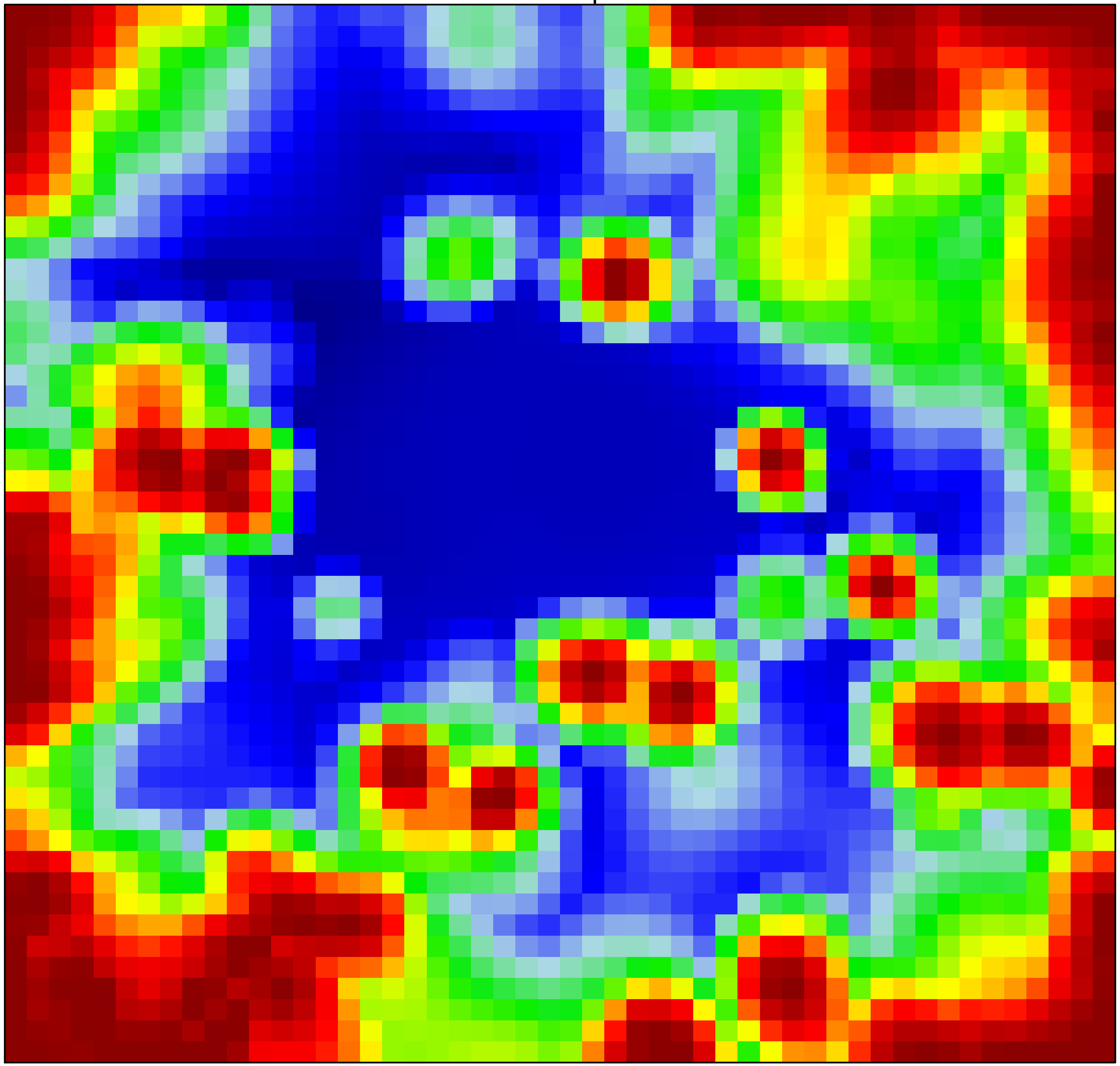
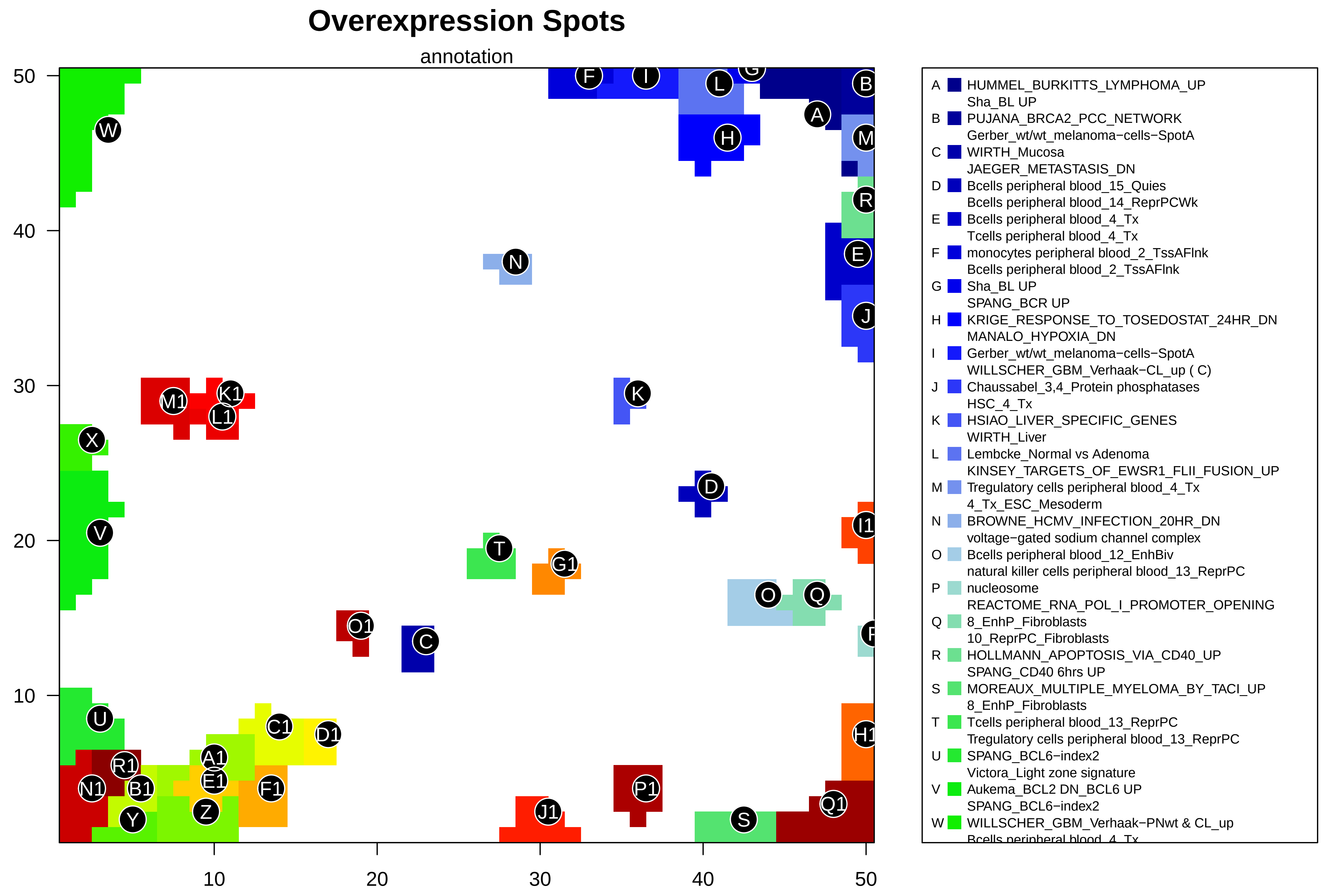
Overexpression Spots

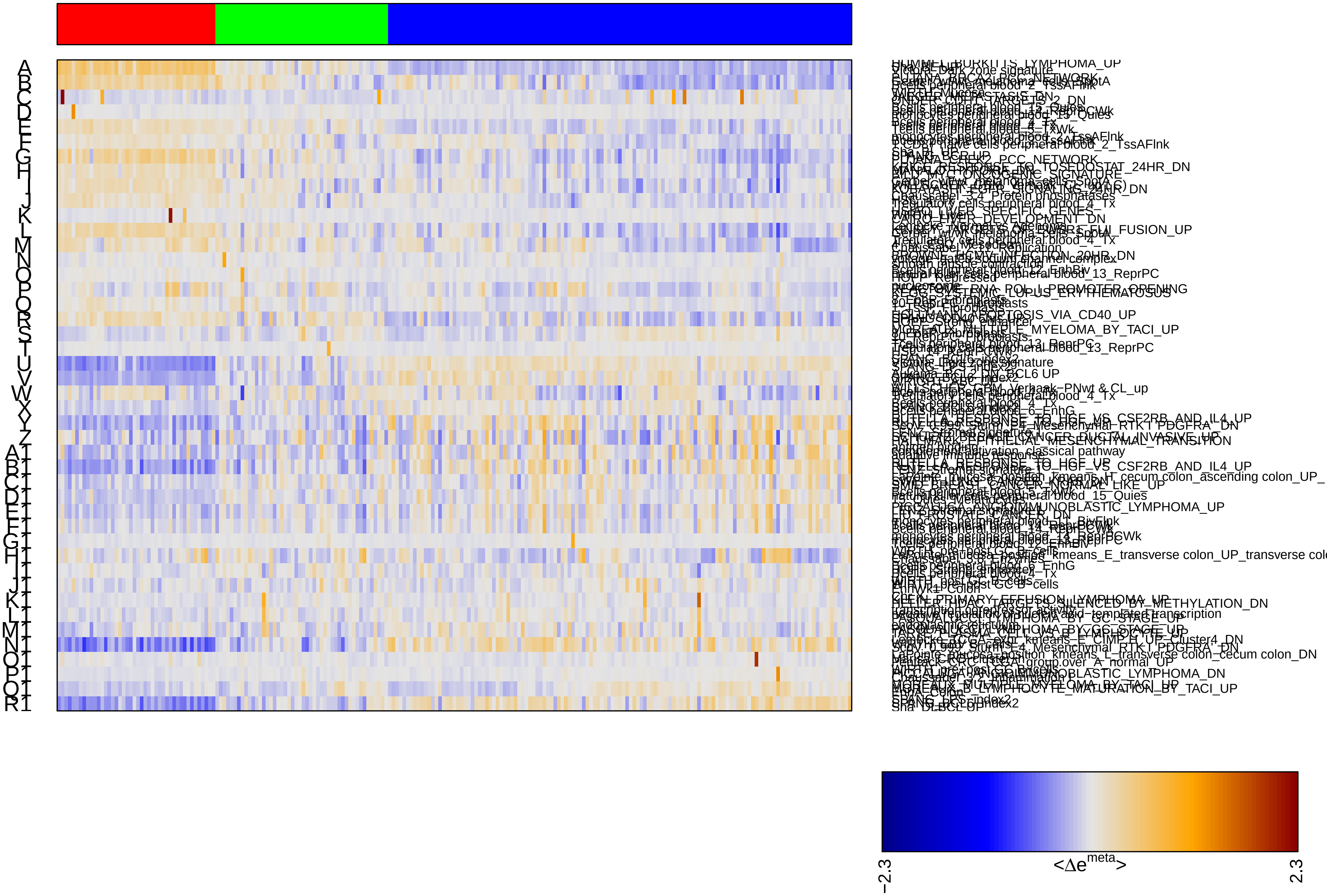
landscape





Overexpression Spots

annotation


A
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E1
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H1
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J1
K1
L1
M1
N1
O1
P1
Q1
R1
HUMMEL_BURKITTS_LYMPHOMA_UP
Sha_BL_UP
Victora Dark zone signature
PUJANA_BRCA2_PCC_NETWORK
Gerber wt/wt melanoma cells SpotA
Bcells peripheral blood_2_TssAFlnk
WIRTH_Mucosa
JAEGER_METASTASIS_DN
ONDER_CDH1_TARGETS_2_DN
Bcells peripheral blood_15_Quies
Bcells peripheral blood_14_ReprPCWk
monocytes peripheral blood_15_Quies
Bcells peripheral blood_4_Tx
Tcells peripheral blood_4_Tx
Tcells peripheral blood_5_TxWk
monocytes peripheral blood_2_TssAFlnk
Bcells peripheral blood_2_TssAFlnk
T CD8 naive cells peripheral blood_2_TssAFlnk
Sha_BL_UP
SPANG_BCR_UP
PUJANA_CHEK2_PCC_NETWORK
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
MANALO_HYPOXIA_DN
BILD_MYC_ONCOGENIC_SIGNATURE
Gerber wt/wt melanoma cells SpotA
KOBAYASHI_EGFR_SIGNALING_24HR_DN
Chaussabel 3,4 Protein phosphatases
Tregulatory cells peripheral blood_4_Tx
HSIAO_LIVER_SPECIFIC_GENES
WIRTH_Liver
CAIRO_LIVER_DEVELOPMENT_DN
Lembcke Normal vs Adenoma
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
Gerber wt/wt melanoma cells SpotA
Tregulatory cells peripheral blood_4_Tx
Chaussabel 2,11 Replication
BROWNE_HCMV_INFECTION_20HR_DN
voltage−gated sodium channel complex
smooth muscle contraction
Bcells peripheral blood_12_EnhBiv
natural killer cells peripheral blood_13_ReprPC
HOPP_Repressed
nucleosome
REACTOME_RNA_POL_I_PROMOTER_OPENING
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
8_EnhP_Fibroblasts
10_ReprPC_Fibroblasts
1_TssP_Fibroblasts
HOLLMANN_APOPTOSIS_VIA_CD40_UP
SPANG_CD40_6hrs_UP
HOPP_Strong_enhancer
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
8_EnhP_Fibroblasts
10_ReprPC_Fibroblasts
Tcells peripheral blood_13_ReprPC
Tregulatory cells peripheral blood_13_ReprPC
HSC_14_ReprPCWk
SPANG_BCL6_index2
Victora Light zone signature
SPANG_LPS_index2
Aukema_BCL2 DN_BCL6 UP
SPANG_BCL6_index2
WRIGHT_ABC_UP
WILLSCHER_GBM_Verhaak−PNwt & CL_up
Bcells peripheral blood_4_Tx
Tregulatory cells peripheral blood_4_Tx
Bcells peripheral blood_4_Tx
SPANG_BCL6_index2
Bcells peripheral blood_6_EnhG
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
Scov 0.999 Sturm E4 Mesenchymal RTK1 'PDGFRA' DN
LENZ_Stromal signature 1
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
antigen binding
complement activation, classical pathway
adaptive immune response
RUTELLA_RESPONSE_TO_HGF_UP
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
LENZ_Stromal signature 1
LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
SWEET_LUNG_CANCER_KRAS_DN
SMID_BREAST_CANCER_NORMAL_LIKE_UP
Bcells peripheral blood_5_TxWk
natural killer cells peripheral blood_15_Quies
15_Quies_Melanocytes
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
LENZ_Stromal signature 1
LIU_PROSTATE_CANCER_DN
monocytes peripheral blood_11_BivFlnk
Tcells peripheral blood_14_ReprPCWk
Bcells peripheral blood_14_ReprPCWk
monocytes peripheral blood_14_ReprPCWk
monocytes peripheral blood_13_ReprPC
Tcells peripheral blood_12_EnhBiv
WIRTH_pre+post GC B−cells
LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
Chaussabel 3,8 Enzymes
Bcells peripheral blood_6_EnhG
HOPP_Strong_enhancer
Bcells peripheral blood_4_Tx
WIRTH_post GC B−cells
WIRTH_pre+post GC B−cells
EnhWk1_Colon
ChrX
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
transcription corepressor activity
negative regulation of nucleic acid−templated transcription
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
endoplasmic reticulum
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
Lembcke_TCGA−expr_kmeans−E_CIMP.H_UP−Cluster4_DN
Scov 0.999 Sturm E4 Mesenchymal RTK1 'PDGFRA' DN
LaPointe_mucosa−position_kmeans_L−transverse colon−cecum colon_DN
group.over_A_normal_UP
WIRTH_pre+post GC B−cells
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
Chaussabel 3,2 Inflammation I
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
EnhA_Colon
SPANG_LPS_index2
SPANG_BCL6_index2
Sha_DLBCL_UP
−2.3
<Δe^meta>
2.3

Overexpression Spots

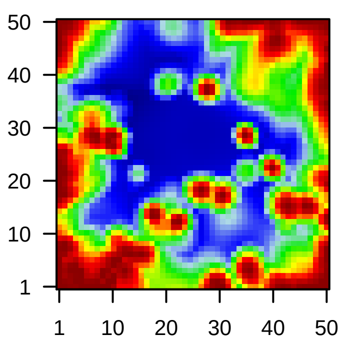
Spot Summary: A

metagenes = 14
genes = 239

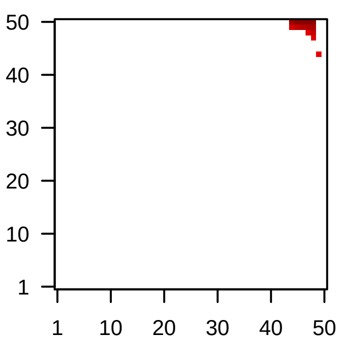
<r> metagenes = 0.95
<r> genes = 0.33
beta: r2= 17.12 / log p= −Inf

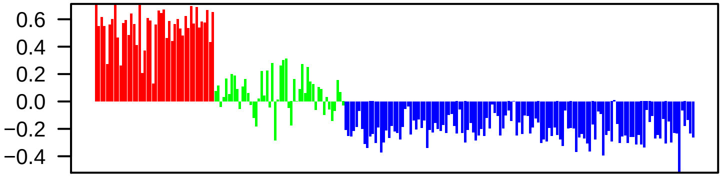
samples with spot = 50 (22.6 %)
mBL : 42 (95.5 %)
intermediate : 8 (16.7 %)

Overview Map



Spot





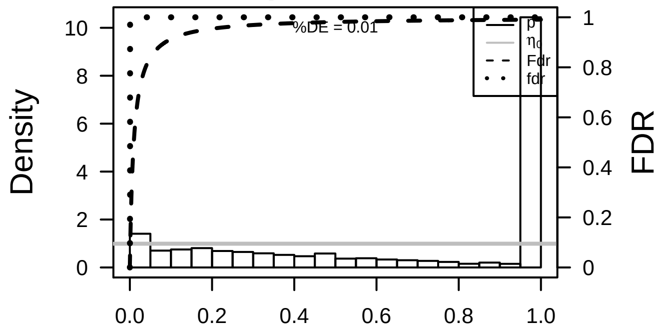
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206660_at	2.83	−0.99	0.51	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy
2	221349_at	2.76	−0.89	0.71	VPREB1	V−set pre−B cell surrogate light chain 1 [Source:HGNC Symb
3	206413_s_at	2.76	−1.22	0.37	TCL1B	T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG
4	204914_s_at	2.24	−0.89	0.67	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
5	213920_at	2.19	−1.02	0.53	CUX2	cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934
6	213674_x_at	2.16	−1.9	0.35		immunoglobulin heavy constant delta [Source:HGNC Symbol
7	38037_at	2.16	−1.11	0.6	HBEGF	heparin binding EGF like growth factor [Source:HGNC Symbo
8	204915_s_at	2.16	−0.86	0.62	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
9	209590_at	2.09	−1.32	0.8	BMP7	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:H
10	210244_at	2.07	−1.33	0.38	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
11	203821_at	2.07	−1.19	0.57	HBEGF	heparin binding EGF like growth factor [Source:HGNC Symbo
12	219737_s_at	2.07	−1.48	0.69	PCDH9	protocadherin 9 [Source:HGNC Symbol;Acc:HGNC:8661]
13	204913_s_at	2.07	−1.11	0.66	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
14	205122_at	2	−1	0.6	TMEFF1	transmembrane protein with EGF like and two follistatin like d
15	209469_at	1.96	−1.84	0.43	GPM6A	glycoprotein M6A [Source:HGNC Symbol;Acc:HGNC:4460]
16	203435_s_at	1.95	−1.72	0.72	MME	membrane metalloendopeptidase [Source:HGNC Symbol;Acc
17	213280_at	1.95	−0.83	0.57	RAP1GAP2	RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac
18	209570_s_at	1.94	−0.79	0.53	NSG1	neuronal vesicle trafficking associated 1 [Source:HGNC Symb
19	217276_x_at	1.91	−1.16	0.57		serine hydrolase−like (pseudogene) [Source:HGNC Symbol;
20	213901_x_at	1.87	−1.27	0.7	RBFOX2	RNA binding fox−1 homolog 2 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−49	31 / 42	GSEA	HUMMEL_BURKITTS_LYMPHOMA_UP
2	6e−29	28 / 99	Lymph	Sha_BL UP
3	6e−24	31 / 192	Lymph	Victora_Dark zone signature
4	8e−23	13 / 15	Lymph	BENTINK_mBL UP
5	4e−19	31 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
6	2e−17	10 / 12	Canc	BENTINK_e2f3.2
7	9e−17	51 / 955	Lymph	SPANG_BCR UP
8	4e−12	23 / 263	Lymph	SPANG_CD40 6hrs UP
9	8e−12	6 / 6	Lymph	MASCQUE_mBL UP
10	9e−12	17 / 135	Lymph	DAVE_BL−vs−DLBCL
11	6e−11	12 / 61	GSEA	BASSO_CD40_SIGNALING_DN
12	5e−09	18 / 227	Lymph	SPANG_IL21 UP
13	7e−09	6 / 12	Canc	BENTINK_ras.1
14	2e−08	29 / 615	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
15	1e−07	15 / 195	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
16	2e−07	9 / 60	GSEA	PYEON_HPV_POSITIVE_TUMORS_UP
17	4e−07	16 / 240	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_DN
18	6e−07	29 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
19	2e−06	26 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
20	3e−06	8 / 61	GSEA	BILBAN_B_CLL_LPL_UP
21	4e−06	12 / 160	GSEA	PUJANA_XPRSS_INT_NETWORK
22	5e−06	4 / 9	Lymph	DAVE_BL UP
23	5e−06	19 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
24	6e−06	33 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
25	8e−06	17 / 337	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
26	9e−06	12 / 176	GSEA	BILD_E2F3_ONCOGENIC_SIGNATURE
27	2e−05	7 / 57	Pneu	Burnham_day1_vs_5_UP
28	2e−05	96 / 4701	CC	cytoplasm
29	2e−05	19 / 444	GSEA	MARTINEZ_RB1_AND_TP53_TARGETS_DN
30	3e−05	16 / 335	GSEA	BENPORATH_ES_1
31	3e−05	11 / 169	GSEA	YAMAZAKI_TCEB3_TARGETS_DN
32	3e−05	16 / 340	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
33	4e−05	8 / 87	miRN	hsa−miR−449b
34	4e−05	4 / 14	Canc	BENTINK_src.10
35	5e−05	25 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
36	6e−05	41 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
37	7e−05	11 / 183	GSEA	PROVENZANI_METASTASIS_UP
38	7e−05	8 / 96	Lymph	SPANG_LPS 6hrs UP
39	9e−05	4 / 17	Lymph	Aukema_BCL2 UP_BCL6 DN
40	1e−04	3 / 7	GSEA	PHESSE_TARGETS_OF_APC_AND_MBD2_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 92	HORVATH_aging_genes meth DOWN
2	0.5	2 / 107	HORVATH_aging_genes meth UP
3	0.5	1 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	2e−05	96 / 4701	cytoplasm
2	9e−04	55 / 2541	nucleoplasm
3	1e−03	87 / 4579	nucleus
4	3e−03	12 / 326	nuclear speck
5	1e−02	3 / 33	cytosolic small ribosomal subunit
6	2e−02	3 / 39	cell leading edge
7	2e−02	2 / 15	NuRD complex
8	2e−02	2 / 16	neuron projection terminus
9	3e−02	21 / 936	cytoskeleton
10	3e−02	6 / 163	transcription factor complex
11	3e−02	2 / 20	small ribosomal subunit
12	5e−02	3 / 55	recycling endosome membrane
13	5e−02	2 / 25	condensed chromosome
14	7e−02	2 / 29	histone deacetylase complex
15	7e−02	9 / 354	centrosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−06	33 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	6e−03	24 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
3	1e−02	108 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	2e−02	14 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
5	3e−02	10 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
6	3e−02	6 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
7	4e−02	34 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	4e−02	19 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
9	4e−02	7 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
10	9e−02	3 / 72	Ang_CRC−CIMPH−vs−L_hyper
11	9e−02	11 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	1e−01	1 / 7	Juehling−MSI−enriched−in−7
13	1e−01	3 / 77	Ang_CRC_Hypermethylated
14	1e−01	1 / 8	KIM_MSI−in−EC
15	1e−01	1 / 11	Kaneda_CIMP−group2

HM

Rank	p−value	#in/all	Geneset
1	0.02	7 / 195	HALLMARK_G2M_CHECKPOINT
2	0.05	5 / 141	HALLMARK_UV_RESPONSE_DN
3	0.05	6 / 187	HALLMARK_E2F_TARGETS
4	0.06	6 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.07	2 / 29	HALLMARK_NOTCH_SIGNALING
6	0.10	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	0.17	2 / 51	HALLMARK_TGF_BETA_SIGNALING
8	0.25	4 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	0.31	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.31	4 / 194	HALLMARK_MYOGENESIS
11	0.31	4 / 194	HALLMARK_KRAS_SIGNALING_UP
12	0.40	2 / 94	HALLMARK_PROTEIN_SECRETION
13	0.46	3 / 173	HALLMARK_MITOTIC_SPINDLE
14	0.46	3 / 174	HALLMARK_APICAL_JUNCTION
15	0.51	3 / 188	HALLMARK_HYPOXIA

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−29	28 / 99	Sha_BL UP
2	6e−24	31 / 192	Victora_Dark zone signature
3	8e−23	13 / 15	BENTINK_mBL UP
4	9e−17	51 / 955	SPANG_BCR UP
5	4e−12	23 / 263	SPANG_CD40 6hrs UP
6	8e−12	6 / 6	MASCQUE_mBL UP
7	9e−12	17 / 135	DAVE_BL−vs−DLBCL
8	5e−09	18 / 227	SPANG_IL21 UP
9	5e−06	4 / 9	DAVE_BL UP
10	7e−05	8 / 96	SPANG_LPS 6hrs UP
11	9e−05	4 / 17	Aukema_BCL2 UP_BCL6 DN
12	5e−04	101 / 5404	HOPP_Strong_enhancer
13	6e−04	105 / 5682	HOPP_Weak_promoter
14	6e−04	11 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	6e−04	108 / 5908	HOPP_Active_promoter

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−05	8 / 87	hsa−miR−449b
2	2e−04	12 / 236	hsa−miR−34a
3	2e−03	3 / 17	hsa−miR−151−5p
4	2e−03	10 / 232	hsa−miR−186
5	2e−03	6 / 93	hsa−miR−605
6	2e−03	7 / 126	hsa−miR−338−3p
7	3e−03	9 / 203	hsa−miR−449a
8	3e−03	5 / 68	hsa−miR−1265
9	3e−03	8 / 171	hsa−miR−203
10	4e−03	6 / 103	hsa−miR−576−3p
11	5e−03	4 / 47	hsa−miR−370
12	5e−03	7 / 145	hsa−miR−607
13	5e−03	6 / 111	hsa−miR−656
14	7e−03	5 / 82	hsa−miR−653
15	7e−03	7 / 155	hsa−miR−586

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−04	16 / 414	negative regulation of transcription, DNA−templated
2	8e−04	3 / 13	replicative senescence
3	2e−03	3 / 18	negative regulation of phosphorylation
4	4e−03	18 / 621	negative regulation of transcription from RNA polymerase II promoter
5	4e−03	3 / 23	positive regulation of pri−miRNA transcription from RNA polymerase II promot
6	5e−03	6 / 110	regulation of cell cycle
7	6e−03	3 / 26	positive regulation of glucose import
8	6e−03	3 / 26	sphingolipid metabolic process
9	7e−03	3 / 27	positive regulation of Wnt signaling pathway
10	8e−03	3 / 29	spinal cord development
11	9e−03	7 / 160	negative regulation of gene expression
12	9e−03	15 / 521	transcription from RNA polymerase II promoter
13	9e−03	3 / 30	response to testosterone
14	1e−02	2 / 11	establishment or maintenance of epithelial cell apical/basal polarity
15	1e−02	2 / 11	muscle fiber development

Chr

Rank	p−value	#in/all	Geneset
1	0.002	16 / 480	Chr 4
2	0.021	3 / 41	Chr Y
3	0.033	11 / 403	Chr 14
4	0.053	9 / 333	Chr 22
5	0.062	7 / 242	Chr 13
6	0.262	12 / 669	Chr 6
7	0.283	9 / 492	Chr 9
8	0.314	12 / 700	Chr 12
9	0.410	9 / 554	Chr 5
10	0.609	6 / 437	Chr 8
11	0.622	5 / 369	Chr 20
12	0.647	18 / 1325	Chr 1
13	0.665	11 / 832	Chr 2
14	0.667	11 / 833	Chr 19
15	0.685	7 / 548	Chr 16

Glioma

Rank	p−value	#in/all	Geneset
1	0.02	3 / 41	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
2	0.03	22 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	0.04	11 / 421	Down_b
4	0.05	3 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
5	0.05	6 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
6	0.05	3 / 59	GIEZELT_GBM_STS_up_VS_LTS
7	0.07	2 / 30	Shaw_responders_down_in_oligo_glioma
8	0.07	3 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	0.08	2 / 32	WIRTH_PN subtype
10	0.08	2 / 32	Shaw_down_in_1p19q
11	0.08	1 / 6	Shaw_responders_up_in_oligo_glioma
12	0.10	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
13	0.11	1 / 8	Shaw_up_in_1p19qdel
14	0.11	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
15	0.15	1 / 11	KIM amplified & overexpressed in LTS

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	2 / 25	Angelova_immune−metagene−DC
2	0.14	1 / 10	Angelova_immune−metagene−neutrophils
3	0.17	1 / 13	Angelova_immune−metagene−activated_B−cells
4	0.17	1 / 13	Angelova_immune−metagene−immature_B−cells
5	0.22	1 / 17	Angelova_immune−metagene−central_memory_CD8
6	0.23	1 / 18	Angelova_CRC_immunostimulators
7	0.32	1 / 26	Angelova_immune−metagene−activated_CD4
8	0.48	1 / 45	Angelova_immune−metagene−MDSC
9	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
10	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
14	1.00	0 / 14	Angelova_immune−metagene−eosinophil
15	1.00	0 / 19	Angelova_immune−metagene−iDC

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	10 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	0.03	13 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	0.03	4 / 83	TCGA_melanoma_immune_high
4	0.06	1 / 4	Melanoma Epi−Enzyme Cluster 5
5	0.08	3 / 68	Tirosh_housekeeping_genes
6	0.17	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	0.24	4 / 171	Landsberg_dedifferentiation_up
8	0.24	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	0.30	1 / 24	Gerami_melanoma−metastatic−risk_DN
10	0.37	5 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	0.38	1 / 33	Tirosh_T−cell specific genes−melanoma
12	0.43	1 / 38	Tirosh_G1/S phase specific genes
13	0.45	4 / 236	Gerber_wt/wt_group3−specific
14	0.46	2 / 107	Tirosh_Exhaustion program in Mel75
15	0.50	1 / 47	Tirosh_G2/M phase specific genes

Pneumonia

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

TF

Rank	p−value	#in/all	Geneset
1	0.06	1 / 4	MYC_TF and cofactors
2	0.10	58 / 3435	ICGC_Ebfsc137065_targets
3	0.12	1 / 9	MYC_Targets DOWN
4	0.12	1 / 9	MYC_DNA repair UP
5	0.18	51 / 3121	ICGC_Egr1_targets
6	0.19	22 / 1241	KIM_MYC targets
7	0.21	31 / 1848	ICGC_Pbx3_targets
8	0.22	37 / 2254	ICGC_BatfPcr1_targets
9	0.23	60 / 3796	ICGC_Nficsc81335_targets
10	0.24	18 / 1032	ICGC_Usf1_targets
11	0.30	49 / 3150	ICGC_Creb1_targets
12	0.33	70 / 4602	ICGC_Elf1_targets
13	0.34	62 / 4072	ICGC_Mta3_targets
14	0.34	24 / 1508	ICGC_Mef2_targets
15	0.35	46 / 2994	ICGC_Zeb1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−17	10 / 12	BENTINK_e2f3.2
2	7e−09	6 / 12	BENTINK_ras.1
3	4e−05	4 / 14	BENTINK_src.10
4	2e−03	9 / 186	SPANG_LPS−index2
5	2e−02	2 / 14	BENTINK_src.2
6	3e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
7	4e−02	11 / 409	Lembcke_Normal vs Adenoma
8	4e−02	0 / 14	LIU_PROSTATE_CANCER_DN
9	8e−02	2 / 32	KUIPER_MM good survival
10	9e−02	3 / 72	PanCan_Wnt_geneset_nanostring
11	9e−02	0 / 11	LIU_PROSTATE_CANCER_UP
12	1e−01	2 / 41	PanCan_DNARepair_geneset_nanostring
13	1e−01	4 / 130	PanCan_CC+Apop_geneset_nanostring
14	1e−01	5 / 187	PanCan_PI3K_geneset_nanostring
15	1e−01	1 / 10	GENTLES_modul3

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−07	154 / 8406	Bcells peripheral blood_2_TssAFlnk
2	2e−07	163 / 9160	2_TssA_Neuronal_Progenitor
3	1e−06	151 / 8322	T CD8+ naive cells peripheral blood_1_TssA
4	2e−06	147 / 8068	Thelper cells peripheral blood_1_TssA
5	4e−06	143 / 7833	Bcells peripheral blood_1_TssA
6	6e−06	88 / 4062	T CD8+ naive cells peripheral blood_15_Quies
7	8e−06	56 / 2197	monocytes peripheral blood_11_BivFlnk
8	1e−05	160 / 9298	Bcells peripheral blood_7_Enh
9	2e−05	155 / 8918	1_TssA_ESC_Mesoderm
10	2e−05	153 / 8766	2_TssA_Melanocytes
11	2e−05	44 / 1611	natural killer cells peripheral blood_11_BivFlnk
12	2e−05	121 / 6389	4_Tx_ESC_Mesoderm
13	2e−05	82 / 3819	natural killer cells peripheral blood_15_Quies
14	2e−05	82 / 3825	Bcells peripheral blood_15_Quies
15	3e−05	151 / 8641	1_TssA_ESC_Endoderm

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−49	31 / 42	HUMMEL_BURKITTS_LYMPHOMA_UP
2	4e−19	31 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
3	6e−11	12 / 61	BASSO_CD40_SIGNALING_DN
4	2e−08	29 / 615	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
5	1e−07	15 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
6	2e−07	9 / 60	PYEON_HPV_POSITIVE_TUMORS_UP
7	4e−07	16 / 240	MITSIADES_RESPONSE_TO_APLIDIN_DN
8	6e−07	29 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
9	2e−06	26 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
10	3e−06	8 / 61	BILBAN_B_CLL_LPL_UP
11	4e−06	12 / 160	PUJANA_XPRSS_INT_NETWORK
12	5e−06	19 / 400	PUJANA_BRCA2_PCC_NETWORK
13	8e−06	17 / 337	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP
14	9e−06	12 / 176	BILD_E2F3_ONCOGENIC_SIGNATURE
15	2e−05	19 / 444	MARTINEZ_RB1_AND_TP53_TARGETS_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	3 / 32	Marjolein_ageing−genes_DN
2	0.27	1 / 22	DUMEAUX_Fasting enriched genes
3	0.36	4 / 210	Homuth_BMI−associated−genes_DN
4	0.60	1 / 62	DUMEAUX_Smoking enriched genes
5	0.89	1 / 150	Homuth_BMI−associated−genes_UP
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 22	DUMEAUX_High bmi enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	5e−04	12 / 268	transcription factor binding
2	2e−03	36 / 1541	DNA binding
3	6e−03	18 / 644	protein homodimerization activity
4	9e−03	2 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
5	1e−02	2 / 11	DNA−(apurinic or apyrimidinic site) lyase activity
6	1e−02	3 / 32	histone deacetylase activity
7	1e−02	2 / 12	protein kinase A catalytic subunit binding
8	1e−02	2 / 13	enhancer binding
9	2e−02	26 / 1161	RNA binding
10	2e−02	2 / 14	protein kinase C activity
11	2e−02	10 / 329	RNA polymerase II proximal promoter sequence−specific DNA binding
12	2e−02	2 / 16	dynein light intermediate chain binding
13	2e−02	2 / 16	immunoglobulin receptor binding
14	2e−02	20 / 852	nucleic acid binding
15	2e−02	2 / 17	cAMP binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	2 / 5	JONGENEEL_Fetal Brain
2	0.003	4 / 42	Chaussabel_1,3_B−cells
3	0.003	6 / 100	Chaussabel_2,8_T−cells
4	0.012	2 / 12	WIRTH_Cortex cerebri
5	0.014	11 / 352	WIRTH_Nervous System
6	0.014	16 / 604	PROTEINATLAS_hippocampus
7	0.018	15 / 569	PROTEINATLAS_salivary gland
8	0.023	3 / 42	VAQUERIZAS_Fetal brain_TF
9	0.037	2 / 21	VAQUERIZAS_Tonsil_TF
10	0.037	16 / 678	PROTEINATLAS_lymph node
11	0.039	22 / 1022	PROTEINATLAS_placenta
12	0.039	7 / 218	WIRTH_pre+post GC B−cells
13	0.051	16 / 708	PROTEINATLAS_thyroid gland
14	0.062	22 / 1076	PROTEINATLAS_stomach
15	0.063	15 / 671	PROTEINATLAS_cervix, uterine

Overexpression Spots

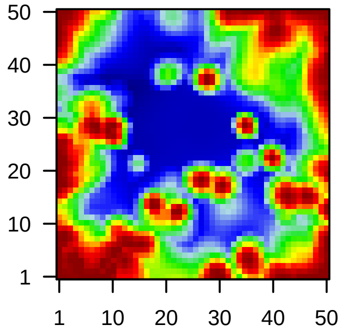
Spot Summary: B

metagenes = 6
genes = 112

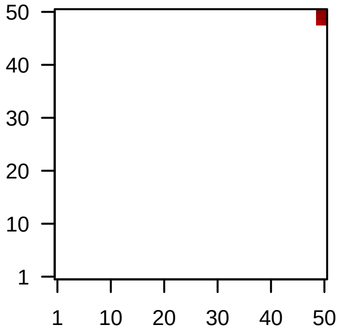
<r> metagenes = 0.99
<r> genes = 0.36
beta: r2= 14.46 / log p= −Inf

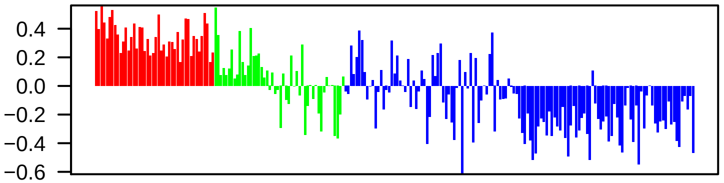
samples with spot = 62 (28.1 %)
mBL : 41 (93.2 %)
intermediate : 10 (20.8 %)
non−mBL : 11 (8.5 %)

Overview Map



Spot





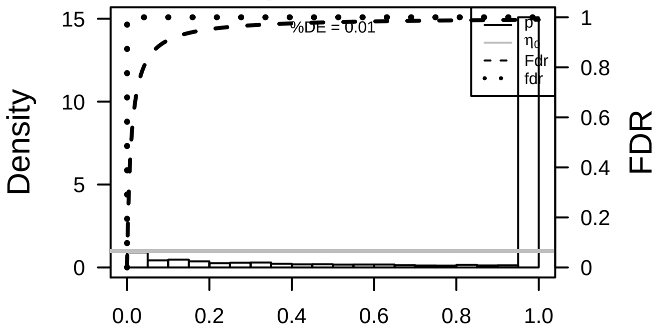
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	AFFX−r2−Hs1	3.22	−1.13	0.58		
2	AFFX−r2−Hs1	3.07	−1.49	0.5		
3	AFFX−HUMR	2.91	−0.94	0.58		microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835
4	AFFX−HUMR	2.85	−1.18	0.48		
5	AFFX−r2−Hs1	2.71	−1.22	0.66		
6	AFFX−M2783	2.6	−1.58	0.57		
7	AFFX−HUMR	2.6	−1.04	0.59		
8	AFFX−r2−Hs2	2.21	−1.56	0.55		
9	215767_at	1.86	−2.03	0.34	ZNF804A	zinc finger protein 804A [Source:HGNC Symbol;Acc:HGNC:2
10	211071_s_at	1.55	−1.35	0.44	MLLT11	MLLT11, transcription factor 7 cofactor [Source:HGNC Symbo
11	220214_at	1.53	−1.31	0.49	ZNF215	zinc finger protein 215 [Source:HGNC Symbol;Acc:HGNC:13
12	215907_at	1.52	−1.29	0.48		
13	219703_at	1.3	−1.06	0.65	MNS1	meiosis specific nuclear structural 1 [Source:HGNC Symbol;
14	215143_at	1.28	−1.14	0.59		
15	208580_x_at	1.24	−0.83	0.54	HIST1H4K	histone cluster 1 H4 family member k [Source:HGNC Symbol
16	AFFX−BioB−3	1.19	−1.03	0.56		
17	214220_s_at	1.16	−0.96	0.64	ALMS1	ALMS1, centrosome and basal body associated protein [Sou
18	204087_s_at	1.15	−1.02	0.64	SLC5A6	solute carrier family 5 member 6 [Source:HGNC Symbol;Acc:
19	212290_at	1.1	−1.52	0.61	SLC7A1	solute carrier family 7 member 1 [Source:HGNC Symbol;Acc:
20	218848_at	1.1	−1.13	0.57	THOC6	THO complex 6 [Source:HGNC Symbol;Acc:HGNC:28369]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−14	22 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
2	1e−13	20 / 319	Melar	Gerber_wt/wt_melanoma−cells−SpotA
3	4e−11	30 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	9e−11	16 / 267	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
5	4e−10	71 / 5529	Lympl	HOPP_Txn_elongation
6	2e−09	18 / 431	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
7	7e−09	19 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
8	2e−08	17 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	2e−08	12 / 195	HM	HALLMARK_G2M_CHECKPOINT
10	4e−08	16 / 409	Canc	Lembcke_Normal vs Adenoma
11	6e−08	9 / 102	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
12	7e−08	14 / 314	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_1_DN
13	8e−08	24 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	2e−07	41 / 2541	CC	nucleoplasm
15	4e−07	58 / 4579	CC	nucleus
16	9e−07	29 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
17	1e−06	12 / 281	BP	DNA repair
18	1e−06	6 / 47	GSEA	OXFORD_RALA_OR_RALB_TARGETS_UP
19	1e−06	9 / 147	GSEA	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
20	2e−06	8 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
21	4e−06	17 / 641	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
22	4e−06	12 / 321	GSEA	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C
23	4e−06	14 / 442	GSEA	KIM_WT1_TARGETS_DN
24	4e−06	8 / 128	GSEA	BENPORATH_PROLIFERATION
25	7e−06	17 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
26	9e−06	9 / 187	HM	HALLMARK_E2F_TARGETS
27	1e−05	12 / 351	BP	cellular response to DNA damage stimulus
28	1e−05	52 / 4261	Lympl	HOPP_Txn_transition
29	1e−05	5 / 41	GSEA	PARK_HSC_AND_MULTIPOTENT_PROGENITORS
30	1e−05	7 / 106	GSEA	VANTVEER_BREAST_CANCER_METASTASIS_DN
31	2e−05	14 / 497	BP	cell cycle
32	2e−05	10 / 254	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
33	2e−05	17 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
34	2e−05	3 / 8	GSEA	SEMBA_FHIT_TARGETS_DN
35	2e−05	8 / 160	GSEA	PUJANA_XPRSS_INT_NETWORK
36	2e−05	11 / 324	CC	chromosome
37	4e−05	10 / 280	GSEA	MANALO_HYPOXIA_DN
38	4e−05	8 / 173	HM	HALLMARK_MITOTIC_SPINDLE
39	4e−05	9 / 226	GSEA	ZHANG_TLX_TARGETS_60HR_DN
40	4e−05	3 / 10	BP	kinetochore assembly

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 92	HORVATH_aging_genes meth DOWN
2	0.5	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−06	12 / 281	DNA repair
2	1e−05	12 / 351	cellular response to DNA damage stimulus
3	2e−05	14 / 497	cell cycle
4	4e−05	3 / 10	kinetochore assembly
5	2e−04	5 / 71	regulation of G2/M transition of mitotic cell cycle
6	2e−04	5 / 76	DNA recombination
7	2e−04	3 / 17	replication fork processing
8	4e−04	9 / 307	cell division
9	6e−04	4 / 52	double−strand break repair via nonhomologous end joining
10	8e−04	4 / 57	double−strand break repair via homologous recombination
11	1e−03	3 / 27	DNA biosynthetic process
12	1e−03	4 / 62	meiotic cell cycle
13	1e−03	3 / 30	mitotic spindle organization
14	2e−03	4 / 70	chromosome segregation
15	2e−03	3 / 33	regulation of cytokinesis

Cancer

Rank	p−value	#in/all	Geneset
1	4e−08	16 / 409	Lembcke_Normal vs Adenoma
2	7e−04	1 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	2e−03	2 / 10	GENTLES_modul3
4	3e−03	3 / 41	PanCan_DNARepair_geneset_nanostring
5	4e−02	2 / 45	KUIPER_MM poor survival
6	5e−02	1 / 14	LIU_COMMON_CANCER_GENES
7	8e−02	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
8	8e−02	1 / 12	BENTINK_ras.1
9	9e−02	1 / 13	GENTLES_modul11
10	1e−01	1 / 15	BEN−PORATH_UP
11	2e−01	0 / 16	LIU_LIVER_CANCER
12	2e−01	1 / 32	KUIPER_MM good survival
13	2e−01	2 / 130	PanCan_CC+Apop_geneset_nanostring
14	3e−01	0 / 15	RHODES_CANCER_META_SIGNATURE
15	3e−01	1 / 58	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	2e−07	41 / 2541	nucleoplasm
2	4e−07	58 / 4579	nucleus
3	2e−05	11 / 324	chromosome
4	2e−04	6 / 118	chromosome, centromeric region
5	3e−04	6 / 121	midbody
6	9e−04	5 / 101	kinetochore
7	2e−03	2 / 10	chromocenter
8	2e−03	4 / 77	condensed chromosome kinetochore
9	3e−03	2 / 11	Fanconi anaemia nuclear complex
10	4e−03	3 / 44	nuclear chromosome
11	4e−03	8 / 354	centrosome
12	6e−03	7 / 292	microtubule organizing center
13	6e−03	4 / 98	spindle pole
14	7e−03	4 / 103	nuclear chromosome, telomeric region
15	1e−02	2 / 21	mitotic spindle pole

Chr

Rank	p−value	#in/all	Geneset
1	0.02	9 / 548	Chr 16
2	0.06	10 / 776	Chr 17
3	0.06	15 / 1325	Chr 1
4	0.08	10 / 833	Chr 19
5	0.10	4 / 242	Chr 13
6	0.37	6 / 669	Chr 6
7	0.47	4 / 480	Chr 4
8	0.49	4 / 492	Chr 9
9	0.58	5 / 689	Chr 3
10	0.64	1 / 139	Chr 21
11	0.71	2 / 333	Chr 22
12	0.76	2 / 369	Chr 20
13	0.76	4 / 700	Chr 12
14	0.78	2 / 382	Chr 15
15	0.80	2 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−11	90 / 8406	Bcells peripheral blood_2_TssAFlnk
2	1e−10	79 / 6590	Tregulatory cells peripheral blood_5_TxWk
3	2e−10	88 / 8200	monocytes peripheral blood_2_TssAFlnk
4	5e−10	88 / 8322	T CD8+ naive cells peripheral blood_1_TssA
5	9e−10	85 / 7833	Bcells peripheral blood_1_TssA
6	1e−09	87 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
7	3e−09	85 / 7957	Tcells peripheral blood_2_TssAFlnk
8	3e−09	83 / 7635	monocytes peripheral blood_1_TssA
9	5e−09	75 / 6389	4_Tx_ESC_Mesoderm
10	7e−09	80 / 7225	Overlap_fetal_midbrain_ReprPC
11	8e−09	86 / 8275	2_TssA_Fibroblasts
12	9e−09	84 / 7930	Tregulatory cells peripheral blood_1_TssA
13	1e−08	72 / 6068	4_Tx_ESC_Endoderm
14	2e−08	81 / 7489	monocytes peripheral blood_5_TxWk
15	3e−08	87 / 8641	1_TssA_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	12 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	0.002	18 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	0.006	2 / 16	Budinska_B_Lower crypt−like_UP
4	0.008	10 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
5	0.022	2 / 31	Marisa_CRC−cluster−c
6	0.036	1 / 5	Marisa_CRC−C5
7	0.045	19 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	0.047	4 / 184	Kosinski_lower−crypt−long−list
9	0.096	10 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
10	0.098	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	0.124	2 / 83	Marisa_CRC−cluster−d
12	0.154	6 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
13	0.205	1 / 31	Kosinski_lower−crypt−short−list
14	0.271	9 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
15	0.304	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Glioma

Rank	p−value	#in/all	Geneset
1	2e−06	8 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	5e−03	3 / 47	developing astrocytes
3	9e−03	3 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
4	7e−02	15 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	1e−01	1 / 16	VERHAAK_PN subtype
6	1e−01	1 / 22	Martinez_Glio_hypermeth
7	2e−01	14 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
8	3e−01	1 / 45	OL vs. MOG− OL
9	3e−01	1 / 53	Christensen_hypermethylated_in_primary_glioblastoma
10	3e−01	3 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	3e−01	1 / 58	Stuehler_Proteins_up_in_STS
12	4e−01	4 / 421	Down_b
13	4e−01	1 / 66	Weller_LGG_gradeII−vs−III_DOWN
14	4e−01	1 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
15	4e−01	1 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−14	22 / 400	PUJANA_BRCA2_PCC_NETWORK
2	4e−11	30 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	9e−11	16 / 267	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
4	2e−09	18 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	7e−09	19 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
6	2e−08	17 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
7	6e−08	9 / 102	WHITEFORD_PEDIATRIC_CANCER_MARKERS
8	7e−08	14 / 314	LINDGREN_BLADDER_CANCER_CLUSTER_1_DN
9	8e−08	24 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	9e−07	29 / 1527	PUJANA_BRCA1_PCC_NETWORK
11	1e−06	6 / 47	OXFORD_RALA_OR_RALB_TARGETS_UP
12	1e−06	9 / 147	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
13	4e−06	17 / 641	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
14	4e−06	12 / 321	TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C
15	4e−06	14 / 442	KIM_WT1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−08	12 / 195	HALLMARK_G2M_CHECKPOINT
2	9e−06	9 / 187	HALLMARK_E2F_TARGETS
3	4e−05	8 / 173	HALLMARK_MITOTIC_SPINDLE
4	7e−02	3 / 133	HALLMARK_DNA_REPAIR
5	2e−01	3 / 192	HALLMARK_MTORC1_SIGNALING
6	3e−01	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	3e−01	1 / 55	HALLMARK_MYC_TARGETS_V2
8	5e−01	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	6e−01	1 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	6e−01	1 / 141	HALLMARK_UV_RESPONSE_DN
11	7e−01	1 / 174	HALLMARK_ADIPOGENESIS
12	7e−01	1 / 176	HALLMARK_ALLOGRAFT_REJECTION
13	7e−01	1 / 182	HALLMARK_GLYCOLYSIS
14	7e−01	1 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
15	8e−01	1 / 187	HALLMARK_INFLAMMATORY_RESPONSE

Immunome

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

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−10	71 / 5529	HOPP_Txn_elongation
2	1e−05	52 / 4261	HOPP_Txn_transition
3	2e−04	61 / 5908	HOPP_Active_promoter
4	3e−03	6 / 192	Victora_Dark zone signature
5	4e−03	15 / 955	SPANG_BCR UP
6	4e−02	3 / 99	Sha_BL UP
7	5e−02	6 / 353	SPANG_CD40 6hrs DN
8	1e−01	4 / 237	ZHANG_DLBCL mutated
9	1e−01	38 / 4357	HOPP_Weak_txn
10	1e−01	48 / 5682	HOPP_Weak_promoter
11	2e−01	45 / 5404	HOPP_Strong_enhancer
12	2e−01	2 / 102	ROSOLOWSKI_blue total
13	2e−01	17 / 1814	HOPP_Repetitive
14	2e−01	9 / 906	SPANG_BCR DN
15	3e−01	37 / 4559	HOPP_Weak_enhancer

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−13	20 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	4e−04	4 / 47	Tirosh_G2/M phase specific genes
3	1e−02	1 / 2	Melanoma Epi−Enzyme Cluster 6
4	3e−02	1 / 4	Melanoma Epi−Enzyme Cluster 3
5	4e−02	2 / 44	Tirosh_top50 correlated genes PC2
6	4e−02	2 / 46	Tirosh_top50 correlated genes PC5
7	8e−02	2 / 65	Harbst_melanoma_highgrade_up
8	1e−01	2 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
9	3e−01	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
10	3e−01	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	5e−01	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	8e−01	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
13	8e−01	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
14	8e−01	1 / 236	Gerber_wt/wt_group3−specific
15	1e+00	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD

MF

Rank	p−value	#in/all	Geneset
1	0.003	5 / 132	methyltransferase activity
2	0.003	4 / 81	single−stranded DNA binding
3	0.003	2 / 12	S−adenosylmethionine−dependent methyltransferase activity
4	0.003	2 / 12	ubiquitin−ubiquitin ligase activity
5	0.004	21 / 1541	DNA binding
6	0.006	4 / 97	double−stranded DNA binding
7	0.009	2 / 20	dynein complex binding
8	0.010	2 / 21	gamma−tubulin binding
9	0.010	7 / 328	chromatin binding
10	0.013	2 / 24	NF−kappaB binding
11	0.019	2 / 29	ribonucleoprotein complex binding
12	0.020	2 / 30	histone−lysine N−methyltransferase activity
13	0.020	68 / 7864	protein binding
14	0.022	12 / 852	nucleic acid binding
15	0.023	2 / 32	aminoacyl−tRNA ligase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	7 / 260	hsa−let−7e
2	0.011	2 / 22	hsa−miR−1225−3p
3	0.017	2 / 27	hsa−miR−770−5p
4	0.022	3 / 82	hsa−miR−210
5	0.027	2 / 35	hsa−miR−1224−5p
6	0.032	2 / 38	hsa−miR−518a−3p
7	0.032	3 / 94	hsa−miR−875−3p
8	0.035	4 / 167	hsa−miR−221
9	0.036	1 / 5	hsa−miR−339−3p
10	0.050	2 / 49	hsa−miR−940
11	0.052	2 / 50	hsa−miR−384
12	0.055	4 / 194	hsa−miR−124
13	0.055	3 / 117	hsa−miR−200a
14	0.057	1 / 8	hsa−miR−638
15	0.061	3 / 122	hsa−miR−506

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.3	1 / 52	Burnham_day1_vs_5_DN
2	0.3	1 / 54	Burnham_timecourse
3	0.4	1 / 68	Burnham_sep_vs_con_UP
4	0.4	1 / 71	Burnham_cap_fp_vs_con_UP
5	0.6	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.7	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	1.0	0 / 56	Burnham_sep_vs_con_DN
8	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.0	0 / 48	Burnham_viral_DN
10	1.0	0 / 57	Burnham_viral_UP
11	1.0	0 / 57	Burnham_day1_vs_5_UP
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.005	6 / 219	WIRTH_GC B−cells
2	0.106	4 / 245	Chaussabel_3,9_Kinases
3	0.109	11 / 989	PROTEINATLAS_tonsil
4	0.111	1 / 16	VAQUERIZAS_Fetal liver_TF
5	0.124	1 / 18	JONGENEEL_Monocytes
6	0.125	8 / 678	PROTEINATLAS_lymph node
7	0.127	10 / 905	PROTEINATLAS_appendix
8	0.137	1 / 20	Chaussabel_2,7_Unknown function
9	0.159	5 / 390	PROTEINATLAS_ovary
10	0.160	3 / 188	Chaussabel_3,8_Enzymes
11	0.202	2 / 113	Chaussabel_1,8_Metabolism Biosynthesis
12	0.210	1 / 32	VAQUERIZAS_Liver_TF
13	0.229	2 / 123	Chaussabel_3,7_Spliceosome
14	0.240	10 / 1048	PROTEINATLAS_rectum
15	0.256	1 / 40	VAQUERIZAS_Testis_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.09	1 / 13	Alternative lengthening of telomeres
2	0.18	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	7e−05	22 / 1241	KIM_MYC targets
2	1e−04	40 / 3150	ICGC_Creb1_targets
3	2e−04	43 / 3564	ICGC_Taf1_targets
4	4e−04	24 / 1578	ICGC_GabpPcr2_targets
5	6e−04	43 / 3769	ICGC_Pmlsc71910_targets
6	9e−04	18 / 1089	ICGC_Ets1_targets
7	2e−03	42 / 3796	ICGC_Nficsc81335_targets
8	2e−03	41 / 3703	ICGC_Foxm1_targets
9	2e−03	11 / 549	ICGC_Atf3_targets
10	2e−03	40 / 3630	ICGC_Sp1_targets
11	3e−03	41 / 3804	ICGC_Stat5_targets
12	4e−03	16 / 1044	ICGC_Six5_targets
13	4e−03	35 / 3121	ICGC_Egr1_targets
14	5e−03	37 / 3420	ICGC_Bclaf101388_targets
15	6e−03	42 / 4072	ICGC_Mta3_targets

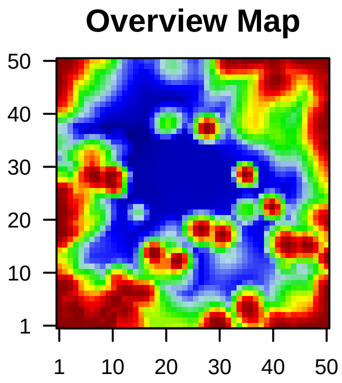
Overexpression Spots

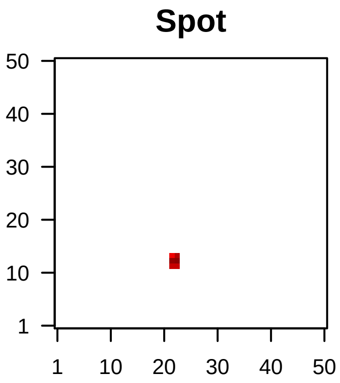
Spot Summary: C

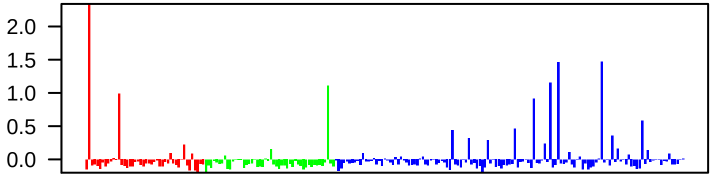
metagenes = 6
genes = 60

<r> metagenes = 0.99
<r> genes = 0.41
beta: r2= 2.26 / log p= −Inf

samples with spot = 15 (6.8 %)
mBL : 3 (6.8 %)
intermediate : 1 (2.1 %)
non−mBL : 11 (8.5 %)


Overview Map


Spot

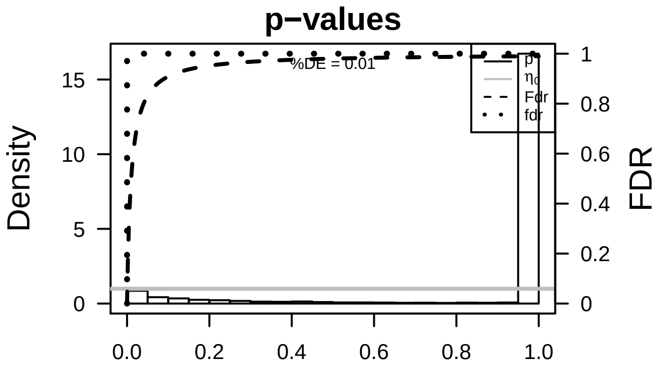


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209351_at	3.74	−0.88	0.84	KRT14	keratin 14 [Source:HGNC Symbol;Acc:HGNC:6416]
2	207935_s_at	3.59	−0.75	0.87	KRT13	keratin 13 [Source:HGNC Symbol;Acc:HGNC:6415]
3	209125_at	3.52	−0.85	0.86	KRT6A	keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
4	213796_at	3.5	−0.56	0.89	SPRR1A	small proline rich protein 1A [Source:HGNC Symbol;Acc:HGN
5	214580_x_at	3.41	−0.74	0.85	KRT6A	keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
6	213240_s_at	3.27	−0.54	0.77	KRT4	keratin 4 [Source:HGNC Symbol;Acc:HGNC:6441]
7	209126_x_at	3.19	−0.85	0.87	KRT6B	keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
8	218990_s_at	3.14	−0.5	0.84	SPRR3	small proline rich protein 3 [Source:HGNC Symbol;Acc:HGNC
9	205064_at	3.11	−0.84	0.85	SPRR1B	small proline rich protein 1B [Source:HGNC Symbol;Acc:HGN
10	204268_at	3.09	−0.94	0.87	S100A2	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
11	213680_at	2.96	−0.86	0.82	KRT6B	keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
12	208539_x_at	2.91	−0.65	0.77	SPRR2D	small proline rich protein 2D [Source:HGNC Symbol;Acc:HGN
13	205916_at	2.87	−0.49	0.65	S100A7A	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
14	205185_at	2.83	−0.74	0.78	SPINK5	serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
15	205157_s_at	2.82	−0.57	0.73	KRT17	keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
16	202504_at	2.8	−1.08	0.74	TRIM29	tripartite motif containing 29 [Source:HGNC Symbol;Acc:HGN
17	205595_at	2.76	−0.98	0.75	DSG3	desmoglein 3 [Source:HGNC Symbol;Acc:HGNC:3050]
18	202286_s_at	2.75	−0.69	0.81	TACSTD2	tumor associated calcium signal transducer 2 [Source:HGNC
19	219554_at	2.73	−0.66	0.75	RHCG	Rh family C glycoprotein [Source:HGNC Symbol;Acc:HGNC:
20	220090_at	2.72	−1.01	0.72	CRNN	cornulin [Source:HGNC Symbol;Acc:HGNC:1230]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−73	38 / 105	Refer	WIRTH_Mucosa
2	3e−46	33 / 248	GSEA	JAEGER_METASTASIS_DN
3	5e−39	34 / 453	GSEA	ONDER_CDH1_TARGETS_2_DN
4	3e−35	21 / 78	BP	cornification
5	8e−34	20 / 72	BP	keratinization
6	2e−26	15 / 46	GSEA	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
7	1e−21	12 / 35	CC	cornified envelope
8	2e−20	22 / 422	GSEA	DELYS_THYROID_CANCER_UP
9	2e−17	16 / 208	GSEA	RICKMAN_METASTASIS_DN
10	5e−16	12 / 93	GSEA	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
11	7e−16	10 / 46	BP	keratinocyte differentiation
12	7e−16	21 / 608	GSEA	SMID_BREAST_CANCER_BASAL_UP
13	2e−15	10 / 51	GSEA	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	6e−15	11 / 82	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
15	7e−15	10 / 57	GSEA	ONDER_CDH1_TARGETS_3_DN
16	1e−14	29 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
17	3e−14	13 / 169	MF	structural molecule activity
18	3e−14	8 / 26	GSEA	AIGNER_ZEB1_TARGETS
19	6e−14	8 / 28	BP	peptide cross−linking
20	8e−14	9 / 47	GSEA	CROMER_TUMORIGENESIS_DN
21	8e−14	20 / 677	Refer	PROTEINATLAS_esophagus
22	9e−14	15 / 294	GSEA	LEI_MYB_TARGETS
23	1e−13	10 / 74	BP	epidermis development
24	1e−13	18 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
25	2e−13	16 / 374	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
26	2e−13	11 / 113	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
27	1e−12	14 / 282	GSEA	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
28	4e−12	30 / 2239	CC	extracellular exosome
29	7e−12	9 / 76	CC	intermediate filament
30	2e−11	9 / 83	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
31	2e−11	21 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
32	3e−11	16 / 527	Refer	PROTEINATLAS_oral mucosa
33	4e−11	11 / 178	GSEA	WU_CELL_MIGRATION
34	4e−11	8 / 59	Melan	TCGA_melanoma_keratin_high
35	5e−11	10 / 134	GSEA	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
36	5e−11	8 / 61	GSEA	CHANG_IMMORTALIZED_BY_HPV31_DN
37	7e−11	17 / 648	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
38	9e−11	15 / 474	Refer	PROTEINATLAS_vagina
39	2e−10	6 / 23	CC	desmosome
40	3e−10	12 / 282	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	3e−35	21 / 78	cornification
2	8e−34	20 / 72	keratinization
3	7e−16	10 / 46	keratinocyte differentiation
4	6e−14	8 / 28	peptide cross−linking
5	1e−13	10 / 74	epidermis development
6	1e−06	7 / 146	cytoskeleton organization
7	2e−06	6 / 104	cell−cell adhesion
8	8e−06	3 / 11	hemidesmosome assembly
9	9e−06	4 / 36	skin development
10	1e−05	5 / 78	wound healing
11	2e−04	4 / 78	negative regulation of peptidase activity
12	7e−04	2 / 11	regulation of ventricular cardiac muscle cell action potential
13	1e−03	2 / 14	intermediate filament organization
14	2e−03	2 / 16	morphogenesis of an epithelium
15	2e−03	2 / 17	hair follicle morphogenesis

Cancer

Rank	p−value	#in/all	Geneset
1	7e−06	0 / 14	LIU_PROSTATE_CANCER_DN
2	3e−02	5 / 480	Lembcke_Colonic Inflammation
3	6e−02	4 / 409	Lembcke_Normal vs Adenoma
4	9e−02	2 / 134	PanCan_RAS_geneset_nanostring
5	2e−01	2 / 187	PanCan_PI3K_geneset_nanostring
6	2e−01	1 / 45	KUIPER_MM poor survival
7	3e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
8	4e−01	1 / 130	PanCan_CC+Apop_geneset_nanostring
9	4e−01	1 / 147	PanCan_MAPK_geneset_nanostring
10	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1e+00	0 / 12	LIU_BREAST_CANCER
15	1e+00	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	1e−21	12 / 35	cornified envelope
2	4e−12	30 / 2239	extracellular exosome
3	7e−12	9 / 76	intermediate filament
4	2e−10	6 / 23	desmosome
5	5e−10	6 / 27	keratin filament
6	3e−04	9 / 595	cell junction
7	5e−04	3 / 41	intermediate filament cytoskeleton
8	2e−03	14 / 1611	extracellular region
9	2e−03	3 / 73	cell−cell adherens junction
10	3e−03	21 / 3210	plasma membrane
11	7e−03	6 / 462	cell surface
12	1e−02	2 / 43	intercalated disc
13	1e−02	22 / 3805	cytosol
14	2e−02	2 / 56	specific granule lumen
15	4e−02	1 / 10	fascia adherens

Chr

Rank	p−value	#in/all	Geneset
1	0.008	11 / 1325	Chr 1
2	0.031	3 / 184	Chr 18
3	0.145	4 / 548	Chr 16
4	0.157	3 / 369	Chr 20
5	0.159	5 / 776	Chr 17
6	0.261	4 / 700	Chr 12
7	0.536	2 / 480	Chr 4
8	0.538	3 / 756	Chr 11
9	0.548	2 / 490	Chr 10
10	0.597	1 / 242	Chr 13
11	0.718	2 / 669	Chr 6
12	0.763	1 / 382	Chr 15
13	0.782	1 / 403	Chr 14
14	0.808	1 / 437	Chr 8
15	0.824	2 / 832	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−06	22 / 2148	10_ReprPC_Skeletal_Muscle
2	3e−06	21 / 1984	10_ReprPC_Melanocytes
3	3e−06	23 / 2375	10_ReprPC_Fibroblasts
4	7e−05	27 / 3734	Tcells peripheral blood_13_ReprPC
5	2e−04	19 / 2254	10_ReprPC_MSC_Adipocyte
6	6e−04	16 / 1813	8_EnhP_Fibroblasts
7	6e−04	19 / 2417	9_ReprPCWk_Melanocytes
8	6e−04	10 / 808	Mid_Frontal_Lobe_TssP
9	7e−04	21 / 2867	9_ReprPCWk_MSC_Adipocyte
10	1e−02	16 / 2408	9_ReprPCWk_Skeletal_Muscle
11	2e−02	4 / 258	Mid_Frontal_Lobe_TxTrans
12	2e−02	15 / 2405	Bcells peripheral blood_13_ReprPC
13	3e−02	11 / 1611	natural killer cells peripheral blood_11_BivFlnk
14	3e−02	16 / 2724	Tcells peripheral blood_11_BivFlnk
15	3e−02	11 / 1634	8_EnhP_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−08	12 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
2	1e−07	12 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
3	6e−07	11 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
4	3e−04	3 / 35	Ang_CRC_Hypomethylated
5	1e−02	5 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	2e−02	5 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
7	4e−02	1 / 10	Budinska_E_Mixed_UP
8	7e−02	3 / 255	Kosinski_top−crypt−long−list
9	9e−02	1 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
10	9e−02	1 / 25	Ang_CRC−CIMPH−vs−L_hypo
11	1e−01	1 / 43	Marisa_CRC−cluster−f
12	2e−01	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	2e−01	4 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
14	2e−01	5 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	3e−01	1 / 92	Marisa_CRC−cluster−h

Glioma

Rank	p−value	#in/all	Geneset
1	1e−14	29 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	3e−07	11 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	7e−06	8 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	3e−04	3 / 36	Christensen_hypomethylated_in_ependymoma
5	8e−04	3 / 50	Christensen_hypomethylated_in_primary_glioblastoma
6	2e−03	4 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	4e−03	3 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
8	4e−03	3 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
9	9e−03	3 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
10	1e−02	3 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
11	1e−02	1 / 4	Martinez_Glio_hypometh
12	2e−02	2 / 53	Christensen_hypermethylated_in_primary_glioblastoma
13	2e−02	2 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
14	4e−02	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
15	4e−02	2 / 82	laffaire_hypermeth_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−46	33 / 248	JAEGER_METASTASIS_DN
2	5e−39	34 / 453	ONDER_CDH1_TARGETS_2_DN
3	2e−26	15 / 46	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
4	2e−20	22 / 422	DELYS_THYROID_CANCER_UP
5	2e−17	16 / 208	RICKMAN_METASTASIS_DN
6	5e−16	12 / 93	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
7	7e−16	21 / 608	SMID_BREAST_CANCER_BASAL_UP
8	2e−15	10 / 51	HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	6e−15	11 / 82	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
10	7e−15	10 / 57	ONDER_CDH1_TARGETS_3_DN
11	3e−14	8 / 26	AIGNER_ZEB1_TARGETS
12	8e−14	9 / 47	CROMER_TUMORIGENESIS_DN
13	9e−14	15 / 294	LEI_MYB_TARGETS
14	1e−13	18 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
15	2e−13	16 / 374	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN

HM

Rank	p−value	#in/all	Geneset
1	5e−07	8 / 195	HALLMARK_KRAS_SIGNALING_DN
2	7e−06	7 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
3	7e−05	6 / 191	HALLMARK_P53_PATHWAY
4	6e−03	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	1e−01	1 / 34	HALLMARK_APICAL_SURFACE
6	1e−01	2 / 174	HALLMARK_APICAL_JUNCTION
7	1e−01	2 / 182	HALLMARK_GLYCOLYSIS
8	2e−01	2 / 194	HALLMARK_KRAS_SIGNALING_UP
9	3e−01	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	4e−01	1 / 130	HALLMARK_COAGULATION
11	4e−01	1 / 149	HALLMARK_UV_RESPONSE_UP
12	5e−01	1 / 170	HALLMARK_IL2_STAT5_SIGNALING
13	5e−01	1 / 178	HALLMARK_COMPLEMENT
14	5e−01	1 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	5e−01	1 / 194	HALLMARK_MYOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.002	2 / 19	Angelova_immune−metagene−iDC
2	0.102	1 / 29	Angelova_immune−metagene−Th1
3	0.132	1 / 38	Angelova_immune−metagene−mast−cells
4	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
6	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
7	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
8	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
9	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
10	1.000	0 / 25	Angelova_immune−metagene−DC
11	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
12	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
13	1.000	0 / 14	Angelova_immune−metagene−eosinophil
14	1.000	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.000	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−08	7 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
2	5e−07	7 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
3	7e−04	3 / 46	Subero_DLBCL_hypo_meth
4	1e−03	22 / 3168	HOPP_Repressed
5	7e−03	2 / 33	Subero_T−PLL_hypo_meth
6	5e−02	1 / 14	Subero_B−CLL_hypo_meth
7	5e−02	4 / 378	TARTE_Mature plasma cell signature
8	6e−02	13 / 2206	HOPP_Heterochrom
9	6e−02	3 / 237	ZHANG_DLBCL mutated
10	7e−02	1 / 19	Subero_MCL_hypo_meth
11	2e−01	1 / 45	Subero_INT_hypo_meth
12	2e−01	1 / 47	Subero_B−ALL_hyper_meth
13	2e−01	1 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
14	2e−01	1 / 56	Subero_mBL_hyper_meth
15	2e−01	1 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−11	8 / 59	TCGA_melanoma_keratin_high
2	2e−08	5 / 24	Gerami_melanoma−metastatic−risk_DN
3	6e−06	3 / 10	Joensson_Melanoma Normal like subtype
4	2e−03	3 / 64	Harbst_melanoma_lowgrade_up
5	1e−02	1 / 3	Gerami_melanoma−metastatic−risk_UP
6	4e−02	2 / 85	Tirosh_AXL−signature
7	1e−01	2 / 171	Landsberg_dedifferentiation_up
8	2e−01	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
9	6e−01	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
10	1e+00	0 / 17	Hugo_melanoma−all−MET_UP
11	1e+00	0 / 37	Hugo_melanoma−all−MET_DN
12	1e+00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	1e+00	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1e+00	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1e+00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	3e−14	13 / 169	structural molecule activity
2	2e−09	8 / 96	structural constituent of cytoskeleton
3	2e−05	3 / 15	transition metal ion binding
4	7e−05	4 / 61	serine−type endopeptidase inhibitor activity
5	1e−04	9 / 517	calcium ion binding
6	2e−04	4 / 77	peptidase inhibitor activity
7	7e−04	2 / 11	structural constituent of epidermis
8	9e−04	3 / 52	scaffold protein binding
9	2e−03	2 / 16	cadherin binding involved in cell−cell adhesion
10	2e−03	2 / 19	fibroblast growth factor binding
11	3e−03	3 / 74	protein binding, bridging
12	7e−03	2 / 33	endopeptidase inhibitor activity
13	7e−03	3 / 104	serine−type peptidase activity
14	2e−02	3 / 154	serine−type endopeptidase activity
15	2e−02	2 / 59	cell adhesion molecule binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	2 / 18	hsa−miR−591
2	0.092	1 / 26	hsa−miR−626
3	0.116	1 / 33	hsa−miR−483−5p
4	0.142	1 / 41	hsa−miR−504
5	0.145	1 / 42	hsa−miR−660
6	0.154	1 / 45	hsa−miR−891b
7	0.176	1 / 52	hsa−miR−1246
8	0.203	1 / 61	hsa−miR−1290
9	0.203	1 / 61	hsa−miR−939
10	0.203	1 / 61	hsa−miR−620
11	0.224	1 / 68	hsa−miR−505
12	0.230	1 / 70	hsa−miR−1303
13	0.255	1 / 79	hsa−miR−888
14	0.264	1 / 82	hsa−miR−516b
15	0.266	1 / 83	hsa−miR−513b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.001	3 / 57	Burnham_day1_vs_5_UP
2	0.002	3 / 71	Burnham_cap_fp_vs_con_UP
3	0.026	2 / 68	Burnham_sep_vs_con_UP
4	0.065	1 / 18	Scicluna_UP
5	0.089	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	1.000	0 / 56	Burnham_sep_vs_con_DN
7	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
8	1.000	0 / 48	Burnham_viral_DN
9	1.000	0 / 57	Burnham_viral_UP
10	1.000	0 / 52	Burnham_day1_vs_5_DN
11	1.000	0 / 54	Burnham_timecourse
12	1.000	0 / 41	Scicluna_DN
13	1.000	0 / 37	Sweeney_viral_up
14	1.000	0 / 33	Sweeney_viral_dn
15	1.000	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−73	38 / 105	WIRTH_Mucosa
2	8e−14	20 / 677	PROTEINATLAS_esophagus
3	3e−11	16 / 527	PROTEINATLAS_oral mucosa
4	9e−11	15 / 474	PROTEINATLAS_vagina
5	1e−09	16 / 671	PROTEINATLAS_cervix, uterine
6	9e−09	16 / 776	PROTEINATLAS_skin
7	8e−08	4 / 12	WIRTH_Tonsil
8	9e−06	14 / 989	PROTEINATLAS_tonsil
9	3e−04	3 / 37	Chaussabel_2,2_Neutrophils
10	1e−03	2 / 13	WIRTH_Prim. lymphoid organs
11	4e−02	3 / 209	Chaussabel_2,5_Immune related molecules
12	5e−02	1 / 15	WIRTH_Cerebellum
13	6e−02	1 / 18	JONGENEEL_Monocytes
14	1e−01	1 / 30	JONGENEEL_Bone Marrow
15	2e−01	4 / 595	PROTEINATLAS_breast

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	0.009	10 / 1148	HEBENSTREIT_low expression TF
2	0.557	14 / 3778	ICGC_Pol24_targets
3	0.630	15 / 4212	ICGC_Pol2_targets
4	0.650	8 / 2321	ICGC_Rad21_targets
5	0.759	14 / 4264	ICGC_Pax5_targets
6	0.841	1 / 485	ICGC_NrsfPcr2_targets
7	0.876	1 / 549	ICGC_Atf3_targets
8	0.884	12 / 4131	ICGC_Tcf3_targets
9	0.903	2 / 1025	ICGC_NrsfPcr1_targets
10	0.920	12 / 4319	ICGC_Pou2_targets
11	0.962	8 / 3435	ICGC_Ebfsc137065_targets
12	0.977	4 / 2254	ICGC_BatfPcr1_targets
13	0.981	2 / 1508	ICGC_Mef2_targets
14	0.982	1 / 1032	ICGC_Usf1_targets
15	0.982	1 / 1041	ICGC_P300_targets

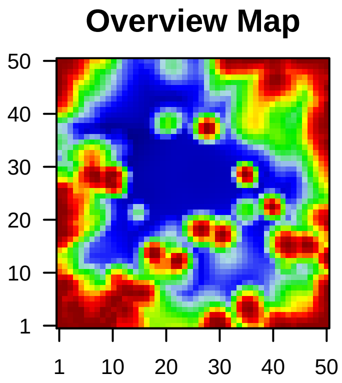
Overexpression Spots

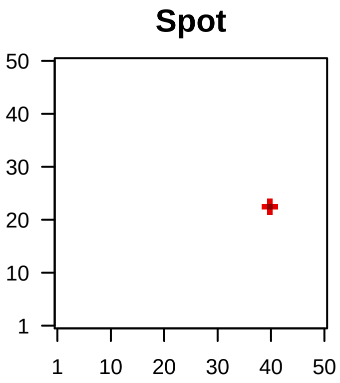
Spot Summary: D

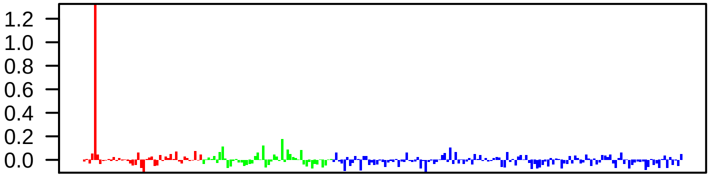
metagenes = 5
genes = 69

<r> metagenes = 0.97
<r> genes = 0.13
beta: r2= 0.2 / log p= −11.38

samples with spot = 1 (0.5 %)
mBL : 1 (2.3 %)


Overview Map


Spot

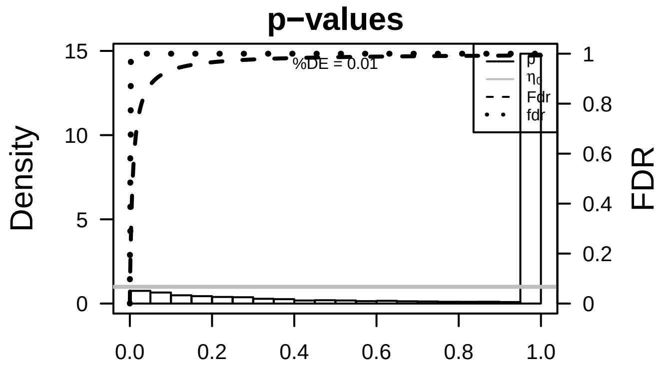


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	210487_at	2.85	−0.57	0.66	DNTT	DNA nucleotidylexotransferase [Source:HGNC Symbol;Acc:H
2	220389_at	2.51	−0.53	0.64	CCDC81	coiled−coil domain containing 81 [Source:HGNC Symbol;Acc
3	216840_s_at	2.51	−0.6	0.54	LAMA2	laminin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:6
4	219564_at	2.44	−0.48	0.44	KCNJ16	potassium voltage−gated channel subfamily J member 16 [Sc
5	213519_s_at	2.31	−1.09	0.45	LAMA2	laminin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:6
6	206674_at	2.26	−0.64	0.46	FLT3	fms related tyrosine kinase 3 [Source:HGNC Symbol;Acc:HG
7	203354_s_at	2.26	−0.57	0.61	PSD3	pleckstrin and Sec7 domain containing 3 [Source:HGNC Sym
8	206771_at	2.25	−0.74	0.34	UPK3A	uroplakin 3A [Source:HGNC Symbol;Acc:HGNC:12580]
9	203726_s_at	2.24	−0.76	0.51	LAMA3	laminin subunit alpha 3 [Source:HGNC Symbol;Acc:HGNC:6
10	206591_at	2.18	−0.65	0.54	RAG1	recombination activating 1 [Source:HGNC Symbol;Acc:HGNC
11	212113_at	2.1	−0.88	0.3	ATXN7L3B	ataxin 7 like 3B [Source:HGNC Symbol;Acc:HGNC:37931]
12	214539_at	2.07	−0.69	0.31	SERPINB10	serpin family B member 10 [Source:HGNC Symbol;Acc:HGN
13	210473_s_at	2.05	−0.69	0.4	ADGRA3	adhesion G protein−coupled receptor A3 [Source:HGNC Sym
14	214761_at	2.04	−0.75	0.49	ZNF423	zinc finger protein 423 [Source:HGNC Symbol;Acc:HGNC:16
15	211341_at	2.01	−0.78	0.34	POU4F1	POU class 4 homeobox 1 [Source:HGNC Symbol;Acc:HGNC
16	217056_at	1.98	−0.73	0.45		T cell receptor alpha variable 36/delta variable 7 [Source:HGN
17	213880_at	1.92	−0.59	0.53	LGR5	leucine rich repeat containing G protein−coupled receptor 5 [
18	209195_s_at	1.9	−0.91	0.42	ADCY6	adenylate cyclase 6 [Source:HGNC Symbol;Acc:HGNC:237]
19	206067_s_at	1.89	−0.57	0.48	WT1	Wilms tumor 1 [Source:HGNC Symbol;Acc:HGNC:12796]
20	206089_at	1.87	−0.45	0.5	NELL1	neural EGFL like 1 [Source:HGNC Symbol;Acc:HGNC:7750]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−08	11 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
2	2e−06	50 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
3	8e−06	32 / 3168	Lymph	HOPP_Repressed
4	6e−05	22 / 1894	Lymph	HOPP_Poised_promoter
5	7e−05	7 / 209	GSEA	BROWNE_HCMV_INFECTION_1HR_DN
6	1e−04	4 / 49	BP	cellular response to cytokine stimulus
7	1e−04	3 / 19	Refer	JONGENEEL_Thymus
8	3e−04	4 / 65	GSEA	MORI_MATURE_B_LYMPHOCYTE_DN
9	4e−04	3 / 29	BP	positive regulation of bone mineralization
10	6e−04	3 / 33	miRN	hsa−miR−588
11	6e−04	4 / 78	GSEA	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF
12	6e−04	4 / 80	GSEA	PID_CMYB_PATHWAY
13	7e−04	4 / 83	GSEA	SMID_BREAST_CANCER_LUMINAL_A_UP
14	8e−04	5 / 148	MF	ubiquitin protein ligase activity
15	8e−04	2 / 9	GSEA	REACTOME_PROSTANOID_LIGAND_RECEPTORS
16	9e−04	6 / 227	BP	regulation of molecular function
17	1e−03	6 / 234	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_DN
18	1e−03	2 / 10	CC	intrinsic component of the cytoplasmic side of the plasma membrane
19	1e−03	2 / 10	GSEA	PID_INTEGRIN4_PATHWAY
20	1e−03	2 / 10	GSEA	SHANK_TAL1_TARGETS_DN
21	1e−03	3 / 41	GSEA	PID_A6B1_A6B4_INTEGRIN_PATHWAY
22	1e−03	5 / 168	BP	regulation of gene expression
23	2e−03	2 / 12	BP	regulation of embryonic development
24	2e−03	2 / 12	Cance	BENTINK_e2f3.2
25	2e−03	2 / 13	BP	dentate gyrus development
26	2e−03	2 / 13	BP	negative regulation of cell migration involved in sprouting angiogenesis
27	2e−03	2 / 13	GSEA	REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS
28	2e−03	10 / 697	GSEA	BENPORATH_SUZ12_TARGETS
29	2e−03	2 / 14	MF	C2H2 zinc finger domain binding
30	2e−03	15 / 1361	BP	signal transduction
31	2e−03	1 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
32	2e−03	1 / 16	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
33	2e−03	2 / 15	BP	sympathetic nervous system development
34	2e−03	7 / 376	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
35	2e−03	9 / 595	BP	G−protein coupled receptor signaling pathway
36	3e−03	6 / 283	GSEA	CHYLA_CBFA2T3_TARGETS_UP
37	3e−03	4 / 121	GSEA	RODWELL_AGING_KIDNEY_DN
38	3e−03	2 / 17	BP	cellular response to prostaglandin E stimulus
39	3e−03	2 / 17	BP	regulation of long−term neuronal synaptic plasticity
40	3e−03	7 / 394	GSEA	YAGI_AML_WITH_INV_16_TRANSLOCATION


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 107	HORVATH_aging_genes meth UP
2	1.0	0 / 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	0.001	2 / 10	intrinsic component of the cytoplasmic side of the plasma membrane
2	0.005	2 / 22	ciliary base
3	0.010	3 / 90	nuclear matrix
4	0.011	8 / 623	cell projection
5	0.011	6 / 382	synapse
6	0.016	32 / 4701	cytoplasm
7	0.025	2 / 50	extrinsic component of membrane
8	0.030	23 / 3210	plasma membrane
9	0.041	2 / 65	voltage−gated potassium channel complex
10	0.042	2 / 66	basement membrane
11	0.053	1 / 11	Cul4A−RING E3 ubiquitin ligase complex
12	0.054	3 / 174	postsynaptic membrane
13	0.059	33 / 5339	membrane
14	0.067	1 / 14	basal lamina
15	0.067	1 / 14	cyclin−dependent protein kinase holoenzyme complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	50 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	2e−03	7 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
3	5e−03	6 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
4	3e−02	8 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
5	3e−02	5 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
6	5e−02	6 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
7	5e−02	2 / 72	Ang_CRC−CIMPH−vs−L_hyper
8	6e−02	2 / 77	Ang_CRC_Hypermethylated
9	6e−02	8 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
10	6e−02	1 / 12	Juehling_HNPCC−mutated−in−4
11	9e−02	1 / 20	Kosinski_top−crypt−short−list
12	1e−01	8 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
13	3e−01	6 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	3e−01	2 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
15	4e−01	6 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_

HM

Rank	p−value	#in/all	Geneset
1	0.01	2 / 35	HALLMARK_HEDGEHOG_SIGNALING
2	0.08	2 / 96	HALLMARK_ANDROGEN_RESPONSE
3	0.17	2 / 150	HALLMARK_APOPTOSIS
4	0.17	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.21	2 / 173	HALLMARK_MITOTIC_SPINDLE
6	0.21	2 / 174	HALLMARK_APICAL_JUNCTION
7	0.22	1 / 51	HALLMARK_TGF_BETA_SIGNALING
8	0.24	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	0.24	2 / 191	HALLMARK_P53_PATHWAY
10	0.25	2 / 193	HALLMARK_HEME_METABOLISM
11	0.25	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.25	2 / 194	HALLMARK_MYOGENESIS
13	0.25	2 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.34	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	0.41	1 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−06	32 / 3168	HOPP_Repressed
2	6e−05	22 / 1894	HOPP_Poised_promoter
3	2e−02	3 / 118	Subero_INT_hyper_meth
4	3e−02	3 / 132	Subero_DLBCL_hyper_meth
5	4e−02	2 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
6	5e−02	1 / 10	MASCQUE_ABC UP
7	6e−02	1 / 13	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
8	9e−02	2 / 99	Sha_BL UP
9	1e−01	3 / 237	ZHANG_DLBCL mutated
10	1e−01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
11	1e−01	1 / 26	DAVE_Immune response 1
12	2e−01	1 / 35	Subero_MM_hyper_meth
13	2e−01	12 / 1814	HOPP_Repetitive
14	2e−01	1 / 41	ROSOLOWSKI_blue DOWN
15	2e−01	1 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 33	hsa−miR−588
2	1e−02	3 / 90	hsa−miR−22
3	1e−02	2 / 31	hsa−miR−661
4	2e−02	5 / 320	hsa−miR−519a
5	3e−02	2 / 52	hsa−miR−1278
6	3e−02	3 / 136	hsa−miR−511
7	3e−02	2 / 59	hsa−miR−643
8	4e−02	1 / 8	hsa−miR−639
9	4e−02	2 / 65	hsa−miR−557
10	4e−02	3 / 159	hsa−miR−568
11	5e−02	2 / 75	hsa−miR−10b
12	6e−02	2 / 78	hsa−miR−133b
13	6e−02	2 / 79	hsa−miR−133a
14	6e−02	5 / 435	hsa−miR−93
15	6e−02	3 / 185	hsa−miR−182

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 49	cellular response to cytokine stimulus
2	4e−04	3 / 29	positive regulation of bone mineralization
3	9e−04	6 / 227	regulation of molecular function
4	1e−03	5 / 168	regulation of gene expression
5	2e−03	2 / 12	regulation of embryonic development
6	2e−03	2 / 13	dentate gyrus development
7	2e−03	2 / 13	negative regulation of cell migration involved in sprouting angiogenesis
8	2e−03	15 / 1361	signal transduction
9	2e−03	2 / 15	sympathetic nervous system development
10	2e−03	9 / 595	G−protein coupled receptor signaling pathway
11	3e−03	2 / 17	cellular response to prostaglandin E stimulus
12	3e−03	2 / 17	regulation of long−term neuronal synaptic plasticity
13	4e−03	3 / 64	B cell differentiation
14	4e−03	2 / 19	adrenal gland development
15	5e−03	2 / 21	peripheral nervous system development

Chr

Rank	p−value	#in/all	Geneset
1	0.03	4 / 242	Chr 13
2	0.03	8 / 756	Chr 11
3	0.03	6 / 490	Chr 10
4	0.21	4 / 480	Chr 4
5	0.23	2 / 184	Chr 18
6	0.29	3 / 382	Chr 15
7	0.32	3 / 403	Chr 14
8	0.33	5 / 776	Chr 17
9	0.42	4 / 669	Chr 6
10	0.45	4 / 700	Chr 12
11	0.49	2 / 333	Chr 22
12	0.52	3 / 554	Chr 5
13	0.55	2 / 369	Chr 20
14	0.64	2 / 437	Chr 8
15	0.65	6 / 1325	Chr 1

Glioma

Rank	p−value	#in/all	Geneset
1	0.008	11 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
2	0.010	5 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
3	0.023	2 / 48	in vivo astrocytes vs. cultured astroglia
4	0.031	4 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	0.037	2 / 62	GIEZELT_GBM_STS_down_VS_LTS
6	0.062	11 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	0.068	3 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
8	0.071	1 / 15	Gorovets_LGG_NB_subclass
9	0.076	1 / 16	VERHAAK_CL subtype
10	0.099	1 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)
11	0.099	1 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN
12	0.103	1 / 22	Martinez_Glio_hypermeth
13	0.103	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	0.120	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
15	0.124	11 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN

Immunome

Rank	p−value	#in/all	Geneset
1	0.3	1 / 67	Angelova_immune−metagene−T−cells
2	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
3	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
4	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.0	0 / 25	Angelova_immune−metagene−DC
9	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.0	0 / 14	Angelova_immune−metagene−eosinophil
12	1.0	0 / 19	Angelova_immune−metagene−iDC
13	1.0	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.0	0 / 11	Angelova_immune−metagene−macrophages
15	1.0	0 / 38	Angelova_immune−metagene−mast−cells

Melanoma

Rank	p−value	#in/all	Geneset
1	0.008	5 / 249	Gerber_wt/wt_melanoma−cells−SpotE
2	0.167	1 / 37	Hugo_melanoma−all−MET_DN
3	0.223	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
4	0.229	4 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	0.253	1 / 59	TCGA_melanoma_keratin_high
6	0.271	1 / 64	Harbst_melanoma_lowgrade_up
7	0.313	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
8	0.320	1 / 78	Tirosh_expression higher in CAFs than in T−cells
9	0.446	1 / 119	TCGA_melanoma_MITF_low
10	0.638	1 / 204	Landsberg_dedifferentiation_down
11	0.691	1 / 236	Gerber_wt/wt_group3−specific
12	1.000	0 / 17	Hugo_melanoma−all−MET_UP
13	1.000	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
14	1.000	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
15	1.000	0 / 16	Hugo_melanoma−all−LEF1_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	1 / 41	Scicluna_DN
2	0.2	1 / 56	Burnham_sep_vs_con_DN
3	0.2	1 / 57	Burnham_viral_UP
4	0.2	1 / 57	Burnham_day1_vs_5_UP
5	0.5	1 / 122	Terre_IMS_influenza_meta_signature
6	0.6	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	1.0	0 / 68	Burnham_sep_vs_con_UP
8	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.0	0 / 48	Burnham_viral_DN
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 54	Burnham_timecourse
13	1.0	0 / 18	Scicluna_UP
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

TF

Rank	p−value	#in/all	Geneset
1	0.1	9 / 1148	HEBENSTREIT_low expression TF
2	0.4	9 / 1636	ICGC_Bcl11_targets
3	0.5	8 / 1508	ICGC_Mef2_targets
4	0.5	10 / 1941	ICGC_Bcl3_targets
5	0.6	5 / 1041	ICGC_P300_targets
6	0.6	2 / 415	ICGC_RxraPcr1_targets
7	0.7	2 / 485	ICGC_NrsfPcr2_targets
8	0.7	2 / 522	ICGC_SrfPcr2_targets
9	0.7	14 / 3213	ICGC_Pu1_targets
10	0.8	9 / 2254	ICGC_BatfPcr1_targets
11	0.8	7 / 1848	ICGC_Pbx3_targets
12	0.8	5 / 1387	HEBENSTREIT_high expression TF
13	0.9	3 / 1025	ICGC_NrsfPcr1_targets
14	0.9	3 / 1032	ICGC_Usf1_targets
15	0.9	13 / 3435	ICGC_Ebfsc137065_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	BENTINK_e2f3.2
2	0.002	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.018	3 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.065	3 / 187	PanCan_PI3K_geneset_nanostring
5	0.081	2 / 96	PanCan_TXmisReg_geneset_nanostring
6	0.116	1 / 25	PanCan_HH_geneset_nanostring
7	0.207	1 / 47	PanCan_TGF−B_geneset_nanostring
8	0.249	1 / 58	SHAUGHNESSY_MM high risk
9	0.300	1 / 72	PanCan_Wnt_geneset_nanostring
10	0.475	1 / 130	PanCan_CC+Apop_geneset_nanostring
11	0.486	1 / 134	PanCan_RAS_geneset_nanostring
12	0.518	1 / 147	PanCan_MAPK_geneset_nanostring
13	0.603	2 / 409	Lembcke_Normal vs Adenoma
14	0.603	1 / 186	SPANG_LPS−index2
15	0.795	1 / 317	SPANG_BCL6−index2

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−08	41 / 3825	Bcells peripheral blood_15_Quies
2	5e−08	35 / 3001	Bcells peripheral blood_14_ReprPCWk
3	6e−08	42 / 4214	monocytes peripheral blood_15_Quies
4	1e−07	40 / 3918	Tcells peripheral blood_14_ReprPCWk
5	2e−07	39 / 3819	natural killer cells peripheral blood_15_Quies
6	1e−06	31 / 2747	Bcells peripheral blood_12_EnhBiv
7	1e−06	37 / 3755	HSC_15_Quies
8	2e−06	32 / 2984	natural killer cells peripheral blood_14_ReprPCWk
9	3e−06	28 / 2405	Bcells peripheral blood_13_ReprPC
10	7e−06	28 / 2515	natural killer cells peripheral blood_13_ReprPC
11	8e−06	31 / 2993	monocytes peripheral blood_9_Het
12	1e−05	34 / 3540	Tregulatory cells peripheral blood_15_Quies
13	1e−05	35 / 3734	Tcells peripheral blood_13_ReprPC
14	2e−05	21 / 1611	natural killer cells peripheral blood_11_BivFlnk
15	2e−05	34 / 3616	Thelper cells peripheral blood_15_Quies

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−08	11 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
2	7e−05	7 / 209	BROWNE_HCMV_INFECTION_1HR_DN
3	3e−04	4 / 65	MORI_MATURE_B_LYMPHOCYTE_DN
4	6e−04	4 / 78	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF
5	6e−04	4 / 80	PID_CMYB_PATHWAY
6	7e−04	4 / 83	SMID_BREAST_CANCER_LUMINAL_A_UP
7	8e−04	2 / 9	REACTOME_PROSTANOID_LIGAND_RECEPTORS
8	1e−03	6 / 234	VERHAAK_AML_WITH_NPM1_MUTATED_DN
9	1e−03	2 / 10	PID_INTEGRIN4_PATHWAY
10	1e−03	2 / 10	SHANK_TAL1_TARGETS_DN
11	1e−03	3 / 41	PID_A6B1_A6B4_INTEGRIN_PATHWAY
12	2e−03	2 / 13	REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS
13	2e−03	10 / 697	BENPORATH_SUZ12_TARGETS
14	2e−03	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	3e−03	6 / 283	CHYLA_CBFA2T3_TARGETS_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	3 / 210	Homuth_BMI−associated−genes_DN
2	0.15	1 / 32	Marjolein_ageing−genes_DN
3	0.26	1 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 22	DUMEAUX_High bmi enriched genes
13	1.00	0 / 22	DUMEAUX_Fasting enriched genes
14	1.00	0 / 150	Homuth_BMI−associated−genes_UP
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	8e−04	5 / 148	ubiquitin protein ligase activity
2	2e−03	2 / 14	C2H2 zinc finger domain binding
3	7e−03	6 / 346	receptor binding
4	1e−02	3 / 105	Ras guanyl−nucleotide exchange factor activity
5	2e−02	4 / 202	GTPase activator activity
6	2e−02	5 / 337	G−protein coupled receptor activity
7	3e−02	3 / 130	guanyl−nucleotide exchange factor activity
8	3e−02	4 / 234	transcriptional activator activity, RNA polymerase II proximal promoter seque
9	4e−02	13 / 1541	DNA binding
10	4e−02	6 / 500	signal transducer activity
11	4e−02	2 / 62	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
12	5e−02	3 / 163	magnesium ion binding
13	5e−02	1 / 10	armadillo repeat domain binding
14	5e−02	1 / 10	gamma−catenin binding
15	5e−02	3 / 169	structural molecule activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 19	JONGENEEL_Thymus
2	2e−02	2 / 40	VAQUERIZAS_Testis_TF
3	2e−02	2 / 41	VAQUERIZAS_Thymus_TF
4	2e−02	2 / 49	VAQUERIZAS_Uterus_TF
5	6e−02	1 / 12	WIRTH_Cortex cerebri
6	7e−02	1 / 14	WIRTH_Thalamus
7	8e−02	1 / 16	VAQUERIZAS_Ovary_TF
8	9e−02	2 / 100	Chaussabel_2,8_T−cells
9	9e−02	1 / 20	VAQUERIZAS_Bone marrow_TF
10	1e−01	1 / 21	VAQUERIZAS_Tonsil_TF
11	1e−01	1 / 24	VAQUERIZAS_Spinal cord_TF
12	1e−01	1 / 25	VAQUERIZAS_Adrenal cortex_TF
13	1e−01	1 / 30	VAQUERIZAS_Lymph node_TF
14	2e−01	1 / 36	VAQUERIZAS_Prostate_TF
15	2e−01	2 / 152	VAQUERIZAS_General_TF

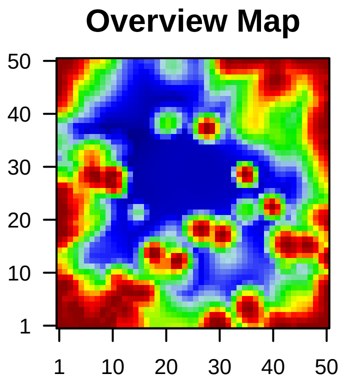
Overexpression Spots

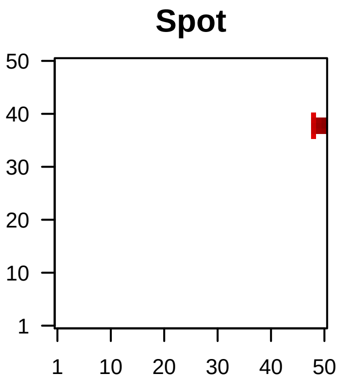
Spot Summary: E

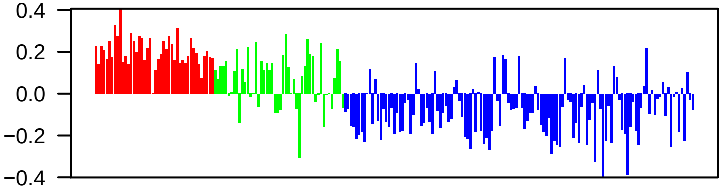
metagenes = 11
genes = 131

<r> metagenes = 0.96
<r> genes = 0.25
beta: r2= 5.45 / log p= −Inf

samples with spot = 28 (12.7 %)
mBL : 20 (45.5 %)
intermediate : 7 (14.6 %)
non−mBL : 1 (0.8 %)


Overview Map


Spot

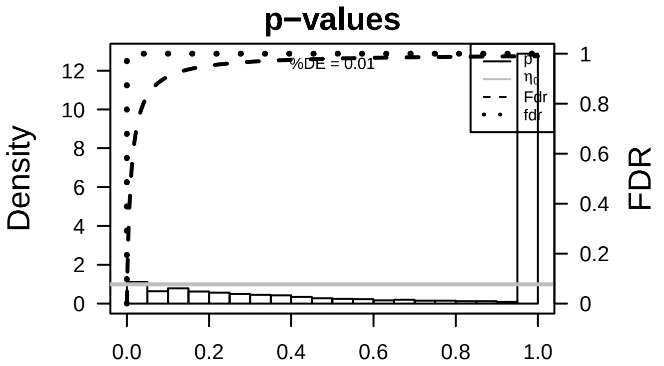


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	211998_at	1.94	−0.89	0.31	H3F3B	H3 histone family member 3B [Source:HGNC Symbol;Acc:HG
2	213436_at	1.92	−1.49	0.45	CNR1	cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21
3	207216_at	1.5	−1.24	0.51	TNFSF8	TNF superfamily member 8 [Source:HGNC Symbol;Acc:HGN
4	205901_at	1.48	−1.42	0.35	PNOC	prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
5	210957_s_at	1.45	−1.17	0.56	AFF2	AF4/FMR2 family member 2 [Source:HGNC Symbol;Acc:HGN
6	205505_at	1.41	−0.91	0.46	GCNT1	glucosaminyl (N−acetyl) transferase 1, core 2 [Source:HGNC
7	213547_at	1.35	−0.78	0.32	CAND2	cullin associated and neddylation dissociated 2 (putative) [So
8	212856_at	1.34	−1.11	0.34	GRAMD4	GRAM domain containing 4 [Source:HGNC Symbol;Acc:HGN
9	218434_s_at	1.28	−1.36	0.39	AACS	acetoacetyl−CoA synthetase [Source:HGNC Symbol;Acc:HG
10	214820_at	1.23	−1.19	0.74	BRWD1	bromodomain and WD repeat domain containing 1 [Source:H
11	204208_at	1.21	−1.1	0.66	RNGTT	RNA guanylyltransferase and 5'−phosphatase [Source:HGNC
12	212068_s_at	1.21	−1.69	0.33	PRRC2B	proline rich coiled−coil 2B [Source:HGNC Symbol;Acc:HGNC
13	220054_at	1.17	−1.18	0.39	IL23A	interleukin 23 subunit alpha [Source:HGNC Symbol;Acc:HGN
14	205306_x_at	1.17	−1.56	0.34	KMO	kynurenine 3−monooxygenase [Source:HGNC Symbol;Acc:H
15	209627_s_at	1.15	−1.47	0.48	OSBPL3	oxysterol binding protein like 3 [Source:HGNC Symbol;Acc:H
16	211138_s_at	1.14	−1.53	0.36	KMO	kynurenine 3−monooxygenase [Source:HGNC Symbol;Acc:H
17	219582_at	1.13	−1.03	0.23	OGFRL1	opioid growth factor receptor like 1 [Source:HGNC Symbol;Ac
18	217513_at	1.12	−0.9	0.4	MILR1	mast cell immunoglobulin like receptor 1 [Source:HGNC Sym
19	209712_at	1.12	−1.02	0.53	SLC35D1	solute carrier family 35 member D1 [Source:HGNC Symbol;A
20	213450_s_at	1.09	−1.3	0.41	LOC102723996	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−13	87 / 5908	Lympl	HOPP_Active_promoter
2	4e−11	70 / 4357	Lympl	HOPP_Weak_txn
3	6e−11	81 / 5682	Lympl	HOPP_Weak_promoter
4	2e−10	79 / 5529	Lympl	HOPP_Txn_elongation
5	6e−10	77 / 5404	Lympl	HOPP_Strong_enhancer
6	8e−09	15 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
7	1e−08	67 / 4559	Lympl	HOPP_Weak_enhancer
8	2e−08	7 / 37	GSEA	ZHAN_MULTIPLE_MYELOMA_CD2_UP
9	4e−08	14 / 263	Lympl	SPANG_CD40 6hrs UP
10	3e−06	19 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
11	5e−06	22 / 906	Lympl	SPANG_BCR DN
12	1e−05	12 / 310	Refer	Chaussabel_3,4_Protein phosphatases
13	1e−05	6 / 61	GSEA	BASSO_CD40_SIGNALING_DN
14	1e−05	10 / 216	miRN	hsa−miR−548l
15	2e−05	14 / 442	GSEA	KIM_WT1_TARGETS_DN
16	3e−05	26 / 1329	MF	transferase activity
17	4e−05	28 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
18	5e−05	19 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
19	6e−05	9 / 207	miRN	hsa−miR−92b
20	7e−05	9 / 213	miRN	hsa−miR−363
21	8e−05	10 / 268	miRN	hsa−miR−367
22	8e−05	9 / 217	miRN	hsa−miR−92a
23	9e−05	25 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
24	1e−04	5 / 56	miRN	hsa−miR−618
25	1e−04	6 / 92	miRN	hsa−miR−491−3p
26	1e−04	5 / 59	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
27	1e−04	6 / 96	HM	HALLMARK_ANDROGEN_RESPONSE
28	2e−04	9 / 235	miRN	hsa−miR−25
29	2e−04	12 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
30	2e−04	8 / 192	Lympl	Victora_Dark zone signature
31	2e−04	11 / 361	GSEA	GARY_CD5_TARGETS_DN
32	3e−04	11 / 369	miRN	hsa−miR−130a
33	3e−04	10 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
34	3e−04	12 / 437	Chr	Chr 8
35	3e−04	3 / 16	BP	negative regulation of T cell receptor signaling pathway
36	3e−04	19 / 955	Lympl	SPANG_BCR UP
37	3e−04	9 / 262	miRN	hsa−miR−32
38	4e−04	10 / 322	GSEA	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP
39	4e−04	53 / 4261	Lympl	HOPP_Txn_transition
40	4e−04	15 / 669	Chr	Chr 6


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 107	HORVATH_aging_genes meth UP
2	1.0	0 / 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	3e−04	3 / 16	negative regulation of T cell receptor signaling pathway
2	2e−03	5 / 104	response to ethanol
3	2e−03	3 / 30	response to organonitrogen compound
4	2e−03	4 / 67	positive regulation of cell growth
5	4e−03	4 / 78	nucleosome assembly
6	5e−03	2 / 13	NAD metabolic process
7	5e−03	2 / 13	response to reactive oxygen species
8	5e−03	2 / 13	stress fiber assembly
9	6e−03	2 / 14	activation of MAPKKK activity
10	6e−03	2 / 14	long term synaptic depression
11	6e−03	2 / 14	regulation of establishment of cell polarity
12	6e−03	4 / 88	osteoblast differentiation
13	8e−03	2 / 16	protein ADP−ribosylation
14	8e−03	3 / 49	cellular response to starvation
15	9e−03	2 / 17	tRNA methylation

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	2 / 11	LIU_PROSTATE_CANCER_UP
2	0.049	1 / 6	ZHANG_MGUS up
3	0.080	1 / 10	GENTLES_modul3
4	0.088	1 / 11	GENTLES_modul14
5	0.111	1 / 14	GUSTAFSON_PI3K_DN
6	0.111	1 / 14	BENTINK_ras.6
7	0.111	1 / 14	BENTINK_src.2
8	0.121	2 / 72	PanCan_Wnt_geneset_nanostring
9	0.125	1 / 16	GENTLES_modul6
10	0.125	1 / 16	GENTLES_modul16
11	0.211	6 / 480	Lembcke_Colonic Inflammation
12	0.235	1 / 32	KUIPER_MM good survival
13	0.291	1 / 41	PanCan_DNARepair_geneset_nanostring
14	0.295	2 / 130	PanCan_CC+Apop_geneset_nanostring
15	0.326	1 / 47	PanCan_TGF−B_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.01	2 / 19	synaptonemal complex
2	0.02	42 / 3805	cytosol
3	0.03	2 / 30	aggresome
4	0.03	2 / 34	condensed nuclear chromosome
5	0.04	9 / 537	perinuclear region of cytoplasm
6	0.04	2 / 39	cell leading edge
7	0.05	6 / 310	dendrite
8	0.05	4 / 163	transcription factor complex
9	0.05	3 / 101	growth cone
10	0.05	2 / 45	chromosome, telomeric region
11	0.06	3 / 104	trans−Golgi network
12	0.06	7 / 416	macromolecular complex
13	0.06	2 / 48	microvillus
14	0.07	3 / 117	cell cortex
15	0.08	4 / 192	membrane raft

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	12 / 437	Chr 8
2	4e−04	15 / 669	Chr 6
3	2e−02	9 / 480	Chr 4
4	2e−02	9 / 490	Chr 10
5	1e−01	3 / 139	Chr 21
6	2e−01	10 / 832	Chr 2
7	2e−01	8 / 700	Chr 12
8	3e−01	6 / 554	Chr 5
9	6e−01	4 / 492	Chr 9
10	6e−01	2 / 242	Chr 13
11	7e−01	10 / 1325	Chr 1
12	8e−01	2 / 333	Chr 22
13	8e−01	1 / 184	Chr 18
14	9e−01	3 / 585	Chr 7
15	9e−01	4 / 776	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−17	91 / 5716	Bcells peripheral blood_4_Tx
2	5e−15	88 / 5753	Tcells peripheral blood_4_Tx
3	4e−14	93 / 6637	Tcells peripheral blood_5_TxWk
4	7e−14	90 / 6244	15_Quies_Fibroblasts
5	8e−14	85 / 5601	Thelper cells peripheral blood_4_Tx
6	1e−13	86 / 5766	natural killer cells peripheral blood_4_Tx
7	1e−12	94 / 7078	Bcells peripheral blood_5_TxWk
8	1e−12	67 / 3767	Bcells peripheral blood_6_EnhG
9	2e−12	96 / 7420	Tcells peripheral blood_1_TssA
10	2e−12	97 / 7581	15_Quies_Melanocytes
11	2e−12	84 / 5738	monocytes peripheral blood_4_Tx
12	2e−12	98 / 7751	natural killer cells peripheral blood_1_TssA
13	2e−12	92 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
14	3e−12	41 / 1535	Bcells peripheral blood_8_ZNF_Rpts
15	3e−12	90 / 6582	Quies3_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.004	15 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
2	0.015	14 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
3	0.020	6 / 255	Kosinski_top−crypt−long−list
4	0.033	9 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
5	0.034	6 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
6	0.047	21 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
7	0.048	7 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	0.055	13 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
9	0.056	17 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	0.063	2 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
11	0.073	1 / 9	Marisa_CRC−C2
12	0.073	13 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
13	0.111	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
14	0.116	7 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
15	0.190	12 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv

Glioma

Rank	p−value	#in/all	Geneset
1	4e−05	28 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	9e−05	25 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	9e−03	3 / 52	GIEZELT_GBM_WT_down_VS_mut
4	5e−02	1 / 6	Shaw_responders_up_in_oligo_glioma
5	6e−02	1 / 7	oligodendrocytes_glio
6	6e−02	6 / 330	Up
7	6e−02	1 / 8	Shaw_up_in_1p19qdel
8	7e−02	9 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	9e−02	5 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
10	1e−01	2 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
11	1e−01	1 / 16	VERHAAK_NL subtype
12	1e−01	1 / 16	VERHAAK_PN subtype
13	2e−01	2 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
14	2e−01	1 / 21	Barbus_GBM_STS_vs._LTS
15	2e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−09	15 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
2	2e−08	7 / 37	ZHAN_MULTIPLE_MYELOMA_CD2_UP
3	3e−06	19 / 673	SCHLOSSER_SERUM_RESPONSE_DN
4	1e−05	6 / 61	BASSO_CD40_SIGNALING_DN
5	2e−05	14 / 442	KIM_WT1_TARGETS_DN
6	5e−05	19 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
7	1e−04	5 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
8	2e−04	12 / 417	SHEN_SMARCA2_TARGETS_UP
9	2e−04	11 / 361	GARY_CD5_TARGETS_DN
10	3e−04	10 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
11	4e−04	10 / 322	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP
12	4e−04	4 / 43	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN
13	5e−04	12 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
14	7e−04	18 / 935	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
15	8e−04	25 / 1550	PILON_KLF1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−04	6 / 96	HALLMARK_ANDROGEN_RESPONSE
2	4e−02	3 / 94	HALLMARK_PROTEIN_SECRETION
3	7e−02	4 / 187	HALLMARK_E2F_TARGETS
4	1e−01	3 / 141	HALLMARK_UV_RESPONSE_DN
5	2e−01	3 / 174	HALLMARK_ADIPOGENESIS
6	2e−01	3 / 192	HALLMARK_MTORC1_SIGNALING
7	2e−01	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	2e−01	3 / 195	HALLMARK_G2M_CHECKPOINT
9	3e−01	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
10	3e−01	1 / 51	HALLMARK_TGF_BETA_SIGNALING
11	4e−01	1 / 55	HALLMARK_MYC_TARGETS_V2
12	4e−01	2 / 176	HALLMARK_ALLOGRAFT_REJECTION
13	5e−01	2 / 188	HALLMARK_HYPOXIA
14	5e−01	1 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	5e−01	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Immunome

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	Angelova_immune−metagene−activated_B−cells
2	0.088	1 / 11	Angelova_immune−metagene−macrophages
3	0.103	1 / 13	Angelova_immune−metagene−immature_B−cells
4	0.125	1 / 16	Angelova_immune−metagene−Th17
5	0.140	1 / 18	Angelova_CRC_immunostimulators
6	0.235	1 / 32	Angelova_immune−metagene−effector_memory_CD8
7	0.297	1 / 42	Angelova_immune−metagene−TGD
8	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
9	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
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 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1.000	0 / 14	Angelova_immune−metagene−eosinophil

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.13	3 / 150	Homuth_BMI−associated−genes_UP
3	0.17	1 / 22	DUMEAUX_High bmi enriched genes
4	0.24	1 / 32	Marjolein_ageing−genes_DN
5	0.52	2 / 210	Homuth_BMI−associated−genes_DN
6	1.00	0 / 62	DUMEAUX_Smoking enriched genes
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 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_Fasting enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−13	87 / 5908	HOPP_Active_promoter
2	4e−11	70 / 4357	HOPP_Weak_txn
3	6e−11	81 / 5682	HOPP_Weak_promoter
4	2e−10	79 / 5529	HOPP_Txn_elongation
5	6e−10	77 / 5404	HOPP_Strong_enhancer
6	1e−08	67 / 4559	HOPP_Weak_enhancer
7	4e−08	14 / 263	SPANG_CD40 6hrs UP
8	5e−06	22 / 906	SPANG_BCR DN
9	2e−04	8 / 192	Victora_Dark zone signature
10	3e−04	19 / 955	SPANG_BCR UP
11	4e−04	53 / 4261	HOPP_Txn_transition
12	1e−03	5 / 96	SPANG_LPS 6hrs UP
13	3e−03	7 / 227	SPANG_IL21 UP
14	6e−03	4 / 88	ROSOLOWSKI_green UP
15	1e−02	2 / 18	SPANG_BAFF 9hrs UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.002	5 / 107	Tirosh_Exhaustion program in Mel75
2	0.114	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	0.152	2 / 83	TCGA_melanoma_immune_high
4	0.182	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
5	0.209	3 / 189	Tirosh_genes preferentially expressed by Tregs
6	0.273	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
7	0.275	4 / 319	Gerber_wt/wt_melanoma−cells−SpotA
8	0.279	1 / 39	Tirosh_top50 correlated genes PC4
9	0.348	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
10	0.399	5 / 497	Gerber_wt/wt_melanoma−cells−SpotD
11	0.509	2 / 204	Landsberg_dedifferentiation_down
12	0.510	1 / 85	Tirosh_AXL−signature
13	0.588	2 / 236	Gerber_wt/wt_group3−specific
14	0.618	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
15	0.674	2 / 276	Gerber_wt/wt_melanoma−cells−SpotB

MF

Rank	p−value	#in/all	Geneset
1	3e−05	26 / 1329	transferase activity
2	2e−03	22 / 1402	nucleotide binding
3	3e−03	2 / 10	MAP kinase kinase kinase kinase activity
4	6e−03	2 / 14	acetyltransferase activity
5	6e−03	2 / 14	SUMO transferase activity
6	7e−03	2 / 15	Notch binding
7	7e−03	2 / 15	phospholipid−translocating ATPase activity
8	8e−03	2 / 16	3'−5' exonuclease activity
9	9e−03	18 / 1185	ATP binding
10	1e−02	2 / 18	NAD+ ADP−ribosyltransferase activity
11	1e−02	2 / 20	ubiquitin conjugating enzyme activity
12	1e−02	3 / 61	nucleotidyltransferase activity
13	2e−02	2 / 23	bHLH transcription factor binding
14	2e−02	3 / 67	drug binding
15	2e−02	13 / 852	nucleic acid binding

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−05	10 / 216	hsa−miR−548l
2	6e−05	9 / 207	hsa−miR−92b
3	7e−05	9 / 213	hsa−miR−363
4	8e−05	10 / 268	hsa−miR−367
5	8e−05	9 / 217	hsa−miR−92a
6	1e−04	5 / 56	hsa−miR−618
7	1e−04	6 / 92	hsa−miR−491−3p
8	2e−04	9 / 235	hsa−miR−25
9	3e−04	11 / 369	hsa−miR−130a
10	3e−04	9 / 262	hsa−miR−32
11	5e−04	7 / 165	hsa−miR−448
12	5e−04	6 / 119	hsa−miR−132
13	5e−04	7 / 169	hsa−miR−148a
14	1e−03	10 / 368	hsa−miR−301a
15	1e−03	9 / 312	hsa−miR−301b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.06	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.29	1 / 41	Scicluna_DN
3	0.37	1 / 56	Burnham_sep_vs_con_DN
4	0.38	1 / 57	Burnham_viral_UP
5	0.38	1 / 57	Burnham_day1_vs_5_UP
6	0.64	1 / 122	Terre_IMS_influenza_meta_signature
7	1.00	0 / 68	Burnham_sep_vs_con_UP
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 48	Burnham_viral_DN
11	1.00	0 / 52	Burnham_day1_vs_5_DN
12	1.00	0 / 54	Burnham_timecourse
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 37	Sweeney_viral_up
15	1.00	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−05	12 / 310	Chaussabel_3,4_Protein phosphatases
2	9e−04	15 / 716	PROTEINATLAS_epididymis
3	1e−03	14 / 678	PROTEINATLAS_lymph node
4	2e−03	14 / 708	PROTEINATLAS_thyroid gland
5	4e−03	12 / 592	PROTEINATLAS_seminal vesicle
6	4e−03	12 / 604	PROTEINATLAS_hippocampus
7	5e−03	2 / 13	WIRTH_B−cells
8	5e−03	3 / 42	Chaussabel_1,3_B−cells
9	7e−03	15 / 893	PROTEINATLAS_pancreas
10	7e−03	18 / 1161	PROTEINATLAS_colon
11	8e−03	16 / 989	PROTEINATLAS_tonsil
12	8e−03	14 / 819	PROTEINATLAS_bronchus
13	9e−03	16 / 1007	PROTEINATLAS_kidney
14	1e−02	4 / 100	Chaussabel_2,8_T−cells
15	1e−02	14 / 848	PROTEINATLAS_adrenal gland

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	MYC_Chromatin_modification UP
2	0.02	19 / 1387	HEBENSTREIT_high expression TF
3	0.04	15 / 1107	ICGC_Myc_targets
4	0.07	8 / 522	ICGC_SrfPcr2_targets
5	0.15	14 / 1241	KIM_MYC targets
6	0.16	12 / 1041	ICGC_P300_targets
7	0.17	23 / 2254	ICGC_BatfPcr1_targets
8	0.18	22 / 2150	ICGC_Irf4_targets
9	0.18	16 / 1494	ICGC_Cebpbsc150_targets
10	0.19	17 / 1630	ICGC_SrfV0416101_targets
11	0.27	15 / 1508	ICGC_Mef2_targets
12	0.29	16 / 1636	ICGC_Bcl11_targets
13	0.34	32 / 3564	ICGC_Taf1_targets
14	0.35	18 / 1941	ICGC_Bcl3_targets
15	0.35	27 / 2994	ICGC_Zeb1_targets

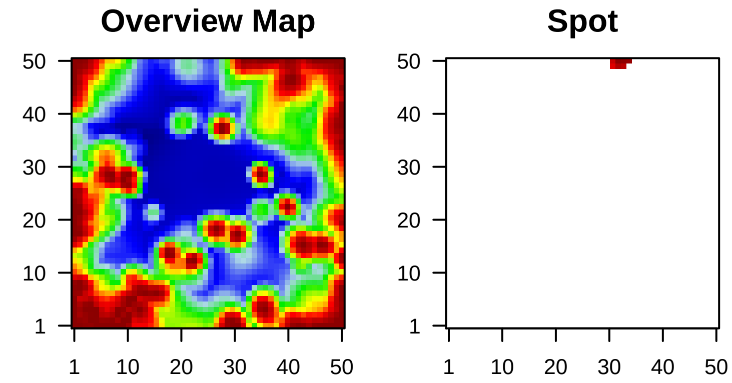
Overexpression Spots

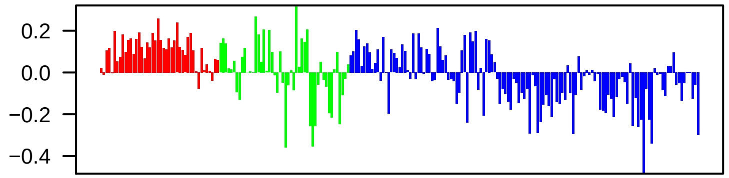
Spot Summary: F

metagenes = 7
genes = 161

<r> metagenes = 0.99
<r> genes = 0.21
beta: r2= 3.45 / log p= −Inf

samples with spot = 7 (3.2 %)
mBL : 2 (4.5 %)
intermediate : 4 (8.3 %)
non−mBL : 1 (0.8 %)



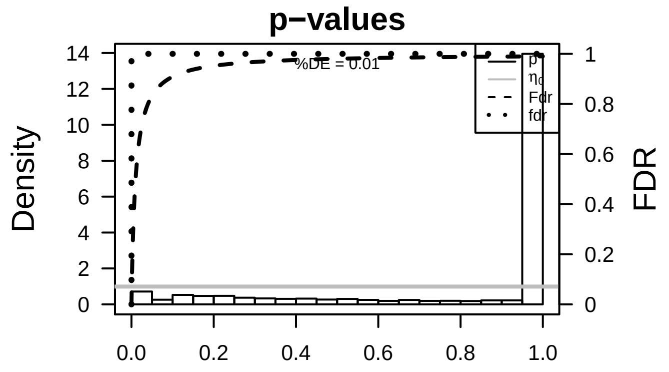


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212436_at	1.64	−1.2	0.37	TRIM33	tripartite motif containing 33 [Source:HGNC Symbol;Acc:HGN
2	209781_s_at	1.63	−1.13	0.4	KHDRBS3	KH RNA binding domain containing, signal transduction asso
3	204282_s_at	1.45	−0.99	0.32	FARS2	phenylalanyl−tRNA synthetase 2, mitochondrial [Source:HGN
4	210041_s_at	1.42	−1.16	0.56	PGM3	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8
5	211697_x_at	1.41	−1.33	0.36	PNO1	partner of NOB1 homolog [Source:HGNC Symbol;Acc:HGNC
6	217551_at	1.4	−1.1	0.25		olfactory receptor family 7 subfamily E member 14 pseudoger
7	217135_x_at	1.38	−0.69	0.54		cytochrome c oxidase subunit 6B1 pseudogene 3 [Source:HG
8	210008_s_at	1.32	−0.99	0.59	MRPS12	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;
9	219741_x_at	1.32	−0.87	0.46	ZNF552	zinc finger protein 552 [Source:HGNC Symbol;Acc:HGNC:26
10	219036_at	1.32	−0.84	0.39	CEP70	centrosomal protein 70 [Source:HGNC Symbol;Acc:HGNC:2
11	219763_at	1.3	−1.3	0.34	DENND1A	DENN domain containing 1A [Source:HGNC Symbol;Acc:HG
12	203672_x_at	1.26	−0.97	0.35	TPMT	thiopurine S−methyltransferase [Source:HGNC Symbol;Acc:H
13	204001_at	1.26	−1.33	0.5	SNAPC3	small nuclear RNA activating complex polypeptide 3 [Source:
14	209646_x_at	1.23	−1.28	0.51	ALDH1B1	aldehyde dehydrogenase 1 family member B1 [Source:HGNC
15	222264_at	1.22	−0.8	0.37	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U like 2 [Source:HG
16	205164_at	1.22	−1.07	0.38	GCAT	glycine C−acetyltransferase [Source:HGNC Symbol;Acc:HGN
17	201618_x_at	1.16	−1.59	0.48	GPAA1	glycosylphosphatidylinositol anchor attachment 1 [Source:HG
18	220212_s_at	1.14	−1.24	0.43	THADA	THADA, armadillo repeat containing [Source:HGNC Symbol;
19	57703_at	1.14	−0.66	0.45	SENP5	SUMO1/sentrin specific peptidase 5 [Source:HGNC Symbol;
20	203702_s_at	1.14	−1	0.4	TTLL4	tubulin tyrosine ligase like 4 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−15	113 / 5529	Lympl	HOPP_Txn_elongation
2	9e−12	111 / 5908	Lympl	HOPP_Active_promoter
3	2e−10	88 / 4261	Lympl	HOPP_Txn_transition
4	2e−09	46 / 1578	TF	ICGC_GabpPcr2_targets
5	4e−08	34 / 1044	TF	ICGC_Six5_targets
6	2e−07	66 / 3150	TF	ICGC_Creb1_targets
7	3e−06	7 / 53	BP	mitochondrial translational termination
8	3e−06	31 / 1089	TF	ICGC_Ets1_targets
9	3e−06	7 / 54	BP	mitochondrial translational elongation
10	8e−06	30 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
11	9e−06	65 / 3420	TF	ICGC_Bclaf101388_targets
12	1e−05	21 / 615	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
13	1e−05	93 / 5682	Lympl	HOPP_Weak_promoter
14	2e−05	69 / 3769	TF	ICGC_Pmlsc71910_targets
15	2e−05	52 / 2541	CC	nucleoplasm
16	2e−05	67 / 3630	TF	ICGC_Sp1_targets
17	2e−05	66 / 3564	TF	ICGC_Taf1_targets
18	2e−05	38 / 1630	TF	ICGC_SrfV0416101_targets
19	3e−05	64 / 3451	TF	ICGC_Atf2_targets
20	3e−05	18 / 510	GSEA	STEIN_ESRRA_TARGETS
21	8e−05	6 / 61	BP	snRNA transcription from RNA polymerase II promoter
22	8e−05	38 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
23	9e−05	4 / 21	CC	mitochondrial small ribosomal subunit
24	9e−05	56 / 2994	TF	ICGC_Zeb1_targets
25	1e−04	10 / 196	CC	nuclear membrane
26	1e−04	3 / 9	GSEA	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
27	1e−04	6 / 67	BP	tRNA processing
28	1e−04	8 / 130	GSEA	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
29	2e−04	31 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
30	2e−04	43 / 2150	TF	ICGC_Irf4_targets
31	2e−04	8 / 139	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
32	2e−04	64 / 3703	TF	ICGC_Foxm1_targets
33	3e−04	9 / 178	GSEA	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
34	3e−04	13 / 361	GSEA	GARY_CD5_TARGETS_DN
35	3e−04	8 / 147	GSEA	WANG_CLIM2_TARGETS_DN
36	3e−04	4 / 29	CC	mitochondrial large ribosomal subunit
37	4e−04	68 / 4072	TF	ICGC_Mta3_targets
38	4e−04	10 / 232	BP	translation
39	4e−04	3 / 13	GSEA	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTH
40	4e−04	13 / 371	GSEA	STEIN_ESRRA_TARGETS_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	2e−05	52 / 2541	nucleoplasm
2	9e−05	4 / 21	mitochondrial small ribosomal subunit
3	1e−04	10 / 196	nuclear membrane
4	3e−04	4 / 29	mitochondrial large ribosomal subunit
5	5e−04	12 / 330	mitochondrial inner membrane
6	1e−03	7 / 139	ribosome
7	2e−03	3 / 20	mitochondrial ribosome
8	4e−03	9 / 268	intracellular ribonucleoprotein complex
9	8e−03	24 / 1221	mitochondrion
10	8e−03	2 / 12	integrator complex
11	1e−02	58 / 3805	cytosol
12	1e−02	2 / 16	neuron projection terminus
13	2e−02	2 / 19	transcriptionally active chromatin
14	2e−02	14 / 653	nucleolus
15	3e−02	3 / 56	proteasome complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−06	30 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	8e−05	38 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
3	2e−04	31 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	2e−02	13 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
5	1e−01	15 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	1e−01	10 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
7	1e−01	9 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
8	3e−01	16 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	3e−01	1 / 31	Marisa_CRC−cluster−c
10	3e−01	13 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
11	4e−01	1 / 43	Marisa_CRC−cluster−f
12	4e−01	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	4e−01	7 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	5e−01	1 / 60	Marisa_CRC−cluster−g
15	6e−01	8 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 97	HALLMARK_PEROXISOME
2	0.2	4 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	0.2	4 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	0.2	3 / 133	HALLMARK_DNA_REPAIR
5	0.3	2 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.3	2 / 97	HALLMARK_BILE_ACID_METABOLISM
7	0.3	3 / 174	HALLMARK_ADIPOGENESIS
8	0.4	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	0.4	3 / 182	HALLMARK_GLYCOLYSIS
10	0.4	3 / 190	HALLMARK_MYC_TARGETS_V1
11	0.5	1 / 51	HALLMARK_TGF_BETA_SIGNALING
12	0.5	2 / 149	HALLMARK_UV_RESPONSE_UP
13	0.6	2 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.6	2 / 173	HALLMARK_MITOTIC_SPINDLE
15	0.6	2 / 178	HALLMARK_COMPLEMENT

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−15	113 / 5529	HOPP_Txn_elongation
2	9e−12	111 / 5908	HOPP_Active_promoter
3	2e−10	88 / 4261	HOPP_Txn_transition
4	1e−05	93 / 5682	HOPP_Weak_promoter
5	4e−03	80 / 5404	HOPP_Strong_enhancer
6	6e−03	33 / 1814	HOPP_Repetitive
7	6e−02	63 / 4559	HOPP_Weak_enhancer
8	1e−01	1 / 9	YAMANE_AICDA_targets_nonrecruited
9	1e−01	59 / 4357	HOPP_Weak_txn
10	1e−01	5 / 227	SPANG_IL21 UP
11	1e−01	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
12	2e−01	14 / 906	SPANG_BCR DN
13	2e−01	14 / 955	SPANG_BCR UP
14	4e−01	1 / 40	CARO_OxPhos_in_DLBCL_UP
15	5e−01	4 / 305	TARTE_Plasmablast signature

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 59	hsa−miR−651
2	6e−03	4 / 61	hsa−miR−1290
3	3e−02	3 / 54	hsa−miR−628−3p
4	3e−02	2 / 25	hsa−miR−892b
5	4e−02	7 / 262	hsa−miR−32
6	4e−02	2 / 26	hsa−miR−1226
7	4e−02	4 / 107	hsa−miR−24
8	4e−02	5 / 160	hsa−miR−545
9	4e−02	3 / 66	hsa−miR−567
10	5e−02	3 / 72	hsa−miR−378
11	6e−02	1 / 5	hsa−miR−126
12	6e−02	2 / 35	hsa−miR−640
13	6e−02	3 / 78	hsa−miR−224
14	7e−02	2 / 36	hsa−miR−553
15	7e−02	2 / 36	hsa−miR−636

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	3e−06	7 / 53	mitochondrial translational termination
2	3e−06	7 / 54	mitochondrial translational elongation
3	8e−05	6 / 61	snRNA transcription from RNA polymerase II promoter
4	1e−04	6 / 67	tRNA processing
5	4e−04	10 / 232	translation
6	8e−04	15 / 502	protein transport
7	2e−03	3 / 21	mitochondrial translation
8	4e−03	4 / 55	negative regulation of DNA binding transcription factor activity
9	5e−03	3 / 30	biosynthetic process
10	6e−03	2 / 10	snRNA processing
11	7e−03	2 / 11	regulation of mRNA splicing, via spliceosome
12	8e−03	3 / 35	cellular amino acid metabolic process
13	8e−03	2 / 12	layer formation in cerebral cortex
14	1e−02	2 / 16	synaptic vesicle endocytosis
15	2e−02	6 / 173	proteasome−mediated ubiquitin−dependent protein catabolic process

Chr

Rank	p−value	#in/all	Geneset
1	5e−04	20 / 756	Chr 11
2	2e−02	16 / 776	Chr 17
3	4e−02	16 / 832	Chr 2
4	4e−02	9 / 382	Chr 15
5	1e−01	8 / 403	Chr 14
6	2e−01	11 / 689	Chr 3
7	2e−01	8 / 492	Chr 9
8	3e−01	7 / 437	Chr 8
9	5e−01	10 / 833	Chr 19
10	6e−01	4 / 369	Chr 20
11	7e−01	6 / 585	Chr 7
12	7e−01	14 / 1325	Chr 1
13	8e−01	3 / 333	Chr 22
14	8e−01	5 / 548	Chr 16
15	8e−01	1 / 139	Chr 21

Glioma

Rank	p−value	#in/all	Geneset
1	0.001	31 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.032	3 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.041	23 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.117	2 / 50	Vishal_subnetwork signature of survival in GBM
5	0.186	10 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.237	5 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
7	0.246	2 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	0.413	1 / 45	Donson−innate immunity−associated with LTS in HGA
9	0.417	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
10	0.460	1 / 52	GIEZELT_GBM_WT_down_VS_mut
11	0.478	1 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	0.497	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
13	0.503	1 / 59	GIEZELT_GBM_STS_up_VS_LTS
14	0.531	1 / 64	Weller_LGG_A_vs_O_DOWN
15	0.542	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl

Immunome

Rank	p−value	#in/all	Geneset
1	0.09	1 / 8	Angelova_immune−metagene−mDC
2	0.11	1 / 10	Angelova_immune−metagene−neutrophils
3	0.20	1 / 19	Angelova_immune−metagene−activated_CD8
4	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Melanoma

Rank	p−value	#in/all	Geneset
1	0.001	9 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.044	7 / 276	Gerber_wt/wt_melanoma−cells−SpotB
3	0.134	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.173	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
5	0.190	2 / 68	Tirosh_housekeeping_genes
6	0.246	2 / 81	Tirosh_Genes in the MITF program
7	0.247	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
8	0.563	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
9	0.635	1 / 85	Tirosh_AXL−signature
10	0.695	2 / 204	Landsberg_dedifferentiation_down
11	0.769	2 / 236	Gerber_wt/wt_group3−specific
12	0.894	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	0.935	3 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	1.000	0 / 17	Hugo_melanoma−all−MET_UP
15	1.000	0 / 37	Hugo_melanoma−all−MET_DN

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 54	Burnham_timecourse
2	0.3	1 / 33	Sweeney_viral_dn
3	0.5	1 / 52	Burnham_day1_vs_5_DN
4	0.5	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
5	0.8	1 / 122	Terre_IMS_influenza_meta_signature
6	0.9	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	1.0	0 / 68	Burnham_sep_vs_con_UP
8	1.0	0 / 56	Burnham_sep_vs_con_DN
9	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
10	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
11	1.0	0 / 48	Burnham_viral_DN
12	1.0	0 / 57	Burnham_viral_UP
13	1.0	0 / 57	Burnham_day1_vs_5_UP
14	1.0	0 / 18	Scicluna_UP
15	1.0	0 / 41	Scicluna_DN

TF

Rank	p−value	#in/all	Geneset
1	2e−09	46 / 1578	ICGC_GabpPcr2_targets
2	4e−08	34 / 1044	ICGC_Six5_targets
3	2e−07	66 / 3150	ICGC_Creb1_targets
4	3e−06	31 / 1089	ICGC_Ets1_targets
5	9e−06	65 / 3420	ICGC_Bclaf101388_targets
6	2e−05	69 / 3769	ICGC_Pmlsc71910_targets
7	2e−05	67 / 3630	ICGC_Sp1_targets
8	2e−05	66 / 3564	ICGC_Taf1_targets
9	2e−05	38 / 1630	ICGC_SrfV0416101_targets
10	3e−05	64 / 3451	ICGC_Atf2_targets
11	9e−05	56 / 2994	ICGC_Zeb1_targets
12	2e−04	43 / 2150	ICGC_Irf4_targets
13	2e−04	64 / 3703	ICGC_Foxm1_targets
14	4e−04	68 / 4072	ICGC_Mta3_targets
15	5e−04	26 / 1107	ICGC_Myc_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.006	2 / 10	GENTLES_modul5
2	0.031	3 / 58	SHAUGHNESSY_MM high risk
3	0.144	0 / 15	RHODES_CANCER_META_SIGNATURE
4	0.152	1 / 14	BENTINK_myc.1
5	0.162	1 / 15	GENTLES_modul2
6	0.162	1 / 15	GENTLES_modul4
7	0.162	1 / 15	GENTLES_modul7
8	0.282	1 / 28	PanCan_HK_geneset_nanostring
9	0.427	0 / 14	LIU_COMMON_CANCER_GENES
10	0.460	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.510	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	0.786	1 / 130	PanCan_CC+Apop_geneset_nanostring
13	0.796	1 / 134	PanCan_RAS_geneset_nanostring
14	0.826	1 / 147	PanCan_MAPK_geneset_nanostring
15	0.863	3 / 409	Lembcke_Normal vs Adenoma

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−24	149 / 8200	monocytes peripheral blood_2_TssAFlnk
2	1e−23	150 / 8406	Bcells peripheral blood_2_TssAFlnk
3	2e−23	150 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
4	3e−23	152 / 8816	Thelper cells peripheral blood_2_TssAFlnk
5	2e−22	146 / 7957	Tcells peripheral blood_2_TssAFlnk
6	2e−22	141 / 7331	TssA_Colon
7	6e−22	148 / 8322	T CD8+ naive cells peripheral blood_1_TssA
8	6e−22	143 / 7635	monocytes peripheral blood_1_TssA
9	2e−21	147 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
10	8e−21	152 / 9146	3_TssF_Skeletal_Muscle
11	1e−20	147 / 8370	natural killer cells peripheral blood_2_TssAFlnk
12	2e−20	143 / 7833	Bcells peripheral blood_1_TssA
13	4e−20	147 / 8430	3_TssF_Melanocytes
14	5e−20	150 / 8918	1_TssA_ESC_Mesoderm
15	6e−20	149 / 8766	2_TssA_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−05	21 / 615	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
2	3e−05	18 / 510	STEIN_ESRRA_TARGETS
3	1e−04	3 / 9	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
4	1e−04	8 / 130	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
5	2e−04	8 / 139	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
6	3e−04	9 / 178	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
7	3e−04	13 / 361	GARY_CD5_TARGETS_DN
8	3e−04	8 / 147	WANG_CLIM2_TARGETS_DN
9	4e−04	3 / 13	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHES
10	4e−04	13 / 371	STEIN_ESRRA_TARGETS_UP
11	2e−03	18 / 703	LEE_BMP2_TARGETS_DN
12	2e−03	3 / 20	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLIC
13	2e−03	13 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
14	2e−03	6 / 112	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN
15	2e−03	3 / 22	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 32	Marjolein_ageing−genes_DN
2	0.5	1 / 62	DUMEAUX_Smoking enriched genes
3	0.5	2 / 150	Homuth_BMI−associated−genes_UP
4	0.7	2 / 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	0.002	6 / 109	structural constituent of ribosome
2	0.008	5 / 106	ligase activity
3	0.008	2 / 12	Lys48−specific deubiquitinase activity
4	0.012	25 / 1329	transferase activity
5	0.019	2 / 18	threonine−type endopeptidase activity
6	0.022	105 / 7864	protein binding
7	0.022	7 / 237	ubiquitin−protein transferase activity
8	0.025	3 / 54	peptide binding
9	0.026	4 / 95	isomerase activity
10	0.027	2 / 22	phospholipase A2 activity
11	0.041	4 / 110	transferase activity, transferring acyl groups
12	0.042	2 / 28	aminopeptidase activity
13	0.042	2 / 28	ephrin receptor binding
14	0.051	2 / 31	SNAP receptor activity
15	0.054	2 / 32	Hsp70 protein binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.04	4 / 113	Chaussabel_1,8_Metabolism Biosynthesis
2	0.06	4 / 123	Chaussabel_3,7_Spliceosome
3	0.07	1 / 6	JONGENEEL_Uterus
4	0.07	6 / 245	Chaussabel_3,9_Kinases
5	0.09	5 / 204	Chaussabel_3,2_Inflammation I
6	0.14	14 / 866	PROTEINATLAS_cerebellum
7	0.14	1 / 13	WIRTH_Prim. lymphoid organs
8	0.16	10 / 592	PROTEINATLAS_seminal vesicle
9	0.16	1 / 15	JONGENEEL_Lung
10	0.20	1 / 19	JONGENEEL_Adrenal Gland
11	0.26	9 / 594	PROTEINATLAS_parathyroid gland
12	0.28	2 / 89	Chaussabel_2,3_Erythrocytes
13	0.29	12 / 848	PROTEINATLAS_adrenal gland
14	0.35	8 / 569	PROTEINATLAS_salivary gland
15	0.36	12 / 893	PROTEINATLAS_pancreas

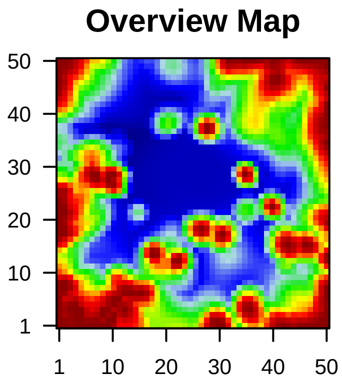
Overexpression Spots

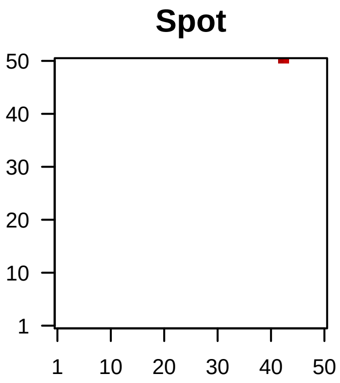
Spot Summary: G

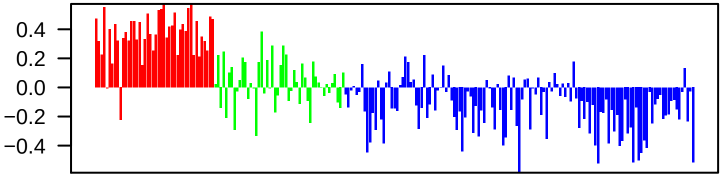
metagenes = 2
genes = 35

<r> metagenes = 0.99
<r> genes = 0.34
beta: r2= 12.38 / log p= −Inf

samples with spot = 49 (22.2 %)
mBL : 40 (90.9 %)
intermediate : 7 (14.6 %)
non−mBL : 2 (1.6 %)


Overview Map


Spot

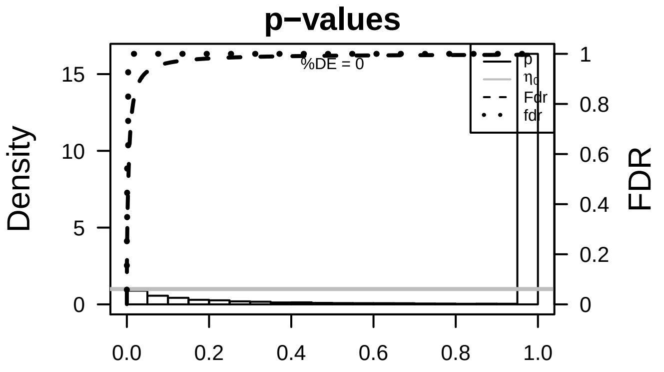


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209470_s_at	1.84	−1.56	0.54	GPM6A	glycoprotein M6A [Source:HGNC Symbol;Acc:HGNC:4460]
2	205001_s_at	1.66	−1.27	0.39	DDX3Y	DEAD−box helicase 3, Y−linked [Source:HGNC Symbol;Acc:
3	218529_at	1.41	−0.99	0.58	CD320	CD320 molecule [Source:HGNC Symbol;Acc:HGNC:16692]
4	216685_s_at	1.33	−1.1	0.4	MTAP	methylthioadenosine phosphorylase [Source:HGNC Symbol;
5	214581_x_at	1.26	−1.08	0.41	TNFRSF21	TNF receptor superfamily member 21 [Source:HGNC Symbol
6	207042_at	1.22	−0.96	0.64	E2F2	E2F transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:
7	91816_f_at	1.19	−1.4	0.6	MEX3D	mex−3 RNA binding family member D [Source:HGNC Symbo
8	207824_s_at	1.17	−1.47	0.63	MAZ	MYC associated zinc finger protein [Source:HGNC Symbol;A
9	202806_at	1.15	−1.5	0.53	DBN1	drebrin 1 [Source:HGNC Symbol;Acc:HGNC:2695]
10	209151_x_at	1.05	−1.73	0.64	TCF3	transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:116
11	200672_x_at	1.05	−1.27	0.56	SPTBN1	spectrin beta, non−erythrocytic 1 [Source:HGNC Symbol;Acc
12	205048_s_at	0.99	−1.39	0.4		phosphoserine phosphatase pseudogene 1 [Source:HGNC S
13	205429_s_at	0.98	−1.08	0.46	MPP6	membrane palmitoylated protein 6 [Source:HGNC Symbol;Ac
14	200894_s_at	0.98	−1.77	0.62	FKBP4	FK506 binding protein 4 [Source:HGNC Symbol;Acc:HGNC:
15	217025_s_at	0.94	−1.16	0.57	DBN1	drebrin 1 [Source:HGNC Symbol;Acc:HGNC:2695]
16	219471_at	0.93	−2.21	0.62	RUBCNL	RUN and cysteine rich domain containing beclin 1 interacting
17	44790_s_at	0.89	−2.07	0.59	RUBCNL	RUN and cysteine rich domain containing beclin 1 interacting
18	211949_s_at	0.88	−1.65	0.7	NOLC1	nucleolar and coiled−body phosphoprotein 1 [Source:HGNC
19	203015_s_at	0.87	−1.09	0.75	SSX2IP	SSX family member 2 interacting protein [Source:HGNC Sym
20	216218_s_at	0.86	−1.36	0.62	PLCL2	phospholipase C like 2 [Source:HGNC Symbol;Acc:HGNC:90

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−07	6 / 99	Lympl	Sha_BL UP
2	6e−06	11 / 955	Lympl	SPANG_BCR UP
3	3e−05	9 / 726	GSE	PUJANA_CHEK2_PCC_NETWORK
4	3e−05	9 / 728	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
5	4e−05	3 / 28	GSE	YU_BAP1_TARGETS
6	5e−05	10 / 966	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	7e−05	3 / 34	GSE	REACTOME_G1_PHASE
8	1e−04	8 / 651	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
9	1e−04	3 / 42	GSE	HUMMEL_BURKITTS_LYMPHOMA_UP
10	3e−04	3 / 53	GSE	GALE_APL_WITH_FLT3_MUTATED_UP
11	3e−04	4 / 135	Lympl	DAVE_BL−vs−DLBCL
12	3e−04	3 / 54	GSE	VERNELL_RETINOBLASTOMA_PATHWAY_UP
13	3e−04	5 / 254	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
14	3e−04	2 / 12	Canc	BENTINK_ras.1
15	4e−04	6 / 417	GSE	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN
16	4e−04	3 / 61	miRN	hsa−miR−1290
17	4e−04	5 / 275	GSE	HADDAD_B_LYMPHOCYTE_PROGENITOR
18	4e−04	5 / 280	GSE	MANALO_HYPOXIA_DN
19	5e−04	5 / 290	GSE	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
20	5e−04	3 / 68	miRN	hsa−miR−608
21	6e−04	4 / 169	GSE	FUJII_YBX1_TARGETS_DN
22	7e−04	20 / 4579	CC	nucleus
23	7e−04	22 / 5404	Lympl	HOPP_Strong_enhancer
24	9e−04	5 / 327	GSE	CUI_TCF21_TARGETS_2_UP
25	9e−04	3 / 82	GSE	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP
26	1e−03	2 / 21	CC	axonal growth cone
27	1e−03	2 / 23	CC	cortical cytoskeleton
28	2e−03	8 / 1007	Refer	PROTEINATLAS_kidney
29	2e−03	6 / 575	GSE	CAIRO_HEPATOBLASTOMA_CLASSES_UP
30	2e−03	2 / 28	GSE	BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_UP
31	2e−03	10 / 1550	GSE	PILON_KLF1_TARGETS_DN
32	2e−03	3 / 110	BP	regulation of cell cycle
33	2e−03	6 / 590	GSE	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
34	2e−03	5 / 400	GSE	PUJANA_BRCA2_PCC_NETWORK
35	2e−03	2 / 30	GSE	VALK_AML_CLUSTER_10
36	2e−03	6 / 593	Refer	PROTEINATLAS_lateral ventricle
37	2e−03	8 / 1048	Refer	PROTEINATLAS_gallbladder
38	2e−03	3 / 114	GSE	KEGG_CELL_CYCLE
39	2e−03	3 / 114	GSE	PUJANA_BRCA_CENTERED_NETWORK
40	2e−03	8 / 1052	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.02	2 / 92	HORVATH_aging_genes meth DOWN
2	0.22	1 / 107	HORVATH_aging_genes meth UP
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	

BP

Rank	p−value	#in/all	Geneset
1	0.002	3 / 110	regulation of cell cycle
2	0.003	2 / 33	nucleotide−excision repair, DNA incision, 5'−to lesion
3	0.003	5 / 421	nervous system development
4	0.003	2 / 35	neuron apoptotic process
5	0.023	1 / 10	regulation of synaptic transmission, GABAergic
6	0.026	1 / 11	copper ion transport
7	0.026	1 / 11	generation of neurons
8	0.026	1 / 11	neural retina development
9	0.026	1 / 11	pre−mRNA cleavage required for polyadenylation
10	0.028	2 / 111	anatomical structure morphogenesis
11	0.028	1 / 12	negative regulation of microtubule polymerization
12	0.029	2 / 113	cell projection organization
13	0.030	1 / 13	muscle cell differentiation
14	0.030	1 / 13	plasma membrane organization
15	0.032	1 / 14	regulation of protein localization to plasma membrane

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	2 / 12	BENTINK_ras.1
2	2e−03	5 / 409	Lembcke_Normal vs Adenoma
3	4e−03	2 / 41	PanCan_DNARepair_geneset_nanostring
4	3e−02	1 / 12	BENTINK_e2f3.2
5	3e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
6	3e−02	1 / 15	GENTLES_modul4
7	4e−02	1 / 16	WOLFER_overlap genes
8	4e−02	2 / 130	PanCan_CC+Apop_geneset_nanostring
9	1e−01	1 / 47	PanCan_TGF−B_geneset_nanostring
10	2e−01	1 / 96	PanCan_TXmisReg_geneset_nanostring
11	4e−01	1 / 186	SPANG_LPS−index2
12	6e−01	0 / 14	LIU_PROSTATE_CANCER_DN
13	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	7e−04	20 / 4579	nucleus
2	1e−03	2 / 21	axonal growth cone
3	1e−03	2 / 23	cortical cytoskeleton
4	3e−03	19 / 4701	cytoplasm
5	6e−03	2 / 49	RNA polymerase II transcription factor complex
6	6e−03	3 / 163	transcription factor complex
7	9e−03	12 / 2541	nucleoplasm
8	2e−02	5 / 653	nucleolus
9	2e−02	6 / 936	cytoskeleton
10	2e−02	3 / 254	axon
11	2e−02	1 / 10	beta−catenin destruction complex
12	3e−02	1 / 11	actomyosin
13	3e−02	2 / 107	fibrillar center
14	3e−02	1 / 13	axolemma
15	3e−02	1 / 13	mRNA cleavage and polyadenylation specificity factor complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	3 / 242	Chr 13
2	0.08	4 / 700	Chr 12
3	0.09	1 / 41	Chr Y
4	0.14	3 / 548	Chr 16
5	0.31	3 / 833	Chr 19
6	0.31	2 / 480	Chr 4
7	0.38	2 / 554	Chr 5
8	0.40	2 / 585	Chr 7
9	0.55	1 / 333	Chr 22
10	0.61	3 / 1325	Chr 1
11	0.65	1 / 437	Chr 8
12	0.69	1 / 490	Chr 10
13	0.69	1 / 492	Chr 9
14	0.80	1 / 669	Chr 6
15	0.81	1 / 689	Chr 3

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−05	27 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
2	2e−04	28 / 7833	Bcells peripheral blood_1_TssA
3	2e−04	27 / 7407	natural killer cells peripheral blood_5_TxWk
4	4e−04	29 / 8766	2_TssA_Melanocytes
5	5e−04	29 / 8865	Thelper cells peripheral blood_7_Enh
6	6e−04	28 / 8275	2_TssA_Fibroblasts
7	6e−04	29 / 8918	1_TssA_ESC_Mesoderm
8	1e−03	29 / 9160	2_TssA_Neuronal_Progenitor
9	2e−03	15 / 3007	14_ZNF_Neuronal_Progenitor
10	2e−03	28 / 8641	1_TssA_ESC_Endoderm
11	2e−03	25 / 7078	Bcells peripheral blood_5_TxWk
12	2e−03	29 / 9298	Bcells peripheral blood_7_Enh
13	2e−03	26 / 7635	monocytes peripheral blood_1_TssA
14	2e−03	24 / 6679	5_Tx_Melanocytes
15	2e−03	28 / 8816	Thelper cells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	1 / 3	Budinska_C_CIMP−H−like_DOWN
2	0.037	1 / 16	Budinska_B_Lower crypt−like_UP
3	0.051	20 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	0.056	2 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
5	0.069	2 / 184	Kosinski_lower−crypt−long−list
6	0.096	1 / 43	Marisa_CRC−cluster−f
7	0.102	7 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	0.146	2 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
9	0.154	2 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
10	0.239	2 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
11	0.357	2 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
12	0.408	1 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	0.416	2 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
14	0.421	3 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
15	0.454	1 / 255	Kosinski_top−crypt−long−list

Glioma

Rank	p−value	#in/all	Geneset
1	0.02	4 / 421	Down_b
2	0.05	1 / 21	KIM deleted & downregulated in LTS
3	0.09	1 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
4	0.10	1 / 43	Patel_stemness signatures
5	0.12	1 / 52	GIEZELT_GBM_WT_down_VS_mut
6	0.14	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.15	1 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	0.20	5 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	0.21	1 / 102	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
10	0.23	1 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
11	0.24	1 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
12	0.27	1 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	0.28	5 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
14	0.29	1 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
15	0.32	1 / 163	ScoV_0.999_Sturm_E1_IDH_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	9 / 726	PUJANA_CHEK2_PCC_NETWORK
2	3e−05	9 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	4e−05	3 / 28	YU_BAP1_TARGETS
4	5e−05	10 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	7e−05	3 / 34	REACTOME_G1_PHASE
6	1e−04	8 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
7	1e−04	3 / 42	HUMMEL_BURKITTS_LYMPHOMA_UP
8	3e−04	3 / 53	GALE_APL_WITH_FLT3_MUTATED_UP
9	3e−04	3 / 54	VERNELL_RETINOBLASTOMA_PATHWAY_UP
10	3e−04	5 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
11	4e−04	6 / 417	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN
12	4e−04	5 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
13	4e−04	5 / 280	MANALO_HYPOXIA_DN
14	5e−04	5 / 290	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
15	6e−04	4 / 169	FUJII_YBX1_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	3 / 195	HALLMARK_G2M_CHECKPOINT
2	0.04	2 / 139	HALLMARK_FATTY_ACID_METABOLISM
3	0.05	2 / 149	HALLMARK_UV_RESPONSE_UP
4	0.07	2 / 187	HALLMARK_E2F_TARGETS
5	0.08	1 / 34	HALLMARK_ANGIOGENESIS
6	0.09	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	0.11	1 / 51	HALLMARK_TGF_BETA_SIGNALING
8	0.12	1 / 55	HALLMARK_MYC_TARGETS_V2
9	0.18	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	0.20	1 / 97	HALLMARK_PEROXISOME
11	0.22	1 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	0.27	1 / 133	HALLMARK_DNA_REPAIR
13	0.33	1 / 170	HALLMARK_IL2_STAT5_SIGNALING
14	0.34	1 / 173	HALLMARK_MITOTIC_SPINDLE
15	0.34	1 / 174	HALLMARK_ADIPOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 21	Angelova_immune−metagene−central_memory_CD4
2	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
3	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
4	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
6	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
7	1.00	0 / 25	Angelova_immune−metagene−DC
8	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
9	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
10	1.00	0 / 14	Angelova_immune−metagene−eosinophil
11	1.00	0 / 19	Angelova_immune−metagene−iDC
12	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
13	1.00	0 / 11	Angelova_immune−metagene−macrophages
14	1.00	0 / 38	Angelova_immune−metagene−mast−cells
15	1.00	0 / 8	Angelova_immune−metagene−mDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 150	Homuth_BMI−associated−genes_UP
2	0.4	1 / 210	Homuth_BMI−associated−genes_DN
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 22	DUMEAUX_High bmi enriched genes
13	1.0	0 / 22	DUMEAUX_Fasting enriched genes
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	1e−07	6 / 99	Sha_BL UP
2	6e−06	11 / 955	SPANG_BCR UP
3	3e−04	4 / 135	DAVE_BL−vs−DLBCL
4	7e−04	22 / 5404	HOPP_Strong_enhancer
5	1e−02	1 / 6	MASCQUE_mBL UP
6	2e−02	2 / 88	ROSOLOWSKI_green UP
7	2e−02	1 / 9	DAVE_BL UP
8	2e−02	20 / 5908	HOPP_Active_promoter
9	2e−02	2 / 102	ROSOLOWSKI_blue total
10	3e−02	2 / 121	ROSOLOWSKI_green total
11	3e−02	1 / 15	BENTINK_mBL UP
12	4e−02	1 / 17	DAVE_c−myc BL UP
13	5e−02	18 / 5529	HOPP_Txn_elongation
14	6e−02	1 / 25	ROSOLOWSKI_red UP
15	7e−02	2 / 192	Victora_Dark zone signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.006	4 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	0.026	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
3	0.055	1 / 24	Tirosh_B−cell specific genes−melanoma
4	0.098	1 / 44	Tirosh_top50 correlated genes PC2
5	0.170	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
6	0.333	1 / 171	Landsberg_dedifferentiation_up
7	0.355	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.420	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	0.446	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
10	0.696	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
11	1.000	0 / 17	Hugo_melanoma−all−MET_UP
12	1.000	0 / 37	Hugo_melanoma−all−MET_DN
13	1.000	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
14	1.000	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
15	1.000	0 / 16	Hugo_melanoma−all−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	0.003	4 / 268	transcription factor binding
2	0.004	8 / 1161	RNA binding
3	0.005	3 / 153	protein dimerization activity
4	0.023	8 / 1541	DNA binding
5	0.023	1 / 10	GABA receptor binding
6	0.023	1 / 10	profilin binding
7	0.026	1 / 11	DNA−(apurinic or apyrimidinic site) lyase activity
8	0.028	5 / 741	DNA binding transcription factor activity
9	0.028	1 / 12	inositol 1,4,5 trisphosphate binding
10	0.029	24 / 7864	protein binding
11	0.030	1 / 13	enhancer binding
12	0.030	1 / 13	mitogen−activated protein kinase kinase kinase binding
13	0.030	1 / 13	NAD+ binding
14	0.032	1 / 14	FK506 binding
15	0.032	1 / 14	tau protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 61	hsa−miR−1290
2	5e−04	3 / 68	hsa−miR−608
3	3e−03	2 / 35	hsa−miR−1224−5p
4	6e−03	2 / 50	hsa−miR−409−5p
5	6e−03	3 / 160	hsa−miR−330−3p
6	6e−03	2 / 51	hsa−miR−492
7	7e−03	2 / 55	hsa−miR−637
8	8e−03	2 / 56	hsa−miR−193b
9	8e−03	2 / 57	hsa−miR−422a
10	8e−03	2 / 58	hsa−miR−1304
11	8e−03	2 / 59	hsa−miR−1179
12	9e−03	2 / 62	hsa−miR−205
13	9e−03	2 / 62	hsa−miR−708
14	1e−02	3 / 189	hsa−miR−214
15	1e−02	2 / 64	hsa−miR−365

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	8 / 1007	PROTEINATLAS_kidney
2	0.002	6 / 593	PROTEINATLAS_lateral ventricle
3	0.002	8 / 1048	PROTEINATLAS_gallbladder
4	0.010	5 / 569	PROTEINATLAS_salivary gland
5	0.011	7 / 1076	PROTEINATLAS_stomach
6	0.012	5 / 592	PROTEINATLAS_seminal vesicle
7	0.012	6 / 840	PROTEINATLAS_urinary bladder
8	0.016	7 / 1161	PROTEINATLAS_colon
9	0.019	5 / 671	PROTEINATLAS_cervix, uterine
10	0.023	5 / 708	PROTEINATLAS_thyroid gland
11	0.031	6 / 1032	PROTEINATLAS_small intestine
12	0.032	1 / 14	WIRTH_Thymus
13	0.033	6 / 1048	PROTEINATLAS_rectum
14	0.034	4 / 527	PROTEINATLAS_oral mucosa
15	0.036	6 / 1072	PROTEINATLAS_duodenum

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	1 / 13	Alternative lengthening of telomeres
2	1.00	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	0.007	8 / 1241	KIM_MYC targets
2	0.012	1 / 5	MYC_TFs
3	0.023	1 / 10	MYC_RNA processing binding UP
4	0.031	6 / 1032	ICGC_Usf1_targets
5	0.136	1 / 62	MYC_Targets UP
6	0.255	2 / 415	ICGC_RxraPcr1_targets
7	0.372	2 / 549	ICGC_Atf3_targets
8	0.456	8 / 3121	ICGC_Egr1_targets
9	0.488	3 / 1107	ICGC_Myc_targets
10	0.537	7 / 2899	ICGC_Nfatc1_targets
11	0.547	4 / 1636	ICGC_Bcl11_targets
12	0.554	9 / 3796	ICGC_Nficsc81335_targets
13	0.575	7 / 2994	ICGC_Zeb1_targets
14	0.646	3 / 1387	HEBENSTREIT_high expression TF
15	0.648	4 / 1848	ICGC_Pbx3_targets

Overexpression Spots

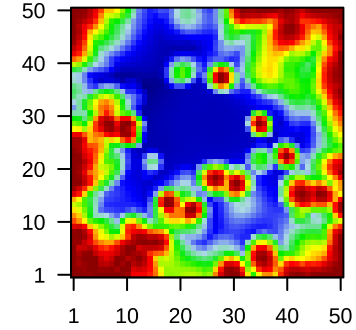
Spot Summary: H

metagenes = 15
genes = 184

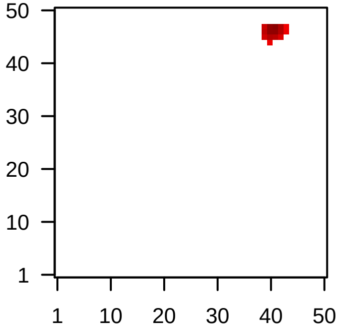
<r> metagenes = 0.97
<r> genes = 0.32
beta: r2= 5.82 / log p= −Inf

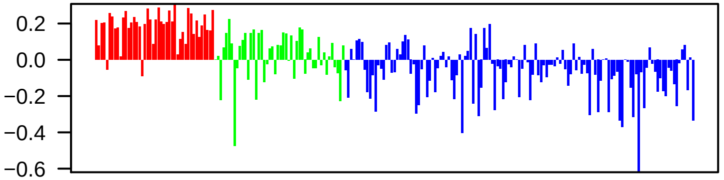
samples with spot = 24 (10.9 %)
mBL : 23 (52.3 %)
intermediate : 1 (2.1 %)

Overview Map



Spot





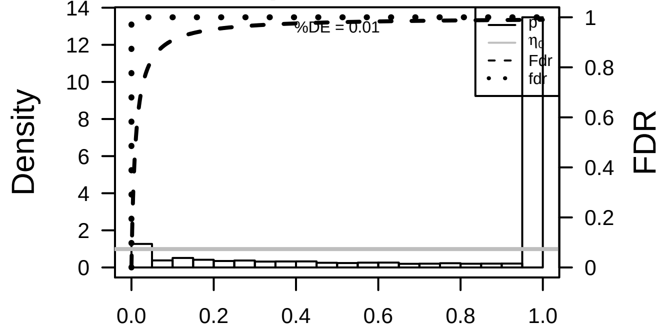
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	219733_s_at	1.48	−1.19	0.53	SLC27A5	solute carrier family 27 member 5 [Source:HGNC Symbol;Acc
2	41037_at	1.43	−0.89	0.31	TEAD4	TEA domain transcription factor 4 [Source:HGNC Symbol;Acc
3	201927_s_at	1.42	−1.07	0.41	PKP4	plakophilin 4 [Source:HGNC Symbol;Acc:HGNC:9026]
4	221239_s_at	1.35	−1.87	0.33	FCRL2	Fc receptor like 2 [Source:HGNC Symbol;Acc:HGNC:14875]
5	213556_at	1.33	−0.71	0.29	PINLYP	phospholipase A2 inhibitor and LY6/PLAUR domain containin
6	207396_s_at	1.29	−1.19	0.46	ALG3	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Symb
7	207621_s_at	1.21	−1.21	0.31	PEMT	phosphatidylethanolamine N−methyltransferase [Source:HGN
8	218296_x_at	1.2	−1.56	0.63	MSTO1	misato 1, mitochondrial distribution and morphology regulator
9	206777_s_at	1.2	−0.95	0.45	CRYBB2	crystallin beta B2 [Source:HGNC Symbol;Acc:HGNC:2398]
10	218944_at	1.16	−0.95	0.57	PYCR3	pyrroline−5−carboxylate reductase 3 [Source:HGNC Symbol;
11	205217_at	1.14	−1.41	0.44	TIMM8A	translocase of inner mitochondrial membrane 8A [Source:HG
12	201802_at	1.13	−1.37	0.35	SLC29A1	solute carrier family 29 member 1 (Augustine blood group) [S
13	203782_s_at	1.09	−0.87	0.51	POLRMT	RNA polymerase mitochondrial [Source:HGNC Symbol;Acc:H
14	221629_x_at	1.05	−0.9	0.45	HGH1	HGH1 homolog [Source:HGNC Symbol;Acc:HGNC:24161]
15	212827_at	1.05	−2.46	0.29		immunoglobulin heavy constant mu [Source:HGNC Symbol;A
16	202482_x_at	1.04	−1.02	0.41	RANBP1	RAN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:98
17	212133_at	1.04	−1.1	0.36	NIPA2	non imprinted in Prader−Willi/Angelman syndrome 2 [Source:
18	202044_at	1.03	−1.01	0.35	ARHGAP35	Rho GTPase activating protein 35 [Source:HGNC Symbol;Acc
19	212996_s_at	1.03	−1.18	0.48	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae) [Source
20	203188_at	1.03	−0.55	0.5	B4GAT1	beta−1,4−glucuronyltransferase 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−38	66 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	6e−27	37 / 280	GSEA	MANALO_HYPOXIA_DN
3	5e−24	28 / 158	GSEA	BILD_MYC_ONCOGENIC_SIGNATURE
4	2e−23	48 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	1e−22	19 / 55	HM	HALLMARK_MYC_TARGETS_V2
6	2e−19	45 / 703	GSEA	LEE_BMP2_TARGETS_DN
7	1e−18	18 / 72	GSEA	SCHUHMACHER_MYC_TARGETS_UP
8	9e−18	39 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	2e−16	61 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
10	5e−14	26 / 314	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
11	6e−14	21 / 190	HM	HALLMARK_MYC_TARGETS_V1
12	4e−13	20 / 186	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
13	6e−13	37 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
14	9e−13	17 / 129	GSEA	WELCSH_BRCA1_TARGETS_DN
15	3e−12	34 / 653	CC	nucleolus
16	3e−11	17 / 159	GSEA	SANSOM_APC_TARGETS_REQUIRE_MYC
17	6e−11	44 / 1161	MF	RNA binding
18	1e−10	30 / 590	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
19	2e−10	39 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
20	1e−09	16 / 174	BP	rRNA processing
21	1e−09	13 / 107	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_DN
22	1e−09	9 / 39	GSEA	IRITANI_MAD1_TARGETS_DN
23	2e−09	18 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
24	2e−09	20 / 295	GSEA	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
25	3e−09	20 / 305	Lymp	TARTE_Plasmablast signature
26	3e−09	8 / 30	CC	small−subunit processome
27	5e−09	28 / 602	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
28	5e−09	16 / 193	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP
29	7e−09	10 / 62	TF	MYC_Targets UP
30	7e−09	28 / 616	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
31	8e−09	20 / 322	GSEA	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
32	1e−08	26 / 546	GSEA	MARTENS_TRETINOIN_RESPONSE_DN
33	2e−08	20 / 335	GSEA	BENPORATH_ES_1
34	3e−08	38 / 1107	TF	ICGC_Myc_targets
35	3e−08	16 / 220	GSEA	BHAT_ESR1_TARGETS_VIA_AKT1_UP
36	4e−08	23 / 466	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
37	6e−08	19 / 327	GSEA	CUI_TCF21_TARGETS_2_UP
38	8e−08	17 / 268	GSEA	MUELLER_PLURINET
39	9e−08	8 / 44	GSEA	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
40	9e−08	9 / 61	GSEA	ZHANG_RESPONSE_TO_CANTHARIDIN_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	3e−12	34 / 653	nucleolus
2	3e−09	8 / 30	small−subunit processome
3	1e−07	17 / 277	mitochondrial matrix
4	2e−07	93 / 4579	nucleus
5	5e−07	61 / 2541	nucleoplasm
6	3e−06	36 / 1221	mitochondrion
7	2e−04	12 / 268	intracellular ribonucleoprotein complex
8	6e−04	3 / 13	exosome (RNase complex)
9	2e−03	3 / 20	preribosome, large subunit precursor
10	3e−03	6 / 107	fibrillar center
11	7e−03	2 / 10	Swr1 complex
12	9e−03	2 / 11	Fanconi anaemia nuclear complex
13	1e−02	2 / 12	Ino80 complex
14	1e−02	3 / 38	mitochondrial nucleoid
15	1e−02	4 / 70	nuclear pore

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−09	28 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	3e−07	24 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	2e−04	10 / 184	Kosinski_lower−crypt−long−list
4	5e−02	12 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	8e−02	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
6	8e−02	1 / 6	Marisa_CRC−C6
7	9e−02	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
8	1e−01	3 / 83	Marisa_CRC−cluster−d
9	1e−01	1 / 12	Juehling−MSI−enriched−in−6
10	2e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	2e−01	27 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	3e−01	18 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	5e−01	4 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	6e−01	9 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	7e−01	6 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

HM

Rank	p−value	#in/all	Geneset
1	1e−22	19 / 55	HALLMARK_MYC_TARGETS_V2
2	6e−14	21 / 190	HALLMARK_MYC_TARGETS_V1
3	2e−07	14 / 187	HALLMARK_E2F_TARGETS
4	1e−05	9 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	4e−03	8 / 195	HALLMARK_G2M_CHECKPOINT
6	1e−02	7 / 192	HALLMARK_MTORC1_SIGNALING
7	3e−02	6 / 174	HALLMARK_ADIPOGENESIS
8	3e−02	6 / 181	HALLMARK_XENOBIOTIC_METABOLISM
9	4e−02	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	4e−02	6 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	1e−01	5 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	1e−01	3 / 97	HALLMARK_BILE_ACID_METABOLISM
13	3e−01	3 / 133	HALLMARK_DNA_REPAIR
14	3e−01	3 / 149	HALLMARK_UV_RESPONSE_UP
15	4e−01	2 / 96	HALLMARK_ANDROGEN_RESPONSE

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−09	20 / 305	TARTE_Plasmablast signature
2	6e−07	87 / 4261	HOPP_Txn_transition
3	9e−05	10 / 173	Victora_Light zone signature
4	2e−04	96 / 5529	HOPP_Txn_elongation
5	6e−04	99 / 5908	HOPP_Active_promoter
6	2e−03	6 / 97	ROSOLOWSKI_red total
7	5e−03	88 / 5404	HOPP_Strong_enhancer
8	1e−02	5 / 99	Sha_BL UP
9	2e−02	2 / 18	WRIGHT_ABC UP
10	3e−02	4 / 85	Aukema_BCL2 DN_BCL6 UP
11	3e−02	4 / 88	ROSOLOWSKI_green UP
12	4e−02	2 / 25	ROSOLOWSKI_red UP
13	4e−02	9 / 353	SPANG_CD40 6hrs DN
14	5e−02	18 / 906	SPANG_BCR DN
15	7e−02	4 / 121	ROSOLOWSKI_green total

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 16	hsa−miR−380*
2	0.03	2 / 19	hsa−miR−943
3	0.03	3 / 49	hsa−miR−671−5p
4	0.03	4 / 87	hsa−miR−146b−5p
5	0.03	4 / 89	hsa−miR−146a
6	0.04	3 / 55	hsa−miR−637
7	0.04	3 / 59	hsa−miR−1266
8	0.05	2 / 26	hsa−miR−934
9	0.05	3 / 64	hsa−miR−486−3p
10	0.06	2 / 30	hsa−miR−518e
11	0.06	1 / 5	hsa−miR−339−3p
12	0.06	1 / 5	hsa−miR−126
13	0.07	3 / 73	hsa−miR−423−5p
14	0.07	2 / 34	hsa−miR−760
15	0.07	5 / 171	hsa−miR−196a

Telomeres

Rank	p−value	#in/all	Geneset
1	0.05	2 / 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	

BP

Rank	p−value	#in/all	Geneset
1	1e−09	16 / 174	rRNA processing
2	2e−05	5 / 27	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
3	1e−04	5 / 38	lactation
4	6e−04	8 / 144	methylation
5	7e−04	3 / 14	positive regulation of telomerase RNA localization to Cajal body
6	7e−04	13 / 351	cellular response to DNA damage stimulus
7	1e−03	5 / 59	positive regulation of protein targeting to mitochondrion
8	1e−03	11 / 281	DNA repair
9	2e−03	3 / 20	ribosomal large subunit biogenesis
10	2e−03	5 / 71	mitochondrion organization
11	3e−03	5 / 76	DNA recombination
12	3e−03	5 / 76	ribosome biogenesis
13	5e−03	3 / 26	exonucleolytic nuclear−transcribed mRNA catabolic process involved in deade
14	5e−03	3 / 27	DNA biosynthetic process
15	6e−03	4 / 56	cellular response to drug

Chr

Rank	p−value	#in/all	Geneset
1	0.006	15 / 548	Chr 16
2	0.013	19 / 833	Chr 19
3	0.024	10 / 369	Chr 20
4	0.071	15 / 756	Chr 11
5	0.110	4 / 139	Chr 21
6	0.148	7 / 333	Chr 22
7	0.392	4 / 242	Chr 13
8	0.418	1 / 41	Chr Y
9	0.463	7 / 490	Chr 10
10	0.553	9 / 689	Chr 3
11	0.612	5 / 403	Chr 14
12	0.657	10 / 832	Chr 2
13	0.683	5 / 437	Chr 8
14	0.695	9 / 776	Chr 17
15	0.742	4 / 382	Chr 15

Glioma

Rank	p−value	#in/all	Geneset
1	1e−06	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	7e−03	16 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
3	3e−02	26 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	4e−02	28 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−01	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
6	1e−01	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
7	1e−01	2 / 52	GIEZELT_GBM_WT_down_VS_mut
8	2e−01	1 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
9	2e−01	2 / 58	Stuehler_Proteins_up_in_STS
10	2e−01	1 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN
11	3e−01	1 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
12	3e−01	1 / 32	WIRTH_PN subtype
13	4e−01	1 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
14	4e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	4e−01	1 / 35	Gorovets_LGG_EPL_subclass

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	2 / 19	Angelova_immune−metagene−activated_CD8
2	0.06	1 / 5	Angelova_immune−metagene−NK56_bright
3	0.16	1 / 13	Angelova_immune−metagene−immature_B−cells
4	0.21	1 / 18	Angelova_immune−metagene−pDC
5	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
6	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
7	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
8	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
9	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
10	1.00	0 / 25	Angelova_immune−metagene−DC
11	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
12	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
13	1.00	0 / 14	Angelova_immune−metagene−eosinophil
14	1.00	0 / 19	Angelova_immune−metagene−iDC
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−07	17 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	9e−02	2 / 38	Tirosh_top50 correlated genes PC1
3	1e−01	7 / 319	Gerber_wt/wt_melanoma−cells−SpotA
4	3e−01	2 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
5	3e−01	2 / 81	Tirosh_Genes in the MITF program
6	3e−01	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
7	4e−01	4 / 230	Gerber_wt/wt_melanoma−cells−SpotC
8	4e−01	1 / 39	Tirosh_melanoma specific genes
9	4e−01	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
10	4e−01	3 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	4e−01	1 / 44	Tirosh_top50 correlated genes PC2
12	6e−01	1 / 65	Harbst_melanoma_highgrade_up
13	6e−01	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
14	7e−01	2 / 189	Tirosh_genes preferentially expressed by Tregs
15	8e−01	2 / 236	Gerber_wt/wt_group3−specific

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.4	1 / 41	Scicluna_DN
3	0.5	1 / 54	Burnham_timecourse
4	0.8	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
5	1.0	0 / 68	Burnham_sep_vs_con_UP
6	1.0	0 / 56	Burnham_sep_vs_con_DN
7	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
8	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
9	1.0	0 / 48	Burnham_viral_DN
10	1.0	0 / 57	Burnham_viral_UP
11	1.0	0 / 57	Burnham_day1_vs_5_UP
12	1.0	0 / 52	Burnham_day1_vs_5_DN
13	1.0	0 / 18	Scicluna_UP
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

TF

Rank	p−value	#in/all	Geneset
1	7e−09	10 / 62	MYC_Targets UP
2	3e−08	38 / 1107	ICGC_Myc_targets
3	4e−06	5 / 19	MYC_Metabolism UP
4	1e−05	35 / 1241	KIM_MYC targets
5	5e−04	61 / 3150	ICGC_Creb1_targets
6	5e−04	67 / 3564	ICGC_Taf1_targets
7	2e−03	16 / 549	ICGC_Atf3_targets
8	3e−03	67 / 3804	ICGC_Stat5_targets
9	3e−03	57 / 3121	ICGC_Egr1_targets
10	4e−03	30 / 1387	HEBENSTREIT_high expression TF
11	6e−03	70 / 4131	ICGC_Tcf3_targets
12	7e−03	2 / 10	MYC_RNA processing binding UP
13	8e−03	72 / 4319	ICGC_Pou2_targets
14	8e−03	23 / 1032	ICGC_Usf1_targets
15	1e−02	31 / 1578	ICGC_GabpPcr2_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	19 / 409	Lembcke_Normal vs Adenoma
2	3e−05	4 / 14	BENTINK_myc.1
3	1e−04	5 / 36	ZHANG_MM up
4	1e−03	3 / 16	WOLFER_overlap genes
5	2e−03	4 / 41	PanCan_DNARepair_geneset_nanostring
6	3e−03	1 / 11	LIU_PROSTATE_CANCER_UP
7	7e−03	4 / 58	SHAUGHNESSY_MM high risk
8	2e−02	2 / 16	GENTLES_modul6
9	2e−02	3 / 45	KUIPER_MM poor survival
10	3e−02	5 / 130	PanCan_CC+Apop_geneset_nanostring
11	4e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
12	5e−02	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1e−01	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1e−01	1 / 10	GENTLES_modul5
15	2e−01	1 / 13	GENTLES_modul1

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−16	156 / 8370	natural killer cells peripheral blood_2_TssAFlnk
2	7e−16	152 / 7957	Tcells peripheral blood_2_TssAFlnk
3	5e−15	155 / 8406	Bcells peripheral blood_2_TssAFlnk
4	6e−15	153 / 8200	monocytes peripheral blood_2_TssAFlnk
5	5e−14	152 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
6	2e−13	147 / 7833	Bcells peripheral blood_1_TssA
7	4e−13	156 / 8816	Thelper cells peripheral blood_2_TssAFlnk
8	1e−12	148 / 8068	Thelper cells peripheral blood_1_TssA
9	6e−12	135 / 6997	Overlap_fetal_midbrain_K9K27me3
10	6e−12	75 / 2704	4_TxTrans_Fibroblasts
11	1e−11	149 / 8322	T CD8+ naive cells peripheral blood_1_TssA
12	1e−11	92 / 3803	6_EnhG_Fibroblasts
13	2e−11	153 / 8766	2_TssA_Melanocytes
14	2e−11	136 / 7165	Tx_Colon
15	2e−11	148 / 8275	2_TssA_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−38	66 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	6e−27	37 / 280	MANALO_HYPOXIA_DN
3	5e−24	28 / 158	BILD_MYC_ONCOGENIC_SIGNATURE
4	2e−23	48 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	2e−19	45 / 703	LEE_BMP2_TARGETS_DN
6	1e−18	18 / 72	SCHUHMACHER_MYC_TARGETS_UP
7	9e−18	39 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	2e−16	61 / 1527	PUJANA_BRCA1_PCC_NETWORK
9	5e−14	26 / 314	PENG_GLUTAMINE_DEPRIVATION_DN
10	4e−13	20 / 186	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
11	6e−13	37 / 726	PUJANA_CHEK2_PCC_NETWORK
12	9e−13	17 / 129	WELCSH_BRCA1_TARGETS_DN
13	3e−11	17 / 159	SANSOM_APC_TARGETS_REQUIRE_MYC
14	1e−10	30 / 590	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
15	2e−10	39 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.3	1 / 22	DUMEAUX_High bmi enriched genes
3	0.3	3 / 150	Homuth_BMI−associated−genes_UP
4	0.3	1 / 32	Marjolein_ageing−genes_DN
5	0.8	2 / 210	Homuth_BMI−associated−genes_DN
6	1.0	0 / 62	DUMEAUX_Smoking enriched genes
7	1.0	0 / 10	DUMEAUX_Smoking literature genes up
8	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
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	6e−11	44 / 1161	RNA binding
2	1e−05	14 / 267	binding
3	5e−05	4 / 16	snoRNA binding
4	5e−04	4 / 28	Ran GTPase binding
5	5e−04	7 / 106	ligase activity
6	1e−03	3 / 16	3'−5'−exoribonuclease activity
7	2e−03	3 / 19	DNA helicase activity
8	2e−03	3 / 20	DNA−directed DNA polymerase activity
9	4e−03	3 / 24	TBP−class protein binding
10	4e−03	3 / 25	nuclear localization sequence binding
11	4e−03	5 / 81	single−stranded DNA binding
12	6e−03	3 / 28	ATP−dependent DNA helicase activity
13	7e−03	2 / 10	neutral amino acid transmembrane transporter activity
14	8e−03	28 / 1329	transferase activity
15	8e−03	6 / 132	methyltransferase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−05	30 / 1076	PROTEINATLAS_stomach
2	8e−05	22 / 678	PROTEINATLAS_lymph node
3	1e−04	31 / 1161	PROTEINATLAS_colon
4	1e−04	20 / 594	PROTEINATLAS_parathyroid gland
5	3e−04	28 / 1072	PROTEINATLAS_duodenum
6	4e−04	27 / 1032	PROTEINATLAS_small intestine
7	5e−04	27 / 1048	PROTEINATLAS_rectum
8	7e−04	24 / 905	PROTEINATLAS_appendix
9	9e−04	23 / 866	PROTEINATLAS_cerebellum
10	1e−03	19 / 677	PROTEINATLAS_esophagus
11	2e−03	18 / 645	PROTEINATLAS_bone marrow
12	2e−03	17 / 593	PROTEINATLAS_lateral ventricle
13	2e−03	17 / 604	PROTEINATLAS_hippocampus
14	3e−03	20 / 776	PROTEINATLAS_skin
15	3e−03	21 / 840	PROTEINATLAS_urinary bladder

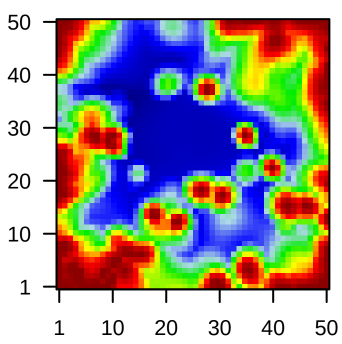
Overexpression Spots

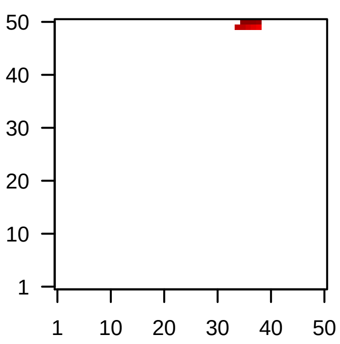
Spot Summary: I

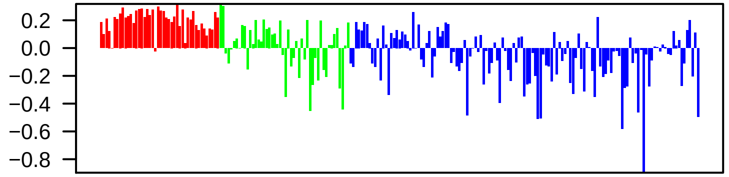
metagenes = 9
genes = 175

<r> metagenes = 0.98
<r> genes = 0.4
beta: r2= 7.91 / log p= −Inf

samples with spot = 31 (14 %)
mBL : 27 (61.4 %)
intermediate : 2 (4.2 %)
non−mBL : 2 (1.6 %)


Overview Map


Spot

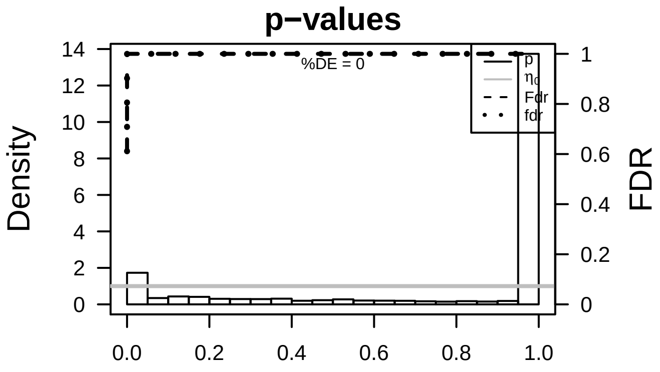


Spot Genelist

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	217127_at	1.5	−1.12	0.4	CTH	cystathionine gamma−lyase [Source:HGNC Symbol;Acc:HGN
3	204720_s_at	1.4	−1.15	0.38	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6 [Source:
4	213610_s_at	1.38	−1.42	0.49	KLHL23	kelch like family member 23 [Source:HGNC Symbol;Acc:HGN
5	204430_s_at	1.22	−1.69	0.22	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
6	222228_s_at	1.16	−0.71	0.31	ALKBH4	alkB homolog 4, lysine demethylase [Source:HGNC Symbol;
7	210389_x_at	1.15	−1.08	0.5	TUBD1	tubulin delta 1 [Source:HGNC Symbol;Acc:HGNC:16811]
8	203946_s_at	1.1	−1.07	0.33	ARG2	arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]
9	207480_s_at	1.09	−1.49	0.3	MEIS2	Meis homeobox 2 [Source:HGNC Symbol;Acc:HGNC:7001]
10	205071_x_at	1.05	−0.85	0.55	XRCC4	X−ray repair cross complementing 4 [Source:HGNC Symbol;
11	202830_s_at	1.02	−0.91	0.46	SLC37A4	solute carrier family 37 member 4 [Source:HGNC Symbol;Ac
12	211793_s_at	1	−0.93	0.34	ABI2	abl interactor 2 [Source:HGNC Symbol;Acc:HGNC:24011]
13	205034_at	1	−1.56	0.72	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
14	218857_s_at	0.98	−1.13	0.44	ASRGL1	asparaginase like 1 [Source:HGNC Symbol;Acc:HGNC:1644
15	215519_x_at	0.97	−0.9	0.36		
16	205628_at	0.96	−1.11	0.54	PRIM2	DNA primase subunit 2 [Source:HGNC Symbol;Acc:HGNC:9
17	203869_at	0.95	−1.05	0.36	USP46	ubiquitin specific peptidase 46 [Source:HGNC Symbol;Acc:H
18	203565_s_at	0.93	−1.18	0.54	MNAT1	MNAT1, CDK activating kinase assembly factor [Source:HGN
19	214358_at	0.92	−0.93	0.52	ACACA	acetyl−CoA carboxylase alpha [Source:HGNC Symbol;Acc:H
20	210559_s_at	0.91	−1.25	0.81	CDK1	cyclin dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−98	85 / 319	Mela	Gerber_wt/wt_melanoma−cells−SpotA
2	2e−86	59 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
3	4e−85	72 / 244	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	2e−82	60 / 137	GSE	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e−74	78 / 431	GSE	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	1e−74	100 / 966	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	6e−65	61 / 254	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	2e−63	8 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	2e−63	8 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	4e−59	68 / 439	GSE	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	4e−56	53 / 219	Refer	WIRTH_GC B−cells
12	4e−55	41 / 95	GSE	ODONNELL_TFRC_TARGETS_DN
13	1e−53	68 / 526	GSE	MARSON_BOUND_BY_E2F4_UNSTIMULATED
14	5e−52	47 / 174	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
15	3e−48	46 / 192	Lymp	Victora_Dark zone signature
16	2e−47	64 / 548	GSE	BENPORATH_CYCLING_GENES
17	2e−46	71 / 758	GSE	NUYTTEN_EZH2_TARGETS_DN
18	2e−45	56 / 400	GSE	PUJANA_BRCA2_PCC_NETWORK
19	8e−45	56 / 409	Canc	Lembcke_Normal vs Adenoma
20	2e−44	35 / 93	GSE	CROONQUIST_IL6_DEPRIVATION_DN
21	2e−42	46 / 250	GSE	HORIUCHI_WTAP_TARGETS_DN
22	3e−41	49 / 321	GSE	BLUM_RESPONSE_TO_SALIRASIB_DN
23	8e−41	27 / 47	Mela	Tirosh_G2/M phase specific genes
24	3e−40	43 / 226	GSE	ZHANG_TLX_TARGETS_60HR_DN
25	6e−40	36 / 131	GSE	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
26	1e−39	31 / 81	GSE	KONG_E2F3_TARGETS
27	2e−39	45 / 271	GSE	REACTOME_CELL_CYCLE_MITOTIC
28	4e−39	27 / 52	GSE	KANG_DOXORUBICIN_RESISTANCE_UP
29	5e−39	43 / 241	GSE	BASAKI_YBX1_TARGETS_UP
30	1e−38	36 / 141	GSE	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
31	1e−38	34 / 117	GSE	CHANG_CYCLING_GENES
32	3e−38	48 / 347	GSE	REACTOME_CELL_CYCLE
33	4e−38	39 / 187	HM	HALLMARK_E2F_TARGETS
34	7e−38	36 / 147	GSE	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
35	8e−38	72 / 1052	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_DN
36	7e−36	31 / 102	GSE	WHITEFORD_PEDIATRIC_CANCER_MARKERS
37	8e−36	30 / 92	GSE	BURTON_ADIPOGENESIS_3
38	8e−36	30 / 92	GSE	LEE_EARLY_T_LYMPHOCYTE_UP
39	2e−35	52 / 497	BP	cell cycle
40	5e−35	43 / 297	GSE	GOLDRATH_ANTIGEN_RESPONSE


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 107	HORVATH_aging_genes meth UP
2	1.0	0 / 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	3e−19	21 / 118	chromosome, centromeric region
2	6e−19	23 / 157	spindle
3	1e−17	29 / 324	chromosome
4	3e−15	17 / 101	kinetochore
5	1e−14	15 / 77	condensed chromosome kinetochore
6	6e−14	17 / 121	midbody
7	3e−13	70 / 2541	nucleoplasm
8	1e−12	98 / 4579	nucleus
9	4e−12	10 / 34	kinesin complex
10	1e−11	38 / 936	cytoskeleton
11	1e−10	13 / 98	spindle pole
12	1e−10	19 / 251	microtubule
13	2e−10	22 / 354	centrosome
14	2e−09	7 / 20	spindle midzone
15	4e−09	80 / 3805	cytosol

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−16	22 / 184	Kosinski_lower−crypt−long−list
2	1e−05	20 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	5e−04	4 / 31	Kosinski_lower−crypt−short−list
4	5e−03	15 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
5	1e−02	31 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
6	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
7	6e−02	17 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	6e−02	20 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	8e−02	15 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
10	8e−02	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
11	9e−02	1 / 8	Boland_CRC−MMR−system
12	9e−02	1 / 8	Marisa_CRC−C1
13	9e−02	1 / 8	Marisa_CRC−C3
14	2e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
15	2e−01	1 / 18	Boland_CRC−MSI−A6−A10

HM

Rank	p−value	#in/all	Geneset
1	4e−38	39 / 187	HALLMARK_E2F_TARGETS
2	4e−33	36 / 195	HALLMARK_G2M_CHECKPOINT
3	8e−17	22 / 173	HALLMARK_MITOTIC_SPINDLE
4	2e−08	12 / 122	HALLMARK_SPERMATOGENESIS
5	2e−03	8 / 192	HALLMARK_MTORC1_SIGNALING
6	6e−03	7 / 182	HALLMARK_GLYCOLYSIS
7	8e−03	7 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
8	2e−02	5 / 133	HALLMARK_DNA_REPAIR
9	8e−02	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	1e−01	2 / 55	HALLMARK_MYC_TARGETS_V2
11	2e−01	4 / 190	HALLMARK_MYC_TARGETS_V1
12	3e−01	3 / 149	HALLMARK_UV_RESPONSE_UP
13	3e−01	3 / 150	HALLMARK_APOPTOSIS
14	3e−01	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
15	3e−01	2 / 97	HALLMARK_PEROXISOME

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−48	46 / 192	Victora_Dark zone signature
2	4e−20	122 / 5529	HOPP_Txn_elongation
3	2e−14	25 / 305	TARTE_Plasmablast signature
4	9e−14	116 / 5908	HOPP_Active_promoter
5	2e−07	82 / 4261	HOPP_Txn_transition
6	7e−06	28 / 955	SPANG_BCR UP
7	1e−05	94 / 5682	HOPP_Weak_promoter
8	2e−04	7 / 102	ROSOLOWSKI_blue total
9	1e−03	6 / 99	Sha_BL UP
10	4e−03	81 / 5404	HOPP_Strong_enhancer
11	5e−03	6 / 135	DAVE_BL−vs−DLBCL
12	2e−02	65 / 4357	HOPP_Weak_txn
13	3e−02	66 / 4559	HOPP_Weak_enhancer
14	4e−02	6 / 213	SPANG_IL21 DN
15	2e−01	1 / 15	BENTINK_mBL UP

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	13 / 474	hsa−miR−20a
2	0.007	8 / 232	hsa−miR−186
3	0.013	3 / 41	hsa−miR−518e*
4	0.016	4 / 82	hsa−miR−210
5	0.017	3 / 46	hsa−miR−208a
6	0.021	2 / 19	hsa−miR−943
7	0.024	5 / 137	hsa−miR−580
8	0.027	8 / 299	hsa−let−7c
9	0.029	4 / 98	hsa−miR−520a−5p
10	0.030	2 / 23	hsa−miR−617
11	0.030	6 / 197	hsa−miR−122
12	0.036	3 / 61	hsa−miR−619
13	0.036	7 / 261	hsa−let−7a
14	0.046	2 / 29	hsa−miR−1231
15	0.048	4 / 115	hsa−miR−135a

Telomeres

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	Alternative lengthening of telomeres
2	0.28	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−35	52 / 497	cell cycle
2	2e−34	43 / 307	cell division
3	1e−21	21 / 91	sister chromatid cohesion
4	2e−15	19 / 137	DNA replication
5	3e−15	15 / 70	chromosome segregation
6	8e−13	15 / 101	mitotic cell cycle
7	6e−11	8 / 21	mitotic sister chromatid segregation
8	6e−11	8 / 21	telomere maintenance via semi−conservative replication
9	9e−11	7 / 14	chromosome condensation
10	1e−10	14 / 119	G2/M transition of mitotic cell cycle
11	7e−10	11 / 71	regulation of G2/M transition of mitotic cell cycle
12	2e−09	8 / 31	DNA replication initiation
13	1e−08	11 / 91	G1/S transition of mitotic cell cycle
14	1e−08	8 / 38	mitotic cytokinesis
15	3e−08	6 / 17	spindle organization

Chr

Rank	p−value	#in/all	Geneset
1	0.05	9 / 403	Chr 14
2	0.07	5 / 184	Chr 18
3	0.13	9 / 490	Chr 10
4	0.17	7 / 382	Chr 15
5	0.21	8 / 480	Chr 4
6	0.23	19 / 1325	Chr 1
7	0.32	11 / 776	Chr 17
8	0.33	8 / 548	Chr 16
9	0.36	5 / 333	Chr 22
10	0.42	6 / 437	Chr 8
11	0.53	6 / 492	Chr 9
12	0.55	9 / 756	Chr 11
13	0.55	3 / 242	Chr 13
14	0.64	4 / 369	Chr 20
15	0.65	6 / 554	Chr 5

Glioma

Rank	p−value	#in/all	Geneset
1	2e−86	59 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	8e−20	16 / 47	developing astrocytes
3	7e−13	13 / 66	Weller_LGG_gradeII−vs−III_DOWN
4	2e−05	37 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−04	6 / 64	cultured astroglia vs. in vivo astrocytes
6	2e−04	31 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	2e−02	3 / 49	OPC
8	2e−02	1 / 2	Phillips Prolif up vs PN & MES
9	6e−02	12 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	2e−01	1 / 15	Mukasa_UP_in_GBM
11	2e−01	1 / 16	VERHAAK_PN subtype
12	2e−01	2 / 64	Weller_LGG_A_vs_O_DOWN
13	4e−01	1 / 45	OL vs. MOG− OL
14	5e−01	1 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
15	5e−01	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl

Immunome

Rank	p−value	#in/all	Geneset
1	5e−21	14 / 26	Angelova_immune−metagene−activated_CD4
2	1e−03	3 / 19	Angelova_immune−metagene−activated_CD8
3	9e−03	2 / 12	Angelova_immune−metagene−memory_B−cells
4	1e−01	1 / 12	Angelova_immune−metagene−effector_memory_CD4
5	4e−01	1 / 38	Angelova_immune−metagene−mast−cells
6	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4
8	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
9	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
10	1e+00	0 / 25	Angelova_immune−metagene−DC
11	1e+00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1e+00	0 / 14	Angelova_immune−metagene−eosinophil
13	1e+00	0 / 19	Angelova_immune−metagene−iDC
14	1e+00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1e+00	0 / 11	Angelova_immune−metagene−macrophages

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−98	85 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	8e−41	27 / 47	Tirosh_G2/M phase specific genes
3	3e−31	26 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
4	2e−29	21 / 44	Tirosh_top50 correlated genes PC2
5	4e−13	11 / 38	Tirosh_G1/S phase specific genes
6	6e−13	13 / 65	Harbst_melanoma_highgrade_up
7	2e−04	5 / 46	Tirosh_top50 correlated genes PC5
8	6e−01	1 / 68	Tirosh_housekeeping_genes
9	6e−01	1 / 81	Tirosh_Genes in the MITF program
10	8e−01	2 / 236	Gerber_wt/wt_group3−specific
11	9e−01	1 / 204	Landsberg_dedifferentiation_down
12	9e−01	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
13	1e+00	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	1e+00	2 / 497	Gerber_wt/wt_melanoma−cells−SpotD
15	1e+00	0 / 17	Hugo_melanoma−all−MET_UP

Pneumonia

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

TF

Rank	p−value	#in/all	Geneset
1	8e−05	59 / 3150	ICGC_Creb1_targets
2	1e−04	64 / 3564	ICGC_Taf1_targets
3	2e−04	66 / 3796	ICGC_Nficsc81335_targets
4	6e−04	64 / 3769	ICGC_Pmlsc71910_targets
5	2e−03	61 / 3703	ICGC_Foxm1_targets
6	4e−03	28 / 1387	HEBENSTREIT_high expression TF
7	4e−03	59 / 3630	ICGC_Sp1_targets
8	5e−03	56 / 3451	ICGC_Atf2_targets
9	6e−03	60 / 3778	ICGC_Pol24_targets
10	6e−03	25 / 1241	KIM_MYC targets
11	8e−03	57 / 3608	ICGC_Tcf12_targets
12	1e−02	33 / 1848	ICGC_Pbx3_targets
13	1e−02	59 / 3804	ICGC_Stat5_targets
14	1e−02	69 / 4602	ICGC_Elf1_targets
15	1e−02	65 / 4319	ICGC_Pou2_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−63	8 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	8e−45	56 / 409	Lembcke_Normal vs Adenoma
3	2e−17	7 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	1e−04	5 / 41	PanCan_DNARepair_geneset_nanostring
5	6e−04	1 / 15	RHODES_CANCER_META_SIGNATURE
6	6e−04	5 / 58	SHAUGHNESSY_MM high risk
7	7e−04	3 / 15	BEN−PORATH_UP
8	8e−04	3 / 16	WOLFER_overlap genes
9	5e−03	6 / 130	PanCan_CC+Apop_geneset_nanostring
10	6e−03	2 / 10	GENTLES_modul3
11	6e−03	3 / 32	KUIPER_MM good survival
12	2e−02	3 / 45	KUIPER_MM poor survival
13	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
14	2e−01	1 / 14	LIU_PROSTATE_CANCER_DN
15	2e−01	1 / 15	WANG_ER_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−19	127 / 6099	HSC_4_Tx
2	3e−19	146 / 8200	monocytes peripheral blood_2_TssAFlnk
3	5e−19	147 / 8370	natural killer cells peripheral blood_2_TssAFlnk
4	2e−17	124 / 6068	4_Tx_ESC_Endoderm
5	5e−17	145 / 8406	Bcells peripheral blood_2_TssAFlnk
6	8e−17	137 / 7489	monocytes peripheral blood_5_TxWk
7	2e−16	143 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
8	4e−16	140 / 7930	Tregulatory cells peripheral blood_1_TssA
9	4e−16	147 / 8816	Thelper cells peripheral blood_2_TssAFlnk
10	3e−15	143 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
11	3e−15	139 / 7957	Tcells peripheral blood_2_TssAFlnk
12	3e−15	136 / 7635	monocytes peripheral blood_1_TssA
13	8e−15	140 / 8143	HSC_5_TxWk
14	1e−14	146 / 8918	1_TssA_ESC_Mesoderm
15	2e−14	141 / 8322	T CD8+ naive cells peripheral blood_1_TssA

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−85	72 / 244	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	2e−82	60 / 137	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	1e−74	78 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	1e−74	100 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
5	6e−65	61 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
6	2e−63	8 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	4e−59	68 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	4e−55	41 / 95	ODONNELL_TFRC_TARGETS_DN
9	1e−53	68 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	5e−52	47 / 174	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	2e−47	64 / 548	BENPORATH_CYCLING_GENES
12	2e−46	71 / 758	NUYTTEN_EZH2_TARGETS_DN
13	2e−45	56 / 400	PUJANA_BRCA2_PCC_NETWORK
14	2e−44	35 / 93	CROONQUIST_IL6_DEPRIVATION_DN
15	2e−42	46 / 250	HORIUCHI_WTAP_TARGETS_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	1 / 8	Marjolein_ageing−genes_UP
2	0.72	2 / 210	Homuth_BMI−associated−genes_DN
3	0.84	1 / 150	Homuth_BMI−associated−genes_UP
4	1.00	0 / 62	DUMEAUX_Smoking enriched genes
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 22	DUMEAUX_High bmi enriched genes
14	1.00	0 / 22	DUMEAUX_Fasting enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	5e−08	10 / 83	microtubule motor activity
2	9e−08	14 / 196	microtubule binding
3	1e−06	34 / 1185	ATP binding
4	3e−06	5 / 20	ATP−dependent microtubule motor activity, plus−end−directed
5	6e−06	36 / 1402	nucleotide binding
6	2e−05	10 / 161	ATPase activity
7	3e−05	118 / 7864	protein binding
8	7e−05	14 / 350	protein kinase binding
9	8e−05	4 / 20	DNA−directed DNA polymerase activity
10	5e−04	6 / 83	motor activity
11	1e−03	4 / 38	4 iron, 4 sulfur cluster binding
12	2e−03	11 / 328	chromatin binding
13	4e−03	3 / 26	cyclin−dependent protein serine/threonine kinase activity
14	4e−03	4 / 53	iron−sulfur cluster binding
15	4e−03	7 / 171	protein C−terminus binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−56	53 / 219	WIRTH_GC B−cells
2	4e−04	26 / 1081	PROTEINATLAS_testis
3	2e−03	15 / 527	PROTEINATLAS_oral mucosa
4	2e−03	19 / 776	PROTEINATLAS_skin
5	3e−03	22 / 989	PROTEINATLAS_tonsil
6	4e−03	16 / 645	PROTEINATLAS_bone marrow
7	6e−03	16 / 671	PROTEINATLAS_cervix, uterine
8	7e−03	16 / 678	PROTEINATLAS_lymph node
9	1e−02	21 / 1032	PROTEINATLAS_small intestine
10	1e−02	2 / 14	WIRTH_Thymus
11	1e−02	15 / 677	PROTEINATLAS_esophagus
12	2e−02	18 / 905	PROTEINATLAS_appendix
13	3e−02	20 / 1072	PROTEINATLAS_duodenum
14	3e−02	19 / 1007	PROTEINATLAS_kidney
15	6e−02	20 / 1161	PROTEINATLAS_colon

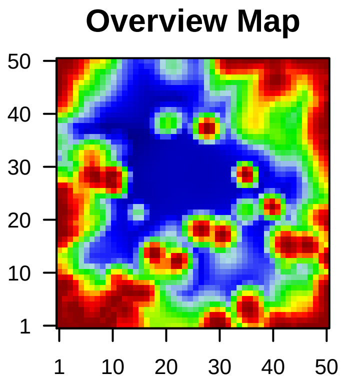
Overexpression Spots

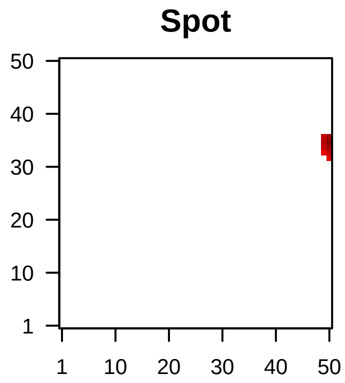
Spot Summary: J

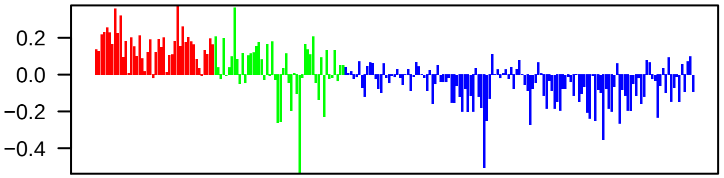
metagenes = 9
genes = 169

<r> metagenes = 0.96
<r> genes = 0.27
beta: r2= 3.95 / log p= −Inf

samples with spot = 14 (6.3 %)
mBL : 11 (25 %)
intermediate : 3 (6.2 %)


Overview Map


Spot

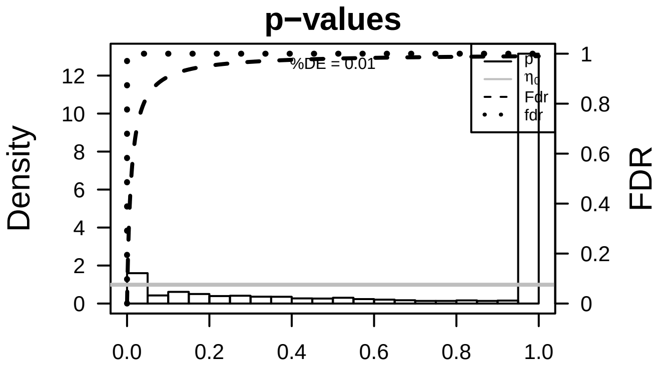


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206233_at	1.81	−0.95	0.2	B4GALT6	beta−1,4−galactosyltransferase 6 [Source:HGNC Symbol;Acc
2	213435_at	1.73	−1.11	0.33	SATB2	SATB homeobox 2 [Source:HGNC Symbol;Acc:HGNC:21637
3	213489_at	1.67	−1.75	0.36	MAPRE2	microtubule associated protein RP/EB family member 2 [Sour
4	221045_s_at	1.42	−0.9	0.15	PER3	period circadian regulator 3 [Source:HGNC Symbol;Acc:HGN
5	202661_at	1.39	−1.1	0.3		
6	214790_at	1.35	−0.72	0.43	SENP6	SUMO1/sentrin specific peptidase 6 [Source:HGNC Symbol;
7	204547_at	1.34	−1.13	0.4	RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Sym
8	208920_at	1.2	−0.9	0.37	SRI	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
9	219312_s_at	1.18	−1.16	0.38	ZBTB10	zinc finger and BTB domain containing 10 [Source:HGNC Sy
10	210379_s_at	1.17	−1.36	0.24	TLK1	tousled like kinase 1 [Source:HGNC Symbol;Acc:HGNC:1184
11	213549_at	1.09	−0.9	0.54	PDZD8	PDZ domain containing 8 [Source:HGNC Symbol;Acc:HGNC
12	203298_s_at	1.07	−1.25	0.27	JARID2	jumonji and AT−rich interaction domain containing 2 [Source:
13	221575_at	1.06	−0.97	0.34	SCLY	selenocysteine lyase [Source:HGNC Symbol;Acc:HGNC:181
14	219676_at	1.05	−0.88	0.37	ZSCAN16	zinc finger and SCAN domain containing 16 [Source:HGNC S
15	208762_at	1.05	−0.78	0.65	SUMO1	small ubiquitin−like modifier 1 [Source:HGNC Symbol;Acc:HG
16	208741_at	1.04	−1.09	0.54	SAP18	Sin3A associated protein 18 [Source:HGNC Symbol;Acc:HGN
17	219342_at	1.03	−1.01	0.46	CASD1	CAS1 domain containing 1 [Source:HGNC Symbol;Acc:HGN
18	213416_at	1.01	−1.54	0.48		
19	216713_at	0.99	−1.62	0.5	KRIT1	KRIT1, ankyrin repeat containing [Source:HGNC Symbol;Acc
20	218247_s_at	0.98	−1.28	0.58	MEX3C	mex−3 RNA binding family member C [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−31	40 / 310	Refer	Chaussabel_3,4_Protein phosphatases
2	1e−24	125 / 5529	Lympl	HOPP_Txn_elongation
3	2e−19	122 / 5908	Lympl	HOPP_Active_promoter
4	2e−17	43 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	4e−15	29 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
6	4e−15	96 / 4261	Lympl	HOPP_Txn_transition
7	1e−14	30 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
8	2e−13	110 / 5682	Lympl	HOPP_Weak_promoter
9	3e−10	43 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
10	3e−10	24 / 448	miRN	hsa−miR−20b
11	4e−10	46 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
12	5e−10	20 / 314	miRN	hsa−miR−372
13	4e−09	22 / 427	miRN	hsa−miR−17
14	4e−09	16 / 216	miRN	hsa−miR−548l
15	4e−09	85 / 4357	Lympl	HOPP_Weak_txn
16	5e−09	23 / 474	miRN	hsa−miR−20a
17	7e−09	16 / 226	miRN	hsa−miR−302b
18	9e−09	87 / 4579	CC	nucleus
19	2e−08	18 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
20	2e−08	12 / 124	miRN	hsa−miR−450b−5p
21	2e−08	43 / 1550	GSEA	PILON_KLF1_TARGETS_DN
22	2e−08	16 / 245	miRN	hsa−miR−302d
23	3e−08	16 / 248	miRN	hsa−miR−520c−3p
24	4e−08	23 / 528	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
25	6e−08	27 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
26	1e−07	17 / 315	miRN	hsa−miR−144
27	1e−07	15 / 245	Refer	Chaussabel_3,9_Kinases
28	2e−07	14 / 212	miRN	hsa−miR−520b
29	2e−07	12 / 150	miRN	hsa−miR−300
30	2e−07	19 / 403	miRN	hsa−miR−106b
31	2e−07	19 / 404	miRN	hsa−miR−103
32	2e−07	18 / 364	miRN	hsa−miR−548n
33	2e−07	19 / 405	miRN	hsa−miR−107
34	2e−07	11 / 126	miRN	hsa−miR−548o
35	2e−07	19 / 407	miRN	hsa−miR−106a
36	2e−07	17 / 328	GSEA	OSMAN_BLADDER_CANCER_UP
37	3e−07	83 / 4559	Lympl	HOPP_Weak_enhancer
38	3e−07	17 / 336	miRN	hsa−miR−519d
39	3e−07	16 / 298	GSEA	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
40	3e−07	15 / 261	miRN	hsa−miR−559


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	1e−05	13 / 260	chromatin organization
2	1e−05	40 / 1764	regulation of transcription, DNA−templated
3	2e−05	38 / 1655	transcription, DNA−templated
4	1e−04	6 / 68	protein sumoylation
5	2e−04	4 / 27	intrinsic apoptotic signaling pathway in response to DNA damage by p53 clas
6	1e−03	3 / 18	regulation of cell morphogenesis
7	2e−03	14 / 497	cell cycle
8	6e−03	3 / 33	autophagosome assembly
9	8e−03	2 / 12	regulation of cardiac muscle cell contraction
10	9e−03	2 / 13	muscle cell differentiation
11	9e−03	2 / 13	regulation of interferon−gamma−mediated signaling pathway
12	1e−02	3 / 39	regulation of cell adhesion
13	1e−02	2 / 14	regulation of establishment of cell polarity
14	1e−02	3 / 42	histone deacetylation
15	1e−02	2 / 15	microtubule nucleation

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	1 / 12	LIU_BREAST_CANCER
2	0.008	2 / 12	BENTINK_ras.1
3	0.011	2 / 14	BENTINK_src.2
4	0.041	2 / 28	PanCan_HK_geneset_nanostring
5	0.064	2 / 36	ZHANG_MM up
6	0.130	1 / 12	GENTLES_modul12
7	0.130	1 / 12	BENTINK_e2f3.2
8	0.150	1 / 14	GENTLES_modul10
9	0.150	1 / 14	BENTINK_myc.1
10	0.252	1 / 25	PanCan_HH_geneset_nanostring
11	0.375	2 / 113	PanCan_Driver_Gene_geneset_nanostring
12	0.407	1 / 45	KUIPER_MM poor survival
13	0.420	0 / 14	LIU_COMMON_CANCER_GENES
14	0.567	1 / 72	PanCan_Wnt_geneset_nanostring
15	0.672	1 / 96	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	9e−09	87 / 4579	nucleus
2	6e−06	8 / 86	PML body
3	3e−04	4 / 29	histone deacetylase complex
4	4e−04	12 / 326	nuclear speck
5	7e−04	46 / 2541	nucleoplasm
6	7e−03	3 / 35	nuclear inner membrane
7	8e−03	6 / 149	nuclear envelope
8	9e−03	4 / 70	nuclear pore
9	9e−03	2 / 13	ESC/E(Z) complex
10	1e−02	4 / 73	ubiquitin ligase complex
11	1e−02	3 / 39	cell leading edge
12	1e−02	3 / 42	transcriptional repressor complex
13	1e−02	2 / 15	phagophore assembly site membrane
14	2e−02	2 / 19	nuclear periphery
15	3e−02	7 / 251	microtubule

Chr

Rank	p−value	#in/all	Geneset
1	0.007	8 / 242	Chr 13
2	0.030	16 / 832	Chr 2
3	0.045	13 / 669	Chr 6
4	0.060	13 / 700	Chr 12
5	0.075	11 / 585	Chr 7
6	0.107	10 / 554	Chr 5
7	0.163	4 / 184	Chr 18
8	0.171	11 / 689	Chr 3
9	0.189	8 / 480	Chr 4
10	0.204	8 / 490	Chr 10
11	0.569	5 / 437	Chr 8
12	0.674	5 / 492	Chr 9
13	0.802	1 / 139	Chr 21
14	0.802	3 / 369	Chr 20
15	0.847	3 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−27	134 / 6099	HSC_4_Tx
2	3e−27	128 / 5527	Tregulatory cells peripheral blood_4_Tx
3	2e−26	116 / 4528	T CD8+ naive cells peripheral blood_4_Tx
4	1e−25	128 / 5716	Bcells peripheral blood_4_Tx
5	2e−24	127 / 5753	Tcells peripheral blood_4_Tx
6	5e−23	125 / 5738	monocytes peripheral blood_4_Tx
7	5e−22	124 / 5766	natural killer cells peripheral blood_4_Tx
8	6e−22	139 / 7420	Tcells peripheral blood_1_TssA
9	9e−22	122 / 5601	Thelper cells peripheral blood_4_Tx
10	2e−21	141 / 7751	natural killer cells peripheral blood_1_TssA
11	2e−21	140 / 7635	monocytes peripheral blood_1_TssA
12	1e−19	124 / 6068	4_Tx_ESC_Endoderm
13	4e−19	139 / 7833	Bcells peripheral blood_1_TssA
14	7e−19	126 / 6389	4_Tx_ESC_Mesoderm
15	1e−18	130 / 6839	T CD8+ naive cells peripheral blood_5_TxWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	41 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
2	9e−06	31 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	1e−04	23 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
4	1e−04	31 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	2e−03	4 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
6	3e−03	20 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	7e−03	20 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	8e−03	13 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
9	9e−03	18 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
10	1e−02	22 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	2e−02	13 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
12	4e−02	18 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
13	7e−02	3 / 83	Marisa_CRC−cluster−d
14	1e−01	10 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	1e−01	9 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans

Glioma

Rank	p−value	#in/all	Geneset
1	3e−10	43 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	4e−10	46 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	3e−05	14 / 330	Up
4	6e−04	5 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	3e−03	4 / 52	GIEZELT_GBM_WT_down_VS_mut
6	1e−02	14 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	4e−02	7 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	7e−02	1 / 6	Donson−adaptive−immunity−associated with LTS in HGA
9	2e−01	1 / 15	neurons_glio
10	2e−01	2 / 64	Weller_LGG_A_vs_O_DOWN
11	2e−01	2 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	2e−01	1 / 21	Barbus_GBM_STS_vs._LTS
13	2e−01	1 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)
14	2e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
15	3e−01	1 / 32	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−17	43 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	4e−15	29 / 417	SHEN_SMARCA2_TARGETS_UP
3	1e−14	30 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
4	2e−08	18 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
5	2e−08	43 / 1550	PILON_KLF1_TARGETS_DN
6	4e−08	23 / 528	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
7	6e−08	27 / 730	ONKEN_UVEAL_MELANOMA_UP
8	2e−07	17 / 328	OSMAN_BLADDER_CANCER_UP
9	3e−07	16 / 298	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
10	6e−07	24 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
11	9e−07	36 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
12	1e−06	11 / 147	WANG_CLIM2_TARGETS_DN
13	1e−06	10 / 122	YAGI_AML_WITH_T_9_11_TRANSLOCATION
14	3e−06	23 / 673	SCHLOSSER_SERUM_RESPONSE_DN
15	3e−06	14 / 269	JOHNSTONE_PARVB_TARGETS_2_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	4 / 96	HALLMARK_ANDROGEN_RESPONSE
2	0.07	5 / 190	HALLMARK_MYC_TARGETS_V1
3	0.07	5 / 195	HALLMARK_G2M_CHECKPOINT
4	0.17	3 / 122	HALLMARK_SPERMATOGENESIS
5	0.18	4 / 192	HALLMARK_MTORC1_SIGNALING
6	0.19	4 / 194	HALLMARK_KRAS_SIGNALING_UP
7	0.32	3 / 173	HALLMARK_MITOTIC_SPINDLE
8	0.35	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	0.37	3 / 187	HALLMARK_E2F_TARGETS
10	0.37	3 / 187	HALLMARK_INFLAMMATORY_RESPONSE
11	0.48	2 / 141	HALLMARK_UV_RESPONSE_DN
12	0.62	2 / 182	HALLMARK_GLYCOLYSIS
13	0.64	2 / 188	HALLMARK_HYPOXIA
14	0.65	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	0.66	1 / 94	HALLMARK_PROTEIN_SECRETION

Immunome

Rank	p−value	#in/all	Geneset
1	0.4	1 / 45	Angelova_immune−metagene−MDSC
2	0.5	1 / 67	Angelova_immune−metagene−T−cells
3	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
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	0.8	1 / 150	Homuth_BMI−associated−genes_UP
2	0.9	1 / 210	Homuth_BMI−associated−genes_DN
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 22	DUMEAUX_High bmi enriched genes
13	1.0	0 / 22	DUMEAUX_Fasting enriched genes
14	1.0	0 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−24	125 / 5529	HOPP_Txn_elongation
2	2e−19	122 / 5908	HOPP_Active_promoter
3	4e−15	96 / 4261	HOPP_Txn_transition
4	2e−13	110 / 5682	HOPP_Weak_promoter
5	4e−09	85 / 4357	HOPP_Weak_txn
6	3e−07	83 / 4559	HOPP_Weak_enhancer
7	2e−04	84 / 5404	HOPP_Strong_enhancer
8	3e−04	23 / 906	SPANG_BCR DN
9	3e−03	21 / 955	SPANG_BCR UP
10	5e−03	8 / 227	SPANG_IL21 UP
11	1e−02	31 / 1814	HOPP_Repetitive
12	3e−02	3 / 57	SPANG_LPS 6hrs DN
13	1e−01	5 / 213	SPANG_IL21 DN
14	1e−01	3 / 102	ROSOLOWSKI_blue total
15	1e−01	7 / 353	SPANG_CD40 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	6 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	0.2	1 / 23	Melanoma Epi−Enzyme Cluster 7
3	0.3	4 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.4	1 / 38	Tirosh_G1/S phase specific genes
5	0.4	3 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	0.4	1 / 39	Tirosh_melanoma specific genes
7	0.4	1 / 46	Tirosh_top50 correlated genes PC5
8	0.4	1 / 47	Tirosh_G2/M phase specific genes
9	0.5	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
10	0.5	1 / 65	Harbst_melanoma_highgrade_up
11	0.5	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	0.6	1 / 81	Tirosh_Genes in the MITF program
13	0.8	4 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	0.9	1 / 204	Landsberg_dedifferentiation_down
15	0.9	1 / 236	Gerber_wt/wt_group3−specific

MF

Rank	p−value	#in/all	Geneset
1	3e−04	111 / 7864	protein binding
2	5e−04	3 / 14	SUMO transferase activity
3	4e−03	5 / 93	histone deacetylase binding
4	6e−03	3 / 32	histone deacetylase activity
5	8e−03	2 / 12	calcium−transporting ATPase activity
6	9e−03	18 / 852	nucleic acid binding
7	9e−03	2 / 13	GTP−Rho binding
8	1e−02	2 / 15	poly(A) binding
9	1e−02	22 / 1161	RNA binding
10	1e−02	6 / 171	protein C−terminus binding
11	1e−02	2 / 16	calcium−dependent cysteine−type endopeptidase activity
12	1e−02	2 / 16	RNA polymerase binding
13	1e−02	9 / 331	protein serine/threonine kinase activity
14	2e−02	27 / 1541	DNA binding
15	2e−02	22 / 1185	ATP binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−10	24 / 448	hsa−miR−20b
2	5e−10	20 / 314	hsa−miR−372
3	4e−09	22 / 427	hsa−miR−17
4	4e−09	16 / 216	hsa−miR−548l
5	5e−09	23 / 474	hsa−miR−20a
6	7e−09	16 / 226	hsa−miR−302b
7	2e−08	12 / 124	hsa−miR−450b−5p
8	2e−08	16 / 245	hsa−miR−302d
9	3e−08	16 / 248	hsa−miR−520c−3p
10	1e−07	17 / 315	hsa−miR−144
11	2e−07	14 / 212	hsa−miR−520b
12	2e−07	12 / 150	hsa−miR−300
13	2e−07	19 / 403	hsa−miR−106b
14	2e−07	19 / 404	hsa−miR−103
15	2e−07	18 / 364	hsa−miR−548n

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	6 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.38	1 / 41	Scicluna_DN
3	0.47	1 / 54	Burnham_timecourse
4	0.48	1 / 57	Burnham_viral_UP
5	1.00	0 / 68	Burnham_sep_vs_con_UP
6	1.00	0 / 56	Burnham_sep_vs_con_DN
7	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
8	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
9	1.00	0 / 48	Burnham_viral_DN
10	1.00	0 / 57	Burnham_day1_vs_5_UP
11	1.00	0 / 52	Burnham_day1_vs_5_DN
12	1.00	0 / 18	Scicluna_UP
13	1.00	0 / 37	Sweeney_viral_up
14	1.00	0 / 33	Sweeney_viral_dn
15	1.00	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−31	40 / 310	Chaussabel_3,4_Protein phosphatases
2	1e−07	15 / 245	Chaussabel_3,9_Kinases
3	2e−04	7 / 106	Chaussabel_2,11_Replication
4	1e−03	8 / 188	Chaussabel_3,8_Enzymes
5	2e−03	6 / 113	Chaussabel_1,8_Metabolism Biosynthesis
6	8e−03	18 / 840	PROTEINATLAS_urinary bladder
7	8e−03	6 / 152	VAQUERIZAS_General_TF
8	2e−02	18 / 923	PROTEINATLAS_cerebral cortex
9	2e−02	13 / 593	PROTEINATLAS_lateral ventricle
10	2e−02	13 / 604	PROTEINATLAS_hippocampus
11	3e−02	16 / 848	PROTEINATLAS_adrenal gland
12	4e−02	3 / 66	VAQUERIZAS_Whole blood_TF
13	4e−02	16 / 866	PROTEINATLAS_cerebellum
14	4e−02	19 / 1081	PROTEINATLAS_testis
15	4e−02	12 / 595	PROTEINATLAS_breast

Telomeres

Rank	p−value	#in/all	Geneset
1	0.009	2 / 13	Alternative lengthening of telomeres
2	0.269	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	0.01	57 / 3778	ICGC_Pol24_targets
2	0.01	54 / 3564	ICGC_Taf1_targets
3	0.02	56 / 3769	ICGC_Pmlsc71910_targets
4	0.02	20 / 1044	ICGC_Six5_targets
5	0.02	56 / 3796	ICGC_Nficsc81335_targets
6	0.02	28 / 1630	ICGC_SrfV0416101_targets
7	0.02	1 / 2	MYC_Chromatin_modification UP
8	0.02	53 / 3608	ICGC_Tcf12_targets
9	0.03	44 / 2899	ICGC_Nfatc1_targets
10	0.03	24 / 1387	HEBENSTREIT_high expression TF
11	0.03	47 / 3150	ICGC_Creb1_targets
12	0.03	25 / 1494	ICGC_Cebpbsc150_targets
13	0.04	50 / 3451	ICGC_Atf2_targets
14	0.04	11 / 522	ICGC_SrfPcr2_targets
15	0.04	54 / 3804	ICGC_Stat5_targets

Overexpression Spots

Spot Summary: K

metagenes = 4
genes = 157

<r> metagenes = 1
<r> genes = 0.29
beta: r2= 2.33 / log p= −Inf

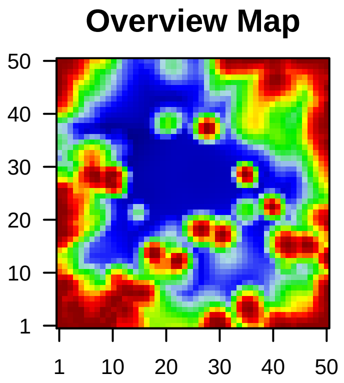
samples with spot = 3 (1.4 %)
mBL : 2 (4.5 %)
non−mBL : 1 (0.8 %)

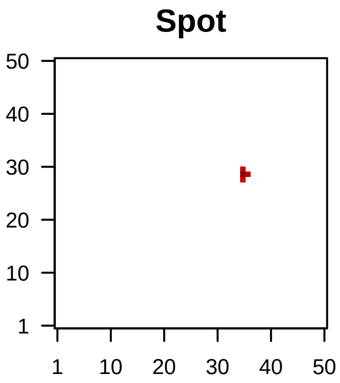
Spot Genelist

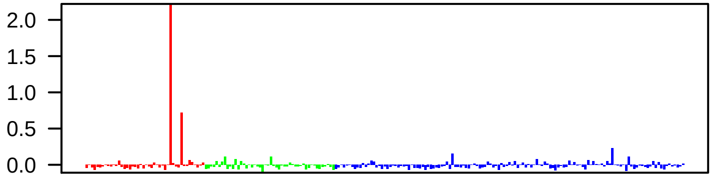
Rank	ID	max e	min e	r	Symbol	Description
1	219465_at	3.55	−0.52	0.79	APOA2	apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
2	208470_s_at	3.52	−0.84	0.63	HPR	haptoglobin−related protein [Source:HGNC Symbol;Acc:HGN
3	219466_s_at	3.5	−0.5	0.82	APOA2	apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
4	211298_s_at	3.41	−0.62	0.78	ALB	albumin [Source:HGNC Symbol;Acc:HGNC:399]
5	203400_s_at	3.34	−0.63	0.74	TF	transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
6	217238_s_at	3.3	−0.55	0.71	ALDOB	aldolase, fructose−bisphosphate B [Source:HGNC Symbol;A
7	205820_s_at	3.27	−0.63	0.7	APOC3	apolipoprotein C3 [Source:HGNC Symbol;Acc:HGNC:610]
8	206697_s_at	3.26	−0.73	0.57	HP	haptoglobin [Source:HGNC Symbol;Acc:HGNC:5141]
9	204988_at	3.25	−0.63	0.7	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	0.76	GC	GC, vitamin D binding protein [Source:HGNC Symbol;Acc:H
12	209937_at	3.14	−0.36	0.78	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	0.69	RBP4	retinol binding protein 4 [Source:HGNC Symbol;Acc:HGNC:
15	206226_at	3.08	−0.56	0.7	HRG	histidine rich glycoprotein [Source:HGNC Symbol;Acc:HGNC
16	210929_s_at	3.08	−0.82	0.67	AHSG	alpha 2−HS glycoprotein [Source:HGNC Symbol;Acc:HGNC:
17	214063_s_at	3.07	−0.61	0.74	TF	transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
18	205650_s_at	3.06	−0.63	0.69	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	0.74	FGB	fibrinogen beta chain [Source:HGNC Symbol;Acc:HGNC:366

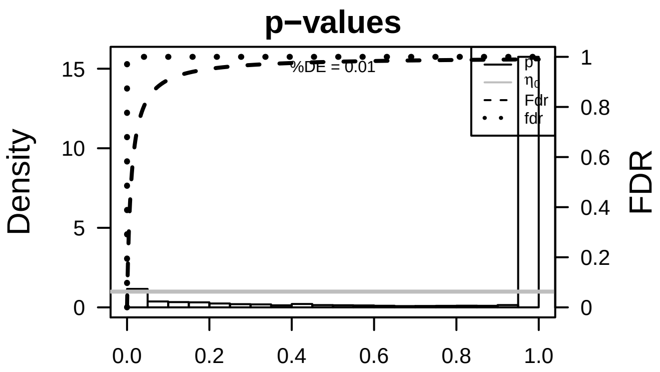
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	79 / 218	GSE	HSIAO_LIVER_SPECIFIC_GENES
2	6e−78	48 / 94	Refer	WIRTH_Liver
3	2e−39	37 / 208	GSE	CAIRO_LIVER_DEVELOPMENT_DN
4	4e−37	30 / 116	CC	blood microparticle
5	9e−34	35 / 243	GSE	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
6	2e−33	35 / 250	GSE	CAIRO_HEPATOBLASTOMA_DN
7	4e−32	29 / 147	GSE	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
8	8e−31	65 / 1611	CC	extracellular region
9	5e−29	38 / 421	GSE	ACEVEDO_LIVER_CANCER_DN
10	2e−28	21 / 64	GSE	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
11	6e−27	52 / 1090	CC	extracellular space
12	6e−27	19 / 52	GSE	SU_LIVER
13	8e−26	35 / 410	GSE	PILON_KLF1_TARGETS_UP
14	3e−24	67 / 2239	CC	extracellular exosome
15	8e−22	22 / 144	GSE	LEE_LIVER_CANCER_SURVIVAL_UP
16	2e−21	21 / 130	HM	HALLMARK_COAGULATION
17	2e−20	18 / 88	BP	negative regulation of endopeptidase activity
18	2e−19	16 / 67	GSE	YAMASHITA_LIVER_CANCER_STEM_CELL_DN
19	6e−19	19 / 124	GSE	SERVITJA_LIVER_HNF1A_TARGETS_DN
20	1e−18	52 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
21	5e−18	14 / 51	BP	hemostasis
22	5e−18	26 / 337	GSE	BOCHKIS_FOXA2_TARGETS
23	8e−18	17 / 100	GSE	OHGUCHI_LIVER_HNF4A_TARGETS_DN
24	2e−17	12 / 32	BP	acute−phase response
25	2e−17	28 / 429	Refer	PROTEINATLAS_liver
26	1e−15	19 / 185	BP	cellular protein metabolic process
27	2e−15	19 / 189	GSE	NABA_ECM_REGULATORS
28	3e−15	13 / 61	MF	serine−type endopeptidase inhibitor activity
29	4e−15	11 / 35	GSE	LEE_LIVER_CANCER
30	4e−15	14 / 79	CC	organelle membrane
31	1e−14	12 / 51	GSE	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
32	2e−14	15 / 110	BP	platelet degranulation
33	5e−14	9 / 21	BP	fibrinolysis
34	8e−14	13 / 77	GSE	WOO_LIVER_CANCER_RECURRENCE_DN
35	8e−14	23 / 376	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
36	2e−13	14 / 103	GSE	REACTOME_BIOLOGICAL_OXIDATIONS
37	2e−13	17 / 181	HM	HALLMARK_XENOBIOTIC_METABOLISM
38	3e−13	9 / 25	GSE	REACTOME_COMPLEMENT_CASCADE
39	5e−13	36 / 1092	GSE	YOSHIMURA_MAPK8_TARGETS_UP
40	1e−12	10 / 41	GSE	KEGG_RETINOL_METABOLISM


Overview Map


Spot




p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 92	HORVATH_aging_genes meth DOWN
2	0.6	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−20	18 / 88	negative regulation of endopeptidase activity
2	5e−18	14 / 51	hemostasis
3	2e−17	12 / 32	acute−phase response
4	1e−15	19 / 185	cellular protein metabolic process
5	2e−14	15 / 110	platelet degranulation
6	5e−14	9 / 21	fibrinolysis
7	4e−11	12 / 98	steroid metabolic process
8	5e−11	11 / 78	negative regulation of peptidase activity
9	2e−10	14 / 172	blood coagulation
10	6e−10	9 / 53	regulation of complement activation
11	4e−09	9 / 66	xenobiotic metabolic process
12	1e−08	15 / 271	post−translational protein modification
13	1e−08	8 / 52	complement activation, classical pathway
14	5e−08	5 / 13	low−density lipoprotein particle remodeling
15	5e−08	5 / 13	regulation of blood coagulation

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 16	LIU_LIVER_CANCER
2	2e−02	9 / 480	Lembcke_Colonic Inflammation
3	1e−01	1 / 13	GENTLES_modul17
4	1e−01	1 / 14	GENTLES_modul13
5	1e−01	1 / 16	GENTLES_modul6
6	5e−01	0 / 11	LIU_PROSTATE_CANCER_UP
7	5e−01	1 / 80	PanCan_JAK−ST_geneset_nanostring
8	8e−01	1 / 187	PanCan_PI3K_geneset_nanostring
9	8e−01	0 / 14	LIU_PROSTATE_CANCER_DN
10	9e−01	2 / 409	Lembcke_Normal vs Adenoma
11	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1e+00	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	4e−37	30 / 116	blood microparticle
2	8e−31	65 / 1611	extracellular region
3	6e−27	52 / 1090	extracellular space
4	3e−24	67 / 2239	extracellular exosome
5	4e−15	14 / 79	organelle membrane
6	2e−12	18 / 241	endoplasmic reticulum lumen
7	1e−10	10 / 63	platelet alpha granule lumen
8	9e−09	6 / 19	high−density lipoprotein particle
9	3e−08	5 / 12	chylomicron
10	4e−08	21 / 604	intracellular membrane−bounded organelle
11	2e−07	5 / 16	very−low−density lipoprotein particle
12	3e−06	4 / 13	endocytic vesicle lumen
13	5e−06	19 / 683	endoplasmic reticulum membrane
14	4e−05	14 / 462	cell surface
15	8e−05	9 / 212	extracellular matrix

Chr

Rank	p−value	#in/all	Geneset
1	0.003	11 / 480	Chr 4
2	0.058	17 / 1325	Chr 1
3	0.071	10 / 689	Chr 3
4	0.127	7 / 490	Chr 10
5	0.235	7 / 585	Chr 7
6	0.420	8 / 832	Chr 2
7	0.517	5 / 554	Chr 5
8	0.558	6 / 700	Chr 12
9	0.612	4 / 492	Chr 9
10	0.634	6 / 756	Chr 11
11	0.675	3 / 403	Chr 14
12	0.696	4 / 548	Chr 16
13	0.797	1 / 184	Chr 18
14	0.829	2 / 369	Chr 20
15	0.831	4 / 669	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−05	39 / 2374	9_ReprPCWk_Fibroblasts
2	2e−05	39 / 2375	10_ReprPC_Fibroblasts
3	4e−05	52 / 3734	Tcells peripheral blood_13_ReprPC
4	3e−04	51 / 3918	Tcells peripheral blood_14_ReprPCWk
5	4e−04	36 / 2417	9_ReprPCWk_Melanocytes
6	1e−03	39 / 2867	9_ReprPCWk_MSC_Adipocyte
7	1e−03	34 / 2408	9_ReprPCWk_Skeletal_Muscle
8	2e−03	19 / 1072	Mid_Frontal_Lobe_ReprPCWk
9	2e−03	32 / 2254	10_ReprPC_MSC_Adipocyte
10	3e−03	36 / 2700	Thelper cells peripheral blood_14_ReprPCWk
11	3e−03	16 / 867	Mid_Frontal_Lobe_Quies
12	4e−03	11 / 502	Mid_Frontal_Lobe_EnhG
13	4e−03	12 / 586	Mid_Frontal_Lobe_Enh
14	6e−03	48 / 4079	15_Quies_ESC_Endoderm
15	3e−02	25 / 1984	10_ReprPC_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−14	23 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
2	8e−09	19 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
3	6e−06	15 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
4	2e−04	74 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
5	2e−02	6 / 255	Kosinski_top−crypt−long−list
6	3e−02	3 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
7	4e−02	6 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	4e−02	2 / 38	Marisa_CRC−cluster−e
9	9e−02	8 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
10	1e−01	7 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
11	1e−01	2 / 77	Ang_CRC_Hypermethylated
12	2e−01	3 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
13	2e−01	1 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
14	2e−01	10 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
15	2e−01	10 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

Glioma

Rank	p−value	#in/all	Geneset
1	1e−18	52 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	3e−10	20 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	3e−08	4 / 5	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
4	9e−05	6 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
5	1e−04	4 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
6	3e−04	13 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
7	5e−03	2 / 12	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
8	9e−03	7 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	1e−02	3 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
10	2e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
11	3e−02	3 / 82	laffaire_hypermeth_LGG_vs_control
12	7e−02	1 / 8	Shaw_up_in_1p19qdel
13	1e−01	1 / 12	VERHAAK_Brain
14	1e−01	1 / 15	Gorovets_LGG_NB_subclass
15	2e−01	1 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−99	79 / 218	HSIAO_LIVER_SPECIFIC_GENES
2	2e−39	37 / 208	CAIRO_LIVER_DEVELOPMENT_DN
3	9e−34	35 / 243	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
4	2e−33	35 / 250	CAIRO_HEPATOBLASTOMA_DN
5	4e−32	29 / 147	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
6	5e−29	38 / 421	ACEVEDO_LIVER_CANCER_DN
7	2e−28	21 / 64	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
8	6e−27	19 / 52	SU_LIVER
9	8e−26	35 / 410	PILON_KLF1_TARGETS_UP
10	8e−22	22 / 144	LEE_LIVER_CANCER_SURVIVAL_UP
11	2e−19	16 / 67	YAMASHITA_LIVER_CANCER_STEM_CELL_DN
12	6e−19	19 / 124	SERVITJA_LIVER_HNF1A_TARGETS_DN
13	5e−18	26 / 337	BOCHKIS_FOXA2_TARGETS
14	8e−18	17 / 100	OHGUCHI_LIVER_HNF4A_TARGETS_DN
15	2e−15	19 / 189	NABA_ECM_REGULATORS

HM

Rank	p−value	#in/all	Geneset
1	2e−21	21 / 130	HALLMARK_COAGULATION
2	2e−13	17 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	2e−06	8 / 97	HALLMARK_BILE_ACID_METABOLISM
4	4e−03	6 / 178	HALLMARK_COMPLEMENT
5	1e−02	4 / 97	HALLMARK_PEROXISOME
6	3e−02	5 / 194	HALLMARK_KRAS_SIGNALING_UP
7	3e−02	2 / 34	HALLMARK_ANGIOGENESIS
8	8e−02	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
9	1e−01	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	2e−01	2 / 96	HALLMARK_ANDROGEN_RESPONSE
11	2e−01	3 / 188	HALLMARK_HYPOXIA
12	3e−01	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
13	5e−01	2 / 182	HALLMARK_GLYCOLYSIS
14	5e−01	2 / 187	HALLMARK_INFLAMMATORY_RESPONSE
15	5e−01	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 16	Angelova_immune−metagene−Th17
2	0.3	1 / 45	Angelova_immune−metagene−MDSC
3	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
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	0.06	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.10	2 / 62	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
9	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
10	1.00	0 / 22	DUMEAUX_High bmi enriched genes
11	1.00	0 / 22	DUMEAUX_Fasting enriched genes
12	1.00	0 / 150	Homuth_BMI−associated−genes_UP
13	1.00	0 / 210	Homuth_BMI−associated−genes_DN
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−09	46 / 2206	HOPP_Heterochrom
2	6e−06	6 / 53	LENZ_Stromal signature 2
3	1e−03	10 / 378	TARTE_Mature plasma cell signature
4	4e−03	40 / 3168	HOPP_Repressed
5	3e−02	4 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
6	5e−02	3 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
7	6e−02	2 / 45	Subero_INT_hypo_meth
8	1e−01	1 / 12	Subero_MM_hypo_meth
9	1e−01	2 / 70	Subero_FL_hyper_meth
10	2e−01	2 / 102	ROSOLOWSKI_blue total
11	3e−01	1 / 46	Subero_DLBCL_hypo_meth
12	3e−01	1 / 47	Subero_B−ALL_hyper_meth
13	4e−01	1 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	5e−01	1 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	5e−01	1 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.002	4 / 64	Harbst_melanoma_lowgrade_up
2	0.165	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
3	0.187	1 / 24	Gerami_melanoma−metastatic−risk_DN
4	0.285	1 / 39	Tirosh_melanoma specific genes
5	0.297	1 / 41	Tirosh_top50 correlated genes PC3
6	0.476	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
7	0.642	1 / 119	TCGA_melanoma_MITF_low
8	0.798	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
9	0.987	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	1.000	0 / 17	Hugo_melanoma−all−MET_UP
11	1.000	0 / 37	Hugo_melanoma−all−MET_DN
12	1.000	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	1.000	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1.000	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1.000	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	3e−15	13 / 61	serine−type endopeptidase inhibitor activity
2	6e−12	9 / 33	endopeptidase inhibitor activity
3	5e−11	11 / 77	peptidase inhibitor activity
4	2e−10	10 / 66	monooxygenase activity
5	7e−10	12 / 126	heparin binding
6	5e−09	7 / 30	oxygen binding
7	4e−08	18 / 447	oxidoreductase activity
8	5e−08	5 / 13	arachidonic acid epoxygenase activity
9	8e−08	11 / 154	serine−type endopeptidase activity
10	2e−07	9 / 103	heme binding
11	3e−07	8 / 76	phospholipid binding
12	5e−07	9 / 113	iron ion binding
13	7e−07	7 / 60	oxidoreductase activity, acting on paired donors, with incorporation or reducti
14	1e−06	14 / 346	receptor binding
15	3e−06	8 / 104	serine−type peptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.5	1 / 83	hsa−miR−33b
2	0.7	1 / 155	hsa−miR−586
3	0.8	1 / 168	hsa−miR−33a
4	0.8	1 / 170	hsa−miR−548m
5	0.9	1 / 299	hsa−let−7c
6	0.9	1 / 329	hsa−let−7b
7	1.0	1 / 344	hsa−miR−19a
8	1.0	0 / 324	hsa−miR−497
9	1.0	0 / 244	hsa−miR−34c−5p
10	1.0	0 / 256	hsa−miR−548c−3p
11	1.0	0 / 295	hsa−miR−373
12	1.0	0 / 140	hsa−miR−520f
13	1.0	0 / 248	hsa−miR−520c−3p
14	1.0	0 / 236	hsa−miR−18b
15	1.0	0 / 75	hsa−miR−425

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 68	Burnham_sep_vs_con_UP
2	0.1	2 / 71	Burnham_cap_fp_vs_con_UP
3	0.1	1 / 18	Scicluna_UP
4	0.3	1 / 48	Burnham_viral_DN
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 57	Burnham_viral_UP
8	1.0	0 / 57	Burnham_day1_vs_5_UP
9	1.0	0 / 52	Burnham_day1_vs_5_DN
10	1.0	0 / 54	Burnham_timecourse
11	1.0	0 / 41	Scicluna_DN
12	1.0	0 / 37	Sweeney_viral_up
13	1.0	0 / 33	Sweeney_viral_dn
14	1.0	0 / 122	Terre_IMS_influenza_meta_signature
15	1.0	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−78	48 / 94	WIRTH_Liver
2	2e−17	28 / 429	PROTEINATLAS_liver
3	2e−08	8 / 55	WIRTH_Homeostasis
4	4e−05	5 / 45	JONGENEEL_Kidney
5	3e−04	3 / 15	JONGENEEL_Lung
6	2e−03	7 / 209	Chaussabel_2,5_Immune related molecules
7	3e−02	1 / 4	JONGENEEL_Mammary Gland
8	4e−02	2 / 37	Chaussabel_2,2_Neutrophils
9	7e−02	1 / 9	JONGENEEL_Colon
10	9e−02	1 / 11	JONGENEEL_Pituitary Gland
11	1e−01	1 / 13	WIRTH_Prim. lymphoid organs
12	2e−01	1 / 19	JONGENEEL_Salivary Gland
13	2e−01	1 / 20	JONGENEEL_Heart
14	2e−01	1 / 28	JONGENEEL_Placenta
15	5e−01	9 / 1007	PROTEINATLAS_kidney

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	3e−06	26 / 1148	HEBENSTREIT_low expression TF
2	5e−01	9 / 1041	ICGC_P300_targets
3	7e−01	3 / 415	ICGC_RxraPcr1_targets
4	9e−01	2 / 522	ICGC_SrfPcr2_targets
5	1e+00	13 / 2321	ICGC_Rad21_targets
6	1e+00	8 / 1636	ICGC_Bcl11_targets
7	1e+00	10 / 2150	ICGC_Irf4_targets
8	1e+00	19 / 3435	ICGC_Ebfsc137065_targets
9	1e+00	25 / 4264	ICGC_Pax5_targets
10	1e+00	17 / 3213	ICGC_Pu1_targets
11	1e+00	21 / 3778	ICGC_Pol24_targets
12	1e+00	5 / 1508	ICGC_Mef2_targets
13	1e+00	3 / 1241	KIM_MYC_targets
14	1e+00	20 / 4212	ICGC_Pol2_targets
15	1e+00	5 / 1941	ICGC_Bcl3_targets

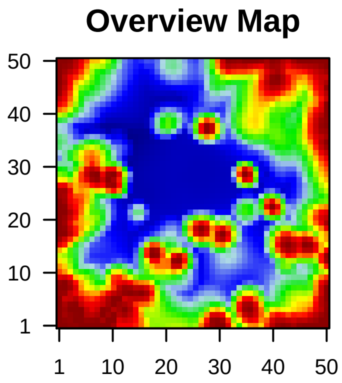
Overexpression Spots

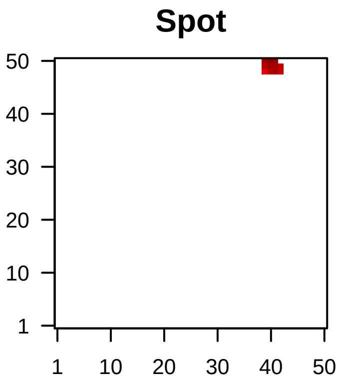
Spot Summary: L

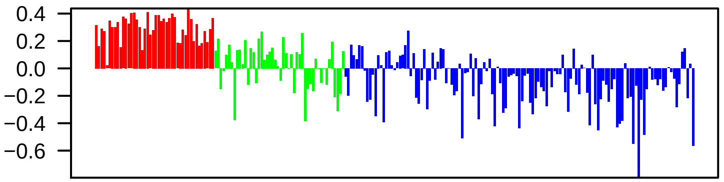
metagenes = 11
genes = 175

<r> metagenes = 0.98
<r> genes = 0.4
beta: r2= 10.02 / log p= −Inf

samples with spot = 40 (18.1 %)
mBL : 34 (77.3 %)
intermediate : 5 (10.4 %)
non−mBL : 1 (0.8 %)


Overview Map


Spot

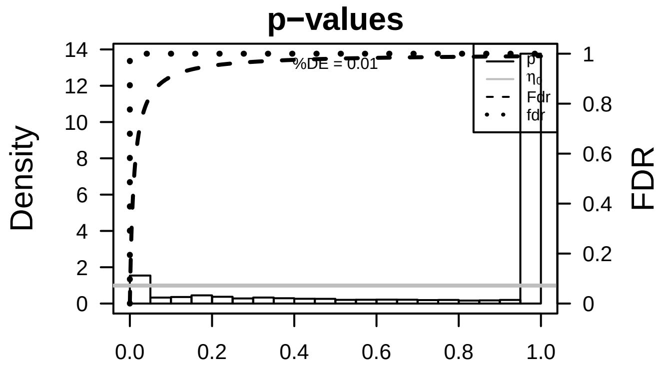


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205229_s_at	1.84	−2.18	0.39	COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
2	209980_s_at	1.66	−1.51	0.73	SHMT1	serine hydroxymethyltransferase 1 [Source:HGNC Symbol;Ac
3	208502_s_at	1.64	−1.55	0.41	PITX1	paired like homeodomain 1 [Source:HGNC Symbol;Acc:HGN
4	219474_at	1.6	−1.32	0.47	C3orf52	chromosome 3 open reading frame 52 [Source:HGNC Symb
5	203790_s_at	1.21	−1.38	0.57	RIDA	reactive intermediate imine deaminase A homolog [Source:H
6	211767_at	1.12	−1.32	0.53	GINS4	GINS complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:
7	219556_at	1.12	−0.87	0.65	TEDC2	tubulin epsilon and delta complex 2 [Source:HGNC Symbol;A
8	208492_at	1.11	−0.78	0.63	RFXAP	regulatory factor X associated protein [Source:HGNC Symbol
9	211814_s_at	1.09	−1.27	0.64	CCNE2	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
10	220258_s_at	1.05	−0.98	0.6	WRAP53	WD repeat containing antisense to TP53 [Source:HGNC Sym
11	212712_at	1.03	−0.91	0.51	CAMSAP1	calmodulin regulated spectrin associated protein 1 [Source:H
12	219311_at	1.03	−0.74	0.65	CEP76	centrosomal protein 76 [Source:HGNC Symbol;Acc:HGNC:2
13	210415_s_at	1.01	−0.81	0.51	ODF2	outer dense fiber of sperm tails 2 [Source:HGNC Symbol;Acc
14	204603_at	0.97	−1.23	0.73	EXO1	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
15	220892_s_at	0.95	−1.71	0.58	PSAT1	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
16	206654_s_at	0.95	−0.83	0.55	POLR3G	RNA polymerase III subunit G [Source:HGNC Symbol;Acc:H
17	201562_s_at	0.95	−0.9	0.46		sorbitol dehydrogenase 2, pseudogene [Source:HGNC Symb
18	213977_s_at	0.95	−1.4	0.47	CIZ1	CDKN1A interacting zinc finger protein 1 [Source:HGNC Sym
19	218051_s_at	0.94	−2.05	0.57	NT5DC2	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
20	205780_at	0.94	−2.54	0.32	BIK	BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:10

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−48	60 / 409	Canc	Lembcke_Normal vs Adenoma
2	3e−45	79 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	4e−41	50 / 319	Mela	Gerber_wt/wt_melanoma−cells−SpotA
4	2e−40	55 / 431	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	3e−37	45 / 280	GSEA	MANALO_HYPOXIA_DN
6	2e−32	60 / 758	GSEA	NUYTTEN_EZH2_TARGETS_DN
7	1e−31	53 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	6e−29	37 / 254	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	1e−28	45 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	2e−28	36 / 244	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
11	3e−28	48 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	5e−28	64 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
13	4e−27	27 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
14	7e−26	33 / 226	GSEA	ZHANG_TLX_TARGETS_60HR_DN
15	2e−25	51 / 703	GSEA	LEE_BMP2_TARGETS_DN
16	1e−24	27 / 140	GSEA	RUIZ_TNC_TARGETS_DN
17	6e−23	49 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
18	2e−22	33 / 290	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
19	3e−22	27 / 169	GSEA	FUJII_YBX1_TARGETS_DN
20	1e−21	33 / 307	GSEA	VECCHI_GASTRIC_CANCER_EARLY_UP
21	2e−21	39 / 466	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_UP
22	4e−21	130 / 5529	Lymp	HOPP_Txn_elongation
23	2e−20	28 / 219	Refer	WIRTH_GC B−cells
24	6e−20	22 / 117	GSEA	CHANG_CYCLING_GENES
25	2e−19	26 / 195	HM	HALLMARK_G2M_CHECKPOINT
26	2e−18	22 / 137	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	2e−18	24 / 174	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
28	4e−18	18 / 79	Mela	Tirosh_core cycling genes in low− and high−proliferation melanoma
29	5e−18	33 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
30	7e−18	30 / 321	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
31	8e−18	62 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
32	6e−17	28 / 294	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
33	1e−16	2 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
34	1e−16	2 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
35	2e−16	38 / 616	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
36	3e−16	17 / 84	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
37	4e−16	25 / 241	GSEA	BASAKI_YBX1_TARGETS_UP
38	5e−16	26 / 267	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
39	1e−15	34 / 509	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
40	2e−15	22 / 187	HM	HALLMARK_E2F_TARGETS


p−values

Aging

Rank	p−value	#in/all	Geneset
1	4e−04	7 / 107	HORVATH_aging_genes meth UP
2	7e−01	1 / 92	HORVATH_aging_genes meth DOWN
3	1e+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	5e−11	69 / 2541	nucleoplasm
2	7e−10	97 / 4579	nucleus
3	8e−07	17 / 324	chromosome
4	3e−06	15 / 277	mitochondrial matrix
5	3e−06	17 / 354	centrosome
6	2e−05	33 / 1221	mitochondrion
7	3e−05	8 / 98	spindle pole
8	8e−05	21 / 653	nucleolus
9	1e−04	8 / 118	chromosome, centromeric region
10	3e−04	7 / 103	nuclear chromosome, telomeric region
11	4e−04	12 / 292	microtubule organizing center
12	1e−03	10 / 251	microtubule
13	2e−03	6 / 100	chromatin
14	2e−03	6 / 101	kinetochore
15	2e−03	66 / 3805	cytosol

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	22 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	2e−05	11 / 184	Kosinski_lower−crypt−long−list
3	2e−04	19 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	7e−02	29 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	7e−02	1 / 6	Marisa_CRC−C6
6	1e−01	1 / 8	KIM_MSI−in−EC
7	1e−01	1 / 8	Boland_CRC−MMR−system
8	1e−01	1 / 12	Juehling−MSI−enriched−in−6
9	1e−01	10 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
10	2e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	2e−01	19 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
12	2e−01	86 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
13	3e−01	1 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
14	3e−01	13 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
15	5e−01	7 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

HM

Rank	p−value	#in/all	Geneset
1	2e−19	26 / 195	HALLMARK_G2M_CHECKPOINT
2	2e−15	22 / 187	HALLMARK_E2F_TARGETS
3	3e−08	9 / 55	HALLMARK_MYC_TARGETS_V2
4	3e−03	8 / 192	HALLMARK_MTORC1_SIGNALING
5	7e−03	7 / 173	HALLMARK_MITOTIC_SPINDLE
6	3e−02	6 / 190	HALLMARK_MYC_TARGETS_V1
7	9e−02	4 / 133	HALLMARK_DNA_REPAIR
8	2e−01	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	2e−01	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
10	4e−01	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
11	4e−01	3 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	5e−01	2 / 139	HALLMARK_FATTY_ACID_METABOLISM
13	5e−01	1 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	6e−01	2 / 149	HALLMARK_UV_RESPONSE_UP
15	7e−01	2 / 182	HALLMARK_GLYCOLYSIS

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−21	130 / 5529	HOPP_Txn_elongation
2	1e−14	26 / 305	TARTE_Plasmablast signature
3	1e−13	16 / 99	Sha_BL UP
4	5e−13	121 / 5908	HOPP_Active_promoter
5	4e−11	18 / 192	Victora_Dark zone signature
6	8e−09	90 / 4261	HOPP_Txn_transition
7	1e−07	12 / 135	DAVE_BL−vs−DLBCL
8	4e−07	32 / 955	SPANG_BCR UP
9	5e−05	4 / 17	DAVE_c−myc BL UP
10	2e−03	6 / 102	ROSOLOWSKI_blue total
11	3e−03	4 / 45	SPANG_BAFF 9hrs DN
12	1e−02	87 / 5682	HOPP_Weak_promoter
13	3e−02	4 / 88	ROSOLOWSKI_green UP
14	7e−02	4 / 121	ROSOLOWSKI_green total
15	8e−02	8 / 353	SPANG_CD40 6hrs DN

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	4 / 31	hsa−miR−661
2	4e−03	7 / 160	hsa−miR−330−3p
3	7e−03	4 / 59	hsa−miR−184
4	1e−02	4 / 72	hsa−miR−378
5	2e−02	6 / 157	hsa−miR−374a
6	2e−02	5 / 115	hsa−miR−28−5p
7	2e−02	6 / 166	hsa−miR−29b
8	3e−02	2 / 20	hsa−miR−662
9	3e−02	2 / 20	hsa−miR−220b
10	3e−02	3 / 51	hsa−miR−492
11	3e−02	3 / 52	hsa−miR−324−5p
12	3e−02	4 / 95	hsa−miR−376a
13	4e−02	2 / 24	hsa−miR−197
14	4e−02	3 / 58	hsa−miR−331−3p
15	4e−02	5 / 145	hsa−miR−374b

Telomeres

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	Alternative lengthening of telomeres
2	0.29	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	1e−13	18 / 137	DNA replication
2	2e−08	24 / 497	cell cycle
3	4e−07	17 / 307	cell division
4	6e−07	16 / 281	DNA repair
5	2e−06	6 / 31	DNA replication initiation
6	2e−06	17 / 351	cellular response to DNA damage stimulus
7	9e−06	5 / 23	regulation of transcription involved in G1/S transition of mitotic cell cycle
8	2e−05	8 / 91	G1/S transition of mitotic cell cycle
9	3e−04	6 / 70	chromosome segregation
10	4e−04	4 / 27	DNA damage checkpoint
11	4e−04	9 / 174	rRNA processing
12	5e−04	7 / 110	regulation of cell cycle
13	6e−04	7 / 113	regulation of signal transduction by p53 class mediator
14	7e−04	3 / 14	purine nucleotide biosynthetic process
15	7e−04	3 / 14	purine ribonucleoside monophosphate biosynthetic process

Chr

Rank	p−value	#in/all	Geneset
1	1e−04	15 / 382	Chr 15
2	4e−03	9 / 242	Chr 13
3	2e−02	12 / 492	Chr 9
4	5e−02	12 / 548	Chr 16
5	5e−02	24 / 1325	Chr 1
6	5e−02	10 / 437	Chr 8
7	1e−01	7 / 333	Chr 22
8	2e−01	13 / 776	Chr 17
9	4e−01	3 / 184	Chr 18
10	6e−01	7 / 554	Chr 5
11	7e−01	8 / 700	Chr 12
12	7e−01	5 / 480	Chr 4
13	7e−01	9 / 833	Chr 19
14	8e−01	4 / 403	Chr 14
15	8e−01	1 / 139	Chr 21

Glioma

Rank	p−value	#in/all	Geneset
1	4e−27	27 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	3e−05	6 / 47	developing astrocytes
3	2e−04	33 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−03	5 / 66	Weller_LGG_gradeII−vs−III_DOWN
5	3e−03	32 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	5e−02	13 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	1e−01	2 / 49	OPC
8	2e−01	2 / 58	Stuehler_Proteins_up_in_STS
9	2e−01	2 / 64	cultured astroglia vs. in vivo astrocytes
10	2e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
11	4e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
12	4e−01	1 / 35	Gorovets_LGG_EPL_subclass
13	5e−01	4 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
14	5e−01	1 / 52	GIEZELT_GBM_WT_down_VS_mut
15	5e−01	1 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up

Immunome

Rank	p−value	#in/all	Geneset
1	0.004	3 / 26	Angelova_immune−metagene−activated_CD4
2	0.216	1 / 19	Angelova_immune−metagene−activated_CD8
3	0.386	1 / 38	Angelova_immune−metagene−mast−cells
4	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.000	0 / 25	Angelova_immune−metagene−DC
9	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.000	0 / 14	Angelova_immune−metagene−eosinophil
12	1.000	0 / 19	Angelova_immune−metagene−iDC
13	1.000	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.000	0 / 11	Angelova_immune−metagene−macrophages
15	1.000	0 / 8	Angelova_immune−metagene−mDC

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−41	50 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	4e−18	18 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
3	5e−15	13 / 44	Tirosh_top50 correlated genes PC2
4	8e−09	10 / 65	Harbst_melanoma_highgrade_up
5	2e−08	8 / 38	Tirosh_G1/S phase specific genes
6	3e−04	5 / 47	Tirosh_G2/M phase specific genes
7	3e−03	4 / 46	Tirosh_top50 correlated genes PC5
8	5e−02	1 / 4	Melanoma Epi−Enzyme Cluster 3
9	5e−02	1 / 4	Melanoma Epi−Enzyme Cluster 5
10	1e−01	6 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	4e−01	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	5e−01	1 / 59	TCGA_melanoma_keratin_high
13	6e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
14	7e−01	1 / 85	Tirosh_AXL−signature
15	8e−01	1 / 119	TCGA_melanoma_MITF_low

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.03	5 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.19	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.35	1 / 33	Sweeney_viral_dn
4	0.46	1 / 48	Burnham_viral_DN
5	0.46	2 / 122	Terre_IMS_influenza_meta_signature
6	1.00	0 / 68	Burnham_sep_vs_con_UP
7	1.00	0 / 56	Burnham_sep_vs_con_DN
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 57	Burnham_viral_UP
11	1.00	0 / 57	Burnham_day1_vs_5_UP
12	1.00	0 / 52	Burnham_day1_vs_5_DN
13	1.00	0 / 54	Burnham_timecourse
14	1.00	0 / 18	Scicluna_UP
15	1.00	0 / 41	Scicluna_DN

TF

Rank	p−value	#in/all	Geneset
1	8e−09	41 / 1241	KIM_MYC targets
2	9e−06	32 / 1107	ICGC_Myc_targets
3	7e−03	61 / 3608	ICGC_Tcf12_targets
4	8e−03	60 / 3564	ICGC_Taf1_targets
5	8e−03	52 / 2994	ICGC_Zeb1_targets
6	8e−03	4 / 62	MYC_Targets UP
7	1e−02	60 / 3630	ICGC_Sp1_targets
8	2e−02	61 / 3769	ICGC_Pmlsc71910_targets
9	2e−02	52 / 3150	ICGC_Creb1_targets
10	2e−02	30 / 1630	ICGC_SrfV0416101_targets
11	2e−02	2 / 19	MYC_Metabolism UP
12	2e−02	21 / 1044	ICGC_Six5_targets
13	2e−02	65 / 4131	ICGC_Tcf3_targets
14	3e−02	71 / 4602	ICGC_Elf1_targets
15	3e−02	60 / 3796	ICGC_Nficsc81335_targets

Cancer

Rank	p−value	#in/all	Geneset
1	5e−48	60 / 409	Lembcke_Normal vs Adenoma
2	1e−16	2 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	3e−05	4 / 15	GENTLES_modul2
4	2e−04	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
5	2e−04	3 / 10	GENTLES_modul3
6	3e−03	4 / 45	KUIPER_MM poor survival
7	6e−03	6 / 130	PanCan_CC+Apop_geneset_nanostring
8	1e−02	2 / 13	GENTLES_modul1
9	1e−02	2 / 14	LIU_COMMON_CANCER_GENES
10	1e−02	2 / 14	BENTINK_myc.1
11	2e−02	2 / 15	GENTLES_modul7
12	4e−02	3 / 58	SHAUGHNESSY_MM high risk
13	1e−01	2 / 41	PanCan_DNARepair_geneset_nanostring
14	1e−01	1 / 12	BENTINK_ras.1
15	2e−01	1 / 14	GENTLES_modul10

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−22	156 / 7957	Tcells peripheral blood_2_TssAFlnk
2	2e−21	155 / 7930	Tregulatory cells peripheral blood_1_TssA
3	6e−21	158 / 8370	natural killer cells peripheral blood_2_TssAFlnk
4	1e−19	157 / 8406	Bcells peripheral blood_2_TssAFlnk
5	2e−19	155 / 8200	monocytes peripheral blood_2_TssAFlnk
6	4e−19	155 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
7	5e−19	126 / 5456	5_Tx_Neuronal_Progenitor
8	1e−18	156 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
9	1e−18	159 / 8816	Thelper cells peripheral blood_2_TssAFlnk
10	1e−18	155 / 8322	T CD8+ naive cells peripheral blood_1_TssA
11	3e−18	147 / 7489	monocytes peripheral blood_5_TxWk
12	5e−18	150 / 7833	Bcells peripheral blood_1_TssA
13	6e−18	152 / 8068	Thelper cells peripheral blood_1_TssA
14	8e−18	135 / 6389	4_Tx_ESC_Mesoderm
15	1e−17	131 / 6068	4_Tx_ESC_Endoderm

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−45	79 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	2e−40	55 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	3e−37	45 / 280	MANALO_HYPOXIA_DN
4	2e−32	60 / 758	NUYTTEN_EZH2_TARGETS_DN
5	1e−31	53 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	6e−29	37 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
7	1e−28	45 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
8	2e−28	36 / 244	KOBAYASHI_EGFR_SIGNALING_24HR_DN
9	3e−28	48 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	5e−28	64 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	7e−26	33 / 226	ZHANG_TLX_TARGETS_60HR_DN
12	2e−25	51 / 703	LEE_BMP2_TARGETS_DN
13	1e−24	27 / 140	RUIZ_TNC_TARGETS_DN
14	6e−23	49 / 726	PUJANA_CHEK2_PCC_NETWORK
15	2e−22	33 / 290	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN

Lifestyle

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

MF

Rank	p−value	#in/all	Geneset
1	3e−06	34 / 1161	RNA binding
2	2e−05	15 / 328	chromatin binding
3	1e−04	5 / 37	exonuclease activity
4	4e−04	7 / 106	ligase activity
5	6e−04	6 / 81	single−stranded DNA binding
6	7e−04	4 / 32	DNA−directed 5'−3' RNA polymerase activity
7	1e−03	28 / 1185	ATP binding
8	2e−03	3 / 21	gamma−tubulin binding
9	5e−03	3 / 28	Ran GTPase binding
10	6e−03	5 / 90	nuclease activity
11	6e−03	31 / 1541	DNA binding
12	7e−03	116 / 7864	protein binding
13	8e−03	3 / 32	aminoacyl−tRNA ligase activity
14	8e−03	2 / 11	MAP kinase tyrosine/serine/threonine phosphatase activity
15	9e−03	3 / 34	tRNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−20	28 / 219	WIRTH_GC B−cells
2	2e−03	18 / 677	PROTEINATLAS_esophagus
3	5e−03	12 / 399	PROTEINATLAS_soft tissue
4	1e−02	16 / 678	PROTEINATLAS_lymph node
5	1e−02	22 / 1048	PROTEINATLAS_rectum
6	2e−02	10 / 355	PROTEINATLAS_skeletal muscle
7	2e−02	2 / 16	VAQUERIZAS_Fetal liver_TF
8	2e−02	15 / 645	PROTEINATLAS_bone marrow
9	2e−02	21 / 1022	PROTEINATLAS_placenta
10	2e−02	17 / 776	PROTEINATLAS_skin
11	4e−02	17 / 848	PROTEINATLAS_adrenal gland
12	5e−02	14 / 671	PROTEINATLAS_cervix, uterine
13	5e−02	17 / 861	PROTEINATLAS_nasopharynx
14	6e−02	16 / 819	PROTEINATLAS_bronchus
15	6e−02	12 / 569	PROTEINATLAS_salivary gland

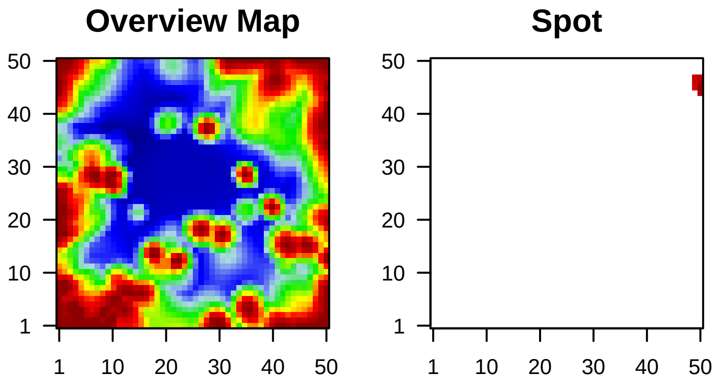
Overexpression Spots

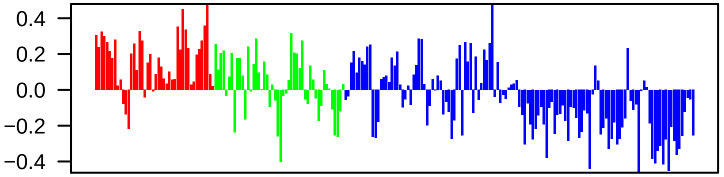
Spot Summary: M

metagenes = 7
genes = 172

<r> metagenes = 0.98
<r> genes = 0.26
beta: r2= 8.66 / log p= −Inf

samples with spot = 41 (18.6 %)
mBL : 19 (43.2 %)
intermediate : 9 (18.8 %)
non−mBL : 13 (10.1 %)



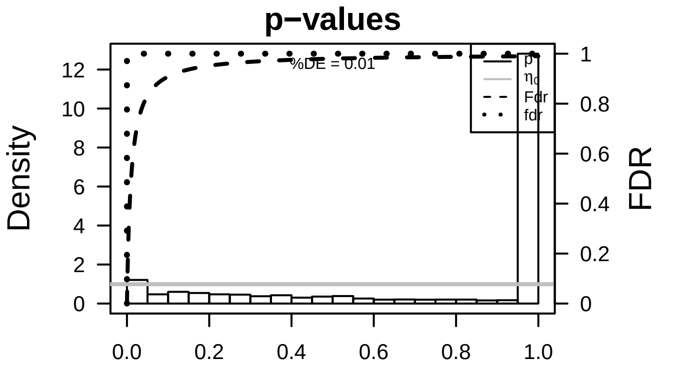


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	AFFX−r2−Hs2	2.62	−0.97	0.51		
2	208719_s_at	2	−1.36	0.47	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:27
3	213668_s_at	1.86	−1.12	0.53	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
4	201418_s_at	1.77	−1.36	0.36	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
5	208151_x_at	1.73	−1.48	0.55	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:27
6	AFFX−M2783	1.67	−1.23	0.58		
7	AFFX−r2−Hs2	1.66	−1.04	0.45		
8	221496_s_at	1.6	−1.41	0.67	TOB2	transducer of ERBB2, 2 [Source:HGNC Symbol;Acc:HGNC:1
9	206500_s_at	1.46	−1.04	0.65	MIS18BP1	MIS18 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2
10	213789_at	1.44	−0.92	0.44		
11	203938_s_at	1.41	−1.47	0.5	TAF1C	TATA−box binding protein associated factor, RNA polymerase
12	213328_at	1.34	−1.04	0.59	NEK1	NIMA related kinase 1 [Source:HGNC Symbol;Acc:HGNC:774
13	202048_s_at	1.31	−1.09	0.53	CBX6	chromobox 6 [Source:HGNC Symbol;Acc:HGNC:1556]
14	213998_s_at	1.25	−1.33	0.52	DDX17	DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:27
15	219437_s_at	1.25	−1.33	0.64	ANKRD11	ankyrin repeat domain 11 [Source:HGNC Symbol;Acc:HGNC
16	213979_s_at	1.24	−1.43	0.44		
17	213577_at	1.24	−1.21	0.47	SQLE	squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127
18	212468_at	1.23	−0.81	0.76	SPAG9	sperm associated antigen 9 [Source:HGNC Symbol;Acc:HGN
19	220085_at	1.22	−2.09	0.81	HELLS	helicase, lymphoid specific [Source:HGNC Symbol;Acc:HGNC
20	222158_s_at	1.21	−1.32	0.7	DESI2	desumoylating isopeptidase 2 [Source:HGNC Symbol;Acc:HC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−20	21 / 106	Refer	Chaussabel_2,11_Replication
2	9e−20	55 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
3	1e−13	112 / 5529	Lympl	HOPP_Txn_elongation
4	4e−11	91 / 4261	Lympl	HOPP_Txn_transition
5	5e−11	22 / 328	GSEA	OSMAN_BLADDER_CANCER_UP
6	4e−09	19 / 303	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
7	1e−08	76 / 3564	TF	ICGC_Taf1_targets
8	1e−08	31 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
9	3e−08	60 / 2541	CC	nucleoplasm
10	3e−08	69 / 3150	TF	ICGC_Creb1_targets
11	4e−08	11 / 102	Lympl	ROSOLOWSKI_blue total
12	2e−07	103 / 5908	Lympl	HOPP_Active_promoter
13	2e−07	33 / 1044	TF	ICGC_Six5_targets
14	2e−07	22 / 516	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
15	2e−06	8 / 72	GSEA	BILD_CTNNB1_ONCOGENIC_SIGNATURE
16	3e−06	27 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
17	3e−06	83 / 4579	CC	nucleus
18	6e−06	11 / 171	miRN	hsa−miR−196a
19	7e−06	35 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
20	9e−06	20 / 549	TF	ICGC_Atf3_targets
21	9e−06	78 / 4319	TF	ICGC_Pou2_targets
22	1e−05	66 / 3451	TF	ICGC_Atf2_targets
23	1e−05	18 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
24	2e−05	22 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
25	2e−05	70 / 3769	TF	ICGC_Pmlsc71910_targets
26	2e−05	38 / 1578	TF	ICGC_GabpPcr2_targets
27	2e−05	30 / 1107	TF	ICGC_Myc_targets
28	2e−05	61 / 3121	TF	ICGC_Egr1_targets
29	2e−05	14 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
30	2e−05	70 / 3804	TF	ICGC_Stat5_targets
31	2e−05	15 / 354	CC	centrosome
32	2e−05	4 / 15	BP	protein localization to centrosome
33	3e−05	13 / 278	miRN	hsa−let−7d
34	3e−05	29 / 1089	TF	ICGC_Ets1_targets
35	4e−05	67 / 3630	TF	ICGC_Sp1_targets
36	4e−05	5 / 32	BP	centrosome cycle
37	4e−05	4 / 17	GSEA	REACTOME_FANCONI_ANEMIA_PATHWAY
38	4e−05	69 / 3796	TF	ICGC_Nficsc81335_targets
39	4e−05	19 / 564	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
40	4e−05	118 / 7864	MF	protein binding



Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 107	HORVATH_aging_genes meth UP
2	1.0	0 / 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	2e−05	4 / 15	protein localization to centrosome
2	4e−05	5 / 32	centrosome cycle
3	7e−05	12 / 260	chromatin organization
4	5e−04	35 / 1655	transcription, DNA−templated
5	7e−04	4 / 34	DNA damage response, detection of DNA damage
6	1e−03	4 / 37	interstrand cross−link repair
7	1e−03	12 / 351	cellular response to DNA damage stimulus
8	1e−03	11 / 307	cell division
9	1e−03	4 / 39	RNA secondary structure unwinding
10	1e−03	5 / 69	chromatin remodeling
11	1e−03	3 / 19	DNA replication−independent nucleosome assembly
12	2e−03	3 / 21	DNA methylation
13	2e−03	3 / 21	positive regulation of intracellular protein transport
14	2e−03	6 / 113	cell projection organization
15	3e−03	4 / 48	regulation of megakaryocyte differentiation

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	4 / 113	PanCan_Driver_Gene_geneset_nanostring
2	0.10	2 / 45	KUIPER_MM poor survival
3	0.16	1 / 14	BENTINK_myc.1
4	0.16	1 / 14	BENTINK_ras.6
5	0.17	1 / 15	WANG_ER_UP
6	0.21	1 / 20	PanCan_ChromMod_geneset_nanostring
7	0.26	1 / 25	PanCan_HH_geneset_nanostring
8	0.27	0 / 16	LIU_LIVER_CANCER
9	0.39	1 / 41	PanCan_DNARepair_geneset_nanostring
10	0.46	2 / 130	PanCan_CC+Apop_geneset_nanostring
11	0.50	0 / 15	RHODES_CANCER_META_SIGNATURE
12	0.54	5 / 409	Lembcke_Normal vs Adenoma
13	0.60	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.83	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	0.99	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−08	60 / 2541	nucleoplasm
2	3e−06	83 / 4579	nucleus
3	2e−05	15 / 354	centrosome
4	6e−05	7 / 83	centriole
5	8e−05	4 / 20	centriolar satellite
6	2e−04	12 / 292	microtubule organizing center
7	2e−03	4 / 44	nuclear chromosome
8	2e−03	17 / 653	nucleolus
9	4e−03	21 / 936	cytoskeleton
10	6e−03	10 / 324	chromosome
11	6e−03	5 / 98	spindle pole
12	7e−03	8 / 233	nuclear body
13	7e−03	2 / 11	pericentric heterochromatin
14	9e−03	2 / 12	integrator complex
15	1e−02	2 / 13	Ada2/Gcn5/Ada3 transcription activator complex

Chr

Rank	p−value	#in/all	Geneset
1	9e−04	16 / 548	Chr 16
2	1e−01	7 / 333	Chr 22
3	2e−01	20 / 1325	Chr 1
4	2e−01	13 / 833	Chr 19
5	2e−01	11 / 689	Chr 3
6	3e−01	11 / 756	Chr 11
7	3e−01	11 / 776	Chr 17
8	4e−01	6 / 437	Chr 8
9	5e−01	2 / 139	Chr 21
10	6e−01	8 / 700	Chr 12
11	6e−01	4 / 369	Chr 20
12	6e−01	2 / 184	Chr 18
13	7e−01	6 / 554	Chr 5
14	7e−01	9 / 832	Chr 2
15	7e−01	5 / 480	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−20	123 / 5527	Tregulatory cells peripheral blood_4_Tx
2	3e−20	132 / 6389	4_Tx_ESC_Mesoderm
3	4e−20	125 / 5753	Tcells peripheral blood_4_Tx
4	2e−19	144 / 7833	Bcells peripheral blood_1_TssA
5	2e−18	126 / 6068	4_Tx_ESC_Endoderm
6	5e−18	125 / 6034	5_Tx_Fibroblasts
7	6e−18	122 / 5766	natural killer cells peripheral blood_4_Tx
8	1e−17	121 / 5716	Bcells peripheral blood_4_Tx
9	2e−17	138 / 7420	Tcells peripheral blood_1_TssA
10	9e−17	139 / 7635	monocytes peripheral blood_1_TssA
11	9e−17	140 / 7751	natural killer cells peripheral blood_1_TssA
12	1e−16	107 / 4683	Overlap_fetal_midbrain_HetRpts
13	1e−16	118 / 5601	Thelper cells peripheral blood_4_Tx
14	1e−16	144 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
15	2e−16	116 / 5456	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−20	55 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	3e−06	27 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	5e−04	36 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	6e−03	13 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
5	2e−02	6 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Damage_signaling
7	3e−02	17 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
8	4e−02	12 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	4e−02	18 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
10	4e−02	21 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	1e−01	1 / 10	KIM_CRC−MSI−regulated_DN
12	1e−01	2 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
13	1e−01	1 / 11	KIM_MSI−in−CRC
14	1e−01	21 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	2e−01	2 / 60	Marisa_CRC−cluster−g

Glioma

Rank	p−value	#in/all	Geneset
1	7e−06	35 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	1e−04	35 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−03	5 / 64	Weller_LGG_A_vs_O_DOWN
4	9e−03	2 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
5	5e−02	7 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	7e−02	1 / 6	WILLSCHER_GBM_Verhaak−PNmut_up (M)
7	9e−02	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
8	1e−01	3 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	1e−01	11 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	1e−01	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
11	1e−01	6 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
12	1e−01	1 / 12	Christensen_hypermethylated_in_ependymoma
13	1e−01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	1e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	2e−01	1 / 16	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−11	22 / 328	OSMAN_BLADDER_CANCER_UP
2	4e−09	19 / 303	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
3	1e−08	31 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
4	2e−07	22 / 516	HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	2e−06	8 / 72	BILD_CTNNB1_ONCOGENIC_SIGNATURE
6	1e−05	18 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
7	2e−05	22 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
8	2e−05	14 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
9	4e−05	4 / 17	REACTOME_FANCONI_ANEMIA_PATHWAY
10	4e−05	19 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
11	8e−05	18 / 539	PARENT_MTOR_SIGNALING_UP
12	9e−05	15 / 398	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
13	1e−04	11 / 230	BRUINS_UVC_RESPONSE_EARLY_LATE
14	1e−04	9 / 159	CHANDRAN_METASTASIS_UP
15	1e−04	5 / 42	PID_FANCONI_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.06	5 / 173	HALLMARK_MITOTIC_SPINDLE
2	0.16	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
3	0.20	4 / 192	HALLMARK_MTORC1_SIGNALING
4	0.34	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
5	0.35	3 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	0.37	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
7	0.39	3 / 187	HALLMARK_E2F_TARGETS
8	0.41	3 / 193	HALLMARK_HEME_METABOLISM
9	0.41	3 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.41	3 / 195	HALLMARK_G2M_CHECKPOINT
11	0.46	1 / 51	HALLMARK_TGF_BETA_SIGNALING
12	0.51	2 / 141	HALLMARK_UV_RESPONSE_DN
13	0.61	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
14	0.63	2 / 178	HALLMARK_COMPLEMENT
15	0.69	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.02	2 / 18	Angelova_immune−metagene−pDC
2	0.05	1 / 4	Angelova_CRC_MSS−neoantigens
3	0.08	1 / 7	Angelova_CRC_MSI−neoantigens
4	0.14	1 / 13	Angelova_CRC_MSS^−neoantigens
5	0.27	1 / 26	Angelova_immune−metagene−activated_CD4
6	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
8	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
9	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
10	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
11	1.00	0 / 25	Angelova_immune−metagene−DC
12	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
14	1.00	0 / 14	Angelova_immune−metagene−eosinophil
15	1.00	0 / 19	Angelova_immune−metagene−iDC

Lifestyle

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

Lymphnoma

Rank	p−value	#in/all	Geneset
1	1e−13	112 / 5529	HOPP_Txn_elongation
2	4e−11	91 / 4261	HOPP_Txn_transition
3	4e−08	11 / 102	ROSOLOWSKI_blue total
4	2e−07	103 / 5908	HOPP_Active_promoter
5	1e−03	87 / 5682	HOPP_Weak_promoter
6	8e−03	80 / 5404	HOPP_Strong_enhancer
7	2e−02	7 / 227	SPANG_IL21 UP
8	2e−02	19 / 955	SPANG_BCR UP
9	3e−02	9 / 353	SPANG_CD40 6hrs DN
10	3e−02	64 / 4357	HOPP_Weak_txn
11	4e−02	17 / 906	SPANG_BCR DN
12	7e−02	2 / 35	Subero_MM_hyper_meth
13	7e−02	64 / 4559	HOPP_Weak_enhancer
14	1e−01	27 / 1814	HOPP_Repetitive
15	3e−01	2 / 88	ROSOLOWSKI_green UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.005	8 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.024	1 / 2	Melanoma Epi−Enzyme Cluster 2
3	0.031	2 / 23	Melanoma Epi−Enzyme Cluster 7
4	0.058	6 / 230	Gerber_wt/wt_melanoma−cells−SpotC
5	0.076	2 / 38	Tirosh_top50 correlated genes PC1
6	0.076	2 / 38	Tirosh_G1/S phase specific genes
7	0.181	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.251	1 / 24	Tirosh_B−cell specific genes−melanoma
9	0.313	4 / 236	Gerber_wt/wt_group3−specific
10	0.443	3 / 204	Landsberg_dedifferentiation_down
11	0.533	4 / 319	Gerber_wt/wt_melanoma−cells−SpotA
12	0.633	1 / 83	TCGA_melanoma_immune_high
13	0.646	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	0.803	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
15	0.851	4 / 497	Gerber_wt/wt_melanoma−cells−SpotD

MF

Rank	p−value	#in/all	Geneset
1	4e−05	118 / 7864	protein binding
2	2e−04	5 / 44	methylated histone binding
3	6e−04	27 / 1161	RNA binding
4	1e−03	4 / 38	core promoter sequence−specific DNA binding
5	3e−03	20 / 852	nucleic acid binding
6	6e−03	2 / 10	peroxisome proliferator activated receptor binding
7	6e−03	10 / 328	chromatin binding
8	7e−03	10 / 331	protein serine/threonine kinase activity
9	8e−03	3 / 34	kinesin binding
10	9e−03	2 / 12	histone methyltransferase activity (H3−K4 specific)
11	9e−03	2 / 12	RNA helicase activity
12	9e−03	29 / 1541	DNA binding
13	1e−02	3 / 37	ribosome binding
14	1e−02	2 / 13	vitamin D receptor binding
15	1e−02	2 / 14	retinoic acid receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−06	11 / 171	hsa−miR−196a
2	3e−05	13 / 278	hsa−let−7d
3	6e−05	5 / 36	hsa−miR−541
4	7e−05	9 / 148	hsa−miR−539
5	1e−04	9 / 155	hsa−miR−381
6	1e−04	7 / 92	hsa−miR−199a−5p
7	1e−04	11 / 234	hsa−miR−570
8	4e−04	8 / 150	hsa−miR−300
9	5e−04	5 / 56	hsa−miR−1275
10	8e−04	4 / 35	hsa−miR−329
11	9e−04	5 / 63	hsa−miR−657
12	1e−03	6 / 100	hsa−miR−519e
13	2e−03	6 / 105	hsa−miR−335
14	2e−03	8 / 185	hsa−miR−182
15	2e−03	4 / 44	hsa−miR−575

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.03	3 / 54	Burnham_timecourse
2	0.44	1 / 48	Burnham_viral_DN
3	0.63	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	0.77	1 / 122	Terre_IMS_influenza_meta_signature
5	0.80	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	1.00	0 / 68	Burnham_sep_vs_con_UP
7	1.00	0 / 56	Burnham_sep_vs_con_DN
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 57	Burnham_viral_UP
11	1.00	0 / 57	Burnham_day1_vs_5_UP
12	1.00	0 / 52	Burnham_day1_vs_5_DN
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−20	21 / 106	Chaussabel_2,11_Replication
2	7e−04	25 / 1048	PROTEINATLAS_rectum
3	9e−03	22 / 1072	PROTEINATLAS_duodenum
4	2e−02	22 / 1161	PROTEINATLAS_colon
5	2e−02	20 / 1032	PROTEINATLAS_small intestine
6	2e−02	7 / 233	PROTEINATLAS_smooth muscle
7	2e−02	2 / 20	Chaussabel_2,7_Unknown function
8	3e−02	19 / 1007	PROTEINATLAS_kidney
9	3e−02	20 / 1076	PROTEINATLAS_stomach
10	3e−02	8 / 310	Chaussabel_3,4_Protein phosphatases
11	4e−02	17 / 905	PROTEINATLAS_appendix
12	4e−02	19 / 1048	PROTEINATLAS_gallbladder
13	5e−02	2 / 30	VAQUERIZAS_Smooth muscle_TF
14	6e−02	2 / 32	VAQUERIZAS_Liver_TF
15	6e−02	15 / 809	PROTEINATLAS_fallopian tube

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−08	76 / 3564	ICGC_Taf1_targets
2	3e−08	69 / 3150	ICGC_Creb1_targets
3	2e−07	33 / 1044	ICGC_Six5_targets
4	9e−06	20 / 549	ICGC_Atf3_targets
5	9e−06	78 / 4319	ICGC_Pou2_targets
6	1e−05	66 / 3451	ICGC_Atf2_targets
7	2e−05	70 / 3769	ICGC_Pmlsc71910_targets
8	2e−05	38 / 1578	ICGC_GabpPcr2_targets
9	2e−05	30 / 1107	ICGC_Myc_targets
10	2e−05	61 / 3121	ICGC_Egr1_targets
11	2e−05	70 / 3804	ICGC_Stat5_targets
12	3e−05	29 / 1089	ICGC_Ets1_targets
13	4e−05	67 / 3630	ICGC_Sp1_targets
14	4e−05	69 / 3796	ICGC_Nficsc81335_targets
15	6e−05	73 / 4131	ICGC_Tcf3_targets

Overexpression Spots

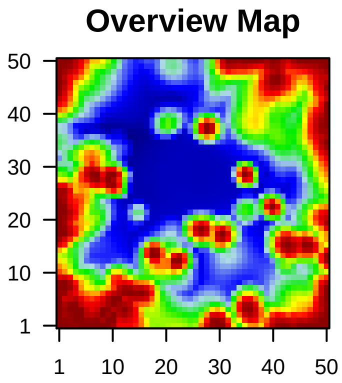
Spot Summary: N

metagenes = 5
genes = 44

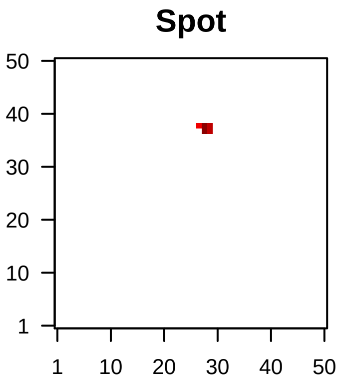
<r> metagenes = 0.98
<r> genes = 0.13
beta: r2= 0.17 / log p= −9.7

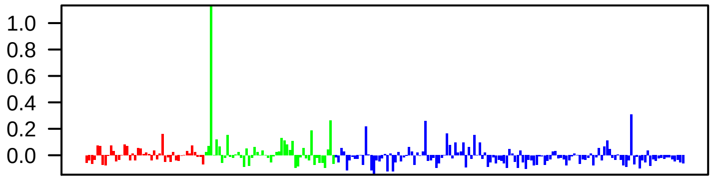
samples with spot = 5 (2.3 %)
intermediate : 2 (4.2 %)
non−mBL : 3 (2.3 %)

Overview Map



Spot





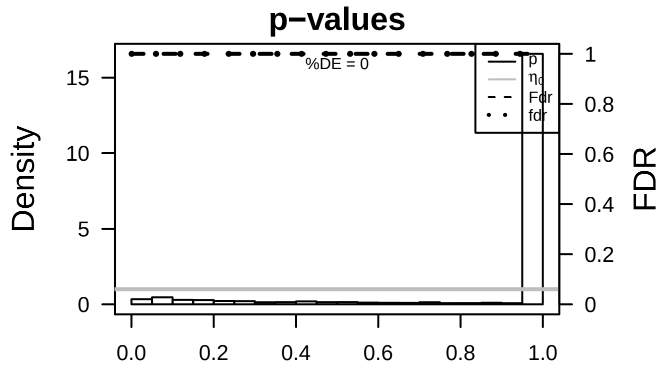
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	220231_at	2.36	−0.6	0.44	PPP1R17	protein phosphatase 1 regulatory subunit 17 [Source:HGNC
2	206163_at	2.29	−0.52	0.38	MAB21L1	mab−21 like 1 [Source:HGNC Symbol;Acc:HGNC:6757]
3	220196_at	2.26	−0.67	0.47	MUC16	mucin 16, cell surface associated [Source:HGNC Symbol;Acc
4	211102_s_at	2.16	−0.7	0.45	LILRA2	leukocyte immunoglobulin like receptor A2 [Source:HGNC Sy
5	206523_at	2.08	−0.71	0.42	CYTH3	cytohesin 3 [Source:HGNC Symbol;Acc:HGNC:9504]
6	206981_at	2.07	−0.55	0.46	SCN4A	sodium voltage−gated channel alpha subunit 4 [Source:HGN
7	219643_at	2.06	−0.5	0.54	LRP1B	LDL receptor related protein 1B [Source:HGNC Symbol;Acc:
8	214961_at	2.01	−0.68	0.49	MTUS2	microtubule associated scaffold protein 2 [Source:HGNC Sym
9	208389_s_at	1.98	−0.75	0.3	SLC1A2	solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:
10	208037_s_at	1.97	−0.95	0.29	MADCAM1	mucosal vascular addressin cell adhesion molecule 1 [Source
11	219695_at	1.97	−0.94	0.33	SMPD3	sphingomyelin phosphodiesterase 3 [Source:HGNC Symbol;
12	205870_at	1.94	−0.75	0.42	BDKRB2	bradykinin receptor B2 [Source:HGNC Symbol;Acc:HGNC:10
13	221843_s_at	1.73	−0.65	0.55	TLDC1	TBC/LysM−associated domain containing 1 [Source:HGNC S
14	210761_s_at	1.69	−0.95	0.33	GRB7	growth factor receptor bound protein 7 [Source:HGNC Symb
15	206594_at	1.66	−1.13	0.39	PASK	PAS domain containing serine/threonine kinase [Source:HGN
16	206638_at	1.65	−0.59	0.4	HTR2B	5−hydroxytryptamine receptor 2B [Source:HGNC Symbol;Acc
17	221345_at	1.62	−0.41	0.4	FFAR2	free fatty acid receptor 2 [Source:HGNC Symbol;Acc:HGNC:
18	207229_at	1.54	−0.72	0.38		killer cell lectin like receptor A1, pseudogene [Source:HGNC
19	207047_s_at	1.35	−0.56	0.37	CLCNKA	chloride voltage−gated channel Ka [Source:HGNC Symbol;A
20	202821_s_at	1.34	−0.68	0.53	LPP	LIM domain containing preferred translocation partner in lipo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−04	4 / 97	GSE	BROWNE_HCMV_INFECTION_20HR_DN
2	8e−04	2 / 13	CC	voltage−gated sodium channel complex
3	1e−03	2 / 17	BP	smooth muscle contraction
4	2e−03	2 / 18	BP	vasoconstriction
5	2e−03	2 / 20	MF	voltage−gated sodium channel activity
6	3e−03	2 / 23	BP	membrane depolarization during action potential
7	3e−03	2 / 26	MF	sodium channel activity
8	3e−03	2 / 26	GSE	ST_INTERLEUKIN_4_PATHWAY
9	4e−03	2 / 29	BP	neuronal action potential
10	5e−03	2 / 32	GSE	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION
11	5e−03	2 / 32	GSE	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES
12	5e−03	8 / 832	Chr	Chr 2
13	5e−03	3 / 107	MF	voltage−gated ion channel activity
14	5e−03	2 / 33	Lymp	Subero_T−PLL_hypo_meth
15	5e−03	2 / 33	GSE	ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY
16	5e−03	9 / 1029	GSE	DODD_NASOPHARYNGEAL_CARCINOMA_UP
17	5e−03	4 / 217	MF	lipid binding
18	5e−03	2 / 34	GSE	ONO_AML1_TARGETS_DN
19	6e−03	3 / 112	BP	regulation of ion transmembrane transport
20	6e−03	2 / 36	GSE	SHIPP_DLBCL_CURED_VS_FATAL_UP
21	6e−03	2 / 36	GSE	ONO_FOXP3_TARGETS_DN
22	7e−03	2 / 38	GSE	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
23	9e−03	2 / 44	BP	calcium−mediated signaling
24	9e−03	3 / 134	CC	vesicle
25	1e−02	2 / 46	GSE	BROWNE_HCMV_INFECTION_2HR_DN
26	1e−02	2 / 47	GSE	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES
27	1e−02	3 / 146	GSE	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS
28	1e−02	4 / 277	CC	neuron projection
29	1e−02	4 / 277	GSE	BROWNE_HCMV_INFECTION_14HR_DN
30	1e−02	2 / 56	BP	negative regulation of translation
31	1e−02	2 / 56	Lymp	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
32	2e−02	2 / 58	BP	sodium ion transmembrane transport
33	2e−02	2 / 58	GSE	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA
34	2e−02	1 / 5	GSE	REACTOME_NEGATIVE_REGULATION_OF_THE_PI3K_AKT_NETWOR
35	2e−02	1 / 5	GSE	KREPPEL_CD99_TARGETS_UP
36	2e−02	7 / 826	GSE	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
37	2e−02	3 / 166	GSE	REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND
38	2e−02	2 / 61	GSE	JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN
39	2e−02	2 / 62	BP	positive regulation of translation
40	2e−02	4 / 307	GSE	RATTENBACHER_BOUND_BY_CELF1

p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	0.001	2 / 17	smooth muscle contraction
2	0.002	2 / 18	vasoconstriction
3	0.003	2 / 23	membrane depolarization during action potential
4	0.004	2 / 29	neuronal action potential
5	0.006	3 / 112	regulation of ion transmembrane transport
6	0.009	2 / 44	calcium−mediated signaling
7	0.014	2 / 56	negative regulation of translation
8	0.015	2 / 58	sodium ion transmembrane transport
9	0.017	2 / 62	positive regulation of translation
10	0.018	2 / 64	multicellular organism growth
11	0.018	2 / 64	positive regulation of endothelial cell proliferation
12	0.032	1 / 10	magnesium ion transmembrane transport
13	0.032	1 / 10	mitochondrial genome maintenance
14	0.032	1 / 10	positive regulation of nuclear−transcribed mRNA catabolic process, deadenyla
15	0.032	1 / 10	positive regulation of nuclear−transcribed mRNA poly(A) tail shortening

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 41	PanCan_DNARepair_geneset_nanostring
2	0.2	1 / 80	PanCan_JAK−ST_geneset_nanostring
3	0.3	1 / 130	PanCan_CC+Apop_geneset_nanostring
4	0.4	1 / 134	PanCan_RAS_geneset_nanostring
5	0.4	1 / 147	PanCan_MAPK_geneset_nanostring
6	0.5	1 / 187	PanCan_PI3K_geneset_nanostring
7	0.6	1 / 317	SPANG_BCL6−index2
8	0.7	1 / 409	Lembcke_Normal vs Adenoma
9	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
10	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.0	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.0	0 / 12	LIU_BREAST_CANCER
14	1.0	0 / 14	LIU_COMMON_CANCER_GENES
15	1.0	0 / 16	LIU_LIVER_CANCER

CC

Rank	p−value	#in/all	Geneset
1	8e−04	2 / 13	voltage−gated sodium channel complex
2	9e−03	3 / 134	vesicle
3	1e−02	4 / 277	neuron projection
4	3e−02	1 / 10	VCP−NPL4−UFD1 AAA ATPase complex
5	4e−02	1 / 11	CCR4−NOT complex
6	4e−02	1 / 12	apical dendrite
7	4e−02	16 / 3210	plasma membrane
8	4e−02	1 / 13	axolemma
9	4e−02	5 / 595	cell junction
10	4e−02	2 / 103	nuclear chromosome, telomeric region
11	5e−02	1 / 15	pericentriolar material
12	6e−02	23 / 5339	membrane
13	6e−02	1 / 18	cytoplasmic dynein complex
14	6e−02	1 / 18	transcription elongation factor complex
15	7e−02	1 / 21	mitotic spindle pole

Chr

Rank	p−value	#in/all	Geneset
1	0.005	8 / 832	Chr 2
2	0.186	2 / 242	Chr 13
3	0.213	3 / 490	Chr 10
4	0.287	4 / 833	Chr 19
5	0.366	1 / 139	Chr 21
6	0.391	3 / 689	Chr 3
7	0.419	2 / 437	Chr 8
8	0.538	2 / 548	Chr 16
9	0.544	2 / 554	Chr 5
10	0.574	2 / 585	Chr 7
11	0.639	4 / 1325	Chr 1
12	0.667	1 / 333	Chr 22
13	0.714	2 / 756	Chr 11
14	0.718	1 / 382	Chr 15
15	0.728	2 / 776	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.01	28 / 6114	7_Enh_Fibroblasts
2	0.01	16 / 2825	9_Het_ESC_Mesoderm
3	0.01	14 / 2338	Bcells peripheral blood_9_Het
4	0.02	32 / 7583	15_Quies_Skeletal_Muscle
5	0.02	29 / 6637	Tcells peripheral blood_5_TxWk
6	0.02	19 / 3838	15_Quies_ESC_Mesoderm
7	0.03	16 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
8	0.03	29 / 6906	3_TssF_Fibroblasts
9	0.04	18 / 3755	HSC_15_Quies
10	0.05	29 / 7078	7_Enh_ESC_Mesoderm
11	0.05	17 / 3540	Tregulatory cells peripheral blood_15_Quies
12	0.05	12 / 2269	9_ReprPCWk_Neuronal_Progenitor
13	0.05	14 / 2792	EnhWk2_Colon
14	0.06	13 / 2548	HSC_9_Het
15	0.06	18 / 3918	Tcells peripheral blood_14_ReprPCWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 6	Juehling_HNPCC−mutated−in−5
2	0.04	2 / 103	Marisa_CRC−cluster−b
3	0.05	1 / 15	TCGA−CRC_less−agressive−disease−markers
4	0.06	6 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
5	0.08	1 / 25	Ang_CRC−CIMPH−vs−L_hypo
6	0.11	1 / 35	Ang_CRC_Hypomethylated
7	0.14	5 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
8	0.15	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
9	0.20	2 / 255	Kosinski_top−crypt−long−list
10	0.22	4 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
11	0.24	2 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
12	0.25	3 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
13	0.26	1 / 92	Marisa_CRC−cluster−h
14	0.28	2 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
15	0.30	23 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_

Glioma

Rank	p−value	#in/all	Geneset
1	0.02	2 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
2	0.03	2 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
3	0.04	2 / 102	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
4	0.04	1 / 14	astrocytes_glio
5	0.05	2 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
6	0.05	2 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
7	0.07	2 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	0.08	2 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	0.11	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
10	0.13	2 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
11	0.14	1 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
12	0.16	1 / 52	GIEZELT_GBM_WT_down_VS_mut
13	0.16	3 / 423	Down_a
14	0.18	1 / 59	GIEZELT_GBM_STS_up_VS_LTS
15	0.18	1 / 61	Christensen_hypomethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 97	BROWNE_HCMV_INFECTION_20HR_DN
2	3e−03	2 / 26	ST_INTERLEUKIN_4_PATHWAY
3	5e−03	2 / 32	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION
4	5e−03	2 / 32	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES
5	5e−03	2 / 33	ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY
6	5e−03	9 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
7	5e−03	2 / 34	ONO_AML1_TARGETS_DN
8	6e−03	2 / 36	SHIPP_DLBCL_CURED_VS_FATAL_UP
9	6e−03	2 / 36	ONO_FOXP3_TARGETS_DN
10	7e−03	2 / 38	MANTOVANI_VIRAL_GPCR_SIGNALING_DN
11	1e−02	2 / 46	BROWNE_HCMV_INFECTION_2HR_DN
12	1e−02	2 / 47	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES
13	1e−02	3 / 146	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS
14	1e−02	4 / 277	BROWNE_HCMV_INFECTION_14HR_DN
15	2e−02	2 / 58	TAYLOR_METHYLATED_IN_ACUTE_LYMPHOBLASTIC_LEUKEMIA

HM

Rank	p−value	#in/all	Geneset
1	0.02	3 / 174	HALLMARK_APICAL_JUNCTION
2	0.12	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
3	0.12	2 / 187	HALLMARK_INFLAMMATORY_RESPONSE
4	0.27	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	0.37	1 / 141	HALLMARK_UV_RESPONSE_DN
6	0.42	1 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.44	1 / 174	HALLMARK_ADIPOGENESIS
8	0.44	1 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	0.46	1 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.47	1 / 191	HALLMARK_P53_PATHWAY
11	0.47	1 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	0.47	1 / 194	HALLMARK_MYOGENESIS
13	0.47	1 / 195	HALLMARK_KRAS_SIGNALING_DN
14	1.00	0 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	1.00	0 / 188	HALLMARK_HYPOXIA

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 15	Angelova_immune−metagene−NK
2	0.07	1 / 23	Angelova_immune−metagene−Th2
3	0.07	1 / 23	Angelova_immune−metagene−Treg
4	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
6	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
7	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
8	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
9	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
10	1.00	0 / 25	Angelova_immune−metagene−DC
11	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
12	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
13	1.00	0 / 14	Angelova_immune−metagene−eosinophil
14	1.00	0 / 19	Angelova_immune−metagene−iDC
15	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.005	2 / 33	Subero_T−PLL_hypo_meth
2	0.014	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
3	0.037	3 / 227	SPANG_IL21 UP
4	0.042	1 / 13	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
5	0.054	1 / 17	Aukema_BCL2 UP_BCL6 DN
6	0.072	1 / 23	Subero_mBL_hypo_meth
7	0.123	1 / 40	CARO_OxPhos_in_DLBCL_UP
8	0.129	2 / 192	Victora_Dark zone signature
9	0.137	1 / 45	Subero_INT_hypo_meth
10	0.140	1 / 46	Subero_DLBCL_hypo_meth
11	0.142	18 / 4357	HOPP_Weak_txn
12	0.170	10 / 2206	HOPP_Heterochrom
13	0.196	18 / 4559	HOPP_Weak_enhancer
14	0.268	21 / 5682	HOPP_Weak_promoter
15	0.320	2 / 353	SPANG_CD40 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 204	Landsberg_dedifferentiation_down
2	0.2	2 / 236	Gerber_wt/wt_group3−specific
3	0.3	1 / 119	TCGA_melanoma_MITF_low
4	0.5	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
5	0.5	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
6	0.8	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
7	1.0	0 / 17	Hugo_melanoma−all−MET_UP
8	1.0	0 / 37	Hugo_melanoma−all−MET_DN
9	1.0	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
10	1.0	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
11	1.0	0 / 16	Hugo_melanoma−all−LEF1_UP
12	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
13	1.0	0 / 85	Tirosh_AXL−signature
14	1.0	0 / 107	Tirosh_Exhaustion program in Mel75
15	1.0	0 / 68	Tirosh_housekeeping_genes

MF

Rank	p−value	#in/all	Geneset
1	0.002	2 / 20	voltage−gated sodium channel activity
2	0.003	2 / 26	sodium channel activity
3	0.005	3 / 107	voltage−gated ion channel activity
4	0.005	4 / 217	lipid binding
5	0.018	2 / 64	phosphatidylinositol binding
6	0.032	1 / 10	anion transmembrane transporter activity
7	0.032	1 / 10	type 1 angiotensin receptor binding
8	0.032	1 / 10	voltage−gated chloride channel activity
9	0.035	1 / 11	dynein heavy chain binding
10	0.035	1 / 11	L−glutamate transmembrane transporter activity
11	0.035	1 / 11	magnesium ion transmembrane transporter activity
12	0.035	1 / 11	mRNA 3'−UTR AU−rich region binding
13	0.035	1 / 11	RNA stem−loop binding
14	0.035	1 / 11	serotonin binding
15	0.035	1 / 11	tropomyosin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	1 / 16	hsa−miR−380*
2	0.07	2 / 134	hsa−miR−31
3	0.08	1 / 26	hsa−miR−127−3p
4	0.11	1 / 35	hsa−miR−1224−5p
5	0.11	1 / 36	hsa−miR−766
6	0.13	1 / 41	hsa−miR−1201
7	0.13	1 / 43	hsa−miR−328
8	0.13	2 / 197	hsa−miR−152
9	0.14	3 / 404	hsa−miR−103
10	0.14	3 / 405	hsa−miR−107
11	0.15	1 / 49	hsa−miR−330−5p
12	0.16	1 / 54	hsa−miR−1184
13	0.16	1 / 54	hsa−miR−1262
14	0.17	1 / 57	hsa−miR−935
15	0.17	1 / 57	hsa−miR−9*

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	1.00	0 / 68	Burnham_sep_vs_con_UP
3	1.00	0 / 56	Burnham_sep_vs_con_DN
4	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
5	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
6	1.00	0 / 48	Burnham_viral_DN
7	1.00	0 / 57	Burnham_viral_UP
8	1.00	0 / 57	Burnham_day1_vs_5_UP
9	1.00	0 / 52	Burnham_day1_vs_5_DN
10	1.00	0 / 54	Burnham_timecourse
11	1.00	0 / 18	Scicluna_UP
12	1.00	0 / 41	Scicluna_DN
13	1.00	0 / 37	Sweeney_viral_up
14	1.00	0 / 33	Sweeney_viral_dn
15	1.00	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.04	2 / 100	Chaussabel_2,8_T−cells
2	0.11	3 / 352	WIRTH_Nervous System
3	0.12	1 / 40	VAQUERIZAS_Testis_TF
4	0.16	1 / 55	WIRTH_Homeostasis
5	0.36	2 / 390	PROTEINATLAS_ovary
6	0.39	1 / 152	VAQUERIZAS_General_TF
7	0.46	1 / 188	Chaussabel_3,8_Enzymes
8	0.50	1 / 209	Chaussabel_2,5_Immune related molecules
9	0.51	1 / 218	WIRTH_pre+post GC B−cells
10	0.54	1 / 233	PROTEINATLAS_smooth muscle
11	0.55	1 / 245	Chaussabel_3,9_Kinases
12	0.59	3 / 923	PROTEINATLAS_cerebral cortex
13	0.69	1 / 355	WIRTH_Immune system
14	0.72	2 / 770	PROTEINATLAS_endometrium
15	0.73	1 / 399	PROTEINATLAS_soft tissue

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	0.08	8 / 1387	HEBENSTREIT_high expression TF
2	0.26	9 / 2150	ICGC_Irf4_targets
3	0.35	12 / 3213	ICGC_Pu1_targets
4	0.44	4 / 1032	ICGC_Usf1_targets
5	0.45	4 / 1044	ICGC_Six5_targets
6	0.46	8 / 2254	ICGC_BatfPcr1_targets
7	0.51	2 / 522	ICGC_SrfPcr2_targets
8	0.55	5 / 1508	ICGC_Mef2_targets
9	0.66	3 / 1025	ICGC_NrsfPcr1_targets
10	0.70	3 / 1089	ICGC_Ets1_targets
11	0.73	11 / 3796	ICGC_Nficsc81335_targets
12	0.73	3 / 1148	HEBENSTREIT_low expression TF
13	0.75	1 / 415	ICGC_RxraPcr1_targets
14	0.79	6 / 2321	ICGC_Rad21_targets
15	0.80	4 / 1636	ICGC_Bcl11_targets

Overexpression Spots

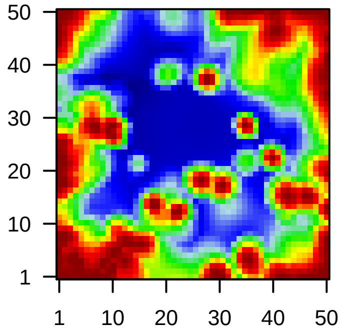
Spot Summary: O

metagenes = 10
genes = 156

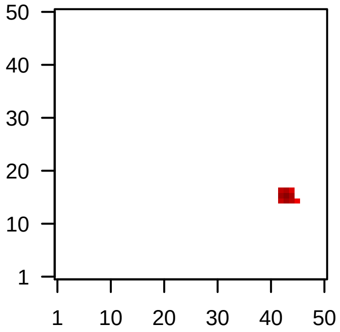
<r> metagenes = 0.97
<r> genes = 0.13
beta: r2= 0.95 / log p= −Inf

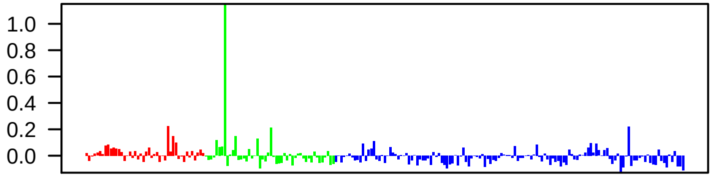
samples with spot = 4 (1.8 %)
mBL : 1 (2.3 %)
intermediate : 2 (4.2 %)
non−mBL : 1 (0.8 %)

Overview Map



Spot





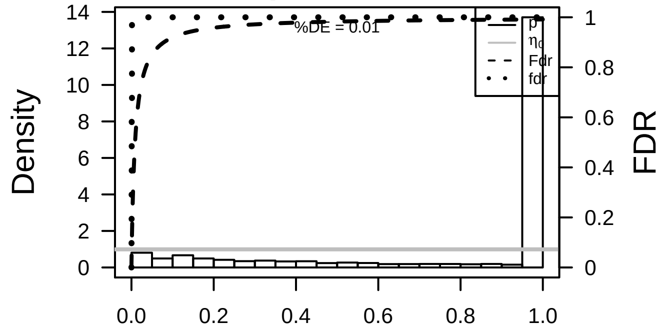
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204865_at	2.65	−0.72	0.5	CA3	carbonic anhydrase 3 [Source:HGNC Symbol;Acc:HGNC:137
2	205363_at	2.4	−0.69	0.39	BBOX1	gamma−butyrobetaine hydroxylase 1 [Source:HGNC Symbol;
3	206045_s_at	2.39	−0.93	0.31	NOL4	nucleolar protein 4 [Source:HGNC Symbol;Acc:HGNC:7870]
4	209840_s_at	2.32	−0.65	0.4	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
5	205951_at	2.23	−0.46	0.45	MYH1	myosin heavy chain 1 [Source:HGNC Symbol;Acc:HGNC:756
6	219692_at	2.17	−1.61	0.12	KREMEN2	kringle containing transmembrane protein 2 [Source:HGNC S
7	209841_s_at	2.16	−0.89	0.39	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
8	206502_s_at	2.15	−0.97	0.17	INSM1	INSM transcriptional repressor 1 [Source:HGNC Symbol;Acc:
9	205529_s_at	2.09	−0.74	0.17	RUNX1T1	RUNX1 translocation partner 1 [Source:HGNC Symbol;Acc:H
10	205347_s_at	1.97	−1.15	0.18	TMSB15A	thymosin beta 15a [Source:HGNC Symbol;Acc:HGNC:30744]
11	209757_s_at	1.94	−0.99	0.24	MYCN	MYCN proto−oncogene, bHLH transcription factor [Source:HC
12	207445_s_at	1.92	−0.85	0.35	CCR9	C−C motif chemokine receptor 9 [Source:HGNC Symbol;Acc:
13	206318_at	1.84	−0.63	0.61	EPPIN	epididymal peptidase inhibitor [Source:HGNC Symbol;Acc:HC
14	213894_at	1.84	−0.59	0.4	THSD7A	thrombospondin type 1 domain containing 7A [Source:HGNC
15	214920_at	1.79	−0.73	0.43	THSD7A	thrombospondin type 1 domain containing 7A [Source:HGNC
16	206404_at	1.78	−0.73	0.38	FGF9	fibroblast growth factor 9 [Source:HGNC Symbol;Acc:HGNC:
17	203296_s_at	1.69	−0.67	0.37	ATP1A2	ATPase Na+/K+ transporting subunit alpha 2 [Source:HGNC
18	222101_s_at	1.69	−0.65	0.31	DCHS1	dachsous cadherin−related 1 [Source:HGNC Symbol;Acc:HG
19	204948_s_at	1.66	−0.82	0.2	FST	follistatin [Source:HGNC Symbol;Acc:HGNC:3971]
20	211585_at	1.65	−0.71	0.55		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−10	59 / 3168	Lymph	HOPP_Repressed
2	9e−07	83 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
3	2e−06	37 / 1894	Lymph	HOPP_Poised_promoter
4	8e−06	16 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
5	4e−05	18 / 697	GSEA	BENPORATH_SUZ12_TARGETS
6	6e−05	7 / 110	GSEA	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
7	8e−05	5 / 50	GSEA	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN
8	2e−04	11 / 329	MF	RNA polymerase II proximal promoter sequence−specific DNA binding
9	2e−04	4 / 32	Gliom	WIRTH_PN subtype
10	2e−04	16 / 657	GSEA	SMID_BREAST_CANCER_BASAL_DN
11	2e−04	8 / 184	Chr	Chr 18
12	3e−04	17 / 730	GSEA	BENPORATH_ES_WITH_H3K27ME3
13	3e−04	20 / 958	Colon	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
14	3e−04	7 / 146	GSEA	LEE_NEURAL_CREST_STEM_CELL_UP
15	4e−04	3 / 16	Refer	WIRTH_Hippocampus
16	5e−04	22 / 1148	TF	HEBENSTREIT_low expression TF
17	6e−04	10 / 318	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
18	7e−04	3 / 20	BP	striated muscle contraction
19	7e−04	5 / 80	BP	lung development
20	1e−03	9 / 284	GSEA	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
21	1e−03	8 / 242	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
22	2e−03	3 / 26	GSEA	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY
23	2e−03	2 / 7	GSEA	PHESSE_TARGETS_OF_APC_AND_MBD2_DN
24	2e−03	19 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
25	2e−03	4 / 59	GSEA	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP
26	2e−03	4 / 62	BP	negative regulation of protein phosphorylation
27	2e−03	4 / 62	Lifesty	DUMEAUX_Smoking enriched genes
28	3e−03	4 / 64	GSEA	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP
29	3e−03	3 / 31	GSEA	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
30	3e−03	7 / 209	Refer	Chaussabel_2,5_Immune related molecules
31	3e−03	2 / 9	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16
32	3e−03	2 / 9	GSEA	MCCABE_HOXC6_TARGETS_UP
33	3e−03	12 / 532	Colon	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_
34	3e−03	8 / 271	GSEA	VECCHI_GASTRIC_CANCER_EARLY_DN
35	3e−03	4 / 67	GSEA	KONDO_PROSTATE_CANCER_HCP_WITH_H3K27ME3
36	3e−03	3 / 33	MF	NADP binding
37	3e−03	3 / 33	GSEA	YANG_BREAST_CANCER_ESR1_UP
38	3e−03	18 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
39	3e−03	2 / 10	BP	exogenous drug catabolic process
40	3e−03	2 / 10	BP	regulation of DNA methylation

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.02	4 / 107	HORVATH_aging_genes meth UP
2	0.07	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.56	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	7e−04	3 / 20	striated muscle contraction
2	7e−04	5 / 80	lung development
3	2e−03	4 / 62	negative regulation of protein phosphorylation
4	3e−03	2 / 10	exogenous drug catabolic process
5	3e−03	2 / 10	regulation of DNA methylation
6	3e−03	2 / 10	relaxation of cardiac muscle
7	3e−03	2 / 10	seminiferous tubule development
8	4e−03	2 / 11	microtubule polymerization
9	4e−03	2 / 11	neuron fate specification
10	5e−03	2 / 12	maternal behavior
11	5e−03	2 / 12	positive regulation of vascular endothelial growth factor receptor signaling patl
12	5e−03	3 / 39	branching involved in ureteric bud morphogenesis
13	6e−03	2 / 13	nitric oxide biosynthetic process
14	6e−03	2 / 13	supramolecular fiber organization
15	6e−03	3 / 42	negative regulation of Wnt signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	5 / 147	PanCan_MAPK_geneset_nanostring
2	0.07	2 / 47	PanCan_TGF−B_geneset_nanostring
3	0.08	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.12	1 / 14	LIU_PROSTATE_CANCER_DN
5	0.12	1 / 14	GUSTAFSON_PI3K_DN
6	0.13	1 / 15	BEN−PORATH_UP
7	0.21	2 / 96	PanCan_TXmisReg_geneset_nanostring
8	0.34	2 / 134	PanCan_RAS_geneset_nanostring
9	0.48	1 / 72	PanCan_Wnt_geneset_nanostring
10	0.49	0 / 11	LIU_PROSTATE_CANCER_UP
11	0.50	2 / 187	PanCan_PI3K_geneset_nanostring
12	0.64	1 / 113	PanCan_Driver_Gene_geneset_nanostring
13	0.69	1 / 130	PanCan_CC+Apop_geneset_nanostring
14	0.71	3 / 409	Lembcke_Normal vs Adenoma
15	0.81	1 / 186	SPANG_LPS−index2

CC

Rank	p−value	#in/all	Geneset
1	0.006	2 / 13	somatodendritic compartment
2	0.007	9 / 382	synapse
3	0.014	2 / 20	centriolar satellite
4	0.016	4 / 109	dendritic spine
5	0.018	2 / 23	voltage−gated calcium channel complex
6	0.019	2 / 24	heterochromatin
7	0.024	11 / 623	cell projection
8	0.026	6 / 254	axon
9	0.027	2 / 29	sarcoplasmic reticulum membrane
10	0.033	8 / 416	macromolecular complex
11	0.035	2 / 33	myofibril
12	0.037	3 / 82	sarcolemma
13	0.043	2 / 37	T−tubule
14	0.054	2 / 42	sarcoplasmic reticulum
15	0.056	2 / 43	intercalated disc

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	8 / 184	Chr 18
2	9e−02	11 / 776	Chr 17
3	2e−01	6 / 403	Chr 14
4	2e−01	10 / 833	Chr 19
5	2e−01	5 / 369	Chr 20
6	4e−01	5 / 437	Chr 8
7	4e−01	6 / 554	Chr 5
8	4e−01	6 / 556	Chr X
9	4e−01	4 / 382	Chr 15
10	6e−01	3 / 333	Chr 22
11	6e−01	6 / 689	Chr 3
12	6e−01	7 / 832	Chr 2
13	6e−01	2 / 242	Chr 13
14	6e−01	4 / 490	Chr 10
15	6e−01	4 / 492	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−10	55 / 2747	Bcells peripheral blood_12_EnhBiv
2	4e−10	52 / 2515	natural killer cells peripheral blood_13_ReprPC
3	9e−10	50 / 2405	Bcells peripheral blood_13_ReprPC
4	1e−09	52 / 2602	natural killer cells peripheral blood_12_EnhBiv
5	2e−09	51 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
6	2e−09	56 / 2984	natural killer cells peripheral blood_14_ReprPCWk
7	2e−09	64 / 3724	Tcells peripheral blood_12_EnhBiv
8	4e−09	43 / 1943	TssP_Colon
9	4e−09	53 / 2765	Tregulatory cells peripheral blood_13_ReprPC
10	5e−09	41 / 1799	T CD8+ naive cells peripheral blood_13_ReprPC
11	5e−09	52 / 2700	Thelper cells peripheral blood_14_ReprPCWk
12	8e−09	56 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
13	2e−08	64 / 3918	Tcells peripheral blood_14_ReprPCWk
14	2e−08	62 / 3734	Tcells peripheral blood_13_ReprPC
15	3e−08	54 / 3001	Bcells peripheral blood_14_ReprPCWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−07	83 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	8e−06	16 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
3	3e−04	20 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
4	6e−04	10 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
5	3e−03	12 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
6	3e−03	18 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
7	2e−02	2 / 25	Ang_CRC−CIMPH−vs−L_hypo
8	4e−02	2 / 35	Ang_CRC_Hypomethylated
9	5e−02	8 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
10	6e−02	4 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
11	6e−02	1 / 7	Budinska_D_Mesenchymal_UP
12	7e−02	1 / 8	Marisa_CRC−C3
13	1e−01	7 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	1e−01	1 / 13	Vilar_hypermutated−in−CRC
15	1e−01	3 / 132	Marisa_CRC−cluster−a

Glioma

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 32	WIRTH_PN subtype
2	4e−03	2 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
3	1e−02	2 / 21	Barbus_GBM_STS_vs._LTS
4	2e−02	3 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
5	2e−02	4 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
6	2e−02	4 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
7	4e−02	3 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	4e−02	4 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	5e−02	2 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP
10	6e−02	4 / 163	ScoV_0.999_Sturm_E1_IDH_DN
11	7e−02	2 / 50	Christensen_hypomethylated_in_primary_glioblastoma
12	7e−02	2 / 50	Vishal_subnetwork signature of survival in GBM
13	1e−01	20 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	1e−01	1 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	1e−01	3 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	18 / 697	BENPORATH_SUZ12_TARGETS
2	6e−05	7 / 110	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
3	8e−05	5 / 50	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASSIC_DN
4	2e−04	16 / 657	SMID_BREAST_CANCER_BASAL_DN
5	3e−04	17 / 730	BENPORATH_ES_WITH_H3K27ME3
6	3e−04	7 / 146	LEE_NEURAL_CREST_STEM_CELL_UP
7	1e−03	9 / 284	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
8	1e−03	8 / 242	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
9	2e−03	3 / 26	DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY
10	2e−03	2 / 7	PHESSE_TARGETS_OF_APC_AND_MBD2_DN
11	2e−03	19 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
12	2e−03	4 / 59	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP
13	3e−03	4 / 64	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP
14	3e−03	3 / 31	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
15	3e−03	2 / 9	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16

HM

Rank	p−value	#in/all	Geneset
1	0.008	6 / 194	HALLMARK_MYOGENESIS
2	0.079	4 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	0.229	1 / 29	HALLMARK_NOTCH_SIGNALING
4	0.237	3 / 188	HALLMARK_HYPOXIA
5	0.251	3 / 194	HALLMARK_KRAS_SIGNALING_UP
6	0.270	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
7	0.296	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
8	0.298	2 / 122	HALLMARK_SPERMATOGENESIS
9	0.360	2 / 141	HALLMARK_UV_RESPONSE_DN
10	0.500	2 / 187	HALLMARK_INFLAMMATORY_RESPONSE
11	0.512	2 / 191	HALLMARK_P53_PATHWAY
12	0.514	2 / 192	HALLMARK_MTORC1_SIGNALING
13	0.520	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.523	2 / 195	HALLMARK_KRAS_SIGNALING_DN
15	0.583	1 / 97	HALLMARK_BILE_ACID_METABOLISM

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	1 / 21	Angelova_immune−metagene−central_memory_CD4
2	0.2	1 / 23	Angelova_immune−metagene−Th2
3	0.3	1 / 38	Angelova_immune−metagene−mast−cells
4	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
6	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
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	0.002	4 / 62	DUMEAUX_Smoking enriched genes
2	0.134	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.250	1 / 32	Marjolein_ageing−genes_DN
4	0.742	1 / 150	Homuth_BMI−associated−genes_UP
5	0.851	1 / 210	Homuth_BMI−associated−genes_DN
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.000	0 / 22	DUMEAUX_High bmi enriched genes
14	1.000	0 / 22	DUMEAUX_Fasting enriched genes
15	1.000	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−10	59 / 3168	HOPP_Repressed
2	2e−06	37 / 1894	HOPP_Poised_promoter
3	1e−02	3 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
4	4e−02	2 / 35	Subero_MM_hyper_meth
5	4e−02	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
6	5e−02	23 / 1814	HOPP_Repetitive
7	6e−02	5 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
8	6e−02	2 / 45	Subero_INT_hypo_meth
9	7e−02	2 / 49	LEE_Developmental_regulators
10	8e−02	2 / 53	LENZ_Stromal signature 2
11	9e−02	1 / 10	MASCQUE_ABC UP
12	9e−02	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
13	1e−01	6 / 378	TARTE_Mature plasma cell signature
14	1e−01	1 / 15	Subero_T−ALL_hypo_meth
15	1e−01	2 / 70	Subero_FL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	Melanoma Epi−Enzyme Cluster 2
2	0.03	3 / 78	Tirosh_CAF−cell specific genes
3	0.07	4 / 171	Landsberg_dedifferentiation_up
4	0.11	2 / 65	Harbst_melanoma_highgrade_up
5	0.28	1 / 37	Hugo_melanoma−all−MET_DN
6	0.29	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
7	0.30	1 / 39	Tirosh_melanoma specific genes
8	0.34	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	0.34	1 / 46	Tirosh_top50 correlated genes PC5
10	0.45	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	0.52	1 / 81	Tirosh_Genes in the MITF program
12	0.53	1 / 83	TCGA_melanoma_immune_high
13	0.55	2 / 204	Landsberg_dedifferentiation_down
14	0.66	1 / 119	TCGA_melanoma_MITF_low
15	0.78	2 / 319	Gerber_wt/wt_melanoma−cells−SpotA

MF

Rank	p−value	#in/all	Geneset
1	2e−04	11 / 329	RNA polymerase II proximal promoter sequence−specific DNA binding
2	3e−03	3 / 33	NADP binding
3	4e−03	2 / 11	transcription factor activity, RNA polymerase II transcription factor binding
4	5e−03	3 / 38	1−phosphatidylinositol−3−kinase activity
5	5e−03	2 / 12	carbonate dehydratase activity
6	5e−03	2 / 12	methyl−CpG binding
7	8e−03	3 / 46	SH3/SH2 adaptor activity
8	8e−03	6 / 196	microtubule binding
9	1e−02	3 / 49	transmembrane receptor protein tyrosine kinase activity
10	1e−02	2 / 17	heparan sulfate proteoglycan binding
11	1e−02	2 / 19	fibronectin binding
12	1e−02	2 / 19	Wnt−activated receptor activity
13	1e−02	2 / 20	receptor ligand activity
14	2e−02	4 / 107	voltage−gated ion channel activity
15	2e−02	2 / 23	alpha−tubulin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 22	hsa−miR−941
2	0.05	2 / 38	hsa−miR−628−5p
3	0.06	2 / 44	hsa−miR−455−5p
4	0.07	3 / 107	hsa−miR−24
5	0.07	2 / 50	hsa−miR−384
6	0.10	2 / 59	hsa−miR−375
7	0.11	2 / 62	hsa−miR−1254
8	0.11	2 / 64	hsa−miR−1261
9	0.11	6 / 369	hsa−miR−15b
10	0.12	2 / 68	hsa−miR−942
11	0.14	3 / 146	hsa−miR−582−5p
12	0.14	6 / 397	hsa−miR−15a
13	0.15	6 / 404	hsa−miR−103
14	0.15	2 / 78	hsa−miR−224
15	0.15	6 / 405	hsa−miR−107

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	1 / 18	Scicluna_UP
2	0.3	1 / 41	Scicluna_DN
3	0.4	1 / 48	Burnham_viral_DN
4	0.5	1 / 68	Burnham_sep_vs_con_UP
5	0.5	1 / 71	Burnham_cap_fp_vs_con_UP
6	1.0	0 / 56	Burnham_sep_vs_con_DN
7	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
8	1.0	0 / 57	Burnham_viral_UP
9	1.0	0 / 57	Burnham_day1_vs_5_UP
10	1.0	0 / 52	Burnham_day1_vs_5_DN
11	1.0	0 / 54	Burnham_timecourse
12	1.0	0 / 37	Sweeney_viral_up
13	1.0	0 / 33	Sweeney_viral_dn
14	1.0	0 / 122	Terre_IMS_influenza_meta_signature
15	1.0	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 16	WIRTH_Hippocampus
2	3e−03	7 / 209	Chaussabel_2,5_Immune related molecules
3	6e−03	4 / 83	WIRTH_Muscle
4	2e−02	2 / 24	VAQUERIZAS_Pituitary_TF
5	3e−02	4 / 133	JONGENEEL_Testis
6	4e−02	3 / 82	WIRTH_Testis
7	5e−02	4 / 152	VAQUERIZAS_General_TF
8	5e−02	2 / 42	VAQUERIZAS_Fetal brain_TF
9	9e−02	1 / 11	JONGENEEL_Pituitary Gland
10	1e−01	6 / 352	WIRTH_Nervous System
11	1e−01	1 / 12	WIRTH_Globus pallidus
12	1e−01	1 / 14	WIRTH_Thalamus
13	2e−01	1 / 19	JONGENEEL_Adrenal Gland
14	2e−01	1 / 19	JONGENEEL_Prostate
15	2e−01	2 / 81	Chaussabel_1,2_Platelets

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	5e−04	22 / 1148	HEBENSTREIT_low expression TF
2	4e−02	1 / 5	MYC_TFs
3	7e−02	14 / 1025	ICGC_NrsfPcr1_targets
4	1e−01	37 / 3435	ICGC_Ebfsc137065_targets
5	3e−01	41 / 4212	ICGC_Pol2_targets
6	3e−01	44 / 4602	ICGC_Elf1_targets
7	3e−01	23 / 2321	ICGC_Rad21_targets
8	3e−01	46 / 4851	ICGC_Runx3_targets
9	4e−01	22 / 2254	ICGC_BatfPcr1_targets
10	4e−01	19 / 1941	ICGC_Bcl3_targets
11	4e−01	39 / 4131	ICGC_Tcf3_targets
12	4e−01	18 / 1848	ICGC_Pbx3_targets
13	4e−01	5 / 485	ICGC_NrsfPcr2_targets
14	5e−01	10 / 1041	ICGC_P300_targets
15	5e−01	4 / 415	ICGC_RxraPcr1_targets

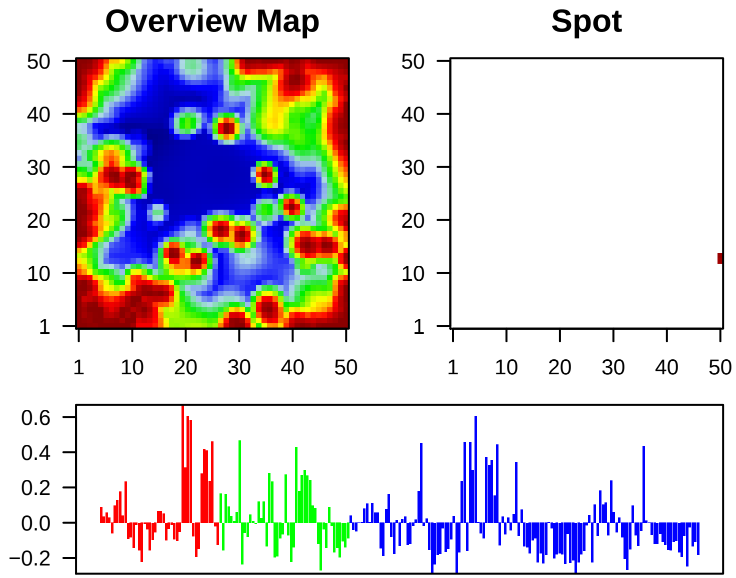
Overexpression Spots

Spot Summary: P

metagenes = 2
genes = 87

<r> metagenes = 0.99
<r> genes = 0.34
beta: r2= 3.54 / log p= −Inf

samples with spot = 32 (14.5 %)
mBL : 10 (22.7 %)
intermediate : 9 (18.8 %)
non−mBL : 13 (10.1 %)

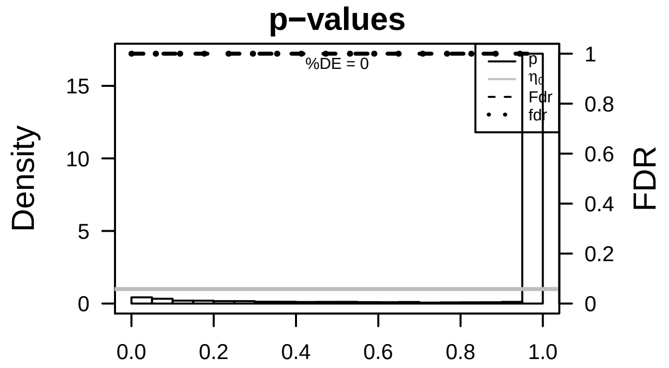


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	213350_at	2.55	−0.86	0.8		
2	214469_at	1.7	−0.75	0.44	HIST1H2AE	histone cluster 1 H2A family member e [Source:HGNC Symb
3	202648_at	1.66	−0.64	0.71		
4	214522_x_at	1.64	−1.21	0.49	HIST1H2AD	histone cluster 1 H2A family member d [Source:HGNC Symb
5	215779_s_at	1.62	−0.92	0.38	HIST1H2BG	histone cluster 1 H2B family member g [Source:HGNC Symb
6	216153_x_at	1.57	−0.93	0.54		
7	222027_at	1.57	−1.19	0.7		
8	219138_at	1.52	−0.72	0.76		
9	214123_s_at	1.49	−0.59	0.61		NOP14 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
10	216563_at	1.43	−0.82	0.61		
11	206035_at	1.43	−0.73	0.66		
12	200908_s_at	1.41	−0.7	0.78		
13	217619_x_at	1.34	−1.37	0.38		
14	214056_at	1.34	−1.23	0.51		
15	214149_s_at	1.32	−1.11	0.65		
16	214395_x_at	1.31	−0.82	0.76		
17	213642_at	1.28	−0.98	0.84		
18	213813_x_at	1.27	−0.74	0.74		
19	214057_at	1.26	−0.82	0.63		
20	213087_s_at	1.26	−0.52	0.68		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−17	11 / 70	CC	nucleosome
2	2e−13	8 / 42	GSEA	REACTOME_RNA_POL_I_PROMOTER_OPENING
3	3e−12	9 / 92	GSEA	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
4	4e−12	8 / 60	GSEA	REACTOME_AMYLOIDS
5	5e−12	8 / 62	GSEA	REACTOME_RNA_POL_I_TRANSCRIPTION
6	5e−12	8 / 62	GSEA	REACTOME_MEIOTIC_RECOMBINATION
7	6e−12	7 / 36	GSEA	REACTOME_PACKAGING_OF_TELOMERE_ENDS
8	4e−11	7 / 46	GSEA	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOS
9	4e−11	12 / 324	CC	chromosome
10	9e−11	8 / 88	GSEA	REACTOME_MEIOSIS
11	1e−10	8 / 91	GSEA	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRAN
12	2e−10	7 / 57	GSEA	REACTOME_MEIOTIC_SYNAPSIS
13	3e−10	7 / 61	GSEA	REACTOME_TELOMERE_MAINTENANCE
14	2e−09	7 / 78	BP	nucleosome assembly
15	9e−09	7 / 98	GSEA	REACTOME_CHROMOSOME_MAINTENANCE
16	1e−08	8 / 164	GSEA	REACTOME_TRANSCRIPTION
17	3e−08	7 / 118	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
18	1e−07	12 / 645	Refer	PROTEINATLAS_bone marrow
19	4e−07	11 / 593	Refer	PROTEINATLAS_lateral ventricle
20	1e−06	11 / 669	Chr	Chr 6
21	1e−06	9 / 408	MF	protein heterodimerization activity
22	2e−06	4 / 31	CC	nuclear nucleosome
23	2e−06	5 / 76	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN
24	3e−06	4 / 36	BP	chromatin silencing
25	4e−06	13 / 1076	Refer	PROTEINATLAS_stomach
26	8e−06	11 / 809	Refer	PROTEINATLAS_fallopian tube
27	1e−05	9 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
28	2e−05	10 / 708	Refer	PROTEINATLAS_thyroid gland
29	2e−05	12 / 1072	Refer	PROTEINATLAS_duodenum
30	3e−05	3 / 22	BP	telomere organization
31	4e−05	7 / 347	GSEA	REACTOME_CELL_CYCLE
32	5e−05	3 / 26	BP	DNA replication−dependent nucleosome assembly
33	5e−05	9 / 642	Refer	PROTEINATLAS_lung
34	6e−05	3 / 27	BP	chromatin silencing at rDNA
35	7e−05	11 / 1022	Refer	PROTEINATLAS_placenta
36	1e−04	5 / 171	CC	nuclear chromatin
37	1e−04	3 / 34	miRN	hsa−miR−760
38	1e−04	11 / 1081	Refer	PROTEINATLAS_testis
39	1e−04	3 / 37	BP	negative regulation of gene expression, epigenetic
40	2e−04	10 / 923	Refer	PROTEINATLAS_cerebral cortex



Aging

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

CC

Rank	p−value	#in/all	Geneset
1	3e−17	11 / 70	nucleosome
2	4e−11	12 / 324	chromosome
3	2e−06	4 / 31	nuclear nucleosome
4	1e−04	5 / 171	nuclear chromatin
5	2e−04	3 / 44	nuclear chromosome
6	3e−03	3 / 103	nuclear chromosome, telomeric region
7	2e−02	12 / 2239	extracellular exosome
8	3e−02	1 / 10	catenin complex
9	3e−02	4 / 416	macromolecular complex
10	3e−02	1 / 11	axon initial segment
11	3e−02	1 / 12	endoplasmic reticulum exit site
12	4e−02	1 / 15	node of Ranvier
13	4e−02	1 / 15	nuclear heterochromatin
14	4e−02	1 / 15	phagophore assembly site membrane
15	6e−02	1 / 21	nuclear euchromatin

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.1	6 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	0.2	1 / 60	Marisa_CRC−cluster−g
3	0.2	3 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
4	0.2	7 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
5	0.3	4 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
6	0.3	5 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	0.4	1 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
8	0.4	2 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
9	0.6	1 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	0.7	1 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	0.8	16 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	0.9	1 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
13	0.9	1 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
14	0.9	1 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
15	0.9	1 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

HM

Rank	p−value	#in/all	Geneset
1	0.09	1 / 34	HALLMARK_APICAL_SURFACE
2	0.10	2 / 193	HALLMARK_HEME_METABOLISM
3	0.24	1 / 96	HALLMARK_ANDROGEN_RESPONSE
4	0.24	1 / 97	HALLMARK_PEROXISOME
5	0.31	1 / 133	HALLMARK_DNA_REPAIR
6	0.39	1 / 174	HALLMARK_APICAL_JUNCTION
7	0.40	1 / 181	HALLMARK_XENOBIOTIC_METABOLISM
8	0.40	1 / 182	HALLMARK_GLYCOLYSIS
9	0.42	1 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	0.42	1 / 192	HALLMARK_MTORC1_SIGNALING
11	0.42	1 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	1.00	0 / 188	HALLMARK_HYPOXIA
13	1.00	0 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	1.00	0 / 173	HALLMARK_MITOTIC_SPINDLE
15	1.00	0 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.02	1 / 9	YAMANE_AICDA_targets_nonrecruited
2	0.03	3 / 237	ZHANG_DLBCL mutated
3	0.09	1 / 33	Subero_T−PLL_hypo_meth
4	0.14	2 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
5	0.19	1 / 77	TARTE_Plasma cell signature
6	0.24	1 / 97	ROSOLOWSKI_red total
7	0.41	13 / 4261	HOPP_Txn_transition
8	0.45	16 / 5404	HOPP_Strong_enhancer
9	0.45	1 / 213	SPANG_IL21 DN
10	0.47	3 / 906	SPANG_BCR DN
11	0.63	16 / 5908	HOPP_Active_promoter
12	0.66	1 / 378	TARTE_Mature plasma cell signature
13	0.91	12 / 5529	HOPP_Txn_elongation
14	0.92	3 / 1894	HOPP_Poised_promoter
15	0.93	9 / 4559	HOPP_Weak_enhancer

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 34	hsa−miR−760
2	1e−02	2 / 57	hsa−miR−518c*
3	1e−02	2 / 63	hsa−miR−30a*
4	2e−02	2 / 77	hsa−miR−526a
5	2e−02	3 / 223	hsa−miR−1244
6	3e−02	1 / 11	hsa−miR−574−3p
7	3e−02	2 / 100	hsa−miR−519e
8	3e−02	3 / 254	hsa−miR−520d−3p
9	5e−02	1 / 17	hsa−miR−323−5p
10	5e−02	2 / 126	hsa−miR−338−3p
11	5e−02	2 / 134	hsa−miR−323b−5p
12	6e−02	2 / 139	hsa−miR−548e
13	6e−02	2 / 141	hsa−miR−573
14	6e−02	1 / 22	hsa−miR−24−1*
15	7e−02	2 / 149	hsa−miR−548a−3p

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	2e−09	7 / 78	nucleosome assembly
2	3e−06	4 / 36	chromatin silencing
3	3e−05	3 / 22	telomere organization
4	5e−05	3 / 26	DNA replication−dependent nucleosome assembly
5	6e−05	3 / 27	chromatin silencing at rDNA
6	1e−04	3 / 37	negative regulation of gene expression, epigenetic
7	2e−04	3 / 42	protein heterotetramerization
8	3e−04	3 / 48	regulation of megakaryocyte differentiation
9	3e−04	3 / 49	positive regulation of gene expression, epigenetic
10	4e−04	3 / 52	double−strand break repair via nonhomologous end joining
11	5e−04	2 / 12	negative regulation of megakaryocyte differentiation
12	6e−04	2 / 13	histone H3−K4 trimethylation
13	7e−04	2 / 14	innate immune response in mucosa
14	9e−04	3 / 67	regulation of gene silencing by miRNA
15	1e−03	2 / 19	DNA replication−independent nucleosome assembly

Chr

Rank	p−value	#in/all	Geneset
1	1e−06	11 / 669	Chr 6
2	8e−02	5 / 833	Chr 19
3	3e−01	2 / 369	Chr 20
4	3e−01	2 / 382	Chr 15
5	3e−01	3 / 689	Chr 3
6	4e−01	3 / 776	Chr 17
7	5e−01	2 / 554	Chr 5
8	7e−01	1 / 403	Chr 14
9	7e−01	3 / 1325	Chr 1
10	7e−01	1 / 480	Chr 4
11	8e−01	1 / 492	Chr 9
12	9e−01	1 / 756	Chr 11
13	9e−01	1 / 832	Chr 2
14	1e+00	0 / 490	Chr 10
15	1e+00	0 / 700	Chr 12

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	3 / 101	Hopp_Sturm_GBM_Epi3_E_G34_UP
2	0.030	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
3	0.046	3 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
4	0.055	1 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
5	0.091	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	0.111	1 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP
7	0.169	2 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
8	0.539	1 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	0.609	1 / 330	Up
10	0.817	3 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
11	0.859	3 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
12	0.902	2 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
13	0.942	1 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
14	1.000	0 / 16	VERHAAK_CL subtype
15	1.000	0 / 16	VERHAAK_MES subtype

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	1 / 12	Angelova_immune−metagene−NK56_dim
2	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
3	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
4	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.00	0 / 25	Angelova_immune−metagene−DC
9	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.00	0 / 14	Angelova_immune−metagene−eosinophil
12	1.00	0 / 19	Angelova_immune−metagene−iDC
13	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.00	0 / 11	Angelova_immune−metagene−macrophages
15	1.00	0 / 38	Angelova_immune−metagene−mast−cells

Melanoma

Rank	p−value	#in/all	Geneset
1	0.06	1 / 23	Melanoma Epi−Enzyme Cluster 7
2	0.13	2 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	0.14	2 / 236	Gerber_wt/wt_group3−specific
4	0.41	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
5	0.41	1 / 189	Tirosh_genes preferentially expressed by Tregs
6	0.51	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
7	0.54	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
8	0.60	1 / 319	Gerber_wt/wt_melanoma−cells−SpotA
9	0.76	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	1.00	0 / 17	Hugo_melanoma−all−MET_UP
11	1.00	0 / 37	Hugo_melanoma−all−MET_DN
12	1.00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	1.00	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1.00	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

Pneumonia

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

TF

Rank	p−value	#in/all	Geneset
1	0.03	11 / 2150	ICGC_Irf4_targets
2	0.09	12 / 2899	ICGC_Nfatc1_targets
3	0.15	13 / 3451	ICGC_Atf2_targets
4	0.15	7 / 1578	ICGC_GabpPcr2_targets
5	0.19	5 / 1107	ICGC_Myc_targets
6	0.22	13 / 3703	ICGC_Foxm1_targets
7	0.23	12 / 3420	ICGC_Bclaf101388_targets
8	0.25	13 / 3796	ICGC_Nficsc81335_targets
9	0.28	11 / 3213	ICGC_Pu1_targets
10	0.28	12 / 3564	ICGC_Taf1_targets
11	0.30	7 / 1941	ICGC_Bcl3_targets
12	0.30	12 / 3608	ICGC_Tcf12_targets
13	0.30	6 / 1630	ICGC_SrfV0416101_targets
14	0.31	6 / 1636	ICGC_Bcl11_targets
15	0.33	4 / 1041	ICGC_P300_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.05	1 / 20	PanCan_ChromMod_geneset_nanostring
2	0.41	1 / 186	SPANG_LPS−index2
3	0.59	1 / 317	SPANG_BCL6−index2
4	0.75	1 / 480	Lembcke_Colonic Inflammation
5	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
6	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
7	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	1.00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	1.00	0 / 12	LIU_BREAST_CANCER
10	1.00	0 / 14	LIU_COMMON_CANCER_GENES
11	1.00	0 / 16	LIU_LIVER_CANCER
12	1.00	0 / 14	LIU_PROSTATE_CANCER_DN
13	1.00	0 / 11	LIU_PROSTATE_CANCER_UP
14	1.00	0 / 15	WANG_ER_UP
15	1.00	0 / 9	WANG_ER_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.04	6 / 932	Tcells peripheral blood_3_TxFlnk
2	0.06	17 / 4266	3_TssF_Neuronal_Progenitor
3	0.06	12 / 2704	4_TxTrans_Fibroblasts
4	0.07	10 / 2144	T CD8+ naive cells peripheral blood_6_EnhG
5	0.12	14 / 3682	natural killer cells peripheral blood_6_EnhG
6	0.12	27 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
7	0.14	26 / 7957	Tcells peripheral blood_2_TssAFlnk
8	0.15	9 / 2204	3_TxFlnk_ESC_Mesoderm
9	0.17	23 / 6997	Overlap_fetal_midbrain_K9K27me3
10	0.18	16 / 4595	6_EnhG_Melanocytes
11	0.19	14 / 3938	Thelper cells peripheral blood_6_EnhG
12	0.21	14 / 4009	6_EnhG_ESC_Mesoderm
13	0.22	25 / 7930	Tregulatory cells peripheral blood_1_TssA
14	0.24	13 / 3767	Bcells peripheral blood_6_EnhG
15	0.25	26 / 8370	natural killer cells peripheral blood_2_TssAFlnk

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−13	8 / 42	REACTOME_RNA_POL_I_PROMOTER_OPENING
2	3e−12	9 / 92	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
3	4e−12	8 / 60	REACTOME_AMYLOIDS
4	5e−12	8 / 62	REACTOME_RNA_POL_I_TRANSCRIPTION
5	5e−12	8 / 62	REACTOME_MEIOTIC_RECOMBINATION
6	6e−12	7 / 36	REACTOME_PACKAGING_OF_TELOMERE_ENDS
7	4e−11	7 / 46	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSO
8	9e−11	8 / 88	REACTOME_MEIOSIS
9	1e−10	8 / 91	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSC
10	2e−10	7 / 57	REACTOME_MEIOTIC_SYNAPSIS
11	3e−10	7 / 61	REACTOME_TELOMERE_MAINTENANCE
12	9e−09	7 / 98	REACTOME_CHROMOSOME_MAINTENANCE
13	1e−08	8 / 164	REACTOME_TRANSCRIPTION
14	3e−08	7 / 118	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
15	2e−06	5 / 76	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 150	Homuth_BMI−associated−genes_UP
2	1.0	0 / 62	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 22	DUMEAUX_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

MF

Rank	p−value	#in/all	Geneset
1	1e−06	9 / 408	protein heterodimerization activity
2	2e−04	13 / 1541	DNA binding
3	9e−03	2 / 52	chromatin DNA binding
4	3e−02	2 / 88	histone binding
5	3e−02	3 / 239	protein domain specific binding
6	3e−02	1 / 11	transmembrane receptor protein serine/threonine kinase activity
7	3e−02	1 / 12	activin binding
8	3e−02	1 / 12	GTPase inhibitor activity
9	3e−02	1 / 12	signal transducer, downstream of receptor, with serine/threonine kinase activi
10	4e−02	1 / 14	retinoic acid receptor binding
11	4e−02	1 / 16	galactosyltransferase activity
12	4e−02	1 / 16	retinoid X receptor binding
13	5e−02	1 / 17	ankyrin binding
14	7e−02	1 / 26	thyroid hormone receptor binding
15	8e−02	1 / 28	protein serine/threonine/tyrosine kinase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−07	12 / 645	PROTEINATLAS_bone marrow
2	4e−07	11 / 593	PROTEINATLAS_lateral ventricle
3	4e−06	13 / 1076	PROTEINATLAS_stomach
4	8e−06	11 / 809	PROTEINATLAS_fallopian tube
5	2e−05	10 / 708	PROTEINATLAS_thyroid gland
6	2e−05	12 / 1072	PROTEINATLAS_duodenum
7	5e−05	9 / 642	PROTEINATLAS_lung
8	7e−05	11 / 1022	PROTEINATLAS_placenta
9	1e−04	11 / 1081	PROTEINATLAS_testis
10	2e−04	10 / 923	PROTEINATLAS_cerebral cortex
11	2e−04	8 / 604	PROTEINATLAS_hippocampus
12	5e−04	9 / 866	PROTEINATLAS_cerebellum
13	6e−04	9 / 893	PROTEINATLAS_pancreas
14	7e−04	6 / 390	PROTEINATLAS_ovary
15	1e−03	6 / 429	PROTEINATLAS_liver

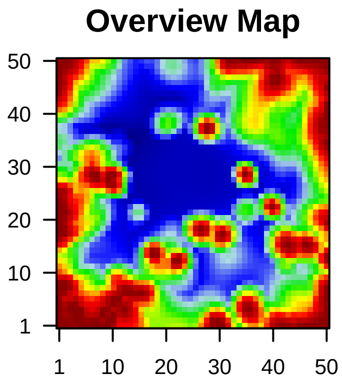
Overexpression Spots

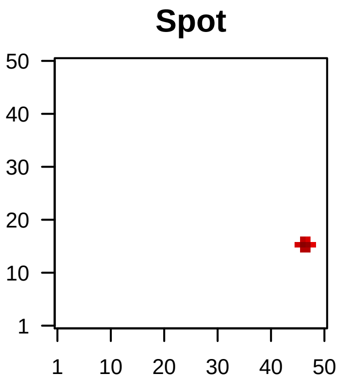
Spot Summary: Q

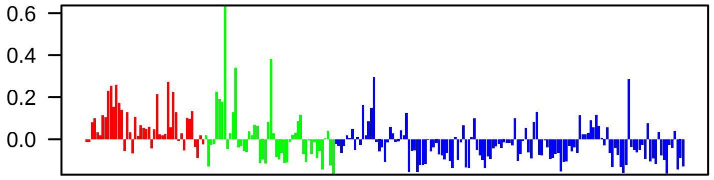
metagenes = 8
genes = 123

<r> metagenes = 0.97
<r> genes = 0.19
beta: r2= 1.55 / log p= −Inf

samples with spot = 12 (5.4 %)
mBL : 6 (13.6 %)
intermediate : 4 (8.3 %)
non−mBL : 2 (1.6 %)





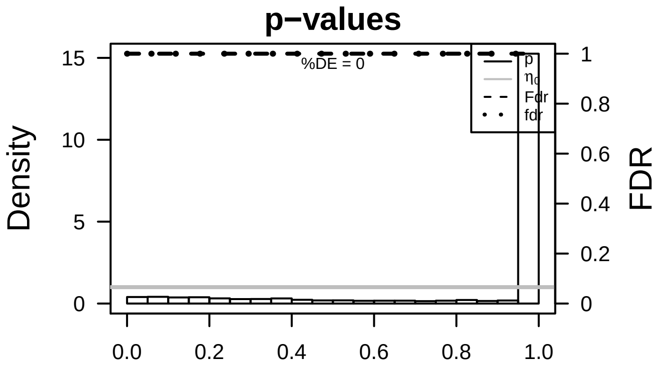


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	208014_x_at	1.81	−0.93	0.42		
2	215607_x_at	1.8	−1.14	0.58		
3	206213_at	1.57	−0.82	0.22	WNT10B	Wnt family member 10B [Source:HGNC Symbol;Acc:HGNC:1
4	207608_x_at	1.54	−0.78	0.53		
5	216054_x_at	1.46	−0.61	0.44	MYL4	myosin light chain 4 [Source:HGNC Symbol;Acc:HGNC:7585
6	209057_x_at	1.37	−1.1	0.64	CDC5L	cell division cycle 5 like [Source:HGNC Symbol;Acc:HGNC:1
7	216981_x_at	1.31	−0.98	0.32	SPN	sialophorin [Source:HGNC Symbol;Acc:HGNC:11249]
8	213066_at	1.22	−0.83	0.37	RUSC2	RUN and SH3 domain containing 2 [Source:HGNC Symbol;A
9	220944_at	1.22	−0.7	0.52	PGLYRP4	peptidoglycan recognition protein 4 [Source:HGNC Symbol;A
10	204776_at	1.22	−1.32	0.27	THBS4	thrombospondin 4 [Source:HGNC Symbol;Acc:HGNC:11788]
11	217473_x_at	1.21	−1.05	0.61	SLC11A1	solute carrier family 11 member 1 [Source:HGNC Symbol;Ac
12	43427_at	1.15	−0.63	0.4	ACACB	acetyl−CoA carboxylase beta [Source:HGNC Symbol;Acc:HG
13	215582_x_at	1.12	−0.91	0.66		
14	211465_x_at	1.11	−0.53	0.56	FUT6	fucosyltransferase 6 [Source:HGNC Symbol;Acc:HGNC:4017
15	215133_s_at	1.08	−0.67	0.39		
16	217117_x_at	1.07	−0.91	0.53		
17	217261_at	1.07	−0.7	0.42		testis−specific transcript, Y−linked 2 (non−protein coding) [So
18	208242_at	1.06	−0.58	0.49	RAX	retina and anterior neural fold homeobox [Source:HGNC Sym
19	215491_at	1.06	−0.65	0.37	MYCL	MYCL proto−oncogene, bHLH transcription factor [Source:HG
20	217580_x_at	1.03	−1.15	0.64	ATL2	atlastin GTPase 2 [Source:HGNC Symbol;Acc:HGNC:24047]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−06	70 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
2	6e−05	13 / 483	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
3	3e−04	9 / 290	Colon	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	8e−04	38 / 3168	Lympl	HOPP_Repressed
5	8e−04	3 / 25	GSEA	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN
6	9e−04	4 / 58	GSEA	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN
7	1e−03	5 / 105	MF	Ras guanyl−nucleotide exchange factor activity
8	1e−03	26 / 1894	Lympl	HOPP_Poised_promoter
9	1e−03	4 / 63	GSEA	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH
10	2e−03	3 / 36	BP	cardiac conduction
11	3e−03	4 / 78	Gliom	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
12	3e−03	13 / 730	GSEA	BENPORATH_ES_WITH_H3K27ME3
13	3e−03	3 / 39	GSEA	REACTOME_NCAM1_INTERACTIONS
14	4e−03	10 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
15	4e−03	2 / 13	BP	protein localization to organelle
16	4e−03	4 / 88	GSEA	KEGG_MELANOGENESIS
17	4e−03	7 / 273	GSEA	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
18	5e−03	2 / 14	BP	ceramide biosynthetic process
19	5e−03	2 / 14	Canc	LIU_PROSTATE_CANCER_DN
20	5e−03	2 / 14	Canc	LIU_PROSTATE_CANCER_DN
21	5e−03	8 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
22	5e−03	2 / 15	BP	ceramide metabolic process
23	5e−03	2 / 15	CC	node of Ranvier
24	6e−03	3 / 50	GSEA	LUI_THYROID_CANCER_CLUSTER_1
25	6e−03	2 / 16	BP	regulation of sodium ion transport
26	8e−03	5 / 168	CC	postsynaptic density
27	9e−03	2 / 19	BP	cartilage condensation
28	1e−02	2 / 20	BP	adult behavior
29	1e−02	5 / 174	CC	postsynaptic membrane
30	1e−02	2 / 21	GSEA	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS
31	1e−02	2 / 21	GSEA	NAKAMURA_CANCER_MICROENVIRONMENT_UP
32	1e−02	9 / 492	Chr	Chr 9
33	1e−02	2 / 22	BP	sensory perception of taste
34	1e−02	9 / 501	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
35	1e−02	2 / 23	BP	membrane depolarization
36	1e−02	2 / 23	GSEA	PID_RXR_VDR_PATHWAY
37	1e−02	4 / 121	GSEA	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_DN
38	1e−02	4 / 122	GSEA	MIKKELSEN_MEF_ICP_WITH_H3K27ME3
39	1e−02	4 / 123	GSEA	GAL_LEUKEMIC_STEM_CELL_UP
40	1e−02	8 / 423	Gliom	Down_a



Aging

Rank	p−value	#in/all	Geneset
1	0.3	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.6	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	0.005	2 / 15	node of Ranvier
2	0.008	5 / 168	postsynaptic density
3	0.010	5 / 174	postsynaptic membrane
4	0.024	3 / 83	centriole
5	0.032	9 / 595	cell junction
6	0.040	2 / 43	intercalated disc
7	0.047	3 / 109	dendritic spine
8	0.071	2 / 59	adherens junction
9	0.072	1 / 10	beta−catenin destruction complex
10	0.072	1 / 10	chromocenter
11	0.072	1 / 10	ciliary rootlet
12	0.072	1 / 10	DNA replication factor A complex
13	0.072	1 / 10	synaptic cleft
14	0.079	1 / 11	axon initial segment
15	0.079	1 / 11	paranode region of axon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−06	70 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	6e−05	13 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
3	3e−04	9 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
4	4e−03	10 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
5	1e−01	6 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
6	1e−01	2 / 92	Marisa_CRC−cluster−h
7	2e−01	1 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
8	2e−01	1 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
9	2e−01	2 / 103	Marisa_CRC−cluster−b
10	2e−01	9 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
11	3e−01	4 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
12	3e−01	4 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
13	3e−01	9 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	3e−01	3 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	3e−01	2 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

HM

Rank	p−value	#in/all	Geneset
1	0.2	3 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	0.2	1 / 34	HALLMARK_APICAL_SURFACE
3	0.2	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
4	0.3	2 / 149	HALLMARK_UV_RESPONSE_UP
5	0.4	2 / 174	HALLMARK_ADIPOGENESIS
6	0.4	2 / 182	HALLMARK_GLYCOLYSIS
7	0.4	2 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
8	0.4	2 / 193	HALLMARK_HEME_METABOLISM
9	0.4	2 / 194	HALLMARK_MYOGENESIS
10	0.4	2 / 195	HALLMARK_KRAS_SIGNALING_DN
11	0.5	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.5	1 / 97	HALLMARK_BILE_ACID_METABOLISM
13	0.5	1 / 97	HALLMARK_PEROXISOME
14	0.6	1 / 122	HALLMARK_SPERMATOGENESIS
15	0.6	1 / 130	HALLMARK_COAGULATION

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−04	38 / 3168	HOPP_Repressed
2	1e−03	26 / 1894	HOPP_Poised_promoter
3	5e−02	2 / 49	LEE_Developmental_regulators
4	6e−02	6 / 378	TARTE_Mature plasma cell signature
5	1e−01	1 / 14	YAMANE_AICDA_targets_recruited
6	1e−01	1 / 15	BENTINK_mBL UP
7	1e−01	1 / 17	Aukema_BCL2 UP_BCL6 DN
8	2e−01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
9	3e−01	19 / 2206	HOPP_Heterochrom
10	3e−01	1 / 45	Monti_BCR_cluster
11	4e−01	2 / 173	Victora_Light zone signature
12	4e−01	1 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
13	4e−01	1 / 70	Subero_FL_hyper_meth
14	4e−01	1 / 77	TARTE_Plasma cell signature
15	5e−01	34 / 4559	HOPP_Weak_enhancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	3 / 77	hsa−miR−526a
2	0.04	2 / 41	hsa−miR−518e*
3	0.04	2 / 41	hsa−miR−519b−5p
4	0.04	2 / 41	hsa−miR−519c−5p
5	0.04	5 / 251	hsa−let−7g
6	0.04	2 / 43	hsa−miR−518d−5p
7	0.04	2 / 43	hsa−miR−520c−5p
8	0.06	1 / 9	hsa−miR−887
9	0.10	3 / 148	hsa−miR−539
10	0.10	5 / 329	hsa−let−7b
11	0.10	2 / 73	hsa−miR−423−5p
12	0.11	1 / 15	hsa−miR−551b
13	0.11	1 / 16	hsa−miR−551a
14	0.12	4 / 257	hsa−let−7i
15	0.15	1 / 22	hsa−miR−663

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	0.002	3 / 36	cardiac conduction
2	0.004	2 / 13	protein localization to organelle
3	0.005	2 / 14	ceramide biosynthetic process
4	0.005	2 / 15	ceramide metabolic process
5	0.006	2 / 16	regulation of sodium ion transport
6	0.009	2 / 19	cartilage condensation
7	0.010	2 / 20	adult behavior
8	0.011	2 / 22	sensory perception of taste
9	0.012	2 / 23	membrane depolarization
10	0.014	13 / 885	positive regulation of transcription from RNA polymerase II promoter
11	0.015	5 / 195	brain development
12	0.021	2 / 30	cellular response to fibroblast growth factor stimulus
13	0.027	5 / 227	regulation of molecular function
14	0.029	2 / 36	negative regulation of cell adhesion
15	0.035	4 / 166	axon guidance

Chr

Rank	p−value	#in/all	Geneset
1	0.01	9 / 492	Chr 9
2	0.09	10 / 833	Chr 19
3	0.15	8 / 700	Chr 12
4	0.23	6 / 554	Chr 5
5	0.26	1 / 41	Chr Y
6	0.28	12 / 1325	Chr 1
7	0.38	5 / 548	Chr 16
8	0.41	4 / 437	Chr 8
9	0.45	3 / 333	Chr 22
10	0.52	6 / 776	Chr 17
11	0.56	5 / 669	Chr 6
12	0.59	6 / 832	Chr 2
13	0.65	1 / 139	Chr 21
14	0.71	3 / 490	Chr 10
15	0.75	1 / 184	Chr 18

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	4 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
2	0.013	8 / 423	Down_a
3	0.025	3 / 85	ScoV_0.999_Sturm_E2_IDH_DN
4	0.033	19 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
5	0.043	3 / 105	WIRTH_Normal Brain
6	0.076	7 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
7	0.079	1 / 11	KIM amplified & overexpressed in LTS
8	0.082	2 / 64	Weller_LGG_gradeII−vs−III_UP
9	0.121	2 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	0.173	2 / 101	Hopp_Sturm_GBM_Epi3_E_G34_UP
11	0.175	2 / 102	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
12	0.194	2 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	0.194	5 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
14	0.201	1 / 30	KIM prognostic signature LTS vs. STS
15	0.202	2 / 112	Christensen_hypermethylated_in_grade3_astrocytoma

Immunome

Rank	p−value	#in/all	Geneset
1	0.09	1 / 12	Angelova_immune−metagene−NK56_dim
2	0.09	1 / 13	Angelova_immune−metagene−activated_B−cells
3	0.19	1 / 29	Angelova_immune−metagene−Th1
4	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	4 / 204	Landsberg_dedifferentiation_down
2	0.16	1 / 24	Tirosh_B−cell specific genes−melanoma
3	0.24	1 / 37	Hugo_melanoma−all−MET_DN
4	0.25	1 / 39	Tirosh_top50 correlated genes PC4
5	0.38	1 / 64	Harbst_melanoma_lowgrade_up
6	0.38	1 / 65	Harbst_melanoma_highgrade_up
7	0.41	1 / 71	Tirosh_Macrophage specific genes−melanoma
8	0.44	1 / 78	Tirosh_CAF−cell specific genes
9	0.45	1 / 81	Tirosh_Genes in the MITF program
10	0.46	1 / 83	TCGA_melanoma_immune_high
11	0.72	1 / 171	Landsberg_dedifferentiation_up
12	0.75	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
13	0.76	1 / 189	Tirosh_genes preferentially expressed by Tregs
14	0.82	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
15	0.83	1 / 236	Gerber_wt/wt_group3−specific

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.3	1 / 48	Burnham_viral_DN
2	0.3	1 / 54	Burnham_timecourse
3	0.7	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	1.0	0 / 68	Burnham_sep_vs_con_UP
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
8	1.0	0 / 57	Burnham_viral_UP
9	1.0	0 / 57	Burnham_day1_vs_5_UP
10	1.0	0 / 52	Burnham_day1_vs_5_DN
11	1.0	0 / 18	Scicluna_UP
12	1.0	0 / 41	Scicluna_DN
13	1.0	0 / 37	Sweeney_viral_up
14	1.0	0 / 33	Sweeney_viral_dn
15	1.0	0 / 122	Terre_IMS_influenza_meta_signature

TF

Rank	p−value	#in/all	Geneset
1	0.08	13 / 1148	HEBENSTREIT_low expression TF
2	0.27	17 / 1941	ICGC_Bcl3_targets
3	0.34	26 / 3213	ICGC_Pu1_targets
4	0.36	9 / 1032	ICGC_Usf1_targets
5	0.37	4 / 415	ICGC_RxraPcr1_targets
6	0.57	17 / 2321	ICGC_Rad21_targets
7	0.59	4 / 549	ICGC_Atf3_targets
8	0.59	31 / 4264	ICGC_Pax5_targets
9	0.65	30 / 4212	ICGC_Pol2_targets
10	0.65	7 / 1025	ICGC_NrsfPcr1_targets
11	0.66	21 / 2994	ICGC_Zeb1_targets
12	0.67	24 / 3435	ICGC_Ebfsc137065_targets
13	0.68	20 / 2899	ICGC_Nfatc1_targets
14	0.69	25 / 3608	ICGC_Tcf12_targets
15	0.70	3 / 485	ICGC_NrsfPcr2_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	2 / 14	LIU_PROSTATE_CANCER_DN
2	0.015	2 / 25	PanCan_HH_geneset_nanostring
3	0.050	4 / 187	PanCan_PI3K_geneset_nanostring
4	0.065	1 / 9	WANG_ER_DN
5	0.086	1 / 12	BENTINK_e2f3.2
6	0.096	3 / 147	PanCan_MAPK_geneset_nanostring
7	0.099	1 / 14	GENTLES_modul10
8	0.099	1 / 14	GUSTAFSON_PI3K_DN
9	0.100	2 / 72	PanCan_Wnt_geneset_nanostring
10	0.106	1 / 15	WANG_ER_UP
11	0.176	0 / 16	LIU_LIVER_CANCER
12	0.205	2 / 113	PanCan_Driver_Gene_geneset_nanostring
13	0.262	2 / 134	PanCan_RAS_geneset_nanostring
14	0.296	0 / 14	LIU_COMMON_CANCER_GENES
15	0.512	1 / 96	PanCan_TXmisReg_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−11	40 / 1813	8_EnhP_Fibroblasts
2	6e−10	44 / 2375	10_ReprPC_Fibroblasts
3	7e−07	37 / 2240	1_TssP_Fibroblasts
4	1e−06	34 / 1984	10_ReprPC_Melanocytes
5	1e−06	30 / 1634	8_EnhP_Melanocytes
6	1e−06	34 / 2015	ReprPC_Colon
7	2e−06	35 / 2148	10_ReprPC_Skeletal_Muscle
8	4e−06	37 / 2417	9_ReprPCWk_Melanocytes
9	5e−06	30 / 1729	8_EnhP_Skeletal_Muscle
10	5e−06	30 / 1744	ReprPCWk_Colon
11	8e−06	36 / 2374	9_ReprPCWk_Fibroblasts
12	1e−05	48 / 3724	Tcells peripheral blood_12_EnhBiv
13	2e−05	19 / 884	12_EnhBiv_ESC_Mesoderm
14	2e−05	18 / 808	Mid_Frontal_Lobe_TssP
15	3e−05	43 / 3272	monocytes peripheral blood_14_ReprPCWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−04	3 / 25	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN
2	9e−04	4 / 58	JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN
3	1e−03	4 / 63	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH
4	3e−03	13 / 730	BENPORATH_ES_WITH_H3K27ME3
5	3e−03	3 / 39	REACTOME_NCAM1_INTERACTIONS
6	4e−03	4 / 88	KEGG_MELANOGENESIS
7	4e−03	7 / 273	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
8	5e−03	2 / 14	LIU_PROSTATE_CANCER_DN
9	5e−03	8 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
10	6e−03	3 / 50	LUI_THYROID_CANCER_CLUSTER_1
11	1e−02	2 / 21	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS
12	1e−02	2 / 21	NAKAMURA_CANCER_MICROENVIRONMENT_UP
13	1e−02	9 / 501	MARTENS_TRETINOIN_RESPONSE_UP
14	1e−02	2 / 23	PID_RXR_VDR_PATHWAY
15	1e−02	4 / 121	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	1 / 10	DUMEAUX_Smoking literature genes up
2	0.68	1 / 150	Homuth_BMI−associated−genes_UP
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 22	DUMEAUX_High bmi enriched genes
12	1.00	0 / 22	DUMEAUX_Fasting enriched genes
13	1.00	0 / 210	Homuth_BMI−associated−genes_DN
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.001	5 / 105	Ras guanyl−nucleotide exchange factor activity
2	0.017	2 / 27	frizzled binding
3	0.021	4 / 141	growth factor activity
4	0.034	2 / 39	nuclear receptor activity
5	0.044	6 / 346	receptor binding
6	0.057	2 / 52	steroid hormone receptor activity
7	0.072	1 / 10	ATPase−coupled anion transmembrane transporter activity
8	0.072	1 / 10	fucosyltransferase activity
9	0.072	1 / 10	glutamate binding
10	0.072	1 / 10	leucine zipper domain binding
11	0.079	1 / 11	high voltage−gated calcium channel activity
12	0.079	1 / 11	metal ion transmembrane transporter activity
13	0.079	1 / 11	peptidase activator activity
14	0.079	1 / 11	peptidoglycan binding
15	0.082	2 / 64	hydrolase activity, acting on glycosyl bonds

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.02	5 / 209	Chaussabel_2,5_Immune related molecules
2	0.04	1 / 5	JONGENEEL_Fetal Brain
3	0.08	1 / 11	JONGENEEL_Pituitary Gland
4	0.09	1 / 12	WIRTH_Globus pallidus
5	0.11	1 / 15	JONGENEEL_Small Intestine
6	0.14	2 / 89	Chaussabel_2,3_Erythrocytes
7	0.16	1 / 24	VAQUERIZAS_Spinal cord_TF
8	0.17	1 / 25	VAQUERIZAS_Adrenal cortex_TF
9	0.20	2 / 113	Chaussabel_1,8_Metabolism Biosynthesis
10	0.24	1 / 37	Chaussabel_2,2_Neutrophils
11	0.27	4 / 352	WIRTH_Nervous System
12	0.27	1 / 42	VAQUERIZAS_Fetal brain_TF
13	0.27	1 / 42	Chaussabel_1,3_B−cells
14	0.28	1 / 44	WIRTH_Pancreas
15	0.29	1 / 45	VAQUERIZAS_Whole brain_TF

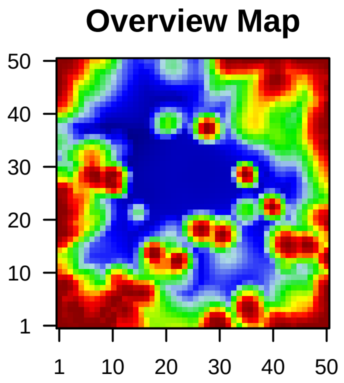
Overexpression Spots

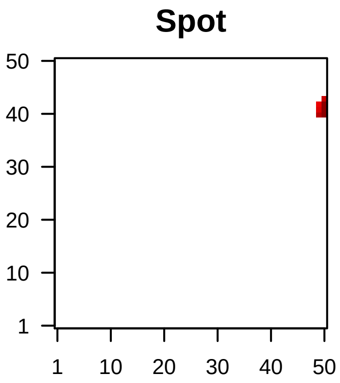
Spot Summary: R

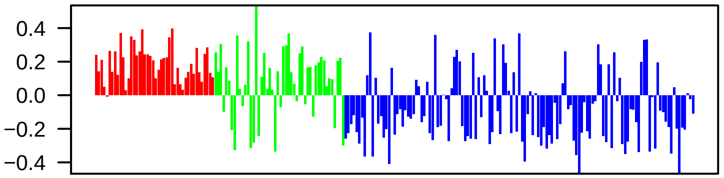
metagenes = 7
genes = 149

<r> metagenes = 0.97
<r> genes = 0.23
beta: r2= 6.61 / log p= −Inf

samples with spot = 50 (22.6 %)
mBL : 23 (52.3 %)
intermediate : 14 (29.2 %)
non−mBL : 13 (10.1 %)





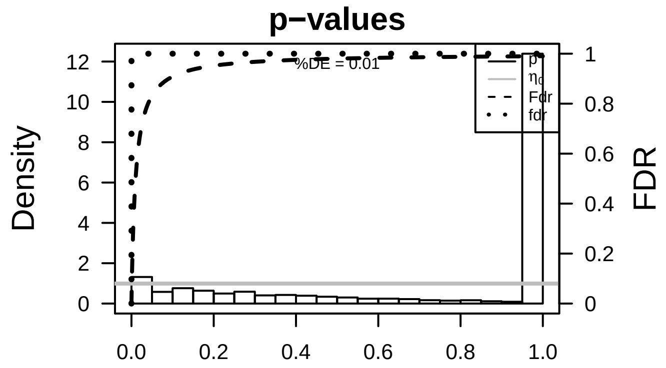


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	220448_at	2.35	−0.95	0.57	KCNK12	potassium two pore domain channel subfamily K member 12
2	203865_s_at	2.33	−1.02	0.39	ADARB1	adenosine deaminase, RNA specific B1 [Source:HGNC Sym
3	221879_at	2.18	−0.84	0.32		
4	205902_at	2.03	−0.94	0.52	KCNN3	potassium calcium−activated channel subfamily N member 3
5	220432_s_at	1.97	−0.86	0.55	CYP39A1	cytochrome P450 family 39 subfamily A member 1 [Source:H
6	210461_s_at	1.78	−0.98	0.53	ABLIM1	actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGN
7	218862_at	1.71	−1.7	0.72	ASB13	ankyrin repeat and SOCS box containing 13 [Source:HGNC
8	218922_s_at	1.62	−1.16	0.63	CERS4	ceramide synthase 4 [Source:HGNC Symbol;Acc:HGNC:237
9	203769_s_at	1.62	−0.95	0.56	STS	steroid sulfatase [Source:HGNC Symbol;Acc:HGNC:11425]
10	219753_at	1.54	−1.48	0.57	STAG3	stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356]
11	219304_s_at	1.54	−1.46	0.44	PDGFD	platelet derived growth factor D [Source:HGNC Symbol;Acc:
12	213122_at	1.5	−1.06	0.37	TSPYL5	TSPY like 5 [Source:HGNC Symbol;Acc:HGNC:29367]
13	208353_x_at	1.49	−0.86	0.43	ANK1	ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492]
14	214806_at	1.47	−0.92	0.54	BICD1	BICD cargo adaptor 1 [Source:HGNC Symbol;Acc:HGNC:10
15	213906_at	1.47	−1.54	0.85	MYBL1	MYB proto−oncogene like 1 [Source:HGNC Symbol;Acc:HGN
16	205425_at	1.45	−1.2	0.33	HIP1	huntingtin interacting protein 1 [Source:HGNC Symbol;Acc:H
17	212719_at	1.43	−1.02	0.48	PHLPP1	PH domain and leucine rich repeat protein phosphatase 1 [S
18	205187_at	1.42	−0.95	0.54	SMAD5	SMAD family member 5 [Source:HGNC Symbol;Acc:HGNC:6
19	212599_at	1.41	−1.6	0.53	AUTS2	AUTS2, activator of transcription and developmental regulato
20	208107_s_at	1.4	−0.84	0.42	REXO5	RNA exonuclease 5 [Source:HGNC Symbol;Acc:HGNC:2466

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−18	22 / 195	GSE	HOLLMANN_APOPTOSIS_VIA_CD40_UP
2	4e−16	23 / 263	Lymp	SPANG_CD40 6hrs UP
3	6e−14	93 / 5404	Lymp	HOPP_Strong_enhancer
4	6e−14	37 / 955	Lymp	SPANG_BCR UP
5	2e−11	16 / 186	GSE	PENG_RAPAMYCIN_RESPONSE_UP
6	3e−10	91 / 5908	Lymp	HOPP_Active_promoter
7	4e−09	5 / 8	Lymp	MASCQUE_GCB UP
8	5e−09	6 / 16	GSE	ZHAN_LATE_DIFFERENTIATION_GENES_DN
9	8e−09	6 / 17	Lymp	Aukema_BCL2 UP_BCL6 DN
10	8e−09	86 / 5682	Lymp	HOPP_Weak_promoter
11	2e−08	10 / 96	Lymp	SPANG_LPS 6hrs UP
12	5e−08	11 / 133	GSE	PENG_LEUCINE_DEPRIVATION_UP
13	2e−07	13 / 219	Refer	WIRTH_GC B−cells
14	8e−07	9 / 107	GSE	SMIRNOV_RESPONSE_TO_IR_6HR_DN
15	2e−06	7 / 61	GSE	BASSO_CD40_SIGNALING_DN
16	3e−06	3 / 4	Lymp	WRIGHT_custom GCB−DLBCL UP
17	8e−06	7 / 76	GSE	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN
18	8e−06	3 / 5	Lymp	Shaknovich_ABC_hyper_meth
19	1e−05	4 / 15	Lymp	DAVE_BL Inter
20	1e−05	65 / 4357	Lymp	HOPP_Weak_txn
21	1e−05	14 / 376	GSE	GARY_CD5_TARGETS_UP
22	1e−05	15 / 429	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
23	2e−05	22 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
24	2e−05	3 / 6	Lymp	Care_GCB UP
25	2e−05	6 / 59	GSE	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
26	2e−05	8 / 121	GSE	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
27	2e−05	8 / 122	GSE	GAVIN_FOXP3_TARGETS_CLUSTER_P3
28	2e−05	35 / 1814	Lymp	HOPP_Repetitive
29	4e−05	13 / 361	BP	intracellular signal transduction
30	4e−05	5 / 41	GSE	BIOCARTA_TCR_PATHWAY
31	5e−05	5 / 42	Refer	Chaussabel_1,3_B−cells
32	5e−05	13 / 368	GSE	ZHENG_BOUND_BY_FOXP3
33	5e−05	62 / 4261	Lymp	HOPP_Txn_transition
34	6e−05	65 / 4559	Lymp	HOPP_Weak_enhancer
35	7e−05	23 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
36	8e−05	16 / 560	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
37	1e−04	52 / 3451	TF	ICGC_Atf2_targets
38	2e−04	29 / 1508	TF	ICGC_Mef2_targets
39	2e−04	5 / 56	miRN	hsa−miR−193b
40	2e−04	5 / 56	GSE	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.6	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−05	13 / 361	intracellular signal transduction
2	3e−04	3 / 14	regulation of establishment of cell polarity
3	3e−04	14 / 507	protein phosphorylation
4	5e−04	7 / 146	cytoskeleton organization
5	5e−04	7 / 147	endocytosis
6	5e−04	3 / 17	T cell proliferation
7	1e−03	4 / 49	negative regulation of signal transduction
8	3e−03	13 / 576	phosphorylation
9	4e−03	3 / 33	T cell differentiation
10	4e−03	3 / 34	vesicle fusion
11	6e−03	2 / 12	negative regulation of actin filament polymerization
12	6e−03	3 / 38	regulation of G−protein coupled receptor protein signaling pathway
13	1e−02	2 / 16	clathrin coat assembly
14	1e−02	2 / 16	negative regulation of Rho protein signal transduction
15	1e−02	11 / 520	positive regulation of transcription, DNA−templated

Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	13 / 480	Lembcke_Colonic Inflammation
2	2e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
3	1e−01	1 / 12	GENTLES_modul12
4	1e−01	1 / 13	GENTLES_modul17
5	1e−01	1 / 14	GUSTAFSON_PI3K_DN
6	1e−01	3 / 130	PanCan_CC+Apop_geneset_nanostring
7	1e−01	1 / 15	RHODES_CANCER_META_SIGNATURE
8	1e−01	1 / 15	WANG_ER_UP
9	1e−01	1 / 15	GENTLES_modul4
10	1e−01	3 / 134	PanCan_RAS_geneset_nanostring
11	1e−01	1 / 16	LIU_LIVER_CANCER
12	2e−01	2 / 72	PanCan_Wnt_geneset_nanostring
13	2e−01	1 / 18	PanCan_Notch_geneset_nanostring
14	2e−01	0 / 12	LIU_BREAST_CANCER
15	3e−01	3 / 187	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.001	4 / 51	clathrin−coated vesicle
2	0.004	60 / 4701	cytoplasm
3	0.006	50 / 3805	cytosol
4	0.008	17 / 936	cytoskeleton
5	0.013	5 / 146	lamellipodium
6	0.016	4 / 101	growth cone
7	0.017	4 / 104	trans−Golgi network
8	0.018	3 / 58	P−body
9	0.021	3 / 62	extrinsic component of cytoplasmic side of plasma membrane
10	0.022	10 / 503	cytoplasmic vesicle
11	0.022	55 / 4579	nucleus
12	0.040	5 / 196	nuclear membrane
13	0.061	2 / 42	azurophil granule membrane
14	0.063	14 / 938	Golgi apparatus
15	0.069	2 / 45	stress fiber

Chr

Rank	p−value	#in/all	Geneset
1	0.01	21 / 1325	Chr 1
2	0.02	11 / 585	Chr 7
3	0.07	11 / 700	Chr 12
4	0.10	8 / 490	Chr 10
5	0.12	7 / 437	Chr 8
6	0.16	6 / 382	Chr 15
7	0.19	9 / 669	Chr 6
8	0.21	9 / 689	Chr 3
9	0.38	2 / 139	Chr 21
10	0.62	3 / 333	Chr 22
11	0.69	7 / 832	Chr 2
12	0.69	3 / 369	Chr 20
13	0.81	6 / 833	Chr 19
14	0.83	1 / 184	Chr 18
15	0.84	3 / 480	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−13	115 / 8370	natural killer cells peripheral blood_2_TssAFlnk
2	6e−13	118 / 8865	Thelper cells peripheral blood_7_Enh
3	1e−12	111 / 7833	Bcells peripheral blood_1_TssA
4	7e−12	104 / 7078	Bcells peripheral blood_5_TxWk
5	1e−11	119 / 9298	Bcells peripheral blood_7_Enh
6	1e−11	112 / 8208	Tcells peripheral blood_7_Enh
7	1e−11	116 / 8816	Thelper cells peripheral blood_2_TssAFlnk
8	2e−11	110 / 7957	Tcells peripheral blood_2_TssAFlnk
9	2e−11	113 / 8406	Bcells peripheral blood_2_TssAFlnk
10	4e−11	91 / 5716	Bcells peripheral blood_4_Tx
11	7e−11	91 / 5766	natural killer cells peripheral blood_4_Tx
12	2e−10	105 / 7489	monocytes peripheral blood_5_TxWk
13	3e−10	104 / 7407	natural killer cells peripheral blood_5_TxWk
14	3e−10	108 / 7930	Tregulatory cells peripheral blood_1_TssA
15	5e−10	107 / 7851	Tregulatory cells peripheral blood_7_Enh

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	22 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
2	7e−05	23 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	6e−03	27 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	1e−02	12 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
5	2e−02	5 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	3e−02	72 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	5e−02	17 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
8	6e−02	1 / 7	TCGA−CRC_agressive−disease−markers
9	7e−02	1 / 8	Marisa_CRC−C1
10	1e−01	3 / 132	Marisa_CRC−cluster−a
11	1e−01	8 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
12	1e−01	8 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	2e−01	5 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
14	2e−01	10 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	2e−01	11 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

Glioma

Rank	p−value	#in/all	Geneset
1	2e−04	13 / 421	Down_b
2	1e−02	7 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
3	2e−02	7 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
4	3e−02	6 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
5	4e−02	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_down (A)
6	6e−02	1 / 6	Shaw_responders_up_in_oligo_glioma
7	6e−02	8 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
8	7e−02	2 / 45	OL vs. MOG− OL
9	7e−02	10 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	7e−02	1 / 8	Shaw_up_in_1p19qdel
11	8e−02	5 / 242	ScoV_0.5_Sturm_C1_IDH_DN
12	8e−02	2 / 50	Vishal_subnetwork signature of survival in GBM
13	1e−01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
14	1e−01	1 / 11	KIM amplified & overexpressed in LTS
15	1e−01	1 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−18	22 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
2	2e−11	16 / 186	PENG_RAPAMYCIN_RESPONSE_UP
3	5e−09	6 / 16	ZHAN_LATE_DIFFERENTIATION_GENES_DN
4	5e−08	11 / 133	PENG_LEUCINE_DEPRIVATION_UP
5	8e−07	9 / 107	SMIRNOV_RESPONSE_TO_IR_6HR_DN
6	2e−06	7 / 61	BASSO_CD40_SIGNALING_DN
7	8e−06	7 / 76	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN
8	1e−05	14 / 376	GARY_CD5_TARGETS_UP
9	1e−05	15 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	2e−05	6 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
11	2e−05	8 / 121	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
12	2e−05	8 / 122	GAVIN_FOXP3_TARGETS_CLUSTER_P3
13	4e−05	5 / 41	BIOCARTA_TCR_PATHWAY
14	5e−05	13 / 368	ZHENG_BOUND_BY_FOXP3
15	8e−05	16 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP

HM

Rank	p−value	#in/all	Geneset
1	0.006	6 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.025	5 / 173	HALLMARK_MITOTIC_SPINDLE
3	0.110	4 / 191	HALLMARK_P53_PATHWAY
4	0.115	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.237	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	0.237	2 / 97	HALLMARK_BILE_ACID_METABOLISM
7	0.242	3 / 178	HALLMARK_COMPLEMENT
8	0.243	1 / 29	HALLMARK_NOTCH_SIGNALING
9	0.280	3 / 193	HALLMARK_HEME_METABOLISM
10	0.283	3 / 194	HALLMARK_KRAS_SIGNALING_UP
11	0.353	2 / 130	HALLMARK_COAGULATION
12	0.363	2 / 133	HALLMARK_DNA_REPAIR
13	0.387	1 / 51	HALLMARK_TGF_BETA_SIGNALING
14	0.391	2 / 141	HALLMARK_UV_RESPONSE_DN
15	0.411	1 / 55	HALLMARK_MYC_TARGETS_V2

Immunome

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 13	Angelova_immune−metagene−immature_B−cells
2	7e−02	1 / 8	Angelova_immune−metagene−mDC
3	9e−02	1 / 10	Angelova_immune−metagene−neutrophils
4	9e−02	1 / 10	Angelova_immune−metagene−TFH
5	1e−01	1 / 12	Angelova_immune−metagene−memory_B−cells
6	1e−01	1 / 15	Angelova_immune−metagene−NK
7	1e−01	1 / 16	Angelova_immune−metagene−Th17
8	2e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
9	3e−01	1 / 38	Angelova_immune−metagene−mast−cells
10	5e−01	1 / 67	Angelova_immune−metagene−T−cells
11	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
12	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
13	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
14	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
15	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	5 / 210	Homuth_BMI−associated−genes_DN
2	0.07	1 / 8	Marjolein_ageing−genes_UP
3	0.19	1 / 22	DUMEAUX_Fasting enriched genes
4	0.26	1 / 32	Marjolein_ageing−genes_DN
5	1.00	0 / 62	DUMEAUX_Smoking enriched genes
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 22	DUMEAUX_High bmi enriched genes
15	1.00	0 / 150	Homuth_BMI−associated−genes_UP

Lymphnoma

Rank	p−value	#in/all	Geneset
1	4e−16	23 / 263	SPANG_CD40 6hrs UP
2	6e−14	93 / 5404	HOPP_Strong_enhancer
3	6e−14	37 / 955	SPANG_BCR UP
4	3e−10	91 / 5908	HOPP_Active_promoter
5	4e−09	5 / 8	MASCQUE_GCB UP
6	8e−09	6 / 17	Aukema_BCL2 UP_BCL6 DN
7	8e−09	86 / 5682	HOPP_Weak_promoter
8	2e−08	10 / 96	SPANG_LPS 6hrs UP
9	3e−06	3 / 4	WRIGHT_custom GCB−DLBCL UP
10	8e−06	3 / 5	Shaknovich_ABC_hyper_meth
11	1e−05	4 / 15	DAVE_BL Inter
12	1e−05	65 / 4357	HOPP_Weak_txn
13	2e−05	3 / 6	Care_GCB UP
14	2e−05	35 / 1814	HOPP_Repetitive
15	5e−05	62 / 4261	HOPP_Txn_transition

Melanoma

Rank	p−value	#in/all	Geneset
1	0.001	3 / 24	Tirosh_B−cell specific genes−melanoma
2	0.019	1 / 2	Melanoma Epi−Enzyme Cluster 2
3	0.051	2 / 38	Hugo_melanoma−BRAFmut−MET_UP
4	0.085	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
5	0.188	2 / 83	TCGA_melanoma_immune_high
6	0.270	4 / 276	Gerber_wt/wt_melanoma−cells−SpotB
7	0.272	1 / 33	Tirosh_T−cell specific genes−melanoma
8	0.272	2 / 107	Tirosh_Exhaustion program in Mel75
9	0.338	6 / 497	Gerber_wt/wt_melanoma−cells−SpotD
10	0.356	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	0.377	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
12	0.460	1 / 64	Harbst_melanoma_lowgrade_up
13	0.488	2 / 171	Landsberg_dedifferentiation_up
14	0.514	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
15	0.541	1 / 81	Tirosh_Genes in the MITF program

MF

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 20	phosphatidylinositol−3,4−bisphosphate binding
2	2e−03	9 / 291	actin binding
3	3e−03	3 / 29	clathrin binding
4	3e−03	11 / 437	protein kinase activity
5	3e−03	4 / 64	phosphatidylinositol binding
6	3e−03	13 / 573	kinase activity
7	4e−03	2 / 10	clathrin adaptor activity
8	4e−03	3 / 34	histone acetyltransferase activity
9	5e−03	6 / 165	calmodulin binding
10	6e−03	2 / 12	cytoskeletal adaptor activity
11	6e−03	3 / 39	receptor tyrosine kinase binding
12	8e−03	6 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
13	8e−03	3 / 44	protein serine/threonine phosphatase activity
14	1e−02	2 / 18	phosphatidylinositol−3,5−bisphosphate binding
15	1e−02	6 / 202	GTPase activator activity

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 56	hsa−miR−193b
2	4e−04	6 / 101	hsa−miR−199b−5p
3	9e−04	4 / 46	hsa−miR−193a−3p
4	2e−03	5 / 92	hsa−miR−199a−5p
5	3e−03	3 / 32	hsa−miR−450a
6	4e−03	6 / 157	hsa−miR−222
7	4e−03	4 / 69	hsa−miR−125a−5p
8	5e−03	4 / 73	hsa−miR−125b
9	5e−03	6 / 167	hsa−miR−221
10	6e−03	9 / 344	hsa−miR−19b
11	7e−03	3 / 41	hsa−miR−504
12	8e−03	3 / 43	hsa−miR−208b
13	9e−03	4 / 86	hsa−miR−1259
14	1e−02	3 / 46	hsa−miR−208a
15	1e−02	3 / 47	hsa−miR−634

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.03	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.27	1 / 33	Sweeney_viral_dn
3	0.33	1 / 41	Scicluna_DN
4	0.69	1 / 122	Terre_IMS_influenza_meta_signature
5	0.73	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	1.00	0 / 68	Burnham_sep_vs_con_UP
7	1.00	0 / 56	Burnham_sep_vs_con_DN
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 48	Burnham_viral_DN
11	1.00	0 / 57	Burnham_viral_UP
12	1.00	0 / 57	Burnham_day1_vs_5_UP
13	1.00	0 / 52	Burnham_day1_vs_5_DN
14	1.00	0 / 54	Burnham_timecourse
15	1.00	0 / 18	Scicluna_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−07	13 / 219	WIRTH_GC B−cells
2	5e−05	5 / 42	Chaussabel_1,3_B−cells
3	3e−02	3 / 68	Chaussabel_2,1_Cytotoxic cells
4	3e−02	12 / 678	PROTEINATLAS_lymph node
5	3e−02	5 / 188	Chaussabel_3,8_Enzymes
6	4e−02	2 / 32	Chaussabel_1,1_Plasma Cells
7	5e−02	15 / 989	PROTEINATLAS_tonsil
8	5e−02	7 / 355	WIRTH_Immune system
9	7e−02	2 / 44	JONGENEEL_Retina
10	7e−02	3 / 99	Chaussabel_1,5_Myeloid lineage
11	7e−02	3 / 100	Chaussabel_2,8_T−cells
12	9e−02	3 / 109	Chaussabel_2,6_Myeloid lineage
13	9e−02	1 / 10	VAQUERIZAS_Skeletal muscle_TF
14	1e−01	1 / 11	JONGENEEL_Spleen
15	1e−01	8 / 496	PROTEINATLAS_spleen

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−04	52 / 3451	ICGC_Atf2_targets
2	2e−04	29 / 1508	ICGC_Mef2_targets
3	2e−04	38 / 2254	ICGC_BatfPcr1_targets
4	2e−04	33 / 1848	ICGC_Pbx3_targets
5	2e−04	55 / 3796	ICGC_Nficsc81335_targets
6	6e−04	44 / 2899	ICGC_Nfatc1_targets
7	1e−03	58 / 4319	ICGC_Pou2_targets
8	1e−03	28 / 1636	ICGC_Bcl11_targets
9	2e−03	26 / 1494	ICGC_Cebpbsc150_targets
10	2e−03	51 / 3703	ICGC_Foxm1_targets
11	2e−03	52 / 3804	ICGC_Stat5_targets
12	2e−03	50 / 3630	ICGC_Sp1_targets
13	2e−03	55 / 4131	ICGC_Tcf3_targets
14	2e−03	49 / 3564	ICGC_Taf1_targets
15	3e−03	51 / 3769	ICGC_Pmlsc71910_targets

Overexpression Spots

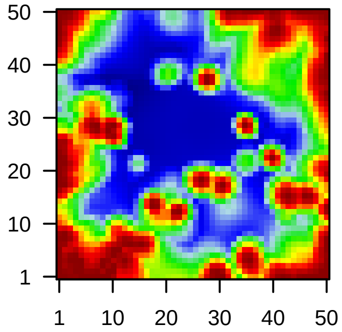
Spot Summary: S

metagenes = 10
genes = 215

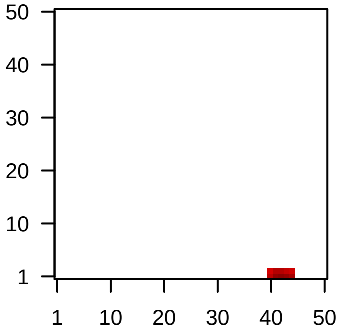
<r> metagenes = 0.98
<r> genes = 0.26
beta: r2= 4.44 / log p= −Inf

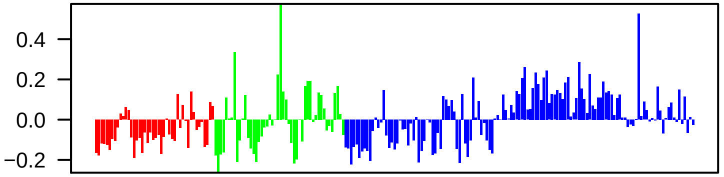
samples with spot = 12 (5.4 %)
intermediate : 3 (6.2 %)
non−mBL : 9 (7 %)

Overview Map



Spot





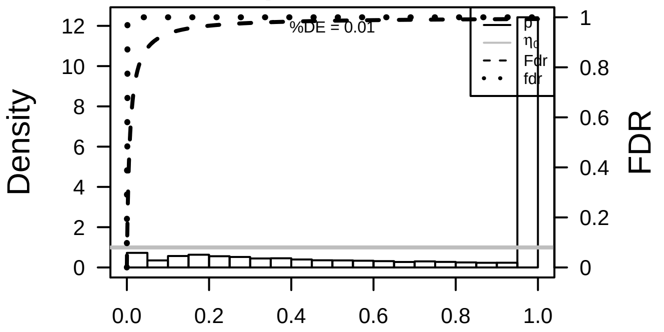
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205033_s_at	2.2	−0.66	0.46	DEFA1	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
2	207337_at	1.83	−1.04	0.49	CTAG2	cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
3	206012_at	1.77	−0.72	0.39	LEFTY2	left−right determination factor 2 [Source:HGNC Symbol;Acc:
4	218687_s_at	1.71	−0.55	0.55	MUC13	mucin 13, cell surface associated [Source:HGNC Symbol;Acc
5	205334_at	1.65	−0.71	0.49	S100A1	S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:
6	205409_at	1.51	−0.76	0.5	FOSL2	FOS like 2, AP−1 transcription factor subunit [Source:HGNC
7	217052_x_at	1.49	−0.92	0.43		
8	36829_at	1.48	−0.66	0.4	PER1	period circadian regulator 1 [Source:HGNC Symbol;Acc:HGN
9	208868_s_at	1.41	−0.86	0.35	GABARAPL1	GABA type A receptor associated protein like 1 [Source:HGN
10	218211_s_at	1.4	−0.63	0.49	MLPH	melanophilin [Source:HGNC Symbol;Acc:HGNC:29643]
11	216873_s_at	1.37	−0.62	0.58	ATP8B2	ATPase phospholipid transporting 8B2 [Source:HGNC Symbo
12	206130_s_at	1.37	−0.45	0.51	ASGR2	asialoglycoprotein receptor 2 [Source:HGNC Symbol;Acc:HG
13	211900_x_at	1.31	−0.62	0.51	CD6	CD6 molecule [Source:HGNC Symbol;Acc:HGNC:1691]
14	218881_s_at	1.28	−1.15	0.58	FOSL2	FOS like 2, AP−1 transcription factor subunit [Source:HGNC
15	211531_x_at	1.27	−0.96	0.33	PRB1	proline rich protein BstNI subfamily 1 [Source:HGNC Symbol;
16	212772_s_at	1.27	−0.57	0.39	ABCA2	ATP binding cassette subfamily A member 2 [Source:HGNC
17	208090_s_at	1.26	−0.81	0.38	AIRE	autoimmune regulator [Source:HGNC Symbol;Acc:HGNC:36
18	209008_x_at	1.25	−0.56	0.59		keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:3
19	209710_at	1.2	−0.71	0.51	GATA2	GATA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:41
20	209768_s_at	1.17	−1.14	0.57		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−11	24 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	4e−07	116 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
3	2e−06	69 / 3168	Lymph	HOPP_Repressed
4	2e−05	7 / 65	BP	excitatory postsynaptic potential
5	4e−05	52 / 2321	TF	ICGC_Rad21_targets
6	3e−04	42 / 1894	Lymph	HOPP_Poised_promoter
7	4e−04	6 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
8	6e−04	7 / 109	CC	dendritic spine
9	7e−04	4 / 31	GSEA	WEIGEL_OXIDATIVE_STRESS_RESPONSE
10	7e−04	3 / 14	BP	positive regulation of blood coagulation
11	1e−03	4 / 34	CC	cortical actin cytoskeleton
12	1e−03	4 / 34	BP	regulation of synaptic plasticity
13	1e−03	27 / 1092	GSEA	YOSHIMURA_MAPK8_TARGETS_UP
14	1e−03	8 / 155	BP	response to hypoxia
15	1e−03	9 / 195	BP	chemical synaptic transmission
16	1e−03	3 / 16	Immu	Angelova_immune−metagene−Th17
17	1e−03	3 / 16	GSEA	STARK_HYPPOCAMPUS_22Q11_DELETION_DN
18	1e−03	7 / 125	MF	transcriptional activator activity, RNA polymerase II transcription regulatory
19	1e−03	36 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
20	1e−03	14 / 423	Gliom	Down_a
21	1e−03	5 / 63	BP	regulation of insulin secretion
22	2e−03	7 / 129	GSEA	ONDER_CDH1_TARGETS_1_UP
23	2e−03	9 / 212	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
24	2e−03	6 / 101	CC	endomembrane system
25	2e−03	3 / 20	BP	positive regulation of blood pressure
26	2e−03	3 / 20	BP	regulation of Wnt signaling pathway
27	2e−03	5 / 70	BP	locomotory behavior
28	2e−03	15 / 501	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
29	2e−03	13 / 402	GSEA	REACTOME_HEMOSTASIS
30	2e−03	3 / 21	BP	receptor clustering
31	3e−03	5 / 72	CC	cell body
32	3e−03	11 / 310	CC	dendrite
33	3e−03	8 / 182	MF	RNA polymerase II regulatory region sequence−specific DNA binding
34	3e−03	3 / 22	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN
35	3e−03	4 / 46	BP	activation of MAPKK activity
36	3e−03	3 / 23	BP	neuromuscular synaptic transmission
37	3e−03	4 / 47	BP	cellular response to cAMP
38	3e−03	4 / 47	BP	learning or memory
39	3e−03	4 / 47	CC	postsynapse
40	3e−03	2 / 7	GSEA	MIKI_COEXPRESSED_WITH_CYP19A1

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 107	HORVATH_aging_genes meth UP
2	0.5	1 / 47	TESCHENDORFF_age_hypermethylated
3	0.7	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−05	7 / 65	excitatory postsynaptic potential
2	7e−04	3 / 14	positive regulation of blood coagulation
3	1e−03	4 / 34	regulation of synaptic plasticity
4	1e−03	8 / 155	response to hypoxia
5	1e−03	9 / 195	chemical synaptic transmission
6	1e−03	5 / 63	regulation of insulin secretion
7	2e−03	3 / 20	positive regulation of blood pressure
8	2e−03	3 / 20	regulation of Wnt signaling pathway
9	2e−03	5 / 70	locomotory behavior
10	2e−03	3 / 21	receptor clustering
11	3e−03	4 / 46	activation of MAPKK activity
12	3e−03	3 / 23	neuromuscular synaptic transmission
13	3e−03	4 / 47	cellular response to cAMP
14	3e−03	4 / 47	learning or memory
15	4e−03	3 / 24	cellular response to amyloid−beta

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	2 / 14	LIU_COMMON_CANCER_GENES
2	0.06	4 / 113	PanCan_Driver_Gene_geneset_nanostring
3	0.13	3 / 96	PanCan_TXmisReg_geneset_nanostring
4	0.15	1 / 12	LIU_BREAST_CANCER
5	0.16	1 / 13	GENTLES_modul18
6	0.21	1 / 18	PanCan_Notch_geneset_nanostring
7	0.26	0 / 11	LIU_PROSTATE_CANCER_UP
8	0.29	0 / 16	LIU_LIVER_CANCER
9	0.31	1 / 28	PanCan_HK_geneset_nanostring
10	0.34	1 / 32	KUIPER_MM good survival
11	0.42	1 / 41	PanCan_DNARepair_geneset_nanostring
12	0.46	1 / 47	PanCan_TGF−B_geneset_nanostring
13	0.50	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	0.51	2 / 130	PanCan_CC+Apop_geneset_nanostring
15	0.65	1 / 80	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−04	7 / 109	dendritic spine
2	1e−03	4 / 34	cortical actin cytoskeleton
3	2e−03	6 / 101	endomembrane system
4	3e−03	5 / 72	cell body
5	3e−03	11 / 310	dendrite
6	3e−03	4 / 47	postsynapse
7	4e−03	4 / 50	terminal bouton
8	4e−03	4 / 51	presynaptic membrane
9	5e−03	5 / 84	Golgi lumen
10	6e−03	57 / 3210	plasma membrane
11	7e−03	7 / 168	postsynaptic density
12	1e−02	11 / 382	synapse
13	1e−02	24 / 1128	integral component of plasma membrane
14	2e−02	5 / 113	receptor complex
15	2e−02	2 / 16	dendrite membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.01	6 / 139	Chr 21
2	0.07	8 / 333	Chr 22
3	0.20	9 / 492	Chr 9
4	0.21	12 / 700	Chr 12
5	0.26	11 / 669	Chr 6
6	0.29	12 / 756	Chr 11
7	0.30	13 / 833	Chr 19
8	0.32	12 / 776	Chr 17
9	0.35	7 / 437	Chr 8
10	0.42	1 / 41	Chr Y
11	0.43	3 / 184	Chr 18
12	0.53	5 / 369	Chr 20
13	0.55	9 / 689	Chr 3
14	0.56	5 / 382	Chr 15
15	0.59	7 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−11	57 / 1813	8_EnhP_Fibroblasts
2	7e−10	65 / 2375	10_ReprPC_Fibroblasts
3	4e−09	85 / 3724	Tcells peripheral blood_12_EnhBiv
4	6e−09	59 / 2148	10_ReprPC_Skeletal_Muscle
5	7e−09	61 / 2269	9_ReprPCWk_Neuronal_Progenitor
6	3e−08	55 / 2015	ReprPC_Colon
7	8e−08	58 / 2240	1_TssP_Fibroblasts
8	2e−07	60 / 2417	9_ReprPCWk_Melanocytes
9	3e−07	65 / 2747	Bcells peripheral blood_12_EnhBiv
10	3e−07	46 / 1634	8_EnhP_Melanocytes
11	3e−07	43 / 1473	10_ReprPC_Neuronal_Progenitor
12	5e−07	47 / 1729	8_EnhP_Skeletal_Muscle
13	6e−07	54 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
14	7e−07	47 / 1747	10_TssBiv_ESC_Mesoderm
15	8e−07	72 / 3272	monocytes peripheral blood_14_ReprPCWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−07	116 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	6e−03	13 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
3	1e−02	14 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
4	1e−02	13 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
5	3e−02	12 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
6	3e−02	8 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
7	5e−02	7 / 255	Kosinski_top−crypt−long−list
8	7e−02	6 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
9	8e−02	18 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
10	1e−01	1 / 8	Marisa_CRC−C3
11	1e−01	1 / 8	Marisa_CRC−C4
12	2e−01	17 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
13	2e−01	13 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	2e−01	4 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	2e−01	1 / 16	Budinska_B_Lower crypt−like_UP

Glioma

Rank	p−value	#in/all	Geneset
1	0.001	36 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	0.001	14 / 423	Down_a
3	0.004	5 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
4	0.012	2 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
5	0.012	2 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma
6	0.012	2 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
7	0.012	2 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
8	0.027	8 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	0.036	2 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
10	0.043	7 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
11	0.081	2 / 36	Christensen_hypomethylated_in_ependymoma
12	0.088	1 / 7	oligodendrocytes_glio
13	0.091	18 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
14	0.098	5 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	0.135	2 / 49	OPC

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−11	24 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	4e−04	6 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	7e−04	4 / 31	WEIGEL_OXIDATIVE_STRESS_RESPONSE
4	1e−03	27 / 1092	YOSHIMURA_MAPK8_TARGETS_UP
5	1e−03	3 / 16	STARK_HYPPOCAMPUS_22Q11_DELETION_DN
6	2e−03	7 / 129	ONDER_CDH1_TARGETS_1_UP
7	2e−03	9 / 212	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
8	2e−03	15 / 501	MARTENS_TRETINOIN_RESPONSE_UP
9	2e−03	13 / 402	REACTOME_HEMOSTASIS
10	3e−03	3 / 22	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN
11	3e−03	2 / 7	MIKI_COEXPRESSED_WITH_CYP19A1
12	4e−03	3 / 25	MCCABE_HOXC6_TARGETS_CANCER_UP
13	5e−03	2 / 8	MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP
14	6e−03	2 / 9	ZHOU_PANCREATIC_BETA_CELL
15	7e−03	5 / 91	LABBE_TGFB1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.01	7 / 194	HALLMARK_MYOGENESIS
2	0.03	5 / 130	HALLMARK_COAGULATION
3	0.03	6 / 181	HALLMARK_XENOBIOTIC_METABOLISM
4	0.14	2 / 51	HALLMARK_TGF_BETA_SIGNALING
5	0.25	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	0.25	4 / 195	HALLMARK_KRAS_SIGNALING_DN
7	0.28	3 / 141	HALLMARK_UV_RESPONSE_DN
8	0.36	1 / 34	HALLMARK_APICAL_SURFACE
9	0.36	1 / 34	HALLMARK_ANGIOGENESIS
10	0.36	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.36	2 / 97	HALLMARK_BILE_ACID_METABOLISM
12	0.39	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
13	0.39	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	0.40	3 / 174	HALLMARK_ADIPOGENESIS
15	0.40	3 / 174	HALLMARK_APICAL_JUNCTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.001	3 / 16	Angelova_immune−metagene−Th17
2	0.100	1 / 8	Angelova_immune−metagene−mDC
3	0.201	1 / 17	Angelova_immune−metagene−central_memory_CD8
4	0.262	1 / 23	Angelova_immune−metagene−Treg
5	0.318	1 / 29	Angelova_immune−metagene−Th1
6	0.448	1 / 45	Angelova_immune−metagene−MDSC
7	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
8	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
9	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
10	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.000	0 / 25	Angelova_immune−metagene−DC
13	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
14	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.000	0 / 14	Angelova_immune−metagene−eosinophil

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.6	1 / 62	DUMEAUX_Smoking enriched genes
2	0.9	1 / 150	Homuth_BMI−associated−genes_UP
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 22	DUMEAUX_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	2e−06	69 / 3168	HOPP_Repressed
2	3e−04	42 / 1894	HOPP_Poised_promoter
3	5e−03	4 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
4	2e−02	3 / 45	Subero_INT_hypo_meth
5	3e−02	3 / 53	LENZ_Stromal signature 2
6	1e−01	4 / 132	Subero_DLBCL_hyper_meth
7	1e−01	2 / 41	ROSOLOWSKI_blue DOWN
8	1e−01	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
9	1e−01	1 / 10	MASCQUE_ABC UP
10	1e−01	3 / 96	SPANG_LPS 6hrs UP
11	1e−01	1 / 12	Subero_MM_hypo_meth
12	2e−01	1 / 14	YAMANE_AICDA_targets_recruited
13	2e−01	3 / 118	Subero_INT_hyper_meth
14	2e−01	2 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
15	2e−01	1 / 19	Subero_MCL_hypo_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.005	8 / 204	Landsberg_dedifferentiation_down
2	0.029	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
3	0.084	2 / 37	Hugo_melanoma−all−MET_DN
4	0.092	2 / 39	Tirosh_melanoma specific genes
5	0.135	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
6	0.272	2 / 78	Tirosh_CAF−cell specific genes
7	0.297	2 / 83	TCGA_melanoma_immune_high
8	0.353	1 / 33	Tirosh_T−cell specific genes−melanoma
9	0.403	1 / 39	Tirosh_top50 correlated genes PC4
10	0.412	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
11	0.418	1 / 41	Tirosh_top50 correlated genes PC3
12	0.464	2 / 119	TCGA_melanoma_MITF_low
13	0.629	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
14	0.658	1 / 81	Tirosh_Genes in the MITF program
15	0.659	2 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	0.001	7 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
2	0.003	8 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
3	0.005	4 / 53	extracellular matrix structural constituent
4	0.006	11 / 346	receptor binding
5	0.006	4 / 56	calcium−dependent protein binding
6	0.010	2 / 12	phospholipase C activity
7	0.011	3 / 35	scavenger receptor activity
8	0.012	2 / 13	glutamate receptor activity
9	0.014	17 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindi
10	0.014	2 / 14	S100 protein binding
11	0.016	2 / 15	phospholipid−translocating ATPase activity
12	0.018	2 / 16	G−protein coupled peptide receptor activity
13	0.024	3 / 47	transcription regulatory region sequence−specific DNA binding
14	0.025	8 / 268	transcription factor binding
15	0.026	3 / 49	transmembrane receptor protein tyrosine kinase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	4 / 64	hsa−miR−510
2	0.01	3 / 35	hsa−miR−532−3p
3	0.02	3 / 43	hsa−miR−328
4	0.02	4 / 78	hsa−miR−133b
5	0.03	5 / 132	hsa−miR−298
6	0.04	7 / 235	hsa−let−7f
7	0.04	6 / 191	hsa−miR−185
8	0.04	8 / 299	hsa−let−7c
9	0.06	7 / 260	hsa−let−7e
10	0.07	2 / 33	hsa−miR−654−3p
11	0.08	2 / 36	hsa−miR−636
12	0.09	3 / 79	hsa−miR−133a
13	0.10	3 / 83	hsa−miR−147
14	0.10	3 / 84	hsa−miR−410
15	0.10	1 / 8	hsa−miR−638

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.5	1 / 54	Burnham_timecourse
2	0.5	1 / 56	Burnham_sep_vs_con_DN
3	0.5	1 / 57	Burnham_viral_UP
4	0.5	1 / 57	Burnham_day1_vs_5_UP
5	0.6	1 / 71	Burnham_cap_fp_vs_con_UP
6	0.8	1 / 122	Terre_IMS_influenza_meta_signature
7	1.0	0 / 68	Burnham_sep_vs_con_UP
8	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.0	0 / 48	Burnham_viral_DN
10	1.0	0 / 52	Burnham_day1_vs_5_DN
11	1.0	0 / 18	Scicluna_UP
12	1.0	0 / 41	Scicluna_DN
13	1.0	0 / 37	Sweeney_viral_up
14	1.0	0 / 33	Sweeney_viral_dn
15	1.0	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.01	2 / 12	WIRTH_Globus pallidus
2	0.02	3 / 42	VAQUERIZAS_Fetal brain_TF
3	0.02	10 / 352	WIRTH_Nervous System
4	0.02	2 / 16	VAQUERIZAS_Ovary_TF
5	0.02	7 / 209	Chaussabel_2,5_Immune related molecules
6	0.02	2 / 17	VAQUERIZAS_Heart_TF
7	0.06	3 / 66	VAQUERIZAS_Whole blood_TF
8	0.07	2 / 32	VAQUERIZAS_Liver_TF
9	0.08	1 / 6	VAQUERIZAS_Appendix_TF
10	0.08	2 / 36	VAQUERIZAS_Prostate_TF
11	0.09	1 / 7	VAQUERIZAS_Tongue_TF
12	0.09	3 / 81	Chaussabel_1,2_Platelets
13	0.10	2 / 40	VAQUERIZAS_Testis_TF
14	0.12	2 / 45	VAQUERIZAS_Placenta_TF
15	0.13	5 / 204	Chaussabel_3,2_Inflammation I

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−05	52 / 2321	ICGC_Rad21_targets
2	1e−02	13 / 485	ICGC_NrsfPcr2_targets
3	1e−02	24 / 1148	HEBENSTREIT_low expression TF
4	1e−01	1 / 12	NOWICK_TF
5	2e−01	69 / 4851	ICGC_Runx3_targets
6	3e−01	54 / 3804	ICGC_Stat5_targets
7	3e−01	16 / 1025	ICGC_NrsfPcr1_targets
8	3e−01	64 / 4602	ICGC_Elf1_targets
9	3e−01	48 / 3435	ICGC_Ebfsc137065_targets
10	3e−01	59 / 4278	ICGC_Yy1_targets
11	4e−01	31 / 2254	ICGC_BatfPcr1_targets
12	5e−01	42 / 3121	ICGC_Egr1_targets
13	5e−01	43 / 3213	ICGC_Pu1_targets
14	5e−01	55 / 4131	ICGC_Tcf3_targets
15	5e−01	22 / 1636	ICGC_Bcl11_targets

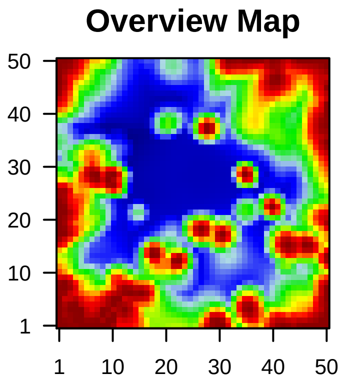
Overexpression Spots

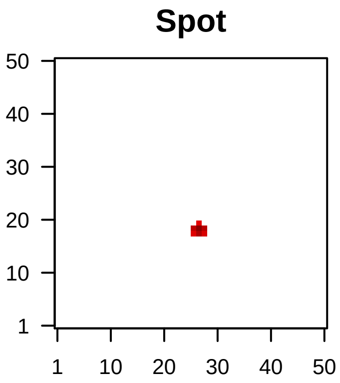
Spot Summary: T

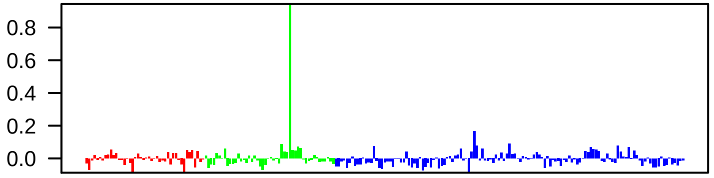
metagenes = 7
genes = 156

<r> metagenes = 0.98
<r> genes = 0.09
beta: r2= 0.28 / log p= −Inf

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


Overview Map


Spot

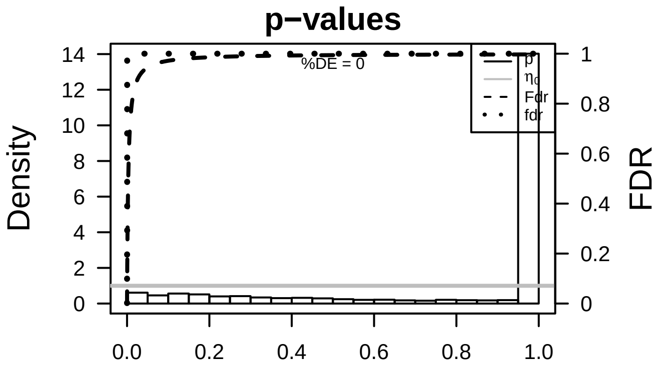


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	203215_s_at	2.09	−0.79	0.21	MYO6	myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]
2	205177_at	2.03	−0.59	0.48	TNNI1	troponin I1, slow skeletal type [Source:HGNC Symbol;Acc:HG
3	220179_at	1.97	−0.73	0.13	DPEP3	dipeptidase 3 [Source:HGNC Symbol;Acc:HGNC:23029]
4	216573_at	1.88	−0.75	0.18		
5	206569_at	1.6	−0.7	0.29	IL24	interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
6	210094_s_at	1.58	−0.67	0.2	PARD3	par−3 family cell polarity regulator [Source:HGNC Symbol;Ac
7	211781_x_at	1.55	−0.85	0.26		
8	216293_at	1.47	−1.03	0.41		
9	214954_at	1.47	−0.61	0.2	SUSD5	sushi domain containing 5 [Source:HGNC Symbol;Acc:HGNC
10	218537_at	1.44	−1.31	0.22	HCFC1R1	host cell factor C1 regulator 1 [Source:HGNC Symbol;Acc:HG
11	207442_at	1.42	−0.88	0.39	CSF3	colony stimulating factor 3 [Source:HGNC Symbol;Acc:HGNC
12	210400_at	1.42	−0.63	0.46	GRIN2C	glutamate ionotropic receptor NMDA type subunit 2C [Source
13	205426_s_at	1.39	−1.12	0.13	HIP1	huntingtin interacting protein 1 [Source:HGNC Symbol;Acc:H
14	211690_at	1.37	−0.72	0.37		
15	205522_at	1.36	−0.56	0.35		
16	217230_at	1.33	−0.82	0.21		
17	217270_s_at	1.32	−0.8	0.25	DYRK1B	dual specificity tyrosine phosphorylation regulated kinase 1B
18	215085_x_at	1.32	−0.71	0.36	DLEC1	deleted in lung and esophageal cancer 1 [Source:HGNC Sym
19	221195_at	1.31	−0.74	0.37	RNFT1	ring finger protein, transmembrane 1 [Source:HGNC Symbol;
20	204046_at	1.31	−1.15	0.28	PLCB2	phospholipase C beta 2 [Source:HGNC Symbol;Acc:HGNC:9

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−05	5 / 46	BP	retinoid metabolic process
2	1e−04	47 / 3168	Lympl	HOPP_Repressed
3	2e−04	77 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
4	2e−04	32 / 1894	Lympl	HOPP_Poised_promoter
5	3e−04	3 / 15	MF	extracellularly glutamate−gated ion channel activity
6	3e−04	3 / 15	MF	ionotropic glutamate receptor activity
7	5e−04	3 / 18	BP	ionotropic glutamate receptor signaling pathway
8	6e−04	5 / 75	CC	apical part of cell
9	6e−04	3 / 19	MF	steroid binding
10	9e−04	4 / 48	BP	bone development
11	9e−04	5 / 83	Refer	WIRTH_Muscle
12	1e−03	4 / 49	BP	regulation of protein stability
13	1e−03	3 / 23	GSEA	LOPES_METHYLATED_IN_COLON_CANCER_UP
14	1e−03	2 / 6	GSEA	REACTOME_OPSINS
15	1e−03	3 / 25	BP	ventricular cardiac muscle tissue morphogenesis
16	2e−03	3 / 26	BP	glycosaminoglycan metabolic process
17	2e−03	3 / 28	GSEA	NEWMAN_ERCC6_TARGETS_DN
18	2e−03	2 / 8	GSEA	OXFORD_RALB_TARGETS_UP
19	3e−03	2 / 9	GSEA	OXFORD_RALA_AND_RALB_TARGETS_DN
20	3e−03	2 / 9	GSEA	MATZUK_PREOVULATORY_FOLLICLE
21	3e−03	3 / 34	BP	regulation of synaptic plasticity
22	4e−03	6 / 164	GSEA	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES
23	4e−03	3 / 36	GSEA	REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABO
24	4e−03	5 / 117	GSEA	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOW
25	4e−03	2 / 11	CC	basal part of cell
26	4e−03	2 / 11	BP	myofibril assembly
27	4e−03	2 / 11	BP	suckling behavior
28	4e−03	4 / 73	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
29	5e−03	7 / 230	GSEA	REACTOME_NEURONAL_SYSTEM
30	5e−03	3 / 38	GSEA	PID_ER_NONGENOMIC_PATHWAY
31	5e−03	8 / 291	MF	actin binding
32	5e−03	2 / 12	CC	Golgi−associated vesicle membrane
33	5e−03	2 / 12	BP	positive regulation of myelination
34	5e−03	2 / 12	Immu	Angelova_immune−metagene−NK56_dim
35	5e−03	3 / 39	MF	SNARE binding
36	6e−03	11 / 501	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
37	6e−03	2 / 13	MF	fatty−acyl−CoA binding
38	6e−03	2 / 13	MF	glutamate receptor activity
39	6e−03	3 / 41	Melar	Tirosh_top50 correlated genes PC3
40	6e−03	7 / 240	GSEA	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	6e−05	5 / 46	retinoid metabolic process
2	5e−04	3 / 18	ionotropic glutamate receptor signaling pathway
3	9e−04	4 / 48	bone development
4	1e−03	4 / 49	regulation of protein stability
5	1e−03	3 / 25	ventricular cardiac muscle tissue morphogenesis
6	2e−03	3 / 26	glycosaminoglycan metabolic process
7	3e−03	3 / 34	regulation of synaptic plasticity
8	4e−03	2 / 11	myofibril assembly
9	4e−03	2 / 11	suckling behavior
10	5e−03	2 / 12	positive regulation of myelination
11	8e−03	2 / 15	regulation of gene expression, epigenetic
12	8e−03	2 / 15	response to peptide
13	9e−03	2 / 16	actin filament−based movement
14	9e−03	2 / 16	regulation of dendrite morphogenesis
15	1e−02	5 / 145	response to stimulus

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	3 / 80	PanCan_JAK−ST_geneset_nanostring
2	0.12	3 / 134	PanCan_RAS_geneset_nanostring
3	0.13	1 / 15	WANG_ER_UP
4	0.13	1 / 16	LIU_LIVER_CANCER
5	0.17	1 / 20	PanCan_ChromMod_geneset_nanostring
6	0.24	3 / 187	PanCan_PI3K_geneset_nanostring
7	0.27	2 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.28	1 / 36	ZHANG_MM up
9	0.33	2 / 130	PanCan_CC+Apop_geneset_nanostring
10	0.35	0 / 14	LIU_COMMON_CANCER_GENES
11	0.35	1 / 47	PanCan_TGF−B_geneset_nanostring
12	0.38	2 / 147	PanCan_MAPK_geneset_nanostring
13	0.49	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.58	1 / 96	PanCan_TXmisReg_geneset_nanostring
15	0.65	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 75	apical part of cell
2	4e−03	2 / 11	basal part of cell
3	5e−03	2 / 12	Golgi−associated vesicle membrane
4	7e−03	4 / 84	Golgi lumen
5	8e−03	8 / 315	neuronal cell body
6	8e−03	3 / 46	clathrin−coated vesicle membrane
7	1e−02	2 / 17	photoreceptor disc membrane
8	1e−02	3 / 51	clathrin−coated vesicle
9	1e−02	3 / 52	clathrin−coated pit
10	1e−02	4 / 101	endomembrane system
11	1e−02	3 / 55	recycling endosome membrane
12	1e−02	2 / 20	excitatory synapse
13	2e−02	3 / 59	adherens junction
14	2e−02	15 / 938	Golgi apparatus
15	2e−02	7 / 310	dendrite

Chr

Rank	p−value	#in/all	Geneset
1	0.01	9 / 403	Chr 14
2	0.15	9 / 669	Chr 6
3	0.27	9 / 776	Chr 17
4	0.28	6 / 490	Chr 10
5	0.28	8 / 689	Chr 3
6	0.37	8 / 756	Chr 11
7	0.37	6 / 548	Chr 16
8	0.45	4 / 382	Chr 15
9	0.48	8 / 833	Chr 19
10	0.57	5 / 556	Chr X
11	0.58	3 / 333	Chr 22
12	0.61	6 / 700	Chr 12
13	0.65	3 / 369	Chr 20
14	0.66	11 / 1325	Chr 1
15	0.78	4 / 585	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−08	61 / 3734	Tcells peripheral blood_13_ReprPC
2	4e−07	49 / 2765	Tregulatory cells peripheral blood_13_ReprPC
3	5e−07	47 / 2600	HSC_14_ReprPCWk
4	1e−06	52 / 3150	monocytes peripheral blood_13_ReprPC
5	2e−06	36 / 1799	T CD8+ naive cells peripheral blood_13_ReprPC
6	2e−06	40 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
7	4e−06	44 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
8	8e−06	44 / 2602	natural killer cells peripheral blood_12_EnhBiv
9	8e−06	43 / 2515	natural killer cells peripheral blood_13_ReprPC
10	1e−05	49 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
11	2e−05	34 / 1813	8_EnhP_Fibroblasts
12	2e−05	47 / 2984	natural killer cells peripheral blood_14_ReprPCWk
13	2e−05	31 / 1604	HSC_11_BivFlnk
14	3e−05	50 / 3272	monocytes peripheral blood_14_ReprPCWk
15	3e−05	38 / 2194	Thelper cells peripheral blood_12_EnhBiv

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	77 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	2e−02	14 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	6e−02	4 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
4	1e−01	7 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
5	1e−01	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
6	1e−01	1 / 16	Budinska_B_Lower crypt−like_UP
7	2e−01	5 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
8	2e−01	2 / 103	Marisa_CRC−cluster−b
9	2e−01	10 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
10	2e−01	4 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
11	2e−01	11 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
12	3e−01	6 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
13	3e−01	5 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
14	4e−01	12 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	5e−01	1 / 72	Ang_CRC−CIMPH−vs−L_hyper

Glioma

Rank	p−value	#in/all	Geneset
1	0.006	4 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	0.008	6 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
3	0.010	3 / 49	OPC
4	0.045	6 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
5	0.070	2 / 48	in vivo astrocytes vs. cultured astroglia
6	0.095	1 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
7	0.096	3 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
8	0.099	2 / 59	GIEZELT_GBM_STS_up_VS_LTS
9	0.122	2 / 67	Weller_LGG_1p19qDel−vs−intact_UP
10	0.127	1 / 15	Gorovets_LGG_NB_subclass
11	0.161	7 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
12	0.173	1 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)
13	0.178	2 / 85	ScoV_0.999_Sturm_E2_IDH_DN
14	0.180	6 / 421	Down_b
15	0.182	2 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	3 / 23	LOPES_METHYLATED_IN_COLON_CANCER_UP
2	0.001	2 / 6	REACTOME_OPSINS
3	0.002	3 / 28	NEWMAN_ERCC6_TARGETS_DN
4	0.002	2 / 8	OXFORD_RALB_TARGETS_UP
5	0.003	2 / 9	OXFORD_RALA_AND_RALB_TARGETS_DN
6	0.003	2 / 9	MATZUK_PREOVULATORY_FOLLICLE
7	0.004	6 / 164	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES
8	0.004	3 / 36	REACTOME_CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOL
9	0.004	5 / 117	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNS
10	0.004	4 / 73	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
11	0.005	7 / 230	REACTOME_NEURONAL_SYSTEM
12	0.005	3 / 38	PID_ER_NONGENOMIC_PATHWAY
13	0.006	11 / 501	MARTENS_TRETINOIN_RESPONSE_UP
14	0.006	7 / 240	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
15	0.007	2 / 14	BIOCARTA_ERYTH_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.1	3 / 122	HALLMARK_SPERMATOGENESIS
2	0.2	3 / 187	HALLMARK_INFLAMMATORY_RESPONSE
3	0.3	3 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	0.3	2 / 130	HALLMARK_COAGULATION
5	0.5	2 / 174	HALLMARK_APICAL_JUNCTION
6	0.5	2 / 176	HALLMARK_ALLOGRAFT_REJECTION
7	0.5	2 / 178	HALLMARK_COMPLEMENT
8	0.5	2 / 188	HALLMARK_HYPOXIA
9	0.5	2 / 191	HALLMARK_P53_PATHWAY
10	0.5	2 / 193	HALLMARK_HEME_METABOLISM
11	0.5	2 / 195	HALLMARK_KRAS_SIGNALING_DN
12	0.6	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	0.6	1 / 97	HALLMARK_PEROXISOME
14	0.7	1 / 141	HALLMARK_UV_RESPONSE_DN
15	0.7	1 / 150	HALLMARK_APOPTOSIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.005	2 / 12	Angelova_immune−metagene−NK56_dim
2	0.095	1 / 11	Angelova_immune−metagene−macrophages
3	0.119	1 / 14	Angelova_immune−metagene−eosinophil
4	0.158	1 / 19	Angelova_immune−metagene−iDC
5	0.456	1 / 67	Angelova_immune−metagene−T−cells
6	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
8	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
9	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
10	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
11	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.000	0 / 25	Angelova_immune−metagene−DC
13	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
14	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.000	0 / 13	Angelova_immune−metagene−immature_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 62	DUMEAUX_Smoking enriched genes
2	0.7	1 / 150	Homuth_BMI−associated−genes_UP
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 22	DUMEAUX_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−04	47 / 3168	HOPP_Repressed
2	2e−04	32 / 1894	HOPP_Poised_promoter
3	1e−01	1 / 14	Subero_B−ALL_hypo_meth
4	1e−01	21 / 1814	HOPP_Repetitive
5	2e−01	1 / 19	Subero_MCL_hypo_meth
6	2e−01	4 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
7	2e−01	1 / 20	Subero_MCL_hyper_meth
8	2e−01	1 / 23	Subero_mBL_hypo_meth
9	2e−01	2 / 91	Subero_T−ALL_hyper_meth
10	3e−01	1 / 33	Subero_T−PLL_hypo_meth
11	3e−01	2 / 118	Subero_INT_hyper_meth
12	3e−01	2 / 132	Subero_DLBCL_hyper_meth
13	3e−01	1 / 45	Subero_INT_hypo_meth
14	3e−01	1 / 46	Subero_DLBCL_hypo_meth
15	3e−01	1 / 47	Subero_B−ALL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.006	3 / 41	Tirosh_top50 correlated genes PC3
2	0.141	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
3	0.164	4 / 236	Gerber_wt/wt_group3−specific
4	0.279	3 / 204	Landsberg_dedifferentiation_down
5	0.291	2 / 119	TCGA_melanoma_MITF_low
6	0.298	1 / 39	Tirosh_melanoma specific genes
7	0.390	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
8	0.446	1 / 65	Harbst_melanoma_highgrade_up
9	0.461	1 / 68	Tirosh_housekeeping_genes
10	0.466	5 / 497	Gerber_wt/wt_melanoma−cells−SpotD
11	0.494	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
12	0.521	1 / 81	Tirosh_Genes in the MITF program
13	0.538	1 / 85	Tirosh_AXL−signature
14	0.790	1 / 171	Landsberg_dedifferentiation_up
15	0.878	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC

MF

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 15	extracellularly glutamate−gated ion channel activity
2	3e−04	3 / 15	ionotropic glutamate receptor activity
3	6e−04	3 / 19	steroid binding
4	5e−03	8 / 291	actin binding
5	5e−03	3 / 39	SNARE binding
6	6e−03	2 / 13	fatty−acyl−CoA binding
7	6e−03	2 / 13	glutamate receptor activity
8	1e−02	2 / 17	heparan sulfate proteoglycan binding
9	1e−02	2 / 17	HMG box domain binding
10	1e−02	2 / 17	hyaluronic acid binding
11	1e−02	3 / 52	steroid hormone receptor activity
12	1e−02	2 / 19	fibroblast growth factor binding
13	1e−02	33 / 2529	metal ion binding
14	2e−02	13 / 741	DNA binding transcription factor activity
15	2e−02	2 / 22	cation channel activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 25	hsa−miR−635
2	0.03	2 / 28	hsa−miR−296−5p
3	0.06	2 / 43	hsa−miR−328
4	0.08	2 / 51	hsa−miR−648
5	0.10	2 / 61	hsa−miR−939
6	0.11	2 / 64	hsa−miR−510
7	0.12	3 / 135	hsa−miR−29c
8	0.13	1 / 15	hsa−miR−542−5p
9	0.14	2 / 73	hsa−miR−423−5p
10	0.15	1 / 18	hsa−miR−1250
11	0.17	5 / 324	hsa−miR−497
12	0.18	1 / 22	hsa−miR−663
13	0.19	2 / 88	hsa−miR−613
14	0.19	2 / 90	hsa−miR−1301
15	0.20	2 / 92	hsa−miR−190b

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−04	5 / 83	WIRTH_Muscle
2	9e−03	2 / 16	WIRTH_Hippocampus
3	3e−02	2 / 28	JONGENEEL_Placenta
4	6e−02	2 / 43	WIRTH_Placenta
5	1e−01	6 / 352	WIRTH_Nervous System
6	2e−01	1 / 20	JONGENEEL_Heart
7	2e−01	10 / 809	PROTEINATLAS_fallopian tube
8	2e−01	10 / 840	PROTEINATLAS_urinary bladder
9	2e−01	1 / 30	JONGENEEL_Bone Marrow
10	3e−01	1 / 36	VAQUERIZAS_Prostate_TF
11	3e−01	1 / 40	VAQUERIZAS_Testis_TF
12	3e−01	8 / 716	PROTEINATLAS_epididymis
13	3e−01	10 / 923	PROTEINATLAS_cerebral cortex
14	3e−01	1 / 44	JONGENEEL_Retina
15	3e−01	1 / 45	VAQUERIZAS_Placenta_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.05	16 / 1148	HEBENSTREIT_low expression TF
2	0.27	6 / 485	ICGC_NrsfPcr2_targets
3	0.37	6 / 549	ICGC_Atf3_targets
4	0.43	22 / 2321	ICGC_Rad21_targets
5	0.48	20 / 2150	ICGC_Irf4_targets
6	0.52	4 / 415	ICGC_RxraPcr1_targets
7	0.59	17 / 1941	ICGC_Bcl3_targets
8	0.70	4 / 522	ICGC_SrfPcr2_targets
9	0.82	12 / 1636	ICGC_Bcl11_targets
10	0.83	7 / 1032	ICGC_Usf1_targets
11	0.83	37 / 4602	ICGC_Elf1_targets
12	0.84	7 / 1041	ICGC_P300_targets
13	0.86	33 / 4212	ICGC_Pol2_targets
14	0.88	26 / 3435	ICGC_Ebfsc137065_targets
15	0.89	23 / 3121	ICGC_Egr1_targets

Overexpression Spots

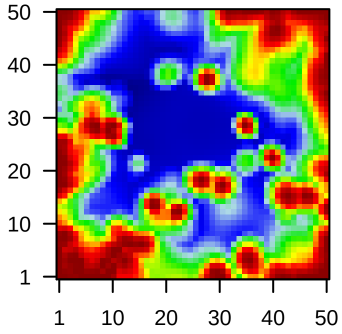
Spot Summary: U

metagenes = 14
genes = 200

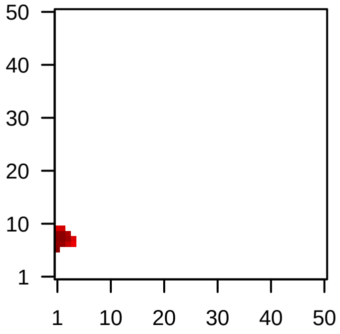
<r> metagenes = 0.98
<r> genes = 0.34
beta: r2= 14.1 / log p= −Inf

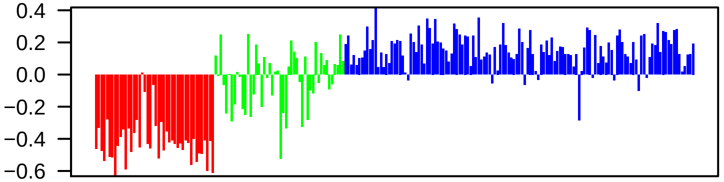
samples with spot = 41 (18.6 %)
intermediate : 4 (8.3 %)
non−mBL : 37 (28.7 %)

Overview Map



Spot





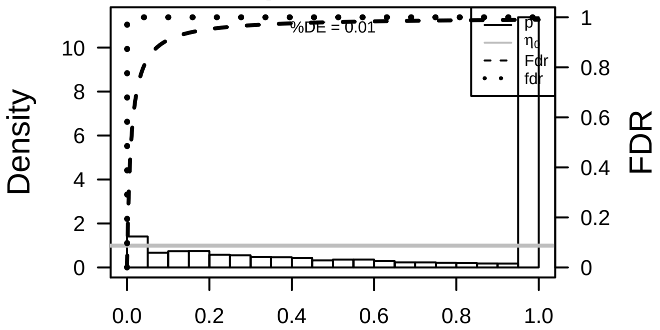
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207900_at	2.93	−0.94	0.34	CCL17	C−C motif chemokine ligand 17 [Source:HGNC Symbol;Acc:H
2	207245_at	2.21	−1.2	0.46	UGT2B17	UDP glucuronosyltransferase family 2 member B17 [Source:H
3	210517_s_at	1.9	−1.34	0.35	AKAP12	A−kinase anchoring protein 12 [Source:HGNC Symbol;Acc:H
4	210437_at	1.88	−1.26	0.43	MAGEA9B	MAGE family member A9B [Source:HGNC Symbol;Acc:HGN
5	203404_at	1.73	−1.41	0.48	ARMCX2	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
6	203562_at	1.7	−1.4	0.56	FEZ1	fasciculation and elongation protein zeta 1 [Source:HGNC Sy
7	203835_at	1.7	−1.1	0.46	LRRC32	leucine rich repeat containing 32 [Source:HGNC Symbol;Acc:
8	217966_s_at	1.67	−0.98	0.59	FAM129A	family with sequence similarity 129 member A [Source:HGNC
9	205997_at	1.63	−1.62	0.64	ADAM28	ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
10	203642_s_at	1.63	−1.51	0.61	COBLL1	cordon−bleu WH2 repeat protein like 1 [Source:HGNC Symb
11	203216_s_at	1.54	−0.93	0.44	MYO6	myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]
12	213534_s_at	1.52	−1.17	0.58	PASK	PAS domain containing serine/threonine kinase [Source:HGN
13	218706_s_at	1.52	−1.14	0.66	GRAMD2B	GRAM domain containing 2B [Source:HGNC Symbol;Acc:HG
14	205691_at	1.5	−1.1	0.51	SYNGR3	synaptogyrin 3 [Source:HGNC Symbol;Acc:HGNC:11501]
15	212445_s_at	1.48	−1.16	0.51	NEDD4L	neural precursor cell expressed, developmentally down−regul
16	221218_s_at	1.46	−0.98	0.39	TPK1	thiamin pyrophosphokinase 1 [Source:HGNC Symbol;Acc:HG
17	203271_s_at	1.46	−1.46	0.65	UNC119	unc−119 lipid binding chaperone [Source:HGNC Symbol;Acc:
18	205469_s_at	1.44	−1.36	0.5	IRF5	interferon regulatory factor 5 [Source:HGNC Symbol;Acc:HG
19	217504_at	1.43	−1.32	0.43	ABCA6	ATP binding cassette subfamily A member 6 [Source:HGNC
20	203641_s_at	1.41	−1.13	0.56	COBLL1	cordon−bleu WH2 repeat protein like 1 [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−27	38 / 317	Cance	SPANG_BCL6−index2
2	3e−22	27 / 173	Lymp	Victora_Light zone signature
3	2e−21	27 / 186	Cance	SPANG_LPS−index2
4	6e−19	32 / 353	Lymp	SPANG_CD40 6hrs DN
5	3e−16	17 / 85	Lymp	Sha_DLBCL UP
6	1e−15	118 / 5404	Lymp	HOPP_Strong_enhancer
7	1e−14	9 / 14	GSE	HUMMEL_BURKITTS_LYMPHOMA_DN
8	2e−13	21 / 213	Lymp	SPANG_IL21 DN
9	3e−13	15 / 90	GSE	BASSO_CD40_SIGNALING_UP
10	9e−13	17 / 135	Lymp	DAVE_BL−vs−DLBCL
11	3e−11	7 / 12	Lymp	BENTINK_mBL DOWN
12	3e−10	28 / 560	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
13	4e−10	36 / 906	Lymp	SPANG_BCR DN
14	4e−09	23 / 431	BP	immune system process
15	7e−09	17 / 238	GSE	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
16	9e−09	110 / 5908	Lymp	HOPP_Active_promoter
17	3e−08	8 / 40	BP	antigen processing and presentation
18	5e−08	14 / 178	GSE	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
19	1e−07	18 / 321	GSE	PHONG_TNF_RESPONSE_NOT_VIA_P38
20	1e−07	9 / 66	BP	interferon−gamma−mediated signaling pathway
21	1e−07	18 / 327	GSE	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
22	2e−07	8 / 50	GSE	LINDSTEDT_DENDRITIC_CELL_MATURATION_B
23	2e−07	15 / 229	GSE	QI_PLASMACYTOMA_UP
24	2e−07	8 / 51	GSE	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
25	2e−07	6 / 22	MF	peptide antigen binding
26	2e−07	6 / 22	Lymp	DAVE_NFkB BL DN
27	3e−07	9 / 72	GSE	MORI_MATURE_B_LYMPHOCYTE_UP
28	3e−07	6 / 23	CC	integral component of lumenal side of endoplasmic reticulum membrane
29	3e−07	4 / 6	Lymp	DAVE_MHCCII BL DN
30	4e−07	8 / 55	GSE	DIRMEIER_LMP1_RESPONSE_EARLY
31	4e−07	8 / 55	GSE	DIRMEIER_LMP1_RESPONSE_LATE_UP
32	7e−07	6 / 26	BP	antigen processing and presentation of peptide antigen via MHC class I
33	7e−07	19 / 404	GSE	RUTELLA_RESPONSE_TO_HGF_UP
34	7e−07	13 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
35	8e−07	7 / 42	GSE	VILIMAS_NOTCH1_TARGETS_UP
36	1e−06	23 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
37	2e−06	25 / 694	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
38	2e−06	101 / 5682	Lymp	HOPP_Weak_promoter
39	4e−06	19 / 453	GSE	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
40	5e−06	15 / 297	Colon	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−09	23 / 431	immune system process
2	3e−08	8 / 40	antigen processing and presentation
3	1e−07	9 / 66	interferon−gamma−mediated signaling pathway
4	7e−07	6 / 26	antigen processing and presentation of peptide antigen via MHC class I
5	1e−05	7 / 63	type I interferon signaling pathway
6	2e−05	15 / 336	immune response
7	5e−05	4 / 17	antigen processing and presentation of peptide or polysaccharide antigen via
8	8e−05	8 / 113	regulation of immune response
9	3e−04	3 / 11	positive regulation of interferon−alpha production
10	9e−04	5 / 60	T cell costimulation
11	1e−03	6 / 98	protein localization to plasma membrane
12	2e−03	5 / 69	antigen processing and presentation of exogenous peptide antigen via MHC c
13	2e−03	13 / 407	viral process
14	2e−03	3 / 20	positive regulation of interleukin−12 production
15	2e−03	3 / 22	positive regulation of interferon−beta production

Cancer

Rank	p−value	#in/all	Geneset
1	7e−27	38 / 317	SPANG_BCL6−index2
2	2e−21	27 / 186	SPANG_LPS−index2
3	1e−04	17 / 480	Lembcke_Colonic Inflammation
4	4e−04	3 / 12	HLA2_signature
5	7e−03	2 / 10	BENTINK_ras.4
6	1e−02	6 / 147	PanCan_MAPK_geneset_nanostring
7	1e−02	2 / 14	BENTINK_src.10
8	2e−02	1 / 12	LIU_BREAST_CANCER
9	2e−02	5 / 130	PanCan_CC+Apop_geneset_nanostring
10	2e−02	1 / 2	HLA1_signature
11	1e−01	3 / 96	PanCan_TXmisReg_geneset_nanostring
12	1e−01	1 / 12	GENTLES_modul12
13	2e−01	1 / 13	GENTLES_modul11
14	2e−01	1 / 14	LIU_PROSTATE_CANCER_DN
15	2e−01	1 / 14	GUSTAFSON_PI3K_UP

CC

Rank	p−value	#in/all	Geneset
1	3e−07	6 / 23	integral component of lumenal side of endoplasmic reticulum membrane
2	4e−05	6 / 51	ER to Golgi transport vesicle membrane
3	6e−05	4 / 18	MHC class II protein complex
4	8e−05	6 / 58	phagocytic vesicle membrane
5	6e−04	5 / 55	recycling endosome membrane
6	8e−04	11 / 281	lysosome
7	2e−03	65 / 3805	cytosol
8	3e−03	56 / 3210	plasma membrane
9	4e−03	16 / 604	intracellular membrane−bounded organelle
10	7e−03	2 / 10	catenin complex
11	7e−03	21 / 938	Golgi apparatus
12	2e−02	5 / 117	cell cortex
13	2e−02	3 / 43	intercalated disc
14	2e−02	4 / 79	organelle membrane
15	2e−02	12 / 479	Golgi membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.002	21 / 832	Chr 2
2	0.004	15 / 556	Chr X
3	0.076	13 / 669	Chr 6
4	0.260	11 / 700	Chr 12
5	0.378	11 / 776	Chr 17
6	0.474	10 / 756	Chr 11
7	0.597	16 / 1325	Chr 1
8	0.601	7 / 585	Chr 7
9	0.673	2 / 184	Chr 18
10	0.686	6 / 548	Chr 16
11	0.722	5 / 480	Chr 4
12	0.746	4 / 403	Chr 14
13	0.764	7 / 689	Chr 3
14	0.800	4 / 437	Chr 8
15	0.809	2 / 242	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−11	87 / 3767	Bcells peripheral blood_6_EnhG
2	1e−08	138 / 8406	Bcells peripheral blood_2_TssAFlnk
3	2e−07	129 / 7833	Bcells peripheral blood_1_TssA
4	4e−07	134 / 8370	natural killer cells peripheral blood_2_TssAFlnk
5	1e−06	131 / 8200	monocytes peripheral blood_2_TssAFlnk
6	3e−06	127 / 7930	Tregulatory cells peripheral blood_1_TssA
7	4e−06	36 / 1308	Mid_Frontal_Lobe_K9K27me3
8	7e−06	124 / 7751	natural killer cells peripheral blood_1_TssA
9	7e−06	129 / 8208	Tcells peripheral blood_7_Enh
10	2e−05	23 / 693	Bcells peripheral blood_3_TxFlnk
11	2e−05	121 / 7635	monocytes peripheral blood_1_TssA
12	3e−05	134 / 8816	Thelper cells peripheral blood_2_TssAFlnk
13	3e−05	109 / 6651	Thelper cells peripheral blood_5_TxWk
14	3e−05	21 / 626	natural killer cells peripheral blood_3_TxFlnk
15	4e−05	53 / 2507	Mid_Frontal_Lobe_ReprPC

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−06	23 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	5e−06	15 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
3	2e−04	28 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
4	6e−04	23 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
5	1e−03	11 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
6	6e−03	7 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
7	1e−02	3 / 38	Marisa_CRC−cluster−e
8	1e−02	21 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	2e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
10	4e−02	7 / 255	Kosinski_top−crypt−long−list
11	6e−02	2 / 31	Marisa_CRC−cluster−c
12	6e−02	16 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	8e−02	10 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	9e−02	20 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	1e−01	1 / 8	Marisa_CRC−C3

Glioma

Rank	p−value	#in/all	Geneset
1	1e−05	18 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	8e−05	27 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	5e−04	11 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
4	2e−03	10 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
5	2e−03	9 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
6	3e−03	9 / 242	ScoV_0.5_Sturm_C1_IDH_DN
7	4e−03	3 / 27	Donson−Misc immune function−associated with LTS in HGA
8	8e−03	6 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
9	9e−03	7 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
10	1e−02	3 / 38	OL vs. OPC
11	1e−02	8 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
12	1e−02	5 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
13	1e−02	5 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
14	2e−02	9 / 330	Up
15	2e−02	4 / 87	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−14	9 / 14	HUMMEL_BURKITTS_LYMPHOMA_DN
2	3e−13	15 / 90	BASSO_CD40_SIGNALING_UP
3	3e−10	28 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
4	7e−09	17 / 238	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
5	5e−08	14 / 178	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
6	1e−07	18 / 321	PHONG_TNF_RESPONSE_NOT_VIA_P38
7	1e−07	18 / 327	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
8	2e−07	8 / 50	LINDSTEDT_DENDRITIC_CELL_MATURATION_B
9	2e−07	15 / 229	QI_PLASMACYTOMA_UP
10	2e−07	8 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
11	3e−07	9 / 72	MORI_MATURE_B_LYMPHOCYTE_UP
12	4e−07	8 / 55	DIRMEIER_LMP1_RESPONSE_EARLY
13	4e−07	8 / 55	DIRMEIER_LMP1_RESPONSE_LATE_UP
14	7e−07	19 / 404	RUTELLA_RESPONSE_TO_HGF_UP
15	8e−07	7 / 42	VILIMAS_NOTCH1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	7e−07	13 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	2e−04	9 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	9e−03	7 / 188	HALLMARK_HYPOXIA
4	2e−02	6 / 173	HALLMARK_MITOTIC_SPINDLE
5	2e−02	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	2e−02	6 / 174	HALLMARK_APICAL_JUNCTION
7	4e−02	6 / 194	HALLMARK_KRAS_SIGNALING_UP
8	4e−02	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	7e−02	3 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	7e−02	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
11	7e−02	5 / 178	HALLMARK_COMPLEMENT
12	8e−02	4 / 130	HALLMARK_COAGULATION
13	1e−01	4 / 150	HALLMARK_APOPTOSIS
14	1e−01	3 / 97	HALLMARK_BILE_ACID_METABOLISM
15	2e−01	4 / 187	HALLMARK_INFLAMMATORY_RESPONSE

Immunome

Rank	p−value	#in/all	Geneset
1	0.002	4 / 45	Angelova_immune−metagene−MDSC
2	0.007	3 / 32	Angelova_immune−metagene−effector_memory_CD8
3	0.019	2 / 17	Angelova_immune−metagene−central_memory_CD8
4	0.021	2 / 18	Angelova_CRC_immunostimulators
5	0.061	1 / 5	Angelova_immune−metagene−NKT
6	0.073	1 / 6	Immunity_immune−checkpoint−inhibitors
7	0.084	1 / 7	Angelova_immune−metagene−cytotoxic_cells
8	0.084	1 / 7	Angelova_CRC_MSI−neoantigens
9	0.097	2 / 42	Angelova_immune−metagene−TGD
10	0.118	1 / 10	Angelova_immune−metagene−TFH
11	0.151	1 / 13	Angelova_immune−metagene−activated_B−cells
12	0.151	1 / 13	Angelova_CRC_MSS^−neoantigens
13	0.172	1 / 15	Angelova_immune−metagene−NK
14	0.182	1 / 16	Angelova_immune−metagene−Th17
15	0.204	2 / 67	Angelova_immune−metagene−T−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 22	DUMEAUX_High bmi enriched genes
2	0.14	1 / 12	DUMEAUX_Women normal BMI literature genes up
3	0.33	1 / 32	Marjolein_ageing−genes_DN
4	0.49	3 / 210	Homuth_BMI−associated−genes_DN
5	0.85	1 / 150	Homuth_BMI−associated−genes_UP
6	1.00	0 / 62	DUMEAUX_Smoking enriched genes
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 22	DUMEAUX_Fasting enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−22	27 / 173	Victora_Light zone signature
2	6e−19	32 / 353	SPANG_CD40 6hrs DN
3	3e−16	17 / 85	Sha_DLBCL UP
4	1e−15	118 / 5404	HOPP_Strong_enhancer
5	2e−13	21 / 213	SPANG_IL21 DN
6	9e−13	17 / 135	DAVE_BL−vs−DLBCL
7	3e−11	7 / 12	BENTINK_mBL DOWN
8	4e−10	36 / 906	SPANG_BCR DN
9	9e−09	110 / 5908	HOPP_Active_promoter
10	2e−07	6 / 22	DAVE_NFkB BL DN
11	3e−07	4 / 6	DAVE_MHCCII BL DN
12	2e−06	101 / 5682	HOPP_Weak_promoter
13	7e−06	7 / 57	SPANG_LPS 6hrs DN
14	1e−05	4 / 12	DAVE_BL_DN
15	1e−04	76 / 4261	HOPP_Txn_transition

Melanoma

Rank	p−value	#in/all	Geneset
1	0.002	6 / 107	Tirosh_Exhaustion program in Mel75
2	0.026	7 / 230	Gerber_wt/wt_melanoma−cells−SpotC
3	0.026	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
4	0.043	6 / 204	Landsberg_dedifferentiation_down
5	0.060	6 / 222	Gerber_wt/wt_melanoma−cells−SpotF
6	0.061	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
7	0.064	2 / 33	Tirosh_T−cell specific genes−melanoma
8	0.067	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma
9	0.081	2 / 38	Hugo_melanoma−BRAFmut−MET_UP
10	0.083	5 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
11	0.086	3 / 83	TCGA_melanoma_immune_high
12	0.088	5 / 189	Tirosh_genes preferentially expressed by Tregs
13	0.166	4 / 171	Landsberg_dedifferentiation_up
14	0.182	1 / 16	Hugo_melanoma−all−LEF1_UP
15	0.251	1 / 23	Melanoma Epi−Enzyme Cluster 7

MF

Rank	p−value	#in/all	Geneset
1	2e−07	6 / 22	peptide antigen binding
2	4e−04	3 / 12	MHC class II receptor activity
3	2e−03	3 / 21	WW domain binding
4	3e−03	3 / 24	hydrolase activity, hydrolyzing O−glycosyl compounds
5	6e−03	3 / 29	SH2 domain binding
6	6e−03	6 / 130	guanyl−nucleotide exchange factor activity
7	8e−03	2 / 11	MAP kinase tyrosine/serine/threonine phosphatase activity
8	1e−02	3 / 41	protein kinase C binding
9	2e−02	2 / 16	MHC class II protein complex binding
10	2e−02	2 / 19	ATPase activator activity
11	2e−02	2 / 19	tumor necrosis factor−activated receptor activity
12	2e−02	3 / 50	cysteine−type endopeptidase activity
13	3e−02	2 / 20	polyubiquitin modification−dependent protein binding
14	3e−02	5 / 135	actin filament binding
15	3e−02	4 / 93	protein N−terminus binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 22	hsa−miR−24−1*
2	0.005	2 / 9	hsa−miR−604
3	0.006	3 / 29	hsa−miR−647
4	0.009	4 / 66	hsa−miR−567
5	0.009	2 / 12	hsa−miR−191*
6	0.012	4 / 71	hsa−miR−188−3p
7	0.026	3 / 51	hsa−miR−648
8	0.030	2 / 22	hsa−miR−941
9	0.065	3 / 74	hsa−miR−595
10	0.071	2 / 35	hsa−miR−640
11	0.074	3 / 78	hsa−miR−133b
12	0.081	2 / 38	hsa−miR−518a−3p
13	0.093	2 / 41	hsa−miR−337−3p
14	0.093	2 / 41	hsa−miR−519b−5p
15	0.093	2 / 41	hsa−miR−519c−5p

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−05	16 / 355	WIRTH_Immune system
2	1e−03	9 / 204	Chaussabel_3,2_Inflammation I
3	1e−02	21 / 989	PROTEINATLAS_tonsil
4	1e−02	7 / 198	Chaussabel_3,3_Inflammation II
5	2e−02	7 / 218	WIRTH_pre+post GC B−cells
6	2e−02	7 / 219	WIRTH_GC B−cells
7	3e−02	6 / 182	WIRTH_post GC B−cells
8	3e−02	10 / 399	PROTEINATLAS_soft tissue
9	3e−02	18 / 905	PROTEINATLAS_appendix
10	4e−02	14 / 678	PROTEINATLAS_lymph node
11	5e−02	21 / 1161	PROTEINATLAS_colon
12	6e−02	3 / 72	Chaussabel_3,1_Interferon−inducible
13	8e−02	3 / 81	Chaussabel_1,2_Platelets
14	8e−02	15 / 809	PROTEINATLAS_fallopian tube
15	8e−02	1 / 7	VAQUERIZAS_Tongue_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	9e−05	36 / 1508	ICGC_Mef2_targets
2	2e−04	35 / 1494	ICGC_Cebpbsc150_targets
3	4e−04	41 / 1941	ICGC_Bcl3_targets
4	9e−04	35 / 1636	ICGC_Bcl11_targets
5	2e−03	43 / 2254	ICGC_BatfPcr1_targets
6	3e−03	41 / 2150	ICGC_Irf4_targets
7	1e−02	49 / 2899	ICGC_Nfatc1_targets
8	1e−02	53 / 3213	ICGC_Pu1_targets
9	1e−02	56 / 3435	ICGC_Ebfsc137065_targets
10	2e−02	60 / 3778	ICGC_Pol24_targets
11	2e−02	55 / 3420	ICGC_Bclaf101388_targets
12	2e−02	33 / 1848	ICGC_Pbx3_targets
13	3e−02	59 / 3796	ICGC_Nficsc81335_targets
14	3e−02	63 / 4131	ICGC_Tcf3_targets
15	4e−02	58 / 3769	ICGC_Pmlsc71910_targets

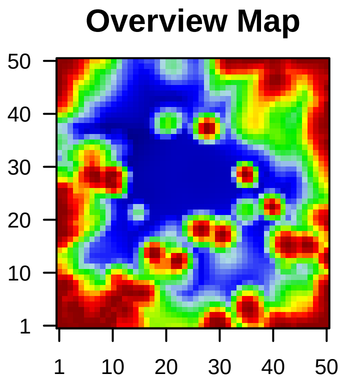
Overexpression Spots

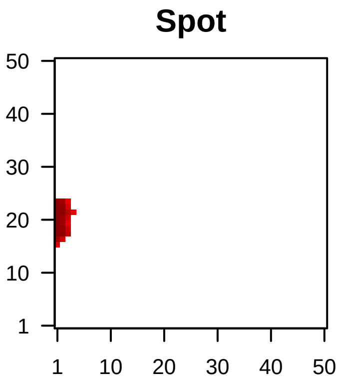
Spot Summary: V

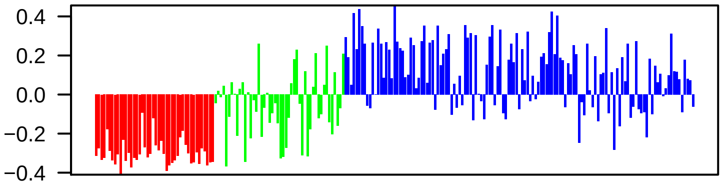
metagenes = 25
genes = 318

<r> metagenes = 0.93
<r> genes = 0.22
beta: r2= 7.82 / log p= −Inf

samples with spot = 53 (24 %)
intermediate : 5 (10.4 %)
non−mBL : 48 (37.2 %)





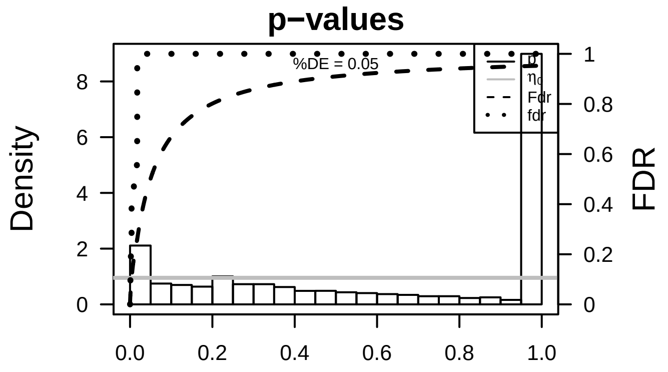


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209810_at	3.13	−1.02	0.46	SFTPB	surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080
2	207861_at	2.76	−1.26	0.54	CCL22	C−C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:
3	204753_s_at	2.57	−0.91	0.41	HLF	HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Ac
4	201839_s_at	2.49	−1.02	0.28	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
5	210551_s_at	2.43	−0.93	0.43	ASMT	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
6	219360_s_at	2.4	−1.57	0.49	TRPM4	transient receptor potential cation channel subfamily M mem
7	37004_at	2.39	−0.69	0.3	SFTPB	surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080
8	207534_at	2.39	−0.99	0.24	MAGEB1	MAGE family member B1 [Source:HGNC Symbol;Acc:HGNC
9	219836_at	2.38	−1.24	0.57	ZBED2	zinc finger BED−type containing 2 [Source:HGNC Symbol;Ac
10	218186_at	2.28	−1.29	0.35	RAB25	RAB25, member RAS oncogene family [Source:HGNC Symb
11	217523_at	2.2	−1.4	0.69	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;
12	219255_x_at	2.16	−1.57	0.44	IL17RB	interleukin 17 receptor B [Source:HGNC Symbol;Acc:HGNC:
13	206478_at	2.15	−1.11	0.26		family with sequence similarity 30 member A [Source:HGNC
14	221728_x_at	2.14	−1.53	0.12		X inactive specific transcript (non−protein coding) [Source:H
15	206218_at	2.12	−0.98	0.28	MAGEB2	MAGE family member B2 [Source:HGNC Symbol;Acc:HGNC
16	204086_at	2.11	−1.29	0.44	PRAME	preferentially expressed antigen in melanoma [Source:HGNC
17	207392_x_at	2.06	−0.9	0.3	UGT2B15	UDP glucuronosyltransferase family 2 member B15 [Source:
18	200951_s_at	2.05	−1.43	0.71	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
19	206779_s_at	2.01	−1.2	0.37	ASMT	acetylserotonin O−methyltransferase [Source:HGNC Symbol;
20	210313_at	2.01	−0.9	0.34	LILRA4	leukocyte immunoglobulin like receptor A4 [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−17	21 / 85	Lymp	Aukema_BCL2 DN_BCL6 UP
2	1e−16	35 / 317	Canc	SPANG_BCL6−index2
3	5e−15	11 / 18	Lymp	WRIGHT_ABC UP
4	1e−12	8 / 10	Lymp	Care_ABC UP
5	1e−10	15 / 85	Lymp	Sha_DLBCL UP
6	5e−10	158 / 5404	Lymp	HOPP_Strong_enhancer
7	2e−09	22 / 234	GSE	HOLLMANN_APOPTOSIS_VIA_CD40_DN
8	2e−08	16 / 139	GSE	BROCKE_APOPTOSIS_REVERSED_BY_IL6
9	6e−08	19 / 213	Lymp	SPANG_IL21 DN
10	7e−08	17 / 173	Lymp	Victora_Light zone signature
11	1e−07	9 / 42	Refer	Chaussabel_1,3_B−cells
12	2e−07	19 / 227	GSE	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP
13	2e−07	4 / 4	Lymp	WRIGHT_custom ABC−DLBCL UP
14	2e−07	24 / 353	Lymp	SPANG_CD40 6hrs DN
15	2e−07	12 / 90	GSE	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
16	3e−07	20 / 262	GSE	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
17	8e−07	16 / 182	Refer	WIRTH_post GC B−cells
18	8e−07	10 / 67	Immu	Angelova_immune−metagene−T−cells
19	1e−06	27 / 480	Canc	Lembcke_Colonic Inflammation
20	2e−06	9 / 56	GSE	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
21	2e−06	25 / 429	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
22	2e−06	5 / 12	BP	leukocyte chemotaxis
23	3e−06	39 / 885	BP	positive regulation of transcription from RNA polymerase II promoter
24	3e−06	57 / 1541	MF	DNA binding
25	5e−06	9 / 64	GSE	GEORGANTAS_HSC_MARKERS
26	6e−06	6 / 24	Mela	Tirosh_B−cell specific genes−melanoma
27	6e−06	7 / 36	GSE	REACTOME_PACKAGING_OF_TELOMERE_ENDS
28	6e−06	19 / 290	GSE	ODONNELL_TFRC_TARGETS_UP
29	7e−06	9 / 67	GSE	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
30	1e−05	73 / 2254	TF	ICGC_BatfPcr1_targets
31	1e−05	14 / 175	GSE	OKUMURA_INFLAMMATORY_RESPONSE_LPS
32	1e−05	10 / 90	GSE	BASSO_CD40_SIGNALING_UP
33	1e−05	17 / 251	GSE	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
34	2e−05	7 / 42	GSE	REACTOME_RNA_POL_I_PROMOTER_OPENING
35	2e−05	57 / 1636	TF	ICGC_Bcl11_targets
36	2e−05	16 / 234	GSE	VERHAAK_AML_WITH_NPM1_MUTATED_DN
37	2e−05	20 / 346	GSE	YAGI_AML_WITH_T_8_21_TRANSLOCATION
38	3e−05	27 / 564	GSE	GOZGIT_ESR1_TARGETS_DN
39	3e−05	8 / 61	GSE	REACTOME_TELOMERE_MAINTENANCE
40	3e−05	17 / 269	GSE	HELLER_HDAC_TARGETS_DN



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	2e−06	5 / 12	leukocyte chemotaxis
2	3e−06	39 / 885	positive regulation of transcription from RNA polymerase II promoter
3	4e−05	59 / 1764	regulation of transcription, DNA−templated
4	5e−05	56 / 1655	transcription, DNA−templated
5	9e−05	16 / 264	positive regulation of GTPase activity
6	1e−04	5 / 25	antibacterial humoral response
7	2e−04	12 / 169	cell migration
8	3e−04	4 / 17	regulation of cell size
9	3e−04	23 / 520	positive regulation of transcription, DNA−templated
10	6e−04	6 / 52	positive regulation of signal transduction
11	8e−04	22 / 521	transcription from RNA polymerase II promoter
12	1e−03	8 / 106	regulation of small GTPase mediated signal transduction
13	2e−03	6 / 64	regulation of GTPase activity
14	2e−03	12 / 223	angiogenesis
15	2e−03	3 / 14	innate immune response in mucosa

Cancer

Rank	p−value	#in/all	Geneset
1	1e−16	35 / 317	SPANG_BCL6−index2
2	1e−06	27 / 480	Lembcke_Colonic Inflammation
3	1e−03	7 / 80	PanCan_JAK−ST_geneset_nanostring
4	4e−03	10 / 186	SPANG_LPS−index2
5	1e−02	6 / 96	PanCan_TXmisReg_geneset_nanostring
6	1e−02	1 / 14	LIU_COMMON_CANCER_GENES
7	2e−02	0 / 14	LIU_PROSTATE_CANCER_DN
8	2e−02	2 / 12	GENTLES_modul12
9	3e−02	6 / 113	PanCan_Driver_Gene_geneset_nanostring
10	3e−02	2 / 13	BENTINK_e2f3.1
11	3e−02	2 / 14	GUSTAFSON_PI3K_UP
12	3e−02	2 / 14	BENTINK_src.10
13	4e−02	3 / 36	ZHANG_MM up
14	1e−01	1 / 6	ZHANG_MGUS up
15	2e−01	6 / 187	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	8e−05	8 / 70	nucleosome
2	1e−02	18 / 494	endosome
3	1e−02	3 / 24	stereocilium
4	2e−02	4 / 48	ficolin−1−rich granule membrane
5	2e−02	92 / 3805	cytosol
6	3e−02	4 / 57	cytoplasmic ribonucleoprotein granule
7	3e−02	3 / 34	peroxisomal matrix
8	3e−02	12 / 324	chromosome
9	3e−02	2 / 14	filopodium membrane
10	4e−02	4 / 62	extrinsic component of cytoplasmic side of plasma membrane
11	4e−02	4 / 62	filopodium
12	5e−02	7 / 163	transcription factor complex
13	5e−02	2 / 18	phagocytic cup
14	6e−02	76 / 3210	plasma membrane
15	6e−02	2 / 20	lamellipodium membrane

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	12 / 184	Chr 18
2	3e−02	18 / 556	Chr X
3	4e−02	21 / 689	Chr 3
4	5e−02	18 / 585	Chr 7
5	5e−02	20 / 669	Chr 6
6	7e−02	23 / 833	Chr 19
7	8e−02	12 / 382	Chr 15
8	3e−01	10 / 403	Chr 14
9	5e−01	27 / 1325	Chr 1
10	5e−01	7 / 333	Chr 22
11	5e−01	10 / 490	Chr 10
12	5e−01	3 / 139	Chr 21
13	6e−01	15 / 756	Chr 11
14	7e−01	10 / 548	Chr 16
15	8e−01	8 / 492	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−12	83 / 1930	Fetal_TssA
2	7e−09	64 / 1535	Bcells peripheral blood_8_ZNF_Rpts
3	1e−08	211 / 8406	Bcells peripheral blood_2_TssAFlnk
4	1e−08	105 / 3184	monocytes peripheral blood_12_EnhBiv
5	1e−08	38 / 693	Bcells peripheral blood_3_TxFlnk
6	2e−08	80 / 2197	monocytes peripheral blood_11_BivFlnk
7	3e−08	117 / 3767	Bcells peripheral blood_6_EnhG
8	6e−08	126 / 4214	monocytes peripheral blood_15_Quies
9	1e−07	100 / 3106	Quies1_Colon
10	1e−07	41 / 847	Fetal_TssP
11	2e−07	79 / 2269	9_ReprPCWk_Neuronal_Progenitor
12	3e−07	77 / 2203	EnhA_Colon
13	7e−07	225 / 9544	HSC_2_TssAFlnk
14	7e−07	80 / 2374	9_ReprPCWk_Fibroblasts
15	9e−07	175 / 6791	7_Enh_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−05	27 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	7e−05	43 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
3	2e−03	3 / 13	Vilar_hypermutated−in−CRC
4	1e−02	17 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
5	2e−02	47 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
6	3e−02	29 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
7	3e−02	11 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	3e−02	10 / 255	Kosinski_top−crypt−long−list
9	4e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
10	4e−02	17 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	5e−02	12 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
12	5e−02	2 / 18	Boland_CRC−MSI−A6−A10
13	6e−02	13 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
14	6e−02	7 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
15	7e−02	31 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	13 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	0.006	6 / 82	laffaire_hypermeth_LGG_vs_control
3	0.007	5 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
4	0.008	7 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	0.009	8 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	0.009	17 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
7	0.011	3 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
8	0.011	11 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
9	0.013	30 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	0.017	7 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
11	0.018	4 / 50	Christensen_hypomethylated_in_primary_glioblastoma
12	0.027	2 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
13	0.027	2 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma
14	0.027	2 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
15	0.027	2 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−09	22 / 234	HOLLMANN_APOPTOSIS_VIA_CD40_DN
2	2e−08	16 / 139	BROCKE_APOPTOSIS_REVERSED_BY_IL6
3	2e−07	19 / 227	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP
4	2e−07	12 / 90	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
5	3e−07	20 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
6	2e−06	9 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
7	2e−06	25 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
8	5e−06	9 / 64	GEORGANTAS_HSC_MARKERS
9	6e−06	7 / 36	REACTOME_PACKAGING_OF_TELOMERE_ENDS
10	6e−06	19 / 290	ODONNELL_TFRC_TARGETS_UP
11	7e−06	9 / 67	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
12	1e−05	14 / 175	OKUMURA_INFLAMMATORY_RESPONSE_LPS
13	1e−05	10 / 90	BASSO_CD40_SIGNALING_UP
14	1e−05	17 / 251	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
15	2e−05	7 / 42	REACTOME_RNA_POL_I_PROMOTER_OPENING

HM

Rank	p−value	#in/all	Geneset
1	6e−04	12 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	2e−03	7 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	2e−03	11 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	2e−03	10 / 170	HALLMARK_IL2_STAT5_SIGNALING
5	5e−03	10 / 191	HALLMARK_P53_PATHWAY
6	9e−03	9 / 176	HALLMARK_ALLOGRAFT_REJECTION
7	1e−02	4 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	2e−02	8 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	2e−02	7 / 141	HALLMARK_UV_RESPONSE_DN
10	4e−02	8 / 193	HALLMARK_HEME_METABOLISM
11	1e−01	5 / 139	HALLMARK_FATTY_ACID_METABOLISM
12	1e−01	2 / 34	HALLMARK_ANGIOGENESIS
13	2e−01	3 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
14	3e−01	2 / 51	HALLMARK_TGF_BETA_SIGNALING
15	3e−01	5 / 178	HALLMARK_COMPLEMENT

Immunome

Rank	p−value	#in/all	Geneset
1	8e−07	10 / 67	Angelova_immune−metagene−T−cells
2	2e−03	3 / 13	Angelova_immune−metagene−activated_B−cells
3	2e−03	3 / 13	Angelova_immune−metagene−immature_B−cells
4	3e−02	2 / 14	Angelova_immune−metagene−eosinophil
5	4e−02	2 / 16	Angelova_immune−metagene−Th17
6	5e−02	2 / 18	Angelova_immune−metagene−pDC
7	5e−02	2 / 19	Angelova_immune−metagene−iDC
8	6e−02	3 / 45	Angelova_immune−metagene−MDSC
9	8e−02	1 / 4	Angelova_CRC_MSS−neoantigens
10	1e−01	2 / 29	Angelova_immune−metagene−Th1
11	2e−01	1 / 10	Angelova_immune−metagene−TFH
12	2e−01	1 / 10	Angelova_CRC_immonoinhibitors
13	2e−01	1 / 11	Angelova_immune−metagene−macrophages
14	2e−01	1 / 12	Angelova_immune−metagene−memory_B−cells
15	2e−01	1 / 12	Angelova_immune−metagene−NK56_dim

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.07	2 / 22	DUMEAUX_Fasting enriched genes
2	0.17	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.18	1 / 10	DUMEAUX_Smoking literature genes up
4	0.36	4 / 150	Homuth_BMI−associated−genes_UP
5	0.36	1 / 22	DUMEAUX_High bmi enriched genes
6	0.72	1 / 62	DUMEAUX_Smoking enriched genes
7	0.80	3 / 210	Homuth_BMI−associated−genes_DN
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−17	21 / 85	Aukema_BCL2 DN_BCL6 UP
2	5e−15	11 / 18	WRIGHT_ABC UP
3	1e−12	8 / 10	Care_ABC UP
4	1e−10	15 / 85	Sha_DLBCL UP
5	5e−10	158 / 5404	HOPP_Strong_enhancer
6	6e−08	19 / 213	SPANG_IL21 DN
7	7e−08	17 / 173	Victora_Light zone signature
8	2e−07	4 / 4	WRIGHT_custom ABC−DLBCL UP
9	2e−07	24 / 353	SPANG_CD40 6hrs DN
10	9e−05	11 / 135	DAVE_BL−vs−DLBCL
11	9e−05	61 / 1894	HOPP_Poised_promoter
12	1e−04	35 / 906	SPANG_BCR DN
13	9e−04	3 / 10	MASCQUE_ABC UP
14	9e−04	4 / 22	DAVE_NFkB BL DN
15	2e−03	7 / 88	ROSOLOWSKI_green UP

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−06	6 / 24	Tirosh_B−cell specific genes−melanoma
2	1e−03	4 / 24	Tirosh_exhuastion−associated genes consitent across tumors
3	6e−03	6 / 83	TCGA_melanoma_immune_high
4	7e−03	11 / 230	Gerber_wt/wt_melanoma−cells−SpotC
5	2e−02	17 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	4e−02	1 / 2	Melanoma Epi−Enzyme Cluster 1
7	4e−02	2 / 16	Hugo_melanoma−all−LEF1_UP
8	4e−02	3 / 39	Tirosh_top50 correlated genes PC4
9	4e−02	3 / 39	Tirosh_melanoma specific genes
10	4e−02	2 / 17	Hugo_melanoma−all−MET_UP
11	8e−02	4 / 81	Tirosh_Genes in the MITF program
12	1e−01	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
13	1e−01	1 / 5	Joensson_Melanoma Proliferative subtype
14	1e−01	7 / 204	Landsberg_dedifferentiation_down
15	1e−01	6 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	3e−06	57 / 1541	DNA binding
2	3e−04	6 / 46	SH3/SH2 adaptor activity
3	7e−04	8 / 96	SH3 domain binding
4	7e−04	11 / 172	transcription corepressor activity
5	8e−04	12 / 202	GTPase activator activity
6	2e−03	6 / 65	protein phosphatase binding
7	4e−03	8 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
8	4e−03	18 / 450	sequence−specific DNA binding
9	8e−03	25 / 741	DNA binding transcription factor activity
10	8e−03	11 / 234	transcriptional activator activity, RNA polymerase II proximal promoter sequer
11	8e−03	67 / 2529	metal ion binding
12	1e−02	24 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindir
13	1e−02	9 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
14	1e−02	15 / 393	molecular_function
15	2e−02	2 / 10	dipeptidase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	7 / 88	hsa−miR−600
2	0.005	12 / 251	hsa−let−7g
3	0.006	15 / 361	hsa−miR−130b
4	0.011	14 / 350	hsa−miR−424
5	0.012	9 / 185	hsa−miR−182
6	0.013	2 / 9	hsa−miR−887
7	0.015	3 / 26	hsa−miR−1292
8	0.015	11 / 257	hsa−let−7i
9	0.016	7 / 130	hsa−miR−96
10	0.017	15 / 404	hsa−miR−103
11	0.017	15 / 405	hsa−miR−107
12	0.017	14 / 369	hsa−miR−15b
13	0.017	14 / 369	hsa−miR−130a
14	0.018	13 / 336	hsa−miR−519d
15	0.020	3 / 29	hsa−miR−1269

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.05	3 / 41	Scicluna_DN
2	0.29	4 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.31	1 / 18	Scicluna_UP
4	0.32	2 / 57	Burnham_viral_UP
5	0.32	2 / 57	Burnham_day1_vs_5_UP
6	0.49	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	0.62	1 / 48	Burnham_cap_fp_vs_con_DN
8	0.62	1 / 48	Burnham_viral_DN
9	0.65	1 / 52	Burnham_day1_vs_5_DN
10	0.67	1 / 54	Burnham_timecourse
11	0.68	1 / 56	Burnham_sep_vs_con_DN
12	0.71	2 / 122	Terre_IMS_influenza_meta_signature
13	0.75	1 / 68	Burnham_sep_vs_con_UP
14	0.76	1 / 71	Burnham_cap_fp_vs_con_UP
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−07	9 / 42	Chaussabel_1,3_B−cells
2	8e−07	16 / 182	WIRTH_post GC B−cells
3	1e−04	14 / 218	WIRTH_pre+post GC B−cells
4	1e−03	7 / 81	Chaussabel_1,2_Platelets
5	2e−03	5 / 45	VAQUERIZAS_Placenta_TF
6	3e−03	4 / 30	VAQUERIZAS_Smooth muscle_TF
7	3e−03	4 / 30	VAQUERIZAS_Fetal lung_TF
8	5e−03	19 / 496	PROTEINATLAS_spleen
9	6e−03	17 / 429	PROTEINATLAS_liver
10	8e−03	5 / 62	VAQUERIZAS_Lung_TF
11	1e−02	3 / 24	VAQUERIZAS_Pituitary_TF
12	1e−02	4 / 45	VAQUERIZAS_Whole brain_TF
13	1e−02	3 / 25	VAQUERIZAS_Adrenal cortex_TF
14	2e−02	4 / 49	VAQUERIZAS_Uterus_TF
15	2e−02	3 / 30	VAQUERIZAS_Lymph node_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	1e−05	73 / 2254	ICGC_BatfPcr1_targets
2	2e−05	57 / 1636	ICGC_Bcl11_targets
3	3e−04	60 / 1941	ICGC_Bcl3_targets
4	4e−03	84 / 3213	ICGC_Pu1_targets
5	6e−03	33 / 1041	ICGC_P300_targets
6	1e−02	43 / 1508	ICGC_Mef2_targets
7	1e−02	76 / 2994	ICGC_Zeb1_targets
8	2e−02	85 / 3435	ICGC_Ebfsc137065_targets
9	3e−02	72 / 2899	ICGC_Nfatc1_targets
10	4e−02	82 / 3420	ICGC_Bclaf101388_targets
11	4e−02	58 / 2321	ICGC_Rad21_targets
12	4e−02	98 / 4212	ICGC_Pol2_targets
13	5e−02	89 / 3796	ICGC_Nficsc81335_targets
14	6e−02	81 / 3451	ICGC_Atf2_targets
15	7e−02	87 / 3769	ICGC_Pmlsc71910_targets

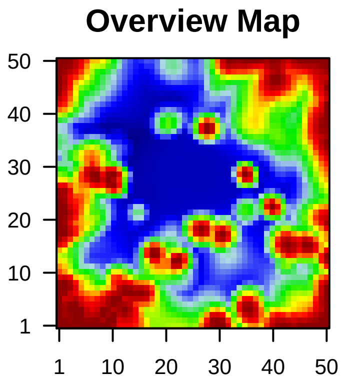
Overexpression Spots

Spot Summary: W

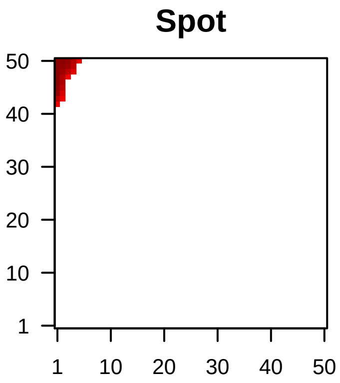
metagenes = 25
genes = 503

<r> metagenes = 0.9
<r> genes = 0.32
beta: r2= 11.05 / log p= −Inf

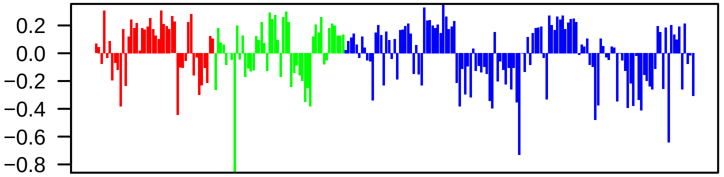
samples with spot = 37 (16.7 %)
mBL : 10 (22.7 %)
intermediate : 10 (20.8 %)
non−mBL : 17 (13.2 %)



Overview Map



Spot

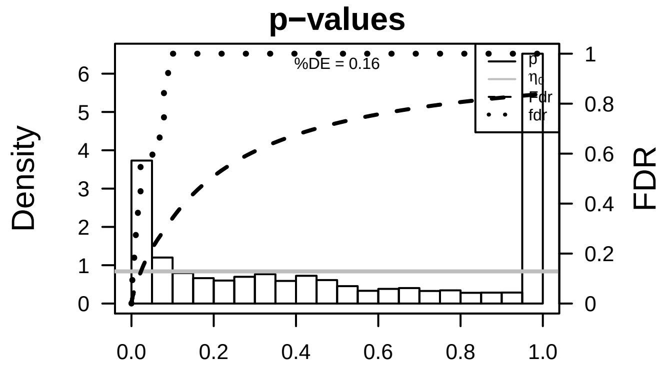


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	210360_s_at	1.7	−1.07	0.48	MTSS1	MTSS1, I−BAR domain containing [Source:HGNC Symbol;Ac
2	212389_at	1.62	−1.05	0.64	SBF1	SET binding factor 1 [Source:HGNC Symbol;Acc:HGNC:105
3	207686_s_at	1.62	−1.44	0.61	CASP8	caspase 8 [Source:HGNC Symbol;Acc:HGNC:1509]
4	203293_s_at	1.51	−1.49	0.53	LMAN1	lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC
5	218811_at	1.49	−1.6	0.62	ORAI2	ORAI calcium release−activated calcium modulator 2 [Source
6	209664_x_at	1.48	−1.43	0.37	NFATC1	nuclear factor of activated T cells 1 [Source:HGNC Symbol;A
7	211708_s_at	1.43	−1.2	0.59	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
8	203294_s_at	1.4	−1.25	0.58	LMAN1	lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC
9	214971_s_at	1.4	−1.95	0.77	ST6GAL1	ST6 beta−galactoside alpha−2,6−sialyltransferase 1 [Source:
10	200831_s_at	1.39	−1.42	0.38	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
11	211162_x_at	1.39	−1.05	0.56	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
12	215050_x_at	1.36	−1.7	0.49	MAPKAPK2	mitogen−activated protein kinase−activated protein kinase 2 [
13	213562_s_at	1.35	−1.44	0.57	SQLE	squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127
14	212497_at	1.34	−0.93	0.55		
15	203826_s_at	1.32	−0.98	0.22	PITPNM1	phosphatidylinositol transfer protein membrane associated 1 [
16	216986_s_at	1.32	−1.21	0.49	IRF4	interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGN
17	204429_s_at	1.31	−2.03	0.44	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
18	208653_s_at	1.3	−1.11	0.53	CD164	CD164 molecule [Source:HGNC Symbol;Acc:HGNC:1632]
19	201718_s_at	1.29	−1.09	0.3	EPB41L2	erythrocyte membrane protein band 4.1 like 2 [Source:HGNC
20	216734_s_at	1.29	−1.59	0.43	CXCR5	C−X−C motif chemokine receptor 5 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−83	105 / 282	Gliom	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	4e−53	299 / 4261	Lymp	HOPP_Txn_transition
3	2e−52	60 / 136	Refer	Chaussabel_2,9_Cytosceleton
4	2e−48	86 / 372	GSE	SENESE_HDAC1_TARGETS_UP
5	2e−47	334 / 5529	Lymp	HOPP_Txn_elongation
6	2e−42	83 / 405	GSE	SENESE_HDAC3_TARGETS_UP
7	7e−31	66 / 355	Refer	WIRTH_Immune system
8	1e−27	294 / 5404	Lymp	HOPP_Strong_enhancer
9	2e−22	55 / 344	GSE	THUM_SYSTOLIC_HEART_FAILURE_UP
10	2e−21	114 / 1338	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	1e−20	295 / 5908	Lymp	HOPP_Active_promoter
12	2e−20	219 / 3805	CC	cytosol
13	3e−20	309 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
14	7e−20	67 / 564	GSE	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
15	4e−19	53 / 376	GSE	GARY_CD5_TARGETS_UP
16	2e−17	70 / 678	Refer	PROTEINATLAS_lymph node
17	2e−16	114 / 1550	GSE	PILON_KLF1_TARGETS_DN
18	2e−15	120 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
19	2e−15	24 / 92	GSE	SENESE_HDAC2_TARGETS_UP
20	4e−15	83 / 989	Refer	PROTEINATLAS_tonsil
21	4e−14	97 / 1312	GSE	PUJANA_ATM_PCC_NETWORK
22	5e−14	28 / 146	GSE	ELVIDGE_HYPOXIA_DN
23	8e−14	234 / 4701	CC	cytoplasm
24	1e−13	52 / 485	GSE	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
25	1e−13	106 / 1527	GSE	PUJANA_BRCA1_PCC_NETWORK
26	2e−13	56 / 560	GSE	MARTINEZ_RB1_TARGETS_UP
27	2e−13	31 / 189	GSE	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
28	2e−12	47 / 439	GSE	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
29	5e−12	69 / 848	Refer	PROTEINATLAS_adrenal gland
30	5e−12	31 / 213	GSE	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
31	7e−12	23 / 118	GSE	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP
32	8e−12	35 / 272	GSE	LIU_SOX4_TARGETS_DN
33	1e−11	332 / 7864	MF	protein binding
34	1e−11	185 / 3564	TF	ICGC_Taf1_targets
35	1e−11	66 / 809	Refer	PROTEINATLAS_fallopian tube
36	3e−11	221 / 4579	CC	nucleus
37	3e−11	17 / 65	GSE	FALVELLA_SMOKERS_WITH_LUNG_CANCER
38	3e−11	60 / 708	Refer	PROTEINATLAS_thyroid gland
39	3e−11	13 / 34	GSE	LOPEZ_TRANSLATION_VIA_FN1_SIGNALING
40	5e−11	259 / 5682	Lymp	HOPP_Weak_promoter



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	4 / 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	2e−20	219 / 3805	cytosol
2	8e−14	234 / 4701	cytoplasm
3	3e−11	221 / 4579	nucleus
4	2e−09	137 / 2541	nucleoplasm
5	1e−07	40 / 479	Golgi membrane
6	2e−07	36 / 416	macromolecular complex
7	2e−07	62 / 938	Golgi apparatus
8	3e−06	21 / 196	nuclear membrane
9	4e−05	27 / 345	focal adhesion
10	7e−05	36 / 537	perinuclear region of cytoplasm
11	9e−05	34 / 503	cytoplasmic vesicle
12	1e−04	9 / 57	cytoplasmic ribonucleoprotein granule
13	1e−04	23 / 292	microtubule organizing center
14	3e−04	24 / 326	nuclear speck
15	3e−04	4 / 11	npBAF complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−20	309 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	2e−15	120 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
3	7e−08	70 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
4	7e−07	79 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	2e−06	69 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
6	1e−05	67 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	8e−05	50 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	1e−03	46 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
9	9e−03	43 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	2e−02	27 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
11	3e−02	43 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
12	8e−02	2 / 14	TCGA_Mutated−in−CRC_hypermutated
13	9e−02	2 / 15	TCGA−CRC_less−agressive−disease−markers
14	1e−01	1 / 4	Juehling−MSI−enriched−in−8−to−9
15	1e−01	23 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	4e−07	21 / 173	HALLMARK_MITOTIC_SPINDLE
2	5e−07	15 / 94	HALLMARK_PROTEIN_SECRETION
3	5e−07	22 / 192	HALLMARK_MTORC1_SIGNALING
4	3e−05	19 / 195	HALLMARK_G2M_CHECKPOINT
5	1e−04	9 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	9e−04	11 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e−03	10 / 96	HALLMARK_ANDROGEN_RESPONSE
8	2e−03	13 / 149	HALLMARK_UV_RESPONSE_UP
9	5e−03	12 / 150	HALLMARK_APOPTOSIS
10	6e−03	13 / 174	HALLMARK_APICAL_JUNCTION
11	2e−02	8 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	6e−02	10 / 170	HALLMARK_IL2_STAT5_SIGNALING
13	7e−02	3 / 29	HALLMARK_NOTCH_SIGNALING
14	1e−01	10 / 187	HALLMARK_E2F_TARGETS
15	1e−01	8 / 141	HALLMARK_UV_RESPONSE_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−53	299 / 4261	HOPP_Txn_transition
2	2e−47	334 / 5529	HOPP_Txn_elongation
3	1e−27	294 / 5404	HOPP_Strong_enhancer
4	1e−20	295 / 5908	HOPP_Active_promoter
5	5e−11	259 / 5682	HOPP_Weak_promoter
6	1e−08	35 / 353	SPANG_CD40 6hrs DN
7	5e−08	17 / 102	ROSOLOWSKI_blue total
8	3e−06	22 / 213	SPANG_IL21 DN
9	3e−06	57 / 906	SPANG_BCR DN
10	2e−05	9 / 45	Monti_BCR_cluster
11	2e−04	13 / 121	ROSOLOWSKI_green total
12	4e−04	52 / 955	SPANG_BCR UP
13	3e−03	175 / 4357	HOPP_Weak_txn
14	6e−03	16 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	1e−02	3 / 14	YAMANE_AICDA_targets_recruited

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−08	40 / 448	hsa−miR−20b
2	2e−08	35 / 364	hsa−miR−548n
3	7e−08	21 / 157	hsa−miR−206
4	1e−07	20 / 148	hsa−miR−1
5	2e−07	28 / 275	hsa−miR−590−3p
6	2e−07	18 / 127	hsa−miR−1297
7	3e−07	20 / 157	hsa−miR−34b
8	4e−07	35 / 407	hsa−miR−106a
9	4e−07	28 / 285	hsa−miR−548b−5p
10	4e−07	36 / 427	hsa−miR−17
11	6e−07	22 / 194	hsa−miR−124
12	8e−07	34 / 403	hsa−miR−106b
13	1e−06	27 / 284	hsa−miR−548d−5p
14	1e−06	26 / 267	hsa−miR−142−5p
15	2e−06	31 / 361	hsa−miR−130b

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	2e−08	43 / 507	protein phosphorylation
2	4e−07	40 / 502	protein transport
3	7e−07	9 / 32	regulation of cholesterol biosynthetic process
4	2e−06	42 / 576	phosphorylation
5	6e−06	10 / 51	retrograde transport, endosome to Golgi
6	1e−05	13 / 91	mRNA transport
7	1e−05	10 / 55	response to cytokine
8	1e−05	37 / 520	positive regulation of transcription, DNA−templated
9	2e−05	15 / 124	peptidyl−serine phosphorylation
10	3e−05	6 / 19	cortical actin cytoskeleton organization
11	3e−05	11 / 74	regulation of mitotic cell cycle
12	6e−05	52 / 885	positive regulation of transcription from RNA polymerase II promoter
13	7e−05	10 / 66	phosphatidylinositol biosynthetic process
14	7e−05	34 / 497	cell cycle
15	8e−05	18 / 190	vesicle−mediated transport

Chr

Rank	p−value	#in/all	Geneset
1	0.002	44 / 833	Chr 19
2	0.053	34 / 756	Chr 11
3	0.138	32 / 776	Chr 17
4	0.174	51 / 1325	Chr 1
5	0.253	26 / 669	Chr 6
6	0.264	15 / 369	Chr 20
7	0.328	6 / 139	Chr 21
8	0.377	30 / 832	Chr 2
9	0.384	15 / 403	Chr 14
10	0.427	7 / 184	Chr 18
11	0.582	23 / 700	Chr 12
12	0.601	19 / 585	Chr 7
13	0.656	15 / 480	Chr 4
14	0.690	10 / 333	Chr 22
15	0.718	13 / 437	Chr 8

Glioma

Rank	p−value	#in/all	Geneset
1	2e−83	105 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−09	87 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−08	91 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	3e−07	10 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
5	2e−03	35 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	6e−03	6 / 50	Vishal_subnetwork signature of survival in GBM
7	7e−03	11 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	2e−02	6 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	3e−02	6 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	4e−02	5 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	5e−02	6 / 78	Weller_LGG_A_vs_O_UP
12	5e−02	2 / 11	KIM amplified & overexpressed in LTS
13	9e−02	5 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
14	1e−01	6 / 99	GIEZELT_GBM_WT_up_VS_mut
15	1e−01	13 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	6 / 67	Angelova_immune−metagene−T−cells
2	0.06	4 / 45	Angelova_immune−metagene−MDSC
3	0.07	2 / 13	Angelova_immune−metagene−immature_B−cells
4	0.29	1 / 10	Angelova_immune−metagene−neutrophils
5	0.29	1 / 10	Angelova_immune−metagene−TFH
6	0.38	1 / 14	Angelova_immune−metagene−eosinophil
7	0.40	1 / 15	Angelova_immune−metagene−NK
8	0.44	1 / 17	Angelova_immune−metagene−central_memory_CD8
9	0.46	1 / 18	Angelova_immune−metagene−pDC
10	0.48	1 / 19	Angelova_immune−metagene−activated_CD8
11	0.48	1 / 19	Angelova_immune−metagene−iDC
12	0.76	1 / 42	Angelova_immune−metagene−TGD
13	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
14	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
15	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4

Melanoma

Rank	p−value	#in/all	Geneset
1	0.004	14 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
2	0.007	6 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
3	0.011	15 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.018	14 / 222	Gerber_wt/wt_melanoma−cells−SpotF
5	0.029	14 / 236	Gerber_wt/wt_group3−specific
6	0.030	25 / 497	Gerber_wt/wt_melanoma−cells−SpotD
7	0.041	3 / 23	Melanoma Epi−Enzyme Cluster 7
8	0.048	4 / 41	Tirosh_top50 correlated genes PC3
9	0.066	1 / 2	Melanoma Epi−Enzyme Cluster 1
10	0.069	4 / 46	Tirosh_top50 correlated genes PC5
11	0.073	4 / 47	Tirosh_G2/M phase specific genes
12	0.135	3 / 38	Tirosh_top50 correlated genes PC1
13	0.153	6 / 107	Tirosh_Exhaustion program in Mel75
14	0.184	3 / 44	Tirosh_top50 correlated genes PC2
15	0.193	2 / 24	Tirosh_B−cell specific genes−melanoma

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.08	10 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.09	8 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.27	3 / 54	Burnham_timecourse
4	0.30	3 / 57	Burnham_day1_vs_5_UP
5	0.48	2 / 48	Burnham_viral_DN
6	0.59	4 / 122	Terre_IMS_influenza_meta_signature
7	0.76	1 / 41	Scicluna_DN
8	0.90	1 / 68	Burnham_sep_vs_con_UP
9	0.91	1 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 56	Burnham_sep_vs_con_DN
11	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.00	0 / 57	Burnham_viral_UP
13	1.00	0 / 52	Burnham_day1_vs_5_DN
14	1.00	0 / 18	Scicluna_UP
15	1.00	0 / 37	Sweeney_viral_up

TF

Rank	p−value	#in/all	Geneset
1	1e−11	185 / 3564	ICGC_Taf1_targets
2	1e−09	161 / 3121	ICGC_Egr1_targets
3	1e−09	162 / 3150	ICGC_Creb1_targets
4	9e−09	183 / 3796	ICGC_Nficsc81335_targets
5	1e−08	183 / 3804	ICGC_Stat5_targets
6	3e−08	147 / 2899	ICGC_Nfatc1_targets
7	9e−08	178 / 3769	ICGC_Pmlsc71910_targets
8	9e−08	166 / 3451	ICGC_Atf2_targets
9	1e−07	164 / 3420	ICGC_Bclaf101388_targets
10	4e−07	69 / 1107	ICGC_Myc_targets
11	9e−07	171 / 3703	ICGC_Foxm1_targets
12	1e−06	168 / 3630	ICGC_Sp1_targets
13	2e−06	84 / 1508	ICGC_Mef2_targets
14	2e−06	183 / 4072	ICGC_Mta3_targets
15	2e−06	185 / 4131	ICGC_Tcf3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	2 / 2	GENTLES_modul8
2	0.001	4 / 15	GENTLES_modul2
3	0.004	11 / 130	PanCan_CC+Apop_geneset_nanostring
4	0.010	3 / 14	BENTINK_src.2
5	0.011	11 / 147	PanCan_MAPK_geneset_nanostring
6	0.015	10 / 134	PanCan_RAS_geneset_nanostring
7	0.022	18 / 317	SPANG_BCL6−index2
8	0.037	8 / 113	PanCan_Driver_Gene_geneset_nanostring
9	0.045	5 / 58	SHAUGHNESSY_MM high risk
10	0.051	2 / 11	LIU_PROSTATE_CANCER_UP
11	0.060	2 / 12	GENTLES_modul12
12	0.073	1 / 14	LIU_COMMON_CANCER_GENES
13	0.079	2 / 14	GENTLES_modul10
14	0.100	2 / 16	GENTLES_modul16
15	0.101	10 / 187	PanCan_PI3K_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−63	362 / 5716	Bcells peripheral blood_4_Tx
2	4e−59	351 / 5527	Tregulatory cells peripheral blood_4_Tx
3	1e−56	365 / 6099	HSC_4_Tx
4	2e−55	399 / 7420	Tcells peripheral blood_1_TssA
5	1e−54	352 / 5753	Tcells peripheral blood_4_Tx
6	4e−53	406 / 7833	Bcells peripheral blood_1_TssA
7	6e−53	349 / 5738	monocytes peripheral blood_4_Tx
8	8e−53	401 / 7635	monocytes peripheral blood_1_TssA
9	1e−52	308 / 4528	T CD8+ naive cells peripheral blood_4_Tx
10	3e−52	349 / 5766	natural killer cells peripheral blood_4_Tx
11	8e−52	278 / 3767	Bcells peripheral blood_6_EnhG
12	2e−49	407 / 8068	Thelper cells peripheral blood_1_TssA
13	1e−48	384 / 7165	Tx_Colon
14	9e−48	337 / 5601	Thelper cells peripheral blood_4_Tx
15	5e−47	267 / 3682	natural killer cells peripheral blood_6_EnhG

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−48	86 / 372	SENESE_HDAC1_TARGETS_UP
2	2e−42	83 / 405	SENESE_HDAC3_TARGETS_UP
3	2e−22	55 / 344	THUM_SYSTOLIC_HEART_FAILURE_UP
4	2e−21	114 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	7e−20	67 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
6	4e−19	53 / 376	GARY_CD5_TARGETS_UP
7	2e−16	114 / 1550	PILON_KLF1_TARGETS_DN
8	2e−15	24 / 92	SENESE_HDAC2_TARGETS_UP
9	4e−14	97 / 1312	PUJANA_ATM_PCC_NETWORK
10	5e−14	28 / 146	ELVIDGE_HYPOXIA_DN
11	1e−13	52 / 485	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
12	1e−13	106 / 1527	PUJANA_BRCA1_PCC_NETWORK
13	2e−13	56 / 560	MARTINEZ_RB1_TARGETS_UP
14	2e−13	31 / 189	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
15	2e−12	47 / 439	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	9e−05	19 / 210	Homuth_BMI−associated−genes_DN
2	4e−02	3 / 22	DUMEAUX_Fasting enriched genes
3	1e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	1e−01	8 / 150	Homuth_BMI−associated−genes_UP
5	4e−01	1 / 14	Huan_blood−pressure_SBP−signature
6	5e−01	1 / 22	DUMEAUX_High bmi enriched genes
7	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 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	1e−11	332 / 7864	protein binding
2	2e−09	89 / 1402	nucleotide binding
3	1e−08	29 / 256	cadherin binding
4	6e−08	75 / 1185	ATP binding
5	8e−08	32 / 331	protein serine/threonine kinase activity
6	7e−07	36 / 437	protein kinase activity
7	7e−07	30 / 328	chromatin binding
8	1e−06	77 / 1329	transferase activity
9	2e−06	42 / 573	kinase activity
10	2e−06	23 / 225	transcription coactivator activity
11	4e−06	11 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
12	1e−04	22 / 268	transcription factor binding
13	1e−04	19 / 214	GTPase activity
14	1e−04	9 / 58	cytoskeletal protein binding
15	1e−04	78 / 1541	DNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−52	60 / 136	Chaussabel_2,9_Cytosceleton
2	7e−31	66 / 355	WIRTH_Immune system
3	2e−17	70 / 678	PROTEINATLAS_lymph node
4	4e−15	83 / 989	PROTEINATLAS_tonsil
5	5e−12	69 / 848	PROTEINATLAS_adrenal gland
6	1e−11	66 / 809	PROTEINATLAS_fallopian tube
7	3e−11	60 / 708	PROTEINATLAS_thyroid gland
8	5e−11	60 / 716	PROTEINATLAS_epididymis
9	1e−10	62 / 770	PROTEINATLAS_endometrium
10	3e−10	75 / 1048	PROTEINATLAS_rectum
11	4e−10	80 / 1161	PROTEINATLAS_colon
12	4e−10	46 / 496	PROTEINATLAS_spleen
13	5e−10	73 / 1022	PROTEINATLAS_placenta
14	1e−09	63 / 840	PROTEINATLAS_urinary bladder
15	2e−09	73 / 1048	PROTEINATLAS_gallbladder

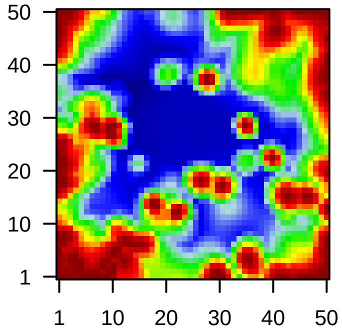
Overexpression Spots

Spot Summary: X

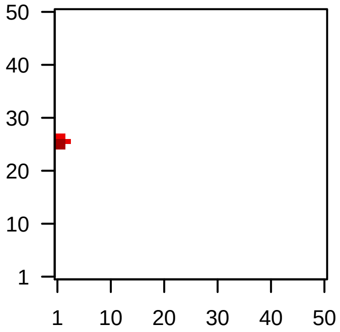
metagenes = 7
genes = 92

<r> metagenes = 0.99
<r> genes = 0.19
beta: r2= 3.66 / log p= −Inf

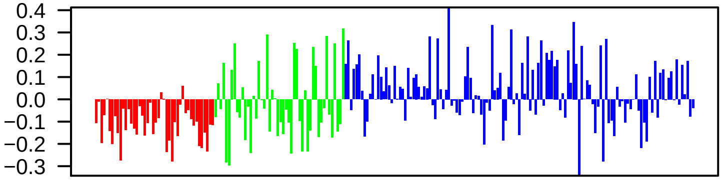
samples with spot = 24 (10.9 %)
intermediate : 8 (16.7 %)
non−mBL : 16 (12.4 %)



Overview Map



Spot

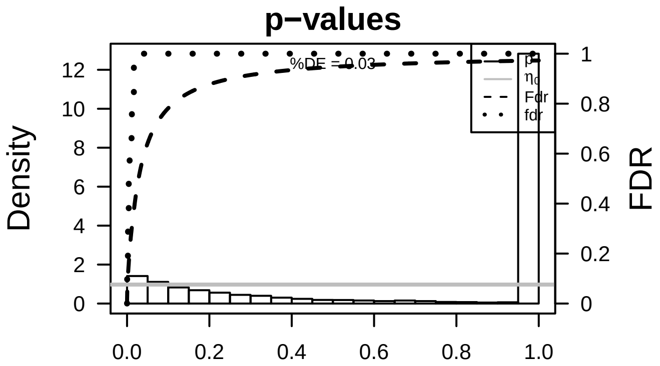


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	203440_at	2.45	−0.91	0.27	CDH2	cadherin 2 [Source:HGNC Symbol;Acc:HGNC:1759]
2	213110_s_at	2.3	−0.71	0.38	COL4A5	collagen type IV alpha 5 chain [Source:HGNC Symbol;Acc:H
3	210889_s_at	2.27	−1.18	0.32	FCGR2B	Fc fragment of IgG receptor IIb [Source:HGNC Symbol;Acc:H
4	203684_s_at	2.03	−1.19	0.55	BCL2	BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC
5	207005_s_at	1.88	−1.01	0.42	BCL2	BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC
6	206983_at	1.72	−1.12	0.5		
7	203695_s_at	1.63	−1.51	0.3	GSDME	gasdermin E [Source:HGNC Symbol;Acc:HGNC:2810]
8	207059_at	1.63	−0.78	0.42	PAX9	paired box 9 [Source:HGNC Symbol;Acc:HGNC:8623]
9	210355_at	1.58	−0.84	0.29	PTHLH	parathyroid hormone like hormone [Source:HGNC Symbol;Ac
10	209795_at	1.57	−1.39	0.49	CD69	CD69 molecule [Source:HGNC Symbol;Acc:HGNC:1694]
11	205139_s_at	1.49	−0.66	0.43	UST	uronyl 2−sulfotransferase [Source:HGNC Symbol;Acc:HGNC:
12	215537_x_at	1.46	−0.78	0.34	DDAH2	dimethylarginine dimethylaminohydrolase 2 [Source:HGNC S
13	219748_at	1.46	−0.98	0.46	TREML2	triggering receptor expressed on myeloid cells like 2 [Source:
14	205466_s_at	1.46	−1.05	0.31	HS3ST1	heparan sulfate−glucosamine 3−sulfotransferase 1 [Source:H
15	203220_s_at	1.41	−0.78	0.37	TLE1	transducin like enhancer of split 1 [Source:HGNC Symbol;Ac
16	205841_at	1.41	−0.89	0.52	JAK2	Janus kinase 2 [Source:HGNC Symbol;Acc:HGNC:6192]
17	210643_at	1.37	−1.36	0.39	TNFSF11	TNF superfamily member 11 [Source:HGNC Symbol;Acc:HG
18	207112_s_at	1.35	−1.12	0.41	GAB1	GRB2 associated binding protein 1 [Source:HGNC Symbol;A
19	210162_s_at	1.34	−1.62	0.39	NFATC1	nuclear factor of activated T cells 1 [Source:HGNC Symbol;A
20	216399_s_at	1.3	−0.87	0.51	SCAPER	S−phase cyclin A associated protein in the ER [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−09	14 / 317	Canc	SPANG_BCL6−index2
2	5e−08	54 / 5404	Lymp	HOPP_Strong_enhancer
3	1e−07	7 / 68	GSEA	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY
4	4e−07	5 / 27	GSEA	SHIN_B_CELL_LYMPHOMA_CLUSTER_3
5	4e−07	8 / 121	GSEA	HUANG_GATA2_TARGETS_UP
6	1e−06	52 / 5529	Lymp	HOPP_Txn_elongation
7	2e−05	5 / 59	GSEA	PID_BCR_5PATHWAY
8	2e−05	3 / 10	GSEA	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_
9	2e−05	5 / 60	GSEA	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
10	3e−05	50 / 5682	Lymp	HOPP_Weak_promoter
11	3e−05	4 / 33	GSEA	PID_EPO_PATHWAY
12	3e−05	6 / 109	BP	animal organ morphogenesis
13	5e−05	9 / 300	GSEA	OSMAN_BLADDER_CANCER_DN
14	5e−05	15 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
15	6e−05	7 / 175	GSEA	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
16	7e−05	4 / 39	BP	B cell receptor signaling pathway
17	8e−05	7 / 184	Chr	Chr 18
18	9e−05	4 / 42	Refer	Chaussabel_1,3_B−cells
19	1e−04	4 / 43	GSEA	SIG_BCR_SIGNALING_PATHWAY
20	1e−04	5 / 83	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN
21	1e−04	4 / 46	GSEA	MARSON_FOXP3_TARGETS_DN
22	1e−04	3 / 18	BP	positive regulation of T cell activation
23	2e−04	3 / 19	GSEA	ZHANG_RESPONSE_TO_CANTHARIDIN_UP
24	2e−04	4 / 49	GSEA	PID_KIT_PATHWAY
25	2e−04	9 / 368	GSEA	ZHENG_BOUND_BY_FOXP3
26	2e−04	5 / 99	GSEA	PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP
27	2e−04	12 / 642	GSEA	CUI_TCF21_TARGETS_2_DN
28	3e−04	49 / 5908	Lymp	HOPP_Active_promoter
29	3e−04	4 / 57	GSEA	MORI_PRE_BI_LYMPHOCYTE_DN
30	3e−04	39 / 4261	Lymp	HOPP_Txn_transition
31	3e−04	8 / 303	miRN	hsa−miR−454
32	3e−04	2 / 5	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
33	4e−04	7 / 234	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_DN
34	4e−04	3 / 25	BP	endoderm development
35	5e−04	4 / 64	BP	regulation of GTPase activity
36	5e−04	14 / 906	Lymp	SPANG_BCR DN
37	5e−04	5 / 118	miRN	hsa−miR−548f
38	6e−04	7 / 252	GSEA	LU_AGING_BRAIN_UP
39	6e−04	5 / 121	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
40	7e−04	2 / 7	GSEA	MIKKELSEN_PLURIPOTENT_STATE_DN



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.02	3 / 107	HORVATH_aging_genes meth UP
2	1.00	0 / 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	

BP

Rank	p−value	#in/all	Geneset
1	3e−05	6 / 109	animal organ morphogenesis
2	7e−05	4 / 39	B cell receptor signaling pathway
3	1e−04	3 / 18	positive regulation of T cell activation
4	4e−04	3 / 25	endoderm development
5	5e−04	4 / 64	regulation of GTPase activity
6	1e−03	2 / 10	glutathione biosynthetic process
7	2e−03	2 / 11	axon regeneration
8	2e−03	2 / 11	intrinsic apoptotic signaling pathway in response to oxidative stress
9	2e−03	3 / 44	signal transduction by protein phosphorylation
10	2e−03	2 / 12	ectoderm development
11	2e−03	2 / 12	negative regulation of immune response
12	2e−03	2 / 13	developmental pigmentation
13	2e−03	2 / 13	establishment of endothelial barrier
14	2e−03	2 / 13	regulation of cytokine production
15	2e−03	7 / 324	cell proliferation

Cancer

Rank	p−value	#in/all	Geneset
1	2e−09	14 / 317	SPANG_BCL6−index2
2	2e−03	9 / 480	Lembcke_Colonic Inflammation
3	5e−02	3 / 147	PanCan_MAPK_geneset_nanostring
4	6e−02	2 / 72	PanCan_Wnt_geneset_nanostring
5	7e−02	1 / 12	GENTLES_modul12
6	8e−02	1 / 15	BEN−PORATH_UP
7	9e−02	3 / 186	SPANG_LPS−index2
8	9e−02	3 / 187	PanCan_PI3K_geneset_nanostring
9	1e−01	1 / 18	PanCan_Notch_geneset_nanostring
10	1e−01	2 / 96	PanCan_TXmisReg_geneset_nanostring
11	1e−01	2 / 113	PanCan_Driver_Gene_geneset_nanostring
12	2e−01	1 / 32	KUIPER_MM good survival
13	2e−01	0 / 14	LIU_COMMON_CANCER_GENES
14	2e−01	1 / 47	PanCan_TGF−B_geneset_nanostring
15	4e−01	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 73	cell−cell adherens junction
2	5e−03	2 / 19	Flemming body
3	5e−03	3 / 63	caveola
4	7e−03	32 / 3805	cytosol
5	2e−02	2 / 34	cortical actin cytoskeleton
6	2e−02	2 / 37	T−tubule
7	2e−02	4 / 179	external side of plasma membrane
8	2e−02	2 / 43	protein−DNA complex
9	3e−02	2 / 48	microvillus
10	5e−02	2 / 62	extrinsic component of cytoplasmic side of plasma membrane
11	5e−02	2 / 62	filopodium
12	5e−02	3 / 146	lamellipodium
13	6e−02	1 / 10	catenin complex
14	6e−02	1 / 10	CD40 receptor complex
15	6e−02	1 / 10	fascia adherens

Chr

Rank	p−value	#in/all	Geneset
1	8e−05	7 / 184	Chr 18
2	5e−02	7 / 585	Chr 7
3	1e−01	7 / 689	Chr 3
4	1e−01	7 / 700	Chr 12
5	1e−01	5 / 490	Chr 10
6	3e−01	5 / 669	Chr 6
7	3e−01	6 / 832	Chr 2
8	4e−01	2 / 242	Chr 13
9	5e−01	3 / 480	Chr 4
10	5e−01	3 / 492	Chr 9
11	6e−01	2 / 382	Chr 15
12	7e−01	2 / 403	Chr 14
13	7e−01	2 / 437	Chr 8
14	8e−01	3 / 756	Chr 11
15	8e−01	2 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−11	60 / 5716	Bcells peripheral blood_4_Tx
2	1e−08	45 / 3767	Bcells peripheral blood_6_EnhG
3	5e−08	56 / 5766	natural killer cells peripheral blood_4_Tx
4	5e−08	66 / 7833	Bcells peripheral blood_1_TssA
5	9e−08	68 / 8406	Bcells peripheral blood_2_TssAFlnk
6	1e−07	72 / 9544	HSC_2_TssAFlnk
7	7e−07	35 / 2792	EnhWk2_Colon
8	1e−06	62 / 7407	natural killer cells peripheral blood_5_TxWk
9	1e−06	56 / 6244	15_Quies_Fibroblasts
10	1e−06	16 / 693	Bcells peripheral blood_3_TxFlnk
11	2e−06	66 / 8370	natural killer cells peripheral blood_2_TssAFlnk
12	2e−06	60 / 7078	7_Enh_ESC_Mesoderm
13	2e−06	63 / 7751	natural killer cells peripheral blood_1_TssA
14	3e−06	62 / 7581	15_Quies_Melanocytes
15	6e−06	59 / 7078	Bcells peripheral blood_5_TxWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.007	4 / 132	Marisa_CRC−cluster−a
2	0.018	8 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	0.023	1 / 4	Juehling−MSI−enriched−in−8−to−9
4	0.032	16 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	0.034	1 / 6	Hewish_dMMR−secondary−mutations_Signal_transduction
6	0.034	1 / 6	Juehling_HNPCC−mutated−in−5
7	0.046	2 / 60	Marisa_CRC−cluster−g
8	0.056	10 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	0.061	1 / 11	KIM_MSI−in−CRC
10	0.067	3 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
11	0.077	1 / 14	TCGA_Mutated−in−CRC_hypermutated
12	0.087	1 / 16	Budinska_B_Lower crypt−like_UP
13	0.098	1 / 18	Boland_CRC−MSI−A6−A10
14	0.107	8 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
15	0.123	10 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a

Glioma

Rank	p−value	#in/all	Geneset
1	0.004	6 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	0.006	3 / 66	Weller_LGG_gradeII−vs−III_DOWN
3	0.009	12 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
4	0.010	5 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
5	0.017	1 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
6	0.023	8 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	0.028	2 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
8	0.043	2 / 58	Stuehler_Proteins_up_in_STS
9	0.048	2 / 62	GIEZELT_GBM_STS_down_VS_LTS
10	0.054	2 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
11	0.059	2 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
12	0.062	2 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
13	0.073	2 / 78	Weller_LGG_A_vs_O_UP
14	0.076	4 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
15	0.079	2 / 82	laffaire_hypermeth_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−07	7 / 68	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY
2	4e−07	5 / 27	SHIN_B_CELL_LYMPHOMA_CLUSTER_3
3	4e−07	8 / 121	HUANG_GATA2_TARGETS_UP
4	2e−05	5 / 59	PID_BCR_5PATHWAY
5	2e−05	3 / 10	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLACK_DN
6	2e−05	5 / 60	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
7	3e−05	4 / 33	PID_EPO_PATHWAY
8	5e−05	9 / 300	OSMAN_BLADDER_CANCER_DN
9	5e−05	15 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	6e−05	7 / 175	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
11	1e−04	4 / 43	SIG_BCR_SIGNALING_PATHWAY
12	1e−04	5 / 83	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN
13	1e−04	4 / 46	MARSON_FOXP3_TARGETS_DN
14	2e−04	3 / 19	ZHANG_RESPONSE_TO_CANTHARIDIN_UP
15	2e−04	4 / 49	PID_KIT_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	1e−03	5 / 141	HALLMARK_UV_RESPONSE_DN
3	2e−03	3 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	2e−03	4 / 96	HALLMARK_ANDROGEN_RESPONSE
5	3e−03	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	1e−02	4 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	2e−02	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	8e−02	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
9	9e−02	3 / 187	HALLMARK_INFLAMMATORY_RESPONSE
10	1e−01	2 / 94	HALLMARK_PROTEIN_SECRETION
11	1e−01	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	2e−01	1 / 29	HALLMARK_NOTCH_SIGNALING
13	2e−01	1 / 34	HALLMARK_APICAL_SURFACE
14	2e−01	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
15	3e−01	2 / 170	HALLMARK_IL2_STAT5_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.007	3 / 67	Angelova_immune−metagene−T−cells
2	0.082	1 / 15	Angelova_immune−metagene−NK
3	0.092	1 / 17	Angelova_immune−metagene−central_memory_CD8
4	0.103	1 / 19	Angelova_immune−metagene−iDC
5	0.113	1 / 21	Angelova_immune−metagene−central_memory_CD4
6	0.123	1 / 23	Angelova_immune−metagene−Treg
7	0.213	1 / 42	Angelova_immune−metagene−TGD
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 / 19	Angelova_immune−metagene−activated_CD8
11	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.000	0 / 25	Angelova_immune−metagene−DC
13	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
14	1.000	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.000	0 / 14	Angelova_immune−metagene−eosinophil

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	3 / 210	Homuth_BMI−associated−genes_DN
2	0.2	1 / 32	Marjolein_ageing−genes_DN
3	0.6	1 / 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 / 22	DUMEAUX_Fasting enriched genes
15	1.0	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−08	54 / 5404	HOPP_Strong_enhancer
2	1e−06	52 / 5529	HOPP_Txn_elongation
3	3e−05	50 / 5682	HOPP_Weak_promoter
4	3e−04	49 / 5908	HOPP_Active_promoter
5	3e−04	39 / 4261	HOPP_Txn_transition
6	5e−04	14 / 906	SPANG_BCR DN
7	9e−04	3 / 34	TARTE_B−cell signature
8	1e−03	39 / 4559	HOPP_Weak_enhancer
9	1e−03	4 / 85	Aukema_BCL2 DN_BCL6 UP
10	2e−03	37 / 4357	HOPP_Weak_txn
11	4e−03	7 / 353	SPANG_CD40 6hrs DN
12	1e−02	3 / 85	Sha_DLBCL UP
13	2e−02	5 / 263	SPANG_CD40 6hrs UP
14	3e−02	4 / 213	SPANG_IL21 DN
15	4e−02	4 / 227	SPANG_IL21 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.07	3 / 171	Landsberg_dedifferentiation_up
2	0.08	2 / 81	Tirosh_Genes in the MITF program
3	0.09	3 / 189	Tirosh_genes preferentially expressed by Tregs
4	0.12	2 / 107	Tirosh_Exhaustion program in Mel75
5	0.15	5 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	0.17	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
7	0.21	1 / 41	Tirosh_top50 correlated genes PC3
8	0.25	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
9	0.32	2 / 204	Landsberg_dedifferentiation_down
10	0.35	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
11	0.38	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
12	0.49	1 / 119	TCGA_melanoma_MITF_low
13	0.74	1 / 236	Gerber_wt/wt_group3−specific
14	0.80	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
15	1.00	0 / 17	Hugo_melanoma−all−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	0.001	2 / 10	peptide hormone receptor binding
2	0.002	4 / 88	histone binding
3	0.002	2 / 11	transmembrane receptor protein serine/threonine kinase activity
4	0.002	2 / 12	signal transducer, downstream of receptor, with serine/threonine kinase activi
5	0.002	3 / 46	SH3/SH2 adaptor activity
6	0.006	3 / 65	protein phosphatase binding
7	0.008	11 / 851	identical protein binding
8	0.009	2 / 26	transcriptional activator activity, RNA polymerase II distal enhancer sequence
9	0.011	23 / 2529	metal ion binding
10	0.012	2 / 29	sulfotransferase activity
11	0.013	2 / 30	tumor necrosis factor receptor binding
12	0.016	3 / 93	protease binding
13	0.020	4 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
14	0.020	8 / 601	zinc ion binding
15	0.027	2 / 45	SMAD binding

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	8 / 303	hsa−miR−454
2	5e−04	5 / 118	hsa−miR−548f
3	1e−03	4 / 78	hsa−miR−216a
4	1e−03	5 / 139	hsa−miR−548e
5	2e−03	5 / 149	hsa−miR−548a−3p
6	2e−03	4 / 89	hsa−miR−624
7	2e−03	7 / 312	hsa−miR−301b
8	2e−03	3 / 44	hsa−miR−552
9	3e−03	7 / 344	hsa−miR−19a
10	3e−03	7 / 344	hsa−miR−19b
11	3e−03	6 / 259	hsa−miR−18a
12	4e−03	4 / 115	hsa−miR−409−3p
13	5e−03	7 / 368	hsa−miR−301a
14	6e−03	4 / 126	hsa−miR−548o
15	8e−03	4 / 137	hsa−miR−190

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	2 / 37	Sweeney_viral_up
2	0.08	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.26	1 / 52	Burnham_day1_vs_5_DN
4	0.28	1 / 57	Burnham_viral_UP
5	0.32	1 / 68	Burnham_sep_vs_con_UP
6	0.50	1 / 122	Terre_IMS_influenza_meta_signature
7	1.00	0 / 56	Burnham_sep_vs_con_DN
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 48	Burnham_viral_DN
11	1.00	0 / 57	Burnham_day1_vs_5_UP
12	1.00	0 / 54	Burnham_timecourse
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−05	4 / 42	Chaussabel_1,3_B−cells
2	8e−03	3 / 72	Chaussabel_3,1_Interferon−inducible
3	8e−03	5 / 218	WIRTH_pre+post GC B−cells
4	5e−02	5 / 355	WIRTH_Immune system
5	5e−02	2 / 66	VAQUERIZAS_Whole blood_TF
6	7e−02	1 / 13	WIRTH_Prim. lymphoid organs
7	8e−02	1 / 14	WIRTH_Thalamus
8	8e−02	3 / 182	WIRTH_post GC B−cells
9	9e−02	1 / 16	VAQUERIZAS_Fetal liver_TF
10	9e−02	1 / 16	VAQUERIZAS_Fetal thyroid_TF
11	9e−02	7 / 678	PROTEINATLAS_lymph node
12	1e−01	1 / 18	JONGENEEL_Monocytes
13	1e−01	2 / 93	Chaussabel_1,4_Replication
14	1e−01	1 / 19	JONGENEEL_Adrenal Gland
15	1e−01	1 / 21	VAQUERIZAS_Tonsil_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.07	1 / 13	Alternative lengthening of telomeres
2	1.00	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	0.005	30 / 3420	ICGC_Bclaf101388_targets
2	0.005	13 / 1041	ICGC_P300_targets
3	0.006	30 / 3435	ICGC_Ebfsc137065_targets
4	0.006	19 / 1848	ICGC_Pbx3_targets
5	0.008	26 / 2899	ICGC_Nfatc1_targets
6	0.008	28 / 3213	ICGC_Pu1_targets
7	0.011	19 / 1941	ICGC_Bcl3_targets
8	0.012	31 / 3769	ICGC_Pmlsc71910_targets
9	0.012	21 / 2254	ICGC_BatfPcr1_targets
10	0.015	20 / 2150	ICGC_Irf4_targets
11	0.018	29 / 3564	ICGC_Taf1_targets
12	0.020	32 / 4072	ICGC_Mta3_targets
13	0.020	26 / 3121	ICGC_Egr1_targets
14	0.021	28 / 3451	ICGC_Atf2_targets
15	0.024	30 / 3804	ICGC_Stat5_targets

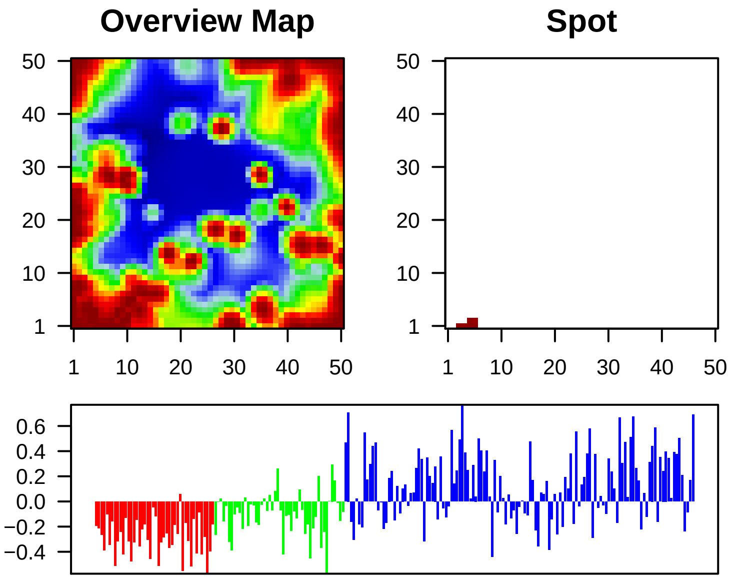
Overexpression Spots

Spot Summary: Y

metagenes = 6
genes = 120

<r> metagenes = 0.97
<r> genes = 0.42
beta: r2= 20.7 / log p= −Inf

samples with spot = 53 (24 %)
intermediate : 2 (4.2 %)
non−mBL : 51 (39.5 %)

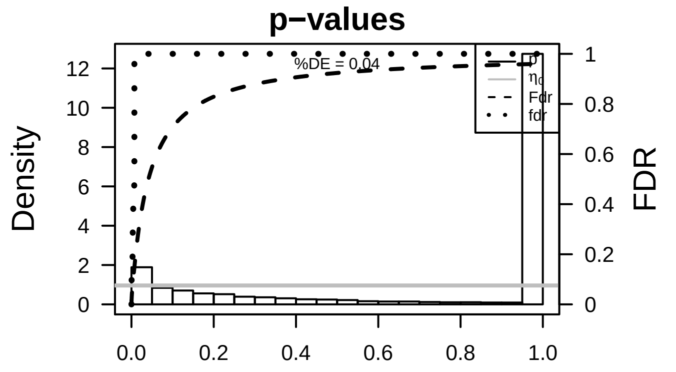


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205040_at	2.98	−1.17	0.61	ORM1	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
2	205041_s_at	2.9	−1.48	0.66	ORM1	orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498]
3	219316_s_at	2.46	−0.79	0.65	FLVCR2	feline leukemia virus subgroup C cellular receptor family mem
4	217546_at	2.25	−0.88	0.61		metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296
5	208168_s_at	2.22	−1.13	0.56	CHIT1	chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936]
6	204561_x_at	2.19	−1.95	0.41		APOC4−APOC2 readthrough (NMD candidate) [Source:HGN
7	221841_s_at	2.08	−1.17	0.52	KLF4	Kruppel like factor 4 [Source:HGNC Symbol;Acc:HGNC:6348
8	202357_s_at	1.99	−1.29	0.64	CFB	complement factor B [Source:HGNC Symbol;Acc:HGNC:103
9	212657_s_at	1.91	−0.87	0.5	IL1RN	interleukin 1 receptor antagonist [Source:HGNC Symbol;Acc:
10	221766_s_at	1.65	−0.98	0.51	FAM46A	family with sequence similarity 46 member A [Source:HGNC
11	203827_at	1.63	−0.75	0.56	WIPI1	WD repeat domain, phosphoinositide interacting 1 [Source:H
12	204745_x_at	1.58	−1.14	0.69	MT1G	metallothionein 1G [Source:HGNC Symbol;Acc:HGNC:7399]
13	222088_s_at	1.58	−1.2	0.62	SLC2A14	solute carrier family 2 member 14 [Source:HGNC Symbol;Ac
14	206631_at	1.55	−1.15	0.68	PTGER2	prostaglandin E receptor 2 [Source:HGNC Symbol;Acc:HGN
15	202497_x_at	1.54	−1.67	0.63	SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:
16	210222_s_at	1.54	−1.12	0.67	RTN1	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]
17	202827_s_at	1.53	−1.17	0.7	MMP14	matrix metallopeptidase 14 [Source:HGNC Symbol;Acc:HGN
18	206100_at	1.48	−1.24	0.55	CPM	carboxypeptidase M [Source:HGNC Symbol;Acc:HGNC:2311
19	202912_at	1.47	−1.35	0.43	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
20	211581_x_at	1.46	−1.1	0.57	LST1	leukocyte specific transcript 1 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−24	31 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	2e−19	27 / 404	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
3	4e−17	26 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
4	2e−14	20 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
5	3e−14	18 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
6	3e−13	17 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
7	5e−13	20 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
8	4e−12	14 / 154	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
9	6e−12	17 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
10	7e−12	11 / 78	Melan	Tirosh_expression higher in CAFs than in T−cells
11	4e−11	15 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
12	1e−10	14 / 202	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
13	2e−10	17 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
14	7e−10	21 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
15	9e−10	19 / 480	Canc	Lembcke_Colonic Inflammation
16	1e−09	16 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
17	2e−09	9 / 71	Melan	Tirosh_Macrophage specific genes−melanoma
18	2e−09	13 / 204	Refer	Chaussabel_3,2_Inflammation I
19	2e−09	12 / 166	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
20	3e−09	10 / 104	GSEA	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
21	4e−09	12 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
22	6e−09	8 / 57	GSEA	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
23	9e−09	11 / 150	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_U
24	1e−08	12 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
25	1e−08	19 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
26	1e−08	11 / 156	GSEA	PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN
27	3e−08	15 / 354	GSEA	RODWELL_AGING_KIDNEY_UP
28	3e−08	22 / 795	GSEA	NUYTTEN_EZH2_TARGETS_UP
29	3e−08	9 / 99	Refer	Chaussabel_1,5_Myeloid lineage
30	5e−08	7 / 49	GSEA	DAUER_STAT3_TARGETS_UP
31	7e−08	7 / 51	GSEA	PRAMOONJAGO_SOX4_TARGETS_UP
32	1e−07	12 / 242	Gliom	ScoV_0.5_Sturm_C1_IDH_DN
33	1e−07	9 / 117	GSEA	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
34	2e−07	13 / 294	GSEA	LEI_MYB_TARGETS
35	2e−07	8 / 86	GSEA	HINATA_NFKB_TARGETS_KERATINOCYTE_UP
36	2e−07	5 / 19	Immu	Angelova_immune−metagene−iDC
37	2e−07	10 / 163	GSEA	WIERENGA_STAT5A_TARGETS_UP
38	3e−07	15 / 422	GSEA	DELYS_THYROID_CANCER_UP
39	3e−07	10 / 166	GSEA	ELVIDGE_HYPOXIA_UP
40	3e−07	10 / 169	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF



Aging

Rank	p−value	#in/all	Geneset
1	0.3	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.5	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−07	14 / 403	neutrophil degranulation
2	2e−06	4 / 14	cellular response to zinc ion
3	2e−06	4 / 14	negative regulation of growth
4	4e−06	8 / 131	chemotaxis
5	6e−05	11 / 368	negative regulation of cell proliferation
6	8e−05	5 / 63	chemokine−mediated signaling pathway
7	1e−04	3 / 14	positive regulation of monocyte chemotaxis
8	1e−04	10 / 336	immune response
9	2e−04	3 / 17	response to metal ion
10	3e−04	13 / 595	G−protein coupled receptor signaling pathway
11	4e−04	3 / 21	fibrinolysis
12	5e−04	9 / 323	inflammatory response
13	8e−04	4 / 59	cell chemotaxis
14	9e−04	6 / 156	positive regulation of ERK1 and ERK2 cascade
15	9e−04	6 / 157	positive regulation of cell migration

Cancer

Rank	p−value	#in/all	Geneset
1	9e−10	19 / 480	Lembcke_Colonic Inflammation
2	2e−03	8 / 317	SPANG_BCL6−index2
3	2e−03	6 / 186	SPANG_LPS−index2
4	2e−02	0 / 14	LIU_PROSTATE_CANCER_DN
5	9e−02	1 / 13	GENTLES_modul18
6	9e−02	1 / 13	BENTINK_e2f3.1
7	1e−01	1 / 14	BENTINK_myc.1
8	1e−01	1 / 14	BENTINK_ras.6
9	1e−01	1 / 15	WANG_ER_UP
10	1e−01	1 / 15	GENTLES_modul4
11	1e−01	0 / 12	LIU_BREAST_CANCER
12	1e−01	2 / 96	PanCan_TXmisReg_geneset_nanostring
13	2e−01	2 / 113	PanCan_Driver_Gene_geneset_nanostring
14	7e−01	1 / 147	PanCan_MAPK_geneset_nanostring
15	8e−01	2 / 409	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	2e−05	6 / 77	specific granule membrane
2	7e−05	5 / 60	tertiary granule membrane
3	2e−04	6 / 116	blood microparticle
4	2e−04	5 / 74	secretory granule membrane
5	2e−04	19 / 1090	extracellular space
6	3e−04	39 / 3270	integral component of membrane
7	4e−04	4 / 50	tertiary granule lumen
8	6e−04	29 / 2239	extracellular exosome
9	8e−04	37 / 3210	plasma membrane
10	9e−04	18 / 1128	integral component of plasma membrane
11	3e−03	8 / 345	focal adhesion
12	5e−03	51 / 5339	membrane
13	5e−03	3 / 48	ficolin−1−rich granule membrane
14	7e−03	3 / 56	specific granule lumen
15	2e−02	3 / 77	cell

Chr

Rank	p−value	#in/all	Geneset
1	0.05	9 / 669	Chr 6
2	0.07	10 / 833	Chr 19
3	0.14	6 / 492	Chr 9
4	0.16	5 / 403	Chr 14
5	0.27	4 / 369	Chr 20
6	0.35	5 / 548	Chr 16
7	0.38	2 / 184	Chr 18
8	0.38	6 / 700	Chr 12
9	0.46	4 / 490	Chr 10
10	0.47	10 / 1325	Chr 1
11	0.48	6 / 776	Chr 17
12	0.55	6 / 832	Chr 2
13	0.76	3 / 554	Chr 5
14	0.82	2 / 437	Chr 8
15	0.83	1 / 242	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−06	29 / 1700	Bcells peripheral blood_11_BivFlnk
2	4e−06	39 / 2747	Bcells peripheral blood_12_EnhBiv
3	9e−06	36 / 2507	Mid_Frontal_Lobe_ReprPC
4	1e−05	13 / 432	monocytes peripheral blood_3_TxFlnk
5	2e−05	37 / 2724	Tcells peripheral blood_11_BivFlnk
6	3e−05	27 / 1676	Fetal_TxTrans
7	3e−05	24 / 1405	4_TxTrans_MSC_Adipocyte
8	9e−05	44 / 3724	Tcells peripheral blood_12_EnhBiv
9	2e−04	32 / 2405	Bcells peripheral blood_13_ReprPC
10	2e−04	25 / 1660	T CD8+ naive cells peripheral blood_12_EnhBiv
11	5e−04	36 / 3001	Bcells peripheral blood_14_ReprPCWk
12	7e−04	26 / 1930	Fetal_TssA
13	8e−04	20 / 1308	Mid_Frontal_Lobe_K9K27me3
14	8e−04	28 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
15	9e−04	37 / 3223	monocytes peripheral blood_6_EnhG

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−10	21 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e−06	8 / 132	Marisa_CRC−cluster−a
3	4e−05	10 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	4e−05	18 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
5	5e−05	10 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	2e−04	4 / 43	Marisa_CRC−cluster−f
7	1e−03	10 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	8e−03	5 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	9e−03	15 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
10	1e−02	7 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
11	2e−02	13 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	3e−02	2 / 38	Marisa_CRC−cluster−e
13	4e−02	5 / 255	Kosinski_top−crypt−long−list
14	4e−02	3 / 103	Marisa_CRC−cluster−b
15	6e−02	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	4e−17	26 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	3e−14	18 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	6e−12	17 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	1e−07	12 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	6e−06	7 / 99	GIEZELT_GBM_WT_up_VS_mut
6	1e−03	3 / 30	KIM prognostic signature LTS vs. STS
7	2e−03	2 / 9	Colman_survival_robust
8	2e−03	3 / 35	Colman_survival_associated
9	2e−03	3 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
10	3e−03	2 / 11	KIM amplified & overexpressed in LTS
11	3e−03	7 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
12	4e−03	3 / 45	Donson−innate immunity−associated with LTS in HGA
13	9e−03	4 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
14	9e−03	14 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
15	1e−02	3 / 64	cultured astroglia vs. in vivo astrocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−24	31 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	2e−19	27 / 404	RUTELLA_RESPONSE_TO_HGF_UP
3	2e−14	20 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
4	3e−13	17 / 223	MCLACHLAN_DENTAL_CARIES_UP
5	5e−13	20 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
6	4e−12	14 / 154	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
7	4e−11	15 / 219	MCLACHLAN_DENTAL_CARIES_DN
8	1e−10	14 / 202	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
9	2e−10	17 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	1e−09	16 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
11	2e−09	12 / 166	VERHAAK_AML_WITH_NPM1_MUTATED_UP
12	3e−09	10 / 104	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
13	4e−09	12 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	6e−09	8 / 57	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
15	9e−09	11 / 150	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−08	12 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	7e−06	9 / 187	HALLMARK_INFLAMMATORY_RESPONSE
3	7e−06	9 / 188	HALLMARK_HYPOXIA
4	1e−05	9 / 194	HALLMARK_KRAS_SIGNALING_UP
5	2e−05	8 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
6	4e−05	8 / 178	HALLMARK_COMPLEMENT
7	2e−04	7 / 170	HALLMARK_IL2_STAT5_SIGNALING
8	4e−04	7 / 191	HALLMARK_P53_PATHWAY
9	2e−03	4 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	2e−03	5 / 130	HALLMARK_COAGULATION
11	4e−03	5 / 150	HALLMARK_APOPTOSIS
12	1e−02	5 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	4e−02	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	7e−02	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	8e−02	3 / 141	HALLMARK_UV_RESPONSE_DN

Immunome

Rank	p−value	#in/all	Geneset
1	2e−07	5 / 19	Angelova_immune−metagene−iDC
2	1e−03	3 / 32	Angelova_immune−metagene−effector_memory_CD8
3	4e−02	2 / 42	Angelova_immune−metagene−TGD
4	4e−02	2 / 45	Angelova_immune−metagene−MDSC
5	7e−02	1 / 10	Angelova_immune−metagene−neutrophils
6	8e−02	1 / 11	Angelova_immune−metagene−macrophages
7	8e−02	2 / 67	Angelova_immune−metagene−T−cells
8	1e−01	1 / 18	Angelova_immune−metagene−pDC
9	2e−01	1 / 23	Angelova_immune−metagene−monocytes
10	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
11	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
12	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
13	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4
14	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
15	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	2 / 10	DUMEAUX_Smoking literature genes up
2	0.010	3 / 62	DUMEAUX_Smoking enriched genes
3	0.035	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	0.443	2 / 210	Homuth_BMI−associated−genes_DN
5	0.660	1 / 150	Homuth_BMI−associated−genes_UP
6	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.000	0 / 22	DUMEAUX_High bmi enriched genes
13	1.000	0 / 22	DUMEAUX_Fasting enriched genes
14	1.000	0 / 14	Huan_blood−pressure_SBP−signature
15	1.000	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 214	LENZ_Stromal signature 1
2	7e−05	6 / 97	ROSOLOWSKI_red total
3	2e−04	4 / 41	ROSOLOWSKI_blue DOWN
4	3e−04	38 / 3168	HOPP_Repressed
5	1e−03	4 / 62	Monti_Host_response_cluster
6	1e−03	25 / 1894	HOPP_Poised_promoter
7	3e−03	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
8	6e−03	4 / 102	ROSOLOWSKI_blue total
9	1e−02	3 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
10	1e−02	4 / 132	Subero_DLBCL_hyper_meth
11	2e−02	7 / 378	TARTE_Mature plasma cell signature
12	2e−02	2 / 33	Care_Extended T−cell
13	4e−02	2 / 47	Subero_B−ALL_hyper_meth
14	5e−02	47 / 5404	HOPP_Strong_enhancer
15	5e−02	1 / 7	CARO_OxPhos_vs_BCR_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	7e−12	11 / 78	Tirosh_expression higher in CAFs than in T−cells
2	2e−09	9 / 71	Tirosh_Macrophage specific genes−melanoma
3	3e−05	8 / 171	Landsberg_dedifferentiation_up
4	5e−05	13 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	5e−05	8 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	3e−04	5 / 85	Tirosh_AXL−signature
7	5e−02	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	8e−02	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
9	8e−02	2 / 65	Harbst_melanoma_highgrade_up
10	2e−01	3 / 204	Landsberg_dedifferentiation_down
11	2e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
12	2e−01	1 / 39	Tirosh_top50 correlated genes PC4
13	3e−01	1 / 41	Tirosh_top50 correlated genes PC3
14	4e−01	2 / 189	Tirosh_genes preferentially expressed by Tregs
15	4e−01	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 20	chemokine receptor activity
2	8e−04	8 / 276	GTP binding
3	8e−04	7 / 214	GTPase activity
4	2e−03	2 / 10	diacylglycerol binding
5	2e−03	2 / 10	glutamate binding
6	3e−03	2 / 11	glucose transmembrane transporter activity
7	3e−03	10 / 500	signal transducer activity
8	5e−03	9 / 447	oxidoreductase activity
9	5e−03	2 / 15	phosphatidic acid binding
10	6e−03	4 / 103	heme binding
11	6e−03	2 / 17	guanyl nucleotide binding
12	9e−03	4 / 113	iron ion binding
13	9e−03	3 / 60	oxidoreductase activity, acting on paired donors, with incorporation or reductio
14	1e−02	2 / 21	G−protein beta/gamma−subunit complex binding
15	1e−02	2 / 21	phosphatidylinositol phospholipase C activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	5 / 128	hsa−miR−200b
2	0.005	4 / 99	hsa−miR−543
3	0.011	4 / 123	hsa−miR−338−5p
4	0.011	4 / 123	hsa−miR−429
5	0.011	4 / 123	hsa−miR−200c
6	0.016	4 / 135	hsa−miR−7
7	0.026	2 / 35	hsa−miR−331−5p
8	0.027	2 / 36	hsa−miR−412
9	0.041	2 / 45	hsa−miR−891b
10	0.041	2 / 45	hsa−miR−431
11	0.042	3 / 108	hsa−miR−421
12	0.046	3 / 112	hsa−miR−383
13	0.049	3 / 115	hsa−miR−409−3p
14	0.049	2 / 50	hsa−miR−371−5p
15	0.052	4 / 197	hsa−miR−122

Pneumonia

Rank	p−value	#in/all	Geneset
1	5e−06	8 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	2e−04	6 / 122	Terre_IMS_influenza_meta_signature
3	7e−04	4 / 57	Burnham_viral_UP
4	6e−03	3 / 52	Burnham_day1_vs_5_DN
5	1e−02	3 / 71	Burnham_cap_fp_vs_con_UP
6	5e−02	2 / 48	Burnham_viral_DN
7	8e−02	2 / 68	Burnham_sep_vs_con_UP
8	1e−01	1 / 18	Scicluna_UP
9	2e−01	1 / 33	Sweeney_viral_dn
10	2e−01	1 / 37	Sweeney_viral_up
11	3e−01	1 / 57	Burnham_day1_vs_5_UP
12	1e+00	0 / 56	Burnham_sep_vs_con_DN
13	1e+00	0 / 48	Burnham_cap_fp_vs_con_DN
14	1e+00	0 / 54	Burnham_timecourse
15	1e+00	0 / 41	Scicluna_DN

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−09	13 / 204	Chaussabel_3,2_Inflammation I
2	3e−08	9 / 99	Chaussabel_1,5_Myeloid lineage
3	8e−06	7 / 102	WIRTH_EBV B−cells
4	1e−04	6 / 109	Chaussabel_2,6_Myeloid lineage
5	1e−03	4 / 62	VAQUERIZAS_Lung_TF
6	4e−03	3 / 45	VAQUERIZAS_Placenta_TF
7	9e−03	3 / 59	Chaussabel_2,10_Immune related cell surface molecules
8	1e−02	5 / 182	WIRTH_post GC B−cells
9	1e−02	2 / 22	VAQUERIZAS_Trachea_TF
10	1e−02	5 / 198	Chaussabel_3,3_Inflammation II
11	1e−02	3 / 72	Chaussabel_3,1_Interferon−inducible
12	2e−02	2 / 30	VAQUERIZAS_Fetal lung_TF
13	4e−02	1 / 6	VAQUERIZAS_Appendix_TF
14	7e−02	4 / 218	WIRTH_pre+post GC B−cells
15	9e−02	1 / 13	WIRTH_Sec. lymphoid organs

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.003	37 / 3435	ICGC_Ebfsc137065_targets
2	0.012	33 / 3213	ICGC_Pu1_targets
3	0.032	14 / 1148	HEBENSTREIT_low expression TF
4	0.048	41 / 4602	ICGC_Elf1_targets
5	0.059	33 / 3608	ICGC_Tcf12_targets
6	0.065	15 / 1387	HEBENSTREIT_high expression TF
7	0.069	42 / 4851	ICGC_Runx3_targets
8	0.074	36 / 4072	ICGC_Mta3_targets
9	0.089	37 / 4264	ICGC_Pax5_targets
10	0.089	36 / 4131	ICGC_Tcf3_targets
11	0.113	21 / 2254	ICGC_BatfPcr1_targets
12	0.146	32 / 3778	ICGC_Pol24_targets
13	0.148	36 / 4319	ICGC_Pou2_targets
14	0.158	35 / 4212	ICGC_Pol2_targets
15	0.185	35 / 4278	ICGC_Yy1_targets

Overexpression Spots

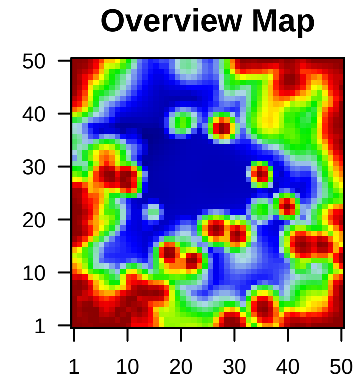
Spot Summary: Z

metagenes = 13
genes = 215

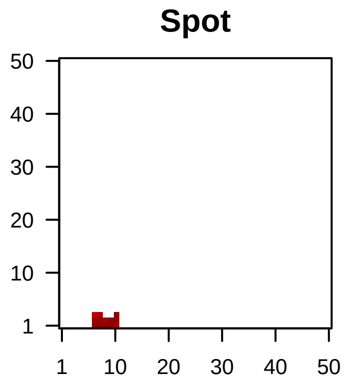
<r> metagenes = 0.96
<r> genes = 0.43
beta: r2= 16.19 / log p= −Inf

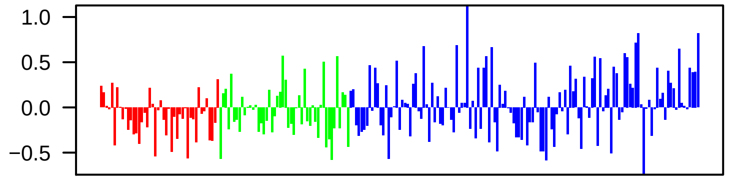
samples with spot = 54 (24.4 %)
mBL : 6 (13.6 %)
intermediate : 7 (14.6 %)
non−mBL : 41 (31.8 %)

Overview Map



Spot





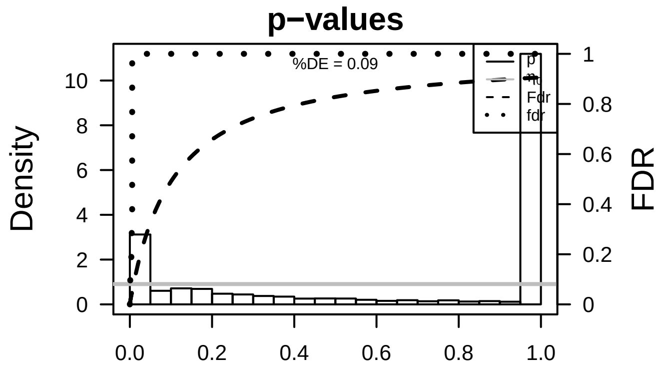
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204475_at	2.81	−1.25	0.46	MMP1	matrix metallopeptidase 1 [Source:HGNC Symbol;Acc:HGNC
2	209875_s_at	2.33	−1.91	0.5	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
3	202718_at	2.31	−1.6	0.53	IGFBP2	insulin like growth factor binding protein 2 [Source:HGNC Sy
4	203290_at	2.16	−1.91	0.18	HLA−DQA1	major histocompatibility complex, class II, DQ alpha 2 [Sourc
5	206025_s_at	2.09	−0.91	0.6	TNFAIP6	TNF alpha induced protein 6 [Source:HGNC Symbol;Acc:HG
6	206026_s_at	2.03	−0.79	0.62	TNFAIP6	TNF alpha induced protein 6 [Source:HGNC Symbol;Acc:HG
7	215646_s_at	2.03	−1.63	0.71	VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]
8	204457_s_at	2	−1.36	0.68	GAS1	growth arrest specific 1 [Source:HGNC Symbol;Acc:HGNC:4
9	206227_at	1.94	−1.63	0.58		cartilage intermediate layer protein [Source:HGNC Symbol;A
10	211813_x_at	1.94	−1.99	0.79	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
11	209616_s_at	1.92	−0.76	0.53	LOC107987423	carboxylesterase 1 pseudogene 1 [Source:HGNC Symbol;Ac
12	219454_at	1.92	−1.06	0.67	EGFL6	EGF like domain multiple 6 [Source:HGNC Symbol;Acc:HGN
13	209621_s_at	1.92	−1.24	0.53	PDLIM3	PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:HGNC:2
14	211571_s_at	1.91	−1.5	0.73	VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]
15	203417_at	1.84	−1.16	0.76	MFAP2	microfibril associated protein 2 [Source:HGNC Symbol;Acc:H
16	201325_s_at	1.82	−1.23	0.69	EMP1	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:H
17	204879_at	1.79	−1.13	0.67	PDPN	podoplanin [Source:HGNC Symbol;Acc:HGNC:29602]
18	212488_at	1.77	−1.28	0.75	COL5A1	collagen type V alpha 1 chain [Source:HGNC Symbol;Acc:H
19	203083_at	1.75	−1.25	0.81	THBS2	thrombospondin 2 [Source:HGNC Symbol;Acc:HGNC:11786]
20	215867_x_at	1.73	−1.13	0.67	CA12	carbonic anhydrase 12 [Source:HGNC Symbol;Acc:HGNC:1

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−99	76 / 214	Lymp	LENZ_Stromal signature 1
2	2e−97	85 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	6e−81	65 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	5e−66	41 / 63	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
5	1e−57	53 / 212	CC	extracellular matrix
6	1e−54	50 / 197	GSEA	NABA_CORE_MATRISOME
7	4e−52	37 / 78	Mela	Tirosh_CAF−cell specific genes
8	5e−52	43 / 132	Colon	Marisa_CRC−cluster−a
9	1e−51	52 / 253	CC	proteinaceous extracellular matrix
10	1e−50	46 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
11	3e−50	73 / 747	GSEA	NABA_MATRISOME
12	3e−48	45 / 183	BP	extracellular matrix organization
13	3e−46	56 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
14	3e−44	39 / 138	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
15	2e−43	46 / 247	GSEA	BOQUEST_STEM_CELL_UP
16	7e−42	76 / 1090	CC	extracellular space
17	1e−37	42 / 249	GSEA	ONDER_CDH1_TARGETS_2_UP
18	9e−34	48 / 443	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
19	1e−33	80 / 1611	CC	extracellular region
20	2e−33	32 / 136	GSEA	NABA_ECM_GLYCOPROTEINS
21	2e−33	53 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
22	5e−32	24 / 58	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
23	8e−31	36 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
24	2e−30	42 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
25	9e−30	23 / 60	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
26	9e−29	41 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
27	9e−29	29 / 138	GSEA	IGLESIAS_E2F_TARGETS_UP
28	3e−28	60 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
29	5e−28	27 / 117	GSEA	ZHU_CMV_ALL_DN
30	5e−28	22 / 60	GSEA	CROMER_TUMORIGENESIS_UP
31	2e−27	38 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
32	3e−27	36 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
33	2e−26	21 / 59	GSEA	PID_INTEGRIN1_PATHWAY
34	3e−26	22 / 70	GSEA	KIM_GLIS2_TARGETS_UP
35	1e−25	23 / 85	Gliom	ScoV_0.999_Sturm_E2_IDH_DN
36	1e−25	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
37	1e−25	0 / 14	Canc	LIU_PROSTATE_CANCER_DN
38	1e−25	23 / 86	GSEA	ZHU_CMV_24_HR_DN
39	3e−25	21 / 66	CC	basement membrane
40	7e−25	36 / 338	GSEA	GRUETZMANN_PANCREATIC_CANCER_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	2 / 47	TESCHENDORFF_age_hypermethylated
2	0.1	3 / 107	HORVATH_aging_genes meth UP
3	0.7	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	3e−48	45 / 183	extracellular matrix organization
2	6e−22	39 / 500	cell adhesion
3	3e−18	16 / 58	collagen catabolic process
4	3e−14	20 / 185	cellular protein metabolic process
5	1e−13	11 / 35	collagen fibril organization
6	5e−12	12 / 62	extracellular matrix disassembly
7	3e−11	16 / 157	positive regulation of cell migration
8	8e−10	17 / 223	angiogenesis
9	1e−09	9 / 42	cellular response to amino acid stimulus
10	1e−09	11 / 78	wound healing
11	1e−08	7 / 25	endodermal cell differentiation
12	3e−08	12 / 130	skeletal system development
13	7e−08	10 / 88	osteoblast differentiation
14	5e−07	6 / 27	positive regulation of cell−substrate adhesion
15	6e−07	12 / 169	cell migration

Cancer

Rank	p−value	#in/all	Geneset
1	1e−25	0 / 14	LIU_PROSTATE_CANCER_DN
2	1e−21	38 / 480	Lembcke_Colonic Inflammation
3	2e−06	12 / 187	PanCan_PI3K_geneset_nanostring
4	1e−05	4 / 13	GENTLES_modul17
5	1e−02	2 / 15	RHODES_CANCER_META_SIGNATURE
6	9e−02	4 / 147	PanCan_MAPK_geneset_nanostring
7	1e−01	1 / 13	GENTLES_modul1
8	2e−01	1 / 14	GUSTAFSON_PI3K_DN
9	2e−01	1 / 14	BENTINK_myc.1
10	2e−01	1 / 14	BENTINK_ras.6
11	2e−01	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	2e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	2e−01	1 / 16	GENTLES_modul16
14	2e−01	1 / 18	PanCan_Notch_geneset_nanostring
15	2e−01	0 / 11	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	1e−57	53 / 212	extracellular matrix
2	1e−51	52 / 253	proteinaceous extracellular matrix
3	7e−42	76 / 1090	extracellular space
4	1e−33	80 / 1611	extracellular region
5	3e−25	21 / 66	basement membrane
6	6e−24	31 / 241	endoplasmic reticulum lumen
7	6e−19	17 / 65	collagen trimer
8	5e−15	67 / 2239	extracellular exosome
9	8e−08	21 / 462	cell surface
10	2e−06	16 / 345	focal adhesion
11	6e−06	8 / 85	lysosomal lumen
12	8e−06	7 / 63	platelet alpha granule lumen
13	5e−05	7 / 84	Golgi lumen
14	2e−04	5 / 47	extracellular vesicle
15	5e−04	3 / 14	basal lamina

Chr

Rank	p−value	#in/all	Geneset
1	0.03	12 / 554	Chr 5
2	0.05	10 / 480	Chr 4
3	0.10	14 / 832	Chr 2
4	0.14	10 / 585	Chr 7
5	0.16	7 / 382	Chr 15
6	0.22	3 / 139	Chr 21
7	0.28	10 / 689	Chr 3
8	0.29	10 / 700	Chr 12
9	0.38	10 / 756	Chr 11
10	0.51	6 / 492	Chr 9
11	0.53	3 / 242	Chr 13
12	0.69	4 / 403	Chr 14
13	0.75	3 / 333	Chr 22
14	0.75	4 / 437	Chr 8
15	0.77	5 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−33	101 / 2765	Tregulatory cells peripheral blood_13_ReprPC
2	9e−33	114 / 3724	Tcells peripheral blood_12_EnhBiv
3	1e−32	114 / 3734	Tcells peripheral blood_13_ReprPC
4	8e−32	93 / 2405	Bcells peripheral blood_13_ReprPC
5	4e−29	88 / 2300	Thelper cells peripheral blood_13_ReprPC
6	3e−27	110 / 3918	Tcells peripheral blood_14_ReprPCWk
7	1e−26	83 / 2194	Thelper cells peripheral blood_12_EnhBiv
8	7e−26	95 / 2984	natural killer cells peripheral blood_14_ReprPCWk
9	1e−25	95 / 3001	Bcells peripheral blood_14_ReprPCWk
10	1e−25	91 / 2747	Bcells peripheral blood_12_EnhBiv
11	1e−24	86 / 2515	natural killer cells peripheral blood_13_ReprPC
12	3e−24	70 / 1660	T CD8+ naive cells peripheral blood_12_EnhBiv
13	6e−24	94 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
14	3e−23	94 / 3150	monocytes peripheral blood_13_ReprPC
15	6e−23	87 / 2724	Tcells peripheral blood_11_BivFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−52	43 / 132	Marisa_CRC−cluster−a
2	3e−28	60 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	3e−27	36 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	5e−19	29 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	3e−07	10 / 103	Marisa_CRC−cluster−b
6	2e−05	14 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	3e−05	7 / 77	Ang_CRC_Hypermethylated
8	1e−04	2 / 2	Budinska_A_Surface crypt−like_DOWN
9	2e−04	6 / 72	Ang_CRC−CIMPH−vs−L_hyper
10	8e−04	10 / 255	Kosinski_top−crypt−long−list
11	2e−03	33 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	2e−03	11 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	4e−03	2 / 8	Marisa_CRC−C3
14	4e−03	8 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
15	1e−02	6 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

Glioma

Rank	p−value	#in/all	Geneset
1	8e−31	36 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
2	1e−25	23 / 85	ScoV_0.999_Sturm_E2_IDH_DN
3	5e−18	27 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	1e−13	11 / 35	Colman_survival_associated
5	1e−12	27 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
6	8e−12	14 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	1e−10	13 / 99	GIEZELT_GBM_WT_up_VS_mut
8	2e−10	11 / 64	cultured astroglia vs. in vivo astrocytes
9	4e−10	6 / 10	Phillips MES up vs Prolif & PN
10	1e−08	13 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	3e−08	10 / 82	laffaire_hypermeth_LGG_vs_control
12	4e−08	12 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	8e−08	11 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
14	1e−07	15 / 242	ScoV_0.5_Sturm_C1_IDH_DN
15	3e−06	5 / 21	KIM deleted & downregulated in LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−97	85 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	5e−66	41 / 63	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
3	1e−54	50 / 197	NABA_CORE_MATRISOME
4	1e−50	46 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
5	3e−50	73 / 747	NABA_MATRISOME
6	3e−46	56 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
7	3e−44	39 / 138	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
8	2e−43	46 / 247	BOQUEST_STEM_CELL_UP
9	1e−37	42 / 249	ONDER_CDH1_TARGETS_2_UP
10	9e−34	48 / 443	CHICAS_RB1_TARGETS_CONFLUENT
11	2e−33	32 / 136	NABA_ECM_GLYCOPROTEINS
12	2e−33	53 / 589	WONG_ADULT_TISSUE_STEM_MODULE
13	5e−32	24 / 58	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_
14	2e−30	42 / 366	LIM_MAMMARY_STEM_CELL_UP
15	9e−30	23 / 60	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL

HM

Rank	p−value	#in/all	Geneset
1	6e−81	65 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	1e−13	17 / 130	HALLMARK_COAGULATION
3	5e−13	19 / 188	HALLMARK_HYPOXIA
4	8e−11	15 / 141	HALLMARK_UV_RESPONSE_DN
5	1e−10	9 / 34	HALLMARK_ANGIOGENESIS
6	2e−05	11 / 194	HALLMARK_MYOGENESIS
7	3e−05	10 / 174	HALLMARK_APICAL_JUNCTION
8	6e−05	10 / 187	HALLMARK_INFLAMMATORY_RESPONSE
9	7e−05	10 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	3e−04	9 / 182	HALLMARK_GLYCOLYSIS
11	3e−04	5 / 51	HALLMARK_TGF_BETA_SIGNALING
12	4e−04	8 / 150	HALLMARK_APOPTOSIS
13	4e−04	9 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
14	2e−03	8 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	7e−03	7 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 25	Angelova_immune−metagene−DC
2	1e−02	3 / 38	Angelova_immune−metagene−mast−cells
3	1e−02	3 / 42	Angelova_immune−metagene−TGD
4	2e−02	2 / 21	Angelova_immune−metagene−central_memory_CD4
5	9e−02	1 / 8	Immunity_HLA−class−II
6	1e−01	1 / 11	Angelova_immune−metagene−macrophages
7	2e−01	1 / 18	Angelova_immune−metagene−pDC
8	2e−01	1 / 19	Angelova_immune−metagene−iDC
9	2e−01	1 / 23	Angelova_immune−metagene−Th2
10	3e−01	1 / 29	Angelova_immune−metagene−Th1
11	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
12	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
13	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
14	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
15	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	2 / 10	DUMEAUX_Smoking literature genes up
2	0.089	1 / 8	Marjolein_ageing−genes_UP
3	0.151	1 / 14	Huan_blood−pressure_SBP−signature
4	0.161	2 / 62	DUMEAUX_Smoking enriched genes
5	0.312	1 / 32	Marjolein_ageing−genes_DN
6	0.441	3 / 210	Homuth_BMI−associated−genes_DN
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 22	DUMEAUX_High bmi enriched genes
15	1.000	0 / 22	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−99	76 / 214	LENZ_Stromal signature 1
2	5e−21	91 / 3168	HOPP_Repressed
3	3e−19	21 / 121	ROSOLOWSKI_green total
4	4e−16	63 / 1894	HOPP_Poised_promoter
5	8e−11	14 / 118	Subero_INT_hyper_meth
6	4e−10	14 / 132	Subero_DLBCL_hyper_meth
7	5e−09	11 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
8	8e−09	11 / 91	Subero_T−ALL_hyper_meth
9	1e−07	9 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
10	2e−07	8 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
11	2e−06	17 / 378	TARTE_Mature plasma cell signature
12	6e−05	45 / 2206	HOPP_Heterochrom
13	1e−04	6 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	3e−03	3 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
15	3e−03	3 / 26	DAVE_Immune response 1

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−52	37 / 78	Tirosh_CAF−cell specific genes
2	2e−11	27 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	2e−10	12 / 85	Tirosh_AXL−signature
4	2e−04	9 / 171	Landsberg_dedifferentiation_up
5	9e−04	4 / 37	Hugo_melanoma−all−MET_DN
6	2e−03	5 / 75	Tirosh_Endothelial−cell specific genes−melanoma
7	2e−02	2 / 17	Hugo_melanoma−all−MET_UP
8	2e−02	6 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
9	3e−02	1 / 3	Gerami_melanoma−metastatic−risk_UP
10	6e−02	3 / 78	Tirosh_expression higher in CAFs than in T−cells
11	8e−02	2 / 41	Tirosh_top50 correlated genes PC3
12	1e−01	1 / 10	Joensson_Melanoma Normal like subtype
13	2e−01	2 / 71	Tirosh_Macrophage specific genes−melanoma
14	2e−01	2 / 81	Tirosh_Genes in the MITF program
15	2e−01	1 / 24	Gerami_melanoma−metastatic−risk_DN

MF

Rank	p−value	#in/all	Geneset
1	4e−24	19 / 53	extracellular matrix structural constituent
2	8e−16	11 / 24	extracellular matrix binding
3	4e−15	17 / 106	integrin binding
4	4e−14	8 / 11	platelet−derived growth factor binding
5	1e−11	11 / 52	collagen binding
6	2e−10	14 / 126	heparin binding
7	2e−10	26 / 517	calcium ion binding
8	1e−09	7 / 19	fibronectin binding
9	7e−08	6 / 20	insulin−like growth factor binding
10	1e−07	10 / 93	protease binding
11	3e−06	5 / 21	glycosaminoglycan binding
12	4e−06	6 / 37	growth factor binding
13	5e−06	4 / 11	peptidase activator activity
14	8e−06	4 / 12	proteoglycan binding
15	2e−05	4 / 14	platelet−derived growth factor receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	4 / 47	hsa−miR−1279
2	0.004	6 / 129	hsa−miR−29a
3	0.005	6 / 135	hsa−miR−29c
4	0.013	6 / 166	hsa−miR−29b
5	0.013	6 / 167	hsa−miR−221
6	0.015	3 / 45	hsa−miR−487a
7	0.017	5 / 128	hsa−miR−583
8	0.020	2 / 19	hsa−miR−596
9	0.020	5 / 135	hsa−miR−548g
10	0.021	5 / 136	hsa−miR−511
11	0.023	3 / 53	hsa−miR−485−3p
12	0.032	4 / 103	hsa−miR−576−3p
13	0.033	7 / 262	hsa−miR−32
14	0.036	5 / 157	hsa−miR−222
15	0.041	4 / 112	hsa−miR−218

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 57	Burnham_day1_vs_5_UP
2	0.3	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.4	1 / 41	Scicluna_DN
4	0.4	1 / 48	Burnham_cap_fp_vs_con_DN
5	0.5	1 / 52	Burnham_day1_vs_5_DN
6	0.5	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	0.5	1 / 54	Burnham_timecourse
8	0.5	1 / 56	Burnham_sep_vs_con_DN
9	0.5	1 / 68	Burnham_sep_vs_con_UP
10	0.6	1 / 71	Burnham_cap_fp_vs_con_UP
11	0.8	1 / 122	Terre_IMS_influenza_meta_signature
12	1.0	0 / 48	Burnham_viral_DN
13	1.0	0 / 57	Burnham_viral_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	4e−04	3 / 13	WIRTH_Sec. lymphoid organs
2	2e−03	5 / 81	Chaussabel_1,2_Platelets
3	1e−02	7 / 209	Chaussabel_2,5_Immune related molecules
4	2e−02	10 / 399	PROTEINATLAS_soft tissue
5	2e−02	2 / 18	JONGENEEL_Monocytes
6	3e−02	2 / 22	VAQUERIZAS_Trachea_TF
7	4e−02	3 / 62	VAQUERIZAS_Lung_TF
8	5e−02	2 / 30	VAQUERIZAS_Smooth muscle_TF
9	5e−02	2 / 30	VAQUERIZAS_Fetal lung_TF
10	5e−02	6 / 233	PROTEINATLAS_smooth muscle
11	7e−02	2 / 36	VAQUERIZAS_Prostate_TF
12	8e−02	2 / 41	VAQUERIZAS_Thyroid_TF
13	9e−02	2 / 43	WIRTH_Placenta
14	1e−01	3 / 99	Chaussabel_1,5_Myeloid lineage
15	1e−01	2 / 49	VAQUERIZAS_Uterus_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	2e−05	30 / 1148	HEBENSTREIT_low expression TF
2	8e−02	34 / 2321	ICGC_Rad21_targets
3	7e−01	11 / 1032	ICGC_Usf1_targets
4	8e−01	22 / 2254	ICGC_BatfPcr1_targets
5	9e−01	4 / 522	ICGC_SrfPcr2_targets
6	9e−01	9 / 1041	ICGC_P300_targets
7	9e−01	3 / 415	ICGC_RxraPcr1_targets
8	9e−01	12 / 1387	HEBENSTREIT_high expression TF
9	9e−01	30 / 3213	ICGC_Pu1_targets
10	9e−01	12 / 1508	ICGC_Mef2_targets
11	1e+00	13 / 1636	ICGC_Bcl11_targets
12	1e+00	18 / 2150	ICGC_Irf4_targets
13	1e+00	40 / 4264	ICGC_Pax5_targets
14	1e+00	31 / 3435	ICGC_Ebfsc137065_targets
15	1e+00	15 / 1941	ICGC_Bcl3_targets

Overexpression Spots

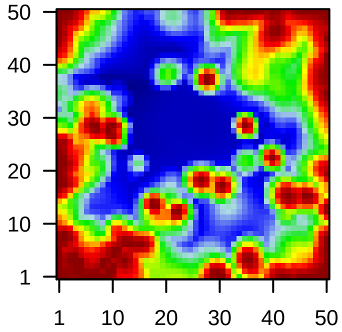
Spot Summary: A1

metagenes = 12
genes = 108

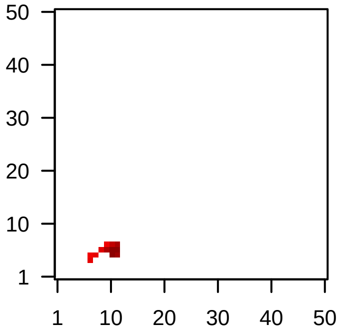
<r> metagenes = 0.93
<r> genes = 0.24
beta: r2= 8.96 / log p= −Inf

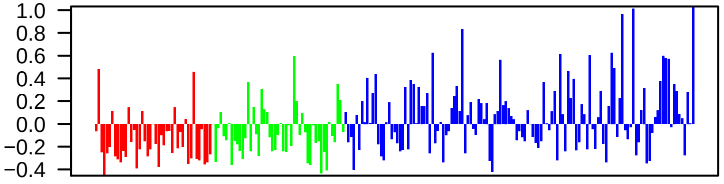
samples with spot = 43 (19.5 %)
mBL : 2 (4.5 %)
intermediate : 5 (10.4 %)
non−mBL : 36 (27.9 %)

Overview Map



Spot





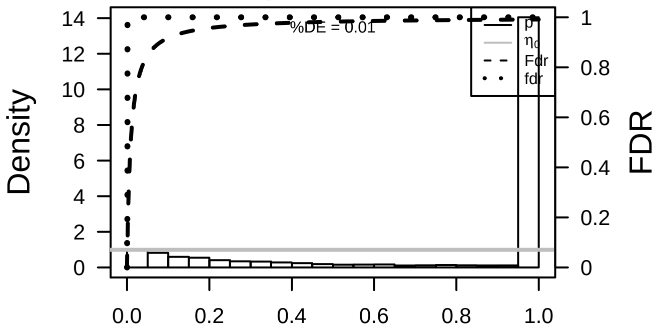
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	216853_x_at	3.78	−1.3	0.56		immunoglobulin lambda variable 3−19 [Source:HGNC Symbo
2	214777_at	3.45	−1.71	0.56		immunoglobulin kappa variable 4−1 [Source:HGNC Symbol;A
3	216560_x_at	3.43	−1.18	0.64		immunoglobulin lambda variable 3−10 [Source:HGNC Symbo
4	204259_at	3.15	−0.97	0.3	MMP7	matrix metallopeptidase 7 [Source:HGNC Symbol;Acc:HGNC
5	217281_x_at	3.13	−1.46	0.65		immunoglobulin heavy variable 3−7 [Source:HGNC Symbol;A
6	202018_s_at	3.09	−0.86	0.39	LTF	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
7	211634_x_at	2.97	−1.71	0.65		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
8	216365_x_at	2.94	−0.92	0.47		
9	216984_x_at	2.81	−1.47	0.68		
10	211650_x_at	2.76	−1.14	0.66		immunoglobulin heavy variable 3−23 [Source:HGNC Symbol;
11	216412_x_at	2.72	−0.9	0.39		
12	214768_x_at	2.67	−1.59	0.66		immunoglobulin kappa variable 2−28 [Source:HGNC Symbol;
13	215214_at	2.64	−1.12	0.72		immunoglobulin lambda variable 3−25 [Source:HGNC Symbo
14	211640_x_at	2.62	−1.03	0.62		
15	211635_x_at	2.55	−1.67	0.62		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
16	211643_x_at	2.53	−1.39	0.65		
17	217179_x_at	2.49	−1.3	0.51		
18	217148_x_at	2.47	−1.36	0.58		immunoglobulin lambda variable 2−14 [Source:HGNC Symbo
19	211798_x_at	2.47	−1.18	0.7		
20	216401_x_at	2.41	−1.34	0.66		immunoglobulin kappa variable 1−37 (non−functional) [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−23	15 / 44	MF	antigen binding
2	4e−20	14 / 52	BP	complement activation, classical pathway
3	6e−17	17 / 161	BP	adaptive immune response
4	3e−16	11 / 39	BP	complement activation
5	1e−14	11 / 53	BP	regulation of complement activation
6	2e−14	12 / 76	BP	Fc−gamma receptor signaling pathway involved in phagocytosis
7	2e−13	9 / 32	Refer	Chaussabel_1,1_Plasma Cells
8	1e−12	18 / 336	BP	immune response
9	3e−12	12 / 113	BP	regulation of immune response
10	7e−12	13 / 154	MF	serine−type endopeptidase activity
11	7e−11	18 / 431	BP	immune system process
12	9e−11	12 / 150	BP	leukocyte migration
13	1e−10	11 / 119	BP	receptor−mediated endocytosis
14	2e−10	46 / 3210	CC	plasma membrane
15	3e−10	11 / 129	BP	Fc−epsilon receptor signaling pathway
16	4e−10	12 / 169	GSEA	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
17	1e−09	31 / 1611	CC	extracellular region
18	2e−09	10 / 116	CC	blood microparticle
19	3e−09	16 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
20	3e−09	17 / 480	Canc	Lembcke_Colonic Inflammation
21	6e−09	12 / 214	Lympl	LENZ_Stromal signature 1
22	2e−08	5 / 15	BP	immunoglobulin production
23	1e−07	10 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
24	4e−07	4 / 11	CC	immunoglobulin complex, circulating
25	4e−07	13 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
26	6e−07	7 / 82	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
27	7e−07	13 / 397	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
28	7e−07	10 / 218	GSEA	DELYS_THYROID_CANCER_DN
29	7e−07	14 / 469	BP	proteolysis
30	1e−06	5 / 32	GSEA	ONGUSAHA_TP53_TARGETS
31	1e−06	12 / 354	GSEA	RODWELL_AGING_KIDNEY_UP
32	2e−06	4 / 16	MF	immunoglobulin receptor binding
33	2e−06	14 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
34	2e−06	5 / 36	BP	phagocytosis, engulfment
35	5e−06	4 / 19	BP	positive regulation of B cell activation
36	5e−06	11 / 333	GSEA	BERENJENO_TRANSFORMED_BY_RHOA_DN
37	7e−06	4 / 21	BP	phagocytosis, recognition
38	8e−06	11 / 352	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
39	1e−05	4 / 23	CC	podosome
40	2e−05	9 / 247	GSEA	BOQUEST_STEM_CELL_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	2 / 107	HORVATH_aging_genes meth UP
2	0.2	1 / 47	TESCHENDORFF_age_hypermethylated
3	0.4	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	

CC

Rank	p−value	#in/all	Geneset
1	2e−10	46 / 3210	plasma membrane
2	1e−09	31 / 1611	extracellular region
3	2e−09	10 / 116	blood microparticle
4	4e−07	4 / 11	immunoglobulin complex, circulating
5	1e−05	4 / 23	podosome
6	2e−05	19 / 1090	extracellular space
7	7e−04	47 / 5339	membrane
8	1e−03	3 / 34	cortical actin cytoskeleton
9	2e−03	5 / 146	lamellipodium
10	3e−03	24 / 2239	extracellular exosome
11	5e−03	2 / 17	apicolateral plasma membrane
12	5e−03	5 / 180	actin cytoskeleton
13	7e−03	8 / 462	cell surface
14	1e−02	3 / 80	ruffle
15	2e−02	13 / 1128	integral component of plasma membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−07	7 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
2	7e−07	13 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
3	3e−04	8 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	8e−03	4 / 132	Marisa_CRC−cluster−a
5	1e−02	1 / 2	Juehling_HNPCC−mutated−in−6−to−8
6	2e−02	1 / 3	Budinska_C_CIMP−H−like_DOWN
7	3e−02	7 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
8	6e−02	1 / 11	Kaneda_CIMP−group2
9	7e−02	4 / 255	Kosinski_top−crypt−long−list
10	8e−02	1 / 13	Budinska_B_Lower crypt−like_DOWN
11	8e−02	10 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	1e−01	4 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
13	1e−01	6 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
14	1e−01	1 / 20	Kosinski_top−crypt−short−list
15	1e−01	5 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

HM

Rank	p−value	#in/all	Geneset
1	6e−04	6 / 174	HALLMARK_APICAL_JUNCTION
2	1e−03	6 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	4e−03	5 / 173	HALLMARK_MITOTIC_SPINDLE
4	2e−02	2 / 34	HALLMARK_ANGIOGENESIS
5	3e−02	4 / 188	HALLMARK_HYPOXIA
6	3e−02	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
7	3e−02	4 / 194	HALLMARK_KRAS_SIGNALING_UP
8	3e−02	4 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
9	4e−02	3 / 130	HALLMARK_COAGULATION
10	5e−02	3 / 141	HALLMARK_UV_RESPONSE_DN
11	8e−02	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
12	9e−02	3 / 174	HALLMARK_ADIPOGENESIS
13	9e−02	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	1e−01	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
15	1e−01	3 / 191	HALLMARK_P53_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−09	12 / 214	LENZ_Stromal signature 1
2	2e−03	3 / 41	ROSOLOWSKI_blue DOWN
3	5e−03	6 / 263	SPANG_CD40 6hrs UP
4	2e−02	36 / 4357	HOPP_Weak_txn
5	2e−02	37 / 4559	HOPP_Weak_enhancer
6	2e−02	21 / 2206	HOPP_Heterochrom
7	2e−02	3 / 97	ROSOLOWSKI_red total
8	4e−02	2 / 53	LENZ_Stromal signature 2
9	6e−02	17 / 1894	HOPP_Poised_promoter
10	7e−02	1 / 12	DAVE_BL_DN
11	8e−02	5 / 378	TARTE_Mature plasma cell signature
12	8e−02	25 / 3168	HOPP_Repressed
13	9e−02	3 / 173	Victora_Light zone signature
14	1e−01	2 / 102	ROSOLOWSKI_blue total
15	2e−01	2 / 132	Subero_DLBCL_hyper_meth

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 36	hsa−miR−146b−3p
2	0.03	2 / 45	hsa−miR−889
3	0.04	2 / 51	hsa−miR−648
4	0.05	2 / 60	hsa−miR−548b−3p
5	0.05	3 / 141	hsa−miR−369−3p
6	0.06	2 / 64	hsa−miR−562
7	0.06	3 / 145	hsa−miR−374b
8	0.07	3 / 157	hsa−miR−374a
9	0.09	1 / 16	hsa−miR−380*
10	0.09	1 / 16	hsa−miR−564
11	0.09	1 / 16	hsa−miR−563
12	0.10	2 / 87	hsa−miR−449b
13	0.10	1 / 17	hsa−miR−151−5p
14	0.10	1 / 17	hsa−miR−609
15	0.11	2 / 94	hsa−miR−875−3p

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−20	14 / 52	complement activation, classical pathway
2	6e−17	17 / 161	adaptive immune response
3	3e−16	11 / 39	complement activation
4	1e−14	11 / 53	regulation of complement activation
5	2e−14	12 / 76	Fc−gamma receptor signaling pathway involved in phagocytosis
6	1e−12	18 / 336	immune response
7	3e−12	12 / 113	regulation of immune response
8	7e−11	18 / 431	immune system process
9	9e−11	12 / 150	leukocyte migration
10	1e−10	11 / 119	receptor−mediated endocytosis
11	3e−10	11 / 129	Fc−epsilon receptor signaling pathway
12	2e−08	5 / 15	immunoglobulin production
13	7e−07	14 / 469	proteolysis
14	2e−06	5 / 36	phagocytosis, engulfment
15	5e−06	4 / 19	positive regulation of B cell activation

Chr

Rank	p−value	#in/all	Geneset
1	0.004	7 / 333	Chr 22
2	0.011	11 / 832	Chr 2
3	0.078	6 / 492	Chr 9
4	0.346	4 / 490	Chr 10
5	0.412	9 / 1325	Chr 1
6	0.434	4 / 554	Chr 5
7	0.497	3 / 437	Chr 8
8	0.561	3 / 480	Chr 4
9	0.572	1 / 139	Chr 21
10	0.607	4 / 689	Chr 3
11	0.661	3 / 556	Chr X
12	0.695	3 / 585	Chr 7
13	0.773	1 / 242	Chr 13
14	0.851	2 / 548	Chr 16
15	0.897	1 / 369	Chr 20

Glioma

Rank	p−value	#in/all	Geneset
1	2e−05	3 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
2	4e−03	2 / 16	Shinawi_with_increased_methylation_in_STS
3	2e−02	2 / 32	Shaw_down_in_1p19q
4	2e−02	7 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
5	2e−02	5 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
6	3e−02	3 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	4e−02	2 / 50	Vishal_subnetwork signature of survival in GBM
8	5e−02	5 / 330	Up
9	5e−02	1 / 9	Colman_survival_robust
10	6e−02	2 / 64	cultured astroglia vs. in vivo astrocytes
11	6e−02	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
12	7e−02	2 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
13	7e−02	10 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
14	8e−02	1 / 14	astrocytes_glio
15	9e−02	1 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA

Immunome

Rank	p−value	#in/all	Geneset
1	0.01	2 / 25	Angelova_immune−metagene−DC
2	0.07	1 / 12	Angelova_immune−metagene−NK56_dim
3	0.10	1 / 17	Angelova_immune−metagene−central_memory_CD8
4	0.13	1 / 23	Angelova_immune−metagene−Th2
5	0.23	1 / 42	Angelova_immune−metagene−TGD
6	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
8	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
9	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
10	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
11	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
12	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
13	1.00	0 / 14	Angelova_immune−metagene−eosinophil
14	1.00	0 / 19	Angelova_immune−metagene−iDC
15	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−04	4 / 64	Harbst_melanoma_lowgrade_up
2	8e−04	10 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	5e−03	2 / 17	Hugo_melanoma−all−MET_UP
4	9e−03	2 / 24	Gerami_melanoma−metastatic−risk_DN
5	1e−02	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma
6	1e−02	3 / 78	Tirosh_CAF−cell specific genes
7	1e−02	3 / 81	Tirosh_Genes in the MITF program
8	2e−02	2 / 39	Tirosh_melanoma specific genes
9	4e−02	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
10	5e−02	4 / 236	Gerber_wt/wt_group3−specific
11	6e−02	1 / 10	Joensson_Melanoma Normal like subtype
12	1e−01	2 / 107	Tirosh_Exhaustion program in Mel75
13	2e−01	1 / 39	Tirosh_top50 correlated genes PC4
14	2e−01	1 / 41	Tirosh_top50 correlated genes PC3
15	2e−01	1 / 46	Tirosh_top50 correlated genes PC5

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.008	3 / 68	Burnham_sep_vs_con_UP
2	0.009	3 / 71	Burnham_cap_fp_vs_con_UP
3	0.182	1 / 33	Sweeney_viral_dn
4	0.253	1 / 48	Burnham_cap_fp_vs_con_DN
5	0.253	1 / 48	Burnham_viral_DN
6	0.271	1 / 52	Burnham_day1_vs_5_DN
7	0.293	1 / 57	Burnham_day1_vs_5_UP
8	0.666	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
9	1.000	0 / 56	Burnham_sep_vs_con_DN
10	1.000	0 / 57	Burnham_viral_UP
11	1.000	0 / 54	Burnham_timecourse
12	1.000	0 / 18	Scicluna_UP
13	1.000	0 / 41	Scicluna_DN
14	1.000	0 / 37	Sweeney_viral_up
15	1.000	0 / 122	Terre_IMS_influenza_meta_signature

TF

Rank	p−value	#in/all	Geneset
1	0.09	11 / 1148	HEBENSTREIT_low expression TF
2	0.45	7 / 1041	ICGC_P300_targets
3	0.54	10 / 1636	ICGC_Bcl11_targets
4	0.60	6 / 1032	ICGC_Usf1_targets
5	0.70	10 / 1848	ICGC_Pbx3_targets
6	0.71	8 / 1508	ICGC_Mef2_targets
7	0.72	2 / 415	ICGC_RxraPcr1_targets
8	0.75	5 / 1025	ICGC_NrsfPcr1_targets
9	0.76	10 / 1941	ICGC_Bcl3_targets
10	0.78	6 / 1241	KIM_MYC targets
11	0.80	2 / 485	ICGC_NrsfPcr2_targets
12	0.83	11 / 2254	ICGC_BatfPcr1_targets
13	0.83	2 / 522	ICGC_SrfPcr2_targets
14	0.85	11 / 2321	ICGC_Rad21_targets
15	0.90	6 / 1494	ICGC_Cebpbsc150_targets

Cancer

Rank	p−value	#in/all	Geneset
1	3e−09	17 / 480	Lembcke_Colonic Inflammation
2	4e−04	0 / 14	LIU_PROSTATE_CANCER_DN
3	7e−02	1 / 12	BEN−PORATH_DN
4	8e−02	1 / 13	GENTLES_modul17
5	8e−02	1 / 14	GENTLES_modul13
6	8e−02	1 / 14	GUSTAFSON_PI3K_UP
7	2e−01	4 / 409	Lembcke_Normal vs Adenoma
8	3e−01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	3e−01	1 / 58	SHAUGHNESSY_MM high risk
10	4e−01	1 / 72	PanCan_Wnt_geneset_nanostring
11	5e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
12	6e−01	2 / 317	SPANG_BCL6−index2
13	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
15	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−05	40 / 3734	Tcells peripheral blood_13_ReprPC
2	5e−05	21 / 1372	Tregulatory cells peripheral blood_10_TssBiv
3	1e−04	28 / 2300	Thelper cells peripheral blood_13_ReprPC
4	1e−04	25 / 1930	Fetal_TssA
5	1e−04	31 / 2700	Thelper cells peripheral blood_14_ReprPCWk
6	2e−04	11 / 493	T CD8+ naive cells peripheral blood_10_TssBiv
7	2e−04	29 / 2515	natural killer cells peripheral blood_13_ReprPC
8	3e−04	29 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
9	4e−04	30 / 2747	Bcells peripheral blood_12_EnhBiv
10	6e−04	38 / 3918	Tcells peripheral blood_14_ReprPCWk
11	7e−04	25 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
12	9e−04	25 / 2194	Thelper cells peripheral blood_12_EnhBiv
13	9e−04	25 / 2197	monocytes peripheral blood_11_BivFlnk
14	1e−03	36 / 3724	Tcells peripheral blood_12_EnhBiv
15	1e−03	31 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−10	12 / 169	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
2	3e−09	16 / 412	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
3	1e−07	10 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	4e−07	13 / 381	SWEET_LUNG_CANCER_KRAS_DN
5	7e−07	10 / 218	DELYS_THYROID_CANCER_DN
6	1e−06	5 / 32	ONGUSAHA_TP53_TARGETS
7	1e−06	12 / 354	RODWELL_AGING_KIDNEY_UP
8	2e−06	14 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
9	5e−06	11 / 333	BERENJENO_TRANSFORMED_BY_RHOA_DN
10	8e−06	11 / 352	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_UP
11	2e−05	9 / 247	BOQUEST_STEM_CELL_UP
12	4e−05	11 / 415	HAN_SATB1_TARGETS_DN
13	5e−05	11 / 424	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
14	5e−05	11 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
15	6e−05	8 / 223	UDAYAKUMAR_MED1_TARGETS_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 32	Marjolein_ageing−genes_DN
2	0.2	2 / 150	Homuth_BMI−associated−genes_UP
3	0.7	1 / 210	Homuth_BMI−associated−genes_DN
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 / 22	DUMEAUX_Fasting enriched genes
15	1.0	0 / 14	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	3e−23	15 / 44	antigen binding
2	7e−12	13 / 154	serine−type endopeptidase activity
3	2e−06	4 / 16	immunoglobulin receptor binding
4	6e−03	2 / 19	lipopolysaccharide binding
5	6e−03	3 / 61	serine−type endopeptidase inhibitor activity
6	7e−03	4 / 126	heparin binding
7	8e−03	5 / 205	receptor activity
8	2e−02	6 / 337	G−protein coupled receptor activity
9	2e−02	4 / 172	transcription corepressor activity
10	2e−02	4 / 173	cytokine activity
11	2e−02	2 / 38	cytokine receptor activity
12	2e−02	2 / 39	chemokine activity
13	3e−02	5 / 291	actin binding
14	3e−02	7 / 500	signal transducer activity
15	6e−02	1 / 10	gamma−catenin binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−13	9 / 32	Chaussabel_1,1_Plasma Cells
2	3e−03	2 / 13	WIRTH_Sec. lymphoid organs
3	8e−03	5 / 204	Chaussabel_3,2_Inflammation I
4	2e−02	3 / 99	Chaussabel_1,5_Myeloid lineage
5	4e−02	2 / 49	VAQUERIZAS_Uterus_TF
6	5e−02	2 / 62	VAQUERIZAS_Lung_TF
7	8e−02	1 / 14	WIRTH_Thymus
8	9e−02	1 / 16	VAQUERIZAS_Ovary_TF
9	9e−02	1 / 16	VAQUERIZAS_Fetal thyroid_TF
10	9e−02	1 / 16	VAQUERIZAS_Salivary gland_TF
11	1e−01	1 / 17	VAQUERIZAS_Heart_TF
12	1e−01	2 / 89	Chaussabel_2,3_Erythrocytes
13	1e−01	1 / 19	JONGENEEL_Prostate
14	1e−01	1 / 22	VAQUERIZAS_Trachea_TF
15	1e−01	2 / 109	Chaussabel_2,6_Myeloid lineage

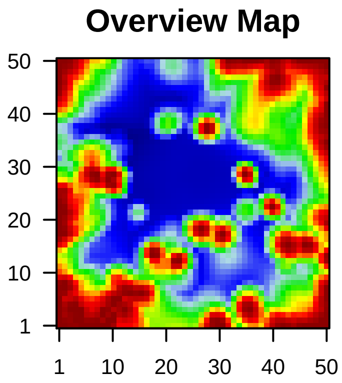
Overexpression Spots

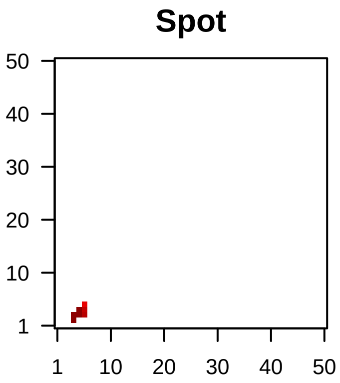
Spot Summary: B1

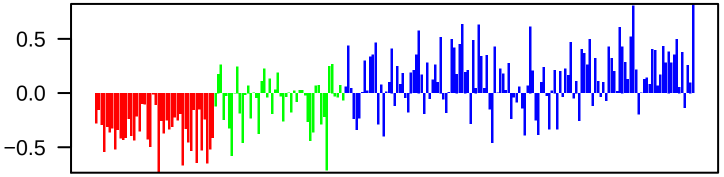
metagenes = 7
genes = 71

<r> metagenes = 0.98
<r> genes = 0.46
beta: r2= 17.81 / log p= −Inf

samples with spot = 60 (27.1 %)
intermediate : 5 (10.4 %)
non−mBL : 55 (42.6 %)





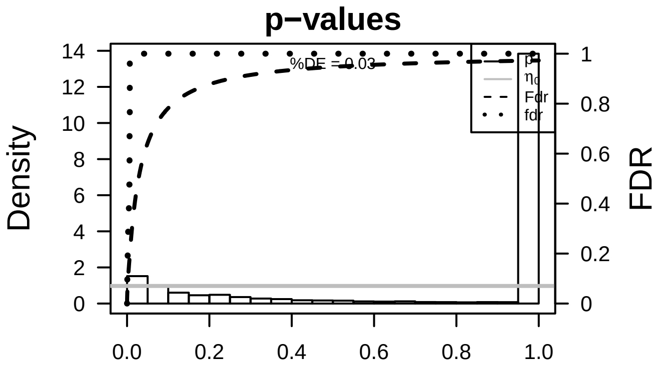


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	215856_at	1.83	−0.82	0.58	SIGLEC15	sialic acid binding Ig like lectin 15 [Source:HGNC Symbol;Acc
2	208893_s_at	1.76	−1.09	0.56	DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:H
3	202498_s_at	1.65	−1.31	0.52	SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:
4	208078_s_at	1.5	−1.36	0.39	SIK1B	salt inducible kinase 1B (putative) [Source:HGNC Symbol;Acc
5	212974_at	1.49	−1.36	0.57	DENND3	DENN domain containing 3 [Source:HGNC Symbol;Acc:HGN
6	210904_s_at	1.45	−1.46	0.64	IL13RA1	interleukin 13 receptor subunit alpha 1 [Source:HGNC Symbo
7	202988_s_at	1.42	−1.31	0.64	RGS1	regulator of G protein signaling 1 [Source:HGNC Symbol;Acc
8	205844_at	1.42	−1.65	0.65	VNN1	vanin 1 [Source:HGNC Symbol;Acc:HGNC:12705]
9	204971_at	1.42	−1.58	0.78	CSTA	cystatin A [Source:HGNC Symbol;Acc:HGNC:2481]
10	208450_at	1.39	−1.07	0.63	LGALS2	galectin 2 [Source:HGNC Symbol;Acc:HGNC:6562]
11	207085_x_at	1.39	−1.2	0.84	CSF2RA	colony stimulating factor 2 receptor alpha subunit [Source:HG
12	221530_s_at	1.38	−1.5	0.61	BHLHE41	basic helix−loop−helix family member e41 [Source:HGNC Sy
13	201169_s_at	1.38	−1.64	0.55	BHLHE40	basic helix−loop−helix family member e40 [Source:HGNC Sy
14	64942_at	1.37	−0.78	0.54	GPR153	G protein−coupled receptor 153 [Source:HGNC Symbol;Acc:
15	220088_at	1.35	−1.23	0.68	C5AR1	complement C5a receptor 1 [Source:HGNC Symbol;Acc:HGN
16	209396_s_at	1.35	−2.29	0.74	CHI3L1	chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
17	202499_s_at	1.3	−0.92	0.56	SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:
18	212975_at	1.29	−0.93	0.55	DENND3	DENN domain containing 3 [Source:HGNC Symbol;Acc:HGN
19	221584_s_at	1.29	−1.18	0.7	KCNMA1	potassium calcium−activated channel subfamily M alpha 1 [S
20	211612_s_at	1.28	−1.57	0.75	IL13RA1	interleukin 13 receptor subunit alpha 1 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−21	24 / 404	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
2	2e−20	23 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
3	5e−20	19 / 214	Lymph	LENZ_Stromal signature 1
4	3e−14	14 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
5	8e−13	16 / 327	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
6	8e−12	17 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
7	1e−11	11 / 132	Colon	Marisa_CRC−cluster−a
8	2e−11	13 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
9	3e−11	13 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
10	4e−11	14 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	6e−11	9 / 78	Melan	Tirosh_expression higher in CAFs than in T−cells
12	9e−11	13 / 255	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
13	2e−10	12 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
14	3e−10	10 / 131	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
15	6e−10	7 / 41	Lymph	ROSOLOWSKI_blue DOWN
16	1e−09	11 / 194	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
17	5e−09	12 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
18	1e−08	8 / 97	Lymph	ROSOLOWSKI_red total
19	3e−08	7 / 71	Melan	Tirosh_Macrophage specific genes−melanoma
20	4e−08	15 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
21	5e−08	8 / 117	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_DN
22	8e−08	5 / 25	GSEA	WILENSKY_RESPONSE_TO_DARAPLADIB
23	9e−08	6 / 50	GSEA	ROSS_AML_WITH_CBFB_MYH11_FUSION
24	2e−07	13 / 480	Cance	Lembcke_Colonic Inflammation
25	2e−07	12 / 403	BP	neutrophil degranulation
26	3e−07	6 / 60	CC	tertiary granule membrane
27	3e−07	10 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
28	4e−07	8 / 154	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
29	5e−07	6 / 67	GSEA	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
30	6e−07	7 / 109	Refer	Chaussabel_2,6_Myeloid lineage
31	6e−07	8 / 162	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
32	7e−07	6 / 69	GSEA	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
33	7e−07	12 / 453	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
34	8e−07	10 / 297	Colon	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
35	9e−07	7 / 116	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
36	1e−06	8 / 171	GSEA	MARKEY_RB1_ACUTE_LOF_UP
37	2e−06	8 / 193	GSEA	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP
38	4e−06	9 / 274	BP	cytokine−mediated signaling pathway
39	6e−06	9 / 290	GSEA	ODONNELL_TFRC_TARGETS_UP
40	6e−06	8 / 218	GSEA	HSIAO_LIVER_SPECIFIC_GENES



Aging

Rank	p−value	#in/all	Geneset
1	0.3	1 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	3e−07	6 / 60	tertiary granule membrane
2	6e−05	4 / 48	ficolin−1−rich granule membrane
3	4e−04	4 / 77	specific granule membrane
4	9e−04	26 / 3210	plasma membrane
5	1e−03	26 / 3270	integral component of membrane
6	1e−03	2 / 12	chylomicron
7	1e−03	2 / 12	low−density lipoprotein particle
8	1e−03	3 / 49	RNA polymerase II transcription factor complex
9	2e−03	3 / 58	phagocytic vesicle membrane
10	2e−03	2 / 16	very−low−density lipoprotein particle
11	3e−03	12 / 1090	extracellular space
12	3e−03	2 / 19	high−density lipoprotein particle
13	3e−03	2 / 19	plasma membrane raft
14	4e−03	19 / 2239	extracellular exosome
15	5e−03	3 / 74	secretory granule membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−11	11 / 132	Marisa_CRC−cluster−a
2	5e−09	12 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	4e−08	15 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	8e−07	10 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	2e−03	2 / 13	Budinska_B_Lower crypt−like_DOWN
6	9e−03	1 / 2	Juehling_HNPCC−mutated−in−6−to−8
7	1e−02	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	1e−02	2 / 35	Ang_CRC_Hypomethylated
9	2e−02	5 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
10	4e−02	9 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
11	4e−02	1 / 10	Budinska_E_Mixed_UP
12	5e−02	8 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	8e−02	9 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	9e−02	1 / 20	Kosinski_top−crypt−short−list
15	1e−01	5 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−05	7 / 178	HALLMARK_COMPLEMENT
2	2e−05	7 / 187	HALLMARK_INFLAMMATORY_RESPONSE
3	3e−05	6 / 130	HALLMARK_COAGULATION
4	2e−04	6 / 194	HALLMARK_KRAS_SIGNALING_UP
5	4e−04	5 / 141	HALLMARK_UV_RESPONSE_DN
6	1e−03	5 / 170	HALLMARK_IL2_STAT5_SIGNALING
7	1e−03	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
8	1e−02	4 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	1e−02	4 / 192	HALLMARK_MTORC1_SIGNALING
10	4e−02	3 / 174	HALLMARK_APICAL_JUNCTION
11	5e−02	3 / 176	HALLMARK_ALLOGRAFT_REJECTION
12	5e−02	3 / 188	HALLMARK_HYPOXIA
13	6e−02	3 / 191	HALLMARK_P53_PATHWAY
14	6e−02	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	6e−02	3 / 193	HALLMARK_HEME_METABOLISM

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−20	19 / 214	LENZ_Stromal signature 1
2	6e−10	7 / 41	ROSOLOWSKI_blue DOWN
3	1e−08	8 / 97	ROSOLOWSKI_red total
4	2e−04	4 / 62	Monti_Host_response_cluster
5	3e−04	8 / 378	TARTE_Mature plasma cell signature
6	4e−03	17 / 1894	HOPP_Poised_promoter
7	4e−03	24 / 3168	HOPP_Repressed
8	6e−03	2 / 26	DAVE_Immune response 1
9	3e−02	1 / 6	Care_GCB UP
10	6e−02	2 / 85	Sha_DLBCL UP
11	6e−02	31 / 5404	HOPP_Strong_enhancer
12	6e−02	2 / 88	ROSOLOWSKI_green UP
13	7e−02	15 / 2206	HOPP_Heterochrom
14	7e−02	1 / 15	Subero_T−ALL_hypo_meth
15	8e−02	2 / 102	ROSOLOWSKI_blue total

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	2 / 24	hsa−miR−193a−5p
2	0.005	3 / 78	hsa−miR−216b
3	0.014	4 / 205	hsa−miR−1252
4	0.017	2 / 44	hsa−miR−629
5	0.020	5 / 344	hsa−miR−19a
6	0.020	5 / 344	hsa−miR−19b
7	0.033	4 / 267	hsa−miR−142−5p
8	0.034	2 / 64	hsa−miR−365
9	0.060	3 / 197	hsa−miR−152
10	0.079	1 / 18	hsa−miR−591
11	0.082	3 / 224	hsa−miR−503
12	0.095	1 / 22	hsa−miR−663
13	0.109	2 / 124	hsa−miR−633
14	0.112	1 / 26	hsa−miR−1226
15	0.120	1 / 28	hsa−miR−1274b

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	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	2e−07	12 / 403	neutrophil degranulation
2	4e−06	9 / 274	cytokine−mediated signaling pathway
3	1e−05	9 / 323	inflammatory response
4	1e−05	3 / 11	amyloid−beta clearance
5	2e−05	6 / 121	positive regulation of angiogenesis
6	2e−04	3 / 24	lipid homeostasis
7	2e−04	3 / 27	endothelial cell migration
8	5e−04	4 / 81	cholesterol metabolic process
9	6e−04	3 / 36	phagocytosis, engulfment
10	6e−04	5 / 150	leukocyte migration
11	9e−04	2 / 10	phospholipid efflux
12	1e−03	3 / 43	positive regulation of cell death
13	1e−03	2 / 11	positive regulation of macrophage chemotaxis
14	1e−03	2 / 11	white fat cell differentiation
15	1e−03	2 / 12	acute inflammatory response

Chr

Rank	p−value	#in/all	Geneset
1	0.09	6 / 689	Chr 3
2	0.11	5 / 556	Chr X
3	0.13	5 / 585	Chr 7
4	0.13	2 / 139	Chr 21
5	0.33	5 / 832	Chr 2
6	0.33	5 / 833	Chr 19
7	0.39	4 / 700	Chr 12
8	0.50	2 / 369	Chr 20
9	0.57	6 / 1325	Chr 1
10	0.57	1 / 184	Chr 18
11	0.59	3 / 669	Chr 6
12	0.65	2 / 480	Chr 4
13	0.66	2 / 490	Chr 10
14	0.66	2 / 492	Chr 9
15	0.67	1 / 242	Chr 13

Glioma

Rank	p−value	#in/all	Geneset
1	8e−12	17 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	3e−11	13 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	3e−07	10 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	6e−04	3 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
5	8e−04	6 / 242	ScoV_0.5_Sturm_C1_IDH_DN
6	8e−04	3 / 41	Gorovets_LGG_PG_subclass
7	1e−03	6 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
8	4e−03	3 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
9	5e−03	5 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
10	9e−03	2 / 32	Shaw_down_in_1p19q
11	1e−02	3 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
12	1e−02	1 / 3	laffaire_hypometh_LGG_vs_control
13	2e−02	1 / 4	Martinez_Glio_hypometh
14	2e−02	2 / 50	Christensen_hypomethylated_in_primary_glioblastoma
15	3e−02	9 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN

Immunome

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 29	Angelova_immune−metagene−Th1
2	9e−04	3 / 42	Angelova_immune−metagene−TGD
3	6e−03	2 / 25	Angelova_immune−metagene−DC
4	6e−02	1 / 13	Angelova_immune−metagene−immature_B−cells
5	7e−02	1 / 17	Angelova_immune−metagene−central_memory_CD8
6	8e−02	1 / 18	Angelova_immune−metagene−pDC
7	8e−02	1 / 18	Angelova_CRC_immunostimulators
8	1e−01	1 / 23	Angelova_immune−metagene−Th2
9	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
10	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
11	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
12	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4
13	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
14	1e+00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1e+00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−11	9 / 78	Tirosh_expression higher in CAFs than in T−cells
2	3e−08	7 / 71	Tirosh_Macrophage specific genes−melanoma
3	3e−05	5 / 78	Tirosh_CAF−cell specific genes
4	5e−04	4 / 81	Tirosh_Genes in the MITF program
5	7e−04	2 / 9	Joensson_Melanoma Pigmentation subtype
6	1e−03	5 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
7	8e−03	4 / 171	Landsberg_dedifferentiation_up
8	1e−02	2 / 39	Tirosh_top50 correlated genes PC4
9	2e−02	2 / 46	Tirosh_top50 correlated genes PC5
10	2e−02	4 / 230	Gerber_wt/wt_melanoma−cells−SpotC
11	5e−02	2 / 83	TCGA_melanoma_immune_high
12	6e−02	2 / 85	Tirosh_AXL−signature
13	1e−01	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
14	2e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	2e−01	1 / 39	Tirosh_melanoma specific genes

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.001	3 / 48	Burnham_viral_DN
2	0.028	2 / 57	Burnham_day1_vs_5_UP
3	0.038	2 / 68	Burnham_sep_vs_con_UP
4	0.041	2 / 71	Burnham_cap_fp_vs_con_UP
5	0.125	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.140	1 / 33	Sweeney_viral_dn
7	0.197	1 / 48	Burnham_cap_fp_vs_con_DN
8	0.211	1 / 52	Burnham_day1_vs_5_DN
9	0.218	1 / 54	Burnham_timecourse
10	0.226	1 / 56	Burnham_sep_vs_con_DN
11	0.428	1 / 122	Terre_IMS_influenza_meta_signature
12	0.560	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
13	1.000	0 / 57	Burnham_viral_UP
14	1.000	0 / 18	Scicluna_UP
15	1.000	0 / 41	Scicluna_DN

TF

Rank	p−value	#in/all	Geneset
1	0.01	11 / 1148	HEBENSTREIT_low expression TF
2	0.07	28 / 4851	ICGC_Runx3_targets
3	0.08	15 / 2254	ICGC_BatfPcr1_targets
4	0.12	11 / 1636	ICGC_Bcl11_targets
5	0.19	7 / 1041	ICGC_P300_targets
6	0.23	9 / 1494	ICGC_Cebpbsc150_targets
7	0.25	13 / 2321	ICGC_Rad21_targets
8	0.26	11 / 1941	ICGC_Bcl3_targets
9	0.28	17 / 3213	ICGC_Pu1_targets
10	0.38	3 / 485	ICGC_NrsfPcr2_targets
11	0.39	11 / 2150	ICGC_Irf4_targets
12	0.39	17 / 3435	ICGC_Ebfsc137065_targets
13	0.47	9 / 1848	ICGC_Pbx3_targets
14	0.49	19 / 4072	ICGC_Mta3_targets
15	0.54	7 / 1508	ICGC_Mef2_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−07	13 / 480	Lembcke_Colonic Inflammation
2	9e−04	4 / 96	PanCan_TXmisReg_geneset_nanostring
3	2e−03	2 / 15	WANG_ER_UP
4	7e−03	0 / 14	LIU_PROSTATE_CANCER_DN
5	1e−02	5 / 317	SPANG_BCL6−index2
6	4e−02	1 / 10	BENTINK_ras.4
7	6e−02	1 / 13	BENTINK_e2f3.1
8	6e−02	1 / 14	BENTINK_src.10
9	1e−01	1 / 32	KUIPER_MM good survival
10	2e−01	0 / 15	RHODES_CANCER_META_SIGNATURE
11	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
12	4e−01	1 / 130	PanCan_CC+Apop_geneset_nanostring
13	5e−01	1 / 147	PanCan_MAPK_geneset_nanostring
14	6e−01	1 / 186	SPANG_LPS−index2
15	6e−01	1 / 187	PanCan_PI3K_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−06	34 / 3724	Tcells peripheral blood_12_EnhBiv
2	1e−05	34 / 3918	Tcells peripheral blood_14_ReprPCWk
3	3e−05	20 / 1676	Fetal_TxTrans
4	9e−05	22 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
5	1e−04	31 / 3734	Tcells peripheral blood_13_ReprPC
6	1e−04	22 / 2194	Thelper cells peripheral blood_12_EnhBiv
7	2e−04	25 / 2747	Bcells peripheral blood_12_EnhBiv
8	3e−04	16 / 1372	Tregulatory cells peripheral blood_10_TssBiv
9	3e−04	21 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
10	4e−04	27 / 3223	monocytes peripheral blood_6_EnhG
11	6e−04	17 / 1611	natural killer cells peripheral blood_11_BivFlnk
12	6e−04	23 / 2602	natural killer cells peripheral blood_12_EnhBiv
13	1e−03	11 / 847	Fetal_TssP
14	2e−03	23 / 2765	Tregulatory cells peripheral blood_13_ReprPC
15	2e−03	15 / 1473	10_ReprPC_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−21	24 / 404	RUTELLA_RESPONSE_TO_HGF_UP
2	2e−20	23 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
3	3e−14	14 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	8e−13	16 / 327	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
5	2e−11	13 / 223	MCLACHLAN_DENTAL_CARIES_UP
6	4e−11	14 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
7	9e−11	13 / 255	HELLER_SILENCED_BY_METHYLATION_UP
8	2e−10	12 / 219	MCLACHLAN_DENTAL_CARIES_DN
9	3e−10	10 / 131	BROWN_MYELOID_CELL_DEVELOPMENT_UP
10	1e−09	11 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
11	5e−08	8 / 117	LENAOUR_DENDRITIC_CELL_MATURATION_DN
12	8e−08	5 / 25	WILENSKY_RESPONSE_TO_DARAPLADIB
13	9e−08	6 / 50	ROSS_AML_WITH_CBFB_MYH11_FUSION
14	4e−07	8 / 154	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
15	5e−07	6 / 67	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	2e−02	4 / 210	Homuth_BMI−associated−genes_DN
3	6e−02	1 / 13	Huan_blood−pressure_DBP−signature
4	6e−02	1 / 14	Huan_blood−pressure_SBP−signature
5	2e−01	1 / 62	DUMEAUX_Smoking enriched genes
6	5e−01	1 / 150	Homuth_BMI−associated−genes_UP
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1e+00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 22	DUMEAUX_High bmi enriched genes
15	1e+00	0 / 22	DUMEAUX_Fasting enriched genes

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 62	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
2	4e−04	4 / 76	phospholipid binding
3	4e−04	3 / 33	E−box binding
4	6e−04	5 / 153	protein dimerization activity
5	9e−04	2 / 10	phospholipase inhibitor activity
6	3e−03	2 / 19	G−protein alpha−subunit binding
7	5e−03	2 / 23	bHLH transcription factor binding
8	8e−03	4 / 172	transcription corepressor activity
9	1e−02	2 / 33	endopeptidase inhibitor activity
10	1e−02	2 / 33	RNA polymerase II activating transcription factor binding
11	1e−02	6 / 408	protein heterodimerization activity
12	1e−02	2 / 36	cholesterol binding
13	1e−02	3 / 107	voltage−gated ion channel activity
14	1e−02	2 / 38	cytokine receptor activity
15	1e−02	2 / 39	nuclear receptor activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−07	7 / 109	Chaussabel_2,6_Myeloid lineage
2	2e−05	7 / 182	WIRTH_post GC B−cells
3	2e−03	2 / 13	WIRTH_Prim. lymphoid organs
4	2e−03	5 / 198	Chaussabel_3,3_Inflammation II
5	2e−03	5 / 204	Chaussabel_3,2_Inflammation I
6	9e−03	2 / 32	VAQUERIZAS_Liver_TF
7	1e−02	3 / 99	Chaussabel_1,5_Myeloid lineage
8	3e−02	2 / 59	Chaussabel_2,10_Immune related cell surface molecules
9	5e−02	1 / 12	VAQUERIZAS_Kidney_TF
10	6e−02	1 / 13	WIRTH_Sec. lymphoid organs
11	7e−02	2 / 93	Chaussabel_1,4_Replication
12	8e−02	3 / 218	WIRTH_pre+post GC B−cells
13	8e−02	2 / 102	WIRTH_EBV B−cells
14	1e−01	1 / 22	VAQUERIZAS_Trachea_TF
15	1e−01	1 / 24	VAQUERIZAS_Spinal cord_TF

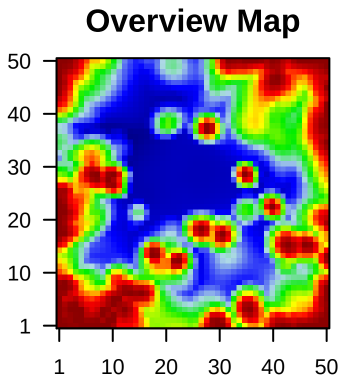
Overexpression Spots

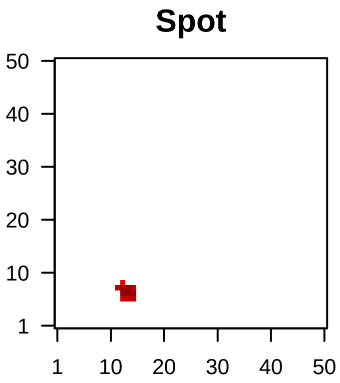
Spot Summary: C1

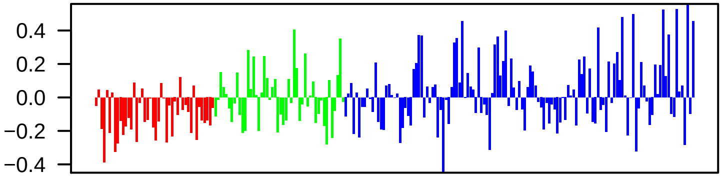
metagenes = 11
genes = 63

<r> metagenes = 0.96
<r> genes = 0.23
beta: r2= 4.31 / log p= −Inf

samples with spot = 31 (14 %)
intermediate : 6 (12.5 %)
non−mBL : 25 (19.4 %)


Overview Map


Spot

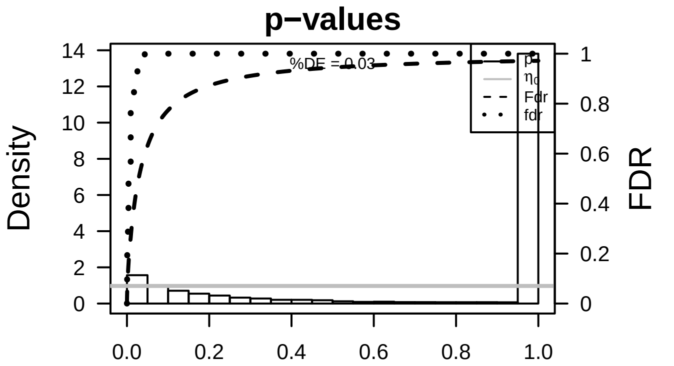


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204271_s_at	2.45	−0.82	0.48	EDNRB	endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC
2	209278_s_at	2.34	−0.69	0.39	TFPI2	tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:H
3	203697_at	2.26	−0.97	0.55	FRZB	frizzled related protein [Source:HGNC Symbol;Acc:HGNC:39
4	203698_s_at	2.21	−0.92	0.45	FRZB	frizzled related protein [Source:HGNC Symbol;Acc:HGNC:39
5	206210_s_at	1.88	−1.47	0.51	CETP	cholesteryl ester transfer protein [Source:HGNC Symbol;Acc:
6	220952_s_at	1.81	−0.93	0.42	PLEKHA5	pleckstrin homology domain containing A5 [Source:HGNC Sy
7	203231_s_at	1.8	−1.05	0.56	ATXN1	ataxin 1 [Source:HGNC Symbol;Acc:HGNC:10548]
8	209277_at	1.8	−0.82	0.33	TFPI2	tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:H
9	206002_at	1.79	−0.99	0.64	ADGRG2	adhesion G protein−coupled receptor G2 [Source:HGNC Sym
10	204273_at	1.78	−1.04	0.56	EDNRB	endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC
11	209894_at	1.77	−0.75	0.44	LEPR	leptin receptor [Source:HGNC Symbol;Acc:HGNC:6554]
12	205399_at	1.75	−0.79	0.57	DCLK1	doublecortin like kinase 1 [Source:HGNC Symbol;Acc:HGNC
13	206291_at	1.75	−0.77	0.52	NTS	neurotensin [Source:HGNC Symbol;Acc:HGNC:8038]
14	205110_s_at	1.74	−1.18	0.55	FGF13	fibroblast growth factor 13 [Source:HGNC Symbol;Acc:HGNC
15	218546_at	1.72	−0.8	0.45	C1orf115	chromosome 1 open reading frame 115 [Source:HGNC Symb
16	216035_x_at	1.64	−0.99	0.57	TCF7L2	transcription factor 7 like 2 [Source:HGNC Symbol;Acc:HGNC
17	201341_at	1.63	−0.98	0.4	ENC1	ectodermal−neural cortex 1 [Source:HGNC Symbol;Acc:HGN
18	212761_at	1.56	−1.02	0.64	TCF7L2	transcription factor 7 like 2 [Source:HGNC Symbol;Acc:HGNC
19	202350_s_at	1.55	−0.76	0.55	MATN2	matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
20	201983_s_at	1.52	−1.23	0.46	EGFR	epidermal growth factor receptor [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−12	22 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
2	2e−10	14 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
3	9e−10	14 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	1e−09	15 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
5	6e−09	13 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
6	2e−08	7 / 75	GSEA	HOELZEL_NF1_TARGETS_DN
7	2e−07	4 / 14	Canc	GENTLES_modul13
8	4e−07	30 / 3168	Lymph	HOPP_Repressed
9	2e−06	12 / 565	GSEA	LEE_BMP2_TARGETS_UP
10	3e−06	7 / 160	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
11	3e−06	6 / 103	GSEA	HOELZEL_NF1_TARGETS_UP
12	5e−06	21 / 1894	Lymph	HOPP_Poised_promoter
13	6e−06	9 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
14	1e−05	7 / 194	GSEA	PLASARI_TGFB1_TARGETS_10HR_DN
15	1e−05	11 / 564	GSEA	GOZGIT_ESR1_TARGETS_DN
16	2e−05	4 / 39	GSEA	TOMLINS_PROSTATE_CANCER_DN
17	2e−05	5 / 84	GSEA	BROWNE_HCMV_INFECTION_16HR_DN
18	2e−05	4 / 42	GSEA	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
19	2e−05	10 / 497	Melan	Gerber_wt/wt_melanoma−cells−SpotD
20	2e−05	7 / 218	GSEA	DELYS_THYROID_CANCER_DN
21	3e−05	4 / 43	GSEA	STREICHER_LSM1_TARGETS_UP
22	3e−05	3 / 15	Gliom	Mukasa_UP_in_GBM
23	3e−05	3 / 15	GSEA	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3
24	3e−05	5 / 90	GSEA	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
25	4e−05	6 / 156	GSEA	PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
26	4e−05	7 / 232	BP	cell surface receptor signaling pathway
27	5e−05	3 / 18	GSEA	NIELSEN_LEIOMYOSARCOMA_CNN1_UP
28	5e−05	6 / 167	BP	Wnt signaling pathway
29	6e−05	9 / 443	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
30	7e−05	6 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
31	7e−05	6 / 178	GSEA	WU_CELL_MIGRATION
32	1e−04	8 / 366	GSEA	HAN_SATB1_TARGETS_UP
33	1e−04	8 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
34	1e−04	4 / 62	Refer	VAQUERIZAS_Lung_TF
35	1e−04	10 / 600	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
36	1e−04	8 / 383	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
37	1e−04	3 / 25	GSEA	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY
38	2e−04	2 / 6	GSEA	PLASARI_TGFB1_TARGETS_1HR_DN
39	3e−04	8 / 421	BP	nervous system development
40	3e−04	6 / 223	miRN	hsa−miR−1244


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	4e−05	7 / 232	cell surface receptor signaling pathway
2	5e−05	6 / 167	Wnt signaling pathway
3	3e−04	8 / 421	nervous system development
4	4e−04	4 / 88	neuron migration
5	7e−04	3 / 43	skeletal muscle tissue development
6	8e−04	2 / 11	cerebral cortex cell migration
7	1e−03	2 / 14	somite development
8	2e−03	10 / 833	multicellular organism development
9	2e−03	3 / 60	response to glucose
10	2e−03	4 / 130	positive regulation of protein kinase B signaling
11	2e−03	3 / 62	forebrain development
12	2e−03	2 / 18	protein localization to cell surface
13	2e−03	3 / 66	canonical Wnt signaling pathway
14	3e−03	2 / 19	non−canonical Wnt signaling pathway
15	3e−03	3 / 69	positive regulation of peptidyl−serine phosphorylation

Cancer

Rank	p−value	#in/all	Geneset
1	2e−07	4 / 14	GENTLES_modul13
2	4e−03	0 / 14	LIU_PROSTATE_CANCER_DN
3	4e−02	0 / 11	LIU_PROSTATE_CANCER_UP
4	1e−01	2 / 134	PanCan_RAS_geneset_nanostring
5	1e−01	2 / 147	PanCan_MAPK_geneset_nanostring
6	2e−01	0 / 14	LIU_COMMON_CANCER_GENES
7	2e−01	2 / 187	PanCan_PI3K_geneset_nanostring
8	3e−01	1 / 72	PanCan_Wnt_geneset_nanostring
9	3e−01	1 / 80	PanCan_JAK−ST_geneset_nanostring
10	3e−01	3 / 480	Lembcke_Colonic Inflammation
11	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
12	5e−01	2 / 409	Lembcke_Normal vs Adenoma
13	7e−01	1 / 317	SPANG_BCL6−index2
14	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
15	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 152	basolateral plasma membrane
2	1e−03	15 / 1611	extracellular region
3	2e−03	2 / 15	A band
4	2e−03	2 / 18	costamere
5	4e−03	22 / 3210	plasma membrane
6	4e−03	3 / 82	sarcolemma
7	6e−03	3 / 90	nuclear matrix
8	8e−03	3 / 101	Z disc
9	9e−03	7 / 595	cell junction
10	1e−02	2 / 37	T−tubule
11	1e−02	3 / 113	receptor complex
12	1e−02	5 / 345	focal adhesion
13	1e−02	2 / 43	intercalated disc
14	1e−02	4 / 231	apical plasma membrane
15	3e−02	9 / 1128	integral component of plasma membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.008	7 / 585	Chr 7
2	0.016	4 / 242	Chr 13
3	0.023	6 / 554	Chr 5
4	0.133	4 / 490	Chr 10
5	0.158	8 / 1325	Chr 1
6	0.309	4 / 700	Chr 12
7	0.387	3 / 556	Chr X
8	0.430	1 / 139	Chr 21
9	0.579	2 / 480	Chr 4
10	0.593	2 / 492	Chr 9
11	0.658	3 / 832	Chr 2
12	0.757	2 / 669	Chr 6
13	0.772	2 / 689	Chr 3
14	0.790	1 / 382	Chr 15
15	0.807	1 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−08	16 / 741	Fetal_Enh
2	2e−08	32 / 3184	monocytes peripheral blood_12_EnhBiv
3	2e−08	35 / 3825	Bcells peripheral blood_15_Quies
4	5e−08	26 / 2197	monocytes peripheral blood_11_BivFlnk
5	7e−08	34 / 3755	HSC_15_Quies
6	1e−07	20 / 1372	Tregulatory cells peripheral blood_10_TssBiv
7	2e−07	31 / 3272	monocytes peripheral blood_14_ReprPCWk
8	2e−07	34 / 3918	Tcells peripheral blood_14_ReprPCWk
9	3e−07	35 / 4214	monocytes peripheral blood_15_Quies
10	5e−07	33 / 3819	natural killer cells peripheral blood_15_Quies
11	8e−07	29 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
12	1e−06	27 / 2747	Bcells peripheral blood_12_EnhBiv
13	1e−06	26 / 2600	HSC_14_ReprPCWk
14	2e−06	28 / 3001	Bcells peripheral blood_14_ReprPCWk
15	7e−06	19 / 1604	HSC_11_BivFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−12	22 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	3e−04	2 / 7	Budinska_D_Mesenchymal_UP
3	8e−04	4 / 103	Marisa_CRC−cluster−b
4	1e−03	7 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
5	1e−03	2 / 14	TCGA_Mutated−in−CRC_non−hypermutated
6	2e−03	2 / 16	Vilar_non−hypermutated−in−CRC
7	4e−02	1 / 9	Marisa_CRC−C2
8	4e−02	2 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
9	5e−02	5 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
10	5e−02	1 / 12	Juehling_HNPCC−mutated−in−4
11	5e−02	1 / 14	TCGA_Mutated−in−CRC_hypermutated
12	6e−02	7 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	6e−02	1 / 16	Vilar_mutated−in−CRC−CamP
14	6e−02	4 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
15	6e−02	5 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	3e−05	3 / 15	Mukasa_UP_in_GBM
2	4e−03	4 / 163	ScoV_0.999_Sturm_E1_IDH_DN
3	6e−03	2 / 30	Shaw_responders_down_in_oligo_glioma
4	1e−02	3 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	2e−02	3 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	2e−02	4 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
7	3e−02	2 / 64	cultured astroglia vs. in vivo astrocytes
8	4e−02	1 / 9	Colman_survival_robust
9	4e−02	3 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
10	4e−02	2 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
11	4e−02	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
12	4e−02	2 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
13	5e−02	1 / 12	Christensen_hypermethylated_in_ependymoma
14	5e−02	2 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
15	6e−02	1 / 15	neurons_glio

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−10	14 / 381	SWEET_LUNG_CANCER_KRAS_DN
2	9e−10	14 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	1e−09	15 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
4	6e−09	13 / 412	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
5	2e−08	7 / 75	HOELZEL_NF1_TARGETS_DN
6	2e−06	12 / 565	LEE_BMP2_TARGETS_UP
7	3e−06	7 / 160	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
8	3e−06	6 / 103	HOELZEL_NF1_TARGETS_UP
9	6e−06	9 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
10	1e−05	7 / 194	PLASARI_TGFB1_TARGETS_10HR_DN
11	1e−05	11 / 564	GOZGIT_ESR1_TARGETS_DN
12	2e−05	4 / 39	TOMLINS_PROSTATE_CANCER_DN
13	2e−05	5 / 84	BROWNE_HCMV_INFECTION_16HR_DN
14	2e−05	4 / 42	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
15	2e−05	7 / 218	DELYS_THYROID_CANCER_DN

HM

Rank	p−value	#in/all	Geneset
1	0.001	5 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.002	4 / 141	HALLMARK_UV_RESPONSE_DN
3	0.006	2 / 29	HALLMARK_NOTCH_SIGNALING
4	0.008	4 / 194	HALLMARK_KRAS_SIGNALING_UP
5	0.008	4 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	0.122	2 / 150	HALLMARK_APOPTOSIS
7	0.142	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.153	2 / 173	HALLMARK_MITOTIC_SPINDLE
9	0.154	2 / 174	HALLMARK_APICAL_JUNCTION
10	0.157	2 / 176	HALLMARK_ALLOGRAFT_REJECTION
11	0.174	2 / 188	HALLMARK_HYPOXIA
12	0.179	2 / 191	HALLMARK_P53_PATHWAY
13	0.183	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.264	1 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
15	0.290	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 13	Angelova_immune−metagene−immature_B−cells
2	0.05	1 / 14	Angelova_immune−metagene−eosinophil
3	0.07	1 / 17	Angelova_immune−metagene−central_memory_CD8
4	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
5	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
6	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
7	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 19	Angelova_immune−metagene−iDC
13	1.00	0 / 11	Angelova_immune−metagene−macrophages
14	1.00	0 / 38	Angelova_immune−metagene−mast−cells
15	1.00	0 / 8	Angelova_immune−metagene−mDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	1 / 22	DUMEAUX_Fasting enriched genes
2	0.22	1 / 62	DUMEAUX_Smoking enriched genes
3	0.57	1 / 210	Homuth_BMI−associated−genes_DN
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 22	DUMEAUX_High bmi enriched genes
13	1.00	0 / 150	Homuth_BMI−associated−genes_UP
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−07	30 / 3168	HOPP_Repressed
2	5e−06	21 / 1894	HOPP_Poised_promoter
3	3e−04	3 / 33	Care_Extended T−cell
4	4e−04	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
5	6e−04	4 / 96	SPANG_LPS 6hrs UP
6	6e−04	6 / 263	SPANG_CD40 6hrs UP
7	1e−03	3 / 53	LENZ_Stromal signature 2
8	2e−03	4 / 132	Subero_DLBCL_hyper_meth
9	2e−03	2 / 18	SPANG_BAFF 9hrs UP
10	1e−02	4 / 214	LENZ_Stromal signature 1
11	2e−02	2 / 47	Subero_B−ALL_hyper_meth
12	2e−02	2 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
13	2e−02	2 / 56	Subero_mBL_hyper_meth
14	3e−02	3 / 173	Victora_Light zone signature
15	5e−02	14 / 2206	HOPP_Heterochrom

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−05	10 / 497	Gerber_wt/wt_melanoma−cells−SpotD
2	2e−02	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
3	3e−02	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
4	4e−02	2 / 75	Tirosh_Endothelial−cell specific genes−melanoma
5	4e−02	2 / 78	Tirosh_CAF−cell specific genes
6	7e−02	3 / 236	Gerber_wt/wt_group3−specific
7	8e−02	2 / 119	TCGA_melanoma_MITF_low
8	1e−01	1 / 33	Tirosh_T−cell specific genes−melanoma
9	1e−01	1 / 37	Hugo_melanoma−all−MET_DN
10	1e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
11	2e−01	1 / 46	Tirosh_top50 correlated genes PC5
12	2e−01	2 / 204	Landsberg_dedifferentiation_down
13	2e−01	1 / 59	TCGA_melanoma_keratin_high
14	2e−01	1 / 64	Harbst_melanoma_lowgrade_up
15	2e−01	1 / 65	Harbst_melanoma_highgrade_up

MF

Rank	p−value	#in/all	Geneset
1	0.001	5 / 191	transmembrane signaling receptor activity
2	0.001	2 / 12	neuropilin binding
3	0.003	2 / 19	Wnt−activated receptor activity
4	0.003	6 / 350	protein kinase binding
5	0.003	3 / 70	beta−catenin binding
6	0.003	3 / 75	PDZ domain binding
7	0.004	2 / 23	spectrin binding
8	0.004	2 / 25	Wnt−protein binding
9	0.005	2 / 26	sodium channel regulator activity
10	0.007	3 / 97	double−stranded DNA binding
11	0.008	2 / 33	enzyme inhibitor activity
12	0.009	3 / 106	integrin binding
13	0.017	3 / 135	actin filament binding
14	0.025	7 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
15	0.025	2 / 61	serine−type endopeptidase inhibitor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	6 / 223	hsa−miR−1244
2	3e−04	5 / 143	hsa−miR−183
3	6e−04	6 / 259	hsa−miR−18a
4	2e−03	4 / 136	hsa−miR−153
5	2e−03	5 / 234	hsa−miR−101
6	2e−03	4 / 141	hsa−miR−369−3p
7	2e−03	5 / 236	hsa−miR−18b
8	3e−03	2 / 22	hsa−miR−1287
9	5e−03	3 / 84	hsa−miR−410
10	5e−03	4 / 171	hsa−miR−196a
11	5e−03	3 / 89	hsa−miR−624
12	6e−03	2 / 28	hsa−miR−1237
13	6e−03	4 / 185	hsa−miR−199a−3p
14	7e−03	3 / 95	hsa−miR−376a
15	7e−03	2 / 32	hsa−miR−501−3p

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 62	VAQUERIZAS_Lung_TF
2	6e−04	3 / 41	VAQUERIZAS_Thymus_TF
3	7e−04	4 / 100	Chaussabel_2,8_T−cells
4	1e−03	3 / 49	VAQUERIZAS_Uterus_TF
5	3e−03	2 / 22	VAQUERIZAS_Trachea_TF
6	6e−03	2 / 28	JONGENEEL_Placenta
7	6e−03	4 / 182	WIRTH_post GC B−cells
8	6e−03	2 / 30	VAQUERIZAS_Fetal lung_TF
9	9e−03	2 / 36	VAQUERIZAS_Prostate_TF
10	5e−02	8 / 1007	PROTEINATLAS_kidney
11	5e−02	1 / 12	WIRTH_Cortex cerebri
12	5e−02	1 / 12	VAQUERIZAS_Kidney_TF
13	5e−02	1 / 13	WIRTH_Sec. lymphoid organs
14	5e−02	1 / 14	WIRTH_Thymus
15	6e−02	1 / 16	VAQUERIZAS_Ovary_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.07	14 / 2321	ICGC_Rad21_targets
2	0.41	5 / 1041	ICGC_P300_targets
3	0.46	18 / 4278	ICGC_Yy1_targets
4	0.49	5 / 1148	HEBENSTREIT_low expression TF
5	0.53	8 / 1941	ICGC_Bcl3_targets
6	0.58	2 / 485	ICGC_NrsfPcr2_targets
7	0.62	14 / 3630	ICGC_Sp1_targets
8	0.63	2 / 522	ICGC_SrfPcr2_targets
9	0.63	7 / 1848	ICGC_Pbx3_targets
10	0.64	11 / 2899	ICGC_Nfatc1_targets
11	0.64	13 / 3420	ICGC_Bclaf101388_targets
12	0.65	8 / 2150	ICGC_Irf4_targets
13	0.66	6 / 1636	ICGC_Bcl11_targets
14	0.68	11 / 2994	ICGC_Zeb1_targets
15	0.69	14 / 3778	ICGC_Pol24_targets

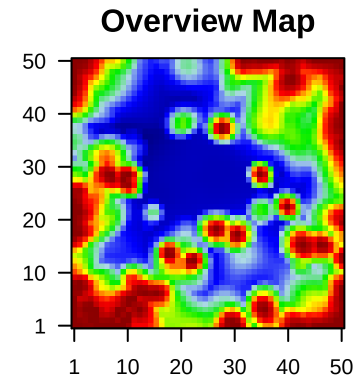
Overexpression Spots

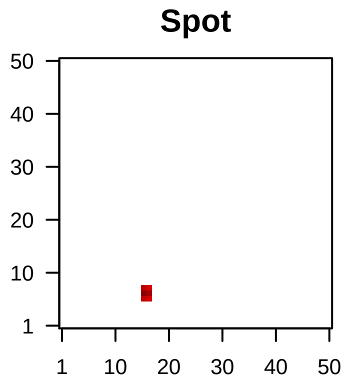
Spot Summary: D1

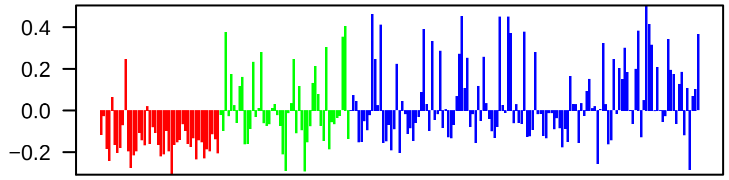
metagenes = 6
genes = 59

<r> metagenes = 0.99
<r> genes = 0.22
beta: r2= 2.64 / log p= −Inf

samples with spot = 35 (15.8 %)
mBL : 1 (2.3 %)
intermediate : 8 (16.7 %)
non−mBL : 26 (20.2 %)





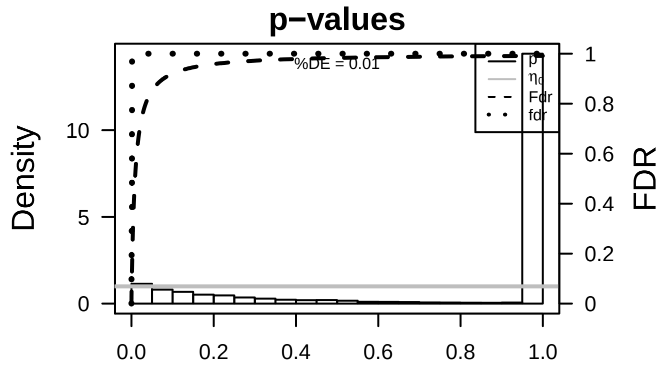


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207599_at	2.71	−0.65	0.5	MMP20	matrix metallopeptidase 20 [Source:HGNC Symbol;Acc:HGN
2	215813_s_at	2.25	−0.94	0.64	PTGS1	prostaglandin−endoperoxide synthase 1 [Source:HGNC Sym
3	204392_at	2.18	−1.11	0.52	CAMK1	calcium/calmodulin dependent protein kinase I [Source:HGN
4	205128_x_at	2.13	−1.29	0.6	PTGS1	prostaglandin−endoperoxide synthase 1 [Source:HGNC Sym
5	218532_s_at	2.06	−1.12	0.55	RETREG1	reticulophagy regulator 1 [Source:HGNC Symbol;Acc:HGNC:
6	218510_x_at	2.04	−0.72	0.57	RETREG1	reticulophagy regulator 1 [Source:HGNC Symbol;Acc:HGNC:
7	213924_at	1.95	−0.87	0.42	GNAL	G protein subunit alpha L [Source:HGNC Symbol;Acc:HGNC:
8	204221_x_at	1.9	−0.87	0.4	GLIPR1	GLI pathogenesis related 1 [Source:HGNC Symbol;Acc:HGN
9	211031_s_at	1.74	−1.01	0.63	CLIP2	CAP−Gly domain containing linker protein 2 [Source:HGNC
10	205225_at	1.73	−0.97	0.57	ESR1	estrogen receptor 1 [Source:HGNC Symbol;Acc:HGNC:3467]
11	219954_s_at	1.67	−0.97	0.39	GBA3	glucosylceramidase beta 3 (gene/pseudogene) [Source:HGN
12	212828_at	1.62	−0.97	0.42	SYNJ2	synaptojanin 2 [Source:HGNC Symbol;Acc:HGNC:11504]
13	206385_s_at	1.51	−0.86	0.6	ANK3	ankyrin 3 [Source:HGNC Symbol;Acc:HGNC:494]
14	204217_s_at	1.5	−0.71	0.45	RTN2	reticulon 2 [Source:HGNC Symbol;Acc:HGNC:10468]
15	204813_at	1.5	−0.81	0.51		
16	204491_at	1.42	−1.03	0.6	PDE4D	phosphodiesterase 4D [Source:HGNC Symbol;Acc:HGNC:87
17	204334_at	1.37	−0.88	0.56	KLF7	Kruppel like factor 7 [Source:HGNC Symbol;Acc:HGNC:6350
18	205407_at	1.35	−1.08	0.51	RECK	reversion inducing cysteine rich protein with kazal motifs [Sou
19	34408_at	1.31	−1.05	0.49	RTN2	reticulon 2 [Source:HGNC Symbol;Acc:HGNC:10468]
20	219313_at	1.22	−1.04	0.55	GRAMD1C	GRAM domain containing 1C [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−07	13 / 642	GSEA	CUI_TCF21_TARGETS_2_DN
2	2e−05	37 / 5682	Lymph	HOPP_Weak_promoter
3	7e−05	14 / 1142	GSEA	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
4	8e−05	4 / 59	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
5	8e−05	10 / 600	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
6	1e−04	8 / 383	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
7	1e−04	30 / 4357	Lymph	HOPP_Weak_txn
8	1e−04	3 / 26	GSEA	BIOCARTA_HDAC_PATHWAY
9	1e−04	7 / 297	GSEA	BASAKI_YBX1_TARGETS_DN
10	2e−04	11 / 788	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
11	2e−04	34 / 5404	Lymph	HOPP_Strong_enhancer
12	2e−04	8 / 434	GSEA	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
13	2e−04	3 / 32	miRN	hsa−miR−501−3p
14	4e−04	3 / 38	GSEA	PID_ER_NONGENOMIC_PATHWAY
15	4e−04	4 / 92	GSEA	HOEBEKE_LYMPHOID_STEM_CELL_UP
16	5e−04	7 / 373	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
17	6e−04	5 / 175	GSEA	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
18	6e−04	8 / 497	Melan	Gerber_wt/wt_melanoma−cells−SpotD
19	6e−04	14 / 1390	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
20	6e−04	7 / 383	GSEA	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS
21	7e−04	6 / 281	CC	lysosome
22	9e−04	29 / 4559	Lymph	HOPP_Weak_enhancer
23	1e−03	3 / 51	GSEA	BIOCARTA_NFAT_PATHWAY
24	1e−03	7 / 421	GSEA	ACEVEDO_LIVER_CANCER_DN
25	1e−03	4 / 121	GSEA	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_DN
26	1e−03	8 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
27	1e−03	2 / 14	BP	positive regulation of interleukin−2 production
28	1e−03	34 / 5908	Lymph	HOPP_Active_promoter
29	1e−03	4 / 127	GSEA	ELVIDGE_HYPOXIA_BY_DMOG_UP
30	2e−03	5 / 223	miRN	hsa−miR−1244
31	2e−03	2 / 16	GSEA	BIOCARTA_ERK5_PATHWAY
32	2e−03	5 / 226	GSEA	GABRIELY_MIR21_TARGETS
33	2e−03	4 / 135	MF	actin filament binding
34	2e−03	2 / 17	MF	guanyl nucleotide binding
35	2e−03	2 / 17	GSEA	BRACHAT_RESPONSE_TO_CISPLATIN
36	2e−03	3 / 66	MF	dioxygenase activity
37	2e−03	3 / 66	Gliom	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
38	2e−03	4 / 141	GSEA	REACTOME_PHOSPHOLIPID_METABOLISM
39	2e−03	2 / 18	CC	costamere
40	2e−03	2 / 18	GSEA	BRACHAT_RESPONSE_TO_METHOTREXATE_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	1 / 92	HORVATH_aging_genes meth DOWN
2	1.0	0 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	2 / 14	positive regulation of interleukin−2 production
2	0.002	2 / 19	Golgi to plasma membrane protein transport
3	0.003	2 / 21	cholesterol efflux
4	0.004	2 / 24	positive regulation of muscle cell differentiation
5	0.006	2 / 29	blood vessel remodeling
6	0.007	2 / 33	autophagosome assembly
7	0.007	3 / 103	platelet activation
8	0.008	2 / 34	positive regulation of interferon−gamma production
9	0.008	2 / 35	pigmentation
10	0.008	3 / 108	cellular response to lipopolysaccharide
11	0.011	2 / 41	positive regulation of tumor necrosis factor production
12	0.012	2 / 43	skeletal muscle tissue development
13	0.013	2 / 45	phosphatidylinositol−3−phosphate biosynthetic process
14	0.013	3 / 128	fatty acid metabolic process
15	0.014	2 / 47	positive regulation of protein ubiquitination

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	0 / 14	LIU_PROSTATE_CANCER_DN
2	0.04	1 / 11	GENTLES_modul14
3	0.11	4 / 480	Lembcke_Colonic Inflammation
4	0.12	3 / 317	SPANG_BCL6−index2
5	0.18	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.27	1 / 80	PanCan_JAK−ST_geneset_nanostring
7	0.31	1 / 96	PanCan_TXmisReg_geneset_nanostring
8	0.36	1 / 113	PanCan_Driver_Gene_geneset_nanostring
9	0.40	1 / 130	PanCan_CC+Apop_geneset_nanostring
10	0.41	1 / 134	PanCan_RAS_geneset_nanostring
11	0.47	2 / 409	Lembcke_Normal vs Adenoma
12	0.52	1 / 186	SPANG_LPS−index2
13	0.52	1 / 187	PanCan_PI3K_geneset_nanostring
14	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
15	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	7e−04	6 / 281	lysosome
2	2e−03	2 / 18	costamere
3	6e−03	2 / 31	heterotrimeric G−protein complex
4	8e−03	2 / 35	cis−Golgi network
5	9e−03	2 / 37	T−tubule
6	9e−03	9 / 938	Golgi apparatus
7	1e−02	2 / 42	sarcoplasmic reticulum
8	1e−02	2 / 44	brush border membrane
9	2e−02	2 / 50	lateral plasma membrane
10	3e−02	3 / 180	actin cytoskeleton
11	3e−02	25 / 4701	cytoplasm
12	4e−02	2 / 79	integral component of endoplasmic reticulum membrane
13	4e−02	3 / 192	membrane raft
14	4e−02	1 / 10	vacuolar membrane
15	4e−02	1 / 11	axon initial segment

Chr

Rank	p−value	#in/all	Geneset
1	0.1	6 / 832	Chr 2
2	0.1	4 / 490	Chr 10
3	0.2	4 / 554	Chr 5
4	0.2	4 / 585	Chr 7
5	0.2	3 / 403	Chr 14
6	0.2	3 / 437	Chr 8
7	0.4	4 / 776	Chr 17
8	0.4	3 / 556	Chr X
9	0.4	1 / 139	Chr 21
10	0.5	3 / 669	Chr 6
11	0.5	3 / 689	Chr 3
12	0.5	1 / 184	Chr 18
13	0.5	3 / 700	Chr 12
14	0.6	2 / 492	Chr 9
15	0.6	1 / 242	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−08	46 / 7078	Bcells peripheral blood_5_TxWk
2	3e−08	34 / 3819	natural killer cells peripheral blood_15_Quies
3	4e−08	47 / 7581	15_Quies_Melanocytes
4	4e−08	47 / 7583	15_Quies_Skeletal_Muscle
5	4e−08	43 / 6244	15_Quies_Fibroblasts
6	8e−08	35 / 4214	monocytes peripheral blood_15_Quies
7	2e−07	34 / 4079	15_Quies_ESC_Endoderm
8	3e−07	43 / 6582	Quies3_Colon
9	6e−07	33 / 4062	T CD8+ naive cells peripheral blood_15_Quies
10	6e−07	47 / 8088	15_Quies_MSC_Adipocyte
11	9e−07	48 / 8550	7_Enh_Skeletal_Muscle
12	2e−06	30 / 3554	8_ZNF_Rpts_ESC_Endoderm
13	2e−06	42 / 6637	Tcells peripheral blood_5_TxWk
14	2e−06	27 / 2974	9_Het_ESC_Endoderm
15	4e−06	44 / 7407	natural killer cells peripheral blood_5_TxWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	9 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	0.02	8 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
3	0.03	2 / 72	Ang_CRC−CIMPH−vs−L_hyper
4	0.04	2 / 77	Ang_CRC_Hypermethylated
5	0.05	7 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
6	0.05	8 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
7	0.08	8 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
8	0.09	4 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
9	0.11	1 / 31	Marisa_CRC−cluster−c
10	0.12	4 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
11	0.15	5 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
12	0.16	7 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	0.16	6 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
14	0.20	3 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
15	0.21	1 / 60	Marisa_CRC−cluster−g

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	3 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
2	0.006	2 / 30	KIM prognostic signature LTS vs. STS
3	0.011	2 / 41	mature astrocytes
4	0.022	2 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	0.030	6 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	0.042	1 / 11	KIM amplified & overexpressed in LTS
7	0.075	1 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
8	0.078	1 / 21	KIM deleted & downregulated in LTS
9	0.081	7 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	0.117	1 / 32	Shaw_down_in_1p19q
11	0.160	1 / 45	OL vs. MOG− OL
12	0.168	2 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
13	0.173	1 / 49	OPC
14	0.176	1 / 50	Christensen_hypomethylated_in_primary_glioblastoma
15	0.183	1 / 52	GIEZELT_GBM_WT_down_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−07	13 / 642	CUI_TCF21_TARGETS_2_DN
2	7e−05	14 / 1142	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
3	8e−05	4 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
4	8e−05	10 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
5	1e−04	8 / 383	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
6	1e−04	3 / 26	BIOCARTA_HDAC_PATHWAY
7	1e−04	7 / 297	BASAKI_YBX1_TARGETS_DN
8	2e−04	11 / 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
9	2e−04	8 / 434	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
10	4e−04	3 / 38	PID_ER_NONGENOMIC_PATHWAY
11	4e−04	4 / 92	HOEBEKE_LYMPHOID_STEM_CELL_UP
12	5e−04	7 / 373	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_5
13	6e−04	5 / 175	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_UP
14	6e−04	14 / 1390	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
15	6e−04	7 / 383	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS

HM

Rank	p−value	#in/all	Geneset
1	0.007	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	0.039	3 / 194	HALLMARK_MYOGENESIS
3	0.051	2 / 94	HALLMARK_PROTEIN_SECRETION
4	0.054	2 / 97	HALLMARK_BILE_ACID_METABOLISM
5	0.081	2 / 122	HALLMARK_SPERMATOGENESIS
6	0.145	2 / 174	HALLMARK_ADIPOGENESIS
7	0.157	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	0.164	2 / 188	HALLMARK_HYPOXIA
9	0.171	2 / 193	HALLMARK_HEME_METABOLISM
10	0.255	1 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
11	0.397	1 / 130	HALLMARK_COAGULATION
12	0.422	1 / 141	HALLMARK_UV_RESPONSE_DN
13	0.476	1 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
14	0.490	1 / 173	HALLMARK_MITOTIC_SPINDLE
15	0.496	1 / 176	HALLMARK_ALLOGRAFT_REJECTION

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 38	Angelova_immune−metagene−mast−cells
2	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
3	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
4	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.0	0 / 25	Angelova_immune−metagene−DC
9	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.0	0 / 14	Angelova_immune−metagene−eosinophil
12	1.0	0 / 19	Angelova_immune−metagene−iDC
13	1.0	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.0	0 / 11	Angelova_immune−metagene−macrophages
15	1.0	0 / 8	Angelova_immune−metagene−mDC

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	37 / 5682	HOPP_Weak_promoter
2	1e−04	30 / 4357	HOPP_Weak_txn
3	2e−04	34 / 5404	HOPP_Strong_enhancer
4	9e−04	29 / 4559	HOPP_Weak_enhancer
5	1e−03	34 / 5908	HOPP_Active_promoter
6	2e−02	13 / 1814	HOPP_Repetitive
7	2e−02	2 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
8	2e−02	8 / 906	SPANG_BCR DN
9	4e−02	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
10	5e−02	18 / 3168	HOPP_Repressed
11	5e−02	1 / 14	WRIGHT_GCB UP
12	6e−02	1 / 15	DAVE_BL Inter
13	6e−02	3 / 237	ZHANG_DLBCL mutated
14	7e−02	27 / 5529	HOPP_Txn_elongation
15	9e−02	2 / 132	Subero_DLBCL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−04	8 / 497	Gerber_wt/wt_melanoma−cells−SpotD
2	6e−02	3 / 236	Gerber_wt/wt_group3−specific
3	6e−02	2 / 107	Tirosh_Exhaustion program in Mel75
4	9e−02	1 / 23	Melanoma Epi−Enzyme Cluster 7
5	9e−02	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
6	1e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
7	1e−01	2 / 171	Landsberg_dedifferentiation_up
8	2e−01	1 / 59	TCGA_melanoma_keratin_high
9	2e−01	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
10	2e−01	1 / 65	Harbst_melanoma_highgrade_up
11	3e−01	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	3e−01	1 / 81	Tirosh_Genes in the MITF program
13	3e−01	1 / 85	Tirosh_AXL−signature
14	5e−01	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
15	1e+00	0 / 17	Hugo_melanoma−all−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	4 / 135	actin filament binding
2	0.002	2 / 17	guanyl nucleotide binding
3	0.002	3 / 66	dioxygenase activity
4	0.003	2 / 21	G−protein beta/gamma−subunit complex binding
5	0.005	18 / 2529	metal ion binding
6	0.008	7 / 601	zinc ion binding
7	0.009	2 / 38	core promoter sequence−specific DNA binding
8	0.014	2 / 46	SH3/SH2 adaptor activity
9	0.017	2 / 51	G−protein coupled receptor binding
10	0.023	2 / 61	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
11	0.026	4 / 291	actin binding
12	0.029	5 / 447	oxidoreductase activity
13	0.029	2 / 69	ATPase binding
14	0.038	1 / 10	calcium channel inhibitor activity
15	0.042	1 / 11	sodium ion binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 32	hsa−miR−501−3p
2	2e−03	5 / 223	hsa−miR−1244
3	2e−03	5 / 240	hsa−miR−548j
4	4e−03	5 / 269	hsa−miR−548a−5p
5	5e−03	3 / 88	hsa−miR−600
6	7e−03	2 / 33	hsa−miR−502−3p
7	8e−03	3 / 107	hsa−miR−204
8	1e−02	4 / 217	hsa−miR−92a
9	1e−02	3 / 119	hsa−miR−140−5p
10	1e−02	3 / 123	hsa−miR−338−5p
11	1e−02	4 / 235	hsa−miR−25
12	2e−02	4 / 251	hsa−miR−548i
13	2e−02	2 / 51	hsa−miR−502−5p
14	2e−02	4 / 256	hsa−miR−548c−3p
15	2e−02	2 / 52	hsa−miR−1246

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	2 / 54	Burnham_timecourse
2	0.38	1 / 122	Terre_IMS_influenza_meta_signature
3	0.50	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	1.00	0 / 68	Burnham_sep_vs_con_UP
5	1.00	0 / 56	Burnham_sep_vs_con_DN
6	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
8	1.00	0 / 48	Burnham_viral_DN
9	1.00	0 / 57	Burnham_viral_UP
10	1.00	0 / 57	Burnham_day1_vs_5_UP
11	1.00	0 / 52	Burnham_day1_vs_5_DN
12	1.00	0 / 18	Scicluna_UP
13	1.00	0 / 41	Scicluna_DN
14	1.00	0 / 37	Sweeney_viral_up
15	1.00	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.007	4 / 198	Chaussabel_3,3_Inflammation II
2	0.031	2 / 72	Chaussabel_3,1_Interferon−inducible
3	0.039	2 / 81	Chaussabel_1,2_Platelets
4	0.044	3 / 204	Chaussabel_3,2_Inflammation I
5	0.063	2 / 106	Chaussabel_2,11_Replication
6	0.071	1 / 19	JONGENEEL_Thymus
7	0.078	1 / 21	VAQUERIZAS_Tonsil_TF
8	0.082	1 / 22	Chaussabel_1,6_Signaling molecules
9	0.117	2 / 152	VAQUERIZAS_General_TF
10	0.118	3 / 310	Chaussabel_3,4_Protein phosphatases
11	0.130	1 / 36	VAQUERIZAS_Prostate_TF
12	0.134	1 / 37	Chaussabel_2,2_Neutrophils
13	0.150	1 / 42	VAQUERIZAS_Fetal brain_TF
14	0.160	1 / 45	VAQUERIZAS_Whole brain_TF
15	0.173	1 / 49	VAQUERIZAS_Uterus_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.02	12 / 1636	ICGC_Bcl11_targets
2	0.05	12 / 1848	ICGC_Pbx3_targets
3	0.05	5 / 522	ICGC_SrfPcr2_targets
4	0.10	13 / 2321	ICGC_Rad21_targets
5	0.12	9 / 1508	ICGC_Mef2_targets
6	0.15	12 / 2254	ICGC_BatfPcr1_targets
7	0.33	15 / 3420	ICGC_Bclaf101388_targets
8	0.35	15 / 3451	ICGC_Atf2_targets
9	0.39	16 / 3796	ICGC_Nficsc81335_targets
10	0.39	16 / 3804	ICGC_Stat5_targets
11	0.40	17 / 4072	ICGC_Mta3_targets
12	0.44	7 / 1630	ICGC_SrfV0416101_targets
13	0.45	6 / 1387	HEBENSTREIT_high expression TF
14	0.45	9 / 2150	ICGC_Irf4_targets
15	0.46	14 / 3435	ICGC_Ebfsc137065_targets

Overexpression Spots

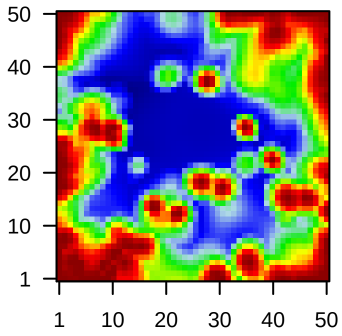
Spot Summary: E1

metagenes = 8
genes = 66

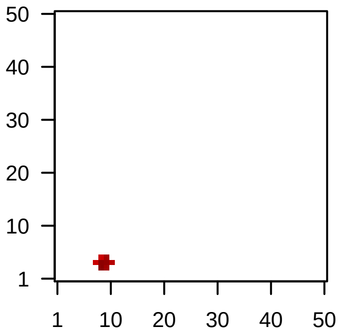
<r> metagenes = 0.97
<r> genes = 0.35
beta: r2= 11.07 / log p= −Inf

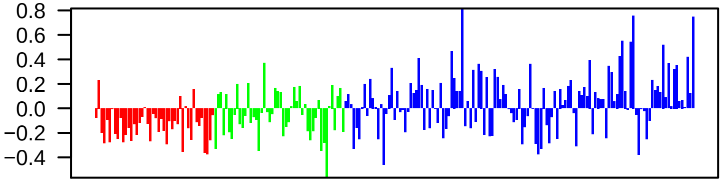
samples with spot = 31 (14 %)
mBL : 1 (2.3 %)
intermediate : 1 (2.1 %)
non−mBL : 29 (22.5 %)

Overview Map



Spot





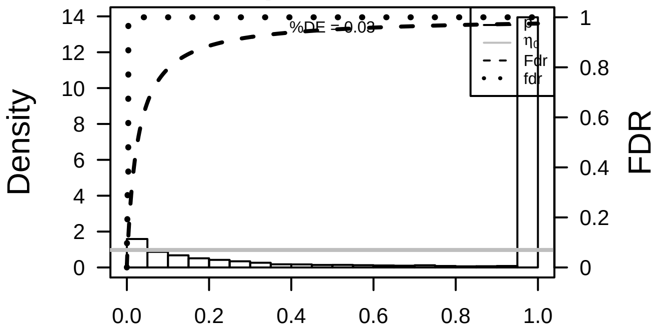
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205755_at	2.49	−0.9	0.54	ITIH3	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
2	205569_at	1.94	−1.1	0.58	LAMP3	lysosomal associated membrane protein 3 [Source:HGNC Sy
3	212624_s_at	1.93	−1.32	0.67	CHN1	chimerin 1 [Source:HGNC Symbol;Acc:HGNC:1943]
4	211458_s_at	1.69	−1.08	0.4	GABARAPL1	GABA type A receptor associated protein like 1 [Source:HGN
5	212158_at	1.62	−1.46	0.56	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
6	219825_at	1.61	−0.96	0.55	CYP26B1	cytochrome P450 family 26 subfamily B member 1 [Source:H
7	210605_s_at	1.52	−0.92	0.56	MFGE8	milk fat globule−EGF factor 8 protein [Source:HGNC Symbol;
8	201012_at	1.43	−0.92	0.63	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
9	202949_s_at	1.43	−1.04	0.54	FHL2	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:H
10	203038_at	1.42	−0.96	0.7	PTPRK	protein tyrosine phosphatase, receptor type K [Source:HGNC
11	212942_s_at	1.38	−1.23	0.49	CEMIP	cell migration inducing hyaluronan binding protein [Source:H
12	219229_at	1.36	−0.77	0.39	SLCO3A1	solute carrier organic anion transporter family member 3A1 [
13	209487_at	1.35	−1.07	0.77	RBPMS	RNA binding protein, mRNA processing factor [Source:HGNC
14	208869_s_at	1.35	−0.97	0.43	GABARAPL1	GABA type A receptor associated protein like 1 [Source:HGN
15	214880_x_at	1.3	−1.4	0.53		
16	219181_at	1.28	−0.78	0.63	LIPG	lipase G, endothelial type [Source:HGNC Symbol;Acc:HGNC
17	202555_s_at	1.28	−1.41	0.6	MYLK	myosin light chain kinase [Source:HGNC Symbol;Acc:HGNC:
18	209488_s_at	1.27	−0.94	0.72	RBPMS	RNA binding protein, mRNA processing factor [Source:HGNC
19	209210_s_at	1.26	−1.29	0.7	FERMT2	fermitin family member 2 [Source:HGNC Symbol;Acc:HGNC:
20	213071_at	1.25	−0.81	0.6	DPT	dermatopontin [Source:HGNC Symbol;Acc:HGNC:3011]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−23	20 / 176	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
2	4e−23	21 / 214	Lymp	LENZ_Stromal signature 1
3	1e−15	1 / 14	Canc	LIU_PROSTATE_CANCER_DN
4	1e−15	1 / 14	Canc	LIU_PROSTATE_CANCER_DN
5	5e−15	19 / 397	GSE	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
6	3e−14	12 / 103	Colon	Marisa_CRC−cluster−b
7	1e−12	16 / 335	GSE	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
8	6e−12	19 / 589	GSE	WONG_ADULT_TISSUE_STEM_MODULE
9	9e−11	9 / 81	GSE	SWEET_KRAS_TARGETS_UP
10	1e−09	21 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
11	3e−09	36 / 3168	Lymp	HOPP_Repressed
12	7e−09	13 / 366	GSE	LIM_MAMMARY_STEM_CELL_UP
13	1e−08	13 / 376	GSE	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
14	1e−08	27 / 1894	Lymp	HOPP_Poised_promoter
15	1e−08	11 / 251	GSE	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
16	2e−08	10 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
17	2e−08	12 / 331	GSE	LINDGREN_BLADDER_CANCER_CLUSTER_2B
18	3e−08	9 / 155	GSE	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
19	5e−08	14 / 516	GSE	SMID_BREAST_CANCER_LUMINAL_B_DN
20	9e−08	12 / 374	GSE	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
21	2e−07	10 / 249	GSE	ONDER_CDH1_TARGETS_2_UP
22	3e−07	14 / 600	GSE	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
23	4e−07	11 / 345	CC	focal adhesion
24	4e−07	9 / 212	CC	extracellular matrix
25	6e−07	12 / 443	GSE	CHICAS_RB1_TARGETS_CONFLUENT
26	1e−06	8 / 176	GSE	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
27	1e−06	6 / 77	GSE	BURTON_ADIPOGENESIS_9
28	1e−06	6 / 78	Mela	Tirosh_CAF−cell specific genes
29	2e−06	7 / 132	Colon	Marisa_CRC−cluster−a
30	2e−06	11 / 415	GSE	BAELDE_DIABETIC_NEPHROPATHY_DN
31	3e−06	6 / 88	Lymp	ROSOLOWSKI_green UP
32	3e−06	7 / 138	GSE	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
33	4e−06	8 / 207	GSE	WANG_SMARCE1_TARGETS_UP
34	6e−06	9 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
35	6e−06	9 / 291	MF	actin binding
36	7e−06	8 / 224	GSE	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
37	9e−06	7 / 165	GSE	CAIRO_LIVER_DEVELOPMENT_UP
38	1e−05	5 / 64	GSE	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
39	1e−05	11 / 491	GSE	ENK_UV_RESPONSE_EPIDERMIS_DN
40	1e−05	10 / 400	GSE	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	3 / 107	HORVATH_aging_genes meth UP
2	0.34	1 / 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	4e−07	11 / 345	focal adhesion
2	4e−07	9 / 212	extracellular matrix
3	2e−05	7 / 180	actin cytoskeleton
4	5e−05	4 / 45	stress fiber
5	1e−04	7 / 241	endoplasmic reticulum lumen
6	1e−04	28 / 3210	plasma membrane
7	2e−04	9 / 462	cell surface
8	2e−04	4 / 66	basement membrane
9	3e−04	4 / 73	cell−cell adherens junction
10	6e−04	21 / 2239	extracellular exosome
11	2e−03	4 / 118	cytoplasmic vesicle membrane
12	2e−03	2 / 16	dendrite membrane
13	3e−03	3 / 60	actin filament
14	3e−03	11 / 936	cytoskeleton
15	3e−03	2 / 19	dendrite cytoplasm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−14	12 / 103	Marisa_CRC−cluster−b
2	1e−09	21 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	2e−06	7 / 132	Marisa_CRC−cluster−a
4	6e−06	9 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
5	4e−04	7 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	4e−04	2 / 7	Budinska_D_Mesenchymal_UP
7	2e−03	7 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	1e−02	5 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
9	2e−02	2 / 43	Marisa_CRC−cluster−f
10	4e−02	1 / 8	Marisa_CRC−C4
11	4e−02	11 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
12	5e−02	3 / 184	Kosinski_lower−crypt−long−list
13	6e−02	1 / 14	TCGA_Mutated−in−CRC_non−hypermutated
14	7e−02	1 / 16	Vilar_non−hypermutated−in−CRC
15	9e−02	1 / 20	Kosinski_top−crypt−short−list

HM

Rank	p−value	#in/all	Geneset
1	2e−08	10 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	4e−05	6 / 141	HALLMARK_UV_RESPONSE_DN
3	2e−04	6 / 194	HALLMARK_MYOGENESIS
4	5e−04	3 / 34	HALLMARK_ANGIOGENESIS
5	5e−03	4 / 150	HALLMARK_APOPTOSIS
6	7e−03	4 / 170	HALLMARK_IL2_STAT5_SIGNALING
7	8e−03	4 / 174	HALLMARK_APICAL_JUNCTION
8	1e−02	4 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	4e−02	3 / 174	HALLMARK_ADIPOGENESIS
10	6e−02	3 / 191	HALLMARK_P53_PATHWAY
11	6e−02	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	6e−02	3 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	1e−01	2 / 130	HALLMARK_COAGULATION
14	2e−01	2 / 173	HALLMARK_MITOTIC_SPINDLE
15	2e−01	2 / 181	HALLMARK_XENOBIOTIC_METABOLISM

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−23	21 / 214	LENZ_Stromal signature 1
2	3e−09	36 / 3168	HOPP_Repressed
3	1e−08	27 / 1894	HOPP_Poised_promoter
4	3e−06	6 / 88	ROSOLOWSKI_green UP
5	2e−05	6 / 121	ROSOLOWSKI_green total
6	2e−04	22 / 2206	HOPP_Heterochrom
7	2e−03	7 / 378	TARTE_Mature plasma cell signature
8	5e−03	2 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
9	1e−02	3 / 102	ROSOLOWSKI_blue total
10	2e−02	3 / 118	Subero_INT_hyper_meth
11	2e−02	3 / 132	Subero_DLBCL_hyper_meth
12	6e−02	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	6e−02	13 / 1814	HOPP_Repetitive
14	8e−02	1 / 18	DAVE_Immune response 2
15	9e−02	3 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	5 / 217	hsa−miR−92a
2	0.005	3 / 78	hsa−miR−219−2−3p
3	0.007	5 / 262	hsa−miR−32
4	0.007	4 / 170	hsa−miR−548m
5	0.008	4 / 171	hsa−miR−196a
6	0.010	2 / 34	hsa−miR−581
7	0.011	4 / 191	hsa−miR−185
8	0.013	3 / 107	hsa−miR−198
9	0.015	2 / 41	hsa−miR−346
10	0.017	5 / 329	hsa−let−7b
11	0.017	3 / 119	hsa−miR−142−3p
12	0.022	4 / 235	hsa−miR−25
13	0.023	3 / 135	hsa−miR−7
14	0.023	4 / 240	hsa−miR−202
15	0.024	2 / 53	hsa−miR−485−3p

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	8e−05	6 / 157	positive regulation of cell migration
2	2e−04	6 / 185	cellular protein metabolic process
3	6e−04	4 / 85	transforming growth factor beta receptor signaling pathway
4	9e−04	2 / 10	ventricular cardiac muscle cell development
5	1e−03	5 / 167	Wnt signaling pathway
6	1e−03	5 / 169	cell migration
7	1e−03	2 / 11	positive regulation of SMAD protein import into nucleus
8	1e−03	2 / 11	positive regulation of wound healing
9	1e−03	3 / 46	positive regulation of pathway−restricted SMAD protein phosphorylation
10	1e−03	2 / 12	cell adhesion mediated by integrin
11	1e−03	6 / 271	post−translational protein modification
12	1e−03	5 / 183	extracellular matrix organization
13	2e−03	4 / 112	regulation of cell shape
14	2e−03	3 / 52	embryonic limb morphogenesis
15	2e−03	8 / 500	cell adhesion

Chr

Rank	p−value	#in/all	Geneset
1	0.04	7 / 700	Chr 12
2	0.05	5 / 437	Chr 8
3	0.05	3 / 184	Chr 18
4	0.10	4 / 382	Chr 15
5	0.17	4 / 480	Chr 4
6	0.18	6 / 832	Chr 2
7	0.25	8 / 1325	Chr 1
8	0.28	5 / 776	Chr 17
9	0.46	3 / 554	Chr 5
10	0.61	3 / 689	Chr 3
11	0.66	2 / 492	Chr 9
12	0.73	2 / 556	Chr X
13	0.78	1 / 333	Chr 22
14	0.85	1 / 403	Chr 14
15	0.87	2 / 756	Chr 11

Glioma

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 32	Shaw_down_in_1p19q
2	1e−03	4 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
3	4e−03	6 / 330	Up
4	6e−03	4 / 163	ScoV_0.999_Sturm_E1_IDH_DN
5	7e−03	3 / 85	ScoV_0.999_Sturm_E2_IDH_DN
6	8e−03	2 / 30	Shaw_responders_down_in_oligo_glioma
7	1e−02	2 / 35	Colman_survival_associated
8	2e−02	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_down (A)
9	3e−02	3 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	3e−02	2 / 64	cultured astroglia vs. in vivo astrocytes
11	5e−02	3 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
12	5e−02	2 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
13	7e−02	1 / 16	VERHAAK_MES subtype
14	7e−02	8 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
15	7e−02	2 / 99	GIEZELT_GBM_WT_up_VS_mut

Immunome

Rank	p−value	#in/all	Geneset
1	0.003	2 / 17	Angelova_immune−metagene−central_memory_CD8
2	0.005	2 / 23	Angelova_immune−metagene−Th2
3	0.023	1 / 5	Angelova_immune−metagene−NK56_bright
4	0.079	1 / 18	Angelova_immune−metagene−pDC
5	0.100	1 / 23	Angelova_immune−metagene−Treg
6	0.174	1 / 42	Angelova_immune−metagene−TGD
7	1.000	0 / 13	Angelova_immune−metagene−activated_B−cells
8	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
9	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
10	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.000	0 / 25	Angelova_immune−metagene−DC
13	1.000	0 / 12	Angelova_immune−metagene−effector_memory_CD4
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	1e−06	6 / 78	Tirosh_CAF−cell specific genes
2	4e−04	9 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	1e−03	5 / 171	Landsberg_dedifferentiation_up
4	2e−03	5 / 204	Landsberg_dedifferentiation_down
5	3e−02	2 / 64	Harbst_melanoma_lowgrade_up
6	9e−02	3 / 236	Gerber_wt/wt_group3−specific
7	2e−01	1 / 41	Tirosh_top50 correlated genes PC3
8	3e−01	1 / 78	Tirosh_expression higher in CAFs than in T−cells
9	3e−01	1 / 81	Tirosh_Genes in the MITF program
10	3e−01	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
11	3e−01	1 / 85	Tirosh_AXL−signature
12	6e−01	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
13	7e−01	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
14	7e−01	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
15	8e−01	1 / 319	Gerber_wt/wt_melanoma−cells−SpotA

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	2 / 48	Burnham_viral_DN
2	0.08	1 / 18	Scicluna_UP
3	0.11	2 / 122	Terre_IMS_influenza_meta_signature
4	0.21	1 / 52	Burnham_day1_vs_5_DN
5	0.23	1 / 57	Burnham_viral_UP
6	0.46	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	0.56	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
8	1.00	0 / 68	Burnham_sep_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 / 71	Burnham_cap_fp_vs_con_UP
12	1.00	0 / 57	Burnham_day1_vs_5_UP
13	1.00	0 / 54	Burnham_timecourse
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

TF

Rank	p−value	#in/all	Geneset
1	0.05	15 / 2150	ICGC_Irf4_targets
2	0.26	11 / 1941	ICGC_Bcl3_targets
3	0.28	17 / 3213	ICGC_Pu1_targets
4	0.32	9 / 1636	ICGC_Bcl11_targets
5	0.36	12 / 2321	ICGC_Rad21_targets
6	0.37	18 / 3608	ICGC_Tcf12_targets
7	0.39	17 / 3435	ICGC_Ebfsc137065_targets
8	0.42	6 / 1148	HEBENSTREIT_low expression TF
9	0.45	11 / 2254	ICGC_BatfPcr1_targets
10	0.45	20 / 4212	ICGC_Pol2_targets
11	0.48	20 / 4264	ICGC_Pax5_targets
12	0.50	6 / 1241	KIM_MYC targets
13	0.54	7 / 1508	ICGC_Mef2_targets
14	0.55	22 / 4851	ICGC_Runx3_targets
15	0.57	2 / 415	ICGC_RxraPcr1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	1e−15	1 / 14	LIU_PROSTATE_CANCER_DN
2	3e−04	9 / 480	Lembcke_Colonic Inflammation
3	2e−03	2 / 13	GENTLES_modul17
4	4e−02	1 / 10	GENTLES_modul3
5	5e−02	3 / 187	PanCan_PI3K_geneset_nanostring
6	6e−02	1 / 14	LIU_COMMON_CANCER_GENES
7	6e−02	1 / 14	GUSTAFSON_PI3K_UP
8	7e−02	1 / 16	GENTLES_modul16
9	1e−01	4 / 409	Lembcke_Normal vs Adenoma
10	1e−01	2 / 134	PanCan_RAS_geneset_nanostring
11	2e−01	1 / 47	PanCan_TGF−B_geneset_nanostring
12	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
13	5e−01	1 / 147	PanCan_MAPK_geneset_nanostring
14	8e−01	1 / 317	SPANG_BCL6−index2
15	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−10	41 / 3734	Tcells peripheral blood_13_ReprPC
2	3e−10	37 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
3	7e−10	34 / 2700	Thelper cells peripheral blood_14_ReprPCWk
4	3e−09	39 / 3724	Tcells peripheral blood_12_EnhBiv
5	5e−09	31 / 2405	Bcells peripheral blood_13_ReprPC
6	1e−08	34 / 2984	natural killer cells peripheral blood_14_ReprPCWk
7	1e−08	34 / 3001	Bcells peripheral blood_14_ReprPCWk
8	2e−08	31 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
9	2e−08	32 / 2724	Tcells peripheral blood_11_BivFlnk
10	3e−08	32 / 2747	Bcells peripheral blood_12_EnhBiv
11	3e−08	32 / 2765	Tregulatory cells peripheral blood_13_ReprPC
12	5e−08	34 / 3150	monocytes peripheral blood_13_ReprPC
13	6e−08	38 / 3906	6_EnhG_MSC_Adipocyte
14	6e−08	30 / 2515	natural killer cells peripheral blood_13_ReprPC
15	2e−07	28 / 2300	Thelper cells peripheral blood_13_ReprPC

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−23	20 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
2	1e−15	1 / 14	LIU_PROSTATE_CANCER_DN
3	5e−15	19 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
4	1e−12	16 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
5	6e−12	19 / 589	WONG_ADULT_TISSUE_STEM_MODULE
6	9e−11	9 / 81	SWEET_KRAS_TARGETS_UP
7	7e−09	13 / 366	LIM_MAMMARY_STEM_CELL_UP
8	1e−08	13 / 376	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
9	1e−08	11 / 251	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
10	2e−08	12 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
11	3e−08	9 / 155	MCBRYAN_PUBERTAL_TGFB1_TARGETS_UP
12	5e−08	14 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
13	9e−08	12 / 374	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
14	2e−07	10 / 249	ONDER_CDH1_TARGETS_2_UP
15	3e−07	14 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.06	1 / 13	Huan_blood−pressure_DBP−signature
3	0.14	1 / 32	Marjolein_ageing−genes_DN
4	1.00	0 / 62	DUMEAUX_Smoking enriched genes
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 22	DUMEAUX_High bmi enriched genes
13	1.00	0 / 22	DUMEAUX_Fasting enriched genes
14	1.00	0 / 150	Homuth_BMI−associated−genes_UP
15	1.00	0 / 210	Homuth_BMI−associated−genes_DN

MF

Rank	p−value	#in/all	Geneset
1	6e−06	9 / 291	actin binding
2	1e−03	2 / 12	activin binding
3	2e−03	2 / 16	cadherin binding involved in cell−cell adhesion
4	3e−03	2 / 19	fibroblast growth factor binding
5	4e−03	3 / 70	beta−catenin binding
6	4e−03	46 / 7864	protein binding
7	7e−03	4 / 165	calmodulin binding
8	1e−02	3 / 103	heme binding
9	1e−02	2 / 37	growth factor binding
10	1e−02	3 / 106	integrin binding
11	2e−02	2 / 45	SMAD binding
12	2e−02	3 / 126	heparin binding
13	2e−02	3 / 135	actin filament binding
14	3e−02	2 / 61	serine−type endopeptidase inhibitor activity
15	4e−02	2 / 70	electron transfer activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 81	Chaussabel_1,2_Platelets
2	2e−03	5 / 204	Chaussabel_3,2_Inflammation I
3	1e−02	3 / 109	Chaussabel_2,6_Myeloid lineage
4	2e−02	4 / 233	PROTEINATLAS_smooth muscle
5	6e−02	1 / 13	WIRTH_Sec. lymphoid organs
6	6e−02	3 / 198	Chaussabel_3,3_Inflammation II
7	7e−02	3 / 209	Chaussabel_2,5_Immune related molecules
8	1e−01	1 / 22	VAQUERIZAS_Trachea_TF
9	1e−01	1 / 30	VAQUERIZAS_Smooth muscle_TF
10	2e−01	1 / 59	Chaussabel_2,10_Immune related cell surface molecules
11	3e−01	3 / 390	PROTEINATLAS_ovary
12	3e−01	3 / 399	PROTEINATLAS_soft tissue
13	3e−01	1 / 89	Chaussabel_2,3_Erythrocytes
14	4e−01	1 / 102	WIRTH_EBV B−cells
15	5e−01	3 / 553	PROTEINATLAS_prostate

Overexpression Spots

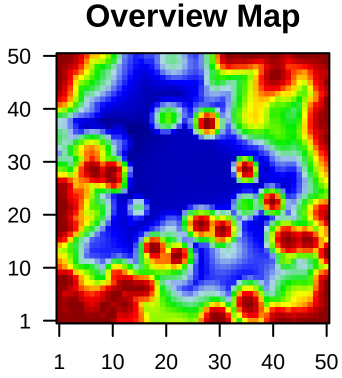
Spot Summary: F1

metagenes = 11
genes = 103

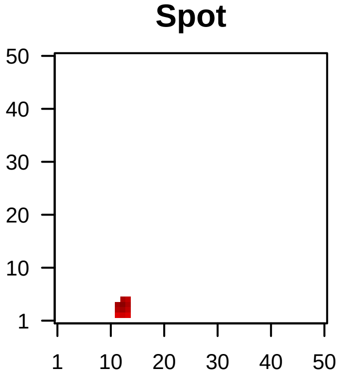
<r> metagenes = 0.96
<r> genes = 0.26
beta: r2= 5.95 / log p= −Inf

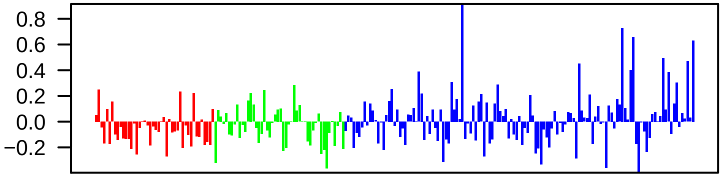
samples with spot = 24 (10.9 %)
mBL : 3 (6.8 %)
intermediate : 3 (6.2 %)
non−mBL : 18 (14 %)

Overview Map



Spot





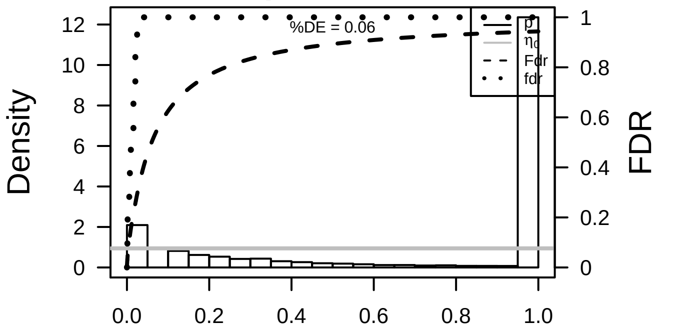
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	214465_at	3.11	−0.71	0.4	ORM2	orosomucoid 2 [Source:HGNC Symbol;Acc:HGNC:8499]
2	203789_s_at	2.15	−0.8	0.45	SEMA3C	semaphorin 3C [Source:HGNC Symbol;Acc:HGNC:10725]
3	202888_s_at	2.08	−0.72	0.46	ANPEP	alanyl aminopeptidase, membrane [Source:HGNC Symbol;Ac
4	222288_at	2.05	−0.78	0.7		
5	207738_s_at	2.04	−0.97	0.68	NCKAP1	NCK associated protein 1 [Source:HGNC Symbol;Acc:HGNC
6	218468_s_at	2.04	−0.87	0.47	GREM1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbo
7	212771_at	2.03	−0.89	0.52	FAM171A1	family with sequence similarity 171 member A1 [Source:HGN
8	203903_s_at	2	−0.91	0.76	HEPH	hephaestin [Source:HGNC Symbol;Acc:HGNC:4866]
9	204363_at	1.96	−0.74	0.65	F3	coagulation factor III, tissue factor [Source:HGNC Symbol;Ac
10	209436_at	1.86	−0.96	0.46	SPON1	spondin 1 [Source:HGNC Symbol;Acc:HGNC:11252]
11	202177_at	1.86	−1.06	0.62	GAS6	growth arrest specific 6 [Source:HGNC Symbol;Acc:HGNC:4
12	202973_x_at	1.84	−0.71	0.6	FAM13A	family with sequence similarity 13 member A [Source:HGNC
13	205573_s_at	1.79	−0.88	0.72	SNX7	sorting nexin 7 [Source:HGNC Symbol;Acc:HGNC:14971]
14	204041_at	1.74	−0.87	0.61	MAOB	monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
15	203548_s_at	1.72	−0.99	0.44	LPL	lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
16	218469_at	1.7	−1.02	0.49	GREM1	gremlin 1, DAN family BMP antagonist [Source:HGNC Symbo
17	201125_s_at	1.68	−0.8	0.51	ITGB5	integrin subunit beta 5 [Source:HGNC Symbol;Acc:HGNC:61
18	201939_at	1.64	−0.84	0.56	PLK2	polo like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
19	212865_s_at	1.63	−0.85	0.63	COL14A1	collagen type XIV alpha 1 chain [Source:HGNC Symbol;Acc:
20	219087_at	1.6	−0.85	0.45	ASPN	asporin [Source:HGNC Symbol;Acc:HGNC:14872]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−16	19 / 214	Lympl	LENZ_Stromal signature 1
2	6e−16	23 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
3	1e−15	46 / 1894	Lympl	HOPP_Poised_promoter
4	9e−15	1 / 14	Cance	LIU_PROSTATE_CANCER_DN
5	9e−15	1 / 14	Cance	LIU_PROSTATE_CANCER_DN
6	9e−14	16 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	8e−13	31 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
8	8e−13	55 / 3168	Lympl	HOPP_Repressed
9	2e−11	19 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
10	1e−10	18 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
11	2e−10	17 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
12	5e−10	22 / 642	GSEA	CUI_TCF21_TARGETS_2_DN
13	7e−10	21 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
14	1e−09	17 / 374	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
15	1e−09	16 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
16	3e−09	10 / 103	Colon	Marisa_CRC−cluster−b
17	1e−08	16 / 383	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
18	1e−08	18 / 500	BP	cell adhesion
19	2e−08	18 / 512	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
20	2e−08	16 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
21	2e−08	13 / 247	GSEA	BOQUEST_STEM_CELL_UP
22	3e−08	13 / 252	GSEA	LU_AGING_BRAIN_UP
23	3e−08	8 / 68	GSEA	HUANG_DASATINIB_RESISTANCE_UP
24	4e−08	13 / 262	GSEA	PASINI_SUZ12_TARGETS_DN
25	6e−08	8 / 75	Melar	Tirosh_Endothelial−cell specific genes−melanoma
26	7e−08	17 / 497	Melar	Gerber_wt/wt_melanoma−cells−SpotD
27	9e−08	7 / 53	Lympl	LENZ_Stromal signature 2
28	1e−07	8 / 82	GSEA	ONDER_CDH1_SIGNALING_VIA_CTNNB1
29	1e−07	17 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
30	2e−07	7 / 58	GSEA	BURTON_ADIPOGENESIS_PEAK_AT_0HR
31	2e−07	6 / 36	GSEA	KUNINGER_IGF1_VS_PDGFB_TARGETS_DN
32	2e−07	46 / 3210	CC	plasma membrane
33	2e−07	9 / 121	GSEA	CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_DN
34	2e−07	12 / 249	GSEA	ONDER_CDH1_TARGETS_2_UP
35	2e−07	37 / 2239	CC	extracellular exosome
36	2e−07	15 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
37	2e−07	11 / 207	GSEA	WANG_SMARCE1_TARGETS_UP
38	3e−07	10 / 169	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
39	3e−07	15 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
40	4e−07	8 / 95	GSEA	TSENG_IRS1_TARGETS_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.04	3 / 107	HORVATH_aging_genes meth UP
2	0.14	2 / 92	HORVATH_aging_genes meth DOWN
3	0.29	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	1e−08	18 / 500	cell adhesion
2	4e−06	10 / 223	angiogenesis
3	3e−04	7 / 183	extracellular matrix organization
4	4e−04	4 / 49	negative regulation of neuron differentiation
5	4e−04	3 / 21	positive regulation of NF−kappaB import into nucleus
6	7e−04	6 / 150	leukocyte migration
7	8e−04	3 / 26	blood vessel morphogenesis
8	1e−03	5 / 107	response to oxidative stress
9	1e−03	5 / 109	animal organ morphogenesis
10	1e−03	5 / 110	platelet degranulation
11	1e−03	3 / 29	activation of protein kinase B activity
12	1e−03	3 / 29	blood vessel remodeling
13	1e−03	6 / 167	Wnt signaling pathway
14	2e−03	3 / 35	collagen fibril organization
15	2e−03	6 / 185	cellular protein metabolic process

Cancer

Rank	p−value	#in/all	Geneset
1	9e−15	1 / 14	LIU_PROSTATE_CANCER_DN
2	9e−05	3 / 13	GENTLES_modul17
3	1e−04	3 / 14	GENTLES_modul13
4	2e−04	3 / 16	GENTLES_modul16
5	2e−03	10 / 480	Lembcke_Colonic Inflammation
6	7e−03	2 / 18	PanCan_Notch_geneset_nanostring
7	1e−02	1 / 16	LIU_LIVER_CANCER
8	3e−02	3 / 96	PanCan_TXmisReg_geneset_nanostring
9	5e−02	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	6e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
11	1e−01	1 / 14	GUSTAFSON_PI3K_DN
12	1e−01	3 / 187	PanCan_PI3K_geneset_nanostring
13	2e−01	1 / 32	KUIPER_MM good survival
14	2e−01	2 / 134	PanCan_RAS_geneset_nanostring
15	3e−01	1 / 47	PanCan_TGF−B_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−07	46 / 3210	plasma membrane
2	2e−07	37 / 2239	extracellular exosome
3	2e−06	23 / 1090	extracellular space
4	3e−06	10 / 212	extracellular matrix
5	5e−06	14 / 462	cell surface
6	6e−06	12 / 345	focal adhesion
7	1e−05	27 / 1611	extracellular region
8	8e−05	5 / 63	platelet alpha granule lumen
9	2e−04	5 / 75	apical part of cell
10	1e−03	4 / 62	filopodium
11	2e−03	7 / 241	endoplasmic reticulum lumen
12	2e−03	7 / 253	proteinaceous extracellular matrix
13	6e−03	2 / 17	apicolateral plasma membrane
14	9e−03	2 / 20	lamellipodium membrane
15	9e−03	3 / 60	actin filament

Chr

Rank	p−value	#in/all	Geneset
1	0.01	8 / 437	Chr 8
2	0.14	5 / 382	Chr 15
3	0.23	12 / 1325	Chr 1
4	0.24	8 / 832	Chr 2
5	0.25	3 / 242	Chr 13
6	0.26	5 / 480	Chr 4
7	0.27	4 / 369	Chr 20
8	0.27	5 / 490	Chr 10
9	0.27	5 / 492	Chr 9
10	0.36	5 / 556	Chr X
11	0.40	5 / 585	Chr 7
12	0.45	6 / 756	Chr 11
13	0.55	5 / 689	Chr 3
14	0.55	3 / 403	Chr 14
15	0.63	1 / 139	Chr 21

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−18	53 / 2197	monocytes peripheral blood_11_BivFlnk
2	2e−18	69 / 3918	Tcells peripheral blood_14_ReprPCWk
3	1e−17	60 / 3001	Bcells peripheral blood_14_ReprPCWk
4	1e−16	54 / 2515	natural killer cells peripheral blood_13_ReprPC
5	7e−16	54 / 2602	natural killer cells peripheral blood_12_EnhBiv
6	2e−15	59 / 3184	monocytes peripheral blood_12_EnhBiv
7	2e−15	58 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
8	6e−15	48 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
9	2e−14	53 / 2700	Thelper cells peripheral blood_14_ReprPCWk
10	3e−14	57 / 3150	monocytes peripheral blood_13_ReprPC
11	3e−14	58 / 3272	monocytes peripheral blood_14_ReprPCWk
12	4e−14	53 / 2747	Bcells peripheral blood_12_EnhBiv
13	1e−13	52 / 2724	Tcells peripheral blood_11_BivFlnk
14	1e−13	61 / 3724	Tcells peripheral blood_12_EnhBiv
15	2e−13	50 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−13	31 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	3e−09	10 / 103	Marisa_CRC−cluster−b
3	4e−05	18 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
4	1e−04	11 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
5	3e−04	5 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
6	2e−03	2 / 10	KIM_CRC−MSI−regulated_DN
7	9e−03	2 / 20	Kosinski_top−crypt−short−list
8	1e−02	4 / 132	Marisa_CRC−cluster−a
9	2e−02	6 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	2e−02	2 / 31	Kosinski_lower−crypt−short−list
11	2e−02	8 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	3e−02	6 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	4e−02	5 / 255	Kosinski_top−crypt−long−list
14	4e−02	1 / 6	Hewish_dMMR−secondary−mutations_Signal_transduction
15	5e−02	1 / 7	Budinska_C_CIMP−H−like_UP

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	4 / 85	ScoV_0.999_Sturm_E2_IDH_DN
2	0.005	3 / 50	Vishal_subnetwork signature of survival in GBM
3	0.009	4 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
4	0.012	3 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
5	0.012	6 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
6	0.015	4 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	0.019	4 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	0.026	2 / 35	Gorovets_LGG_EPL_subclass
9	0.034	3 / 99	GIEZELT_GBM_WT_up_VS_mut
10	0.034	2 / 41	Gorovets_LGG_PG_subclass
11	0.041	2 / 45	OL vs. MOG− OL
12	0.042	1 / 6	WILLSCHER_GBM_STSwt_proteomics−N_UP
13	0.064	2 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
14	0.070	2 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
15	0.076	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−16	23 / 366	LIM_MAMMARY_STEM_CELL_UP
2	9e−15	1 / 14	LIU_PROSTATE_CANCER_DN
3	9e−14	16 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	2e−11	19 / 381	SWEET_LUNG_CANCER_KRAS_DN
5	1e−10	18 / 376	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	2e−10	17 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
7	5e−10	22 / 642	CUI_TCF21_TARGETS_2_DN
8	7e−10	21 / 589	WONG_ADULT_TISSUE_STEM_MODULE
9	1e−09	17 / 374	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
10	1e−09	16 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
11	1e−08	16 / 383	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
12	2e−08	18 / 512	WEST_ADRENOCORTICAL_TUMOR_DN
13	2e−08	16 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
14	2e−08	13 / 247	BOQUEST_STEM_CELL_UP
15	3e−08	13 / 252	LU_AGING_BRAIN_UP

HM

Rank	p−value	#in/all	Geneset
1	7e−05	8 / 194	HALLMARK_KRAS_SIGNALING_UP
2	8e−05	8 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	9e−05	4 / 34	HALLMARK_ANGIOGENESIS
4	3e−04	6 / 130	HALLMARK_COAGULATION
5	2e−03	3 / 34	HALLMARK_APICAL_SURFACE
6	3e−03	6 / 194	HALLMARK_MYOGENESIS
7	3e−03	5 / 141	HALLMARK_UV_RESPONSE_DN
8	9e−03	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
9	2e−02	2 / 29	HALLMARK_NOTCH_SIGNALING
10	3e−02	4 / 170	HALLMARK_IL2_STAT5_SIGNALING
11	5e−02	4 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	5e−02	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	5e−02	2 / 51	HALLMARK_TGF_BETA_SIGNALING
14	7e−02	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	1e−01	3 / 174	HALLMARK_ADIPOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	2 / 38	Angelova_immune−metagene−mast−cells
2	0.04	1 / 5	Angelova_immune−metagene−NK56_bright
3	0.08	1 / 11	Angelova_immune−metagene−macrophages
4	0.13	1 / 19	Angelova_immune−metagene−iDC
5	0.15	1 / 23	Angelova_immune−metagene−Th2
6	0.16	1 / 25	Angelova_immune−metagene−DC
7	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
8	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
9	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
10	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
11	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
12	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
14	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
15	1.00	0 / 14	Angelova_immune−metagene−eosinophil

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 32	Marjolein_ageing−genes_DN
2	0.3	2 / 150	Homuth_BMI−associated−genes_UP
3	0.4	1 / 62	DUMEAUX_Smoking enriched genes
4	0.8	1 / 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−16	19 / 214	LENZ_Stromal signature 1
2	1e−15	46 / 1894	HOPP_Poised_promoter
3	8e−13	55 / 3168	HOPP_Repressed
4	9e−08	7 / 53	LENZ_Stromal signature 2
5	4e−05	6 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
6	5e−05	6 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
7	8e−05	31 / 2206	HOPP_Heterochrom
8	4e−04	5 / 88	ROSOLOWSKI_green UP
9	2e−03	5 / 121	ROSOLOWSKI_green total
10	3e−03	2 / 12	Subero_MM_hypo_meth
11	4e−03	23 / 1814	HOPP_Repetitive
12	7e−03	3 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
13	7e−03	2 / 18	DAVE_Immune response 2
14	7e−03	3 / 56	Subero_mBL_hyper_meth
15	2e−02	3 / 77	TARTE_Plasma cell signature

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−08	8 / 75	Tirosh_Endothelial−cell specific genes−melanoma
2	7e−08	17 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	2e−05	6 / 78	Tirosh_CAF−cell specific genes
4	3e−02	5 / 236	Gerber_wt/wt_group3−specific
5	3e−02	2 / 41	Tirosh_top50 correlated genes PC3
6	4e−02	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
7	8e−02	2 / 64	Harbst_melanoma_lowgrade_up
8	1e−01	3 / 171	Landsberg_dedifferentiation_up
9	2e−01	1 / 24	Gerami_melanoma−metastatic−risk_DN
10	2e−01	3 / 204	Landsberg_dedifferentiation_down
11	2e−01	1 / 39	Tirosh_top50 correlated genes PC4
12	4e−01	1 / 68	Tirosh_housekeeping_genes
13	4e−01	1 / 71	Tirosh_Macrophage specific genes−melanoma
14	4e−01	1 / 81	Tirosh_Genes in the MITF program
15	5e−01	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC

MF

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 52	collagen binding
2	2e−03	12 / 644	protein homodimerization activity
3	3e−03	2 / 11	peptidase activator activity
4	4e−03	69 / 7864	protein binding
5	5e−03	2 / 15	Notch binding
6	5e−03	3 / 49	transmembrane receptor protein tyrosine kinase activity
7	7e−03	4 / 106	integrin binding
8	9e−03	2 / 20	insulin−like growth factor binding
9	9e−03	2 / 20	receptor ligand activity
10	1e−02	2 / 21	gamma−tubulin binding
11	1e−02	9 / 517	calcium ion binding
12	1e−02	7 / 346	receptor binding
13	1e−02	8 / 437	protein kinase activity
14	1e−02	3 / 69	virus receptor activity
15	1e−02	3 / 70	electron transfer activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	7 / 226	hsa−miR−548h
2	0.002	7 / 251	hsa−miR−548i
3	0.002	7 / 253	hsa−miR−548c−5p
4	0.003	7 / 261	hsa−miR−559
5	0.003	7 / 269	hsa−miR−548a−5p
6	0.003	4 / 87	hsa−miR−1206
7	0.004	4 / 88	hsa−miR−1271
8	0.004	5 / 148	hsa−miR−196b
9	0.004	7 / 284	hsa−miR−548d−5p
10	0.004	7 / 285	hsa−miR−548b−5p
11	0.005	5 / 157	hsa−miR−374a
12	0.007	6 / 240	hsa−miR−548j
13	0.007	5 / 171	hsa−miR−196a
14	0.009	2 / 20	hsa−miR−99a
15	0.010	2 / 21	hsa−miR−483−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.05	2 / 48	Burnham_viral_DN
2	0.21	1 / 33	Sweeney_viral_dn
3	0.25	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.34	1 / 57	Burnham_day1_vs_5_UP
5	0.58	1 / 122	Terre_IMS_influenza_meta_signature
6	1.00	0 / 68	Burnham_sep_vs_con_UP
7	1.00	0 / 56	Burnham_sep_vs_con_DN
8	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
9	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
10	1.00	0 / 57	Burnham_viral_UP
11	1.00	0 / 52	Burnham_day1_vs_5_DN
12	1.00	0 / 54	Burnham_timecourse
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−06	4 / 13	WIRTH_Sec. lymphoid organs
2	3e−04	5 / 81	Chaussabel_1,2_Platelets
3	1e−03	4 / 62	VAQUERIZAS_Lung_TF
4	4e−03	6 / 209	Chaussabel_2,5_Immune related molecules
5	6e−03	6 / 233	PROTEINATLAS_smooth muscle
6	6e−03	2 / 17	VAQUERIZAS_Heart_TF
7	2e−02	2 / 30	VAQUERIZAS_Fetal lung_TF
8	3e−02	2 / 36	VAQUERIZAS_Prostate_TF
9	3e−02	2 / 41	VAQUERIZAS_Thyroid_TF
10	3e−02	3 / 100	Chaussabel_2,8_T−cells
11	4e−02	2 / 45	VAQUERIZAS_Placenta_TF
12	4e−02	1 / 6	JONGENEEL_Uterus
13	5e−02	1 / 7	VAQUERIZAS_Tongue_TF
14	5e−02	4 / 198	Chaussabel_3,3_Inflammation II
15	8e−02	1 / 12	WIRTH_Tonsil

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	4e−06	23 / 1148	HEBENSTREIT_low expression TF
2	3e−01	5 / 485	ICGC_NrsfPcr2_targets
3	4e−01	18 / 2321	ICGC_Rad21_targets
4	5e−01	8 / 1041	ICGC_P300_targets
5	6e−01	3 / 415	ICGC_RxraPcr1_targets
6	6e−01	7 / 1032	ICGC_Usf1_targets
7	7e−01	15 / 2254	ICGC_BatfPcr1_targets
8	7e−01	9 / 1387	HEBENSTREIT_high expression TF
9	7e−01	14 / 2150	ICGC_Irf4_targets
10	7e−01	10 / 1636	ICGC_Bcl11_targets
11	8e−01	22 / 3435	ICGC_Ebfsc137065_targets
12	9e−01	6 / 1241	KIM_MYC targets
13	9e−01	2 / 549	ICGC_Atf3_targets
14	9e−01	9 / 1848	ICGC_Pbx3_targets
15	9e−01	20 / 3608	ICGC_Tcf12_targets

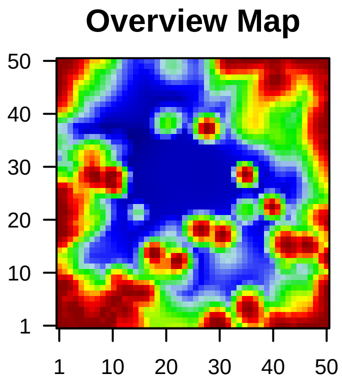
Overexpression Spots

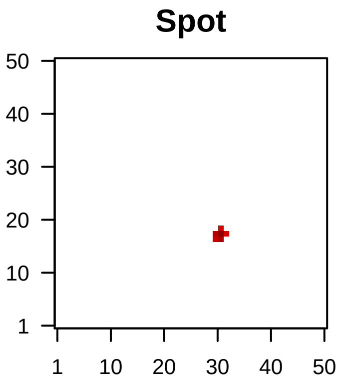
Spot Summary: G1

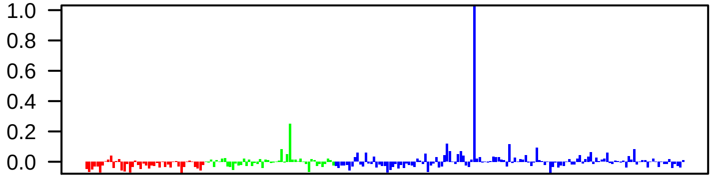
metagenes = 6
genes = 147

<r> metagenes = 0.99
<r> genes = 0.09
beta: r2= 0.34 / log p= −Inf

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


Overview Map


Spot

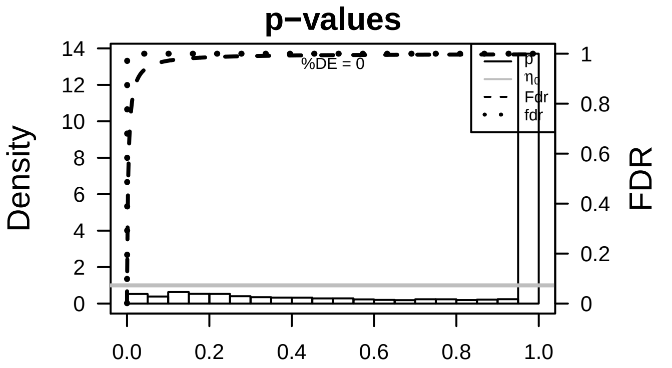


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	216430_x_at	2.85	−0.73	0.41		
2	207213_s_at	2.46	−0.66	0.45	USP2	ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG
3	219511_s_at	2.03	−0.78	0.4	SNCAIP	synuclein alpha interacting protein [Source:HGNC Symbol;Ac
4	206001_at	2	−0.74	0.42	NPY	neuropeptide Y [Source:HGNC Symbol;Acc:HGNC:7955]
5	204454_at	1.99	−0.8	0.39	LDOC1	LDOC1, regulator of NFKB signaling [Source:HGNC Symbol;
6	205817_at	1.85	−0.72	0.37	SIX1	SIX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10887]
7	203458_at	1.84	−1.13	0.35	SPR	sepiapterin reductase [Source:HGNC Symbol;Acc:HGNC:112
8	210402_at	1.83	−0.64	0.42	KCNJ1	potassium voltage−gated channel subfamily J member 1 [Sou
9	219658_at	1.79	−0.81	0.21	PTCD2	pentatricopeptide repeat domain 2 [Source:HGNC Symbol;Ac
10	221526_x_at	1.74	−0.59	0.3	PARD3	par−3 family cell polarity regulator [Source:HGNC Symbol;Ac
11	203441_s_at	1.73	−0.91	0.33	CDH2	cadherin 2 [Source:HGNC Symbol;Acc:HGNC:1759]
12	219412_at	1.73	−0.59	0.41	RAB38	RAB38, member RAS oncogene family [Source:HGNC Symb
13	201481_s_at	1.7	−1.17	0.33	PYGB	glycogen phosphorylase B [Source:HGNC Symbol;Acc:HGN
14	214481_at	1.7	−0.74	0.2	HIST1H2AM	histone cluster 1 H2A family member m [Source:HGNC Symb
15	219527_at	1.69	−0.63	0.32	MARC2	mitochondrial amidoxime reducing component 2 [Source:HGN
16	206876_at	1.68	−0.46	0.36	SIM1	single−minded family bHLH transcription factor 1 [Source:HG
17	205464_at	1.66	−0.64	0.41	SCNN1B	sodium channel epithelial 1 beta subunit [Source:HGNC Sym
18	211197_s_at	1.58	−1.07	0.27	LOC102723996	
19	215184_at	1.54	−0.56	0.42	DAPK2	death associated protein kinase 2 [Source:HGNC Symbol;Ac
20	220002_at	1.54	−0.88	0.36	KIF26B	kinesin family member 26B [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	4 / 17	BP	regulation of long−term neuronal synaptic plasticity
2	4e−05	25 / 1092	GSEA	YOSHIMURA_MAPK8_TARGETS_UP
3	2e−04	4 / 32	BP	excretion
4	3e−04	6 / 92	Colon	Marisa_CRC−cluster−h
5	4e−04	33 / 1894	Lympl	HOPP_Poised_promoter
6	5e−04	3 / 17	MF	inward rectifier potassium channel activity
7	6e−04	5 / 71	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
8	7e−04	3 / 18	BP	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion
9	8e−04	47 / 3168	Lympl	HOPP_Repressed
10	1e−03	3 / 21	BP	potassium ion import
11	1e−03	7 / 164	Colon	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	1e−03	7 / 165	MF	calmodulin binding
13	1e−03	5 / 81	CC	synaptic vesicle
14	1e−03	3 / 23	BP	leukocyte cell−cell adhesion
15	1e−03	7 / 172	GSEA	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN
16	2e−03	3 / 24	BP	positive regulation of blood vessel diameter
17	2e−03	3 / 24	GSEA	REACTOME_INWARDLY_RECTIFYING_K_CHANNELS
18	2e−03	7 / 179	CC	external side of plasma membrane
19	2e−03	8 / 231	CC	apical plasma membrane
20	3e−03	2 / 8	GSEA	MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP
21	3e−03	5 / 99	GSEA	REACTOME_CELL_CELL_COMMUNICATION
22	3e−03	4 / 63	GSEA	REACTOME_CELL_JUNCTION_ORGANIZATION
23	4e−03	3 / 33	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_5_DN
24	4e−03	2 / 10	BP	magnesium ion transmembrane transport
25	4e−03	2 / 10	BP	positive regulation of hormone secretion
26	4e−03	6 / 156	GSEA	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
27	4e−03	10 / 385	GSEA	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1
28	4e−03	4 / 68	Pneu	Burnham_sep_vs_con_UP
29	5e−03	7 / 213	GSEA	SABATES_COLORECTAL_ADENOMA_DN
30	5e−03	2 / 11	MF	magnesium ion transmembrane transporter activity
31	5e−03	2 / 11	BP	regulation of fat cell differentiation
32	5e−03	3 / 36	GSEA	GNATENKO_PLATELET_SIGNATURE
33	5e−03	3 / 37	BP	placenta development
34	6e−03	2 / 12	CC	platelet alpha granule membrane
35	6e−03	2 / 12	CC	trans−Golgi network transport vesicle
36	6e−03	2 / 12	GSEA	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
37	6e−03	3 / 38	BP	positive regulation of insulin secretion
38	6e−03	9 / 344	GSEA	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
39	6e−03	3 / 39	BP	branching involved in ureteric bud morphogenesis
40	6e−03	7 / 225	BP	ion transmembrane transport


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.01	4 / 92	HORVATH_aging_genes meth DOWN
2	0.37	1 / 47	TESCHENDORFF_age_hypermethylated
3	0.65	1 / 107	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	0.001	5 / 81	synaptic vesicle
2	0.002	7 / 179	external side of plasma membrane
3	0.002	8 / 231	apical plasma membrane
4	0.006	2 / 12	platelet alpha granule membrane
5	0.006	2 / 12	trans−Golgi network transport vesicle
6	0.011	43 / 3210	plasma membrane
7	0.014	2 / 19	plasma membrane raft
8	0.016	5 / 152	basolateral plasma membrane
9	0.018	3 / 57	cytoplasmic ribonucleoprotein granule
10	0.018	7 / 277	neuron projection
11	0.019	2 / 22	multivesicular body
12	0.022	2 / 24	dynein complex
13	0.026	2 / 26	integrin complex
14	0.028	2 / 27	Golgi stack
15	0.035	3 / 74	secretory granule membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	6 / 92	Marisa_CRC−cluster−h
2	1e−03	7 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
3	1e−02	75 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	1e−02	11 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
5	3e−02	8 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
6	4e−02	6 / 255	Kosinski_top−crypt−long−list
7	5e−02	6 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
8	7e−02	1 / 7	Budinska_C_CIMP−H−like_UP
9	2e−01	7 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
10	3e−01	6 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
11	3e−01	10 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
12	3e−01	10 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	3e−01	6 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	4e−01	12 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	4e−01	4 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_

HM

Rank	p−value	#in/all	Geneset
1	0.04	2 / 34	HALLMARK_APICAL_SURFACE
2	0.09	4 / 174	HALLMARK_APICAL_JUNCTION
3	0.17	2 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	0.22	3 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	0.24	2 / 97	HALLMARK_BILE_ACID_METABOLISM
6	0.25	1 / 29	HALLMARK_NOTCH_SIGNALING
7	0.28	3 / 191	HALLMARK_P53_PATHWAY
8	0.29	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
9	0.29	3 / 194	HALLMARK_MYOGENESIS
10	0.29	3 / 194	HALLMARK_KRAS_SIGNALING_UP
11	0.29	3 / 195	HALLMARK_KRAS_SIGNALING_DN
12	0.31	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	0.49	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
14	0.51	2 / 174	HALLMARK_ADIPOGENESIS
15	0.51	2 / 176	HALLMARK_ALLOGRAFT_REJECTION

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−04	33 / 1894	HOPP_Poised_promoter
2	8e−04	47 / 3168	HOPP_Repressed
3	1e−01	1 / 15	DAVE_BL Inter
4	2e−01	4 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
5	2e−01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
6	2e−01	1 / 26	DAVE_Immune response 1
7	3e−01	1 / 35	Subero_MM_hyper_meth
8	4e−01	23 / 2206	HOPP_Heterochrom
9	4e−01	1 / 53	LENZ_Stromal signature 2
10	5e−01	1 / 77	TARTE_Plasma cell signature
11	6e−01	1 / 85	Sha_DLBCL UP
12	6e−01	1 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	6e−01	2 / 213	SPANG_IL21 DN
14	6e−01	2 / 227	SPANG_IL21 UP
15	7e−01	2 / 237	ZHANG_DLBCL mutated

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	2 / 16	hsa−miR−564
2	0.08	3 / 104	hsa−miR−1272
3	0.12	1 / 13	hsa−miR−671−3p
4	0.15	1 / 17	hsa−miR−151−5p
5	0.17	2 / 78	hsa−miR−216a
6	0.19	1 / 22	hsa−miR−941
7	0.20	3 / 160	hsa−miR−330−3p
8	0.21	2 / 88	hsa−miR−600
9	0.22	1 / 26	hsa−miR−1293
10	0.22	1 / 26	hsa−miR−631
11	0.23	1 / 27	hsa−miR−621
12	0.25	1 / 30	hsa−miR−601
13	0.27	1 / 32	hsa−miR−517*
14	0.27	1 / 32	hsa−miR−525−3p
15	0.28	1 / 33	hsa−miR−502−3p

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	2e−05	4 / 17	regulation of long−term neuronal synaptic plasticity
2	2e−04	4 / 32	excretion
3	7e−04	3 / 18	calcium−dependent cell−cell adhesion via plasma membrane cell adhesion m
4	1e−03	3 / 21	potassium ion import
5	1e−03	3 / 23	leukocyte cell−cell adhesion
6	2e−03	3 / 24	positive regulation of blood vessel diameter
7	4e−03	2 / 10	magnesium ion transmembrane transport
8	4e−03	2 / 10	positive regulation of hormone secretion
9	5e−03	2 / 11	regulation of fat cell differentiation
10	5e−03	3 / 37	placenta development
11	6e−03	3 / 38	positive regulation of insulin secretion
12	6e−03	3 / 39	branching involved in ureteric bud morphogenesis
13	6e−03	7 / 225	ion transmembrane transport
14	7e−03	2 / 13	positive regulation of leukocyte migration
15	7e−03	2 / 13	striated muscle cell differentiation

Chr

Rank	p−value	#in/all	Geneset
1	0.04	7 / 333	Chr 22
2	0.07	7 / 369	Chr 20
3	0.16	8 / 548	Chr 16
4	0.18	11 / 832	Chr 2
5	0.29	7 / 556	Chr X
6	0.31	9 / 756	Chr 11
7	0.34	6 / 492	Chr 9
8	0.39	2 / 139	Chr 21
9	0.42	9 / 833	Chr 19
10	0.47	7 / 669	Chr 6
11	0.48	8 / 776	Chr 17
12	0.54	2 / 184	Chr 18
13	0.66	6 / 689	Chr 3
14	0.70	4 / 490	Chr 10
15	0.75	11 / 1325	Chr 1

Glioma

Rank	p−value	#in/all	Geneset
1	0.05	2 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
2	0.08	2 / 47	developing astrocytes
3	0.09	1 / 10	Phillips MES up vs Prolif & PN
4	0.09	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
5	0.10	1 / 11	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
6	0.11	1 / 12	VERHAAK_Brain
7	0.11	1 / 12	Donson−immune cell intra signaling−associated with LTS in HGA
8	0.12	7 / 423	Down_a
9	0.12	2 / 62	GIEZELT_GBM_STS_down_VS_LTS
10	0.13	1 / 14	astrocytes_glio
11	0.14	1 / 16	VERHAAK_CL subtype
12	0.17	2 / 78	Weller_LGG_A_vs_O_UP
13	0.19	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	0.27	3 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	0.27	2 / 105	WIRTH_Normal Brain

Immunome

Rank	p−value	#in/all	Geneset
1	0.03	1 / 3	Angelova_CRC_MHC_class_I
2	0.11	1 / 12	Angelova_immune−metagene−NK56_dim
3	0.14	1 / 15	Angelova_immune−metagene−NK
4	0.17	1 / 19	Angelova_immune−metagene−iDC
5	0.20	1 / 23	Angelova_immune−metagene−Th2
6	0.20	1 / 23	Angelova_immune−metagene−Treg
7	0.25	1 / 29	Angelova_immune−metagene−Th1
8	0.34	1 / 42	Angelova_immune−metagene−TGD
9	0.36	1 / 45	Angelova_immune−metagene−MDSC
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 / 7	Angelova_immune−metagene−cytotoxic_cells

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	3 / 64	Harbst_melanoma_lowgrade_up
2	0.05	2 / 37	Hugo_melanoma−all−MET_DN
3	0.05	2 / 39	Tirosh_melanoma specific genes
4	0.06	1 / 6	Joensson_Melanoma high immune response subtype
5	0.17	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
6	0.32	3 / 204	Landsberg_dedifferentiation_down
7	0.33	1 / 41	Tirosh_top50 correlated genes PC3
8	0.47	1 / 65	Harbst_melanoma_highgrade_up
9	0.52	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
10	0.55	1 / 81	Tirosh_Genes in the MITF program
11	0.56	1 / 85	Tirosh_AXL−signature
12	0.69	1 / 119	TCGA_melanoma_MITF_low
13	0.75	2 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	0.84	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
15	0.84	1 / 189	Tirosh_genes preferentially expressed by Tregs

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.004	4 / 68	Burnham_sep_vs_con_UP
2	0.032	3 / 71	Burnham_cap_fp_vs_con_UP
3	0.050	2 / 37	Sweeney_viral_up
4	0.079	2 / 48	Burnham_viral_DN
5	0.090	2 / 52	Burnham_day1_vs_5_DN
6	0.161	1 / 18	Scicluna_UP
7	0.251	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
8	0.330	1 / 41	Scicluna_DN
9	0.332	2 / 122	Terre_IMS_influenza_meta_signature
10	0.374	1 / 48	Burnham_cap_fp_vs_con_DN
11	0.421	1 / 56	Burnham_sep_vs_con_DN
12	0.427	1 / 57	Burnham_viral_UP
13	0.733	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
14	1.000	0 / 57	Burnham_day1_vs_5_UP
15	1.000	0 / 54	Burnham_timecourse

TF

Rank	p−value	#in/all	Geneset
1	0.03	18 / 1148	HEBENSTREIT_low expression TF
2	0.12	18 / 1387	HEBENSTREIT_high expression TF
3	0.12	28 / 2321	ICGC_Rad21_targets
4	0.16	8 / 549	ICGC_Atf3_targets
5	0.18	23 / 1941	ICGC_Bcl3_targets
6	0.19	7 / 485	ICGC_NrsfPcr2_targets
7	0.20	45 / 4131	ICGC_Tcf3_targets
8	0.20	38 / 3435	ICGC_Ebfsc137065_targets
9	0.20	13 / 1032	ICGC_Usf1_targets
10	0.32	50 / 4851	ICGC_Runx3_targets
11	0.34	44 / 4264	ICGC_Pax5_targets
12	0.36	47 / 4602	ICGC_Elf1_targets
13	0.38	33 / 3213	ICGC_Pu1_targets
14	0.48	15 / 1494	ICGC_Cebpbsc150_targets
15	0.49	42 / 4278	ICGC_Yy1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.2	1 / 20	PanCan_ChromMod_geneset_nanostring
2	0.2	2 / 96	PanCan_TXmisReg_geneset_nanostring
3	0.3	1 / 32	KUIPER_MM good survival
4	0.5	0 / 14	LIU_PROSTATE_CANCER_DN
5	0.5	1 / 72	PanCan_Wnt_geneset_nanostring
6	0.5	1 / 80	PanCan_JAK−ST_geneset_nanostring
7	0.7	1 / 134	PanCan_RAS_geneset_nanostring
8	0.8	3 / 409	Lembcke_Normal vs Adenoma
9	0.8	1 / 187	PanCan_PI3K_geneset_nanostring
10	0.9	2 / 480	Lembcke_Colonic Inflammation
11	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1.0	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.0	0 / 12	LIU_BREAST_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−07	59 / 3272	monocytes peripheral blood_14_ReprPCWk
2	2e−07	57 / 3150	monocytes peripheral blood_13_ReprPC
3	9e−07	62 / 3724	Tcells peripheral blood_12_EnhBiv
4	2e−06	45 / 2374	9_ReprPCWk_Fibroblasts
5	6e−06	44 / 2375	10_ReprPC_Fibroblasts
6	1e−05	53 / 3184	monocytes peripheral blood_12_EnhBiv
7	1e−05	59 / 3734	Tcells peripheral blood_13_ReprPC
8	1e−05	36 / 1813	8_EnhP_Fibroblasts
9	3e−05	33 / 1649	13_ReprPC_ESC_Mesoderm
10	5e−05	35 / 1841	HSC_12_EnhBiv
11	6e−05	39 / 2173	HSC_13_ReprPC
12	7e−05	44 / 2602	natural killer cells peripheral blood_12_EnhBiv
13	7e−05	39 / 2197	monocytes peripheral blood_11_BivFlnk
14	1e−04	36 / 1984	10_ReprPC_Melanocytes
15	1e−04	45 / 2747	Bcells peripheral blood_12_EnhBiv

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−05	25 / 1092	YOSHIMURA_MAPK8_TARGETS_UP
2	6e−04	5 / 71	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
3	1e−03	7 / 172	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_DN
4	2e−03	3 / 24	REACTOME_INWARDLY_RECTIFYING_K_CHANNELS
5	3e−03	2 / 8	MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP
6	3e−03	5 / 99	REACTOME_CELL_CELL_COMMUNICATION
7	3e−03	4 / 63	REACTOME_CELL_JUNCTION_ORGANIZATION
8	4e−03	3 / 33	FIGUEROA_AML_METHYLATION_CLUSTER_5_DN
9	4e−03	6 / 156	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
10	4e−03	10 / 385	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1
11	5e−03	7 / 213	SABATES_COLORECTAL_ADENOMA_DN
12	5e−03	3 / 36	GNATENKO_PLATELET_SIGNATURE
13	6e−03	2 / 12	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
14	6e−03	9 / 344	MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED
15	7e−03	3 / 40	MCCLUNG_DELTA_FOSB_TARGETS_8WK

Lifestyle

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

MF

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 17	inward rectifier potassium channel activity
2	1e−03	7 / 165	calmodulin binding
3	5e−03	2 / 11	magnesium ion transmembrane transporter activity
4	9e−03	4 / 83	microtubule motor activity
5	9e−03	4 / 83	motor activity
6	9e−03	4 / 84	hormone activity
7	2e−02	2 / 20	polyubiquitin modification−dependent protein binding
8	2e−02	3 / 56	calcium−dependent protein binding
9	2e−02	2 / 21	WW domain binding
10	2e−02	2 / 22	cation channel activity
11	2e−02	2 / 24	extracellular matrix binding
12	3e−02	3 / 65	protein phosphatase binding
13	3e−02	2 / 26	neuropeptide hormone activity
14	3e−02	21 / 1402	nucleotide binding
15	3e−02	3 / 70	calcium channel activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.009	6 / 182	WIRTH_post GC B−cells
2	0.066	1 / 7	VAQUERIZAS_Tongue_TF
3	0.070	2 / 45	JONGENEEL_Kidney
4	0.099	2 / 55	WIRTH_Homeostasis
5	0.102	1 / 11	JONGENEEL_Thyroid
6	0.110	1 / 12	VAQUERIZAS_Kidney_TF
7	0.119	1 / 13	WIRTH_B−cells
8	0.119	1 / 13	WIRTH_Bone marrow
9	0.119	1 / 13	VAQUERIZAS_Skin_TF
10	0.136	1 / 15	WIRTH_Telencephalon
11	0.136	1 / 15	JONGENEEL_Lung
12	0.144	1 / 16	VAQUERIZAS_Fetal thyroid_TF
13	0.144	1 / 16	VAQUERIZAS_Salivary gland_TF
14	0.169	1 / 19	JONGENEEL_Adrenal Gland
15	0.169	1 / 19	JONGENEEL_Prostate

Overexpression Spots

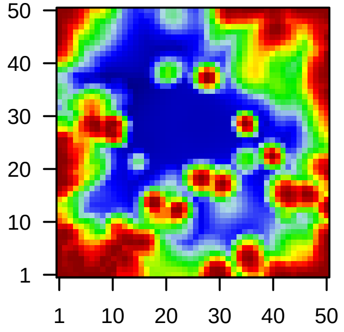
Spot Summary: H1

metagenes = 10
genes = 275

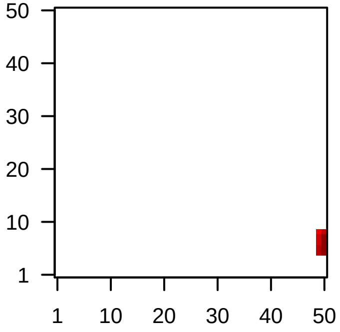
<r> metagenes = 0.98
<r> genes = 0.42
beta: r2= 8.99 / log p= −Inf

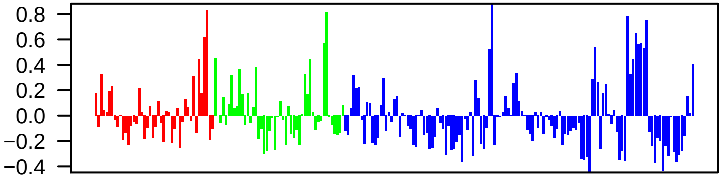
samples with spot = 37 (16.7 %)
mBL : 7 (15.9 %)
intermediate : 8 (16.7 %)
non−mBL : 22 (17.1 %)

Overview Map



Spot





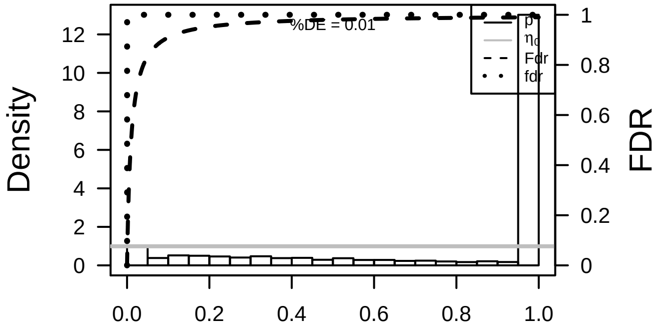
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	214753_at	2.14	−1.23	0.73		
2	207492_at	2.1	−1.01	0.76		
3	205316_at	2.09	−0.97	0.56	SLC15A2	solute carrier family 15 member 2 [Source:HGNC Symbol;Acc
4	220918_at	2.03	−0.81	0.79		
5	208268_at	1.89	−0.91	0.51	ADAM28	ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
6	208195_at	1.84	−1.07	0.36	TTN	titin [Source:HGNC Symbol;Acc:HGNC:12403]
7	220940_at	1.83	−1.2	0.77		
8	215164_at	1.82	−1.12	0.57		
9	215768_at	1.81	−0.79	0.44		
10	217534_at	1.8	−0.88	0.75	FAM49B	family with sequence similarity 49 member B [Source:HGNC
11	216197_at	1.78	−0.87	0.77		
12	221616_s_at	1.78	−0.7	0.76		
13	222358_x_at	1.78	−0.81	0.83		
14	216614_at	1.77	−0.95	0.74		
15	220704_at	1.76	−1.2	0.8	IKZF1	IKAROS family zinc finger 1 [Source:HGNC Symbol;Acc:HGN
16	210230_at	1.75	−1.07	0.63		
17	213089_at	1.75	−1.37	0.89		
18	215221_at	1.74	−0.82	0.62		
19	215599_at	1.73	−0.9	0.83		glucuronidase, beta pseudogene 3 [Source:HGNC Symbol;Ac
20	215024_at	1.72	−0.92	0.78	CCZ1	CCZ1 homolog, vacuolar protein trafficking and biogenesis as

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−25	31 / 218	Refer	WIRTH_pre+post GC B−cells
2	1e−21	57 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
3	2e−19	25 / 188	Refer	Chaussabel_3,8_Enzymes
4	3e−16	33 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
5	5e−15	14 / 59	Gliom	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	2e−13	5 / 14	Canc	LIU_COMMON_CANCER_GENES
7	2e−13	5 / 14	Canc	LIU_COMMON_CANCER_GENES
8	5e−13	9 / 20	Refer	Chaussabel_2,7_Unknown function
9	2e−12	93 / 4261	Lymp	HOPP_Txn_transition
10	1e−11	16 / 143	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
11	3e−10	14 / 127	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
12	3e−10	104 / 5529	Lymp	HOPP_Txn_elongation
13	5e−10	7 / 17	GSEA	SPIRA_SMOKERS_LUNG_CANCER_DN
14	3e−09	12 / 102	Lymp	ROSOLOWSKI_blue total
15	4e−09	7 / 22	Refer	Chaussabel_1,6_Signaling molecules
16	4e−08	22 / 477	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
17	6e−08	30 / 852	MF	nucleic acid binding
18	6e−07	11 / 136	GSEA	REACTOME_MRNA_PROCESSING
19	7e−07	29 / 906	Lymp	SPANG_BCR DN
20	1e−06	36 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
21	5e−06	38 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
22	8e−06	5 / 24	GSEA	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
23	8e−06	21 / 600	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
24	1e−05	9 / 120	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
25	1e−05	31 / 1161	MF	RNA binding
26	1e−05	13 / 261	GSEA	WANG_LMO4_TARGETS_UP
27	1e−05	80 / 4579	CC	nucleus
28	2e−05	23 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
29	2e−05	11 / 198	BP	mRNA splicing, via spliceosome
30	3e−05	13 / 281	BP	mRNA processing
31	4e−05	8 / 106	Refer	Chaussabel_2,11_Replication
32	4e−05	37 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
33	7e−05	16 / 445	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
34	8e−05	17 / 496	Refer	PROTEINATLAS_spleen
35	8e−05	9 / 152	Refer	VAQUERIZAS_General_TF
36	9e−05	3 / 8	Gliom	WILLSCHER_GBM_LTSmut_proteomics−A_UP
37	9e−05	5 / 39	GSEA	BILBAN_B_CLL_LPL_DN
38	9e−05	7 / 90	BP	RNA processing
39	1e−04	7 / 92	GSEA	REACTOME_MRNA_SPLICING
40	1e−04	7 / 92	GSEA	HOEBEKE_LYMPHOID_STEM_CELL_UP

p−values



Aging

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

CC

Rank	p−value	#in/all	Geneset
1	1e−05	80 / 4579	nucleus
2	5e−04	12 / 326	nuclear speck
3	1e−03	46 / 2541	nucleoplasm
4	5e−03	9 / 268	intracellular ribonucleoprotein complex
5	7e−03	5 / 101	kinetochore
6	7e−03	2 / 11	holo TFIIH complex
7	1e−02	3 / 41	cytosolic large ribosomal subunit
8	1e−02	5 / 118	chromosome, centromeric region
9	1e−02	4 / 77	condensed chromosome kinetochore
10	1e−02	3 / 42	cleavage furrow
11	2e−02	5 / 139	ribosome
12	3e−02	2 / 21	M band
13	3e−02	4 / 100	chromatin
14	3e−02	2 / 24	stereocilium
15	4e−02	5 / 157	spindle

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−21	57 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	3e−16	33 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
3	1e−03	21 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
4	2e−03	20 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
5	3e−03	15 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	8e−03	2 / 12	Juehling_HNPCC−mutated−in−4
7	1e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
8	5e−02	28 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	5e−02	2 / 31	Marisa_CRC−cluster−c
10	9e−02	1 / 8	KIM_MSI−in−EC
11	1e−01	10 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
12	1e−01	1 / 10	KIM_CRC−MSI−regulated_DN
13	2e−01	1 / 14	TCGA_Mutated−in−CRC_non−hypermutated
14	2e−01	2 / 60	Marisa_CRC−cluster−g
15	2e−01	15 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_

HM

Rank	p−value	#in/all	Geneset
1	0.07	5 / 190	HALLMARK_MYC_TARGETS_V1
2	0.08	5 / 195	HALLMARK_G2M_CHECKPOINT
3	0.10	2 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	0.33	1 / 34	HALLMARK_APICAL_SURFACE
5	0.33	1 / 34	HALLMARK_ANGIOGENESIS
6	0.34	3 / 173	HALLMARK_MITOTIC_SPINDLE
7	0.38	3 / 187	HALLMARK_E2F_TARGETS
8	0.40	3 / 193	HALLMARK_HEME_METABOLISM
9	0.46	1 / 51	HALLMARK_TGF_BETA_SIGNALING
10	0.47	2 / 133	HALLMARK_DNA_REPAIR
11	0.59	2 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	0.60	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
13	0.65	2 / 188	HALLMARK_HYPOXIA
14	0.67	2 / 194	HALLMARK_KRAS_SIGNALING_UP
15	0.69	1 / 97	HALLMARK_BILE_ACID_METABOLISM

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−12	93 / 4261	HOPP_Txn_transition
2	3e−10	104 / 5529	HOPP_Txn_elongation
3	3e−09	12 / 102	ROSOLOWSKI_blue total
4	7e−07	29 / 906	SPANG_BCR DN
5	2e−03	4 / 45	Monti_BCR_cluster
6	2e−03	2 / 6	MASCQUE_mBL UP
7	3e−03	2 / 7	Shaknovich_ABC_hypo_meth
8	4e−03	87 / 5908	HOPP_Active_promoter
9	6e−03	5 / 99	Sha_BL UP
10	9e−03	79 / 5404	HOPP_Strong_enhancer
11	1e−02	2 / 15	BENTINK_mBL UP
12	1e−02	2 / 15	DAVE_BL Inter
13	2e−02	2 / 19	Subero_MCL_hypo_meth
14	1e−01	2 / 45	SPANG_BAFF 9hrs DN
15	1e−01	1 / 12	BENTINK_mBL DOWN

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	7 / 111	hsa−miR−656
2	6e−04	4 / 33	hsa−miR−654−3p
3	1e−03	7 / 136	hsa−miR−511
4	2e−03	6 / 106	hsa−miR−223
5	2e−03	5 / 72	hsa−miR−339−5p
6	2e−03	9 / 234	hsa−miR−101
7	3e−03	4 / 51	hsa−miR−502−5p
8	3e−03	10 / 301	hsa−miR−519b−3p
9	4e−03	6 / 124	hsa−miR−655
10	5e−03	4 / 58	hsa−miR−1304
11	5e−03	4 / 59	hsa−miR−499−3p
12	6e−03	4 / 62	hsa−miR−489
13	6e−03	10 / 333	hsa−miR−519c−3p
14	6e−03	8 / 232	hsa−miR−186
15	7e−03	7 / 189	hsa−miR−27a

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	2e−05	11 / 198	mRNA splicing, via spliceosome
2	3e−05	13 / 281	mRNA processing
3	9e−05	7 / 90	RNA processing
4	8e−04	3 / 16	programmed cell death
5	1e−03	4 / 42	RNA metabolic process
6	2e−03	9 / 233	RNA splicing
7	5e−03	3 / 30	positive regulation of telomere maintenance via telomerase
8	6e−03	8 / 232	translation
9	8e−03	2 / 12	mitotic chromosome condensation
10	9e−03	11 / 407	viral process
11	1e−02	5 / 110	translational initiation
12	1e−02	2 / 13	cellular response to cholesterol
13	1e−02	30 / 1655	transcription, DNA−templated
14	1e−02	5 / 113	rhythmic process
15	1e−02	2 / 14	regulation of establishment of cell polarity

Chr

Rank	p−value	#in/all	Geneset
1	0.02	17 / 833	Chr 19
2	0.06	11 / 548	Chr 16
3	0.15	8 / 437	Chr 8
4	0.15	10 / 585	Chr 7
5	0.16	5 / 242	Chr 13
6	0.28	12 / 832	Chr 2
7	0.37	3 / 184	Chr 18
8	0.43	9 / 689	Chr 3
9	0.45	9 / 700	Chr 12
10	0.49	2 / 139	Chr 21
11	0.52	5 / 403	Chr 14
12	0.57	9 / 776	Chr 17
13	0.67	4 / 382	Chr 15
14	0.68	7 / 669	Chr 6
15	0.76	3 / 333	Chr 22

Glioma

Rank	p−value	#in/all	Geneset
1	5e−15	14 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	9e−05	3 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
3	1e−02	28 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	1e−02	2 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
5	2e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
6	7e−02	22 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	1e−01	1 / 10	Phillips PN up vs MES & Prolif
8	1e−01	1 / 10	WILLSCHER_GBM_LTSmut_proteomics−B_UP
9	1e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	1e−01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	2e−01	1 / 16	VERHAAK_PN subtype
12	2e−01	2 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
13	2e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	2e−01	2 / 78	Weller_LGG_A_vs_O_UP
15	3e−01	2 / 82	laffaire_hypermeth_LGG_vs_control

Immunome

Rank	p−value	#in/all	Geneset
1	0.06	1 / 5	Angelova_immune−metagene−NKT
2	0.08	1 / 7	Angelova_immune−metagene−cytotoxic_cells
3	0.10	2 / 45	Angelova_immune−metagene−MDSC
4	0.11	1 / 10	Angelova_immune−metagene−neutrophils
5	0.14	1 / 13	Angelova_immune−metagene−immature_B−cells
6	0.19	1 / 18	Angelova_CRC_immunostimulators
7	0.24	1 / 23	Angelova_immune−metagene−monocytes
8	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
9	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
10	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
11	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
12	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
13	1.00	0 / 25	Angelova_immune−metagene−DC
14	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	Melanoma Epi−Enzyme Cluster 6
2	0.03	2 / 24	Tirosh_B−cell specific genes−melanoma
3	0.17	5 / 249	Gerber_wt/wt_melanoma−cells−SpotE
4	0.17	1 / 16	Hugo_melanoma−all−LEF1_UP
5	0.18	6 / 319	Gerber_wt/wt_melanoma−cells−SpotA
6	0.19	2 / 68	Tirosh_housekeeping_genes
7	0.23	5 / 276	Gerber_wt/wt_melanoma−cells−SpotB
8	0.24	1 / 23	Melanoma Epi−Enzyme Cluster 7
9	0.27	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
10	0.36	1 / 38	Tirosh_top50 correlated genes PC1
11	0.37	1 / 39	Tirosh_top50 correlated genes PC4
12	0.39	1 / 41	Tirosh_top50 correlated genes PC3
13	0.43	1 / 47	Tirosh_G2/M phase specific genes
14	0.51	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
15	0.60	2 / 171	Landsberg_dedifferentiation_up

Pneumonia

Rank	p−value	#in/all	Geneset
1	3e−04	9 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	4e−01	1 / 41	Scicluna_DN
3	1e+00	0 / 68	Burnham_sep_vs_con_UP
4	1e+00	0 / 56	Burnham_sep_vs_con_DN
5	1e+00	0 / 48	Burnham_cap_fp_vs_con_DN
6	1e+00	0 / 71	Burnham_cap_fp_vs_con_UP
7	1e+00	0 / 48	Burnham_viral_DN
8	1e+00	0 / 57	Burnham_viral_UP
9	1e+00	0 / 57	Burnham_day1_vs_5_UP
10	1e+00	0 / 52	Burnham_day1_vs_5_DN
11	1e+00	0 / 54	Burnham_timecourse
12	1e+00	0 / 18	Scicluna_UP
13	1e+00	0 / 37	Sweeney_viral_up
14	1e+00	0 / 33	Sweeney_viral_dn
15	1e+00	0 / 122	Terre_IMS_influenza_meta_signature

TF

Rank	p−value	#in/all	Geneset
1	0.03	53 / 3564	ICGC_Taf1_targets
2	0.04	47 / 3150	ICGC_Creb1_targets
3	0.08	25 / 1578	ICGC_GabpPcr2_targets
4	0.08	52 / 3703	ICGC_Foxm1_targets
5	0.10	59 / 4319	ICGC_Pou2_targets
6	0.11	52 / 3769	ICGC_Pmlsc71910_targets
7	0.11	1 / 10	MYC_RNA processing binding UP
8	0.12	10 / 549	ICGC_Atf3_targets
9	0.16	51 / 3804	ICGC_Stat5_targets
10	0.17	2 / 62	MYC_Targets UP
11	0.17	1 / 16	MYC_Protein synthesis degradation UP
12	0.17	22 / 1508	ICGC_Mef2_targets
13	0.19	46 / 3451	ICGC_Atf2_targets
14	0.19	60 / 4602	ICGC_Elf1_targets
15	0.19	63 / 4851	ICGC_Runx3_targets

Cancer

Rank	p−value	#in/all	Geneset
1	2e−13	5 / 14	LIU_COMMON_CANCER_GENES
2	5e−04	3 / 14	GUSTAFSON_PI3K_DN
3	1e−01	2 / 45	KUIPER_MM poor survival
4	1e−01	1 / 12	LIU_BREAST_CANCER
5	1e−01	1 / 12	BENTINK_e2f3.2
6	2e−01	1 / 14	GENTLES_modul10
7	2e−01	1 / 14	BENTINK_myc.1
8	3e−01	2 / 96	PanCan_TXmisReg_geneset_nanostring
9	4e−01	1 / 41	PanCan_DNARepair_geneset_nanostring
10	5e−01	2 / 134	PanCan_RAS_geneset_nanostring
11	5e−01	6 / 480	Lembcke_Colonic Inflammation
12	6e−01	0 / 11	LIU_PROSTATE_CANCER_UP
13	6e−01	0 / 14	LIU_PROSTATE_CANCER_DN
14	7e−01	2 / 187	PanCan_PI3K_geneset_nanostring
15	7e−01	4 / 409	Lembcke_Normal vs Adenoma

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−11	83 / 3682	natural killer cells peripheral blood_6_EnhG
2	4e−11	108 / 5716	Bcells peripheral blood_4_Tx
3	5e−11	80 / 3524	Tregulatory cells peripheral blood_6_EnhG
4	2e−10	63 / 2450	HSC_6_EnhG
5	2e−10	107 / 5766	natural killer cells peripheral blood_4_Tx
6	5e−10	30 / 693	Bcells peripheral blood_3_TxFlnk
7	6e−10	81 / 3767	Bcells peripheral blood_6_EnhG
8	8e−10	83 / 3938	Thelper cells peripheral blood_6_EnhG
9	2e−09	109 / 6099	HSC_4_Tx
10	2e−09	56 / 2144	T CD8+ naive cells peripheral blood_6_EnhG
11	2e−09	103 / 5601	Thelper cells peripheral blood_4_Tx
12	3e−09	127 / 7833	Bcells peripheral blood_1_TssA
13	1e−08	88 / 4528	T CD8+ naive cells peripheral blood_4_Tx
14	1e−08	103 / 5753	Tcells peripheral blood_4_Tx
15	1e−08	115 / 6839	T CD8+ naive cells peripheral blood_5_TxWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−13	5 / 14	LIU_COMMON_CANCER_GENES
2	1e−11	16 / 143	LEE_DIFFERENTIATING_T_LYMPHOCYTE
3	3e−10	14 / 127	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
4	5e−10	7 / 17	SPIRA_SMOKERS_LUNG_CANCER_DN
5	4e−08	22 / 477	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
6	6e−07	11 / 136	REACTOME_MRNA_PROCESSING
7	1e−06	36 / 1312	PUJANA_ATM_PCC_NETWORK
8	5e−06	38 / 1527	PUJANA_BRCA1_PCC_NETWORK
9	8e−06	5 / 24	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
10	8e−06	21 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
11	1e−05	9 / 120	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
12	1e−05	13 / 261	WANG_LMO4_TARGETS_UP
13	2e−05	23 / 730	ONKEN_UVEAL_MELANOMA_UP
14	4e−05	37 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
15	7e−05	16 / 445	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 22	DUMEAUX_High bmi enriched genes
2	0.2	1 / 22	DUMEAUX_Fasting enriched genes
3	0.5	2 / 150	Homuth_BMI−associated−genes_UP
4	0.7	2 / 210	Homuth_BMI−associated−genes_DN
5	1.0	0 / 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	6e−08	30 / 852	nucleic acid binding
2	1e−05	31 / 1161	RNA binding
3	1e−02	2 / 14	C2H2 zinc finger domain binding
4	1e−02	2 / 14	endodeoxyribonuclease activity
5	1e−02	28 / 1541	DNA binding
6	2e−02	2 / 19	miRNA binding
7	2e−02	2 / 20	RNA polymerase II transcription corepressor activity
8	3e−02	2 / 22	translation factor activity, RNA binding
9	3e−02	2 / 23	telomeric DNA binding
10	4e−02	6 / 206	transcription regulatory region DNA binding
11	4e−02	3 / 65	protein phosphatase binding
12	4e−02	5 / 163	magnesium ion binding
13	5e−02	2 / 29	SH2 domain binding
14	5e−02	2 / 30	histone−lysine N−methyltransferase activity
15	6e−02	2 / 33	DNA−dependent ATPase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−25	31 / 218	WIRTH_pre+post GC B−cells
2	2e−19	25 / 188	Chaussabel_3,8_Enzymes
3	5e−13	9 / 20	Chaussabel_2,7_Unknown function
4	4e−09	7 / 22	Chaussabel_1,6_Signaling molecules
5	4e−05	8 / 106	Chaussabel_2,11_Replication
6	8e−05	17 / 496	PROTEINATLAS_spleen
7	8e−05	9 / 152	VAQUERIZAS_General_TF
8	2e−04	25 / 989	PROTEINATLAS_tonsil
9	4e−04	19 / 678	PROTEINATLAS_lymph node
10	6e−04	17 / 593	PROTEINATLAS_lateral ventricle
11	2e−03	17 / 642	PROTEINATLAS_lung
12	2e−03	20 / 819	PROTEINATLAS_bronchus
13	2e−03	24 / 1076	PROTEINATLAS_stomach
14	2e−03	12 / 390	PROTEINATLAS_ovary
15	2e−03	17 / 671	PROTEINATLAS_cervix, uterine

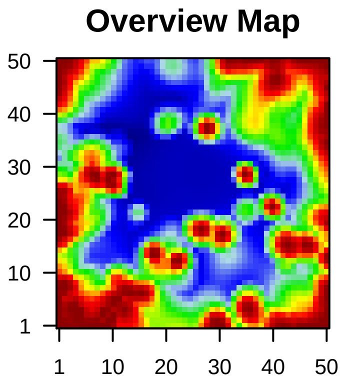
Overexpression Spots

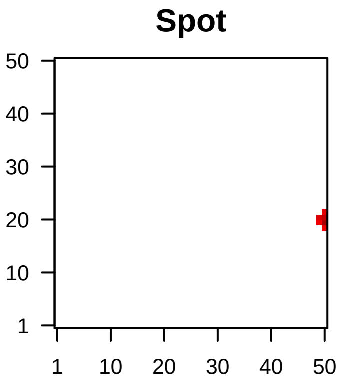
Spot Summary: I1

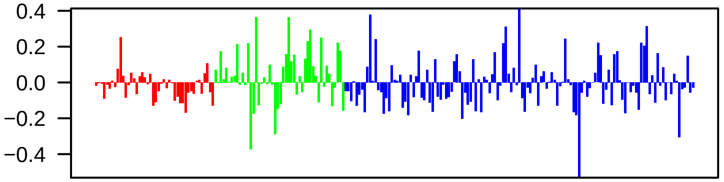
metagenes = 6
genes = 149

<r> metagenes = 0.98
<r> genes = 0.16
beta: r2= 1.84 / log p= −Inf

samples with spot = 18 (8.1 %)
mBL : 1 (2.3 %)
intermediate : 8 (16.7 %)
non−mBL : 9 (7 %)





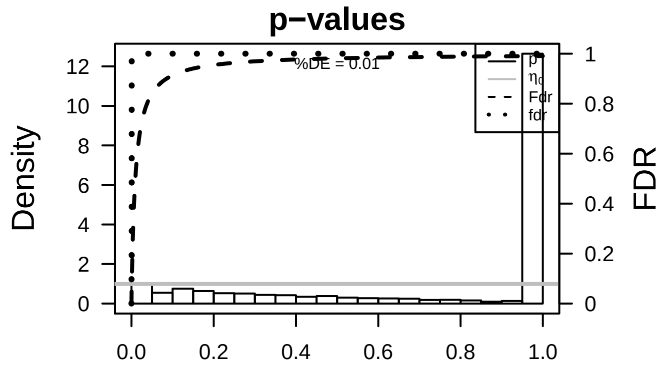


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	217469_at	2.61	−1.06	0.38		immunoglobulin heavy constant epsilon [Source:HGNC Symb
2	205593_s_at	2.17	−0.78	0.43	PDE9A	phosphodiesterase 9A [Source:HGNC Symbol;Acc:HGNC:87
3	211010_s_at	2.09	−0.89	0.18	NCR3	natural cytotoxicity triggering receptor 3 [Source:HGNC Symb
4	218692_at	2.03	−1.04	0.38	SYBU	syntabulin [Source:HGNC Symbol;Acc:HGNC:26011]
5	207819_s_at	1.84	−1.12	0.29	ABCB4	ATP binding cassette subfamily B member 4 [Source:HGNC
6	209739_s_at	1.82	−1.43	0.36	PNPLA4	patatin like phospholipase domain containing 4 [Source:HGN
7	219820_at	1.81	−0.83	0.51	SLC6A16	solute carrier family 6 member 16 [Source:HGNC Symbol;Ac
8	205551_at	1.79	−0.79	0.31	SV2B	synaptic vesicle glycoprotein 2B [Source:HGNC Symbol;Acc:
9	204465_s_at	1.68	−0.74	0.31	INA	internexin neuronal intermediate filament protein alpha [Sour
10	215967_s_at	1.63	−1.03	0.46	LY9	lymphocyte antigen 9 [Source:HGNC Symbol;Acc:HGNC:673
11	214772_at	1.61	−0.73	0.38	KIAA1549L	KIAA1549 like [Source:HGNC Symbol;Acc:HGNC:24836]
12	205389_s_at	1.6	−0.71	0.47	ANK1	ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492]
13	210370_s_at	1.59	−0.95	0.49	LY9	lymphocyte antigen 9 [Source:HGNC Symbol;Acc:HGNC:673
14	212448_at	1.56	−1.11	0.31	NEDD4L	neural precursor cell expressed, developmentally down−regul
15	209498_at	1.52	−1.4	0.36	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1 [S
16	209917_s_at	1.5	−1.09	0.42		TP53 target 1 (non−protein coding) [Source:HGNC Symbol;A
17	207087_x_at	1.47	−0.81	0.41	ANK1	ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492]
18	204530_s_at	1.47	−1.01	0.35	TOX	thymocyte selection associated high mobility group box [Sour
19	214564_s_at	1.44	−0.79	0.38	PCDHGC3	protocadherin gamma subfamily C, 3 [Source:HGNC Symbol;
20	218144_s_at	1.42	−0.72	0.36	INF2	inverted formin, FH2 and WH2 domain containing [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−14	96 / 5404	Lymp	HOPP_Strong_enhancer
2	7e−08	8 / 56	GSE	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
3	1e−07	6 / 24	Mela	Tirosh_B−cell specific genes−melanoma
4	3e−07	7 / 45	Lymp	Monti_BCR_cluster
5	4e−07	87 / 5908	Lymp	HOPP_Active_promoter
6	6e−07	7 / 51	GSE	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
7	9e−07	6 / 34	Lymp	TARTE_B−cell signature
8	9e−07	5 / 19	GSE	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
9	1e−06	70 / 4357	Lymp	HOPP_Weak_txn
10	1e−06	6 / 35	GSE	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
11	1e−06	17 / 429	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
12	3e−06	81 / 5529	Lymp	HOPP_Txn_elongation
13	3e−06	6 / 42	Refe	Chaussabel_1,3_B−cells
14	1e−05	12 / 263	Lymp	SPANG_CD40 6hrs UP
15	3e−05	65 / 4261	Lymp	HOPP_Txn_transition
16	3e−05	9 / 163	GSE	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
17	4e−05	18 / 621	BP	negative regulation of transcription from RNA polymerase II promoter
18	4e−05	33 / 1636	TF	ICGC_Bcl11_targets
19	5e−05	79 / 5682	Lymp	HOPP_Weak_promoter
20	7e−05	26 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
21	7e−05	13 / 368	GSE	ZHENG_BOUND_BY_FOXP3
22	9e−05	10 / 227	Lymp	SPANG_IL21 UP
23	9e−05	10 / 229	GSE	QI_PLASMACYTOMA_UP
24	1e−04	3 / 10	BP	respiratory burst
25	1e−04	30 / 1508	TF	ICGC_Mef2_targets
26	1e−04	9 / 195	GSE	HOLLMANN_APOPTOSIS_VIA_CD40_UP
27	2e−04	5 / 52	GSE	SMIRNOV_RESPONSE_TO_IR_2HR_DN
28	2e−04	7 / 121	GSE	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
29	2e−04	30 / 1550	GSE	PILON_KLF1_TARGETS_DN
30	2e−04	16 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
31	3e−04	5 / 59	GSE	PID_BCR_5PATHWAY
32	3e−04	5 / 61	GSE	BASSO_CD40_SIGNALING_DN
33	4e−04	6 / 96	Lymp	SPANG_LPS 6hrs UP
34	4e−04	3 / 15	GSE	XU_RESPONSE_TO_TRETINOIN_UP
35	4e−04	10 / 275	GSE	HADDAD_B_LYMPHOCYTE_PROGENITOR
36	4e−04	4 / 36	GSE	NAKAYAMA_FRA2_TARGETS
37	4e−04	15 / 560	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
38	5e−04	21 / 955	Lymp	SPANG_BCR UP
39	5e−04	3 / 16	Gliom	VERHAAK_MES subtype
40	5e−04	17 / 694	GSE	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 47	TESCHENDORFF_age_hypermethylated
2	0.7	1 / 107	HORVATH_aging_genes meth UP
3	1.0	0 / 92	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−05	18 / 621	negative regulation of transcription from RNA polymerase II promoter
2	1e−04	3 / 10	respiratory burst
3	6e−04	6 / 106	regulation of small GTPase mediated signal transduction
4	2e−03	3 / 26	cellular response to dexamethasone stimulus
5	2e−03	4 / 56	regulation of Rho protein signal transduction
6	2e−03	9 / 288	positive regulation of apoptotic process
7	5e−03	2 / 11	leukotriene biosynthetic process
8	6e−03	5 / 115	actin cytoskeleton organization
9	6e−03	2 / 12	actin polymerization or depolymerization
10	6e−03	2 / 12	negative regulation of fatty acid biosynthetic process
11	7e−03	3 / 39	B cell receptor signaling pathway
12	9e−03	2 / 15	negative regulation of cell−matrix adhesion
13	9e−03	2 / 15	oogenesis
14	1e−02	9 / 361	intracellular signal transduction
15	1e−02	2 / 16	defense response to protozoan

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	2 / 6	ZHANG_MGUS up
2	0.021	10 / 480	Lembcke_Colonic Inflammation
3	0.113	1 / 12	GENTLES_modul12
4	0.113	1 / 12	HLA2_signature
5	0.122	1 / 13	GENTLES_modul11
6	0.122	1 / 13	GENTLES_modul18
7	0.122	1 / 13	BENTINK_e2f3.1
8	0.148	1 / 16	LIU_LIVER_CANCER
9	0.221	1 / 25	PanCan_HH_geneset_nanostring
10	0.362	1 / 45	KUIPER_MM poor survival
11	0.440	1 / 58	SHAUGHNESSY_MM high risk
12	0.513	1 / 72	PanCan_Wnt_geneset_nanostring
13	0.557	2 / 187	PanCan_PI3K_geneset_nanostring
14	0.582	4 / 409	Lembcke_Normal vs Adenoma
15	0.617	1 / 96	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 17	T cell receptor complex
2	3e−03	53 / 3805	cytosol
3	6e−03	2 / 12	HOPS complex
4	1e−02	3 / 51	clathrin−coated vesicle
5	2e−02	3 / 56	lipid droplet
6	3e−02	10 / 494	endosome
7	3e−02	2 / 25	basal plasma membrane
8	5e−02	5 / 196	nuclear membrane
9	6e−02	4 / 146	lamellipodium
10	6e−02	7 / 354	centrosome
11	7e−02	2 / 42	Cul3−RING ubiquitin ligase complex
12	7e−02	2 / 42	sarcoplasmic reticulum
13	7e−02	2 / 43	myosin complex
14	8e−02	15 / 1016	intracellular
15	9e−02	10 / 623	cell projection

Chr

Rank	p−value	#in/all	Geneset
1	0.004	13 / 556	Chr X
2	0.013	12 / 585	Chr 7
3	0.203	11 / 832	Chr 2
4	0.211	6 / 403	Chr 14
5	0.220	4 / 242	Chr 13
6	0.302	7 / 548	Chr 16
7	0.402	2 / 139	Chr 21
8	0.473	6 / 554	Chr 5
9	0.528	4 / 382	Chr 15
10	0.530	7 / 689	Chr 3
11	0.539	5 / 490	Chr 10
12	0.542	5 / 492	Chr 9
13	0.635	4 / 437	Chr 8
14	0.646	3 / 333	Chr 22
15	0.707	4 / 480	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−15	81 / 3767	Bcells peripheral blood_6_EnhG
2	1e−10	93 / 5716	Bcells peripheral blood_4_Tx
3	1e−08	87 / 5527	Tregulatory cells peripheral blood_4_Tx
4	5e−08	103 / 7407	natural killer cells peripheral blood_5_TxWk
5	2e−07	85 / 5601	Thelper cells peripheral blood_4_Tx
6	3e−07	23 / 693	Bcells peripheral blood_3_TxFlnk
7	6e−07	109 / 8406	Bcells peripheral blood_2_TssAFlnk
8	6e−07	63 / 3682	natural killer cells peripheral blood_6_EnhG
9	8e−07	104 / 7833	Bcells peripheral blood_1_TssA
10	8e−07	101 / 7489	monocytes peripheral blood_5_TxWk
11	1e−06	93 / 6637	Tcells peripheral blood_5_TxWk
12	3e−06	102 / 7751	natural killer cells peripheral blood_1_TssA
13	3e−06	83 / 5738	monocytes peripheral blood_4_Tx
14	4e−06	83 / 5766	natural killer cells peripheral blood_4_Tx
15	5e−06	26 / 1009	Tcells peripheral blood_8_ZNF_Rpts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−05	26 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
2	2e−04	16 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	6e−03	28 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	3e−02	2 / 25	Ang_CRC−CIMPH−vs−L_hypo
5	4e−02	6 / 255	Kosinski_top−crypt−long−list
6	5e−02	2 / 35	Ang_CRC_Hypomethylated
7	8e−02	13 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	1e−01	71 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9	1e−01	11 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	1e−01	14 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
11	1e−01	1 / 15	TCGA−CRC_less−agressive−disease−markers
12	1e−01	12 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	2e−01	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	2e−01	3 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	2e−01	2 / 92	Marisa_CRC−cluster−h

Glioma

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 16	VERHAAK_MES subtype
2	5e−04	5 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
3	1e−03	9 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
4	5e−03	4 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
5	8e−03	4 / 78	Weller_LGG_A_vs_O_UP
6	1e−02	3 / 45	Donson−innate immunity−associated with LTS in HGA
7	1e−02	10 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
8	2e−02	3 / 55	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
9	2e−02	7 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
10	3e−02	6 / 239	ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN
11	4e−02	2 / 30	Shaw_responders_down_in_oligo_glioma
12	4e−02	5 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
13	5e−02	6 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
14	5e−02	4 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	6e−02	1 / 6	WILLSCHER_GBM_Verhaak−PNmut_up (M)

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−08	8 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
2	6e−07	7 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
3	9e−07	5 / 19	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
4	1e−06	6 / 35	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
5	1e−06	17 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	3e−05	9 / 163	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
7	7e−05	13 / 368	ZHENG_BOUND_BY_FOXP3
8	9e−05	10 / 229	QI_PLASMACYTOMA_UP
9	1e−04	9 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
10	2e−04	5 / 52	SMIRNOV_RESPONSE_TO_IR_2HR_DN
11	2e−04	7 / 121	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
12	2e−04	30 / 1550	PILON_KLF1_TARGETS_DN
13	3e−04	5 / 59	PID_BCR_5PATHWAY
14	3e−04	5 / 61	BASSO_CD40_SIGNALING_DN
15	4e−04	3 / 15	XU_RESPONSE_TO_TRETINOIN_UP

HM

Rank	p−value	#in/all	Geneset
1	0.03	5 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.08	4 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.16	3 / 141	HALLMARK_UV_RESPONSE_DN
4	0.25	3 / 174	HALLMARK_APICAL_JUNCTION
5	0.25	2 / 97	HALLMARK_PEROXISOME
6	0.27	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
7	0.29	3 / 188	HALLMARK_HYPOXIA
8	0.29	1 / 34	HALLMARK_APICAL_SURFACE
9	0.29	1 / 34	HALLMARK_ANGIOGENESIS
10	0.29	3 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
11	0.29	3 / 191	HALLMARK_P53_PATHWAY
12	0.30	3 / 192	HALLMARK_MTORC1_SIGNALING
13	0.30	3 / 193	HALLMARK_HEME_METABOLISM
14	0.30	3 / 194	HALLMARK_KRAS_SIGNALING_UP
15	0.32	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.004	2 / 10	Angelova_immune−metagene−TFH
2	0.007	2 / 13	Angelova_immune−metagene−activated_B−cells
3	0.007	2 / 13	Angelova_immune−metagene−immature_B−cells
4	0.039	1 / 4	Angelova_CRC_MHC_class_II
5	0.077	1 / 8	Immunity_HLA−class−II
6	0.164	1 / 18	Angelova_immune−metagene−pDC
7	0.205	1 / 23	Angelova_immune−metagene−Treg
8	0.251	1 / 29	Angelova_immune−metagene−Th1
9	0.273	1 / 32	Angelova_immune−metagene−effector_memory_CD8
10	0.488	1 / 67	Angelova_immune−metagene−T−cells
11	1.000	0 / 26	Angelova_immune−metagene−activated_CD4
12	1.000	0 / 19	Angelova_immune−metagene−activated_CD8
13	1.000	0 / 21	Angelova_immune−metagene−central_memory_CD4
14	1.000	0 / 17	Angelova_immune−metagene−central_memory_CD8
15	1.000	0 / 7	Angelova_immune−metagene−cytotoxic_cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.001	8 / 210	Homuth_BMI−associated−genes_DN
2	0.004	3 / 32	Marjolein_ageing−genes_DN
3	0.113	1 / 12	DUMEAUX_Women normal BMI literature genes up
4	0.148	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.462	1 / 62	DUMEAUX_Smoking enriched genes
6	0.778	1 / 150	Homuth_BMI−associated−genes_UP
7	1.000	0 / 10	DUMEAUX_Smoking literature genes up
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.000	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.000	0 / 22	DUMEAUX_High bmi enriched genes
14	1.000	0 / 22	DUMEAUX_Fasting enriched genes
15	1.000	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−14	96 / 5404	HOPP_Strong_enhancer
2	3e−07	7 / 45	Monti_BCR_cluster
3	4e−07	87 / 5908	HOPP_Active_promoter
4	9e−07	6 / 34	TARTE_B−cell signature
5	1e−06	70 / 4357	HOPP_Weak_txn
6	3e−06	81 / 5529	HOPP_Txn_elongation
7	1e−05	12 / 263	SPANG_CD40 6hrs UP
8	3e−05	65 / 4261	HOPP_Txn_transition
9	5e−05	79 / 5682	HOPP_Weak_promoter
10	9e−05	10 / 227	SPANG_IL21 UP
11	4e−04	6 / 96	SPANG_LPS 6hrs UP
12	5e−04	21 / 955	SPANG_BCR UP
13	6e−04	3 / 17	Aukema_BCL2 UP_BCL6 DN
14	2e−03	19 / 906	SPANG_BCR DN
15	1e−02	9 / 378	TARTE_Mature plasma cell signature

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−07	6 / 24	Tirosh_B−cell specific genes−melanoma
2	9e−02	5 / 236	Gerber_wt/wt_group3−specific
3	9e−02	3 / 107	Tirosh_Exhaustion program in Mel75
4	9e−02	4 / 171	Landsberg_dedifferentiation_up
5	9e−02	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	1e−01	8 / 497	Gerber_wt/wt_melanoma−cells−SpotD
7	2e−01	2 / 83	TCGA_melanoma_immune_high
8	2e−01	1 / 23	Melanoma Epi−Enzyme Cluster 7
9	3e−01	1 / 33	Tirosh_T−cell specific genes−melanoma
10	4e−01	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	4e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
12	5e−01	1 / 64	Harbst_melanoma_lowgrade_up
13	6e−01	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
14	6e−01	1 / 81	Tirosh_Genes in the MITF program
15	6e−01	2 / 189	Tirosh_genes preferentially expressed by Tregs

MF

Rank	p−value	#in/all	Geneset
1	0.002	4 / 54	Rho guanyl−nucleotide exchange factor activity
2	0.003	5 / 96	SH3 domain binding
3	0.004	5 / 104	transcriptional repressor activity, RNA polymerase II proximal promoter seque
4	0.004	2 / 10	profilin binding
5	0.006	9 / 331	protein serine/threonine kinase activity
6	0.006	3 / 38	signal transducer activity, downstream of receptor
7	0.010	5 / 130	guanyl−nucleotide exchange factor activity
8	0.011	2 / 16	phospholipid transporter activity
9	0.015	2 / 19	steroid binding
10	0.015	6 / 202	GTPase activator activity
11	0.017	2 / 20	phosphatidylinositol−3,4−bisphosphate binding
12	0.020	2 / 22	protein phosphatase 2A binding
13	0.026	3 / 64	phosphatidylinositol binding
14	0.027	11 / 573	kinase activity
15	0.029	89 / 7864	protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	7 / 194	hsa−miR−124
2	0.004	3 / 31	hsa−miR−34c−3p
3	0.004	4 / 64	hsa−miR−562
4	0.005	5 / 109	hsa−miR−194
5	0.010	3 / 45	hsa−miR−891b
6	0.016	5 / 148	hsa−miR−1
7	0.016	6 / 205	hsa−miR−548p
8	0.018	4 / 101	hsa−miR−155
9	0.018	3 / 56	hsa−miR−618
10	0.021	3 / 59	hsa−miR−643
11	0.021	8 / 344	hsa−miR−19b
12	0.022	5 / 160	hsa−miR−545
13	0.024	3 / 62	hsa−miR−578
14	0.027	4 / 114	hsa−miR−494
15	0.030	3 / 68	hsa−miR−767−5p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.002	7 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.336	1 / 41	Scicluna_DN
3	0.381	1 / 48	Burnham_cap_fp_vs_con_DN
4	0.381	1 / 48	Burnham_viral_DN
5	0.388	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.405	1 / 52	Burnham_day1_vs_5_DN
7	0.417	1 / 54	Burnham_timecourse
8	0.429	1 / 56	Burnham_sep_vs_con_DN
9	0.493	1 / 68	Burnham_sep_vs_con_UP
10	0.508	1 / 71	Burnham_cap_fp_vs_con_UP
11	1.000	0 / 57	Burnham_viral_UP
12	1.000	0 / 57	Burnham_day1_vs_5_UP
13	1.000	0 / 18	Scicluna_UP
14	1.000	0 / 37	Sweeney_viral_up
15	1.000	0 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−06	6 / 42	Chaussabel_1,3_B−cells
2	6e−04	8 / 188	Chaussabel_3,8_Enzymes
3	1e−03	3 / 21	VAQUERIZAS_Tonsil_TF
4	3e−03	10 / 355	WIRTH_Immune system
5	4e−03	12 / 496	PROTEINATLAS_spleen
6	7e−03	2 / 13	WIRTH_B−cells
7	1e−02	2 / 16	VAQUERIZAS_Ovary_TF
8	1e−02	3 / 49	VAQUERIZAS_Uterus_TF
9	2e−02	17 / 989	PROTEINATLAS_tonsil
10	2e−02	2 / 24	VAQUERIZAS_Pituitary_TF
11	3e−02	3 / 66	VAQUERIZAS_Whole blood_TF
12	3e−02	15 / 905	PROTEINATLAS_appendix
13	4e−02	2 / 30	VAQUERIZAS_Smooth muscle_TF
14	4e−02	12 / 678	PROTEINATLAS_lymph node
15	4e−02	2 / 32	VAQUERIZAS_Liver_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	4e−05	33 / 1636	ICGC_Bcl11_targets
2	1e−04	30 / 1508	ICGC_Mef2_targets
3	8e−04	36 / 2150	ICGC_Irf4_targets
4	8e−04	38 / 2321	ICGC_Rad21_targets
5	9e−04	37 / 2254	ICGC_BatfPcr1_targets
6	1e−03	48 / 3213	ICGC_Pu1_targets
7	1e−03	33 / 1941	ICGC_Bcl3_targets
8	1e−03	27 / 1494	ICGC_Cebpbsc150_targets
9	3e−03	45 / 3121	ICGC_Egr1_targets
10	4e−03	30 / 1848	ICGC_Pbx3_targets
11	5e−03	48 / 3435	ICGC_Ebfsc137065_targets
12	6e−03	19 / 1032	ICGC_Usf1_targets
13	7e−03	47 / 3420	ICGC_Bclaf101388_targets
14	8e−03	51 / 3796	ICGC_Nficsc81335_targets
15	8e−03	49 / 3630	ICGC_Sp1_targets

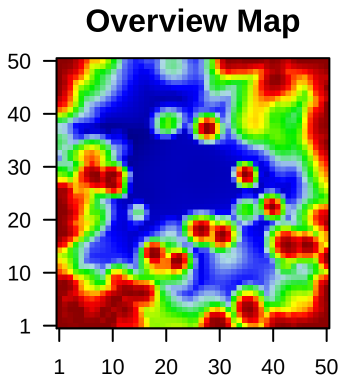
Overexpression Spots

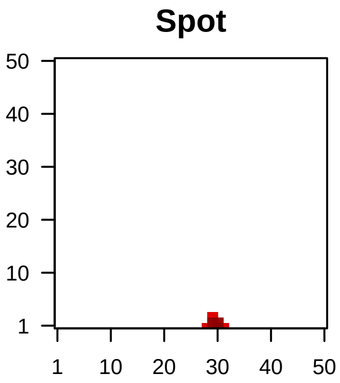
Spot Summary: J1

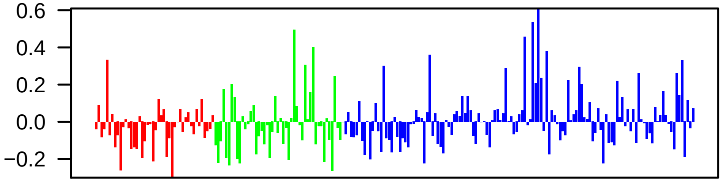
metagenes = 10
genes = 110

<r> metagenes = 0.98
<r> genes = 0.14
beta: r2= 2.05 / log p= −Inf

samples with spot = 20 (9 %)
mBL : 1 (2.3 %)
intermediate : 4 (8.3 %)
non−mBL : 15 (11.6 %)


Overview Map


Spot

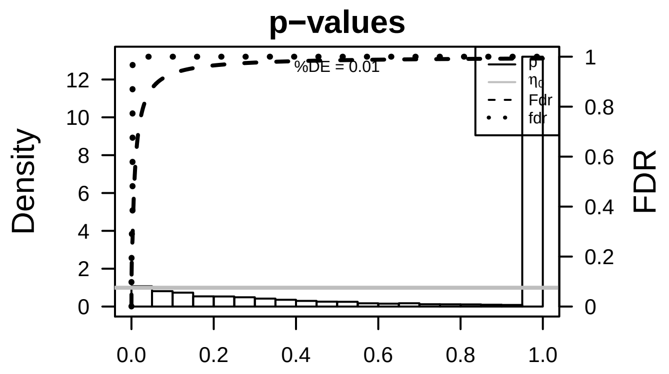


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209988_s_at	3.22	−0.78	0.39	ASCL1	achaete−scute family bHLH transcription factor 1 [Source:HG
2	219463_at	3.17	−0.88	0.48	LAMP5	lysosomal associated membrane protein family member 5 [Sc
3	209987_s_at	2.71	−0.72	0.37	ASCL1	achaete−scute family bHLH transcription factor 1 [Source:HG
4	215118_s_at	2.52	−1.42	0.27		
5	201525_at	2.5	−0.99	0.43	APOD	apolipoprotein D [Source:HGNC Symbol;Acc:HGNC:612]
6	206759_at	2.49	−0.94	0.44	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HG
7	218613_at	2.4	−0.84	0.36	PSD3	pleckstrin and Sec7 domain containing 3 [Source:HGNC Sym
8	210763_x_at	2.4	−1.08	0.21	NCR3	natural cytotoxicity triggering receptor 3 [Source:HGNC Symb
9	209695_at	2.28	−0.87	0.45	PTP4A3	protein tyrosine phosphatase type IVA, member 3 [Source:HG
10	219168_s_at	2.19	−1.1	0.45	PRR5	proline rich 5 [Source:HGNC Symbol;Acc:HGNC:31682]
11	204040_at	2.15	−0.68	0.28	RNF144A	ring finger protein 144A [Source:HGNC Symbol;Acc:HGNC:2
12	210617_at	2.14	−1.06	0.35	PHEX	phosphate regulating endopeptidase homolog X−linked [Sour
13	206498_at	2.11	−0.99	0.27	OCA2	OCA2 melanosomal transmembrane protein [Source:HGNC S
14	203355_s_at	1.96	−0.95	0.37	PSD3	pleckstrin and Sec7 domain containing 3 [Source:HGNC Sym
15	220146_at	1.89	−0.99	0.44	TLR7	toll like receptor 7 [Source:HGNC Symbol;Acc:HGNC:15631]
16	221880_s_at	1.86	−1.04	0.38	FAM174B	family with sequence similarity 174 member B [Source:HGNC
17	213348_at	1.84	−0.8	0.43	CDKN1C	cyclin dependent kinase inhibitor 1C [Source:HGNC Symbol;
18	219014_at	1.76	−1.51	0.45	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254
19	221704_s_at	1.74	−0.99	0.47	VPS37B	VPS37B, ESCRT−I subunit [Source:HGNC Symbol;Acc:HGN
20	210298_x_at	1.74	−0.9	0.45	FHL1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−12	15 / 182	Refer	WIRTH_post GC B−cells
2	2e−08	12 / 218	Refer	WIRTH_pre+post GC B−cells
3	2e−05	17 / 785	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
4	2e−05	13 / 491	GSEA	ENK_UV_RESPONSE_EPIDERMIS_DN
5	3e−05	16 / 741	GSEA	PEREZ_TP53_TARGETS
6	9e−05	10 / 336	BP	immune response
7	1e−04	38 / 3210	CC	plasma membrane
8	1e−04	23 / 1508	TF	ICGC_Mef2_targets
9	1e−04	54 / 5404	Lympl	HOPP_Strong_enhancer
10	2e−04	24 / 1636	TF	ICGC_Bcl11_targets
11	2e−04	6 / 121	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
12	2e−04	9 / 306	GSEA	SANSOM_APC_TARGETS_DN
13	3e−04	3 / 19	BP	regulation of protein binding
14	4e−04	5 / 92	BP	Notch signaling pathway
15	4e−04	3 / 22	MF	14−3−3 protein binding
16	4e−04	3 / 22	BP	positive regulation of NIK/NF−kappaB signaling
17	5e−04	3 / 23	BP	membrane depolarization
18	5e−04	5 / 97	BP	positive regulation of DNA binding transcription factor activity
19	5e−04	4 / 55	MF	core promoter binding
20	6e−04	3 / 25	GSEA	LU_TUMOR_ANGIOGENESIS_UP
21	7e−04	7 / 220	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
22	7e−04	9 / 361	BP	intracellular signal transduction
23	8e−04	25 / 1941	TF	ICGC_Bcl3_targets
24	8e−04	5 / 109	BP	neuron differentiation
25	9e−04	3 / 28	BP	ventricular septum morphogenesis
26	9e−04	5 / 111	GSEA	QI_HYPOXIA
27	9e−04	2 / 7	GSEA	SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN
28	1e−03	7 / 234	Lympl	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
29	1e−03	4 / 66	GSEA	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
30	1e−03	7 / 236	Melar	Gerber_wt/wt_group3−specific
31	1e−03	3 / 31	Colon	Kosinski_lower−crypt−short−list
32	1e−03	16 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
33	1e−03	5 / 121	GSEA	HUANG_GATA2_TARGETS_UP
34	1e−03	38 / 3630	TF	ICGC_Sp1_targets
35	1e−03	7 / 249	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
36	2e−03	3 / 35	GSEA	PID_RET_PATHWAY
37	2e−03	3 / 35	GSEA	ZHAN_MULTIPLE_MYELOMA_HP_DN
38	2e−03	4 / 76	GSEA	GRADE_COLON_AND_RECTAL_CANCER_DN
39	2e−03	6 / 189	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
40	2e−03	5 / 129	GSEA	ONDER_CDH1_TARGETS_1_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 107	HORVATH_aging_genes meth UP
2	0.5	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	9e−05	10 / 336	immune response
2	3e−04	3 / 19	regulation of protein binding
3	4e−04	5 / 92	Notch signaling pathway
4	4e−04	3 / 22	positive regulation of NIK/NF−kappaB signaling
5	5e−04	3 / 23	membrane depolarization
6	5e−04	5 / 97	positive regulation of DNA binding transcription factor activity
7	7e−04	9 / 361	intracellular signal transduction
8	8e−04	5 / 109	neuron differentiation
9	9e−04	3 / 28	ventricular septum morphogenesis
10	2e−03	3 / 36	negative regulation of cell adhesion
11	2e−03	2 / 10	negative regulation of peptidyl−tyrosine phosphorylation
12	2e−03	2 / 10	response to dexamethasone
13	3e−03	4 / 85	transforming growth factor beta receptor signaling pathway
14	3e−03	2 / 12	cardiac muscle cell proliferation
15	3e−03	2 / 12	pathway−restricted SMAD protein phosphorylation

Cancer

Rank	p−value	#in/all	Geneset
1	0.08	1 / 13	GENTLES_modul11
2	0.09	1 / 14	GENTLES_modul13
3	0.09	1 / 14	GUSTAFSON_PI3K_DN
4	0.10	1 / 16	LIU_LIVER_CANCER
5	0.10	1 / 16	GENTLES_modul16
6	0.11	1 / 18	PanCan_Notch_geneset_nanostring
7	0.13	1 / 20	PanCan_ChromMod_geneset_nanostring
8	0.22	5 / 480	Lembcke_Colonic Inflammation
9	0.24	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.27	0 / 14	LIU_COMMON_CANCER_GENES
11	0.30	4 / 409	Lembcke_Normal vs Adenoma
12	0.39	1 / 72	PanCan_Wnt_geneset_nanostring
13	0.40	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.48	1 / 96	PanCan_TXmisReg_geneset_nanostring
15	0.54	1 / 113	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−04	38 / 3210	plasma membrane
2	2e−03	2 / 11	basal part of cell
3	3e−03	2 / 12	uropod
4	4e−03	3 / 47	cell periphery
5	4e−03	3 / 48	microvillus
6	4e−03	3 / 49	RNA polymerase II transcription factor complex
7	7e−03	4 / 113	receptor complex
8	9e−03	5 / 188	endosome membrane
9	1e−02	2 / 24	stereocilium
10	1e−02	32 / 3270	integral component of membrane
11	1e−02	7 / 382	synapse
12	2e−02	3 / 79	ruffle membrane
13	2e−02	3 / 82	transport vesicle
14	2e−02	14 / 1128	integral component of plasma membrane
15	2e−02	9 / 623	cell projection

Chr

Rank	p−value	#in/all	Geneset
1	0.05	7 / 492	Chr 9
2	0.11	9 / 833	Chr 19
3	0.17	6 / 556	Chr X
4	0.20	6 / 585	Chr 7
5	0.42	4 / 490	Chr 10
6	0.48	3 / 382	Chr 15
7	0.49	2 / 242	Chr 13
8	0.51	5 / 700	Chr 12
9	0.51	3 / 403	Chr 14
10	0.57	3 / 437	Chr 8
11	0.61	5 / 776	Chr 17
12	0.63	3 / 480	Chr 4
13	0.72	2 / 369	Chr 20
14	0.73	3 / 554	Chr 5
15	0.76	4 / 756	Chr 11

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−05	48 / 4219	EnhWk1_Colon
2	3e−05	43 / 3682	natural killer cells peripheral blood_6_EnhG
3	1e−04	27 / 1911	Mid_Frontal_Lobe_HetRpts
4	1e−04	32 / 2507	Mid_Frontal_Lobe_ReprPC
5	1e−04	26 / 1833	12_EnhBiv_ESC_Endoderm
6	1e−04	65 / 7078	Bcells peripheral blood_5_TxWk
7	2e−04	29 / 2203	EnhA_Colon
8	2e−04	44 / 4079	15_Quies_ESC_Endoderm
9	3e−04	72 / 8370	natural killer cells peripheral blood_2_TssAFlnk
10	3e−04	24 / 1700	Bcells peripheral blood_11_BivFlnk
11	3e−04	63 / 6906	3_TssF_Fibroblasts
12	3e−04	72 / 8406	Bcells peripheral blood_2_TssAFlnk
13	3e−04	8 / 258	T CD8+ naive cells peripheral blood_3_TxFlnk
14	4e−04	31 / 2531	10_TssBiv_ESC_Endoderm
15	4e−04	16 / 932	Tcells peripheral blood_3_TxFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.001	3 / 31	Kosinski_lower−crypt−short−list
2	0.002	17 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
3	0.071	7 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
4	0.073	10 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
5	0.087	5 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
6	0.103	1 / 16	Vilar_mutated−in−CRC−CamP
7	0.108	2 / 83	Marisa_CRC−cluster−d
8	0.127	1 / 20	Kosinski_top−crypt−short−list
9	0.132	4 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
10	0.165	11 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	0.226	5 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	0.227	1 / 38	Marisa_CRC−cluster−e
13	0.229	7 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
14	0.238	5 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
15	0.247	3 / 255	Kosinski_top−crypt−long−list

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	3 / 38	OL vs. OPC
2	0.009	2 / 21	KIM deleted & downregulated in LTS
3	0.016	3 / 78	Weller_LGG_A_vs_O_UP
4	0.017	2 / 30	KIM prognostic signature LTS vs. STS
5	0.021	2 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
6	0.024	4 / 163	ScoV_0.999_Sturm_E1_IDH_DN
7	0.035	5 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
8	0.037	2 / 45	Donson−innate immunity−associated with LTS in HGA
9	0.053	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
10	0.059	1 / 9	Donson−migration tethering and rolling−associated with LTS in HGA
11	0.064	11 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
12	0.079	2 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	0.097	1 / 15	VERHAAK_PN_Brain
14	0.097	1 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
15	0.103	1 / 16	VERHAAK_CL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	17 / 785	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
2	2e−05	13 / 491	ENK_UV_RESPONSE_EPIDERMIS_DN
3	3e−05	16 / 741	PEREZ_TP53_TARGETS
4	2e−04	6 / 121	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
5	2e−04	9 / 306	SANSOM_APC_TARGETS_DN
6	6e−04	3 / 25	LU_TUMOR_ANGIOGENESIS_UP
7	7e−04	7 / 220	RUTELLA_RESPONSE_TO_HGF_DN
8	9e−04	5 / 111	QI_HYPOXIA
9	9e−04	2 / 7	SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN
10	1e−03	4 / 66	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
11	1e−03	16 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
12	1e−03	5 / 121	HUANG_GATA2_TARGETS_UP
13	1e−03	7 / 249	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
14	2e−03	3 / 35	PID_RET_PATHWAY
15	2e−03	3 / 35	ZHAN_MULTIPLE_MYELOMA_HP_DN

HM

Rank	p−value	#in/all	Geneset
1	0.009	5 / 191	HALLMARK_P53_PATHWAY
2	0.010	5 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.010	5 / 194	HALLMARK_MYOGENESIS
4	0.015	4 / 141	HALLMARK_UV_RESPONSE_DN
5	0.027	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.030	4 / 174	HALLMARK_APICAL_JUNCTION
7	0.038	4 / 187	HALLMARK_INFLAMMATORY_RESPONSE
8	0.038	4 / 188	HALLMARK_HYPOXIA
9	0.119	3 / 178	HALLMARK_COMPLEMENT
10	0.125	3 / 182	HALLMARK_GLYCOLYSIS
11	0.137	3 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.139	2 / 97	HALLMARK_BILE_ACID_METABOLISM
13	0.141	3 / 193	HALLMARK_HEME_METABOLISM
14	0.178	1 / 29	HALLMARK_NOTCH_SIGNALING
15	0.206	1 / 34	HALLMARK_ANGIOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.05	1 / 8	Angelova_immune−metagene−mDC
2	0.11	1 / 18	Angelova_CRC_immunostimulators
3	0.14	1 / 23	Angelova_immune−metagene−Treg
4	0.18	1 / 29	Angelova_immune−metagene−Th1
5	0.19	1 / 32	Angelova_immune−metagene−effector_memory_CD8
6	0.26	1 / 45	Angelova_immune−metagene−MDSC
7	0.37	1 / 67	Angelova_immune−metagene−T−cells
8	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
9	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
10	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
11	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
12	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
13	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
14	1.00	0 / 25	Angelova_immune−metagene−DC
15	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	2 / 22	DUMEAUX_High bmi enriched genes
2	0.05	1 / 8	Marjolein_ageing−genes_UP
3	0.05	4 / 210	Homuth_BMI−associated−genes_DN
4	0.07	2 / 62	DUMEAUX_Smoking enriched genes
5	0.08	1 / 12	DUMEAUX_Women normal BMI literature genes up
6	0.19	1 / 32	Marjolein_ageing−genes_DN
7	0.27	2 / 150	Homuth_BMI−associated−genes_UP
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_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 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
15	1.00	0 / 22	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−04	54 / 5404	HOPP_Strong_enhancer
2	1e−03	7 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
3	2e−03	7 / 263	SPANG_CD40 6hrs UP
4	8e−03	3 / 62	Monti_Host_response_cluster
5	1e−02	40 / 4357	HOPP_Weak_txn
6	2e−02	50 / 5908	HOPP_Active_promoter
7	3e−02	4 / 173	Victora_Light zone signature
8	4e−02	47 / 5682	HOPP_Weak_promoter
9	9e−02	1 / 14	Subero_B−ALL_hypo_meth
10	9e−02	1 / 14	Subero_B−CLL_hypo_meth
11	1e−01	2 / 77	TARTE_Plasma cell signature
12	1e−01	17 / 1814	HOPP_Repetitive
13	1e−01	10 / 955	SPANG_BCR UP
14	1e−01	1 / 19	Subero_MCL_hypo_meth
15	1e−01	17 / 1894	HOPP_Poised_promoter

Melanoma

Rank	p−value	#in/all	Geneset
1	0.001	7 / 236	Gerber_wt/wt_group3−specific
2	0.033	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
3	0.049	4 / 204	Landsberg_dedifferentiation_down
4	0.200	1 / 33	Tirosh_T−cell specific genes−melanoma
5	0.244	5 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	0.292	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	0.365	2 / 189	Tirosh_genes preferentially expressed by Tregs
8	0.399	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
9	0.423	1 / 81	Tirosh_Genes in the MITF program
10	0.431	1 / 83	TCGA_melanoma_immune_high
11	0.438	1 / 85	Tirosh_AXL−signature
12	0.503	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
13	0.517	1 / 107	Tirosh_Exhaustion program in Mel75
14	0.688	1 / 171	Landsberg_dedifferentiation_up
15	0.780	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF

MF

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 22	14−3−3 protein binding
2	5e−04	4 / 55	core promoter binding
3	2e−03	6 / 191	transmembrane signaling receptor activity
4	2e−03	8 / 346	receptor binding
5	3e−03	3 / 45	SMAD binding
6	4e−03	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
7	8e−03	3 / 61	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
8	9e−03	2 / 21	transcription factor activity, transcription factor binding
9	2e−02	2 / 30	protein tyrosine/serine/threonine phosphatase activity
10	2e−02	3 / 81	protein tyrosine phosphatase activity
11	2e−02	2 / 33	phosphotyrosine residue binding
12	2e−02	2 / 34	phosphatase binding
13	2e−02	5 / 239	protein domain specific binding
14	2e−02	3 / 92	phosphatase activity
15	3e−02	3 / 94	ion channel binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.009	2 / 21	hsa−miR−483−3p
2	0.013	4 / 136	hsa−miR−153
3	0.028	4 / 170	hsa−miR−548m
4	0.033	3 / 104	hsa−miR−212
5	0.036	3 / 108	hsa−miR−421
6	0.046	1 / 7	hsa−miR−566
7	0.046	3 / 119	hsa−miR−132
8	0.051	2 / 54	hsa−miR−299−5p
9	0.056	2 / 57	hsa−miR−9*
10	0.062	2 / 60	hsa−miR−622
11	0.066	2 / 62	hsa−miR−205
12	0.066	2 / 62	hsa−miR−1254
13	0.066	2 / 62	hsa−miR−489
14	0.069	2 / 64	hsa−miR−1305
15	0.078	1 / 12	hsa−miR−147b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.03	2 / 41	Scicluna_DN
2	0.20	1 / 33	Sweeney_viral_dn
3	0.28	1 / 48	Burnham_cap_fp_vs_con_DN
4	0.28	1 / 48	Burnham_viral_DN
5	0.30	1 / 52	Burnham_day1_vs_5_DN
6	0.31	1 / 54	Burnham_timecourse
7	0.32	1 / 56	Burnham_sep_vs_con_DN
8	0.34	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
9	0.37	1 / 68	Burnham_sep_vs_con_UP
10	0.56	1 / 122	Terre_IMS_influenza_meta_signature
11	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
12	1.00	0 / 57	Burnham_viral_UP
13	1.00	0 / 57	Burnham_day1_vs_5_UP
14	1.00	0 / 18	Scicluna_UP
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−12	15 / 182	WIRTH_post GC B−cells
2	2e−08	12 / 218	WIRTH_pre+post GC B−cells
3	8e−03	2 / 20	VAQUERIZAS_Bone marrow_TF
4	1e−02	7 / 355	WIRTH_Immune system
5	3e−02	3 / 100	Chaussabel_2,8_T−cells
6	5e−02	4 / 204	Chaussabel_3,2_Inflammation I
7	6e−02	5 / 310	Chaussabel_3,4_Protein phosphatases
8	8e−02	2 / 68	Chaussabel_2,1_Cytotoxic cells
9	8e−02	2 / 72	Chaussabel_3,1_Interferon−inducible
10	9e−02	5 / 352	WIRTH_Nervous System
11	1e−01	1 / 15	WIRTH_Telencephalon
12	1e−01	1 / 15	JONGENEEL_Lung
13	1e−01	1 / 16	VAQUERIZAS_Ovary_TF
14	1e−01	7 / 604	PROTEINATLAS_hippocampus
15	1e−01	2 / 89	Chaussabel_2,3_Erythrocytes

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−04	23 / 1508	ICGC_Mef2_targets
2	2e−04	24 / 1636	ICGC_Bcl11_targets
3	8e−04	25 / 1941	ICGC_Bcl3_targets
4	1e−03	38 / 3630	ICGC_Sp1_targets
5	2e−03	36 / 3435	ICGC_Ebfsc137065_targets
6	5e−03	41 / 4264	ICGC_Pax5_targets
7	6e−03	37 / 3769	ICGC_Pmlsc71910_targets
8	7e−03	24 / 2150	ICGC_Irf4_targets
9	9e−03	35 / 3608	ICGC_Tcf12_targets
10	9e−03	32 / 3213	ICGC_Pu1_targets
11	9e−03	25 / 2321	ICGC_Rad21_targets
12	1e−02	18 / 1494	ICGC_Cebpbsc150_targets
13	1e−02	39 / 4212	ICGC_Pol2_targets
14	2e−02	39 / 4278	ICGC_Yy1_targets
15	2e−02	35 / 3778	ICGC_Pol24_targets

Overexpression Spots

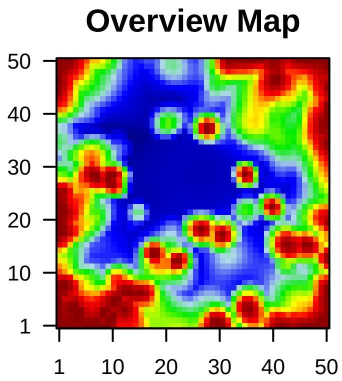
Spot Summary: K1

metagenes = 7
genes = 88

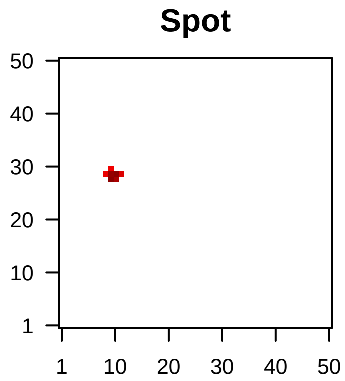
<r> metagenes = 0.98
<r> genes = 0.18
beta: r2= 1.53 / log p= −Inf

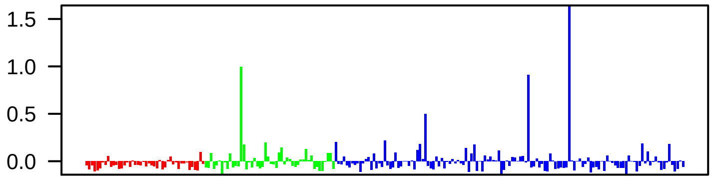
samples with spot = 5 (2.3 %)
intermediate : 1 (2.1 %)
non−mBL : 4 (3.1 %)

Overview Map



Spot





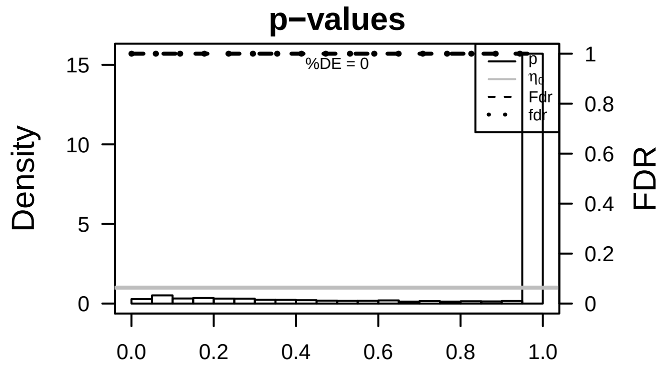
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	207663_x_at	3.8	−0.83	0.47	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
2	206640_x_at	3.58	−0.65	0.45	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
3	211425_x_at	3.5	−0.75	0.75		SSX family member 6, pseudogene [Source:HGNC Symbol;A
4	208235_x_at	3.42	−0.72	0.38	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
5	207739_s_at	3.42	−1.01	0.45	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
6	207086_x_at	3.38	−0.68	0.45	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	208155_x_at	3.36	−0.82	0.45	GAGE12J	G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
8	209942_x_at	3.13	−0.71	0.64	MAGEA3	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
9	210394_x_at	3.08	−0.76	0.72		SSX family member 6, pseudogene [Source:HGNC Symbol;A
10	207666_x_at	3	−0.6	0.67	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:113
11	210497_x_at	3	−0.67	0.7	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:113
12	214612_x_at	3	−0.72	0.65	MAGEA3	MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
13	206626_x_at	2.85	−0.74	0.7	SSX1	SSX family member 1 [Source:HGNC Symbol;Acc:HGNC:113
14	207325_x_at	2.83	−0.79	0.66	MAGEA1	MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC
15	206574_s_at	2.79	−1.22	0.37	PTP4A3	protein tyrosine phosphatase type IVA, member 3 [Source:HG
16	206834_at	2.78	−0.67	0.51	HBD	hemoglobin subunit delta [Source:HGNC Symbol;Acc:HGNC:
17	217339_x_at	2.78	−0.86	0.6	CTAG1A	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2
18	216471_x_at	2.77	−0.78	0.64	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:113
19	220062_s_at	2.72	−0.8	0.41	MAGEC2	MAGE family member C2 [Source:HGNC Symbol;Acc:HGNC
20	211674_x_at	2.72	−0.68	0.59	CTAG1A	cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−09	17 / 556	Chr	Chr X
2	1e−07	6 / 46	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
3	1e−06	10 / 262	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
4	5e−06	3 / 7	Immu	Angelova_CRC_MSI−neoantigens
5	3e−05	6 / 115	GSEA	YEGNASUBRAMANIAN_PROSTATE_CANCER
6	4e−05	3 / 13	Immu	Angelova_CRC_MSS^−neoantigens
7	4e−05	5 / 75	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
8	5e−05	3 / 14	GSEA	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
9	5e−05	5 / 77	Lymp	TARTE_Plasma cell signature
10	5e−05	8 / 255	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
11	8e−05	8 / 269	GSEA	HELLER_HDAC_TARGETS_DN
12	2e−04	2 / 4	Immu	Angelova_CRC_MSS−neoantigens
13	2e−04	3 / 22	GSEA	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
14	3e−04	6 / 171	GSEA	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
15	6e−04	5 / 133	Refer	JONGENEEL_Testis
16	7e−04	2 / 8	GSEA	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
17	9e−04	3 / 36	GSEA	MUELLER_METHYLATED_IN_GLIOBLASTOMA
18	9e−04	3 / 36	GSEA	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS
19	9e−04	4 / 83	Mela	TCGA_melanoma_immune_high
20	9e−04	3 / 37	BP	positive regulation of interleukin−6 production
21	1e−03	3 / 42	BP	negative regulation of nucleic acid−templated transcription
22	2e−03	8 / 424	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
23	2e−03	2 / 12	CC	low−density lipoprotein particle
24	2e−03	3 / 50	BP	response to unfolded protein
25	2e−03	3 / 50	GSEA	YANG_BREAST_CANCER_ESR1_LASER_DN
26	2e−03	2 / 14	BP	cellular protein catabolic process
27	3e−03	2 / 15	BP	cellular response to interleukin−6
28	3e−03	2 / 15	GSEA	MCGOWAN_RSP6_TARGETS_UP
29	3e−03	2 / 16	GSEA	KEGG_STEROID_BIOSYNTHESIS
30	3e−03	2 / 17	BP	positive regulation of ubiquitin−protein transferase activity
31	4e−03	7 / 385	GSEA	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1
32	4e−03	2 / 18	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G6_DN
33	4e−03	7 / 387	GSEA	LIAO_METASTASIS
34	4e−03	9 / 608	GSEA	SMID_BREAST_CANCER_BASAL_UP
35	4e−03	2 / 19	BP	low−density lipoprotein particle clearance
36	4e−03	4 / 127	GSEA	BIDUS_METASTASIS_DN
37	5e−03	3 / 64	GSEA	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPH
38	5e−03	2 / 20	BP	lipoprotein metabolic process
39	5e−03	2 / 20	GSEA	HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP
40	6e−03	27 / 3270	CC	integral component of membrane

p−values



Aging

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

CC

Rank	p−value	#in/all	Geneset
1	0.002	2 / 12	low−density lipoprotein particle
2	0.006	27 / 3270	integral component of membrane
3	0.006	2 / 22	smooth endoplasmic reticulum
4	0.007	12 / 1035	endoplasmic reticulum
5	0.014	2 / 35	nuclear inner membrane
6	0.030	2 / 52	clathrin−coated pit
7	0.037	4 / 241	endoplasmic reticulum lumen
8	0.045	2 / 65	collagen trimer
9	0.051	1 / 10	endolysosome membrane
10	0.051	1 / 10	vacuolar membrane
11	0.056	1 / 11	gamma−tubulin complex
12	0.059	2 / 75	apical part of cell
13	0.059	4 / 281	lysosome
14	0.061	1 / 12	chylomicron
15	0.061	1 / 12	trans−Golgi network transport vesicle

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.01	12 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	0.02	2 / 43	Marisa_CRC−cluster−f
3	0.04	41 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
4	0.04	1 / 8	Marisa_CRC−C1
5	0.05	1 / 9	Marisa_CRC−C2
6	0.05	5 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
7	0.05	1 / 10	KIM_CRC−MSI−regulated_DN
8	0.06	5 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
9	0.07	2 / 83	Marisa_CRC−cluster−d
10	0.07	1 / 14	TCGA_Mutated−in−CRC_non−hypermutated
11	0.08	1 / 15	TCGA−CRC_less−agressive−disease−markers
12	0.08	1 / 16	Vilar_non−hypermutated−in−CRC
13	0.08	1 / 16	Budinska_B_Lower crypt−like_UP
14	0.08	4 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP
15	0.09	6 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	0.02	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.14	1 / 29	HALLMARK_NOTCH_SIGNALING
4	0.18	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.21	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
6	0.22	2 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.25	2 / 182	HALLMARK_GLYCOLYSIS
8	0.27	2 / 192	HALLMARK_MTORC1_SIGNALING
9	0.27	1 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	0.40	1 / 96	HALLMARK_ANDROGEN_RESPONSE
11	0.40	1 / 97	HALLMARK_BILE_ACID_METABOLISM
12	0.40	1 / 97	HALLMARK_PEROXISOME
13	0.47	1 / 122	HALLMARK_SPERMATOGENESIS
14	0.52	1 / 139	HALLMARK_FATTY_ACID_METABOLISM
15	0.52	1 / 141	HALLMARK_UV_RESPONSE_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 77	TARTE_Plasma cell signature
2	4e−02	2 / 62	Monti_Host_response_cluster
3	9e−02	1 / 18	SPANG_BAFF 9hrs UP
4	1e−01	1 / 23	Subero_mBL_hypo_meth
5	2e−01	1 / 45	Subero_INT_hypo_meth
6	3e−01	1 / 57	SPANG_LPS 6hrs DN
7	3e−01	2 / 213	SPANG_IL21 DN
8	4e−01	1 / 85	Aukema_BCL2 DN_BCL6 UP
9	4e−01	1 / 85	Sha_DLBCL UP
10	4e−01	1 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
11	4e−01	1 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
12	4e−01	1 / 96	SPANG_LPS 6hrs UP
13	4e−01	2 / 263	SPANG_CD40 6hrs UP
14	5e−01	1 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
15	5e−01	1 / 135	DAVE_BL−vs−DLBCL

miRNA target

Rank	p−value	#in/all	Geneset
1	0.1	1 / 22	hsa−miR−1227
2	0.1	1 / 22	hsa−miR−24−1*
3	0.1	1 / 26	hsa−miR−517b
4	0.2	1 / 36	hsa−miR−412
5	0.2	1 / 41	hsa−miR−504
6	0.2	1 / 47	hsa−miR−1200
7	0.2	1 / 49	hsa−miR−219−1−3p
8	0.2	1 / 50	hsa−miR−219−5p
9	0.2	1 / 50	hsa−miR−409−5p
10	0.2	1 / 54	hsa−miR−628−3p
11	0.3	1 / 55	hsa−miR−637
12	0.3	1 / 56	hsa−miR−1826
13	0.3	1 / 57	hsa−miR−422a
14	0.3	1 / 57	hsa−miR−876−3p
15	0.3	1 / 61	hsa−miR−620

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−04	3 / 37	positive regulation of interleukin−6 production
2	1e−03	3 / 42	negative regulation of nucleic acid−templated transcription
3	2e−03	3 / 50	response to unfolded protein
4	2e−03	2 / 14	cellular protein catabolic process
5	3e−03	2 / 15	cellular response to interleukin−6
6	3e−03	2 / 17	positive regulation of ubiquitin−protein transferase activity
7	4e−03	2 / 19	low−density lipoprotein particle clearance
8	5e−03	2 / 20	lipoprotein metabolic process
9	1e−02	3 / 91	cellular protein modification process
10	1e−02	2 / 32	negative regulation of Notch signaling pathway
11	1e−02	2 / 33	protein N−linked glycosylation via asparagine
12	3e−02	2 / 49	negative regulation of ERK1 and ERK2 cascade
13	3e−02	2 / 51	cholesterol homeostasis
14	3e−02	2 / 54	IRE1−mediated unfolded protein response
15	3e−02	2 / 56	positive regulation of inflammatory response

Chr

Rank	p−value	#in/all	Geneset
1	3e−09	17 / 556	Chr X
2	4e−02	5 / 369	Chr 20
3	1e−01	3 / 242	Chr 13
4	5e−01	1 / 139	Chr 21
5	6e−01	4 / 776	Chr 17
6	6e−01	3 / 585	Chr 7
7	6e−01	2 / 382	Chr 15
8	6e−01	4 / 833	Chr 19
9	7e−01	2 / 437	Chr 8
10	7e−01	3 / 700	Chr 12
11	7e−01	2 / 480	Chr 4
12	7e−01	2 / 492	Chr 9
13	8e−01	3 / 756	Chr 11
14	8e−01	2 / 554	Chr 5
15	8e−01	1 / 333	Chr 22

Glioma

Rank	p−value	#in/all	Geneset
1	0.04	2 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
2	0.05	1 / 9	Donson−migration tethering and rolling−associated with LTS in HGA
3	0.05	4 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	0.08	1 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
5	0.08	1 / 15	Gorovets_LGG_NB_subclass
6	0.08	1 / 16	VERHAAK_MES subtype
7	0.08	5 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
8	0.13	3 / 239	ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN
9	0.13	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
10	0.15	1 / 30	Shaw_responders_down_in_oligo_glioma
11	0.16	3 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
12	0.18	4 / 421	Down_b
13	0.18	4 / 423	Down_a
14	0.21	2 / 163	ScoV_0.999_Sturm_E1_IDH_DN
15	0.26	2 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN

Immunome

Rank	p−value	#in/all	Geneset
1	5e−06	3 / 7	Angelova_CRC_MSI−neoantigens
2	4e−05	3 / 13	Angelova_CRC_MSS^−neoantigens
3	2e−04	2 / 4	Angelova_CRC_MSS−neoantigens
4	6e−02	1 / 12	Angelova_immune−metagene−NK56_dim
5	9e−02	1 / 18	Angelova_CRC_immunostimulators
6	1e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
7	2e−01	1 / 45	Angelova_immune−metagene−MDSC
8	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
9	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
10	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
11	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8
12	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
13	1e+00	0 / 25	Angelova_immune−metagene−DC
14	1e+00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
15	1e+00	0 / 32	Angelova_immune−metagene−effector_memory_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 83	TCGA_melanoma_immune_high
2	2e−02	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
3	2e−02	3 / 119	TCGA_melanoma_MITF_low
4	5e−02	2 / 65	Harbst_melanoma_highgrade_up
5	9e−02	1 / 17	Hugo_melanoma−all−MET_UP
6	9e−02	3 / 204	Landsberg_dedifferentiation_down
7	1e−01	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
8	2e−01	1 / 46	Tirosh_top50 correlated genes PC5
9	2e−01	2 / 171	Landsberg_dedifferentiation_up
10	3e−01	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
11	3e−01	1 / 81	Tirosh_Genes in the MITF program
12	6e−01	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	7e−01	1 / 236	Gerber_wt/wt_group3−specific
14	9e−01	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
15	1e+00	0 / 37	Hugo_melanoma−all−MET_DN

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	1 / 33	Sweeney_viral_dn
2	0.2	1 / 54	Burnham_timecourse
3	0.3	1 / 57	Burnham_day1_vs_5_UP
4	0.5	1 / 122	Terre_IMS_influenza_meta_signature
5	1.0	0 / 68	Burnham_sep_vs_con_UP
6	1.0	0 / 56	Burnham_sep_vs_con_DN
7	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
8	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
9	1.0	0 / 48	Burnham_viral_DN
10	1.0	0 / 57	Burnham_viral_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

TF

Rank	p−value	#in/all	Geneset
1	0.09	17 / 2321	ICGC_Rad21_targets
2	0.10	27 / 4131	ICGC_Tcf3_targets
3	0.17	8 / 1041	ICGC_P300_targets
4	0.23	22 / 3608	ICGC_Tcf12_targets
5	0.24	21 / 3435	ICGC_Ebfsc137065_targets
6	0.25	12 / 1848	ICGC_Pbx3_targets
7	0.31	12 / 1941	ICGC_Bcl3_targets
8	0.33	13 / 2150	ICGC_Irf4_targets
9	0.35	10 / 1636	ICGC_Bcl11_targets
10	0.37	24 / 4264	ICGC_Pax5_targets
11	0.37	21 / 3703	ICGC_Foxm1_targets
12	0.39	9 / 1508	ICGC_Mef2_targets
13	0.39	17 / 2994	ICGC_Zeb1_targets
14	0.40	13 / 2254	ICGC_BatfPcr1_targets
15	0.40	20 / 3564	ICGC_Taf1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	0 / 11	LIU_PROSTATE_CANCER_UP
2	0.012	7 / 480	Lembcke_Colonic Inflammation
3	0.066	1 / 13	GENTLES_modul11
4	0.071	1 / 14	GENTLES_modul13
5	0.210	1 / 45	KUIPER_MM poor survival
6	0.239	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.259	0 / 15	RHODES_CANCER_META_SIGNATURE
8	0.286	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
9	0.305	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.315	1 / 72	PanCan_Wnt_geneset_nanostring
11	0.343	1 / 80	PanCan_JAK−ST_geneset_nanostring
12	0.396	1 / 96	PanCan_TXmisReg_geneset_nanostring
13	0.534	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	0.627	1 / 187	PanCan_PI3K_geneset_nanostring
15	0.635	2 / 409	Lembcke_Normal vs Adenoma

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.004	9 / 595	13_HetRpts_Fibroblasts
2	0.017	17 / 1911	Mid_Frontal_Lobe_HetRpts
3	0.037	14 / 1611	natural killer cells peripheral blood_11_BivFlnk
4	0.044	27 / 3825	Bcells peripheral blood_15_Quies
5	0.046	27 / 3838	15_Quies_ESC_Mesoderm
6	0.064	6 / 544	12_Het_Fibroblasts
7	0.069	8 / 836	Fetal_K9K27me3
8	0.073	8 / 847	Fetal_TssP
9	0.091	18 / 2507	Mid_Frontal_Lobe_ReprPC
10	0.092	13 / 1676	Fetal_TxTrans
11	0.100	13 / 1700	Bcells peripheral blood_11_BivFlnk
12	0.107	10 / 1233	13_HetRpts_Melanocytes
13	0.114	16 / 2240	1_TssP_Fibroblasts
14	0.124	14 / 1930	Fetal_TssA
15	0.150	24 / 3755	HSC_15_Quies

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−07	6 / 46	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
2	1e−06	10 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
3	3e−05	6 / 115	YEGNASUBRAMANIAN_PROSTATE_CANCER
4	4e−05	5 / 75	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
5	5e−05	3 / 14	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
6	5e−05	8 / 255	HELLER_SILENCED_BY_METHYLATION_UP
7	8e−05	8 / 269	HELLER_HDAC_TARGETS_DN
8	2e−04	3 / 22	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
9	3e−04	6 / 171	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
10	7e−04	2 / 8	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
11	9e−04	3 / 36	MUELLER_METHYLATED_IN_GLIOBLASTOMA
12	9e−04	3 / 36	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS
13	2e−03	8 / 424	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
14	2e−03	3 / 50	YANG_BREAST_CANCER_ESR1_LASER_DN
15	3e−03	2 / 15	MCGOWAN_RSP6_TARGETS_UP

Lifestyle

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

MF

Rank	p−value	#in/all	Geneset
1	0.02	2 / 40	protein complex scaffold activity
2	0.02	3 / 110	transferase activity, transferring acyl groups
3	0.05	2 / 69	virus receptor activity
4	0.05	1 / 10	protein membrane anchor
5	0.05	1 / 10	type 1 angiotensin receptor binding
6	0.05	3 / 163	transferase activity, transferring glycosyl groups
7	0.06	1 / 11	1−acylglycerol−3−phosphate O−acyltransferase activity
8	0.06	1 / 12	low−density lipoprotein particle binding
9	0.06	1 / 12	low−density lipoprotein receptor activity
10	0.06	1 / 12	misfolded protein binding
11	0.06	3 / 172	transcription corepressor activity
12	0.07	1 / 13	calcium−activated potassium channel activity
13	0.07	1 / 13	fatty−acyl−CoA binding
14	0.07	1 / 13	MAP kinase activity
15	0.07	1 / 13	NAD+ binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 133	JONGENEEL_Testis
2	6e−03	2 / 23	JONGENEEL_Pancreas
3	4e−02	2 / 59	Chaussabel_2,10_Immune related cell surface molecules
4	6e−02	1 / 12	WIRTH_Cortex cerebri
5	7e−02	2 / 82	WIRTH_Testis
6	7e−02	1 / 14	WIRTH_Thyroid gland
7	2e−01	1 / 32	Chaussabel_1,1_Plasma Cells
8	2e−01	1 / 37	Chaussabel_2,2_Neutrophils
9	2e−01	8 / 1081	PROTEINATLAS_testis
10	2e−01	1 / 44	WIRTH_Pancreas
11	2e−01	2 / 182	WIRTH_post GC B−cells
12	3e−01	2 / 209	Chaussabel_2,5_Immune related molecules
13	3e−01	1 / 68	Chaussabel_2,1_Cytotoxic cells
14	4e−01	1 / 83	WIRTH_Muscle
15	4e−01	1 / 102	WIRTH_EBV B−cells

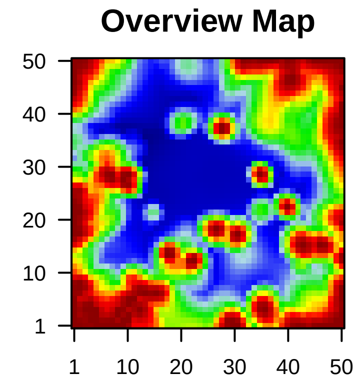
Overexpression Spots

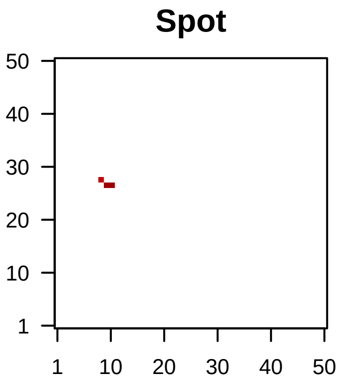
Spot Summary: L1

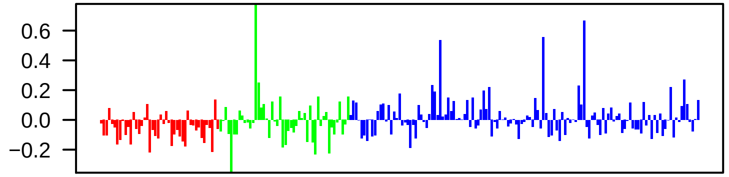
metagenes = 3
genes = 10

<r> metagenes = 0.98
<r> genes = 0.22
beta: r2= 1.55 / log p= −Inf

samples with spot = 10 (4.5 %)
intermediate : 2 (4.2 %)
non−mBL : 8 (6.2 %)





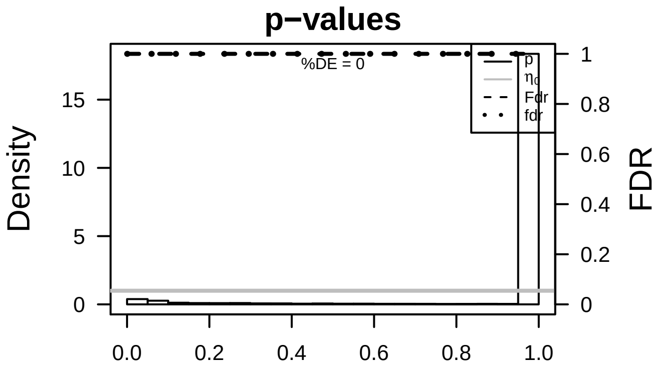


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	208586_s_at	2.01	−0.61	0.45	SSX4	SSX family member 4 [Source:HGNC Symbol;Acc:HGNC:11
2	211670_x_at	1.95	−0.64	0.57	SSX3	SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:11
3	207794_at	1.43	−0.73	0.48	CCR2	C−C motif chemokine receptor 2 [Source:HGNC Symbol;Acc:
4	213763_at	1.4	−0.84	0.53	HIPK2	homeodomain interacting protein kinase 2 [Source:HGNC Sy
5	214151_s_at	1.36	−0.73	0.46	CCPG1	cell cycle progression 1 [Source:HGNC Symbol;Acc:HGNC:2
6	219435_at	0.88	−0.86	0.43	CTC1	CST telomere replication complex component 1 [Source:HG
7	217927_at	0.75	−0.46	0.47	SPCS1	signal peptidase complex subunit 1 [Source:HGNC Symbol;A
8	204129_at	0.63	−0.67	0.34	BCL9	B cell CLL/lymphoma 9 [Source:HGNC Symbol;Acc:HGNC:1
9	209744_x_at	0.62	−0.51	0.44	ITCH	itchy E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:
10	208757_at	0.61	−0.56	0.43	TMED9	transmembrane p24 trafficking protein 9 [Source:HGNC Sym

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−04	3 / 172	MF	transcription corepressor activity
2	4e−04	2 / 42	BP	negative regulation of nucleic acid−templated transcription
3	5e−04	3 / 216	GSE	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
4	7e−04	3 / 244	GSE	RIZKI_TUMOR_INVASIVENESS_3D_DN
5	9e−04	3 / 269	GSE	HELLER_HDAC_TARGETS_DN
6	1e−03	2 / 73	GSE	SU_TESTIS
7	2e−03	2 / 93	GSE	JUBAN_TARGETS_OF_SPI1_AND_FLI1_UP
8	4e−03	1 / 5	GSE	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
9	5e−03	1 / 6	GSE	REACTOME_BETA_DEFENSINS
10	5e−03	1 / 6	GSE	CHESLER_BRAIN_QTL_TRANS
11	5e−03	1 / 7	GSE	KONDO_HYPOXIA
12	5e−03	1 / 7	GSE	ROETH_TERT_TARGETS_DN
13	6e−03	1 / 8	miRN	hsa−miR−886−3p
14	6e−03	1 / 8	GSE	KRISHNAN_FURIN_TARGETS_DN
15	7e−03	2 / 171	GSE	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
16	8e−03	1 / 10	MF	G−rich strand telomeric DNA binding
17	8e−03	1 / 10	GSE	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GIP
18	8e−03	1 / 11	MF	C−C chemokine receptor activity
19	8e−03	1 / 11	BP	hematopoietic stem cell proliferation
20	8e−03	1 / 11	BP	positive regulation of tumor necrosis factor biosynthetic process
21	8e−03	1 / 11	GSE	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24
22	8e−03	1 / 11	GSE	TIAN_BHLHA15_TARGETS
23	9e−03	1 / 12	BP	embryonic camera−type eye morphogenesis
24	9e−03	1 / 12	BP	negative regulation of protein ubiquitination involved in ubiquitin−dependen
25	9e−03	1 / 12	CC	trans−Golgi network transport vesicle
26	9e−03	1 / 12	GSE	REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHR
27	1e−02	1 / 13	BP	replicative senescence
28	1e−02	1 / 13	Immu	Angelova_CRC_MSS^−neoantigens
29	1e−02	1 / 13	GSE	REACTOME_DEFENSINS
30	1e−02	1 / 14	BP	dendritic cell chemotaxis
31	1e−02	1 / 14	BP	positive regulation of interleukin−2 production
32	1e−02	1 / 14	BP	positive regulation of monocyte chemotaxis
33	1e−02	1 / 14	GSE	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GLP1
34	1e−02	1 / 14	GSE	GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_UP
35	1e−02	1 / 15	BP	negative regulation of telomere maintenance via telomerase
36	1e−02	1 / 15	MF	ubiquitin−like protein ligase binding
37	1e−02	1 / 16	BP	DNA damage response, signal transduction by p53 class mediator resultin
38	1e−02	1 / 16	BP	retina layer formation
39	1e−02	1 / 16	BP	signal peptide processing
40	1e−02	1 / 16	GSE	SUZUKI_AMPLIFIED_IN_ORAL_CANCER



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	4e−04	2 / 42	negative regulation of nucleic acid−templated transcription
2	8e−03	1 / 11	hematopoietic stem cell proliferation
3	8e−03	1 / 11	positive regulation of tumor necrosis factor biosynthetic process
4	9e−03	1 / 12	embryonic camera−type eye morphogenesis
5	9e−03	1 / 12	negative regulation of protein ubiquitination involved in ubiquitin−dependent p
6	1e−02	1 / 13	replicative senescence
7	1e−02	1 / 14	dendritic cell chemotaxis
8	1e−02	1 / 14	positive regulation of interleukin−2 production
9	1e−02	1 / 14	positive regulation of monocyte chemotaxis
10	1e−02	1 / 15	negative regulation of telomere maintenance via telomerase
11	1e−02	1 / 16	DNA damage response, signal transduction by p53 class mediator resulting in
12	1e−02	1 / 16	retina layer formation
13	1e−02	1 / 16	signal peptide processing
14	1e−02	1 / 18	positive regulation of T cell activation
15	2e−02	1 / 20	negative regulation of adenylate cyclase activity

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	0.3	1 / 480	Lembcke_Colonic Inflammation
3	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
4	1.0	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
5	1.0	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	1.0	0 / 12	LIU_BREAST_CANCER
7	1.0	0 / 14	LIU_COMMON_CANCER_GENES
8	1.0	0 / 16	LIU_LIVER_CANCER
9	1.0	0 / 14	LIU_PROSTATE_CANCER_DN
10	1.0	0 / 11	LIU_PROSTATE_CANCER_UP
11	1.0	0 / 15	WANG_ER_UP
12	1.0	0 / 9	WANG_ER_DN
13	1.0	0 / 16	WOLFER_overlap genes
14	1.0	0 / 12	BEN−PORATH_DN
15	1.0	0 / 15	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	0.009	1 / 12	trans−Golgi network transport vesicle
2	0.026	1 / 35	cis−Golgi network
3	0.034	1 / 45	chromosome, telomeric region
4	0.037	1 / 49	RNA polymerase II transcription factor complex
5	0.038	1 / 51	endoplasmic reticulum−Golgi intermediate compartment
6	0.040	1 / 54	endoplasmic reticulum−Golgi intermediate compartment membrane
7	0.058	1 / 79	integral component of endoplasmic reticulum membrane
8	0.058	1 / 79	organelle membrane
9	0.060	1 / 82	transport vesicle
10	0.063	1 / 86	PML body
11	0.073	1 / 99	perikaryon
12	0.074	2 / 604	intracellular membrane−bounded organelle
13	0.075	1 / 103	nuclear chromosome, telomeric region
14	0.080	1 / 109	early endosome membrane
15	0.085	1 / 117	cell cortex

Chr

Rank	p−value	#in/all	Geneset
1	0.06	2 / 556	Chr X
2	0.09	2 / 689	Chr 3
3	0.25	1 / 369	Chr 20
4	0.25	1 / 382	Chr 15
5	0.35	1 / 554	Chr 5
6	0.36	1 / 585	Chr 7
7	0.45	1 / 776	Chr 17
8	0.65	1 / 1325	Chr 1
9	1.00	0 / 490	Chr 10
10	1.00	0 / 756	Chr 11
11	1.00	0 / 700	Chr 12
12	1.00	0 / 242	Chr 13
13	1.00	0 / 403	Chr 14
14	1.00	0 / 548	Chr 16
15	1.00	0 / 184	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.02	5 / 2249	3_TxFlnk_ESC_Endoderm
2	0.06	6 / 4138	6_EnhG_Skeletal_Muscle
3	0.07	5 / 3223	monocytes peripheral blood_6_EnhG
4	0.08	2 / 636	TxEnhG2_Colon
5	0.08	3 / 1405	4_TxTrans_MSC_Adipocyte
6	0.09	2 / 666	Overlap_fetal_midbrain_ZNF
7	0.10	4 / 2450	HSC_6_EnhG
8	0.11	2 / 741	Fetal_Enh
9	0.11	8 / 7420	Tcells peripheral blood_1_TssA
10	0.12	5 / 3682	natural killer cells peripheral blood_6_EnhG
11	0.13	5 / 3767	Bcells peripheral blood_6_EnhG
12	0.13	8 / 7635	monocytes peripheral blood_1_TssA
13	0.15	5 / 3938	Thelper cells peripheral blood_6_EnhG
14	0.15	8 / 7751	natural killer cells peripheral blood_1_TssA
15	0.17	8 / 7930	Tregulatory cells peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 31	Marisa_CRC−cluster−c
2	0.12	1 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
3	0.13	2 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
4	0.14	2 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
5	0.20	1 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	0.22	2 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
7	0.22	2 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
8	0.32	1 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
9	0.33	6 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
10	0.37	1 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
11	0.49	1 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
12	0.66	1 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
13	1.00	0 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
14	1.00	0 / 14	TCGA_Mutated−in−CRC_hypermutated
15	1.00	0 / 14	TCGA_Mutated−in−CRC_non−hypermutated

Glioma

Rank	p−value	#in/all	Geneset
1	0.04	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
2	0.10	3 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	0.27	2 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.27	1 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
5	0.29	1 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
6	0.32	1 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
7	0.36	2 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
8	1.00	0 / 16	VERHAAK_CL subtype
9	1.00	0 / 16	VERHAAK_MES subtype
10	1.00	0 / 16	VERHAAK_NL subtype
11	1.00	0 / 16	VERHAAK_PN subtype
12	1.00	0 / 32	WIRTH_PN subtype
13	1.00	0 / 105	WIRTH_Normal Brain
14	1.00	0 / 12	VERHAAK_Brain
15	1.00	0 / 15	VERHAAK_PN_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 216	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
2	7e−04	3 / 244	RIZKI_TUMOR_INVASIVENESS_3D_DN
3	9e−04	3 / 269	HELLER_HDAC_TARGETS_DN
4	1e−03	2 / 73	SU_TESTIS
5	2e−03	2 / 93	JUBAN_TARGETS_OF_SPI1_AND_FLI1_UP
6	4e−03	1 / 5	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
7	5e−03	1 / 6	REACTOME_BETA_DEFENSINS
8	5e−03	1 / 6	CHESLER_BRAIN_QTL_TRANS
9	5e−03	1 / 7	KONDO_HYPOXIA
10	5e−03	1 / 7	ROETH_TERT_TARGETS_DN
11	6e−03	1 / 8	KRISHNAN_FURIN_TARGETS_DN
12	7e−03	2 / 171	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_UP
13	8e−03	1 / 10	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF_GIP
14	8e−03	1 / 11	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_24
15	8e−03	1 / 11	TIAN_BHLHA15_TARGETS

HM

Rank	p−value	#in/all	Geneset
1	0.03	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
2	0.04	1 / 51	HALLMARK_TGF_BETA_SIGNALING
3	0.08	1 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	0.12	1 / 170	HALLMARK_IL2_STAT5_SIGNALING
5	0.13	1 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	1.00	0 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	1.00	0 / 188	HALLMARK_HYPOXIA
8	1.00	0 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	1.00	0 / 173	HALLMARK_MITOTIC_SPINDLE
10	1.00	0 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	1.00	0 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	1.00	0 / 133	HALLMARK_DNA_REPAIR
13	1.00	0 / 195	HALLMARK_G2M_CHECKPOINT
14	1.00	0 / 150	HALLMARK_APOPTOSIS
15	1.00	0 / 29	HALLMARK_NOTCH_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	0.01	1 / 13	Angelova_CRC_MSS^−neoantigens
2	0.02	1 / 23	Angelova_immune−metagene−Th2
3	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.06	1 / 77	TARTE_Plasma cell signature
2	0.18	6 / 5404	HOPP_Strong_enhancer
3	0.20	4 / 3168	HOPP_Repressed
4	0.41	4 / 4261	HOPP_Txn_transition
5	0.41	5 / 5529	HOPP_Txn_elongation
6	0.47	4 / 4559	HOPP_Weak_enhancer
7	0.49	5 / 5908	HOPP_Active_promoter
8	0.51	1 / 906	SPANG_BCR DN
9	0.69	4 / 5682	HOPP_Weak_promoter
10	0.69	3 / 4357	HOPP_Weak_txn
11	0.77	1 / 1814	HOPP_Repetitive
12	0.79	1 / 1894	HOPP_Poised_promoter
13	0.84	1 / 2206	HOPP_Heterochrom
14	1.00	0 / 15	BENTINK_mBL UP
15	1.00	0 / 12	BENTINK_mBL DOWN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	1 / 189	Tirosh_genes preferentially expressed by Tregs
2	0.2	1 / 236	Gerber_wt/wt_group3−specific
3	0.2	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
4	1.0	0 / 17	Hugo_melanoma−all−MET_UP
5	1.0	0 / 37	Hugo_melanoma−all−MET_DN
6	1.0	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
7	1.0	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
8	1.0	0 / 16	Hugo_melanoma−all−LEF1_UP
9	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
10	1.0	0 / 85	Tirosh_AXL−signature
11	1.0	0 / 107	Tirosh_Exhaustion program in Mel75
12	1.0	0 / 68	Tirosh_housekeeping_genes
13	1.0	0 / 81	Tirosh_Genes in the MITF program
14	1.0	0 / 38	Tirosh_top50 correlated genes PC1
15	1.0	0 / 44	Tirosh_top50 correlated genes PC2

MF

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 172	transcription corepressor activity
2	8e−03	1 / 10	G−rich strand telomeric DNA binding
3	8e−03	1 / 11	C−C chemokine receptor activity
4	1e−02	1 / 15	ubiquitin−like protein ligase binding
5	1e−02	1 / 18	cytokine binding
6	2e−02	1 / 20	chemokine receptor activity
7	2e−02	1 / 23	telomeric DNA binding
8	2e−02	1 / 29	ribonucleoprotein complex binding
9	2e−02	1 / 33	RNA polymerase II activating transcription factor binding
10	3e−02	1 / 37	ribosome binding
11	3e−02	1 / 38	RNA polymerase II transcription coactivator activity
12	3e−02	1 / 45	SMAD binding
13	3e−02	1 / 45	syntaxin binding
14	3e−02	2 / 393	molecular_function
15	4e−02	9 / 7864	protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.006	1 / 8	hsa−miR−886−3p
2	0.020	1 / 27	hsa−miR−1296
3	0.027	1 / 36	hsa−miR−146b−3p
4	0.027	1 / 36	hsa−miR−766
5	0.027	1 / 36	hsa−miR−636
6	0.033	1 / 44	hsa−miR−610
7	0.035	1 / 47	hsa−miR−370
8	0.037	1 / 49	hsa−miR−30e*
9	0.037	1 / 49	hsa−miR−550
10	0.041	1 / 55	hsa−miR−140−3p
11	0.047	1 / 63	hsa−miR−30a*
12	0.055	1 / 74	hsa−miR−496
13	0.055	1 / 75	hsa−miR−188−5p
14	0.055	1 / 75	hsa−miR−587
15	0.065	1 / 89	hsa−miR−376c

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.05	1 / 68	Burnham_sep_vs_con_UP
2	0.05	1 / 71	Burnham_cap_fp_vs_con_UP
3	1.00	0 / 56	Burnham_sep_vs_con_DN
4	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
5	1.00	0 / 48	Burnham_viral_DN
6	1.00	0 / 57	Burnham_viral_UP
7	1.00	0 / 57	Burnham_day1_vs_5_UP
8	1.00	0 / 52	Burnham_day1_vs_5_DN
9	1.00	0 / 54	Burnham_timecourse
10	1.00	0 / 18	Scicluna_UP
11	1.00	0 / 41	Scicluna_DN
12	1.00	0 / 37	Sweeney_viral_up
13	1.00	0 / 33	Sweeney_viral_dn
14	1.00	0 / 122	Terre_IMS_influenza_meta_signature
15	1.00	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.05	2 / 496	PROTEINATLAS_spleen
2	0.06	1 / 82	WIRTH_Testis
3	0.07	2 / 604	PROTEINATLAS_hippocampus
4	0.13	1 / 182	WIRTH_post GC B−cells
5	0.14	1 / 198	Chaussabel_3,3_Inflammation II
6	0.15	2 / 923	PROTEINATLAS_cerebral cortex
7	0.16	1 / 233	PROTEINATLAS_smooth muscle
8	0.18	2 / 1022	PROTEINATLAS_placenta
9	0.18	2 / 1032	PROTEINATLAS_small intestine
10	0.19	2 / 1072	PROTEINATLAS_duodenum
11	0.19	2 / 1076	PROTEINATLAS_stomach
12	0.24	1 / 355	PROTEINATLAS_skeletal muscle
13	0.26	1 / 390	PROTEINATLAS_ovary
14	0.26	1 / 399	PROTEINATLAS_soft tissue
15	0.33	1 / 527	PROTEINATLAS_oral mucosa

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	0.08	3 / 1387	HEBENSTREIT_high expression TF
2	0.12	3 / 1636	ICGC_Bcl11_targets
3	0.17	4 / 2994	ICGC_Zeb1_targets
4	0.21	4 / 3213	ICGC_Pu1_targets
5	0.25	3 / 2321	ICGC_Rad21_targets
6	0.27	4 / 3564	ICGC_Taf1_targets
7	0.29	4 / 3630	ICGC_Sp1_targets
8	0.32	2 / 1508	ICGC_Mef2_targets
9	0.33	1 / 522	ICGC_SrfPcr2_targets
10	0.37	4 / 4072	ICGC_Mta3_targets
11	0.38	3 / 2899	ICGC_Nfatc1_targets
12	0.39	4 / 4131	ICGC_Tcf3_targets
13	0.41	4 / 4264	ICGC_Pax5_targets
14	0.42	4 / 4278	ICGC_Yy1_targets
15	0.42	4 / 4319	ICGC_Pou2_targets

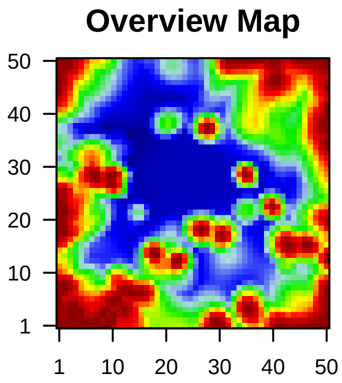
Overexpression Spots

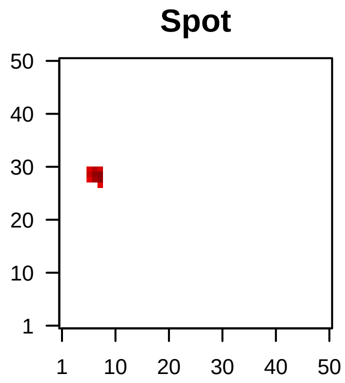
Spot Summary: M1

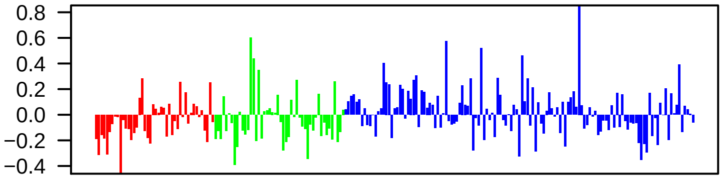
metagenes = 10
genes = 70

<r> metagenes = 0.97
<r> genes = 0.24
beta: r2= 2.24 / log p= −Inf

samples with spot = 25 (11.3 %)
mBL : 3 (6.8 %)
intermediate : 5 (10.4 %)
non−mBL : 17 (13.2 %)


Overview Map


Spot

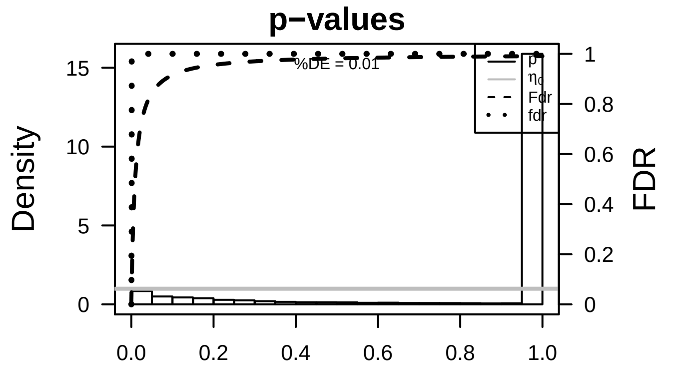


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	220377_at	2.84	−1.15	0.22		family with sequence similarity 30 member A [Source:HGNC
2	206691_s_at	2.31	−0.7	0.35	PDIA2	protein disulfide isomerase family A member 2 [Source:HGN
3	217414_x_at	2.09	−2.18	0.66	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
4	217192_s_at	1.98	−0.81	0.34	PRDM1	PR/SET domain 1 [Source:HGNC Symbol;Acc:HGNC:9346]
5	217232_x_at	1.87	−1.68	0.63	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
6	209458_x_at	1.77	−1.81	0.66	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
7	211699_x_at	1.76	−1.79	0.68	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
8	209116_x_at	1.75	−1.74	0.64	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
9	204018_x_at	1.74	−1.94	0.65	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
10	39248_at	1.74	−1.59	0.36	AQP3	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:H
11	211696_x_at	1.67	−1.34	0.62	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
12	211745_x_at	1.66	−1.57	0.66	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
13	208906_at	1.54	−0.94	0.29	BSCL2	BSCL2, seipin lipid droplet biogenesis associated [Source:H
14	202064_s_at	1.54	−0.89	0.45	SEL1L	SEL1L ERAD E3 ligase adaptor subunit [Source:HGNC Sym
15	214414_x_at	1.47	−1.7	0.65	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HGN
16	216450_x_at	1.45	−1.06	0.56		
17	208363_s_at	1.35	−0.64	0.4	INPP4A	inositol polyphosphate−4−phosphatase type I A [Source:HGN
18	202843_at	1.34	−1.15	0.46	DNAJB9	DnaJ heat shock protein family (Hsp40) member B9 [Source:
19	218681_s_at	1.27	−1.26	0.54	SDF2L1	stromal cell derived factor 2 like 1 [Source:HGNC Symbol;Acc
20	207542_s_at	1.25	−0.94	0.34	AQP1	aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−19	30 / 1035	CC	endoplasmic reticulum
2	6e−18	17 / 216	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
3	1e−16	12 / 75	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
4	2e−16	12 / 77	Lymph	TARTE_Plasma cell signature
5	5e−15	20 / 518	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
6	6e−15	22 / 683	CC	endoplasmic reticulum membrane
7	4e−12	8 / 41	GSEA	MORI_PLASMA_CELL_UP
8	5e−11	13 / 273	GSEA	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
9	4e−10	8 / 71	BP	response to endoplasmic reticulum stress
10	9e−08	8 / 140	BP	protein folding
11	1e−07	9 / 198	GSEA	TIEN_INTESTINE_PROBIOTICS_24HR_DN
12	4e−07	4 / 16	MF	protein disulfide isomerase activity
13	5e−07	9 / 241	CC	endoplasmic reticulum lumen
14	7e−07	10 / 325	GSEA	REACTOME_METABOLISM_OF_PROTEINS
15	8e−07	6 / 79	CC	integral component of endoplasmic reticulum membrane
16	1e−06	7 / 137	GSEA	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
17	2e−06	6 / 95	MF	isomerase activity
18	5e−06	18 / 1387	TF	HEBENSTREIT_high expression TF
19	8e−06	5 / 68	GSEA	REACTOME_UNFOLDED_PROTEIN_RESPONSE
20	1e−05	5 / 71	GSEA	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
21	1e−05	3 / 12	BP	retrograde protein transport, ER to cytosol
22	2e−05	3 / 13	CC	endocytic vesicle lumen
23	3e−05	5 / 88	GSEA	QI_PLASMACYTOMA_DN
24	4e−05	6 / 153	GSEA	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
25	4e−05	5 / 95	GSEA	HELLER_SILENCED_BY_METHYLATION_DN
26	4e−05	7 / 233	GSEA	BLUM_RESPONSE_TO_SALIRASIB_UP
27	6e−05	4 / 52	BP	ubiquitin−dependent ERAD pathway
28	6e−05	6 / 169	GSEA	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
29	7e−05	4 / 54	BP	IRE1−mediated unfolded protein response
30	8e−05	5 / 110	GSEA	REACTOME_DIABETES_PATHWAYS
31	8e−05	4 / 57	BP	cell redox homeostasis
32	9e−05	36 / 5339	CC	membrane
33	1e−04	5 / 119	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
34	1e−04	38 / 5908	Lymph	HOPP_Active_promoter
35	1e−04	4 / 64	GSEA	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPH
36	1e−04	4 / 64	GSEA	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL
37	2e−04	8 / 384	GSEA	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
38	2e−04	3 / 26	GSEA	CHOW_RASSF1_TARGETS_DN
39	2e−04	26 / 3270	CC	integral component of membrane
40	2e−04	5 / 129	GSEA	WELCSH_BRCA1_TARGETS_DN


p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	4e−10	8 / 71	response to endoplasmic reticulum stress
2	9e−08	8 / 140	protein folding
3	1e−05	3 / 12	retrograde protein transport, ER to cytosol
4	6e−05	4 / 52	ubiquitin−dependent ERAD pathway
5	7e−05	4 / 54	IRE1−mediated unfolded protein response
6	8e−05	4 / 57	cell redox homeostasis
7	4e−04	3 / 34	bicarbonate transport
8	7e−04	4 / 99	cellular response to hypoxia
9	7e−04	3 / 43	positive regulation of cell death
10	9e−04	2 / 11	oxygen transport
11	1e−03	2 / 12	ER−associated misfolded protein catabolic process
12	1e−03	3 / 50	response to unfolded protein
13	1e−03	2 / 13	ERAD pathway
14	1e−03	2 / 13	protein folding in endoplasmic reticulum
15	1e−03	2 / 14	water transport

Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	0 / 11	LIU_PROSTATE_CANCER_UP
2	4e−02	3 / 186	SPANG_LPS−index2
3	4e−02	1 / 11	GENTLES_modul14
4	5e−02	1 / 12	GENTLES_modul12
5	5e−02	1 / 13	BENTINK_e2f3.1
6	6e−02	1 / 14	GENTLES_modul13
7	6e−02	1 / 16	GENTLES_modul6
8	1e−01	1 / 32	KUIPER_MM good survival
9	2e−01	0 / 15	RHODES_CANCER_META_SIGNATURE
10	3e−01	3 / 480	Lembcke_Colonic Inflammation
11	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
12	4e−01	0 / 14	LIU_PROSTATE_CANCER_DN
13	4e−01	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	5e−01	1 / 187	PanCan_PI3K_geneset_nanostring
15	7e−01	1 / 317	SPANG_BCL6−index2

CC

Rank	p−value	#in/all	Geneset
1	1e−19	30 / 1035	endoplasmic reticulum
2	6e−15	22 / 683	endoplasmic reticulum membrane
3	5e−07	9 / 241	endoplasmic reticulum lumen
4	8e−07	6 / 79	integral component of endoplasmic reticulum membrane
5	2e−05	3 / 13	endocytic vesicle lumen
6	9e−05	36 / 5339	membrane
7	2e−04	26 / 3270	integral component of membrane
8	3e−04	4 / 77	cell
9	6e−04	4 / 96	melanosome
10	1e−03	3 / 53	rough endoplasmic reticulum
11	3e−03	18 / 2239	extracellular exosome
12	6e−03	7 / 537	perinuclear region of cytoplasm
13	2e−02	2 / 51	endoplasmic reticulum−Golgi intermediate compartment
14	2e−02	2 / 56	lipid droplet
15	4e−02	2 / 77	specific granule membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.007	8 / 689	Chr 3
2	0.047	4 / 333	Chr 22
3	0.054	6 / 669	Chr 6
4	0.157	5 / 700	Chr 12
5	0.431	3 / 585	Chr 7
6	0.436	1 / 139	Chr 21
7	0.494	2 / 403	Chr 14
8	0.538	2 / 437	Chr 8
9	0.589	2 / 480	Chr 4
10	0.605	3 / 756	Chr 11
11	0.623	3 / 776	Chr 17
12	0.662	2 / 548	Chr 16
13	0.784	1 / 369	Chr 20
14	0.796	1 / 382	Chr 15
15	0.805	4 / 1325	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−07	47 / 7331	TssA_Colon
2	2e−06	48 / 7833	Bcells peripheral blood_1_TssA
3	3e−06	49 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
4	3e−06	48 / 7930	Tregulatory cells peripheral blood_1_TssA
5	3e−06	47 / 7635	monocytes peripheral blood_1_TssA
6	5e−06	49 / 8370	natural killer cells peripheral blood_2_TssAFlnk
7	5e−06	26 / 2704	4_TxTrans_Fibroblasts
8	5e−06	46 / 7420	Tcells peripheral blood_1_TssA
9	6e−06	49 / 8406	Bcells peripheral blood_2_TssAFlnk
10	6e−06	47 / 7751	natural killer cells peripheral blood_1_TssA
11	7e−06	49 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
12	8e−06	50 / 8816	Thelper cells peripheral blood_2_TssAFlnk
13	9e−06	23 / 2249	3_TxFlnk_ESC_Endoderm
14	9e−06	33 / 4208	Tcells peripheral blood_6_EnhG
15	1e−05	31 / 3803	6_EnhG_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.003	13 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	0.005	4 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
3	0.008	14 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	0.025	2 / 60	Marisa_CRC−cluster−g
5	0.033	4 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	0.119	1 / 31	Marisa_CRC−cluster−c
7	0.172	4 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
8	0.196	4 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
9	0.196	7 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	0.231	4 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
11	0.277	3 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
12	0.281	6 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	0.286	1 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
14	0.293	5 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
15	0.435	3 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN

Glioma

Rank	p−value	#in/all	Geneset
1	0.02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
2	0.03	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
3	0.04	1 / 9	Colman_survival_robust
4	0.06	1 / 15	Mukasa_UP_in_GBM
5	0.06	2 / 101	Hopp_Sturm_GBM_Epi3_E_G34_UP
6	0.09	9 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	0.13	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
8	0.13	1 / 35	Gorovets_LGG_EPL_subclass
9	0.13	1 / 35	Colman_survival_associated
10	0.20	1 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	0.21	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.24	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	0.24	1 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
14	0.25	1 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
15	0.26	2 / 242	ScoV_0.5_Sturm_C1_IDH_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−18	17 / 216	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
2	1e−16	12 / 75	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
3	5e−15	20 / 518	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
4	4e−12	8 / 41	MORI_PLASMA_CELL_UP
5	5e−11	13 / 273	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
6	1e−07	9 / 198	TIEN_INTESTINE_PROBIOTICS_24HR_DN
7	7e−07	10 / 325	REACTOME_METABOLISM_OF_PROTEINS
8	1e−06	7 / 137	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
9	8e−06	5 / 68	REACTOME_UNFOLDED_PROTEIN_RESPONSE
10	1e−05	5 / 71	REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION
11	3e−05	5 / 88	QI_PLASMACYTOMA_DN
12	4e−05	6 / 153	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
13	4e−05	5 / 95	HELLER_SILENCED_BY_METHYLATION_DN
14	4e−05	7 / 233	BLUM_RESPONSE_TO_SALIRASIB_UP
15	6e−05	6 / 169	RODWELL_AGING_KIDNEY_NO_BLOOD_UP

HM

Rank	p−value	#in/all	Geneset
1	0.003	4 / 149	HALLMARK_UV_RESPONSE_UP
2	0.009	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	0.019	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
4	0.044	3 / 192	HALLMARK_MTORC1_SIGNALING
5	0.059	2 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.169	2 / 181	HALLMARK_XENOBIOTIC_METABOLISM
7	0.187	2 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
8	0.187	2 / 193	HALLMARK_HEME_METABOLISM
9	0.188	2 / 194	HALLMARK_KRAS_SIGNALING_UP
10	0.321	1 / 94	HALLMARK_PROTEIN_SECRETION
11	0.329	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.329	1 / 97	HALLMARK_PEROXISOME
13	0.422	1 / 133	HALLMARK_DNA_REPAIR
14	0.504	1 / 170	HALLMARK_IL2_STAT5_SIGNALING
15	0.512	1 / 174	HALLMARK_ADIPOGENESIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.2	1 / 67	Angelova_immune−metagene−T−cells
2	1.0	0 / 13	Angelova_immune−metagene−activated_B−cells
3	1.0	0 / 26	Angelova_immune−metagene−activated_CD4
4	1.0	0 / 19	Angelova_immune−metagene−activated_CD8
5	1.0	0 / 21	Angelova_immune−metagene−central_memory_CD4
6	1.0	0 / 17	Angelova_immune−metagene−central_memory_CD8
7	1.0	0 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1.0	0 / 25	Angelova_immune−metagene−DC
9	1.0	0 / 12	Angelova_immune−metagene−effector_memory_CD4
10	1.0	0 / 32	Angelova_immune−metagene−effector_memory_CD8
11	1.0	0 / 14	Angelova_immune−metagene−eosinophil
12	1.0	0 / 19	Angelova_immune−metagene−iDC
13	1.0	0 / 13	Angelova_immune−metagene−immature_B−cells
14	1.0	0 / 11	Angelova_immune−metagene−macrophages
15	1.0	0 / 38	Angelova_immune−metagene−mast−cells

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−16	12 / 77	TARTE_Plasma cell signature
2	1e−04	38 / 5908	HOPP_Active_promoter
3	4e−04	36 / 5682	HOPP_Weak_promoter
4	6e−04	35 / 5529	HOPP_Txn_elongation
5	2e−03	28 / 4261	HOPP_Txn_transition
6	7e−03	27 / 4357	HOPP_Weak_txn
7	8e−03	3 / 102	ROSOLOWSKI_blue total
8	1e−02	31 / 5404	HOPP_Strong_enhancer
9	1e−02	27 / 4559	HOPP_Weak_enhancer
10	1e−02	2 / 45	SPANG_BAFF 9hrs DN
11	2e−02	4 / 237	ZHANG_DLBCL mutated
12	2e−02	2 / 57	SPANG_LPS 6hrs DN
13	3e−02	3 / 173	Victora_Light zone signature
14	5e−02	2 / 85	Aukema_BCL2 DN_BCL6 UP
15	7e−02	7 / 906	SPANG_BCR DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.007	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
2	0.042	3 / 189	Tirosh_genes preferentially expressed by Tregs
3	0.068	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.094	1 / 24	Gerami_melanoma−metastatic−risk_DN
5	0.127	1 / 33	Tirosh_T−cell specific genes−melanoma
6	0.155	1 / 41	Tirosh_top50 correlated genes PC3
7	0.203	2 / 204	Landsberg_dedifferentiation_down
8	0.251	2 / 236	Gerber_wt/wt_group3−specific
9	0.265	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
10	0.274	1 / 78	Tirosh_CAF−cell specific genes
11	0.277	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
12	0.289	1 / 83	TCGA_melanoma_immune_high
13	0.332	3 / 497	Gerber_wt/wt_melanoma−cells−SpotD
14	0.601	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
15	1.000	0 / 17	Hugo_melanoma−all−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	4e−07	4 / 16	protein disulfide isomerase activity
2	2e−06	6 / 95	isomerase activity
3	7e−04	2 / 10	water channel activity
4	1e−03	2 / 12	misfolded protein binding
5	4e−03	2 / 23	channel activity
6	4e−03	2 / 23	peroxidase activity
7	4e−03	3 / 80	chaperone binding
8	4e−03	4 / 163	transferase activity, transferring glycosyl groups
9	7e−03	2 / 30	oxygen binding
10	8e−03	2 / 32	Hsp70 protein binding
11	8e−03	2 / 32	peptidyl−prolyl cis−trans isomerase activity
12	3e−02	2 / 64	hydrolase activity, acting on glycosyl bonds
13	3e−02	2 / 69	ATPase binding
14	4e−02	1 / 11	metal ion transmembrane transporter activity
15	4e−02	1 / 11	polypeptide N−acetylgalactosaminyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	4 / 93	hsa−miR−605
2	7e−04	4 / 100	hsa−miR−493
3	2e−03	3 / 59	hsa−miR−326
4	3e−03	5 / 240	hsa−miR−202
5	3e−03	2 / 20	hsa−miR−99a
6	3e−03	2 / 20	hsa−miR−100
7	4e−03	2 / 23	hsa−miR−99b
8	6e−03	6 / 407	hsa−miR−106a
9	8e−03	6 / 435	hsa−miR−93
10	9e−03	2 / 36	hsa−miR−146b−3p
11	1e−02	2 / 38	hsa−miR−1291
12	1e−02	4 / 217	hsa−miR−577
13	1e−02	2 / 41	hsa−miR−571
14	1e−02	4 / 223	hsa−miR−1244
15	2e−02	2 / 46	hsa−miR−193a−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	1 / 37	Sweeney_viral_up
2	0.2	1 / 68	Burnham_sep_vs_con_UP
3	0.3	1 / 71	Burnham_cap_fp_vs_con_UP
4	0.5	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 48	Burnham_viral_DN
8	1.0	0 / 57	Burnham_viral_UP
9	1.0	0 / 57	Burnham_day1_vs_5_UP
10	1.0	0 / 52	Burnham_day1_vs_5_DN
11	1.0	0 / 54	Burnham_timecourse
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 33	Sweeney_viral_dn
15	1.0	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−04	12 / 893	PROTEINATLAS_pancreas
2	3e−04	3 / 32	Chaussabel_1,1_Plasma Cells
3	9e−04	2 / 11	JONGENEEL_Peripheral Blood Lymphocytes
4	9e−04	2 / 11	Chaussabel_3,5_Hemoglobin genes
5	4e−03	11 / 1076	PROTEINATLAS_stomach
6	7e−03	2 / 30	JONGENEEL_Bone Marrow
7	8e−03	10 / 1022	PROTEINATLAS_placenta
8	5e−02	1 / 12	WIRTH_Globus pallidus
9	6e−02	1 / 14	WIRTH_Thyroid gland
10	9e−02	1 / 23	JONGENEEL_Pancreas
11	1e−01	7 / 1032	PROTEINATLAS_small intestine
12	1e−01	2 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
13	1e−01	7 / 1072	PROTEINATLAS_duodenum
14	2e−01	1 / 44	WIRTH_Pancreas
15	2e−01	2 / 188	Chaussabel_3,8_Enzymes

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	5e−06	18 / 1387	HEBENSTREIT_high expression TF
2	2e−03	23 / 3150	ICGC_Creb1_targets
3	2e−03	26 / 3796	ICGC_Nficsc81335_targets
4	3e−03	28 / 4319	ICGC_Pou2_targets
5	7e−03	17 / 2254	ICGC_BatfPcr1_targets
6	7e−03	26 / 4131	ICGC_Tcf3_targets
7	8e−03	10 / 1032	ICGC_Usf1_targets
8	9e−03	10 / 1044	ICGC_Six5_targets
9	9e−03	23 / 3564	ICGC_Taf1_targets
10	1e−02	24 / 3804	ICGC_Stat5_targets
11	1e−02	20 / 2994	ICGC_Zeb1_targets
12	2e−02	27 / 4602	ICGC_Elf1_targets
13	2e−02	19 / 2899	ICGC_Nfatc1_targets
14	2e−02	6 / 522	ICGC_SrfPcr2_targets
15	2e−02	12 / 1578	ICGC_GabpPcr2_targets

Overexpression Spots

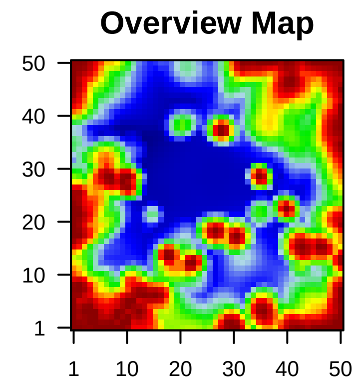
Spot Summary: N1

metagenes = 13
genes = 298

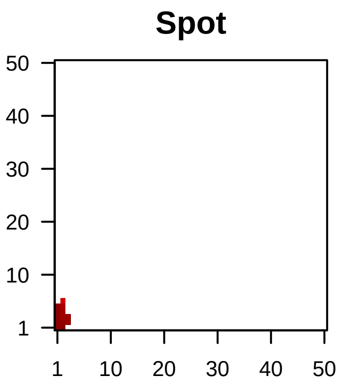
<r> metagenes = 0.97
<r> genes = 0.42
beta: r2= 25.74 / log p= −Inf

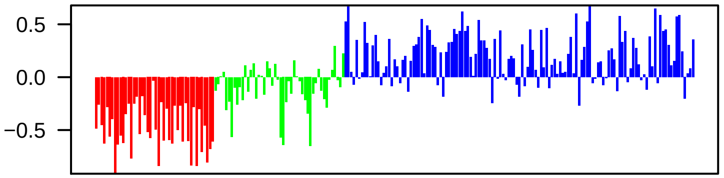
samples with spot = 63 (28.5 %)
intermediate : 2 (4.2 %)
non−mBL : 61 (47.3 %)

Overview Map



Spot





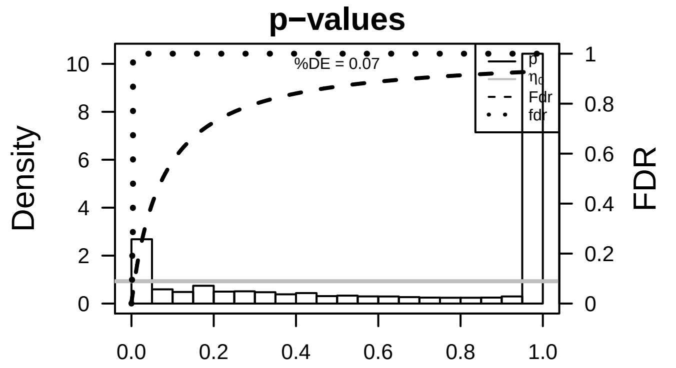
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	211644_x_at	2.59	−1.77	0.36		immunoglobulin kappa variable 3−20 [Source:HGNC Symbol;
2	221185_s_at	2.57	−1.49	0.55	IQCG	IQ motif containing G [Source:HGNC Symbol;Acc:HGNC:252
3	214551_s_at	2.53	−1.11	0.67	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
4	208451_s_at	2.38	−1.57	0.64	C4A	complement C4A (Rodgers blood group) [Source:HGNC Sym
5	203535_at	2.34	−1.86	0.61	S100A9	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
6	217022_s_at	2.33	−2.54	0.5		immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
7	205819_at	2.09	−0.95	0.53	MARCO	macrophage receptor with collagenous structure [Source:HGI
8	202833_s_at	2.04	−2.04	0.77	SERPINA1	serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC
9	212062_at	1.97	−1.07	0.48	ATP9A	ATPase phospholipid transporting 9A (putative) [Source:HGN
10	202917_s_at	1.96	−1.75	0.64	S100A8	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:
11	214049_x_at	1.96	−1.08	0.64	CD7	CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
12	210116_at	1.95	−1.66	0.55	SH2D1A	SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGN
13	207979_s_at	1.93	−1.42	0.46	CD8B	CD8b molecule [Source:HGNC Symbol;Acc:HGNC:1707]
14	202274_at	1.93	−2	0.36	ACTG2	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
15	204787_at	1.89	−1.35	0.48	VSIG4	V−set and immunoglobulin domain containing 4 [Source:HGN
16	204006_s_at	1.87	−1.43	0.49	FCGR3A	Fc fragment of IgG receptor IIIa [Source:HGNC Symbol;Acc:
17	205403_at	1.87	−1.01	0.51	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGN
18	206974_at	1.84	−1.08	0.7	CXCR6	C−X−C motif chemokine receptor 6 [Source:HGNC Symbol;A
19	206486_at	1.79	−1.26	0.66	LAG3	lymphocyte activating 3 [Source:HGNC Symbol;Acc:HGNC:6
20	210916_s_at	1.78	−1.66	0.71	CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−87	108 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−68	53 / 102	Refer	WIRTH_EBV B−cells
3	9e−59	78 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
4	1e−38	34 / 85	Lympl	Sha_DLBCL UP
5	3e−32	45 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
6	4e−31	39 / 194	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
7	5e−31	29 / 83	Melar	TCGA_melanoma_immune_high
8	3e−30	43 / 265	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
9	1e−28	35 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	1e−27	38 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
11	6e−27	25 / 71	Melar	Tirosh_Macrophage specific genes−melanoma
12	7e−27	51 / 480	Canc	Lembcke_Colonic Inflammation
13	1e−26	34 / 176	HM	HALLMARK_ALLOGRAFT_REJECTION
14	8e−26	37 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
15	2e−25	23 / 62	Lympl	Monti_Host_response_cluster
16	3e−25	47 / 431	BP	immune system process
17	7e−24	22 / 62	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
18	8e−24	39 / 299	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
19	2e−23	40 / 323	BP	inflammatory response
20	8e−23	24 / 88	GSEA	WIELAND_UP_BY_HBV_INFECTION
21	8e−23	23 / 78	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
22	2e−22	44 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
23	3e−22	33 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
24	4e−22	17 / 33	Melar	Tirosh_T−cell specific genes−melanoma
25	7e−22	38 / 317	Canc	SPANG_BCL6−index2
26	5e−21	39 / 355	Refer	WIRTH_Immune system
27	6e−21	38 / 336	BP	immune response
28	9e−21	34 / 261	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
29	5e−20	29 / 186	Canc	SPANG_LPS−index2
30	2e−19	34 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
31	3e−19	37 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
32	7e−19	21 / 87	GSEA	BOSCO_TH1_CYTOTOXIC_MODULE
33	8e−19	18 / 56	Pneu	Burnham_sep_vs_con_DN
34	1e−18	20 / 78	Melar	Tirosh_expression higher in CAFs than in T−cells
35	2e−18	43 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
36	2e−18	30 / 229	GSEA	QI_PLASMACYTOMA_UP
37	4e−18	31 / 255	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
38	5e−18	17 / 52	GSEA	SANA_RESPONSE_TO_IFNG_UP
39	8e−18	27 / 187	HM	HALLMARK_INFLAMMATORY_RESPONSE
40	4e−17	18 / 68	Refer	Chaussabel_2,1_Cytotoxic cells

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 47	TESCHENDORFF_age_hypermethylated
2	0.5	2 / 92	HORVATH_aging_genes meth DOWN
3	0.8	1 / 107	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−25	47 / 431	immune system process
2	2e−23	40 / 323	inflammatory response
3	6e−21	38 / 336	immune response
4	2e−14	32 / 367	innate immune response
5	5e−13	18 / 113	regulation of immune response
6	7e−13	19 / 131	chemotaxis
7	9e−13	26 / 274	cytokine−mediated signaling pathway
8	2e−12	14 / 63	chemokine−mediated signaling pathway
9	3e−12	20 / 161	adaptive immune response
10	8e−12	20 / 169	response to lipopolysaccharide
11	6e−11	22 / 232	cell surface receptor signaling pathway
12	3e−10	13 / 75	cellular response to interferon−gamma
13	2e−09	14 / 104	response to virus
14	4e−09	31 / 553	apoptotic process
15	8e−09	16 / 156	positive regulation of ERK1 and ERK2 cascade

Cancer

Rank	p−value	#in/all	Geneset
1	7e−27	51 / 480	Lembcke_Colonic Inflammation
2	7e−22	38 / 317	SPANG_BCL6−index2
3	5e−20	29 / 186	SPANG_LPS−index2
4	6e−10	7 / 13	GENTLES_modul18
5	9e−07	10 / 80	PanCan_JAK−ST_geneset_nanostring
6	2e−05	4 / 10	BENTINK_ras.4
7	3e−05	9 / 96	PanCan_TXmisReg_geneset_nanostring
8	1e−03	3 / 13	GENTLES_modul11
9	2e−02	2 / 12	HLA2_signature
10	2e−02	2 / 14	GUSTAFSON_PI3K_UP
11	2e−02	1 / 14	LIU_PROSTATE_CANCER_DN
12	4e−02	6 / 147	PanCan_MAPK_geneset_nanostring
13	4e−02	7 / 187	PanCan_PI3K_geneset_nanostring
14	7e−02	0 / 16	LIU_LIVER_CANCER
15	1e−01	1 / 9	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−14	70 / 1611	extracellular region
2	3e−12	21 / 179	external side of plasma membrane
3	4e−11	50 / 1090	extracellular space
4	6e−09	93 / 3210	plasma membrane
5	2e−07	6 / 17	T cell receptor complex
6	3e−07	43 / 1128	integral component of plasma membrane
7	4e−07	10 / 74	secretory granule membrane
8	4e−06	23 / 462	cell surface
9	6e−06	85 / 3270	integral component of membrane
10	7e−06	6 / 29	immunological synapse
11	1e−05	122 / 5339	membrane
12	1e−04	22 / 537	perinuclear region of cytoplasm
13	1e−04	6 / 48	ficolin−1−rich granule membrane
14	5e−04	3 / 10	amyloid−beta complex
15	8e−04	8 / 116	blood microparticle

Chr

Rank	p−value	#in/all	Geneset
1	0.02	32 / 1325	Chr 1
2	0.13	12 / 490	Chr 10
3	0.17	9 / 369	Chr 20
4	0.24	16 / 776	Chr 17
5	0.33	11 / 554	Chr 5
6	0.40	14 / 756	Chr 11
7	0.40	11 / 585	Chr 7
8	0.42	9 / 480	Chr 4
9	0.44	15 / 832	Chr 2
10	0.49	6 / 333	Chr 22
11	0.52	12 / 700	Chr 12
12	0.68	6 / 403	Chr 14
13	0.73	10 / 689	Chr 3
14	0.82	2 / 184	Chr 18
15	0.82	7 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−16	44 / 626	natural killer cells peripheral blood_3_TxFlnk
2	1e−15	36 / 432	monocytes peripheral blood_3_TxFlnk
3	3e−10	44 / 932	Tcells peripheral blood_3_TxFlnk
4	7e−10	81 / 2507	Mid_Frontal_Lobe_ReprPC
5	4e−07	18 / 258	T CD8+ naive cells peripheral blood_3_TxFlnk
6	6e−07	22 / 383	K9acLow_Colon
7	7e−07	55 / 1676	Fetal_TxTrans
8	1e−06	29 / 642	Thelper cells peripheral blood_3_TxFlnk
9	2e−06	86 / 3223	monocytes peripheral blood_6_EnhG
10	4e−06	39 / 1072	Mid_Frontal_Lobe_ReprPCWk
11	6e−06	44 / 1308	Mid_Frontal_Lobe_K9K27me3
12	2e−05	32 / 867	Mid_Frontal_Lobe_Quies
13	2e−04	87 / 3682	natural killer cells peripheral blood_6_EnhG
14	8e−04	63 / 2555	Tregulatory cells peripheral blood_3_TxFlnk
15	1e−03	67 / 2792	EnhWk2_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−87	108 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−19	34 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	6e−12	26 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	5e−07	8 / 43	Marisa_CRC−cluster−f
5	7e−07	9 / 60	Marisa_CRC−cluster−g
6	1e−06	22 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
7	2e−06	18 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	1e−05	9 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
9	1e−03	3 / 13	Budinska_B_Lower crypt−like_DOWN
10	2e−03	3 / 15	TCGA−CRC_less−agressive−disease−markers
11	3e−03	4 / 35	Ang_CRC_Hypomethylated
12	3e−03	44 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	6e−03	2 / 7	Budinska_C_CIMP−H−like_UP
14	9e−03	2 / 9	Marisa_CRC−C2
15	1e−02	17 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	9e−59	78 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	3e−32	45 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	8e−26	37 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
4	3e−12	24 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	9e−10	22 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
6	1e−09	7 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
7	6e−09	20 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
8	1e−08	12 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
9	5e−08	9 / 45	Donson−innate immunity−associated with LTS in HGA
10	9e−07	5 / 12	Donson−immune cell intra signaling−associated with LTS in HGA
11	1e−06	54 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
12	3e−06	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
13	2e−05	10 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
14	2e−05	8 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
15	8e−05	5 / 27	Donson−Misc immune function−associated with LTS in HGA

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−31	39 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
2	3e−30	43 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
3	1e−27	38 / 223	MCLACHLAN_DENTAL_CARIES_UP
4	7e−24	22 / 62	BROWNE_INTERFERON_RESPONSIVE_GENES
5	8e−24	39 / 299	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
6	8e−23	24 / 88	WIELAND_UP_BY_HBV_INFECTION
7	8e−23	23 / 78	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
8	2e−22	44 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
9	3e−22	33 / 219	MCLACHLAN_DENTAL_CARIES_DN
10	9e−21	34 / 261	POOLA_INVASIVE_BREAST_CANCER_UP
11	3e−19	37 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
12	7e−19	21 / 87	BOSCO_TH1_CYTOTOXIC_MODULE
13	2e−18	43 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
14	2e−18	30 / 229	QI_PLASMACYTOMA_UP
15	4e−18	31 / 255	HELLER_SILENCED_BY_METHYLATION_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−28	35 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	1e−26	34 / 176	HALLMARK_ALLOGRAFT_REJECTION
3	8e−18	27 / 187	HALLMARK_INFLAMMATORY_RESPONSE
4	2e−16	19 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	1e−14	23 / 170	HALLMARK_IL2_STAT5_SIGNALING
6	8e−12	21 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	5e−08	11 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	6e−08	16 / 178	HALLMARK_COMPLEMENT
9	2e−06	13 / 150	HALLMARK_APOPTOSIS
10	2e−02	8 / 194	HALLMARK_KRAS_SIGNALING_UP
11	2e−02	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	4e−02	7 / 191	HALLMARK_P53_PATHWAY
13	5e−02	7 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
14	7e−02	6 / 174	HALLMARK_APICAL_JUNCTION
15	1e−01	6 / 188	HALLMARK_HYPOXIA

Immunome

Rank	p−value	#in/all	Geneset
1	3e−13	15 / 67	Angelova_immune−metagene−T−cells
2	4e−08	8 / 32	Angelova_immune−metagene−effector_memory_CD8
3	4e−07	7 / 29	Angelova_immune−metagene−Th1
4	7e−05	6 / 42	Angelova_immune−metagene−TGD
5	9e−05	3 / 6	Immunity_immune−checkpoint−inhibitors
6	1e−04	6 / 45	Angelova_immune−metagene−MDSC
7	2e−04	3 / 7	Angelova_immune−metagene−cytotoxic_cells
8	4e−04	4 / 21	Angelova_immune−metagene−central_memory_CD4
9	5e−04	3 / 10	Angelova_immune−metagene−TFH
10	5e−04	4 / 23	Angelova_immune−metagene−Treg
11	1e−03	3 / 13	Angelova_immune−metagene−activated_B−cells
12	4e−03	3 / 19	Angelova_immune−metagene−iDC
13	8e−03	3 / 25	Angelova_immune−metagene−DC
14	1e−02	2 / 10	Angelova_CRC_immonoinhibitors
15	4e−02	2 / 18	Angelova_CRC_immunostimulators

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−06	5 / 14	Huan_blood−pressure_SBP−signature
2	4e−05	4 / 12	DUMEAUX_Women normal BMI literature genes up
3	5e−04	4 / 22	DUMEAUX_High bmi enriched genes
4	8e−04	2 / 3	Huan_blood−pressure_HTN−signature
5	1e−03	3 / 13	Huan_blood−pressure_DBP−signature
6	7e−03	2 / 8	Marjolein_ageing−genes_UP
7	9e−03	2 / 9	DUMEAUX_Monocytes in smokers literature genes up
8	8e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e−01	2 / 32	Marjolein_ageing−genes_DN
10	3e−01	5 / 210	Homuth_BMI−associated−genes_DN
11	5e−01	3 / 150	Homuth_BMI−associated−genes_UP
12	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
13	1e+00	0 / 10	DUMEAUX_Smoking literature 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

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−38	34 / 85	Sha_DLBCL UP
2	2e−25	23 / 62	Monti_Host_response_cluster
3	6e−17	23 / 135	DAVE_BL−vs−DLBCL
4	2e−15	26 / 213	SPANG_IL21 DN
5	4e−13	9 / 15	Care_Polarized immune response
6	1e−10	10 / 33	Care_Extended T−cell
7	2e−07	15 / 173	Victora_Light zone signature
8	3e−07	11 / 88	ROSOLOWSKI_green UP
9	9e−07	12 / 121	ROSOLOWSKI_green total
10	9e−07	5 / 12	BENTINK_mBL DOWN
11	2e−06	10 / 85	Aukema_BCL2 DN_BCL6 UP
12	6e−06	20 / 378	TARTE_Mature plasma cell signature
13	9e−06	34 / 906	SPANG_BCR DN
14	9e−06	5 / 18	DAVE_Immune response 2
15	2e−05	4 / 10	MASCQUE_ABC UP

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−31	29 / 83	TCGA_melanoma_immune_high
2	6e−27	25 / 71	Tirosh_Macrophage specific genes−melanoma
3	4e−22	17 / 33	Tirosh_T−cell specific genes−melanoma
4	1e−18	20 / 78	Tirosh_expression higher in CAFs than in T−cells
5	1e−14	24 / 189	Tirosh_genes preferentially expressed by Tregs
6	2e−12	17 / 107	Tirosh_Exhaustion program in Mel75
7	6e−10	18 / 171	Landsberg_dedifferentiation_up
8	4e−07	4 / 5	Joensson_Melanoma Proliferative subtype
9	2e−06	6 / 24	Tirosh_exhuastion−associated genes consitent across tumors
10	6e−03	10 / 230	Gerber_wt/wt_melanoma−cells−SpotC
11	1e−02	4 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
12	1e−02	5 / 85	Tirosh_AXL−signature
13	2e−02	8 / 204	Landsberg_dedifferentiation_down
14	3e−02	3 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	4e−02	7 / 185	Tirosh_genes from malignant cells in Mel79−melanoma

MF

Rank	p−value	#in/all	Geneset
1	6e−10	10 / 39	chemokine activity
2	8e−10	18 / 173	cytokine activity
3	3e−05	26 / 644	protein homodimerization activity
4	1e−04	4 / 16	CCR chemokine receptor binding
5	2e−04	4 / 17	MHC class I protein binding
6	2e−04	6 / 50	amyloid−beta binding
7	3e−04	10 / 154	serine−type endopeptidase activity
8	3e−04	4 / 20	chemokine receptor activity
9	3e−04	20 / 500	signal transducer activity
10	4e−04	5 / 38	cytokine receptor activity
11	1e−03	4 / 29	coreceptor activity
12	2e−03	10 / 191	transmembrane signaling receptor activity
13	2e−03	14 / 346	receptor binding
14	3e−03	10 / 205	receptor activity
15	3e−03	5 / 59	cell adhesion molecule binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	5 / 64	hsa−miR−890
2	0.036	2 / 18	hsa−miR−1228
3	0.036	2 / 18	hsa−miR−591
4	0.056	5 / 122	hsa−miR−506
5	0.113	4 / 109	hsa−miR−485−5p
6	0.118	3 / 71	hsa−miR−188−3p
7	0.122	3 / 72	hsa−miR−378
8	0.157	1 / 10	hsa−miR−369−5p
9	0.207	2 / 50	hsa−miR−384
10	0.207	2 / 50	hsa−miR−892a
11	0.213	6 / 237	hsa−miR−302c
12	0.221	6 / 240	hsa−miR−302a
13	0.226	1 / 15	hsa−miR−598
14	0.231	5 / 194	hsa−miR−124
15	0.244	2 / 56	hsa−miR−592

Pneumonia

Rank	p−value	#in/all	Geneset
1	8e−19	18 / 56	Burnham_sep_vs_con_DN
2	3e−14	14 / 48	Burnham_cap_fp_vs_con_DN
3	1e−08	10 / 52	Burnham_day1_vs_5_DN
4	2e−08	14 / 122	Terre_IMS_influenza_meta_signature
5	3e−05	6 / 37	Sweeney_viral_up
6	4e−04	6 / 57	Burnham_viral_UP
7	5e−04	9 / 135	Terre_MSV_multiple_respiratory_viruses_up
8	3e−03	3 / 18	Scicluna_UP
9	5e−03	4 / 41	Scicluna_DN
10	9e−03	4 / 48	Burnham_viral_DN
11	3e−02	4 / 68	Burnham_sep_vs_con_UP
12	1e−01	3 / 71	Burnham_cap_fp_vs_con_UP
13	2e−01	2 / 54	Burnham_timecourse
14	3e−01	2 / 57	Burnham_day1_vs_5_UP
15	4e−01	1 / 33	Sweeney_viral_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−68	53 / 102	WIRTH_EBV B−cells
2	5e−21	39 / 355	WIRTH_Immune system
3	4e−17	18 / 68	Chaussabel_2,1_Cytotoxic cells
4	3e−09	12 / 72	Chaussabel_3,1_Interferon−inducible
5	1e−08	13 / 99	Chaussabel_1,5_Myeloid lineage
6	8e−08	27 / 496	PROTEINATLAS_spleen
7	1e−05	13 / 182	WIRTH_post GC B−cells
8	2e−05	10 / 109	Chaussabel_2,6_Myeloid lineage
9	5e−04	6 / 59	Chaussabel_2,10_Immune related cell surface molecules
10	1e−03	30 / 989	PROTEINATLAS_tonsil
11	2e−03	10 / 198	Chaussabel_3,3_Inflammation II
12	2e−03	10 / 204	Chaussabel_3,2_Inflammation I
13	3e−03	22 / 678	PROTEINATLAS_lymph node
14	4e−03	10 / 219	WIRTH_GC B−cells
15	7e−03	20 / 645	PROTEINATLAS_bone marrow

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	1e−04	60 / 2254	ICGC_BatfPcr1_targets
2	3e−04	46 / 1636	ICGC_Bcl11_targets
3	4e−04	43 / 1508	ICGC_Mef2_targets
4	6e−04	76 / 3213	ICGC_Pu1_targets
5	7e−04	51 / 1941	ICGC_Bcl3_targets
6	1e−03	31 / 1041	ICGC_P300_targets
7	2e−03	53 / 2150	ICGC_Irf4_targets
8	7e−03	75 / 3435	ICGC_Ebfsc137065_targets
9	2e−02	79 / 3778	ICGC_Pol24_targets
10	2e−02	36 / 1494	ICGC_Cebpbsc150_targets
11	3e−02	51 / 2321	ICGC_Rad21_targets
12	5e−02	76 / 3796	ICGC_Nficsc81335_targets
13	5e−02	75 / 3769	ICGC_Pmlsc71910_targets
14	6e−02	80 / 4072	ICGC_Mta3_targets
15	6e−02	69 / 3451	ICGC_Atf2_targets

Overexpression Spots

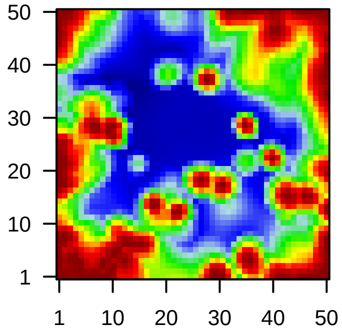
Spot Summary: O1

metagenes = 5
genes = 87

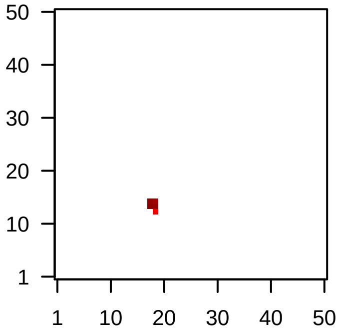
<r> metagenes = 0.99
<r> genes = 0.23
beta: r2= 1.83 / log p= −Inf

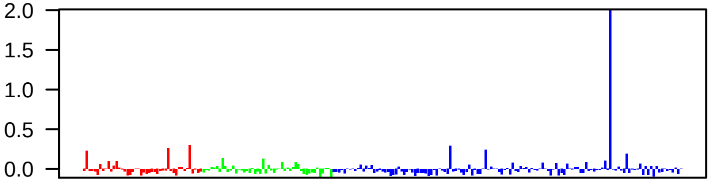
samples with spot = 6 (2.7 %)
mBL : 3 (6.8 %)
non−mBL : 3 (2.3 %)

Overview Map



Spot





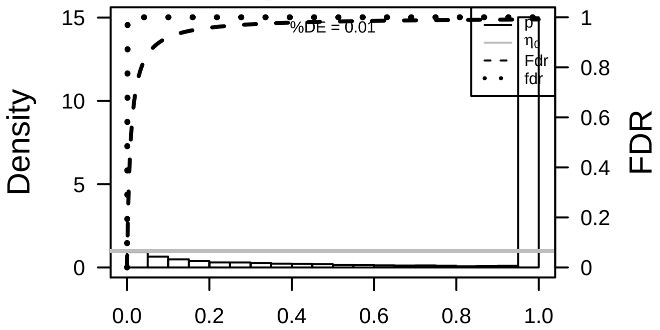
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212768_s_at	3.21	−0.59	0.64	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
2	203824_at	3.13	−0.55	0.68	TSPAN8	tetraspanin 8 [Source:HGNC Symbol;Acc:HGNC:11855]
3	210107_at	3.12	−1.18	0.64	CLCA1	chloride channel accessory 1 [Source:HGNC Symbol;Acc:HG
4	206199_at	2.96	−0.74	0.73	CEACAM7	carcinoembryonic antigen related cell adhesion molecule 7 [S
5	204272_at	2.94	−0.65	0.69	LGALS4	galectin 4 [Source:HGNC Symbol;Acc:HGNC:6565]
6	206262_at	2.91	−0.55	0.7	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
7	206143_at	2.89	−0.51	0.66	SLC26A3	solute carrier family 26 member 3 [Source:HGNC Symbol;Acc
8	214142_at	2.86	−0.46	0.66	ZG16	zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGN
9	206198_s_at	2.82	−0.6	0.64	CEACAM7	carcinoembryonic antigen related cell adhesion molecule 7 [S
10	209752_at	2.77	−0.58	0.7	REG1A	regenerating family member 1 alpha [Source:HGNC Symbol;
11	205009_at	2.76	−0.89	0.37	TFF1	trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	209847_at	2.74	−0.64	0.54	CDH17	cadherin 17 [Source:HGNC Symbol;Acc:HGNC:1756]
13	213953_at	2.71	−0.64	0.68	KRT20	keratin 20 [Source:HGNC Symbol;Acc:HGNC:20412]
14	209173_at	2.66	−0.63	0.55	AGR2	anterior gradient 2, protein disulphide isomerase family memb
15	211848_s_at	2.64	−0.56	0.6	CEACAM7	carcinoembryonic antigen related cell adhesion molecule 7 [S
16	204213_at	2.64	−0.74	0.31	PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
17	203240_at	2.57	−0.63	0.47	FCGBP	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
18	206664_at	2.57	−0.63	0.66	SI	sucrase−isomaltase [Source:HGNC Symbol;Acc:HGNC:1085
19	204623_at	2.56	−0.76	0.57	TFF3	trefoil factor 3 [Source:HGNC Symbol;Acc:HGNC:11757]
20	212741_at	2.49	−0.63	0.57	MAOA	monoamine oxidase A [Source:HGNC Symbol;Acc:HGNC:68

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−25	39 / 883	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
2	8e−18	15 / 92	Colon	Marisa_CRC−cluster−h
3	2e−15	13 / 82	Colon	Pentrack_CRC_TCGA_group.over_A_normal_UP
4	7e−14	20 / 376	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
5	2e−12	20 / 448	Colon	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
6	2e−12	19 / 397	Colon	Pentrack_CRC_TCGA_corr_C_normal_UP
7	2e−11	19 / 452	Colon	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	5e−11	27 / 1048	Refer	PROTEINATLAS_rectum
9	2e−10	10 / 91	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
10	2e−10	18 / 453	GSEA	ONDER_CDH1_TARGETS_2_DN
11	2e−10	26 / 1032	Refer	PROTEINATLAS_small intestine
12	5e−10	26 / 1072	Refer	PROTEINATLAS_duodenum
13	7e−10	13 / 218	GSEA	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
14	1e−09	12 / 182	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	2e−09	12 / 196	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
16	1e−08	11 / 178	GSEA	WU_CELL_MIGRATION
17	1e−08	25 / 1161	Refer	PROTEINATLAS_colon
18	1e−08	9 / 104	GSEA	DOANE_BREAST_CANCER_ESR1_UP
19	8e−08	21 / 905	Refer	PROTEINATLAS_appendix
20	2e−07	28 / 1652	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
21	3e−07	16 / 564	GSEA	GOZGIT_ESR1_TARGETS_DN
22	4e−07	17 / 657	GSEA	SMID_BREAST_CANCER_BASAL_DN
23	9e−07	3 / 4	GSEA	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX6_DN
24	1e−06	9 / 174	GSEA	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP
25	1e−06	21 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
26	2e−06	5 / 33	GSEA	LIU_CDX2_TARGETS_UP
27	2e−06	17 / 738	Colon	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
28	2e−06	8 / 140	GSEA	RODRIGUES_NTN1_TARGETS_DN
29	2e−06	7 / 99	GSEA	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
30	3e−06	5 / 38	Colon	Marisa_CRC−cluster−e
31	5e−06	11 / 329	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
32	5e−06	8 / 157	GSEA	SMID_BREAST_CANCER_LUMINAL_B_UP
33	5e−06	5 / 42	GSEA	WANG_BARRETTS_ESOPHAGUS_UP
34	6e−06	9 / 213	GSEA	SABATES_COLORECTAL_ADENOMA_DN
35	6e−06	7 / 115	GSEA	YEGNASUBRAMANIAN_PROSTATE_CANCER
36	8e−06	14 / 565	GSEA	LEE_BMP2_TARGETS_UP
37	1e−05	19 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
38	1e−05	30 / 2239	CC	extracellular exosome
39	2e−05	4 / 25	GSEA	JI_METASTASIS_REPRESSED_BY_STK11
40	2e−05	37 / 3168	Lymp	HOPP_Repressed

p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 36	antimicrobial humoral response
2	0.002	2 / 10	limb bud formation
3	0.002	2 / 12	epithelial cell morphogenesis
4	0.002	2 / 12	sperm capacitation
5	0.004	2 / 15	negative regulation of epithelial to mesenchymal transition
6	0.004	3 / 52	negative regulation of epithelial cell proliferation
7	0.004	2 / 16	anion transport
8	0.004	3 / 54	epidermal growth factor receptor signaling pathway
9	0.006	3 / 59	chloride transport
10	0.006	5 / 189	carbohydrate metabolic process
11	0.007	2 / 20	lymphocyte chemotaxis
12	0.007	3 / 63	cellular response to interleukin−1
13	0.007	2 / 21	defense response to fungus
14	0.007	2 / 21	regulation of ERK1 and ERK2 cascade
15	0.008	2 / 22	digestion

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	1 / 14	LIU_PROSTATE_CANCER_DN
2	0.034	2 / 47	PanCan_TGF−B_geneset_nanostring
3	0.074	6 / 480	Lembcke_Colonic Inflammation
4	0.077	1 / 13	GENTLES_modul17
5	0.117	2 / 96	PanCan_TXmisReg_geneset_nanostring
6	0.153	2 / 113	PanCan_Driver_Gene_geneset_nanostring
7	0.199	2 / 134	PanCan_RAS_geneset_nanostring
8	0.228	2 / 147	PanCan_MAPK_geneset_nanostring
9	0.371	0 / 11	LIU_PROSTATE_CANCER_UP
10	0.686	1 / 187	PanCan_PI3K_geneset_nanostring
11	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1.000	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	1.000	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	1.000	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	1.000	0 / 12	LIU_BREAST_CANCER

CC

Rank	p−value	#in/all	Geneset
1	1e−05	30 / 2239	extracellular exosome
2	2e−05	19 / 1090	extracellular space
3	7e−05	23 / 1611	extracellular region
4	8e−05	36 / 3270	integral component of membrane
5	1e−04	35 / 3210	plasma membrane
6	4e−04	17 / 1128	integral component of plasma membrane
7	5e−04	7 / 231	apical plasma membrane
8	2e−03	2 / 11	zymogen granule membrane
9	5e−03	3 / 55	brush border
10	6e−03	2 / 19	microvillus membrane
11	1e−02	3 / 84	Golgi lumen
12	3e−02	2 / 48	microvillus
13	4e−02	2 / 50	lateral plasma membrane
14	4e−02	41 / 5339	membrane
15	5e−02	2 / 56	specific granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.03	14 / 1325	Chr 1
2	0.05	3 / 139	Chr 21
3	0.13	5 / 437	Chr 8
4	0.25	5 / 548	Chr 16
5	0.25	7 / 833	Chr 19
6	0.35	4 / 490	Chr 10
7	0.44	4 / 554	Chr 5
8	0.49	4 / 585	Chr 7
9	0.57	3 / 480	Chr 4
10	0.62	4 / 689	Chr 3
11	0.63	4 / 700	Chr 12
12	0.67	2 / 369	Chr 20
13	0.68	1 / 184	Chr 18
14	0.71	4 / 776	Chr 17
15	0.71	2 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−05	31 / 2408	9_ReprPCWk_Skeletal_Muscle
2	2e−05	41 / 3734	Tcells peripheral blood_13_ReprPC
3	2e−05	31 / 2417	9_ReprPCWk_Melanocytes
4	6e−05	41 / 3918	Tcells peripheral blood_14_ReprPCWk
5	6e−05	13 / 595	13_HetRpts_Fibroblasts
6	1e−04	29 / 2374	9_ReprPCWk_Fibroblasts
7	1e−04	39 / 3755	HSC_15_Quies
8	3e−04	28 / 2375	10_ReprPC_Fibroblasts
9	4e−04	33 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
10	6e−04	24 / 1984	10_ReprPC_Melanocytes
11	1e−03	18 / 1352	11_K9K27me3_Melanocytes
12	2e−03	27 / 2515	natural killer cells peripheral blood_13_ReprPC
13	2e−03	10 / 544	12_Het_Fibroblasts
14	2e−03	24 / 2194	Thelper cells peripheral blood_12_EnhBiv
15	2e−03	30 / 3001	Bcells peripheral blood_14_ReprPCWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−25	39 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
2	8e−18	15 / 92	Marisa_CRC−cluster−h
3	2e−15	13 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
4	7e−14	20 / 376	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
5	2e−12	20 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
6	2e−12	19 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
7	2e−11	19 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	1e−06	21 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
9	2e−06	17 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
10	3e−06	5 / 38	Marisa_CRC−cluster−e
11	3e−05	9 / 255	Kosinski_top−crypt−long−list
12	4e−04	2 / 5	Marisa_CRC−C5
13	3e−02	2 / 43	Marisa_CRC−cluster−f
14	3e−02	1 / 5	Budinska_A_Surface crypt−like_UP
15	4e−02	1 / 6	Marisa_CRC−C6

Glioma

Rank	p−value	#in/all	Geneset
1	2e−07	28 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	4e−03	8 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	7e−03	6 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	6e−02	4 / 239	ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN
5	6e−02	1 / 10	Phillips PN up vs MES & Prolif
6	7e−02	2 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
7	8e−02	4 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
8	8e−02	1 / 14	astrocytes_glio
9	1e−01	1 / 21	Barbus_GBM_STS_vs._LTS
10	2e−01	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
11	2e−01	1 / 35	Gorovets_LGG_EPL_subclass
12	2e−01	1 / 36	Christensen_hypomethylated_in_ependymoma
13	3e−01	1 / 49	OPC
14	3e−01	1 / 50	Christensen_hypomethylated_in_primary_glioblastoma
15	3e−01	1 / 55	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−10	10 / 91	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
2	2e−10	18 / 453	ONDER_CDH1_TARGETS_2_DN
3	7e−10	13 / 218	MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
4	1e−09	12 / 182	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
5	2e−09	12 / 196	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
6	1e−08	11 / 178	WU_CELL_MIGRATION
7	1e−08	9 / 104	DOANE_BREAST_CANCER_ESR1_UP
8	3e−07	16 / 564	GOZGIT_ESR1_TARGETS_DN
9	4e−07	17 / 657	SMID_BREAST_CANCER_BASAL_DN
10	9e−07	3 / 4	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX6_DN
11	1e−06	9 / 174	MCBRYAN_PUBERTAL_BREAST_3_4WK_UP
12	2e−06	5 / 33	LIU_CDX2_TARGETS_UP
13	2e−06	8 / 140	RODRIGUES_NTN1_TARGETS_DN
14	2e−06	7 / 99	WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
15	5e−06	11 / 329	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP

HM

Rank	p−value	#in/all	Geneset
1	0.001	6 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.001	6 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.005	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
4	0.007	5 / 194	HALLMARK_KRAS_SIGNALING_UP
5	0.101	3 / 182	HALLMARK_GLYCOLYSIS
6	0.113	2 / 94	HALLMARK_PROTEIN_SECRETION
7	0.194	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
8	0.210	2 / 139	HALLMARK_FATTY_ACID_METABOLISM
9	0.319	2 / 187	HALLMARK_INFLAMMATORY_RESPONSE
10	0.326	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
11	0.408	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
12	0.451	1 / 97	HALLMARK_PEROXISOME
13	0.552	1 / 130	HALLMARK_COAGULATION
14	0.602	1 / 149	HALLMARK_UV_RESPONSE_UP
15	0.605	1 / 150	HALLMARK_APOPTOSIS

Immunome

Rank	p−value	#in/all	Geneset
1	0.02	2 / 38	Angelova_immune−metagene−mast−cells
2	0.34	1 / 67	Angelova_immune−metagene−T−cells
3	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−04	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	2e−02	2 / 32	Marjolein_ageing−genes_DN
3	2e−02	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	8e−02	1 / 13	Huan_blood−pressure_DBP−signature
5	9e−02	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
6	3e−01	1 / 62	DUMEAUX_Smoking enriched genes
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1e+00	0 / 22	DUMEAUX_High bmi enriched genes
13	1e+00	0 / 22	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 150	Homuth_BMI−associated−genes_UP
15	1e+00	0 / 210	Homuth_BMI−associated−genes_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−05	37 / 3168	HOPP_Repressed
2	2e−03	22 / 1894	HOPP_Poised_promoter
3	6e−03	23 / 2206	HOPP_Heterochrom
4	3e−02	1 / 5	Shaknovich_ABC_hyper_meth
5	5e−02	3 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
6	1e−01	2 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
7	1e−01	1 / 18	SPANG_BAFF 9hrs UP
8	1e−01	2 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
9	1e−01	1 / 20	Subero_MCL_hyper_meth
10	1e−01	1 / 23	Subero_mBL_hypo_meth
11	2e−01	1 / 45	Subero_INT_hypo_meth
12	3e−01	1 / 47	Subero_B−ALL_hyper_meth
13	3e−01	1 / 53	LENZ_Stromal signature 2
14	3e−01	1 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
15	3e−01	1 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−05	5 / 64	Harbst_melanoma_lowgrade_up
2	6e−02	1 / 10	Joensson_Melanoma Normal like subtype
3	2e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	2e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
5	3e−01	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
6	4e−01	4 / 497	Gerber_wt/wt_melanoma−cells−SpotD
7	4e−01	2 / 236	Gerber_wt/wt_group3−specific
8	5e−01	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
9	7e−01	1 / 204	Landsberg_dedifferentiation_down
10	7e−01	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	1e+00	0 / 17	Hugo_melanoma−all−MET_UP
12	1e+00	0 / 37	Hugo_melanoma−all−MET_DN
13	1e+00	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1e+00	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1e+00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	3e−05	7 / 143	carbohydrate binding
2	2e−03	2 / 11	retinol dehydrogenase activity
3	4e−03	2 / 15	inorganic anion exchanger activity
4	5e−03	3 / 55	chloride channel activity
5	7e−03	4 / 126	heparin binding
6	2e−02	3 / 86	metalloendopeptidase activity
7	2e−02	9 / 644	protein homodimerization activity
8	2e−02	2 / 39	chemokine activity
9	2e−02	2 / 40	antiporter activity
10	4e−02	7 / 517	calcium ion binding
11	4e−02	3 / 125	metallopeptidase activity
12	5e−02	2 / 61	serine−type endopeptidase inhibitor activity
13	6e−02	3 / 141	growth factor activity
14	6e−02	6 / 447	oxidoreductase activity
15	6e−02	1 / 10	anion transmembrane transporter activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	2 / 38	hsa−miR−658
2	0.04	2 / 53	hsa−miR−873
3	0.06	1 / 10	hsa−miR−487b
4	0.06	1 / 10	hsa−miR−369−5p
5	0.10	2 / 86	hsa−miR−1259
6	0.13	1 / 23	hsa−miR−486−5p
7	0.13	2 / 104	hsa−miR−1272
8	0.15	1 / 26	hsa−miR−558
9	0.16	2 / 117	hsa−miR−320c
10	0.16	2 / 117	hsa−miR−522
11	0.17	1 / 31	hsa−miR−661
12	0.18	2 / 126	hsa−miR−338−3p
13	0.19	1 / 35	hsa−miR−532−3p
14	0.20	2 / 133	hsa−miR−320b
15	0.20	1 / 36	hsa−miR−146b−3p

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.008	3 / 68	Burnham_sep_vs_con_UP
2	0.009	3 / 71	Burnham_cap_fp_vs_con_UP
3	0.048	2 / 57	Burnham_day1_vs_5_UP
4	0.256	1 / 48	Burnham_cap_fp_vs_con_DN
5	0.274	1 / 52	Burnham_day1_vs_5_DN
6	0.292	1 / 56	Burnham_sep_vs_con_DN
7	0.670	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
8	1.000	0 / 48	Burnham_viral_DN
9	1.000	0 / 57	Burnham_viral_UP
10	1.000	0 / 54	Burnham_timecourse
11	1.000	0 / 18	Scicluna_UP
12	1.000	0 / 41	Scicluna_DN
13	1.000	0 / 37	Sweeney_viral_up
14	1.000	0 / 33	Sweeney_viral_dn
15	1.000	0 / 122	Terre_IMS_influenza_meta_signature

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−11	27 / 1048	PROTEINATLAS_rectum
2	2e−10	26 / 1032	PROTEINATLAS_small intestine
3	5e−10	26 / 1072	PROTEINATLAS_duodenum
4	1e−08	25 / 1161	PROTEINATLAS_colon
5	8e−08	21 / 905	PROTEINATLAS_appendix
6	1e−04	3 / 15	JONGENEEL_Small Intestine
7	1e−03	2 / 9	JONGENEEL_Colon
8	2e−03	15 / 1048	PROTEINATLAS_gallbladder
9	2e−03	15 / 1076	PROTEINATLAS_stomach
10	2e−03	12 / 770	PROTEINATLAS_endometrium
11	5e−03	2 / 17	VAQUERIZAS_Pancreas_TF
12	8e−03	2 / 22	VAQUERIZAS_Trachea_TF
13	1e−02	2 / 30	VAQUERIZAS_Fetal lung_TF
14	2e−02	7 / 429	PROTEINATLAS_liver
15	2e−02	2 / 37	Chaussabel_2,2_Neutrophils

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	0.01	14 / 1148	HEBENSTREIT_low expression TF
2	0.69	9 / 1636	ICGC_Bcl11_targets
3	0.75	12 / 2254	ICGC_BatfPcr1_targets
4	0.78	5 / 1041	ICGC_P300_targets
5	0.79	12 / 2321	ICGC_Rad21_targets
6	0.83	7 / 1508	ICGC_Mef2_targets
7	0.88	17 / 3435	ICGC_Ebfsc137065_targets
8	0.93	1 / 415	ICGC_RxraPcr1_targets
9	0.93	9 / 2150	ICGC_Irf4_targets
10	0.96	3 / 1025	ICGC_NrsfPcr1_targets
11	0.96	3 / 1032	ICGC_Usf1_targets
12	0.97	1 / 549	ICGC_Atf3_targets
13	0.97	3 / 1107	ICGC_Myc_targets
14	0.97	16 / 3778	ICGC_Pol24_targets
15	0.99	6 / 1941	ICGC_Bcl3_targets

Overexpression Spots

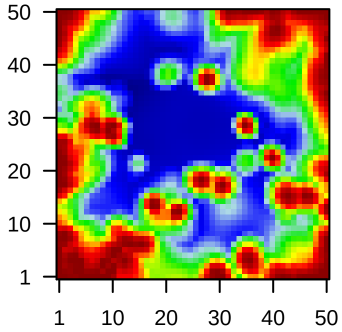
Spot Summary: P1

metagenes = 10
genes = 153

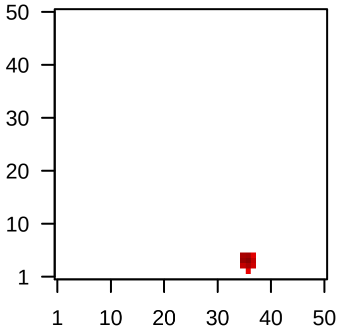
<r> metagenes = 0.98
<r> genes = 0.13
beta: r2= 1.11 / log p= −Inf

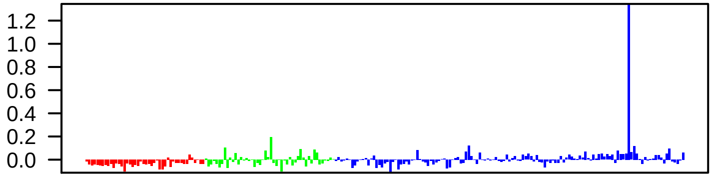
samples with spot = 1 (0.5 %)
non−mBL : 1 (0.8 %)

Overview Map



Spot





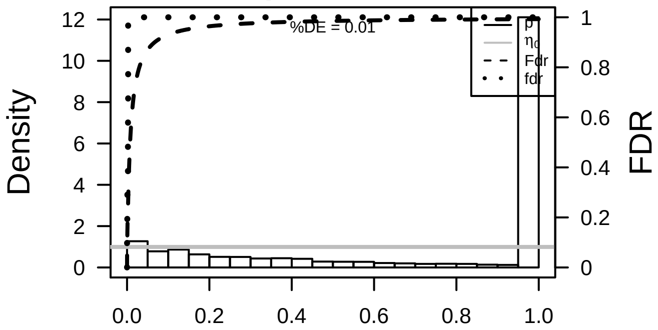
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202768_at	2.75	−0.96	0.4	FOSB	FosB proto−oncogene, AP−1 transcription factor subunit [Sou
2	218332_at	2.62	−0.7	0.29	BEX1	brain expressed X−linked 1 [Source:HGNC Symbol;Acc:HGN
3	205767_at	2.62	−0.51	0.62	EREG	epiregulin [Source:HGNC Symbol;Acc:HGNC:3443]
4	216248_s_at	2.32	−0.9	0.44	NR4A2	nuclear receptor subfamily 4 group A member 2 [Source:HGN
5	204622_x_at	2.28	−0.78	0.44	NR4A2	nuclear receptor subfamily 4 group A member 2 [Source:HGN
6	205051_s_at	2.19	−0.76	0.3	KIT	KIT proto−oncogene receptor tyrosine kinase [Source:HGNC
7	203949_at	2.03	−0.73	0.36	MPO	myeloperoxidase [Source:HGNC Symbol;Acc:HGNC:7218]
8	210426_x_at	2.01	−0.68	0.39	RORA	RAR related orphan receptor A [Source:HGNC Symbol;Acc:
9	201465_s_at	1.99	−0.91	0.26	JUN	Jun proto−oncogene, AP−1 transcription factor subunit [Sour
10	207857_at	1.99	−0.76	0.23	LILRA2	leukocyte immunoglobulin like receptor A2 [Source:HGNC Sy
11	210254_at	1.98	−0.67	0.51	MS4A3	membrane spanning 4−domains A3 [Source:HGNC Symbol;
12	60084_at	1.96	−0.57	0.51	CYLD	CYLD lysine 63 deubiquitinase [Source:HGNC Symbol;Acc:H
13	214651_s_at	1.95	−0.58	0.26	HOXA9	homeobox A9 [Source:HGNC Symbol;Acc:HGNC:5109]
14	222309_at	1.95	−0.89	0.3		
15	207723_s_at	1.94	−0.77	0.2	KLRC3	killer cell lectin like receptor C3 [Source:HGNC Symbol;Acc:
16	216015_s_at	1.9	−0.45	0.55	NLRP3	NLR family pyrin domain containing 3 [Source:HGNC Symbol
17	210123_s_at	1.88	−0.81	0.39	CHRFAM7A	CHRNA7 (exons 5−10) and FAM7A (exons A−E) fusion [Sour
18	209369_at	1.87	−0.57	0.42	ANXA3	annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
19	205239_at	1.86	−0.59	0.44	AREG	amphiregulin [Source:HGNC Symbol;Acc:HGNC:651]
20	202861_at	1.86	−0.88	0.3	PER1	period circadian regulator 1 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−12	17 / 218	Refer	WIRTH_pre+post GC B−cells
2	4e−09	11 / 112	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
3	2e−07	12 / 204	Refer	Chaussabel_3,2_Inflammation I
4	2e−06	8 / 93	Refer	Chaussabel_1,4_Replication
5	3e−06	7 / 71	Pneu	Burnham_cap_fp_vs_con_UP
6	8e−06	6 / 54	GSEA	NAGASHIMA_EGF_SIGNALING_UP
7	2e−05	5 / 36	Refer	VAQUERIZAS_Prostate_TF
8	2e−05	5 / 36	GSEA	SHIPP_DLBCL_CURED_VS_FATAL_UP
9	3e−05	10 / 220	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
10	3e−05	5 / 40	BP	intracellular receptor signaling pathway
11	3e−05	6 / 68	Pneu	Burnham_sep_vs_con_UP
12	3e−05	4 / 21	GSEA	ST_GA12_PATHWAY
13	3e−05	5 / 42	GSEA	AMIT_EGF_RESPONSE_60_HELA
14	6e−05	8 / 150	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_U
15	9e−05	8 / 160	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
16	9e−05	22 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
17	1e−04	8 / 166	GSEA	NAGASHIMA_NRG1_SIGNALING_UP
18	1e−04	4 / 29	HM	HALLMARK_NOTCH_SIGNALING
19	1e−04	8 / 169	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
20	1e−04	5 / 57	Pneu	Burnham_day1_vs_5_UP
21	1e−04	9 / 220	GSEA	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP
22	2e−04	8 / 176	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
23	2e−04	4 / 32	GSEA	AMIT_SERUM_RESPONSE_40_MCF10A
24	3e−04	12 / 407	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_UP
25	3e−04	19 / 885	BP	positive regulation of transcription from RNA polymerase II promoter
26	3e−04	8 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
27	3e−04	3 / 15	MF	transcription coactivator binding
28	3e−04	4 / 37	GSEA	REACTOME_NUCLEAR_SIGNALING_BY_ERBB4
29	3e−04	8 / 194	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
30	3e−04	45 / 3168	Lymp	HOPP_Repressed
31	3e−04	3 / 16	GSEA	BIOCARTA_NKCELLS_PATHWAY
32	4e−04	4 / 39	MF	nuclear receptor activity
33	4e−04	4 / 39	GSEA	ST_JNK_MAPK_PATHWAY
34	4e−04	4 / 40	GSEA	RIZ_ERYTHROID_DIFFERENTIATION_12HR
35	4e−04	3 / 17	Refer	VAQUERIZAS_Pancreas_TF
36	5e−04	5 / 74	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP
37	5e−04	3 / 18	GSEA	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
38	5e−04	4 / 42	BP	response to cAMP
39	5e−04	8 / 209	GSEA	REACTOME_INNATE_IMMUNE_SYSTEM
40	6e−04	6 / 116	GSEA	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.05	3 / 92	HORVATH_aging_genes meth DOWN
2	0.62	1 / 107	HORVATH_aging_genes meth UP
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	

BP

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 40	intracellular receptor signaling pathway
2	3e−04	19 / 885	positive regulation of transcription from RNA polymerase II promoter
3	5e−04	4 / 42	response to cAMP
4	7e−04	4 / 46	regulation of circadian rhythm
5	9e−04	3 / 22	positive regulation of interleukin−1 beta secretion
6	1e−03	3 / 24	stem cell differentiation
7	2e−03	4 / 56	steroid hormone mediated signaling pathway
8	2e−03	3 / 29	cAMP−mediated signaling
9	3e−03	3 / 33	negative regulation of I−kappaB kinase/NF−kappaB signaling
10	3e−03	3 / 34	positive regulation of interferon−gamma production
11	3e−03	2 / 10	negative regulation of NF−kappaB import into nucleus
12	3e−03	2 / 10	positive regulation of pseudopodium assembly
13	3e−03	2 / 10	regulation of smooth muscle cell proliferation
14	4e−03	2 / 11	mast cell degranulation
15	5e−03	3 / 38	positive regulation of DNA replication

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	5 / 113	PanCan_Driver_Gene_geneset_nanostring
2	0.010	4 / 96	PanCan_TXmisReg_geneset_nanostring
3	0.060	2 / 45	KUIPER_MM poor survival
4	0.078	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.101	1 / 12	LIU_BREAST_CANCER
6	0.116	3 / 134	PanCan_RAS_geneset_nanostring
7	0.117	1 / 14	GUSTAFSON_PI3K_UP
8	0.134	2 / 72	PanCan_Wnt_geneset_nanostring
9	0.148	1 / 18	PanCan_Notch_geneset_nanostring
10	0.158	2 / 80	PanCan_JAK−ST_geneset_nanostring
11	0.321	2 / 130	PanCan_CC+Apop_geneset_nanostring
12	0.375	2 / 147	PanCan_MAPK_geneset_nanostring
13	0.496	2 / 187	PanCan_PI3K_geneset_nanostring
14	0.707	3 / 409	Lembcke_Normal vs Adenoma
15	0.803	3 / 480	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	0.002	43 / 3210	plasma membrane
2	0.005	42 / 3270	integral component of membrane
3	0.011	5 / 152	basolateral plasma membrane
4	0.012	2 / 19	mast cell granule
5	0.012	2 / 19	synaptic membrane
6	0.017	2 / 23	voltage−gated calcium channel complex
7	0.018	3 / 62	filopodium
8	0.018	3 / 63	caveola
9	0.021	17 / 1128	integral component of plasma membrane
10	0.025	6 / 254	axon
11	0.026	9 / 479	Golgi membrane
12	0.027	2 / 29	dendritic shaft
13	0.028	58 / 5339	membrane
14	0.028	3 / 74	secretory granule
15	0.037	6 / 277	neuron projection

Chr

Rank	p−value	#in/all	Geneset
1	0.009	14 / 776	Chr 17
2	0.054	9 / 548	Chr 16
3	0.126	3 / 139	Chr 21
4	0.251	5 / 382	Chr 15
5	0.306	1 / 41	Chr Y
6	0.318	9 / 832	Chr 2
7	0.363	3 / 242	Chr 13
8	0.422	5 / 480	Chr 4
9	0.443	5 / 492	Chr 9
10	0.508	7 / 756	Chr 11
11	0.514	12 / 1325	Chr 1
12	0.570	3 / 333	Chr 22
13	0.592	6 / 700	Chr 12
14	0.636	4 / 490	Chr 10
15	0.698	3 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−05	39 / 2327	14_ReprPCWk_ESC_Mesoderm
2	1e−04	38 / 2375	10_ReprPC_Fibroblasts
3	1e−04	26 / 1352	11_K9K27me3_Melanocytes
4	3e−04	51 / 3734	Tcells peripheral blood_13_ReprPC
5	4e−04	30 / 1813	8_EnhP_Fibroblasts
6	5e−04	36 / 2374	9_ReprPCWk_Fibroblasts
7	6e−04	51 / 3838	15_Quies_ESC_Mesoderm
8	7e−04	28 / 1700	Bcells peripheral blood_11_BivFlnk
9	2e−03	48 / 3724	Tcells peripheral blood_12_EnhBiv
10	2e−03	36 / 2548	HSC_9_Het
11	2e−03	4 / 60	Overlap_fetal_midbrain_Tx
12	2e−03	33 / 2269	9_ReprPCWk_Neuronal_Progenitor
13	2e−03	18 / 967	11_K9K27me3_MSC_Adipocyte
14	2e−03	15 / 735	HetRpts_Colon
15	2e−03	14 / 666	Overlap_fetal_midbrain_ZNF

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	74 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	5e−03	2 / 12	Juehling_HNPCC−mutated−in−4
3	6e−03	12 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	2e−02	2 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
5	4e−02	13 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
6	5e−02	8 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
7	5e−02	1 / 6	Marisa_CRC−C6
8	7e−02	8 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	9e−02	12 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	1e−01	1 / 14	TCGA_Mutated−in−CRC_hypermutated
11	1e−01	1 / 14	TCGA_Mutated−in−CRC_non−hypermutated
12	1e−01	11 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	1e−01	1 / 16	Vilar_mutated−in−CRC−CamP
14	1e−01	1 / 16	Vilar_non−hypermutated−in−CRC
15	1e−01	2 / 72	Ang_CRC−CIMPH−vs−L_hyper

Glioma

Rank	p−value	#in/all	Geneset
1	0.01	7 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	0.02	2 / 22	Martinez_Glio_hypermeth
3	0.02	4 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
4	0.03	5 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
5	0.03	4 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	0.04	3 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
7	0.06	21 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
8	0.07	2 / 50	Christensen_hypomethylated_in_primary_glioblastoma
9	0.08	2 / 53	Christensen_hypermethylated_in_primary_glioblastoma
10	0.08	7 / 421	Down_b
11	0.08	3 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
12	0.09	1 / 10	Phillips PN up vs MES & Prolif
13	0.09	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
14	0.09	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
15	0.10	2 / 61	Christensen_hypomethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−09	11 / 112	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
2	8e−06	6 / 54	NAGASHIMA_EGF_SIGNALING_UP
3	2e−05	5 / 36	SHIPP_DLBCL_CURED_VS_FATAL_UP
4	3e−05	10 / 220	RUTELLA_RESPONSE_TO_HGF_DN
5	3e−05	4 / 21	ST_GA12_PATHWAY
6	3e−05	5 / 42	AMIT_EGF_RESPONSE_60_HELA
7	6e−05	8 / 150	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP
8	9e−05	8 / 160	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
9	9e−05	22 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
10	1e−04	8 / 166	NAGASHIMA_NRG1_SIGNALING_UP
11	1e−04	8 / 169	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
12	1e−04	9 / 220	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP
13	2e−04	8 / 176	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
14	2e−04	4 / 32	AMIT_SERUM_RESPONSE_40_MCF10A
15	3e−04	12 / 407	MITSIADES_RESPONSE_TO_APLIDIN_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 29	HALLMARK_NOTCH_SIGNALING
2	3e−04	8 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	6e−03	6 / 187	HALLMARK_INFLAMMATORY_RESPONSE
4	1e−02	5 / 150	HALLMARK_APOPTOSIS
5	2e−02	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	9e−02	4 / 194	HALLMARK_MYOGENESIS
7	1e−01	3 / 141	HALLMARK_UV_RESPONSE_DN
8	2e−01	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	2e−01	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
10	2e−01	3 / 173	HALLMARK_MITOTIC_SPINDLE
11	2e−01	3 / 188	HALLMARK_HYPOXIA
12	2e−01	3 / 193	HALLMARK_HEME_METABOLISM
13	3e−01	3 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	3e−01	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
15	3e−01	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Immunome

Rank	p−value	#in/all	Geneset
1	0.01	2 / 21	Angelova_immune−metagene−central_memory_CD4
2	0.04	2 / 38	Angelova_immune−metagene−mast−cells
3	0.10	1 / 12	Angelova_immune−metagene−memory_B−cells
4	0.10	1 / 12	Angelova_immune−metagene−NK56_dim
5	0.11	1 / 13	Angelova_immune−metagene−activated_B−cells
6	0.19	1 / 23	Angelova_immune−metagene−Th2
7	0.25	1 / 32	Angelova_immune−metagene−effector_memory_CD8
8	0.33	1 / 45	Angelova_immune−metagene−MDSC
9	0.45	1 / 67	Angelova_immune−metagene−T−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 / 17	Angelova_immune−metagene−central_memory_CD8
13	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
14	1.00	0 / 25	Angelova_immune−metagene−DC
15	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.10	2 / 62	DUMEAUX_Smoking enriched genes
3	0.12	4 / 210	Homuth_BMI−associated−genes_DN
4	0.15	3 / 150	Homuth_BMI−associated−genes_UP
5	0.18	1 / 22	DUMEAUX_High bmi 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 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 22	DUMEAUX_Fasting enriched genes
14	1.00	0 / 14	Huan_blood−pressure_SBP−signature
15	1.00	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−04	45 / 3168	HOPP_Repressed
2	2e−03	29 / 1894	HOPP_Poised_promoter
3	7e−03	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
4	2e−02	29 / 2206	HOPP_Heterochrom
5	3e−02	4 / 132	Subero_DLBCL_hyper_meth
6	4e−02	2 / 35	Subero_MM_hyper_meth
7	8e−02	1 / 9	YAMANE_AICDA_targets_nonrecruited
8	8e−02	2 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
9	9e−02	3 / 118	Subero_INT_hyper_meth
10	9e−02	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
11	1e−01	6 / 378	TARTE_Mature plasma cell signature
12	2e−01	4 / 237	ZHANG_DLBCL mutated
13	2e−01	20 / 1814	HOPP_Repetitive
14	2e−01	53 / 5404	HOPP_Strong_enhancer
15	2e−01	2 / 91	Subero_T−ALL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.004	2 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
2	0.024	5 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
3	0.035	3 / 81	Tirosh_Genes in the MITF program
4	0.051	2 / 41	Tirosh_top50 correlated genes PC3
5	0.054	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC
6	0.075	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
7	0.108	4 / 204	Landsberg_dedifferentiation_down
8	0.131	2 / 71	Tirosh_Macrophage specific genes−melanoma
9	0.168	2 / 83	TCGA_melanoma_immune_high
10	0.194	3 / 171	Landsberg_dedifferentiation_up
11	0.245	2 / 107	Tirosh_Exhaustion program in Mel75
12	0.281	1 / 37	Hugo_melanoma−all−MET_DN
13	0.287	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
14	0.409	1 / 59	TCGA_melanoma_keratin_high
15	0.435	1 / 64	Harbst_melanoma_lowgrade_up

MF

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 15	transcription coactivator binding
2	4e−04	4 / 39	nuclear receptor activity
3	1e−03	4 / 52	steroid hormone receptor activity
4	2e−03	7 / 191	transmembrane signaling receptor activity
5	2e−03	4 / 61	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
6	3e−03	8 / 268	transcription factor binding
7	3e−03	2 / 10	inositol−1,3,4,5−tetrakisphosphate 5−phosphatase activity
8	3e−03	4 / 70	beta−catenin binding
9	5e−03	3 / 38	core promoter sequence−specific DNA binding
10	5e−03	2 / 12	3',5'−cyclic−AMP phosphodiesterase activity
11	6e−03	2 / 13	MAP kinase activity
12	7e−03	10 / 450	sequence−specific DNA binding
13	8e−03	2 / 15	glucocorticoid receptor binding
14	9e−03	8 / 329	RNA polymerase II proximal promoter sequence−specific DNA binding
15	1e−02	2 / 17	cAMP binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	4 / 64	hsa−miR−365
2	0.003	8 / 278	hsa−let−7d
3	0.004	4 / 71	hsa−miR−134
4	0.006	3 / 41	hsa−miR−346
5	0.009	7 / 262	hsa−miR−32
6	0.011	3 / 52	hsa−miR−514
7	0.012	3 / 54	hsa−miR−1184
8	0.018	6 / 234	hsa−miR−101
9	0.020	4 / 117	hsa−miR−200a
10	0.021	4 / 119	hsa−miR−140−5p
11	0.027	8 / 404	hsa−miR−103
12	0.028	8 / 405	hsa−miR−107
13	0.028	3 / 74	hsa−miR−595
14	0.028	6 / 260	hsa−let−7e
15	0.029	2 / 30	hsa−miR−1258

Pneumonia

Rank	p−value	#in/all	Geneset
1	3e−06	7 / 71	Burnham_cap_fp_vs_con_UP
2	3e−05	6 / 68	Burnham_sep_vs_con_UP
3	1e−04	5 / 57	Burnham_day1_vs_5_UP
4	2e−02	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
5	7e−02	2 / 48	Burnham_cap_fp_vs_con_DN
6	7e−02	2 / 48	Burnham_viral_DN
7	9e−02	2 / 56	Burnham_sep_vs_con_DN
8	4e−01	1 / 52	Burnham_day1_vs_5_DN
9	4e−01	1 / 54	Burnham_timecourse
10	7e−01	1 / 122	Terre_IMS_influenza_meta_signature
11	7e−01	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
12	1e+00	0 / 57	Burnham_viral_UP
13	1e+00	0 / 18	Scicluna_UP
14	1e+00	0 / 41	Scicluna_DN
15	1e+00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−12	17 / 218	WIRTH_pre+post GC B−cells
2	2e−07	12 / 204	Chaussabel_3,2_Inflammation I
3	2e−06	8 / 93	Chaussabel_1,4_Replication
4	2e−05	5 / 36	VAQUERIZAS_Prostate_TF
5	4e−04	3 / 17	VAQUERIZAS_Pancreas_TF
6	9e−04	4 / 49	VAQUERIZAS_Uterus_TF
7	1e−03	3 / 25	VAQUERIZAS_Adrenal cortex_TF
8	3e−03	4 / 68	Chaussabel_2,1_Cytotoxic cells
9	6e−03	2 / 13	WIRTH_Bone marrow
10	6e−03	2 / 13	VAQUERIZAS_Skin_TF
11	1e−02	2 / 17	VAQUERIZAS_Adrenal gland_TF
12	2e−02	2 / 22	VAQUERIZAS_Trachea_TF
13	2e−02	3 / 62	VAQUERIZAS_Lung_TF
14	2e−02	3 / 66	VAQUERIZAS_Whole blood_TF
15	3e−02	2 / 30	JONGENEEL_Bone Marrow

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	6e−04	30 / 1848	ICGC_Pbx3_targets
2	8e−04	20 / 1041	ICGC_P300_targets
3	4e−03	32 / 2254	ICGC_BatfPcr1_targets
4	4e−03	25 / 1636	ICGC_Bcl11_targets
5	5e−03	47 / 3778	ICGC_Pol24_targets
6	6e−03	40 / 3121	ICGC_Egr1_targets
7	7e−03	43 / 3435	ICGC_Ebfsc137065_targets
8	1e−02	49 / 4131	ICGC_Tcf3_targets
9	1e−02	22 / 1508	ICGC_Mef2_targets
10	1e−02	49 / 4212	ICGC_Pol2_targets
11	2e−02	39 / 3213	ICGC_Pu1_targets
12	2e−02	26 / 1941	ICGC_Bcl3_targets
13	2e−02	47 / 4072	ICGC_Mta3_targets
14	2e−02	41 / 3451	ICGC_Atf2_targets
15	2e−02	28 / 2150	ICGC_Irf4_targets

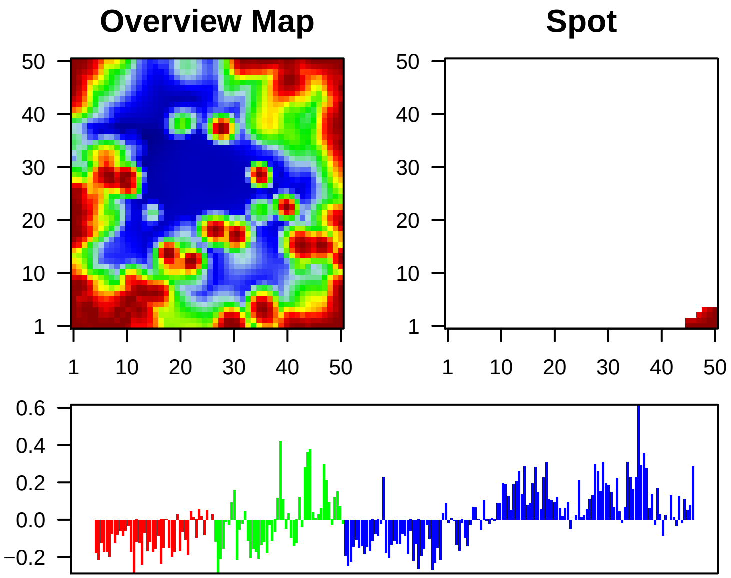
Overexpression Spots

Spot Summary: Q1

metagenes = 19
genes = 381

<r> metagenes = 0.92
<r> genes = 0.31
beta: r2= 7.22 / log p= −Inf

samples with spot = 25 (11.3 %)
intermediate : 6 (12.5 %)
non−mBL : 19 (14.7 %)

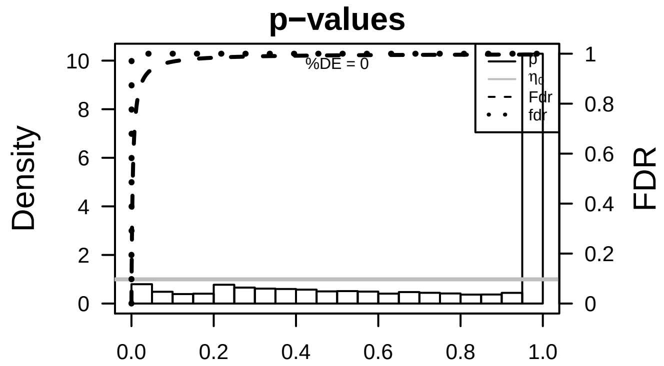


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212236_x_at	2.22	−0.68	0.5	KRT17	keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
2	209800_at	2.16	−0.6	0.49	KRT16	keratin 16 [Source:HGNC Symbol;Acc:HGNC:6423]
3	214532_x_at	2.06	−0.84	0.35	POU5F1	POU class 5 homeobox 1 [Source:HGNC Symbol;Acc:HGNC
4	202222_s_at	1.96	−0.73	0.57	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
5	206760_s_at	1.74	−0.74	0.47	FCER2	Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HG
6	214027_x_at	1.73	−0.87	0.52	DES	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
7	213936_x_at	1.69	−0.59	0.41	SFTPB	surfactant protein B [Source:HGNC Symbol;Acc:HGNC:1080
8	209957_s_at	1.66	−0.88	0.64	NPPA	natriuretic peptide A [Source:HGNC Symbol;Acc:HGNC:7939
9	205116_at	1.66	−0.71	0.48	LAMA2	laminin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:6
10	64408_s_at	1.59	−0.71	0.25		
11	207388_s_at	1.59	−1.07	0.51	PTGES	prostaglandin E synthase [Source:HGNC Symbol;Acc:HGNC
12	222015_at	1.58	−0.94	0.37	CSNK1E	casein kinase 1 epsilon [Source:HGNC Symbol;Acc:HGNC:2
13	204692_at	1.55	−0.85	0.5	SAP25	Sin3A associated protein 25 [Source:HGNC Symbol;Acc:HGN
14	208607_s_at	1.55	−0.64	0.42	SAA2	serum amyloid A2 [Source:HGNC Symbol;Acc:HGNC:10514]
15	214403_x_at	1.53	−1.06	0.64		
16	207961_x_at	1.51	−1.16	0.51	MYH11	myosin heavy chain 11 [Source:HGNC Symbol;Acc:HGNC:75
17	210424_s_at	1.46	−1.02	0.35	GOLGA8A	golgin A8 family member A [Source:HGNC Symbol;Acc:HGN
18	202014_at	1.44	−0.67	0.4	PPP1R15A	protein phosphatase 1 regulatory subunit 15A [Source:HGNC
19	213075_at	1.42	−0.99	0.36	OLFML2A	olfactomedin like 2A [Source:HGNC Symbol;Acc:HGNC:2727
20	219664_s_at	1.41	−0.91	0.28	DECR2	2,4−dienoyl−CoA reductase 2 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−15	38 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	6e−12	16 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	3e−06	19 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	7e−06	28 / 483	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	1e−05	21 / 311	GSEA	SHEN_SMARCA2_TARGETS_DN
6	3e−05	62 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
7	3e−05	182 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
8	4e−05	5 / 18	GSEA	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
9	5e−05	4 / 10	BP	cerebellar Purkinje cell differentiation
10	5e−05	28 / 539	Colon	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	6e−05	7 / 44	GSEA	PARENT_MTOR_SIGNALING_DN
12	2e−04	14 / 194	HM	HALLMARK_MYOGENESIS
13	2e−04	5 / 24	GSEA	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLAC
14	2e−04	9 / 88	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
15	3e−04	46 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
16	3e−04	8 / 73	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
17	3e−04	19 / 333	Chr	Chr 22
18	3e−04	5 / 26	GSEA	CHO_NR4A1_TARGETS
19	3e−04	8 / 75	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_DN
20	4e−04	3 / 7	Gliom	Sturm_GBM_Meth_overexpression_C_G34_UP
21	4e−04	26 / 548	Chr	Chr 16
22	4e−04	17 / 290	GSEA	ODONNELL_TFRC_TARGETS_UP
23	7e−04	5 / 31	GSEA	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS
24	8e−04	9 / 106	GSEA	SENGUPTA_EBNA1_ANTICORRELATED
25	8e−04	21 / 421	Gliom	Down_b
26	1e−03	11 / 163	MF	transferase activity, transferring glycosyl groups
27	1e−03	8 / 94	GSEA	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
28	2e−03	33 / 833	BP	multicellular organism development
29	2e−03	3 / 11	MF	platelet−derived growth factor binding
30	2e−03	23 / 512	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
31	2e−03	6 / 57	GSEA	PID_HDAC_CLASSI_PATHWAY
32	2e−03	12 / 198	GSEA	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
33	2e−03	33 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
34	2e−03	3 / 12	BP	regulation of embryonic development
35	2e−03	4 / 25	BP	positive regulation of mitotic nuclear division
36	2e−03	9 / 125	BP	protein glycosylation
37	3e−03	5 / 42	BP	histone deacetylation
38	3e−03	5 / 42	GSEA	RASHI_RESPONSE_TO_IONIZING_RADIATION_3
39	3e−03	4 / 26	BP	neural crest cell migration
40	3e−03	3 / 13	MF	NAD+ binding



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 107	HORVATH_aging_genes meth UP
2	0.7	1 / 47	TESCHENDORFF_age_hypermethylated
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	5e−05	4 / 10	cerebellar Purkinje cell differentiation
2	2e−03	33 / 833	multicellular organism development
3	2e−03	3 / 12	regulation of embryonic development
4	2e−03	4 / 25	positive regulation of mitotic nuclear division
5	2e−03	9 / 125	protein glycosylation
6	3e−03	5 / 42	histone deacetylation
7	3e−03	4 / 26	neural crest cell migration
8	3e−03	3 / 13	regulation of myelination
9	4e−03	4 / 29	response to ischemia
10	5e−03	3 / 16	histone H3 deacetylation
11	8e−03	4 / 34	respiratory gaseous exchange
12	8e−03	3 / 18	cell recognition
13	9e−03	5 / 56	regulation of cell migration
14	1e−02	8 / 128	fatty acid metabolic process
15	1e−02	5 / 58	activation of protein kinase activity

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	3 / 16	LIU_LIVER_CANCER
2	0.069	8 / 187	PanCan_PI3K_geneset_nanostring
3	0.118	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.125	6 / 147	PanCan_MAPK_geneset_nanostring
5	0.182	4 / 96	PanCan_TXmisReg_geneset_nanostring
6	0.190	1 / 9	WANG_ER_DN
7	0.245	1 / 12	LIU_BREAST_CANCER
8	0.262	1 / 13	GENTLES_modul18
9	0.265	4 / 113	PanCan_Driver_Gene_geneset_nanostring
10	0.279	1 / 14	LIU_COMMON_CANCER_GENES
11	0.279	1 / 14	LIU_PROSTATE_CANCER_DN
12	0.279	1 / 14	GUSTAFSON_PI3K_DN
13	0.279	1 / 14	BENTINK_ras.6
14	0.344	1 / 18	PanCan_Notch_geneset_nanostring
15	0.374	1 / 20	PanCan_ChromMod_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.01	6 / 82	sarcolemma
2	0.01	38 / 1128	integral component of plasma membrane
3	0.02	4 / 42	sarcoplasmic reticulum
4	0.02	5 / 65	collagen trimer
5	0.02	2 / 10	beta−catenin destruction complex
6	0.03	90 / 3270	integral component of membrane
7	0.04	2 / 13	axolemma
8	0.04	88 / 3210	plasma membrane
9	0.04	2 / 14	basal lamina
10	0.04	2 / 14	filopodium membrane
11	0.04	2 / 14	sperm midpiece
12	0.04	4 / 58	Golgi cisterna membrane
13	0.05	2 / 15	contractile fiber
14	0.05	3 / 35	ciliary membrane
15	0.05	5 / 86	PML body

Chr

Rank	p−value	#in/all	Geneset
1	3e−04	19 / 333	Chr 22
2	4e−04	26 / 548	Chr 16
3	1e−02	30 / 833	Chr 19
4	6e−02	25 / 776	Chr 17
5	2e−01	21 / 756	Chr 11
6	3e−01	19 / 700	Chr 12
7	3e−01	16 / 585	Chr 7
8	3e−01	13 / 492	Chr 9
9	4e−01	11 / 437	Chr 8
10	5e−01	9 / 369	Chr 20
11	5e−01	13 / 556	Chr X
12	6e−01	15 / 669	Chr 6
13	6e−01	1 / 41	Chr Y
14	6e−01	3 / 139	Chr 21
15	6e−01	12 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−10	94 / 2203	EnhA_Colon
2	3e−09	106 / 2704	4_TxTrans_Fibroblasts
3	2e−08	60 / 1239	EnhP_Colon
4	9e−08	96 / 2507	Mid_Frontal_Lobe_ReprPC
5	1e−07	92 / 2380	TxEnhG1_Colon
6	3e−07	225 / 7943	Enh_Colon
7	4e−07	77 / 1911	Mid_Frontal_Lobe_HetRpts
8	7e−07	67 / 1600	4_TxTrans_Melanocytes
9	2e−06	126 / 3803	6_EnhG_Fibroblasts
10	5e−06	122 / 3724	Tcells peripheral blood_12_EnhBiv
11	7e−06	70 / 1813	8_EnhP_Fibroblasts
12	3e−05	32 / 634	Mid_Frontal_Lobe_Het
13	4e−05	89 / 2602	natural killer cells peripheral blood_12_EnhBiv
14	4e−05	71 / 1943	TssP_Colon
15	4e−05	92 / 2724	Tcells peripheral blood_11_BivFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−06	28 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
2	3e−05	182 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
3	5e−05	28 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
4	3e−04	46 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
5	2e−03	33 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
6	2e−02	15 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
7	2e−02	13 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	7e−02	35 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	1e−01	16 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
10	1e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation
11	2e−01	14 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
12	2e−01	4 / 92	Marisa_CRC−cluster−h
13	2e−01	1 / 8	Marisa_CRC−C3
14	2e−01	2 / 38	Marisa_CRC−cluster−e
15	2e−01	1 / 12	Juehling−MSI−enriched−in−6

Glioma

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
2	8e−04	21 / 421	Down_b
3	5e−02	5 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
4	6e−02	3 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
5	7e−02	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
6	9e−02	6 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
7	1e−01	5 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	1e−01	3 / 53	Christensen_hypermethylated_in_primary_glioblastoma
9	1e−01	28 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	2e−01	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
11	2e−01	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
12	2e−01	3 / 64	Weller_LGG_gradeII−vs−III_UP
13	2e−01	3 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
14	2e−01	4 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	2e−01	3 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−15	38 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	6e−12	16 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	3e−06	19 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	1e−05	21 / 311	SHEN_SMARCA2_TARGETS_DN
5	3e−05	62 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
6	4e−05	5 / 18	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
7	6e−05	7 / 44	PARENT_MTOR_SIGNALING_DN
8	2e−04	5 / 24	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO
9	2e−04	9 / 88	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
10	3e−04	8 / 73	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
11	3e−04	5 / 26	CHO_NR4A1_TARGETS
12	3e−04	8 / 75	LAIHO_COLORECTAL_CANCER_SERRATED_DN
13	4e−04	17 / 290	ODONNELL_TFRC_TARGETS_UP
14	7e−04	5 / 31	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS
15	8e−04	9 / 106	SENGUPTA_EBNA1_ANTICORRELATED

HM

Rank	p−value	#in/all	Geneset
1	2e−04	14 / 194	HALLMARK_MYOGENESIS
2	1e−02	4 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	8e−02	8 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	1e−01	7 / 174	HALLMARK_APICAL_JUNCTION
5	2e−01	2 / 34	HALLMARK_APICAL_SURFACE
6	2e−01	6 / 174	HALLMARK_ADIPOGENESIS
7	2e−01	6 / 182	HALLMARK_GLYCOLYSIS
8	3e−01	2 / 51	HALLMARK_TGF_BETA_SIGNALING
9	4e−01	3 / 96	HALLMARK_ANDROGEN_RESPONSE
10	4e−01	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
11	4e−01	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
12	4e−01	5 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	5e−01	5 / 191	HALLMARK_P53_PATHWAY
14	5e−01	4 / 150	HALLMARK_APOPTOSIS
15	5e−01	5 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE

Immunome

Rank	p−value	#in/all	Geneset
1	0.04	2 / 14	Angelova_immune−metagene−eosinophil
2	0.13	1 / 6	Immunity_immune−checkpoint−inhibitors
3	0.14	2 / 29	Angelova_immune−metagene−Th1
4	0.21	1 / 10	Angelova_immune−metagene−TFH
5	0.21	1 / 10	Angelova_CRC_immonoinhibitors
6	0.24	1 / 12	Angelova_immune−metagene−NK56_dim
7	0.44	1 / 25	Angelova_immune−metagene−DC
8	0.65	1 / 45	Angelova_immune−metagene−MDSC
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 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.09	2 / 22	DUMEAUX_Fasting enriched genes
3	0.28	1 / 14	Huan_blood−pressure_SBP−signature
4	0.36	6 / 210	Homuth_BMI−associated−genes_DN
5	0.40	1 / 22	DUMEAUX_High bmi enriched genes
6	0.68	3 / 150	Homuth_BMI−associated−genes_UP
7	0.77	1 / 62	DUMEAUX_Smoking enriched genes
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	0.03	15 / 378	TARTE_Mature plasma cell signature
2	0.04	4 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
3	0.04	3 / 33	Subero_T−PLL_hypo_meth
4	0.04	4 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
5	0.09	3 / 45	Subero_INT_hypo_meth
6	0.09	5 / 102	ROSOLOWSKI_blue total
7	0.09	3 / 46	Subero_DLBCL_hypo_meth
8	0.14	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
9	0.17	50 / 1894	HOPP_Poised_promoter
10	0.23	79 / 3168	HOPP_Repressed
11	0.24	2 / 41	ROSOLOWSKI_blue DOWN
12	0.24	1 / 12	BENTINK_mBL DOWN
13	0.28	2 / 45	SPANG_BAFF 9hrs DN
14	0.28	1 / 14	Subero_B−ALL_hypo_meth
15	0.34	1 / 18	WRIGHT_ABC UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	2 / 10	Joensson_Melanoma Normal like subtype
2	0.05	5 / 85	Tirosh_AXL−signature
3	0.05	3 / 37	Hugo_melanoma−all−MET_DN
4	0.11	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
5	0.23	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
6	0.23	2 / 39	Tirosh_top50 correlated genes PC4
7	0.26	6 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.27	3 / 78	Tirosh_CAF−cell specific genes
9	0.43	1 / 24	Gerami_melanoma−metastatic−risk_DN
10	0.44	2 / 64	Harbst_melanoma_lowgrade_up
11	0.45	2 / 65	Harbst_melanoma_highgrade_up
12	0.49	2 / 71	Tirosh_Macrophage specific genes−melanoma
13	0.51	5 / 204	Landsberg_dedifferentiation_down
14	0.54	1 / 33	Tirosh_T−cell specific genes−melanoma
15	0.56	4 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	0.001	11 / 163	transferase activity, transferring glycosyl groups
2	0.002	3 / 11	platelet−derived growth factor binding
3	0.003	3 / 13	NAD+ binding
4	0.004	3 / 14	C2H2 zinc finger domain binding
5	0.004	14 / 268	transcription factor binding
6	0.005	3 / 16	galactosyltransferase activity
7	0.007	16 / 346	receptor binding
8	0.007	11 / 202	GTPase activator activity
9	0.009	3 / 19	enhancer sequence−specific DNA binding
10	0.009	3 / 19	receptor signaling complex scaffold activity
11	0.009	27 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
12	0.012	4 / 39	nuclear receptor activity
13	0.014	9 / 165	calmodulin binding
14	0.021	2 / 10	anion transmembrane transporter activity
15	0.021	2 / 10	fucosyltransferase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	4 / 28	hsa−miR−296−5p
2	0.008	2 / 6	hsa−miR−886−5p
3	0.013	5 / 61	hsa−miR−939
4	0.021	3 / 26	hsa−miR−558
5	0.025	5 / 72	hsa−miR−339−5p
6	0.037	3 / 32	hsa−miR−615−5p
7	0.040	4 / 56	hsa−miR−1275
8	0.047	4 / 59	hsa−miR−361−3p
9	0.058	2 / 17	hsa−miR−323−5p
10	0.088	4 / 73	hsa−miR−299−3p
11	0.109	3 / 50	hsa−miR−1285
12	0.109	3 / 50	hsa−miR−371−5p
13	0.120	2 / 26	hsa−miR−1293
14	0.120	2 / 26	hsa−miR−555
15	0.126	4 / 83	hsa−miR−147

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.4	2 / 54	Burnham_timecourse
2	0.4	2 / 57	Burnham_day1_vs_5_UP
3	0.5	1 / 33	Sweeney_viral_dn
4	0.6	1 / 37	Sweeney_viral_up
5	0.6	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
6	0.6	1 / 41	Scicluna_DN
7	0.7	1 / 56	Burnham_sep_vs_con_DN
8	0.8	2 / 122	Terre_IMS_influenza_meta_signature
9	1.0	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
10	1.0	0 / 68	Burnham_sep_vs_con_UP
11	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
13	1.0	0 / 48	Burnham_viral_DN
14	1.0	0 / 57	Burnham_viral_UP
15	1.0	0 / 52	Burnham_day1_vs_5_DN

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.01	11 / 218	WIRTH_pre+post GC B−cells
2	0.02	10 / 209	Chaussabel_2,5_Immune related molecules
3	0.02	8 / 152	VAQUERIZAS_General_TF
4	0.05	3 / 36	VAQUERIZAS_Prostate_TF
5	0.06	2 / 17	VAQUERIZAS_Heart_TF
6	0.06	8 / 182	WIRTH_post GC B−cells
7	0.09	1 / 4	JONGENEEL_Bladder
8	0.11	2 / 25	VAQUERIZAS_Adrenal cortex_TF
9	0.15	7 / 188	Chaussabel_3,8_Enzymes
10	0.20	3 / 66	VAQUERIZAS_Whole blood_TF
11	0.23	1 / 11	JONGENEEL_Peripheral Blood Lymphocytes
12	0.23	1 / 11	JONGENEEL_Spleen
13	0.23	1 / 11	JONGENEEL_Thyroid
14	0.24	2 / 40	VAQUERIZAS_Testis_TF
15	0.24	2 / 41	VAQUERIZAS_Thymus_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.01	90 / 3121	ICGC_Egr1_targets
2	0.03	57 / 1941	ICGC_Bcl3_targets
3	0.03	18 / 485	ICGC_NrsfPcr2_targets
4	0.04	121 / 4602	ICGC_Elf1_targets
5	0.05	35 / 1148	HEBENSTREIT_low expression TF
6	0.12	104 / 4072	ICGC_Mta3_targets
7	0.12	45 / 1636	ICGC_Bcl11_targets
8	0.13	122 / 4851	ICGC_Runx3_targets
9	0.13	105 / 4131	ICGC_Tcf3_targets
10	0.14	88 / 3435	ICGC_Ebfsc137065_targets
11	0.20	81 / 3213	ICGC_Pu1_targets
12	0.24	94 / 3804	ICGC_Stat5_targets
13	0.27	89 / 3630	ICGC_Sp1_targets
14	0.27	58 / 2321	ICGC_Rad21_targets
15	0.28	27 / 1032	ICGC_Usf1_targets

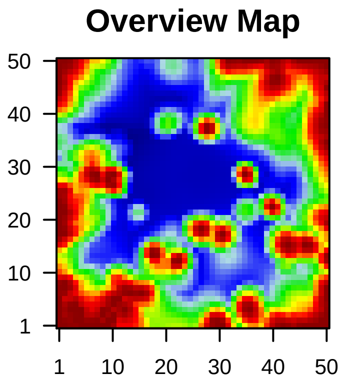
Overexpression Spots

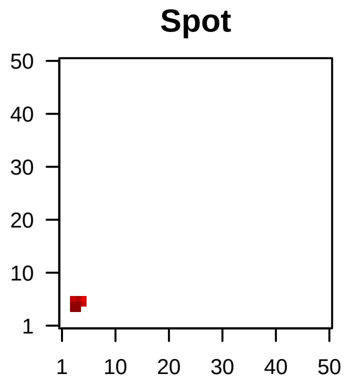
Spot Summary: R1

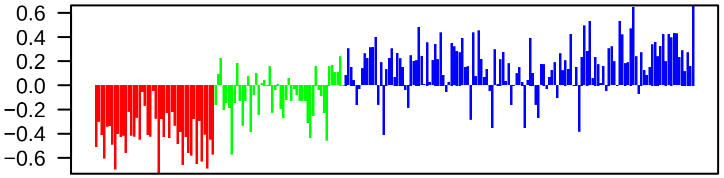
metagenes = 8
genes = 73

<r> metagenes = 0.99
<r> genes = 0.42
beta: r2= 18.04 / log p= −Inf

samples with spot = 62 (28.1 %)
intermediate : 2 (4.2 %)
non−mBL : 60 (46.5 %)





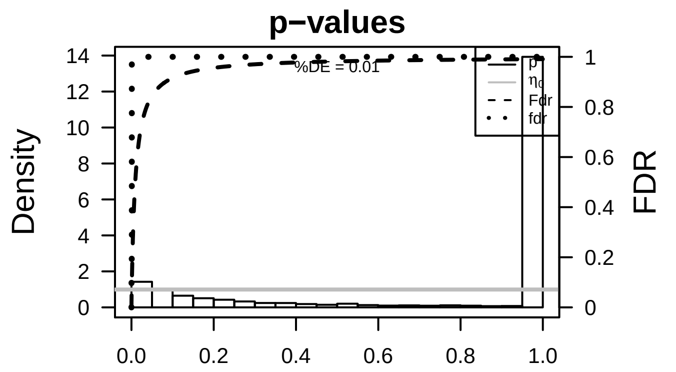


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	217002_s_at	2.74	−1.28	0.49	HTR3A	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
2	216615_s_at	2.49	−1.56	0.57	HTR3A	5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc
3	207113_s_at	1.77	−1.49	0.66	TNF	tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:118
4	214508_x_at	1.59	−1.16	0.52	CREM	cAMP responsive element modulator [Source:HGNC Symbol;
5	206975_at	1.59	−1.2	0.64	LTA	lymphotoxin alpha [Source:HGNC Symbol;Acc:HGNC:6709]
6	210184_at	1.59	−0.83	0.6	ITGAX	integrin subunit alpha X [Source:HGNC Symbol;Acc:HGNC:6
7	221211_s_at	1.42	−1.4	0.59	MAP3K7CL	MAP3K7 C−terminal like [Source:HGNC Symbol;Acc:HGNC:
8	217897_at	1.39	−1.06	0.62	FXYD6	FXYD domain containing ion transport regulator 6 [Source:H
9	209683_at	1.33	−1.18	0.57	FAM49A	family with sequence similarity 49 member A [Source:HGNC
10	208322_s_at	1.33	−1.19	0.59	ST3GAL1	ST3 beta−galactoside alpha−2,3−sialyltransferase 1 [Source:
11	212960_at	1.3	−1.05	0.43	TBC1D9	TBC1 domain family member 9 [Source:HGNC Symbol;Acc:
12	204385_at	1.29	−0.89	0.56	KYNU	kynureninase [Source:HGNC Symbol;Acc:HGNC:6469]
13	208763_s_at	1.28	−1.75	0.54	TSC22D3	TSC22 domain family member 3 [Source:HGNC Symbol;Acc:
14	208092_s_at	1.27	−1.29	0.58	FAM49A	family with sequence similarity 49 member A [Source:HGNC
15	206295_at	1.23	−1.51	0.82	IL18	interleukin 18 [Source:HGNC Symbol;Acc:HGNC:5986]
16	203665_at	1.2	−1.5	0.45	HMOX1	heme oxygenase 1 [Source:HGNC Symbol;Acc:HGNC:5013]
17	204249_s_at	1.19	−1.43	0.79	LMO2	LIM domain only 2 [Source:HGNC Symbol;Acc:HGNC:6642]
18	220423_at	1.18	−2.1	0.76	PLA2G2D	phospholipase A2 group IID [Source:HGNC Symbol;Acc:HGN
19	219013_at	1.15	−1.46	0.55	GALNT11	polypeptide N−acetylgalactosaminyltransferase 11 [Source:H
20	201301_s_at	1.15	−1.55	0.76	ANXA4	annexin A4 [Source:HGNC Symbol;Acc:HGNC:542]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−11	12 / 186	Canc	SPANG_LPS−index2
2	1e−09	13 / 317	Canc	SPANG_BCL6−index2
3	4e−09	8 / 85	Lymp	Sha_DLBCL UP
4	2e−08	14 / 480	Canc	Lembcke_Colonic Inflammation
5	4e−08	15 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	9e−08	9 / 176	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	1e−07	10 / 242	Gliom	ScoV_0.5_Sturm_C1_IDH_DN
8	2e−07	12 / 404	GSE	RUTELLA_RESPONSE_TO_HGF_UP
9	2e−07	9 / 198	Refer	Chaussabel_3,3_Inflammation II
10	5e−07	11 / 354	GSE	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
11	8e−07	9 / 229	GSE	QI_PLASMACYTOMA_UP
12	1e−06	8 / 173	Lymp	Victora_Light zone signature
13	1e−06	11 / 386	GSE	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
14	2e−06	9 / 251	GSE	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
15	2e−06	8 / 190	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
16	2e−06	10 / 335	GSE	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
17	3e−06	6 / 90	GSE	BASSO_CD40_SIGNALING_UP
18	4e−06	10 / 353	Lymp	SPANG_CD40 6hrs DN
19	5e−06	11 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
20	7e−06	12 / 565	GSE	LEE_BMP2_TARGETS_UP
21	9e−06	5 / 62	GSE	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
22	1e−05	4 / 30	BP	negative regulation of extrinsic apoptotic signaling pathway via death doma
23	1e−05	5 / 67	GSE	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
24	1e−05	5 / 67	GSE	VANLOO_SP3_TARGETS_DN
25	1e−05	8 / 246	Gliom	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
26	2e−05	10 / 422	GSE	DELYS_THYROID_CANCER_UP
27	2e−05	8 / 255	GSE	HELLER_SILENCED_BY_METHYLATION_UP
28	3e−05	9 / 348	GSE	MARTENS_BOUND_BY_PML_RARA_FUSION
29	3e−05	9 / 353	GSE	JOHNSTONE_PARVB_TARGETS_3_UP
30	4e−05	3 / 15	BP	regulation of extrinsic apoptotic signaling pathway via death domain recept
31	4e−05	10 / 462	CC	cell surface
32	4e−05	14 / 902	GSE	CHEN_METABOLIC_SYNDROM_NETWORK
33	4e−05	11 / 564	GSE	GOZGIT_ESR1_TARGETS_DN
34	5e−05	8 / 290	GSE	ODONNELL_TFRC_TARGETS_UP
35	5e−05	7 / 212	GSE	KIM_WT1_TARGETS_UP
36	5e−05	7 / 213	Lymp	SPANG_IL21 DN
37	5e−05	7 / 214	Lymp	LENZ_Stromal signature 1
38	8e−05	5 / 97	GSE	KOBAYASHI_EGFR_SIGNALING_24HR_UP
39	1e−04	8 / 324	GSE	FOSTER_TOLERANT_MACROPHAGE_DN
40	1e−04	5 / 104	GSE	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION



Aging

Rank	p−value	#in/all	Geneset
1	0.07	2 / 92	HORVATH_aging_genes meth DOWN
2	0.09	2 / 107	HORVATH_aging_genes meth UP
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	

BP

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 30	negative regulation of extrinsic apoptotic signaling pathway via death domain
2	4e−05	3 / 15	regulation of extrinsic apoptotic signaling pathway via death domain receptors
3	1e−04	3 / 21	negative regulation of interleukin−6 production
4	1e−04	3 / 21	positive regulation of NF−kappaB import into nucleus
5	1e−04	8 / 336	immune response
6	3e−04	3 / 30	lipopolysaccharide−mediated signaling pathway
7	3e−04	3 / 30	regulation of tumor necrosis factor−mediated signaling pathway
8	5e−04	5 / 143	positive regulation of I−kappaB kinase/NF−kappaB signaling
9	5e−04	6 / 225	ion transmembrane transport
10	6e−04	3 / 36	negative regulation of tumor necrosis factor production
11	8e−04	3 / 41	extrinsic apoptotic signaling pathway
12	9e−04	2 / 10	T−helper 1 type immune response
13	1e−03	2 / 11	interferon−gamma production
14	1e−03	2 / 12	activation of cysteine−type endopeptidase activity involved in apoptotic signali
15	1e−03	6 / 274	cytokine−mediated signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	3e−11	12 / 186	SPANG_LPS−index2
2	1e−09	13 / 317	SPANG_BCL6−index2
3	2e−08	14 / 480	Lembcke_Colonic Inflammation
4	7e−03	0 / 14	LIU_PROSTATE_CANCER_DN
5	4e−02	1 / 10	BENTINK_ras.4
6	6e−02	1 / 14	BENTINK_src.10
7	7e−02	1 / 15	WANG_ER_UP
8	7e−02	1 / 16	GENTLES_modul16
9	9e−02	2 / 113	PanCan_Driver_Gene_geneset_nanostring
10	1e−01	2 / 130	PanCan_CC+Apop_geneset_nanostring
11	1e−01	1 / 32	KUIPER_MM good survival
12	1e−01	2 / 147	PanCan_MAPK_geneset_nanostring
13	2e−01	1 / 45	KUIPER_MM poor survival
14	2e−01	1 / 47	PanCan_TGF−B_geneset_nanostring
15	3e−01	0 / 11	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	4e−05	10 / 462	cell surface
2	6e−04	21 / 2239	extracellular exosome
3	6e−04	17 / 1611	extracellular region
4	1e−03	3 / 48	ficolin−1−rich granule membrane
5	4e−03	12 / 1128	integral component of plasma membrane
6	5e−03	3 / 74	secretory granule membrane
7	9e−03	4 / 179	external side of plasma membrane
8	9e−03	5 / 281	lysosome
9	1e−02	4 / 192	membrane raft
10	2e−02	22 / 3210	plasma membrane
11	2e−02	10 / 1090	extracellular space
12	3e−02	22 / 3270	integral component of membrane
13	3e−02	32 / 5339	membrane
14	6e−02	2 / 85	lysosomal lumen
15	8e−02	1 / 18	costamere

Chr

Rank	p−value	#in/all	Geneset
1	0.05	5 / 437	Chr 8
2	0.06	4 / 333	Chr 22
3	0.13	2 / 139	Chr 21
4	0.18	4 / 490	Chr 10
5	0.18	4 / 492	Chr 9
6	0.25	4 / 556	Chr X
7	0.26	5 / 756	Chr 11
8	0.37	3 / 480	Chr 4
9	0.46	3 / 548	Chr 16
10	0.50	3 / 585	Chr 7
11	0.53	4 / 832	Chr 2
12	0.59	3 / 669	Chr 6
13	0.61	3 / 689	Chr 3
14	0.67	1 / 242	Chr 13
15	0.82	1 / 369	Chr 20

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−06	21 / 1639	Fetal_TssF
2	6e−06	53 / 8200	monocytes peripheral blood_2_TssAFlnk
3	8e−06	21 / 1676	Fetal_TxTrans
4	2e−05	10 / 432	monocytes peripheral blood_3_TxFlnk
5	3e−05	56 / 9440	HSC_7_Enh
6	5e−05	17 / 1308	Mid_Frontal_Lobe_K9K27me3
7	5e−05	29 / 3223	monocytes peripheral blood_6_EnhG
8	8e−05	49 / 7635	monocytes peripheral blood_1_TssA
9	9e−05	13 / 847	Fetal_TssP
10	2e−04	20 / 1930	Fetal_TssA
11	2e−04	51 / 8406	Bcells peripheral blood_2_TssAFlnk
12	4e−04	53 / 9114	natural killer cells peripheral blood_7_Enh
13	7e−04	54 / 9544	HSC_2_TssAFlnk
14	9e−04	53 / 9298	Bcells peripheral blood_7_Enh
15	9e−04	53 / 9299	monocytes peripheral blood_7_Enh

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−08	15 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−03	6 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	2e−03	6 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	8e−03	4 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
5	9e−03	15 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
6	2e−02	3 / 132	Marisa_CRC−cluster−a
7	2e−02	1 / 5	Kaneda_CIMP−group1
8	2e−02	1 / 5	Hewish_dMMR−secondary−mutations_Apoptosis
9	2e−02	10 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
10	3e−02	1 / 7	Boland_CRC−MSI−TGC
11	4e−02	6 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
12	4e−02	8 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	6e−02	1 / 13	Budinska_B_Lower crypt−like_DOWN
14	7e−02	5 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
15	8e−02	10 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

Glioma

Rank	p−value	#in/all	Geneset
1	1e−07	10 / 242	ScoV_0.5_Sturm_C1_IDH_DN
2	5e−06	11 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
3	1e−05	8 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
4	5e−04	4 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
5	6e−04	6 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
6	2e−03	4 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	7e−03	2 / 27	Donson−Misc immune function−associated with LTS in HGA
8	7e−03	5 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
9	7e−03	5 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
10	1e−02	3 / 99	GIEZELT_GBM_WT_up_VS_mut
11	1e−02	2 / 36	Christensen_hypomethylated_in_ependymoma
12	3e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
13	4e−02	1 / 9	Colman_survival_robust
14	4e−02	2 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
15	5e−02	1 / 12	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−08	9 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
2	2e−07	12 / 404	RUTELLA_RESPONSE_TO_HGF_UP
3	5e−07	11 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
4	8e−07	9 / 229	QI_PLASMACYTOMA_UP
5	1e−06	11 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
6	2e−06	9 / 251	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP
7	2e−06	10 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
8	3e−06	6 / 90	BASSO_CD40_SIGNALING_UP
9	7e−06	12 / 565	LEE_BMP2_TARGETS_UP
10	9e−06	5 / 62	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
11	1e−05	5 / 67	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
12	1e−05	5 / 67	VANLOO_SP3_TARGETS_DN
13	2e−05	10 / 422	DELYS_THYROID_CANCER_UP
14	2e−05	8 / 255	HELLER_SILENCED_BY_METHYLATION_UP
15	3e−05	9 / 348	MARTENS_BOUND_BY_PML_RARA_FUSION

HM

Rank	p−value	#in/all	Geneset
1	2e−06	8 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	6e−04	5 / 150	HALLMARK_APOPTOSIS
3	6e−04	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	9e−04	5 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	1e−03	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
6	2e−03	5 / 188	HALLMARK_HYPOXIA
7	4e−03	4 / 141	HALLMARK_UV_RESPONSE_DN
8	9e−03	4 / 178	HALLMARK_COMPLEMENT
9	1e−02	4 / 187	HALLMARK_INFLAMMATORY_RESPONSE
10	1e−02	4 / 191	HALLMARK_P53_PATHWAY
11	4e−02	3 / 170	HALLMARK_IL2_STAT5_SIGNALING
12	5e−02	3 / 176	HALLMARK_ALLOGRAFT_REJECTION
13	6e−02	3 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	7e−02	2 / 96	HALLMARK_ANDROGEN_RESPONSE
15	2e−01	1 / 39	HALLMARK_PANCREAS_BETA_CELLS

Immunome

Rank	p−value	#in/all	Geneset
1	0.02	2 / 42	Angelova_immune−metagene−TGD
2	0.11	1 / 25	Angelova_immune−metagene−DC
3	0.12	1 / 29	Angelova_immune−metagene−Th1
4	0.14	1 / 32	Angelova_immune−metagene−effector_memory_CD8
5	0.19	1 / 45	Angelova_immune−metagene−MDSC
6	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
7	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
8	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
9	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
10	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
11	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
12	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
13	1.00	0 / 14	Angelova_immune−metagene−eosinophil
14	1.00	0 / 19	Angelova_immune−metagene−iDC
15	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.05	1 / 12	DUMEAUX_Women normal BMI literature genes up
2	0.06	1 / 13	Huan_blood−pressure_DBP−signature
3	0.06	1 / 14	Huan_blood−pressure_SBP−signature
4	0.07	3 / 210	Homuth_BMI−associated−genes_DN
5	0.10	1 / 22	DUMEAUX_High bmi enriched genes
6	0.50	1 / 150	Homuth_BMI−associated−genes_UP
7	1.00	0 / 62	DUMEAUX_Smoking enriched genes
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_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 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
15	1.00	0 / 22	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−09	8 / 85	Sha_DLBCL UP
2	1e−06	8 / 173	Victora_Light zone signature
3	4e−06	10 / 353	SPANG_CD40 6hrs DN
4	5e−05	7 / 213	SPANG_IL21 DN
5	5e−05	7 / 214	LENZ_Stromal signature 1
6	1e−04	3 / 22	DAVE_NFkB BL DN
7	4e−04	5 / 135	DAVE_BL−vs−DLBCL
8	7e−04	12 / 906	SPANG_BCR DN
9	9e−04	37 / 5404	HOPP_Strong_enhancer
10	2e−03	2 / 14	WRIGHT_GCB UP
11	2e−03	2 / 15	Subero_T−ALL_hypo_meth
12	7e−03	3 / 88	ROSOLOWSKI_green UP
13	1e−02	2 / 33	Subero_T−PLL_hypo_meth
14	1e−02	3 / 102	ROSOLOWSKI_blue total
15	2e−02	3 / 121	ROSOLOWSKI_green total

Melanoma

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 71	Tirosh_Macrophage specific genes−melanoma
2	2e−03	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
3	2e−03	5 / 189	Tirosh_genes preferentially expressed by Tregs
4	2e−03	5 / 204	Landsberg_dedifferentiation_down
5	7e−03	3 / 85	Tirosh_AXL−signature
6	2e−02	4 / 230	Gerber_wt/wt_melanoma−cells−SpotC
7	4e−02	4 / 276	Gerber_wt/wt_melanoma−cells−SpotB
8	5e−02	2 / 78	Tirosh_expression higher in CAFs than in T−cells
9	7e−02	1 / 17	Hugo_melanoma−all−MET_UP
10	2e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
11	2e−01	1 / 39	Tirosh_top50 correlated genes PC4
12	3e−01	1 / 75	Tirosh_Endothelial−cell specific genes−melanoma
13	3e−01	2 / 236	Gerber_wt/wt_group3−specific
14	3e−01	1 / 78	Tirosh_CAF−cell specific genes
15	4e−01	3 / 497	Gerber_wt/wt_melanoma−cells−SpotD

MF

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 30	tumor necrosis factor receptor binding
2	8e−04	3 / 41	protein kinase C binding
3	4e−03	2 / 22	cation channel activity
4	5e−03	2 / 23	bHLH transcription factor binding
5	6e−03	2 / 26	sodium channel regulator activity
6	6e−03	3 / 83	kinase binding
7	1e−02	2 / 33	E−box binding
8	1e−02	2 / 33	RNA polymerase II activating transcription factor binding
9	1e−02	4 / 205	receptor activity
10	3e−02	7 / 644	protein homodimerization activity
11	3e−02	2 / 56	calcium−dependent protein binding
12	3e−02	6 / 517	calcium ion binding
13	3e−02	3 / 151	ion channel activity
14	4e−02	43 / 7864	protein binding
15	4e−02	10 / 1201	hydrolase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.008	2 / 29	hsa−miR−647
2	0.013	2 / 38	hsa−miR−769−3p
3	0.017	2 / 44	hsa−miR−455−5p
4	0.023	3 / 134	hsa−miR−31
5	0.034	2 / 64	hsa−miR−562
6	0.039	3 / 165	hsa−miR−448
7	0.040	1 / 9	hsa−miR−604
8	0.066	3 / 205	hsa−miR−1252
9	0.070	1 / 16	hsa−miR−563
10	0.074	2 / 99	hsa−miR−664
11	0.079	1 / 18	hsa−miR−668
12	0.079	1 / 18	hsa−miR−591
13	0.082	3 / 224	hsa−miR−503
14	0.087	4 / 369	hsa−miR−15b
15	0.093	4 / 378	hsa−miR−16

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.08	1 / 18	Scicluna_UP
2	0.14	1 / 33	Sweeney_viral_dn
3	0.20	1 / 48	Burnham_viral_DN
4	0.21	1 / 52	Burnham_day1_vs_5_DN
5	0.22	1 / 54	Burnham_timecourse
6	0.27	1 / 68	Burnham_sep_vs_con_UP
7	0.28	1 / 71	Burnham_cap_fp_vs_con_UP
8	0.43	1 / 122	Terre_IMS_influenza_meta_signature
9	0.56	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
10	1.00	0 / 56	Burnham_sep_vs_con_DN
11	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.00	0 / 57	Burnham_viral_UP
13	1.00	0 / 57	Burnham_day1_vs_5_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−07	9 / 198	Chaussabel_3,3_Inflammation II
2	1e−03	4 / 99	Chaussabel_1,5_Myeloid lineage
3	1e−03	5 / 182	WIRTH_post GC B−cells
4	2e−03	5 / 204	Chaussabel_3,2_Inflammation I
5	9e−03	3 / 93	Chaussabel_1,4_Replication
6	1e−02	3 / 102	WIRTH_EBV B−cells
7	1e−02	3 / 109	Chaussabel_2,6_Myeloid lineage
8	3e−02	2 / 62	VAQUERIZAS_Lung_TF
9	4e−02	1 / 9	JONGENEEL_Colon
10	5e−02	1 / 11	JONGENEEL_Peripheral Blood Lymphocytes
11	5e−02	1 / 12	VAQUERIZAS_Kidney_TF
12	7e−02	1 / 15	JONGENEEL_Small Intestine
13	7e−02	1 / 17	VAQUERIZAS_Adrenal gland_TF
14	1e−01	1 / 22	VAQUERIZAS_Trachea_TF
15	1e−01	1 / 25	VAQUERIZAS_Adrenal cortex_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.04	16 / 2254	ICGC_BatfPcr1_targets
2	0.12	27 / 4851	ICGC_Runx3_targets
3	0.12	19 / 3213	ICGC_Pu1_targets
4	0.20	19 / 3435	ICGC_Ebfsc137065_targets
5	0.25	13 / 2321	ICGC_Rad21_targets
6	0.30	22 / 4319	ICGC_Pou2_targets
7	0.32	9 / 1636	ICGC_Bcl11_targets
8	0.35	19 / 3778	ICGC_Pol24_targets
9	0.35	19 / 3796	ICGC_Nficsc81335_targets
10	0.41	20 / 4131	ICGC_Tcf3_targets
11	0.42	6 / 1148	HEBENSTREIT_low expression TF
12	0.43	22 / 4602	ICGC_Elf1_targets
13	0.45	7 / 1387	HEBENSTREIT_high expression TF
14	0.50	5 / 1025	ICGC_NrsfPcr1_targets
15	0.51	5 / 1032	ICGC_Usf1_targets