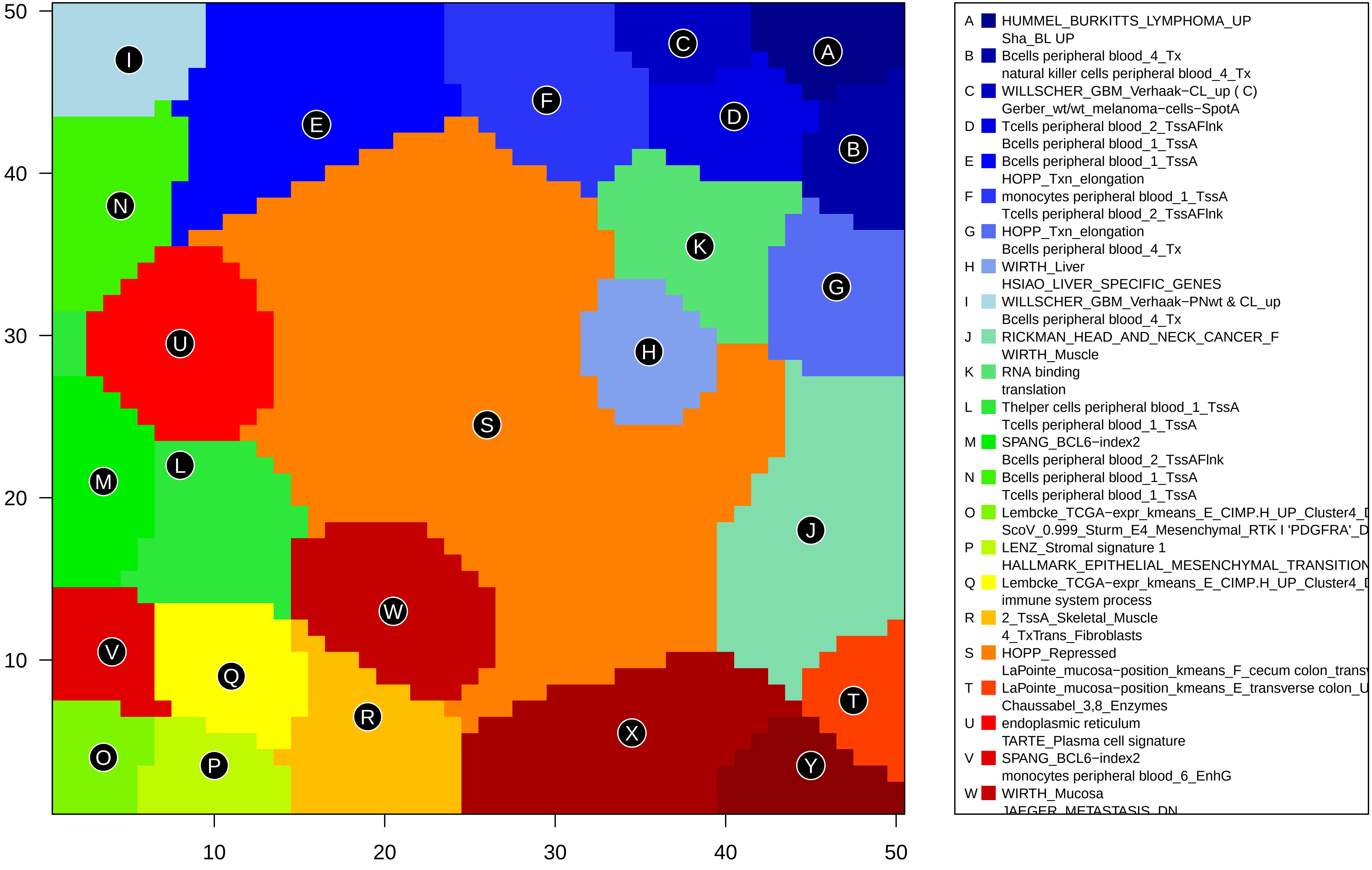
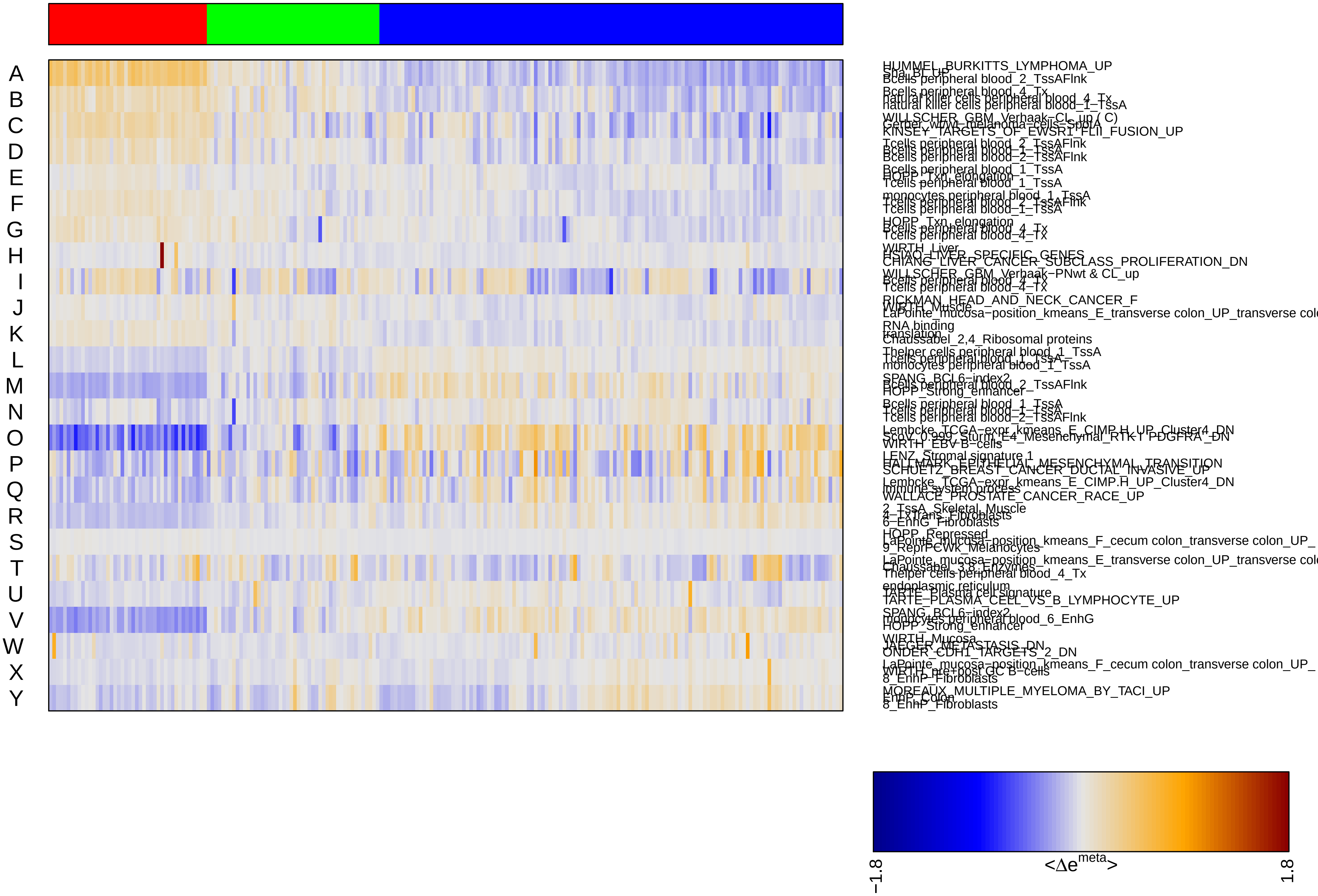
K−Means Cluster

annotation





A
B
C
D
E
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G
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I
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K
L
M
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P
Q
R
S
T
U
V
W
X
Y
HUMMEL_BURKITTS_LYMPHOMA_UP
Sha_BL_UP
Bcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_4_Tx
natural killer cells peripheral blood_4_Tx
natural killer cells peripheral blood_1_TssA
WILLSCHER_GBM_Verhaak−CL_up (C)
Gerber_wt/wt−melanoma−cells−SpotA
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
Tcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_1_TssA
Bcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_1_TssA
HOPP_Txn_elongation
Tcells peripheral blood_1_TssA
monocytes peripheral blood_1_TssA
Tcells peripheral blood_2_TssAFlnk
Tcells peripheral blood_1_TssA
HOPP_Txn_elongation
Bcells peripheral blood_4_Tx
Tcells peripheral blood_4_Tx
WIRTH_Liver
HSIAO_LIVER_SPECIFIC_GENES
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
WILLSCHER_GBM_Verhaak−PNwt & CL_up
Bcells peripheral blood_4_Tx
Tcells peripheral blood_4_Tx
RICKMAN_HEAD_AND_NECK_CANCER_F
WIRTH_Muscle
LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse col
RNA binding
translation
Chaussabel_2,4_Ribosomal proteins
Thelper cells peripheral blood_1_TssA
Tcells peripheral blood_1_TssA
monocytes peripheral blood_1_TssA
SPANG_BCL6−index2
Bcells peripheral blood_2_TssAFlnk
HOPP_Strong_enhancer
Bcells peripheral blood_1_TssA
Tcells peripheral blood_1_TssA
Tcells peripheral blood_2_TssAFlnk
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
ScoV_0.999_Sturm_E4_Mesenchymal_RTK1 PDGFRA_DN
WIRTH_EBV B−cells
LENZ_Stromal signature 1
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
immune system process
WALLACE_PROSTATE_CANCER_RACE_UP
2_TssA_Skeletal_Muscle
4−TxTrans_Fibroblasts
6−EnhG_Fibroblasts
HOPP_Repressed
LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9_ReprPCWk_Melanocytes
LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse col
Chaussabel_3,8_Enzymes
Thelper cells peripheral blood_4_Tx
endoplasmic reticulum
TARTE_Plasma cell signature
TARTE−PLASMA_CELL_VS_B_LYMPHOCYTE_UP
SPANG_BCL6−index2
monocytes peripheral blood_6_EnhG
HOPP_Strong_enhancer
WIRTH_Mucosa
JAEGER_METASTASIS_DN
ONDER_CDH1_TARGETS_2_DN
LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
WIRTH_pre+post GC B−cells
8_EnhP_Fibroblasts
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
EnhP_Colon
8_EnhP_Fibroblasts
−1.8
<Δe^meta>
1.8

K−Means Cluster

Spot Summary: A

metagenes = 43
genes = 607

<r> metagenes = 0.94
<r> genes = 0.27
beta: r2= 13.5 / log p= −Inf

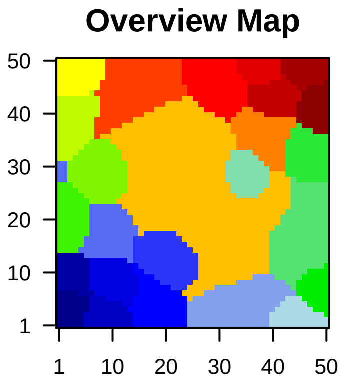
samples with spot = 51 (23.1 %)
mBL : 43 (97.7 %)
intermediate : 8 (16.7 %)

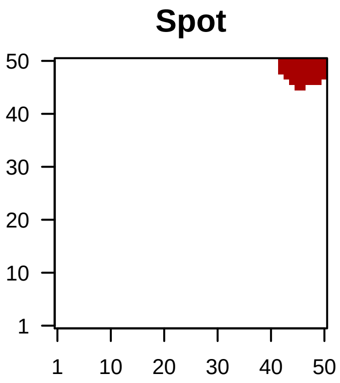
Spot Genelist

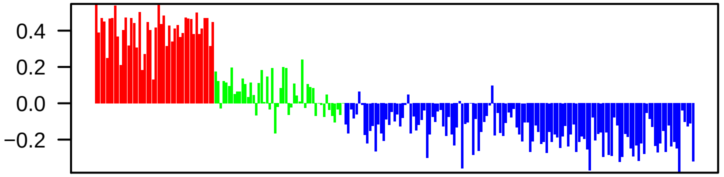
Rank	ID	max e	min e	r	Symbol	Description
1	AFFX−r2−Hs1	3.22	−1.13	0.3		
2	AFFX−r2−Hs1	3.07	−1.49	0.23		
3	AFFX−HUMR	2.91	−0.94	0.31		microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835
4	AFFX−HUMR	2.85	−1.18	0.21		
5	206660_at	2.83	−0.99	0.48	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
6	221349_at	2.76	−0.89	0.71	VPREB1	V−set pre−B cell surrogate light chain 1 [Source:HGNC Symb
7	206413_s_at	2.76	−1.22	0.37	TCL1B	T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG
8	AFFX−r2−Hs1	2.71	−1.22	0.36		
9	AFFX−r2−Hs2	2.62	−0.97	0.32		
10	AFFX−M2783	2.6	−1.58	0.34		
11	AFFX−HUMR	2.6	−1.04	0.31		
12	203980_at	2.41	−1.55	0.28	FABP4	fatty acid binding protein 4 [Source:HGNC Symbol;Acc:HGNC
13	204914_s_at	2.24	−0.89	0.64	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
14	AFFX−r2−Hs2	2.21	−1.56	0.32		
15	213920_at	2.19	−1.02	0.49	CUX2	cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934
16	219855_at	2.18	−0.78	0.45	NUDT11	nudix hydrolase 11 [Source:HGNC Symbol;Acc:HGNC:18011
17	213674_x_at	2.16	−1.9	0.32		immunoglobulin heavy constant delta [Source:HGNC Symbol
18	38037_at	2.16	−1.11	0.55	HBEGF	heparin binding EGF like growth factor [Source:HGNC Symb
19	204915_s_at	2.16	−0.86	0.57	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
20	209598_at	2.13	−0.99	0.2	PNMA2	PNMA family member 2 [Source:HGNC Symbol;Acc:HGNC:9

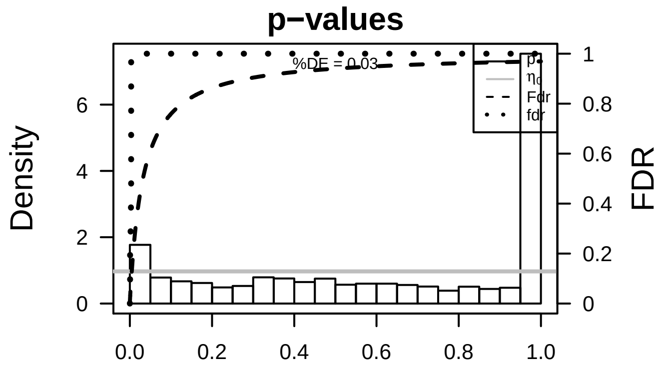
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−48	37 / 42	GSEA	HUMMEL_BURKITTS_LYMPHOMA_UP
2	2e−31	40 / 99	Lympl	Sha_BL UP
3	1e−25	107 / 955	Lympl	SPANG_BCR UP
4	8e−22	43 / 192	Lympl	Victora_Dark zone signature
5	4e−19	58 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
6	1e−18	80 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
7	3e−17	13 / 15	Lympl	BENTINK_mBL UP
8	2e−16	71 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
9	8e−16	120 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
10	8e−15	92 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	9e−15	87 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	3e−14	41 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
13	3e−14	37 / 227	Lympl	SPANG_IL21 UP
14	7e−14	71 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
15	3e−13	63 / 615	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
16	3e−13	10 / 12	Cance	BENTINK_e2f3.2
17	4e−12	297 / 5908	Lympl	HOPP_Active_promoter
18	5e−12	26 / 135	Lympl	DAVE_BL−vs−DLBCL
19	6e−12	158 / 2541	CC	nucleoplasm
20	2e−11	34 / 240	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_DN
21	2e−11	37 / 280	GSEA	MANALO_HYPOXIA_DN
22	8e−11	45 / 409	Cance	Lembcke_Normal vs Adenoma
23	3e−10	38 / 319	Melar	Gerber_wt/wt_melanoma−cells−SpotA
24	3e−10	34 / 263	Lympl	SPANG_CD40 6hrs UP
25	4e−10	275 / 5529	Lympl	HOPP_Txn_elongation
26	4e−10	51 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
27	7e−10	59 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
28	8e−10	45 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
29	1e−09	236 / 4579	CC	nucleus
30	1e−09	53 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
31	2e−09	8 / 12	Cance	BENTINK_ras.1
32	2e−09	54 / 602	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
33	3e−09	6 / 6	Lympl	MASCQUE_mBL UP
34	4e−09	15 / 60	GSEA	PYEON_HPV_POSITIVE_TUMORS_UP
35	4e−09	36 / 321	GSEA	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C
36	5e−09	43 / 431	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
37	3e−08	57 / 703	GSEA	LEE_BMP2_TARGETS_DN
38	3e−08	23 / 160	GSEA	PUJANA_XPRSS_INT_NETWORK
39	8e−08	25 / 195	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
40	8e−08	41 / 442	GSEA	KIM_WT1_TARGETS_DN









Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 92	HORVATH_aging_genes meth DOWN
2	0.2	6 / 107	HORVATH_aging_genes meth UP
3	0.8	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	

BP

Rank	p−value	#in/all	Geneset
1	8e−06	27 / 281	DNA repair
2	3e−05	38 / 497	cell cycle
3	5e−05	7 / 27	DNA biosynthetic process
4	6e−05	11 / 71	regulation of G2/M transition of mitotic cell cycle
5	2e−04	13 / 110	regulation of cell cycle
6	3e−04	27 / 351	cellular response to DNA damage stimulus
7	8e−04	4 / 12	centriole replication
8	1e−03	29 / 414	negative regulation of transcription, DNA−templated
9	1e−03	14 / 144	methylation
10	1e−03	4 / 13	replicative senescence
11	1e−03	6 / 32	centrosome cycle
12	2e−03	5 / 24	chromosome organization
13	2e−03	8 / 62	meiotic cell cycle
14	2e−03	6 / 37	interstrand cross−link repair
15	3e−03	5 / 27	positive regulation of Wnt signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	3e−13	10 / 12	BENTINK_e2f3.2
2	8e−11	45 / 409	Lembcke_Normal vs Adenoma
3	2e−09	8 / 12	BENTINK_ras.1
4	1e−04	8 / 41	PanCan_DNARepair_geneset_nanostring
5	3e−04	4 / 10	GENTLES_modul3
6	4e−04	14 / 130	PanCan_CC+Apop_geneset_nanostring
7	1e−03	4 / 14	BENTINK_myc.1
8	1e−03	4 / 14	BENTINK_src.10
9	1e−02	14 / 186	SPANG_LPS−index2
10	3e−02	5 / 45	KUIPER_MM poor survival
11	3e−02	4 / 32	KUIPER_MM good survival
12	4e−02	3 / 20	PanCan_ChromMod_geneset_nanostring
13	8e−02	2 / 13	GENTLES_modul11
14	1e−01	2 / 14	LIU_COMMON_CANCER_GENES
15	1e−01	4 / 47	PanCan_TGF−B_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−12	158 / 2541	nucleoplasm
2	1e−09	236 / 4579	nucleus
3	3e−04	26 / 326	nuclear speck
4	3e−04	24 / 292	microtubule organizing center
5	3e−04	12 / 98	spindle pole
6	4e−04	27 / 354	centrosome
7	5e−04	4 / 11	Fanconi anaemia nuclear complex
8	5e−04	25 / 324	chromosome
9	2e−03	40 / 653	nucleolus
10	2e−03	12 / 118	chromosome, centromeric region
11	2e−03	53 / 936	cytoskeleton
12	3e−03	206 / 4701	cytoplasm
13	5e−03	3 / 10	lateral element
14	6e−03	4 / 20	centriolar satellite
15	7e−03	4 / 21	mitotic spindle pole

Chr

Rank	p−value	#in/all	Geneset
1	1e−04	22 / 242	Chr 13
2	9e−03	32 / 548	Chr 16
3	1e−02	28 / 480	Chr 4
4	3e−02	20 / 333	Chr 22
5	1e−01	32 / 700	Chr 12
6	1e−01	21 / 437	Chr 8
7	2e−01	3 / 41	Chr Y
8	3e−01	54 / 1325	Chr 1
9	3e−01	17 / 403	Chr 14
10	4e−01	27 / 669	Chr 6
11	4e−01	20 / 490	Chr 10
12	6e−01	18 / 492	Chr 9
13	6e−01	21 / 585	Chr 7
14	7e−01	27 / 776	Chr 17
15	7e−01	29 / 833	Chr 19

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−26	421 / 8406	Bcells peripheral blood_2_TssAFlnk
2	2e−26	403 / 7833	Bcells peripheral blood_1_TssA
3	6e−24	413 / 8322	T CD8+ naive cells peripheral blood_1_TssA
4	5e−22	401 / 8068	Thelper cells peripheral blood_1_TssA
5	4e−21	432 / 9160	2_TssA_Neuronal_Progenitor
6	4e−19	366 / 7225	Overlap_fetal_midbrain_ReprPC
7	1e−18	415 / 8766	2_TssA_Melanocytes
8	2e−18	382 / 7751	natural killer cells peripheral blood_1_TssA
9	2e−18	399 / 8275	2_TssA_Fibroblasts
10	5e−18	415 / 8816	Thelper cells peripheral blood_2_TssAFlnk
11	1e−17	400 / 8370	natural killer cells peripheral blood_2_TssAFlnk
12	2e−17	297 / 5456	5_Tx_Neuronal_Progenitor
13	2e−17	408 / 8641	1_TssA_ESC_Endoderm
14	3e−17	395 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
15	4e−17	416 / 8918	1_TssA_ESC_Mesoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−09	54 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	2e−05	97 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
3	3e−05	41 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	9e−04	65 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
5	1e−03	55 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
6	3e−03	55 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
7	3e−03	48 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	1e−02	45 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
9	2e−02	3 / 16	Budinska_B_Lower crypt−like_UP
10	2e−02	13 / 184	Kosinski_lower−crypt−long−list
11	5e−02	28 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
12	6e−02	257 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
13	7e−02	19 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	7e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
15	9e−02	35 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	5e−04	82 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−03	12 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
3	3e−03	70 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−02	25 / 421	Down_b
5	2e−02	6 / 59	GIEZELT_GBM_STS_up_VS_LTS
6	3e−02	4 / 32	WIRTH_PN subtype
7	5e−02	3 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
8	6e−02	9 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
9	7e−02	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
10	7e−02	1 / 2	Phillips Prolif up vs PN & MES
11	9e−02	9 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	1e−01	2 / 16	VERHAAK_PN subtype
13	1e−01	7 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
14	1e−01	4 / 52	GIEZELT_GBM_WT_down_VS_mut
15	2e−01	6 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−48	37 / 42	HUMMEL_BURKITTS_LYMPHOMA_UP
2	4e−19	58 / 400	PUJANA_BRCA2_PCC_NETWORK
3	1e−18	80 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4	2e−16	71 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	8e−16	120 / 1527	PUJANA_BRCA1_PCC_NETWORK
6	8e−15	92 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
7	9e−15	87 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	3e−14	41 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
9	7e−14	71 / 726	PUJANA_CHEK2_PCC_NETWORK
10	3e−13	63 / 615	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
11	2e−11	34 / 240	MITSIADES_RESPONSE_TO_APLIDIN_DN
12	2e−11	37 / 280	MANALO_HYPOXIA_DN
13	4e−10	51 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
14	7e−10	59 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
15	8e−10	45 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6

HM

Rank	p−value	#in/all	Geneset
1	3e−07	24 / 195	HALLMARK_G2M_CHECKPOINT
2	5e−07	23 / 187	HALLMARK_E2F_TARGETS
3	2e−03	15 / 173	HALLMARK_MITOTIC_SPINDLE
4	5e−02	4 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	5e−02	5 / 55	HALLMARK_MYC_TARGETS_V2
6	5e−02	12 / 190	HALLMARK_MYC_TARGETS_V1
7	1e−01	11 / 192	HALLMARK_MTORC1_SIGNALING
8	1e−01	11 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	1e−01	4 / 51	HALLMARK_TGF_BETA_SIGNALING
10	2e−01	8 / 141	HALLMARK_UV_RESPONSE_DN
11	2e−01	10 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	3e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
13	3e−01	8 / 174	HALLMARK_ADIPOGENESIS
14	5e−01	6 / 149	HALLMARK_UV_RESPONSE_UP
15	5e−01	7 / 176	HALLMARK_ALLOGRAFT_REJECTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	2 / 25	Angelova_immune−metagene−DC
2	0.3	2 / 26	Angelova_immune−metagene−activated_CD4
3	0.3	1 / 10	Angelova_immune−metagene−neutrophils
4	0.4	1 / 12	Angelova_immune−metagene−memory_B−cells
5	0.4	1 / 13	Angelova_immune−metagene−activated_B−cells
6	0.4	1 / 13	Angelova_immune−metagene−immature_B−cells
7	0.5	1 / 17	Angelova_immune−metagene−central_memory_CD8
8	0.5	1 / 18	Angelova_immune−metagene−pDC
9	0.5	1 / 18	Angelova_CRC_immunostimulators
10	0.6	1 / 21	Angelova_immune−metagene−central_memory_CD4
11	0.6	1 / 23	Angelova_immune−metagene−Th2
12	0.8	1 / 45	Angelova_immune−metagene−MDSC
13	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
14	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
15	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	4 / 32	Marjolein_ageing−genes_DN
2	0.20	8 / 150	Homuth_BMI−associated−genes_UP
3	0.54	8 / 210	Homuth_BMI−associated−genes_DN
4	0.57	1 / 22	DUMEAUX_Fasting enriched genes
5	0.68	2 / 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 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−31	40 / 99	Sha_BL UP
2	1e−25	107 / 955	SPANG_BCR UP
3	8e−22	43 / 192	Victora_Dark zone signature
4	3e−17	13 / 15	BENTINK_mBL UP
5	3e−14	37 / 227	SPANG_IL21 UP
6	4e−12	297 / 5908	HOPP_Active_promoter
7	5e−12	26 / 135	DAVE_BL−vs−DLBCL
8	3e−10	34 / 263	SPANG_CD40 6hrs UP
9	4e−10	275 / 5529	HOPP_Txn_elongation
10	3e−09	6 / 6	MASCQUE_mBL UP
11	2e−06	264 / 5682	HOPP_Weak_promoter
12	8e−06	5 / 9	DAVE_BL UP
13	2e−04	198 / 4261	HOPP_Txn_transition
14	3e−04	241 / 5404	HOPP_Strong_enhancer
15	3e−04	5 / 17	DAVE_c−myc BL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	3e−10	38 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	3e−02	5 / 47	Tirosh_G2/M phase specific genes
3	4e−02	6 / 68	Tirosh_housekeeping_genes
4	7e−02	1 / 2	Melanoma Epi−Enzyme Cluster 6
5	1e−01	1 / 4	Melanoma Epi−Enzyme Cluster 3
6	1e−01	1 / 4	Melanoma Epi−Enzyme Cluster 5
7	2e−01	14 / 276	Gerber_wt/wt_melanoma−cells−SpotB
8	2e−01	3 / 38	Tirosh_G1/S phase specific genes
9	2e−01	5 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
10	2e−01	5 / 83	TCGA_melanoma_immune_high
11	2e−01	2 / 24	Tirosh_B−cell specific genes−melanoma
12	2e−01	4 / 65	Harbst_melanoma_highgrade_up
13	2e−01	3 / 44	Tirosh_top50 correlated genes PC2
14	3e−01	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
15	3e−01	4 / 75	Tirosh_Endothelial−cell specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	2e−06	75 / 1161	RNA binding
2	4e−06	92 / 1541	DNA binding
3	4e−04	52 / 852	nucleic acid binding
4	8e−04	4 / 12	S−adenosylmethionine−dependent methyltransferase activity
5	9e−04	10 / 81	single−stranded DNA binding
6	1e−03	13 / 132	methyltransferase activity
7	3e−03	10 / 97	double−stranded DNA binding
8	4e−03	4 / 18	translation elongation factor activity
9	4e−03	5 / 29	ribonucleoprotein complex binding
10	6e−03	4 / 20	dynein complex binding
11	7e−03	10 / 107	mRNA binding
12	7e−03	3 / 11	DNA−(apurinic or apyrimidinic site) lyase activity
13	7e−03	322 / 7864	protein binding
14	9e−03	3 / 12	protein kinase A catalytic subunit binding
15	1e−02	5 / 38	4 iron, 4 sulfur cluster binding

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−05	12 / 87	hsa−miR−449b
2	2e−03	6 / 35	hsa−miR−1224−5p
3	2e−03	15 / 171	hsa−miR−203
4	3e−03	4 / 17	hsa−miR−609
5	4e−03	18 / 236	hsa−miR−34a
6	4e−03	19 / 260	hsa−let−7e
7	5e−03	10 / 103	hsa−miR−576−3p
8	7e−03	9 / 90	hsa−miR−507
9	7e−03	10 / 107	hsa−miR−24
10	8e−03	6 / 47	hsa−miR−370
11	9e−03	12 / 145	hsa−miR−607
12	1e−02	15 / 203	hsa−miR−449a
13	1e−02	13 / 166	hsa−miR−29b
14	1e−02	12 / 148	hsa−miR−196b
15	1e−02	17 / 244	hsa−miR−34c−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.005	7 / 57	Burnham_day1_vs_5_UP
2	0.067	4 / 41	Scicluna_DN
3	0.362	3 / 57	Burnham_viral_UP
4	0.473	3 / 68	Burnham_sep_vs_con_UP
5	0.498	1 / 18	Scicluna_UP
6	0.608	2 / 54	Burnham_timecourse
7	0.627	2 / 56	Burnham_sep_vs_con_DN
8	0.752	2 / 71	Burnham_cap_fp_vs_con_UP
9	0.841	1 / 48	Burnham_cap_fp_vs_con_DN
10	0.864	1 / 52	Burnham_day1_vs_5_DN
11	0.887	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
12	0.967	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
13	0.991	1 / 122	Terre_IMS_influenza_meta_signature
14	1.000	0 / 48	Burnham_viral_DN
15	1.000	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−04	7 / 42	Chaussabel_1,3_B−cells
2	3e−03	26 / 390	PROTEINATLAS_ovary
3	4e−03	36 / 604	PROTEINATLAS_hippocampus
4	5e−03	6 / 42	VAQUERIZAS_Fetal brain_TF
5	5e−03	35 / 593	PROTEINATLAS_lateral ventricle
6	6e−03	35 / 595	PROTEINATLAS_breast
7	6e−03	5 / 32	VAQUERIZAS_Liver_TF
8	9e−03	33 / 569	PROTEINATLAS_salivary gland
9	9e−03	38 / 678	PROTEINATLAS_lymph node
10	1e−02	17 / 245	Chaussabel_3,9_Kinases
11	1e−02	14 / 188	Chaussabel_3,8_Enzymes
12	1e−02	55 / 1076	PROTEINATLAS_stomach
13	1e−02	37 / 671	PROTEINATLAS_cervix, uterine
14	1e−02	55 / 1081	PROTEINATLAS_testis
15	1e−02	9 / 100	Chaussabel_2,8_T−cells

Telomeres

Rank	p−value	#in/all	Geneset
1	0.08	3 / 27	Nabetani_alt len telomeres_genes_ko
2	0.08	2 / 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−05	75 / 1241	KIM_MYC targets
2	6e−05	64 / 1044	ICGC_Six5_targets
3	1e−03	61 / 1089	ICGC_Ets1_targets
4	1e−03	164 / 3564	ICGC_Taf1_targets
5	2e−03	145 / 3121	ICGC_Egr1_targets
6	2e−03	146 / 3150	ICGC_Creb1_targets
7	2e−03	60 / 1107	ICGC_Myc_targets
8	8e−03	2 / 4	MYC_TF and cofactors
9	8e−03	7 / 62	MYC_Targets UP
10	9e−03	32 / 549	ICGC_Atf3_targets
11	1e−02	166 / 3796	ICGC_Nficsc81335_targets
12	1e−02	162 / 3703	ICGC_Foxm1_targets
13	2e−02	133 / 2994	ICGC_Zeb1_targets
14	2e−02	158 / 3630	ICGC_Sp1_targets
15	2e−02	77 / 1630	ICGC_SrfV0416101_targets

K−Means Cluster

Spot Summary: B

metagenes = 47
genes = 579

<r> metagenes = 0.88
<r> genes = 0.17
beta: r2= 5.84 / log p= −Inf

samples with spot = 46 (20.8 %)
mBL : 31 (70.5 %)
intermediate : 11 (22.9 %)
non−mBL : 4 (3.1 %)

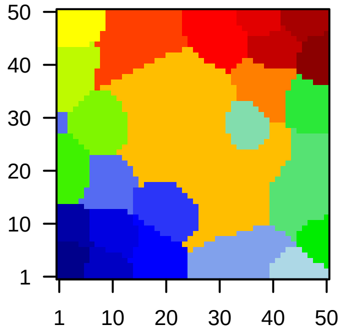
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	219655_at	2.48	−0.74	0.5	SUGCT	succinyl−CoA:glutarate−CoA transferase [Source:HGNC Sym
2	221933_at	2.43	−0.83	0.26	NLGN4X	neuroligin 4, X−linked [Source:HGNC Symbol;Acc:HGNC:14
3	220448_at	2.35	−0.95	0.52	KCNK12	potassium two pore domain channel subfamily K member 12
4	203865_s_at	2.33	−1.02	0.38	ADARB1	adenosine deaminase, RNA specific B1 [Source:HGNC Sym
5	221879_at	2.18	−0.84	0.29		
6	205902_at	2.03	−0.94	0.48	KCNN3	potassium calcium−activated channel subfamily N member 3
7	208719_s_at	2	−1.36	0.2	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
8	210640_s_at	1.98	−0.91	0.41	GPER1	G protein−coupled estrogen receptor 1 [Source:HGNC Symb
9	220432_s_at	1.97	−0.86	0.51	CYP39A1	cytochrome P450 family 39 subfamily A member 1 [Source:H
10	211998_at	1.94	−0.89	0.24	H3F3B	H3 histone family member 3B [Source:HGNC Symbol;Acc:H
11	217373_x_at	1.92	−1.07	0.41	MDM2	MDM2 proto−oncogene [Source:HGNC Symbol;Acc:HGNC:6
12	213436_at	1.92	−1.49	0.38	CNR1	cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21
13	212186_at	1.91	−1.42	0.36	ACACA	acetyl−CoA carboxylase alpha [Source:HGNC Symbol;Acc:H
14	218980_at	1.88	−0.67	0.47	FHOD3	formin homology 2 domain containing 3 [Source:HGNC Sym
15	209493_at	1.88	−1.38	0.35	PDZD2	PDZ domain containing 2 [Source:HGNC Symbol;Acc:HGNC
16	213668_s_at	1.86	−1.12	0.27	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
17	205340_at	1.82	−0.76	0.28	ZBTB24	zinc finger and BTB domain containing 24 [Source:HGNC Sy
18	210461_s_at	1.78	−0.98	0.5	ABLIM1	actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGN
19	208151_x_at	1.73	−1.48	0.27	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2
20	218862_at	1.71	−1.7	0.59	ASB13	ankyrin repeat and SOCS box containing 13 [Source:HGNC

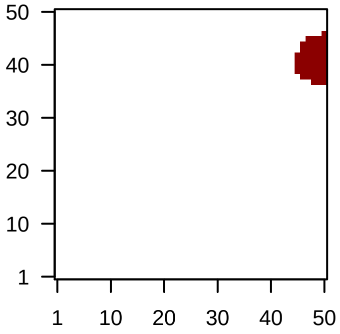
Geneset Overrepresentation

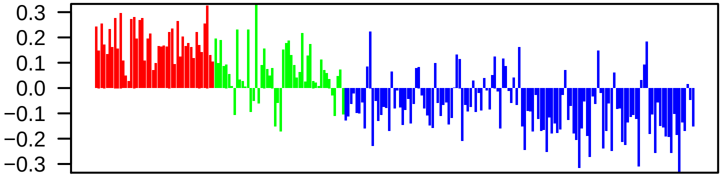
Rank	p−value	#in/all	Geneset	
1	2e−32	346 / 5908	Lymp	HOPP_Active_promoter
2	2e−30	328 / 5529	Lymp	HOPP_Txn_elongation
3	2e−24	310 / 5404	Lymp	HOPP_Strong_enhancer
4	5e−24	264 / 4261	Lymp	HOPP_Txn_transition
5	3e−21	49 / 263	Lymp	SPANG_CD40 6hrs UP
6	4e−21	312 / 5682	Lymp	HOPP_Weak_promoter
7	6e−19	94 / 955	Lymp	SPANG_BCR UP
8	4e−16	81 / 830	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
9	5e−15	35 / 195	GSE	HOLLMANN_APOPTOSIS_VIA_CD40_UP
10	1e−14	242 / 4357	Lymp	HOPP_Weak_txn
11	1e−13	247 / 4559	Lymp	HOPP_Weak_enhancer
12	6e−13	24 / 106	Refer	Chaussabel_2,11_Replication
13	2e−12	92 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
14	4e−12	40 / 309	GSE	DAZARD_RESPONSE_TO_UV_NHEK_DN
15	8e−12	200 / 3564	TF	ICGC_Taf1_targets
16	1e−11	108 / 1527	GSE	PUJANA_BRCA1_PCC_NETWORK
17	6e−11	238 / 4579	CC	nucleus
18	2e−10	35 / 275	GSE	HADDAD_B_LYMPHOCYTE_PROGENITOR
19	2e−10	151 / 2541	CC	nucleoplasm
20	1e−09	46 / 469	GSE	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
21	2e−09	19 / 96	Lymp	SPANG_LPS 6hrs UP
22	9e−09	89 / 1312	GSE	PUJANA_ATM_PCC_NETWORK
23	2e−08	197 / 3796	TF	ICGC_Nficsc81335_targets
24	2e−08	14 / 59	GSE	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
25	3e−08	168 / 3121	TF	ICGC_Egr1_targets
26	3e−08	14 / 61	GSE	BASSO_CD40_SIGNALING_DN
27	5e−08	98 / 1550	GSE	PILON_KLF1_TARGETS_DN
28	7e−08	6 / 8	Lymp	MASCQUE_GCB UP
29	8e−08	180 / 3451	TF	ICGC_Atf2_targets
30	9e−08	20 / 133	GSE	PENG_LEUCINE_DEPRIVATION_UP
31	1e−07	24 / 186	GSE	PENG_RAPAMYCIN_RESPONSE_UP
32	2e−07	128 / 2254	TF	ICGC_BatfPcr1_targets
33	2e−07	193 / 3804	TF	ICGC_Stat5_targets
34	2e−07	24 / 192	Lymp	Victora_Dark zone signature
35	2e−07	62 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
36	3e−07	94 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
37	4e−07	190 / 3769	TF	ICGC_Pmlsc71910_targets
38	5e−07	11 / 45	Lymp	Monti_BCR_cluster
39	5e−07	94 / 1541	MF	DNA binding
40	6e−07	10 / 37	GSE	ZHAN_MULTIPLE_MYELOMA_CD2_UP

Overview Map

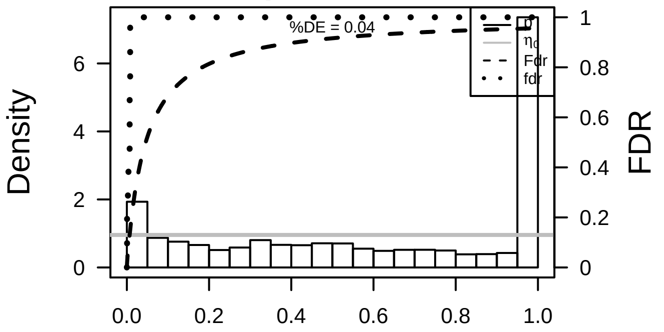


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	4 / 107	HORVATH_aging_genes meth UP
2	0.8	1 / 47	TESCHENDORFF_age_hypermethylated
3	1.0	1 / 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−06	97 / 1655	transcription, DNA−templated
2	6e−06	100 / 1764	regulation of transcription, DNA−templated
3	1e−04	23 / 260	chromatin organization
4	1e−04	36 / 507	protein phosphorylation
5	3e−04	5 / 17	T cell proliferation
6	4e−04	10 / 74	regulation of mitotic cell cycle
7	2e−03	36 / 576	phosphorylation
8	2e−03	33 / 520	positive regulation of transcription, DNA−templated
9	2e−03	12 / 124	peptidyl−serine phosphorylation
10	2e−03	13 / 141	protein dephosphorylation
11	2e−03	22 / 307	cell division
12	3e−03	6 / 38	negative regulation of fat cell differentiation
13	3e−03	37 / 621	negative regulation of transcription from RNA polymerase II promoter
14	3e−03	4 / 17	cell−cell junction organization
15	3e−03	11 / 113	regulation of signal transduction by p53 class mediator

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	8 / 72	PanCan_Wnt_geneset_nanostring
2	0.009	11 / 130	PanCan_CC+Apop_geneset_nanostring
3	0.014	3 / 14	BENTINK_src.2
4	0.019	2 / 6	ZHANG_MGUS up
5	0.024	9 / 113	PanCan_Driver_Gene_geneset_nanostring
6	0.060	2 / 11	LIU_PROSTATE_CANCER_UP
7	0.105	2 / 15	RHODES_CANCER_META_SIGNATURE
8	0.105	2 / 15	WANG_ER_UP
9	0.124	23 / 480	Lembcke_Colonic Inflammation
10	0.168	2 / 20	PanCan_ChromMod_geneset_nanostring
11	0.232	3 / 45	KUIPER_MM poor survival
12	0.250	1 / 16	LIU_LIVER_CANCER
13	0.252	0 / 14	LIU_COMMON_CANCER_GENES
14	0.314	1 / 10	GENTLES_modul3
15	0.340	1 / 11	GENTLES_modul14

CC

Rank	p−value	#in/all	Geneset
1	6e−11	238 / 4579	nucleus
2	2e−10	151 / 2541	nucleoplasm
3	6e−05	180 / 3805	cytosol
4	2e−04	212 / 4701	cytoplasm
5	5e−04	4 / 11	pericentric heterochromatin
6	2e−03	52 / 936	cytoskeleton
7	3e−03	18 / 233	nuclear body
8	4e−03	4 / 18	replication fork
9	4e−03	5 / 29	immunological synapse
10	1e−02	13 / 171	nuclear chromatin
11	1e−02	8 / 86	PML body
12	2e−02	3 / 15	NuRD complex
13	2e−02	3 / 15	pericentriolar material
14	2e−02	9 / 107	fibrillar center
15	2e−02	20 / 324	chromosome

Chr

Rank	p−value	#in/all	Geneset
1	0.003	39 / 669	Chr 6
2	0.007	27 / 437	Chr 8
3	0.054	40 / 832	Chr 2
4	0.068	29 / 585	Chr 7
5	0.092	33 / 700	Chr 12
6	0.100	58 / 1325	Chr 1
7	0.254	15 / 333	Chr 22
8	0.257	7 / 139	Chr 21
9	0.276	21 / 490	Chr 10
10	0.468	21 / 548	Chr 16
11	0.513	18 / 480	Chr 4
12	0.654	24 / 689	Chr 3
13	0.663	13 / 382	Chr 15
14	0.681	6 / 184	Chr 18
15	0.751	18 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−51	372 / 5716	Bcells peripheral blood_4_Tx
2	9e−47	367 / 5766	natural killer cells peripheral blood_4_Tx
3	4e−45	427 / 7751	natural killer cells peripheral blood_1_TssA
4	7e−45	429 / 7833	Bcells peripheral blood_1_TssA
5	1e−44	417 / 7420	Tcells peripheral blood_1_TssA
6	1e−44	363 / 5753	Tcells peripheral blood_4_Tx
7	3e−44	416 / 7407	natural killer cells peripheral blood_5_TxWk
8	2e−43	391 / 6637	Tcells peripheral blood_5_TxWk
9	3e−43	442 / 8406	Bcells peripheral blood_2_TssAFlnk
10	9e−42	428 / 7957	Tcells peripheral blood_2_TssAFlnk
11	9e−42	350 / 5527	Tregulatory cells peripheral blood_4_Tx
12	5e−41	401 / 7078	Bcells peripheral blood_5_TxWk
13	8e−41	351 / 5601	Thelper cells peripheral blood_4_Tx
14	4e−39	432 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
15	4e−39	434 / 8322	T CD8+ naive cells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	92 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	2e−07	62 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	2e−05	63 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	2e−04	92 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	4e−03	61 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
6	5e−03	264 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	1e−02	49 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	1e−02	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
9	3e−02	12 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
10	3e−02	27 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
11	3e−02	2 / 8	Boland_CRC−MMR−system
12	5e−02	41 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	6e−02	27 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	1e−01	4 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
15	1e−01	40 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

Glioma

Rank	p−value	#in/all	Geneset
1	3e−07	94 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−06	83 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−03	21 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	3e−03	23 / 330	Up
5	6e−03	7 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	1e−02	6 / 50	Vishal_subnetwork signature of survival in GBM
7	2e−02	2 / 6	WILLSCHER_GBM_Verhaak−PNmut_up (M)
8	2e−02	33 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	3e−02	6 / 64	Weller_LGG_A_vs_O_DOWN
10	5e−02	5 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	7e−02	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
12	1e−01	21 / 421	Down_b
13	1e−01	13 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
14	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_down (A)
15	2e−01	14 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−16	81 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	5e−15	35 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
3	4e−12	40 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
4	1e−11	108 / 1527	PUJANA_BRCA1_PCC_NETWORK
5	2e−10	35 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
6	1e−09	46 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
7	9e−09	89 / 1312	PUJANA_ATM_PCC_NETWORK
8	2e−08	14 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
9	3e−08	14 / 61	BASSO_CD40_SIGNALING_DN
10	5e−08	98 / 1550	PILON_KLF1_TARGETS_DN
11	9e−08	20 / 133	PENG_LEUCINE_DEPRIVATION_UP
12	1e−07	24 / 186	PENG_RAPAMYCIN_RESPONSE_UP
13	6e−07	10 / 37	ZHAN_MULTIPLE_MYELOMA_CD2_UP
14	7e−07	51 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
15	8e−07	7 / 16	ZHAN_LATE_DIFFERENTIATION_GENES_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	14 / 187	HALLMARK_E2F_TARGETS
2	0.03	8 / 96	HALLMARK_ANDROGEN_RESPONSE
3	0.05	4 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
4	0.11	11 / 195	HALLMARK_G2M_CHECKPOINT
5	0.12	4 / 51	HALLMARK_TGF_BETA_SIGNALING
6	0.15	8 / 141	HALLMARK_UV_RESPONSE_DN
7	0.17	10 / 191	HALLMARK_P53_PATHWAY
8	0.18	10 / 192	HALLMARK_MTORC1_SIGNALING
9	0.18	9 / 170	HALLMARK_IL2_STAT5_SIGNALING
10	0.18	10 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.19	9 / 173	HALLMARK_MITOTIC_SPINDLE
12	0.20	9 / 174	HALLMARK_ADIPOGENESIS
13	0.27	5 / 94	HALLMARK_PROTEIN_SECRETION
14	0.29	2 / 29	HALLMARK_NOTCH_SIGNALING
15	0.33	8 / 176	HALLMARK_ALLOGRAFT_REJECTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.001	4 / 13	Angelova_immune−metagene−immature_B−cells
2	0.033	2 / 8	Angelova_immune−metagene−mDC
3	0.082	2 / 13	Angelova_immune−metagene−activated_B−cells
4	0.117	2 / 16	Angelova_immune−metagene−Th17
5	0.140	1 / 4	Angelova_CRC_MSS−neoantigens
6	0.232	1 / 7	Angelova_CRC_MSI−neoantigens
7	0.314	1 / 10	Angelova_immune−metagene−neutrophils
8	0.314	1 / 10	Angelova_immune−metagene−TFH
9	0.340	1 / 11	Angelova_immune−metagene−macrophages
10	0.364	1 / 12	Angelova_immune−metagene−memory_B−cells
11	0.388	1 / 13	Angelova_CRC_MSS^−neoantigens
12	0.411	1 / 14	Angelova_immune−metagene−eosinophil
13	0.432	1 / 15	Angelova_immune−metagene−NK
14	0.493	1 / 18	Angelova_immune−metagene−pDC
15	0.493	1 / 18	Angelova_CRC_immunostimulators

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.005	16 / 210	Homuth_BMI−associated−genes_DN
2	0.105	9 / 150	Homuth_BMI−associated−genes_UP
3	0.117	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.172	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	0.195	2 / 22	DUMEAUX_Fasting enriched genes
6	0.261	1 / 8	Marjolein_ageing−genes_UP
7	0.333	2 / 32	Marjolein_ageing−genes_DN
8	0.564	1 / 22	DUMEAUX_High bmi enriched genes
9	1.000	0 / 62	DUMEAUX_Smoking enriched genes
10	1.000	0 / 10	DUMEAUX_Smoking literature genes up
11	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
15	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−32	346 / 5908	HOPP_Active_promoter
2	2e−30	328 / 5529	HOPP_Txn_elongation
3	2e−24	310 / 5404	HOPP_Strong_enhancer
4	5e−24	264 / 4261	HOPP_Txn_transition
5	3e−21	49 / 263	SPANG_CD40 6hrs UP
6	4e−21	312 / 5682	HOPP_Weak_promoter
7	6e−19	94 / 955	SPANG_BCR UP
8	1e−14	242 / 4357	HOPP_Weak_txn
9	1e−13	247 / 4559	HOPP_Weak_enhancer
10	2e−09	19 / 96	SPANG_LPS 6hrs UP
11	7e−08	6 / 8	MASCQUE_GCB UP
12	2e−07	24 / 192	Victora_Dark zone signature
13	5e−07	11 / 45	Monti_BCR_cluster
14	9e−06	6 / 15	DAVE_BL Inter
15	1e−05	59 / 906	SPANG_BCR DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.05	8 / 107	Tirosh_Exhaustion program in Mel75
2	0.05	3 / 23	Melanoma Epi−Enzyme Cluster 7
3	0.06	3 / 24	Tirosh_B−cell specific genes−melanoma
4	0.07	13 / 222	Gerber_wt/wt_melanoma−cells−SpotF
5	0.07	1 / 2	Melanoma Epi−Enzyme Cluster 2
6	0.09	13 / 230	Gerber_wt/wt_melanoma−cells−SpotC
7	0.12	4 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	0.14	1 / 4	Melanoma Epi−Enzyme Cluster 3
9	0.17	3 / 38	Hugo_melanoma−BRAFmut−MET_UP
10	0.17	3 / 38	Tirosh_top50 correlated genes PC1
11	0.17	12 / 236	Gerber_wt/wt_group3−specific
12	0.17	1 / 5	Joensson_Melanoma Proliferative subtype
13	0.21	15 / 319	Gerber_wt/wt_melanoma−cells−SpotA
14	0.25	9 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
15	0.25	3 / 47	Tirosh_G2/M phase specific genes

MF

Rank	p−value	#in/all	Geneset
1	5e−07	94 / 1541	DNA binding
2	4e−06	10 / 44	methylated histone binding
3	1e−05	336 / 7864	protein binding
4	4e−05	28 / 331	protein serine/threonine kinase activity
5	8e−05	76 / 1329	transferase activity
6	4e−04	31 / 437	protein kinase activity
7	4e−04	7 / 38	core promoter sequence−specific DNA binding
8	5e−04	51 / 852	nucleic acid binding
9	1e−03	20 / 249	ubiquitin protein ligase binding
10	1e−03	19 / 237	ubiquitin−protein transferase activity
11	1e−03	4 / 14	SUMO transferase activity
12	2e−03	62 / 1161	RNA binding
13	2e−03	63 / 1185	ATP binding
14	2e−03	20 / 268	transcription factor binding
15	2e−03	8 / 64	phosphatidylinositol binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−05	29 / 344	hsa−miR−19a
2	3e−05	29 / 344	hsa−miR−19b
3	3e−05	13 / 92	hsa−miR−199a−5p
4	9e−05	13 / 101	hsa−miR−199b−5p
5	1e−04	24 / 278	hsa−let−7d
6	1e−04	29 / 369	hsa−miR−130a
7	1e−04	9 / 53	hsa−miR−606
8	1e−04	7 / 32	hsa−miR−450a
9	2e−04	16 / 155	hsa−miR−381
10	2e−04	25 / 312	hsa−miR−301b
11	3e−04	7 / 35	hsa−miR−518f
12	3e−04	25 / 315	hsa−miR−144
13	5e−04	15 / 150	hsa−miR−300
14	5e−04	11 / 90	hsa−miR−22
15	7e−04	12 / 109	hsa−miR−485−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.007	14 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.193	3 / 41	Scicluna_DN
3	0.600	2 / 54	Burnham_timecourse
4	0.629	2 / 57	Burnham_viral_UP
5	0.667	4 / 122	Terre_IMS_influenza_meta_signature
6	0.713	1 / 33	Sweeney_viral_dn
7	0.753	1 / 37	Sweeney_viral_up
8	0.837	1 / 48	Burnham_viral_DN
9	0.880	1 / 56	Burnham_sep_vs_con_DN
10	0.884	1 / 57	Burnham_day1_vs_5_UP
11	0.994	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
12	1.000	0 / 68	Burnham_sep_vs_con_UP
13	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
14	1.000	0 / 71	Burnham_cap_fp_vs_con_UP
15	1.000	0 / 52	Burnham_day1_vs_5_DN

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−13	24 / 106	Chaussabel_2,11_Replication
2	4e−06	29 / 310	Chaussabel_3,4_Protein phosphatases
3	5e−06	49 / 678	PROTEINATLAS_lymph node
4	1e−05	63 / 989	PROTEINATLAS_tonsil
5	2e−05	9 / 42	Chaussabel_1,3_B−cells
6	2e−05	22 / 219	WIRTH_GC B−cells
7	8e−05	13 / 100	Chaussabel_2,8_T−cells
8	1e−04	43 / 645	PROTEINATLAS_bone marrow
9	2e−04	18 / 188	Chaussabel_3,8_Enzymes
10	3e−04	27 / 355	WIRTH_Immune system
11	2e−03	37 / 604	PROTEINATLAS_hippocampus
12	2e−03	19 / 245	Chaussabel_3,9_Kinases
13	3e−03	26 / 390	PROTEINATLAS_ovary
14	3e−03	56 / 1048	PROTEINATLAS_rectum
15	4e−03	47 / 848	PROTEINATLAS_adrenal gland

Telomeres

Rank	p−value	#in/all	Geneset
1	0.08	2 / 13	Alternative lengthening of telomeres
2	0.64	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	8e−12	200 / 3564	ICGC_Taf1_targets
2	2e−08	197 / 3796	ICGC_Nficsc81335_targets
3	3e−08	168 / 3121	ICGC_Egr1_targets
4	8e−08	180 / 3451	ICGC_Atf2_targets
5	2e−07	128 / 2254	ICGC_BatfPcr1_targets
6	2e−07	193 / 3804	ICGC_Stat5_targets
7	4e−07	190 / 3769	ICGC_Pmlsc71910_targets
8	8e−07	182 / 3608	ICGC_Tcf12_targets
9	9e−07	174 / 3420	ICGC_Bclaf101388_targets
10	1e−06	182 / 3630	ICGC_Sp1_targets
11	1e−06	162 / 3150	ICGC_Creb1_targets
12	1e−06	209 / 4319	ICGC_Pou2_targets
13	2e−06	184 / 3703	ICGC_Foxm1_targets
14	2e−06	201 / 4131	ICGC_Tcf3_targets
15	5e−06	89 / 1508	ICGC_Mef2_targets

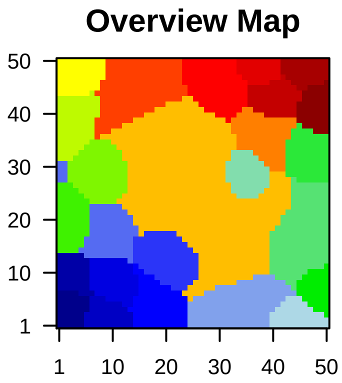
K−Means Cluster

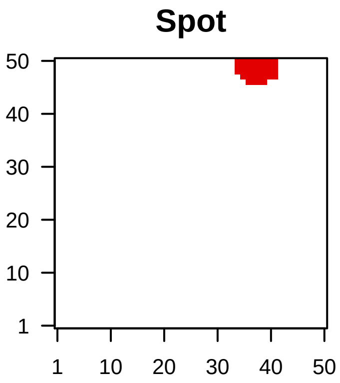
Spot Summary: C

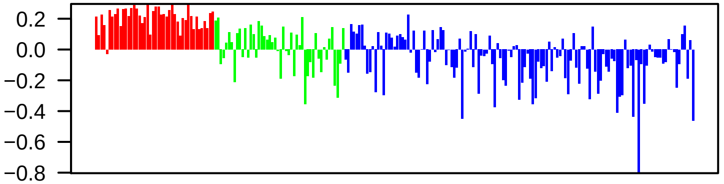
metagenes = 35
genes = 550

<r> metagenes = 0.95
<r> genes = 0.34
beta: r2= 7.28 / log p= −Inf

samples with spot = 49 (22.2 %)
mBL : 36 (81.8 %)
intermediate : 7 (14.6 %)
non−mBL : 6 (4.7 %)





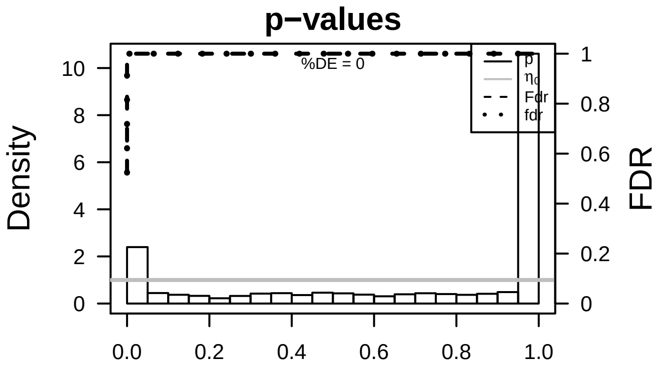


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205190_at	1.86	−1.09	0.47	PLS1	plastin 1 [Source:HGNC Symbol;Acc:HGNC:9090]
2	205229_s_at	1.84	−2.18	0.38	COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
3	209980_s_at	1.66	−1.51	0.73	SHMT1	serine hydroxymethyltransferase 1 [Source:HGNC Symbol;Ac
4	208502_s_at	1.64	−1.55	0.39	PITX1	paired like homeodomain 1 [Source:HGNC Symbol;Acc:HGN
5	212436_at	1.64	−1.2	0.31	TRIM33	tripartite motif containing 33 [Source:HGNC Symbol;Acc:HGN
6	219474_at	1.6	−1.32	0.48	C3orf52	chromosome 3 open reading frame 52 [Source:HGNC Symbo
7	218507_at	1.58	−1.34	0.21	HILPDA	hypoxia inducible lipid droplet associated [Source:HGNC Sym
8	217127_at	1.5	−1.12	0.39	CTH	cystathionine gamma−lyase [Source:HGNC Symbol;Acc:HGN
9	219733_s_at	1.48	−1.19	0.47	SLC27A5	solute carrier family 27 member 5 [Source:HGNC Symbol;Acc
10	204720_s_at	1.4	−1.15	0.37	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6 [Source:
11	213610_s_at	1.38	−1.42	0.47	KLHL23	kelch like family member 23 [Source:HGNC Symbol;Acc:HGN
12	204001_at	1.26	−1.33	0.36	SNAPC3	small nuclear RNA activating complex polypeptide 3 [Source:
13	201791_s_at	1.24	−1.39	0.33	DHCR7	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
14	204430_s_at	1.22	−1.69	0.23	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
15	203790_s_at	1.21	−1.38	0.55	RIDA	reactive intermediate imine deaminase A homolog [Source:H
16	222228_s_at	1.16	−0.71	0.32	ALKBH4	alkB homolog 4, lysine demethylase [Source:HGNC Symbol;
17	210389_x_at	1.15	−1.08	0.51	TUBD1	tubulin delta 1 [Source:HGNC Symbol;Acc:HGNC:16811]
18	205217_at	1.14	−1.41	0.48	TIMM8A	translocase of inner mitochondrial membrane 8A [Source:HG
19	211767_at	1.12	−1.32	0.55	GINS4	GINS complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:2
20	220160_s_at	1.11	−1.35	0.42	KPTN	kaptin, actin binding protein [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	91 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−99	167 / 319	Melar	Gerber_wt/wt_melanoma−cells−SpotA
3	1e−99	223 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	1e−99	99 / 137	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e−99	132 / 244	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	1e−99	121 / 254	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
7	1e−99	162 / 431	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	3e−94	149 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	2e−93	138 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	3e−93	12 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	3e−93	12 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	2e−88	130 / 409	Canc	Lembcke_Normal vs Adenoma
13	1e−85	100 / 219	Refer	WIRTH_GC B−cells
14	4e−83	108 / 280	GSEA	MANALO_HYPOXIA_DN
15	1e−81	89 / 174	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	9e−80	97 / 226	GSEA	ZHANG_TLX_TARGETS_60HR_DN
17	1e−77	157 / 758	GSEA	NUYTTEN_EZH2_TARGETS_DN
18	3e−74	136 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
19	3e−73	106 / 321	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
20	5e−71	114 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
21	7e−71	84 / 187	HM	HALLMARK_E2F_TARGETS
22	8e−70	146 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
23	4e−68	171 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
24	4e−67	99 / 307	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
25	6e−67	62 / 93	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
26	1e−66	58 / 79	Melar	Tirosh_core cycling genes in low− and high−proliferation melanoma
27	9e−66	125 / 548	GSEA	BENPORATH_CYCLING_GENES
28	9e−66	67 / 117	GSEA	CHANG_CYCLING_GENES
29	3e−62	57 / 84	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
30	3e−60	91 / 290	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
31	4e−60	111 / 466	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
32	2e−59	193 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
33	6e−58	45 / 52	GSEA	KANG_DOXORUBICIN_RESISTANCE_UP
34	2e−57	82 / 241	GSEA	BASAKI_YBX1_TARGETS_UP
35	3e−57	71 / 169	GSEA	FUJII_YBX1_TARGETS_DN
36	1e−56	58 / 102	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
37	2e−56	50 / 70	GSEA	CROONQUIST_NRAS_SIGNALING_DN
38	4e−56	129 / 703	GSEA	LEE_BMP2_TARGETS_DN
39	4e−55	73 / 192	Lympl	Victora_Dark zone signature
40	9e−55	81 / 250	GSEA	HORIUCHI_WTAP_TARGETS_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.02	9 / 107	HORVATH_aging_genes meth UP
2	0.86	2 / 92	HORVATH_aging_genes meth DOWN
3	1.00	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	3e−29	289 / 4579	nucleus
2	5e−29	199 / 2541	nucleoplasm
3	6e−25	59 / 324	chromosome
4	2e−20	33 / 118	chromosome, centromeric region
5	2e−16	24 / 77	condensed chromosome kinetochore
6	2e−16	27 / 101	kinetochore
7	5e−16	70 / 653	nucleolus
8	9e−16	49 / 354	centrosome
9	2e−15	32 / 157	spindle
10	8e−13	23 / 98	spindle pole
11	5e−11	37 / 292	microtubule organizing center
12	5e−10	22 / 121	midbody
13	7e−10	203 / 3805	cytosol
14	4e−09	31 / 251	microtubule
15	1e−08	70 / 936	cytoskeleton

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−25	46 / 184	Kosinski_lower−crypt−long−list
2	8e−14	60 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	5e−10	55 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	8e−04	6 / 31	Kosinski_lower−crypt−short−list
5	1e−03	4 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
6	2e−03	87 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
7	3e−02	3 / 18	Boland_CRC−MSI−A6−A10
8	3e−02	29 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
9	3e−02	2 / 8	Boland_CRC−MMR−system
10	7e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
11	7e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
12	2e−01	24 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
13	2e−01	1 / 6	Marisa_CRC−C6
14	2e−01	49 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	2e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes

HM

Rank	p−value	#in/all	Geneset
1	7e−71	84 / 187	HALLMARK_E2F_TARGETS
2	3e−53	72 / 195	HALLMARK_G2M_CHECKPOINT
3	3e−14	32 / 173	HALLMARK_MITOTIC_SPINDLE
4	5e−13	18 / 55	HALLMARK_MYC_TARGETS_V2
5	2e−09	27 / 190	HALLMARK_MYC_TARGETS_V1
6	2e−07	24 / 192	HALLMARK_MTORC1_SIGNALING
7	2e−06	18 / 133	HALLMARK_DNA_REPAIR
8	6e−04	13 / 122	HALLMARK_SPERMATOGENESIS
9	2e−02	13 / 182	HALLMARK_GLYCOLYSIS
10	7e−02	5 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	9e−02	11 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	1e−01	7 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
13	1e−01	9 / 149	HALLMARK_UV_RESPONSE_UP
14	1e−01	11 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
15	1e−01	8 / 139	HALLMARK_FATTY_ACID_METABOLISM

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−55	73 / 192	Victora_Dark zone signature
2	3e−45	356 / 5529	HOPP_Txn_elongation
3	2e−34	68 / 305	TARTE_Plasmablast signature
4	2e−30	342 / 5908	HOPP_Active_promoter
5	1e−21	258 / 4261	HOPP_Txn_transition
6	1e−16	27 / 99	Sha_BL UP
7	2e−11	78 / 955	SPANG_BCR UP
8	2e−08	21 / 135	DAVE_BL−vs−DLBCL
9	7e−08	268 / 5682	HOPP_Weak_promoter
10	4e−06	249 / 5404	HOPP_Strong_enhancer
11	5e−06	15 / 102	ROSOLOWSKI_blue total
12	3e−03	4 / 17	DAVE_c−myc BL UP
13	2e−02	5 / 45	Monti_BCR_cluster
14	7e−02	177 / 4357	HOPP_Weak_txn
15	8e−02	4 / 45	SPANG_BAFF 9hrs DN

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 31	hsa−miR−661
2	9e−03	9 / 95	hsa−miR−376a
3	9e−03	13 / 167	hsa−miR−432
4	1e−02	16 / 232	hsa−miR−186
5	2e−02	5 / 41	hsa−miR−518e*
6	2e−02	13 / 181	hsa−miR−520g
7	2e−02	6 / 59	hsa−miR−184
8	2e−02	7 / 77	hsa−miR−526a
9	2e−02	4 / 30	hsa−miR−518e
10	3e−02	5 / 46	hsa−miR−208a
11	3e−02	9 / 115	hsa−miR−28−5p
12	3e−02	10 / 134	hsa−miR−520h
13	3e−02	11 / 154	hsa−miR−452
14	3e−02	8 / 98	hsa−miR−520a−5p
15	3e−02	5 / 47	hsa−miR−151−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.001	4 / 13	Alternative lengthening of telomeres
2	0.003	5 / 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	2e−40	93 / 497	cell cycle
2	5e−38	72 / 307	cell division
3	2e−34	48 / 137	DNA replication
4	4e−22	31 / 91	sister chromatid cohesion
5	5e−20	49 / 281	DNA repair
6	3e−14	13 / 21	mitotic sister chromatid segregation
7	3e−14	13 / 21	telomere maintenance via semi−conservative replication
8	4e−14	21 / 70	chromosome segregation
9	2e−13	24 / 101	mitotic cell cycle
10	2e−13	45 / 351	cellular response to DNA damage stimulus
11	1e−12	14 / 31	DNA replication initiation
12	4e−12	10 / 14	chromosome condensation
13	4e−11	13 / 32	DNA synthesis involved in DNA repair
14	6e−11	23 / 119	G2/M transition of mitotic cell cycle
15	7e−11	10 / 17	spindle organization

Chr

Rank	p−value	#in/all	Geneset
1	6e−06	33 / 382	Chr 15
2	3e−03	68 / 1325	Chr 1
3	2e−02	30 / 548	Chr 16
4	1e−01	36 / 776	Chr 17
5	1e−01	17 / 333	Chr 22
6	2e−01	12 / 242	Chr 13
7	3e−01	19 / 437	Chr 8
8	3e−01	21 / 492	Chr 9
9	4e−01	20 / 490	Chr 10
10	4e−01	8 / 184	Chr 18
11	4e−01	30 / 756	Chr 11
12	4e−01	6 / 139	Chr 21
13	4e−01	16 / 403	Chr 14
14	7e−01	16 / 480	Chr 4
15	8e−01	23 / 700	Chr 12

Glioma

Rank	p−value	#in/all	Geneset
1	1e−99	91 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	2e−22	24 / 47	developing astrocytes
3	4e−18	24 / 66	Weller_LGG_gradeII−vs−III_DOWN
4	1e−11	99 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	1e−10	105 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	2e−03	8 / 64	cultured astroglia vs. in vivo astrocytes
7	4e−03	36 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
8	3e−02	5 / 49	OPC
9	6e−02	5 / 58	Stuehler_Proteins_up_in_STS
10	7e−02	1 / 2	Phillips Prolif up vs PN & MES
11	2e−01	2 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
12	3e−01	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
13	4e−01	2 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
14	4e−01	3 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
15	4e−01	2 / 35	Gorovets_LGG_EPL_subclass

Immunome

Rank	p−value	#in/all	Geneset
1	3e−24	20 / 26	Angelova_immune−metagene−activated_CD4
2	5e−04	5 / 19	Angelova_immune−metagene−activated_CD8
3	7e−02	2 / 12	Angelova_immune−metagene−memory_B−cells
4	2e−01	1 / 5	Angelova_immune−metagene−NK56_bright
5	4e−01	1 / 12	Angelova_immune−metagene−effector_memory_CD4
6	4e−01	2 / 38	Angelova_immune−metagene−mast−cells
7	5e−01	1 / 18	Angelova_immune−metagene−pDC
8	8e−01	1 / 45	Angelova_immune−metagene−MDSC
9	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
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 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1e+00	0 / 14	Angelova_immune−metagene−eosinophil

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−99	167 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	1e−66	58 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
3	6e−49	38 / 44	Tirosh_top50 correlated genes PC2
4	8e−41	35 / 47	Tirosh_G2/M phase specific genes
5	6e−29	26 / 38	Tirosh_G1/S phase specific genes
6	2e−18	24 / 65	Harbst_melanoma_highgrade_up
7	3e−04	8 / 46	Tirosh_top50 correlated genes PC5
8	3e−02	17 / 276	Gerber_wt/wt_melanoma−cells−SpotB
9	1e−01	1 / 4	Melanoma Epi−Enzyme Cluster 3
10	1e−01	1 / 4	Melanoma Epi−Enzyme Cluster 5
11	2e−01	3 / 38	Tirosh_top50 correlated genes PC1
12	6e−01	3 / 81	Tirosh_Genes in the MITF program
13	8e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
14	8e−01	6 / 204	Landsberg_dedifferentiation_down
15	8e−01	7 / 249	Gerber_wt/wt_melanoma−cells−SpotE

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.002	13 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.298	6 / 122	Terre_IMS_influenza_meta_signature
3	0.323	3 / 54	Burnham_timecourse
4	0.345	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	0.629	2 / 57	Burnham_day1_vs_5_UP
6	0.713	1 / 33	Sweeney_viral_dn
7	0.837	1 / 48	Burnham_viral_DN
8	0.884	1 / 57	Burnham_viral_UP
9	0.932	1 / 71	Burnham_cap_fp_vs_con_UP
10	1.000	0 / 68	Burnham_sep_vs_con_UP
11	1.000	0 / 56	Burnham_sep_vs_con_DN
12	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
13	1.000	0 / 52	Burnham_day1_vs_5_DN
14	1.000	0 / 18	Scicluna_UP
15	1.000	0 / 41	Scicluna_DN

TF

Rank	p−value	#in/all	Geneset
1	6e−16	104 / 1241	KIM_MYC targets
2	7e−10	193 / 3564	ICGC_Taf1_targets
3	2e−09	174 / 3150	ICGC_Creb1_targets
4	2e−08	78 / 1107	ICGC_Myc_targets
5	4e−07	191 / 3796	ICGC_Nficsc81335_targets
6	2e−06	187 / 3769	ICGC_Pmlsc71910_targets
7	7e−06	185 / 3804	ICGC_Stat5_targets
8	7e−06	178 / 3630	ICGC_Sp1_targets
9	1e−05	11 / 62	MYC_Targets UP
10	3e−05	174 / 3608	ICGC_Tcf12_targets
11	3e−05	213 / 4602	ICGC_Elf1_targets
12	4e−05	177 / 3703	ICGC_Foxm1_targets
13	5e−05	201 / 4319	ICGC_Pou2_targets
14	1e−04	191 / 4131	ICGC_Tcf3_targets
15	2e−04	63 / 1089	ICGC_Ets1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	3e−93	12 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	2e−88	130 / 409	Lembcke_Normal vs Adenoma
3	1e−23	7 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	1e−09	9 / 16	WOLFER_overlap genes
5	2e−07	11 / 41	PanCan_DNARepair_geneset_nanostring
6	1e−06	12 / 58	SHAUGHNESSY_MM high risk
7	4e−06	10 / 45	KUIPER_MM poor survival
8	9e−06	6 / 15	GENTLES_modul2
9	1e−05	5 / 10	GENTLES_modul3
10	9e−05	15 / 130	PanCan_CC+Apop_geneset_nanostring
11	2e−04	5 / 15	BEN−PORATH_UP
12	2e−04	1 / 15	RHODES_CANCER_META_SIGNATURE
13	1e−03	4 / 13	GENTLES_modul1
14	5e−03	3 / 10	GENTLES_modul5
15	6e−03	5 / 32	KUIPER_MM good survival

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−54	445 / 7957	Tcells peripheral blood_2_TssAFlnk
2	8e−54	450 / 8200	monocytes peripheral blood_2_TssAFlnk
3	7e−53	450 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
4	6e−52	452 / 8370	natural killer cells peripheral blood_2_TssAFlnk
5	3e−51	452 / 8406	Bcells peripheral blood_2_TssAFlnk
6	4e−48	436 / 7930	Tregulatory cells peripheral blood_1_TssA
7	3e−47	457 / 8816	Thelper cells peripheral blood_2_TssAFlnk
8	5e−45	445 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
9	4e−44	428 / 7833	Bcells peripheral blood_1_TssA
10	4e−44	441 / 8322	T CD8+ naive cells peripheral blood_1_TssA
11	3e−43	421 / 7635	monocytes peripheral blood_1_TssA
12	4e−43	433 / 8068	Thelper cells peripheral blood_1_TssA
13	3e−42	371 / 6099	HSC_4_Tx
14	1e−41	449 / 8766	2_TssA_Melanocytes
15	2e−40	451 / 8918	1_TssA_ESC_Mesoderm

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	223 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	1e−99	99 / 137	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	1e−99	132 / 244	KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	1e−99	121 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
5	1e−99	162 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	3e−94	149 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	2e−93	138 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	3e−93	12 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	4e−83	108 / 280	MANALO_HYPOXIA_DN
10	1e−81	89 / 174	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	9e−80	97 / 226	ZHANG_TLX_TARGETS_60HR_DN
12	1e−77	157 / 758	NUYTTEN_EZH2_TARGETS_DN
13	3e−74	136 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
14	3e−73	106 / 321	BLUM_RESPONSE_TO_SALIRASIB_DN
15	5e−71	114 / 400	PUJANA_BRCA2_PCC_NETWORK

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 8	Marjolein_ageing−genes_UP
2	0.9	1 / 62	DUMEAUX_Smoking enriched genes
3	0.9	3 / 150	Homuth_BMI−associated−genes_UP
4	1.0	4 / 210	Homuth_BMI−associated−genes_DN
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 22	DUMEAUX_High bmi enriched genes
14	1.0	0 / 22	DUMEAUX_Fasting enriched genes
15	1.0	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−08	82 / 1185	ATP binding
2	2e−08	349 / 7864	protein binding
3	2e−07	89 / 1402	nucleotide binding
4	2e−07	15 / 81	single−stranded DNA binding
5	3e−06	7 / 19	DNA helicase activity
6	4e−06	73 / 1161	RNA binding
7	5e−06	30 / 328	chromatin binding
8	6e−06	9 / 37	exonuclease activity
9	1e−05	21 / 196	microtubule binding
10	5e−05	12 / 83	microtubule motor activity
11	6e−05	6 / 20	DNA−directed DNA polymerase activity
12	1e−04	17 / 161	ATPase activity
13	1e−04	5 / 14	four−way junction DNA binding
14	1e−04	12 / 90	nuclease activity
15	1e−04	13 / 106	ligase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−85	100 / 219	WIRTH_GC B−cells
2	8e−10	57 / 645	PROTEINATLAS_bone marrow
3	2e−09	58 / 678	PROTEINATLAS_lymph node
4	3e−09	79 / 1081	PROTEINATLAS_testis
5	8e−08	54 / 677	PROTEINATLAS_esophagus
6	9e−07	67 / 989	PROTEINATLAS_tonsil
7	1e−06	56 / 776	PROTEINATLAS_skin
8	7e−06	67 / 1048	PROTEINATLAS_rectum
9	7e−06	68 / 1072	PROTEINATLAS_duodenum
10	1e−05	57 / 861	PROTEINATLAS_nasopharynx
11	1e−05	40 / 527	PROTEINATLAS_oral mucosa
12	2e−05	54 / 819	PROTEINATLAS_bronchus
13	9e−05	61 / 1007	PROTEINATLAS_kidney
14	1e−04	64 / 1076	PROTEINATLAS_stomach
15	2e−04	61 / 1032	PROTEINATLAS_small intestine

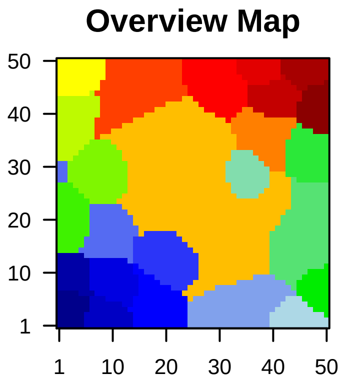
K−Means Cluster

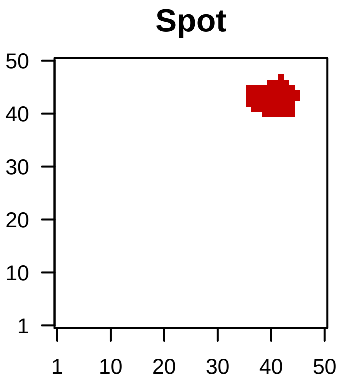
Spot Summary: D

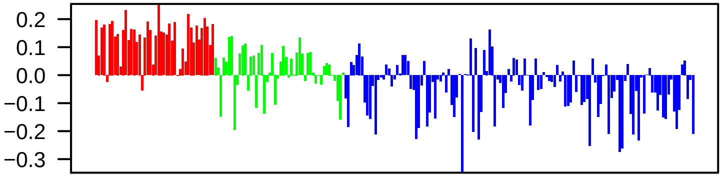
metagenes = 57
genes = 610

<r> metagenes = 0.92
<r> genes = 0.21
beta: r2= 3.32 / log p= −Inf

samples with spot = 25 (11.3 %)
mBL : 24 (54.5 %)
non−mBL : 1 (0.8 %)


Overview Map


Spot

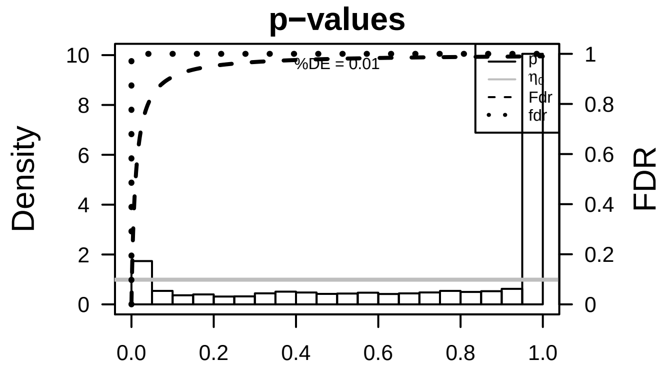


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205123_s_at	2.4	−0.7	0.4	TMEFF1	transmembrane protein with EGF like and two follistatin like d
2	219743_at	1.91	−0.7	0.52	HEY2	hes related family bHLH transcription factor with YRPW motif
3	211363_s_at	1.76	−1.12	0.41	MTAP	methylthioadenosine phosphorylase [Source:HGNC Symbol;
4	209587_at	1.65	−1.24	0.45	PITX1	paired like homeodomain 1 [Source:HGNC Symbol;Acc:HGN
5	204993_at	1.61	−1.23	0.28	GNAZ	G protein subunit alpha z [Source:HGNC Symbol;Acc:HGNC:
6	205789_at	1.51	−1.42	0.14	CD1D	CD1d molecule [Source:HGNC Symbol;Acc:HGNC:1637]
7	221591_s_at	1.45	−0.81	0.27	PIMREG	PICALM interacting mitotic regulator [Source:HGNC Symbol;
8	41037_at	1.43	−0.89	0.25	TEAD4	TEA domain transcription factor 4 [Source:HGNC Symbol;Acc
9	208244_at	1.42	−0.88	0.46	BMP3	bone morphogenetic protein 3 [Source:HGNC Symbol;Acc:H
10	201927_s_at	1.42	−1.07	0.34	PKP4	plakophilin 4 [Source:HGNC Symbol;Acc:HGNC:9026]
11	221967_at	1.41	−0.93	0.28	NXPH4	neurexophilin 4 [Source:HGNC Symbol;Acc:HGNC:8078]
12	215379_x_at	1.41	−2.47	0.21		immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
13	215946_x_at	1.37	−1.38	0.27		immunoglobulin lambda like polypeptide 3, pseudogene [Sou
14	221239_s_at	1.35	−1.87	0.41	FCRL2	Fc receptor like 2 [Source:HGNC Symbol;Acc:HGNC:14875]
15	213556_at	1.33	−0.71	0.3	PINLYP	phospholipase A2 inhibitor and LY6/PLAUR domain containin
16	218885_s_at	1.32	−1.4	0.22	GALNT12	polypeptide N−acetylgalactosaminyltransferase 12 [Source:H
17	214158_s_at	1.3	−1.03	0.3	PRDM10	PR/SET domain 10 [Source:HGNC Symbol;Acc:HGNC:1399
18	207396_s_at	1.29	−1.19	0.37	ALG3	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Sym
19	205262_at	1.28	−0.6	0.44	KCNH2	potassium voltage−gated channel subfamily H member 2 [So
20	217656_at	1.24	−0.69	0.49		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−37	114 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	1e−28	62 / 280	GSEA	MANALO_HYPOXIA_DN
3	7e−28	131 / 1161	MF	RNA binding
4	1e−27	154 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
5	2e−27	310 / 4579	CC	nucleus
6	7e−26	97 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
7	4e−25	206 / 2541	CC	nucleoplasm
8	5e−25	84 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	2e−24	89 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
10	2e−22	58 / 314	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
11	3e−20	86 / 703	GSEA	LEE_BMP2_TARGETS_DN
12	4e−20	82 / 653	CC	nucleolus
13	3e−19	274 / 4261	Lymp	HOPP_Txn_transition
14	5e−18	23 / 55	HM	HALLMARK_MYC_TARGETS_V2
15	3e−17	44 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
16	2e−16	35 / 158	GSEA	BILD_MYC_ONCOGENIC_SIGNATURE
17	5e−16	71 / 602	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
18	6e−16	68 / 561	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
19	3e−15	44 / 268	GSEA	MUELLER_PLURINET
20	6e−15	316 / 5529	Lymp	HOPP_Txn_elongation
21	7e−15	65 / 546	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
22	1e−14	36 / 190	HM	HALLMARK_MYC_TARGETS_V1
23	2e−14	34 / 174	BP	rRNA processing
24	1e−13	225 / 3564	TF	ICGC_Taf1_targets
25	6e−13	21 / 72	GSEA	SCHUHMACHER_MYC_TARGETS_UP
26	2e−12	27 / 129	GSEA	WELCSH_BRCA1_TARGETS_DN
27	2e−12	30 / 159	GSEA	SANSOM_APC_TARGETS_REQUIRE_MYC
28	3e−12	95 / 1107	TF	ICGC_Myc_targets
29	5e−12	91 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
30	2e−11	73 / 776	Refer	PROTEINATLAS_skin
31	3e−11	18 / 62	TF	MYC_Targets UP
32	4e−11	77 / 852	MF	nucleic acid binding
33	6e−11	56 / 527	Refer	PROTEINATLAS_oral mucosa
34	8e−11	47 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
35	1e−10	37 / 270	GSEA	FOURNIER_ACINAR_DEVELOPMENT_LATE_2
36	1e−10	34 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
37	2e−10	15 / 45	GSEA	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN
38	2e−10	24 / 123	GSEA	DANG_MYC_TARGETS_UP
39	2e−10	26 / 144	BP	methylation
40	2e−10	50 / 453	GSEA	FEVR_CTNNB1_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	3 / 92	HORVATH_aging_genes meth DOWN
2	1.0	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	2e−14	34 / 174	rRNA processing
2	2e−10	26 / 144	methylation
3	4e−10	37 / 281	DNA repair
4	1e−09	36 / 281	mRNA processing
5	2e−09	41 / 351	cellular response to DNA damage stimulus
6	1e−08	28 / 198	mRNA splicing, via spliceosome
7	1e−07	29 / 233	RNA splicing
8	2e−06	14 / 76	ribosome biogenesis
9	3e−06	13 / 67	tRNA processing
10	3e−06	19 / 137	DNA replication
11	9e−06	7 / 20	tRNA modification
12	8e−05	13 / 90	RNA processing
13	1e−04	6 / 20	ribosomal large subunit biogenesis
14	1e−04	11 / 71	mitochondrion organization
15	2e−04	5 / 14	nucleosome disassembly

Cancer

Rank	p−value	#in/all	Geneset
1	5e−07	7 / 14	BENTINK_myc.1
2	2e−04	33 / 409	Lembcke_Normal vs Adenoma
3	2e−04	8 / 41	PanCan_DNARepair_geneset_nanostring
4	3e−04	5 / 16	WOLFER_overlap genes
5	9e−03	7 / 58	SHAUGHNESSY_MM high risk
6	2e−02	3 / 15	GENTLES_modul2
7	2e−02	3 / 15	GENTLES_modul4
8	2e−02	3 / 15	GENTLES_modul7
9	3e−02	2 / 15	RHODES_CANCER_META_SIGNATURE
10	5e−02	3 / 20	PanCan_ChromMod_geneset_nanostring
11	6e−02	4 / 36	ZHANG_MM up
12	6e−02	2 / 10	GENTLES_modul3
13	1e−01	2 / 13	GENTLES_modul1
14	1e−01	2 / 14	GENTLES_modul10
15	1e−01	4 / 45	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	2e−27	310 / 4579	nucleus
2	4e−25	206 / 2541	nucleoplasm
3	4e−20	82 / 653	nucleolus
4	6e−10	95 / 1221	mitochondrion
5	3e−07	20 / 128	spliceosomal complex
6	2e−06	9 / 30	small−subunit processome
7	3e−06	14 / 77	catalytic step 2 spliceosome
8	6e−06	28 / 268	intracellular ribonucleoprotein complex
9	1e−05	28 / 277	mitochondrial matrix
10	8e−05	6 / 19	histone methyltransferase complex
11	2e−04	233 / 4701	cytoplasm
12	4e−04	27 / 324	chromosome
13	5e−04	27 / 326	nuclear speck
14	7e−04	4 / 11	methylosome
15	8e−04	5 / 19	nuclear periphery

Chr

Rank	p−value	#in/all	Geneset
1	2e−05	33 / 369	Chr 20
2	3e−05	59 / 833	Chr 19
3	2e−03	37 / 548	Chr 16
4	2e−02	22 / 333	Chr 22
5	7e−02	23 / 403	Chr 14
6	2e−01	37 / 756	Chr 11
7	2e−01	33 / 689	Chr 3
8	2e−01	24 / 492	Chr 9
9	5e−01	2 / 41	Chr Y
10	5e−01	32 / 776	Chr 17
11	6e−01	28 / 700	Chr 12
12	6e−01	53 / 1325	Chr 1
13	6e−01	7 / 184	Chr 18
14	7e−01	9 / 242	Chr 13
15	7e−01	5 / 139	Chr 21

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−43	471 / 7957	Tcells peripheral blood_2_TssAFlnk
2	1e−41	465 / 7833	Bcells peripheral blood_1_TssA
3	3e−41	482 / 8406	Bcells peripheral blood_2_TssAFlnk
4	1e−38	477 / 8370	natural killer cells peripheral blood_2_TssAFlnk
5	2e−37	471 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
6	5e−37	469 / 8200	monocytes peripheral blood_2_TssAFlnk
7	3e−35	440 / 7420	Tcells peripheral blood_1_TssA
8	1e−34	484 / 8816	Thelper cells peripheral blood_2_TssAFlnk
9	2e−34	472 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
10	4e−34	468 / 8322	T CD8+ naive cells peripheral blood_1_TssA
11	5e−34	445 / 7635	monocytes peripheral blood_1_TssA
12	7e−33	323 / 4595	6_EnhG_Melanocytes
13	9e−33	420 / 6997	Overlap_fetal_midbrain_K9K27me3
14	2e−32	446 / 7751	natural killer cells peripheral blood_1_TssA
15	5e−31	454 / 8068	Thelper cells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−16	71 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	6e−16	68 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	4e−08	87 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
4	1e−03	4 / 12	Juehling−MSI−enriched−in−6
5	3e−03	3 / 8	KIM_MSI−in−EC
6	9e−03	15 / 184	Kosinski_lower−crypt−long−list
7	1e−02	72 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
8	2e−02	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
9	2e−02	8 / 83	Marisa_CRC−cluster−d
10	3e−02	2 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
11	6e−02	30 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
12	2e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
13	2e−01	4 / 60	Marisa_CRC−cluster−g
14	3e−01	1 / 8	Boland_CRC−MMR−system
15	3e−01	1 / 8	Marisa_CRC−C1

Glioma

Rank	p−value	#in/all	Geneset
1	2e−08	12 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
2	6e−05	46 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
3	1e−04	12 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	3e−03	3 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
5	6e−03	82 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	2e−02	71 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	7e−02	2 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
8	7e−02	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
9	2e−01	3 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	2e−01	5 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
11	2e−01	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
12	2e−01	2 / 21	Barbus_GBM_STS_vs._LTS
13	2e−01	1 / 6	Donson−adaptive−immunity−associated with LTS in HGA
14	2e−01	2 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
15	3e−01	3 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−37	114 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	1e−28	62 / 280	MANALO_HYPOXIA_DN
3	1e−27	154 / 1527	PUJANA_BRCA1_PCC_NETWORK
4	7e−26	97 / 726	PUJANA_CHEK2_PCC_NETWORK
5	5e−25	84 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	2e−24	89 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	2e−22	58 / 314	PENG_GLUTAMINE_DEPRIVATION_DN
8	3e−20	86 / 703	LEE_BMP2_TARGETS_DN
9	3e−17	44 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
10	2e−16	35 / 158	BILD_MYC_ONCOGENIC_SIGNATURE
11	3e−15	44 / 268	MUELLER_PLURINET
12	7e−15	65 / 546	MARTENS_TRETINOIN_RESPONSE_DN
13	6e−13	21 / 72	SCHUHMACHER_MYC_TARGETS_UP
14	2e−12	27 / 129	WELCSH_BRCA1_TARGETS_DN
15	2e−12	30 / 159	SANSOM_APC_TARGETS_REQUIRE_MYC

HM

Rank	p−value	#in/all	Geneset
1	5e−18	23 / 55	HALLMARK_MYC_TARGETS_V2
2	1e−14	36 / 190	HALLMARK_MYC_TARGETS_V1
3	1e−08	27 / 187	HALLMARK_E2F_TARGETS
4	2e−06	24 / 195	HALLMARK_G2M_CHECKPOINT
5	3e−03	13 / 133	HALLMARK_DNA_REPAIR
6	4e−03	11 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	2e−01	9 / 149	HALLMARK_UV_RESPONSE_UP
8	2e−01	3 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	2e−01	8 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	2e−01	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	3e−01	10 / 192	HALLMARK_MTORC1_SIGNALING
12	3e−01	10 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
13	4e−01	9 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	4e−01	8 / 173	HALLMARK_MITOTIC_SPINDLE
15	4e−01	8 / 174	HALLMARK_ADIPOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.007	4 / 19	Angelova_immune−metagene−activated_CD8
2	0.155	1 / 4	Angelova_CRC_MSS−neoantigens
3	0.190	1 / 5	Angelova_immune−metagene−NKT
4	0.255	1 / 7	Angelova_CRC_MSI−neoantigens
5	0.344	1 / 10	Angelova_immune−metagene−neutrophils
6	0.397	1 / 12	Angelova_immune−metagene−effector_memory_CD4
7	0.397	1 / 12	Angelova_immune−metagene−NK56_dim
8	0.422	1 / 13	Angelova_immune−metagene−immature_B−cells
9	0.422	1 / 13	Angelova_CRC_MSS^−neoantigens
10	0.620	1 / 23	Angelova_immune−metagene−Treg
11	0.666	1 / 26	Angelova_immune−metagene−activated_CD4
12	0.850	1 / 45	Angelova_immune−metagene−MDSC
13	0.941	1 / 67	Angelova_immune−metagene−T−cells
14	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
15	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	3 / 32	Marjolein_ageing−genes_DN
2	0.2	2 / 22	DUMEAUX_Fasting enriched genes
3	0.3	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.5	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.6	1 / 22	DUMEAUX_High bmi enriched genes
6	0.7	5 / 150	Homuth_BMI−associated−genes_UP
7	0.8	7 / 210	Homuth_BMI−associated−genes_DN
8	1.0	0 / 62	DUMEAUX_Smoking enriched genes
9	1.0	0 / 10	DUMEAUX_Smoking literature genes up
10	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1.0	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−19	274 / 4261	HOPP_Txn_transition
2	6e−15	316 / 5529	HOPP_Txn_elongation
3	2e−09	311 / 5908	HOPP_Active_promoter
4	3e−06	31 / 305	TARTE_Plasmablast signature
5	7e−04	60 / 955	SPANG_BCR UP
6	7e−04	12 / 99	Sha_BL UP
7	8e−04	17 / 173	Victora_Light zone signature
8	1e−03	3 / 6	MASCQUE_mBL UP
9	4e−03	12 / 121	ROSOLOWSKI_green total
10	2e−02	4 / 25	ROSOLOWSKI_red UP
11	2e−02	50 / 906	SPANG_BCR DN
12	3e−02	8 / 88	ROSOLOWSKI_green UP
13	3e−02	256 / 5682	HOPP_Weak_promoter
14	3e−02	3 / 17	DAVE_c−myc BL UP
15	4e−02	5 / 45	Monti_BCR_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	8e−05	26 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	3e−03	24 / 319	Gerber_wt/wt_melanoma−cells−SpotA
3	4e−02	7 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
4	1e−01	14 / 236	Gerber_wt/wt_group3−specific
5	1e−01	11 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	2e−01	3 / 38	Tirosh_top50 correlated genes PC1
7	2e−01	3 / 38	Tirosh_G1/S phase specific genes
8	3e−01	2 / 24	Tirosh_B−cell specific genes−melanoma
9	3e−01	3 / 44	Tirosh_top50 correlated genes PC2
10	4e−01	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
11	5e−01	10 / 230	Gerber_wt/wt_melanoma−cells−SpotC
12	6e−01	9 / 222	Gerber_wt/wt_melanoma−cells−SpotF
13	6e−01	2 / 47	Tirosh_G2/M phase specific genes
14	6e−01	1 / 23	Melanoma Epi−Enzyme Cluster 7
15	6e−01	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma

MF

Rank	p−value	#in/all	Geneset
1	7e−28	131 / 1161	RNA binding
2	4e−11	77 / 852	nucleic acid binding
3	2e−08	22 / 132	methyltransferase activity
4	2e−06	29 / 267	binding
5	2e−05	16 / 116	helicase activity
6	3e−05	6 / 16	3'−5' exonuclease activity
7	5e−05	10 / 53	ATP−dependent RNA helicase activity
8	1e−04	8 / 37	exonuclease activity
9	1e−04	92 / 1541	DNA binding
10	3e−04	7 / 32	DNA−directed 5'−3' RNA polymerase activity
11	3e−04	5 / 16	snoRNA binding
12	4e−04	7 / 34	tRNA binding
13	4e−04	83 / 1402	nucleotide binding
14	5e−04	72 / 1185	ATP binding
15	5e−04	79 / 1329	transferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	6 / 36	hsa−miR−541
2	0.004	8 / 62	hsa−miR−489
3	0.005	7 / 51	hsa−miR−492
4	0.005	5 / 28	hsa−miR−654−5p
5	0.006	5 / 29	hsa−miR−1231
6	0.008	5 / 31	hsa−miR−661
7	0.009	8 / 72	hsa−miR−149
8	0.010	7 / 59	hsa−miR−1266
9	0.012	4 / 22	hsa−miR−1225−3p
10	0.012	11 / 122	hsa−miR−491−5p
11	0.012	6 / 47	hsa−miR−370
12	0.012	18 / 244	hsa−miR−34c−5p
13	0.014	10 / 109	hsa−miR−485−5p
14	0.015	6 / 49	hsa−miR−940
15	0.015	6 / 49	hsa−miR−671−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	1e−04	19 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	5e−01	2 / 41	Scicluna_DN
3	7e−01	2 / 54	Burnham_timecourse
4	9e−01	1 / 48	Burnham_viral_DN
5	9e−01	1 / 68	Burnham_sep_vs_con_UP
6	1e+00	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	1e+00	1 / 122	Terre_IMS_influenza_meta_signature
8	1e+00	0 / 56	Burnham_sep_vs_con_DN
9	1e+00	0 / 48	Burnham_cap_fp_vs_con_DN
10	1e+00	0 / 71	Burnham_cap_fp_vs_con_UP
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−11	73 / 776	PROTEINATLAS_skin
2	6e−11	56 / 527	PROTEINATLAS_oral mucosa
3	2e−10	76 / 866	PROTEINATLAS_cerebellum
4	7e−10	87 / 1081	PROTEINATLAS_testis
5	2e−09	84 / 1048	PROTEINATLAS_rectum
6	2e−09	62 / 677	PROTEINATLAS_esophagus
7	3e−09	85 / 1076	PROTEINATLAS_stomach
8	1e−08	88 / 1161	PROTEINATLAS_colon
9	2e−08	47 / 474	PROTEINATLAS_vagina
10	2e−08	69 / 840	PROTEINATLAS_urinary bladder
11	3e−08	59 / 671	PROTEINATLAS_cervix, uterine
12	4e−08	80 / 1048	PROTEINATLAS_gallbladder
13	8e−08	68 / 848	PROTEINATLAS_adrenal gland
14	1e−07	80 / 1072	PROTEINATLAS_duodenum
15	1e−07	77 / 1022	PROTEINATLAS_placenta

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	2 / 13	Alternative lengthening of telomeres
2	0.3	2 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−13	225 / 3564	ICGC_Taf1_targets
2	3e−12	95 / 1107	ICGC_Myc_targets
3	3e−11	18 / 62	MYC_Targets UP
4	6e−10	192 / 3150	ICGC_Creb1_targets
5	9e−09	186 / 3121	ICGC_Egr1_targets
6	2e−08	81 / 1044	ICGC_Six5_targets
7	2e−08	216 / 3804	ICGC_Stat5_targets
8	5e−08	177 / 2994	ICGC_Zeb1_targets
9	6e−08	90 / 1241	KIM_MYC targets
10	2e−07	210 / 3769	ICGC_Pmlsc71910_targets
11	2e−07	106 / 1578	ICGC_GabpPcr2_targets
12	2e−07	234 / 4319	ICGC_Pou2_targets
13	4e−07	245 / 4602	ICGC_Elf1_targets
14	4e−07	202 / 3630	ICGC_Sp1_targets
15	4e−07	224 / 4131	ICGC_Tcf3_targets

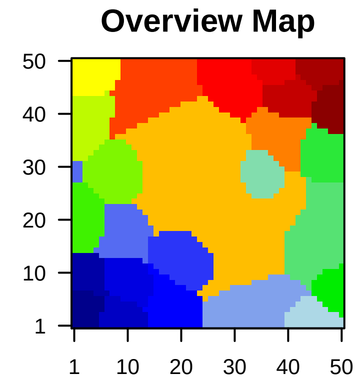
K−Means Cluster

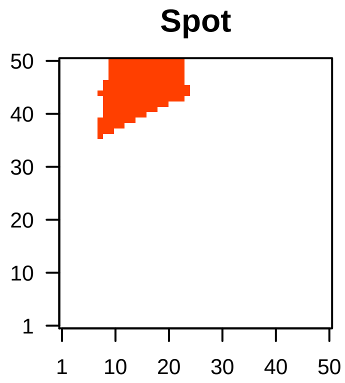
Spot Summary: E

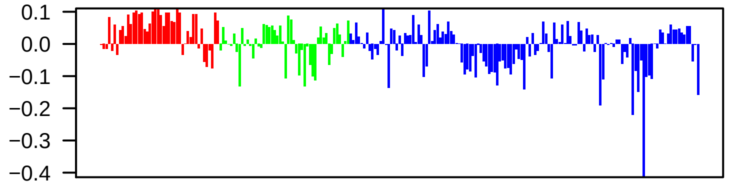
metagenes = 165
genes = 572

<r> metagenes = 0.79
<r> genes = 0.12
beta: r2= 1.24 / log p= −Inf

samples with spot = 0 (0 %)


Overview Map


Spot

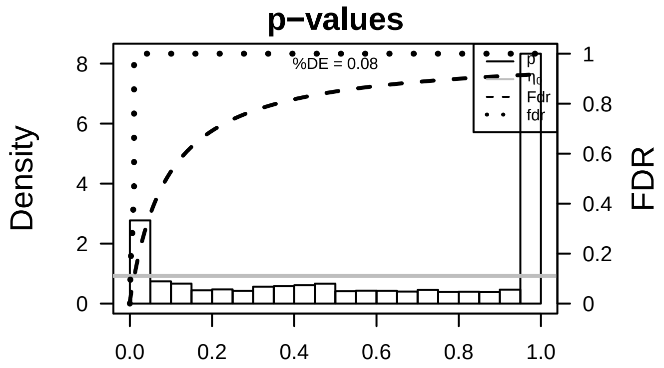


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206624_at	1.74	−1.1	0.16	USP9Y	ubiquitin specific peptidase 9, Y−linked [Source:HGNC Symb
2	205149_s_at	1.57	−0.85	0.43	CLCN4	chloride voltage−gated channel 4 [Source:HGNC Symbol;Acc
3	214831_at	1.57	−0.86	0.44	ELK4	ELK4, ETS transcription factor [Source:HGNC Symbol;Acc:H
4	205414_s_at	1.45	−0.96	0.15	ARHGAP44	Rho GTPase activating protein 44 [Source:HGNC Symbol;Ac
5	211823_s_at	1.43	−0.78	0.32	PXN	paxillin [Source:HGNC Symbol;Acc:HGNC:9718]
6	203067_at	1.41	−0.69	0.31	PDHX	pyruvate dehydrogenase complex component X [Source:HGN
7	217556_at	1.35	−0.88	0.26	CLCN4	chloride voltage−gated channel 4 [Source:HGNC Symbol;Acc
8	206220_s_at	1.35	−0.91	0.21	RASA3	RAS p21 protein activator 3 [Source:HGNC Symbol;Acc:HGN
9	208608_s_at	1.34	−0.79	0.25	SNTB1	syntrophin beta 1 [Source:HGNC Symbol;Acc:HGNC:11168]
10	220615_s_at	1.27	−0.69	0.09	FAR2	fatty acyl−CoA reductase 2 [Source:HGNC Symbol;Acc:HGN
11	214012_at	1.25	−1.11	0.14	ERAP1	endoplasmic reticulum aminopeptidase 1 [Source:HGNC Sym
12	210544_s_at	1.23	−0.85	0.29	ALDH3A2	aldehyde dehydrogenase 3 family member A2 [Source:HGNC
13	210349_at	1.2	−1.13	0.21	CAMK4	calcium/calmodulin dependent protein kinase IV [Source:HGN
14	204849_at	1.19	−1.27	0.13	TCFL5	transcription factor like 5 [Source:HGNC Symbol;Acc:HGNC:
15	215150_at	1.17	−0.74	0.49	YOD1	YOD1 deubiquitinase [Source:HGNC Symbol;Acc:HGNC:250
16	206907_at	1.15	−1.4	0.08	TNFSF9	TNF superfamily member 9 [Source:HGNC Symbol;Acc:HGN
17	220119_at	1.15	−0.65	0.27	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A [Source:HGN
18	214901_at	1.15	−0.87	0.27	ZNF8	zinc finger protein 8 [Source:HGNC Symbol;Acc:HGNC:1315
19	202485_s_at	1.14	−1.08	0.3	MBD2	methyl−CpG binding domain protein 2 [Source:HGNC Symbo
20	32128_at	1.12	−1.78	0.21	CCL18	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−58	396 / 5529	Lympl	HOPP_Txn_elongation
2	3e−42	384 / 5908	Lympl	HOPP_Active_promoter
3	1e−41	316 / 4261	Lympl	HOPP_Txn_transition
4	6e−41	162 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
5	4e−39	158 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	7e−32	91 / 564	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
7	3e−28	151 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
8	1e−22	120 / 1190	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
9	3e−21	103 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	7e−20	62 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
11	6e−19	133 / 1550	GSEA	PILON_KLF1_TARGETS_DN
12	9e−18	68 / 540	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_UP
13	9e−17	99 / 1044	TF	ICGC_Six5_targets
14	9e−17	317 / 5682	Lympl	HOPP_Weak_promoter
15	2e−16	226 / 3564	TF	ICGC_Taf1_targets
16	1e−15	99 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran
17	2e−15	73 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
18	3e−15	76 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
19	5e−15	125 / 1578	TF	ICGC_GabpPcr2_targets
20	2e−14	66 / 594	Refer	PROTEINATLAS_parathyroid gland
21	3e−14	44 / 297	GSEA	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
22	2e−13	169 / 2541	CC	nucleoplasm
23	4e−13	91 / 1048	Refer	PROTEINATLAS_gallbladder
24	5e−13	79 / 848	Refer	PROTEINATLAS_adrenal gland
25	8e−13	70 / 708	Refer	PROTEINATLAS_thyroid gland
26	8e−13	208 / 3420	TF	ICGC_Bclaf101388_targets
27	9e−13	101 / 1241	TF	KIM_MYC targets
28	1e−12	109 / 1390	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
29	2e−12	37 / 245	Refer	Chaussabel_3,9_Kinases
30	2e−12	87 / 1007	Refer	PROTEINATLAS_kidney
31	2e−12	91 / 1081	Refer	PROTEINATLAS_testis
32	3e−12	91 / 1089	TF	ICGC_Ets1_targets
33	9e−12	220 / 3769	TF	ICGC_Pmlsc71910_targets
34	9e−12	48 / 406	GSEA	MOOTHA_HUMAN_MITODB_6_2002
35	1e−11	56 / 527	GSEA	KIM_ALL_DISORDERS_CALB1_CORR_UP
36	1e−11	180 / 2899	TF	ICGC_Nfatc1_targets
37	1e−11	254 / 4579	CC	nucleus
38	2e−11	11 / 19	GSEA	DEN_INTERACT_WITH_LCA5
39	2e−11	220 / 3805	CC	cytosol
40	3e−11	66 / 699	GSEA	BENPORATH_MYC_MAX_TARGETS


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	5 / 92	HORVATH_aging_genes meth DOWN
2	1.0	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	2e−13	169 / 2541	nucleoplasm
2	1e−11	254 / 4579	nucleus
3	2e−11	220 / 3805	cytosol
4	7e−10	92 / 1221	mitochondrion
5	2e−07	13 / 56	proteasome complex
6	9e−07	33 / 330	mitochondrial inner membrane
7	8e−06	27 / 268	intracellular ribonucleoprotein complex
8	9e−06	8 / 28	microtubule associated complex
9	4e−05	26 / 277	mitochondrial matrix
10	7e−05	9 / 46	peroxisomal membrane
11	1e−04	6 / 21	mitochondrial small ribosomal subunit
12	1e−04	5 / 14	integral component of peroxisomal membrane
13	2e−04	225 / 4701	cytoplasm
14	2e−04	27 / 326	nuclear speck
15	3e−04	12 / 92	peroxisome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−41	162 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	1e−15	99 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
3	6e−08	50 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	5e−06	104 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
5	6e−06	47 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
6	3e−03	65 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	8e−03	53 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	1e−02	49 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	1e−02	61 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	2e−02	3 / 14	TCGA_Mutated−in−CRC_hypermutated
11	2e−02	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
12	2e−02	46 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	2e−02	2 / 6	Hewish_dMMR−secondary−mutations_Signal_transduction
14	2e−02	3 / 16	Vilar_mutated−in−CRC−CamP
15	4e−02	5 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN

HM

Rank	p−value	#in/all	Geneset
1	7e−09	27 / 190	HALLMARK_MYC_TARGETS_V1
2	4e−08	26 / 192	HALLMARK_MTORC1_SIGNALING
3	1e−06	23 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	3e−05	17 / 139	HALLMARK_FATTY_ACID_METABOLISM
5	2e−04	15 / 133	HALLMARK_DNA_REPAIR
6	5e−03	10 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
7	5e−03	10 / 97	HALLMARK_PEROXISOME
8	9e−03	10 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	4e−02	12 / 174	HALLMARK_ADIPOGENESIS
10	5e−02	13 / 195	HALLMARK_G2M_CHECKPOINT
11	9e−02	7 / 96	HALLMARK_ANDROGEN_RESPONSE
12	1e−01	4 / 51	HALLMARK_TGF_BETA_SIGNALING
13	1e−01	10 / 173	HALLMARK_MITOTIC_SPINDLE
14	2e−01	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	2e−01	10 / 187	HALLMARK_E2F_TARGETS

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−58	396 / 5529	HOPP_Txn_elongation
2	3e−42	384 / 5908	HOPP_Active_promoter
3	1e−41	316 / 4261	HOPP_Txn_transition
4	9e−17	317 / 5682	HOPP_Weak_promoter
5	9e−10	281 / 5404	HOPP_Strong_enhancer
6	1e−08	35 / 305	TARTE_Plasmablast signature
7	3e−07	235 / 4559	HOPP_Weak_enhancer
8	1e−04	8 / 40	CARO_OxPhos_in_DLBCL_UP
9	2e−04	210 / 4357	HOPP_Weak_txn
10	1e−03	7 / 42	Monti_OxPhos_cluster
11	2e−03	3 / 7	CARO_OxPhos_vs_BCR_UP
12	4e−03	18 / 227	SPANG_IL21 UP
13	5e−03	54 / 955	SPANG_BCR UP
14	2e−02	3 / 15	DAVE_BL Inter
15	3e−02	3 / 17	DAVE_c−myc BL UP

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−10	45 / 405	hsa−miR−107
2	9e−09	42 / 404	hsa−miR−103
3	3e−07	22 / 160	hsa−miR−330−3p
4	4e−07	15 / 79	hsa−miR−888
5	2e−06	23 / 189	hsa−miR−214
6	3e−06	34 / 363	hsa−miR−195
7	4e−06	16 / 107	hsa−miR−24
8	5e−06	24 / 216	hsa−miR−548l
9	6e−06	26 / 248	hsa−miR−520c−3p
10	6e−06	14 / 86	hsa−miR−297
11	8e−06	35 / 397	hsa−miR−15a
12	8e−06	33 / 364	hsa−miR−548n
13	1e−05	33 / 369	hsa−miR−15b
14	1e−05	20 / 170	hsa−miR−548m
15	1e−05	30 / 324	hsa−miR−497

Telomeres

Rank	p−value	#in/all	Geneset
1	0.01	3 / 13	Alternative lengthening of telomeres
2	0.02	4 / 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	3e−07	25 / 198	mRNA splicing, via spliceosome
2	6e−07	22 / 166	ubiquitin−dependent protein catabolic process
3	2e−06	29 / 281	DNA repair
4	2e−06	29 / 281	mRNA processing
5	1e−05	20 / 167	protein polyubiquitination
6	1e−05	18 / 140	protein folding
7	1e−05	17 / 129	Fc−epsilon receptor signaling pathway
8	1e−05	35 / 407	viral process
9	1e−05	6 / 15	chaperone cofactor−dependent protein refolding
10	1e−05	12 / 69	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
11	1e−05	12 / 69	regulation of cellular response to heat
12	2e−05	20 / 173	proteasome−mediated ubiquitin−dependent protein catabolic process
13	2e−05	12 / 70	regulation of transcription from RNA polymerase II promoter in response to hy
14	2e−05	24 / 233	RNA splicing
15	2e−05	10 / 49	regulation of cellular amino acid metabolic process

Chr

Rank	p−value	#in/all	Geneset
1	0.001	29 / 403	Chr 14
2	0.030	23 / 382	Chr 15
3	0.031	13 / 184	Chr 18
4	0.050	30 / 554	Chr 5
5	0.097	25 / 480	Chr 4
6	0.114	40 / 832	Chr 2
7	0.146	33 / 689	Chr 3
8	0.220	3 / 41	Chr Y
9	0.362	11 / 242	Chr 13
10	0.371	55 / 1325	Chr 1
11	0.389	16 / 369	Chr 20
12	0.391	21 / 492	Chr 9
13	0.405	28 / 669	Chr 6
14	0.443	31 / 756	Chr 11
15	0.569	19 / 490	Chr 10

Glioma

Rank	p−value	#in/all	Geneset
1	1e−10	101 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	1e−10	110 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−08	33 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	2e−06	12 / 58	Stuehler_Proteins_up_in_STS
5	7e−03	37 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	1e−02	22 / 330	Up
7	4e−02	8 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	5e−02	5 / 50	Vishal_subnetwork signature of survival in GBM
9	7e−02	5 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
10	1e−01	9 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
12	1e−01	4 / 52	GIEZELT_GBM_WT_down_VS_mut
13	3e−01	4 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	3e−01	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
15	3e−01	19 / 421	Down_b

Immunome

Rank	p−value	#in/all	Geneset
1	0.01	2 / 5	Angelova_immune−metagene−NK56_bright
2	0.08	2 / 12	Angelova_immune−metagene−NK56_dim
3	0.17	2 / 19	Angelova_immune−metagene−activated_CD8
4	0.38	1 / 12	Angelova_immune−metagene−effector_memory_CD4
5	0.43	1 / 14	Angelova_immune−metagene−eosinophil
6	0.52	1 / 18	Angelova_immune−metagene−pDC
7	0.52	1 / 18	Angelova_CRC_immunostimulators
8	0.60	1 / 23	Angelova_immune−metagene−monocytes
9	0.60	1 / 23	Angelova_immune−metagene−Th2
10	0.65	1 / 26	Angelova_immune−metagene−activated_CD4
11	0.82	1 / 42	Angelova_immune−metagene−TGD
12	0.84	1 / 45	Angelova_immune−metagene−MDSC
13	0.93	1 / 67	Angelova_immune−metagene−T−cells
14	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
15	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−05	27 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	6e−04	7 / 38	Tirosh_top50 correlated genes PC1
3	2e−03	19 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	7e−03	15 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
5	5e−02	5 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	8e−02	1 / 2	Melanoma Epi−Enzyme Cluster 2
7	1e−01	1 / 4	Melanoma Epi−Enzyme Cluster 5
8	2e−01	12 / 222	Gerber_wt/wt_melanoma−cells−SpotF
9	2e−01	10 / 189	Tirosh_genes preferentially expressed by Tregs
10	3e−01	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
11	4e−01	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
12	4e−01	11 / 249	Gerber_wt/wt_melanoma−cells−SpotE
13	4e−01	4 / 81	Tirosh_Genes in the MITF program
14	4e−01	5 / 107	Tirosh_Exhaustion program in Mel75
15	5e−01	1 / 16	Hugo_melanoma−all−LEF1_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.3	7 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.4	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.6	2 / 54	Burnham_timecourse
4	0.9	1 / 48	Burnham_viral_DN
5	0.9	3 / 122	Terre_IMS_influenza_meta_signature
6	0.9	1 / 52	Burnham_day1_vs_5_DN
7	0.9	1 / 71	Burnham_cap_fp_vs_con_UP
8	1.0	0 / 68	Burnham_sep_vs_con_UP
9	1.0	0 / 56	Burnham_sep_vs_con_DN
10	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
11	1.0	0 / 57	Burnham_viral_UP
12	1.0	0 / 57	Burnham_day1_vs_5_UP
13	1.0	0 / 18	Scicluna_UP
14	1.0	0 / 41	Scicluna_DN
15	1.0	0 / 37	Sweeney_viral_up

TF

Rank	p−value	#in/all	Geneset
1	9e−17	99 / 1044	ICGC_Six5_targets
2	2e−16	226 / 3564	ICGC_Taf1_targets
3	5e−15	125 / 1578	ICGC_GabpPcr2_targets
4	8e−13	208 / 3420	ICGC_Bclaf101388_targets
5	9e−13	101 / 1241	KIM_MYC targets
6	3e−12	91 / 1089	ICGC_Ets1_targets
7	9e−12	220 / 3769	ICGC_Pmlsc71910_targets
8	1e−11	180 / 2899	ICGC_Nfatc1_targets
9	3e−11	219 / 3796	ICGC_Nficsc81335_targets
10	4e−11	219 / 3804	ICGC_Stat5_targets
11	6e−11	214 / 3703	ICGC_Foxm1_targets
12	7e−11	189 / 3150	ICGC_Creb1_targets
13	2e−10	186 / 3121	ICGC_Egr1_targets
14	3e−10	208 / 3630	ICGC_Sp1_targets
15	3e−10	207 / 3608	ICGC_Tcf12_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	3 / 15	GENTLES_modul7
2	0.08	5 / 58	SHAUGHNESSY_MM high risk
3	0.08	8 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.10	3 / 28	PanCan_HK_geneset_nanostring
5	0.10	4 / 45	KUIPER_MM poor survival
6	0.10	2 / 14	BENTINK_src.2
7	0.11	1 / 14	LIU_COMMON_CANCER_GENES
8	0.11	4 / 47	PanCan_TGF−B_geneset_nanostring
9	0.12	2 / 15	BEN−PORATH_UP
10	0.17	3 / 36	ZHANG_MM up
11	0.19	1 / 15	RHODES_CANCER_META_SIGNATURE
12	0.22	3 / 41	PanCan_DNARepair_geneset_nanostring
13	0.33	1 / 10	GENTLES_modul5
14	0.36	1 / 11	GENTLES_modul14
15	0.41	1 / 13	GENTLES_modul1

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−60	474 / 7833	Bcells peripheral blood_1_TssA
2	9e−58	459 / 7420	Tcells peripheral blood_1_TssA
3	1e−57	355 / 4528	T CD8+ naive cells peripheral blood_4_Tx
4	6e−55	465 / 7751	natural killer cells peripheral blood_1_TssA
5	2e−54	461 / 7635	monocytes peripheral blood_1_TssA
6	3e−53	468 / 7930	Tregulatory cells peripheral blood_1_TssA
7	5e−53	409 / 6099	HSC_4_Tx
8	1e−52	478 / 8322	T CD8+ naive cells peripheral blood_1_TssA
9	5e−51	469 / 8068	Thelper cells peripheral blood_1_TssA
10	4e−49	390 / 5753	Tcells peripheral blood_4_Tx
11	4e−49	441 / 7225	Overlap_fetal_midbrain_ReprPC
12	2e−47	461 / 7957	Tcells peripheral blood_2_TssAFlnk
13	7e−47	425 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
14	8e−47	441 / 7331	TssA_Colon
15	5e−46	466 / 8200	monocytes peripheral blood_2_TssAFlnk

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−39	158 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	7e−32	91 / 564	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
3	3e−28	151 / 1527	PUJANA_BRCA1_PCC_NETWORK
4	1e−22	120 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
5	3e−21	103 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
6	7e−20	62 / 417	SHEN_SMARCA2_TARGETS_UP
7	6e−19	133 / 1550	PILON_KLF1_TARGETS_DN
8	9e−18	68 / 540	TIEN_INTESTINE_PROBIOTICS_24HR_UP
9	2e−15	73 / 673	SCHLOSSER_SERUM_RESPONSE_DN
10	3e−15	76 / 726	PUJANA_CHEK2_PCC_NETWORK
11	3e−14	44 / 297	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
12	1e−12	109 / 1390	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
13	9e−12	48 / 406	MOOTHA_HUMAN_MITODB_6_2002
14	1e−11	56 / 527	KIM_ALL_DISORDERS_CALB1_CORR_UP
15	2e−11	11 / 19	DEN_INTERACT_WITH_LCA5

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	9 / 150	Homuth_BMI−associated−genes_UP
2	0.2	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.3	1 / 10	DUMEAUX_Smoking literature genes up
4	0.5	9 / 210	Homuth_BMI−associated−genes_DN
5	0.5	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
6	1.0	0 / 62	DUMEAUX_Smoking enriched genes
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 9	DUMEAUX_Monocytes in 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	3e−10	90 / 1161	RNA binding
2	6e−07	364 / 7864	protein binding
3	2e−05	18 / 148	ubiquitin protein ligase activity
4	6e−05	57 / 852	nucleic acid binding
5	2e−04	23 / 256	cadherin binding
6	3e−04	13 / 107	mRNA binding
7	4e−04	22 / 249	ubiquitin protein ligase binding
8	1e−03	10 / 81	single−stranded DNA binding
9	2e−03	6 / 33	GTPase binding
10	2e−03	4 / 15	poly(A) binding
11	2e−03	8 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
12	3e−03	10 / 90	unfolded protein binding
13	5e−03	4 / 18	threonine−type endopeptidase activity
14	6e−03	7 / 55	damaged DNA binding
15	6e−03	22 / 312	enzyme binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−14	66 / 594	PROTEINATLAS_parathyroid gland
2	4e−13	91 / 1048	PROTEINATLAS_gallbladder
3	5e−13	79 / 848	PROTEINATLAS_adrenal gland
4	8e−13	70 / 708	PROTEINATLAS_thyroid gland
5	2e−12	37 / 245	Chaussabel_3,9_Kinases
6	2e−12	87 / 1007	PROTEINATLAS_kidney
7	2e−12	91 / 1081	PROTEINATLAS_testis
8	4e−11	86 / 1048	PROTEINATLAS_rectum
9	5e−11	92 / 1161	PROTEINATLAS_colon
10	5e−11	59 / 595	PROTEINATLAS_breast
11	7e−11	87 / 1076	PROTEINATLAS_stomach
12	1e−10	69 / 770	PROTEINATLAS_endometrium
13	1e−10	73 / 840	PROTEINATLAS_urinary bladder
14	2e−10	26 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
15	3e−10	58 / 604	PROTEINATLAS_hippocampus

K−Means Cluster

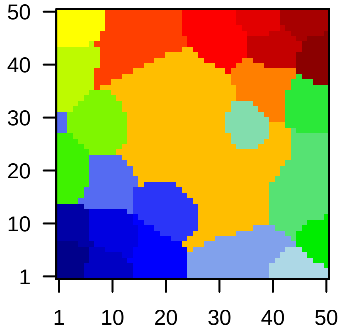
Spot Summary: F

metagenes = 106
genes = 794

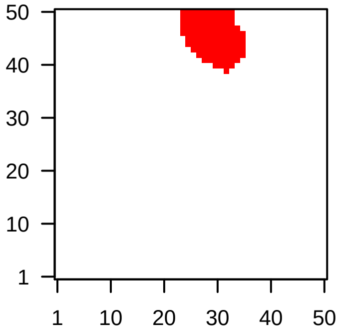
<r> metagenes = 0.87
<r> genes = 0.17
beta: r2= 1.47 / log p= −Inf

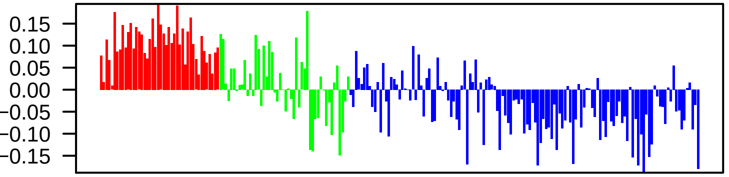
samples with spot = 9 (4.1 %)
mBL : 8 (18.2 %)
intermediate : 1 (2.1 %)

Overview Map



Spot





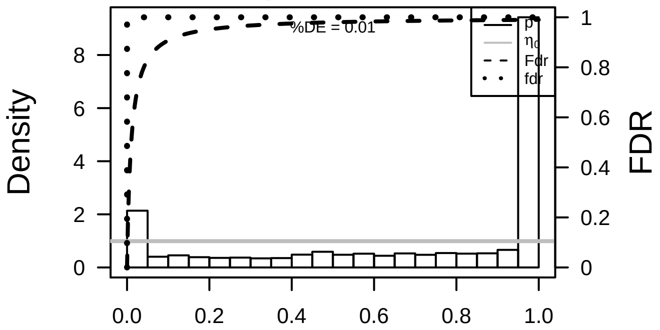
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206023_at	2.55	−1.15	0.2	NMU	neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
2	220595_at	2.14	−0.73	0.31	PDZRN4	PDZ domain containing ring finger 4 [Source:HGNC Symbol;A
3	205130_at	2	−0.95	0.22	MOK	MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833
4	215783_s_at	1.96	−1.21	0.17	ALPL	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
5	203673_at	1.92	−0.8	0.1	TG	thyroglobulin [Source:HGNC Symbol;Acc:HGNC:11764]
6	207949_s_at	1.9	−0.94	0.21	ICA1	islet cell autoantigen 1 [Source:HGNC Symbol;Acc:HGNC:53
7	205622_at	1.89	−0.95	0.19	SMPD2	sphingomyelin phosphodiesterase 2 [Source:HGNC Symbol;A
8	214243_s_at	1.88	−0.75	0.4		serine hydrolase−like (pseudogene) [Source:HGNC Symbol;A
9	221810_at	1.87	−1.12	0.23	RAB15	RAB15, member RAS oncogene family [Source:HGNC Symb
10	208496_x_at	1.86	−0.87	0.18	HIST1H3G	histone cluster 1 H3 family member g [Source:HGNC Symbol
11	220158_at	1.85	−0.68	0.17	LGALS14	galectin 14 [Source:HGNC Symbol;Acc:HGNC:30054]
12	205888_s_at	1.79	−0.75	0.4	JAKMIP2	janus kinase and microtubule interacting protein 2 [Source:HG
13	203770_s_at	1.76	−0.79	0.18	STS	steroid sulfatase [Source:HGNC Symbol;Acc:HGNC:11425]
14	222044_at	1.74	−1.01	0.49	PCIF1	PDX1 C−terminal inhibiting factor 1 [Source:HGNC Symbol;A
15	220744_s_at	1.72	−1.03	0.31	IFT122	intraflagellar transport 122 [Source:HGNC Symbol;Acc:HGNC
16	219370_at	1.67	−0.85	−0.02	RPRM	reprimo, TP53 dependent G2 arrest mediator homolog [Sourc
17	210571_s_at	1.66	−1.07	0.24		cytidine monophospho−N−acetylneuraminic acid hydroxylase
18	214554_at	1.64	−0.71	0.46	HIST1H2AL	histone cluster 1 H2A family member l [Source:HGNC Symbo
19	204679_at	1.64	−1	0.18	KCNK1	potassium two pore domain channel subfamily K member 1 [S
20	59697_at	1.64	−1.28	0.14	RAB15	RAB15, member RAS oncogene family [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−42	483 / 5529	Lympl	HOPP_Txn_elongation
2	5e−35	392 / 4261	Lympl	HOPP_Txn_transition
3	4e−34	186 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
4	2e−32	126 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
5	6e−31	194 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
6	8e−30	474 / 5908	Lympl	HOPP_Active_promoter
7	4e−27	156 / 1161	MF	RNA binding
8	1e−24	254 / 2541	CC	nucleoplasm
9	7e−24	71 / 330	CC	mitochondrial inner membrane
10	6e−23	92 / 540	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_UP
11	1e−22	149 / 1190	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
12	1e−22	140 / 1081	Refer	PROTEINATLAS_testis
13	3e−22	160 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
14	6e−22	51 / 190	HM	HALLMARK_MYC_TARGETS_V1
15	1e−21	97 / 616	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
16	8e−21	70 / 361	GSEA	GARY_CD5_TARGETS_DN
17	6e−20	48 / 186	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
18	2e−19	146 / 1241	TF	KIM_MYC targets
19	4e−19	57 / 268	CC	intracellular ribonucleoprotein complex
20	5e−19	129 / 1044	TF	ICGC_Six5_targets
21	1e−18	365 / 4579	CC	nucleus
22	1e−18	97 / 677	Refer	PROTEINATLAS_esophagus
23	2e−18	96 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
24	2e−18	33 / 95	GSEA	KEGG_OXIDATIVE_PHOSPHORYLATION
25	3e−18	44 / 172	GSEA	REACTOME_HIV_INFECTION
26	6e−18	47 / 198	BP	mRNA splicing, via spliceosome
27	7e−18	70 / 406	GSEA	MOOTHA_HUMAN_MITODB_6_2002
28	2e−17	71 / 422	GSEA	MOOTHA_MITOCHONDRIA
29	5e−17	298 / 3564	TF	ICGC_Taf1_targets
30	6e−17	40 / 154	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
31	1e−16	124 / 1048	Refer	PROTEINATLAS_gallbladder
32	1e−16	67 / 396	GSEA	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
33	1e−16	35 / 120	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
34	2e−16	43 / 181	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
35	2e−16	137 / 1221	CC	mitochondrion
36	2e−16	37 / 136	GSEA	REACTOME_MRNA_PROCESSING
37	2e−16	101 / 776	Refer	PROTEINATLAS_skin
38	2e−16	28 / 77	GSEA	MOOTHA_VOXPHOS
39	4e−16	116 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
40	4e−16	26 / 67	GSEA	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHES

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.8	4 / 92	HORVATH_aging_genes meth DOWN
2	1.0	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	1e−24	254 / 2541	nucleoplasm
2	7e−24	71 / 330	mitochondrial inner membrane
3	4e−19	57 / 268	intracellular ribonucleoprotein complex
4	1e−18	365 / 4579	nucleus
5	2e−16	137 / 1221	mitochondrion
6	6e−13	21 / 56	proteasome complex
7	2e−12	13 / 20	mitochondrial ribosome
8	3e−10	28 / 128	spliceosomal complex
9	3e−10	11 / 18	mitochondrial proton−transporting ATP synthase complex
10	4e−10	15 / 37	mitochondrial respiratory chain complex I
11	6e−10	16 / 44	respiratory chain
12	9e−10	75 / 653	nucleolus
13	3e−09	8 / 10	proton−transporting ATP synthase complex, coupling factor F(o)
14	1e−08	10 / 19	proteasome core complex
15	2e−08	19 / 77	catalytic step 2 spliceosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−34	186 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	4e−12	73 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	3e−10	72 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	2e−05	134 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
5	1e−04	88 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
6	3e−03	4 / 12	Juehling−MSI−enriched−in−6
7	7e−02	2 / 8	KIM_MSI−in−EC
8	9e−02	4 / 31	Marisa_CRC−cluster−c
9	2e−01	1 / 5	Kaneda_CIMP−group1
10	3e−01	4 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
11	3e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
12	3e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
13	3e−01	1 / 7	Boland_CRC−MSI−TGC
14	4e−01	1 / 8	Boland_CRC−MMR−system
15	4e−01	55 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_

HM

Rank	p−value	#in/all	Geneset
1	6e−22	51 / 190	HALLMARK_MYC_TARGETS_V1
2	6e−20	48 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	9e−06	27 / 195	HALLMARK_G2M_CHECKPOINT
4	1e−04	24 / 187	HALLMARK_E2F_TARGETS
5	4e−04	18 / 133	HALLMARK_DNA_REPAIR
6	1e−02	12 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e−01	15 / 192	HALLMARK_MTORC1_SIGNALING
8	2e−01	13 / 174	HALLMARK_ADIPOGENESIS
9	2e−01	8 / 97	HALLMARK_PEROXISOME
10	4e−01	8 / 122	HALLMARK_SPERMATOGENESIS
11	4e−01	6 / 96	HALLMARK_ANDROGEN_RESPONSE
12	5e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
13	6e−01	3 / 55	HALLMARK_MYC_TARGETS_V2
14	6e−01	10 / 191	HALLMARK_P53_PATHWAY
15	6e−01	5 / 97	HALLMARK_BILE_ACID_METABOLISM

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−42	483 / 5529	HOPP_Txn_elongation
2	5e−35	392 / 4261	HOPP_Txn_transition
3	8e−30	474 / 5908	HOPP_Active_promoter
4	3e−12	50 / 305	TARTE_Plasmablast signature
5	2e−11	401 / 5682	HOPP_Weak_promoter
6	3e−09	15 / 42	Monti_OxPhos_cluster
7	3e−08	11 / 25	ROSOLOWSKI_red UP
8	1e−06	12 / 40	CARO_OxPhos_in_DLBCL_UP
9	9e−04	14 / 97	ROSOLOWSKI_red total
10	2e−03	12 / 85	Aukema_BCL2 DN_BCL6 UP
11	5e−02	2 / 7	CARO_OxPhos_vs_BCR_UP
12	6e−02	61 / 906	SPANG_BCR DN
13	7e−02	16 / 192	Victora_Dark zone signature
14	1e−01	266 / 4559	HOPP_Weak_enhancer
15	3e−01	57 / 955	SPANG_BCR UP

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	11 / 59	hsa−miR−643
2	4e−04	16 / 112	hsa−miR−383
3	7e−04	12 / 74	hsa−miR−496
4	9e−04	14 / 98	hsa−miR−154
5	1e−03	10 / 57	hsa−miR−422a
6	1e−03	15 / 111	hsa−miR−656
7	1e−03	13 / 89	hsa−miR−376c
8	2e−03	15 / 117	hsa−miR−200a
9	2e−03	15 / 118	hsa−miR−548f
10	2e−03	18 / 155	hsa−miR−381
11	2e−03	9 / 53	hsa−miR−873
12	2e−03	6 / 26	hsa−miR−1178
13	3e−03	12 / 86	hsa−miR−297
14	3e−03	7 / 35	hsa−miR−640
15	3e−03	12 / 87	hsa−miR−501−5p

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	6e−18	47 / 198	mRNA splicing, via spliceosome
2	1e−15	26 / 70	regulation of transcription from RNA polymerase II promoter in response to hy
3	2e−15	22 / 49	regulation of cellular amino acid metabolic process
4	2e−15	25 / 65	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
5	5e−15	47 / 233	RNA splicing
6	1e−14	28 / 88	regulation of hematopoietic stem cell differentiation
7	3e−14	51 / 281	mRNA processing
8	6e−14	22 / 56	negative regulation of G2/M transition of mitotic cell cycle
9	1e−13	24 / 69	positive regulation of ubiquitin−protein ligase activity involved in regulation of r
10	2e−13	24 / 71	anaphase−promoting complex−dependent catabolic process
11	7e−13	37 / 173	proteasome−mediated ubiquitin−dependent protein catabolic process
12	2e−12	20 / 53	mitochondrial translational termination
13	2e−12	22 / 65	SCF−dependent proteasomal ubiquitin−dependent protein catabolic process
14	2e−12	27 / 99	regulation of mRNA stability
15	3e−12	20 / 54	mitochondrial translational elongation

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	63 / 756	Chr 11
2	2e−03	37 / 403	Chr 14
3	3e−03	61 / 776	Chr 17
4	1e−02	61 / 832	Chr 2
5	1e−02	39 / 490	Chr 10
6	6e−02	86 / 1325	Chr 1
7	1e−01	24 / 333	Chr 22
8	1e−01	26 / 369	Chr 20
9	2e−01	10 / 139	Chr 21
10	3e−01	29 / 480	Chr 4
11	4e−01	26 / 437	Chr 8
12	6e−01	36 / 669	Chr 6
13	6e−01	20 / 382	Chr 15
14	8e−01	24 / 492	Chr 9
15	9e−01	39 / 833	Chr 19

Glioma

Rank	p−value	#in/all	Geneset
1	2e−14	154 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	3e−11	131 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	4e−07	15 / 58	Stuehler_Proteins_up_in_STS
4	2e−03	17 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	1e−02	8 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	1e−02	7 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	3e−02	45 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
8	4e−02	5 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
9	6e−02	6 / 50	Vishal_subnetwork signature of survival in GBM
10	7e−02	6 / 52	GIEZELT_GBM_WT_down_VS_mut
11	7e−02	2 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
12	1e−01	2 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
13	1e−01	3 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	2e−01	2 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
15	3e−01	2 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)

Immunome

Rank	p−value	#in/all	Geneset
1	0.003	5 / 19	Angelova_immune−metagene−activated_CD8
2	0.025	3 / 12	Angelova_immune−metagene−effector_memory_CD4
3	0.365	1 / 8	Angelova_immune−metagene−mDC
4	0.433	1 / 10	Angelova_immune−metagene−neutrophils
5	0.641	1 / 18	Angelova_immune−metagene−pDC
6	0.730	1 / 23	Angelova_immune−metagene−monocytes
7	0.923	1 / 45	Angelova_immune−metagene−MDSC
8	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
9	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
10	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
12	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1.000	0 / 25	Angelova_immune−metagene−DC
14	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.000	0 / 14	Angelova_immune−metagene−eosinophil

Melanoma

Rank	p−value	#in/all	Geneset
1	3e−04	30 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	3e−03	30 / 319	Gerber_wt/wt_melanoma−cells−SpotA
3	4e−03	7 / 38	Tirosh_top50 correlated genes PC1
4	2e−02	6 / 38	Tirosh_G1/S phase specific genes
5	3e−02	17 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	7e−02	18 / 222	Gerber_wt/wt_melanoma−cells−SpotF
7	1e−01	3 / 24	Tirosh_exhuastion−associated genes consitent across tumors
8	1e−01	7 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
9	2e−01	1 / 4	Melanoma Epi−Enzyme Cluster 5
10	3e−01	1 / 6	Joensson_Melanoma high immune response subtype
11	4e−01	12 / 189	Tirosh_genes preferentially expressed by Tregs
12	4e−01	1 / 10	Joensson_Melanoma Normal like subtype
13	6e−01	2 / 39	Tirosh_melanoma specific genes
14	7e−01	12 / 236	Gerber_wt/wt_group3−specific
15	7e−01	4 / 81	Tirosh_Genes in the MITF program

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.5	7 / 122	Terre_IMS_influenza_meta_signature
2	0.6	2 / 33	Sweeney_viral_dn
3	0.6	3 / 54	Burnham_timecourse
4	0.7	9 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	0.8	6 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.8	2 / 52	Burnham_day1_vs_5_DN
7	0.9	1 / 41	Scicluna_DN
8	1.0	1 / 68	Burnham_sep_vs_con_UP
9	1.0	1 / 71	Burnham_cap_fp_vs_con_UP
10	1.0	0 / 56	Burnham_sep_vs_con_DN
11	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.0	0 / 48	Burnham_viral_DN
13	1.0	0 / 57	Burnham_viral_UP
14	1.0	0 / 57	Burnham_day1_vs_5_UP
15	1.0	0 / 18	Scicluna_UP

TF

Rank	p−value	#in/all	Geneset
1	2e−19	146 / 1241	KIM_MYC targets
2	5e−19	129 / 1044	ICGC_Six5_targets
3	5e−17	298 / 3564	ICGC_Taf1_targets
4	6e−16	162 / 1578	ICGC_GabpPcr2_targets
5	6e−14	261 / 3150	ICGC_Creb1_targets
6	1e−12	275 / 3451	ICGC_Atf2_targets
7	6e−12	293 / 3796	ICGC_Nficsc81335_targets
8	2e−11	268 / 3420	ICGC_Bclaf101388_targets
9	4e−11	290 / 3804	ICGC_Stat5_targets
10	7e−11	150 / 1630	ICGC_SrfV0416101_targets
11	1e−10	286 / 3769	ICGC_Pmlsc71910_targets
12	9e−10	278 / 3703	ICGC_Foxm1_targets
13	9e−10	108 / 1089	ICGC_Ets1_targets
14	3e−08	266 / 3630	ICGC_Sp1_targets
15	4e−08	104 / 1107	ICGC_Myc_targets

Cancer

Rank	p−value	#in/all	Geneset
1	1e−06	1 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	5e−06	6 / 10	GENTLES_modul5
3	3e−03	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	4e−03	6 / 28	PanCan_HK_geneset_nanostring
5	1e−02	4 / 16	WOLFER_overlap genes
6	1e−02	4 / 16	GENTLES_modul6
7	4e−02	0 / 15	RHODES_CANCER_META_SIGNATURE
8	4e−02	3 / 14	LIU_COMMON_CANCER_GENES
9	4e−02	3 / 14	GENTLES_modul10
10	1e−01	6 / 58	SHAUGHNESSY_MM high risk
11	1e−01	1 / 2	GENTLES_modul8
12	2e−01	2 / 13	GENTLES_modul1
13	2e−01	2 / 14	BENTINK_myc.1
14	2e−01	2 / 14	BENTINK_ras.6
15	2e−01	2 / 14	BENTINK_src.2

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−57	616 / 7635	monocytes peripheral blood_1_TssA
2	3e−53	624 / 7957	Tcells peripheral blood_2_TssAFlnk
3	4e−53	600 / 7420	Tcells peripheral blood_1_TssA
4	1e−52	622 / 7930	Tregulatory cells peripheral blood_1_TssA
5	3e−52	617 / 7833	Bcells peripheral blood_1_TssA
6	9e−52	632 / 8200	monocytes peripheral blood_2_TssAFlnk
7	6e−51	592 / 7331	TssA_Colon
8	2e−49	630 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
9	7e−49	636 / 8406	Bcells peripheral blood_2_TssAFlnk
10	2e−48	607 / 7751	natural killer cells peripheral blood_1_TssA
11	9e−47	629 / 8322	T CD8+ naive cells peripheral blood_1_TssA
12	9e−47	618 / 8068	Thelper cells peripheral blood_1_TssA
13	2e−45	577 / 7225	Overlap_fetal_midbrain_ReprPC
14	5e−44	629 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
15	9e−43	426 / 4528	T CD8+ naive cells peripheral blood_4_Tx

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−32	126 / 726	PUJANA_CHEK2_PCC_NETWORK
2	6e−31	194 / 1527	PUJANA_BRCA1_PCC_NETWORK
3	6e−23	92 / 540	TIEN_INTESTINE_PROBIOTICS_24HR_UP
4	1e−22	149 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
5	3e−22	160 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	1e−21	97 / 616	WEI_MYCN_TARGETS_WITH_E_BOX
7	8e−21	70 / 361	GARY_CD5_TARGETS_DN
8	2e−18	96 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
9	2e−18	33 / 95	KEGG_OXIDATIVE_PHOSPHORYLATION
10	3e−18	44 / 172	REACTOME_HIV_INFECTION
11	7e−18	70 / 406	MOOTHA_HUMAN_MITODB_6_2002
12	2e−17	71 / 422	MOOTHA_MITOCHONDRIA
13	6e−17	40 / 154	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
14	1e−16	67 / 396	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
15	1e−16	35 / 120	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M

Lifestyle

Rank	p−value	#in/all	Geneset
1	7e−07	25 / 150	Homuth_BMI−associated−genes_UP
2	2e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	4e−01	13 / 210	Homuth_BMI−associated−genes_DN
4	4e−01	1 / 10	DUMEAUX_Smoking literature genes up
5	5e−01	2 / 32	Marjolein_ageing−genes_DN
6	5e−01	1 / 14	Huan_blood−pressure_SBP−signature
7	7e−01	1 / 22	DUMEAUX_Fasting enriched genes
8	9e−01	2 / 62	DUMEAUX_Smoking enriched genes
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 22	DUMEAUX_High bmi enriched genes

MF

Rank	p−value	#in/all	Geneset
1	4e−27	156 / 1161	RNA binding
2	7e−09	10 / 18	threonine−type endopeptidase activity
3	8e−09	13 / 33	NADH dehydrogenase (ubiquinone) activity
4	1e−06	9 / 22	hydrogen ion transmembrane transporter activity
5	2e−06	493 / 7864	protein binding
6	5e−06	19 / 107	mRNA binding
7	7e−06	7 / 15	NADH dehydrogenase activity
8	1e−05	7 / 16	2 iron, 2 sulfur cluster binding
9	3e−05	18 / 109	structural constituent of ribosome
10	3e−05	8 / 24	TBP−class protein binding
11	3e−05	6 / 13	proton−transporting ATP synthase activity, rotational mechanism
12	1e−04	14 / 81	single−stranded DNA binding
13	1e−04	9 / 37	single−stranded RNA binding
14	2e−04	11 / 55	double−stranded RNA binding
15	2e−04	6 / 17	telomerase RNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−22	140 / 1081	PROTEINATLAS_testis
2	1e−18	97 / 677	PROTEINATLAS_esophagus
3	1e−16	124 / 1048	PROTEINATLAS_gallbladder
4	2e−16	101 / 776	PROTEINATLAS_skin
5	6e−16	122 / 1048	PROTEINATLAS_rectum
6	8e−16	124 / 1076	PROTEINATLAS_stomach
7	4e−15	104 / 848	PROTEINATLAS_adrenal gland
8	4e−15	110 / 923	PROTEINATLAS_cerebral cortex
9	6e−15	103 / 840	PROTEINATLAS_urinary bladder
10	4e−14	103 / 866	PROTEINATLAS_cerebellum
11	5e−14	80 / 592	PROTEINATLAS_seminal vesicle
12	6e−14	80 / 594	PROTEINATLAS_parathyroid gland
13	9e−14	90 / 716	PROTEINATLAS_epididymis
14	1e−13	115 / 1032	PROTEINATLAS_small intestine
15	1e−13	89 / 708	PROTEINATLAS_thyroid gland

K−Means Cluster

Spot Summary: G

metagenes = 74
genes = 844

<r> metagenes = 0.87
<r> genes = 0.2
beta: r2= 2.24 / log p= −Inf

samples with spot = 8 (3.6 %)
mBL : 6 (13.6 %)
intermediate : 2 (4.2 %)

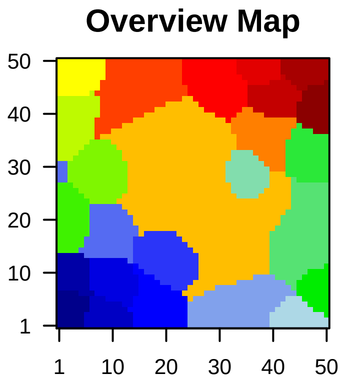
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206233_at	1.81	−0.95	0.17	B4GALT6	beta−1,4−galactosyltransferase 6 [Source:HGNC Symbol;Acc
2	213435_at	1.73	−1.11	0.29	SATB2	SATB homeobox 2 [Source:HGNC Symbol;Acc:HGNC:21637
3	213489_at	1.67	−1.75	0.31	MAPRE2	microtubule associated protein RP/EB family member 2 [Sour
4	213839_at	1.52	−0.78	0.19	CLMN	calmin [Source:HGNC Symbol;Acc:HGNC:19972]
5	221045_s_at	1.42	−0.9	0.12	PER3	period circadian regulator 3 [Source:HGNC Symbol;Acc:HGN
6	206738_at	1.41	−0.97	0.34		APOC4−APOC2 readthrough (NMD candidate) [Source:HGN
7	202661_at	1.39	−1.1	0.29		
8	221207_s_at	1.38	−0.94	0.37	NBEA	neurobeachin [Source:HGNC Symbol;Acc:HGNC:7648]
9	208358_s_at	1.36	−1	0.31	UGT8	UDP glycosyltransferase 8 [Source:HGNC Symbol;Acc:HGN
10	214790_at	1.35	−0.72	0.37	SENP6	SUMO1/sentrin specific peptidase 6 [Source:HGNC Symbol;
11	204547_at	1.34	−1.13	0.32	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
12	206314_at	1.34	−1.07	0.33	ZKSCAN7	zinc finger with KRAB and SCAN domains 7 [Source:HGNC
13	210733_at	1.33	−1	0.35		
14	220181_x_at	1.3	−1.03	0.4	SLC30A5	solute carrier family 30 member 5 [Source:HGNC Symbol;Ac
15	218183_at	1.27	−0.93	0.29	CDIP1	cell death inducing p53 target 1 [Source:HGNC Symbol;Acc:
16	208920_at	1.2	−0.9	0.31	SRI	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
17	219312_s_at	1.18	−1.16	0.33	ZBTB10	zinc finger and BTB domain containing 10 [Source:HGNC Sy
18	210379_s_at	1.17	−1.36	0.23	TLK1	tousled like kinase 1 [Source:HGNC Symbol;Acc:HGNC:1184
19	209750_at	1.16	−0.94	0.41	NR1D2	nuclear receptor subfamily 1 group D member 2 [Source:HG
20	204155_s_at	1.15	−1.45	0.18	SIK3	SIK family kinase 3 [Source:HGNC Symbol;Acc:HGNC:2916

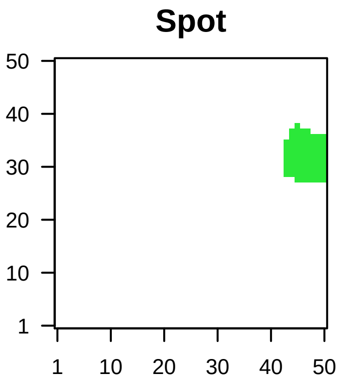
Geneset Overrepresentation

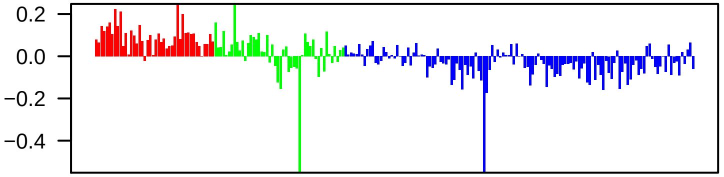
Rank	p−value	#in/all	Geneset	
1	1e−99	597 / 5529	Lympl	HOPP_Txn_elongation
2	2e−98	144 / 310	Refer	Chaussabel_3,4_Protein phosphatases
3	2e−87	589 / 5908	Lympl	HOPP_Active_promoter
4	3e−59	449 / 4261	Lympl	HOPP_Txn_transition
5	2e−57	175 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
6	6e−53	119 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
7	1e−47	510 / 5682	Lympl	HOPP_Weak_promoter
8	3e−41	200 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
9	3e−40	80 / 245	Refer	Chaussabel_3,9_Kinases
10	2e−39	215 / 1550	GSEA	PILON_KLF1_TARGETS_DN
11	5e−35	109 / 516	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
12	7e−35	126 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
13	1e−34	103 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
14	2e−33	93 / 398	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
15	3e−32	199 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
16	1e−31	409 / 4579	CC	nucleus
17	2e−31	120 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
18	6e−30	103 / 528	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
19	1e−27	385 / 4357	Lympl	HOPP_Weak_txn
20	4e−26	172 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
21	1e−25	116 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
22	7e−25	144 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
23	3e−24	153 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
24	1e−23	180 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
25	1e−23	163 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
26	4e−23	384 / 4559	Lympl	HOPP_Weak_enhancer
27	7e−23	149 / 1161	MF	RNA binding
28	8e−22	81 / 442	GSEA	KIM_WT1_TARGETS_DN
29	1e−21	161 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
30	8e−21	247 / 2541	CC	nucleoplasm
31	4e−20	58 / 260	miRN	hsa−miR−561
32	8e−20	62 / 297	GSEA	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
33	3e−19	57 / 261	miRN	hsa−miR−559
34	7e−19	62 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
35	8e−19	59 / 284	miRN	hsa−miR−548d−5p
36	2e−18	78 / 468	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_DN
37	2e−18	50 / 214	GSEA	CHEN_HOXA5_TARGETS_9HR_UP
38	2e−18	40 / 139	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
39	4e−18	57 / 275	miRN	hsa−miR−590−3p
40	5e−18	122 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP

Overview Map

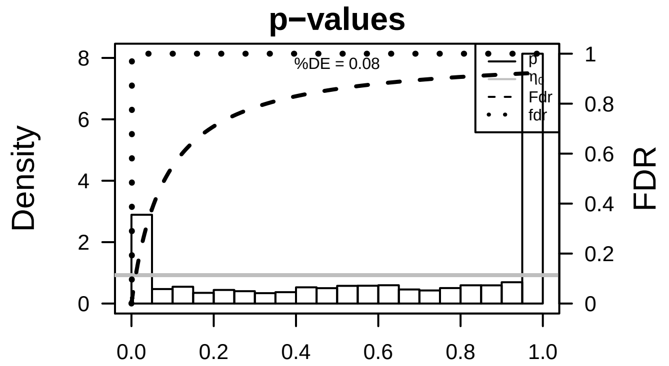


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	2 / 92	HORVATH_aging_genes meth DOWN
2	1	1 / 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	2e−13	170 / 1764	regulation of transcription, DNA−templated
2	1e−12	160 / 1655	transcription, DNA−templated
3	1e−11	47 / 281	mRNA processing
4	7e−10	39 / 233	RNA splicing
5	8e−08	64 / 569	regulation of transcription from RNA polymerase II promoter
6	2e−07	37 / 260	chromatin organization
7	6e−07	30 / 198	mRNA splicing, via spliceosome
8	8e−07	16 / 68	protein sumoylation
9	1e−06	16 / 69	chromatin remodeling
10	2e−06	54 / 497	cell cycle
11	5e−06	10 / 31	tRNA export from nucleus
12	9e−06	17 / 90	RNA processing
13	1e−05	17 / 91	mRNA transport
14	2e−05	36 / 307	cell division
15	2e−05	14 / 69	regulation of cellular response to heat

Cancer

Rank	p−value	#in/all	Geneset
1	8e−09	9 / 14	BENTINK_src.2
2	2e−05	10 / 36	ZHANG_MM up
3	6e−05	6 / 14	BENTINK_ras.6
4	2e−04	5 / 11	GENTLES_modul14
5	1e−03	5 / 16	GENTLES_modul6
6	4e−03	14 / 113	PanCan_Driver_Gene_geneset_nanostring
7	2e−02	4 / 18	PanCan_Notch_geneset_nanostring
8	2e−02	2 / 12	LIU_BREAST_CANCER
9	3e−02	3 / 12	GENTLES_modul12
10	4e−02	6 / 45	KUIPER_MM poor survival
11	7e−02	4 / 28	PanCan_HK_geneset_nanostring
12	1e−01	3 / 20	PanCan_ChromMod_geneset_nanostring
13	1e−01	1 / 2	GENTLES_modul8
14	1e−01	2 / 12	BENTINK_ras.1
15	2e−01	1 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	1e−31	409 / 4579	nucleus
2	8e−21	247 / 2541	nucleoplasm
3	2e−07	43 / 326	nuclear speck
4	6e−07	23 / 128	spliceosomal complex
5	2e−06	18 / 90	nuclear matrix
6	6e−06	15 / 70	nuclear pore
7	9e−06	64 / 653	nucleolus
8	3e−05	37 / 324	chromosome
9	4e−05	6 / 13	ESC/E(Z) complex
10	4e−05	17 / 100	chromatin
11	8e−05	15 / 86	PML body
12	9e−05	21 / 149	nuclear envelope
13	1e−04	260 / 3805	cytosol
14	1e−04	18 / 118	chromosome, centromeric region
15	1e−04	9 / 35	nuclear inner membrane

Chr

Rank	p−value	#in/all	Geneset
1	6e−06	32 / 242	Chr 13
2	5e−04	45 / 480	Chr 4
3	6e−04	50 / 554	Chr 5
4	3e−03	55 / 669	Chr 6
5	8e−03	54 / 689	Chr 3
6	4e−02	59 / 832	Chr 2
7	5e−02	50 / 700	Chr 12
8	5e−02	33 / 437	Chr 8
9	2e−01	14 / 184	Chr 18
10	3e−01	26 / 403	Chr 14
11	3e−01	30 / 490	Chr 10
12	4e−01	35 / 585	Chr 7
13	7e−01	7 / 139	Chr 21
14	8e−01	18 / 382	Chr 15
15	8e−01	27 / 556	Chr X

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−99	603 / 5716	Bcells peripheral blood_4_Tx
2	1e−99	600 / 5753	Tcells peripheral blood_4_Tx
3	1e−99	551 / 4528	T CD8+ naive cells peripheral blood_4_Tx
4	1e−99	615 / 6099	HSC_4_Tx
5	9e−94	578 / 5527	Tregulatory cells peripheral blood_4_Tx
6	1e−91	579 / 5601	Thelper cells peripheral blood_4_Tx
7	5e−89	584 / 5766	natural killer cells peripheral blood_4_Tx
8	7e−89	661 / 7420	Tcells peripheral blood_1_TssA
9	1e−88	582 / 5738	monocytes peripheral blood_4_Tx
10	7e−87	672 / 7751	natural killer cells peripheral blood_1_TssA
11	4e−85	518 / 4683	Overlap_fetal_midbrain_HetRpts
12	6e−85	665 / 7635	monocytes peripheral blood_1_TssA
13	1e−81	669 / 7833	Bcells peripheral blood_1_TssA
14	1e−76	637 / 7225	Overlap_fetal_midbrain_ReprPC
15	5e−75	617 / 6839	T CD8+ naive cells peripheral blood_5_TxWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−26	172 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	3e−24	153 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	3e−08	95 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
4	3e−08	149 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	5e−08	86 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
6	1e−07	63 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
7	2e−06	13 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
8	3e−06	91 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	3e−05	50 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
10	1e−04	56 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
11	2e−04	73 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
12	3e−03	69 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	5e−03	4 / 13	Vilar_hypermutated−in−CRC
14	7e−03	44 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
15	3e−02	81 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a

Glioma

Rank	p−value	#in/all	Geneset
1	1e−23	180 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−21	161 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	5e−15	58 / 330	Up
4	2e−11	47 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	2e−08	69 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	9e−05	12 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	6e−04	10 / 52	GIEZELT_GBM_WT_down_VS_mut
8	4e−02	2 / 6	Donson−adaptive−immunity−associated with LTS in HGA
9	8e−02	7 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	9e−02	5 / 43	Patel_stemness signatures
11	1e−01	6 / 58	Stuehler_Proteins_up_in_STS
12	1e−01	1 / 2	Phillips Prolif up vs PN & MES
13	1e−01	3 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	2e−01	5 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
15	2e−01	2 / 16	VERHAAK_NL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−57	175 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	6e−53	119 / 417	SHEN_SMARCA2_TARGETS_UP
3	3e−41	200 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	2e−39	215 / 1550	PILON_KLF1_TARGETS_DN
5	5e−35	109 / 516	HAMAI_APOPTOSIS_VIA_TRAIL_UP
6	7e−35	126 / 673	SCHLOSSER_SERUM_RESPONSE_DN
7	1e−34	103 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
8	2e−33	93 / 398	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
9	3e−32	199 / 1527	PUJANA_BRCA1_PCC_NETWORK
10	2e−31	120 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
11	6e−30	103 / 528	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
12	1e−25	116 / 726	PUJANA_CHEK2_PCC_NETWORK
13	7e−25	144 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	1e−23	163 / 1312	PUJANA_ATM_PCC_NETWORK
15	8e−22	81 / 442	KIM_WT1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−07	30 / 190	HALLMARK_MYC_TARGETS_V1
2	1e−05	27 / 195	HALLMARK_G2M_CHECKPOINT
3	9e−03	19 / 187	HALLMARK_E2F_TARGETS
4	2e−02	12 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	6e−02	15 / 173	HALLMARK_MITOTIC_SPINDLE
6	2e−01	5 / 51	HALLMARK_TGF_BETA_SIGNALING
7	2e−01	8 / 94	HALLMARK_PROTEIN_SECRETION
8	2e−01	8 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	3e−01	13 / 192	HALLMARK_MTORC1_SIGNALING
10	3e−01	7 / 96	HALLMARK_ANDROGEN_RESPONSE
11	4e−01	12 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	4e−01	8 / 122	HALLMARK_SPERMATOGENESIS
13	4e−01	9 / 139	HALLMARK_FATTY_ACID_METABOLISM
14	7e−01	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	8e−01	9 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	2 / 12	Angelova_immune−metagene−effector_memory_CD4
2	0.3	2 / 18	Angelova_immune−metagene−pDC
3	0.3	2 / 21	Angelova_immune−metagene−central_memory_CD4
4	0.4	1 / 8	Angelova_immune−metagene−mDC
5	0.4	2 / 23	Angelova_immune−metagene−monocytes
6	0.4	1 / 10	Angelova_immune−metagene−neutrophils
7	0.6	1 / 14	Angelova_immune−metagene−eosinophil
8	0.7	1 / 19	Angelova_immune−metagene−activated_CD8
9	0.7	1 / 19	Angelova_immune−metagene−iDC
10	0.7	2 / 45	Angelova_immune−metagene−MDSC
11	0.8	1 / 32	Angelova_immune−metagene−effector_memory_CD8
12	0.9	1 / 38	Angelova_immune−metagene−mast−cells
13	1.0	1 / 67	Angelova_immune−metagene−T−cells
14	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
15	1.0	0 / 26	Angelova_immune−metagene−activated_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	3 / 22	DUMEAUX_Fasting enriched genes
2	0.1	16 / 210	Homuth_BMI−associated−genes_DN
3	1.0	4 / 150	Homuth_BMI−associated−genes_UP
4	1.0	0 / 62	DUMEAUX_Smoking enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 22	DUMEAUX_High bmi enriched genes
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	1e−99	597 / 5529	HOPP_Txn_elongation
2	2e−87	589 / 5908	HOPP_Active_promoter
3	3e−59	449 / 4261	HOPP_Txn_transition
4	1e−47	510 / 5682	HOPP_Weak_promoter
5	1e−27	385 / 4357	HOPP_Weak_txn
6	4e−23	384 / 4559	HOPP_Weak_enhancer
7	7e−11	389 / 5404	HOPP_Strong_enhancer
8	6e−08	20 / 88	ROSOLOWSKI_green UP
9	4e−06	21 / 121	ROSOLOWSKI_green total
10	1e−05	85 / 955	SPANG_BCR UP
11	6e−05	79 / 906	SPANG_BCR DN
12	2e−03	24 / 227	SPANG_IL21 UP
13	1e−02	124 / 1814	HOPP_Repetitive
14	1e−02	4 / 17	DAVE_c−myc BL UP
15	4e−02	25 / 305	TARTE_Plasmablast signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.007	22 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.017	12 / 107	Tirosh_Exhaustion program in Mel75
3	0.020	21 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.037	26 / 319	Gerber_wt/wt_melanoma−cells−SpotA
5	0.160	1 / 3	Gerami_melanoma−metastatic−risk_UP
6	0.207	1 / 4	Melanoma Epi−Enzyme Cluster 3
7	0.207	1 / 4	Melanoma Epi−Enzyme Cluster 5
8	0.259	4 / 46	Tirosh_top50 correlated genes PC5
9	0.285	6 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
10	0.348	12 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	0.371	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
12	0.374	2 / 23	Melanoma Epi−Enzyme Cluster 7
13	0.448	29 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	0.471	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
15	0.498	3 / 47	Tirosh_G2/M phase specific genes

MF

Rank	p−value	#in/all	Geneset
1	7e−23	149 / 1161	RNA binding
2	3e−15	106 / 852	nucleic acid binding
3	5e−13	534 / 7864	protein binding
4	1e−09	42 / 267	binding
5	3e−06	128 / 1541	DNA binding
6	3e−06	31 / 225	transcription coactivator activity
7	7e−06	19 / 107	mRNA binding
8	8e−06	39 / 328	chromatin binding
9	1e−04	12 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
10	8e−04	16 / 116	helicase activity
11	9e−04	26 / 237	ubiquitin−protein transferase activity
12	1e−03	5 / 15	poly(A) binding
13	1e−03	9 / 48	translation initiation factor activity
14	2e−03	18 / 148	ubiquitin protein ligase activity
15	2e−03	5 / 17	lysine−acetylated histone binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−20	58 / 260	hsa−miR−561
2	3e−19	57 / 261	hsa−miR−559
3	8e−19	59 / 284	hsa−miR−548d−5p
4	4e−18	57 / 275	hsa−miR−590−3p
5	7e−18	54 / 253	hsa−miR−548c−5p
6	1e−17	66 / 364	hsa−miR−548n
7	3e−17	50 / 226	hsa−miR−548h
8	9e−17	56 / 285	hsa−miR−548b−5p
9	4e−16	50 / 240	hsa−miR−548j
10	6e−16	51 / 251	hsa−miR−548i
11	2e−15	57 / 314	hsa−miR−372
12	7e−15	49 / 248	hsa−miR−520c−3p
13	1e−14	51 / 269	hsa−miR−548a−5p
14	1e−14	69 / 448	hsa−miR−20b
15	2e−14	47 / 235	hsa−miR−30e

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	5 / 54	Burnham_timecourse
2	0.3	12 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.6	7 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.7	2 / 41	Scicluna_DN
5	0.9	1 / 48	Burnham_viral_DN
6	1.0	1 / 52	Burnham_day1_vs_5_DN
7	1.0	1 / 57	Burnham_viral_UP
8	1.0	1 / 68	Burnham_sep_vs_con_UP
9	1.0	1 / 71	Burnham_cap_fp_vs_con_UP
10	1.0	2 / 122	Terre_IMS_influenza_meta_signature
11	1.0	0 / 56	Burnham_sep_vs_con_DN
12	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
13	1.0	0 / 57	Burnham_day1_vs_5_UP
14	1.0	0 / 18	Scicluna_UP
15	1.0	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−98	144 / 310	Chaussabel_3,4_Protein phosphatases
2	3e−40	80 / 245	Chaussabel_3,9_Kinases
3	2e−14	103 / 840	PROTEINATLAS_urinary bladder
4	4e−14	103 / 848	PROTEINATLAS_adrenal gland
5	2e−13	115 / 1022	PROTEINATLAS_placenta
6	4e−13	79 / 593	PROTEINATLAS_lateral ventricle
7	1e−12	85 / 677	PROTEINATLAS_esophagus
8	1e−12	78 / 595	PROTEINATLAS_breast
9	1e−12	72 / 527	PROTEINATLAS_oral mucosa
10	2e−12	100 / 861	PROTEINATLAS_nasopharynx
11	2e−12	117 / 1081	PROTEINATLAS_testis
12	2e−12	84 / 671	PROTEINATLAS_cervix, uterine
13	3e−12	114 / 1048	PROTEINATLAS_gallbladder
14	3e−12	114 / 1048	PROTEINATLAS_rectum
15	3e−12	29 / 113	Chaussabel_1,8_Metabolism Biosynthesis

Telomeres

Rank	p−value	#in/all	Geneset
1	0.02	5 / 27	Nabetani_alt len telomeres_genes_ko
2	0.16	2 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−16	301 / 3564	ICGC_Taf1_targets
2	6e−16	127 / 1089	ICGC_Ets1_targets
3	4e−12	275 / 3420	ICGC_Bclaf101388_targets
4	3e−11	293 / 3769	ICGC_Pmlsc71910_targets
5	4e−11	273 / 3451	ICGC_Atf2_targets
6	3e−10	250 / 3150	ICGC_Creb1_targets
7	3e−09	274 / 3608	ICGC_Tcf12_targets
8	3e−09	286 / 3804	ICGC_Stat5_targets
9	5e−09	243 / 3121	ICGC_Egr1_targets
10	6e−09	145 / 1630	ICGC_SrfV0416101_targets
11	7e−09	284 / 3796	ICGC_Nficsc81335_targets
12	7e−09	108 / 1107	ICGC_Myc_targets
13	8e−09	278 / 3703	ICGC_Foxm1_targets
14	9e−09	300 / 4072	ICGC_Mta3_targets
15	1e−08	282 / 3778	ICGC_Pol24_targets

K−Means Cluster

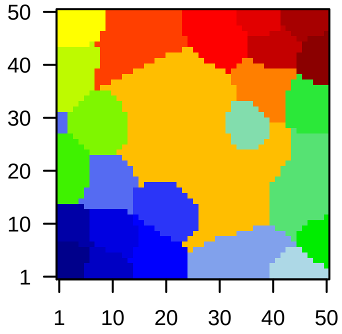
Spot Summary: H

metagenes = 57
genes = 279

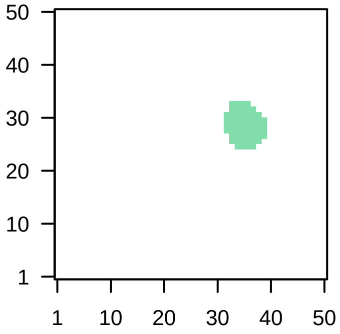
<r> metagenes = 0.93
<r> genes = 0.19
beta: r2= 1.69 / log p= −Inf

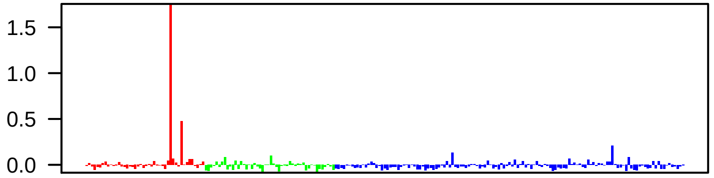
samples with spot = 3 (1.4 %)
mBL : 2 (4.5 %)
non−mBL : 1 (0.8 %)

Overview Map



Spot





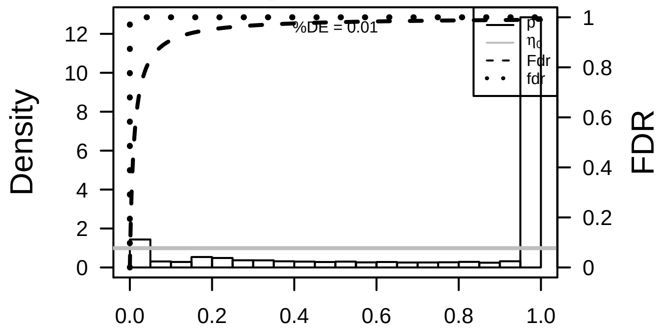
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	219465_at	3.55	−0.52	0.78	APOA2	apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
2	208470_s_at	3.52	−0.84	0.62	HPR	haptoglobin−related protein [Source:HGNC Symbol;Acc:HGN
3	219466_s_at	3.5	−0.5	0.81	APOA2	apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
4	211298_s_at	3.41	−0.62	0.76	ALB	albumin [Source:HGNC Symbol;Acc:HGNC:399]
5	203400_s_at	3.34	−0.63	0.73	TF	transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
6	217238_s_at	3.3	−0.55	0.69	ALDOB	aldolase, fructose−bisphosphate B [Source:HGNC Symbol;Ac
7	205820_s_at	3.27	−0.63	0.68	APOC3	apolipoprotein C3 [Source:HGNC Symbol;Acc:HGNC:610]
8	206697_s_at	3.26	−0.73	0.56	HP	haptoglobin [Source:HGNC Symbol;Acc:HGNC:5141]
9	204988_at	3.25	−0.63	0.68	FGB	fibrinogen beta chain [Source:HGNC Symbol;Acc:HGNC:366
10	205892_s_at	3.21	−0.45	0.68	FABP1	fatty acid binding protein 1 [Source:HGNC Symbol;Acc:HGN
11	204965_at	3.18	−0.53	0.74	GC	GC, vitamin D binding protein [Source:HGNC Symbol;Acc:H
12	209937_at	3.14	−0.36	0.77	TM4SF4	transmembrane 4 L six family member 4 [Source:HGNC Sym
13	208383_s_at	3.1	−0.64	0.61	PCK1	phosphoenolpyruvate carboxykinase 1 [Source:HGNC Symb
14	219140_s_at	3.1	−0.66	0.68	RBP4	retinol binding protein 4 [Source:HGNC Symbol;Acc:HGNC:
15	206226_at	3.08	−0.56	0.68	HRG	histidine rich glycoprotein [Source:HGNC Symbol;Acc:HGNC
16	210929_s_at	3.08	−0.82	0.66	AHSG	alpha 2−HS glycoprotein [Source:HGNC Symbol;Acc:HGNC:
17	214063_s_at	3.07	−0.61	0.72	TF	transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
18	205650_s_at	3.06	−0.63	0.68	FGA	fibrinogen alpha chain [Source:HGNC Symbol;Acc:HGNC:36
19	219612_s_at	3.01	−0.47	0.74	FGG	fibrinogen gamma chain [Source:HGNC Symbol;Acc:HGNC:
20	216238_s_at	2.97	−0.52	0.72	FGB	fibrinogen beta chain [Source:HGNC Symbol;Acc:HGNC:366

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	70 / 94	Refer	WIRTH_Liver
2	1e−99	113 / 218	GSEA	HSIAO_LIVER_SPECIFIC_GENES
3	4e−52	49 / 147	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
4	1e−46	51 / 208	GSEA	CAIRO_LIVER_DEVELOPMENT_DN
5	3e−44	52 / 243	GSEA	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
6	3e−42	51 / 250	GSEA	CAIRO_HEPATOBLASTOMA_DN
7	4e−41	30 / 52	GSEA	SU_LIVER
8	3e−40	41 / 144	GSEA	LEE_LIVER_CANCER_SURVIVAL_UP
9	4e−38	58 / 421	GSEA	ACEVEDO_LIVER_CANCER_DN
10	1e−35	29 / 64	GSEA	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
11	6e−34	34 / 116	CC	blood microparticle
12	3e−30	92 / 1611	CC	extracellular region
13	7e−29	29 / 100	GSEA	OHGUCHI_LIVER_HNF4A_TARGETS_DN
14	3e−28	74 / 1090	CC	extracellular space
15	1e−26	30 / 130	HM	HALLMARK_COAGULATION
16	4e−26	46 / 410	GSEA	PILON_KLF1_TARGETS_UP
17	5e−25	23 / 67	GSEA	YAMASHITA_LIVER_CANCER_STEM_CELL_DN
18	7e−25	24 / 77	GSEA	WOO_LIVER_CANCER_RECURRENCE_DN
19	3e−23	27 / 124	GSEA	SERVITJA_LIVER_HNF1A_TARGETS_DN
20	5e−22	96 / 2239	CC	extracellular exosome
21	1e−21	19 / 51	BP	hemostasis
22	1e−20	37 / 337	GSEA	BOCHKIS_FOXA2_TARGETS
23	8e−20	28 / 181	HM	HALLMARK_XENOBIOTIC_METABOLISM
24	1e−19	40 / 429	Refer	PROTEINATLAS_liver
25	4e−19	30 / 229	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
26	2e−18	17 / 51	GSEA	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
27	2e−18	76 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
28	2e−18	15 / 35	GSEA	LEE_LIVER_CANCER
29	3e−18	27 / 189	GSEA	NABA_ECM_REGULATORS
30	7e−18	20 / 88	BP	negative regulation of endopeptidase activity
31	1e−17	14 / 31	GSEA	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
32	3e−17	35 / 376	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
33	7e−17	18 / 73	GSEA	LEE_LIVER_CANCER_DENA_DN
34	3e−16	12 / 23	GSEA	BIOCARTA_INTRINSIC_PATHWAY
35	3e−16	26 / 205	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_DN
36	3e−16	18 / 79	CC	organelle membrane
37	4e−16	15 / 47	GSEA	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
38	9e−16	13 / 32	BP	acute−phase response
39	1e−15	12 / 25	GSEA	REACTOME_COMPLEMENT_CASCADE
40	1e−15	14 / 41	GSEA	KEGG_RETINOL_METABOLISM

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.8	1 / 92	HORVATH_aging_genes meth DOWN
2	0.8	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	1e−21	19 / 51	hemostasis
2	7e−18	20 / 88	negative regulation of endopeptidase activity
3	9e−16	13 / 32	acute−phase response
4	3e−13	10 / 21	fibrinolysis
5	3e−13	36 / 542	oxidation−reduction process
6	5e−13	21 / 172	blood coagulation
7	2e−12	17 / 110	platelet degranulation
8	2e−12	21 / 185	cellular protein metabolic process
9	4e−12	16 / 98	steroid metabolic process
10	3e−11	12 / 53	regulation of complement activation
11	2e−10	8 / 18	blood coagulation, intrinsic pathway
12	5e−10	11 / 52	complement activation, classical pathway
13	5e−10	12 / 66	xenobiotic metabolic process
14	2e−09	26 / 402	lipid metabolic process
15	3e−09	6 / 10	plasminogen activation

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	3 / 16	LIU_LIVER_CANCER
2	0.004	3 / 20	PanCan_ChromMod_geneset_nanostring
3	0.048	13 / 480	Lembcke_Colonic Inflammation
4	0.177	1 / 12	LIU_BREAST_CANCER
5	0.191	1 / 13	GENTLES_modul17
6	0.191	1 / 13	BENTINK_e2f3.1
7	0.204	1 / 14	LIU_PROSTATE_CANCER_DN
8	0.204	1 / 14	GENTLES_modul13
9	0.229	1 / 16	GENTLES_modul6
10	0.371	2 / 80	PanCan_JAK−ST_geneset_nanostring
11	0.444	1 / 36	ZHANG_MM up
12	0.572	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	0.584	3 / 187	PanCan_PI3K_geneset_nanostring
14	0.640	2 / 134	PanCan_RAS_geneset_nanostring
15	0.706	0 / 11	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	6e−34	34 / 116	blood microparticle
2	3e−30	92 / 1611	extracellular region
3	3e−28	74 / 1090	extracellular space
4	5e−22	96 / 2239	extracellular exosome
5	3e−16	18 / 79	organelle membrane
6	5e−11	22 / 241	endoplasmic reticulum lumen
7	3e−10	8 / 19	high−density lipoprotein particle
8	4e−09	11 / 63	platelet alpha granule lumen
9	1e−08	31 / 604	intracellular membrane−bounded organelle
10	8e−07	5 / 12	chylomicron
11	4e−06	5 / 16	very−low−density lipoprotein particle
12	3e−05	4 / 12	low−density lipoprotein particle
13	4e−05	4 / 13	endocytic vesicle lumen
14	4e−05	4 / 13	platelet dense granule lumen
15	6e−05	20 / 462	cell surface

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	22 / 480	Chr 4
2	6e−03	16 / 490	Chr 10
3	3e−02	18 / 700	Chr 12
4	5e−02	17 / 689	Chr 3
5	8e−02	28 / 1325	Chr 1
6	3e−01	11 / 554	Chr 5
7	5e−01	1 / 41	Chr Y
8	6e−01	6 / 382	Chr 15
9	6e−01	13 / 832	Chr 2
10	6e−01	9 / 585	Chr 7
11	7e−01	2 / 139	Chr 21
12	8e−01	5 / 403	Chr 14
13	8e−01	2 / 184	Chr 18
14	8e−01	10 / 776	Chr 17
15	9e−01	9 / 756	Chr 11

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−14	115 / 3918	Tcells peripheral blood_14_ReprPCWk
2	3e−12	108 / 3734	Tcells peripheral blood_13_ReprPC
3	1e−10	84 / 2700	Thelper cells peripheral blood_14_ReprPCWk
4	1e−09	76 / 2417	9_ReprPCWk_Melanocytes
5	2e−08	82 / 2867	9_ReprPCWk_MSC_Adipocyte
6	1e−07	70 / 2374	9_ReprPCWk_Fibroblasts
7	1e−07	70 / 2375	10_ReprPC_Fibroblasts
8	2e−07	70 / 2408	9_ReprPCWk_Skeletal_Muscle
9	2e−06	78 / 2984	natural killer cells peripheral blood_14_ReprPCWk
10	4e−06	79 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
11	4e−06	97 / 4079	15_Quies_ESC_Endoderm
12	1e−05	76 / 3001	Bcells peripheral blood_14_ReprPCWk
13	1e−05	81 / 3272	monocytes peripheral blood_14_ReprPCWk
14	1e−05	68 / 2600	HSC_14_ReprPCWk
15	1e−04	87 / 3819	natural killer cells peripheral blood_15_Quies

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−17	35 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	8e−12	31 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
3	3e−07	139 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	4e−05	20 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
5	3e−03	12 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
6	8e−03	10 / 255	Kosinski_top−crypt−long−list
7	2e−02	3 / 38	Marisa_CRC−cluster−e
8	5e−02	14 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
9	8e−02	1 / 5	Kaneda_CIMP−group1
10	1e−01	10 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
11	1e−01	5 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	1e−01	16 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	1e−01	3 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	2e−01	18 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	2e−01	3 / 92	Marisa_CRC−cluster−h

Glioma

Rank	p−value	#in/all	Geneset
1	2e−18	76 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	1e−09	5 / 5	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
3	1e−08	25 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	5e−04	13 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	1e−03	18 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
6	1e−03	4 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
7	3e−03	6 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
8	1e−02	4 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
9	2e−02	2 / 12	VERHAAK_Brain
10	2e−02	2 / 12	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
11	2e−02	2 / 15	Gorovets_LGG_NB_subclass
12	3e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
13	4e−02	4 / 82	laffaire_hypermeth_LGG_vs_control
14	4e−02	2 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN
15	5e−02	4 / 85	ScoV_0.999_Sturm_E2_IDH_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	113 / 218	HSIAO_LIVER_SPECIFIC_GENES
2	4e−52	49 / 147	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
3	1e−46	51 / 208	CAIRO_LIVER_DEVELOPMENT_DN
4	3e−44	52 / 243	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
5	3e−42	51 / 250	CAIRO_HEPATOBLASTOMA_DN
6	4e−41	30 / 52	SU_LIVER
7	3e−40	41 / 144	LEE_LIVER_CANCER_SURVIVAL_UP
8	4e−38	58 / 421	ACEVEDO_LIVER_CANCER_DN
9	1e−35	29 / 64	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
10	7e−29	29 / 100	OHGUCHI_LIVER_HNF4A_TARGETS_DN
11	4e−26	46 / 410	PILON_KLF1_TARGETS_UP
12	5e−25	23 / 67	YAMASHITA_LIVER_CANCER_STEM_CELL_DN
13	7e−25	24 / 77	WOO_LIVER_CANCER_RECURRENCE_DN
14	3e−23	27 / 124	SERVITJA_LIVER_HNF1A_TARGETS_DN
15	1e−20	37 / 337	BOCHKIS_FOXA2_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	1e−26	30 / 130	HALLMARK_COAGULATION
2	8e−20	28 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	5e−08	12 / 97	HALLMARK_BILE_ACID_METABOLISM
4	2e−03	9 / 178	HALLMARK_COMPLEMENT
5	4e−03	9 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
6	1e−02	8 / 194	HALLMARK_KRAS_SIGNALING_UP
7	2e−02	5 / 97	HALLMARK_PEROXISOME
8	1e−01	2 / 34	HALLMARK_ANGIOGENESIS
9	1e−01	2 / 35	HALLMARK_HEDGEHOG_SIGNALING
10	2e−01	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
11	2e−01	5 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	3e−01	4 / 182	HALLMARK_GLYCOLYSIS
13	4e−01	4 / 187	HALLMARK_INFLAMMATORY_RESPONSE
14	4e−01	4 / 188	HALLMARK_HYPOXIA
15	4e−01	4 / 195	HALLMARK_KRAS_SIGNALING_DN

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	Angelova_immune−metagene−NK56_dim
2	0.2	1 / 16	Angelova_immune−metagene−Th17
3	0.3	1 / 23	Angelova_immune−metagene−Treg
4	0.5	1 / 45	Angelova_immune−metagene−MDSC
5	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
6	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
7	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
8	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
9	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
10	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
11	1.0	0 / 25	Angelova_immune−metagene−DC
12	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
14	1.0	0 / 14	Angelova_immune−metagene−eosinophil
15	1.0	0 / 19	Angelova_immune−metagene−iDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.1	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.3	2 / 62	DUMEAUX_Smoking enriched genes
4	0.9	1 / 150	Homuth_BMI−associated−genes_UP
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 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_High bmi enriched genes
12	1.0	0 / 22	DUMEAUX_Fasting enriched genes
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	1e−12	78 / 2206	HOPP_Heterochrom
2	2e−06	8 / 53	LENZ_Stromal signature 2
3	4e−05	77 / 3168	HOPP_Repressed
4	2e−02	12 / 378	TARTE_Mature plasma cell signature
5	1e−01	3 / 70	Subero_FL_hyper_meth
6	2e−01	4 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
7	2e−01	2 / 45	Subero_INT_hypo_meth
8	2e−01	1 / 12	Subero_MM_hypo_meth
9	2e−01	6 / 237	ZHANG_DLBCL mutated
10	2e−01	3 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
11	3e−01	2 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
12	3e−01	1 / 25	ROSOLOWSKI_red UP
13	4e−01	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
14	4e−01	2 / 91	Subero_T−ALL_hyper_meth
15	5e−01	2 / 102	ROSOLOWSKI_blue total

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−04	6 / 64	Harbst_melanoma_lowgrade_up
2	1e−01	7 / 249	Gerber_wt/wt_melanoma−cells−SpotE
3	2e−01	1 / 16	Hugo_melanoma−all−LEF1_UP
4	3e−01	1 / 23	Melanoma Epi−Enzyme Cluster 7
5	3e−01	1 / 24	Gerami_melanoma−metastatic−risk_DN
6	4e−01	2 / 78	Tirosh_CAF−cell specific genes
7	5e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
8	5e−01	1 / 39	Tirosh_melanoma specific genes
9	5e−01	1 / 41	Tirosh_top50 correlated genes PC3
10	5e−01	4 / 230	Gerber_wt/wt_melanoma−cells−SpotC
11	6e−01	2 / 119	TCGA_melanoma_MITF_low
12	7e−01	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
13	8e−01	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
14	8e−01	2 / 204	Landsberg_dedifferentiation_down
15	9e−01	1 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	6e−15	35 / 447	oxidoreductase activity
2	3e−14	15 / 61	serine−type endopeptidase inhibitor activity
3	5e−14	21 / 154	serine−type endopeptidase activity
4	2e−12	14 / 66	monooxygenase activity
5	2e−11	17 / 126	heparin binding
6	1e−10	15 / 104	serine−type peptidase activity
7	4e−10	7 / 13	arachidonic acid epoxygenase activity
8	7e−10	9 / 30	oxygen binding
9	1e−09	14 / 103	heme binding
10	2e−09	9 / 33	endopeptidase inhibitor activity
11	3e−09	11 / 60	oxidoreductase activity, acting on paired donors, with incorporation or reductio
12	3e−09	12 / 77	peptidase inhibitor activity
13	4e−09	14 / 113	iron ion binding
14	4e−08	6 / 14	oxidoreductase activity, acting on paired donors, with incorporation or reductio
15	2e−07	6 / 17	steroid hydroxylase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.07	2 / 26	hsa−miR−934
2	0.15	2 / 43	hsa−miR−328
3	0.23	2 / 56	hsa−miR−1826
4	0.23	1 / 16	hsa−miR−563
5	0.27	1 / 19	hsa−miR−943
6	0.28	2 / 65	hsa−miR−557
7	0.30	1 / 22	hsa−miR−1227
8	0.31	1 / 23	hsa−miR−99b
9	0.32	2 / 72	hsa−miR−339−5p
10	0.33	1 / 25	hsa−miR−635
11	0.33	1 / 25	hsa−miR−892b
12	0.37	1 / 28	hsa−miR−654−5p
13	0.37	1 / 28	hsa−miR−1274b
14	0.37	3 / 135	hsa−miR−7
15	0.38	1 / 29	hsa−miR−215

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	2 / 48	Burnham_viral_DN
2	0.3	1 / 18	Scicluna_UP
3	0.3	2 / 68	Burnham_sep_vs_con_UP
4	0.3	2 / 71	Burnham_cap_fp_vs_con_UP
5	0.6	1 / 57	Burnham_day1_vs_5_UP
6	0.8	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	0.9	1 / 122	Terre_IMS_influenza_meta_signature
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 / 57	Burnham_viral_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 54	Burnham_timecourse
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	1e−99	70 / 94	WIRTH_Liver
2	1e−19	40 / 429	PROTEINATLAS_liver
3	1e−13	14 / 55	WIRTH_Homeostasis
4	5e−07	8 / 45	JONGENEEL_Kidney
5	2e−03	2 / 4	JONGENEEL_Mammary Gland
6	2e−03	3 / 15	JONGENEEL_Lung
7	2e−02	8 / 209	Chaussabel_2,5_Immune related molecules
8	1e−01	2 / 37	Chaussabel_2,2_Neutrophils
9	1e−01	21 / 1007	PROTEINATLAS_kidney
10	1e−01	1 / 9	JONGENEEL_Colon
11	2e−01	1 / 11	JONGENEEL_Pituitary Gland
12	2e−01	1 / 11	JONGENEEL_Spleen
13	2e−01	1 / 11	JONGENEEL_Thyroid
14	2e−01	1 / 13	WIRTH_Prim. lymphoid organs
15	2e−01	1 / 14	WIRTH_Thalamus

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	1e−07	43 / 1148	HEBENSTREIT_low expression TF
2	9e−01	12 / 1041	ICGC_P300_targets
3	1e+00	4 / 485	ICGC_NrsfPcr2_targets
4	1e+00	3 / 415	ICGC_RxraPcr1_targets
5	1e+00	28 / 2321	ICGC_Rad21_targets
6	1e+00	15 / 1636	ICGC_Bcl11_targets
7	1e+00	2 / 522	ICGC_SrfPcr2_targets
8	1e+00	2 / 549	ICGC_Atf3_targets
9	1e+00	42 / 3778	ICGC_Pol24_targets
10	1e+00	7 / 1107	ICGC_Myc_targets
11	1e+00	6 / 1032	ICGC_Usf1_targets
12	1e+00	47 / 4264	ICGC_Pax5_targets
13	1e+00	34 / 3435	ICGC_Ebfsc137065_targets
14	1e+00	7 / 1241	KIM_MYC targets
15	1e+00	8 / 1387	HEBENSTREIT_high expression TF

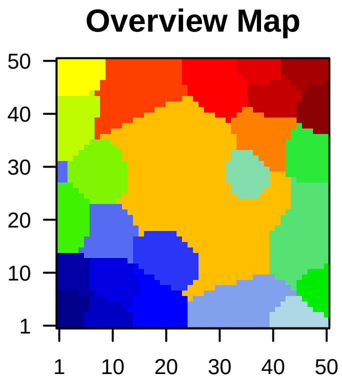
K−Means Cluster

Spot Summary: I

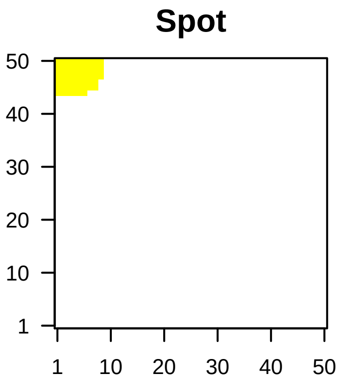
metagenes = 58
genes = 842

<r> metagenes = 0.91
<r> genes = 0.29
beta: r2= 8.6 / log p= −Inf

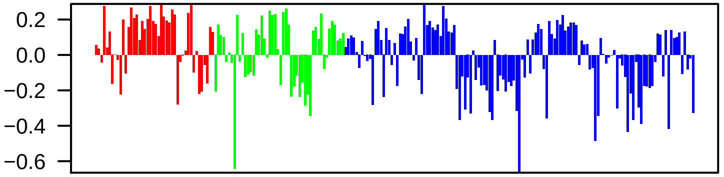
samples with spot = 56 (25.3 %)
mBL : 20 (45.5 %)
intermediate : 14 (29.2 %)
non−mBL : 22 (17.1 %)



Overview Map



Spot



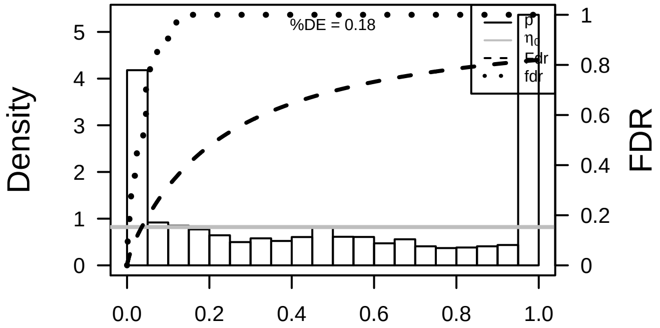
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	215489_x_at	1.98	−1.03	0.42	HOMER3	homer scaffolding protein 3 [Source:HGNC Symbol;Acc:HGN
2	213060_s_at	1.81	−1.28	0.21	CHI3L2	chitinase 3 like 2 [Source:HGNC Symbol;Acc:HGNC:1933]
3	210360_s_at	1.7	−1.07	0.45	MTSS1	MTSS1, I−BAR domain containing [Source:HGNC Symbol;Ac
4	212389_at	1.62	−1.05	0.59	SBF1	SET binding factor 1 [Source:HGNC Symbol;Acc:HGNC:105
5	207686_s_at	1.62	−1.44	0.59	CASP8	caspase 8 [Source:HGNC Symbol;Acc:HGNC:1509]
6	215621_s_at	1.56	−1.08	0.17		immunoglobulin heavy constant delta [Source:HGNC Symbol
7	208595_s_at	1.54	−1.23	0.42	MBD1	methyl−CpG binding domain protein 1 [Source:HGNC Symbo
8	203293_s_at	1.51	−1.49	0.58	LMAN1	lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC
9	218811_at	1.49	−1.6	0.6	ORAI2	ORAI calcium release−activated calcium modulator 2 [Source
10	209664_x_at	1.48	−1.43	0.34	NFATC1	nuclear factor of activated T cells 1 [Source:HGNC Symbol;A
11	220086_at	1.45	−1.15	0.42	IKZF5	IKAROS family zinc finger 5 [Source:HGNC Symbol;Acc:HGN
12	211708_s_at	1.43	−1.2	0.6	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
13	203294_s_at	1.4	−1.25	0.59	LMAN1	lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC
14	214971_s_at	1.4	−1.95	0.75	ST6GAL1	ST6 beta−galactoside alpha−2,6−sialyltransferase 1 [Source:
15	200831_s_at	1.39	−1.42	0.39	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
16	211162_x_at	1.39	−1.05	0.55	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
17	215050_x_at	1.36	−1.7	0.4	MAPKAPK2	mitogen−activated protein kinase−activated protein kinase 2 [
18	213562_s_at	1.35	−1.44	0.61	SQLE	squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127
19	212497_at	1.34	−0.93	0.51		
20	221703_at	1.32	−1.12	0.51	BRIP1	BRCA1 interacting protein C−terminal helicase 1 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	144 / 282	Gliom	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−98	575 / 5529	Lympl	HOPP_Txn_elongation
3	2e−85	93 / 136	Refer	Chaussabel_2,9_Cytosceleton
4	2e−81	479 / 4261	Lympl	HOPP_Txn_transition
5	3e−55	528 / 5908	Lympl	HOPP_Active_promoter
6	6e−48	106 / 372	GSEA	SENESE_HDAC1_TARGETS_UP
7	7e−43	98 / 355	Refer	WIRTH_Immune system
8	1e−40	102 / 405	GSEA	SENESE_HDAC3_TARGETS_UP
9	9e−39	193 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	1e−33	201 / 1550	GSEA	PILON_KLF1_TARGETS_DN
11	1e−33	111 / 564	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
12	6e−33	453 / 5404	Lympl	HOPP_Strong_enhancer
13	5e−30	461 / 5682	Lympl	HOPP_Weak_promoter
14	8e−28	78 / 344	GSEA	THUM_SYSTOLIC_HEART_FAILURE_UP
15	7e−27	185 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
16	2e−25	323 / 3564	TF	ICGC_Taf1_targets
17	1e−24	163 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
18	3e−24	335 / 3805	CC	cytosol
19	1e−22	69 / 328	GSEA	OSMAN_BLADDER_CANCER_UP
20	1e−22	130 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
21	5e−22	189 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
22	2e−20	90 / 564	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
23	4e−20	84 / 509	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
24	4e−20	470 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
25	2e−18	315 / 3769	TF	ICGC_Pmlsc71910_targets
26	2e−18	151 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
27	4e−18	109 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
28	5e−18	315 / 3796	TF	ICGC_Nficsc81335_targets
29	1e−17	95 / 678	Refer	PROTEINATLAS_lymph node
30	3e−17	313 / 3804	TF	ICGC_Stat5_targets
31	4e−17	232 / 2541	CC	nucleoplasm
32	6e−17	271 / 3150	TF	ICGC_Creb1_targets
33	8e−17	54 / 272	GSEA	LIU_SOX4_TARGETS_DN
34	9e−17	160 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
35	3e−16	356 / 4579	CC	nucleus
36	5e−16	113 / 935	GSEA	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
37	1e−15	69 / 439	GSEA	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
38	2e−15	285 / 3451	TF	ICGC_Atf2_targets
39	2e−15	283 / 3420	TF	ICGC_Bclaf101388_targets
40	3e−15	104 / 848	Refer	PROTEINATLAS_adrenal gland

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	7 / 92	HORVATH_aging_genes meth DOWN
2	0.8	4 / 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	3e−24	335 / 3805	cytosol
2	4e−17	232 / 2541	nucleoplasm
3	3e−16	356 / 4579	nucleus
4	2e−12	348 / 4701	cytoplasm
5	2e−08	52 / 416	macromolecular complex
6	5e−06	15 / 70	nuclear pore
7	1e−05	27 / 196	nuclear membrane
8	1e−05	38 / 326	nuclear speck
9	2e−04	36 / 345	focal adhesion
10	2e−04	47 / 494	endosome
11	2e−04	34 / 324	chromosome
12	3e−04	36 / 354	centrosome
13	4e−04	15 / 100	chromatin
14	4e−04	15 / 101	kinetochore
15	5e−04	8 / 35	cytoplasmic stress granule

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−22	189 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
2	4e−20	470 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
3	5e−14	140 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	4e−13	124 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
5	4e−08	102 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
6	4e−08	85 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
7	2e−06	87 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	1e−05	77 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
9	2e−05	97 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	1e−04	75 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	7e−04	5 / 14	TCGA_Mutated−in−CRC_hypermutated
12	2e−03	5 / 18	Boland_CRC−MSI−A6−A10
13	3e−03	42 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
14	1e−02	4 / 16	Vilar_non−hypermutated−in−CRC
15	3e−02	40 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

HM

Rank	p−value	#in/all	Geneset
1	3e−10	33 / 173	HALLMARK_MITOTIC_SPINDLE
2	6e−08	31 / 192	HALLMARK_MTORC1_SIGNALING
3	3e−07	30 / 195	HALLMARK_G2M_CHECKPOINT
4	7e−07	19 / 94	HALLMARK_PROTEIN_SECRETION
5	7e−04	15 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	2e−03	17 / 141	HALLMARK_UV_RESPONSE_DN
7	6e−03	12 / 96	HALLMARK_ANDROGEN_RESPONSE
8	8e−03	16 / 149	HALLMARK_UV_RESPONSE_UP
9	2e−02	18 / 187	HALLMARK_E2F_TARGETS
10	2e−02	8 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	2e−02	11 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	3e−02	17 / 190	HALLMARK_MYC_TARGETS_V1
13	4e−02	14 / 150	HALLMARK_APOPTOSIS
14	9e−02	5 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	1e−01	14 / 174	HALLMARK_ADIPOGENESIS

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−98	575 / 5529	HOPP_Txn_elongation
2	2e−81	479 / 4261	HOPP_Txn_transition
3	3e−55	528 / 5908	HOPP_Active_promoter
4	6e−33	453 / 5404	HOPP_Strong_enhancer
5	5e−30	461 / 5682	HOPP_Weak_promoter
6	5e−11	322 / 4357	HOPP_Weak_txn
7	4e−09	96 / 955	SPANG_BCR UP
8	9e−09	323 / 4559	HOPP_Weak_enhancer
9	1e−08	91 / 906	SPANG_BCR DN
10	2e−08	47 / 353	SPANG_CD40 6hrs DN
11	6e−07	20 / 102	ROSOLOWSKI_blue total
12	2e−05	11 / 45	Monti_BCR_cluster
13	2e−04	134 / 1814	HOPP_Repetitive
14	1e−03	16 / 121	ROSOLOWSKI_green total
15	2e−03	23 / 213	SPANG_IL21 DN

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−14	59 / 364	hsa−miR−548n
2	2e−13	50 / 285	hsa−miR−548b−5p
3	1e−12	31 / 127	hsa−miR−1297
4	3e−12	48 / 284	hsa−miR−548d−5p
5	1e−11	62 / 448	hsa−miR−20b
6	2e−11	30 / 133	hsa−miR−495
7	8e−11	42 / 251	hsa−miR−548i
8	1e−10	58 / 427	hsa−miR−17
9	3e−10	26 / 112	hsa−miR−136
10	3e−10	36 / 202	hsa−miR−26b
11	3e−10	35 / 193	hsa−miR−26a
12	4e−10	47 / 315	hsa−miR−144
13	4e−10	31 / 157	hsa−miR−206
14	5e−10	43 / 275	hsa−miR−590−3p
15	5e−10	32 / 167	hsa−miR−432

Telomeres

Rank	p−value	#in/all	Geneset
1	0.5	1 / 13	Alternative lengthening of telomeres
2	0.8	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−09	62 / 507	protein phosphorylation
2	1e−08	60 / 502	protein transport
3	8e−08	20 / 91	mRNA transport
4	1e−07	57 / 497	cell cycle
5	1e−07	63 / 576	phosphorylation
6	3e−07	38 / 281	mRNA processing
7	5e−07	33 / 233	RNA splicing
8	5e−06	10 / 32	regulation of cholesterol biosynthetic process
9	1e−05	27 / 198	mRNA splicing, via spliceosome
10	1e−05	20 / 124	peptidyl−serine phosphorylation
11	4e−05	12 / 56	negative regulation of translation
12	5e−05	134 / 1764	regulation of transcription, DNA−templated
13	5e−05	127 / 1655	transcription, DNA−templated
14	6e−05	15 / 86	mRNA export from nucleus
15	8e−05	11 / 51	retrograde transport, endosome to Golgi

Chr

Rank	p−value	#in/all	Geneset
1	0.001	67 / 832	Chr 2
2	0.022	56 / 776	Chr 17
3	0.025	49 / 669	Chr 6
4	0.048	40 / 554	Chr 5
5	0.074	85 / 1325	Chr 1
6	0.155	45 / 700	Chr 12
7	0.215	13 / 184	Chr 18
8	0.297	25 / 403	Chr 14
9	0.358	9 / 139	Chr 21
10	0.370	29 / 490	Chr 10
11	0.500	42 / 756	Chr 11
12	0.536	21 / 382	Chr 15
13	0.578	13 / 242	Chr 13
14	0.644	25 / 480	Chr 4
15	0.701	22 / 437	Chr 8

Glioma

Rank	p−value	#in/all	Geneset
1	1e−99	144 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	2e−18	151 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	9e−17	160 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	3e−07	65 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
5	2e−05	21 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	9e−03	29 / 330	Up
7	2e−02	7 / 50	Vishal_subnetwork signature of survival in GBM
8	2e−02	3 / 11	KIM amplified & overexpressed in LTS
9	3e−02	8 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	3e−02	7 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	6e−02	8 / 78	Weller_LGG_A_vs_O_UP
12	7e−02	7 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	1e−01	7 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
14	1e−01	9 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	1e−01	6 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up

Immunome

Rank	p−value	#in/all	Geneset
1	0.07	3 / 18	Angelova_immune−metagene−pDC
2	0.16	2 / 13	Angelova_immune−metagene−immature_B−cells
3	0.16	6 / 67	Angelova_immune−metagene−T−cells
4	0.20	2 / 15	Angelova_immune−metagene−NK
5	0.20	1 / 4	Angelova_CRC_MSS−neoantigens
6	0.23	4 / 45	Angelova_immune−metagene−MDSC
7	0.33	1 / 7	Angelova_CRC_MSI−neoantigens
8	0.43	1 / 10	Angelova_immune−metagene−neutrophils
9	0.43	1 / 10	Angelova_immune−metagene−TFH
10	0.49	1 / 12	Angelova_immune−metagene−memory_B−cells
11	0.52	1 / 13	Angelova_CRC_MSS^−neoantigens
12	0.53	2 / 32	Angelova_immune−metagene−effector_memory_CD8
13	0.55	1 / 14	Angelova_immune−metagene−eosinophil
14	0.62	1 / 17	Angelova_immune−metagene−central_memory_CD8
15	0.66	1 / 19	Angelova_immune−metagene−activated_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−07	32 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	7e−05	28 / 230	Gerber_wt/wt_melanoma−cells−SpotC
3	1e−03	6 / 23	Melanoma Epi−Enzyme Cluster 7
4	2e−02	7 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
5	3e−02	11 / 107	Tirosh_Exhaustion program in Mel75
6	4e−02	6 / 46	Tirosh_top50 correlated genes PC5
7	5e−02	16 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	6e−02	5 / 38	Tirosh_top50 correlated genes PC1
9	2e−01	33 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	2e−01	4 / 41	Tirosh_top50 correlated genes PC3
11	2e−01	16 / 236	Gerber_wt/wt_group3−specific
12	3e−01	4 / 47	Tirosh_G2/M phase specific genes
13	3e−01	18 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	3e−01	3 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	3e−01	3 / 38	Tirosh_G1/S phase specific genes

Pneumonia

Rank	p−value	#in/all	Geneset
1	2e−05	25 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	3e−02	7 / 54	Burnham_timecourse
3	5e−01	8 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	5e−01	3 / 48	Burnham_viral_DN
5	5e−01	7 / 122	Terre_IMS_influenza_meta_signature
6	5e−01	2 / 33	Sweeney_viral_dn
7	6e−01	3 / 57	Burnham_day1_vs_5_UP
8	7e−01	2 / 41	Scicluna_DN
9	9e−01	1 / 48	Burnham_cap_fp_vs_con_DN
10	1e+00	1 / 56	Burnham_sep_vs_con_DN
11	1e+00	1 / 68	Burnham_sep_vs_con_UP
12	1e+00	1 / 71	Burnham_cap_fp_vs_con_UP
13	1e+00	0 / 57	Burnham_viral_UP
14	1e+00	0 / 52	Burnham_day1_vs_5_DN
15	1e+00	0 / 18	Scicluna_UP

TF

Rank	p−value	#in/all	Geneset
1	2e−25	323 / 3564	ICGC_Taf1_targets
2	2e−18	315 / 3769	ICGC_Pmlsc71910_targets
3	5e−18	315 / 3796	ICGC_Nficsc81335_targets
4	3e−17	313 / 3804	ICGC_Stat5_targets
5	6e−17	271 / 3150	ICGC_Creb1_targets
6	2e−15	285 / 3451	ICGC_Atf2_targets
7	2e−15	283 / 3420	ICGC_Bclaf101388_targets
8	4e−15	299 / 3703	ICGC_Foxm1_targets
9	6e−15	321 / 4072	ICGC_Mta3_targets
10	2e−14	246 / 2899	ICGC_Nfatc1_targets
11	5e−14	259 / 3121	ICGC_Egr1_targets
12	7e−14	299 / 3778	ICGC_Pol24_targets
13	7e−14	121 / 1107	ICGC_Myc_targets
14	1e−13	328 / 4278	ICGC_Yy1_targets
15	5e−13	147 / 1494	ICGC_Cebpbsc150_targets

Cancer

Rank	p−value	#in/all	Geneset
1	9e−05	19 / 130	PanCan_CC+Apop_geneset_nanostring
2	9e−04	5 / 15	GENTLES_modul2
3	3e−03	2 / 2	GENTLES_modul8
4	4e−03	14 / 113	PanCan_Driver_Gene_geneset_nanostring
5	1e−02	8 / 58	SHAUGHNESSY_MM high risk
6	2e−02	15 / 147	PanCan_MAPK_geneset_nanostring
7	3e−02	13 / 134	PanCan_RAS_geneset_nanostring
8	4e−02	3 / 14	BENTINK_src.2
9	4e−02	8 / 72	PanCan_Wnt_geneset_nanostring
10	5e−02	3 / 15	GENTLES_modul4
11	9e−02	2 / 15	RHODES_CANCER_META_SIGNATURE
12	1e−01	5 / 45	KUIPER_MM poor survival
13	1e−01	1 / 14	LIU_COMMON_CANCER_GENES
14	1e−01	2 / 11	LIU_PROSTATE_CANCER_UP
15	1e−01	2 / 12	GENTLES_modul12

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−99	604 / 5716	Bcells peripheral blood_4_Tx
2	1e−99	592 / 5753	Tcells peripheral blood_4_Tx
3	1e−99	611 / 6099	HSC_4_Tx
4	1e−99	587 / 5527	Tregulatory cells peripheral blood_4_Tx
5	1e−99	542 / 4528	T CD8+ naive cells peripheral blood_4_Tx
6	8e−99	579 / 5601	Thelper cells peripheral blood_4_Tx
7	1e−97	659 / 7420	Tcells peripheral blood_1_TssA
8	5e−97	585 / 5766	natural killer cells peripheral blood_4_Tx
9	7e−92	661 / 7635	monocytes peripheral blood_1_TssA
10	2e−91	668 / 7833	Bcells peripheral blood_1_TssA
11	4e−89	625 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
12	5e−87	570 / 5738	monocytes peripheral blood_4_Tx
13	2e−85	658 / 7751	natural killer cells peripheral blood_1_TssA
14	4e−82	661 / 7930	Tregulatory cells peripheral blood_1_TssA
15	4e−81	665 / 8068	Thelper cells peripheral blood_1_TssA

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−48	106 / 372	SENESE_HDAC1_TARGETS_UP
2	1e−40	102 / 405	SENESE_HDAC3_TARGETS_UP
3	9e−39	193 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	1e−33	201 / 1550	PILON_KLF1_TARGETS_DN
5	1e−33	111 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
6	8e−28	78 / 344	THUM_SYSTOLIC_HEART_FAILURE_UP
7	7e−27	185 / 1527	PUJANA_BRCA1_PCC_NETWORK
8	1e−24	163 / 1312	PUJANA_ATM_PCC_NETWORK
9	1e−22	69 / 328	OSMAN_BLADDER_CANCER_UP
10	1e−22	130 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
11	2e−20	90 / 564	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
12	4e−20	84 / 509	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
13	4e−18	109 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
14	8e−17	54 / 272	LIU_SOX4_TARGETS_DN
15	5e−16	113 / 935	MARSON_BOUND_BY_FOXP3_UNSTIMULATED

Lifestyle

Rank	p−value	#in/all	Geneset
1	9e−05	26 / 210	Homuth_BMI−associated−genes_DN
2	3e−02	4 / 22	DUMEAUX_Fasting enriched genes
3	2e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	2e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	3e−01	10 / 150	Homuth_BMI−associated−genes_UP
6	3e−01	2 / 22	DUMEAUX_High bmi enriched genes
7	4e−01	1 / 10	DUMEAUX_Smoking literature genes up
8	5e−01	1 / 14	Huan_blood−pressure_SBP−signature
9	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
10	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 13	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	6e−13	523 / 7864	protein binding
2	6e−11	134 / 1402	nucleotide binding
3	1e−09	114 / 1185	ATP binding
4	2e−09	47 / 331	protein serine/threonine kinase activity
5	7e−08	34 / 225	transcription coactivator activity
6	1e−07	63 / 573	kinase activity
7	1e−07	52 / 437	protein kinase activity
8	1e−07	117 / 1329	transferase activity
9	7e−07	41 / 328	chromatin binding
10	1e−06	102 / 1161	RNA binding
11	2e−05	13 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
12	3e−05	121 / 1541	DNA binding
13	3e−05	31 / 256	cadherin binding
14	4e−05	16 / 93	protein N−terminus binding
15	7e−05	17 / 107	mRNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−85	93 / 136	Chaussabel_2,9_Cytosceleton
2	7e−43	98 / 355	WIRTH_Immune system
3	1e−17	95 / 678	PROTEINATLAS_lymph node
4	3e−15	104 / 848	PROTEINATLAS_adrenal gland
5	5e−15	115 / 989	PROTEINATLAS_tonsil
6	5e−15	92 / 708	PROTEINATLAS_thyroid gland
7	8e−15	37 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
8	5e−14	98 / 809	PROTEINATLAS_fallopian tube
9	5e−14	119 / 1076	PROTEINATLAS_stomach
10	1e−13	79 / 594	PROTEINATLAS_parathyroid gland
11	2e−13	117 / 1072	PROTEINATLAS_duodenum
12	3e−13	115 / 1048	PROTEINATLAS_rectum
13	3e−13	113 / 1022	PROTEINATLAS_placenta
14	2e−12	91 / 770	PROTEINATLAS_endometrium
15	2e−12	115 / 1081	PROTEINATLAS_testis

K−Means Cluster

Spot Summary: J

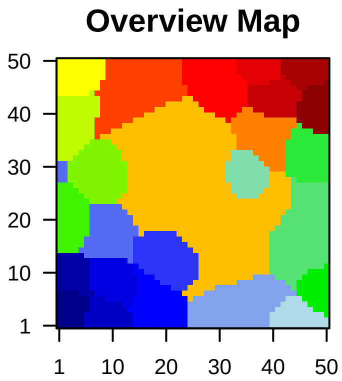
metagenes = 163
genes = 1565

<r> metagenes = 0.59

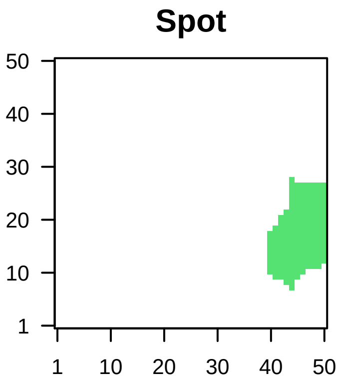
beta: r2= 1.21 / log p= −Inf

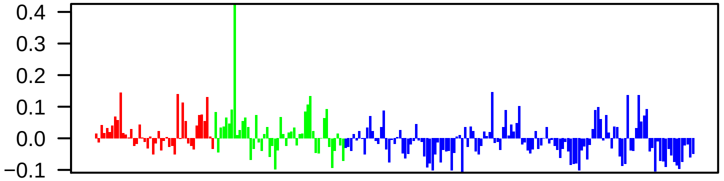
samples with spot = 2 (0.9 %)
intermediate : 1 (2.1 %)
non−mBL : 1 (0.8 %)

Overview Map



Spot





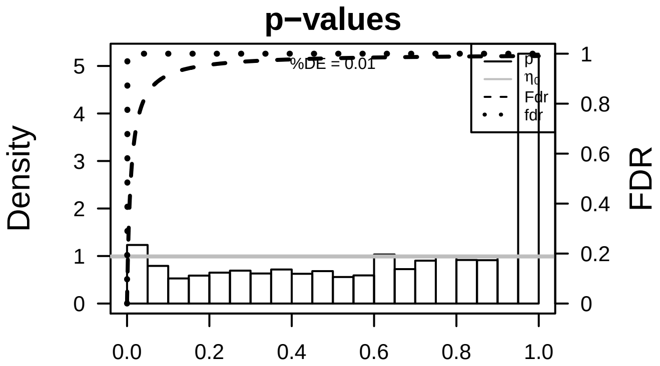
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206835_at	3.38	−0.64	0.02	STATH	statherin [Source:HGNC Symbol;Acc:HGNC:11369]
2	219106_s_at	2.74	−0.57	0.38	KLHL41	kelch like family member 41 [Source:HGNC Symbol;Acc:HGN
3	209888_s_at	2.71	−0.65	0.4	MYL1	myosin light chain 1 [Source:HGNC Symbol;Acc:HGNC:7582
4	205553_s_at	2.65	−0.64	0.28	CSRP3	cysteine and glycine rich protein 3 [Source:HGNC Symbol;Ac
5	204865_at	2.65	−0.72	0.4	CA3	carbonic anhydrase 3 [Source:HGNC Symbol;Acc:HGNC:137
6	217469_at	2.61	−1.06	0.09		immunoglobulin heavy constant epsilon [Source:HGNC Symb
7	205374_at	2.56	−0.68	0.29	SLN	sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]
8	206793_at	2.56	−0.94	0.05	PNMT	phenylethanolamine N−methyltransferase [Source:HGNC Syr
9	213350_at	2.55	−0.86	0.52		
10	203872_at	2.52	−0.86	0.16	ACTA1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:H
11	214087_s_at	2.5	−0.61	0.25	MYBPC1	myosin binding protein C, slow type [Source:HGNC Symbol;A
12	204631_at	2.49	−0.59	0.28	MYH2	myosin heavy chain 2 [Source:HGNC Symbol;Acc:HGNC:757
13	204810_s_at	2.44	−0.61	0.15	CKM	creatine kinase, M−type [Source:HGNC Symbol;Acc:HGNC:1
14	205054_at	2.41	−0.73	0.2	NEB	nebulin [Source:HGNC Symbol;Acc:HGNC:7720]
15	205363_at	2.4	−0.69	0.22	BBOX1	gamma−butyrobetaine hydroxylase 1 [Source:HGNC Symbol;
16	205132_at	2.4	−1.02	0.09	ACTC1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:H
17	206045_s_at	2.39	−0.93	0.2	NOL4	nucleolar protein 4 [Source:HGNC Symbol;Acc:HGNC:7870]
18	205272_s_at	2.34	−0.52	0.01	PRH2	proline rich protein HaeIII subfamily 2 [Source:HGNC Symbol
19	209840_s_at	2.32	−0.65	0.27	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:H
20	209904_at	2.29	−0.83	0.29	TNNC1	troponin C1, slow skeletal and cardiac type [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−16	26 / 47	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_F
2	4e−15	34 / 83	Refer	WIRTH_Muscle
3	2e−13	179 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
4	5e−11	217 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
5	1e−10	675 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
6	1e−08	19 / 49	GSEA	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
7	2e−08	82 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
8	3e−08	17 / 41	MF	structural constituent of muscle
9	3e−08	29 / 106	Refer	Chaussabel_2,11_Replication
10	4e−08	158 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
11	5e−08	42 / 194	HM	HALLMARK_MYOGENESIS
12	5e−08	16 / 38	BP	muscle filament sliding
13	1e−07	13 / 27	GSEA	REACTOME_STRIATED_MUSCLE_CONTRACTION
14	2e−07	10 / 16	Refer	WIRTH_Hippocampus
15	2e−07	20 / 61	GSEA	KUNINGER_IGF1_VS_PDGFB_TARGETS_UP
16	3e−07	56 / 310	Refer	Chaussabel_3,4_Protein phosphatases
17	5e−07	55 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
18	1e−06	15 / 41	BP	cardiac muscle contraction
19	3e−06	113 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
20	3e−06	34 / 165	GSEA	THUM_SYSTOLIC_HEART_FAILURE_DN
21	4e−06	10 / 21	CC	muscle myosin complex
22	5e−06	58 / 355	Refer	PROTEINATLAS_skeletal muscle
23	5e−06	38 / 198	GSEA	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
24	7e−06	12 / 31	GSEA	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP
25	8e−06	9 / 18	GSEA	HUMMERICH_BENIGN_SKIN_TUMOR_DN
26	1e−05	7 / 11	GSEA	DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4
27	2e−05	23 / 99	miRN	hsa−miR−664
28	2e−05	11 / 29	BP	sarcomere organization
29	2e−05	111 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
30	2e−05	14 / 45	GSEA	REACTOME_MUSCLE_CONTRACTION
31	2e−05	69 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
32	2e−05	9 / 20	BP	striated muscle contraction
33	3e−05	8 / 16	GSEA	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN
34	5e−05	18 / 72	GSEA	BILD_CTNNB1_ONCOGENIC_SIGNATURE
35	5e−05	55 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
36	6e−05	4 / 4	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
37	7e−05	84 / 621	BP	negative regulation of transcription from RNA polymerase II promoter
38	8e−05	120 / 958	Colon	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
39	8e−05	8 / 18	BP	regulation of muscle contraction
40	8e−05	13 / 44	CC	sarcomere

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	10 / 107	HORVATH_aging_genes meth UP
2	0.6	4 / 47	TESCHENDORFF_age_hypermethylated
3	0.9	5 / 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	5e−08	16 / 38	muscle filament sliding
2	1e−06	15 / 41	cardiac muscle contraction
3	2e−05	11 / 29	sarcomere organization
4	2e−05	9 / 20	striated muscle contraction
5	7e−05	84 / 621	negative regulation of transcription from RNA polymerase II promoter
6	8e−05	8 / 18	regulation of muscle contraction
7	4e−04	197 / 1764	regulation of transcription, DNA−templated
8	6e−04	185 / 1655	transcription, DNA−templated
9	6e−04	11 / 40	protein K48−linked ubiquitination
10	7e−04	19 / 95	muscle contraction
11	1e−03	5 / 10	histone H2A monoubiquitination
12	1e−03	5 / 10	respiratory burst
13	1e−03	5 / 10	UV−damage excision repair
14	1e−03	8 / 25	gastrulation
15	2e−03	5 / 11	membrane depolarization during cardiac muscle cell action potential

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	5 / 12	HLA2_signature
2	0.012	3 / 6	ZHANG_MGUS up
3	0.023	17 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.031	4 / 14	GUSTAFSON_PI3K_DN
5	0.055	2 / 14	LIU_COMMON_CANCER_GENES
6	0.069	3 / 11	GENTLES_modul14
7	0.103	7 / 45	KUIPER_MM poor survival
8	0.124	3 / 14	LIU_PROSTATE_CANCER_DN
9	0.145	3 / 15	BEN−PORATH_UP
10	0.180	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.190	2 / 9	WANG_ER_DN
12	0.242	6 / 47	PanCan_TGF−B_geneset_nanostring
13	0.293	2 / 12	LIU_BREAST_CANCER
14	0.304	5 / 41	PanCan_DNARepair_geneset_nanostring
15	0.321	4 / 32	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	4e−06	10 / 21	muscle myosin complex
2	8e−05	13 / 44	sarcomere
3	9e−05	11 / 33	myofibril
4	2e−04	21 / 101	Z disc
5	2e−04	49 / 326	nuclear speck
6	3e−04	8 / 21	M band
7	6e−04	7 / 18	myosin filament
8	9e−04	18 / 90	nuclear matrix
9	3e−03	10 / 42	sarcoplasmic reticulum
10	4e−03	8 / 30	SCF ubiquitin ligase complex
11	8e−03	5 / 15	A band
12	8e−03	5 / 15	contractile fiber
13	9e−03	13 / 70	nucleosome
14	1e−02	26 / 180	actin cytoskeleton
15	1e−02	7 / 28	microtubule associated complex

Chr

Rank	p−value	#in/all	Geneset
1	0.002	29 / 184	Chr 18
2	0.004	68 / 554	Chr 5
3	0.015	65 / 556	Chr X
4	0.071	45 / 403	Chr 14
5	0.146	60 / 585	Chr 7
6	0.179	16 / 139	Chr 21
7	0.181	77 / 776	Chr 17
8	0.254	25 / 242	Chr 13
9	0.257	37 / 369	Chr 20
10	0.295	53 / 548	Chr 16
11	0.400	77 / 833	Chr 19
12	0.463	45 / 492	Chr 9
13	0.504	62 / 689	Chr 3
14	0.601	38 / 437	Chr 8
15	0.613	33 / 382	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−11	436 / 3767	Bcells peripheral blood_6_EnhG
2	1e−07	275 / 2325	HSC_8_ZNF_Rpts
3	6e−07	497 / 4683	Overlap_fetal_midbrain_HetRpts
4	1e−06	299 / 2626	8_ZNF_Rpts_ESC_Mesoderm
5	1e−06	710 / 7066	Overlap_fetal_midbrain_ReprPCWk
6	5e−06	668 / 6643	5_Tx_Skeletal_Muscle
7	7e−06	615 / 6068	4_Tx_ESC_Endoderm
8	1e−05	473 / 4528	T CD8+ naive cells peripheral blood_4_Tx
9	2e−05	663 / 6637	Tcells peripheral blood_5_TxWk
10	2e−05	563 / 5527	Tregulatory cells peripheral blood_4_Tx
11	2e−05	579 / 5716	Bcells peripheral blood_4_Tx
12	3e−05	582 / 5766	natural killer cells peripheral blood_4_Tx
13	6e−05	659 / 6651	Thelper cells peripheral blood_5_TxWk
14	7e−05	564 / 5601	Thelper cells peripheral blood_4_Tx
15	9e−05	374 / 3554	8_ZNF_Rpts_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−13	179 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	1e−10	675 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
3	2e−08	82 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
4	4e−08	158 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
5	2e−05	111 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
6	8e−05	120 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
7	3e−03	67 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
8	4e−03	40 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
9	1e−02	110 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
10	2e−02	94 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
11	4e−02	2 / 4	Juehling−MSI−enriched−in−8−to−9
12	5e−02	4 / 16	Vilar_non−hypermutated−in−CRC
13	5e−02	6 / 31	Marisa_CRC−cluster−c
14	7e−02	5 / 25	Ang_CRC−CIMPH−vs−L_hypo
15	9e−02	2 / 6	Juehling_HNPCC−mutated−in−5

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	7 / 21	Barbus_GBM_STS_vs._LTS
2	0.002	13 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.013	4 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
4	0.023	36 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
5	0.028	5 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
6	0.036	49 / 423	Down_a
7	0.042	5 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
8	0.051	67 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	0.054	9 / 55	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
10	0.069	3 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
11	0.074	10 / 67	Weller_LGG_1p19qDel−vs−intact_UP
12	0.106	150 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
13	0.123	7 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	0.145	3 / 15	neurons_glio
15	0.154	5 / 32	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−16	26 / 47	RICKMAN_HEAD_AND_NECK_CANCER_F
2	5e−11	217 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
3	1e−08	19 / 49	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
4	1e−07	13 / 27	REACTOME_STRIATED_MUSCLE_CONTRACTION
5	2e−07	20 / 61	KUNINGER_IGF1_VS_PDGFB_TARGETS_UP
6	5e−07	55 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
7	3e−06	113 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
8	3e−06	34 / 165	THUM_SYSTOLIC_HEART_FAILURE_DN
9	5e−06	38 / 198	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
10	7e−06	12 / 31	CHEMELLO_SOLEUS_VS_EDL_MYOFIBERS_UP
11	8e−06	9 / 18	HUMMERICH_BENIGN_SKIN_TUMOR_DN
12	1e−05	7 / 11	DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4
13	2e−05	14 / 45	REACTOME_MUSCLE_CONTRACTION
14	2e−05	69 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
15	3e−05	8 / 16	HUMMERICH_MALIGNANT_SKIN_TUMOR_DN

HM

Rank	p−value	#in/all	Geneset
1	5e−08	42 / 194	HALLMARK_MYOGENESIS
2	2e−01	22 / 195	HALLMARK_KRAS_SIGNALING_DN
3	2e−01	16 / 141	HALLMARK_UV_RESPONSE_DN
4	4e−01	4 / 34	HALLMARK_APICAL_SURFACE
5	4e−01	4 / 35	HALLMARK_HEDGEHOG_SIGNALING
6	5e−01	4 / 39	HALLMARK_PANCREAS_BETA_CELLS
7	5e−01	16 / 173	HALLMARK_MITOTIC_SPINDLE
8	5e−01	3 / 29	HALLMARK_NOTCH_SIGNALING
9	5e−01	9 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	6e−01	17 / 193	HALLMARK_HEME_METABOLISM
11	6e−01	17 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	6e−01	8 / 97	HALLMARK_PEROXISOME
13	7e−01	3 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	7e−01	4 / 51	HALLMARK_TGF_BETA_SIGNALING
15	7e−01	14 / 174	HALLMARK_APICAL_JUNCTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.04	2 / 4	Angelova_CRC_MHC_class_II
2	0.16	2 / 8	Immunity_HLA−class−II
3	0.22	2 / 10	Angelova_immune−metagene−TFH
4	0.25	1 / 3	Angelova_CRC_MHC_class_I
5	0.26	4 / 29	Angelova_immune−metagene−Th1
6	0.29	2 / 12	Angelova_immune−metagene−effector_memory_CD4
7	0.29	2 / 12	Angelova_immune−metagene−NK56_dim
8	0.33	2 / 13	Angelova_immune−metagene−activated_B−cells
9	0.33	2 / 13	Angelova_immune−metagene−immature_B−cells
10	0.34	3 / 23	Angelova_immune−metagene−Th2
11	0.49	2 / 18	Angelova_immune−metagene−pDC
12	0.57	2 / 21	Angelova_immune−metagene−central_memory_CD4
13	0.61	1 / 10	Angelova_immune−metagene−neutrophils
14	0.64	1 / 11	Angelova_immune−metagene−macrophages
15	0.67	3 / 38	Angelova_immune−metagene−mast−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	3 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.3	3 / 22	DUMEAUX_Fasting enriched genes
3	0.3	4 / 32	Marjolein_ageing−genes_DN
4	0.3	21 / 210	Homuth_BMI−associated−genes_DN
5	0.6	1 / 10	DUMEAUX_Smoking literature genes up
6	0.7	5 / 62	DUMEAUX_Smoking enriched genes
7	0.7	1 / 12	DUMEAUX_Women normal BMI literature genes up
8	0.7	1 / 13	Huan_blood−pressure_DBP−signature
9	0.8	11 / 150	Homuth_BMI−associated−genes_UP
10	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
15	1.0	0 / 22	DUMEAUX_High bmi enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	534 / 5404	HOPP_Strong_enhancer
2	0.001	544 / 5529	HOPP_Txn_elongation
3	0.002	427 / 4261	HOPP_Txn_transition
4	0.006	10 / 45	Monti_BCR_cluster
5	0.007	36 / 263	SPANG_CD40 6hrs UP
6	0.009	8 / 34	TARTE_B−cell signature
7	0.011	567 / 5908	HOPP_Active_promoter
8	0.020	46 / 378	TARTE_Mature plasma cell signature
9	0.046	14 / 96	SPANG_LPS 6hrs UP
10	0.050	416 / 4357	HOPP_Weak_txn
11	0.079	28 / 237	ZHANG_DLBCL mutated
12	0.163	25 / 227	SPANG_IL21 UP
13	0.169	5 / 33	Subero_T−PLL_hypo_meth
14	0.182	524 / 5682	HOPP_Weak_promoter
15	0.186	89 / 906	SPANG_BCR DN

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−04	9 / 24	Tirosh_B−cell specific genes−melanoma
2	5e−03	32 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	8e−03	2 / 2	Melanoma Epi−Enzyme Cluster 1
4	5e−02	5 / 23	Melanoma Epi−Enzyme Cluster 7
5	2e−01	1 / 2	Melanoma Epi−Enzyme Cluster 2
6	3e−01	8 / 68	Tirosh_housekeeping_genes
7	3e−01	24 / 236	Gerber_wt/wt_group3−specific
8	4e−01	20 / 204	Landsberg_dedifferentiation_down
9	4e−01	4 / 37	Hugo_melanoma−all−MET_DN
10	5e−01	4 / 39	Tirosh_top50 correlated genes PC4
11	5e−01	10 / 107	Tirosh_Exhaustion program in Mel75
12	5e−01	21 / 230	Gerber_wt/wt_melanoma−cells−SpotC
13	5e−01	6 / 65	Harbst_melanoma_highgrade_up
14	6e−01	1 / 9	Joensson_Melanoma Pigmentation subtype
15	6e−01	7 / 81	Tirosh_Genes in the MITF program

MF

Rank	p−value	#in/all	Geneset
1	3e−08	17 / 41	structural constituent of muscle
2	7e−04	173 / 1541	DNA binding
3	1e−03	42 / 291	actin binding
4	2e−03	35 / 237	ubiquitin−protein transferase activity
5	3e−03	100 / 852	nucleic acid binding
6	4e−03	5 / 13	arachidonic acid epoxygenase activity
7	4e−03	5 / 13	muscle alpha−actinin binding
8	5e−03	10 / 44	methylated histone binding
9	7e−03	43 / 329	RNA polymerase II proximal promoter sequence−specific DNA binding
10	1e−02	6 / 22	histone demethylase activity
11	1e−02	4 / 11	titin binding
12	1e−02	32 / 239	protein domain specific binding
13	2e−02	10 / 52	chromatin DNA binding
14	2e−02	10 / 52	protein transporter activity
15	2e−02	27 / 196	microtubule binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−05	23 / 99	hsa−miR−664
2	3e−04	47 / 312	hsa−miR−301b
3	3e−04	31 / 181	hsa−miR−181a
4	4e−04	29 / 167	hsa−miR−181c
5	4e−04	12 / 45	hsa−miR−891b
6	6e−04	52 / 368	hsa−miR−301a
7	8e−04	18 / 89	hsa−miR−624
8	9e−04	44 / 303	hsa−miR−454
9	1e−03	27 / 160	hsa−miR−330−3p
10	2e−03	16 / 80	hsa−miR−590−5p
11	3e−03	16 / 84	hsa−miR−1284
12	3e−03	43 / 315	hsa−miR−144
13	3e−03	18 / 101	hsa−miR−515−3p
14	4e−03	16 / 86	hsa−miR−297
15	4e−03	8 / 30	hsa−miR−518b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	10 / 54	Burnham_timecourse
2	0.16	6 / 41	Scicluna_DN
3	0.44	17 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	0.74	5 / 68	Burnham_sep_vs_con_UP
5	0.77	5 / 71	Burnham_cap_fp_vs_con_UP
6	0.82	1 / 18	Scicluna_UP
7	0.82	3 / 48	Burnham_cap_fp_vs_con_DN
8	0.82	3 / 48	Burnham_viral_DN
9	0.89	3 / 56	Burnham_sep_vs_con_DN
10	0.93	8 / 135	Terre_MSV_multiple_respiratory_viruses_up
11	0.95	2 / 52	Burnham_day1_vs_5_DN
12	0.97	2 / 57	Burnham_viral_UP
13	0.97	2 / 57	Burnham_day1_vs_5_UP
14	1.00	2 / 122	Terre_IMS_influenza_meta_signature
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−15	34 / 83	WIRTH_Muscle
2	3e−08	29 / 106	Chaussabel_2,11_Replication
3	2e−07	10 / 16	WIRTH_Hippocampus
4	3e−07	56 / 310	Chaussabel_3,4_Protein phosphatases
5	5e−06	58 / 355	PROTEINATLAS_skeletal muscle
6	3e−04	32 / 188	Chaussabel_3,8_Enzymes
7	9e−04	17 / 83	Chaussabel_1,7_MHC Ribosomal proteins
8	2e−03	25 / 152	VAQUERIZAS_General_TF
9	4e−03	31 / 209	Chaussabel_2,5_Immune related molecules
10	4e−03	7 / 24	VAQUERIZAS_Pituitary_TF
11	7e−03	61 / 496	PROTEINATLAS_spleen
12	9e−03	49 / 390	PROTEINATLAS_ovary
13	1e−02	6 / 22	Chaussabel_1,6_Signaling molecules
14	1e−02	69 / 593	PROTEINATLAS_lateral ventricle
15	2e−02	31 / 233	PROTEINATLAS_smooth muscle

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	2 / 13	Alternative lengthening of telomeres
2	0.7	2 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	303 / 3121	ICGC_Egr1_targets
2	0.05	311 / 3213	ICGC_Pu1_targets
3	0.06	212 / 2150	ICGC_Irf4_targets
4	0.16	107 / 1089	ICGC_Ets1_targets
5	0.18	321 / 3435	ICGC_Ebfsc137065_targets
6	0.21	390 / 4212	ICGC_Pol2_targets
7	0.22	318 / 3420	ICGC_Bclaf101388_targets
8	0.22	337 / 3630	ICGC_Sp1_targets
9	0.23	183 / 1941	ICGC_Bcl3_targets
10	0.24	330 / 3564	ICGC_Taf1_targets
11	0.26	333 / 3608	ICGC_Tcf12_targets
12	0.27	142 / 1508	ICGC_Mef2_targets
13	0.28	148 / 1578	ICGC_GabpPcr2_targets
14	0.32	97 / 1032	ICGC_Usf1_targets
15	0.32	152 / 1636	ICGC_Bcl11_targets

K−Means Cluster

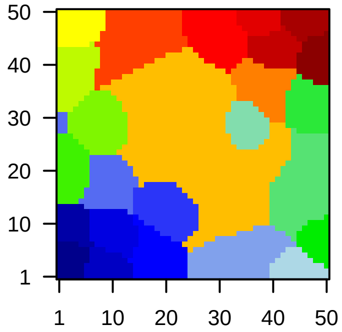
Spot Summary: K

metagenes = 88
genes = 675

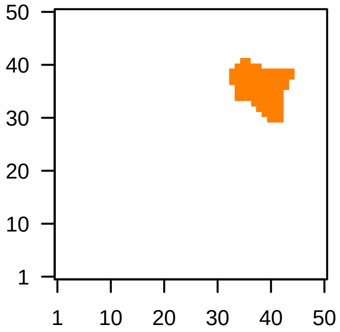
<r> metagenes = 0.78
<r> genes = 0.13
beta: r2= 1.06 / log p= −Inf

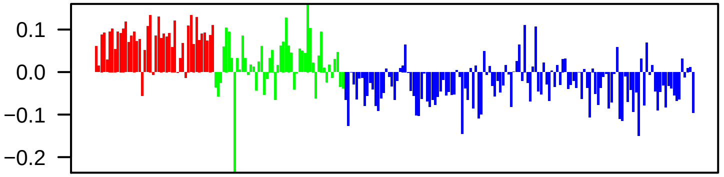
samples with spot = 1 (0.5 %)
intermediate : 1 (2.1 %)

Overview Map



Spot





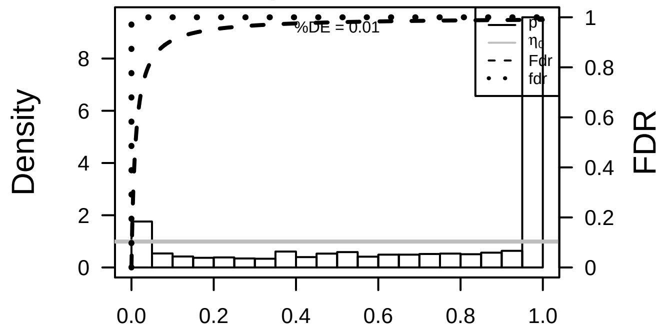
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206424_at	2.81	−0.68	0.37	CYP26A1	cytochrome P450 family 26 subfamily A member 1 [Source:H
2	204550_x_at	2.33	−1.15	0.16	GSTM4	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
3	204281_at	2.28	−1.06	0.27	TEAD4	TEA domain transcription factor 4 [Source:HGNC Symbol;Ac
4	203962_s_at	2.23	−1.27	0.23	NEBL	nebulette [Source:HGNC Symbol;Acc:HGNC:16932]
5	215333_x_at	2.19	−1.28	0.18	GSTM4	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
6	204418_x_at	2.18	−1.41	0.19	GSTM4	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
7	210445_at	2.14	−0.95	0.23	FABP6	fatty acid binding protein 6 [Source:HGNC Symbol;Acc:HGN
8	204099_at	1.93	−0.74	0.07	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulat
9	209859_at	1.78	−0.9	0.25	TRIM9	tripartite motif containing 9 [Source:HGNC Symbol;Acc:HGN
10	203961_at	1.76	−0.66	0.32	NEBL	nebulette [Source:HGNC Symbol;Acc:HGNC:16932]
11	220051_at	1.68	−0.94	0.09	PRSS21	serine protease 21 [Source:HGNC Symbol;Acc:HGNC:9485]
12	214862_x_at	1.68	−0.7	0.42		
13	32137_at	1.53	−0.57	0.26	JAG2	jagged 2 [Source:HGNC Symbol;Acc:HGNC:6189]
14	211829_s_at	1.53	−0.82	0.36	GPER1	G protein−coupled estrogen receptor 1 [Source:HGNC Symb
15	207164_s_at	1.52	−1.06	0.18	ZBTB18	zinc finger and BTB domain containing 18 [Source:HGNC Sy
16	209784_s_at	1.5	−0.74	0.32	JAG2	jagged 2 [Source:HGNC Symbol;Acc:HGNC:6189]
17	206492_at	1.49	−0.86	0.24	FHIT	fragile histidine triad [Source:HGNC Symbol;Acc:HGNC:3701
18	220277_at	1.47	−0.77	0.23	CXXC4	CXXC finger protein 4 [Source:HGNC Symbol;Acc:HGNC:24
19	206264_at	1.45	−0.76	0.43	GPLD1	glycosylphosphatidylinositol specific phospholipase D1 [Sour
20	221868_at	1.42	−0.96	0.4	PAIP2B	poly(A) binding protein interacting protein 2B [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−53	180 / 1161	MF	RNA binding
2	2e−47	78 / 232	BP	translation
3	5e−38	49 / 105	Refer	Chaussabel_2,4_Ribosomal proteins
4	8e−37	49 / 110	BP	translational initiation
5	3e−34	40 / 75	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
6	4e−34	176 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
7	6e−32	45 / 110	GSEA	REACTOME_TRANSLATION
8	7e−30	53 / 174	BP	rRNA processing
9	1e−28	94 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
10	3e−28	63 / 268	CC	intracellular ribonucleoprotein complex
11	1e−27	38 / 90	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
12	2e−27	41 / 109	MF	structural constituent of ribosome
13	2e−26	32 / 64	BP	SRP−dependent cotranslational protein targeting to membrane
14	5e−26	30 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
15	3e−24	33 / 78	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
16	4e−24	64 / 325	GSEA	REACTOME_METABOLISM_OF_PROTEINS
17	4e−24	49 / 190	HM	HALLMARK_MYC_TARGETS_V1
18	5e−24	29 / 58	GSEA	KEGG_RIBOSOME
19	2e−23	31 / 71	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
20	3e−23	33 / 83	BP	viral transcription
21	9e−23	41 / 139	CC	ribosome
22	2e−22	305 / 4261	Lymph	HOPP_Txn_transition
23	3e−22	24 / 41	CC	cytosolic large ribosomal subunit
24	3e−21	362 / 5529	Lymph	HOPP_Txn_elongation
25	3e−21	61 / 335	GSEA	HSIAO_HOUSEKEEPING_GENES
26	4e−21	81 / 561	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
27	2e−20	23 / 42	GSEA	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
28	2e−20	46 / 200	GSEA	REACTOME_METABOLISM_OF_RNA
29	7e−20	41 / 163	GSEA	REACTOME_METABOLISM_OF_MRNA
30	9e−20	29 / 77	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
31	9e−19	32 / 103	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
32	1e−18	29 / 83	Refer	Chaussabel_1,7_MHC Ribosomal proteins
33	9e−18	22 / 47	GSEA	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
34	5e−17	129 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
35	1e−16	20 / 41	GSEA	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_
36	2e−16	85 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
37	3e−16	18 / 33	GSEA	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
38	4e−16	111 / 1107	TF	ICGC_Myc_targets
39	4e−16	16 / 25	BP	cytoplasmic translation
40	6e−16	114 / 1161	Refer	PROTEINATLAS_colon

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	5 / 92	HORVATH_aging_genes meth DOWN
2	0.7	4 / 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−47	78 / 232	translation
2	8e−37	49 / 110	translational initiation
3	7e−30	53 / 174	rRNA processing
4	1e−27	38 / 90	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
5	2e−26	32 / 64	SRP−dependent cotranslational protein targeting to membrane
6	3e−23	33 / 83	viral transcription
7	4e−16	16 / 25	cytoplasmic translation
8	1e−11	34 / 198	mRNA splicing, via spliceosome
9	8e−11	36 / 233	RNA splicing
10	1e−10	40 / 281	mRNA processing
11	3e−08	12 / 36	tRNA aminoacylation for protein translation
12	3e−08	17 / 76	ribosome biogenesis
13	4e−08	7 / 10	IRES−dependent viral translational initiation
14	5e−08	11 / 31	protein targeting to mitochondrion
15	8e−07	12 / 47	mRNA 3'−end processing

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 14	GENTLES_modul10
2	1e−03	7 / 36	ZHANG_MM up
3	5e−03	4 / 16	WOLFER_overlap genes
4	1e−01	2 / 15	RHODES_CANCER_META_SIGNATURE
5	1e−01	2 / 13	GENTLES_modul1
6	1e−01	2 / 14	LIU_COMMON_CANCER_GENES
7	1e−01	2 / 14	BENTINK_src.2
8	1e−01	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
9	1e−01	2 / 15	GENTLES_modul4
10	1e−01	2 / 15	GENTLES_modul7
11	2e−01	2 / 16	GENTLES_modul6
12	2e−01	2 / 18	PanCan_Notch_geneset_nanostring
13	3e−01	4 / 58	SHAUGHNESSY_MM high risk
14	4e−01	2 / 28	PanCan_HK_geneset_nanostring
15	4e−01	1 / 10	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	3e−28	63 / 268	intracellular ribonucleoprotein complex
2	9e−23	41 / 139	ribosome
3	3e−22	24 / 41	cytosolic large ribosomal subunit
4	3e−15	116 / 1221	mitochondrion
5	1e−13	74 / 653	nucleolus
6	7e−13	186 / 2541	nucleoplasm
7	8e−11	10 / 15	eukaryotic translation initiation factor 3 complex
8	1e−10	44 / 330	mitochondrial inner membrane
9	2e−10	11 / 20	small ribosomal subunit
10	7e−10	240 / 3805	cytosol
11	7e−10	13 / 33	cytosolic small ribosomal subunit
12	3e−09	275 / 4579	nucleus
13	1e−08	23 / 128	spliceosomal complex
14	3e−08	35 / 277	mitochondrial matrix
15	5e−08	9 / 19	polysomal ribosome

Chr

Rank	p−value	#in/all	Geneset
1	0.003	48 / 700	Chr 12
2	0.003	39 / 548	Chr 16
3	0.004	41 / 585	Chr 7
4	0.007	53 / 833	Chr 19
5	0.092	32 / 554	Chr 5
6	0.120	20 / 333	Chr 22
7	0.225	26 / 490	Chr 10
8	0.282	21 / 403	Chr 14
9	0.301	13 / 242	Chr 13
10	0.407	62 / 1325	Chr 1
11	0.441	7 / 139	Chr 21
12	0.559	2 / 41	Chr Y
13	0.606	16 / 369	Chr 20
14	0.624	24 / 556	Chr X
15	0.794	19 / 492	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−32	486 / 7833	Bcells peripheral blood_1_TssA
2	3e−31	468 / 7420	Tcells peripheral blood_1_TssA
3	3e−30	491 / 8068	Thelper cells peripheral blood_1_TssA
4	3e−29	210 / 2204	3_TxFlnk_ESC_Mesoderm
5	6e−29	483 / 7930	Tregulatory cells peripheral blood_1_TssA
6	6e−29	484 / 7957	Tcells peripheral blood_2_TssAFlnk
7	4e−28	499 / 8406	Bcells peripheral blood_2_TssAFlnk
8	1e−26	329 / 4528	T CD8+ naive cells peripheral blood_4_Tx
9	2e−26	466 / 7635	monocytes peripheral blood_1_TssA
10	3e−26	496 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
11	3e−26	489 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
12	4e−26	453 / 7331	TssA_Colon
13	4e−26	487 / 8200	monocytes peripheral blood_2_TssAFlnk
14	2e−25	490 / 8322	T CD8+ naive cells peripheral blood_1_TssA
15	3e−25	444 / 7165	Tx_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−21	81 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	5e−17	129 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
3	2e−14	72 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	9e−06	115 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
5	7e−04	19 / 184	Kosinski_lower−crypt−long−list
6	5e−03	72 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	5e−02	2 / 8	KIM_MSI−in−EC
8	7e−02	2 / 10	KIM_CRC−MSI−regulated_DN
9	1e−01	2 / 12	Juehling_HNPCC−mutated−in−4
10	1e−01	2 / 12	Juehling−MSI−enriched−in−6
11	2e−01	29 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
12	2e−01	2 / 18	Boland_CRC−MSI−A6−A10
13	2e−01	55 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	2e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
15	3e−01	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes

Glioma

Rank	p−value	#in/all	Geneset
1	0.001	9 / 58	Stuehler_Proteins_up_in_STS
2	0.009	88 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	0.011	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	0.015	24 / 330	Up
5	0.017	7 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	0.017	77 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	0.027	5 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
8	0.048	2 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
9	0.066	36 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	0.072	2 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
11	0.130	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
12	0.162	2 / 16	VERHAAK_CL subtype
13	0.189	4 / 50	Vishal_subnetwork signature of survival in GBM
14	0.201	23 / 421	Down_b
15	0.237	4 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−34	40 / 75	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
2	4e−34	176 / 1527	PUJANA_BRCA1_PCC_NETWORK
3	6e−32	45 / 110	REACTOME_TRANSLATION
4	1e−28	94 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
5	5e−26	30 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	3e−24	33 / 78	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EX
7	4e−24	64 / 325	REACTOME_METABOLISM_OF_PROTEINS
8	5e−24	29 / 58	KEGG_RIBOSOME
9	2e−23	31 / 71	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICA
10	3e−21	61 / 335	HSIAO_HOUSEKEEPING_GENES
11	2e−20	23 / 42	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
12	2e−20	46 / 200	REACTOME_METABOLISM_OF_RNA
13	7e−20	41 / 163	REACTOME_METABOLISM_OF_MRNA
14	9e−20	29 / 77	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGE
15	9e−19	32 / 103	REACTOME_INFLUENZA_LIFE_CYCLE

HM

Rank	p−value	#in/all	Geneset
1	4e−24	49 / 190	HALLMARK_MYC_TARGETS_V1
2	5e−13	35 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	1e−03	19 / 192	HALLMARK_MTORC1_SIGNALING
4	2e−03	17 / 174	HALLMARK_ADIPOGENESIS
5	2e−02	12 / 133	HALLMARK_DNA_REPAIR
6	2e−02	10 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	4e−02	6 / 55	HALLMARK_MYC_TARGETS_V2
8	1e−01	12 / 187	HALLMARK_E2F_TARGETS
9	2e−01	12 / 195	HALLMARK_G2M_CHECKPOINT
10	3e−01	8 / 139	HALLMARK_FATTY_ACID_METABOLISM
11	4e−01	5 / 94	HALLMARK_PROTEIN_SECRETION
12	4e−01	5 / 97	HALLMARK_PEROXISOME
13	5e−01	9 / 193	HALLMARK_HEME_METABOLISM
14	6e−01	2 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	7e−01	5 / 122	HALLMARK_SPERMATOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	2 / 19	Angelova_immune−metagene−activated_CD8
2	0.3	2 / 23	Angelova_immune−metagene−Treg
3	0.3	1 / 8	Angelova_immune−metagene−mDC
4	0.7	1 / 26	Angelova_immune−metagene−activated_CD4
5	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
6	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.0	0 / 25	Angelova_immune−metagene−DC
10	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.0	0 / 14	Angelova_immune−metagene−eosinophil
13	1.0	0 / 19	Angelova_immune−metagene−iDC
14	1.0	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.0	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−09	26 / 150	Homuth_BMI−associated−genes_UP
2	2e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	2e−01	3 / 32	Marjolein_ageing−genes_DN
4	2e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	7e−01	8 / 210	Homuth_BMI−associated−genes_DN
6	8e−01	2 / 62	DUMEAUX_Smoking enriched genes
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 22	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 22	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−22	305 / 4261	HOPP_Txn_transition
2	3e−21	362 / 5529	HOPP_Txn_elongation
3	3e−14	357 / 5908	HOPP_Active_promoter
4	6e−07	315 / 5682	HOPP_Weak_promoter
5	3e−04	28 / 305	TARTE_Plasmablast signature
6	2e−03	7 / 40	CARO_OxPhos_in_DLBCL_UP
7	6e−03	3 / 9	YAMANE_AICDA_targets_nonrecruited
8	1e−02	6 / 42	Monti_OxPhos_cluster
9	2e−02	268 / 5404	HOPP_Strong_enhancer
10	1e−01	3 / 25	ROSOLOWSKI_red UP
11	1e−01	2 / 15	DAVE_BL Inter
12	2e−01	47 / 906	SPANG_BCR DN
13	2e−01	8 / 121	ROSOLOWSKI_green total
14	2e−01	2 / 18	SPANG_BAFF 9hrs UP
15	2e−01	6 / 88	ROSOLOWSKI_green UP

Melanoma

Rank	p−value	#in/all	Geneset
1	8e−16	24 / 68	Tirosh_housekeeping_genes
2	6e−07	11 / 38	Tirosh_top50 correlated genes PC1
3	8e−06	30 / 276	Gerber_wt/wt_melanoma−cells−SpotB
4	2e−02	15 / 189	Tirosh_genes preferentially expressed by Tregs
5	8e−02	3 / 23	Melanoma Epi−Enzyme Cluster 7
6	1e−01	1 / 3	Melanoma Epi−Enzyme Cluster 4
7	2e−01	1 / 4	Melanoma Epi−Enzyme Cluster 3
8	3e−01	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
9	4e−01	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
10	4e−01	11 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	5e−01	1 / 16	Hugo_melanoma−all−LEF1_UP
12	7e−01	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma
13	7e−01	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
14	7e−01	3 / 81	Tirosh_Genes in the MITF program
15	7e−01	4 / 107	Tirosh_Exhaustion program in Mel75

MF

Rank	p−value	#in/all	Geneset
1	1e−53	180 / 1161	RNA binding
2	2e−27	41 / 109	structural constituent of ribosome
3	1e−11	17 / 48	translation initiation factor activity
4	9e−07	10 / 32	aminoacyl−tRNA ligase activity
5	2e−06	10 / 35	rRNA binding
6	6e−06	67 / 852	nucleic acid binding
7	1e−05	15 / 90	unfolded protein binding
8	2e−05	16 / 107	mRNA binding
9	3e−05	18 / 132	methyltransferase activity
10	3e−05	6 / 15	cofactor binding
11	4e−05	402 / 7864	protein binding
12	1e−04	10 / 53	ATP−dependent RNA helicase activity
13	7e−04	7 / 34	tRNA binding
14	7e−04	8 / 44	mRNA 3'−UTR binding
15	1e−03	13 / 106	ligase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	12 / 81	hsa−miR−544
2	1e−03	8 / 47	hsa−miR−1200
3	3e−03	10 / 78	hsa−miR−216b
4	3e−03	8 / 54	hsa−miR−1184
5	3e−03	14 / 134	hsa−miR−323b−5p
6	3e−03	18 / 194	hsa−miR−124
7	4e−03	23 / 278	hsa−let−7d
8	5e−03	19 / 217	hsa−miR−577
9	5e−03	4 / 16	hsa−miR−563
10	5e−03	23 / 284	hsa−miR−548d−5p
11	5e−03	23 / 285	hsa−miR−548b−5p
12	6e−03	5 / 26	hsa−miR−127−3p
13	6e−03	15 / 160	hsa−miR−330−3p
14	6e−03	7 / 49	hsa−miR−30e*
15	9e−03	13 / 136	hsa−miR−511

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	11 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.3	7 / 122	Terre_IMS_influenza_meta_signature
3	0.4	2 / 33	Sweeney_viral_dn
4	0.6	2 / 41	Scicluna_DN
5	0.7	2 / 57	Burnham_day1_vs_5_UP
6	0.9	1 / 48	Burnham_viral_DN
7	0.9	1 / 54	Burnham_timecourse
8	0.9	1 / 57	Burnham_viral_UP
9	0.9	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
10	1.0	0 / 68	Burnham_sep_vs_con_UP
11	1.0	0 / 56	Burnham_sep_vs_con_DN
12	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
13	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
14	1.0	0 / 52	Burnham_day1_vs_5_DN
15	1.0	0 / 18	Scicluna_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−38	49 / 105	Chaussabel_2,4_Ribosomal proteins
2	1e−18	29 / 83	Chaussabel_1,7_MHC Ribosomal proteins
3	6e−16	114 / 1161	PROTEINATLAS_colon
4	1e−15	80 / 677	PROTEINATLAS_esophagus
5	5e−15	94 / 893	PROTEINATLAS_pancreas
6	1e−14	91 / 861	PROTEINATLAS_nasopharynx
7	4e−14	87 / 819	PROTEINATLAS_bronchus
8	3e−13	102 / 1076	PROTEINATLAS_stomach
9	3e−13	100 / 1048	PROTEINATLAS_rectum
10	5e−13	101 / 1072	PROTEINATLAS_duodenum
11	2e−12	85 / 848	PROTEINATLAS_adrenal gland
12	2e−12	67 / 592	PROTEINATLAS_seminal vesicle
13	3e−12	67 / 593	PROTEINATLAS_lateral ventricle
14	3e−12	82 / 809	PROTEINATLAS_fallopian tube
15	3e−12	67 / 594	PROTEINATLAS_parathyroid gland

Telomeres

Rank	p−value	#in/all	Geneset
1	0.7	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	4e−16	111 / 1107	ICGC_Myc_targets
2	7e−16	119 / 1241	KIM_MYC targets
3	5e−10	123 / 1578	ICGC_GabpPcr2_targets
4	1e−09	227 / 3564	ICGC_Taf1_targets
5	1e−09	90 / 1044	ICGC_Six5_targets
6	3e−08	258 / 4319	ICGC_Pou2_targets
7	7e−08	15 / 62	MYC_Targets UP
8	9e−08	198 / 3150	ICGC_Creb1_targets
9	1e−07	212 / 3451	ICGC_Atf2_targets
10	1e−07	229 / 3796	ICGC_Nficsc81335_targets
11	2e−07	245 / 4131	ICGC_Tcf3_targets
12	3e−07	209 / 3420	ICGC_Bclaf101388_targets
13	5e−07	222 / 3703	ICGC_Foxm1_targets
14	5e−07	218 / 3630	ICGC_Sp1_targets
15	7e−07	181 / 2899	ICGC_Nfatc1_targets

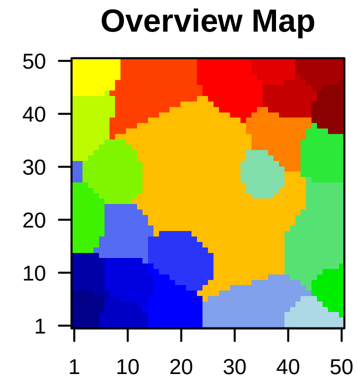
K−Means Cluster

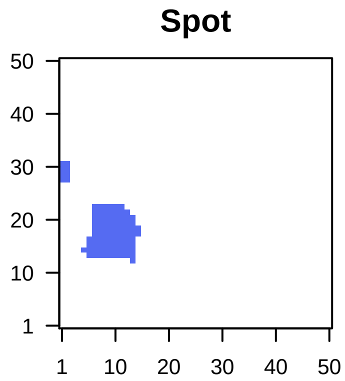
Spot Summary: L

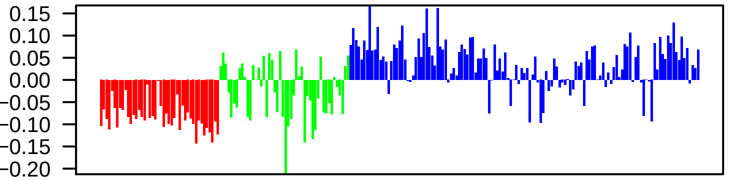
metagenes = 93
genes = 518

<r> metagenes = 0.72
<r> genes = 0.1
beta: r2= 1.08 / log p= −Inf

samples with spot = 3 (1.4 %)
non−mBL : 3 (2.3 %)





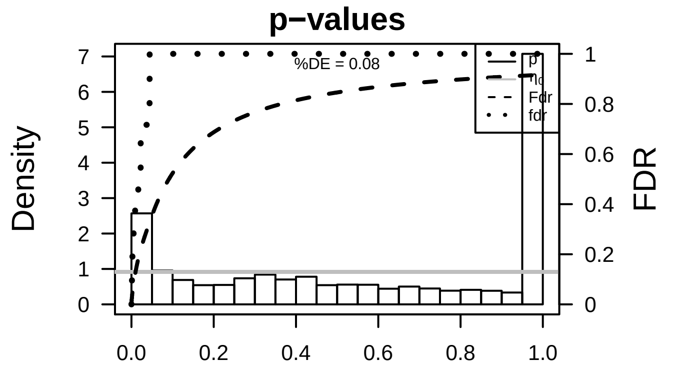


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207901_at	2.53	−0.61	0.27	IL12B	interleukin 12B [Source:HGNC Symbol;Acc:HGNC:5970]
2	211828_s_at	2.43	−0.94	0.43	TNIK	TRAF2 and NCK interacting kinase [Source:HGNC Symbol;A
3	220177_s_at	2.28	−0.71	0.2	TMPRSS3	transmembrane serine protease 3 [Source:HGNC Symbol;Ac
4	219225_at	2.26	−0.75	0.35	PGBD5	piggyBac transposable element derived 5 [Source:HGNC Syr
5	220105_at	2.23	−1.09	0.32	RSPH14	radial spoke head 14 homolog [Source:HGNC Symbol;Acc:H
6	210127_at	2.14	−0.79	0.16	RAB6B	RAB6B, member RAS oncogene family [Source:HGNC Symb
7	210675_s_at	2.13	−0.71	0.31	PTPRR	protein tyrosine phosphatase, receptor type R [Source:HGNC
8	206084_at	2.12	−0.58	0.31	PTPRR	protein tyrosine phosphatase, receptor type R [Source:HGNC
9	204584_at	2.12	−1.05	0.48	L1CAM	L1 cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC
10	214890_s_at	2.09	−0.92	0.35	FAM149A	family with sequence similarity 149 member A [Source:HGNC
11	220384_at	2.07	−0.67	0.05	NME8	NME/NM23 family member 8 [Source:HGNC Symbol;Acc:HG
12	220234_at	1.99	−0.62	0.22	CA8	carbonic anhydrase 8 [Source:HGNC Symbol;Acc:HGNC:138
13	220673_s_at	1.96	−0.53	0.12	PPP4R4	protein phosphatase 4 regulatory subunit 4 [Source:HGNC Sy
14	204587_at	1.92	−1.12	0.13	SLC25A14	solute carrier family 25 member 14 [Source:HGNC Symbol;Ac
15	203798_s_at	1.9	−0.65	0.21	VSNL1	visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
16	214319_at	1.9	−0.68	0.03		
17	207681_at	1.86	−1.01	0.49	CXCR3	C−X−C motif chemokine receptor 3 [Source:HGNC Symbol;A
18	206489_s_at	1.83	−0.43	0.25	DLGAP1	DLG associated protein 1 [Source:HGNC Symbol;Acc:HGNC
19	213651_at	1.82	−0.87	0.13	INPP5J	inositol polyphosphate−5−phosphatase J [Source:HGNC Syn
20	209686_at	1.81	−0.72	0.29	S100B	S100 calcium binding protein B [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−18	281 / 5529	Lymph	HOPP_Txn_elongation
2	1e−17	71 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
3	5e−17	231 / 4261	Lymph	HOPP_Txn_transition
4	7e−16	287 / 5908	Lymph	HOPP_Active_promoter
5	9e−15	207 / 3805	CC	cytosol
6	4e−13	261 / 5404	Lymph	HOPP_Strong_enhancer
7	9e−13	40 / 317	Cance	SPANG_BCL6−index2
8	2e−12	46 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
9	4e−12	72 / 883	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	7e−12	87 / 1190	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
11	7e−12	54 / 564	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
12	7e−12	94 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
13	2e−11	230 / 4701	CC	cytoplasm
14	2e−10	334 / 7864	MF	protein binding
15	4e−10	260 / 5682	Lymph	HOPP_Weak_promoter
16	3e−09	36 / 345	CC	focal adhesion
17	1e−08	38 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
18	3e−08	55 / 726	GSEA	REACTOME_IMMUNE_SYSTEM
19	3e−08	50 / 630	GSEA	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UI
20	5e−08	84 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
21	6e−08	174 / 3564	TF	ICGC_Taf1_targets
22	7e−08	37 / 408	GSEA	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
23	1e−07	43 / 528	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
24	2e−07	91 / 1550	GSEA	PILON_KLF1_TARGETS_DN
25	2e−07	120 / 2239	CC	extracellular exosome
26	2e−07	70 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
27	2e−07	26 / 237	MF	ubiquitin−protein transferase activity
28	2e−07	40 / 479	CC	Golgi membrane
29	3e−07	73 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
30	4e−07	40 / 494	CC	endosome
31	5e−07	17 / 117	BP	autophagy
32	6e−07	60 / 906	Lymph	SPANG_BCR DN
33	6e−07	199 / 4357	Lymph	HOPP_Weak_txn
34	6e−07	40 / 502	BP	protein transport
35	8e−07	61 / 935	GSEA	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
36	1e−06	10 / 42	BP	interleukin−12−mediated signaling pathway
37	1e−06	21 / 182	GSEA	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRE
38	1e−06	15 / 99	GSEA	PID_ERBB1_DOWNSTREAM_PATHWAY
39	2e−06	15 / 100	CC	late endosome
40	2e−06	27 / 282	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.9	2 / 107	HORVATH_aging_genes meth UP
2	1.0	1 / 92	HORVATH_aging_genes meth DOWN
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−07	17 / 117	autophagy
2	6e−07	40 / 502	protein transport
3	1e−06	10 / 42	interleukin−12−mediated signaling pathway
4	2e−06	18 / 143	positive regulation of I−kappaB kinase/NF−kappaB signaling
5	2e−06	17 / 129	Fc−epsilon receptor signaling pathway
6	2e−06	20 / 173	proteasome−mediated ubiquitin−dependent protein catabolic process
7	5e−06	19 / 167	protein polyubiquitination
8	8e−06	7 / 23	viral life cycle
9	1e−05	32 / 403	neutrophil degranulation
10	1e−05	15 / 118	membrane organization
11	3e−05	5 / 12	regulation of necroptotic process
12	5e−05	5 / 13	barbed−end actin filament capping
13	6e−05	15 / 135	T cell receptor signaling pathway
14	7e−05	15 / 136	ER to Golgi vesicle−mediated transport
15	7e−05	10 / 65	vascular endothelial growth factor receptor signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	9e−13	40 / 317	SPANG_BCL6−index2
2	6e−06	20 / 186	SPANG_LPS−index2
3	3e−02	4 / 36	ZHANG_MM up
4	4e−02	9 / 130	PanCan_CC+Apop_geneset_nanostring
5	5e−02	2 / 11	LIU_PROSTATE_CANCER_UP
6	1e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	1e−01	2 / 16	GENTLES_modul16
8	2e−01	2 / 25	PanCan_HH_geneset_nanostring
9	2e−01	1 / 16	LIU_LIVER_CANCER
10	2e−01	4 / 72	PanCan_Wnt_geneset_nanostring
11	3e−01	2 / 28	PanCan_HK_geneset_nanostring
12	3e−01	1 / 10	BENTINK_ras.4
13	3e−01	4 / 80	PanCan_JAK−ST_geneset_nanostring
14	3e−01	6 / 134	PanCan_RAS_geneset_nanostring
15	3e−01	1 / 12	GENTLES_modul12

CC

Rank	p−value	#in/all	Geneset
1	9e−15	207 / 3805	cytosol
2	2e−11	230 / 4701	cytoplasm
3	3e−09	36 / 345	focal adhesion
4	2e−07	120 / 2239	extracellular exosome
5	2e−07	40 / 479	Golgi membrane
6	4e−07	40 / 494	endosome
7	2e−06	15 / 100	late endosome
8	6e−06	13 / 85	late endosome membrane
9	1e−05	19 / 180	actin cytoskeleton
10	1e−05	16 / 134	vesicle
11	7e−05	20 / 219	lysosomal membrane
12	1e−04	9 / 55	phagocytic vesicle
13	1e−04	18 / 192	membrane raft
14	1e−04	54 / 938	Golgi apparatus
15	1e−04	34 / 503	cytoplasmic vesicle

Chr

Rank	p−value	#in/all	Geneset
1	0.005	37 / 689	Chr 3
2	0.017	29 / 556	Chr X
3	0.053	11 / 184	Chr 18
4	0.084	23 / 492	Chr 9
5	0.087	34 / 776	Chr 17
6	0.112	16 / 333	Chr 22
7	0.122	22 / 490	Chr 10
8	0.219	33 / 832	Chr 2
9	0.243	16 / 382	Chr 15
10	0.345	6 / 139	Chr 21
11	0.354	21 / 554	Chr 5
12	0.588	16 / 480	Chr 4
13	0.634	13 / 403	Chr 14
14	0.729	11 / 369	Chr 20
15	0.731	7 / 242	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−32	390 / 8068	Thelper cells peripheral blood_1_TssA
2	2e−30	369 / 7420	Tcells peripheral blood_1_TssA
3	2e−30	375 / 7635	monocytes peripheral blood_1_TssA
4	3e−30	378 / 7751	natural killer cells peripheral blood_1_TssA
5	5e−29	378 / 7833	Bcells peripheral blood_1_TssA
6	1e−27	378 / 7930	Tregulatory cells peripheral blood_1_TssA
7	4e−27	388 / 8322	T CD8+ naive cells peripheral blood_1_TssA
8	3e−26	300 / 5527	Tregulatory cells peripheral blood_4_Tx
9	7e−26	387 / 8370	natural killer cells peripheral blood_2_TssAFlnk
10	1e−25	383 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
11	3e−25	371 / 7835	HSC_1_TssA
12	3e−25	353 / 7225	Overlap_fetal_midbrain_ReprPC
13	1e−24	373 / 7957	Tcells peripheral blood_2_TssAFlnk
14	2e−24	304 / 5753	Tcells peripheral blood_4_Tx
15	2e−24	396 / 8816	Thelper cells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−12	72 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
2	5e−08	84 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
3	2e−07	70 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
4	3e−07	73 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
5	4e−04	3 / 5	Hewish_dMMR−secondary−mutations_Apoptosis
6	1e−03	82 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
7	1e−02	23 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	1e−02	46 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
9	1e−02	3 / 15	TCGA−CRC_less−agressive−disease−markers
10	7e−02	2 / 13	Vilar_hypermutated−in−CRC
11	7e−02	10 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
12	9e−02	4 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	1e−01	2 / 16	Budinska_B_Lower crypt−like_UP
14	1e−01	2 / 18	Boland_CRC−MSI−A6−A10
15	2e−01	4 / 60	Marisa_CRC−cluster−g

Glioma

Rank	p−value	#in/all	Geneset
1	2e−04	70 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	1e−03	23 / 330	Up
3	3e−03	6 / 43	Patel_stemness signatures
4	4e−03	34 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
5	7e−03	70 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	9e−03	3 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
7	4e−02	3 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
8	6e−02	4 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP
9	6e−02	2 / 12	VERHAAK_Brain
10	8e−02	13 / 242	ScoV_0.5_Sturm_C1_IDH_DN
11	1e−01	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
12	1e−01	8 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	1e−01	14 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	1e−01	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−17	71 / 673	SCHLOSSER_SERUM_RESPONSE_DN
2	2e−12	46 / 417	SHEN_SMARCA2_TARGETS_UP
3	7e−12	87 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
4	7e−12	54 / 564	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
5	7e−12	94 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	1e−08	38 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
7	3e−08	55 / 726	REACTOME_IMMUNE_SYSTEM
8	3e−08	50 / 630	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
9	7e−08	37 / 408	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
10	1e−07	43 / 528	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
11	2e−07	91 / 1550	PILON_KLF1_TARGETS_DN
12	8e−07	61 / 935	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
13	1e−06	21 / 182	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRES
14	1e−06	15 / 99	PID_ERBB1_DOWNSTREAM_PATHWAY
15	2e−06	27 / 282	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN

HM

Rank	p−value	#in/all	Geneset
1	9e−05	12 / 94	HALLMARK_PROTEIN_SECRETION
2	1e−04	18 / 192	HALLMARK_MTORC1_SIGNALING
3	1e−04	12 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
4	2e−03	13 / 150	HALLMARK_APOPTOSIS
5	4e−03	6 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
6	4e−03	14 / 182	HALLMARK_GLYCOLYSIS
7	7e−03	13 / 174	HALLMARK_ADIPOGENESIS
8	7e−03	13 / 174	HALLMARK_APICAL_JUNCTION
9	9e−03	13 / 178	HALLMARK_COMPLEMENT
10	3e−02	5 / 51	HALLMARK_TGF_BETA_SIGNALING
11	3e−02	11 / 170	HALLMARK_IL2_STAT5_SIGNALING
12	5e−02	7 / 96	HALLMARK_ANDROGEN_RESPONSE
13	5e−02	7 / 97	HALLMARK_PEROXISOME
14	5e−02	9 / 139	HALLMARK_FATTY_ACID_METABOLISM
15	1e−01	10 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION

Immunome

Rank	p−value	#in/all	Geneset
1	8e−06	7 / 23	Angelova_immune−metagene−monocytes
2	8e−02	2 / 14	Angelova_immune−metagene−eosinophil
3	1e−01	1 / 3	Angelova_CRC_MHC_class_I
4	1e−01	2 / 19	Angelova_immune−metagene−iDC
5	2e−01	2 / 23	Angelova_immune−metagene−Th2
6	2e−01	1 / 8	Angelova_immune−metagene−mDC
7	3e−01	1 / 10	Angelova_immune−metagene−neutrophils
8	3e−01	1 / 10	Angelova_CRC_immonoinhibitors
9	3e−01	1 / 11	Angelova_immune−metagene−macrophages
10	3e−01	1 / 12	Angelova_immune−metagene−effector_memory_CD4
11	3e−01	1 / 12	Angelova_immune−metagene−memory_B−cells
12	5e−01	1 / 18	Angelova_immune−metagene−pDC
13	5e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
14	6e−01	1 / 29	Angelova_immune−metagene−Th1
15	7e−01	2 / 67	Angelova_immune−metagene−T−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−05	20 / 210	Homuth_BMI−associated−genes_DN
2	1e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	1e−01	8 / 150	Homuth_BMI−associated−genes_UP
4	2e−01	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
5	4e−01	3 / 62	DUMEAUX_Smoking enriched genes
6	4e−01	1 / 14	Huan_blood−pressure_SBP−signature
7	5e−01	1 / 22	DUMEAUX_High bmi enriched genes
8	5e−01	1 / 22	DUMEAUX_Fasting enriched genes
9	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
10	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−18	281 / 5529	HOPP_Txn_elongation
2	5e−17	231 / 4261	HOPP_Txn_transition
3	7e−16	287 / 5908	HOPP_Active_promoter
4	4e−13	261 / 5404	HOPP_Strong_enhancer
5	4e−10	260 / 5682	HOPP_Weak_promoter
6	6e−07	60 / 906	SPANG_BCR DN
7	6e−07	199 / 4357	HOPP_Weak_txn
8	6e−03	9 / 97	ROSOLOWSKI_red total
9	2e−02	177 / 4559	HOPP_Weak_enhancer
10	5e−02	5 / 57	SPANG_LPS 6hrs DN
11	6e−02	74 / 1814	HOPP_Repetitive
12	9e−02	2 / 15	Subero_T−ALL_hypo_meth
13	1e−01	12 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
14	1e−01	2 / 18	DAVE_Immune response 2
15	2e−01	2 / 23	Subero_mBL_hypo_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−06	21 / 189	Tirosh_genes preferentially expressed by Tregs
2	1e−03	18 / 230	Gerber_wt/wt_melanoma−cells−SpotC
3	2e−03	17 / 222	Gerber_wt/wt_melanoma−cells−SpotF
4	4e−03	10 / 107	Tirosh_Exhaustion program in Mel75
5	4e−03	29 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	1e−02	5 / 39	Tirosh_melanoma specific genes
7	3e−02	12 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	3e−02	16 / 276	Gerber_wt/wt_melanoma−cells−SpotB
9	7e−02	1 / 2	Melanoma Epi−Enzyme Cluster 2
10	7e−02	6 / 85	Tirosh_AXL−signature
11	8e−02	5 / 68	Tirosh_housekeeping_genes
12	1e−01	2 / 17	Hugo_melanoma−all−MET_UP
13	1e−01	12 / 236	Gerber_wt/wt_group3−specific
14	1e−01	3 / 38	Tirosh_top50 correlated genes PC1
15	1e−01	3 / 39	Tirosh_top50 correlated genes PC4

MF

Rank	p−value	#in/all	Geneset
1	2e−10	334 / 7864	protein binding
2	2e−07	26 / 237	ubiquitin−protein transferase activity
3	1e−05	75 / 1329	transferase activity
4	3e−05	23 / 256	cadherin binding
5	5e−05	16 / 148	ubiquitin protein ligase activity
6	8e−04	13 / 135	actin filament binding
7	8e−04	70 / 1402	nucleotide binding
8	1e−03	4 / 14	death receptor binding
9	1e−03	24 / 350	protein kinase binding
10	1e−03	10 / 93	protease binding
11	1e−03	4 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
12	2e−03	18 / 249	ubiquitin protein ligase binding
13	2e−03	22 / 331	protein serine/threonine kinase activity
14	3e−03	20 / 291	actin binding
15	3e−03	4 / 18	protein kinase activator activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−05	16 / 134	hsa−miR−141
2	2e−05	18 / 165	hsa−miR−448
3	4e−05	14 / 115	hsa−miR−409−3p
4	9e−05	19 / 205	hsa−miR−548p
5	1e−04	22 / 267	hsa−miR−142−5p
6	1e−04	26 / 344	hsa−miR−19a
7	2e−04	16 / 164	hsa−miR−548d−3p
8	2e−04	13 / 117	hsa−miR−200a
9	2e−04	22 / 275	hsa−miR−590−3p
10	3e−04	18 / 205	hsa−miR−1252
11	3e−04	17 / 191	hsa−miR−185
12	3e−04	15 / 157	hsa−miR−206
13	4e−04	25 / 344	hsa−miR−19b
14	4e−04	28 / 405	hsa−miR−107
15	4e−04	8 / 52	hsa−miR−514

Pneumonia

Rank	p−value	#in/all	Geneset
1	6e−05	15 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	1e−01	3 / 33	Sweeney_viral_dn
3	4e−01	5 / 122	Terre_IMS_influenza_meta_signature
4	5e−01	2 / 52	Burnham_day1_vs_5_DN
5	6e−01	2 / 56	Burnham_sep_vs_con_DN
6	6e−01	6 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	7e−01	2 / 68	Burnham_sep_vs_con_UP
8	7e−01	2 / 71	Burnham_cap_fp_vs_con_UP
9	8e−01	1 / 41	Scicluna_DN
10	8e−01	1 / 48	Burnham_cap_fp_vs_con_DN
11	8e−01	1 / 48	Burnham_viral_DN
12	8e−01	1 / 54	Burnham_timecourse
13	1e+00	0 / 57	Burnham_viral_UP
14	1e+00	0 / 57	Burnham_day1_vs_5_UP
15	1e+00	0 / 18	Scicluna_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−04	18 / 198	Chaussabel_3,3_Inflammation II
2	2e−03	16 / 204	Chaussabel_3,2_Inflammation I
3	2e−03	13 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
4	9e−03	3 / 13	WIRTH_B−cells
5	1e−02	16 / 245	Chaussabel_3,9_Kinases
6	1e−02	36 / 716	PROTEINATLAS_epididymis
7	1e−02	8 / 93	Chaussabel_1,4_Replication
8	3e−02	8 / 109	Chaussabel_2,6_Myeloid lineage
9	4e−02	46 / 1032	PROTEINATLAS_small intestine
10	5e−02	9 / 136	Chaussabel_2,9_Cytosceleton
11	5e−02	30 / 642	PROTEINATLAS_lung
12	6e−02	47 / 1081	PROTEINATLAS_testis
13	8e−02	5 / 66	VAQUERIZAS_Whole blood_TF
14	8e−02	39 / 905	PROTEINATLAS_appendix
15	9e−02	7 / 113	Chaussabel_1,8_Metabolism Biosynthesis

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	Alternative lengthening of telomeres
2	0.6	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−08	174 / 3564	ICGC_Taf1_targets
2	8e−06	173 / 3796	ICGC_Nficsc81335_targets
3	2e−05	146 / 3121	ICGC_Egr1_targets
4	2e−05	157 / 3420	ICGC_Bclaf101388_targets
5	2e−05	190 / 4319	ICGC_Pou2_targets
6	2e−05	200 / 4602	ICGC_Elf1_targets
7	5e−05	207 / 4851	ICGC_Runx3_targets
8	6e−05	186 / 4278	ICGC_Yy1_targets
9	8e−05	168 / 3804	ICGC_Stat5_targets
10	8e−05	134 / 2899	ICGC_Nfatc1_targets
11	1e−04	78 / 1494	ICGC_Cebpbsc150_targets
12	2e−04	165 / 3769	ICGC_Pmlsc71910_targets
13	3e−04	140 / 3150	ICGC_Creb1_targets
14	3e−04	157 / 3608	ICGC_Tcf12_targets
15	4e−04	81 / 1630	ICGC_SrfV0416101_targets

K−Means Cluster

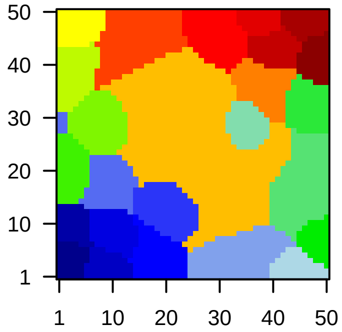
Spot Summary: M

metagenes = 68
genes = 701

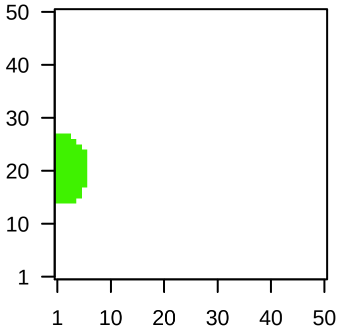
<r> metagenes = 0.85
<r> genes = 0.16
beta: r2= 5.39 / log p= −Inf

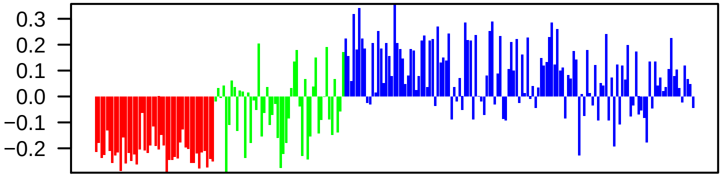
samples with spot = 50 (22.6 %)
intermediate : 5 (10.4 %)
non−mBL : 45 (34.9 %)

Overview Map



Spot





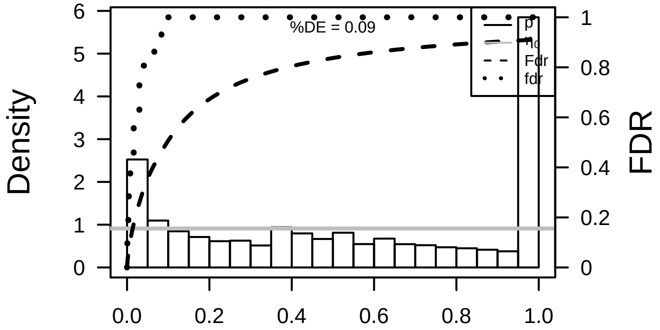
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209810_at	3.13	−1.02	0.45	SFTPB	surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080
2	207861_at	2.76	−1.26	0.53	CCL22	C−C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:
3	220635_at	2.62	−0.68	0.28	PSORS1C2	psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;
4	204755_x_at	2.62	−0.62	0.4	HLF	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
5	204753_s_at	2.57	−0.91	0.41	HLF	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
6	201839_s_at	2.49	−1.02	0.27	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
7	203440_at	2.45	−0.91	0.19	CDH2	cadherin 2 [Source:HGNC Symbol;Acc:HGNC:1759]
8	210551_s_at	2.43	−0.93	0.42	ASMT	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
9	219360_s_at	2.4	−1.57	0.47	TRPM4	transient receptor potential cation channel subfamily M memb
10	37004_at	2.39	−0.69	0.28	SFTPB	surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080
11	207534_at	2.39	−0.99	0.24	MAGEB1	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
12	219836_at	2.38	−1.24	0.57	ZBED2	zinc finger BED−type containing 2 [Source:HGNC Symbol;Ac
13	203797_at	2.31	−1.01	0.27	VSNL1	visinin like 1 [Source:HGNC Symbol;Acc:HGNC:12722]
14	213110_s_at	2.3	−0.71	0.24	COL4A5	collagen type IV alpha 5 chain [Source:HGNC Symbol;Acc:H
15	206881_s_at	2.3	−0.78	0.4	LILRA3	leukocyte immunoglobulin like receptor A3 [Source:HGNC Sy
16	218186_at	2.28	−1.29	0.35	RAB25	RAB25, member RAS oncogene family [Source:HGNC Symb
17	210889_s_at	2.27	−1.18	0.13	FCGR2B	Fc fragment of IgG receptor IIb [Source:HGNC Symbol;Acc:H
18	221690_s_at	2.27	−1.48	0.2	NLRP2	NLR family pyrin domain containing 2 [Source:HGNC Symbol
19	213497_at	2.23	−1.39	0.46	ABTB2	ankyrin repeat and BTB domain containing 2 [Source:HGNC
20	217523_at	2.2	−1.4	0.68	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−24	62 / 317	Canc	SPANG_BCL6−index2
2	9e−23	344 / 5404	Lympl	HOPP_Strong_enhancer
3	4e−20	30 / 85	Lympl	Aukema_BCL2 DN_BCL6 UP
4	4e−14	40 / 234	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_DN
5	5e−12	35 / 213	Lympl	SPANG_IL21 DN
6	2e−11	11 / 18	Lympl	WRIGHT_ABC UP
7	3e−10	138 / 1941	TF	ICGC_Bcl3_targets
8	4e−10	8 / 10	Lympl	Care_ABC UP
9	5e−10	121 / 1636	TF	ICGC_Bcl11_targets
10	9e−10	94 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
11	1e−09	14 / 42	Refer	Chaussabel_1,3_B−cells
12	2e−09	51 / 480	Canc	Lembcke_Colonic Inflammation
13	2e−09	78 / 906	Lympl	SPANG_BCR DN
14	2e−09	248 / 4261	Lympl	HOPP_Txn_transition
15	3e−09	28 / 182	Refer	WIRTH_post GC B−cells
16	4e−09	28 / 184	Chr	Chr 18
17	2e−08	54 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
18	2e−08	40 / 353	Lympl	SPANG_CD40 6hrs DN
19	5e−08	146 / 2254	TF	ICGC_BatfPcr1_targets
20	7e−08	192 / 3213	TF	ICGC_Pu1_targets
21	9e−08	25 / 173	Lympl	Victora_Light zone signature
22	9e−08	17 / 85	Lympl	Sha_DLBCL UP
23	1e−07	15 / 67	Immu	Angelova_immune−metagene−T−cells
24	1e−07	14 / 59	GSEA	PID_BCR_5PATHWAY
25	3e−07	32 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
26	3e−07	31 / 262	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
27	3e−07	44 / 453	GSEA	ONDER_CDH1_TARGETS_2_DN
28	3e−07	70 / 885	BP	positive regulation of transcription from RNA polymerase II promoter
29	4e−07	104 / 1508	TF	ICGC_Mef2_targets
30	4e−07	38 / 368	GSEA	ZHENG_BOUND_BY_FOXP3
31	4e−07	21 / 139	GSEA	BROCKE_APOPTOSIS_REVERSED_BY_IL6
32	4e−07	42 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
33	6e−07	27 / 218	Refer	WIRTH_pre+post GC B−cells
34	7e−07	14 / 67	GSEA	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
35	8e−07	32 / 290	GSEA	ODONNELL_TFRC_TARGETS_UP
36	1e−06	308 / 5908	Lympl	HOPP_Active_promoter
37	1e−06	16 / 90	GSEA	BASSO_CD40_SIGNALING_UP
38	1e−06	36 / 355	Refer	WIRTH_Immune system
39	2e−06	37 / 376	GSEA	GARY_CD5_TARGETS_UP
40	2e−06	35 / 346	GSEA	YAGI_AML_WITH_T_8_21_TRANSLOCATION

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.09	8 / 107	HORVATH_aging_genes meth UP
2	0.56	4 / 92	HORVATH_aging_genes meth DOWN
3	0.87	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	

BP

Rank	p−value	#in/all	Geneset
1	3e−07	70 / 885	positive regulation of transcription from RNA polymerase II promoter
2	5e−06	45 / 520	positive regulation of transcription, DNA−templated
3	1e−05	44 / 521	transcription from RNA polymerase II promoter
4	3e−05	26 / 250	regulation of apoptotic process
5	7e−05	102 / 1655	transcription, DNA−templated
6	8e−05	7 / 26	B cell activation
7	8e−05	107 / 1764	regulation of transcription, DNA−templated
8	9e−05	5 / 12	leukocyte chemotaxis
9	3e−04	18 / 169	cell migration
10	4e−04	10 / 64	regulation of GTPase activity
11	4e−04	41 / 553	apoptotic process
12	4e−04	5 / 16	negative regulation of B cell proliferation
13	6e−04	4 / 10	positive regulation of T cell differentiation in thymus
14	6e−04	13 / 106	regulation of small GTPase mediated signal transduction
15	7e−04	8 / 46	peptidyl−tyrosine autophosphorylation

Cancer

Rank	p−value	#in/all	Geneset
1	1e−24	62 / 317	SPANG_BCL6−index2
2	2e−09	51 / 480	Lembcke_Colonic Inflammation
3	1e−04	20 / 186	SPANG_LPS−index2
4	2e−03	10 / 80	PanCan_JAK−ST_geneset_nanostring
5	2e−02	3 / 13	BENTINK_e2f3.1
6	2e−02	3 / 14	GUSTAFSON_PI3K_UP
7	2e−02	9 / 96	PanCan_TXmisReg_geneset_nanostring
8	2e−02	10 / 113	PanCan_Driver_Gene_geneset_nanostring
9	2e−02	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	5e−02	1 / 14	LIU_COMMON_CANCER_GENES
11	7e−02	0 / 14	LIU_PROSTATE_CANCER_DN
12	9e−02	6 / 72	PanCan_Wnt_geneset_nanostring
13	9e−02	2 / 12	GENTLES_modul12
14	1e−01	3 / 28	PanCan_HK_geneset_nanostring
15	1e−01	2 / 14	GUSTAFSON_PI3K_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−04	200 / 3805	cytosol
2	7e−04	10 / 70	nucleosome
3	1e−03	9 / 62	extrinsic component of cytoplasmic side of plasma membrane
4	1e−03	36 / 494	endosome
5	2e−03	234 / 4701	cytoplasm
6	7e−03	16 / 188	endosome membrane
7	1e−02	14 / 163	transcription factor complex
8	1e−02	11 / 118	cytoplasmic vesicle membrane
9	1e−02	4 / 22	site of double−strand break
10	1e−02	5 / 34	peroxisomal matrix
11	1e−02	14 / 171	nuclear chromatin
12	2e−02	6 / 48	ficolin−1−rich granule membrane
13	2e−02	6 / 48	microvillus
14	2e−02	220 / 4579	nucleus
15	2e−02	7 / 62	filopodium

Chr

Rank	p−value	#in/all	Geneset
1	4e−09	28 / 184	Chr 18
2	2e−03	29 / 382	Chr 15
3	3e−03	45 / 689	Chr 3
4	4e−02	33 / 556	Chr X
5	6e−02	45 / 833	Chr 19
6	1e−01	35 / 669	Chr 6
7	2e−01	29 / 585	Chr 7
8	4e−01	17 / 369	Chr 20
9	5e−01	21 / 490	Chr 10
10	6e−01	17 / 403	Chr 14
11	6e−01	23 / 548	Chr 16
12	6e−01	31 / 756	Chr 11
13	7e−01	19 / 492	Chr 9
14	8e−01	52 / 1325	Chr 1
15	8e−01	12 / 333	Chr 22

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−24	467 / 8406	Bcells peripheral blood_2_TssAFlnk
2	3e−22	441 / 7833	Bcells peripheral blood_1_TssA
3	2e−21	499 / 9544	HSC_2_TssAFlnk
4	4e−21	264 / 3767	Bcells peripheral blood_6_EnhG
5	1e−19	443 / 8068	Thelper cells peripheral blood_1_TssA
6	2e−18	467 / 8816	Thelper cells peripheral blood_2_TssAFlnk
7	5e−18	450 / 8370	natural killer cells peripheral blood_2_TssAFlnk
8	2e−17	425 / 7751	natural killer cells peripheral blood_1_TssA
9	2e−17	342 / 5716	Bcells peripheral blood_4_Tx
10	3e−17	446 / 8322	T CD8+ naive cells peripheral blood_1_TssA
11	3e−16	388 / 6906	3_TssF_Fibroblasts
12	4e−16	440 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
13	5e−16	429 / 7957	Tcells peripheral blood_2_TssAFlnk
14	6e−16	79 / 693	Bcells peripheral blood_3_TxFlnk
15	8e−16	354 / 6114	7_Enh_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−10	94 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
2	6e−06	49 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	2e−04	103 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	6e−03	4 / 18	Boland_CRC−MSI−A6−A10
5	7e−03	59 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
6	9e−03	35 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
7	1e−02	62 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
8	1e−02	19 / 255	Kosinski_top−crypt−long−list
9	1e−02	7 / 60	Marisa_CRC−cluster−g
10	2e−02	3 / 13	Vilar_hypermutated−in−CRC
11	2e−02	2 / 5	Kaneda_CIMP−group1
12	4e−02	5 / 43	Marisa_CRC−cluster−f
13	4e−02	22 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	7e−02	12 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	8e−02	26 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

Glioma

Rank	p−value	#in/all	Geneset
1	5e−04	24 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	7e−04	63 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	3e−03	10 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
4	4e−03	20 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
5	2e−02	7 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
6	2e−02	8 / 82	laffaire_hypermeth_LGG_vs_control
7	3e−02	17 / 242	ScoV_0.5_Sturm_C1_IDH_DN
8	4e−02	4 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
9	4e−02	27 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
10	4e−02	11 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	6e−02	9 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
12	7e−02	6 / 67	Weller_LGG_1p19qDel−vs−intact_UP
13	7e−02	6 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
14	7e−02	15 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
15	7e−02	3 / 23	Christensen_hypomethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−14	40 / 234	HOLLMANN_APOPTOSIS_VIA_CD40_DN
2	2e−08	54 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
3	1e−07	14 / 59	PID_BCR_5PATHWAY
4	3e−07	32 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
5	3e−07	31 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
6	3e−07	44 / 453	ONDER_CDH1_TARGETS_2_DN
7	4e−07	38 / 368	ZHENG_BOUND_BY_FOXP3
8	4e−07	21 / 139	BROCKE_APOPTOSIS_REVERSED_BY_IL6
9	4e−07	42 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	7e−07	14 / 67	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
11	8e−07	32 / 290	ODONNELL_TFRC_TARGETS_UP
12	1e−06	16 / 90	BASSO_CD40_SIGNALING_UP
13	2e−06	37 / 376	GARY_CD5_TARGETS_UP
14	2e−06	35 / 346	YAGI_AML_WITH_T_8_21_TRANSLOCATION
15	2e−06	14 / 73	ROSS_LEUKEMIA_WITH_MLL_FUSIONS

HM

Rank	p−value	#in/all	Geneset
1	2e−04	19 / 176	HALLMARK_ALLOGRAFT_REJECTION
2	3e−04	16 / 141	HALLMARK_UV_RESPONSE_DN
3	1e−03	10 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	2e−03	7 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
5	5e−03	15 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	8e−03	16 / 191	HALLMARK_P53_PATHWAY
7	9e−03	16 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	2e−02	15 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	3e−02	8 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	3e−02	13 / 170	HALLMARK_IL2_STAT5_SIGNALING
11	4e−02	14 / 193	HALLMARK_HEME_METABOLISM
12	1e−01	12 / 187	HALLMARK_INFLAMMATORY_RESPONSE
13	1e−01	10 / 150	HALLMARK_APOPTOSIS
14	1e−01	12 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
15	1e−01	11 / 178	HALLMARK_COMPLEMENT

Immunome

Rank	p−value	#in/all	Geneset
1	1e−07	15 / 67	Angelova_immune−metagene−T−cells
2	2e−03	4 / 13	Angelova_immune−metagene−activated_B−cells
3	2e−02	3 / 13	Angelova_immune−metagene−immature_B−cells
4	4e−02	5 / 45	Angelova_immune−metagene−MDSC
5	1e−01	2 / 14	Angelova_immune−metagene−eosinophil
6	1e−01	3 / 29	Angelova_immune−metagene−Th1
7	1e−01	2 / 16	Angelova_immune−metagene−Th17
8	2e−01	1 / 4	Angelova_CRC_MSS−neoantigens
9	2e−01	2 / 18	Angelova_immune−metagene−pDC
10	2e−01	2 / 19	Angelova_immune−metagene−iDC
11	2e−01	1 / 5	Angelova_immune−metagene−NKT
12	2e−01	2 / 21	Angelova_immune−metagene−central_memory_CD4
13	3e−01	2 / 23	Angelova_immune−metagene−Th2
14	3e−01	2 / 23	Angelova_immune−metagene−Treg
15	3e−01	3 / 42	Angelova_immune−metagene−TGD

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	4 / 22	DUMEAUX_Fasting enriched genes
2	0.19	12 / 210	Homuth_BMI−associated−genes_DN
3	0.33	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.35	1 / 10	DUMEAUX_Smoking literature genes up
5	0.46	7 / 150	Homuth_BMI−associated−genes_UP
6	0.62	1 / 22	DUMEAUX_High bmi enriched genes
7	0.75	2 / 62	DUMEAUX_Smoking enriched genes
8	0.75	1 / 32	Marjolein_ageing−genes_DN
9	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1.00	0 / 7	DUMEAUX_Hormon therapy in non 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 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−23	344 / 5404	HOPP_Strong_enhancer
2	4e−20	30 / 85	Aukema_BCL2 DN_BCL6 UP
3	5e−12	35 / 213	SPANG_IL21 DN
4	2e−11	11 / 18	WRIGHT_ABC UP
5	4e−10	8 / 10	Care_ABC UP
6	2e−09	78 / 906	SPANG_BCR DN
7	2e−09	248 / 4261	HOPP_Txn_transition
8	2e−08	40 / 353	SPANG_CD40 6hrs DN
9	9e−08	25 / 173	Victora_Light zone signature
10	9e−08	17 / 85	Sha_DLBCL UP
11	1e−06	308 / 5908	HOPP_Active_promoter
12	3e−06	4 / 4	WRIGHT_custom ABC−DLBCL UP
13	7e−06	287 / 5529	HOPP_Txn_elongation
14	8e−05	287 / 5682	HOPP_Weak_promoter
15	3e−04	225 / 4357	HOPP_Weak_txn

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−05	7 / 24	Tirosh_B−cell specific genes−melanoma
2	5e−04	19 / 189	Tirosh_genes preferentially expressed by Tregs
3	1e−02	18 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	1e−02	32 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	2e−02	4 / 24	Tirosh_exhuastion−associated genes consitent across tumors
6	2e−02	8 / 81	Tirosh_Genes in the MITF program
7	3e−02	3 / 16	Hugo_melanoma−all−LEF1_UP
8	6e−02	12 / 171	Landsberg_dedifferentiation_up
9	6e−02	7 / 83	TCGA_melanoma_immune_high
10	8e−02	4 / 39	Tirosh_melanoma specific genes
11	8e−02	1 / 2	Melanoma Epi−Enzyme Cluster 1
12	1e−01	13 / 204	Landsberg_dedifferentiation_down
13	1e−01	15 / 249	Gerber_wt/wt_melanoma−cells−SpotE
14	1e−01	5 / 65	Harbst_melanoma_highgrade_up
15	2e−01	2 / 17	Hugo_melanoma−all−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	3e−05	98 / 1541	DNA binding
2	6e−05	380 / 7864	protein binding
3	9e−05	11 / 65	protein phosphatase binding
4	1e−04	9 / 46	SH3/SH2 adaptor activity
5	1e−04	143 / 2529	metal ion binding
6	3e−04	19 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
7	7e−04	8 / 46	non−membrane spanning protein tyrosine kinase activity
8	9e−04	14 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
9	1e−03	72 / 1185	ATP binding
10	2e−03	48 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
11	2e−03	33 / 450	sequence−specific DNA binding
12	3e−03	48 / 741	DNA binding transcription factor activity
13	3e−03	11 / 96	SH3 domain binding
14	3e−03	18 / 202	GTPase activator activity
15	3e−03	29 / 393	molecular_function

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	38 / 474	hsa−miR−20a
2	3e−04	12 / 88	hsa−miR−600
3	5e−04	26 / 299	hsa−let−7c
4	6e−04	30 / 369	hsa−miR−15b
5	6e−04	28 / 336	hsa−miR−519d
6	1e−03	6 / 28	hsa−miR−654−5p
7	1e−03	28 / 350	hsa−miR−424
8	1e−03	29 / 369	hsa−miR−130a
9	1e−03	11 / 89	hsa−miR−1248
10	2e−03	11 / 91	hsa−miR−211
11	2e−03	29 / 378	hsa−miR−16
12	2e−03	28 / 363	hsa−miR−195
13	2e−03	7 / 44	hsa−miR−552
14	2e−03	17 / 185	hsa−miR−182
15	2e−03	13 / 124	hsa−miR−655

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	5 / 37	Sweeney_viral_up
2	0.14	11 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.17	3 / 33	Sweeney_viral_dn
4	0.18	2 / 18	Scicluna_UP
5	0.18	4 / 52	Burnham_day1_vs_5_DN
6	0.23	4 / 57	Burnham_viral_UP
7	0.25	3 / 41	Scicluna_DN
8	0.56	3 / 68	Burnham_sep_vs_con_UP
9	0.60	5 / 122	Terre_IMS_influenza_meta_signature
10	0.61	2 / 48	Burnham_cap_fp_vs_con_DN
11	0.68	2 / 54	Burnham_timecourse
12	0.69	5 / 135	Terre_MSV_multiple_respiratory_viruses_up
13	0.70	2 / 56	Burnham_sep_vs_con_DN
14	0.71	2 / 57	Burnham_day1_vs_5_UP
15	0.81	2 / 71	Burnham_cap_fp_vs_con_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−09	14 / 42	Chaussabel_1,3_B−cells
2	3e−09	28 / 182	WIRTH_post GC B−cells
3	6e−07	27 / 218	WIRTH_pre+post GC B−cells
4	1e−06	36 / 355	WIRTH_Immune system
5	1e−03	9 / 62	VAQUERIZAS_Lung_TF
6	2e−03	9 / 66	VAQUERIZAS_Whole blood_TF
7	3e−03	18 / 204	Chaussabel_3,2_Inflammation I
8	8e−03	9 / 81	Chaussabel_1,2_Platelets
9	1e−02	10 / 100	Chaussabel_2,8_T−cells
10	1e−02	4 / 21	VAQUERIZAS_Tonsil_TF
11	1e−02	8 / 72	Chaussabel_3,1_Interferon−inducible
12	1e−02	6 / 45	VAQUERIZAS_Placenta_TF
13	1e−02	6 / 45	VAQUERIZAS_Whole brain_TF
14	3e−02	3 / 16	VAQUERIZAS_Fetal liver_TF
15	3e−02	27 / 429	PROTEINATLAS_liver

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	3e−10	138 / 1941	ICGC_Bcl3_targets
2	5e−10	121 / 1636	ICGC_Bcl11_targets
3	5e−08	146 / 2254	ICGC_BatfPcr1_targets
4	7e−08	192 / 3213	ICGC_Pu1_targets
5	4e−07	104 / 1508	ICGC_Mef2_targets
6	6e−06	194 / 3451	ICGC_Atf2_targets
7	6e−06	168 / 2899	ICGC_Nfatc1_targets
8	8e−06	209 / 3796	ICGC_Nficsc81335_targets
9	9e−06	192 / 3435	ICGC_Ebfsc137065_targets
10	2e−05	176 / 3121	ICGC_Egr1_targets
11	5e−05	194 / 3564	ICGC_Taf1_targets
12	5e−05	187 / 3420	ICGC_Bclaf101388_targets
13	5e−05	203 / 3769	ICGC_Pmlsc71910_targets
14	7e−05	216 / 4072	ICGC_Mta3_targets
15	9e−05	134 / 2321	ICGC_Rad21_targets

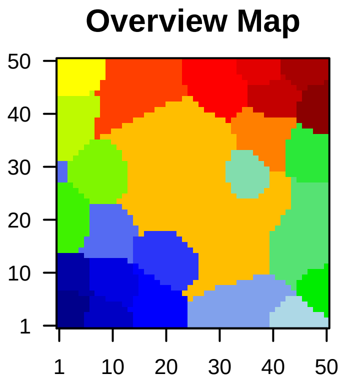
K−Means Cluster

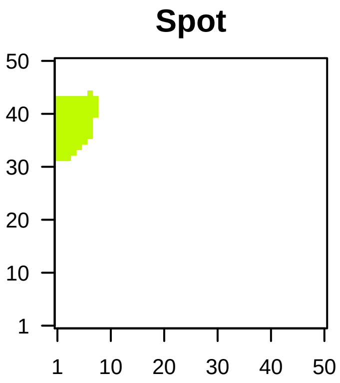
Spot Summary: N

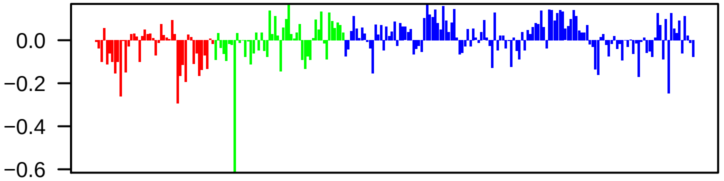
metagenes = 79
genes = 565

<r> metagenes = 0.8
<r> genes = 0.13
beta: r2= 2.22 / log p= −Inf

samples with spot = 3 (1.4 %)
intermediate : 1 (2.1 %)
non−mBL : 2 (1.6 %)


Overview Map


Spot

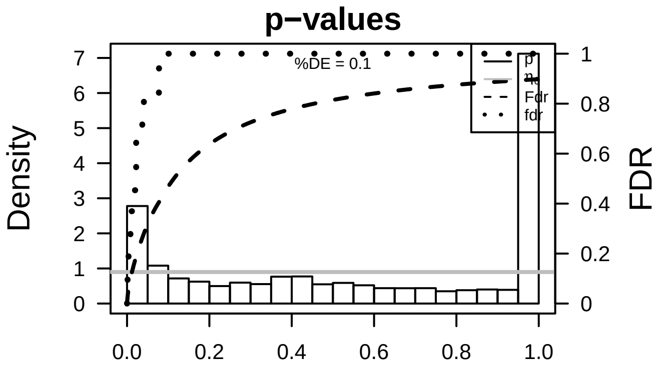


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	220994_s_at	2.07	−1.08	0.12	STXBP6	syntaxin binding protein 6 [Source:HGNC Symbol;Acc:HGNC
2	215666_at	1.84	−0.76	0.08		
3	213816_s_at	1.72	−0.66	0.2	MET	MET proto−oncogene, receptor tyrosine kinase [Source:HGN
4	204149_s_at	1.63	−0.9	0.19	GSTM4	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:H
5	210192_at	1.6	−1.09	0.18	ATP8A1	ATPase phospholipid transporting 8A1 [Source:HGNC Symbo
6	206473_at	1.52	−0.99	0.37	MBTPS2	membrane bound transcription factor peptidase, site 2 [Sourc
7	214860_at	1.52	−0.83	0.35	SLC9A7	solute carrier family 9 member A7 [Source:HGNC Symbol;Ac
8	205775_at	1.5	−1.09	0.1	FAM50B	family with sequence similarity 50 member B [Source:HGNC
9	201868_s_at	1.5	−1.05	0.36	TBL1X	transducin beta like 1 X−linked [Source:HGNC Symbol;Acc:H
10	212940_at	1.49	−0.73	0.37	COL6A1	collagen type VI alpha 1 chain [Source:HGNC Symbol;Acc:H
11	211855_s_at	1.48	−1.16	0.23	SLC25A14	solute carrier family 25 member 14 [Source:HGNC Symbol;A
12	211195_s_at	1.47	−0.96	0.32	TP63	tumor protein p63 [Source:HGNC Symbol;Acc:HGNC:15979]
13	211108_s_at	1.46	−0.84	0.56	JAK3	Janus kinase 3 [Source:HGNC Symbol;Acc:HGNC:6193]
14	205170_at	1.43	−1.44	0.59	STAT2	signal transducer and activator of transcription 2 [Source:HG
15	216017_s_at	1.4	−1.3	0.5	NAB2	NGFI−A binding protein 2 [Source:HGNC Symbol;Acc:HGNC
16	205148_s_at	1.4	−0.91	0.25	CLCN4	chloride voltage−gated channel 4 [Source:HGNC Symbol;Acc
17	208086_s_at	1.4	−0.95	0.14	DMD	dystrophin [Source:HGNC Symbol;Acc:HGNC:2928]
18	214318_s_at	1.39	−0.72	0.08	FRY	FRY microtubule binding protein [Source:HGNC Symbol;Acc:
19	214673_s_at	1.38	−1.31	0.53	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin prot
20	212272_at	1.37	−0.86	0.28	LPIN1	lipin 1 [Source:HGNC Symbol;Acc:HGNC:13345]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−29	285 / 4261	Lympl	HOPP_Txn_transition
2	9e−24	324 / 5529	Lympl	HOPP_Txn_elongation
3	1e−17	236 / 3805	CC	cytosol
4	2e−16	299 / 5404	Lympl	HOPP_Strong_enhancer
5	7e−16	52 / 376	GSEA	GARY_CD5_TARGETS_UP
6	5e−15	386 / 7864	MF	protein binding
7	6e−15	314 / 5908	Lympl	HOPP_Active_promoter
8	1e−14	59 / 502	BP	protein transport
9	3e−13	33 / 190	BP	vesicle−mediated transport
10	1e−12	210 / 3564	TF	ICGC_Taf1_targets
11	2e−12	90 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran
12	4e−12	15 / 38	Gliom	WILLSCHER_GBM_Verhaak−PNwt_up
13	4e−12	123 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
14	5e−12	23 / 102	GSEA	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
15	3e−11	187 / 3150	TF	ICGC_Creb1_targets
16	4e−11	185 / 3121	TF	ICGC_Egr1_targets
17	9e−11	23 / 117	GSEA	JOHNSTONE_PARVB_TARGETS_2_UP
18	3e−10	249 / 4701	CC	cytoplasm
19	4e−10	211 / 3804	TF	ICGC_Stat5_targets
20	5e−10	33 / 249	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
21	9e−10	97 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
22	2e−09	23 / 136	BP	ER to Golgi vesicle−mediated transport
23	2e−09	13 / 41	GSEA	FAELT_B_CLL_WITH_VH3_21_UP
24	1e−08	46 / 479	CC	Golgi membrane
25	1e−08	33 / 280	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
26	1e−08	16 / 73	miRN	hsa−miR−423−5p
27	2e−08	26 / 191	miRN	hsa−miR−185
28	2e−08	26 / 191	GSEA	REACTOME_SIGNALLING_BY_NGF
29	3e−08	71 / 938	CC	Golgi apparatus
30	3e−08	202 / 3769	TF	ICGC_Pmlsc71910_targets
31	3e−08	187 / 3420	TF	ICGC_Bclaf101388_targets
32	3e−08	195 / 3608	TF	ICGC_Tcf12_targets
33	3e−08	27 / 208	GSEA	RICKMAN_METASTASIS_DN
34	4e−08	22 / 146	GSEA	ELVIDGE_HYPOXIA_DN
35	4e−08	279 / 5682	Lympl	HOPP_Weak_promoter
36	5e−08	29 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
37	5e−08	20 / 124	GSEA	SCHLOSSER_SERUM_RESPONSE_UP
38	6e−08	93 / 1387	TF	HEBENSTREIT_high expression TF
39	8e−08	18 / 104	CC	trans−Golgi network
40	9e−08	201 / 3796	TF	ICGC_Nficsc81335_targets


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	4 / 92	HORVATH_aging_genes meth DOWN
2	0.6	4 / 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	1e−14	59 / 502	protein transport
2	3e−13	33 / 190	vesicle−mediated transport
3	2e−09	23 / 136	ER to Golgi vesicle−mediated transport
4	6e−07	7 / 15	membrane protein intracellular domain proteolysis
5	2e−06	22 / 184	intracellular protein transport
6	3e−06	9 / 33	glycolytic process
7	3e−06	11 / 51	retrograde transport, endosome to Golgi
8	4e−06	7 / 19	positive regulation of protein dephosphorylation
9	1e−05	6 / 15	lysosome localization
10	2e−05	7 / 24	canonical glycolysis
11	3e−05	43 / 576	phosphorylation
12	3e−05	5 / 11	cellular response to angiotensin
13	4e−05	15 / 115	actin cytoskeleton organization
14	4e−05	6 / 18	intra−Golgi vesicle−mediated transport
15	5e−05	5 / 12	positive regulation of extrinsic apoptotic signaling pathway in absence of ligan

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	3 / 11	GENTLES_modul14
2	0.012	10 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.015	3 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.015	11 / 134	PanCan_RAS_geneset_nanostring
5	0.018	3 / 15	GENTLES_modul2
6	0.027	11 / 147	PanCan_MAPK_geneset_nanostring
7	0.059	12 / 187	PanCan_PI3K_geneset_nanostring
8	0.092	3 / 28	PanCan_HK_geneset_nanostring
9	0.106	11 / 186	SPANG_LPS−index2
10	0.112	2 / 15	GENTLES_modul7
11	0.125	2 / 16	GENTLES_modul16
12	0.131	8 / 130	PanCan_CC+Apop_geneset_nanostring
13	0.185	4 / 58	SHAUGHNESSY_MM high risk
14	0.245	15 / 317	SPANG_BCL6−index2
15	0.318	18 / 409	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	1e−17	236 / 3805	cytosol
2	3e−10	249 / 4701	cytoplasm
3	1e−08	46 / 479	Golgi membrane
4	3e−08	71 / 938	Golgi apparatus
5	8e−08	18 / 104	trans−Golgi network
6	9e−07	53 / 683	endoplasmic reticulum membrane
7	9e−07	259 / 5339	membrane
8	4e−06	225 / 4579	nucleus
9	7e−06	138 / 2541	nucleoplasm
10	1e−05	9 / 38	SNARE complex
11	8e−05	14 / 109	early endosome membrane
12	9e−05	37 / 494	endosome
13	1e−04	119 / 2239	extracellular exosome
14	2e−04	9 / 55	phagocytic vesicle
15	3e−04	36 / 503	cytoplasmic vesicle

Chr

Rank	p−value	#in/all	Geneset
1	4e−07	62 / 833	Chr 19
2	2e−06	45 / 556	Chr X
3	1e−02	43 / 776	Chr 17
4	5e−02	31 / 585	Chr 7
5	8e−02	37 / 756	Chr 11
6	2e−01	8 / 139	Chr 21
7	3e−01	22 / 492	Chr 9
8	3e−01	24 / 548	Chr 16
9	4e−01	14 / 333	Chr 22
10	7e−01	13 / 369	Chr 20
11	7e−01	14 / 403	Chr 14
12	7e−01	29 / 832	Chr 2
13	8e−01	46 / 1325	Chr 1
14	9e−01	13 / 437	Chr 8
15	9e−01	14 / 490	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−61	466 / 7833	Bcells peripheral blood_1_TssA
2	3e−55	447 / 7420	Tcells peripheral blood_1_TssA
3	3e−55	462 / 7957	Tcells peripheral blood_2_TssAFlnk
4	2e−54	452 / 7635	monocytes peripheral blood_1_TssA
5	3e−54	330 / 4208	Tcells peripheral blood_6_EnhG
6	1e−53	463 / 8068	Thelper cells peripheral blood_1_TssA
7	3e−53	466 / 8200	monocytes peripheral blood_2_TssAFlnk
8	2e−50	450 / 7751	natural killer cells peripheral blood_1_TssA
9	1e−49	467 / 8406	Bcells peripheral blood_2_TssAFlnk
10	9e−49	309 / 3938	Thelper cells peripheral blood_6_EnhG
11	1e−48	301 / 3767	Bcells peripheral blood_6_EnhG
12	3e−48	463 / 8322	T CD8+ naive cells peripheral blood_1_TssA
13	2e−47	451 / 7930	Tregulatory cells peripheral blood_1_TssA
14	9e−47	294 / 3682	natural killer cells peripheral blood_6_EnhG
15	2e−46	462 / 8370	natural killer cells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	90 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	4e−12	123 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
3	9e−10	97 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	1e−07	81 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
5	2e−04	56 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	7e−03	62 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	2e−02	19 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
8	3e−02	2 / 7	Boland_CRC−MSI−TGC
9	4e−02	2 / 8	Marisa_CRC−C1
10	7e−02	11 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
11	7e−02	3 / 25	Ang_CRC−CIMPH−vs−L_hypo
12	1e−01	3 / 31	Marisa_CRC−cluster−c
13	1e−01	15 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
14	2e−01	3 / 35	Ang_CRC_Hypomethylated
15	2e−01	1 / 5	Hewish_dMMR−secondary−mutations_Apoptosis

Glioma

Rank	p−value	#in/all	Geneset
1	4e−12	15 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
2	4e−05	26 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	2e−04	42 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
4	8e−03	12 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	9e−03	5 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	1e−02	76 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	1e−02	3 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
8	3e−02	5 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
9	4e−02	7 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	7e−02	2 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
11	1e−01	60 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
12	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
13	2e−01	4 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	2e−01	4 / 58	Stuehler_Proteins_up_in_STS
15	2e−01	6 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−16	52 / 376	GARY_CD5_TARGETS_UP
2	5e−12	23 / 102	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
3	9e−11	23 / 117	JOHNSTONE_PARVB_TARGETS_2_UP
4	5e−10	33 / 249	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
5	2e−09	13 / 41	FAELT_B_CLL_WITH_VH3_21_UP
6	1e−08	33 / 280	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
7	2e−08	26 / 191	REACTOME_SIGNALLING_BY_NGF
8	3e−08	27 / 208	RICKMAN_METASTASIS_DN
9	4e−08	22 / 146	ELVIDGE_HYPOXIA_DN
10	5e−08	29 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
11	5e−08	20 / 124	SCHLOSSER_SERUM_RESPONSE_UP
12	1e−07	8 / 18	PID_ARF_3PATHWAY
13	2e−07	9 / 25	REACTOME_GLYCOLYSIS
14	2e−07	61 / 798	LOPEZ_MBD_TARGETS
15	3e−07	54 / 675	GRADE_COLON_CANCER_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−05	14 / 94	HALLMARK_PROTEIN_SECRETION
2	3e−04	12 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
3	2e−03	16 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	5e−03	13 / 149	HALLMARK_UV_RESPONSE_UP
5	8e−03	15 / 192	HALLMARK_MTORC1_SIGNALING
6	2e−02	13 / 173	HALLMARK_MITOTIC_SPINDLE
7	3e−02	6 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	4e−02	12 / 174	HALLMARK_ADIPOGENESIS
9	4e−02	12 / 174	HALLMARK_APICAL_JUNCTION
10	4e−02	12 / 178	HALLMARK_COMPLEMENT
11	4e−02	4 / 35	HALLMARK_HEDGEHOG_SIGNALING
12	5e−02	5 / 51	HALLMARK_TGF_BETA_SIGNALING
13	9e−02	4 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
14	9e−02	9 / 139	HALLMARK_FATTY_ACID_METABOLISM
15	1e−01	3 / 29	HALLMARK_NOTCH_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 3	Angelova_CRC_MHC_class_I
2	0.1	1 / 4	Angelova_CRC_MHC_class_II
3	0.2	2 / 19	Angelova_immune−metagene−activated_CD8
4	0.2	2 / 23	Angelova_immune−metagene−monocytes
5	0.2	2 / 23	Angelova_immune−metagene−Treg
6	0.3	1 / 8	Immunity_HLA−class−II
7	0.3	1 / 10	Angelova_immune−metagene−neutrophils
8	0.3	1 / 10	Angelova_CRC_immonoinhibitors
9	0.4	1 / 11	Angelova_immune−metagene−macrophages
10	0.4	1 / 12	Angelova_immune−metagene−memory_B−cells
11	0.4	1 / 12	Angelova_immune−metagene−NK56_dim
12	0.5	1 / 17	Angelova_immune−metagene−central_memory_CD8
13	0.5	1 / 18	Angelova_immune−metagene−pDC
14	0.5	2 / 45	Angelova_immune−metagene−MDSC
15	0.7	2 / 67	Angelova_immune−metagene−T−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−05	22 / 210	Homuth_BMI−associated−genes_DN
2	3e−02	11 / 150	Homuth_BMI−associated−genes_UP
3	1e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	2e−01	2 / 22	DUMEAUX_Fasting enriched genes
5	3e−01	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
6	4e−01	1 / 14	Huan_blood−pressure_SBP−signature
7	7e−01	1 / 32	Marjolein_ageing−genes_DN
8	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
9	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
10	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 22	DUMEAUX_High bmi enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−29	285 / 4261	HOPP_Txn_transition
2	9e−24	324 / 5529	HOPP_Txn_elongation
3	2e−16	299 / 5404	HOPP_Strong_enhancer
4	6e−15	314 / 5908	HOPP_Active_promoter
5	4e−08	279 / 5682	HOPP_Weak_promoter
6	2e−02	48 / 906	SPANG_BCR DN
7	3e−02	5 / 45	SPANG_BAFF 9hrs DN
8	3e−02	8 / 96	SPANG_LPS 6hrs UP
9	3e−02	21 / 353	SPANG_CD40 6hrs DN
10	7e−02	13 / 213	SPANG_IL21 DN
11	9e−02	4 / 45	Monti_BCR_cluster
12	1e−01	2 / 14	YAMANE_AICDA_targets_recruited
13	1e−01	44 / 955	SPANG_BCR UP
14	1e−01	180 / 4357	HOPP_Weak_txn
15	1e−01	3 / 34	TARTE_B−cell signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.005	18 / 236	Gerber_wt/wt_group3−specific
2	0.076	1 / 2	Melanoma Epi−Enzyme Cluster 1
3	0.104	11 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
4	0.110	13 / 230	Gerber_wt/wt_melanoma−cells−SpotC
5	0.115	11 / 189	Tirosh_genes preferentially expressed by Tregs
6	0.116	15 / 276	Gerber_wt/wt_melanoma−cells−SpotB
7	0.120	7 / 107	Tirosh_Exhaustion program in Mel75
8	0.180	3 / 38	Tirosh_top50 correlated genes PC1
9	0.222	2 / 23	Melanoma Epi−Enzyme Cluster 7
10	0.241	11 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	0.256	12 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	0.265	10 / 204	Landsberg_dedifferentiation_down
13	0.270	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
14	0.474	2 / 41	Tirosh_top50 correlated genes PC3
15	0.535	2 / 46	Tirosh_top50 correlated genes PC5

MF

Rank	p−value	#in/all	Geneset
1	5e−15	386 / 7864	protein binding
2	7e−07	28 / 256	cadherin binding
3	2e−05	43 / 573	kinase activity
4	4e−05	80 / 1329	transferase activity
5	9e−05	29 / 350	protein kinase binding
6	1e−04	81 / 1402	nucleotide binding
7	1e−04	7 / 31	SNAP receptor activity
8	2e−04	20 / 214	GTPase activity
9	7e−04	22 / 267	binding
10	7e−04	6 / 29	Rho GTPase binding
11	1e−03	5 / 21	protein serine/threonine kinase activator activity
12	2e−03	8 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
13	3e−03	4 / 16	ARF guanyl−nucleotide exchange factor activity
14	3e−03	5 / 26	transcriptional activator activity, RNA polymerase II distal enhancer sequence
15	3e−03	7 / 51	ubiquitin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−08	16 / 73	hsa−miR−423−5p
2	2e−08	26 / 191	hsa−miR−185
3	1e−07	28 / 234	hsa−miR−570
4	3e−07	24 / 189	hsa−miR−214
5	6e−07	9 / 28	hsa−miR−296−5p
6	4e−06	32 / 344	hsa−miR−19a
7	4e−06	32 / 344	hsa−miR−19b
8	7e−06	11 / 55	hsa−miR−637
9	8e−06	19 / 155	hsa−miR−129−5p
10	2e−05	17 / 134	hsa−miR−323b−5p
11	3e−05	36 / 448	hsa−miR−20b
12	3e−05	35 / 435	hsa−miR−93
13	4e−05	12 / 78	hsa−miR−216a
14	4e−05	23 / 236	hsa−miR−34a
15	5e−05	11 / 68	hsa−miR−608

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.04	4 / 33	Sweeney_viral_dn
2	0.08	9 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.74	2 / 68	Burnham_sep_vs_con_UP
4	0.87	1 / 52	Burnham_day1_vs_5_DN
5	0.88	1 / 54	Burnham_timecourse
6	0.89	1 / 57	Burnham_day1_vs_5_UP
7	0.92	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
8	0.94	1 / 71	Burnham_cap_fp_vs_con_UP
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 / 48	Burnham_viral_DN
12	1.00	0 / 57	Burnham_viral_UP
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	1e−07	36 / 355	WIRTH_Immune system
2	4e−06	51 / 678	PROTEINATLAS_lymph node
3	8e−06	52 / 716	PROTEINATLAS_epididymis
4	2e−05	65 / 989	PROTEINATLAS_tonsil
5	3e−05	55 / 809	PROTEINATLAS_fallopian tube
6	3e−05	53 / 770	PROTEINATLAS_endometrium
7	8e−05	56 / 861	PROTEINATLAS_nasopharynx
8	2e−04	62 / 1022	PROTEINATLAS_placenta
9	6e−04	42 / 642	PROTEINATLAS_lung
10	6e−04	52 / 848	PROTEINATLAS_adrenal gland
11	1e−03	4 / 13	WIRTH_B−cells
12	1e−03	37 / 569	PROTEINATLAS_salivary gland
13	1e−03	42 / 671	PROTEINATLAS_cervix, uterine
14	1e−03	50 / 840	PROTEINATLAS_urinary bladder
15	1e−03	49 / 819	PROTEINATLAS_bronchus

Telomeres

Rank	p−value	#in/all	Geneset
1	0.08	3 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−12	210 / 3564	ICGC_Taf1_targets
2	3e−11	187 / 3150	ICGC_Creb1_targets
3	4e−11	185 / 3121	ICGC_Egr1_targets
4	4e−10	211 / 3804	ICGC_Stat5_targets
5	3e−08	202 / 3769	ICGC_Pmlsc71910_targets
6	3e−08	187 / 3420	ICGC_Bclaf101388_targets
7	3e−08	195 / 3608	ICGC_Tcf12_targets
8	6e−08	93 / 1387	HEBENSTREIT_high expression TF
9	9e−08	201 / 3796	ICGC_Nficsc81335_targets
10	9e−08	215 / 4131	ICGC_Tcf3_targets
11	1e−07	101 / 1578	ICGC_GabpPcr2_targets
12	2e−07	185 / 3451	ICGC_Atf2_targets
13	2e−07	161 / 2899	ICGC_Nfatc1_targets
14	3e−07	220 / 4319	ICGC_Pou2_targets
15	4e−07	191 / 3630	ICGC_Sp1_targets

K−Means Cluster

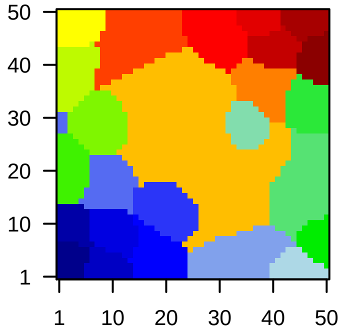
Spot Summary: O

metagenes = 37
genes = 612

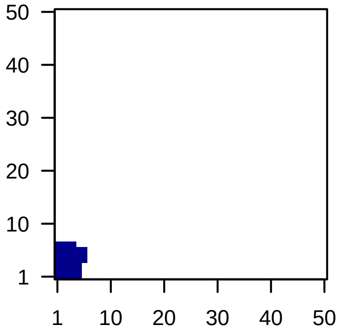
<r> metagenes = 0.94
<r> genes = 0.37
beta: r2= 22.16 / log p= −Inf

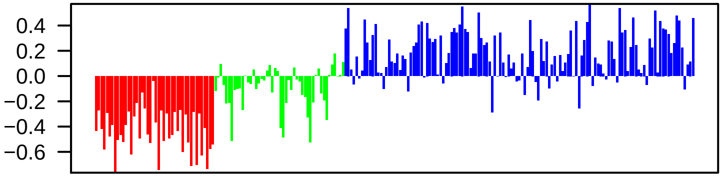
samples with spot = 73 (33 %)
intermediate : 1 (2.1 %)
non−mBL : 72 (55.8 %)

Overview Map



Spot





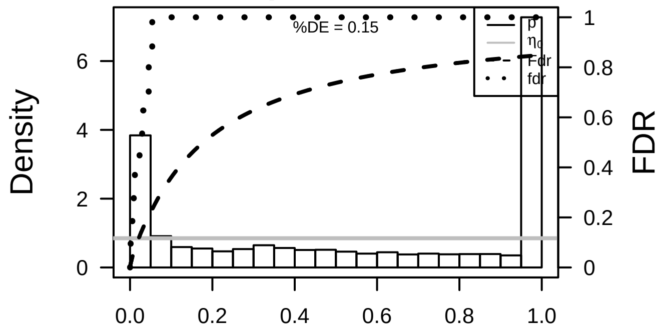
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207900_at	2.93	−0.94	0.32	CCL17	C−C motif chemokine ligand 17 [Source:HGNC Symbol;Acc:H
2	217002_s_at	2.74	−1.28	0.3	HTR3A	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
3	211644_x_at	2.59	−1.77	0.33		immunoglobulin kappa variable 3−20 [Source:HGNC Symbol;
4	221185_s_at	2.57	−1.49	0.57	IQCG	IQ motif containing G [Source:HGNC Symbol;Acc:HGNC:252
5	214551_s_at	2.53	−1.11	0.61	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
6	216615_s_at	2.49	−1.56	0.37	HTR3A	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
7	219316_s_at	2.46	−0.79	0.65	FLVCR2	feline leukemia virus subgroup C cellular receptor family mem
8	208451_s_at	2.38	−1.57	0.58	C4A	complement C4A (Rodgers blood group) [Source:HGNC Sym
9	203535_at	2.34	−1.86	0.58	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
10	217022_s_at	2.33	−2.54	0.46		immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
11	217546_at	2.25	−0.88	0.49		metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296
12	208168_s_at	2.22	−1.13	0.49	CHIT1	chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936]
13	207245_at	2.21	−1.2	0.38	UGT2B17	UDP glucuronosyltransferase family 2 member B17 [Source:H
14	205819_at	2.09	−0.95	0.51	MARCO	macrophage receptor with collagenous structure [Source:HGI
15	202833_s_at	2.04	−2.04	0.77	SERPINA1	serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC
16	202357_s_at	1.99	−1.29	0.58	CFB	complement factor B [Source:HGNC Symbol;Acc:HGNC:1037
17	212062_at	1.97	−1.07	0.46	ATP9A	ATPase phospholipid transporting 9A (putative) [Source:HGN
18	202917_s_at	1.96	−1.75	0.63	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:
19	214049_x_at	1.96	−1.08	0.59	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
20	210116_at	1.95	−1.66	0.48	SH2D1A	SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGN(

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	166 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	9e−87	130 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
3	1e−66	63 / 102	Refer	WIRTH_EBV B−cells
4	2e−56	53 / 85	Lympl	Sha_DLBCL UP
5	9e−51	78 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
6	5e−47	96 / 480	Cance	Lembcke_Colonic Inflammation
7	8e−46	69 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
8	8e−46	68 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
9	5e−45	43 / 71	Melar	Tirosh_Macrophage specific genes−melanoma
10	3e−44	86 / 404	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
11	4e−41	81 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
12	6e−41	42 / 78	Melar	Tirosh_expression higher in CAFs than in T−cells
13	7e−41	74 / 317	Cance	SPANG_BCL6−index2
14	8e−41	60 / 194	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
15	2e−38	61 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
16	4e−35	54 / 186	Cance	SPANG_LPS−index2
17	3e−33	61 / 265	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
18	2e−32	59 / 255	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
19	2e−32	49 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
20	1e−31	40 / 104	GSEA	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
21	1e−31	66 / 336	BP	immune response
22	5e−31	67 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
23	3e−30	60 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
24	4e−29	62 / 323	BP	inflammatory response
25	6e−29	56 / 261	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
26	5e−28	45 / 166	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
27	1e−27	58 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
28	1e−27	47 / 187	HM	HALLMARK_INFLAMMATORY_RESPONSE
29	3e−27	51 / 229	GSEA	QI_PLASMACYTOMA_UP
30	7e−27	33 / 83	Melar	TCGA_melanoma_immune_high
31	8e−27	45 / 176	HM	HALLMARK_ALLOGRAFT_REJECTION
32	5e−26	47 / 202	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
33	1e−25	99 / 902	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
34	3e−24	44 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
35	5e−24	71 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
36	5e−24	30 / 78	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
37	1e−23	64 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
38	1e−23	89 / 795	GSEA	NUYTTEN_EZH2_TARGETS_UP
39	2e−23	58 / 354	GSEA	RODWELL_AGING_KIDNEY_UP
40	2e−23	27 / 62	Lympl	Monti_Host_response_cluster

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	6 / 92	HORVATH_aging_genes meth DOWN
2	0.5	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.7	3 / 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	1e−31	66 / 336	immune response
2	4e−29	62 / 323	inflammatory response
3	5e−22	62 / 431	immune system process
4	3e−19	46 / 274	cytokine−mediated signaling pathway
5	3e−15	50 / 403	neutrophil degranulation
6	6e−15	28 / 131	chemotaxis
7	1e−13	45 / 367	innate immune response
8	2e−13	19 / 63	chemokine−mediated signaling pathway
9	8e−13	29 / 169	response to lipopolysaccharide
10	2e−11	32 / 232	cell surface receptor signaling pathway
11	4e−11	22 / 113	regulation of immune response
12	1e−10	25 / 156	positive regulation of ERK1 and ERK2 cascade
13	5e−10	50 / 553	apoptotic process
14	5e−09	16 / 75	cellular response to interferon−gamma
15	5e−09	8 / 14	cellular response to zinc ion

Cancer

Rank	p−value	#in/all	Geneset
1	5e−47	96 / 480	Lembcke_Colonic Inflammation
2	7e−41	74 / 317	SPANG_BCL6−index2
3	4e−35	54 / 186	SPANG_LPS−index2
4	2e−09	8 / 13	GENTLES_modul18
5	3e−07	6 / 10	BENTINK_ras.4
6	1e−06	15 / 96	PanCan_TXmisReg_geneset_nanostring
7	1e−04	11 / 80	PanCan_JAK−ST_geneset_nanostring
8	1e−04	1 / 14	LIU_PROSTATE_CANCER_DN
9	1e−04	5 / 15	WANG_ER_UP
10	5e−03	12 / 147	PanCan_MAPK_geneset_nanostring
11	9e−03	3 / 13	GENTLES_modul11
12	1e−02	3 / 14	GUSTAFSON_PI3K_UP
13	1e−02	3 / 14	BENTINK_src.10
14	6e−02	1 / 16	LIU_LIVER_CANCER
15	6e−02	2 / 12	HLA2_signature

CC

Rank	p−value	#in/all	Geneset
1	1e−15	91 / 1090	extracellular space
2	1e−14	115 / 1611	extracellular region
3	1e−13	31 / 179	external side of plasma membrane
4	2e−13	181 / 3210	plasma membrane
5	5e−11	18 / 74	secretory granule membrane
6	1e−09	171 / 3270	integral component of membrane
7	5e−09	77 / 1128	integral component of plasma membrane
8	6e−09	13 / 48	ficolin−1−rich granule membrane
9	1e−08	42 / 462	cell surface
10	1e−08	14 / 60	tertiary granule membrane
11	1e−07	240 / 5339	membrane
12	2e−07	121 / 2239	extracellular exosome
13	3e−07	43 / 537	perinuclear region of cytoplasm
14	8e−07	7 / 17	T cell receptor complex
15	2e−05	25 / 281	lysosome

Chr

Rank	p−value	#in/all	Geneset
1	0.2	34 / 832	Chr 2
2	0.2	21 / 490	Chr 10
3	0.2	51 / 1325	Chr 1
4	0.3	30 / 756	Chr 11
5	0.3	22 / 556	Chr X
6	0.3	15 / 369	Chr 20
7	0.4	6 / 139	Chr 21
8	0.4	29 / 776	Chr 17
9	0.5	24 / 669	Chr 6
10	0.6	24 / 700	Chr 12
11	0.6	20 / 585	Chr 7
12	0.6	16 / 480	Chr 4
13	0.6	23 / 689	Chr 3
14	0.6	11 / 333	Chr 22
15	0.7	14 / 437	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−26	68 / 432	monocytes peripheral blood_3_TxFlnk
2	3e−16	122 / 1676	Fetal_TxTrans
3	1e−14	185 / 3223	monocytes peripheral blood_6_EnhG
4	2e−14	63 / 626	natural killer cells peripheral blood_3_TxFlnk
5	4e−14	154 / 2507	Mid_Frontal_Lobe_ReprPC
6	6e−11	91 / 1308	Mid_Frontal_Lobe_K9K27me3
7	5e−09	38 / 383	K9acLow_Colon
8	7e−09	63 / 847	Fetal_TssP
9	3e−08	98 / 1639	Fetal_TssF
10	4e−08	339 / 8200	monocytes peripheral blood_2_TssAFlnk
11	3e−07	107 / 1930	Fetal_TssA
12	5e−07	62 / 932	Tcells peripheral blood_3_TxFlnk
13	8e−07	68 / 1072	Mid_Frontal_Lobe_ReprPCWk
14	1e−06	58 / 867	Mid_Frontal_Lobe_Quies
15	1e−06	152 / 3110	14_ReprPCWk_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	166 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−30	60 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	4e−20	49 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	1e−10	23 / 132	Marisa_CRC−cluster−a
5	2e−09	8 / 13	Budinska_B_Lower crypt−like_DOWN
6	2e−07	11 / 43	Marisa_CRC−cluster−f
7	1e−06	34 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	3e−06	27 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
9	4e−05	10 / 60	Marisa_CRC−cluster−g
10	2e−04	26 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
11	2e−04	51 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	5e−04	55 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
13	5e−04	10 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	6e−04	34 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	1e−03	29 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

Glioma

Rank	p−value	#in/all	Geneset
1	9e−87	130 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	9e−51	78 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	8e−46	69 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
4	1e−21	46 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	7e−19	45 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
6	2e−13	36 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
7	2e−12	10 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
8	5e−12	20 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
9	9e−10	20 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
10	3e−08	12 / 45	Donson−innate immunity−associated with LTS in HGA
11	1e−07	14 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
12	3e−07	7 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
13	4e−06	91 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	3e−05	7 / 27	Donson−Misc immune function−associated with LTS in HGA
15	3e−05	5 / 12	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−46	68 / 223	MCLACHLAN_DENTAL_CARIES_UP
2	3e−44	86 / 404	RUTELLA_RESPONSE_TO_HGF_UP
3	4e−41	81 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
4	8e−41	60 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	2e−38	61 / 219	MCLACHLAN_DENTAL_CARIES_DN
6	3e−33	61 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
7	2e−32	59 / 255	HELLER_SILENCED_BY_METHYLATION_UP
8	1e−31	40 / 104	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
9	5e−31	67 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
10	6e−29	56 / 261	POOLA_INVASIVE_BREAST_CANCER_UP
11	5e−28	45 / 166	VERHAAK_AML_WITH_NPM1_MUTATED_UP
12	1e−27	58 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
13	3e−27	51 / 229	QI_PLASMACYTOMA_UP
14	5e−26	47 / 202	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
15	1e−25	99 / 902	CHEN_METABOLIC_SYNDROM_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	2e−32	49 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	1e−27	47 / 187	HALLMARK_INFLAMMATORY_RESPONSE
3	8e−27	45 / 176	HALLMARK_ALLOGRAFT_REJECTION
4	3e−24	44 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	1e−18	36 / 170	HALLMARK_IL2_STAT5_SIGNALING
6	6e−17	25 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	3e−16	34 / 178	HALLMARK_COMPLEMENT
8	6e−11	25 / 150	HALLMARK_APOPTOSIS
9	4e−08	15 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	4e−06	21 / 194	HALLMARK_KRAS_SIGNALING_UP
11	9e−06	20 / 188	HALLMARK_HYPOXIA
12	5e−05	15 / 130	HALLMARK_COAGULATION
13	1e−04	18 / 191	HALLMARK_P53_PATHWAY
14	2e−02	6 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	2e−02	12 / 181	HALLMARK_XENOBIOTIC_METABOLISM

Immunome

Rank	p−value	#in/all	Geneset
1	8e−12	18 / 67	Angelova_immune−metagene−T−cells
2	3e−10	12 / 32	Angelova_immune−metagene−effector_memory_CD8
3	2e−09	11 / 29	Angelova_immune−metagene−Th1
4	1e−08	12 / 42	Angelova_immune−metagene−TGD
5	3e−08	12 / 45	Angelova_immune−metagene−MDSC
6	2e−06	7 / 19	Angelova_immune−metagene−iDC
7	3e−04	5 / 18	Angelova_CRC_immunostimulators
8	8e−04	3 / 6	Immunity_immune−checkpoint−inhibitors
9	8e−04	4 / 13	Angelova_immune−metagene−activated_B−cells
10	1e−03	5 / 23	Angelova_immune−metagene−Treg
11	1e−03	3 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1e−03	5 / 25	Angelova_immune−metagene−DC
13	2e−03	4 / 17	Angelova_immune−metagene−central_memory_CD8
14	4e−03	3 / 10	Angelova_immune−metagene−TFH
15	5e−03	4 / 21	Angelova_immune−metagene−central_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−06	6 / 14	Huan_blood−pressure_SBP−signature
2	3e−05	5 / 12	DUMEAUX_Women normal BMI literature genes up
3	8e−05	6 / 22	DUMEAUX_High bmi enriched genes
4	2e−04	4 / 9	DUMEAUX_Monocytes in smokers literature genes up
5	8e−04	4 / 13	Huan_blood−pressure_DBP−signature
6	4e−03	2 / 3	Huan_blood−pressure_HTN−signature
7	1e−02	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	3e−02	2 / 8	Marjolein_ageing−genes_UP
9	3e−02	13 / 210	Homuth_BMI−associated−genes_DN
10	1e−01	3 / 32	Marjolein_ageing−genes_DN
11	3e−01	1 / 10	DUMEAUX_Smoking literature genes up
12	4e−01	3 / 62	DUMEAUX_Smoking enriched genes
13	4e−01	6 / 150	Homuth_BMI−associated−genes_UP
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

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−56	53 / 85	Sha_DLBCL UP
2	2e−23	27 / 62	Monti_Host_response_cluster
3	3e−22	36 / 135	DAVE_BL−vs−DLBCL
4	3e−21	39 / 173	Victora_Light zone signature
5	2e−20	42 / 213	SPANG_IL21 DN
6	1e−13	44 / 353	SPANG_CD40 6hrs DN
7	1e−11	9 / 12	BENTINK_mBL DOWN
8	4e−11	11 / 22	DAVE_NFkB BL DN
9	5e−11	14 / 41	ROSOLOWSKI_blue DOWN
10	2e−10	70 / 906	SPANG_BCR DN
11	2e−10	254 / 5404	HOPP_Strong_enhancer
12	3e−10	9 / 15	Care_Polarized immune response
13	3e−10	40 / 378	TARTE_Mature plasma cell signature
14	5e−10	12 / 33	Care_Extended T−cell
15	1e−09	18 / 88	ROSOLOWSKI_green UP

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−45	43 / 71	Tirosh_Macrophage specific genes−melanoma
2	6e−41	42 / 78	Tirosh_expression higher in CAFs than in T−cells
3	7e−27	33 / 83	TCGA_melanoma_immune_high
4	3e−18	18 / 33	Tirosh_T−cell specific genes−melanoma
5	8e−14	32 / 189	Tirosh_genes preferentially expressed by Tregs
6	4e−11	27 / 171	Landsberg_dedifferentiation_up
7	4e−09	19 / 107	Tirosh_Exhaustion program in Mel75
8	7e−06	13 / 85	Tirosh_AXL−signature
9	7e−06	4 / 5	Joensson_Melanoma Proliferative subtype
10	8e−06	10 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
11	1e−05	7 / 24	Tirosh_exhuastion−associated genes consitent across tumors
12	9e−05	19 / 204	Landsberg_dedifferentiation_down
13	3e−04	17 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
14	7e−03	16 / 230	Gerber_wt/wt_melanoma−cells−SpotC
15	1e−02	5 / 38	Hugo_melanoma−BRAFmut−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	1e−09	25 / 173	cytokine activity
2	5e−09	12 / 39	chemokine activity
3	3e−06	46 / 644	protein homodimerization activity
4	3e−06	7 / 20	chemokine receptor activity
5	6e−06	8 / 30	tumor necrosis factor receptor binding
6	1e−05	6 / 16	CCR chemokine receptor binding
7	1e−05	37 / 500	signal transducer activity
8	4e−05	8 / 38	cytokine receptor activity
9	5e−05	9 / 50	amyloid−beta binding
10	1e−04	19 / 205	receptor activity
11	3e−04	15 / 154	serine−type endopeptidase activity
12	4e−04	5 / 19	lipopolysaccharide binding
13	4e−04	5 / 19	tumor necrosis factor−activated receptor activity
14	4e−04	4 / 11	MAP kinase tyrosine/serine/threonine phosphatase activity
15	4e−04	6 / 29	coreceptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	4 / 29	hsa−miR−647
2	0.02	3 / 18	hsa−miR−1228
3	0.02	3 / 18	hsa−miR−591
4	0.03	5 / 50	hsa−miR−384
5	0.03	9 / 128	hsa−miR−200b
6	0.04	4 / 36	hsa−miR−146b−3p
7	0.04	6 / 71	hsa−miR−188−3p
8	0.04	2 / 9	hsa−miR−604
9	0.05	6 / 78	hsa−miR−216b
10	0.06	3 / 26	hsa−miR−1226
11	0.06	8 / 122	hsa−miR−506
12	0.06	8 / 123	hsa−miR−429
13	0.06	8 / 123	hsa−miR−200c
14	0.07	4 / 44	hsa−miR−629
15	0.07	5 / 64	hsa−miR−562

Pneumonia

Rank	p−value	#in/all	Geneset
1	2e−14	19 / 56	Burnham_sep_vs_con_DN
2	3e−12	16 / 48	Burnham_cap_fp_vs_con_DN
3	1e−09	21 / 122	Terre_IMS_influenza_meta_signature
4	2e−09	14 / 52	Burnham_day1_vs_5_DN
5	4e−06	17 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	2e−05	10 / 57	Burnham_viral_UP
7	3e−05	9 / 48	Burnham_viral_DN
8	2e−04	7 / 37	Sweeney_viral_up
9	3e−04	5 / 18	Scicluna_UP
10	2e−03	8 / 68	Burnham_sep_vs_con_UP
11	3e−03	8 / 71	Burnham_cap_fp_vs_con_UP
12	3e−02	4 / 33	Sweeney_viral_dn
13	5e−02	4 / 41	Scicluna_DN
14	3e−01	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
15	3e−01	3 / 54	Burnham_timecourse

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−66	63 / 102	WIRTH_EBV B−cells
2	2e−19	29 / 99	Chaussabel_1,5_Myeloid lineage
3	4e−16	48 / 355	WIRTH_Immune system
4	3e−14	32 / 182	WIRTH_post GC B−cells
5	3e−13	24 / 109	Chaussabel_2,6_Myeloid lineage
6	9e−13	19 / 68	Chaussabel_2,1_Cytotoxic cells
7	2e−11	30 / 204	Chaussabel_3,2_Inflammation I
8	5e−11	29 / 198	Chaussabel_3,3_Inflammation II
9	2e−08	15 / 72	Chaussabel_3,1_Interferon−inducible
10	9e−08	13 / 59	Chaussabel_2,10_Immune related cell surface molecules
11	2e−07	41 / 496	PROTEINATLAS_spleen
12	2e−04	19 / 219	WIRTH_GC B−cells
13	2e−02	33 / 645	PROTEINATLAS_bone marrow
14	2e−02	34 / 678	PROTEINATLAS_lymph node
15	2e−02	3 / 18	JONGENEEL_Monocytes

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−07	120 / 2254	ICGC_BatfPcr1_targets
2	6e−06	153 / 3213	ICGC_Pu1_targets
3	3e−05	158 / 3435	ICGC_Ebfsc137065_targets
4	3e−04	77 / 1508	ICGC_Mef2_targets
5	3e−04	204 / 4851	ICGC_Runx3_targets
6	4e−04	82 / 1636	ICGC_Bcl11_targets
7	4e−04	94 / 1941	ICGC_Bcl3_targets
8	2e−03	105 / 2321	ICGC_Rad21_targets
9	3e−03	53 / 1041	ICGC_P300_targets
10	5e−03	157 / 3778	ICGC_Pol24_targets
11	5e−03	96 / 2150	ICGC_Irf4_targets
12	1e−02	154 / 3796	ICGC_Nficsc81335_targets
13	2e−02	162 / 4072	ICGC_Mta3_targets
14	2e−02	66 / 1494	ICGC_Cebpbsc150_targets
15	3e−02	118 / 2899	ICGC_Nfatc1_targets

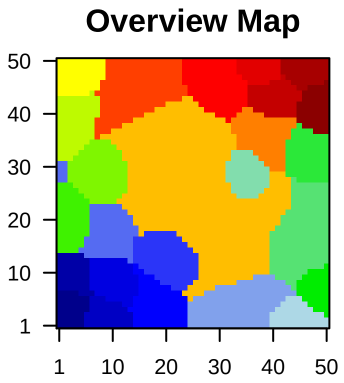
K−Means Cluster

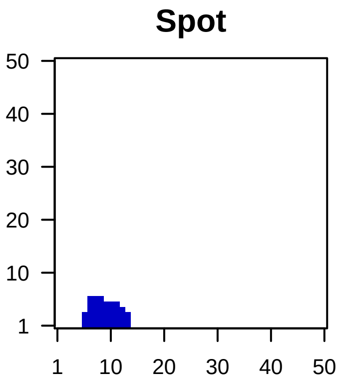
Spot Summary: P

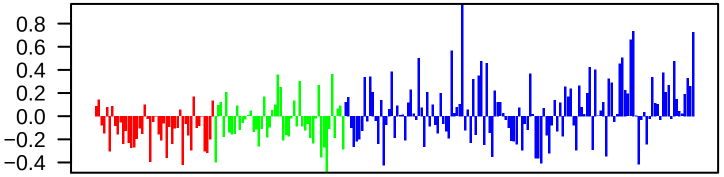
\# metagenes = 43
\# genes = 541

<r> metagenes = 0.91
<r> genes = 0.3
beta: r2= 12.03 / log p= −Inf

\# samples with spot = 50 (22.6 %)
mBL : 1 (2.3 %)
intermediate : 7 (14.6 %)
non−mBL : 42 (32.6 %)





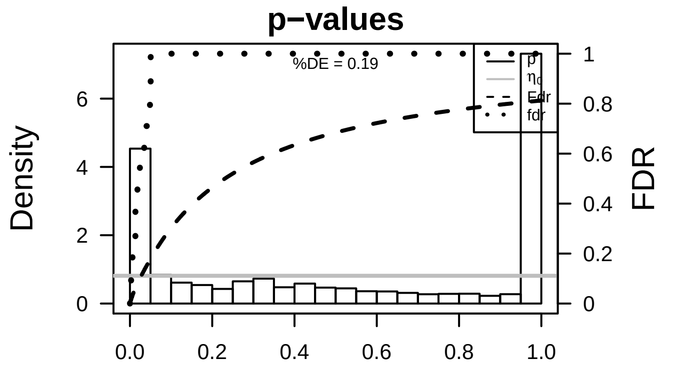


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204259_at	3.15	−0.97	0.39	MMP7	matrix metallopeptidase 7 [Source:HGNC Symbol;Acc:HGNC
2	214465_at	3.11	−0.71	0.48	ORM2	orosomucoid 2 [Source:HGNC Symbol;Acc:HGNC:8499]
3	202018_s_at	3.09	−0.86	0.21	LTF	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
4	205040_at	2.98	−1.17	0.54	ORM1	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
5	205041_s_at	2.9	−1.48	0.54	ORM1	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
6	205828_at	2.88	−0.77	0.35	MMP3	matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC
7	204475_at	2.81	−1.25	0.49	MMP1	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
8	202859_x_at	2.69	−1.11	0.33	CXCL8	C−X−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
9	214974_x_at	2.66	−0.89	0.4	CXCL5	C−X−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc
10	205755_at	2.49	−0.9	0.46	ITIH3	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
11	211597_s_at	2.37	−1.26	0.45	HOPX	HOP homeobox [Source:HGNC Symbol;Acc:HGNC:24961]
12	209875_s_at	2.33	−1.91	0.47	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
13	202718_at	2.31	−1.6	0.49	IGFBP2	insulin like growth factor binding protein 2 [Source:HGNC Sy
14	37892_at	2.31	−0.8	0.56	COL11A1	collagen type XI alpha 1 chain [Source:HGNC Symbol;Acc:H
15	211506_s_at	2.3	−0.85	0.32	CXCL8	C−X−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
16	204470_at	2.29	−1.07	0.35	CXCL1	C−X−C motif chemokine ligand 1 [Source:HGNC Symbol;Acc
17	207850_at	2.25	−0.9	0.34	CXCL3	C−X−C motif chemokine ligand 3 [Source:HGNC Symbol;Acc
18	204561_x_at	2.19	−1.95	0.31		APOC4−APOC2 readthrough (NMD candidate) [Source:HGN
19	218678_at	2.18	−1.04	0.33	NES	nestin [Source:HGNC Symbol;Acc:HGNC:7756]
20	203234_at	2.18	−1.33	0.5	UPP1	uridine phosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:1

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	124 / 214	Lympl	LENZ_Stromal signature 1
2	1e−99	100 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	1e−99	132 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	6e−82	84 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
5	5e−74	107 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
6	3e−69	81 / 212	CC	extracellular matrix
7	3e−63	49 / 63	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
8	2e−62	74 / 197	GSEA	NABA_CORE_MATRISOME
9	5e−61	125 / 747	GSEA	NABA_MATRISOME
10	3e−59	51 / 78	Melar	Tirosh_CAF−cell specific genes
11	8e−58	77 / 247	GSEA	BOQUEST_STEM_CELL_UP
12	1e−55	88 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
13	5e−55	59 / 132	Colon	Marisa_CRC−cluster−a
14	3e−53	74 / 253	CC	proteinaceous extracellular matrix
15	2e−52	138 / 1090	CC	extracellular space
16	6e−52	4 / 14	Cance	LIU_PROSTATE_CANCER_DN
17	6e−52	4 / 14	Cance	LIU_PROSTATE_CANCER_DN
18	2e−51	103 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
19	2e−51	85 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
20	6e−48	55 / 138	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
21	9e−47	159 / 1611	CC	extracellular region
22	2e−45	67 / 249	GSEA	ONDER_CDH1_TARGETS_2_UP
23	4e−45	59 / 183	BP	extracellular matrix organization
24	3e−43	69 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
25	2e−42	82 / 443	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
26	2e−41	50 / 136	GSEA	NABA_ECM_GLYCOPROTEINS
27	2e−41	218 / 3168	Lympl	HOPP_Repressed
28	5e−41	71 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
29	2e−40	58 / 207	GSEA	WANG_SMARCE1_TARGETS_UP
30	1e−39	82 / 480	Cance	Lembcke_Colonic Inflammation
31	1e−38	115 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
32	1e−36	71 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
33	1e−36	34 / 60	GSEA	CROMER_TUMORIGENESIS_UP
34	1e−35	38 / 85	Gliom	ScoV_0.999_Sturm_E2_IDH_DN
35	4e−35	155 / 1894	Lympl	HOPP_Poised_promoter
36	1e−33	31 / 54	GSEA	CROONQUIST_STROMAL_STIMULATION_UP
37	3e−33	57 / 262	GSEA	PASINI_SUZ12_TARGETS_DN
38	4e−33	41 / 117	GSEA	ZHU_CMV_ALL_DN
39	1e−32	69 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
40	4e−32	53 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up



Aging

Rank	p−value	#in/all	Geneset
1	0.04	7 / 107	HORVATH_aging_genes meth UP
2	0.06	6 / 92	HORVATH_aging_genes meth DOWN
3	0.17	3 / 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	3e−69	81 / 212	extracellular matrix
2	3e−53	74 / 253	proteinaceous extracellular matrix
3	2e−52	138 / 1090	extracellular space
4	9e−47	159 / 1611	extracellular region
5	1e−28	30 / 66	basement membrane
6	4e−28	50 / 241	endoplasmic reticulum lumen
7	3e−21	144 / 2239	extracellular exosome
8	7e−21	58 / 462	cell surface
9	5e−17	45 / 345	focal adhesion
10	1e−16	21 / 65	collagen trimer
11	8e−10	150 / 3210	plasma membrane
12	4e−09	14 / 63	platelet alpha granule lumen
13	1e−06	7 / 20	lamellipodium membrane
14	8e−06	16 / 146	lamellipodium
15	4e−05	11 / 84	Golgi lumen

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−55	59 / 132	Marisa_CRC−cluster−a
2	3e−43	69 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	1e−38	115 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	4e−32	59 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	1e−19	28 / 103	Marisa_CRC−cluster−b
6	3e−06	23 / 255	Kosinski_top−crypt−long−list
7	4e−06	26 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
8	5e−05	25 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
9	1e−04	10 / 77	Ang_CRC_Hypermethylated
10	3e−04	9 / 72	Ang_CRC−CIMPH−vs−L_hyper
11	9e−04	3 / 7	Budinska_D_Mesenchymal_UP
12	9e−04	2 / 2	Budinska_A_Surface crypt−like_DOWN
13	9e−04	24 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
14	2e−03	5 / 31	Kosinski_lower−crypt−short−list
15	3e−03	4 / 20	Kosinski_top−crypt−short−list

HM

Rank	p−value	#in/all	Geneset
1	1e−99	100 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	8e−22	33 / 130	HALLMARK_COAGULATION
3	4e−21	38 / 188	HALLMARK_HYPOXIA
4	3e−18	35 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	1e−17	17 / 34	HALLMARK_ANGIOGENESIS
6	1e−17	30 / 141	HALLMARK_UV_RESPONSE_DN
7	7e−10	22 / 150	HALLMARK_APOPTOSIS
8	4e−09	24 / 194	HALLMARK_MYOGENESIS
9	4e−09	24 / 194	HALLMARK_KRAS_SIGNALING_UP
10	4e−08	22 / 187	HALLMARK_INFLAMMATORY_RESPONSE
11	1e−06	19 / 174	HALLMARK_APICAL_JUNCTION
12	1e−06	13 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
13	2e−06	19 / 178	HALLMARK_COMPLEMENT
14	9e−06	18 / 182	HALLMARK_GLYCOLYSIS
15	5e−05	16 / 170	HALLMARK_IL2_STAT5_SIGNALING

Lymphnoma

Rank	p−value	#in/all	Geneset
1	1e−99	124 / 214	LENZ_Stromal signature 1
2	2e−41	218 / 3168	HOPP_Repressed
3	4e−35	155 / 1894	HOPP_Poised_promoter
4	2e−17	28 / 121	ROSOLOWSKI_green total
5	1e−13	17 / 53	LENZ_Stromal signature 2
6	8e−13	41 / 378	TARTE_Mature plasma cell signature
7	5e−12	22 / 118	Subero_INT_hyper_meth
8	7e−12	23 / 132	Subero_DLBCL_hyper_meth
9	2e−09	113 / 2206	HOPP_Heterochrom
10	4e−08	15 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
11	1e−07	13 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
12	3e−06	13 / 91	Subero_T−ALL_hyper_meth
13	4e−06	10 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
14	1e−05	12 / 88	ROSOLOWSKI_green UP
15	2e−05	12 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	10 / 129	hsa−miR−29a
2	0.007	10 / 135	hsa−miR−29c
3	0.008	2 / 5	hsa−miR−126
4	0.012	6 / 64	hsa−miR−562
5	0.013	15 / 262	hsa−miR−32
6	0.013	5 / 47	hsa−miR−1279
7	0.015	9 / 128	hsa−miR−583
8	0.016	7 / 87	hsa−miR−501−5p
9	0.016	7 / 88	hsa−miR−1271
10	0.018	3 / 19	hsa−miR−596
11	0.020	4 / 35	hsa−miR−331−5p
12	0.021	9 / 136	hsa−miR−511
13	0.028	5 / 57	hsa−miR−876−3p
14	0.028	10 / 166	hsa−miR−29b
15	0.031	12 / 217	hsa−miR−92a

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−45	59 / 183	extracellular matrix organization
2	2e−31	74 / 500	cell adhesion
3	5e−22	42 / 223	angiogenesis
4	1e−18	35 / 185	cellular protein metabolic process
5	7e−18	21 / 58	collagen catabolic process
6	8e−16	16 / 35	collagen fibril organization
7	1e−13	27 / 157	positive regulation of cell migration
8	2e−12	17 / 62	extracellular matrix disassembly
9	5e−11	11 / 25	endodermal cell differentiation
10	1e−10	37 / 368	negative regulation of cell proliferation
11	6e−10	19 / 110	platelet degranulation
12	1e−09	16 / 78	wound healing
13	7e−09	22 / 169	cell migration
14	1e−08	16 / 91	ossification
15	1e−08	7 / 12	positive regulation of peptidase activity

Chr

Rank	p−value	#in/all	Geneset
1	0.01	24 / 480	Chr 4
2	0.04	20 / 437	Chr 8
3	0.07	28 / 700	Chr 12
4	0.09	32 / 832	Chr 2
5	0.11	16 / 382	Chr 15
6	0.12	7 / 139	Chr 21
7	0.16	19 / 492	Chr 9
8	0.16	22 / 585	Chr 7
9	0.31	43 / 1325	Chr 1
10	0.33	23 / 689	Chr 3
11	0.40	18 / 554	Chr 5
12	0.59	7 / 242	Chr 13
13	0.67	9 / 333	Chr 22
14	0.80	12 / 490	Chr 10
15	0.81	4 / 184	Chr 18

Glioma

Rank	p−value	#in/all	Geneset
1	1e−35	38 / 85	ScoV_0.999_Sturm_E2_IDH_DN
2	4e−32	53 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	1e−27	52 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	1e−21	58 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
5	6e−19	27 / 99	GIEZELT_GBM_WT_up_VS_mut
6	2e−14	19 / 64	cultured astroglia vs. in vivo astrocytes
7	2e−14	15 / 35	Colman_survival_associated
8	1e−12	21 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	8e−12	31 / 242	ScoV_0.5_Sturm_C1_IDH_DN
10	3e−10	22 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	2e−09	7 / 10	Phillips MES up vs Prolif & PN
12	8e−09	18 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
13	1e−08	19 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	2e−08	11 / 41	Gorovets_LGG_PG_subclass
15	1e−06	15 / 112	Christensen_hypermethylated_in_grade3_astrocytoma

Immunome

Rank	p−value	#in/all	Geneset
1	8e−05	6 / 25	Angelova_immune−metagene−DC
2	2e−04	4 / 11	Angelova_immune−metagene−macrophages
3	5e−03	5 / 38	Angelova_immune−metagene−mast−cells
4	1e−02	3 / 17	Angelova_immune−metagene−central_memory_CD8
5	2e−02	3 / 19	Angelova_immune−metagene−iDC
6	3e−02	3 / 23	Angelova_immune−metagene−Th2
7	4e−02	4 / 42	Angelova_immune−metagene−TGD
8	1e−01	2 / 18	Angelova_immune−metagene−pDC
9	1e−01	2 / 21	Angelova_immune−metagene−central_memory_CD4
10	1e−01	1 / 5	Angelova_immune−metagene−NK56_bright
11	2e−01	1 / 8	Immunity_HLA−class−II
12	3e−01	1 / 12	Angelova_immune−metagene−NK56_dim
13	4e−01	1 / 15	Angelova_immune−metagene−NK
14	4e−01	1 / 18	Angelova_CRC_immunostimulators
15	5e−01	1 / 23	Angelova_immune−metagene−Treg

Melanoma

Rank	p−value	#in/all	Geneset
1	3e−59	51 / 78	Tirosh_CAF−cell specific genes
2	3e−28	70 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	5e−13	20 / 85	Tirosh_AXL−signature
4	4e−08	14 / 75	Tirosh_Endothelial−cell specific genes−melanoma
5	7e−07	20 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	4e−06	18 / 171	Landsberg_dedifferentiation_up
7	2e−04	7 / 41	Tirosh_top50 correlated genes PC3
8	8e−04	17 / 236	Gerber_wt/wt_group3−specific
9	3e−03	8 / 81	Tirosh_Genes in the MITF program
10	1e−02	3 / 17	Hugo_melanoma−all−MET_UP
11	2e−02	6 / 71	Tirosh_Macrophage specific genes−melanoma
12	2e−02	4 / 37	Hugo_melanoma−all−MET_DN
13	3e−02	6 / 78	Tirosh_expression higher in CAFs than in T−cells
14	3e−02	3 / 24	Gerami_melanoma−metastatic−risk_DN
15	3e−02	2 / 10	Joensson_Melanoma Normal like subtype

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.01	5 / 48	Burnham_viral_DN
2	0.09	4 / 57	Burnham_day1_vs_5_UP
3	0.11	7 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.15	4 / 68	Burnham_sep_vs_con_UP
5	0.16	4 / 71	Burnham_cap_fp_vs_con_UP
6	0.20	3 / 52	Burnham_day1_vs_5_DN
7	0.26	2 / 33	Sweeney_viral_dn
8	0.42	1 / 18	Scicluna_UP
9	0.42	2 / 48	Burnham_cap_fp_vs_con_DN
10	0.71	3 / 122	Terre_IMS_influenza_meta_signature
11	0.71	1 / 41	Scicluna_DN
12	0.79	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
13	0.81	1 / 54	Burnham_timecourse
14	0.82	1 / 56	Burnham_sep_vs_con_DN
15	0.82	1 / 57	Burnham_viral_UP

TF

Rank	p−value	#in/all	Geneset
1	6e−09	70 / 1148	HEBENSTREIT_low expression TF
2	3e−02	85 / 2321	ICGC_Rad21_targets
3	5e−01	49 / 1636	ICGC_Bcl11_targets
4	7e−01	65 / 2254	ICGC_BatfPcr1_targets
5	7e−01	29 / 1032	ICGC_Usf1_targets
6	8e−01	59 / 2150	ICGC_Irf4_targets
7	8e−01	10 / 415	ICGC_RxraPcr1_targets
8	8e−01	27 / 1041	ICGC_P300_targets
9	9e−01	11 / 485	ICGC_NrsfPcr2_targets
10	9e−01	94 / 3435	ICGC_Ebfsc137065_targets
11	9e−01	86 / 3213	ICGC_Pu1_targets
12	9e−01	116 / 4264	ICGC_Pax5_targets
13	9e−01	34 / 1387	HEBENSTREIT_high expression TF
14	1e+00	10 / 522	ICGC_SrfPcr2_targets
15	1e+00	46 / 1941	ICGC_Bcl3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	6e−52	4 / 14	LIU_PROSTATE_CANCER_DN
2	1e−39	82 / 480	Lembcke_Colonic Inflammation
3	1e−11	9 / 13	GENTLES_modul17
4	9e−07	20 / 187	PanCan_PI3K_geneset_nanostring
5	9e−03	3 / 15	RHODES_CANCER_META_SIGNATURE
6	1e−02	5 / 47	PanCan_TGF−B_geneset_nanostring
7	2e−02	3 / 18	PanCan_Notch_geneset_nanostring
8	6e−02	2 / 14	GENTLES_modul13
9	7e−02	6 / 96	PanCan_TXmisReg_geneset_nanostring
10	7e−02	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	8e−02	8 / 147	PanCan_MAPK_geneset_nanostring
12	8e−02	2 / 16	GENTLES_modul16
13	1e−01	7 / 134	PanCan_RAS_geneset_nanostring
14	2e−01	4 / 80	PanCan_JAK−ST_geneset_nanostring
15	2e−01	15 / 409	Lembcke_Normal vs Adenoma

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−61	267 / 3724	Tcells peripheral blood_12_EnhBiv
2	3e−58	264 / 3734	Tcells peripheral blood_13_ReprPC
3	5e−56	224 / 2765	Tregulatory cells peripheral blood_13_ReprPC
4	2e−54	221 / 2747	Bcells peripheral blood_12_EnhBiv
5	2e−50	201 / 2405	Bcells peripheral blood_13_ReprPC
6	2e−48	189 / 2194	Thelper cells peripheral blood_12_EnhBiv
7	7e−48	202 / 2515	natural killer cells peripheral blood_13_ReprPC
8	2e−47	205 / 2602	natural killer cells peripheral blood_12_EnhBiv
9	2e−46	253 / 3918	Tcells peripheral blood_14_ReprPCWk
10	2e−45	207 / 2724	Tcells peripheral blood_11_BivFlnk
11	1e−44	188 / 2300	Thelper cells peripheral blood_13_ReprPC
12	1e−43	157 / 1660	T CD8+ naive cells peripheral blood_12_EnhBiv
13	1e−42	217 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
14	3e−42	213 / 3001	Bcells peripheral blood_14_ReprPCWk
15	4e−42	194 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	132 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	6e−82	84 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
3	5e−74	107 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
4	3e−63	49 / 63	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
5	2e−62	74 / 197	NABA_CORE_MATRISOME
6	5e−61	125 / 747	NABA_MATRISOME
7	8e−58	77 / 247	BOQUEST_STEM_CELL_UP
8	1e−55	88 / 366	LIM_MAMMARY_STEM_CELL_UP
9	6e−52	4 / 14	LIU_PROSTATE_CANCER_DN
10	2e−51	103 / 589	WONG_ADULT_TISSUE_STEM_MODULE
11	2e−51	85 / 376	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
12	6e−48	55 / 138	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
13	2e−45	67 / 249	ONDER_CDH1_TARGETS_2_UP
14	2e−42	82 / 443	CHICAS_RB1_TARGETS_CONFLUENT
15	2e−41	50 / 136	NABA_ECM_GLYCOPROTEINS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	3 / 10	DUMEAUX_Smoking literature genes up
2	0.064	2 / 14	Huan_blood−pressure_SBP−signature
3	0.070	3 / 32	Marjolein_ageing−genes_DN
4	0.115	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	0.192	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
6	0.216	1 / 8	Marjolein_ageing−genes_UP
7	0.285	3 / 62	DUMEAUX_Smoking enriched genes
8	0.306	1 / 12	DUMEAUX_Women normal BMI literature genes up
9	0.327	1 / 13	Huan_blood−pressure_DBP−signature
10	0.443	7 / 210	Homuth_BMI−associated−genes_DN
11	0.832	3 / 150	Homuth_BMI−associated−genes_UP
12	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
13	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
14	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
15	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	5e−23	24 / 53	extracellular matrix structural constituent
2	2e−19	16 / 24	extracellular matrix binding
3	5e−16	27 / 126	heparin binding
4	6e−15	24 / 106	integrin binding
5	8e−14	17 / 52	collagen binding
6	7e−13	49 / 517	calcium ion binding
7	2e−11	13 / 37	growth factor binding
8	7e−11	10 / 20	insulin−like growth factor binding
9	9e−11	8 / 11	platelet−derived growth factor binding
10	1e−09	9 / 19	fibronectin binding
11	6e−09	7 / 11	peptidase activator activity
12	1e−07	15 / 93	protease binding
13	6e−07	6 / 12	insulin−like growth factor I binding
14	2e−06	6 / 14	platelet−derived growth factor receptor binding
15	2e−06	28 / 346	receptor binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−11	9 / 13	WIRTH_Sec. lymphoid organs
2	9e−07	21 / 204	Chaussabel_3,2_Inflammation I
3	3e−05	11 / 81	Chaussabel_1,2_Platelets
4	9e−05	9 / 62	VAQUERIZAS_Lung_TF
5	2e−04	17 / 209	Chaussabel_2,5_Immune related molecules
6	4e−04	7 / 45	VAQUERIZAS_Placenta_TF
7	2e−03	10 / 109	Chaussabel_2,6_Myeloid lineage
8	2e−03	5 / 30	VAQUERIZAS_Fetal lung_TF
9	3e−03	14 / 198	Chaussabel_3,3_Inflammation II
10	3e−03	9 / 99	Chaussabel_1,5_Myeloid lineage
11	4e−03	4 / 22	VAQUERIZAS_Trachea_TF
12	4e−03	5 / 36	VAQUERIZAS_Prostate_TF
13	6e−03	3 / 13	VAQUERIZAS_Skin_TF
14	1e−02	14 / 233	PROTEINATLAS_smooth muscle
15	1e−02	4 / 30	VAQUERIZAS_Smooth muscle_TF

K−Means Cluster

Spot Summary: Q

metagenes = 65
genes = 543

<r> metagenes = 0.87
<r> genes = 0.19
beta: r2= 4.55 / log p= −Inf

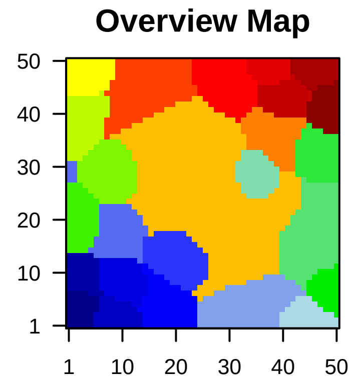
samples with spot = 38 (17.2 %)
intermediate : 3 (6.2 %)
non−mBL : 35 (27.1 %)

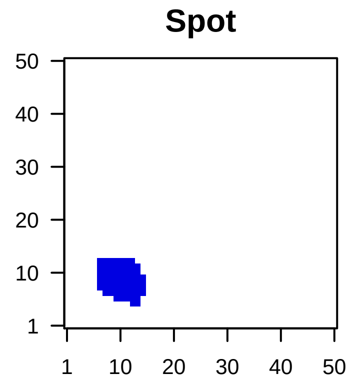
Spot Genelist

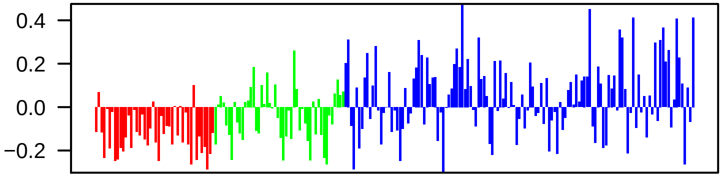
Rank	ID	max e	min e	r	Symbol	Description
1	216853_x_at	3.78	−1.3	0.43		immunoglobulin lambda variable 3−19 [Source:HGNC Symbo
2	214777_at	3.45	−1.71	0.36		immunoglobulin kappa variable 4−1 [Source:HGNC Symbol;A
3	216560_x_at	3.43	−1.18	0.41		immunoglobulin lambda variable 3−10 [Source:HGNC Symbo
4	217281_x_at	3.13	−1.46	0.45		immunoglobulin heavy variable 3−7 [Source:HGNC Symbol;A
5	211634_x_at	2.97	−1.71	0.38		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
6	216365_x_at	2.94	−0.92	0.32		
7	216984_x_at	2.81	−1.47	0.42		
8	211650_x_at	2.76	−1.14	0.4		immunoglobulin heavy variable 3−23 [Source:HGNC Symbol;
9	216412_x_at	2.72	−0.9	0.22		
10	214768_x_at	2.67	−1.59	0.41		immunoglobulin kappa variable 2−28 [Source:HGNC Symbol;
11	215214_at	2.64	−1.12	0.44		immunoglobulin lambda variable 3−25 [Source:HGNC Symbo
12	211640_x_at	2.62	−1.03	0.39		
13	211861_x_at	2.6	−0.7	0.5	CD28	CD28 molecule [Source:HGNC Symbol;Acc:HGNC:1653]
14	214470_at	2.58	−1.02	0.53	KLRB1	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
15	211635_x_at	2.55	−1.67	0.37		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
16	211643_x_at	2.53	−1.39	0.45		
17	211856_x_at	2.52	−0.69	0.45	CD28	CD28 molecule [Source:HGNC Symbol;Acc:HGNC:1653]
18	210439_at	2.5	−0.93	0.5	ICOS	inducible T cell costimulator [Source:HGNC Symbol;Acc:HGN
19	217179_x_at	2.49	−1.3	0.22		
20	210547_x_at	2.48	−1.17	0.31	ICA1	islet cell autoantigen 1 [Source:HGNC Symbol;Acc:HGNC:53

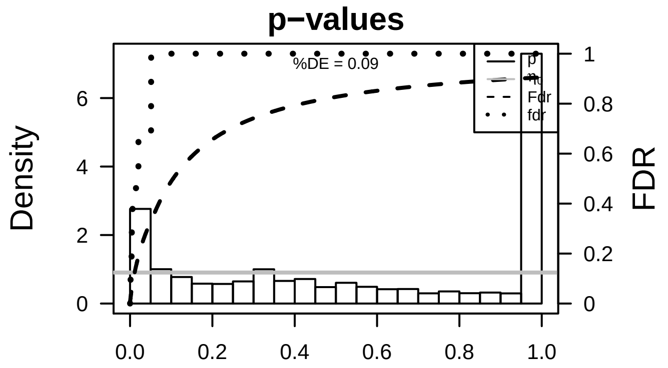
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−30	82 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	7e−26	65 / 431	BP	immune system process
3	2e−25	51 / 265	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
4	7e−23	54 / 336	BP	immune response
5	5e−21	53 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
6	1e−20	58 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
7	2e−20	19 / 33	Lymp	Care_Extended T−cell
8	3e−19	188 / 3210	CC	plasma membrane
9	3e−19	53 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
10	1e−18	28 / 102	Refer	WIRTH_EBV B−cells
11	2e−18	53 / 404	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
12	1e−17	33 / 161	BP	adaptive immune response
13	4e−17	54 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
14	4e−17	23 / 73	GSEA	HECKER_IFNB1_TARGETS
15	2e−16	21 / 62	Lymp	Monti_Host_response_cluster
16	2e−16	15 / 26	GSEA	MOSERLE_IFNA_RESPONSE
17	5e−16	22 / 72	Refer	Chaussabel_3,1_Interferon−inducible
18	5e−16	20 / 57	Pneu	Burnham_viral_UP
19	9e−16	255 / 5339	CC	membrane
20	8e−15	16 / 37	Pneu	Sweeney_viral_up
21	1e−14	17 / 44	MF	antigen binding
22	2e−14	54 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
23	5e−14	46 / 397	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
24	8e−14	74 / 902	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
25	9e−14	39 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
26	2e−13	20 / 76	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
27	3e−13	17 / 52	Pneu	Burnham_day1_vs_5_DN
28	3e−13	26 / 138	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
29	4e−13	67 / 795	GSEA	NUYTTEN_EZH2_TARGETS_UP
30	5e−13	15 / 39	BP	complement activation
31	6e−13	22 / 99	Refer	Chaussabel_1,5_Myeloid lineage
32	1e−12	172 / 3270	CC	integral component of membrane
33	1e−12	22 / 102	GSEA	KEGG_LYSOSOME
34	1e−12	23 / 113	BP	regulation of immune response
35	2e−12	37 / 299	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
36	3e−12	44 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
37	4e−12	27 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
38	4e−12	19 / 78	Mela	Tirosh_expression higher in CAFs than in T−cells
39	4e−12	41 / 367	BP	innate immune response
40	5e−12	40 / 353	GSEA	JOHNSTONE_PARVB_TARGETS_3_UP









Aging

Rank	p−value	#in/all	Geneset
1	0.5	2 / 47	TESCHENDORFF_age_hypermethylated
2	0.6	3 / 92	HORVATH_aging_genes meth DOWN
3	0.7	3 / 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	7e−26	65 / 431	immune system process
2	7e−23	54 / 336	immune response
3	1e−17	33 / 161	adaptive immune response
4	5e−13	15 / 39	complement activation
5	1e−12	23 / 113	regulation of immune response
6	4e−12	41 / 367	innate immune response
7	6e−11	15 / 52	complement activation, classical pathway
8	8e−11	15 / 53	regulation of complement activation
9	1e−10	13 / 38	negative regulation of viral genome replication
10	2e−10	17 / 76	Fc−gamma receptor signaling pathway involved in phagocytosis
11	3e−10	40 / 403	neutrophil degranulation
12	3e−10	23 / 146	defense response to virus
13	1e−08	14 / 63	type I interferon signaling pathway
14	4e−08	17 / 104	response to virus
15	9e−08	20 / 150	leukocyte migration

Cancer

Rank	p−value	#in/all	Geneset
1	9e−10	34 / 317	SPANG_BCL6−index2
2	5e−09	42 / 480	Lembcke_Colonic Inflammation
3	8e−09	24 / 186	SPANG_LPS−index2
4	3e−06	6 / 14	GENTLES_modul13
5	6e−04	4 / 13	GENTLES_modul11
6	8e−03	3 / 13	BENTINK_e2f3.1
7	1e−02	3 / 16	GENTLES_modul16
8	2e−02	0 / 14	LIU_PROSTATE_CANCER_DN
9	2e−02	4 / 32	KUIPER_MM good survival
10	6e−02	2 / 12	LIU_BREAST_CANCER
11	7e−02	2 / 13	GENTLES_modul18
12	1e−01	5 / 80	PanCan_JAK−ST_geneset_nanostring
13	3e−01	6 / 134	PanCan_RAS_geneset_nanostring
14	3e−01	1 / 11	LIU_PROSTATE_CANCER_UP
15	3e−01	1 / 12	GENTLES_modul12

CC

Rank	p−value	#in/all	Geneset
1	3e−19	188 / 3210	plasma membrane
2	9e−16	255 / 5339	membrane
3	1e−12	172 / 3270	integral component of membrane
4	5e−12	103 / 1611	extracellular region
5	4e−11	34 / 281	lysosome
6	4e−09	24 / 179	external side of plasma membrane
7	1e−08	16 / 85	lysosomal lumen
8	4e−08	41 / 494	endosome
9	4e−08	71 / 1128	integral component of plasma membrane
10	8e−08	116 / 2239	extracellular exosome
11	7e−06	9 / 42	azurophil granule membrane
12	3e−05	20 / 219	lysosomal membrane
13	1e−04	13 / 116	blood microparticle
14	1e−04	9 / 60	tertiary granule membrane
15	2e−04	57 / 1090	extracellular space

Chr

Rank	p−value	#in/all	Geneset
1	0.04	9 / 139	Chr 21
2	0.05	36 / 832	Chr 2
3	0.12	51 / 1325	Chr 1
4	0.13	21 / 492	Chr 9
5	0.17	11 / 242	Chr 13
6	0.20	14 / 333	Chr 22
7	0.25	19 / 490	Chr 10
8	0.27	25 / 669	Chr 6
9	0.33	15 / 403	Chr 14
10	0.43	24 / 700	Chr 12
11	0.54	18 / 554	Chr 5
12	0.58	24 / 756	Chr 11
13	0.60	15 / 480	Chr 4
14	0.73	16 / 556	Chr X
15	0.77	12 / 437	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−05	144 / 3223	monocytes peripheral blood_6_EnhG
2	2e−05	41 / 626	natural killer cells peripheral blood_3_TxFlnk
3	2e−05	162 / 3755	HSC_15_Quies
4	2e−05	135 / 3001	Bcells peripheral blood_14_ReprPCWk
5	2e−05	85 / 1676	Fetal_TxTrans
6	2e−05	133 / 2948	TssD1_Colon
7	5e−05	162 / 3825	Bcells peripheral blood_15_Quies
8	7e−05	170 / 4079	15_Quies_ESC_Endoderm
9	1e−04	268 / 7078	7_Enh_ESC_Mesoderm
10	2e−04	69 / 1372	Tregulatory cells peripheral blood_10_TssBiv
11	3e−04	257 / 6791	7_Enh_ESC_Endoderm
12	3e−04	40 / 695	monocytes peripheral blood_10_TssBiv
13	4e−04	157 / 3838	15_Quies_ESC_Mesoderm
14	5e−04	131 / 3110	14_ReprPCWk_ESC_Endoderm
15	5e−04	77 / 1639	Fetal_TssF

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−30	82 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	5e−14	46 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
3	5e−09	31 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	4e−07	14 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
5	1e−06	56 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	2e−05	57 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
7	4e−05	24 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
8	1e−04	83 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	3e−03	7 / 60	Marisa_CRC−cluster−g
10	1e−02	49 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
11	2e−02	4 / 31	Kosinski_lower−crypt−short−list
12	2e−02	7 / 83	Marisa_CRC−cluster−d
13	2e−02	2 / 7	Budinska_D_Mesenchymal_UP
14	3e−02	26 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
15	3e−02	2 / 9	Marisa_CRC−C2

Glioma

Rank	p−value	#in/all	Geneset
1	4e−17	54 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	8e−09	16 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
3	6e−08	28 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	1e−05	14 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
5	1e−05	9 / 45	Donson−innate immunity−associated with LTS in HGA
6	2e−04	20 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
7	6e−04	18 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
8	1e−03	18 / 242	ScoV_0.5_Sturm_C1_IDH_DN
9	1e−03	8 / 64	cultured astroglia vs. in vivo astrocytes
10	1e−03	4 / 15	Mukasa_UP_in_GBM
11	1e−03	19 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
12	3e−03	5 / 30	Shaw_responders_down_in_oligo_glioma
13	4e−03	11 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	4e−03	10 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	6e−03	3 / 12	Donson−immune cell intra signaling−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−25	51 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
2	5e−21	53 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
3	1e−20	58 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	3e−19	53 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
5	2e−18	53 / 404	RUTELLA_RESPONSE_TO_HGF_UP
6	4e−17	23 / 73	HECKER_IFNB1_TARGETS
7	2e−16	15 / 26	MOSERLE_IFNA_RESPONSE
8	2e−14	54 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
9	8e−14	74 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
10	9e−14	39 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	3e−13	26 / 138	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
12	4e−13	67 / 795	NUYTTEN_EZH2_TARGETS_UP
13	1e−12	22 / 102	KEGG_LYSOSOME
14	2e−12	37 / 299	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
15	3e−12	44 / 412	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−13	20 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	4e−12	27 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	5e−06	19 / 176	HALLMARK_ALLOGRAFT_REJECTION
4	6e−06	19 / 178	HALLMARK_COMPLEMENT
5	1e−04	16 / 170	HALLMARK_IL2_STAT5_SIGNALING
6	2e−04	17 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	3e−04	6 / 29	HALLMARK_NOTCH_SIGNALING
8	4e−04	14 / 149	HALLMARK_UV_RESPONSE_UP
9	6e−04	16 / 194	HALLMARK_KRAS_SIGNALING_UP
10	1e−03	15 / 187	HALLMARK_INFLAMMATORY_RESPONSE
11	1e−03	13 / 150	HALLMARK_APOPTOSIS
12	4e−03	14 / 191	HALLMARK_P53_PATHWAY
13	4e−03	9 / 96	HALLMARK_ANDROGEN_RESPONSE
14	4e−03	14 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
15	5e−03	14 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Immunome

Rank	p−value	#in/all	Geneset
1	4e−10	13 / 42	Angelova_immune−metagene−TGD
2	6e−05	7 / 32	Angelova_immune−metagene−effector_memory_CD8
3	1e−04	6 / 25	Angelova_immune−metagene−DC
4	7e−04	5 / 23	Angelova_immune−metagene−monocytes
5	7e−04	5 / 23	Angelova_immune−metagene−Th2
6	1e−03	3 / 7	Angelova_immune−metagene−cytotoxic_cells
7	1e−03	4 / 15	Angelova_immune−metagene−NK
8	4e−03	4 / 21	Angelova_immune−metagene−central_memory_CD4
9	1e−02	4 / 29	Angelova_immune−metagene−Th1
10	2e−02	3 / 17	Angelova_immune−metagene−central_memory_CD8
11	2e−02	3 / 18	Angelova_CRC_immunostimulators
12	2e−02	6 / 67	Angelova_immune−metagene−T−cells
13	4e−02	2 / 10	Angelova_CRC_immonoinhibitors
14	5e−02	2 / 11	Angelova_immune−metagene−macrophages
15	6e−02	4 / 45	Angelova_immune−metagene−MDSC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	6 / 62	DUMEAUX_Smoking enriched genes
2	0.03	2 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.03	3 / 22	DUMEAUX_High bmi enriched genes
4	0.06	2 / 12	DUMEAUX_Women normal BMI literature genes up
5	0.07	2 / 13	Huan_blood−pressure_DBP−signature
6	0.08	3 / 32	Marjolein_ageing−genes_DN
7	0.09	1 / 3	Huan_blood−pressure_HTN−signature
8	0.23	1 / 8	Marjolein_ageing−genes_UP
9	0.38	8 / 210	Homuth_BMI−associated−genes_DN
10	0.52	1 / 22	DUMEAUX_Fasting enriched genes
11	0.87	3 / 150	Homuth_BMI−associated−genes_UP
12	1.00	0 / 10	DUMEAUX_Smoking literature genes up
13	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
14	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
15	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−20	19 / 33	Care_Extended T−cell
2	2e−16	21 / 62	Monti_Host_response_cluster
3	2e−06	31 / 378	TARTE_Mature plasma cell signature
4	4e−06	6 / 15	Care_Polarized immune response
5	5e−06	24 / 263	SPANG_CD40 6hrs UP
6	2e−05	13 / 97	ROSOLOWSKI_red total
7	7e−05	19 / 213	SPANG_IL21 DN
8	2e−04	5 / 18	DAVE_Immune response 2
9	4e−04	87 / 1894	HOPP_Poised_promoter
10	5e−04	10 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
11	1e−03	207 / 5404	HOPP_Strong_enhancer
12	2e−03	178 / 4559	HOPP_Weak_enhancer
13	2e−03	171 / 4357	HOPP_Weak_txn
14	2e−03	6 / 41	ROSOLOWSKI_blue DOWN
15	2e−03	129 / 3168	HOPP_Repressed

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−12	19 / 78	Tirosh_expression higher in CAFs than in T−cells
2	8e−10	16 / 71	Tirosh_Macrophage specific genes−melanoma
3	2e−09	25 / 189	Tirosh_genes preferentially expressed by Tregs
4	8e−06	8 / 33	Tirosh_T−cell specific genes−melanoma
5	1e−04	16 / 171	Landsberg_dedifferentiation_up
6	3e−03	8 / 75	Tirosh_Endothelial−cell specific genes−melanoma
7	8e−03	5 / 39	Tirosh_top50 correlated genes PC4
8	2e−02	13 / 204	Landsberg_dedifferentiation_down
9	2e−02	5 / 46	Tirosh_top50 correlated genes PC5
10	2e−02	25 / 497	Gerber_wt/wt_melanoma−cells−SpotD
11	4e−02	6 / 78	Tirosh_CAF−cell specific genes
12	4e−02	3 / 24	Tirosh_exhuastion−associated genes consitent across tumors
13	4e−02	4 / 41	Tirosh_top50 correlated genes PC3
14	5e−02	6 / 81	Tirosh_Genes in the MITF program
15	6e−02	7 / 107	Tirosh_Exhaustion program in Mel75

MF

Rank	p−value	#in/all	Geneset
1	1e−14	17 / 44	antigen binding
2	4e−06	20 / 191	transmembrane signaling receptor activity
3	1e−05	17 / 154	serine−type endopeptidase activity
4	1e−04	5 / 16	immunoglobulin receptor binding
5	4e−04	4 / 12	proteoglycan binding
6	8e−04	13 / 143	carbohydrate binding
7	1e−03	6 / 36	cholesterol binding
8	1e−03	7 / 50	cysteine−type endopeptidase activity
9	1e−03	16 / 205	receptor activity
10	1e−03	4 / 16	cholesterol transporter activity
11	2e−03	22 / 346	receptor binding
12	3e−03	4 / 19	tumor necrosis factor−activated receptor activity
13	3e−03	3 / 10	serine−type carboxypeptidase activity
14	5e−03	3 / 11	1−phosphatidylinositol binding
15	5e−03	9 / 100	cysteine−type peptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	19 / 223	hsa−miR−1244
2	9e−04	23 / 344	hsa−miR−19a
3	9e−04	23 / 344	hsa−miR−19b
4	3e−03	14 / 185	hsa−miR−199a−3p
5	4e−03	12 / 150	hsa−miR−199b−3p
6	7e−03	23 / 404	hsa−miR−103
7	7e−03	23 / 405	hsa−miR−107
8	7e−03	11 / 143	hsa−miR−183
9	9e−03	12 / 168	hsa−miR−33a
10	1e−02	15 / 236	hsa−miR−18b
11	1e−02	7 / 75	hsa−miR−587
12	1e−02	6 / 61	hsa−miR−1290
13	2e−02	3 / 17	hsa−miR−323−5p
14	2e−02	10 / 141	hsa−miR−369−3p
15	2e−02	8 / 101	hsa−miR−199b−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	5e−16	20 / 57	Burnham_viral_UP
2	8e−15	16 / 37	Sweeney_viral_up
3	3e−13	17 / 52	Burnham_day1_vs_5_DN
4	5e−11	22 / 122	Terre_IMS_influenza_meta_signature
5	5e−06	9 / 41	Scicluna_DN
6	1e−04	14 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	9e−04	7 / 48	Burnham_cap_fp_vs_con_DN
8	2e−03	7 / 56	Burnham_sep_vs_con_DN
9	2e−02	3 / 18	Scicluna_UP
10	2e−02	4 / 33	Sweeney_viral_dn
11	2e−02	6 / 68	Burnham_sep_vs_con_UP
12	3e−02	6 / 71	Burnham_cap_fp_vs_con_UP
13	7e−02	4 / 48	Burnham_viral_DN
14	4e−01	7 / 179	Terre_MSV_multiple_respiratory_viruses_dn
15	5e−01	2 / 54	Burnham_timecourse

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−18	28 / 102	WIRTH_EBV B−cells
2	5e−16	22 / 72	Chaussabel_3,1_Interferon−inducible
3	6e−13	22 / 99	Chaussabel_1,5_Myeloid lineage
4	1e−09	26 / 198	Chaussabel_3,3_Inflammation II
5	3e−09	18 / 100	Chaussabel_2,8_T−cells
6	1e−08	18 / 109	Chaussabel_2,6_Myeloid lineage
7	3e−07	12 / 59	Chaussabel_2,10_Immune related cell surface molecules
8	5e−07	9 / 32	Chaussabel_1,1_Plasma Cells
9	2e−06	12 / 68	Chaussabel_2,1_Cytotoxic cells
10	1e−05	28 / 355	WIRTH_Immune system
11	9e−04	8 / 62	VAQUERIZAS_Lung_TF
12	6e−03	7 / 66	VAQUERIZAS_Whole blood_TF
13	7e−03	14 / 204	Chaussabel_3,2_Inflammation I
14	1e−02	5 / 41	VAQUERIZAS_Thymus_TF
15	1e−02	32 / 642	PROTEINATLAS_lung

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.1	84 / 2254	ICGC_BatfPcr1_targets
2	0.1	41 / 1041	ICGC_P300_targets
3	0.2	84 / 2321	ICGC_Rad21_targets
4	0.2	56 / 1508	ICGC_Mef2_targets
5	0.4	1 / 16	MYC_Protein synthesis degradation UP
6	0.4	55 / 1636	ICGC_Bcl11_targets
7	0.5	106 / 3213	ICGC_Pu1_targets
8	0.5	34 / 1032	ICGC_Usf1_targets
9	0.5	18 / 549	ICGC_Atf3_targets
10	0.5	45 / 1387	HEBENSTREIT_high expression TF
11	0.6	122 / 3796	ICGC_Nficsc81335_targets
12	0.6	15 / 485	ICGC_NrsfPcr2_targets
13	0.7	67 / 2150	ICGC_Irf4_targets
14	0.7	107 / 3451	ICGC_Atf2_targets
15	0.8	30 / 1025	ICGC_NrsfPcr1_targets

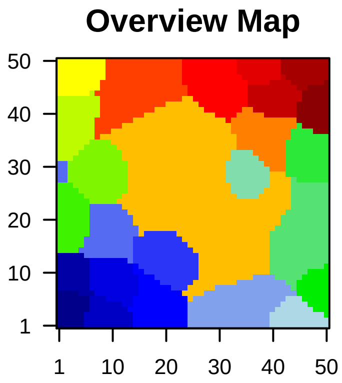
K−Means Cluster

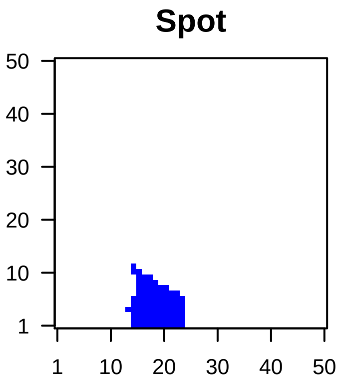
Spot Summary: R

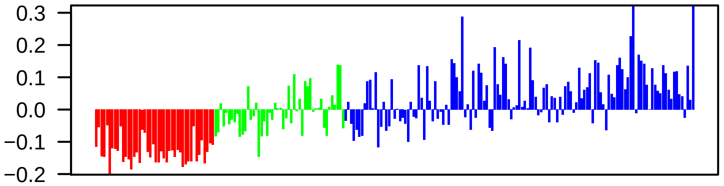
metagenes = 85
genes = 656

<r> metagenes = 0.82
<r> genes = 0.14
beta: r2= 2.28 / log p= −Inf

samples with spot = 13 (5.9 %)
non−mBL : 13 (10.1 %)





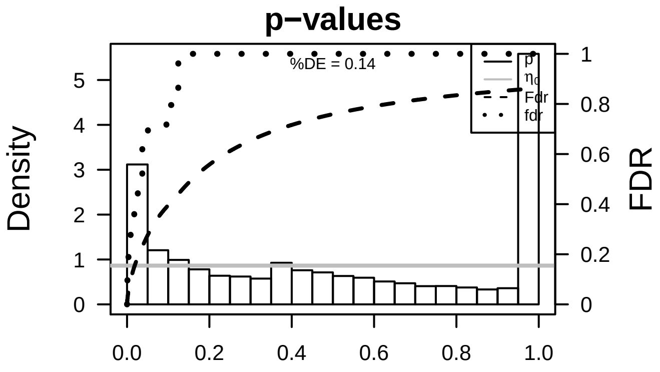


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	211583_x_at	3.03	−1.02	0.08	NCR3	natural cytotoxicity triggering receptor 3 [Source:HGNC Symb
2	207599_at	2.71	−0.65	0.27	MMP20	matrix metallopeptidase 20 [Source:HGNC Symbol;Acc:HGN
3	206310_at	2.54	−0.92	0.29	SPINK2	serine peptidase inhibitor, Kazal type 2 [Source:HGNC Symb
4	205373_at	2.5	−0.78	0.26	CTNNA2	catenin alpha 2 [Source:HGNC Symbol;Acc:HGNC:2510]
5	215101_s_at	2.45	−0.8	0.3	CXCL5	C−X−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc
6	209948_at	2.35	−0.7	0.28	KCNMB1	potassium calcium−activated channel subfamily M regulatory
7	204540_at	2.25	−0.76	0.27	EEF1A2	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
8	215813_s_at	2.25	−0.94	0.62	PTGS1	prostaglandin−endoperoxide synthase 1 [Source:HGNC Sym
9	214460_at	2.23	−0.96	0.24	LSAMP	limbic system−associated membrane protein [Source:HGNC
10	208555_x_at	2.2	−0.9	0.4	CST2	cystatin SA [Source:HGNC Symbol;Acc:HGNC:2474]
11	204392_at	2.18	−1.11	0.43	CAMK1	calcium/calmodulin dependent protein kinase I [Source:HGN
12	204591_at	2.15	−1.03	0.23	CHL1	cell adhesion molecule L1 like [Source:HGNC Symbol;Acc:H
13	205128_x_at	2.13	−1.29	0.54	PTGS1	prostaglandin−endoperoxide synthase 1 [Source:HGNC Sym
14	221259_s_at	2.12	−0.6	0.26	TEX11	testis expressed 11 [Source:HGNC Symbol;Acc:HGNC:1173
15	205990_s_at	2.09	−1.31	0.22	WNT5A	Wnt family member 5A [Source:HGNC Symbol;Acc:HGNC:12
16	212909_at	2.08	−0.77	0.21	LYPD1	LY6/PLAUR domain containing 1 [Source:HGNC Symbol;Acc
17	218532_s_at	2.06	−1.12	0.48	RETREG1	reticulophagy regulator 1 [Source:HGNC Symbol;Acc:HGNC:
18	222288_at	2.05	−0.78	0.51		
19	213338_at	2.05	−0.87	0.42	TMEM158	transmembrane protein 158 (gene/pseudogene) [Source:HGN
20	201984_s_at	2.04	−0.64	0.29	EGFR	epidermal growth factor receptor [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−14	135 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
2	4e−13	53 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
3	3e−12	98 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran
4	7e−11	311 / 5339	CC	membrane
5	1e−10	313 / 5404	Lympl	HOPP_Strong_enhancer
6	2e−10	98 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
7	4e−10	48 / 407	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_UP
8	8e−10	41 / 321	GSEA	PHONG_TNF_RESPONSE_NOT_VIA_P38
9	2e−09	42 / 345	CC	focal adhesion
10	2e−09	78 / 883	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	2e−09	275 / 4701	CC	cytoplasm
12	3e−09	81 / 938	CC	Golgi apparatus
13	4e−09	42 / 353	GSEA	JOHNSTONE_PARVB_TARGETS_3_UP
14	5e−09	78 / 902	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
15	1e−08	317 / 5682	Lympl	HOPP_Weak_promoter
16	2e−08	55 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
17	5e−08	408 / 7864	MF	protein binding
18	1e−07	50 / 512	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
19	1e−07	29 / 218	GSEA	PHONG_TNF_RESPONSE_VIA_P38_COMPLETE
20	1e−07	26 / 183	GSEA	ZHANG_TLX_TARGETS_36HR_UP
21	1e−07	67 / 788	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
22	2e−07	27 / 197	GSEA	MANALO_HYPOXIA_UP
23	2e−07	47 / 477	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
24	2e−07	31 / 251	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
25	3e−07	57 / 642	GSEA	CUI_TCF21_TARGETS_2_DN
26	5e−07	33 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
27	7e−07	20 / 127	GSEA	ELVIDGE_HYPOXIA_BY_DMOG_UP
28	1e−06	49 / 537	CC	perinuclear region of cytoplasm
29	1e−06	23 / 166	GSEA	ELVIDGE_HYPOXIA_UP
30	1e−06	22 / 155	GSEA	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
31	1e−06	10 / 34	GSEA	BIOCARTA_INTEGRIN_PATHWAY
32	1e−06	71 / 906	Lympl	SPANG_BCR DN
33	1e−06	316 / 5908	Lympl	HOPP_Active_promoter
34	1e−06	34 / 317	Cance	SPANG_BCL6−index2
35	2e−06	35 / 333	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_DN
36	2e−06	78 / 1035	CC	endoplasmic reticulum
37	2e−06	20 / 135	MF	actin filament binding
38	2e−06	37 / 364	miRN	hsa−miR−548n
39	2e−06	47 / 518	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
40	2e−06	55 / 648	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3



Aging

Rank	p−value	#in/all	Geneset
1	0.05	9 / 107	HORVATH_aging_genes meth UP
2	0.22	6 / 92	HORVATH_aging_genes meth DOWN
3	0.88	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	

BP

Rank	p−value	#in/all	Geneset
1	4e−06	13 / 65	vascular endothelial growth factor receptor signaling pathway
2	2e−05	12 / 64	positive regulation of endothelial cell proliferation
3	5e−05	36 / 403	neutrophil degranulation
4	7e−05	8 / 33	positive regulation of blood vessel endothelial cell migration
5	9e−05	8 / 34	dendrite morphogenesis
6	1e−04	5 / 12	cellular response to fluid shear stress
7	1e−04	5 / 12	positive regulation of vascular endothelial growth factor receptor signaling patl
8	1e−04	6 / 19	clathrin−dependent endocytosis
9	2e−04	16 / 128	fatty acid metabolic process
10	2e−04	8 / 38	lactation
11	2e−04	10 / 59	fatty acid biosynthetic process
12	3e−04	15 / 121	positive regulation of angiogenesis
13	4e−04	6 / 23	actin filament polymerization
14	4e−04	13 / 99	cellular response to hypoxia
15	5e−04	17 / 155	response to hypoxia

Cancer

Rank	p−value	#in/all	Geneset
1	1e−06	34 / 317	SPANG_BCL6−index2
2	2e−04	1 / 14	LIU_PROSTATE_CANCER_DN
3	8e−04	15 / 134	PanCan_RAS_geneset_nanostring
4	9e−03	16 / 187	PanCan_PI3K_geneset_nanostring
5	1e−02	13 / 147	PanCan_MAPK_geneset_nanostring
6	1e−02	3 / 12	GENTLES_modul12
7	2e−02	31 / 480	Lembcke_Colonic Inflammation
8	3e−02	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	8e−02	2 / 11	LIU_PROSTATE_CANCER_UP
10	8e−02	2 / 11	GENTLES_modul14
11	1e−01	2 / 12	LIU_BREAST_CANCER
12	1e−01	2 / 12	BENTINK_ras.1
13	1e−01	12 / 186	SPANG_LPS−index2
14	1e−01	8 / 113	PanCan_Driver_Gene_geneset_nanostring
15	1e−01	6 / 80	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	7e−11	311 / 5339	membrane
2	2e−09	42 / 345	focal adhesion
3	2e−09	275 / 4701	cytoplasm
4	3e−09	81 / 938	Golgi apparatus
5	1e−06	49 / 537	perinuclear region of cytoplasm
6	2e−06	78 / 1035	endoplasmic reticulum
7	2e−06	57 / 683	endoplasmic reticulum membrane
8	1e−05	16 / 104	trans−Golgi network
9	1e−05	25 / 219	lysosomal membrane
10	1e−05	69 / 936	cytoskeleton
11	2e−05	43 / 494	endosome
12	2e−05	16 / 109	early endosome membrane
13	3e−05	212 / 3805	cytosol
14	4e−05	41 / 479	Golgi membrane
15	7e−05	9 / 42	azurophil granule membrane

Chr

Rank	p−value	#in/all	Geneset
1	3e−05	46 / 556	Chr X
2	4e−02	41 / 700	Chr 12
3	2e−01	24 / 437	Chr 8
4	2e−01	30 / 585	Chr 7
5	3e−01	25 / 490	Chr 10
6	3e−01	19 / 369	Chr 20
7	3e−01	27 / 554	Chr 5
8	3e−01	37 / 776	Chr 17
9	4e−01	35 / 756	Chr 11
10	5e−01	37 / 832	Chr 2
11	5e−01	15 / 333	Chr 22
12	6e−01	29 / 669	Chr 6
13	6e−01	6 / 139	Chr 21
14	7e−01	28 / 689	Chr 3
15	7e−01	22 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−26	511 / 9179	2_TssA_Skeletal_Muscle
2	1e−22	219 / 2704	4_TxTrans_Fibroblasts
3	3e−21	273 / 3803	6_EnhG_Fibroblasts
4	3e−21	514 / 9576	2_TssA_MSC_Adipocyte
5	4e−21	499 / 9146	3_TssF_Skeletal_Muscle
6	3e−20	195 / 2380	TxEnhG1_Colon
7	7e−20	510 / 9544	HSC_2_TssAFlnk
8	2e−19	419 / 7165	Tx_Colon
9	1e−18	485 / 8918	1_TssA_ESC_Mesoderm
10	4e−18	478 / 8766	2_TssA_Melanocytes
11	4e−17	490 / 9160	2_TssA_Neuronal_Progenitor
12	9e−17	382 / 6466	5_Tx_MSC_Adipocyte
13	2e−16	442 / 7943	Enh_Colon
14	6e−16	474 / 8816	Thelper cells peripheral blood_2_TssAFlnk
15	6e−16	267 / 4009	6_EnhG_ESC_Mesoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−12	98 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	2e−10	98 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
3	2e−09	78 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
4	5e−07	33 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	4e−05	71 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
6	3e−04	27 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
7	2e−03	100 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	3e−03	35 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	4e−03	21 / 255	Kosinski_top−crypt−long−list
10	4e−02	2 / 7	TCGA−CRC_agressive−disease−markers
11	4e−02	7 / 72	Ang_CRC−CIMPH−vs−L_hyper
12	4e−02	5 / 43	Marisa_CRC−cluster−f
13	5e−02	4 / 31	Marisa_CRC−cluster−c
14	5e−02	72 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	5e−02	7 / 77	Ang_CRC_Hypermethylated

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	10 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	0.006	6 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
3	0.006	25 / 330	Up
4	0.008	21 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
5	0.008	59 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
6	0.012	4 / 21	Barbus_GBM_STS_vs._LTS
7	0.018	3 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
8	0.021	18 / 242	ScoV_0.5_Sturm_C1_IDH_DN
9	0.024	29 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
10	0.043	11 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	0.044	19 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
12	0.050	16 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
13	0.051	5 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
14	0.056	7 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
15	0.068	13 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−14	135 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
2	4e−13	53 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
3	4e−10	48 / 407	MITSIADES_RESPONSE_TO_APLIDIN_UP
4	8e−10	41 / 321	PHONG_TNF_RESPONSE_NOT_VIA_P38
5	4e−09	42 / 353	JOHNSTONE_PARVB_TARGETS_3_UP
6	5e−09	78 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
7	2e−08	55 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	1e−07	50 / 512	WEST_ADRENOCORTICAL_TUMOR_DN
9	1e−07	29 / 218	PHONG_TNF_RESPONSE_VIA_P38_COMPLETE
10	1e−07	26 / 183	ZHANG_TLX_TARGETS_36HR_UP
11	1e−07	67 / 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
12	2e−07	27 / 197	MANALO_HYPOXIA_UP
13	2e−07	47 / 477	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
14	2e−07	31 / 251	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
15	3e−07	57 / 642	CUI_TCF21_TARGETS_2_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−05	22 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	4e−05	22 / 193	HALLMARK_HEME_METABOLISM
3	2e−04	21 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	4e−04	20 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	4e−04	20 / 194	HALLMARK_MYOGENESIS
6	6e−04	18 / 173	HALLMARK_MITOTIC_SPINDLE
7	7e−04	7 / 35	HALLMARK_HEDGEHOG_SIGNALING
8	2e−03	18 / 188	HALLMARK_HYPOXIA
9	3e−03	11 / 94	HALLMARK_PROTEIN_SECRETION
10	7e−03	15 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	8e−03	5 / 29	HALLMARK_NOTCH_SIGNALING
12	2e−02	15 / 191	HALLMARK_P53_PATHWAY
13	3e−02	14 / 182	HALLMARK_GLYCOLYSIS
14	5e−02	7 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	6e−02	4 / 34	HALLMARK_ANGIOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.02	4 / 23	Angelova_immune−metagene−monocytes
2	0.08	4 / 38	Angelova_immune−metagene−mast−cells
3	0.12	2 / 14	Angelova_immune−metagene−eosinophil
4	0.17	3 / 32	Angelova_immune−metagene−effector_memory_CD8
5	0.20	1 / 5	Angelova_immune−metagene−NK56_bright
6	0.20	2 / 19	Angelova_immune−metagene−iDC
7	0.30	2 / 25	Angelova_immune−metagene−DC
8	0.30	1 / 8	Immunity_HLA−class−II
9	0.36	1 / 10	Angelova_immune−metagene−TFH
10	0.39	1 / 11	Angelova_immune−metagene−macrophages
11	0.42	1 / 12	Angelova_immune−metagene−memory_B−cells
12	0.42	1 / 12	Angelova_immune−metagene−NK56_dim
13	0.51	1 / 16	Angelova_immune−metagene−Th17
14	0.54	1 / 17	Angelova_immune−metagene−central_memory_CD8
15	0.56	1 / 18	Angelova_immune−metagene−pDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	4 / 13	Huan_blood−pressure_DBP−signature
2	0.002	19 / 210	Homuth_BMI−associated−genes_DN
3	0.022	3 / 14	Huan_blood−pressure_SBP−signature
4	0.096	2 / 12	DUMEAUX_Women normal BMI literature genes up
5	0.155	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
6	0.165	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	0.166	3 / 32	Marjolein_ageing−genes_DN
8	0.271	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	0.271	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	0.303	1 / 8	Marjolein_ageing−genes_UP
11	0.629	1 / 22	DUMEAUX_High bmi enriched genes
12	0.629	1 / 22	DUMEAUX_Fasting enriched genes
13	0.765	2 / 62	DUMEAUX_Smoking enriched genes
14	0.902	4 / 150	Homuth_BMI−associated−genes_UP
15	1.000	0 / 10	DUMEAUX_Smoking literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−10	313 / 5404	HOPP_Strong_enhancer
2	1e−08	317 / 5682	HOPP_Weak_promoter
3	1e−06	71 / 906	SPANG_BCR DN
4	1e−06	316 / 5908	HOPP_Active_promoter
5	8e−06	25 / 214	LENZ_Stromal signature 1
6	1e−03	12 / 96	SPANG_LPS 6hrs UP
7	3e−03	22 / 263	SPANG_CD40 6hrs UP
8	3e−03	223 / 4357	HOPP_Weak_txn
9	9e−03	272 / 5529	HOPP_Txn_elongation
10	1e−02	17 / 213	SPANG_IL21 DN
11	2e−02	102 / 1894	HOPP_Poised_promoter
12	2e−02	3 / 14	WRIGHT_GCB UP
13	3e−02	11 / 132	Subero_DLBCL_hyper_meth
14	3e−02	7 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	4e−02	3 / 18	DAVE_Immune response 2

Melanoma

Rank	p−value	#in/all	Geneset
1	8e−05	41 / 497	Gerber_wt/wt_melanoma−cells−SpotD
2	1e−03	18 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
3	3e−03	5 / 24	Tirosh_exhuastion−associated genes consitent across tumors
4	8e−03	19 / 236	Gerber_wt/wt_group3−specific
5	2e−02	14 / 171	Landsberg_dedifferentiation_up
6	2e−02	17 / 222	Gerber_wt/wt_melanoma−cells−SpotF
7	3e−02	8 / 81	Tirosh_Genes in the MITF program
8	5e−02	2 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
9	5e−02	9 / 107	Tirosh_Exhaustion program in Mel75
10	5e−02	17 / 249	Gerber_wt/wt_melanoma−cells−SpotE
11	5e−02	5 / 46	Tirosh_top50 correlated genes PC5
12	8e−02	7 / 85	Tirosh_AXL−signature
13	8e−02	2 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
14	8e−02	4 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	9e−02	4 / 39	Tirosh_top50 correlated genes PC4

MF

Rank	p−value	#in/all	Geneset
1	5e−08	408 / 7864	protein binding
2	2e−06	20 / 135	actin filament binding
3	1e−05	30 / 291	actin binding
4	2e−05	27 / 256	cadherin binding
5	1e−03	5 / 19	ligand−dependent nuclear receptor binding
6	2e−03	22 / 249	ubiquitin protein ligase binding
7	2e−03	27 / 331	protein serine/threonine kinase activity
8	2e−03	5 / 22	phosphatidylinositol−3−phosphate binding
9	2e−03	8 / 54	Rho guanyl−nucleotide exchange factor activity
10	3e−03	10 / 80	chaperone binding
11	3e−03	9 / 70	beta−catenin binding
12	4e−03	7 / 46	SH3/SH2 adaptor activity
13	4e−03	4 / 16	phosphatidylinositol−4−phosphate binding
14	6e−03	24 / 312	enzyme binding
15	6e−03	15 / 165	calmodulin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−06	37 / 364	hsa−miR−548n
2	6e−06	20 / 146	hsa−miR−548k
3	8e−06	29 / 269	hsa−miR−548a−5p
4	1e−04	39 / 474	hsa−miR−20a
5	2e−04	18 / 155	hsa−miR−586
6	2e−04	21 / 197	hsa−miR−152
7	2e−04	13 / 92	hsa−miR−498
8	2e−04	25 / 261	hsa−miR−559
9	2e−04	29 / 324	hsa−miR−497
10	3e−04	7 / 31	hsa−miR−34c−3p
11	3e−04	18 / 164	hsa−miR−148b
12	4e−04	11 / 74	hsa−miR−595
13	4e−04	23 / 240	hsa−miR−548j
14	5e−04	18 / 169	hsa−miR−148a
15	6e−04	17 / 157	hsa−miR−34b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.003	6 / 33	Sweeney_viral_dn
2	0.088	5 / 54	Burnham_timecourse
3	0.142	9 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.187	2 / 18	Scicluna_UP
5	0.352	4 / 68	Burnham_sep_vs_con_UP
6	0.451	3 / 56	Burnham_sep_vs_con_DN
7	0.452	6 / 122	Terre_IMS_influenza_meta_signature
8	0.490	2 / 37	Sweeney_viral_up
9	0.545	2 / 41	Scicluna_DN
10	0.611	3 / 71	Burnham_cap_fp_vs_con_UP
11	0.631	2 / 48	Burnham_viral_DN
12	0.680	7 / 179	Terre_MSV_multiple_respiratory_viruses_dn
13	0.723	2 / 57	Burnham_viral_UP
14	0.886	1 / 48	Burnham_cap_fp_vs_con_DN
15	0.905	1 / 52	Burnham_day1_vs_5_DN

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−05	23 / 198	Chaussabel_3,3_Inflammation II
2	1e−03	9 / 62	VAQUERIZAS_Lung_TF
3	2e−03	11 / 89	Chaussabel_2,3_Erythrocytes
4	3e−03	10 / 81	Chaussabel_1,2_Platelets
5	3e−03	7 / 45	VAQUERIZAS_Placenta_TF
6	4e−03	9 / 72	Chaussabel_3,1_Interferon−inducible
7	4e−03	4 / 16	VAQUERIZAS_Fetal thyroid_TF
8	5e−03	6 / 36	VAQUERIZAS_Prostate_TF
9	6e−03	62 / 1022	PROTEINATLAS_placenta
10	8e−03	18 / 218	WIRTH_pre+post GC B−cells
11	2e−02	3 / 13	WIRTH_Prim. lymphoid organs
12	2e−02	16 / 204	Chaussabel_3,2_Inflammation I
13	2e−02	57 / 989	PROTEINATLAS_tonsil
14	2e−02	10 / 109	Chaussabel_2,6_Myeloid lineage
15	2e−02	4 / 25	VAQUERIZAS_Adrenal cortex_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.7	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.004	94 / 1636	ICGC_Bcl11_targets
2	0.008	209 / 4131	ICGC_Tcf3_targets
3	0.014	123 / 2321	ICGC_Rad21_targets
4	0.027	98 / 1848	ICGC_Pbx3_targets
5	0.029	117 / 2254	ICGC_BatfPcr1_targets
6	0.030	102 / 1941	ICGC_Bcl3_targets
7	0.034	171 / 3435	ICGC_Ebfsc137065_targets
8	0.047	74 / 1387	HEBENSTREIT_high expression TF
9	0.049	186 / 3804	ICGC_Stat5_targets
10	0.057	2 / 9	MYC_Targets DOWN
11	0.061	232 / 4851	ICGC_Runx3_targets
12	0.062	78 / 1494	ICGC_Cebpbsc150_targets
13	0.073	78 / 1508	ICGC_Mef2_targets
14	0.079	183 / 3796	ICGC_Nficsc81335_targets
15	0.086	1 / 2	MYC_Cell cycle DOWN

K−Means Cluster

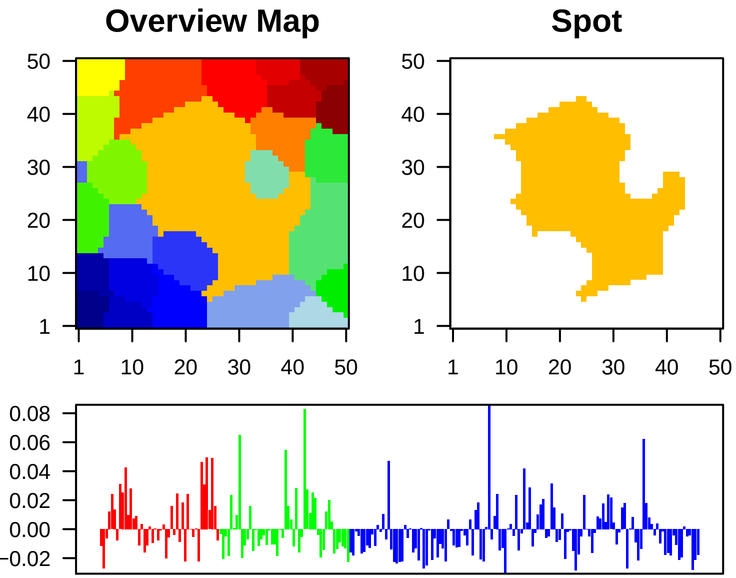
Spot Summary: S

metagenes = 666
genes = 6172

<r> metagenes = 0.12

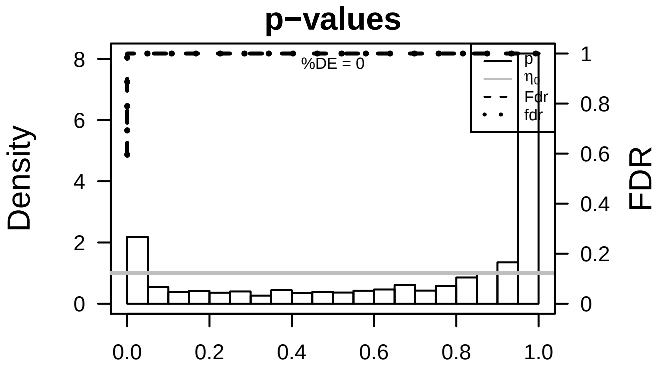
beta: r2= 0.03 / log p= −1.89

samples with spot = 0 (0 %)



Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	1492 / 3168	Lympl	HOPP_Repressed
2	1e−99	2694 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
3	3e−60	600 / 1148	TF	HEBENSTREIT_low expression TF
4	2e−43	240 / 373	GSE	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
5	3e−42	392 / 730	GSE	BENPORATH_ES_WITH_H3K27ME3
6	5e−41	826 / 1894	Lympl	HOPP_Poised_promoter
7	6e−40	218 / 337	MF	G−protein coupled receptor activity
8	2e−38	328 / 595	BP	G−protein coupled receptor signaling pathway
9	2e−37	221 / 352	Refer	WIRTH_Nervous System
10	8e−34	525 / 1128	CC	integral component of plasma membrane
11	3e−33	162 / 240	GSE	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
12	3e−31	245 / 432	GSE	BENPORATH_PRC2_TARGETS
13	4e−31	137 / 195	BP	chemical synaptic transmission
14	8e−31	352 / 697	GSE	BENPORATH_SUZ12_TARGETS
15	5e−29	112 / 151	MF	ion channel activity
16	5e−29	234 / 417	GSE	REACTOME_GPCR_DOWNSTREAM_SIGNALING
17	9e−29	353 / 713	GSE	BENPORATH_EED_TARGETS
18	9e−29	268 / 500	MF	signal transducer activity
19	1e−28	1223 / 3210	CC	plasma membrane
20	6e−27	268 / 510	GSE	REACTOME_SIGNALING_BY_GPCR
21	7e−27	690 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
22	1e−26	106 / 145	BP	response to stimulus
23	1e−25	170 / 284	GSE	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
24	4e−24	577 / 1361	BP	signal transduction
25	1e−23	208 / 382	CC	synapse
26	3e−23	248 / 482	BP	ion transport
27	8e−23	182 / 324	GSE	REACTOME_GPCR_LIGAND_BINDING
28	5e−22	78 / 102	Gliom	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
29	2e−21	79 / 105	Gliom	WIRTH_Normal Brain
30	1e−20	172 / 311	GSE	SHEN_SMARCA2_TARGETS_DN
31	4e−20	88 / 126	Gliom	ScoV_0.999_Sturm_E5_RTK II 'Classic'_UP_RTK I 'PDGFRA'_DN
32	5e−20	65 / 82	Refer	WIRTH_Testis
33	5e−20	136 / 230	GSE	REACTOME_NEURONAL_SYSTEM
34	3e−19	155 / 278	Colon	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
35	3e−18	459 / 1092	GSE	YOSHIMURA_MAPK8_TARGETS_UP
36	5e−18	1185 / 3270	CC	integral component of membrane
37	5e−18	136 / 239	GSE	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
38	8e−18	362 / 826	GSE	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
39	2e−17	206 / 414	Gliom	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
40	7e−17	113 / 191	Gliom	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN



Aging

Rank	p−value	#in/all	Geneset
1	3e−09	34 / 47	TESCHENDORFF_age_hypermethylated
2	6e−03	45 / 107	HORVATH_aging_genes meth UP
3	6e−01	27 / 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	8e−34	525 / 1128	integral component of plasma membrane
2	1e−28	1223 / 3210	plasma membrane
3	1e−23	208 / 382	synapse
4	5e−18	1185 / 3270	integral component of membrane
5	1e−16	105 / 174	postsynaptic membrane
6	8e−12	150 / 310	dendrite
7	2e−11	46 / 65	voltage−gated potassium channel complex
8	5e−11	253 / 595	cell junction
9	3e−09	121 / 254	axon
10	2e−07	138 / 315	neuronal cell body
11	2e−07	28 / 40	chloride channel complex
12	4e−07	54 / 99	perikaryon
13	1e−06	121 / 277	neuron projection
14	3e−06	14 / 16	GABA−A receptor complex
15	6e−06	78 / 168	postsynaptic density

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	2694 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	3e−19	155 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
3	4e−15	185 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
4	6e−15	122 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
5	2e−12	155 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
6	3e−11	345 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
7	1e−08	192 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	2e−06	210 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
9	1e−04	72 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
10	1e−04	183 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	2e−04	16 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
12	3e−04	36 / 72	Ang_CRC−CIMPH−vs−L_hyper
13	1e−03	15 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
14	1e−03	132 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
15	2e−03	36 / 77	Ang_CRC_Hypermethylated

HM

Rank	p−value	#in/all	Geneset
1	2e−05	86 / 195	HALLMARK_KRAS_SIGNALING_DN
2	4e−05	58 / 122	HALLMARK_SPERMATOGENESIS
3	5e−05	24 / 39	HALLMARK_PANCREAS_BETA_CELLS
4	8e−04	20 / 35	HALLMARK_HEDGEHOG_SIGNALING
5	1e−01	49 / 141	HALLMARK_UV_RESPONSE_DN
6	4e−01	55 / 174	HALLMARK_APICAL_JUNCTION
7	6e−01	58 / 194	HALLMARK_MYOGENESIS
8	6e−01	15 / 51	HALLMARK_TGF_BETA_SIGNALING
9	6e−01	10 / 34	HALLMARK_APICAL_SURFACE
10	6e−01	10 / 34	HALLMARK_ANGIOGENESIS
11	6e−01	11 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	7e−01	8 / 29	HALLMARK_NOTCH_SIGNALING
13	8e−01	54 / 193	HALLMARK_HEME_METABOLISM
14	9e−01	50 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	9e−01	23 / 96	HALLMARK_ANDROGEN_RESPONSE

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	1492 / 3168	HOPP_Repressed
2	5e−41	826 / 1894	HOPP_Poised_promoter
3	1e−14	819 / 2206	HOPP_Heterochrom
4	5e−10	74 / 132	Subero_DLBCL_hyper_meth
5	1e−08	65 / 118	Subero_INT_hyper_meth
6	2e−08	34 / 49	LEE_Developmental_regulators
7	2e−08	649 / 1814	HOPP_Repetitive
8	7e−07	41 / 70	Subero_FL_hyper_meth
9	7e−06	33 / 56	Subero_mBL_hyper_meth
10	1e−05	37 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
11	4e−05	46 / 91	Subero_T−ALL_hyper_meth
12	6e−05	37 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
13	8e−04	25 / 47	Subero_B−ALL_hyper_meth
14	5e−03	12 / 20	Subero_MCL_hyper_meth
15	1e−02	13 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	6 / 13	hsa−miR−671−3p
2	0.2	6 / 14	hsa−miR−1282
3	0.3	7 / 19	hsa−miR−943
4	0.3	6 / 16	hsa−miR−551a
5	0.4	3 / 7	hsa−miR−566
6	0.4	25 / 78	hsa−miR−125a−3p
7	0.5	3 / 8	hsa−miR−638
8	0.5	3 / 8	hsa−miR−1306
9	0.5	3 / 8	hsa−miR−202*
10	0.5	11 / 35	hsa−miR−1277
11	0.5	1 / 2	hsa−miR−585
12	0.5	6 / 19	hsa−miR−519e*
13	0.6	7 / 23	hsa−miR−617
14	0.6	17 / 57	hsa−miR−876−3p
15	0.6	2 / 6	hsa−miR−886−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.8	3 / 13	Alternative lengthening of telomeres
2	1.0	4 / 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	2e−38	328 / 595	G−protein coupled receptor signaling pathway
2	4e−31	137 / 195	chemical synaptic transmission
3	1e−26	106 / 145	response to stimulus
4	4e−24	577 / 1361	signal transduction
5	3e−23	248 / 482	ion transport
6	9e−16	75 / 112	regulation of ion transmembrane transport
7	2e−14	172 / 347	regulation of receptor activity
8	3e−14	34 / 38	detection of chemical stimulus involved in sensory perception of smell
9	4e−14	45 / 57	sensory perception of smell
10	2e−13	348 / 833	multicellular organism development
11	5e−13	89 / 153	visual perception
12	7e−13	119 / 225	ion transmembrane transport
13	9e−12	192 / 421	nervous system development
14	4e−11	48 / 70	neuropeptide signaling pathway
15	1e−10	62 / 102	potassium ion transport

Chr

Rank	p−value	#in/all	Geneset
1	0.001	201 / 556	Chr X
2	0.004	21 / 41	Chr Y
3	0.011	229 / 669	Chr 6
4	0.024	165 / 480	Chr 4
5	0.105	181 / 554	Chr 5
6	0.137	189 / 585	Chr 7
7	0.241	122 / 382	Chr 15
8	0.311	77 / 242	Chr 13
9	0.316	116 / 369	Chr 20
10	0.337	257 / 832	Chr 2
11	0.381	152 / 492	Chr 9
12	0.431	134 / 437	Chr 8
13	0.586	226 / 756	Chr 11
14	0.737	39 / 139	Chr 21
15	0.766	95 / 333	Chr 22

Glioma

Rank	p−value	#in/all	Geneset
1	7e−27	690 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e−22	78 / 102	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
3	2e−21	79 / 105	WIRTH_Normal Brain
4	4e−20	88 / 126	ScoV_0.999_Sturm_E5_RTK II 'Classic'_UP_RTK I 'PDGFRA'_DN
5	2e−17	206 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
6	7e−17	113 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
7	1e−14	129 / 239	ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN
8	9e−13	196 / 423	Down_a
9	2e−10	70 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
10	5e−08	121 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
11	2e−07	32 / 48	in vivo astrocytes vs. cultured astroglia
12	3e−07	39 / 64	Weller_LGG_gradeII−vs−III_UP
13	2e−06	17 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)
14	3e−06	118 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
15	4e−06	37 / 64	Weller_LGG_A_vs_O_DOWN

Immunome

Rank	p−value	#in/all	Geneset
1	0.08	16 / 38	Angelova_immune−metagene−mast−cells
2	0.22	6 / 14	Angelova_immune−metagene−eosinophil
3	0.28	6 / 15	Angelova_immune−metagene−NK
4	0.34	7 / 19	Angelova_immune−metagene−iDC
5	0.35	6 / 16	Angelova_immune−metagene−Th17
6	0.35	5 / 13	Angelova_CRC_MSS^−neoantigens
7	0.36	4 / 10	Angelova_immune−metagene−TFH
8	0.39	8 / 23	Angelova_immune−metagene−Th2
9	0.44	4 / 11	Angelova_immune−metagene−macrophages
10	0.45	3 / 8	Angelova_immune−metagene−mDC
11	0.48	2 / 5	Angelova_immune−metagene−NKT
12	0.51	4 / 12	Angelova_immune−metagene−NK56_dim
13	0.57	7 / 23	Angelova_immune−metagene−Treg
14	0.62	3 / 10	Angelova_CRC_immonoinhibitors
15	0.66	1 / 3	Angelova_CRC_MHC_class_I

Melanoma

Rank	p−value	#in/all	Geneset
1	3e−14	76 / 119	TCGA_melanoma_MITF_low
2	1e−05	34 / 59	TCGA_melanoma_keratin_high
3	4e−03	7 / 9	Joensson_Melanoma Pigmentation subtype
4	1e−02	18 / 37	Hugo_melanoma−all−MET_DN
5	5e−02	17 / 39	Tirosh_top50 correlated genes PC4
6	6e−02	87 / 249	Gerber_wt/wt_melanoma−cells−SpotE
7	1e−01	26 / 68	Tirosh_housekeeping_genes
8	1e−01	16 / 39	Tirosh_melanoma specific genes
9	2e−01	7 / 17	Hugo_melanoma−all−MET_UP
10	2e−01	14 / 38	Hugo_melanoma−BRAFmut−MET_UP
11	3e−01	3 / 6	Joensson_Melanoma high immune response subtype
12	5e−01	3 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
13	5e−01	2 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	5e−01	1 / 2	Melanoma Epi−Enzyme Cluster 2
15	5e−01	1 / 2	Melanoma Epi−Enzyme Cluster 6

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.5	15 / 48	Burnham_viral_DN
2	0.7	16 / 57	Burnham_day1_vs_5_UP
3	0.9	17 / 71	Burnham_cap_fp_vs_con_UP
4	0.9	16 / 68	Burnham_sep_vs_con_UP
5	0.9	3 / 18	Scicluna_UP
6	0.9	11 / 52	Burnham_day1_vs_5_DN
7	1.0	7 / 37	Sweeney_viral_up
8	1.0	11 / 54	Burnham_timecourse
9	1.0	8 / 48	Burnham_cap_fp_vs_con_DN
10	1.0	9 / 56	Burnham_sep_vs_con_DN
11	1.0	5 / 41	Scicluna_DN
12	1.0	23 / 122	Terre_IMS_influenza_meta_signature
13	1.0	6 / 57	Burnham_viral_UP
14	1.0	30 / 179	Terre_MSV_multiple_respiratory_viruses_dn
15	1.0	1 / 33	Sweeney_viral_dn

TF

Rank	p−value	#in/all	Geneset
1	3e−60	600 / 1148	HEBENSTREIT_low expression TF
2	1e−04	184 / 485	ICGC_NrsfPcr2_targets
3	2e−01	3 / 5	MYC_TFs
4	3e−01	711 / 2321	ICGC_Rad21_targets
5	5e−01	1 / 2	MYC_ECM cell adhesion DOWN
6	5e−01	4 / 12	NOWICK_TF
7	8e−01	2 / 9	MYC_Targets DOWN
8	9e−01	291 / 1025	ICGC_NrsfPcr1_targets
9	1e+00	1 / 9	MYC_DNA repair UP
10	1e+00	2 / 16	MYC_Protein synthesis degradation UP
11	1e+00	2 / 19	MYC_Metabolism UP
12	1e+00	126 / 522	ICGC_SrfPcr2_targets
13	1e+00	268 / 1041	ICGC_P300_targets
14	1e+00	5 / 62	MYC_Targets UP
15	1e+00	120 / 549	ICGC_Atf3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	58 / 134	PanCan_RAS_geneset_nanostring
2	2e−03	9 / 12	BEN−PORATH_DN
3	4e−03	33 / 72	PanCan_Wnt_geneset_nanostring
4	2e−02	70 / 187	PanCan_PI3K_geneset_nanostring
5	5e−02	12 / 25	PanCan_HH_geneset_nanostring
6	7e−02	53 / 147	PanCan_MAPK_geneset_nanostring
7	1e−01	7 / 14	GUSTAFSON_PI3K_DN
8	2e−01	17 / 47	PanCan_TGF−B_geneset_nanostring
9	4e−01	26 / 80	PanCan_JAK−ST_geneset_nanostring
10	4e−01	7 / 20	PanCan_ChromMod_geneset_nanostring
11	4e−01	30 / 96	PanCan_TXmisReg_geneset_nanostring
12	6e−01	33 / 113	PanCan_Driver_Gene_geneset_nanostring
13	6e−01	4 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	7e−01	4 / 14	GENTLES_modul13
15	8e−01	3 / 12	BENTINK_e2f3.2

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−99	1182 / 2417	9_ReprPCWk_Melanocytes
2	1e−99	1145 / 2254	10_ReprPC_MSC_Adipocyte
3	1e−99	1370 / 2867	9_ReprPCWk_MSC_Adipocyte
4	1e−99	1089 / 2148	10_ReprPC_Skeletal_Muscle
5	1e−99	1187 / 2408	9_ReprPCWk_Skeletal_Muscle
6	1e−99	1058 / 2015	ReprPC_Colon
7	1e−99	921 / 1744	ReprPCWk_Colon
8	1e−99	1477 / 3150	monocytes peripheral blood_13_ReprPC
9	1e−99	1512 / 3272	monocytes peripheral blood_14_ReprPCWk
10	1e−99	1196 / 2405	Bcells peripheral blood_13_ReprPC
11	1e−99	1464 / 3001	Bcells peripheral blood_14_ReprPCWk
12	1e−99	1782 / 3734	Tcells peripheral blood_13_ReprPC
13	1e−99	1763 / 3918	Tcells peripheral blood_14_ReprPCWk
14	1e−99	1156 / 2173	HSC_13_ReprPC
15	1e−99	1309 / 2600	HSC_14_ReprPCWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−43	240 / 373	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
2	3e−42	392 / 730	BENPORATH_ES_WITH_H3K27ME3
3	3e−33	162 / 240	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
4	3e−31	245 / 432	BENPORATH_PRC2_TARGETS
5	8e−31	352 / 697	BENPORATH_SUZ12_TARGETS
6	5e−29	234 / 417	REACTOME_GPCR_DOWNSTREAM_SIGNALING
7	9e−29	353 / 713	BENPORATH_EED_TARGETS
8	6e−27	268 / 510	REACTOME_SIGNALING_BY_GPCR
9	1e−25	170 / 284	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
10	8e−23	182 / 324	REACTOME_GPCR_LIGAND_BINDING
11	1e−20	172 / 311	SHEN_SMARCA2_TARGETS_DN
12	5e−20	136 / 230	REACTOME_NEURONAL_SYSTEM
13	3e−18	459 / 1092	YOSHIMURA_MAPK8_TARGETS_UP
14	5e−18	136 / 239	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
15	8e−18	362 / 826	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−04	32 / 62	DUMEAUX_Smoking enriched genes
2	1e−01	4 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
3	4e−01	3 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	6e−01	3 / 10	DUMEAUX_Smoking literature genes up
5	8e−01	4 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
6	8e−01	5 / 22	DUMEAUX_Fasting enriched genes
7	9e−01	1 / 8	Marjolein_ageing−genes_UP
8	1e+00	3 / 22	DUMEAUX_High bmi enriched genes
9	1e+00	1 / 12	DUMEAUX_Women normal BMI literature genes up
10	1e+00	1 / 14	Huan_blood−pressure_SBP−signature
11	1e+00	4 / 32	Marjolein_ageing−genes_DN
12	1e+00	30 / 150	Homuth_BMI−associated−genes_UP
13	1e+00	27 / 210	Homuth_BMI−associated−genes_DN
14	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
15	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	6e−40	218 / 337	G−protein coupled receptor activity
2	5e−29	112 / 151	ion channel activity
3	9e−29	268 / 500	signal transducer activity
4	9e−17	74 / 107	voltage−gated ion channel activity
5	8e−15	40 / 47	voltage−gated potassium channel activity
6	3e−14	34 / 38	olfactory receptor activity
7	8e−11	38 / 51	potassium channel activity
8	4e−10	53 / 84	hormone activity
9	7e−10	62 / 105	Ras guanyl−nucleotide exchange factor activity
10	4e−09	45 / 70	calcium channel activity
11	4e−08	213 / 517	calcium ion binding
12	4e−08	29 / 40	extracellular ligand−gated ion channel activity
13	6e−08	73 / 141	growth factor activity
14	9e−08	33 / 49	transmembrane receptor protein tyrosine kinase activity
15	1e−07	187 / 450	sequence−specific DNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−37	221 / 352	WIRTH_Nervous System
2	5e−20	65 / 82	WIRTH_Testis
3	5e−12	35 / 43	WIRTH_Placenta
4	1e−10	34 / 44	JONGENEEL_Retina
5	2e−08	71 / 133	JONGENEEL_Testis
6	2e−07	30 / 44	WIRTH_Pancreas
7	1e−06	34 / 55	WIRTH_Homeostasis
8	8e−06	93 / 209	Chaussabel_2,5_Immune related molecules
9	4e−05	19 / 28	JONGENEEL_Placenta
10	2e−04	41 / 83	WIRTH_Muscle
11	3e−03	12 / 19	JONGENEEL_Prostate
12	4e−03	6 / 7	WIRTH_Pituitary gland
13	4e−03	9 / 13	WIRTH_Bone marrow
14	8e−03	13 / 23	JONGENEEL_Pancreas
15	9e−03	9 / 14	WIRTH_Thalamus

K−Means Cluster

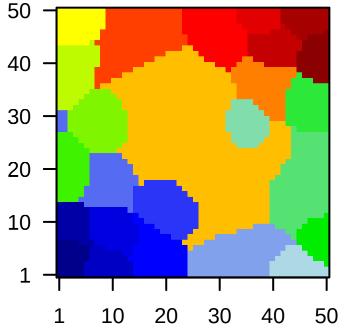
Spot Summary: T

metagenes = 41
genes = 697

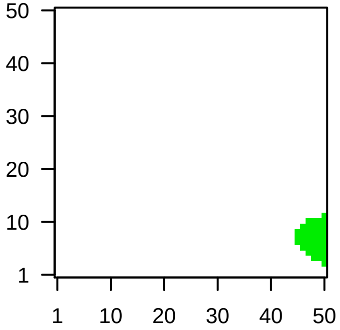
<r> metagenes = 0.92
<r> genes = 0.28
beta: r2= 5.64 / log p= −Inf

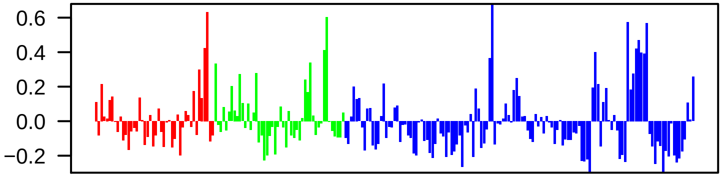
samples with spot = 35 (15.8 %)
mBL : 5 (11.4 %)
intermediate : 9 (18.8 %)
non−mBL : 21 (16.3 %)

Overview Map



Spot





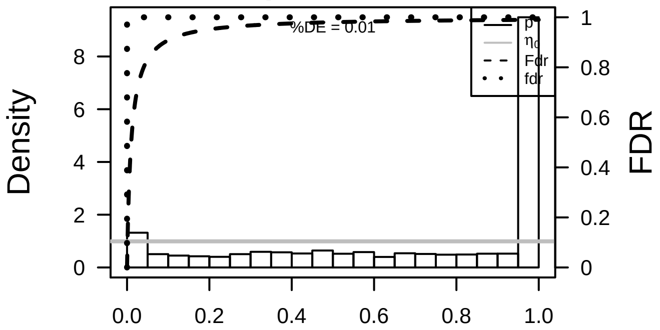
Spot Genelist

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	0.58		
4	222073_at	2.16	−0.87	0.38	COL4A3	collagen type IV alpha 3 chain [Source:HGNC Symbol;Acc:H
5	204073_s_at	2.15	−0.65	0.16	MYRF	myelin regulatory factor [Source:HGNC Symbol;Acc:HGNC:1
6	214753_at	2.14	−1.23	0.73		
7	212225_at	2.11	−0.84	0.45	EIF1	eukaryotic translation initiation factor 1 [Source:HGNC Symb
8	207492_at	2.1	−1.01	0.74		
9	205316_at	2.09	−0.97	0.55	SLC15A2	solute carrier family 15 member 2 [Source:HGNC Symbol;Ac
10	220918_at	2.03	−0.81	0.79		
11	207078_at	1.96	−0.94	0.73	MED6	mediator complex subunit 6 [Source:HGNC Symbol;Acc:HGN
12	208268_at	1.89	−0.91	0.53	ADAM28	ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
13	215392_at	1.89	−0.68	0.77		
14	208195_at	1.84	−1.07	0.35	TTN	titin [Source:HGNC Symbol;Acc:HGNC:12403]
15	222375_at	1.83	−0.72	0.68		
16	220940_at	1.83	−1.2	0.75		
17	215164_at	1.82	−1.12	0.55		
18	213931_at	1.82	−1.03	0.39	ID2	inhibitor of DNA binding 2 [Source:HGNC Symbol;Acc:HGNC
19	215768_at	1.81	−0.79	0.42		
20	217534_at	1.8	−0.88	0.75	FAM49B	family with sequence similarity 49 member B [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−48	149 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
2	7e−42	60 / 188	Refer	Chaussabel_3,8_Enzymes
3	6e−29	261 / 4261	Lymp	HOPP_Txn_transition
4	2e−27	50 / 218	Refer	WIRTH_pre+post GC B−cells
5	7e−22	291 / 5529	Lymp	HOPP_Txn_elongation
6	1e−20	16 / 20	Refer	Chaussabel_2,7_Unknown function
7	3e−19	62 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
8	2e−15	28 / 127	GSE	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
9	6e−15	7 / 14	Canc	LIU_COMMON_CANCER_GENES
10	6e−15	7 / 14	Canc	LIU_COMMON_CANCER_GENES
11	5e−14	19 / 59	Gliom	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	4e−13	35 / 239	GSE	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
13	6e−12	107 / 1602	GSE	BLALOCK_ALZHEIMERS_DISEASE_UP
14	7e−12	70 / 852	MF	nucleic acid binding
15	1e−10	24 / 143	GSE	LEE_DIFFERENTIATING_T_LYMPHOCYTE
16	2e−10	25 / 159	GSE	JISON_SICKLE_CELL_DISEASE_DN
17	8e−10	182 / 3564	TF	ICGC_Taf1_targets
18	1e−09	9 / 17	GSE	SPIRA_SMOKERS_LUNG_CANCER_DN
19	2e−09	19 / 102	Lymp	ROSOLOWSKI_blue total
20	3e−09	32 / 281	BP	mRNA processing
21	3e−09	218 / 4579	CC	nucleus
22	7e−09	264 / 5908	Lymp	HOPP_Active_promoter
23	1e−08	17 / 92	GSE	HOEBEKE_LYMPHOID_STEM_CELL_UP
24	5e−08	11 / 39	GSE	BILBAN_B_CLL_LPL_DN
25	8e−08	60 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
26	1e−07	47 / 600	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
27	1e−07	26 / 233	BP	RNA splicing
28	1e−07	74 / 1161	MF	RNA binding
29	2e−07	40 / 477	GSE	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
30	2e−07	19 / 136	GSE	REACTOME_MRNA_PROCESSING
31	2e−07	14 / 75	GSE	LAIHO_COLORECTAL_CANCER_SERRATED_DN
32	2e−07	21 / 165	GSE	THUM_SYSTOLIC_HEART_FAILURE_DN
33	3e−07	239 / 5404	Lymp	HOPP_Strong_enhancer
34	4e−07	24 / 214	GSE	CHEN_HOXA5_TARGETS_9HR_UP
35	4e−07	8 / 22	Refer	Chaussabel_1,6_Signaling molecules
36	4e−07	155 / 3150	TF	ICGC_Creb1_targets
37	5e−07	52 / 730	GSE	ONKEN_UVEAL_MELANOMA_UP
38	5e−07	79 / 1312	GSE	PUJANA_ATM_PCC_NETWORK
39	8e−07	17 / 120	GSE	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
40	1e−06	178 / 3796	TF	ICGC_Nficsc81335_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	1	1 / 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	

CC

Rank	p−value	#in/all	Geneset
1	3e−09	218 / 4579	nucleus
2	3e−06	29 / 326	nuclear speck
3	6e−06	126 / 2541	nucleoplasm
4	1e−03	24 / 354	centrosome
5	2e−03	12 / 128	spliceosomal complex
6	6e−03	4 / 22	histone acetyltransferase complex
7	7e−03	13 / 174	cilium
8	8e−03	9 / 101	kinetochore
9	8e−03	155 / 3805	cytosol
10	1e−02	6 / 54	axoneme
11	1e−02	5 / 41	cytosolic large ribosomal subunit
12	2e−02	3 / 18	cytoplasmic dynein complex
13	3e−02	17 / 292	microtubule organizing center
14	3e−02	5 / 50	host cell
15	3e−02	6 / 70	nuclear pore

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−48	149 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	3e−19	62 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
3	8e−08	60 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
4	7e−05	7 / 31	Marisa_CRC−cluster−c
5	2e−04	35 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
6	3e−04	49 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
7	2e−03	251 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
8	4e−03	7 / 60	Marisa_CRC−cluster−g
9	7e−03	3 / 12	Juehling_HNPCC−mutated−in−4
10	2e−02	3 / 16	Vilar_non−hypermutated−in−CRC
11	4e−02	73 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	5e−02	51 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	8e−02	2 / 14	TCGA_Mutated−in−CRC_non−hypermutated
14	8e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
15	1e−01	2 / 16	Vilar_mutated−in−CRC−CampP

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 51	HALLMARK_TGF_BETA_SIGNALING
2	0.1	9 / 173	HALLMARK_MITOTIC_SPINDLE
3	0.3	6 / 133	HALLMARK_DNA_REPAIR
4	0.3	8 / 187	HALLMARK_E2F_TARGETS
5	0.3	2 / 34	HALLMARK_APICAL_SURFACE
6	0.4	8 / 193	HALLMARK_HEME_METABOLISM
7	0.4	8 / 195	HALLMARK_G2M_CHECKPOINT
8	0.5	2 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.5	7 / 190	HALLMARK_MYC_TARGETS_V1
10	0.6	6 / 188	HALLMARK_HYPOXIA
11	0.6	6 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.7	3 / 97	HALLMARK_BILE_ACID_METABOLISM
13	0.7	1 / 34	HALLMARK_ANGIOGENESIS
14	0.7	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
15	0.7	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−29	261 / 4261	HOPP_Txn_transition
2	7e−22	291 / 5529	HOPP_Txn_elongation
3	2e−09	19 / 102	ROSOLOWSKI_blue total
4	7e−09	264 / 5908	HOPP_Active_promoter
5	3e−07	239 / 5404	HOPP_Strong_enhancer
6	7e−06	57 / 906	SPANG_BCR DN
7	2e−02	2 / 6	MASCQUE_mBL UP
8	2e−02	5 / 45	Monti_BCR_cluster
9	2e−02	8 / 99	Sha_BL UP
10	2e−02	2 / 7	Shaknovich_ABC_hypo_meth
11	3e−02	216 / 5682	HOPP_Weak_promoter
12	6e−02	42 / 955	SPANG_BCR UP
13	7e−02	14 / 263	SPANG_CD40 6hrs UP
14	9e−02	2 / 15	BENTINK_mBL UP
15	9e−02	2 / 15	DAVE_BL Inter

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	13 / 111	hsa−miR−656
2	2e−04	8 / 49	hsa−miR−330−5p
3	3e−04	27 / 378	hsa−miR−16
4	4e−04	21 / 267	hsa−miR−142−5p
5	8e−04	25 / 363	hsa−miR−195
6	1e−03	30 / 474	hsa−miR−20a
7	1e−03	18 / 232	hsa−miR−186
8	1e−03	28 / 435	hsa−miR−93
9	1e−03	23 / 336	hsa−miR−519d
10	2e−03	24 / 361	hsa−miR−130b
11	2e−03	22 / 324	hsa−miR−497
12	2e−03	5 / 27	hsa−miR−770−5p
13	2e−03	24 / 368	hsa−miR−301a
14	2e−03	24 / 369	hsa−miR−15b
15	2e−03	23 / 350	hsa−miR−424

Telomeres

Rank	p−value	#in/all	Geneset
1	0.6	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	3e−09	32 / 281	mRNA processing
2	1e−07	26 / 233	RNA splicing
3	1e−05	89 / 1655	transcription, DNA−templated
4	1e−05	13 / 90	RNA processing
5	2e−05	20 / 198	mRNA splicing, via spliceosome
6	7e−05	90 / 1764	regulation of transcription, DNA−templated
7	2e−04	8 / 49	RNA export from nucleus
8	4e−04	4 / 11	histone H4−K16 acetylation
9	6e−04	6 / 31	regulation of alternative mRNA splicing, via spliceosome
10	8e−04	4 / 13	alternative mRNA splicing, via spliceosome
11	1e−03	7 / 47	mRNA 3'−end processing
12	1e−03	4 / 15	mRNA splice site selection
13	2e−03	9 / 83	viral transcription
14	2e−03	4 / 17	negative regulation of mRNA splicing, via spliceosome
15	3e−03	9 / 86	mRNA export from nucleus

Chr

Rank	p−value	#in/all	Geneset
1	0.01	29 / 548	Chr 16
2	0.02	40 / 833	Chr 19
3	0.03	29 / 585	Chr 7
4	0.04	36 / 776	Chr 17
5	0.07	20 / 403	Chr 14
6	0.11	30 / 689	Chr 3
7	0.18	15 / 333	Chr 22
8	0.21	7 / 139	Chr 21
9	0.30	27 / 700	Chr 12
10	0.34	15 / 382	Chr 15
11	0.51	29 / 832	Chr 2
12	0.60	8 / 242	Chr 13
13	0.61	6 / 184	Chr 18
14	0.73	17 / 554	Chr 5
15	0.73	11 / 369	Chr 20

Glioma

Rank	p−value	#in/all	Geneset
1	5e−14	19 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	9e−04	75 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−03	3 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
4	4e−03	3 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
5	1e−02	62 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	7e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
7	9e−02	2 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
8	1e−01	27 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	2e−01	2 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
10	2e−01	3 / 50	Vishal_subnetwork signature of survival in GBM
11	3e−01	1 / 10	Phillips PN up vs MES & Prolif
12	3e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
13	4e−01	4 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
14	4e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	4e−01	2 / 38	WILLSCHER_GBM_Verhaak−PNwt_up

Immunome

Rank	p−value	#in/all	Geneset
1	0.07	2 / 13	Angelova_immune−metagene−immature_B−cells
2	0.16	1 / 5	Angelova_immune−metagene−NKT
3	0.20	3 / 45	Angelova_immune−metagene−MDSC
4	0.22	1 / 7	Angelova_immune−metagene−cytotoxic_cells
5	0.30	1 / 10	Angelova_immune−metagene−neutrophils
6	0.39	1 / 14	Angelova_immune−metagene−eosinophil
7	0.47	1 / 18	Angelova_immune−metagene−pDC
8	0.47	1 / 18	Angelova_CRC_immunostimulators
9	0.55	1 / 23	Angelova_immune−metagene−monocytes
10	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
11	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
12	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
13	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
14	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
15	1.00	0 / 25	Angelova_immune−metagene−DC

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	15 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.05	3 / 24	Tirosh_B−cell specific genes−melanoma
3	0.07	1 / 2	Melanoma Epi−Enzyme Cluster 6
4	0.19	2 / 23	Melanoma Epi−Enzyme Cluster 7
5	0.19	9 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	0.21	4 / 68	Tirosh_housekeeping_genes
7	0.26	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	0.32	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
9	0.40	9 / 230	Gerber_wt/wt_melanoma−cells−SpotC
10	0.42	12 / 319	Gerber_wt/wt_melanoma−cells−SpotA
11	0.43	9 / 236	Gerber_wt/wt_group3−specific
12	0.43	1 / 16	Hugo_melanoma−all−LEF1_UP
13	0.49	2 / 47	Tirosh_G2/M phase specific genes
14	0.49	9 / 249	Gerber_wt/wt_melanoma−cells−SpotE
15	0.57	1 / 24	Gerami_melanoma−metastatic−risk_DN

Pneumonia

Rank	p−value	#in/all	Geneset
1	4e−06	20 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	3e−01	3 / 54	Burnham_timecourse
3	4e−01	2 / 41	Scicluna_DN
4	7e−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

TF

Rank	p−value	#in/all	Geneset
1	8e−10	182 / 3564	ICGC_Taf1_targets
2	4e−07	155 / 3150	ICGC_Creb1_targets
3	1e−06	178 / 3796	ICGC_Nficsc81335_targets
4	3e−06	195 / 4319	ICGC_Pou2_targets
5	8e−06	174 / 3804	ICGC_Stat5_targets
6	1e−05	147 / 3121	ICGC_Egr1_targets
7	2e−05	171 / 3769	ICGC_Pmlsc71910_targets
8	3e−05	167 / 3703	ICGC_Foxm1_targets
9	3e−05	200 / 4602	ICGC_Elf1_targets
10	5e−05	182 / 4131	ICGC_Tcf3_targets
11	6e−05	156 / 3451	ICGC_Atf2_targets
12	6e−05	135 / 2899	ICGC_Nfatc1_targets
13	2e−04	108 / 2254	ICGC_BatfPcr1_targets
14	2e−04	83 / 1630	ICGC_SrfV0416101_targets
15	2e−04	184 / 4278	ICGC_Yy1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	6e−15	7 / 14	LIU_COMMON_CANCER_GENES
2	1e−03	4 / 14	GUSTAFSON_PI3K_DN
3	2e−02	3 / 16	LIU_LIVER_CANCER
4	6e−02	2 / 12	LIU_BREAST_CANCER
5	8e−02	2 / 14	BENTINK_ras.6
6	8e−02	2 / 14	BENTINK_src.2
7	2e−01	5 / 96	PanCan_TXmisReg_geneset_nanostring
8	3e−01	1 / 10	GENTLES_modul5
9	3e−01	1 / 12	BENTINK_e2f3.2
10	4e−01	5 / 113	PanCan_Driver_Gene_geneset_nanostring
11	4e−01	1 / 14	GENTLES_modul10
12	4e−01	1 / 14	BENTINK_myc.1
13	4e−01	1 / 15	WANG_ER_UP
14	4e−01	2 / 41	PanCan_DNARepair_geneset_nanostring
15	5e−01	2 / 45	KUIPER_MM poor survival

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−39	329 / 5601	Thelper cells peripheral blood_4_Tx
2	2e−36	330 / 5766	natural killer cells peripheral blood_4_Tx
3	4e−35	327 / 5753	Tcells peripheral blood_4_Tx
4	3e−34	324 / 5716	Bcells peripheral blood_4_Tx
5	2e−32	314 / 5527	Tregulatory cells peripheral blood_4_Tx
6	6e−30	261 / 4208	Tcells peripheral blood_6_EnhG
7	2e−29	272 / 4528	T CD8+ naive cells peripheral blood_4_Tx
8	2e−28	344 / 6679	5_Tx_Melanocytes
9	3e−28	378 / 7833	Bcells peripheral blood_1_TssA
10	1e−27	365 / 7420	Tcells peripheral blood_1_TssA
11	2e−27	347 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
12	1e−26	227 / 3524	Tregulatory cells peripheral blood_6_EnhG
13	1e−26	233 / 3682	natural killer cells peripheral blood_6_EnhG
14	2e−26	320 / 6068	4_Tx_ESC_Endoderm
15	4e−26	390 / 8406	Bcells peripheral blood_2_TssAFlnk

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−15	28 / 127	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
2	6e−15	7 / 14	LIU_COMMON_CANCER_GENES
3	4e−13	35 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	6e−12	107 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
5	1e−10	24 / 143	LEE_DIFFERENTIATING_T_LYMPHOCYTE
6	2e−10	25 / 159	JISON_SICKLE_CELL_DISEASE_DN
7	1e−09	9 / 17	SPIRA_SMOKERS_LUNG_CANCER_DN
8	1e−08	17 / 92	HOEBEKE_LYMPHOID_STEM_CELL_UP
9	5e−08	11 / 39	BILBAN_B_CLL_LPL_DN
10	1e−07	47 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
11	2e−07	40 / 477	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
12	2e−07	19 / 136	REACTOME_MRNA_PROCESSING
13	2e−07	14 / 75	LAIHO_COLORECTAL_CANCER_SERRATED_DN
14	2e−07	21 / 165	THUM_SYSTOLIC_HEART_FAILURE_DN
15	4e−07	24 / 214	CHEN_HOXA5_TARGETS_9HR_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	11 / 210	Homuth_BMI−associated−genes_DN
2	0.2	2 / 22	DUMEAUX_Fasting enriched genes
3	0.5	1 / 22	DUMEAUX_High bmi enriched genes
4	0.6	5 / 150	Homuth_BMI−associated−genes_UP
5	0.9	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

MF

Rank	p−value	#in/all	Geneset
1	7e−12	70 / 852	nucleic acid binding
2	1e−07	74 / 1161	RNA binding
3	2e−04	79 / 1541	DNA binding
4	4e−03	10 / 107	mRNA binding
5	4e−03	4 / 20	RNA polymerase II transcription corepressor activity
6	7e−03	7 / 65	thiol−dependent ubiquitinyl hydrolase activity
7	8e−03	9 / 100	cysteine−type peptidase activity
8	1e−02	4 / 25	cyclin binding
9	1e−02	4 / 25	nuclear localization sequence binding
10	1e−02	20 / 331	protein serine/threonine kinase activity
11	1e−02	6 / 57	thiol−dependent ubiquitin−specific protease activity
12	2e−02	5 / 44	methylated histone binding
13	2e−02	3 / 17	lysine−acetylated histone binding
14	2e−02	5 / 48	translation initiation factor activity
15	3e−02	3 / 19	miRNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−42	60 / 188	Chaussabel_3,8_Enzymes
2	2e−27	50 / 218	WIRTH_pre+post GC B−cells
3	1e−20	16 / 20	Chaussabel_2,7_Unknown function
4	4e−07	8 / 22	Chaussabel_1,6_Signaling molecules
5	1e−06	21 / 182	WIRTH_post GC B−cells
6	3e−06	62 / 989	PROTEINATLAS_tonsil
7	3e−06	15 / 106	Chaussabel_2,11_Replication
8	7e−06	53 / 819	PROTEINATLAS_bronchus
9	1e−05	53 / 840	PROTEINATLAS_urinary bladder
10	2e−05	53 / 848	PROTEINATLAS_adrenal gland
11	7e−05	16 / 152	VAQUERIZAS_General_TF
12	1e−04	51 / 861	PROTEINATLAS_nasopharynx
13	2e−04	58 / 1048	PROTEINATLAS_gallbladder
14	2e−04	43 / 708	PROTEINATLAS_thyroid gland
15	2e−04	50 / 866	PROTEINATLAS_cerebellum

K−Means Cluster

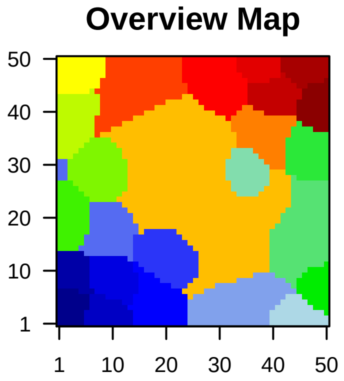
Spot Summary: U

metagenes = 102
genes = 554

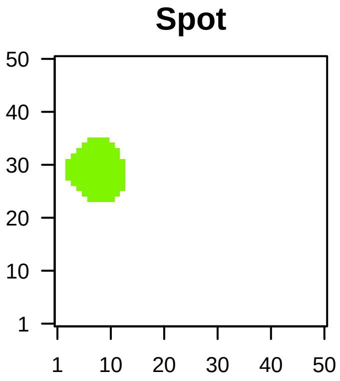
<r> metagenes = 0.76
<r> genes = 0.1
beta: r2= 1.4 / log p= −Inf

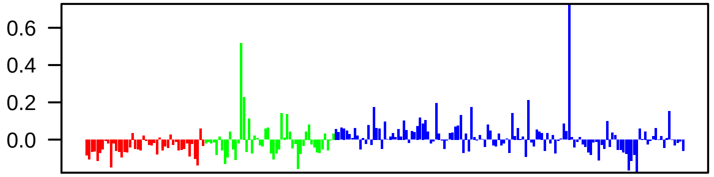
samples with spot = 8 (3.6 %)
intermediate : 2 (4.2 %)
non−mBL : 6 (4.7 %)

Overview Map



Spot





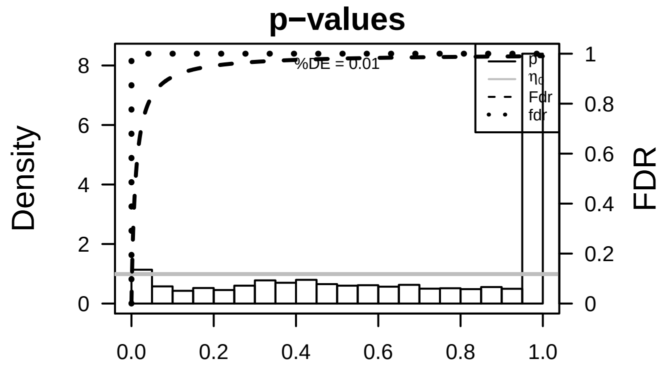
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207663_x_at	3.8	−0.83	0.24	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
2	206640_x_at	3.58	−0.65	0.2	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
3	211425_x_at	3.5	−0.75	0.48		SSX family member 6, pseudogene [Source:HGNC Symbol;A
4	208235_x_at	3.42	−0.72	0.22	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
5	207739_s_at	3.42	−1.01	0.3	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
6	207086_x_at	3.38	−0.68	0.22	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	208155_x_at	3.36	−0.82	0.22	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
8	209942_x_at	3.13	−0.71	0.37	MAGEA3	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
9	210394_x_at	3.08	−0.76	0.47		SSX family member 6, pseudogene [Source:HGNC Symbol;A
10	207666_x_at	3	−0.6	0.39	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:11
11	210497_x_at	3	−0.67	0.43	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:11
12	214612_x_at	3	−0.72	0.37	MAGEA3	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
13	214957_at	2.96	−0.84	0.18	ACTL8	actin like 8 [Source:HGNC Symbol;Acc:HGNC:24018]
14	206018_at	2.95	−0.82	0.13	FOXG1	forkhead box G1 [Source:HGNC Symbol;Acc:HGNC:3811]
15	206626_x_at	2.85	−0.74	0.47	SSX1	SSX family member 1 [Source:HGNC Symbol;Acc:HGNC:11
16	220377_at	2.84	−1.15	0.16		family with sequence similarity 30 member A [Source:HGNC
17	207325_x_at	2.83	−0.79	0.39	MAGEA1	MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC
18	206574_s_at	2.79	−1.22	0.39	PTP4A3	protein tyrosine phosphatase type IVA, member 3 [Source:H
19	206834_at	2.78	−0.67	0.48	HBD	hemoglobin subunit delta [Source:HGNC Symbol;Acc:HGNC:
20	214254_at	2.78	−0.63	0.26	MAGEA4	MAGE family member A4 [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−36	123 / 1035	CC	endoplasmic reticulum
2	5e−31	35 / 77	Lymp	TARTE_Plasma cell signature
3	9e−29	33 / 75	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
4	5e−28	88 / 683	CC	endoplasmic reticulum membrane
5	2e−19	41 / 216	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
6	3e−19	25 / 71	GSEA	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
7	2e−17	61 / 518	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
8	3e−17	31 / 137	GSEA	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
9	2e−13	260 / 5339	CC	membrane
10	4e−13	15 / 37	GSEA	KEGG_N_GLYCAN_BIOSYNTHESIS
11	2e−12	40 / 325	GSEA	REACTOME_METABOLISM_OF_PROTEINS
12	4e−12	178 / 3270	CC	integral component of membrane
13	4e−11	23 / 125	BP	protein glycosylation
14	4e−11	14 / 41	GSEA	MORI_PLASMA_CELL_UP
15	3e−10	46 / 479	CC	Golgi membrane
16	3e−10	16 / 64	GSEA	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPH
17	9e−10	16 / 68	GSEA	REACTOME_UNFOLDED_PROTEIN_RESPONSE
18	9e−10	27 / 198	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
19	2e−09	16 / 71	BP	response to endoplasmic reticulum stress
20	3e−09	14 / 54	BP	IRE1−mediated unfolded protein response
21	3e−09	75 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tra
22	4e−09	29 / 241	CC	endoplasmic reticulum lumen
23	5e−09	11 / 32	BP	protein N−linked glycosylation
24	6e−09	19 / 110	GSEA	REACTOME_DIABETES_PATHWAYS
25	7e−09	11 / 33	BP	protein N−linked glycosylation via asparagine
26	8e−09	30 / 262	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
27	3e−08	17 / 96	GSEA	SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOC
28	4e−08	20 / 136	BP	ER to Golgi vesicle−mediated transport
29	4e−08	65 / 938	CC	Golgi apparatus
30	4e−08	22 / 163	MF	transferase activity, transferring glycosyl groups
31	5e−08	29 / 269	GSEA	HELLER_HDAC_TARGETS_DN
32	7e−08	15 / 79	CC	integral component of endoplasmic reticulum membrane
33	1e−07	12 / 51	CC	endoplasmic reticulum−Golgi intermediate compartment
34	1e−07	17 / 106	HM	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
35	1e−07	194 / 4131	TF	ICGC_Tcf3_targets
36	1e−07	12 / 52	GSEA	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
37	2e−07	13 / 64	GSEA	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL
38	3e−07	11 / 46	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
39	3e−07	19 / 140	BP	protein folding
40	3e−07	171 / 3564	TF	ICGC_Taf1_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	3 / 92	HORVATH_aging_genes meth DOWN
2	0.7	3 / 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	4e−11	23 / 125	protein glycosylation
2	2e−09	16 / 71	response to endoplasmic reticulum stress
3	3e−09	14 / 54	IRE1−mediated unfolded protein response
4	5e−09	11 / 32	protein N−linked glycosylation
5	7e−09	11 / 33	protein N−linked glycosylation via asparagine
6	4e−08	20 / 136	ER to Golgi vesicle−mediated transport
7	3e−07	19 / 140	protein folding
8	6e−07	22 / 190	vesicle−mediated transport
9	1e−05	5 / 10	cargo loading into COPII−coated vesicle
10	1e−05	10 / 53	COPII vesicle coating
11	3e−05	36 / 502	protein transport
12	3e−05	5 / 12	retrograde protein transport, ER to cytosol
13	3e−05	11 / 72	retrograde vesicle−mediated transport, Golgi to ER
14	5e−05	9 / 50	response to unfolded protein
15	6e−05	9 / 52	ubiquitin−dependent ERAD pathway

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	0 / 11	LIU_PROSTATE_CANCER_UP
2	0.003	1 / 15	RHODES_CANCER_META_SIGNATURE
3	0.005	14 / 186	SPANG_LPS−index2
4	0.082	2 / 14	GENTLES_modul13
5	0.082	16 / 317	SPANG_BCL6−index2
6	0.126	3 / 36	ZHANG_MM up
7	0.139	4 / 58	SHAUGHNESSY_MM high risk
8	0.142	5 / 80	PanCan_JAK−ST_geneset_nanostring
9	0.180	7 / 134	PanCan_RAS_geneset_nanostring
10	0.271	1 / 9	WANG_ER_DN
11	0.292	6 / 130	PanCan_CC+Apop_geneset_nanostring
12	0.303	2 / 32	KUIPER_MM good survival
13	0.317	8 / 187	PanCan_PI3K_geneset_nanostring
14	0.320	1 / 11	GENTLES_modul14
15	0.344	1 / 12	GENTLES_modul12

CC

Rank	p−value	#in/all	Geneset
1	3e−36	123 / 1035	endoplasmic reticulum
2	5e−28	88 / 683	endoplasmic reticulum membrane
3	2e−13	260 / 5339	membrane
4	4e−12	178 / 3270	integral component of membrane
5	3e−10	46 / 479	Golgi membrane
6	4e−09	29 / 241	endoplasmic reticulum lumen
7	4e−08	65 / 938	Golgi apparatus
8	7e−08	15 / 79	integral component of endoplasmic reticulum membrane
9	1e−07	12 / 51	endoplasmic reticulum−Golgi intermediate compartment
10	2e−05	12 / 82	transport vesicle
11	3e−05	5 / 12	trans−Golgi network transport vesicle
12	5e−05	5 / 13	COPII vesicle coat
13	8e−05	6 / 22	smooth endoplasmic reticulum
14	2e−04	9 / 58	Golgi cisterna membrane
15	2e−04	7 / 35	cis−Golgi network

Chr

Rank	p−value	#in/all	Geneset
1	3e−05	45 / 689	Chr 3
2	6e−02	31 / 669	Chr 6
3	7e−02	26 / 556	Chr X
4	2e−01	17 / 403	Chr 14
5	3e−01	49 / 1325	Chr 1
6	3e−01	19 / 492	Chr 9
7	3e−01	21 / 548	Chr 16
8	4e−01	28 / 756	Chr 11
9	4e−01	2 / 41	Chr Y
10	5e−01	21 / 585	Chr 7
11	5e−01	12 / 333	Chr 22
12	6e−01	6 / 184	Chr 18
13	6e−01	12 / 369	Chr 20
14	7e−01	4 / 139	Chr 21
15	7e−01	17 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−09	371 / 9179	2_TssA_Skeletal_Muscle
2	5e−09	312 / 7331	TssA_Colon
3	2e−08	338 / 8200	monocytes peripheral blood_2_TssAFlnk
4	2e−08	371 / 9275	3_TssF_MSC_Adipocyte
5	3e−08	319 / 7635	monocytes peripheral blood_1_TssA
6	3e−08	344 / 8430	3_TssF_Melanocytes
7	1e−07	364 / 9146	3_TssF_Skeletal_Muscle
8	1e−07	309 / 7420	Tcells peripheral blood_1_TssA
9	1e−07	352 / 8766	2_TssA_Melanocytes
10	1e−07	364 / 9160	2_TssA_Neuronal_Progenitor
11	3e−07	325 / 7957	Tcells peripheral blood_2_TssAFlnk
12	5e−07	339 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
13	7e−07	374 / 9576	2_TssA_MSC_Adipocyte
14	8e−07	319 / 7833	Bcells peripheral blood_1_TssA
15	8e−07	299 / 7225	Overlap_fetal_midbrain_ReprPC

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−09	75 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	3e−05	18 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
3	6e−04	61 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
4	4e−03	65 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	5e−03	45 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	4e−02	2 / 10	KIM_CRC−MSI−regulated_DN
7	8e−02	70 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
8	9e−02	15 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
9	9e−02	2 / 15	TCGA−CRC_less−agressive−disease−markers
10	2e−01	1 / 6	Hewish_dMMR−secondary−mutations_Signal_transduction
11	2e−01	1 / 7	Boland_CRC−MSI−TGC
12	2e−01	3 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	2e−01	1 / 8	Marisa_CRC−C1
14	3e−01	1 / 9	Marisa_CRC−C2
15	3e−01	3 / 60	Marisa_CRC−cluster−g

Glioma

Rank	p−value	#in/all	Geneset
1	0.001	23 / 330	Up
2	0.007	2 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
3	0.040	15 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
4	0.053	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
5	0.072	2 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
6	0.078	4 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
7	0.089	5 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
8	0.111	9 / 163	ScoV_0.999_Sturm_E1_IDH_DN
9	0.121	4 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
10	0.204	52 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
11	0.245	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
12	0.271	1 / 9	Donson−migration tethering and rolling−associated with LTS in HGA
13	0.271	1 / 9	Colman_survival_robust
14	0.290	2 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
15	0.303	2 / 32	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−29	33 / 75	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
2	2e−19	41 / 216	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
3	3e−19	25 / 71	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
4	2e−17	61 / 518	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
5	3e−17	31 / 137	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
6	4e−13	15 / 37	KEGG_N_GLYCAN_BIOSYNTHESIS
7	2e−12	40 / 325	REACTOME_METABOLISM_OF_PROTEINS
8	4e−11	14 / 41	MORI_PLASMA_CELL_UP
9	3e−10	16 / 64	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHO
10	9e−10	16 / 68	REACTOME_UNFOLDED_PROTEIN_RESPONSE
11	9e−10	27 / 198	TIEN_INTESTINE_PROBIOTICS_24HR_DN
12	6e−09	19 / 110	REACTOME_DIABETES_PATHWAYS
13	8e−09	30 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
14	3e−08	17 / 96	SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYT
15	5e−08	29 / 269	HELLER_HDAC_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−07	17 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	5e−03	9 / 94	HALLMARK_PROTEIN_SECRETION
3	9e−03	11 / 139	HALLMARK_FATTY_ACID_METABOLISM
4	1e−02	13 / 182	HALLMARK_GLYCOLYSIS
5	2e−02	13 / 192	HALLMARK_MTORC1_SIGNALING
6	2e−02	12 / 181	HALLMARK_XENOBIOTIC_METABOLISM
7	9e−02	8 / 133	HALLMARK_DNA_REPAIR
8	1e−01	3 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1e−01	8 / 149	HALLMARK_UV_RESPONSE_UP
10	2e−01	3 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	2e−01	9 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	2e−01	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	2e−01	5 / 97	HALLMARK_PEROXISOME
14	2e−01	6 / 122	HALLMARK_SPERMATOGENESIS
15	3e−01	2 / 29	HALLMARK_NOTCH_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 13	Angelova_CRC_MSS^−neoantigens
2	1e−03	3 / 7	Angelova_CRC_MSI−neoantigens
3	7e−03	2 / 4	Angelova_CRC_MSS−neoantigens
4	4e−02	3 / 23	Angelova_immune−metagene−Th2
5	1e−01	2 / 16	Angelova_immune−metagene−Th17
6	3e−01	1 / 11	Angelova_immune−metagene−macrophages
7	3e−01	1 / 12	Angelova_immune−metagene−effector_memory_CD4
8	3e−01	1 / 12	Angelova_immune−metagene−NK56_dim
9	4e−01	1 / 15	Angelova_immune−metagene−NK
10	5e−01	2 / 45	Angelova_immune−metagene−MDSC
11	5e−01	1 / 18	Angelova_immune−metagene−pDC
12	5e−01	1 / 18	Angelova_CRC_immunostimulators
13	5e−01	1 / 19	Angelova_immune−metagene−iDC
14	5e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
15	8e−01	1 / 42	Angelova_immune−metagene−TGD

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.4	8 / 210	Homuth_BMI−associated−genes_DN
3	0.6	2 / 62	DUMEAUX_Smoking enriched genes
4	1.0	1 / 150	Homuth_BMI−associated−genes_UP
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−31	35 / 77	TARTE_Plasma cell signature
2	2e−06	252 / 5908	HOPP_Active_promoter
3	5e−05	186 / 4261	HOPP_Txn_transition
4	1e−04	235 / 5682	HOPP_Weak_promoter
5	2e−04	228 / 5529	HOPP_Txn_elongation
6	9e−04	189 / 4559	HOPP_Weak_enhancer
7	1e−03	49 / 906	SPANG_BCR DN
8	3e−03	23 / 353	SPANG_CD40 6hrs DN
9	3e−03	215 / 5404	HOPP_Strong_enhancer
10	7e−03	3 / 12	Subero_MM_hypo_meth
11	7e−03	175 / 4357	HOPP_Weak_txn
12	2e−02	5 / 45	SPANG_BAFF 9hrs DN
13	3e−02	7 / 85	Aukema_BCL2 DN_BCL6 UP
14	1e−01	4 / 57	SPANG_LPS 6hrs DN
15	2e−01	5 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.005	15 / 204	Landsberg_dedifferentiation_down
2	0.005	14 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
3	0.024	7 / 83	TCGA_melanoma_immune_high
4	0.053	8 / 119	TCGA_melanoma_MITF_low
5	0.063	11 / 189	Tirosh_genes preferentially expressed by Tregs
6	0.065	13 / 236	Gerber_wt/wt_group3−specific
7	0.083	12 / 222	Gerber_wt/wt_melanoma−cells−SpotF
8	0.150	3 / 39	Tirosh_top50 correlated genes PC4
9	0.211	3 / 46	Tirosh_top50 correlated genes PC5
10	0.257	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
11	0.296	1 / 10	Joensson_Melanoma Normal like subtype
12	0.305	4 / 81	Tirosh_Genes in the MITF program
13	0.354	19 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	0.389	3 / 65	Harbst_melanoma_highgrade_up
15	0.415	2 / 41	Tirosh_top50 correlated genes PC3

MF

Rank	p−value	#in/all	Geneset
1	4e−08	22 / 163	transferase activity, transferring glycosyl groups
2	5e−07	7 / 16	protein disulfide isomerase activity
3	8e−07	15 / 95	isomerase activity
4	6e−04	4 / 12	misfolded protein binding
5	2e−03	9 / 80	chaperone binding
6	6e−03	7 / 64	hydrolase activity, acting on glycosyl bonds
7	7e−03	3 / 12	calcium−transporting ATPase activity
8	9e−03	3 / 13	fatty−acyl−CoA binding
9	1e−02	3 / 14	FK506 binding
10	2e−02	14 / 217	lipid binding
11	2e−02	5 / 45	syntaxin binding
12	2e−02	4 / 30	oxygen binding
13	2e−02	3 / 17	low−density lipoprotein particle receptor binding
14	2e−02	4 / 32	peptidyl−prolyl cis−trans isomerase activity
15	3e−02	54 / 1201	hydrolase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	24 / 369	hsa−miR−15b
2	0.006	15 / 208	hsa−miR−30b
3	0.010	13 / 181	hsa−miR−520g
4	0.016	15 / 235	hsa−miR−30e
5	0.017	14 / 215	hsa−miR−30c
6	0.017	19 / 324	hsa−miR−497
7	0.018	7 / 78	hsa−miR−216b
8	0.019	4 / 30	hsa−miR−1258
9	0.019	20 / 350	hsa−miR−424
10	0.019	13 / 197	hsa−miR−30a
11	0.024	7 / 83	hsa−miR−147
12	0.026	4 / 33	hsa−miR−182*
13	0.027	20 / 363	hsa−miR−195
14	0.028	11 / 165	hsa−miR−448
15	0.029	2 / 8	hsa−miR−886−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.06	8 / 122	Terre_IMS_influenza_meta_signature
2	0.28	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.31	3 / 57	Burnham_day1_vs_5_UP
4	0.42	3 / 68	Burnham_sep_vs_con_UP
5	0.44	3 / 71	Burnham_cap_fp_vs_con_UP
6	0.50	2 / 48	Burnham_viral_DN
7	0.50	5 / 135	Terre_MSV_multiple_respiratory_viruses_up
8	0.54	2 / 52	Burnham_day1_vs_5_DN
9	0.56	2 / 54	Burnham_timecourse
10	0.69	1 / 33	Sweeney_viral_dn
11	0.73	1 / 37	Sweeney_viral_up
12	0.87	1 / 57	Burnham_viral_UP
13	1.00	0 / 56	Burnham_sep_vs_con_DN
14	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
15	1.00	0 / 18	Scicluna_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−06	58 / 893	PROTEINATLAS_pancreas
2	2e−04	59 / 1076	PROTEINATLAS_stomach
3	3e−04	56 / 1022	PROTEINATLAS_placenta
4	7e−04	6 / 32	Chaussabel_1,1_Plasma Cells
5	8e−04	55 / 1032	PROTEINATLAS_small intestine
6	1e−03	4 / 14	WIRTH_Thyroid gland
7	1e−03	56 / 1072	PROTEINATLAS_duodenum
8	2e−03	13 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
9	5e−03	38 / 716	PROTEINATLAS_epididymis
10	2e−02	30 / 592	PROTEINATLAS_seminal vesicle
11	3e−02	37 / 770	PROTEINATLAS_endometrium
12	4e−02	42 / 923	PROTEINATLAS_cerebral cortex
13	4e−02	3 / 23	JONGENEEL_Pancreas
14	5e−02	5 / 59	Chaussabel_2,10_Immune related cell surface molecules
15	5e−02	46 / 1048	PROTEINATLAS_rectum

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	1e−07	194 / 4131	ICGC_Tcf3_targets
2	3e−07	171 / 3564	ICGC_Taf1_targets
3	3e−06	195 / 4319	ICGC_Pou2_targets
4	5e−06	144 / 2994	ICGC_Zeb1_targets
5	9e−06	139 / 2899	ICGC_Nfatc1_targets
6	1e−05	148 / 3150	ICGC_Creb1_targets
7	2e−05	164 / 3608	ICGC_Tcf12_targets
8	3e−05	171 / 3804	ICGC_Stat5_targets
9	3e−05	156 / 3420	ICGC_Bclaf101388_targets
10	4e−05	166 / 3703	ICGC_Foxm1_targets
11	5e−05	156 / 3451	ICGC_Atf2_targets
12	6e−05	179 / 4072	ICGC_Mta3_targets
13	8e−05	59 / 1032	ICGC_Usf1_targets
14	8e−05	167 / 3769	ICGC_Pmlsc71910_targets
15	9e−05	197 / 4602	ICGC_Elf1_targets

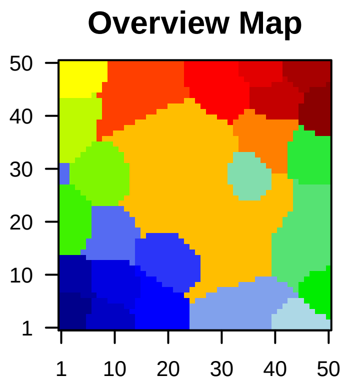
K−Means Cluster

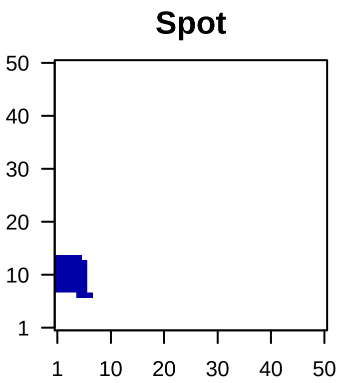
Spot Summary: V

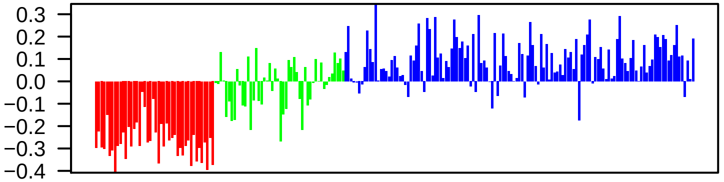
metagenes = 44
genes = 435

<r> metagenes = 0.95
<r> genes = 0.28
beta: r2= 7.33 / log p= −Inf

samples with spot = 41 (18.6 %)
intermediate : 1 (2.1 %)
non−mBL : 40 (31 %)





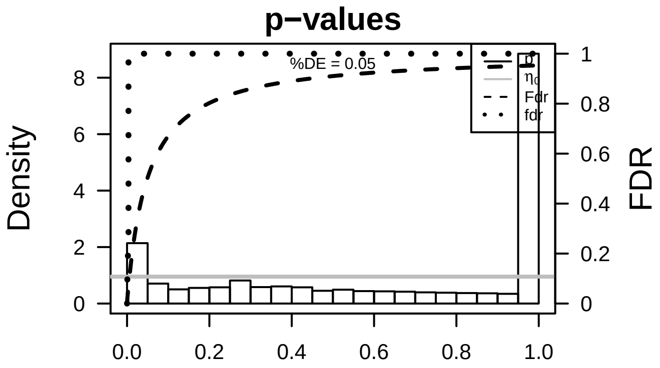


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209728_at	2.5	−1.71	0.29	HLA−DRB4	major histocompatibility complex, class II, DR beta 4 [Source:
2	206140_at	2.21	−0.79	0.29	LHX2	LIM homeobox 2 [Source:HGNC Symbol;Acc:HGNC:6594]
3	205485_at	2.16	−1.09	0.4	RYR1	ryanodine receptor 1 [Source:HGNC Symbol;Acc:HGNC:104
4	206181_at	1.94	−1.03	0.49	SLAMF1	signaling lymphocytic activation molecule family member 1 [S
5	219895_at	1.94	−1.26	0.54	TMEM255A	transmembrane protein 255A [Source:HGNC Symbol;Acc:HG
6	210517_s_at	1.9	−1.34	0.28	AKAP12	A−kinase anchoring protein 12 [Source:HGNC Symbol;Acc:H
7	203485_at	1.86	−1.02	0.58	RTN1	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]
8	211685_s_at	1.86	−1.28	0.45	NCALD	neurocalcin delta [Source:HGNC Symbol;Acc:HGNC:7655]
9	219677_at	1.82	−0.78	0.28	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1
10	205613_at	1.78	−1.32	0.27	SYT17	synaptotagmin 17 [Source:HGNC Symbol;Acc:HGNC:24119]
11	205898_at	1.71	−1.04	0.49	CX3CR1	C−X3−C motif chemokine receptor 1 [Source:HGNC Symbol;
12	206632_s_at	1.69	−1.24	0.41	APOBEC3A	apolipoprotein B mRNA editing enzyme catalytic subunit 3A [
13	213817_at	1.69	−0.93	0.51	IRAK3	interleukin 1 receptor associated kinase 3 [Source:HGNC Sy
14	211194_s_at	1.66	−1.3	0.43	TP63	tumor protein p63 [Source:HGNC Symbol;Acc:HGNC:15979]
15	205997_at	1.63	−1.62	0.63	ADAM28	ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
16	220066_at	1.59	−1.28	0.6	NOD2	nucleotide binding oligomerization domain containing 2 [Sour
17	209967_s_at	1.58	−1.09	0.4	CREM	cAMP responsive element modulator [Source:HGNC Symbol;
18	205174_s_at	1.55	−1.18	0.27	QPCT	glutaminyl−peptide cyclotransferase [Source:HGNC Symbol;
19	203216_s_at	1.54	−0.93	0.41	MYO6	myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]
20	219352_at	1.53	−0.89	0.49	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−47	72 / 317	Cance	SPANG_BCL6−index2
2	2e−23	236 / 5404	Lymp	HOPP_Strong_enhancer
3	4e−23	21 / 40	BP	antigen processing and presentation
4	1e−21	15 / 18	CC	MHC class II protein complex
5	1e−20	16 / 23	CC	integral component of lumenal side of endoplasmic reticulum membrane
6	4e−20	35 / 186	Cance	SPANG_LPS−index2
7	4e−20	23 / 66	BP	interferon−gamma−mediated signaling pathway
8	5e−20	14 / 17	BP	antigen processing and presentation of peptide or polysaccharide antigen
9	2e−19	51 / 431	BP	immune system process
10	1e−18	45 / 353	GSE	JOHNSTONE_PARVB_TARGETS_3_UP
11	3e−18	238 / 5908	Lymp	HOPP_Active_promoter
12	6e−18	73 / 906	Lymp	SPANG_BCR DN
13	2e−17	39 / 281	CC	lysosome
14	2e−17	14 / 22	MF	peptide antigen binding
15	3e−16	42 / 353	Lymp	SPANG_CD40 6hrs DN
16	3e−16	19 / 58	CC	phagocytic vesicle membrane
17	2e−15	52 / 560	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
18	2e−14	16 / 46	GSE	MORI_IMMATURE_B_LYMPHOCYTE_UP
19	7e−14	29 / 198	Refer	Chaussabel_3,3_Inflammation II
20	1e−13	20 / 88	GSE	WIELAND_UP_BY_HBV_INFECTION
21	1e−13	16 / 51	GSE	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
22	2e−13	20 / 90	GSE	BASSO_CD40_SIGNALING_UP
23	2e−13	38 / 354	GSE	RODWELL_AGING_KIDNEY_UP
24	8e−13	26 / 173	Lymp	Victora_Light zone signature
25	1e−12	36 / 336	BP	immune response
26	3e−12	15 / 51	CC	ER to Golgi transport vesicle membrane
27	4e−12	62 / 902	GSE	CHEN_METABOLIC_SYNDROM_NETWORK
28	5e−12	36 / 355	Refer	WIRTH_Immune system
29	1e−11	38 / 403	BP	neutrophil degranulation
30	1e−11	214 / 5682	Lymp	HOPP_Weak_promoter
31	1e−11	37 / 386	GSE	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
32	5e−11	16 / 72	GSE	MORI_MATURE_B_LYMPHOCYTE_UP
33	5e−11	37 / 404	GSE	RUTELLA_RESPONSE_TO_HGF_UP
34	5e−11	27 / 224	GSE	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
35	6e−11	24 / 178	GSE	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
36	1e−10	8 / 12	MF	MHC class II receptor activity
37	1e−10	50 / 694	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
38	2e−10	26 / 219	CC	lysosomal membrane
39	2e−10	35 / 386	GSE	MULLIGHAN_MLL_SIGNATURE_2_UP
40	4e−10	6 / 6	Lymp	DAVE_MHCCII BL DN



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.8	2 / 107	HORVATH_aging_genes meth UP
3	0.9	1 / 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	4e−23	21 / 40	antigen processing and presentation
2	4e−20	23 / 66	interferon−gamma−mediated signaling pathway
3	5e−20	14 / 17	antigen processing and presentation of peptide or polysaccharide antigen via
4	2e−19	51 / 431	immune system process
5	1e−12	36 / 336	immune response
6	1e−11	38 / 403	neutrophil degranulation
7	9e−09	15 / 87	antigen processing and presentation of exogenous peptide antigen via MHC c
8	1e−08	9 / 26	antigen processing and presentation of peptide antigen via MHC class I
9	2e−07	12 / 69	antigen processing and presentation of exogenous peptide antigen via MHC c
10	3e−06	15 / 135	T cell receptor signaling pathway
11	4e−06	10 / 60	T cell costimulation
12	1e−05	27 / 407	viral process
13	4e−05	9 / 63	type I interferon signaling pathway
14	5e−05	12 / 113	regulation of immune response
15	5e−05	24 / 367	innate immune response

Cancer

Rank	p−value	#in/all	Geneset
1	5e−47	72 / 317	SPANG_BCL6−index2
2	4e−20	35 / 186	SPANG_LPS−index2
3	3e−07	6 / 12	HLA2_signature
4	9e−05	4 / 10	BENTINK_ras.4
5	7e−04	2 / 2	HLA1_signature
6	1e−03	25 / 480	Lembcke_Colonic Inflammation
7	3e−03	3 / 12	GENTLES_modul12
8	6e−03	3 / 14	BENTINK_src.10
9	4e−02	2 / 12	LIU_BREAST_CANCER
10	5e−02	2 / 13	GENTLES_modul11
11	5e−02	2 / 13	GENTLES_modul18
12	5e−02	2 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	7e−02	4 / 58	SHAUGHNESSY_MM high risk
14	2e−01	1 / 6	ZHANG_MGUS up
15	2e−01	6 / 147	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−21	15 / 18	MHC class II protein complex
2	1e−20	16 / 23	integral component of lumenal side of endoplasmic reticulum membrane
3	2e−17	39 / 281	lysosome
4	3e−16	19 / 58	phagocytic vesicle membrane
5	3e−12	15 / 51	ER to Golgi transport vesicle membrane
6	2e−10	26 / 219	lysosomal membrane
7	7e−10	16 / 85	lysosomal lumen
8	1e−09	23 / 188	endosome membrane
9	1e−09	10 / 28	clathrin−coated endocytic vesicle membrane
10	5e−08	36 / 494	endosome
11	3e−07	9 / 36	transport vesicle membrane
12	9e−07	51 / 938	Golgi apparatus
13	1e−06	95 / 2239	extracellular exosome
14	1e−06	125 / 3210	plasma membrane
15	7e−06	10 / 64	trans−Golgi network membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.008	25 / 556	Chr X
2	0.015	33 / 832	Chr 2
3	0.022	27 / 669	Chr 6
4	0.219	24 / 756	Chr 11
5	0.246	22 / 700	Chr 12
6	0.439	14 / 490	Chr 10
7	0.486	36 / 1325	Chr 1
8	0.500	16 / 585	Chr 7
9	0.501	15 / 548	Chr 16
10	0.518	15 / 554	Chr 5
11	0.698	9 / 382	Chr 15
12	0.779	5 / 242	Chr 13
13	0.792	7 / 333	Chr 22
14	0.831	9 / 437	Chr 8
15	0.835	17 / 776	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−25	175 / 3223	monocytes peripheral blood_6_EnhG
2	4e−20	179 / 3682	natural killer cells peripheral blood_6_EnhG
3	2e−19	180 / 3767	Bcells peripheral blood_6_EnhG
4	4e−19	295 / 8200	monocytes peripheral blood_2_TssAFlnk
5	2e−18	281 / 7635	monocytes peripheral blood_1_TssA
6	5e−17	295 / 8406	Bcells peripheral blood_2_TssAFlnk
7	2e−16	281 / 7833	Bcells peripheral blood_1_TssA
8	2e−15	291 / 8370	natural killer cells peripheral blood_2_TssAFlnk
9	2e−15	288 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
10	3e−15	162 / 3524	Tregulatory cells peripheral blood_6_EnhG
11	5e−15	58 / 693	Bcells peripheral blood_3_TxFlnk
12	8e−15	280 / 7957	Tcells peripheral blood_2_TssAFlnk
13	1e−14	279 / 7930	Tregulatory cells peripheral blood_1_TssA
14	2e−14	44 / 432	monocytes peripheral blood_3_TxFlnk
15	3e−14	274 / 7751	natural killer cells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−09	42 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	1e−07	59 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
3	2e−07	25 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	1e−05	56 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
5	2e−05	22 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	9e−05	43 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	1e−04	71 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	2e−02	49 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
9	2e−02	2 / 8	Marisa_CRC−C3
10	2e−02	23 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	2e−02	6 / 83	Marisa_CRC−cluster−d
12	4e−02	20 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	5e−02	3 / 31	Marisa_CRC−cluster−c
14	7e−02	16 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
15	8e−02	4 / 60	Marisa_CRC−cluster−g

Glioma

Rank	p−value	#in/all	Geneset
1	9e−10	37 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	1e−05	19 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	6e−05	6 / 27	Donson−Misc immune function−associated with LTS in HGA
4	5e−04	44 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	6e−04	20 / 330	Up
6	9e−04	17 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
7	9e−04	17 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
8	1e−03	6 / 45	Donson−innate immunity−associated with LTS in HGA
9	2e−03	8 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
10	5e−03	10 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	6e−03	14 / 242	ScoV_0.5_Sturm_C1_IDH_DN
12	8e−03	4 / 30	Shaw_responders_down_in_oligo_glioma
13	9e−03	8 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
14	2e−02	7 / 99	GIEZELT_GBM_WT_up_VS_mut
15	3e−02	6 / 87	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−18	45 / 353	JOHNSTONE_PARVB_TARGETS_3_UP
2	2e−15	52 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
3	2e−14	16 / 46	MORI_IMMATURE_B_LYMPHOCYTE_UP
4	1e−13	20 / 88	WIELAND_UP_BY_HBV_INFECTION
5	1e−13	16 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
6	2e−13	20 / 90	BASSO_CD40_SIGNALING_UP
7	2e−13	38 / 354	RODWELL_AGING_KIDNEY_UP
8	4e−12	62 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
9	1e−11	37 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
10	5e−11	16 / 72	MORI_MATURE_B_LYMPHOCYTE_UP
11	5e−11	37 / 404	RUTELLA_RESPONSE_TO_HGF_UP
12	5e−11	27 / 224	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
13	6e−11	24 / 178	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
14	1e−10	50 / 694	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
15	2e−10	35 / 386	MULLIGHAN_MLL_SIGNATURE_2_UP

HM

Rank	p−value	#in/all	Geneset
1	6e−10	22 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	5e−08	20 / 176	HALLMARK_ALLOGRAFT_REJECTION
3	1e−07	13 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	5e−05	16 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	2e−03	13 / 188	HALLMARK_HYPOXIA
6	2e−03	13 / 191	HALLMARK_P53_PATHWAY
7	7e−03	11 / 174	HALLMARK_APICAL_JUNCTION
8	8e−03	11 / 178	HALLMARK_COMPLEMENT
9	1e−02	11 / 187	HALLMARK_INFLAMMATORY_RESPONSE
10	1e−02	7 / 94	HALLMARK_PROTEIN_SECRETION
11	2e−02	9 / 150	HALLMARK_APOPTOSIS
12	2e−02	5 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	7e−02	3 / 35	HALLMARK_HEDGEHOG_SIGNALING
14	7e−02	9 / 193	HALLMARK_HEME_METABOLISM
15	8e−02	9 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome

Rank	p−value	#in/all	Geneset
1	7e−07	5 / 8	Immunity_HLA−class−II
2	1e−03	4 / 18	Angelova_CRC_immunostimulators
3	1e−03	5 / 32	Angelova_immune−metagene−effector_memory_CD8
4	2e−03	4 / 21	Angelova_immune−metagene−central_memory_CD4
5	4e−03	2 / 4	Angelova_CRC_MHC_class_II
6	7e−03	4 / 29	Angelova_immune−metagene−Th1
7	6e−02	2 / 15	Angelova_immune−metagene−NK
8	8e−02	1 / 3	Angelova_CRC_MHC_class_I
9	1e−01	3 / 42	Angelova_immune−metagene−TGD
10	1e−01	3 / 45	Angelova_immune−metagene−MDSC
11	1e−01	2 / 23	Angelova_immune−metagene−monocytes
12	1e−01	1 / 5	Angelova_immune−metagene−NKT
13	2e−01	1 / 6	Immunity_immune−checkpoint−inhibitors
14	2e−01	1 / 7	Angelova_immune−metagene−cytotoxic_cells
15	2e−01	1 / 8	Angelova_immune−metagene−mDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	4 / 22	DUMEAUX_High bmi enriched genes
2	0.026	11 / 210	Homuth_BMI−associated−genes_DN
3	0.195	1 / 8	Marjolein_ageing−genes_UP
4	0.278	1 / 12	DUMEAUX_Women normal BMI literature genes up
5	0.297	1 / 13	Huan_blood−pressure_DBP−signature
6	0.572	4 / 150	Homuth_BMI−associated−genes_UP
7	0.814	1 / 62	DUMEAUX_Smoking enriched genes
8	1.000	0 / 10	DUMEAUX_Smoking literature genes up
9	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
15	1.000	0 / 22	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−23	236 / 5404	HOPP_Strong_enhancer
2	3e−18	238 / 5908	HOPP_Active_promoter
3	6e−18	73 / 906	SPANG_BCR DN
4	3e−16	42 / 353	SPANG_CD40 6hrs DN
5	8e−13	26 / 173	Victora_Light zone signature
6	1e−11	214 / 5682	HOPP_Weak_promoter
7	4e−10	6 / 6	DAVE_MHCCII BL DN
8	2e−09	167 / 4261	HOPP_Txn_transition
9	6e−09	15 / 85	Sha_DLBCL UP
10	1e−08	23 / 213	SPANG_IL21 DN
11	1e−07	196 / 5529	HOPP_Txn_elongation
12	7e−05	13 / 135	DAVE_BL−vs−DLBCL
13	2e−04	4 / 12	BENTINK_mBL DOWN
14	2e−04	8 / 62	Monti_Host_response_cluster
15	2e−04	5 / 22	DAVE_NFkB BL DN

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−07	15 / 107	Tirosh_Exhaustion program in Mel75
2	1e−05	17 / 189	Tirosh_genes preferentially expressed by Tregs
3	1e−03	15 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	2e−03	12 / 171	Landsberg_dedifferentiation_up
5	6e−03	7 / 81	Tirosh_Genes in the MITF program
6	8e−03	7 / 85	Tirosh_AXL−signature
7	1e−02	5 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	2e−02	11 / 204	Landsberg_dedifferentiation_down
9	2e−02	4 / 41	Tirosh_top50 correlated genes PC3
10	3e−02	10 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	6e−02	3 / 33	Tirosh_T−cell specific genes−melanoma
12	1e−01	4 / 71	Tirosh_Macrophage specific genes−melanoma
13	1e−01	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	2e−01	17 / 497	Gerber_wt/wt_melanoma−cells−SpotD
15	2e−01	4 / 83	TCGA_melanoma_immune_high

MF

Rank	p−value	#in/all	Geneset
1	2e−17	14 / 22	peptide antigen binding
2	1e−10	8 / 12	MHC class II receptor activity
3	2e−06	6 / 16	MHC class II protein complex binding
4	2e−05	248 / 7864	protein binding
5	3e−04	8 / 64	hydrolase activity, acting on glycosyl bonds
6	5e−04	4 / 15	proton−transporting ATPase activity, rotational mechanism
7	9e−04	5 / 29	SH2 domain binding
8	1e−03	14 / 202	GTPase activator activity
9	1e−03	9 / 99	Rab GTPase binding
10	2e−03	4 / 21	WW domain binding
11	3e−03	4 / 24	hydrolase activity, hydrolyzing O−glycosyl compounds
12	4e−03	3 / 13	K63−linked polyubiquitin modification−dependent protein binding
13	1e−02	6 / 69	virus receptor activity
14	1e−02	5 / 50	cysteine−type endopeptidase activity
15	1e−02	3 / 18	cytokine binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	11 / 164	hsa−miR−148b
2	0.006	11 / 169	hsa−miR−148a
3	0.007	4 / 29	hsa−miR−647
4	0.010	8 / 112	hsa−miR−218
5	0.014	6 / 74	hsa−miR−595
6	0.017	8 / 122	hsa−miR−506
7	0.017	11 / 197	hsa−miR−152
8	0.032	4 / 45	hsa−miR−513a−5p
9	0.040	16 / 369	hsa−miR−130a
10	0.049	10 / 205	hsa−miR−1252
11	0.050	4 / 52	hsa−miR−1246
12	0.052	6 / 100	hsa−miR−625
13	0.055	8 / 154	hsa−miR−452
14	0.056	18 / 448	hsa−miR−20b
15	0.057	3 / 33	hsa−miR−483−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	1e−05	8 / 41	Scicluna_DN
2	2e−05	9 / 56	Burnham_sep_vs_con_DN
3	1e−04	8 / 57	Burnham_viral_UP
4	3e−04	7 / 48	Burnham_cap_fp_vs_con_DN
5	1e−02	9 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	6e−02	3 / 33	Sweeney_viral_dn
7	8e−02	3 / 37	Sweeney_viral_up
8	1e−01	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
9	1e−01	6 / 122	Terre_IMS_influenza_meta_signature
10	3e−01	3 / 71	Burnham_cap_fp_vs_con_UP
11	4e−01	2 / 52	Burnham_day1_vs_5_DN
12	5e−01	2 / 68	Burnham_sep_vs_con_UP
13	7e−01	1 / 48	Burnham_viral_DN
14	8e−01	1 / 54	Burnham_timecourse
15	1e+00	0 / 57	Burnham_day1_vs_5_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−14	29 / 198	Chaussabel_3,3_Inflammation II
2	5e−12	36 / 355	WIRTH_Immune system
3	3e−06	11 / 72	Chaussabel_3,1_Interferon−inducible
4	3e−06	10 / 59	Chaussabel_2,10_Immune related cell surface molecules
5	3e−05	12 / 109	Chaussabel_2,6_Myeloid lineage
6	7e−05	11 / 99	Chaussabel_1,5_Myeloid lineage
7	4e−03	12 / 182	WIRTH_post GC B−cells
8	7e−03	23 / 496	PROTEINATLAS_spleen
9	1e−02	3 / 17	VAQUERIZAS_Adrenal gland_TF
10	1e−02	7 / 93	Chaussabel_1,4_Replication
11	1e−02	12 / 218	WIRTH_pre+post GC B−cells
12	1e−02	28 / 678	PROTEINATLAS_lymph node
13	2e−02	3 / 22	Chaussabel_1,6_Signaling molecules
14	2e−02	11 / 204	Chaussabel_3,2_Inflammation I
15	2e−02	37 / 989	PROTEINATLAS_tonsil

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	1e−06	75 / 1636	ICGC_Bcl11_targets
2	5e−05	65 / 1494	ICGC_Cebpbsc150_targets
3	6e−05	65 / 1508	ICGC_Mef2_targets
4	2e−04	77 / 1941	ICGC_Bcl3_targets
5	5e−04	46 / 1041	ICGC_P300_targets
6	9e−04	112 / 3213	ICGC_Pu1_targets
7	1e−03	83 / 2254	ICGC_BatfPcr1_targets
8	1e−03	70 / 1848	ICGC_Pbx3_targets
9	2e−03	78 / 2150	ICGC_Irf4_targets
10	2e−03	126 / 3796	ICGC_Nficsc81335_targets
11	4e−03	99 / 2899	ICGC_Nfatc1_targets
12	4e−03	42 / 1032	ICGC_Usf1_targets
13	6e−03	138 / 4319	ICGC_Pou2_targets
14	1e−02	111 / 3435	ICGC_Ebfsc137065_targets
15	1e−02	111 / 3451	ICGC_Atf2_targets

K−Means Cluster

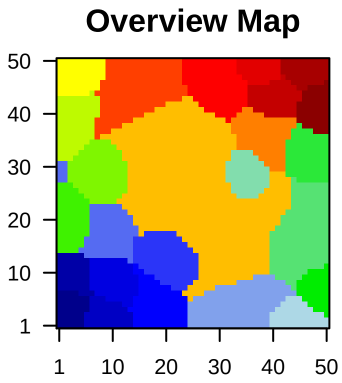
Spot Summary: W

metagenes = 98
genes = 501

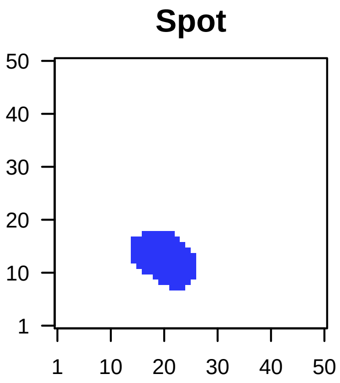
<r> metagenes = 0.75
<r> genes = 0.11
beta: r2= 1.37 / log p= −Inf

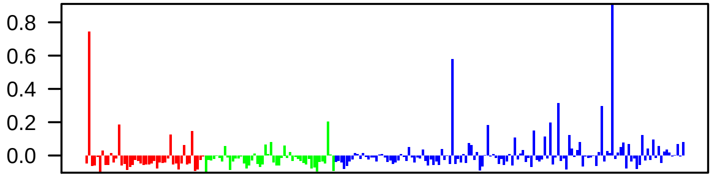
samples with spot = 10 (4.5 %)
mBL : 2 (4.5 %)
intermediate : 1 (2.1 %)
non−mBL : 7 (5.4 %)

Overview Map



Spot





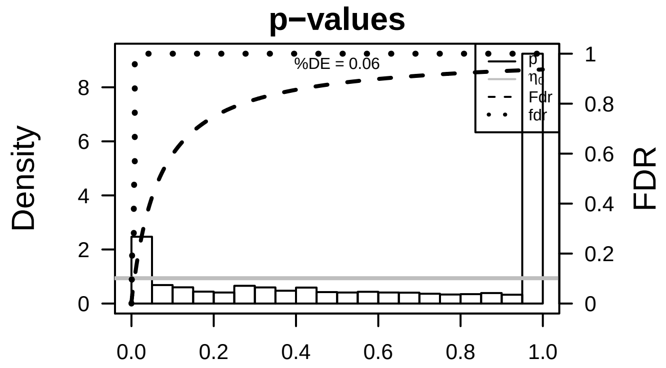
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209351_at	3.74	−0.88	0.5	KRT14	keratin 14 [Source:HGNC Symbol;Acc:HGNC:6416]
2	218835_at	3.68	−0.52	0.34	SFTPA2	surfactant protein A2 [Source:HGNC Symbol;Acc:HGNC:107
3	207935_s_at	3.59	−0.75	0.49	KRT13	keratin 13 [Source:HGNC Symbol;Acc:HGNC:6415]
4	209125_at	3.52	−0.85	0.49	KRT6A	keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
5	213796_at	3.5	−0.56	0.54	SPRR1A	small proline rich protein 1A [Source:HGNC Symbol;Acc:HG
6	214580_x_at	3.41	−0.74	0.49	KRT6A	keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
7	213240_s_at	3.27	−0.54	0.45	KRT4	keratin 4 [Source:HGNC Symbol;Acc:HGNC:6441]
8	212768_s_at	3.21	−0.59	0.42	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
9	209126_x_at	3.19	−0.85	0.55	KRT6B	keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
10	218990_s_at	3.14	−0.5	0.47	SPRR3	small proline rich protein 3 [Source:HGNC Symbol;Acc:HGN
11	203824_at	3.13	−0.55	0.46	TSPAN8	tetraspanin 8 [Source:HGNC Symbol;Acc:HGNC:11855]
12	210107_at	3.12	−1.18	0.37	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
13	205064_at	3.11	−0.84	0.46	SPRR1B	small proline rich protein 1B [Source:HGNC Symbol;Acc:HG
14	204268_at	3.09	−0.94	0.55	S100A2	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
15	211735_x_at	3.02	−0.68	0.25	SFTPC	surfactant protein C [Source:HGNC Symbol;Acc:HGNC:1080
16	206199_at	2.96	−0.74	0.53	CEACAM7	carcinoembryonic antigen related cell adhesion molecule 7 [S
17	213680_at	2.96	−0.86	0.47	KRT6B	keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
18	204272_at	2.94	−0.65	0.44	LGALS4	galectin 4 [Source:HGNC Symbol;Acc:HGNC:6565]
19	208539_x_at	2.91	−0.65	0.48	SPRR2D	small proline rich protein 2D [Source:HGNC Symbol;Acc:HG
20	206262_at	2.91	−0.55	0.42	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−92	76 / 105	Refer	WIRTH_Mucosa
2	5e−74	91 / 248	GSEA	JAEGER_METASTASIS_DN
3	4e−65	107 / 453	GSEA	ONDER_CDH1_TARGETS_2_DN
4	3e−39	222 / 3168	Lymp	HOPP_Repressed
5	1e−33	75 / 452	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
6	4e−33	112 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
7	1e−32	29 / 46	GSEA	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
8	9e−31	34 / 78	BP	cornification
9	2e−28	45 / 178	GSEA	WU_CELL_MIGRATION
10	6e−28	31 / 72	BP	keratinization
11	1e−27	34 / 93	GSEA	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
12	2e−27	95 / 883	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	4e−27	32 / 82	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
14	9e−26	65 / 448	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
15	2e−25	46 / 218	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
16	7e−25	62 / 422	GSEA	DELYS_THYROID_CANCER_UP
17	1e−24	128 / 1611	CC	extracellular region
18	6e−24	38 / 152	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
19	2e−22	71 / 608	GSEA	SMID_BREAST_CANCER_BASAL_UP
20	3e−22	65 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
21	7e−22	39 / 182	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
22	3e−21	54 / 376	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
23	8e−21	4 / 14	Canc	LIU_PROSTATE_CANCER_DN
24	8e−21	4 / 14	Canc	LIU_PROSTATE_CANCER_DN
25	4e−20	22 / 51	GSEA	HUPER_BREAST_BASAL_VS_LUMINAL_UP
26	1e−19	131 / 1894	Lymp	HOPP_Poised_promoter
27	1e−19	120 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
28	2e−19	96 / 1148	TF	HEBENSTREIT_low expression TF
29	7e−19	22 / 57	GSEA	ONDER_CDH1_TARGETS_3_DN
30	3e−18	16 / 26	GSEA	AIGNER_ZEB1_TARGETS
31	5e−18	43 / 282	GSEA	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
32	1e−17	141 / 2239	CC	extracellular exosome
33	1e−17	61 / 565	GSEA	LEE_BMP2_TARGETS_UP
34	3e−17	71 / 747	GSEA	NABA_MATRISOME
35	4e−17	25 / 92	Colon	Marisa_CRC−cluster−h
36	5e−17	33 / 174	GSEA	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP
37	6e−17	17 / 35	CC	cornified envelope
38	9e−17	27 / 113	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
39	2e−16	39 / 255	Colon	Kosinski_top−crypt−long−list
40	4e−16	20 / 58	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_E

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	5 / 107	HORVATH_aging_genes meth UP
2	0.6	3 / 92	HORVATH_aging_genes meth DOWN
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	1e−24	128 / 1611	extracellular region
2	1e−17	141 / 2239	extracellular exosome
3	6e−17	17 / 35	cornified envelope
4	2e−15	85 / 1090	extracellular space
5	1e−10	159 / 3210	plasma membrane
6	7e−10	10 / 23	desmosome
7	1e−09	16 / 76	intermediate filament
8	1e−08	71 / 1128	integral component of plasma membrane
9	4e−08	152 / 3270	integral component of membrane
10	4e−08	45 / 595	cell junction
11	2e−07	8 / 22	anchored component of plasma membrane
12	4e−07	25 / 253	proteinaceous extracellular matrix
13	1e−06	23 / 231	apical plasma membrane
14	1e−06	8 / 27	keratin filament
15	3e−06	10 / 50	lateral plasma membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−33	75 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
2	2e−27	95 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
3	9e−26	65 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
4	3e−21	54 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
5	4e−17	25 / 92	Marisa_CRC−cluster−h
6	2e−16	39 / 255	Kosinski_top−crypt−long−list
7	3e−13	44 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	6e−13	20 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
9	7e−12	77 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
10	8e−08	8 / 20	Kosinski_top−crypt−short−list
11	3e−06	47 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
12	2e−04	7 / 38	Marisa_CRC−cluster−e
13	3e−04	3 / 5	Marisa_CRC−C5
14	6e−04	3 / 6	Marisa_CRC−C6
15	2e−03	10 / 103	Marisa_CRC−cluster−b

HM

Rank	p−value	#in/all	Geneset
1	2e−09	25 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
2	2e−09	25 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	1e−08	24 / 194	HALLMARK_KRAS_SIGNALING_UP
4	6e−05	17 / 181	HALLMARK_XENOBIOTIC_METABOLISM
5	5e−04	16 / 195	HALLMARK_KRAS_SIGNALING_DN
6	1e−03	15 / 191	HALLMARK_P53_PATHWAY
7	3e−03	13 / 174	HALLMARK_APICAL_JUNCTION
8	5e−03	11 / 141	HALLMARK_UV_RESPONSE_DN
9	9e−03	13 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	1e−02	8 / 97	HALLMARK_BILE_ACID_METABOLISM
11	2e−02	4 / 34	HALLMARK_ANGIOGENESIS
12	4e−02	11 / 194	HALLMARK_MYOGENESIS
13	5e−02	8 / 130	HALLMARK_COAGULATION
14	9e−02	9 / 170	HALLMARK_IL2_STAT5_SIGNALING
15	1e−01	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lymphnoma

Rank	p−value	#in/all	Geneset
1	3e−39	222 / 3168	HOPP_Repressed
2	1e−19	131 / 1894	HOPP_Poised_promoter
3	3e−08	16 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
4	7e−08	24 / 214	LENZ_Stromal signature 1
5	4e−07	109 / 2206	HOPP_Heterochrom
6	5e−07	14 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
7	4e−06	16 / 132	Subero_DLBCL_hyper_meth
8	4e−06	15 / 118	Subero_INT_hyper_meth
9	6e−06	10 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
10	1e−05	11 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
11	1e−05	15 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
12	6e−05	10 / 70	Subero_FL_hyper_meth
13	3e−04	8 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
14	6e−04	10 / 91	Subero_T−ALL_hyper_meth
15	6e−04	7 / 47	Subero_B−ALL_hyper_meth

miRNA target

Rank	p−value	#in/all	Geneset
1	0.08	2 / 15	hsa−miR−551b
2	0.09	2 / 16	hsa−miR−551a
3	0.09	4 / 54	hsa−miR−299−5p
4	0.10	8 / 150	hsa−miR−199b−3p
5	0.11	2 / 18	hsa−miR−591
6	0.11	8 / 154	hsa−miR−944
7	0.16	3 / 44	hsa−miR−629
8	0.16	2 / 23	hsa−miR−521
9	0.17	3 / 45	hsa−miR−891b
10	0.19	4 / 72	hsa−miR−339−5p
11	0.19	3 / 48	hsa−miR−1243
12	0.20	2 / 26	hsa−miR−558
13	0.20	4 / 74	hsa−miR−595
14	0.21	2 / 27	hsa−miR−770−5p
15	0.21	4 / 75	hsa−miR−587

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	9e−31	34 / 78	cornification
2	6e−28	31 / 72	keratinization
3	3e−13	16 / 46	keratinocyte differentiation
4	5e−10	19 / 104	cell−cell adhesion
5	6e−10	44 / 500	cell adhesion
6	7e−09	10 / 28	peptide cross−linking
7	8e−09	15 / 74	epidermis development
8	5e−08	17 / 109	animal organ morphogenesis
9	1e−07	13 / 66	epithelial cell differentiation
10	4e−07	6 / 11	hemidesmosome assembly
11	9e−07	13 / 78	wound healing
12	1e−06	20 / 183	extracellular matrix organization
13	2e−06	11 / 59	chloride transport
14	8e−06	12 / 81	cell−matrix adhesion
15	9e−06	6 / 17	hair follicle morphogenesis

Chr

Rank	p−value	#in/all	Geneset
1	0.01	12 / 184	Chr 18
2	0.03	54 / 1325	Chr 1
3	0.05	22 / 480	Chr 4
4	0.14	20 / 490	Chr 10
5	0.15	7 / 139	Chr 21
6	0.19	31 / 833	Chr 19
7	0.28	24 / 669	Chr 6
8	0.35	9 / 242	Chr 13
9	0.38	13 / 369	Chr 20
10	0.39	28 / 832	Chr 2
11	0.40	15 / 437	Chr 8
12	0.57	24 / 776	Chr 17
13	0.59	15 / 492	Chr 9
14	0.66	16 / 548	Chr 16
15	0.73	11 / 403	Chr 14

Glioma

Rank	p−value	#in/all	Geneset
1	1e−19	120 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	7e−14	46 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	6e−10	31 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	2e−07	20 / 163	ScoV_0.999_Sturm_E1_IDH_DN
5	1e−06	9 / 36	Christensen_hypomethylated_in_ependymoma
6	2e−05	9 / 50	Christensen_hypomethylated_in_primary_glioblastoma
7	7e−05	14 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	2e−04	12 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	4e−04	10 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
10	4e−04	4 / 12	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
11	6e−04	13 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	8e−04	49 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
13	3e−03	6 / 45	OL vs. MOG− OL
14	4e−03	8 / 82	laffaire_hypermeth_LGG_vs_control
15	5e−03	7 / 66	Christensen_hypermethylated_in_grade2_astrocytoma

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	4 / 38	Angelova_immune−metagene−mast−cells
2	0.03	3 / 23	Angelova_immune−metagene−Th2
3	0.12	2 / 19	Angelova_immune−metagene−iDC
4	0.19	2 / 25	Angelova_immune−metagene−DC
5	0.30	1 / 11	Angelova_immune−metagene−macrophages
6	0.32	1 / 12	Angelova_immune−metagene−effector_memory_CD4
7	0.61	1 / 29	Angelova_immune−metagene−Th1
8	0.88	1 / 67	Angelova_immune−metagene−T−cells
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 / 7	Angelova_immune−metagene−cytotoxic_cells
15	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−16	20 / 59	TCGA_melanoma_keratin_high
2	4e−11	8 / 10	Joensson_Melanoma Normal like subtype
3	9e−11	16 / 64	Harbst_melanoma_lowgrade_up
4	8e−05	6 / 24	Gerami_melanoma−metastatic−risk_DN
5	7e−04	9 / 78	Tirosh_CAF−cell specific genes
6	4e−03	10 / 119	TCGA_melanoma_MITF_low
7	8e−03	12 / 171	Landsberg_dedifferentiation_up
8	8e−03	26 / 497	Gerber_wt/wt_melanoma−cells−SpotD
9	1e−02	3 / 16	Hugo_melanoma−all−LEF1_UP
10	2e−02	2 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
11	3e−02	14 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	3e−02	4 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	3e−02	4 / 39	Tirosh_melanoma specific genes
14	9e−02	5 / 75	Tirosh_Endothelial−cell specific genes−melanoma
15	9e−02	1 / 3	Gerami_melanoma−metastatic−risk_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	7e−05	10 / 71	Burnham_cap_fp_vs_con_UP
2	3e−04	9 / 68	Burnham_sep_vs_con_UP
3	3e−02	5 / 57	Burnham_day1_vs_5_UP
4	1e−01	2 / 18	Scicluna_UP
5	4e−01	2 / 48	Burnham_cap_fp_vs_con_DN
6	4e−01	2 / 48	Burnham_viral_DN
7	5e−01	2 / 52	Burnham_day1_vs_5_DN
8	5e−01	2 / 56	Burnham_sep_vs_con_DN
9	9e−01	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
10	1e+00	1 / 122	Terre_IMS_influenza_meta_signature
11	1e+00	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
12	1e+00	0 / 57	Burnham_viral_UP
13	1e+00	0 / 54	Burnham_timecourse
14	1e+00	0 / 41	Scicluna_DN
15	1e+00	0 / 37	Sweeney_viral_up

TF

Rank	p−value	#in/all	Geneset
1	2e−19	96 / 1148	HEBENSTREIT_low expression TF
2	9e−01	64 / 2321	ICGC_Rad21_targets
3	1e+00	24 / 1032	ICGC_Usf1_targets
4	1e+00	9 / 522	ICGC_SrfPcr2_targets
5	1e+00	89 / 3435	ICGC_Ebfsc137065_targets
6	1e+00	36 / 1636	ICGC_Bcl11_targets
7	1e+00	8 / 549	ICGC_Atf3_targets
8	1e+00	50 / 2254	ICGC_BatfPcr1_targets
9	1e+00	105 / 4264	ICGC_Pax5_targets
10	1e+00	17 / 1041	ICGC_P300_targets
11	1e+00	72 / 3213	ICGC_Pu1_targets
12	1e+00	26 / 1508	ICGC_Mef2_targets
13	1e+00	98 / 4212	ICGC_Pol2_targets
14	1e+00	85 / 3778	ICGC_Pol24_targets
15	1e+00	33 / 1848	ICGC_Pbx3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	8e−21	4 / 14	LIU_PROSTATE_CANCER_DN
2	1e−03	28 / 480	Lembcke_Colonic Inflammation
3	2e−02	12 / 187	PanCan_PI3K_geneset_nanostring
4	3e−02	8 / 113	PanCan_Driver_Gene_geneset_nanostring
5	3e−02	1 / 11	LIU_PROSTATE_CANCER_UP
6	3e−02	2 / 9	WANG_ER_DN
7	3e−02	20 / 409	Lembcke_Normal vs Adenoma
8	6e−02	4 / 47	PanCan_TGF−B_geneset_nanostring
9	6e−02	2 / 13	GENTLES_modul17
10	6e−02	8 / 134	PanCan_RAS_geneset_nanostring
11	8e−02	6 / 96	PanCan_TXmisReg_geneset_nanostring
12	9e−02	2 / 16	GENTLES_modul16
13	3e−01	1 / 13	BENTINK_e2f3.1
14	4e−01	1 / 14	GENTLES_modul10
15	4e−01	1 / 14	GENTLES_modul13

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−42	249 / 3734	Tcells peripheral blood_13_ReprPC
2	7e−38	248 / 3918	Tcells peripheral blood_14_ReprPCWk
3	3e−36	210 / 3001	Bcells peripheral blood_14_ReprPCWk
4	2e−34	182 / 2405	Bcells peripheral blood_13_ReprPC
5	3e−33	204 / 2984	natural killer cells peripheral blood_14_ReprPCWk
6	1e−32	187 / 2602	natural killer cells peripheral blood_12_EnhBiv
7	2e−32	183 / 2515	natural killer cells peripheral blood_13_ReprPC
8	2e−31	212 / 3272	monocytes peripheral blood_14_ReprPCWk
9	2e−30	227 / 3724	Tcells peripheral blood_12_EnhBiv
10	2e−30	205 / 3150	monocytes peripheral blood_13_ReprPC
11	2e−29	187 / 2747	Bcells peripheral blood_12_EnhBiv
12	3e−29	168 / 2300	Thelper cells peripheral blood_13_ReprPC
13	5e−28	185 / 2765	Tregulatory cells peripheral blood_13_ReprPC
14	6e−26	157 / 2194	Thelper cells peripheral blood_12_EnhBiv
15	9e−26	139 / 1799	T CD8+ naive cells peripheral blood_13_ReprPC

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−74	91 / 248	JAEGER_METASTASIS_DN
2	4e−65	107 / 453	ONDER_CDH1_TARGETS_2_DN
3	4e−33	112 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
4	1e−32	29 / 46	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
5	2e−28	45 / 178	WU_CELL_MIGRATION
6	1e−27	34 / 93	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
7	4e−27	32 / 82	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
8	2e−25	46 / 218	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
9	7e−25	62 / 422	DELYS_THYROID_CANCER_UP
10	6e−24	38 / 152	COLDREN_GEFITINIB_RESISTANCE_DN
11	2e−22	71 / 608	SMID_BREAST_CANCER_BASAL_UP
12	3e−22	65 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
13	7e−22	39 / 182	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	8e−21	4 / 14	LIU_PROSTATE_CANCER_DN
15	4e−20	22 / 51	HUPER_BREAST_BASAL_VS_LUMINAL_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	2 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.019	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.089	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.201	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
5	0.267	2 / 32	Marjolein_ageing−genes_DN
6	0.274	1 / 10	DUMEAUX_Smoking literature genes up
7	0.341	1 / 13	Huan_blood−pressure_DBP−signature
8	0.506	1 / 22	DUMEAUX_High bmi enriched genes
9	0.586	2 / 62	DUMEAUX_Smoking enriched genes
10	0.953	2 / 150	Homuth_BMI−associated−genes_UP
11	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 22	DUMEAUX_Fasting enriched genes
15	1.000	0 / 210	Homuth_BMI−associated−genes_DN

MF

Rank	p−value	#in/all	Geneset
1	7e−14	29 / 169	structural molecule activity
2	2e−08	21 / 154	serine−type endopeptidase activity
3	2e−08	17 / 104	serine−type peptidase activity
4	9e−07	31 / 374	peptidase activity
5	9e−07	11 / 55	chloride channel activity
6	3e−06	37 / 517	calcium ion binding
7	8e−05	11 / 86	metalloendopeptidase activity
8	1e−04	9 / 61	serine−type endopeptidase inhibitor activity
9	1e−04	10 / 77	peptidase inhibitor activity
10	2e−04	14 / 143	carbohydrate binding
11	3e−04	4 / 11	retinol dehydrogenase activity
12	6e−04	12 / 125	metallopeptidase activity
13	8e−04	7 / 49	transmembrane receptor protein tyrosine kinase activity
14	9e−04	10 / 96	structural constituent of cytoskeleton
15	1e−03	4 / 15	transition metal ion binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−92	76 / 105	WIRTH_Mucosa
2	4e−10	8 / 12	WIRTH_Tonsil
3	3e−06	8 / 30	VAQUERIZAS_Fetal lung_TF
4	2e−05	8 / 37	Chaussabel_2,2_Neutrophils
5	5e−05	6 / 22	VAQUERIZAS_Trachea_TF
6	1e−04	9 / 62	VAQUERIZAS_Lung_TF
7	3e−04	17 / 209	Chaussabel_2,5_Immune related molecules
8	4e−04	38 / 677	PROTEINATLAS_esophagus
9	5e−04	7 / 45	VAQUERIZAS_Placenta_TF
10	5e−04	29 / 474	PROTEINATLAS_vagina
11	6e−04	4 / 13	VAQUERIZAS_Skin_TF
12	7e−04	37 / 671	PROTEINATLAS_cervix, uterine
13	1e−03	4 / 15	JONGENEEL_Small Intestine
14	1e−03	52 / 1072	PROTEINATLAS_duodenum
15	1e−03	51 / 1048	PROTEINATLAS_rectum

K−Means Cluster

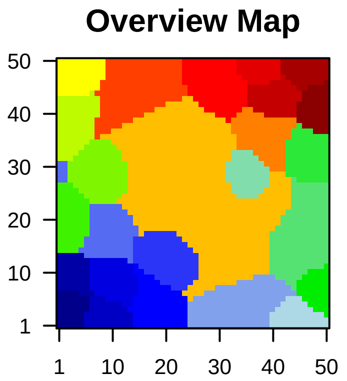
Spot Summary: X

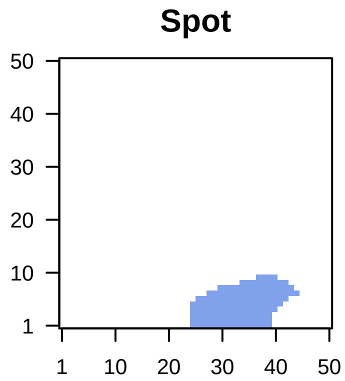
metagenes = 139
genes = 1050

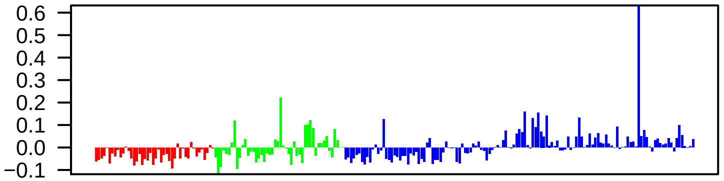
<r> metagenes = 0.66

beta: r2= 1.04 / log p= −Inf

samples with spot = 4 (1.8 %)
intermediate : 1 (2.1 %)
non−mBL : 3 (2.3 %)


Overview Map


Spot

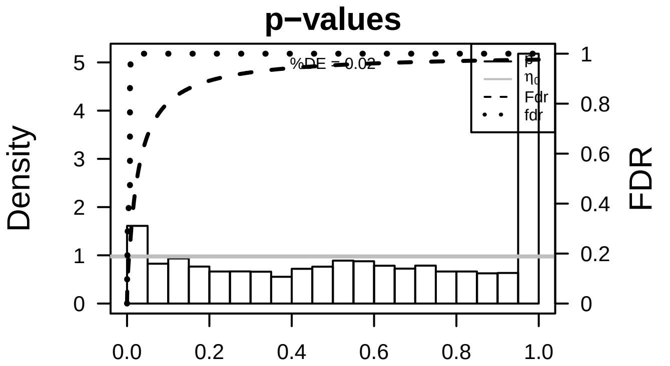


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209988_s_at	3.22	−0.78	0.11	ASCL1	achaete−scute family bHLH transcription factor 1 [Source:HG
2	219463_at	3.17	−0.88	0.24	LAMP5	lysosomal associated membrane protein family member 5 [S
3	202768_at	2.75	−0.96	0.23	FOSB	FosB proto−oncogene, AP−1 transcription factor subunit [Sou
4	213768_s_at	2.71	−0.86	0.23	ASCL1	achaete−scute family bHLH transcription factor 1 [Source:HG
5	209987_s_at	2.71	−0.72	0.14	ASCL1	achaete−scute family bHLH transcription factor 1 [Source:HG
6	218332_at	2.62	−0.7	0.25	BEX1	brain expressed X−linked 1 [Source:HGNC Symbol;Acc:HGN
7	205767_at	2.62	−0.51	0.48	EREG	epiregulin [Source:HGNC Symbol;Acc:HGNC:3443]
8	215118_s_at	2.52	−1.42	0.21		
9	201525_at	2.5	−0.99	0.24	APOD	apolipoprotein D [Source:HGNC Symbol;Acc:HGNC:612]
10	206759_at	2.49	−0.94	0.29	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:H
11	218613_at	2.4	−0.84	0.07	PSD3	pleckstrin and Sec7 domain containing 3 [Source:HGNC Sym
12	210763_x_at	2.4	−1.08	0.04	NCR3	natural cytotoxicity triggering receptor 3 [Source:HGNC Sym
13	216248_s_at	2.32	−0.9	0.31	NR4A2	nuclear receptor subfamily 4 group A member 2 [Source:HG
14	219457_s_at	2.3	−0.85	0.11	RIN3	Ras and Rab interactor 3 [Source:HGNC Symbol;Acc:HGNC:
15	204622_x_at	2.28	−0.78	0.26	NR4A2	nuclear receptor subfamily 4 group A member 2 [Source:HG
16	209695_at	2.28	−0.87	0.25	PTP4A3	protein tyrosine phosphatase type IVA, member 3 [Source:H
17	222315_at	2.23	−0.97	0.09		
18	219168_s_at	2.19	−1.1	0.15	PRR5	proline rich 5 [Source:HGNC Symbol;Acc:HGNC:31682]
19	205051_s_at	2.19	−0.76	0.17	KIT	KIT proto−oncogene receptor tyrosine kinase [Source:HGNC
20	204134_at	2.17	−1.07	0.01	PDE2A	phosphodiesterase 2A [Source:HGNC Symbol;Acc:HGNC:87

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−15	509 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
2	2e−13	46 / 218	Refer	WIRTH_pre+post GC B−cells
3	1e−08	155 / 1602	GSE	BLALOCK_ALZHEIMERS_DISEASE_UP
4	5e−08	35 / 204	Refer	Chaussabel_3,2_Inflammation I
5	5e−07	263 / 3210	CC	plasma membrane
6	1e−06	37 / 251	GSE	PEREZ_TP63_TARGETS
7	5e−06	41 / 311	GSE	SHEN_SMARCA2_TARGETS_DN
8	2e−05	16 / 77	CC	specific granule membrane
9	2e−05	20 / 112	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
10	3e−05	161 / 1894	Lymp	HOPP_Poised_promoter
11	4e−05	54 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
12	6e−05	64 / 621	BP	negative regulation of transcription from RNA polymerase II promoter
13	7e−05	77 / 788	GSE	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
14	7e−05	42 / 358	GSE	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
15	7e−05	6 / 13	Refer	WIRTH_Bone marrow
16	8e−05	27 / 193	HM	HALLMARK_HEME_METABOLISM
17	1e−04	9 / 32	Gliom	WIRTH_PN subtype
18	1e−04	24 / 166	GSE	NAGASHIMA_NRG1_SIGNALING_UP
19	1e−04	245 / 3168	Lymp	HOPP_Repressed
20	2e−04	24 / 169	GSE	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
21	2e−04	15 / 83	GSE	SMID_BREAST_CANCER_LUMINAL_A_UP
22	2e−04	6 / 15	BP	definitive hemopoiesis
23	2e−04	25 / 182	Refer	WIRTH_post GC B−cells
24	2e−04	25 / 183	GSE	ZHANG_TLX_TARGETS_36HR_UP
25	2e−04	16 / 93	Refer	Chaussabel_1,4_Replication
26	2e−04	20 / 132	Lymp	Subero_DLBCL_hyper_meth
27	2e−04	8 / 28	BP	negative chemotaxis
28	2e−04	31 / 251	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
29	3e−04	11 / 52	MF	steroid hormone receptor activity
30	3e−04	5 / 11	BP	positive regulation of calcium ion−dependent exocytosis
31	3e−04	92 / 1029	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_UP
32	3e−04	25 / 189	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
33	4e−04	248 / 3270	CC	integral component of membrane
34	4e−04	13 / 70	GSE	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP
35	4e−04	7 / 23	CC	voltage−gated calcium channel complex
36	4e−04	8 / 30	Refer	JONGENEEL_Bone Marrow
37	4e−04	8 / 30	miRN	hsa−miR−1258
38	4e−04	47 / 450	MF	sequence−specific DNA binding
39	5e−04	11 / 54	miRN	hsa−miR−1184
40	5e−04	11 / 54	GSE	NAGASHIMA_EGF_SIGNALING_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.06	10 / 92	HORVATH_aging_genes meth DOWN
2	0.81	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.81	5 / 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	6e−05	64 / 621	negative regulation of transcription from RNA polymerase II promoter
2	2e−04	6 / 15	definitive hemopoiesis
3	2e−04	8 / 28	negative chemotaxis
4	3e−04	5 / 11	positive regulation of calcium ion−dependent exocytosis
5	5e−04	7 / 24	regulation of exocytosis
6	5e−04	5 / 12	cAMP catabolic process
7	6e−04	9 / 39	erythrocyte differentiation
8	6e−04	11 / 56	steroid hormone mediated signaling pathway
9	7e−04	9 / 40	intracellular receptor signaling pathway
10	1e−03	75 / 833	multicellular organism development
11	1e−03	5 / 14	negative regulation of protein complex assembly
12	1e−03	8 / 35	cellular response to epidermal growth factor stimulus
13	1e−03	16 / 109	neuron differentiation
14	2e−03	11 / 62	hemopoiesis
15	2e−03	21 / 166	axon guidance

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	4 / 16	GENTLES_modul16
2	0.02	4 / 18	PanCan_Notch_geneset_nanostring
3	0.04	11 / 96	PanCan_TXmisReg_geneset_nanostring
4	0.04	3 / 13	GENTLES_modul18
5	0.05	12 / 113	PanCan_Driver_Gene_geneset_nanostring
6	0.08	14 / 147	PanCan_MAPK_geneset_nanostring
7	0.11	2 / 9	WANG_ER_DN
8	0.14	12 / 134	PanCan_RAS_geneset_nanostring
9	0.19	1 / 11	LIU_PROSTATE_CANCER_UP
10	0.21	3 / 25	PanCan_HH_geneset_nanostring
11	0.22	2 / 14	GUSTAFSON_PI3K_UP
12	0.22	2 / 14	GUSTAFSON_PI3K_DN
13	0.22	1 / 16	LIU_LIVER_CANCER
14	0.30	10 / 130	PanCan_CC+Apop_geneset_nanostring
15	0.31	4 / 45	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	5e−07	263 / 3210	plasma membrane
2	2e−05	16 / 77	specific granule membrane
3	4e−04	248 / 3270	integral component of membrane
4	4e−04	7 / 23	voltage−gated calcium channel complex
5	6e−04	41 / 382	synapse
6	6e−04	23 / 174	postsynaptic membrane
7	7e−04	17 / 113	receptor complex
8	3e−03	46 / 479	Golgi membrane
9	4e−03	7 / 33	myofibril
10	4e−03	93 / 1128	integral component of plasma membrane
11	6e−03	9 / 54	endoplasmic reticulum−Golgi intermediate compartment membrane
12	8e−03	6 / 29	dendritic shaft
13	8e−03	8 / 47	synaptic vesicle membrane
14	9e−03	77 / 938	Golgi apparatus
15	1e−02	369 / 5339	membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	36 / 382	Chr 15
2	0.01	65 / 776	Chr 17
3	0.02	47 / 548	Chr 16
4	0.11	27 / 333	Chr 22
5	0.11	5 / 41	Chr Y
6	0.13	29 / 369	Chr 20
7	0.25	35 / 492	Chr 9
8	0.27	89 / 1325	Chr 1
9	0.29	48 / 700	Chr 12
10	0.32	51 / 756	Chr 11
11	0.38	10 / 139	Chr 21
12	0.48	26 / 403	Chr 14
13	0.57	15 / 242	Chr 13
14	0.59	36 / 585	Chr 7
15	0.61	51 / 832	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−11	183 / 1813	8_EnhP_Fibroblasts
2	4e−10	219 / 2375	10_ReprPC_Fibroblasts
3	7e−10	245 / 2747	Bcells peripheral blood_12_EnhBiv
4	1e−09	167 / 1700	Bcells peripheral blood_11_BivFlnk
5	2e−09	204 / 2203	EnhA_Colon
6	6e−09	214 / 2374	9_ReprPCWk_Fibroblasts
7	2e−08	98 / 884	12_EnhBiv_ESC_Mesoderm
8	9e−08	205 / 2327	14_ReprPCWk_ESC_Mesoderm
9	1e−07	119 / 1181	8_EnhP_Neuronal_Progenitor
10	2e−07	300 / 3724	Tcells peripheral blood_12_EnhBiv
11	2e−07	189 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
12	7e−07	188 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
13	1e−06	219 / 2602	natural killer cells peripheral blood_12_EnhBiv
14	1e−06	205 / 2405	Bcells peripheral blood_13_ReprPC
15	1e−06	565 / 7943	Enh_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−15	509 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	4e−05	54 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
3	5e−04	101 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
4	5e−03	11 / 72	Ang_CRC−CIMPH−vs−L_hyper
5	9e−03	11 / 77	Ang_CRC_Hypermethylated
6	2e−02	27 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
7	2e−02	42 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
8	4e−02	89 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	4e−02	5 / 31	Kosinski_lower−crypt−short−list
10	6e−02	4 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
11	7e−02	5 / 35	Ang_CRC_Hypomethylated
12	8e−02	3 / 16	Vilar_mutated−in−CRC−CamP
13	8e−02	66 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	9e−02	5 / 38	Marisa_CRC−cluster−e
15	1e−01	55 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	1e−04	9 / 32	WIRTH_PN subtype
2	4e−03	17 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	4e−03	15 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
4	6e−03	28 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
5	6e−03	40 / 421	Down_b
6	1e−02	14 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
7	1e−02	27 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
8	2e−02	8 / 53	Christensen_hypermethylated_in_primary_glioblastoma
9	2e−02	11 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
10	2e−02	7 / 45	OL vs. MOG− OL
11	2e−02	9 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
12	2e−02	9 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	4e−02	15 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	4e−02	8 / 62	GIEZELT_GBM_STS_down_VS_LTS
15	5e−02	11 / 99	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−08	155 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
2	1e−06	37 / 251	PEREZ_TP63_TARGETS
3	5e−06	41 / 311	SHEN_SMARCA2_TARGETS_DN
4	2e−05	20 / 112	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
5	7e−05	77 / 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
6	7e−05	42 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
7	1e−04	24 / 166	NAGASHIMA_NRG1_SIGNALING_UP
8	2e−04	24 / 169	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
9	2e−04	15 / 83	SMID_BREAST_CANCER_LUMINAL_A_UP
10	2e−04	25 / 183	ZHANG_TLX_TARGETS_36HR_UP
11	2e−04	31 / 251	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
12	3e−04	92 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
13	3e−04	25 / 189	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
14	4e−04	13 / 70	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP
15	5e−04	11 / 54	NAGASHIMA_EGF_SIGNALING_UP

HM

Rank	p−value	#in/all	Geneset
1	8e−05	27 / 193	HALLMARK_HEME_METABOLISM
2	2e−03	7 / 29	HALLMARK_NOTCH_SIGNALING
3	4e−03	22 / 191	HALLMARK_P53_PATHWAY
4	6e−03	22 / 195	HALLMARK_KRAS_SIGNALING_DN
5	5e−02	18 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	6e−02	18 / 194	HALLMARK_MYOGENESIS
7	8e−02	17 / 187	HALLMARK_INFLAMMATORY_RESPONSE
8	9e−02	5 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1e−01	13 / 141	HALLMARK_UV_RESPONSE_DN
10	2e−01	13 / 150	HALLMARK_APOPTOSIS
11	2e−01	16 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	2e−01	12 / 149	HALLMARK_UV_RESPONSE_UP
13	3e−01	13 / 173	HALLMARK_MITOTIC_SPINDLE
14	3e−01	14 / 188	HALLMARK_HYPOXIA
15	3e−01	13 / 174	HALLMARK_APICAL_JUNCTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	3 / 18	Angelova_immune−metagene−pDC
2	0.1	3 / 21	Angelova_immune−metagene−central_memory_CD4
3	0.2	3 / 23	Angelova_immune−metagene−Th2
4	0.2	3 / 23	Angelova_immune−metagene−Treg
5	0.2	4 / 38	Angelova_immune−metagene−mast−cells
6	0.3	3 / 32	Angelova_immune−metagene−effector_memory_CD8
7	0.4	1 / 8	Angelova_immune−metagene−mDC
8	0.5	1 / 10	Angelova_immune−metagene−neutrophils
9	0.5	1 / 12	Angelova_immune−metagene−memory_B−cells
10	0.5	1 / 12	Angelova_immune−metagene−NK56_dim
11	0.5	3 / 45	Angelova_immune−metagene−MDSC
12	0.6	2 / 29	Angelova_immune−metagene−Th1
13	0.6	1 / 13	Angelova_immune−metagene−activated_B−cells
14	0.6	1 / 14	Angelova_immune−metagene−eosinophil
15	0.6	1 / 15	Angelova_immune−metagene−NK

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	9 / 62	DUMEAUX_Smoking enriched genes
2	0.02	21 / 210	Homuth_BMI−associated−genes_DN
3	0.16	3 / 22	DUMEAUX_High bmi enriched genes
4	0.24	12 / 150	Homuth_BMI−associated−genes_UP
5	0.28	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	0.41	1 / 8	Marjolein_ageing−genes_UP
7	0.54	1 / 12	DUMEAUX_Women normal BMI literature genes up
8	0.60	1 / 14	Huan_blood−pressure_SBP−signature
9	0.88	1 / 32	Marjolein_ageing−genes_DN
10	1.00	0 / 10	DUMEAUX_Smoking literature genes up
11	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
15	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−05	161 / 1894	HOPP_Poised_promoter
2	1e−04	245 / 3168	HOPP_Repressed
3	2e−04	20 / 132	Subero_DLBCL_hyper_meth
4	1e−03	14 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
5	3e−03	16 / 118	Subero_INT_hyper_meth
6	4e−03	11 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
7	5e−03	7 / 35	Subero_MM_hyper_meth
8	1e−02	24 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
9	3e−02	11 / 91	Subero_T−ALL_hyper_meth
10	3e−02	9 / 70	Subero_FL_hyper_meth
11	3e−02	133 / 1814	HOPP_Repetitive
12	3e−02	7 / 49	LEE_Developmental_regulators
13	4e−02	366 / 5404	HOPP_Strong_enhancer
14	5e−02	7 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
15	5e−02	5 / 33	Subero_T−PLL_hypo_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	22 / 204	Landsberg_dedifferentiation_down
2	0.04	6 / 41	Tirosh_top50 correlated genes PC3
3	0.07	9 / 81	Tirosh_Genes in the MITF program
4	0.08	5 / 37	Hugo_melanoma−all−MET_DN
5	0.10	6 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	0.12	1 / 2	Melanoma Epi−Enzyme Cluster 2
7	0.14	10 / 107	Tirosh_Exhaustion program in Mel75
8	0.15	2 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
9	0.16	37 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	0.18	1 / 3	Melanoma Epi−Enzyme Cluster 4
11	0.19	7 / 75	Tirosh_Endothelial−cell specific genes−melanoma
12	0.28	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
13	0.32	1 / 6	Joensson_Melanoma high immune response subtype
14	0.35	3 / 33	Tirosh_T−cell specific genes−melanoma
15	0.38	5 / 64	Harbst_melanoma_lowgrade_up

MF

Rank	p−value	#in/all	Geneset
1	3e−04	11 / 52	steroid hormone receptor activity
2	4e−04	47 / 450	sequence−specific DNA binding
3	5e−04	5 / 12	3',5'−cyclic−AMP phosphodiesterase activity
4	6e−04	9 / 39	nuclear receptor activity
5	6e−04	69 / 741	DNA binding transcription factor activity
6	9e−04	67 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
7	9e−04	24 / 191	transmembrane signaling receptor activity
8	1e−03	11 / 61	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
9	2e−03	6 / 23	3',5'−cyclic−nucleotide phosphodiesterase activity
10	4e−03	8 / 42	phosphoric diester hydrolase activity
11	5e−03	4 / 12	Rac guanyl−nucleotide exchange factor activity
12	7e−03	6 / 28	voltage−gated calcium channel activity
13	9e−03	17 / 143	carbohydrate binding
14	1e−02	10 / 70	transcriptional repressor activity, RNA polymerase II transcription regulatory r
15	2e−02	8 / 52	chromatin DNA binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	8 / 30	hsa−miR−1258
2	5e−04	11 / 54	hsa−miR−1184
3	8e−04	17 / 115	hsa−miR−138
4	8e−04	9 / 41	hsa−miR−346
5	1e−03	20 / 151	hsa−miR−1283
6	1e−03	34 / 315	hsa−miR−144
7	1e−03	8 / 36	hsa−miR−146b−3p
8	2e−03	11 / 62	hsa−miR−205
9	2e−03	25 / 216	hsa−miR−524−5p
10	3e−03	40 / 405	hsa−miR−107
11	4e−03	9 / 50	hsa−miR−1285
12	4e−03	7 / 33	hsa−miR−588
13	4e−03	36 / 361	hsa−miR−130b
14	5e−03	9 / 52	hsa−miR−514
15	5e−03	11 / 72	hsa−miR−339−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.001	12 / 71	Burnham_cap_fp_vs_con_UP
2	0.003	9 / 48	Burnham_viral_DN
3	0.003	11 / 68	Burnham_sep_vs_con_UP
4	0.066	7 / 57	Burnham_day1_vs_5_UP
5	0.113	5 / 41	Scicluna_DN
6	0.139	6 / 56	Burnham_sep_vs_con_DN
7	0.183	5 / 48	Burnham_cap_fp_vs_con_DN
8	0.346	3 / 33	Sweeney_viral_dn
9	0.445	4 / 54	Burnham_timecourse
10	0.456	12 / 179	Terre_MSV_multiple_respiratory_viruses_dn
11	0.645	3 / 52	Burnham_day1_vs_5_DN
12	0.690	1 / 18	Scicluna_UP
13	0.954	4 / 122	Terre_IMS_influenza_meta_signature
14	0.974	4 / 135	Terre_MSV_multiple_respiratory_viruses_up
15	0.976	1 / 57	Burnham_viral_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−13	46 / 218	WIRTH_pre+post GC B−cells
2	5e−08	35 / 204	Chaussabel_3,2_Inflammation I
3	7e−05	6 / 13	WIRTH_Bone marrow
4	2e−04	25 / 182	WIRTH_post GC B−cells
5	2e−04	16 / 93	Chaussabel_1,4_Replication
6	4e−04	8 / 30	JONGENEEL_Bone Marrow
7	1e−03	8 / 36	VAQUERIZAS_Prostate_TF
8	2e−03	25 / 209	Chaussabel_2,5_Immune related molecules
9	2e−03	9 / 45	VAQUERIZAS_Whole brain_TF
10	2e−03	4 / 10	VAQUERIZAS_Skeletal muscle_TF
11	3e−03	6 / 24	VAQUERIZAS_Spinal cord_TF
12	5e−03	10 / 62	VAQUERIZAS_Lung_TF
13	8e−03	7 / 37	Chaussabel_2,2_Neutrophils
14	1e−02	8 / 49	VAQUERIZAS_Uterus_TF
15	2e−02	2 / 4	JONGENEEL_Bladder

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.002	253 / 3435	ICGC_Ebfsc137065_targets
2	0.002	145 / 1848	ICGC_Pbx3_targets
3	0.003	130 / 1636	ICGC_Bcl11_targets
4	0.003	230 / 3121	ICGC_Egr1_targets
5	0.004	87 / 1041	ICGC_P300_targets
6	0.004	86 / 1032	ICGC_Usf1_targets
7	0.006	174 / 2321	ICGC_Rad21_targets
8	0.008	232 / 3213	ICGC_Pu1_targets
9	0.009	116 / 1494	ICGC_Cebpbsc150_targets
10	0.013	290 / 4131	ICGC_Tcf3_targets
11	0.016	3 / 9	MYC_Targets DOWN
12	0.019	81 / 1025	ICGC_NrsfPcr1_targets
13	0.022	164 / 2254	ICGC_BatfPcr1_targets
14	0.027	263 / 3778	ICGC_Pol24_targets
15	0.028	282 / 4072	ICGC_Mta3_targets

K−Means Cluster

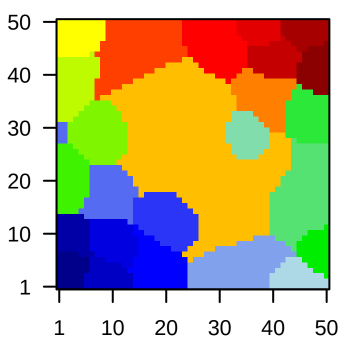
Spot Summary: Y

metagenes = 47
genes = 821

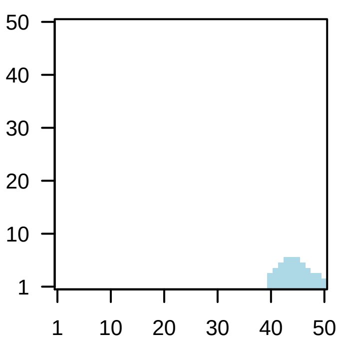
<r> metagenes = 0.92
<r> genes = 0.24
beta: r2= 4.97 / log p= −Inf

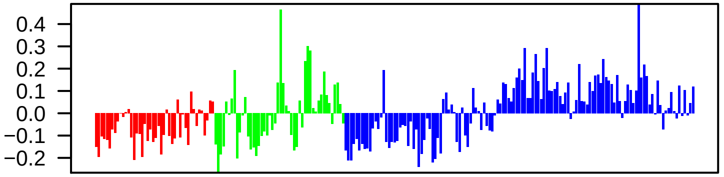
samples with spot = 26 (11.8 %)
intermediate : 6 (12.5 %)
non−mBL : 20 (15.5 %)

Overview Map



Spot





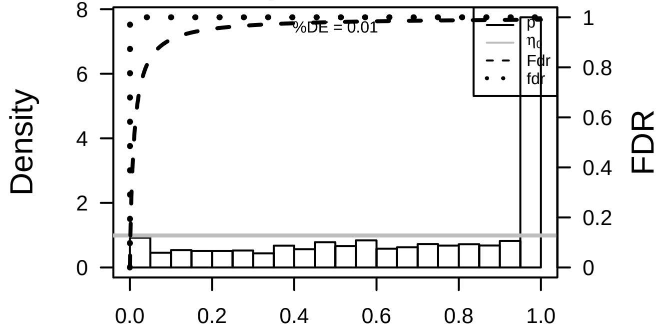
Spot Genelist

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	205033_s_at	2.2	−0.66	0.43	DEFA1	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
3	38691_s_at	2.17	−0.66	0.28	SFTPC	surfactant protein C [Source:HGNC Symbol;Acc:HGNC:1080
4	209800_at	2.16	−0.6	0.49	KRT16	keratin 16 [Source:HGNC Symbol;Acc:HGNC:6423]
5	214532_x_at	2.06	−0.84	0.3	POU5F1	POU class 5 homeobox 1 [Source:HGNC Symbol;Acc:HGNC
6	202222_s_at	1.96	−0.73	0.57	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
7	207337_at	1.83	−1.04	0.48	CTAG2	cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
8	206012_at	1.77	−0.72	0.36	LEFTY2	left−right determination factor 2 [Source:HGNC Symbol;Acc:
9	206760_s_at	1.74	−0.74	0.48	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HG
10	214027_x_at	1.73	−0.87	0.45	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
11	218687_s_at	1.71	−0.55	0.47	MUC13	mucin 13, cell surface associated [Source:HGNC Symbol;Acc
12	209957_s_at	1.66	−0.88	0.62	NPPA	natriuretic peptide A [Source:HGNC Symbol;Acc:HGNC:7939
13	205116_at	1.66	−0.71	0.42	LAMA2	laminin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:6
14	205334_at	1.65	−0.71	0.5	S100A1	S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:
15	64408_s_at	1.59	−0.71	0.21		
16	207388_s_at	1.59	−1.07	0.44	PTGES	prostaglandin E synthase [Source:HGNC Symbol;Acc:HGNC
17	222015_at	1.58	−0.94	0.32	CSNK1E	casein kinase 1 epsilon [Source:HGNC Symbol;Acc:HGNC:2
18	208607_s_at	1.55	−0.64	0.46	SAA2	serum amyloid A2 [Source:HGNC Symbol;Acc:HGNC:10514]
19	214403_x_at	1.53	−1.06	0.6		
20	205409_at	1.51	−0.76	0.45	FOSL2	FOS like 2, AP−1 transcription factor subunit [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−26	73 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	5e−15	412 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
3	2e−12	22 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
4	4e−11	39 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
5	6e−09	55 / 483	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
6	2e−08	55 / 501	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
7	8e−08	39 / 311	GSEA	SHEN_SMARCA2_TARGETS_DN
8	5e−07	42 / 373	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
9	9e−07	121 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
10	4e−06	10 / 34	BP	respiratory gaseous exchange
11	1e−05	204 / 3168	Lymph	HOPP_Repressed
12	1e−05	16 / 94	GSEA	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
13	1e−05	26 / 209	Refer	Chaussabel_2,5_Immune related molecules
14	3e−05	9 / 34	BP	regulation of synaptic plasticity
15	4e−05	49 / 548	Chr	Chr 16
16	4e−05	130 / 1894	Lymph	HOPP_Poised_promoter
17	5e−05	24 / 198	GSEA	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
18	5e−05	34 / 333	Chr	Chr 22
19	7e−05	153 / 2321	TF	ICGC_Rad21_targets
20	8e−05	14 / 86	Gliom	Sturm_GBM_Meth_overexpression_B_adult_UP
21	1e−04	59 / 730	GSEA	BENPORATH_ES_WITH_H3K27ME3
22	1e−04	24 / 212	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
23	2e−04	65 / 833	Chr	Chr 19
24	2e−04	4 / 7	Gliom	Sturm_GBM_Meth_overexpression_C_G34_UP
25	2e−04	12 / 73	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
26	2e−04	22 / 194	HM	HALLMARK_MYOGENESIS
27	3e−04	22 / 195	BP	chemical synaptic transmission
28	3e−04	5 / 13	BP	lens fiber cell differentiation
29	3e−04	42 / 485	TF	ICGC_NrsfPcr2_targets
30	3e−04	11 / 65	BP	excitatory postsynaptic potential
31	5e−04	32 / 346	MF	receptor binding
32	5e−04	34 / 377	GSEA	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP
33	8e−04	8 / 41	GSEA	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER
34	8e−04	5 / 16	BP	histone H3 deacetylation
35	8e−04	5 / 16	BP	regulation of dendrite morphogenesis
36	8e−04	5 / 16	GSEA	STARK_HYPPOCAMPUS_22Q11_DELETION_DN
37	9e−04	12 / 85	BP	glucose homeostasis
38	1e−03	22 / 214	GSEA	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
39	1e−03	4 / 10	BP	cerebellar Purkinje cell differentiation
40	1e−03	4 / 10	CC	synaptic cleft

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.04	10 / 107	HORVATH_aging_genes meth UP
2	0.30	6 / 92	HORVATH_aging_genes meth DOWN
3	0.68	2 / 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−06	10 / 34	respiratory gaseous exchange
2	3e−05	9 / 34	regulation of synaptic plasticity
3	3e−04	22 / 195	chemical synaptic transmission
4	3e−04	5 / 13	lens fiber cell differentiation
5	3e−04	11 / 65	excitatory postsynaptic potential
6	8e−04	5 / 16	histone H3 deacetylation
7	8e−04	5 / 16	regulation of dendrite morphogenesis
8	9e−04	12 / 85	glucose homeostasis
9	1e−03	4 / 10	cerebellar Purkinje cell differentiation
10	1e−03	6 / 26	neural crest cell migration
11	2e−03	19 / 183	extracellular matrix organization
12	2e−03	60 / 833	multicellular organism development
13	2e−03	4 / 12	regulation of embryonic development
14	2e−03	5 / 20	regulation of Wnt signaling pathway
15	3e−03	6 / 29	neuronal action potential

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	2 / 12	LIU_BREAST_CANCER
2	0.1	2 / 16	LIU_LIVER_CANCER
3	0.2	2 / 14	LIU_COMMON_CANCER_GENES
4	0.2	2 / 14	LIU_PROSTATE_CANCER_DN
5	0.2	2 / 14	BENTINK_ras.6
6	0.2	10 / 147	PanCan_MAPK_geneset_nanostring
7	0.2	8 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.2	7 / 96	PanCan_TXmisReg_geneset_nanostring
9	0.2	12 / 187	PanCan_PI3K_geneset_nanostring
10	0.2	2 / 18	PanCan_Notch_geneset_nanostring
11	0.3	2 / 20	PanCan_ChromMod_geneset_nanostring
12	0.3	8 / 134	PanCan_RAS_geneset_nanostring
13	0.4	1 / 9	WANG_ER_DN
14	0.4	2 / 28	PanCan_HK_geneset_nanostring
15	0.4	3 / 47	PanCan_TGF−B_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.001	4 / 10	synaptic cleft
2	0.001	26 / 277	neuron projection
3	0.002	77 / 1128	integral component of plasma membrane
4	0.003	13 / 109	dendritic spine
5	0.004	7 / 42	sarcoplasmic reticulum
6	0.006	190 / 3270	integral component of membrane
7	0.006	26 / 310	dendrite
8	0.007	6 / 35	ciliary membrane
9	0.009	185 / 3210	plasma membrane
10	0.011	44 / 623	cell projection
11	0.011	7 / 50	terminal bouton
12	0.011	3 / 10	beta−catenin destruction complex
13	0.011	11 / 101	endomembrane system
14	0.014	7 / 52	clathrin−coated pit
15	0.015	6 / 41	intermediate filament cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	4e−05	49 / 548	Chr 16
2	5e−05	34 / 333	Chr 22
3	2e−04	65 / 833	Chr 19
4	1e−03	40 / 492	Chr 9
5	3e−02	50 / 776	Chr 17
6	2e−01	43 / 756	Chr 11
7	3e−01	9 / 139	Chr 21
8	4e−01	37 / 700	Chr 12
9	5e−01	19 / 369	Chr 20
10	6e−01	2 / 41	Chr Y
11	7e−01	20 / 437	Chr 8
12	7e−01	31 / 669	Chr 6
13	8e−01	24 / 554	Chr 5
14	9e−01	24 / 585	Chr 7
15	9e−01	22 / 556	Chr X

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−19	135 / 1239	EnhP_Colon
2	2e−18	172 / 1813	8_EnhP_Fibroblasts
3	5e−15	275 / 3724	Tcells peripheral blood_12_EnhBiv
4	1e−14	150 / 1634	8_EnhP_Melanocytes
5	2e−13	192 / 2375	10_ReprPC_Fibroblasts
6	5e−13	151 / 1729	8_EnhP_Skeletal_Muscle
7	7e−13	182 / 2240	1_TssP_Fibroblasts
8	7e−12	165 / 2015	ReprPC_Colon
9	9e−12	194 / 2507	Mid_Frontal_Lobe_ReprPC
10	5e−11	230 / 3184	monocytes peripheral blood_12_EnhBiv
11	6e−11	173 / 2203	EnhA_Colon
12	8e−11	157 / 1943	TssP_Colon
13	2e−10	195 / 2602	natural killer cells peripheral blood_12_EnhBiv
14	2e−10	203 / 2747	Bcells peripheral blood_12_EnhBiv
15	4e−10	167 / 2148	10_ReprPC_Skeletal_Muscle

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−15	412 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	6e−09	55 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
3	9e−03	39 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
4	1e−02	39 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	1e−02	36 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
6	2e−02	55 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
7	2e−02	32 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
8	5e−02	17 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
9	5e−02	19 / 255	Kosinski_top−crypt−long−list
10	6e−02	2 / 8	Marisa_CRC−C3
11	7e−02	69 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	1e−01	21 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	1e−01	22 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
14	2e−01	11 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	2e−01	18 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	8e−05	14 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
2	2e−04	4 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
3	4e−03	34 / 423	Down_a
4	5e−03	104 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
5	6e−03	33 / 421	Down_b
6	7e−03	4 / 16	VERHAAK_CL subtype
7	2e−02	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	4e−02	8 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
9	5e−02	5 / 41	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
10	5e−02	12 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	6e−02	11 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
12	7e−02	3 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
13	8e−02	4 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
14	1e−01	6 / 64	Weller_LGG_gradeII−vs−III_UP
15	1e−01	5 / 50	Christensen_hypomethylated_in_primary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−26	73 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	2e−12	22 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	4e−11	39 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	2e−08	55 / 501	MARTENS_TRETINOIN_RESPONSE_UP
5	8e−08	39 / 311	SHEN_SMARCA2_TARGETS_DN
6	5e−07	42 / 373	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
7	9e−07	121 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
8	1e−05	16 / 94	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
9	5e−05	24 / 198	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
10	1e−04	59 / 730	BENPORATH_ES_WITH_H3K27ME3
11	1e−04	24 / 212	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
12	2e−04	12 / 73	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
13	5e−04	34 / 377	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP
14	8e−04	8 / 41	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER
15	8e−04	5 / 16	STARK_HYPPOCAMPUS_22Q11_DELETION_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−04	22 / 194	HALLMARK_MYOGENESIS
2	3e−02	15 / 174	HALLMARK_APICAL_JUNCTION
3	3e−02	16 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	9e−02	4 / 34	HALLMARK_APICAL_SURFACE
5	1e−01	14 / 195	HALLMARK_KRAS_SIGNALING_DN
6	1e−01	4 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	2e−01	11 / 173	HALLMARK_MITOTIC_SPINDLE
8	2e−01	11 / 174	HALLMARK_ADIPOGENESIS
9	2e−01	4 / 51	HALLMARK_TGF_BETA_SIGNALING
10	3e−01	9 / 139	HALLMARK_FATTY_ACID_METABOLISM
11	3e−01	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	4e−01	11 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
13	5e−01	7 / 130	HALLMARK_COAGULATION
14	5e−01	9 / 170	HALLMARK_IL2_STAT5_SIGNALING
15	5e−01	5 / 96	HALLMARK_ANDROGEN_RESPONSE

Immunome

Rank	p−value	#in/all	Geneset
1	0.007	4 / 16	Angelova_immune−metagene−Th17
2	0.116	2 / 12	Angelova_immune−metagene−NK56_dim
3	0.224	1 / 5	Angelova_immune−metagene−NK56_bright
4	0.263	1 / 6	Immunity_immune−checkpoint−inhibitors
5	0.334	1 / 8	Angelova_immune−metagene−mDC
6	0.353	2 / 25	Angelova_immune−metagene−DC
7	0.398	1 / 10	Angelova_immune−metagene−TFH
8	0.398	1 / 10	Angelova_CRC_immonoinhibitors
9	0.425	2 / 29	Angelova_immune−metagene−Th1
10	0.509	1 / 14	Angelova_immune−metagene−eosinophil
11	0.579	1 / 17	Angelova_immune−metagene−central_memory_CD8
12	0.619	1 / 19	Angelova_immune−metagene−iDC
13	0.661	2 / 45	Angelova_immune−metagene−MDSC
14	0.690	1 / 23	Angelova_immune−metagene−Treg
15	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.30	2 / 22	DUMEAUX_High bmi enriched genes
3	0.30	2 / 22	DUMEAUX_Fasting enriched genes
4	0.37	4 / 62	DUMEAUX_Smoking enriched genes
5	0.51	1 / 14	Huan_blood−pressure_SBP−signature
6	0.62	7 / 150	Homuth_BMI−associated−genes_UP
7	0.90	7 / 210	Homuth_BMI−associated−genes_DN
8	1.00	0 / 10	DUMEAUX_Smoking literature genes up
9	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.00	0 / 5	DUMEAUX_Estrogen related in 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 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−05	204 / 3168	HOPP_Repressed
2	4e−05	130 / 1894	HOPP_Poised_promoter
3	1e−03	9 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
4	6e−03	7 / 45	Subero_INT_hypo_meth
5	1e−02	10 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
6	3e−02	6 / 46	Subero_DLBCL_hypo_meth
7	5e−02	6 / 53	LENZ_Stromal signature 2
8	6e−02	3 / 19	Subero_MCL_hypo_meth
9	8e−02	4 / 33	Subero_T−PLL_hypo_meth
10	1e−01	3 / 23	Subero_mBL_hypo_meth
11	1e−01	8 / 102	ROSOLOWSKI_blue total
12	1e−01	5 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
13	1e−01	4 / 41	ROSOLOWSKI_blue DOWN
14	2e−01	2 / 14	Subero_B−ALL_hypo_meth
15	2e−01	9 / 132	Subero_DLBCL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.009	6 / 37	Hugo_melanoma−all−MET_DN
2	0.011	3 / 10	Joensson_Melanoma Normal like subtype
3	0.082	15 / 204	Landsberg_dedifferentiation_down
4	0.097	1 / 2	Melanoma Epi−Enzyme Cluster 1
5	0.100	2 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
6	0.113	17 / 249	Gerber_wt/wt_melanoma−cells−SpotE
7	0.245	4 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	0.304	3 / 39	Tirosh_top50 correlated genes PC4
9	0.304	3 / 39	Tirosh_melanoma specific genes
10	0.335	4 / 59	TCGA_melanoma_keratin_high
11	0.335	2 / 24	Gerami_melanoma−metastatic−risk_DN
12	0.344	5 / 78	Tirosh_CAF−cell specific genes
13	0.392	4 / 64	Harbst_melanoma_lowgrade_up
14	0.413	5 / 85	Tirosh_AXL−signature
15	0.475	9 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	5e−04	32 / 346	receptor binding
2	2e−03	54 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
3	2e−03	9 / 58	cytoskeletal protein binding
4	3e−03	54 / 741	DNA binding transcription factor activity
5	3e−03	5 / 21	transcription factor activity, transcription factor binding
6	3e−03	8 / 51	ubiquitin binding
7	4e−03	14 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
8	7e−03	4 / 16	G−protein coupled peptide receptor activity
9	7e−03	23 / 268	transcription factor binding
10	8e−03	4 / 17	cAMP binding
11	9e−03	17 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
12	9e−03	34 / 450	sequence−specific DNA binding
13	1e−02	3 / 10	fucosyltransferase activity
14	1e−02	3 / 10	water channel activity
15	1e−02	6 / 39	nuclear receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	5 / 28	hsa−miR−296−5p
2	0.02	4 / 21	hsa−miR−483−3p
3	0.03	8 / 72	hsa−miR−339−5p
4	0.03	2 / 6	hsa−miR−886−5p
5	0.04	6 / 50	hsa−miR−371−5p
6	0.04	4 / 26	hsa−miR−558
7	0.06	5 / 43	hsa−miR−328
8	0.07	6 / 58	hsa−miR−331−3p
9	0.07	4 / 32	hsa−miR−615−5p
10	0.08	6 / 60	hsa−miR−1321
11	0.10	6 / 64	hsa−miR−510
12	0.10	2 / 11	hsa−miR−1249
13	0.10	4 / 36	hsa−miR−146b−3p
14	0.10	4 / 36	hsa−miR−766
15	0.12	2 / 12	hsa−miR−191*

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−05	26 / 209	Chaussabel_2,5_Immune related molecules
2	8e−03	4 / 17	VAQUERIZAS_Heart_TF
3	2e−02	14 / 152	VAQUERIZAS_General_TF
4	7e−02	24 / 352	WIRTH_Nervous System
5	1e−01	2 / 11	JONGENEEL_Thyroid
6	1e−01	2 / 12	WIRTH_Tonsil
7	1e−01	2 / 12	WIRTH_Globus pallidus
8	1e−01	15 / 218	WIRTH_pre+post GC B−cells
9	2e−01	2 / 14	WIRTH_Thalamus
10	2e−01	1 / 4	JONGENEEL_Bladder
11	2e−01	3 / 30	JONGENEEL_Bone Marrow
12	2e−01	2 / 16	VAQUERIZAS_Fetal liver_TF
13	2e−01	2 / 16	VAQUERIZAS_Ovary_TF
14	2e−01	3 / 32	VAQUERIZAS_Liver_TF
15	2e−01	2 / 19	JONGENEEL_Prostate

Telomeres

Rank	p−value	#in/all	Geneset
1	0.7	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	7e−05	153 / 2321	ICGC_Rad21_targets
2	3e−04	42 / 485	ICGC_NrsfPcr2_targets
3	4e−03	273 / 4851	ICGC_Runx3_targets
4	4e−03	260 / 4602	ICGC_Elf1_targets
5	8e−03	75 / 1148	HEBENSTREIT_low expression TF
6	1e−02	232 / 4131	ICGC_Tcf3_targets
7	3e−02	176 / 3121	ICGC_Egr1_targets
8	3e−02	211 / 3804	ICGC_Stat5_targets
9	3e−02	113 / 1941	ICGC_Bcl3_targets
10	5e−02	232 / 4278	ICGC_Yy1_targets
11	6e−02	220 / 4072	ICGC_Mta3_targets
12	8e−02	186 / 3435	ICGC_Ebfsc137065_targets
13	9e−02	195 / 3630	ICGC_Sp1_targets
14	1e−01	171 / 3213	ICGC_Pu1_targets
15	2e−01	223 / 4264	ICGC_Pax5_targets