HGNC Symbo
14	210594_x_at	1.1	−1.23	0.56	MPZL1	myelin protein zero like 1 [Source:HGNC Symbol;Acc:HGNC:
15	215509_s_at	1.08	−1.84	0.71	BUB1	BUB1 mitotic checkpoint serine/threonine kinase [Source:HG
16	204864_s_at	1.08	−1.21	0.73	IL6ST	interleukin 6 signal transducer [Source:HGNC Symbol;Acc:H
17	211540_s_at	1.07	−1.55	0.72	RB1	RB transcriptional corepressor 1 [Source:HGNC Symbol;Acc:
18	215286_s_at	1.06	−1.35	0.66	PHTF2	putative homeodomain transcription factor 2 [Source:HGNC S
19	210756_s_at	1.02	−1.46	0.59	NOTCH2	notch 2 [Source:HGNC Symbol;Acc:HGNC:7882]
20	214336_s_at	1.01	−1.08	0.8	COPA	coatomer protein complex subunit alpha [Source:HGNC Syml

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−55	52 / 282	Gliom	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	2e−38	33 / 136	Refer	Chaussabel_2,9_Cytosceleton
3	6e−32	40 / 372	GSEA	SENESE_HDAC1_TARGETS_UP
4	4e−28	38 / 405	GSEA	SENESE_HDAC3_TARGETS_UP
5	1e−18	99 / 5529	Lympl	HOPP_Txn_elongation
6	7e−18	27 / 344	GSEA	THUM_SYSTOLIC_HEART_FAILURE_UP
7	1e−17	86 / 4261	Lympl	HOPP_Txn_transition
8	2e−15	25 / 355	Refer	WIRTH_Immune system
9	1e−14	16 / 118	GSEA	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP
10	2e−13	95 / 5908	Lympl	HOPP_Active_promoter
11	2e−13	28 / 564	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
12	2e−10	38 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	4e−10	93 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
14	8e−10	11 / 92	GSEA	SENESE_HDAC2_TARGETS_UP
15	4e−09	13 / 163	GSEA	ONDER_CDH1_TARGETS_1_DN
16	4e−09	85 / 5682	Lympl	HOPP_Weak_promoter
17	3e−08	19 / 448	miRN	hsa−miR−20b
18	4e−08	37 / 1550	GSEA	PILON_KLF1_TARGETS_DN
19	4e−08	17 / 361	miRN	hsa−miR−130b
20	5e−08	8 / 57	GSEA	JI_RESPONSE_TO_FSH_DN
21	7e−08	6 / 24	GSEA	AZARE_STAT3_TARGETS
22	9e−08	13 / 213	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
23	2e−07	32 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
24	2e−07	25 / 854	Colon	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
25	3e−07	14 / 275	miRN	hsa−miR−590−3p
26	3e−07	33 / 1390	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
27	4e−07	15 / 329	miRN	hsa−let−7b
28	4e−07	9 / 102	Lympl	ROSOLOWSKI_blue total
29	6e−07	24 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
30	8e−07	13 / 257	GSEA	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN
31	9e−07	61 / 3805	CC	cytosol
32	9e−07	77 / 5404	Lympl	HOPP_Strong_enhancer
33	1e−06	21 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
34	1e−06	16 / 403	miRN	hsa−miR−106b
35	1e−06	18 / 509	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
36	1e−06	10 / 147	GSEA	LU_AGING_BRAIN_DN
37	1e−06	14 / 314	miRN	hsa−miR−372
38	1e−06	8 / 87	miRN	hsa−miR−449b
39	1e−06	11 / 189	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
40	2e−06	17 / 468	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 92	HORVATH_aging_genes meth DOWN
2	0.6	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−06	6 / 47	learning or memory
2	2e−05	16 / 502	protein transport
3	2e−05	7 / 91	mRNA transport
4	2e−04	3 / 13	striated muscle cell differentiation
5	3e−04	14 / 507	protein phosphorylation
6	9e−04	4 / 46	activation of MAPKK activity
7	1e−03	4 / 48	blood vessel development
8	1e−03	3 / 24	positive regulation of muscle cell differentiation
9	2e−03	5 / 91	G1/S transition of mitotic cell cycle
10	2e−03	4 / 55	protein import into nucleus
11	2e−03	4 / 58	activation of protein kinase activity
12	3e−03	3 / 32	positive regulation of neuron death
13	3e−03	3 / 32	regulation of cholesterol biosynthetic process
14	3e−03	4 / 66	Ras protein signal transduction
15	4e−03	2 / 10	Notch receptor processing, ligand−dependent

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	9 / 317	SPANG_BCL6−index2
2	0.004	5 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.007	2 / 14	BENTINK_src.2
4	0.009	2 / 16	GENTLES_modul16
5	0.019	1 / 2	GENTLES_modul8
6	0.049	4 / 147	PanCan_MAPK_geneset_nanostring
7	0.085	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.098	1 / 11	GENTLES_modul14
9	0.106	1 / 12	GENTLES_modul12
10	0.121	3 / 130	PanCan_CC+Apop_geneset_nanostring
11	0.123	1 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	0.123	1 / 14	GENTLES_modul10
13	0.131	1 / 15	BEN−PORATH_UP
14	0.131	1 / 15	GENTLES_modul2
15	0.155	1 / 18	PanCan_Notch_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	9e−07	61 / 3805	cytosol
2	3e−06	69 / 4701	cytoplasm
3	2e−04	14 / 503	cytoplasmic vesicle
4	5e−04	5 / 70	nuclear pore
5	5e−04	7 / 149	nuclear envelope
6	5e−04	8 / 196	nuclear membrane
7	9e−04	4 / 46	clathrin−coated vesicle membrane
8	2e−03	34 / 2239	extracellular exosome
9	3e−03	5 / 101	kinetochore
10	3e−03	58 / 4579	nucleus
11	4e−03	11 / 462	cell surface
12	5e−03	11 / 479	Golgi membrane
13	5e−03	3 / 38	SNARE complex
14	6e−03	2 / 13	SWI/SNF complex
15	7e−03	6 / 180	actin cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.03	10 / 554	Chr 5
2	0.07	18 / 1325	Chr 1
3	0.17	6 / 403	Chr 14
4	0.29	8 / 669	Chr 6
5	0.33	8 / 700	Chr 12
6	0.37	9 / 832	Chr 2
7	0.37	2 / 139	Chr 21
8	0.41	8 / 756	Chr 11
9	0.44	8 / 776	Chr 17
10	0.46	7 / 689	Chr 3
11	0.48	5 / 490	Chr 10
12	0.49	5 / 492	Chr 9
13	0.51	2 / 184	Chr 18
14	0.64	5 / 585	Chr 7
15	0.66	4 / 480	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−23	106 / 5716	Bcells peripheral blood_4_Tx
2	3e−22	108 / 6099	HSC_4_Tx
3	4e−20	101 / 5527	Tregulatory cells peripheral blood_4_Tx
4	2e−19	102 / 5766	natural killer cells peripheral blood_4_Tx
5	1e−18	101 / 5738	monocytes peripheral blood_4_Tx
6	1e−18	101 / 5753	Tcells peripheral blood_4_Tx
7	8e−18	110 / 7078	Bcells peripheral blood_5_TxWk
8	5e−17	104 / 6389	4_Tx_ESC_Mesoderm
9	1e−16	107 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
10	1e−16	97 / 5601	Thelper cells peripheral blood_4_Tx
11	1e−16	87 / 4528	T CD8+ naive cells peripheral blood_4_Tx
12	4e−16	100 / 6034	5_Tx_Fibroblasts
13	5e−15	109 / 7420	Tcells peripheral blood_1_TssA
14	8e−15	103 / 6643	5_Tx_Skeletal_Muscle
15	2e−14	101 / 6466	5_Tx_MSC_Adipocyte

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−10	93 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	2e−07	25 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
3	2e−06	27 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
4	6e−04	25 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	1e−03	18 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	1e−03	19 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
7	2e−03	28 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	7e−03	2 / 14	TCGA_Mutated−in−CRC_hypermutated
9	2e−02	18 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	4e−02	1 / 4	Juehling−MSI−enriched−in−8−to−9
11	4e−02	17 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	5e−02	13 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	5e−02	1 / 6	Hewish_dMMR−secondary−mutations_Signal_transduction
14	5e−02	1 / 6	Juehling_HNPCC−mutated−in−5
15	1e−01	1 / 11	KIM_MSI−in−CRC

Glioma

Rank	p−value	#in/all	Geneset
1	5e−55	52 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	2e−03	14 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
3	4e−02	4 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	7e−02	20 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	7e−02	18 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	8e−02	5 / 242	ScoV_0.5_Sturm_C1_IDH_DN
7	8e−02	5 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
8	1e−01	1 / 11	KIM amplified & overexpressed in LTS
9	1e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	1e−01	2 / 58	Stuehler_Proteins_up_in_STS
11	1e−01	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
12	1e−01	1 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
13	1e−01	1 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma
14	1e−01	1 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
15	1e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−32	40 / 372	SENESE_HDAC1_TARGETS_UP
2	4e−28	38 / 405	SENESE_HDAC3_TARGETS_UP
3	7e−18	27 / 344	THUM_SYSTOLIC_HEART_FAILURE_UP
4	1e−14	16 / 118	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP
5	2e−13	28 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
6	2e−10	38 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	8e−10	11 / 92	SENESE_HDAC2_TARGETS_UP
8	4e−09	13 / 163	ONDER_CDH1_TARGETS_1_DN
9	4e−08	37 / 1550	PILON_KLF1_TARGETS_DN
10	5e−08	8 / 57	JI_RESPONSE_TO_FSH_DN
11	7e−08	6 / 24	AZARE_STAT3_TARGETS
12	9e−08	13 / 213	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
13	2e−07	32 / 1312	PUJANA_ATM_PCC_NETWORK
14	3e−07	33 / 1390	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
15	6e−07	24 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN

HM

Rank	p−value	#in/all	Geneset
1	0.002	5 / 94	HALLMARK_PROTEIN_SECRETION
2	0.002	7 / 192	HALLMARK_MTORC1_SIGNALING
3	0.012	4 / 96	HALLMARK_ANDROGEN_RESPONSE
4	0.013	5 / 149	HALLMARK_UV_RESPONSE_UP
5	0.023	5 / 173	HALLMARK_MITOTIC_SPINDLE
6	0.030	2 / 29	HALLMARK_NOTCH_SIGNALING
7	0.036	5 / 195	HALLMARK_G2M_CHECKPOINT
8	0.043	4 / 141	HALLMARK_UV_RESPONSE_DN
9	0.052	4 / 150	HALLMARK_APOPTOSIS
10	0.103	4 / 191	HALLMARK_P53_PATHWAY
11	0.105	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	0.108	4 / 194	HALLMARK_MYOGENESIS
13	0.158	2 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
14	0.188	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	0.202	3 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE

Immunome

Rank	p−value	#in/all	Geneset
1	0.09	1 / 10	Angelova_immune−metagene−TFH
2	0.11	1 / 13	Angelova_immune−metagene−immature_B−cells
3	0.12	1 / 14	Angelova_immune−metagene−eosinophil
4	0.16	1 / 19	Angelova_immune−metagene−activated_CD8
5	0.16	1 / 19	Angelova_immune−metagene−iDC
6	0.33	1 / 42	Angelova_immune−metagene−TGD
7	0.34	1 / 45	Angelova_immune−metagene−MDSC
8	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
9	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
10	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
12	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1.00	0 / 25	Angelova_immune−metagene−DC
14	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	7 / 210	Homuth_BMI−associated−genes_DN
2	0.186	1 / 22	DUMEAUX_High bmi enriched genes
3	0.186	1 / 22	DUMEAUX_Fasting enriched genes
4	1.000	0 / 62	DUMEAUX_Smoking enriched genes
5	1.000	0 / 10	DUMEAUX_Smoking literature genes up
6	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.000	0 / 150	Homuth_BMI−associated−genes_UP
14	1.000	0 / 14	Huan_blood−pressure_SBP−signature
15	1.000	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−18	99 / 5529	HOPP_Txn_elongation
2	1e−17	86 / 4261	HOPP_Txn_transition
3	2e−13	95 / 5908	HOPP_Active_promoter
4	4e−09	85 / 5682	HOPP_Weak_promoter
5	4e−07	9 / 102	ROSOLOWSKI_blue total
6	9e−07	77 / 5404	HOPP_Strong_enhancer
7	3e−04	20 / 906	SPANG_BCR DN
8	7e−04	58 / 4357	HOPP_Weak_txn
9	7e−04	60 / 4559	HOPP_Weak_enhancer
10	1e−03	19 / 955	SPANG_BCR UP
11	4e−03	28 / 1814	HOPP_Repetitive
12	6e−03	7 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
13	4e−02	2 / 34	TARTE_B−cell signature
14	5e−02	5 / 213	SPANG_IL21 DN
15	6e−02	5 / 227	SPANG_IL21 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 46	Tirosh_top50 correlated genes PC5
2	5e−03	7 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	7e−03	3 / 41	Tirosh_top50 correlated genes PC3
4	7e−03	11 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	7e−02	5 / 236	Gerber_wt/wt_group3−specific
6	8e−02	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	9e−02	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	3e−01	3 / 204	Landsberg_dedifferentiation_down
9	3e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
10	3e−01	1 / 39	Tirosh_melanoma specific genes
11	3e−01	1 / 44	Tirosh_top50 correlated genes PC2
12	3e−01	4 / 319	Gerber_wt/wt_melanoma−cells−SpotA
13	4e−01	1 / 47	Tirosh_G2/M phase specific genes
14	4e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
15	5e−01	1 / 65	Harbst_melanoma_highgrade_up

MF

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 11	RNA stem−loop binding
2	3e−04	92 / 7864	protein binding
3	9e−04	3 / 21	mitogen−activated protein kinase binding
4	1e−03	10 / 331	protein serine/threonine kinase activity
5	2e−03	3 / 28	Ran GTPase binding
6	3e−03	11 / 437	protein kinase activity
7	3e−03	3 / 31	SNAP receptor activity
8	5e−03	23 / 1402	nucleotide binding
9	6e−03	2 / 13	mitogen−activated protein kinase kinase kinase binding
10	6e−03	2 / 13	protein tyrosine kinase binding
11	6e−03	2 / 13	sulfuric ester hydrolase activity
12	6e−03	20 / 1185	ATP binding
13	7e−03	12 / 573	kinase activity
14	7e−03	2 / 14	lamin binding
15	7e−03	2 / 14	MAP kinase kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−08	19 / 448	hsa−miR−20b
2	4e−08	17 / 361	hsa−miR−130b
3	3e−07	14 / 275	hsa−miR−590−3p
4	4e−07	15 / 329	hsa−let−7b
5	1e−06	16 / 403	hsa−miR−106b
6	1e−06	14 / 314	hsa−miR−372
7	1e−06	8 / 87	hsa−miR−449b
8	2e−06	16 / 427	hsa−miR−17
9	3e−06	16 / 435	hsa−miR−93
10	3e−06	12 / 245	hsa−miR−302d
11	4e−06	10 / 167	hsa−miR−181c
12	4e−06	9 / 134	hsa−miR−141
13	5e−06	8 / 103	hsa−miR−576−3p
14	5e−06	11 / 216	hsa−miR−548l
15	6e−06	9 / 140	hsa−miR−520f

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.07	2 / 48	Burnham_viral_DN
2	0.10	2 / 57	Burnham_day1_vs_5_UP
3	0.13	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.23	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	0.40	1 / 54	Burnham_timecourse
6	0.47	1 / 68	Burnham_sep_vs_con_UP
7	0.49	1 / 71	Burnham_cap_fp_vs_con_UP
8	0.68	1 / 122	Terre_IMS_influenza_meta_signature
9	1.00	0 / 56	Burnham_sep_vs_con_DN
10	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
11	1.00	0 / 57	Burnham_viral_UP
12	1.00	0 / 52	Burnham_day1_vs_5_DN
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−38	33 / 136	Chaussabel_2,9_Cytosceleton
2	2e−15	25 / 355	WIRTH_Immune system
3	9e−05	8 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
4	2e−04	17 / 678	PROTEINATLAS_lymph node
5	3e−04	20 / 905	PROTEINATLAS_appendix
6	4e−04	15 / 594	PROTEINATLAS_parathyroid gland
7	5e−04	9 / 245	Chaussabel_3,9_Kinases
8	1e−03	20 / 1032	PROTEINATLAS_small intestine
9	2e−03	17 / 848	PROTEINATLAS_adrenal gland
10	3e−03	15 / 716	PROTEINATLAS_epididymis
11	3e−03	5 / 106	Chaussabel_2,11_Replication
12	3e−03	13 / 592	PROTEINATLAS_seminal vesicle
13	5e−03	18 / 989	PROTEINATLAS_tonsil
14	5e−03	19 / 1076	PROTEINATLAS_stomach
15	6e−03	14 / 708	PROTEINATLAS_thyroid gland

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	9e−05	29 / 1494	ICGC_Cebpbsc150_targets
2	1e−03	49 / 3564	ICGC_Taf1_targets
3	6e−03	19 / 1089	ICGC_Ets1_targets
4	6e−03	24 / 1508	ICGC_Mef2_targets
5	9e−03	48 / 3796	ICGC_Nficsc81335_targets
6	1e−02	24 / 1578	ICGC_GabpPcr2_targets
7	1e−02	30 / 2150	ICGC_Irf4_targets
8	1e−02	38 / 2899	ICGC_Nfatc1_targets
9	1e−02	47 / 3778	ICGC_Pol24_targets
10	1e−02	17 / 1025	ICGC_NrsfPcr1_targets
11	2e−02	47 / 3804	ICGC_Stat5_targets
12	2e−02	43 / 3420	ICGC_Bclaf101388_targets
13	2e−02	40 / 3150	ICGC_Creb1_targets
14	2e−02	45 / 3703	ICGC_Foxm1_targets
15	3e−02	51 / 4319	ICGC_Pou2_targets

D−Cluster

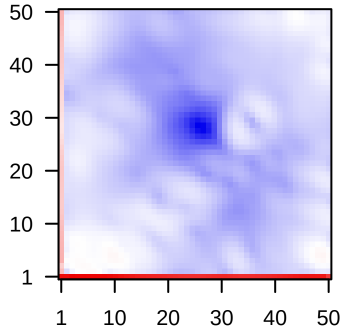
Spot Summary: G

metagenes = 16
genes = 312

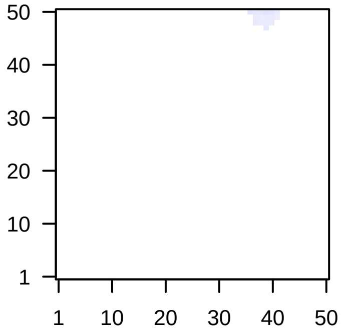
<r> metagenes = 0.98
<r> genes = 0.41
beta: r2= 9.18 / log p= −Inf

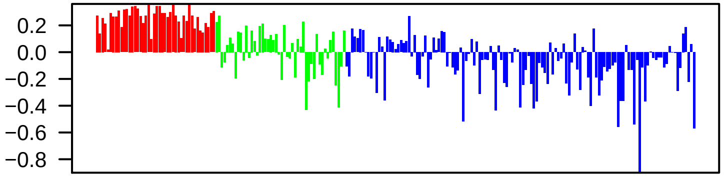
samples with spot = 31 (14 %)
mBL : 29 (65.9 %)
intermediate : 1 (2.1 %)
non−mBL : 1 (0.8 %)

Overview Map



Spot





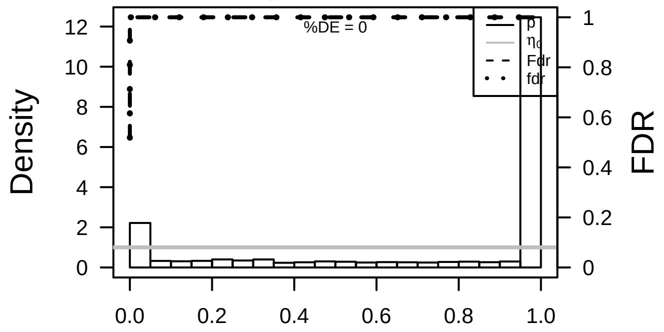
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205229_s_at	1.84	−2.18	0.38	COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
2	209980_s_at	1.66	−1.51	0.74	SHMT1	serine hydroxymethyltransferase 1 [Source:HGNC Symbol;Ac
3	219474_at	1.6	−1.32	0.47	C3orf52	chromosome 3 open reading frame 52 [Source:HGNC Symb
4	213610_s_at	1.38	−1.42	0.45	KLHL23	kelch like family member 23 [Source:HGNC Symbol;Acc:HG
5	203790_s_at	1.21	−1.38	0.53	RIDA	reactive intermediate imine deaminase A homolog [Source:H
6	210389_x_at	1.15	−1.08	0.51	TUBD1	tubulin delta 1 [Source:HGNC Symbol;Acc:HGNC:16811]
7	211767_at	1.12	−1.32	0.55	GINS4	GINS complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:
8	211814_s_at	1.09	−1.27	0.69	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
9	220258_s_at	1.05	−0.98	0.63	WRAP53	WD repeat containing antisense to TP53 [Source:HGNC Sym
10	212712_at	1.03	−0.91	0.46	CAMSAP1	calmodulin regulated spectrin associated protein 1 [Source:H
11	219311_at	1.03	−0.74	0.68	CEP76	centrosomal protein 76 [Source:HGNC Symbol;Acc:HGNC:2
12	202830_s_at	1.02	−0.91	0.43	SLC37A4	solute carrier family 37 member 4 [Source:HGNC Symbol;Ac
13	210415_s_at	1.01	−0.81	0.51	ODF2	outer dense fiber of sperm tails 2 [Source:HGNC Symbol;Acc
14	211793_s_at	1	−0.93	0.33	ABI2	abl interactor 2 [Source:HGNC Symbol;Acc:HGNC:24011]
15	205034_at	1	−1.56	0.65	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
16	218857_s_at	0.98	−1.13	0.39	ASRGL1	asparaginase like 1 [Source:HGNC Symbol;Acc:HGNC:1644
17	221219_s_at	0.97	−1.61	0.38	KLHDC4	kelch domain containing 4 [Source:HGNC Symbol;Acc:HGN
18	204603_at	0.97	−1.23	0.77	EXO1	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
19	215519_x_at	0.97	−0.9	0.38		
20	220892_s_at	0.95	−1.71	0.52	PSAT1	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	83 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−99	125 / 319	Mela	Gerber_wt/wt_melanoma−cells−SpotA
3	1e−99	162 / 966	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	1e−99	101 / 244	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
5	1e−99	125 / 431	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	3e−99	79 / 137	GSE	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
7	6e−89	90 / 254	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	2e−85	103 / 409	Canc	Lembcke_Normal vs Adenoma
9	1e−83	10 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1e−83	10 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1e−79	108 / 526	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	3e−79	101 / 439	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
13	7e−77	121 / 758	GSE	NUYTTEN_EZH2_TARGETS_DN
14	1e−76	78 / 219	Refe	WIRTH_GC B−cells
15	3e−68	67 / 174	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	2e−66	72 / 226	GSE	ZHANG_TLX_TARGETS_60HR_DN
17	1e−63	52 / 93	GSE	CROONQUIST_IL6_DEPRIVATION_DN
18	3e−62	97 / 575	GSE	CAIRO_HEPATOBLASTOMA_CLASSES_UP
19	5e−62	78 / 321	GSE	BLUM_RESPONSE_TO_SALIRASIB_DN
20	5e−62	123 / 1052	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
21	2e−61	84 / 400	GSE	PUJANA_BRCA2_PCC_NETWORK
22	2e−59	50 / 95	GSE	ODONNELL_TFRC_TARGETS_DN
23	2e−58	74 / 307	GSE	VECCHI_GASTRIC_CANCER_EARLY_UP
24	7e−57	62 / 195	HM	HALLMARK_G2M_CHECKPOINT
25	2e−56	90 / 548	GSE	BENPORATH_CYCLING_GENES
26	3e−55	60 / 187	HM	HALLMARK_E2F_TARGETS
27	5e−55	51 / 117	GSE	CHANG_CYCLING_GENES
28	1e−54	83 / 466	GSE	BERENJENO_TRANSFORMED_BY_RHOA_UP
29	2e−54	60 / 192	Lymp	Victora_Dark zone signature
30	3e−53	42 / 70	GSE	CROONQUIST_NRAS_SIGNALING_DN
31	2e−52	67 / 280	GSE	MANALO_HYPOXIA_DN
32	5e−52	64 / 250	GSE	HORIUCHI_WTAP_TARGETS_DN
33	3e−51	37 / 52	GSE	KANG_DOXORUBICIN_RESISTANCE_UP
34	1e−50	95 / 726	GSE	PUJANA_CHEK2_PCC_NETWORK
35	2e−50	62 / 241	GSE	BASAKI_YBX1_TARGETS_UP
36	2e−50	52 / 147	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
37	4e−50	42 / 79	Mela	Tirosh_core cycling genes in low− and high−proliferation melanoma
38	1e−48	42 / 84	GSE	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
39	3e−48	69 / 347	GSE	REACTOME_CELL_CYCLE
40	4e−48	53 / 169	GSE	FUJII_YBX1_TARGETS_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.002	8 / 107	HORVATH_aging_genes meth UP
2	1.000	0 / 92	HORVATH_aging_genes meth DOWN
3	1.000	0 / 47	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−42	74 / 497	cell cycle
2	7e−38	57 / 307	cell division
3	6e−31	37 / 137	DNA replication
4	2e−21	25 / 91	sister chromatid cohesion
5	2e−17	35 / 281	DNA repair
6	2e−16	19 / 70	chromosome segregation
7	2e−14	20 / 101	mitotic cell cycle
8	9e−14	34 / 351	cellular response to DNA damage stimulus
9	2e−11	11 / 31	DNA replication initiation
10	6e−11	18 / 119	G2/M transition of mitotic cell cycle
11	1e−10	8 / 14	chromosome condensation
12	2e−10	9 / 21	mitotic sister chromatid segregation
13	7e−10	15 / 91	G1/S transition of mitotic cell cycle
14	2e−09	16 / 113	regulation of signal transduction by p53 class mediator
15	2e−09	13 / 71	regulation of G2/M transition of mitotic cell cycle

Cancer

Rank	p−value	#in/all	Geneset
1	2e−85	103 / 409	Lembcke_Normal vs Adenoma
2	1e−83	10 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	3e−17	7 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	2e−06	8 / 41	PanCan_DNARepair_geneset_nanostring
5	2e−05	12 / 130	PanCan_CC+Apop_geneset_nanostring
6	4e−05	4 / 10	GENTLES_modul3
7	4e−05	7 / 45	KUIPER_MM poor survival
8	2e−04	7 / 58	SHAUGHNESSY_MM high risk
9	2e−04	4 / 15	BEN−PORATH_UP
10	1e−03	1 / 15	RHODES_CANCER_META_SIGNATURE
11	2e−03	3 / 13	GENTLES_modul1
12	4e−03	3 / 15	GENTLES_modul2
13	4e−03	3 / 16	WOLFER_overlap genes
14	3e−02	3 / 32	KUIPER_MM good survival
15	3e−02	2 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	7e−30	189 / 4579	nucleus
2	7e−27	132 / 2541	nucleoplasm
3	3e−25	46 / 324	chromosome
4	1e−19	26 / 118	chromosome, centromeric region
5	2e−17	27 / 157	spindle
6	1e−16	22 / 101	kinetochore
7	1e−15	19 / 77	condensed chromosome kinetochore
8	4e−15	36 / 354	centrosome
9	2e−12	18 / 98	spindle pole
10	3e−12	55 / 936	cytoskeleton
11	6e−11	11 / 34	kinesin complex
12	1e−10	27 / 292	microtubule organizing center
13	4e−10	129 / 3805	cytosol
14	7e−10	24 / 251	microtubule
15	4e−09	8 / 20	spindle midzone

Chr

Rank	p−value	#in/all	Geneset
1	6e−05	21 / 382	Chr 15
2	7e−02	17 / 548	Chr 16
3	1e−01	11 / 333	Chr 22
4	1e−01	35 / 1325	Chr 1
5	1e−01	8 / 242	Chr 13
6	2e−01	14 / 492	Chr 9
7	2e−01	20 / 776	Chr 17
8	2e−01	13 / 490	Chr 10
9	3e−01	5 / 184	Chr 18
10	4e−01	10 / 437	Chr 8
11	5e−01	9 / 403	Chr 14
12	6e−01	10 / 480	Chr 4
13	6e−01	11 / 554	Chr 5
14	7e−01	16 / 833	Chr 19
15	8e−01	2 / 139	Chr 21

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−33	262 / 8370	natural killer cells peripheral blood_2_TssAFlnk
2	6e−33	259 / 8200	monocytes peripheral blood_2_TssAFlnk
3	2e−32	259 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
4	3e−32	224 / 6099	HSC_4_Tx
5	7e−32	254 / 7930	Tregulatory cells peripheral blood_1_TssA
6	1e−31	254 / 7957	Tcells peripheral blood_2_TssAFlnk
7	2e−31	260 / 8406	Bcells peripheral blood_2_TssAFlnk
8	5e−31	260 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
9	1e−30	248 / 7635	monocytes peripheral blood_1_TssA
10	1e−30	258 / 8322	T CD8+ naive cells peripheral blood_1_TssA
11	3e−30	264 / 8816	Thelper cells peripheral blood_2_TssAFlnk
12	6e−30	220 / 6068	4_Tx_ESC_Endoderm
13	3e−29	244 / 7489	monocytes peripheral blood_5_TxWk
14	1e−28	206 / 5456	5_Tx_Neuronal_Progenitor
15	3e−28	248 / 7833	Bcells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−21	33 / 184	Kosinski_lower−crypt−long−list
2	7e−10	37 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	1e−05	30 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	4e−04	5 / 31	Kosinski_lower−crypt−short−list
5	1e−02	2 / 8	Boland_CRC−MMR−system
6	1e−02	36 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	3e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
8	4e−02	18 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
9	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
10	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
11	5e−02	2 / 18	Boland_CRC−MSI−A6−A10
12	8e−02	45 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	1e−01	1 / 6	Marisa_CRC−C6
14	1e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
15	2e−01	1 / 8	KIM_MSI−in−EC

Glioma

Rank	p−value	#in/all	Geneset
1	1e−99	83 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	9e−22	20 / 47	developing astrocytes
3	1e−19	21 / 66	Weller_LGG_gradeII−vs−III_DOWN
4	3e−08	59 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	1e−06	60 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	4e−04	7 / 64	cultured astroglia vs. in vivo astrocytes
7	4e−03	5 / 49	OPC
8	6e−03	23 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	4e−02	1 / 2	Phillips Prolif up vs PN & MES
10	3e−01	1 / 15	Mukasa_UP_in_GBM
11	3e−01	1 / 16	VERHAAK_PN subtype
12	3e−01	2 / 58	Stuehler_Proteins_up_in_STS
13	4e−01	2 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
14	4e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
15	4e−01	2 / 64	Weller_LGG_A_vs_O_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	162 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	1e−99	101 / 244	KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	1e−99	125 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	3e−99	79 / 137	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	6e−89	90 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
6	1e−83	10 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	1e−79	108 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
8	3e−79	101 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	7e−77	121 / 758	NUYTTEN_EZH2_TARGETS_DN
10	3e−68	67 / 174	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	2e−66	72 / 226	ZHANG_TLX_TARGETS_60HR_DN
12	1e−63	52 / 93	CROONQUIST_IL6_DEPRIVATION_DN
13	3e−62	97 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
14	5e−62	78 / 321	BLUM_RESPONSE_TO_SALIRASIB_DN
15	5e−62	123 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN

HM

Rank	p−value	#in/all	Geneset
1	7e−57	62 / 195	HALLMARK_G2M_CHECKPOINT
2	3e−55	60 / 187	HALLMARK_E2F_TARGETS
3	3e−17	28 / 173	HALLMARK_MITOTIC_SPINDLE
4	2e−07	10 / 55	HALLMARK_MYC_TARGETS_V2
5	6e−05	14 / 192	HALLMARK_MTORC1_SIGNALING
6	3e−04	10 / 122	HALLMARK_SPERMATOGENESIS
7	7e−04	12 / 190	HALLMARK_MYC_TARGETS_V1
8	7e−03	8 / 133	HALLMARK_DNA_REPAIR
9	4e−02	8 / 182	HALLMARK_GLYCOLYSIS
10	5e−02	8 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
11	2e−01	5 / 139	HALLMARK_FATTY_ACID_METABOLISM
12	3e−01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	3e−01	3 / 97	HALLMARK_PEROXISOME
14	4e−01	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	4e−01	5 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION

Immunome

Rank	p−value	#in/all	Geneset
1	5e−25	18 / 26	Angelova_immune−metagene−activated_CD4
2	3e−02	2 / 12	Angelova_immune−metagene−memory_B−cells
3	6e−02	2 / 19	Angelova_immune−metagene−activated_CD8
4	6e−01	1 / 38	Angelova_immune−metagene−mast−cells
5	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
6	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1e+00	0 / 25	Angelova_immune−metagene−DC
10	1e+00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1e+00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1e+00	0 / 14	Angelova_immune−metagene−eosinophil
13	1e+00	0 / 19	Angelova_immune−metagene−iDC
14	1e+00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1e+00	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.8	3 / 210	Homuth_BMI−associated−genes_DN
2	0.8	2 / 150	Homuth_BMI−associated−genes_UP
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 22	DUMEAUX_High bmi enriched genes
13	1.0	0 / 22	DUMEAUX_Fasting enriched genes
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−54	60 / 192	Victora_Dark zone signature
2	1e−31	212 / 5529	HOPP_Txn_elongation
3	2e−27	47 / 305	TARTE_Plasmablast signature
4	1e−20	201 / 5908	HOPP_Active_promoter
5	1e−15	154 / 4261	HOPP_Txn_transition
6	2e−14	20 / 99	Sha_BL UP
7	2e−09	50 / 955	SPANG_BCR UP
8	2e−07	15 / 135	DAVE_BL−vs−DLBCL
9	2e−06	12 / 102	ROSOLOWSKI_blue total
10	7e−05	152 / 5682	HOPP_Weak_promoter
11	5e−03	3 / 17	DAVE_c−myc BL UP
12	1e−02	4 / 45	SPANG_BAFF 9hrs DN
13	2e−02	132 / 5404	HOPP_Strong_enhancer
14	6e−02	105 / 4357	HOPP_Weak_txn
15	7e−02	3 / 45	Monti_BCR_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−99	125 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	4e−50	42 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
3	7e−45	32 / 44	Tirosh_top50 correlated genes PC2
4	2e−41	31 / 47	Tirosh_G2/M phase specific genes
5	9e−21	18 / 38	Tirosh_G1/S phase specific genes
6	8e−20	21 / 65	Harbst_melanoma_highgrade_up
7	5e−06	8 / 46	Tirosh_top50 correlated genes PC5
8	8e−02	1 / 4	Melanoma Epi−Enzyme Cluster 3
9	8e−02	1 / 4	Melanoma Epi−Enzyme Cluster 5
10	5e−01	6 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	8e−01	1 / 68	Tirosh_housekeeping_genes
12	8e−01	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
13	8e−01	1 / 81	Tirosh_Genes in the MITF program
14	8e−01	1 / 85	Tirosh_AXL−signature
15	9e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC

MF

Rank	p−value	#in/all	Geneset
1	4e−11	61 / 1185	ATP binding
2	4e−09	63 / 1402	nucleotide binding
3	4e−08	209 / 7864	protein binding
4	1e−07	24 / 328	chromatin binding
5	2e−07	12 / 83	microtubule motor activity
6	8e−07	8 / 37	exonuclease activity
7	9e−07	17 / 196	microtubule binding
8	8e−06	14 / 161	ATPase activity
9	2e−05	57 / 1541	DNA binding
10	2e−05	10 / 90	nuclease activity
11	5e−05	45 / 1161	RNA binding
12	5e−05	5 / 20	ATP−dependent microtubule motor activity, plus−end−directed
13	5e−05	9 / 81	single−stranded DNA binding
14	3e−04	4 / 16	3'−5' exonuclease activity
15	4e−04	8 / 83	motor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	5 / 31	hsa−miR−661
2	3e−03	5 / 46	hsa−miR−208a
3	9e−03	5 / 61	hsa−miR−619
4	1e−02	4 / 41	hsa−miR−518e*
5	1e−02	2 / 8	hsa−miR−202*
6	1e−02	3 / 24	hsa−miR−197
7	2e−02	6 / 95	hsa−miR−376a
8	2e−02	6 / 98	hsa−miR−520a−5p
9	2e−02	5 / 72	hsa−miR−378
10	2e−02	8 / 157	hsa−miR−374a
11	2e−02	8 / 160	hsa−miR−330−3p
12	2e−02	3 / 29	hsa−miR−1229
13	2e−02	4 / 52	hsa−miR−324−5p
14	3e−02	5 / 84	hsa−miR−525−5p
15	3e−02	4 / 58	hsa−miR−331−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	1e−04	11 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	1e−01	5 / 122	Terre_IMS_influenza_meta_signature
3	2e−01	6 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	7e−01	1 / 54	Burnham_timecourse
5	7e−01	1 / 57	Burnham_viral_UP
6	7e−01	1 / 57	Burnham_day1_vs_5_UP
7	8e−01	1 / 71	Burnham_cap_fp_vs_con_UP
8	1e+00	0 / 68	Burnham_sep_vs_con_UP
9	1e+00	0 / 56	Burnham_sep_vs_con_DN
10	1e+00	0 / 48	Burnham_cap_fp_vs_con_DN
11	1e+00	0 / 48	Burnham_viral_DN
12	1e+00	0 / 52	Burnham_day1_vs_5_DN
13	1e+00	0 / 18	Scicluna_UP
14	1e+00	0 / 41	Scicluna_DN
15	1e+00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−76	78 / 219	WIRTH_GC B−cells
2	1e−08	39 / 677	PROTEINATLAS_esophagus
3	3e−08	38 / 678	PROTEINATLAS_lymph node
4	9e−08	36 / 645	PROTEINATLAS_bone marrow
5	6e−07	48 / 1081	PROTEINATLAS_testis
6	8e−07	30 / 527	PROTEINATLAS_oral mucosa
7	3e−06	37 / 776	PROTEINATLAS_skin
8	4e−06	43 / 989	PROTEINATLAS_tonsil
9	6e−06	45 / 1072	PROTEINATLAS_duodenum
10	2e−05	43 / 1048	PROTEINATLAS_rectum
11	2e−05	37 / 848	PROTEINATLAS_adrenal gland
12	1e−04	40 / 1032	PROTEINATLAS_small intestine
13	1e−04	35 / 861	PROTEINATLAS_nasopharynx
14	2e−04	41 / 1076	PROTEINATLAS_stomach
15	2e−04	43 / 1161	PROTEINATLAS_colon

Telomeres

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 13	Alternative lengthening of telomeres
2	2e−02	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	8e−11	62 / 1241	KIM_MYC targets
2	1e−07	115 / 3564	ICGC_Taf1_targets
3	1e−06	117 / 3796	ICGC_Nficsc81335_targets
4	2e−06	101 / 3150	ICGC_Creb1_targets
5	5e−06	111 / 3630	ICGC_Sp1_targets
6	6e−06	114 / 3769	ICGC_Pmlsc71910_targets
7	1e−05	109 / 3608	ICGC_Tcf12_targets
8	1e−05	111 / 3703	ICGC_Foxm1_targets
9	1e−04	121 / 4319	ICGC_Pou2_targets
10	1e−04	109 / 3804	ICGC_Stat5_targets
11	1e−04	127 / 4602	ICGC_Elf1_targets
12	1e−04	42 / 1107	ICGC_Myc_targets
13	6e−04	113 / 4131	ICGC_Tcf3_targets
14	1e−03	104 / 3778	ICGC_Pol24_targets
15	1e−03	115 / 4278	ICGC_Yy1_targets

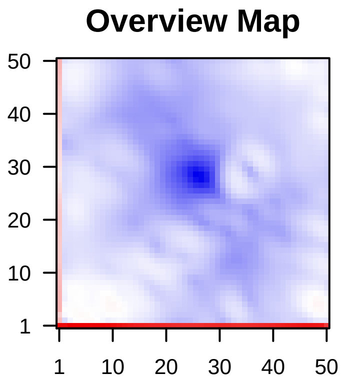
D−Cluster

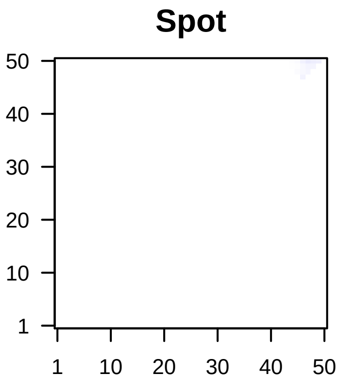
Spot Summary: H

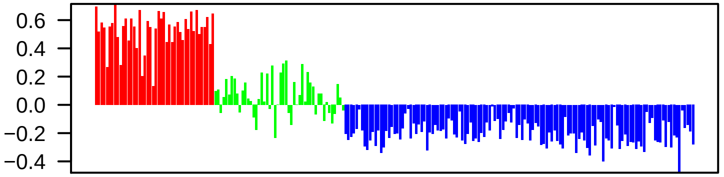
metagenes = 15
genes = 280

<r> metagenes = 0.98
<r> genes = 0.33
beta: r2= 16.92 / log p= −Inf

samples with spot = 46 (20.8 %)
mBL : 42 (95.5 %)
intermediate : 4 (8.3 %)





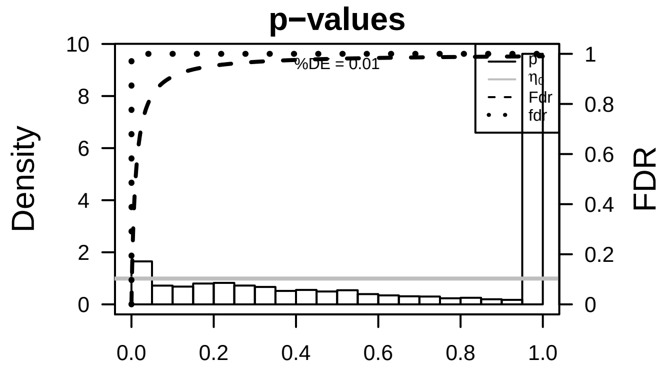


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206660_at	2.83	−0.99	0.51	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
2	221349_at	2.76	−0.89	0.72	VPREB1	V−set pre−B cell surrogate light chain 1 [Source:HGNC Symb
3	206413_s_at	2.76	−1.22	0.37	TCL1B	T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG
4	204914_s_at	2.24	−0.89	0.67	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
5	213920_at	2.19	−1.02	0.52	CUX2	cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934
6	219855_at	2.18	−0.78	0.46	NUDT11	nudix hydrolase 11 [Source:HGNC Symbol;Acc:HGNC:18011
7	213674_x_at	2.16	−1.9	0.35		immunoglobulin heavy constant delta [Source:HGNC Symbol
8	38037_at	2.16	−1.11	0.59	HBEGF	heparin binding EGF like growth factor [Source:HGNC Symbo
9	204915_s_at	2.16	−0.86	0.61	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
10	209590_at	2.09	−1.32	0.8	BMP7	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:H
11	210244_at	2.07	−1.33	0.37	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc
12	203821_at	2.07	−1.19	0.56	HBEGF	heparin binding EGF like growth factor [Source:HGNC Symbo
13	219737_s_at	2.07	−1.48	0.69	PCDH9	protocadherin 9 [Source:HGNC Symbol;Acc:HGNC:8661]
14	204913_s_at	2.07	−1.11	0.66	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
15	205122_at	2	−1	0.61	TMEFF1	transmembrane protein with EGF like and two follistatin like d
16	209469_at	1.96	−1.84	0.43	GPM6A	glycoprotein M6A [Source:HGNC Symbol;Acc:HGNC:4460]
17	203435_s_at	1.95	−1.72	0.71	MME	membrane metalloendopeptidase [Source:HGNC Symbol;Acc
18	213280_at	1.95	−0.83	0.57	RAP1GAP2	RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac
19	209570_s_at	1.94	−0.79	0.52	NSG1	neuronal vesicle trafficking associated 1 [Source:HGNC Sym
20	217276_x_at	1.91	−1.16	0.56		serine hydrolase−like (pseudogene) [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−49	32 / 42	GSEA	HUMMEL_BURKITTS_LYMPHOMA_UP
2	1e−28	37 / 192	Lymph	Victora_Dark zone signature
3	7e−27	28 / 99	Lymph	Sha_BL UP
4	7e−22	13 / 15	Lymph	BENTINK_mBL UP
5	4e−20	61 / 955	Lymph	SPANG_BCR UP
6	5e−17	31 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
7	1e−16	10 / 12	Cance	BENTINK_e2f3.2
8	7e−15	28 / 263	Lymph	SPANG_CD40 6hrs UP
9	6e−12	23 / 227	Lymph	SPANG_IL21 UP
10	2e−11	6 / 6	Lymph	MASCQUE_mBL UP
11	1e−10	20 / 195	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
12	1e−10	17 / 135	Lymph	DAVE_BL−vs−DLBCL
13	4e−10	12 / 61	GSEA	BASSO_CD40_SIGNALING_DN
14	1e−09	34 / 615	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
15	2e−08	6 / 12	Cance	BENTINK_ras.1
16	2e−08	35 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
17	9e−08	24 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
18	2e−07	5 / 9	Lymph	DAVE_BL UP
19	4e−07	21 / 340	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
20	6e−07	30 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
21	7e−07	9 / 60	GSEA	PYEON_HPV_POSITIVE_TUMORS_UP
22	8e−07	9 / 61	GSEA	BILBAN_B_CLL_LPL_UP
23	1e−06	38 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
24	2e−06	38 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
25	3e−06	131 / 5682	Lymph	HOPP_Weak_promoter
26	3e−06	50 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
27	8e−06	21 / 414	BP	negative regulation of transcription, DNA−templated
28	1e−05	13 / 176	GSEA	BILD_E2F3_ONCOGENIC_SIGNATURE
29	1e−05	28 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
30	1e−05	26 / 608	GSEA	SMID_BREAST_CANCER_BASAL_UP
31	2e−05	15 / 240	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_DN
32	2e−05	29 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
33	2e−05	9 / 87	miRN	hsa−miR−449b
34	2e−05	18 / 335	GSEA	BENPORATH_ES_1
35	2e−05	12 / 160	GSEA	PUJANA_XPRSS_INT_NETWORK
36	2e−05	18 / 337	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
37	2e−05	21 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
38	4e−05	26 / 641	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
39	4e−05	36 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
40	5e−05	7 / 57	Pneu	Burnham_day1_vs_5_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	3 / 107	HORVATH_aging_genes meth UP
2	0.5	2 / 92	HORVATH_aging_genes meth DOWN
3	0.6	1 / 47	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	

CC

Rank	p−value	#in/all	Geneset
1	2e−04	66 / 2541	nucleoplasm
2	4e−04	105 / 4701	cytoplasm
3	9e−04	101 / 4579	nucleus
4	9e−03	3 / 25	condensed chromosome
5	1e−02	2 / 11	Fanconi anaemia nuclear complex
6	2e−02	6 / 118	chromosome, centromeric region
7	2e−02	3 / 33	cytosolic small ribosomal subunit
8	3e−02	13 / 416	macromolecular complex
9	3e−02	3 / 39	cell leading edge
10	3e−02	24 / 936	cytoskeleton
11	3e−02	2 / 16	neuron projection terminus
12	3e−02	4 / 71	ciliary basal body
13	4e−02	3 / 44	nuclear chromosome
14	4e−02	9 / 268	intracellular ribonucleoprotein complex
15	4e−02	2 / 20	small ribosomal subunit

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	38 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	2e−04	32 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
3	4e−03	129 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	2e−02	12 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
5	3e−02	20 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	3e−02	2 / 16	Budinska_B_Lower crypt−like_UP
7	5e−02	16 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
8	6e−02	15 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	6e−02	21 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
10	6e−02	38 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
11	6e−02	6 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	8e−02	1 / 5	Marisa_CRC−C5
13	8e−02	7 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	1e−01	6 / 184	Kosinski_lower−crypt−long−list
15	1e−01	1 / 7	Juehling−MSI−enriched−in−7

HM

Rank	p−value	#in/all	Geneset
1	0.006	9 / 195	HALLMARK_G2M_CHECKPOINT
2	0.018	8 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.041	7 / 187	HALLMARK_E2F_TARGETS
4	0.056	3 / 51	HALLMARK_TGF_BETA_SIGNALING
5	0.087	2 / 29	HALLMARK_NOTCH_SIGNALING
6	0.093	5 / 141	HALLMARK_UV_RESPONSE_DN
7	0.109	6 / 191	HALLMARK_P53_PATHWAY
8	0.115	6 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	0.117	6 / 195	HALLMARK_KRAS_SIGNALING_DN
10	0.137	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.174	5 / 173	HALLMARK_MITOTIC_SPINDLE
12	0.176	5 / 174	HALLMARK_ADIPOGENESIS
13	0.182	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
14	0.230	5 / 192	HALLMARK_MTORC1_SIGNALING
15	0.399	4 / 188	HALLMARK_HYPOXIA

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−28	37 / 192	Victora_Dark zone signature
2	7e−27	28 / 99	Sha_BL UP
3	7e−22	13 / 15	BENTINK_mBL UP
4	4e−20	61 / 955	SPANG_BCR UP
5	7e−15	28 / 263	SPANG_CD40 6hrs UP
6	6e−12	23 / 227	SPANG_IL21 UP
7	2e−11	6 / 6	MASCQUE_mBL UP
8	1e−10	17 / 135	DAVE_BL−vs−DLBCL
9	2e−07	5 / 9	DAVE_BL UP
10	3e−06	131 / 5682	HOPP_Weak_promoter
11	9e−05	129 / 5908	HOPP_Active_promoter
12	2e−04	4 / 17	Aukema_BCL2 UP_BCL6 DN
13	2e−04	8 / 96	SPANG_LPS 6hrs UP
14	7e−04	12 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	8e−04	116 / 5404	HOPP_Strong_enhancer

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 87	hsa−miR−449b
2	2e−04	13 / 236	hsa−miR−34a
3	3e−03	10 / 203	hsa−miR−449a
4	3e−03	9 / 171	hsa−miR−203
5	3e−03	3 / 17	hsa−miR−151−5p
6	3e−03	7 / 111	hsa−miR−656
7	3e−03	8 / 145	hsa−miR−607
8	6e−03	5 / 68	hsa−miR−1265
9	8e−03	4 / 47	hsa−miR−370
10	9e−03	10 / 244	hsa−miR−34c−5p
11	1e−02	3 / 26	hsa−miR−934
12	1e−02	4 / 49	hsa−miR−671−5p
13	1e−02	6 / 107	hsa−miR−24
14	1e−02	7 / 151	hsa−miR−1283
15	2e−02	5 / 86	hsa−miR−297

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	

BP

Rank	p−value	#in/all	Geneset
1	8e−06	21 / 414	negative regulation of transcription, DNA−templated
2	1e−03	3 / 12	positive regulation of endothelial cell apoptotic process
3	1e−03	3 / 13	replicative senescence
4	3e−03	7 / 110	regulation of cell cycle
5	3e−03	3 / 18	negative regulation of phosphorylation
6	4e−03	3 / 19	translational elongation
7	4e−03	3 / 20	negative regulation of cell cycle arrest
8	6e−03	4 / 42	interleukin−12−mediated signaling pathway
9	7e−03	3 / 23	positive regulation of pri−miRNA transcription from RNA polymerase II promot
10	7e−03	5 / 71	regulation of G2/M transition of mitotic cell cycle
11	8e−03	3 / 24	cellular response to ionizing radiation
12	9e−03	11 / 281	DNA repair
13	9e−03	6 / 105	negative regulation of cell growth
14	1e−02	3 / 26	positive regulation of glucose import
15	1e−02	3 / 26	sphingolipid metabolic process

Chr

Rank	p−value	#in/all	Geneset
1	6e−04	19 / 480	Chr 4
2	3e−02	3 / 41	Chr Y
3	8e−02	11 / 403	Chr 14
4	1e−01	9 / 333	Chr 22
5	1e−01	7 / 242	Chr 13
6	2e−01	15 / 700	Chr 12
7	3e−01	14 / 669	Chr 6
8	3e−01	26 / 1325	Chr 1
9	4e−01	7 / 369	Chr 20
10	5e−01	9 / 492	Chr 9
11	5e−01	8 / 437	Chr 8
12	5e−01	10 / 585	Chr 7
13	6e−01	8 / 490	Chr 10
14	6e−01	9 / 554	Chr 5
15	6e−01	3 / 184	Chr 18

Glioma

Rank	p−value	#in/all	Geneset
1	0.01	6 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	0.03	25 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	0.04	7 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
4	0.05	3 / 47	developing astrocytes
5	0.06	12 / 421	Down_b
6	0.06	2 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
7	0.08	3 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
8	0.08	3 / 59	GIEZELT_GBM_STS_up_VS_LTS
9	0.09	2 / 30	Shaw_responders_down_in_oligo_glioma
10	0.10	1 / 6	Shaw_responders_up_in_oligo_glioma
11	0.10	3 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.10	2 / 32	WIRTH_PN subtype
13	0.10	2 / 32	Shaw_down_in_1p19q
14	0.11	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
15	0.12	32 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN

Immunome

Rank	p−value	#in/all	Geneset
1	0.07	2 / 25	Angelova_immune−metagene−DC
2	0.16	1 / 10	Angelova_immune−metagene−neutrophils
3	0.20	1 / 13	Angelova_immune−metagene−activated_B−cells
4	0.20	1 / 13	Angelova_immune−metagene−immature_B−cells
5	0.25	1 / 17	Angelova_immune−metagene−central_memory_CD8
6	0.27	1 / 18	Angelova_CRC_immunostimulators
7	0.33	1 / 23	Angelova_immune−metagene−Th2
8	0.36	1 / 26	Angelova_immune−metagene−activated_CD4
9	0.54	1 / 45	Angelova_immune−metagene−MDSC
10	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
11	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
12	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
14	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.00	0 / 14	Angelova_immune−metagene−eosinophil

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−04	15 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	2e−02	15 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	3e−02	1 / 2	Melanoma Epi−Enzyme Cluster 6
4	5e−02	3 / 47	Tirosh_G2/M phase specific genes
5	5e−02	4 / 83	TCGA_melanoma_immune_high
6	7e−02	1 / 4	Melanoma Epi−Enzyme Cluster 5
7	1e−01	3 / 65	Harbst_melanoma_highgrade_up
8	1e−01	3 / 68	Tirosh_housekeeping_genes
9	2e−01	3 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
10	2e−01	2 / 44	Tirosh_top50 correlated genes PC2
11	2e−01	2 / 46	Tirosh_top50 correlated genes PC5
12	2e−01	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
13	3e−01	6 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	3e−01	4 / 171	Landsberg_dedifferentiation_up
15	4e−01	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC

Pneumonia

Rank	p−value	#in/all	Geneset
1	5e−05	7 / 57	Burnham_day1_vs_5_UP
2	3e−02	3 / 41	Scicluna_DN
3	7e−02	3 / 57	Burnham_viral_UP
4	2e−01	2 / 56	Burnham_sep_vs_con_DN
5	3e−01	1 / 18	Scicluna_UP
6	3e−01	2 / 68	Burnham_sep_vs_con_UP
7	6e−01	1 / 48	Burnham_cap_fp_vs_con_DN
8	7e−01	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
9	7e−01	1 / 71	Burnham_cap_fp_vs_con_UP
10	1e+00	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
11	1e+00	0 / 48	Burnham_viral_DN
12	1e+00	0 / 52	Burnham_day1_vs_5_DN
13	1e+00	0 / 54	Burnham_timecourse
14	1e+00	0 / 37	Sweeney_viral_up
15	1e+00	0 / 33	Sweeney_viral_dn

TF

Rank	p−value	#in/all	Geneset
1	0.02	67 / 3121	ICGC_Egr1_targets
2	0.02	43 / 1848	ICGC_Pbx3_targets
3	0.03	78 / 3796	ICGC_Nficsc81335_targets
4	0.05	75 / 3703	ICGC_Foxm1_targets
5	0.05	25 / 1032	ICGC_Usf1_targets
6	0.05	70 / 3435	ICGC_Ebfsc137065_targets
7	0.05	29 / 1241	KIM_MYC targets
8	0.05	81 / 4072	ICGC_Mta3_targets
9	0.06	90 / 4602	ICGC_Elf1_targets
10	0.07	1 / 4	MYC_TF and cofactors
11	0.07	71 / 3564	ICGC_Taf1_targets
12	0.08	63 / 3150	ICGC_Creb1_targets
13	0.10	71 / 3630	ICGC_Sp1_targets
14	0.10	83 / 4319	ICGC_Pou2_targets
15	0.11	92 / 4851	ICGC_Runx3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	1e−16	10 / 12	BENTINK_e2f3.2
2	2e−08	6 / 12	BENTINK_ras.1
3	7e−05	4 / 14	BENTINK_src.10
4	3e−04	11 / 186	SPANG_LPS−index2
5	6e−04	17 / 409	Lembcke_Normal vs Adenoma
6	1e−02	2 / 10	GENTLES_modul3
7	2e−02	2 / 13	GENTLES_modul11
8	2e−02	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
9	2e−02	6 / 130	PanCan_CC+Apop_geneset_nanostring
10	4e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
11	5e−02	0 / 14	LIU_PROSTATE_CANCER_DN
12	1e−01	6 / 187	PanCan_PI3K_geneset_nanostring
13	1e−01	2 / 32	KUIPER_MM good survival
14	1e−01	3 / 72	PanCan_Wnt_geneset_nanostring
15	1e−01	0 / 11	LIU_PROSTATE_CANCER_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−11	198 / 9160	2_TssA_Neuronal_Progenitor
2	8e−11	187 / 8406	Bcells peripheral blood_2_TssAFlnk
3	3e−10	181 / 8068	Thelper cells peripheral blood_1_TssA
4	5e−10	184 / 8322	T CD8+ naive cells peripheral blood_1_TssA
5	3e−09	175 / 7833	Bcells peripheral blood_1_TssA
6	5e−09	165 / 7225	Overlap_fetal_midbrain_ReprPC
7	1e−08	187 / 8766	2_TssA_Melanocytes
8	1e−08	189 / 8918	1_TssA_ESC_Mesoderm
9	1e−08	185 / 8641	1_TssA_ESC_Endoderm
10	2e−08	187 / 8816	Thelper cells peripheral blood_2_TssAFlnk
11	6e−08	196 / 9544	HSC_2_TssAFlnk
12	7e−08	178 / 8275	2_TssA_Fibroblasts
13	9e−08	171 / 7835	HSC_1_TssA
14	1e−07	192 / 9298	Bcells peripheral blood_7_Enh
15	7e−07	167 / 7751	natural killer cells peripheral blood_1_TssA

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−49	32 / 42	HUMMEL_BURKITTS_LYMPHOMA_UP
2	5e−17	31 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
3	1e−10	20 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
4	4e−10	12 / 61	BASSO_CD40_SIGNALING_DN
5	1e−09	34 / 615	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
6	2e−08	35 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	9e−08	24 / 400	PUJANA_BRCA2_PCC_NETWORK
8	4e−07	21 / 340	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
9	6e−07	30 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
10	7e−07	9 / 60	PYEON_HPV_POSITIVE_TUMORS_UP
11	8e−07	9 / 61	BILBAN_B_CLL_LPL_UP
12	1e−06	38 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
13	3e−06	50 / 1527	PUJANA_BRCA1_PCC_NETWORK
14	1e−05	13 / 176	BILD_E2F3_ONCOGENIC_SIGNATURE
15	1e−05	28 / 669	JOHNSTONE_PARVB_TARGETS_3_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	3 / 32	Marjolein_ageing−genes_DN
2	0.29	5 / 210	Homuth_BMI−associated−genes_DN
3	0.32	1 / 22	DUMEAUX_Fasting enriched genes
4	0.66	1 / 62	DUMEAUX_Smoking enriched genes
5	0.93	1 / 150	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 22	DUMEAUX_High bmi enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.003	3 / 18	translation elongation factor activity
2	0.003	21 / 644	protein homodimerization activity
3	0.004	40 / 1541	DNA binding
4	0.004	3 / 20	dynein complex binding
5	0.006	25 / 852	nucleic acid binding
6	0.006	11 / 268	transcription factor binding
7	0.012	2 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
8	0.012	5 / 81	single−stranded DNA binding
9	0.014	2 / 11	DNA−(apurinic or apyrimidinic site) lyase activity
10	0.016	150 / 7864	protein binding
11	0.017	2 / 12	protein kinase A catalytic subunit binding
12	0.020	2 / 13	enhancer binding
13	0.021	5 / 93	protein N−terminus binding
14	0.021	9 / 239	protein domain specific binding
15	0.023	2 / 14	protein kinase C activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	7 / 100	Chaussabel_2,8_T−cells
2	0.003	2 / 5	JONGENEEL_Fetal Brain
3	0.006	4 / 42	Chaussabel_1,3_B−cells
4	0.006	21 / 678	PROTEINATLAS_lymph node
5	0.009	18 / 569	PROTEINATLAS_salivary gland
6	0.011	20 / 671	PROTEINATLAS_cervix, uterine
7	0.012	20 / 677	PROTEINATLAS_esophagus
8	0.013	6 / 113	Chaussabel_1,8_Metabolism Biosynthesis
9	0.015	27 / 1022	PROTEINATLAS_placenta
10	0.015	18 / 604	PROTEINATLAS_hippocampus
11	0.017	2 / 12	WIRTH_Cortex cerebri
12	0.018	12 / 352	WIRTH_Nervous System
13	0.023	22 / 819	PROTEINATLAS_bronchus
14	0.026	17 / 595	PROTEINATLAS_breast
15	0.027	27 / 1076	PROTEINATLAS_stomach

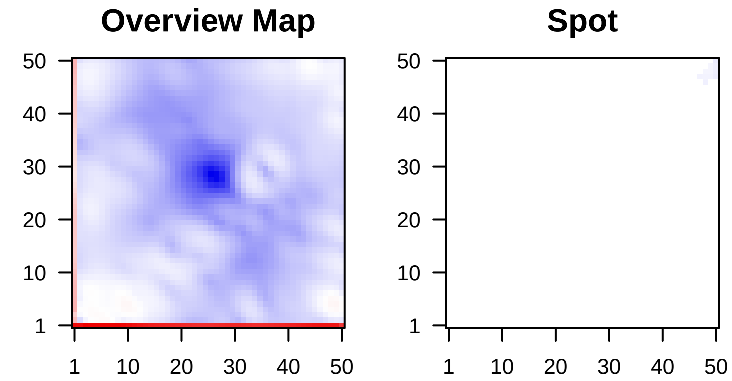
D−Cluster

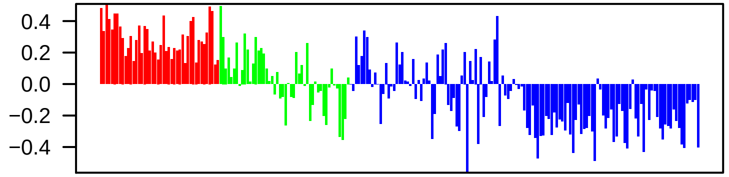
Spot Summary: I

metagenes = 11
genes = 148

<r> metagenes = 0.98
<r> genes = 0.31
beta: r2= 12.6 / log p= −Inf

samples with spot = 37 (16.7 %)
mBL : 25 (56.8 %)
intermediate : 5 (10.4 %)
non−mBL : 7 (5.4 %)



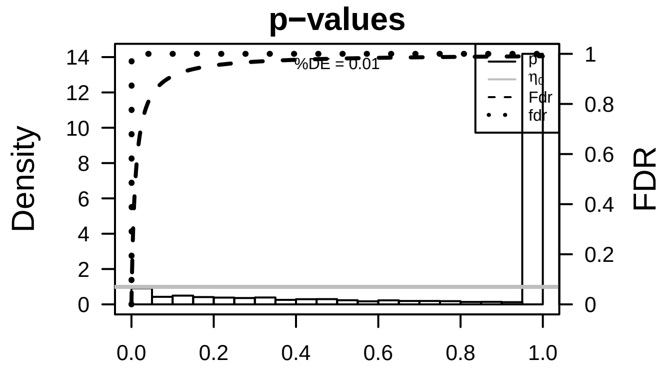


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	AFFX−r2−Hs1	3.22	−1.13	0.61		
2	AFFX−r2−Hs1	3.07	−1.49	0.53		
3	AFFX−HUMR	2.91	−0.94	0.61		microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835
4	AFFX−HUMR	2.85	−1.18	0.5		
5	AFFX−r2−Hs1	2.71	−1.22	0.69		
6	AFFX−r2−Hs2	2.62	−0.97	0.6		
7	AFFX−M2783	2.6	−1.58	0.6		
8	AFFX−HUMR	2.6	−1.04	0.62		
9	AFFX−r2−Hs2	2.21	−1.56	0.59		
10	215767_at	1.86	−2.03	0.34	ZNF804A	zinc finger protein 804A [Source:HGNC Symbol;Acc:HGNC:2
11	201418_s_at	1.77	−1.36	0.38	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
12	AFFX−r2−Hs2	1.66	−1.04	0.51		
13	220214_at	1.53	−1.31	0.46	ZNF215	zinc finger protein 215 [Source:HGNC Symbol;Acc:HGNC:13
14	215907_at	1.52	−1.29	0.5		
15	203938_s_at	1.41	−1.47	0.57	TAF1C	TATA−box binding protein associated factor, RNA polymerase
16	214349_at	1.34	−1.04	0.36		
17	202048_s_at	1.31	−1.09	0.56	CBX6	chromobox 6 [Source:HGNC Symbol;Acc:HGNC:1556]
18	219703_at	1.3	−1.06	0.62	MNS1	meiosis specific nuclear structural 1 [Source:HGNC Symbol;
19	213345_at	1.3	−0.81	0.51	NFATC4	nuclear factor of activated T cells 4 [Source:HGNC Symbol;A
20	207416_s_at	1.29	−0.76	0.5		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−10	21 / 400	GSE	PUJANA_BRCA2_PCC_NETWORK
2	4e−10	90 / 5529	Lymp	HOPP_Txn_elongation
3	2e−09	33 / 1052	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	2e−08	17 / 319	Mela	Gerber_wt/wt_melanoma−cells−SpotA
5	4e−08	76 / 4579	CC	nucleus
6	1e−07	51 / 2541	CC	nucleoplasm
7	2e−07	20 / 526	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
8	4e−07	70 / 4261	Lymp	HOPP_Txn_transition
9	3e−06	16 / 409	Canc	Lembcke_Normal vs Adenoma
10	3e−06	29 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
11	2e−05	4 / 16	GSE	REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS
12	2e−05	4 / 17	GSE	REACTOME_FANCONI_ANEMIA_PATHWAY
13	2e−05	19 / 651	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
14	3e−05	18 / 602	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
15	3e−05	32 / 1527	GSE	PUJANA_BRCA1_PCC_NETWORK
16	6e−05	5 / 42	GSE	RASHI_RESPONSE_TO_IONIZING_RADIATION_3
17	6e−05	19 / 703	GSE	LEE_BMP2_TARGETS_DN
18	7e−05	7 / 102	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	7e−05	11 / 267	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
20	7e−05	6 / 71	GSE	REACTOME_MITOTIC_G2_G2_M_PHASES
21	8e−05	24 / 1044	TF	ICGC_Six5_targets
22	1e−04	5 / 47	GSE	OXFORD_RALA_OR_RALB_TARGETS_UP
23	1e−04	12 / 327	GSE	ZHANG_BREAST_CANCER_PROGENITORS_UP
24	1e−04	19 / 728	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
25	1e−04	9 / 187	HM	HALLMARK_E2F_TARGETS
26	1e−04	16 / 548	Chr	Chr 16
27	1e−04	8 / 147	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
28	1e−04	11 / 280	GSE	MANALO_HYPOXIA_DN
29	1e−04	15 / 497	BP	cell cycle
30	1e−04	13 / 387	GSE	LIAO_METASTASIS
31	1e−04	31 / 1578	TF	ICGC_GabpPcr2_targets
32	1e−04	4 / 27	GSE	REACTOME_SIGNALING_BY_FGFR1_MUTANTS
33	1e−04	10 / 240	GSE	MITSIADES_RESPONSE_TO_APLIDIN_DN
34	1e−04	9 / 195	HM	HALLMARK_G2M_CHECKPOINT
35	1e−04	5 / 51	GSE	REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES
36	2e−04	12 / 347	GSE	REACTOME_CELL_CYCLE
37	2e−04	4 / 29	MF	ribonucleoprotein complex binding
38	2e−04	3 / 12	BP	centriole replication
39	2e−04	5 / 56	GSE	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS
40	2e−04	6 / 88	GSE	REACTOME_DNA_REPAIR



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 92	HORVATH_aging_genes meth DOWN
2	0.7	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	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	

CC

Rank	p−value	#in/all	Geneset
1	4e−08	76 / 4579	nucleus
2	1e−07	51 / 2541	nucleoplasm
3	4e−04	11 / 324	chromosome
4	7e−04	10 / 292	microtubule organizing center
5	1e−03	5 / 83	centriole
6	2e−03	10 / 326	nuclear speck
7	2e−03	15 / 653	nucleolus
8	3e−03	10 / 354	centrosome
9	4e−03	5 / 103	nuclear chromosome, telomeric region
10	5e−03	2 / 11	Fanconi anaemia nuclear complex
11	5e−03	2 / 11	pericentric heterochromatin
12	9e−03	2 / 15	pericentriolar material
13	1e−02	2 / 19	telomerase holoenzyme complex
14	2e−02	2 / 20	centriolar satellite
15	2e−02	2 / 22	PcG protein complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	29 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	3e−05	18 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
3	4e−04	15 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	3e−03	29 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	4e−03	17 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
6	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
7	2e−02	15 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
8	1e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
9	2e−01	7 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
10	3e−01	1 / 31	Marisa_CRC−cluster−c
11	3e−01	1 / 31	Kosinski_lower−crypt−short−list
12	3e−01	3 / 184	Kosinski_lower−crypt−long−list
13	3e−01	7 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	5e−01	10 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
15	5e−01	12 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a

HM

Rank	p−value	#in/all	Geneset
1	1e−04	9 / 187	HALLMARK_E2F_TARGETS
2	1e−04	9 / 195	HALLMARK_G2M_CHECKPOINT
3	3e−04	8 / 173	HALLMARK_MITOTIC_SPINDLE
4	4e−02	4 / 133	HALLMARK_DNA_REPAIR
5	3e−01	3 / 192	HALLMARK_MTORC1_SIGNALING
6	4e−01	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	4e−01	1 / 55	HALLMARK_MYC_TARGETS_V2
8	6e−01	2 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
9	6e−01	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	7e−01	1 / 122	HALLMARK_SPERMATOGENESIS
11	8e−01	1 / 139	HALLMARK_FATTY_ACID_METABOLISM
12	8e−01	1 / 141	HALLMARK_UV_RESPONSE_DN
13	8e−01	1 / 150	HALLMARK_APOPTOSIS
14	8e−01	1 / 176	HALLMARK_ALLOGRAFT_REJECTION
15	8e−01	1 / 182	HALLMARK_GLYCOLYSIS

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−10	90 / 5529	HOPP_Txn_elongation
2	4e−07	70 / 4261	HOPP_Txn_transition
3	4e−04	78 / 5908	HOPP_Active_promoter
4	6e−03	18 / 955	SPANG_BCR UP
5	7e−03	7 / 227	SPANG_IL21 UP
6	9e−03	9 / 353	SPANG_CD40 6hrs DN
7	8e−02	3 / 99	Sha_BL UP
8	8e−02	3 / 102	ROSOLOWSKI_blue total
9	9e−02	5 / 237	ZHANG_DLBCL mutated
10	1e−01	13 / 906	SPANG_BCR DN
11	2e−01	4 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
12	3e−01	1 / 35	Subero_MM_hyper_meth
13	3e−01	3 / 192	Victora_Dark zone signature
14	3e−01	57 / 5404	HOPP_Strong_enhancer
15	3e−01	1 / 42	Monti_OxPhos_cluster

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	9 / 260	hsa−let−7e
2	0.002	5 / 92	hsa−miR−199a−5p
3	0.002	3 / 27	hsa−miR−770−5p
4	0.005	3 / 35	hsa−miR−1224−5p
5	0.011	5 / 134	hsa−miR−141
6	0.012	2 / 17	hsa−miR−323−5p
7	0.013	4 / 91	hsa−miR−211
8	0.017	3 / 55	hsa−miR−637
9	0.018	3 / 56	hsa−miR−1275
10	0.019	3 / 57	hsa−miR−518c*
11	0.019	4 / 103	hsa−miR−576−3p
12	0.020	3 / 58	hsa−miR−331−3p
13	0.020	2 / 22	hsa−miR−1225−3p
14	0.025	5 / 167	hsa−miR−221
15	0.027	2 / 26	hsa−miR−1293

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	2 / 27	Nabetani_alt len telomeres_genes_ko
2	0.12	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	

BP

Rank	p−value	#in/all	Geneset
1	1e−04	15 / 497	cell cycle
2	2e−04	3 / 12	centriole replication
3	5e−04	10 / 281	DNA repair
4	7e−04	5 / 71	regulation of G2/M transition of mitotic cell cycle
5	9e−04	6 / 113	regulation of signal transduction by p53 class mediator
6	1e−03	5 / 79	ciliary basal body−plasma membrane docking
7	1e−03	9 / 260	chromatin organization
8	1e−03	6 / 119	G2/M transition of mitotic cell cycle
9	2e−03	6 / 137	DNA replication
10	3e−03	10 / 351	cellular response to DNA damage stimulus
11	3e−03	4 / 62	meiotic cell cycle
12	4e−03	3 / 32	centrosome cycle
13	4e−03	3 / 32	protein peptidyl−prolyl isomerization
14	4e−03	2 / 10	microtubule anchoring
15	4e−03	2 / 10	positive regulation of cilium assembly

Chr

Rank	p−value	#in/all	Geneset
1	1e−04	16 / 548	Chr 16
2	8e−02	12 / 776	Chr 17
3	9e−02	5 / 242	Chr 13
4	1e−01	6 / 333	Chr 22
5	2e−01	16 / 1325	Chr 1
6	3e−01	10 / 833	Chr 19
7	4e−01	6 / 492	Chr 9
8	5e−01	7 / 669	Chr 6
9	5e−01	4 / 369	Chr 20
10	5e−01	7 / 689	Chr 3
11	7e−01	7 / 832	Chr 2
12	8e−01	1 / 139	Chr 21
13	8e−01	5 / 700	Chr 12
14	8e−01	1 / 184	Chr 18
15	9e−01	3 / 480	Chr 4

Glioma

Rank	p−value	#in/all	Geneset
1	0.006	23 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.008	25 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	0.020	1 / 2	Phillips Prolif up vs PN & MES
4	0.021	3 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	0.028	4 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
6	0.055	4 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	0.095	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
8	0.100	3 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
9	0.104	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
10	0.104	3 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.113	1 / 12	Christensen_hypermethylated_in_ependymoma
12	0.113	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
13	0.126	7 / 421	Down_b
14	0.144	3 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	0.148	1 / 16	VERHAAK_PN subtype

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	1 / 18	Angelova_immune−metagene−pDC
2	0.2	1 / 26	Angelova_immune−metagene−activated_CD4
3	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.0	0 / 25	Angelova_immune−metagene−DC
9	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.0	0 / 14	Angelova_immune−metagene−eosinophil
12	1.0	0 / 19	Angelova_immune−metagene−iDC
13	1.0	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.0	0 / 11	Angelova_immune−metagene−macrophages
15	1.0	0 / 38	Angelova_immune−metagene−mast−cells

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−08	17 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	4e−02	1 / 4	Melanoma Epi−Enzyme Cluster 3
3	8e−02	2 / 47	Tirosh_G2/M phase specific genes
4	3e−01	1 / 38	Tirosh_G1/S phase specific genes
5	4e−01	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	5e−01	1 / 68	Tirosh_housekeeping_genes
7	5e−01	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
8	7e−01	2 / 222	Gerber_wt/wt_melanoma−cells−SpotF
9	7e−01	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
10	7e−01	2 / 236	Gerber_wt/wt_group3−specific
11	7e−01	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	9e−01	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	1e+00	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	1e+00	0 / 17	Hugo_melanoma−all−MET_UP
15	1e+00	0 / 37	Hugo_melanoma−all−MET_DN

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 54	Burnham_timecourse
2	0.4	1 / 52	Burnham_day1_vs_5_DN
3	0.5	1 / 68	Burnham_sep_vs_con_UP
4	0.5	1 / 71	Burnham_cap_fp_vs_con_UP
5	0.5	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
6	0.7	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	1.0	0 / 56	Burnham_sep_vs_con_DN
8	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.0	0 / 48	Burnham_viral_DN
10	1.0	0 / 57	Burnham_viral_UP
11	1.0	0 / 57	Burnham_day1_vs_5_UP
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

TF

Rank	p−value	#in/all	Geneset
1	8e−05	24 / 1044	ICGC_Six5_targets
2	1e−04	31 / 1578	ICGC_GabpPcr2_targets
3	5e−04	53 / 3564	ICGC_Taf1_targets
4	7e−04	48 / 3150	ICGC_Creb1_targets
5	2e−03	21 / 1089	ICGC_Ets1_targets
6	2e−03	23 / 1241	KIM_MYC targets
7	8e−03	12 / 549	ICGC_Atf3_targets
8	1e−02	56 / 4319	ICGC_Pou2_targets
9	1e−02	19 / 1107	ICGC_Myc_targets
10	2e−02	49 / 3769	ICGC_Pmlsc71910_targets
11	2e−02	49 / 3796	ICGC_Nficsc81335_targets
12	2e−02	48 / 3703	ICGC_Foxm1_targets
13	2e−02	47 / 3630	ICGC_Sp1_targets
14	2e−02	52 / 4131	ICGC_Tcf3_targets
15	3e−02	41 / 3121	ICGC_Egr1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	16 / 409	Lembcke_Normal vs Adenoma
2	7e−04	4 / 41	PanCan_DNARepair_geneset_nanostring
3	1e−02	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
4	7e−02	2 / 45	KUIPER_MM poor survival
5	8e−02	1 / 14	LIU_COMMON_CANCER_GENES
6	9e−02	1 / 10	GENTLES_modul3
7	1e−01	1 / 12	BENTINK_e2f3.2
8	1e−01	1 / 12	BENTINK_ras.1
9	1e−01	1 / 14	BENTINK_myc.1
10	1e−01	1 / 14	BENTINK_ras.6
11	1e−01	3 / 130	PanCan_CC+Apop_geneset_nanostring
12	2e−01	1 / 20	PanCan_ChromMod_geneset_nanostring
13	2e−01	0 / 16	LIU_LIVER_CANCER
14	2e−01	2 / 96	PanCan_TXmisReg_geneset_nanostring
15	3e−01	1 / 32	KUIPER_MM good survival

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−10	110 / 7833	Bcells peripheral blood_1_TssA
2	2e−09	114 / 8406	Bcells peripheral blood_2_TssAFlnk
3	2e−09	97 / 6389	4_Tx_ESC_Mesoderm
4	5e−09	87 / 5456	5_Tx_Neuronal_Progenitor
5	9e−09	112 / 8322	T CD8+ naive cells peripheral blood_1_TssA
6	1e−08	87 / 5527	Tregulatory cells peripheral blood_4_Tx
7	2e−08	106 / 7635	monocytes peripheral blood_1_TssA
8	3e−08	110 / 8200	monocytes peripheral blood_2_TssAFlnk
9	3e−08	108 / 7957	Tcells peripheral blood_2_TssAFlnk
10	4e−08	91 / 6068	4_Tx_ESC_Endoderm
11	5e−08	110 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
12	1e−07	87 / 5753	Tcells peripheral blood_4_Tx
13	1e−07	105 / 7751	natural killer cells peripheral blood_1_TssA
14	2e−07	113 / 8766	2_TssA_Melanocytes
15	2e−07	86 / 5716	Bcells peripheral blood_4_Tx

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−10	21 / 400	PUJANA_BRCA2_PCC_NETWORK
2	2e−09	33 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	2e−07	20 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
4	2e−05	4 / 16	REACTOME_SIGNALING_BY_FGFR1_FUSION_MUTANTS
5	2e−05	4 / 17	REACTOME_FANCONI_ANEMIA_PATHWAY
6	2e−05	19 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	3e−05	32 / 1527	PUJANA_BRCA1_PCC_NETWORK
8	6e−05	5 / 42	RASHI_RESPONSE_TO_IONIZING_RADIATION_3
9	6e−05	19 / 703	LEE_BMP2_TARGETS_DN
10	7e−05	7 / 102	WHITEFORD_PEDIATRIC_CANCER_MARKERS
11	7e−05	11 / 267	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
12	7e−05	6 / 71	REACTOME_MITOTIC_G2_G2_M_PHASES
13	1e−04	5 / 47	OXFORD_RALA_OR_RALB_TARGETS_UP
14	1e−04	12 / 327	ZHANG_BREAST_CANCER_PROGENITORS_UP
15	1e−04	19 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.5	1 / 62	DUMEAUX_Smoking enriched genes
2	0.8	1 / 150	Homuth_BMI−associated−genes_UP
3	0.9	1 / 210	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 22	DUMEAUX_High bmi enriched genes
13	1.0	0 / 22	DUMEAUX_Fasting enriched genes
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 29	ribonucleoprotein complex binding
2	5e−04	29 / 1541	DNA binding
3	2e−03	22 / 1161	RNA binding
4	4e−03	3 / 32	peptidyl−prolyl cis−trans isomerase activity
5	6e−03	3 / 37	single−stranded RNA binding
6	6e−03	2 / 12	S−adenosylmethionine−dependent methyltransferase activity
7	6e−03	2 / 12	ubiquitin−ubiquitin ligase activity
8	8e−03	3 / 41	tubulin binding
9	1e−02	5 / 132	methyltransferase activity
10	2e−02	4 / 97	double−stranded DNA binding
11	2e−02	2 / 21	gamma−tubulin binding
12	2e−02	15 / 852	nucleic acid binding
13	2e−02	2 / 24	NF−kappaB binding
14	3e−02	2 / 28	ATP−dependent DNA helicase activity
15	4e−02	2 / 32	aminoacyl−tRNA ligase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.01	2 / 16	VAQUERIZAS_Fetal liver_TF
2	0.01	6 / 188	Chaussabel_3,8_Enzymes
3	0.02	9 / 390	PROTEINATLAS_ovary
4	0.02	16 / 905	PROTEINATLAS_appendix
5	0.02	4 / 106	Chaussabel_2,11_Replication
6	0.03	17 / 1032	PROTEINATLAS_small intestine
7	0.04	6 / 245	Chaussabel_3,9_Kinases
8	0.04	16 / 989	PROTEINATLAS_tonsil
9	0.04	17 / 1072	PROTEINATLAS_duodenum
10	0.04	12 / 678	PROTEINATLAS_lymph node
11	0.04	2 / 32	VAQUERIZAS_Liver_TF
12	0.05	9 / 474	PROTEINATLAS_vagina
13	0.06	16 / 1048	PROTEINATLAS_rectum
14	0.06	2 / 40	VAQUERIZAS_Testis_TF
15	0.06	2 / 41	VAQUERIZAS_Thymus_TF

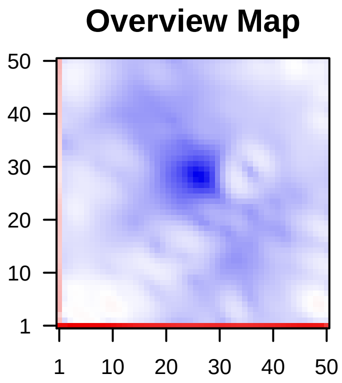
D−Cluster

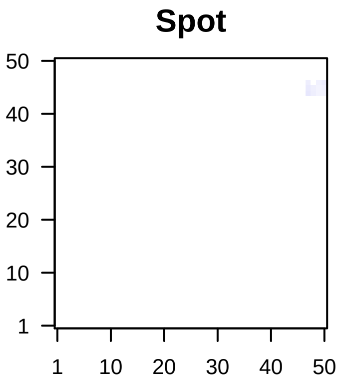
Spot Summary: J

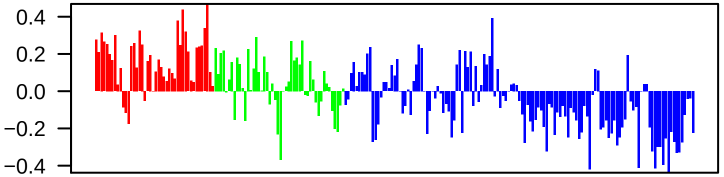
metagenes = 11
genes = 181

<r> metagenes = 0.97
<r> genes = 0.25
beta: r2= 7.68 / log p= −Inf

samples with spot = 14 (6.3 %)
mBL : 10 (22.7 %)
intermediate : 3 (6.2 %)
non−mBL : 1 (0.8 %)





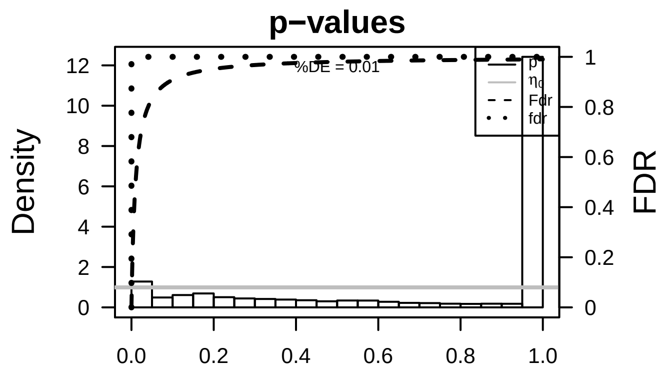


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	208719_s_at	2	−1.36	0.46	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
2	213668_s_at	1.86	−1.12	0.5	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
3	208151_x_at	1.73	−1.48	0.55	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
4	213792_s_at	1.71	−1.1	0.36	INSR	insulin receptor [Source:HGNC Symbol;Acc:HGNC:6091]
5	AFFX−M2783	1.67	−1.23	0.55		
6	221496_s_at	1.6	−1.41	0.67	TOB2	transducer of ERBB2, 2 [Source:HGNC Symbol;Acc:HGNC:1
7	206500_s_at	1.46	−1.04	0.68	MIS18BP1	MIS18 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2
8	213789_at	1.44	−0.92	0.45		
9	213328_at	1.34	−1.04	0.6	NEK1	NIMA related kinase 1 [Source:HGNC Symbol;Acc:HGNC:77
10	219048_at	1.3	−1.15	0.33	PIGN	phosphatidylinositol glycan anchor biosynthesis class N [Sou
11	220938_s_at	1.3	−1.05	0.56	GMEB1	glucocorticoid modulatory element binding protein 1 [Source:
12	213998_s_at	1.25	−1.33	0.53	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
13	219437_s_at	1.25	−1.33	0.62	ANKRD11	ankyrin repeat domain 11 [Source:HGNC Symbol;Acc:HGNC
14	213979_s_at	1.24	−1.43	0.46		
15	213577_at	1.24	−1.21	0.46	SQLE	squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127
16	212468_at	1.23	−0.81	0.77	SPAG9	sperm associated antigen 9 [Source:HGNC Symbol;Acc:HGN
17	222158_s_at	1.21	−1.32	0.73	DESI2	desumoylating isopeptidase 2 [Source:HGNC Symbol;Acc:HG
18	221753_at	1.21	−1.57	0.52	SSH1	slingshot protein phosphatase 1 [Source:HGNC Symbol;Acc:
19	213660_s_at	1.2	−0.79	0.5	TOP3B	DNA topoisomerase III beta [Source:HGNC Symbol;Acc:HGN
20	214723_x_at	1.19	−0.73	0.63	ANKRD36	ankyrin repeat domain 36 [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−19	56 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
2	3e−18	20 / 106	Refer	Chaussabel_2,11_Replication
3	1e−13	118 / 5529	Lymp	HOPP_Txn_elongation
4	4e−12	98 / 4261	Lymp	HOPP_Txn_transition
5	2e−11	37 / 830	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
6	4e−09	81 / 3564	TF	ICGC_Taf1_targets
7	7e−09	20 / 328	GSE	OSMAN_BLADDER_CANCER_UP
8	1e−08	64 / 2541	CC	nucleoplasm
9	3e−08	111 / 5908	Lymp	HOPP_Active_promoter
10	3e−07	17 / 303	GSE	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
11	7e−07	69 / 3150	TF	ICGC_Creb1_targets
12	7e−07	10 / 102	Lymp	ROSOLOWSKI_blue total
13	9e−07	12 / 159	GSE	CHANDRAN_METASTASIS_UP
14	1e−06	89 / 4579	CC	nucleus
15	1e−06	7 / 44	MF	methylated histone binding
16	2e−06	67 / 3121	TF	ICGC_Egr1_targets
17	3e−06	84 / 4319	TF	ICGC_Pou2_targets
18	4e−06	42 / 1602	GSE	BLALOCK_ALZHEIMERS_DISEASE_UP
19	4e−06	76 / 3769	TF	ICGC_Pmlsc71910_targets
20	4e−06	8 / 72	GSE	BILD_CTNNB1_ONCOGENIC_SIGNATURE
21	5e−06	76 / 3796	TF	ICGC_Nficsc81335_targets
22	5e−06	76 / 3804	TF	ICGC_Stat5_targets
23	7e−06	73 / 3630	TF	ICGC_Sp1_targets
24	1e−05	70 / 3451	TF	ICGC_Atf2_targets
25	1e−05	23 / 669	GSE	JOHNSTONE_PARVB_TARGETS_3_DN
26	1e−05	69 / 3420	TF	ICGC_Bclaf101388_targets
27	2e−05	14 / 286	GSE	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
28	2e−05	30 / 1044	TF	ICGC_Six5_targets
29	2e−05	85 / 4602	TF	ICGC_Elf1_targets
30	3e−05	40 / 1630	TF	ICGC_SrfV0416101_targets
31	3e−05	72 / 3703	TF	ICGC_Foxm1_targets
32	3e−05	18 / 469	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
33	3e−05	80 / 4278	TF	ICGC_Yy1_targets
34	4e−05	77 / 4072	TF	ICGC_Mta3_targets
35	4e−05	40 / 1655	BP	transcription, DNA−templated
36	6e−05	13 / 278	miRN	hsa−let−7d
37	6e−05	77 / 4131	TF	ICGC_Tcf3_targets
38	7e−05	10 / 171	miRN	hsa−miR−196a
39	8e−05	5 / 35	miRN	hsa−miR−329
40	8e−05	5 / 35	GSE	PENG_GLUTAMINE_DEPRIVATION_UP



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 92	HORVATH_aging_genes meth DOWN
2	1	0 / 107	HORVATH_aging_genes meth UP
3	1	0 / 47	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−05	40 / 1655	transcription, DNA−templated
2	1e−04	12 / 260	chromatin organization
3	2e−04	40 / 1764	regulation of transcription, DNA−templated
4	6e−04	13 / 351	cellular response to DNA damage stimulus
5	7e−04	4 / 32	centrosome cycle
6	9e−04	4 / 34	DNA damage response, detection of DNA damage
7	2e−03	4 / 39	RNA secondary structure unwinding
8	2e−03	5 / 69	chromatin remodeling
9	2e−03	3 / 21	DNA methylation
10	2e−03	4 / 44	signal transduction by protein phosphorylation
11	3e−03	5 / 74	regulation of mitotic cell cycle
12	3e−03	4 / 46	heart morphogenesis
13	3e−03	6 / 113	cell projection organization
14	4e−03	10 / 284	spermatogenesis
15	4e−03	4 / 50	smoothened signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	4 / 113	PanCan_Driver_Gene_geneset_nanostring
2	0.12	1 / 14	LIU_COMMON_CANCER_GENES
3	0.17	1 / 14	BENTINK_ras.6
4	0.17	1 / 14	BENTINK_src.2
5	0.17	1 / 15	RHODES_CANCER_META_SIGNATURE
6	0.18	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
7	0.18	1 / 15	WANG_ER_UP
8	0.28	1 / 25	PanCan_HH_geneset_nanostring
9	0.30	1 / 28	PanCan_HK_geneset_nanostring
10	0.44	1 / 45	KUIPER_MM poor survival
11	0.62	0 / 11	LIU_PROSTATE_CANCER_UP
12	0.81	1 / 130	PanCan_CC+Apop_geneset_nanostring
13	0.85	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	0.97	2 / 409	Lembcke_Normal vs Adenoma
15	0.99	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	1e−08	64 / 2541	nucleoplasm
2	1e−06	89 / 4579	nucleus
3	6e−04	13 / 354	centrosome
4	8e−04	6 / 86	PML body
5	2e−03	3 / 19	histone methyltransferase complex
6	2e−03	5 / 73	ubiquitin ligase complex
7	6e−03	4 / 56	lipid droplet
8	7e−03	2 / 10	Golgi transport complex
9	8e−03	2 / 11	pericentric heterochromatin
10	9e−03	4 / 63	caveola
11	1e−02	2 / 12	integrator complex
12	1e−02	8 / 233	nuclear body
13	1e−02	9 / 292	microtubule organizing center
14	2e−02	2 / 15	nuclear heterochromatin
15	2e−02	2 / 15	NuRD complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	13 / 548	Chr 16
2	0.04	17 / 833	Chr 19
3	0.12	22 / 1325	Chr 1
4	0.14	7 / 333	Chr 22
5	0.18	14 / 832	Chr 2
6	0.19	12 / 700	Chr 12
7	0.33	7 / 437	Chr 8
8	0.50	10 / 756	Chr 11
9	0.51	5 / 369	Chr 20
10	0.52	9 / 689	Chr 3
11	0.53	2 / 139	Chr 21
12	0.60	3 / 242	Chr 13
13	0.67	9 / 776	Chr 17
14	0.69	2 / 184	Chr 18
15	0.76	5 / 492	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−23	157 / 7833	Bcells peripheral blood_1_TssA
2	3e−22	142 / 6389	4_Tx_ESC_Mesoderm
3	1e−21	134 / 5753	Tcells peripheral blood_4_Tx
4	2e−21	137 / 6034	5_Tx_Fibroblasts
5	3e−21	154 / 7751	natural killer cells peripheral blood_1_TssA
6	2e−20	136 / 6068	4_Tx_ESC_Endoderm
7	2e−20	150 / 7420	Tcells peripheral blood_1_TssA
8	5e−20	129 / 5527	Tregulatory cells peripheral blood_4_Tx
9	1e−19	151 / 7635	monocytes peripheral blood_1_TssA
10	2e−19	135 / 6099	HSC_4_Tx
11	3e−19	156 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
12	3e−19	141 / 6679	5_Tx_Melanocytes
13	3e−19	130 / 5716	Bcells peripheral blood_4_Tx
14	5e−19	157 / 8406	Bcells peripheral blood_2_TssAFlnk
15	7e−19	154 / 8068	Thelper cells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−19	56 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	5e−04	23 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	3e−03	23 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
4	4e−03	35 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	4e−03	26 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
6	7e−03	98 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	1e−02	13 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
8	6e−02	2 / 31	Marisa_CRC−cluster−c
9	7e−02	1 / 6	Juehling_HNPCC−mutated−in−5
10	8e−02	16 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
11	1e−01	1 / 10	KIM_CRC−MSI−regulated_DN
12	1e−01	2 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	1e−01	1 / 11	KIM_MSI−in−CRC
14	1e−01	22 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	2e−01	4 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Glioma

Rank	p−value	#in/all	Geneset
1	2e−04	33 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	2e−04	36 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−03	5 / 64	Weller_LGG_A_vs_O_DOWN
4	4e−03	4 / 50	Vishal_subnetwork signature of survival in GBM
5	1e−02	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
6	3e−02	8 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	6e−02	8 / 330	Up
8	7e−02	1 / 6	WILLSCHER_GBM_Verhaak−PNmut_up (M)
9	1e−01	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
10	1e−01	2 / 47	developing astrocytes
11	1e−01	1 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
12	2e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
13	2e−01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	2e−01	1 / 16	VERHAAK_CL subtype
15	2e−01	1 / 16	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−11	37 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	7e−09	20 / 328	OSMAN_BLADDER_CANCER_UP
3	3e−07	17 / 303	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
4	9e−07	12 / 159	CHANDRAN_METASTASIS_UP
5	4e−06	42 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
6	4e−06	8 / 72	BILD_CTNNB1_ONCOGENIC_SIGNATURE
7	1e−05	23 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
8	2e−05	14 / 286	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
9	3e−05	18 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
10	8e−05	5 / 35	PENG_GLUTAMINE_DEPRIVATION_UP
11	1e−04	15 / 376	GARY_CD5_TARGETS_UP
12	2e−04	13 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
13	2e−04	23 / 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
14	3e−04	9 / 165	THUM_SYSTOLIC_HEART_FAILURE_DN
15	3e−04	18 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP

HM

Rank	p−value	#in/all	Geneset
1	0.04	6 / 195	HALLMARK_G2M_CHECKPOINT
2	0.08	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.09	5 / 187	HALLMARK_E2F_TARGETS
4	0.10	5 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.17	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.18	4 / 173	HALLMARK_MITOTIC_SPINDLE
7	0.36	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
8	0.39	3 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	0.45	3 / 192	HALLMARK_MTORC1_SIGNALING
10	0.45	3 / 193	HALLMARK_HEME_METABOLISM
11	0.48	1 / 51	HALLMARK_TGF_BETA_SIGNALING
12	0.54	2 / 141	HALLMARK_UV_RESPONSE_DN
13	0.64	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
14	0.66	2 / 174	HALLMARK_ADIPOGENESIS
15	0.67	2 / 178	HALLMARK_COMPLEMENT

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 4	Angelova_CRC_MSS−neoantigens
2	0.09	1 / 7	Angelova_CRC_MSI−neoantigens
3	0.15	1 / 13	Angelova_CRC_MSS^−neoantigens
4	0.21	1 / 18	Angelova_immune−metagene−pDC
5	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
6	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
7	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
8	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
9	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
10	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
11	1.00	0 / 25	Angelova_immune−metagene−DC
12	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
14	1.00	0 / 14	Angelova_immune−metagene−eosinophil
15	1.00	0 / 19	Angelova_immune−metagene−iDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.13	5 / 210	Homuth_BMI−associated−genes_DN
3	0.30	3 / 150	Homuth_BMI−associated−genes_UP
4	1.00	0 / 62	DUMEAUX_Smoking enriched genes
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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 22	DUMEAUX_High bmi enriched genes
13	1.00	0 / 22	DUMEAUX_Fasting enriched genes
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	1e−13	118 / 5529	HOPP_Txn_elongation
2	4e−12	98 / 4261	HOPP_Txn_transition
3	3e−08	111 / 5908	HOPP_Active_promoter
4	7e−07	10 / 102	ROSOLOWSKI_blue total
5	1e−03	93 / 5682	HOPP_Weak_promoter
6	2e−03	88 / 5404	HOPP_Strong_enhancer
7	2e−02	20 / 955	SPANG_BCR UP
8	3e−02	68 / 4357	HOPP_Weak_txn
9	5e−02	69 / 4559	HOPP_Weak_enhancer
10	7e−02	17 / 906	SPANG_BCR DN
11	7e−02	2 / 35	Subero_MM_hyper_meth
12	1e−01	6 / 263	SPANG_CD40 6hrs UP
13	1e−01	3 / 96	SPANG_LPS 6hrs UP
14	1e−01	3 / 99	Sha_BL UP
15	2e−01	5 / 227	SPANG_IL21 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	1 / 2	Melanoma Epi−Enzyme Cluster 2
2	0.03	2 / 23	Melanoma Epi−Enzyme Cluster 7
3	0.07	6 / 222	Gerber_wt/wt_melanoma−cells−SpotF
4	0.08	2 / 38	Tirosh_top50 correlated genes PC1
5	0.09	5 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	0.12	2 / 47	Tirosh_G2/M phase specific genes
7	0.17	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC
8	0.27	1 / 24	Tirosh_B−cell specific genes−melanoma
9	0.27	1 / 24	Gerami_melanoma−metastatic−risk_DN
10	0.36	4 / 236	Gerber_wt/wt_group3−specific
11	0.39	1 / 38	Tirosh_G1/S phase specific genes
12	0.39	5 / 319	Gerber_wt/wt_melanoma−cells−SpotA
13	0.45	7 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	0.49	3 / 204	Landsberg_dedifferentiation_down
15	0.64	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma

MF

Rank	p−value	#in/all	Geneset
1	1e−06	7 / 44	methylated histone binding
2	1e−04	124 / 7864	protein binding
3	5e−04	23 / 852	nucleic acid binding
4	1e−03	34 / 1541	DNA binding
5	1e−03	4 / 38	core promoter sequence−specific DNA binding
6	3e−03	11 / 328	chromatin binding
7	3e−03	26 / 1161	RNA binding
8	4e−03	11 / 331	protein serine/threonine kinase activity
9	7e−03	2 / 10	peroxisome proliferator activated receptor binding
10	8e−03	2 / 11	cation binding
11	9e−03	3 / 34	kinesin binding
12	1e−02	2 / 12	histone methyltransferase activity (H3−K4 specific)
13	1e−02	2 / 12	Lys48−specific deubiquitinase activity
14	1e−02	2 / 12	RNA helicase activity
15	1e−02	12 / 437	protein kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−05	13 / 278	hsa−let−7d
2	7e−05	10 / 171	hsa−miR−196a
3	8e−05	5 / 35	hsa−miR−329
4	9e−05	5 / 36	hsa−miR−541
5	1e−04	9 / 148	hsa−miR−539
6	2e−04	9 / 155	hsa−miR−381
7	2e−04	11 / 234	hsa−miR−570
8	3e−04	10 / 204	hsa−miR−30d
9	4e−04	6 / 75	hsa−miR−10b
10	7e−04	8 / 150	hsa−miR−300
11	1e−03	9 / 197	hsa−miR−30a
12	1e−03	8 / 159	hsa−miR−568
13	1e−03	6 / 92	hsa−miR−199a−5p
14	1e−03	5 / 63	hsa−miR−657
15	2e−03	12 / 344	hsa−miR−19a

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	2 / 54	Burnham_timecourse
2	0.5	1 / 48	Burnham_viral_DN
3	0.5	1 / 57	Burnham_viral_UP
4	0.7	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	0.8	1 / 122	Terre_IMS_influenza_meta_signature
6	1.0	0 / 68	Burnham_sep_vs_con_UP
7	1.0	0 / 56	Burnham_sep_vs_con_DN
8	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.0	0 / 57	Burnham_day1_vs_5_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−18	20 / 106	Chaussabel_2,11_Replication
2	2e−03	3 / 20	Chaussabel_2,7_Unknown function
3	1e−02	8 / 245	Chaussabel_3,9_Kinases
4	1e−02	22 / 1048	PROTEINATLAS_rectum
5	2e−02	9 / 310	Chaussabel_3,4_Protein phosphatases
6	3e−02	6 / 188	Chaussabel_3,8_Enzymes
7	6e−02	2 / 30	VAQUERIZAS_Smooth muscle_TF
8	6e−02	2 / 32	VAQUERIZAS_Liver_TF
9	8e−02	6 / 233	PROTEINATLAS_smooth muscle
10	9e−02	8 / 355	WIRTH_Immune system
11	1e−01	2 / 41	VAQUERIZAS_Thymus_TF
12	1e−01	2 / 42	VAQUERIZAS_Fetal brain_TF
13	1e−01	2 / 49	VAQUERIZAS_Uterus_TF
14	1e−01	4 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
15	1e−01	1 / 11	JONGENEEL_Spleen

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−09	81 / 3564	ICGC_Taf1_targets
2	7e−07	69 / 3150	ICGC_Creb1_targets
3	2e−06	67 / 3121	ICGC_Egr1_targets
4	3e−06	84 / 4319	ICGC_Pou2_targets
5	4e−06	76 / 3769	ICGC_Pmlsc71910_targets
6	5e−06	76 / 3796	ICGC_Nficsc81335_targets
7	5e−06	76 / 3804	ICGC_Stat5_targets
8	7e−06	73 / 3630	ICGC_Sp1_targets
9	1e−05	70 / 3451	ICGC_Atf2_targets
10	1e−05	69 / 3420	ICGC_Bclaf101388_targets
11	2e−05	30 / 1044	ICGC_Six5_targets
12	2e−05	85 / 4602	ICGC_Elf1_targets
13	3e−05	40 / 1630	ICGC_SrfV0416101_targets
14	3e−05	72 / 3703	ICGC_Foxm1_targets
15	3e−05	80 / 4278	ICGC_Yy1_targets

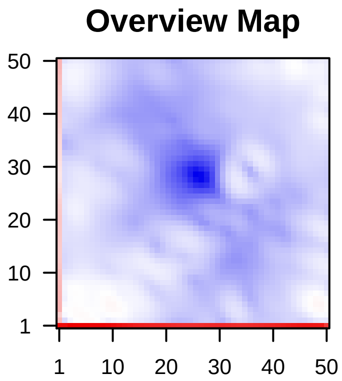
D−Cluster

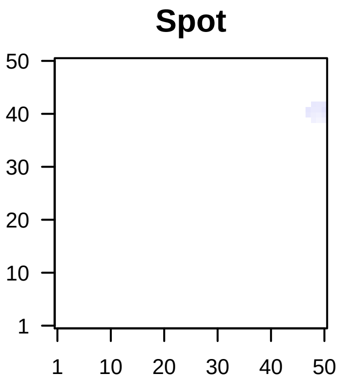
Spot Summary: K

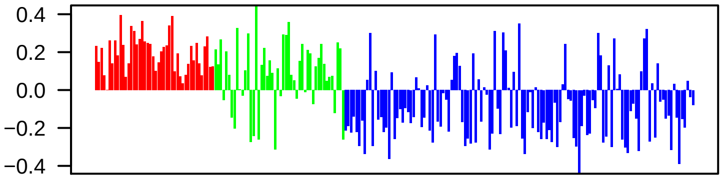
metagenes = 14
genes = 199

<r> metagenes = 0.97
<r> genes = 0.24
beta: r2= 6.27 / log p= −Inf

samples with spot = 26 (11.8 %)
mBL : 10 (22.7 %)
intermediate : 7 (14.6 %)
non−mBL : 9 (7 %)


Overview Map


Spot

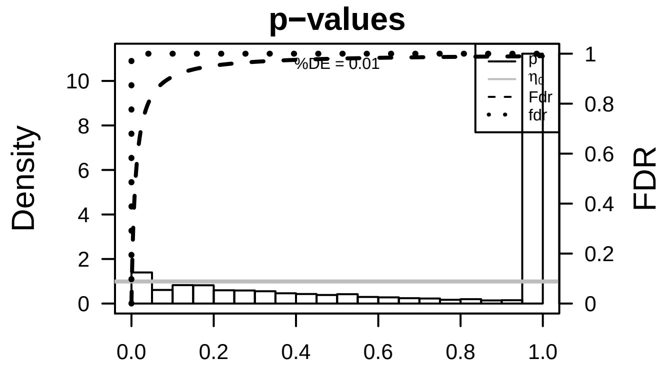


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	219655_at	2.48	−0.74	0.49	SUGCT	succinyl−CoA:glutarate−CoA transferase [Source:HGNC Sym
2	220448_at	2.35	−0.95	0.55	KCNK12	potassium two pore domain channel subfamily K member 12
3	203865_s_at	2.33	−1.02	0.38	ADARB1	adenosine deaminase, RNA specific B1 [Source:HGNC Symb
4	221879_at	2.18	−0.84	0.29		
5	205902_at	2.03	−0.94	0.51	KCNN3	potassium calcium−activated channel subfamily N member 3
6	210640_s_at	1.98	−0.91	0.39	GPER1	G protein−coupled estrogen receptor 1 [Source:HGNC Symb
7	220432_s_at	1.97	−0.86	0.6	CYP39A1	cytochrome P450 family 39 subfamily A member 1 [Source:H
8	213436_at	1.92	−1.49	0.38	CNR1	cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21
9	210461_s_at	1.78	−0.98	0.51	ABLIM1	actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGN
10	218862_at	1.71	−1.7	0.71	ASB13	ankyrin repeat and SOCS box containing 13 [Source:HGNC
11	220351_at	1.66	−0.79	0.42		C−C motif chemokine receptor like 1 pseudogene 1 [Source:
12	218922_s_at	1.62	−1.16	0.62	CERS4	ceramide synthase 4 [Source:HGNC Symbol;Acc:HGNC:237
13	203769_s_at	1.62	−0.95	0.56	STS	steroid sulfatase [Source:HGNC Symbol;Acc:HGNC:11425]
14	219753_at	1.54	−1.48	0.56	STAG3	stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356]
15	219304_s_at	1.54	−1.46	0.42	PDGFD	platelet derived growth factor D [Source:HGNC Symbol;Acc:
16	207216_at	1.5	−1.24	0.45	TNFSF8	TNF superfamily member 8 [Source:HGNC Symbol;Acc:HGN
17	213122_at	1.5	−1.06	0.36	TSPYL5	TSPY like 5 [Source:HGNC Symbol;Acc:HGNC:29367]
18	208353_x_at	1.49	−0.86	0.44	ANK1	ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492]
19	213906_at	1.47	−1.54	0.85	MYBL1	MYB proto−oncogene like 1 [Source:HGNC Symbol;Acc:HGN
20	210957_s_at	1.45	−1.17	0.63	AFF2	AF4/FMR2 family member 2 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−23	32 / 263	Lymp	SPANG_CD40 6hrs UP
2	2e−22	28 / 195	GSE	HOLLMANN_APOPTOSIS_VIA_CD40_UP
3	6e−17	118 / 5404	Lymp	HOPP_Strong_enhancer
4	4e−14	119 / 5908	Lymp	HOPP_Active_promoter
5	3e−13	13 / 61	GSE	BASSO_CD40_SIGNALING_DN
6	7e−13	114 / 5682	Lymp	HOPP_Weak_promoter
7	1e−12	19 / 186	GSE	PENG_RAPAMYCIN_RESPONSE_UP
8	1e−11	39 / 955	Lymp	SPANG_BCR UP
9	2e−10	18 / 219	Refer	WIRTH_GC B−cells
10	8e−10	14 / 133	GSE	PENG_LEUCINE_DEPRIVATION_UP
11	1e−09	19 / 275	GSE	HADDAD_B_LYMPHOCYTE_PROGENITOR
12	1e−08	5 / 8	Lymp	MASCQUE_GCB UP
13	2e−08	6 / 16	GSE	ZHAN_LATE_DIFFERENTIATION_GENES_DN
14	2e−08	9 / 56	GSE	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
15	3e−08	87 / 4357	Lymp	HOPP_Weak_txn
16	3e−08	6 / 17	Lymp	Aukema_BCL2 UP_BCL6 DN
17	4e−08	9 / 59	GSE	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
18	1e−07	88 / 4559	Lymp	HOPP_Weak_enhancer
19	3e−07	10 / 96	Lymp	SPANG_LPS 6hrs UP
20	3e−07	7 / 37	GSE	ZHAN_MULTIPLE_MYELOMA_CD2_UP
21	7e−07	5 / 15	Lymp	DAVE_BL Inter
22	1e−06	7 / 45	Lymp	Monti_BCR_cluster
23	4e−06	8 / 76	GSE	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN
24	4e−06	12 / 192	Lymp	Victora_Dark zone signature
25	6e−06	9 / 107	GSE	SMIRNOV_RESPONSE_TO_IR_6HR_DN
26	7e−06	3 / 4	Lymp	WRIGHT_custom GCB−DLBCL UP
27	8e−06	23 / 678	Refer	PROTEINATLAS_lymph node
28	8e−06	95 / 5529	Lymp	HOPP_Txn_elongation
29	1e−05	11 / 176	GSE	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN
30	1e−05	78 / 4261	Lymp	HOPP_Txn_transition
31	2e−05	9 / 121	GSE	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
32	2e−05	3 / 5	Lymp	Shaknovich_ABC_hyper_meth
33	2e−05	17 / 429	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
34	2e−05	18 / 480	Canc	Lembcke_Colonic Inflammation
35	3e−05	4 / 15	GSE	BIOCARTA_MEF2D_PATHWAY
36	3e−05	3 / 6	Lymp	Care_GCB UP
37	4e−05	10 / 168	GSE	SASAKI_ADULT_T_CELL_LEUKEMIA
38	4e−05	20 / 600	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
39	5e−05	41 / 1814	Lymp	HOPP_Repetitive
40	7e−05	27 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 107	HORVATH_aging_genes meth UP
2	0.4	1 / 47	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 92	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	

CC

Rank	p−value	#in/all	Geneset
1	5e−04	78 / 4701	cytoplasm
2	1e−03	65 / 3805	cytosol
3	2e−03	6 / 104	trans−Golgi network
4	2e−03	22 / 936	cytoskeleton
5	3e−03	55 / 3210	plasma membrane
6	5e−03	72 / 4579	nucleus
7	8e−03	5 / 101	growth cone
8	1e−02	20 / 938	Golgi apparatus
9	1e−02	7 / 196	nuclear membrane
10	1e−02	4 / 72	cell body
11	1e−02	2 / 15	pericentriolar material
12	1e−02	5 / 117	cell cortex
13	1e−02	3 / 42	azurophil granule membrane
14	2e−02	6 / 168	postsynaptic density
15	2e−02	2 / 18	replication fork

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−05	27 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	2e−04	23 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	2e−03	16 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	3e−02	30 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	6e−02	5 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	7e−02	20 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
7	8e−02	4 / 132	Marisa_CRC−cluster−a
8	8e−02	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
9	8e−02	1 / 7	TCGA−CRC_agressive−disease−markers
10	8e−02	1 / 7	Boland_CRC−MSI−TGC
11	9e−02	1 / 8	Boland_CRC−MMR−system
12	9e−02	1 / 8	Marisa_CRC−C1
13	1e−01	10 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	1e−01	6 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
15	2e−01	6 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

HM

Rank	p−value	#in/all	Geneset
1	0.02	6 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.02	6 / 173	HALLMARK_MITOTIC_SPINDLE
3	0.03	5 / 141	HALLMARK_UV_RESPONSE_DN
4	0.03	6 / 191	HALLMARK_P53_PATHWAY
5	0.05	2 / 29	HALLMARK_NOTCH_SIGNALING
6	0.11	3 / 96	HALLMARK_ANDROGEN_RESPONSE
7	0.12	3 / 97	HALLMARK_BILE_ACID_METABOLISM
8	0.17	4 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	0.21	4 / 193	HALLMARK_HEME_METABOLISM
10	0.21	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.37	3 / 178	HALLMARK_COMPLEMENT
12	0.38	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
13	0.40	3 / 187	HALLMARK_E2F_TARGETS
14	0.47	1 / 51	HALLMARK_TGF_BETA_SIGNALING
15	0.47	2 / 130	HALLMARK_COAGULATION

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−23	32 / 263	SPANG_CD40 6hrs UP
2	6e−17	118 / 5404	HOPP_Strong_enhancer
3	4e−14	119 / 5908	HOPP_Active_promoter
4	7e−13	114 / 5682	HOPP_Weak_promoter
5	1e−11	39 / 955	SPANG_BCR UP
6	1e−08	5 / 8	MASCQUE_GCB UP
7	3e−08	87 / 4357	HOPP_Weak_txn
8	3e−08	6 / 17	Aukema_BCL2 UP_BCL6 DN
9	1e−07	88 / 4559	HOPP_Weak_enhancer
10	3e−07	10 / 96	SPANG_LPS 6hrs UP
11	7e−07	5 / 15	DAVE_BL Inter
12	1e−06	7 / 45	Monti_BCR_cluster
13	4e−06	12 / 192	Victora_Dark zone signature
14	7e−06	3 / 4	WRIGHT_custom GCB−DLBCL UP
15	8e−06	95 / 5529	HOPP_Txn_elongation

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−04	6 / 92	hsa−miR−199a−5p
2	1e−03	6 / 101	hsa−miR−199b−5p
3	2e−03	7 / 146	hsa−miR−548k
4	2e−03	3 / 22	hsa−miR−1287
5	4e−03	4 / 53	hsa−miR−606
6	5e−03	4 / 56	hsa−miR−193b
7	1e−02	4 / 69	hsa−miR−125a−5p
8	1e−02	4 / 73	hsa−miR−125b
9	1e−02	3 / 41	hsa−miR−504
10	1e−02	6 / 160	hsa−miR−545
11	2e−02	5 / 124	hsa−miR−633
12	2e−02	3 / 46	hsa−miR−193a−3p
13	2e−02	3 / 47	hsa−miR−634
14	2e−02	3 / 48	hsa−miR−1243
15	2e−02	2 / 19	hsa−miR−517c

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	

BP

Rank	p−value	#in/all	Geneset
1	1e−04	14 / 361	intracellular signal transduction
2	5e−04	16 / 507	protein phosphorylation
3	6e−04	3 / 14	regulation of establishment of cell polarity
4	7e−04	8 / 157	positive regulation of cell migration
5	1e−03	3 / 17	T cell proliferation
6	2e−03	6 / 104	response to ethanol
7	2e−03	7 / 146	cytoskeleton organization
8	5e−03	15 / 576	phosphorylation
9	6e−03	4 / 60	positive regulation of JNK cascade
10	6e−03	2 / 10	filopodium assembly
11	6e−03	2 / 10	protein deacetylation
12	7e−03	4 / 63	regulation of insulin secretion
13	7e−03	3 / 33	T cell differentiation
14	7e−03	3 / 33	Wnt signaling pathway, calcium modulating pathway
15	8e−03	2 / 11	mast cell degranulation

Chr

Rank	p−value	#in/all	Geneset
1	0.008	16 / 669	Chr 6
2	0.012	14 / 585	Chr 7
3	0.017	12 / 490	Chr 10
4	0.018	11 / 437	Chr 8
5	0.084	22 / 1325	Chr 1
6	0.086	13 / 700	Chr 12
7	0.241	3 / 139	Chr 21
8	0.370	7 / 480	Chr 4
9	0.465	9 / 689	Chr 3
10	0.566	10 / 832	Chr 2
11	0.660	2 / 184	Chr 18
12	0.689	4 / 382	Chr 15
13	0.822	7 / 756	Chr 11
14	0.874	3 / 403	Chr 14
15	0.917	2 / 333	Chr 22

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	13 / 421	Down_b
2	0.006	4 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.022	8 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	0.035	10 / 423	Down_a
5	0.061	7 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
6	0.071	1 / 6	Shaw_responders_up_in_oligo_glioma
7	0.081	6 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
8	0.094	1 / 8	Shaw_up_in_1p19qdel
9	0.097	9 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
10	0.104	2 / 45	OL vs. MOG− OL
11	0.109	7 / 330	Up
12	0.110	6 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
13	0.126	1 / 11	KIM amplified & overexpressed in LTS
14	0.126	1 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
15	0.130	11 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP

Immunome

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 13	Angelova_immune−metagene−immature_B−cells
2	1e−02	2 / 13	Angelova_immune−metagene−activated_B−cells
3	9e−02	1 / 8	Angelova_immune−metagene−mDC
4	1e−01	1 / 10	Angelova_immune−metagene−neutrophils
5	1e−01	1 / 10	Angelova_immune−metagene−TFH
6	1e−01	1 / 11	Angelova_immune−metagene−macrophages
7	1e−01	1 / 12	Angelova_immune−metagene−memory_B−cells
8	2e−01	1 / 15	Angelova_immune−metagene−NK
9	2e−01	1 / 16	Angelova_immune−metagene−Th17
10	2e−01	2 / 67	Angelova_immune−metagene−T−cells
11	2e−01	1 / 18	Angelova_CRC_immunostimulators
12	2e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
13	3e−01	1 / 32	Angelova_immune−metagene−effector_memory_CD8
14	4e−01	1 / 38	Angelova_immune−metagene−mast−cells
15	4e−01	1 / 42	Angelova_immune−metagene−TGD

Melanoma

Rank	p−value	#in/all	Geneset
1	0.002	6 / 107	Tirosh_Exhaustion program in Mel75
2	0.003	3 / 24	Tirosh_B−cell specific genes−melanoma
3	0.019	4 / 83	TCGA_melanoma_immune_high
4	0.048	1 / 4	Melanoma Epi−Enzyme Cluster 3
5	0.055	6 / 222	Gerber_wt/wt_melanoma−cells−SpotF
6	0.128	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	0.195	6 / 319	Gerber_wt/wt_melanoma−cells−SpotA
8	0.200	4 / 189	Tirosh_genes preferentially expressed by Tregs
9	0.248	5 / 276	Gerber_wt/wt_melanoma−cells−SpotB
10	0.251	2 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
11	0.255	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
12	0.333	1 / 33	Tirosh_T−cell specific genes−melanoma
13	0.373	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
14	0.381	1 / 39	Tirosh_top50 correlated genes PC4
15	0.404	7 / 497	Gerber_wt/wt_melanoma−cells−SpotD

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.002	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.089	2 / 41	Scicluna_DN
3	0.333	1 / 33	Sweeney_viral_dn
4	0.365	1 / 37	Sweeney_viral_up
5	0.440	2 / 122	Terre_IMS_influenza_meta_signature
6	0.498	1 / 56	Burnham_sep_vs_con_DN
7	0.504	1 / 57	Burnham_viral_UP
8	0.504	1 / 57	Burnham_day1_vs_5_UP
9	0.811	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
10	1.000	0 / 68	Burnham_sep_vs_con_UP
11	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.000	0 / 71	Burnham_cap_fp_vs_con_UP
13	1.000	0 / 48	Burnham_viral_DN
14	1.000	0 / 52	Burnham_day1_vs_5_DN
15	1.000	0 / 54	Burnham_timecourse

TF

Rank	p−value	#in/all	Geneset
1	6e−04	33 / 1508	ICGC_Mef2_targets
2	1e−03	43 / 2254	ICGC_BatfPcr1_targets
3	1e−03	37 / 1848	ICGC_Pbx3_targets
4	8e−03	22 / 1041	ICGC_P300_targets
5	8e−03	31 / 1636	ICGC_Bcl11_targets
6	1e−02	48 / 2899	ICGC_Nfatc1_targets
7	1e−02	55 / 3451	ICGC_Atf2_targets
8	2e−02	39 / 2321	ICGC_Rad21_targets
9	3e−02	20 / 1032	ICGC_Usf1_targets
10	3e−02	58 / 3796	ICGC_Nficsc81335_targets
11	4e−02	11 / 485	ICGC_NrsfPcr2_targets
12	4e−02	26 / 1494	ICGC_Cebpbsc150_targets
13	4e−02	32 / 1941	ICGC_Bcl3_targets
14	5e−02	54 / 3630	ICGC_Sp1_targets
15	6e−02	47 / 3121	ICGC_Egr1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	18 / 480	Lembcke_Colonic Inflammation
2	2e−03	5 / 72	PanCan_Wnt_geneset_nanostring
3	5e−03	6 / 130	PanCan_CC+Apop_geneset_nanostring
4	2e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
5	7e−02	1 / 6	ZHANG_MGUS up
6	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
7	1e−01	1 / 10	GENTLES_modul3
8	1e−01	1 / 11	GENTLES_modul14
9	1e−01	1 / 13	GENTLES_modul17
10	2e−01	1 / 14	GUSTAFSON_PI3K_UP
11	2e−01	1 / 14	GUSTAFSON_PI3K_DN
12	2e−01	1 / 15	RHODES_CANCER_META_SIGNATURE
13	2e−01	1 / 15	WANG_ER_UP
14	2e−01	1 / 15	GENTLES_modul4
15	2e−01	1 / 16	LIU_LIVER_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−14	92 / 3767	Bcells peripheral blood_6_EnhG
2	3e−13	143 / 8406	Bcells peripheral blood_2_TssAFlnk
3	9e−13	137 / 7833	Bcells peripheral blood_1_TssA
4	9e−13	142 / 8370	natural killer cells peripheral blood_2_TssAFlnk
5	1e−12	114 / 5716	Bcells peripheral blood_4_Tx
6	1e−12	138 / 7957	Tcells peripheral blood_2_TssAFlnk
7	2e−12	146 / 8865	Thelper cells peripheral blood_7_Enh
8	2e−12	129 / 7078	Bcells peripheral blood_5_TxWk
9	2e−12	133 / 7489	monocytes peripheral blood_5_TxWk
10	3e−12	132 / 7407	natural killer cells peripheral blood_5_TxWk
11	4e−12	145 / 8816	Thelper cells peripheral blood_2_TssAFlnk
12	5e−12	135 / 7751	natural killer cells peripheral blood_1_TssA
13	8e−12	139 / 8208	Tcells peripheral blood_7_Enh
14	1e−11	131 / 7420	Tcells peripheral blood_1_TssA
15	2e−11	148 / 9298	Bcells peripheral blood_7_Enh

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−22	28 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
2	3e−13	13 / 61	BASSO_CD40_SIGNALING_DN
3	1e−12	19 / 186	PENG_RAPAMYCIN_RESPONSE_UP
4	8e−10	14 / 133	PENG_LEUCINE_DEPRIVATION_UP
5	1e−09	19 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
6	2e−08	6 / 16	ZHAN_LATE_DIFFERENTIATION_GENES_DN
7	2e−08	9 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
8	4e−08	9 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
9	3e−07	7 / 37	ZHAN_MULTIPLE_MYELOMA_CD2_UP
10	4e−06	8 / 76	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN
11	6e−06	9 / 107	SMIRNOV_RESPONSE_TO_IR_6HR_DN
12	1e−05	11 / 176	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN
13	2e−05	9 / 121	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
14	2e−05	17 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
15	3e−05	4 / 15	BIOCARTA_MEF2D_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	6 / 210	Homuth_BMI−associated−genes_DN
2	0.06	2 / 32	Marjolein_ageing−genes_DN
3	0.09	1 / 8	Marjolein_ageing−genes_UP
4	0.84	1 / 150	Homuth_BMI−associated−genes_UP
5	1.00	0 / 62	DUMEAUX_Smoking enriched genes
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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 22	DUMEAUX_High bmi enriched genes
15	1.00	0 / 22	DUMEAUX_Fasting enriched genes

MF

Rank	p−value	#in/all	Geneset
1	9e−04	11 / 291	actin binding
2	9e−04	14 / 437	protein kinase activity
3	9e−04	8 / 165	calmodulin binding
4	4e−03	3 / 26	cyclin−dependent protein serine/threonine kinase activity
5	4e−03	7 / 163	magnesium ion binding
6	4e−03	15 / 573	kinase activity
7	6e−03	2 / 10	inositol−1,3,4,5−tetrakisphosphate 5−phosphatase activity
8	6e−03	2 / 10	MAP kinase kinase kinase kinase activity
9	7e−03	10 / 331	protein serine/threonine kinase activity
10	8e−03	2 / 11	ATPase activity, coupled
11	8e−03	111 / 7864	protein binding
12	1e−02	2 / 15	phospholipid−translocating ATPase activity
13	1e−02	9 / 312	enzyme binding
14	2e−02	3 / 44	protein serine/threonine phosphatase activity
15	2e−02	3 / 46	non−membrane spanning protein tyrosine kinase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−10	18 / 219	WIRTH_GC B−cells
2	8e−06	23 / 678	PROTEINATLAS_lymph node
3	1e−04	5 / 42	Chaussabel_1,3_B−cells
4	5e−04	9 / 188	Chaussabel_3,8_Enzymes
5	9e−04	24 / 989	PROTEINATLAS_tonsil
6	7e−03	3 / 32	Chaussabel_1,1_Plasma Cells
7	9e−03	4 / 68	Chaussabel_2,1_Cytotoxic cells
8	1e−02	10 / 355	WIRTH_Immune system
9	1e−02	2 / 15	WIRTH_Cerebellum
10	3e−02	14 / 645	PROTEINATLAS_bone marrow
11	3e−02	2 / 22	Chaussabel_1,6_Signaling molecules
12	3e−02	4 / 99	Chaussabel_1,5_Myeloid lineage
13	3e−02	4 / 100	Chaussabel_2,8_T−cells
14	4e−02	11 / 496	PROTEINATLAS_spleen
15	4e−02	4 / 109	Chaussabel_2,6_Myeloid lineage

D−Cluster

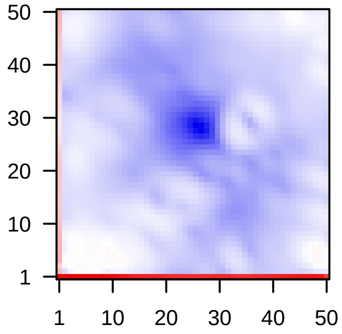
Spot Summary: L

metagenes = 35
genes = 603

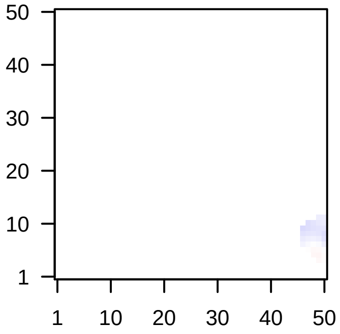
<r> metagenes = 0.93
<r> genes = 0.31
beta: r2= 6.01 / log p= −Inf

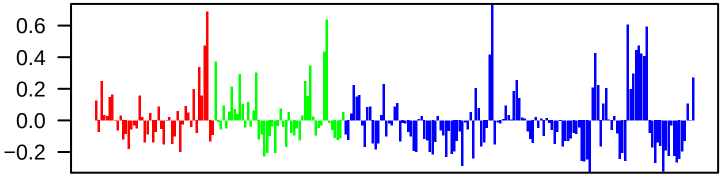
samples with spot = 20 (9 %)
mBL : 3 (6.8 %)
intermediate : 6 (12.5 %)
non−mBL : 11 (8.5 %)

Overview Map



Spot





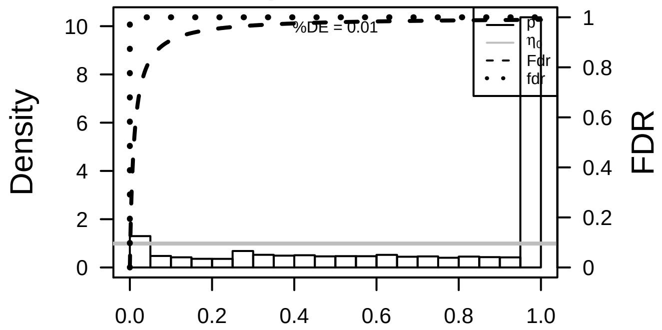
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	216766_at	2.26	−0.64	0.68		
2	222357_at	2.23	−0.66	0.62	ZBTB20	zinc finger and BTB domain containing 20 [Source:HGNC Sy
3	215200_x_at	2.17	−1.11	0.57		
4	222073_at	2.16	−0.87	0.38	COL4A3	collagen type IV alpha 3 chain [Source:HGNC Symbol;Acc:H
5	214753_at	2.14	−1.23	0.74		
6	212225_at	2.11	−0.84	0.45	EIF1	eukaryotic translation initiation factor 1 [Source:HGNC Symb
7	207492_at	2.1	−1.01	0.76		
8	205316_at	2.09	−0.97	0.56	SLC15A2	solute carrier family 15 member 2 [Source:HGNC Symbol;Ac
9	220918_at	2.03	−0.81	0.79		
10	207078_at	1.96	−0.94	0.74	MED6	mediator complex subunit 6 [Source:HGNC Symbol;Acc:HGN
11	208268_at	1.89	−0.91	0.51	ADAM28	ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
12	215392_at	1.89	−0.68	0.77		
13	208195_at	1.84	−1.07	0.36	TTN	titin [Source:HGNC Symbol;Acc:HGNC:12403]
14	222375_at	1.83	−0.72	0.68		
15	220940_at	1.83	−1.2	0.76		
16	215164_at	1.82	−1.12	0.57		
17	213931_at	1.82	−1.03	0.39	ID2	inhibitor of DNA binding 2 [Source:HGNC Symbol;Acc:HGNC
18	215768_at	1.81	−0.79	0.42		
19	217534_at	1.8	−0.88	0.75	FAM49B	family with sequence similarity 49 member B [Source:HGNC
20	216197_at	1.78	−0.87	0.77		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−50	137 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
2	2e−39	54 / 188	Refer	Chaussabel_3,8_Enzymes
3	3e−27	46 / 218	Refer	WIRTH_pre+post GC B−cells
4	2e−26	221 / 4261	Lymph	HOPP_Txn_transition
5	5e−22	250 / 5529	Lymph	HOPP_Txn_elongation
6	7e−20	15 / 20	Refer	Chaussabel_2,7_Unknown function
7	7e−20	57 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
8	2e−15	26 / 127	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
9	2e−14	18 / 59	Gliom	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	3e−13	32 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
11	2e−12	7 / 14	Cance	LIU_COMMON_CANCER_GENES
12	2e−12	7 / 14	Cance	LIU_COMMON_CANCER_GENES
13	2e−12	63 / 852	MF	nucleic acid binding
14	2e−11	23 / 143	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
15	1e−10	90 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
16	1e−10	23 / 159	GSEA	JISON_SICKLE_CELL_DISEASE_DN
17	2e−10	158 / 3564	TF	ICGC_Taf1_targets
18	4e−09	17 / 102	Lymph	ROSOLOWSKI_blue total
19	7e−09	11 / 39	GSEA	BILBAN_B_CLL_LPL_DN
20	8e−09	8 / 17	GSEA	SPIRA_SMOKERS_LUNG_CANCER_DN
21	9e−09	28 / 281	BP	mRNA processing
22	5e−08	23 / 214	GSEA	CHEN_HOXA5_TARGETS_9HR_UP
23	6e−08	181 / 4579	CC	nucleus
24	6e−08	18 / 136	GSEA	REACTOME_MRNA_PROCESSING
25	7e−08	42 / 600	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
26	9e−08	8 / 22	Refer	Chaussabel_1,6_Signaling molecules
27	2e−07	134 / 3150	TF	ICGC_Creb1_targets
28	2e−07	54 / 906	Lymph	SPANG_BCR DN
29	2e−07	218 / 5908	Lymph	HOPP_Active_promoter
30	2e−07	23 / 233	BP	RNA splicing
31	3e−07	16 / 120	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
32	3e−07	14 / 92	GSEA	HOEBEKE_LYMPHOID_STEM_CELL_UP
33	3e−07	15 / 106	Refer	Chaussabel_2,11_Replication
34	3e−07	51 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
35	4e−07	69 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
36	5e−07	63 / 1161	MF	RNA binding
37	9e−07	45 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
38	9e−07	34 / 477	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
39	1e−06	18 / 165	GSEA	THUM_SYSTOLIC_HEART_FAILURE_DN
40	1e−06	151 / 3796	TF	ICGC_Nficsc81335_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.9	1 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	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−09	28 / 281	mRNA processing
2	2e−07	23 / 233	RNA splicing
3	2e−05	18 / 198	mRNA splicing, via spliceosome
4	5e−05	11 / 90	RNA processing
5	9e−05	73 / 1655	transcription, DNA−templated
6	2e−04	6 / 31	regulation of alternative mRNA splicing, via spliceosome
7	3e−04	7 / 47	mRNA 3'−end processing
8	5e−04	7 / 49	RNA export from nucleus
9	7e−04	4 / 15	mRNA splice site selection
10	9e−04	8 / 71	regulation of G2/M transition of mitotic cell cycle
11	1e−03	7 / 56	termination of RNA polymerase II transcription
12	1e−03	72 / 1764	regulation of transcription, DNA−templated
13	1e−03	4 / 17	negative regulation of mRNA splicing, via spliceosome
14	2e−03	8 / 79	ciliary basal body−plasma membrane docking
15	3e−03	8 / 83	viral transcription

Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	7 / 14	LIU_COMMON_CANCER_GENES
2	5e−04	4 / 14	GUSTAFSON_PI3K_DN
3	4e−02	2 / 12	LIU_BREAST_CANCER
4	6e−02	2 / 14	BENTINK_ras.6
5	6e−02	2 / 14	BENTINK_src.2
6	8e−02	2 / 16	LIU_LIVER_CANCER
7	3e−01	1 / 10	GENTLES_modul5
8	3e−01	1 / 12	BENTINK_e2f3.2
9	3e−01	4 / 96	PanCan_TXmisReg_geneset_nanostring
10	3e−01	1 / 14	GENTLES_modul10
11	3e−01	1 / 14	BENTINK_myc.1
12	3e−01	5 / 134	PanCan_RAS_geneset_nanostring
13	4e−01	2 / 45	KUIPER_MM poor survival
14	4e−01	2 / 47	PanCan_TGF−B_geneset_nanostring
15	4e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−08	181 / 4579	nucleus
2	8e−06	25 / 326	nuclear speck
3	5e−05	104 / 2541	nucleoplasm
4	1e−03	21 / 354	centrosome
5	2e−03	9 / 101	kinetochore
6	4e−03	10 / 128	spliceosomal complex
7	4e−03	6 / 54	axoneme
8	4e−03	12 / 174	cilium
9	6e−03	5 / 41	cytosolic large ribosomal subunit
10	1e−02	129 / 3805	cytosol
11	1e−02	3 / 18	cytoplasmic dynein complex
12	2e−02	8 / 118	chromosome, centromeric region
13	2e−02	14 / 268	intracellular ribonucleoprotein complex
14	2e−02	6 / 77	condensed chromosome kinetochore
15	3e−02	2 / 10	azurophil granule

Chr

Rank	p−value	#in/all	Geneset
1	0.005	37 / 833	Chr 19
2	0.008	26 / 548	Chr 16
3	0.012	20 / 403	Chr 14
4	0.058	30 / 776	Chr 17
5	0.104	7 / 139	Chr 21
6	0.117	22 / 585	Chr 7
7	0.186	24 / 689	Chr 3
8	0.276	23 / 700	Chr 12
9	0.413	12 / 382	Chr 15
10	0.484	13 / 437	Chr 8
11	0.485	10 / 333	Chr 22
12	0.516	24 / 832	Chr 2
13	0.543	7 / 242	Chr 13
14	0.616	10 / 369	Chr 20
15	0.697	1 / 41	Chr Y

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−32	276 / 5766	natural killer cells peripheral blood_4_Tx
2	2e−31	271 / 5601	Thelper cells peripheral blood_4_Tx
3	3e−30	273 / 5753	Tcells peripheral blood_4_Tx
4	3e−28	268 / 5716	Bcells peripheral blood_4_Tx
5	1e−26	230 / 4528	T CD8+ naive cells peripheral blood_4_Tx
6	4e−26	318 / 7833	Bcells peripheral blood_1_TssA
7	8e−26	258 / 5527	Tregulatory cells peripheral blood_4_Tx
8	2e−25	307 / 7420	Tcells peripheral blood_1_TssA
9	7e−25	272 / 6099	HSC_4_Tx
10	2e−23	251 / 5456	5_Tx_Neuronal_Progenitor
11	2e−23	213 / 4208	Tcells peripheral blood_6_EnhG
12	4e−23	288 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
13	8e−23	325 / 8406	Bcells peripheral blood_2_TssAFlnk
14	1e−22	283 / 6679	5_Tx_Melanocytes
15	1e−22	194 / 3682	natural killer cells peripheral blood_6_EnhG

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−50	137 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	7e−20	57 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
3	3e−07	51 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
4	4e−04	42 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
5	6e−04	214 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
6	2e−03	5 / 31	Marisa_CRC−cluster−c
7	4e−03	3 / 12	Juehling_HNPCC−mutated−in−4
8	7e−03	6 / 60	Marisa_CRC−cluster−g
9	2e−02	24 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
10	2e−02	63 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
11	6e−02	2 / 14	TCGA_Mutated−in−CRC_non−hypermutated
12	6e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
13	8e−02	2 / 16	Vilar_mutated−in−CRC−CamP
14	8e−02	2 / 16	Vilar_non−hypermutated−in−CRC
15	8e−02	22 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN

Glioma

Rank	p−value	#in/all	Geneset
1	2e−14	18 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	1e−04	68 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−03	3 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
4	2e−03	3 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
5	3e−03	56 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	6e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
7	7e−02	2 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
8	2e−01	22 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	2e−01	3 / 50	Vishal_subnetwork signature of survival in GBM
10	3e−01	1 / 10	Phillips PN up vs MES & Prolif
11	3e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
12	3e−01	3 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
13	3e−01	3 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	3e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	3e−01	4 / 99	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−15	26 / 127	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
2	3e−13	32 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
3	2e−12	7 / 14	LIU_COMMON_CANCER_GENES
4	2e−11	23 / 143	LEE_DIFFERENTIATING_T_LYMPHOCYTE
5	1e−10	90 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
6	1e−10	23 / 159	JISON_SICKLE_CELL_DISEASE_DN
7	7e−09	11 / 39	BILBAN_B_CLL_LPL_DN
8	8e−09	8 / 17	SPIRA_SMOKERS_LUNG_CANCER_DN
9	5e−08	23 / 214	CHEN_HOXA5_TARGETS_9HR_UP
10	6e−08	18 / 136	REACTOME_MRNA_PROCESSING
11	7e−08	42 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
12	3e−07	16 / 120	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
13	3e−07	14 / 92	HOEBEKE_LYMPHOID_STEM_CELL_UP
14	4e−07	69 / 1312	PUJANA_ATM_PCC_NETWORK
15	9e−07	45 / 730	ONKEN_UVEAL_MELANOMA_UP

HM

Rank	p−value	#in/all	Geneset
1	0.1	8 / 173	HALLMARK_MITOTIC_SPINDLE
2	0.2	3 / 51	HALLMARK_TGF_BETA_SIGNALING
3	0.2	8 / 193	HALLMARK_HEME_METABOLISM
4	0.3	2 / 34	HALLMARK_APICAL_SURFACE
5	0.3	7 / 187	HALLMARK_E2F_TARGETS
6	0.3	7 / 195	HALLMARK_G2M_CHECKPOINT
7	0.3	5 / 133	HALLMARK_DNA_REPAIR
8	0.4	2 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.5	6 / 188	HALLMARK_HYPOXIA
10	0.5	6 / 190	HALLMARK_MYC_TARGETS_V1
11	0.5	3 / 97	HALLMARK_BILE_ACID_METABOLISM
12	0.6	1 / 34	HALLMARK_ANGIOGENESIS
13	0.6	5 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	0.6	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
15	0.7	5 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	2 / 13	Angelova_immune−metagene−immature_B−cells
2	0.14	1 / 5	Angelova_immune−metagene−NKT
3	0.18	1 / 7	Angelova_immune−metagene−cytotoxic_cells
4	0.25	1 / 10	Angelova_immune−metagene−neutrophils
5	0.37	2 / 45	Angelova_immune−metagene−MDSC
6	0.41	1 / 18	Angelova_immune−metagene−pDC
7	0.41	1 / 18	Angelova_CRC_immunostimulators
8	0.49	1 / 23	Angelova_immune−metagene−monocytes
9	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
10	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
11	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
12	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
13	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
14	1.00	0 / 25	Angelova_immune−metagene−DC
15	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	2 / 22	DUMEAUX_Fasting enriched genes
2	0.4	7 / 210	Homuth_BMI−associated−genes_DN
3	0.4	5 / 150	Homuth_BMI−associated−genes_UP
4	0.5	1 / 22	DUMEAUX_High bmi enriched genes
5	0.8	1 / 62	DUMEAUX_Smoking enriched genes
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−26	221 / 4261	HOPP_Txn_transition
2	5e−22	250 / 5529	HOPP_Txn_elongation
3	4e−09	17 / 102	ROSOLOWSKI_blue total
4	2e−07	54 / 906	SPANG_BCR DN
5	2e−07	218 / 5908	HOPP_Active_promoter
6	2e−06	199 / 5404	HOPP_Strong_enhancer
7	9e−03	5 / 45	Monti_BCR_cluster
8	1e−02	2 / 6	MASCQUE_mBL UP
9	2e−02	2 / 7	Shaknovich_ABC_hypo_meth
10	2e−02	7 / 99	Sha_BL UP
11	7e−02	2 / 15	BENTINK_mBL UP
12	7e−02	2 / 15	DAVE_BL Inter
13	9e−02	176 / 5682	HOPP_Weak_promoter
14	1e−01	2 / 19	Subero_MCL_hypo_meth
15	1e−01	34 / 955	SPANG_BCR UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	3 / 24	Tirosh_B−cell specific genes−melanoma
2	0.05	11 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	0.06	1 / 2	Melanoma Epi−Enzyme Cluster 6
4	0.13	4 / 68	Tirosh_housekeeping_genes
5	0.14	2 / 23	Melanoma Epi−Enzyme Cluster 7
6	0.16	8 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
7	0.21	12 / 319	Gerber_wt/wt_melanoma−cells−SpotA
8	0.27	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
9	0.34	8 / 230	Gerber_wt/wt_melanoma−cells−SpotC
10	0.36	8 / 236	Gerber_wt/wt_group3−specific
11	0.37	1 / 16	Hugo_melanoma−all−LEF1_UP
12	0.39	2 / 47	Tirosh_G2/M phase specific genes
13	0.43	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
14	0.50	1 / 24	Gerami_melanoma−metastatic−risk_DN
15	0.57	7 / 249	Gerber_wt/wt_melanoma−cells−SpotE

MF

Rank	p−value	#in/all	Geneset
1	2e−12	63 / 852	nucleic acid binding
2	5e−07	63 / 1161	RNA binding
3	5e−04	8 / 65	thiol−dependent ubiquitinyl hydrolase activity
4	6e−04	10 / 100	cysteine−type peptidase activity
5	1e−03	7 / 57	thiol−dependent ubiquitin−specific protease activity
6	2e−03	63 / 1541	DNA binding
7	2e−03	4 / 20	RNA polymerase II transcription corepressor activity
8	4e−03	9 / 107	mRNA binding
9	1e−02	5 / 50	cysteine−type endopeptidase activity
10	2e−02	3 / 19	miRNA binding
11	2e−02	3 / 20	dynein complex binding
12	2e−02	5 / 55	double−stranded RNA binding
13	2e−02	3 / 22	translation factor activity, RNA binding
14	3e−02	3 / 23	telomeric DNA binding
15	3e−02	9 / 150	protein tyrosine kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	13 / 111	hsa−miR−656
2	7e−05	8 / 49	hsa−miR−330−5p
3	3e−04	9 / 75	hsa−miR−188−5p
4	3e−04	23 / 363	hsa−miR−195
5	6e−04	23 / 378	hsa−miR−16
6	7e−04	21 / 336	hsa−miR−519d
7	8e−04	10 / 105	hsa−miR−335
8	9e−04	22 / 368	hsa−miR−301a
9	1e−03	16 / 232	hsa−miR−186
10	1e−03	20 / 324	hsa−miR−497
11	1e−03	26 / 474	hsa−miR−20a
12	1e−03	6 / 44	hsa−miR−455−5p
13	2e−03	17 / 267	hsa−miR−142−5p
14	2e−03	21 / 369	hsa−miR−15b
15	2e−03	5 / 33	hsa−miR−654−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	4e−06	18 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	3e−01	2 / 41	Scicluna_DN
3	5e−01	2 / 54	Burnham_timecourse
4	6e−01	1 / 33	Sweeney_viral_dn
5	1e+00	1 / 122	Terre_IMS_influenza_meta_signature
6	1e+00	0 / 68	Burnham_sep_vs_con_UP
7	1e+00	0 / 56	Burnham_sep_vs_con_DN
8	1e+00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1e+00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1e+00	0 / 48	Burnham_viral_DN
11	1e+00	0 / 57	Burnham_viral_UP
12	1e+00	0 / 57	Burnham_day1_vs_5_UP
13	1e+00	0 / 52	Burnham_day1_vs_5_DN
14	1e+00	0 / 18	Scicluna_UP
15	1e+00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−39	54 / 188	Chaussabel_3,8_Enzymes
2	3e−27	46 / 218	WIRTH_pre+post GC B−cells
3	7e−20	15 / 20	Chaussabel_2,7_Unknown function
4	9e−08	8 / 22	Chaussabel_1,6_Signaling molecules
5	3e−07	15 / 106	Chaussabel_2,11_Replication
6	2e−05	17 / 182	WIRTH_post GC B−cells
7	3e−05	51 / 989	PROTEINATLAS_tonsil
8	8e−05	43 / 819	PROTEINATLAS_bronchus
9	1e−04	14 / 152	VAQUERIZAS_General_TF
10	2e−04	43 / 848	PROTEINATLAS_adrenal gland
11	3e−04	43 / 861	PROTEINATLAS_nasopharynx
12	3e−04	42 / 840	PROTEINATLAS_urinary bladder
13	4e−04	50 / 1076	PROTEINATLAS_stomach
14	5e−04	27 / 474	PROTEINATLAS_vagina
15	9e−04	34 / 671	PROTEINATLAS_cervix, uterine

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	2e−10	158 / 3564	ICGC_Taf1_targets
2	2e−07	134 / 3150	ICGC_Creb1_targets
3	1e−06	151 / 3796	ICGC_Nficsc81335_targets
4	3e−06	166 / 4319	ICGC_Pou2_targets
5	3e−06	150 / 3804	ICGC_Stat5_targets
6	6e−06	173 / 4602	ICGC_Elf1_targets
7	7e−06	147 / 3769	ICGC_Pmlsc71910_targets
8	1e−05	157 / 4131	ICGC_Tcf3_targets
9	2e−05	125 / 3121	ICGC_Egr1_targets
10	2e−05	143 / 3703	ICGC_Foxm1_targets
11	3e−05	160 / 4278	ICGC_Yy1_targets
12	3e−05	177 / 4851	ICGC_Runx3_targets
13	8e−05	132 / 3451	ICGC_Atf2_targets
14	9e−05	151 / 4072	ICGC_Mta3_targets
15	2e−04	113 / 2899	ICGC_Nfatc1_targets

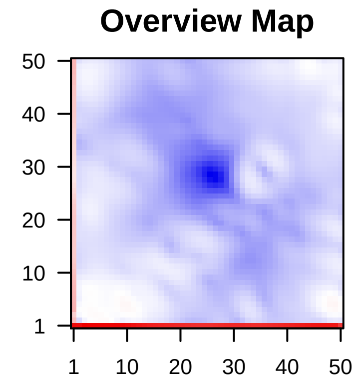
D−Cluster

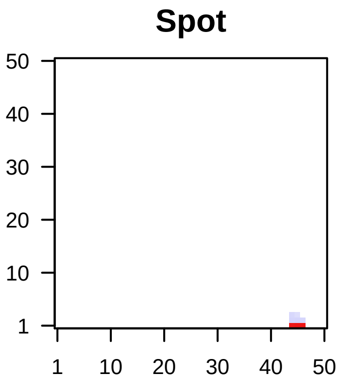
Spot Summary: M

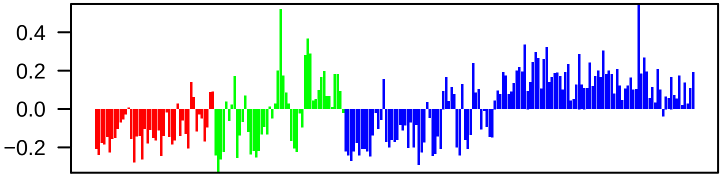
metagenes = 8
genes = 207

<r> metagenes = 0.99
<r> genes = 0.36
beta: r2= 6.91 / log p= −Inf

samples with spot = 12 (5.4 %)
intermediate : 4 (8.3 %)
non−mBL : 8 (6.2 %)





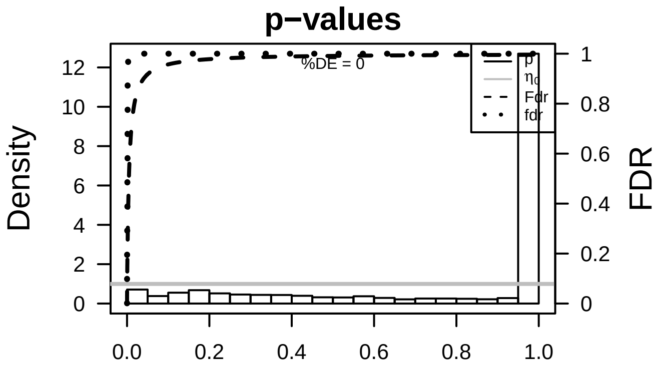


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212236_x_at	2.22	−0.68	0.53	KRT17	keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
2	202222_s_at	1.96	−0.73	0.58	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
3	207337_at	1.83	−1.04	0.54	CTAG2	cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
4	206760_s_at	1.74	−0.74	0.48	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HG
5	205334_at	1.65	−0.71	0.54	S100A1	S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:
6	208607_s_at	1.55	−0.64	0.49	SAA2	serum amyloid A2 [Source:HGNC Symbol;Acc:HGNC:10514]
7	208868_s_at	1.41	−0.86	0.39	GABARAPL1	GABA type A receptor associated protein like 1 [Source:HGN
8	206729_at	1.4	−0.95	0.43	TNFRSF8	TNF receptor superfamily member 8 [Source:HGNC Symbol;
9	211893_x_at	1.38	−0.71	0.45	CD6	CD6 molecule [Source:HGNC Symbol;Acc:HGNC:1691]
10	211900_x_at	1.31	−0.62	0.52	CD6	CD6 molecule [Source:HGNC Symbol;Acc:HGNC:1691]
11	211531_x_at	1.27	−0.96	0.39	PRB1	proline rich protein BstNI subfamily 1 [Source:HGNC Symbol;
12	212772_s_at	1.27	−0.57	0.44	ABCA2	ATP binding cassette subfamily A member 2 [Source:HGNC
13	205674_x_at	1.26	−0.71	0.46	FXYD2	FXYD domain containing ion transport regulator 2 [Source:H
14	209008_x_at	1.25	−0.56	0.58		keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:3
15	220686_s_at	1.22	−0.65	0.63	PIWIL2	piwi like RNA−mediated gene silencing 2 [Source:HGNC Sym
16	209768_s_at	1.17	−1.14	0.59		
17	217597_x_at	1.14	−0.78	0.75	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
18	217389_s_at	1.13	−0.77	0.58		
19	220193_at	1.13	−1.25	0.42	SH3D21	SH3 domain containing 21 [Source:HGNC Symbol;Acc:HGN
20	221605_s_at	1.1	−0.76	0.71	PIPOX	pipecolic acid and sarcosine oxidase [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−10	22 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	3e−07	9 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	4e−06	6 / 34	BP	regulation of synaptic plasticity
4	6e−05	6 / 54	Lympl	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
5	6e−05	5 / 34	BP	respiratory gaseous exchange
6	1e−04	17 / 485	TF	ICGC_NrsfPcr2_targets
7	2e−04	4 / 24	GSEA	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATIO
8	3e−04	3 / 11	MF	platelet−derived growth factor binding
9	4e−04	102 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
10	4e−04	17 / 539	Colon	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	4e−04	4 / 29	GSEA	REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS
12	6e−04	12 / 311	GSEA	SHEN_SMARCA2_TARGETS_DN
13	6e−04	3 / 14	BP	intermediate filament organization
14	6e−04	3 / 14	GSEA	REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA
15	7e−04	4 / 33	GSEA	REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE
16	8e−04	10 / 235	GSEA	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
17	8e−04	27 / 1128	CC	integral component of plasma membrane
18	9e−04	58 / 3168	Lympl	HOPP_Repressed
19	9e−04	4 / 35	BP	blood circulation
20	1e−03	39 / 1894	Lympl	HOPP_Poised_promoter
21	1e−03	4 / 37	GSEA	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION
22	1e−03	3 / 17	BP	regulation of neuronal synaptic plasticity
23	1e−03	6 / 94	GSEA	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
24	1e−03	5 / 65	BP	excitatory postsynaptic potential
25	1e−03	15 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
26	1e−03	7 / 132	Lympl	Subero_DLBCL_hyper_meth
27	2e−03	3 / 20	BP	regulation of axonogenesis
28	2e−03	3 / 20	GSEA	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP
29	2e−03	19 / 730	GSEA	BENPORATH_ES_WITH_H3K27ME3
30	2e−03	4 / 44	GSEA	PARENT_MTOR_SIGNALING_DN
31	2e−03	7 / 144	GSEA	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_DN
32	2e−03	2 / 6	GSEA	NIKOLSKY_BREAST_CANCER_20P13_AMPLICON
33	2e−03	4 / 45	Lympl	Subero_INT_hypo_meth
34	3e−03	3 / 22	BP	neuromuscular process
35	3e−03	13 / 422	GSEA	DELYS_THYROID_CANCER_UP
36	3e−03	5 / 76	BP	ephrin receptor signaling pathway
37	3e−03	5 / 78	Melar	Tirosh_CAF−cell specific genes
38	3e−03	14 / 483	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
39	3e−03	6 / 114	BP	calcium ion transport
40	3e−03	2 / 7	Gliom	Sturm_GBM_Meth_overexpression_C_G34_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.05	4 / 107	HORVATH_aging_genes meth UP
2	0.32	2 / 92	HORVATH_aging_genes meth DOWN
3	0.45	1 / 47	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	

CC

Rank	p−value	#in/all	Geneset
1	8e−04	27 / 1128	integral component of plasma membrane
2	6e−03	10 / 310	dendrite
3	7e−03	2 / 10	synaptic cleft
4	8e−03	9 / 277	neuron projection
5	9e−03	4 / 65	collagen trimer
6	1e−02	2 / 13	axolemma
7	1e−02	3 / 41	intermediate filament cytoskeleton
8	2e−02	2 / 16	dendrite membrane
9	2e−02	6 / 168	postsynaptic density
10	2e−02	3 / 47	postsynapse
11	2e−02	2 / 19	high−density lipoprotein particle
12	2e−02	2 / 19	synaptic membrane
13	2e−02	52 / 3210	plasma membrane
14	3e−02	14 / 623	cell projection
15	3e−02	2 / 20	excitatory synapse

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−04	102 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	4e−04	17 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
3	1e−03	15 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
4	3e−03	14 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	1e−02	10 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
6	4e−02	17 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
7	6e−02	2 / 31	Kosinski_lower−crypt−short−list
8	7e−02	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
9	7e−02	7 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	1e−01	1 / 8	Marisa_CRC−C3
11	1e−01	6 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
12	1e−01	1 / 12	Juehling−MSI−enriched−in−6
13	2e−01	16 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	2e−01	8 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
15	2e−01	9 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

HM

Rank	p−value	#in/all	Geneset
1	0.06	5 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.10	5 / 194	HALLMARK_MYOGENESIS
3	0.10	4 / 141	HALLMARK_UV_RESPONSE_DN
4	0.19	4 / 178	HALLMARK_COMPLEMENT
5	0.35	2 / 97	HALLMARK_BILE_ACID_METABOLISM
6	0.35	1 / 34	HALLMARK_APICAL_SURFACE
7	0.37	3 / 174	HALLMARK_ADIPOGENESIS
8	0.39	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
9	0.43	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
10	0.44	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
11	0.44	3 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.45	3 / 195	HALLMARK_KRAS_SIGNALING_DN
13	0.45	3 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.49	2 / 130	HALLMARK_COAGULATION
15	0.50	1 / 55	HALLMARK_MYC_TARGETS_V2

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−05	6 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
2	9e−04	58 / 3168	HOPP_Repressed
3	1e−03	39 / 1894	HOPP_Poised_promoter
4	1e−03	7 / 132	Subero_DLBCL_hyper_meth
5	2e−03	4 / 45	Subero_INT_hypo_meth
6	5e−03	5 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
7	3e−02	3 / 56	Subero_mBL_hyper_meth
8	4e−02	2 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
9	4e−02	4 / 102	ROSOLOWSKI_blue total
10	5e−02	3 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
11	6e−02	4 / 118	Subero_INT_hyper_meth
12	6e−02	2 / 33	Subero_T−PLL_hypo_meth
13	1e−01	3 / 96	SPANG_LPS 6hrs UP
14	1e−01	5 / 214	LENZ_Stromal signature 1
15	1e−01	1 / 12	Subero_MM_hypo_meth

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	3 / 26	hsa−miR−558
2	0.004	3 / 26	hsa−miR−555
3	0.019	2 / 17	hsa−miR−323−5p
4	0.027	4 / 90	hsa−miR−22
5	0.033	3 / 56	hsa−miR−1275
6	0.036	3 / 58	hsa−miR−331−3p
7	0.041	3 / 61	hsa−miR−939
8	0.045	2 / 27	hsa−miR−1296
9	0.048	2 / 28	hsa−miR−296−5p
10	0.061	2 / 32	hsa−miR−615−5p
11	0.061	1 / 5	hsa−miR−1281
12	0.062	3 / 72	hsa−miR−339−5p
13	0.073	1 / 6	hsa−miR−886−5p
14	0.087	3 / 83	hsa−miR−147
15	0.097	3 / 87	hsa−miR−501−5p

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	

BP

Rank	p−value	#in/all	Geneset
1	4e−06	6 / 34	regulation of synaptic plasticity
2	6e−05	5 / 34	respiratory gaseous exchange
3	6e−04	3 / 14	intermediate filament organization
4	9e−04	4 / 35	blood circulation
5	1e−03	3 / 17	regulation of neuronal synaptic plasticity
6	1e−03	5 / 65	excitatory postsynaptic potential
7	2e−03	3 / 20	regulation of axonogenesis
8	3e−03	3 / 22	neuromuscular process
9	3e−03	5 / 76	ephrin receptor signaling pathway
10	3e−03	6 / 114	calcium ion transport
11	4e−03	3 / 25	positive regulation of mitotic nuclear division
12	4e−03	5 / 85	glucose homeostasis
13	5e−03	4 / 54	memory
14	6e−03	3 / 29	activation of protein kinase B activity
15	6e−03	3 / 29	long−term memory

Chr

Rank	p−value	#in/all	Geneset
1	0.009	18 / 776	Chr 17
2	0.009	10 / 333	Chr 22
3	0.065	12 / 585	Chr 7
4	0.153	10 / 548	Chr 16
5	0.156	13 / 756	Chr 11
6	0.164	14 / 833	Chr 19
7	0.186	8 / 437	Chr 8
8	0.255	3 / 139	Chr 21
9	0.320	6 / 369	Chr 20
10	0.405	1 / 41	Chr Y
11	0.553	7 / 556	Chr X
12	0.575	5 / 403	Chr 14
13	0.584	6 / 490	Chr 10
14	0.589	6 / 492	Chr 9
15	0.784	7 / 700	Chr 12

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	2 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
2	0.006	6 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	0.007	12 / 423	Down_a
4	0.019	4 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
5	0.024	30 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	0.024	4 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
7	0.029	3 / 53	Christensen_hypermethylated_in_primary_glioblastoma
8	0.035	5 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	0.037	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
10	0.047	3 / 64	Weller_LGG_gradeII−vs−III_UP
11	0.050	3 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
12	0.052	3 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	0.053	4 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
14	0.056	4 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	0.084	9 / 421	Down_b

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	2 / 29	Angelova_immune−metagene−Th1
2	0.14	1 / 12	Angelova_immune−metagene−NK56_dim
3	0.18	1 / 16	Angelova_immune−metagene−Th17
4	0.19	1 / 17	Angelova_immune−metagene−central_memory_CD8
5	0.27	1 / 25	Angelova_immune−metagene−DC
6	0.43	1 / 45	Angelova_immune−metagene−MDSC
7	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
8	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
9	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
10	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
14	1.00	0 / 14	Angelova_immune−metagene−eosinophil
15	1.00	0 / 19	Angelova_immune−metagene−iDC

Melanoma

Rank	p−value	#in/all	Geneset
1	0.003	5 / 78	Tirosh_CAF−cell specific genes
2	0.004	8 / 204	Landsberg_dedifferentiation_down
3	0.007	2 / 10	Joensson_Melanoma Normal like subtype
4	0.011	3 / 37	Hugo_melanoma−all−MET_DN
5	0.086	2 / 39	Tirosh_melanoma specific genes
6	0.135	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	0.197	2 / 65	Harbst_melanoma_highgrade_up
8	0.205	5 / 249	Gerber_wt/wt_melanoma−cells−SpotE
9	0.280	2 / 83	TCGA_melanoma_immune_high
10	0.290	2 / 85	Tirosh_AXL−signature
11	0.342	1 / 33	Tirosh_T−cell specific genes−melanoma
12	0.364	3 / 171	Landsberg_dedifferentiation_up
13	0.443	2 / 119	TCGA_melanoma_MITF_low
14	0.527	1 / 59	TCGA_melanoma_keratin_high
15	0.556	1 / 64	Harbst_melanoma_lowgrade_up

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 54	Burnham_timecourse
2	0.2	2 / 57	Burnham_day1_vs_5_UP
3	0.4	1 / 37	Sweeney_viral_up
4	0.5	1 / 56	Burnham_sep_vs_con_DN
5	0.8	1 / 122	Terre_IMS_influenza_meta_signature
6	0.8	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	0.9	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
8	1.0	0 / 68	Burnham_sep_vs_con_UP
9	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
10	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
11	1.0	0 / 48	Burnham_viral_DN
12	1.0	0 / 57	Burnham_viral_UP
13	1.0	0 / 52	Burnham_day1_vs_5_DN
14	1.0	0 / 18	Scicluna_UP
15	1.0	0 / 41	Scicluna_DN

TF

Rank	p−value	#in/all	Geneset
1	1e−04	17 / 485	ICGC_NrsfPcr2_targets
2	5e−03	25 / 1148	HEBENSTREIT_low expression TF
3	5e−02	38 / 2321	ICGC_Rad21_targets
4	9e−02	18 / 1025	ICGC_NrsfPcr1_targets
5	2e−01	29 / 1941	ICGC_Bcl3_targets
6	2e−01	33 / 2254	ICGC_BatfPcr1_targets
7	4e−01	8 / 549	ICGC_Atf3_targets
8	4e−01	41 / 3121	ICGC_Egr1_targets
9	5e−01	44 / 3435	ICGC_Ebfsc137065_targets
10	5e−01	52 / 4131	ICGC_Tcf3_targets
11	6e−01	23 / 1848	ICGC_Pbx3_targets
12	6e−01	60 / 4851	ICGC_Runx3_targets
13	6e−01	56 / 4602	ICGC_Elf1_targets
14	7e−01	49 / 4072	ICGC_Mta3_targets
15	7e−01	19 / 1630	ICGC_SrfV0416101_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	12 / 480	Lembcke_Colonic Inflammation
2	0.09	4 / 134	PanCan_RAS_geneset_nanostring
3	0.12	3 / 96	PanCan_TXmisReg_geneset_nanostring
4	0.14	1 / 12	LIU_BREAST_CANCER
5	0.15	1 / 13	GENTLES_modul18
6	0.16	1 / 14	BENTINK_ras.6
7	0.18	1 / 16	LIU_LIVER_CANCER
8	0.20	1 / 18	PanCan_Notch_geneset_nanostring
9	0.21	4 / 187	PanCan_PI3K_geneset_nanostring
10	0.28	3 / 147	PanCan_MAPK_geneset_nanostring
11	0.32	0 / 14	LIU_PROSTATE_CANCER_DN
12	0.33	1 / 32	KUIPER_MM good survival
13	0.42	2 / 113	PanCan_Driver_Gene_geneset_nanostring
14	0.45	1 / 47	PanCan_TGF−B_geneset_nanostring
15	0.48	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−08	49 / 1813	8_EnhP_Fibroblasts
2	2e−07	38 / 1239	EnhP_Colon
3	4e−07	54 / 2203	EnhA_Colon
4	4e−07	49 / 1911	Mid_Frontal_Lobe_HetRpts
5	5e−07	57 / 2405	Bcells peripheral blood_13_ReprPC
6	1e−06	61 / 2747	Bcells peripheral blood_12_EnhBiv
7	2e−06	75 / 3734	Tcells peripheral blood_13_ReprPC
8	4e−06	54 / 2375	10_ReprPC_Fibroblasts
9	4e−06	47 / 1943	TssP_Colon
10	9e−06	73 / 3724	Tcells peripheral blood_12_EnhBiv
11	1e−05	56 / 2602	natural killer cells peripheral blood_12_EnhBiv
12	2e−05	48 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
13	5e−05	63 / 3184	monocytes peripheral blood_12_EnhBiv
14	5e−05	48 / 2194	Thelper cells peripheral blood_12_EnhBiv
15	8e−05	48 / 2240	1_TssP_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−10	22 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	3e−07	9 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	2e−04	4 / 24	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_
4	4e−04	4 / 29	REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS
5	6e−04	12 / 311	SHEN_SMARCA2_TARGETS_DN
6	6e−04	3 / 14	REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_
7	7e−04	4 / 33	REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_
8	8e−04	10 / 235	NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON
9	1e−03	4 / 37	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION
10	1e−03	6 / 94	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
11	2e−03	3 / 20	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP
12	2e−03	19 / 730	BENPORATH_ES_WITH_H3K27ME3
13	2e−03	4 / 44	PARENT_MTOR_SIGNALING_DN
14	2e−03	7 / 144	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_DN
15	2e−03	2 / 6	NIKOLSKY_BREAST_CANCER_20P13_AMPLICON

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.24	1 / 22	DUMEAUX_High bmi enriched genes
3	0.24	1 / 22	DUMEAUX_Fasting enriched genes
4	0.54	1 / 62	DUMEAUX_Smoking enriched genes
5	0.57	2 / 150	Homuth_BMI−associated−genes_UP
6	0.74	2 / 210	Homuth_BMI−associated−genes_DN
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 11	platelet−derived growth factor binding
2	4e−03	3 / 26	sodium channel activity
3	4e−03	11 / 346	receptor binding
4	4e−03	4 / 53	extracellular matrix structural constituent
5	8e−03	2 / 11	ephrin receptor activity
6	1e−02	3 / 35	scavenger receptor activity
7	1e−02	2 / 12	insulin−like growth factor I binding
8	1e−02	2 / 12	phospholipase C activity
9	1e−02	5 / 105	Ras guanyl−nucleotide exchange factor activity
10	1e−02	2 / 13	alpha−actinin binding
11	2e−02	2 / 19	tumor necrosis factor−activated receptor activity
12	2e−02	3 / 49	transmembrane receptor protein tyrosine kinase activity
13	3e−02	3 / 52	collagen binding
14	3e−02	2 / 21	chemoattractant activity
15	3e−02	2 / 22	cation channel activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.02	2 / 17	VAQUERIZAS_Heart_TF
2	0.05	6 / 209	Chaussabel_2,5_Immune related molecules
3	0.05	1 / 4	JONGENEEL_Bladder
4	0.08	8 / 352	WIRTH_Nervous System
5	0.10	3 / 89	Chaussabel_2,3_Erythrocytes
6	0.13	1 / 11	JONGENEEL_Spleen
7	0.13	1 / 11	Chaussabel_3,5_Hemoglobin genes
8	0.14	1 / 12	WIRTH_Globus pallidus
9	0.15	1 / 13	WIRTH_Bone marrow
10	0.18	1 / 16	VAQUERIZAS_Fetal liver_TF
11	0.20	2 / 66	VAQUERIZAS_Whole blood_TF
12	0.21	1 / 19	JONGENEEL_Thymus
13	0.22	1 / 20	VAQUERIZAS_Bone marrow_TF
14	0.23	2 / 72	Chaussabel_3,1_Interferon−inducible
15	0.27	2 / 81	Chaussabel_1,2_Platelets