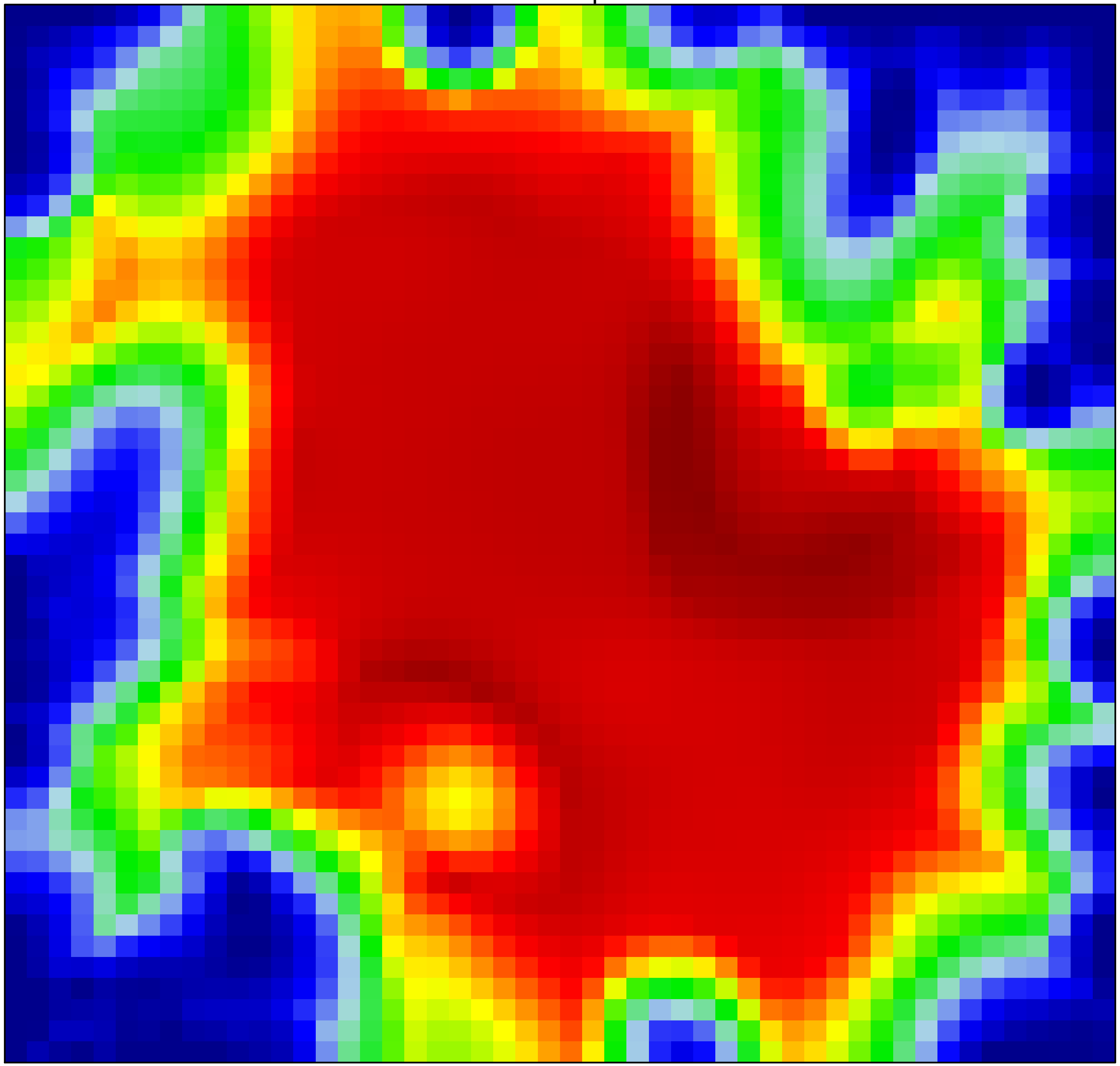
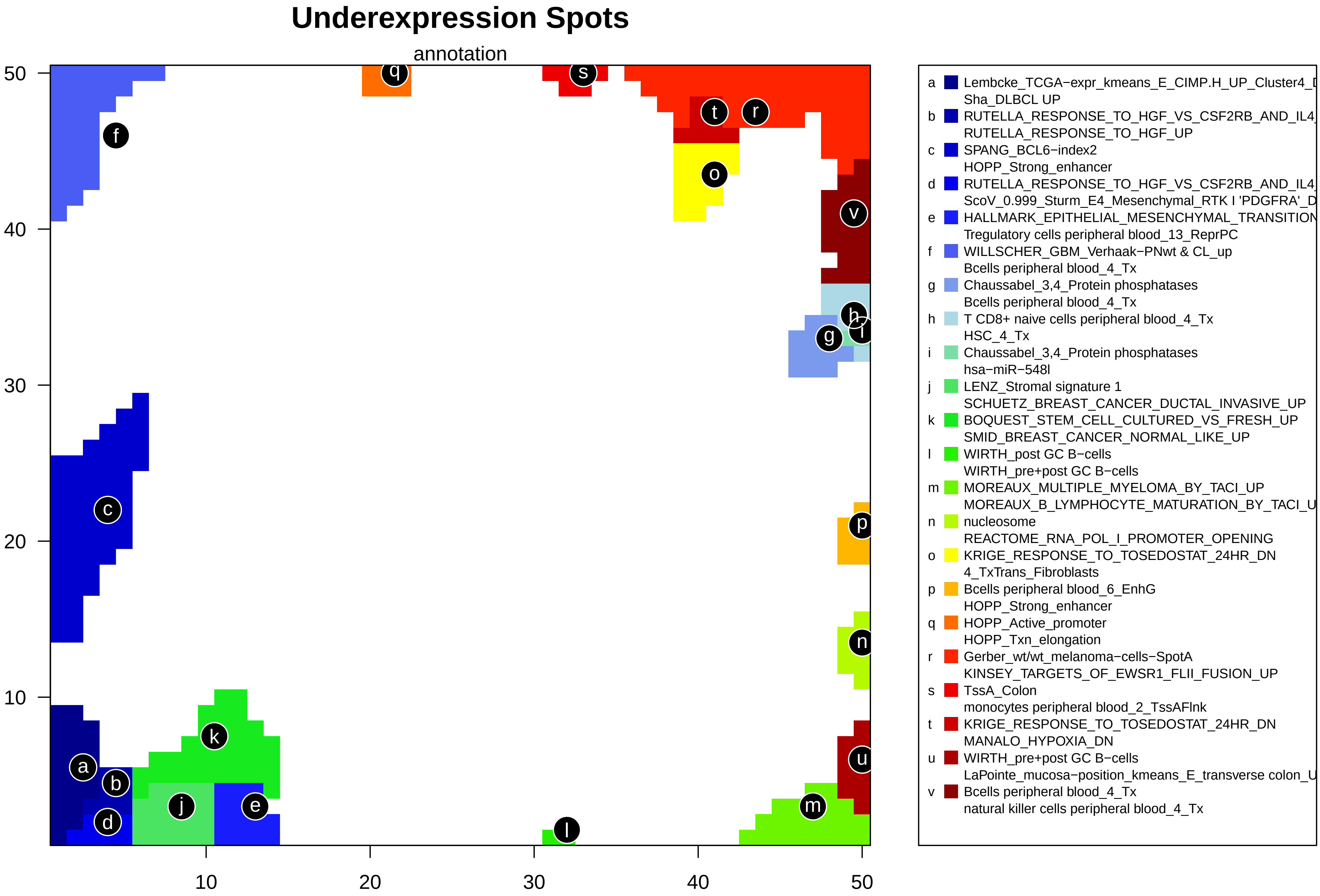
Underexpression Spots

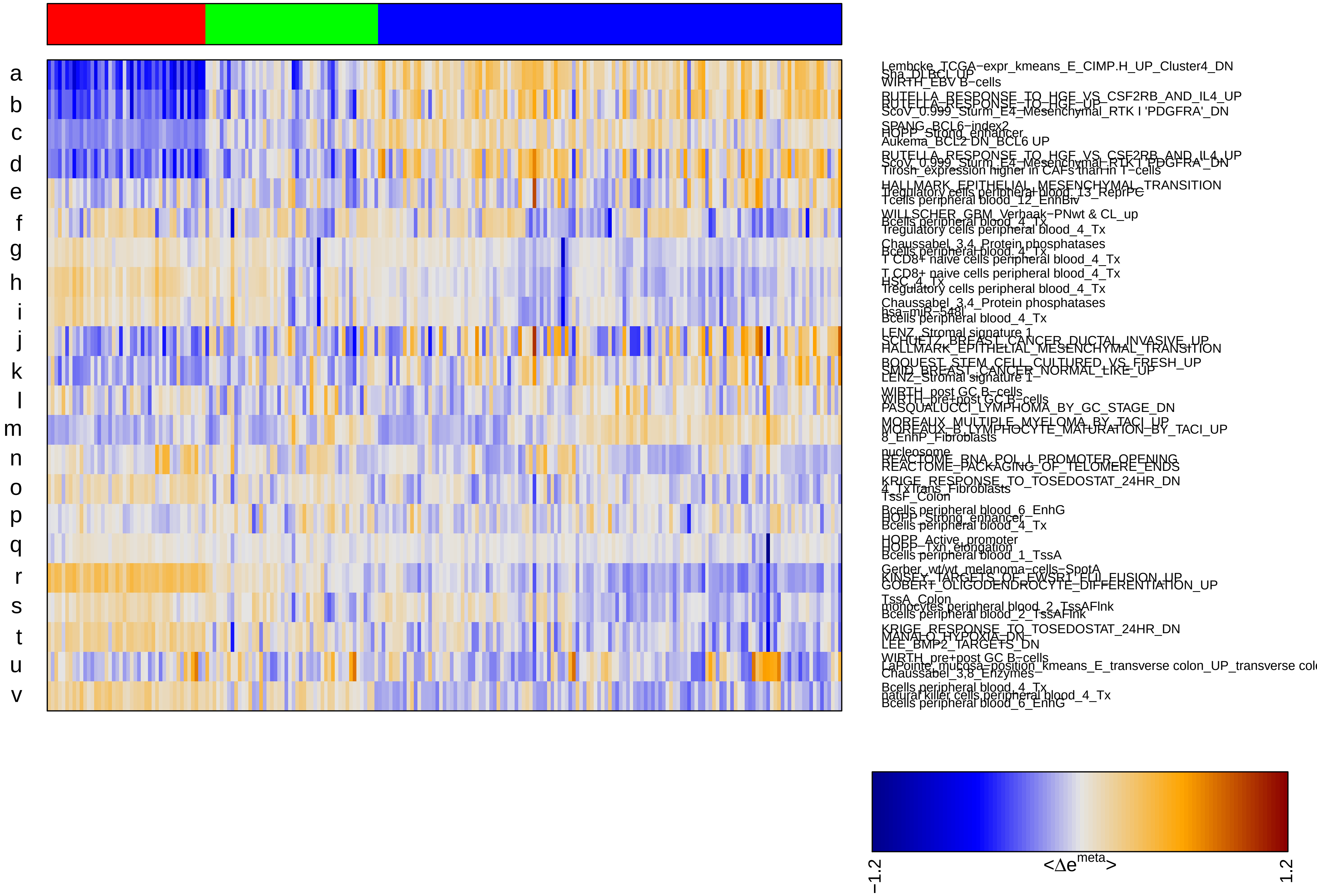
landscape





Underexpression Spots

annotation


a
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u
v
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
Sha_DLBCL UP
WIRTH_EBV B−cells
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
RUTELLA_RESPONSE_TO_HGF_UP
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
SPANG_BCL6−index2
HOPP_Strong_enhancer
Aukema_BCL2 DN_BCL6 UP
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
Tirosh_expression higher in CAFs than in T−cells
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
Tregulatory cells peripheral blood_13_ReprPC
Tcells peripheral blood_12_EnhBiv
WILLSCHER_GBM_Verhaak−PNwt & CL_up
Bcells peripheral blood_4_Tx
Tregulatory cells peripheral blood_4_Tx
Chaussabel_3,4_Protein phosphatases
Bcells peripheral blood_4_Tx
T CD8+ naive cells peripheral blood_4_Tx
T CD8+ naive cells peripheral blood_4_Tx
HSC_4_Tx
Tregulatory cells peripheral blood_4_Tx
Chaussabel_3,4_Protein phosphatases
hsa−miR−548l
Bcells peripheral blood_4_Tx
LENZ_Stromal signature 1
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
SMID_BREAST_CANCER_NORMAL_LIKE_UP
LENZ_Stromal signature 1
WIRTH_post GC B−cells
WIRTH_pre+post GC B−cells
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
8_EnhP_Fibroblasts
nucleosome
REACTOME_RNA_POL_I_PROMOTER_OPENING
REACTOME_PACKAGING_OF_TELOMERE_ENDS
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
4_TxTrans_Fibroblasts
TssF_Colon
Bcells peripheral blood_6_EnhG
HOPP_Strong_enhancer
Bcells peripheral blood_4_Tx
HOPP_Active_promoter
HOPP_Txn_elongation
Bcells peripheral blood_1_TssA
Gerber_wt/wt_melanoma−cells−SpotA
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
TssA_Colon
monocytes peripheral blood_2_TssAFlnk
Bcells peripheral blood_2_TssAFlnk
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
MANALO_HYPOXIA_DN
LEE_BMP2_TARGETS_DN
WIRTH_pre+post GC B−cells
LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse col
Chaussabel_3,8_Enzymes
Bcells peripheral blood_4_Tx
natural killer cells peripheral blood_4_Tx
Bcells peripheral blood_6_EnhG
−1.2
$<\Delta e^{meta}>$
1.2

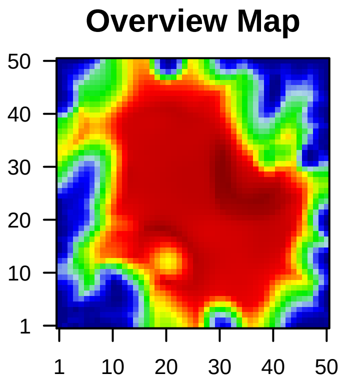
Underexpression Spots

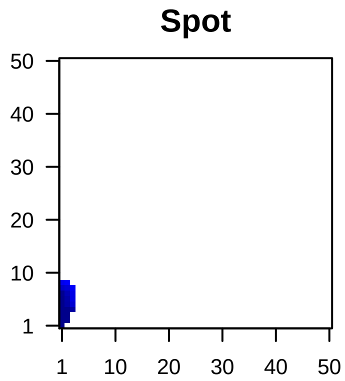
Spot Summary: a

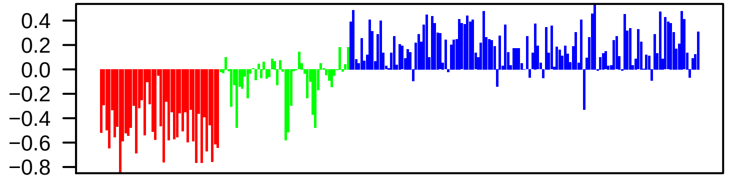
metagenes = 22
genes = 420

<r> metagenes = 0.96
<r> genes = 0.36
beta: r2= 22.18 / log p= −Inf

samples with spot = 52 (23.5 %)
mBL : 42 (95.5 %)
intermediate : 9 (18.8 %)
non−mBL : 1 (0.8 %)


Overview Map


Spot

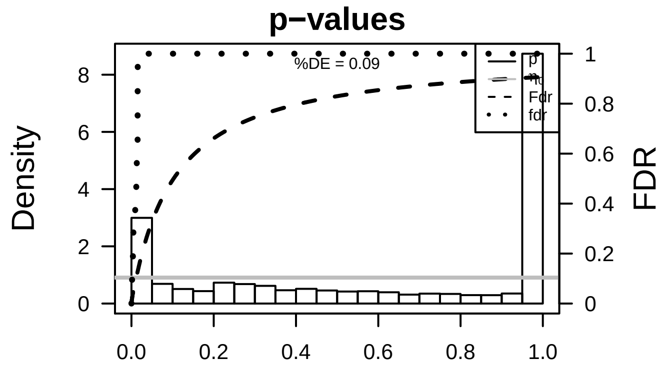


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	221671_x_at	1.08	−3.54	0.45		immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
2	221651_x_at	1.07	−3.48	0.44		immunoglobulin kappa constant [Source:HGNC Symbol;Acc:
3	211430_s_at	1.43	−3.25	0.6		immunoglobulin heavy constant gamma 2 (G2m marker) [So
4	214669_x_at	1.2	−2.67	0.42		
5	203915_at	1.15	−2.65	0.66	CXCL9	C−X−C motif chemokine ligand 9 [Source:HGNC Symbol;Acc
6	217022_s_at	2.33	−2.54	0.49		immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
7	210072_at	0.99	−2.47	0.7	CCL19	C−C motif chemokine ligand 19 [Source:HGNC Symbol;Acc:
8	206666_at	1.46	−2.38	0.68	GZMK	granzyme K [Source:HGNC Symbol;Acc:HGNC:4711]
9	205242_at	1.5	−2.36	0.7	CXCL13	C−X−C motif chemokine ligand 13 [Source:HGNC Symbol;Ac
10	202270_at	0.94	−2.24	0.74	GBP1	guanylate binding protein 1 [Source:HGNC Symbol;Acc:HGN
11	206461_x_at	1.76	−2.22	0.66	MT1H	metallothionein 1H [Source:HGNC Symbol;Acc:HGNC:7400]
12	204533_at	1.34	−2.21	0.7	CXCL10	C−X−C motif chemokine ligand 10 [Source:HGNC Symbol;Ac
13	208791_at	1.61	−2.17	0.69	CLU	clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
14	211663_x_at	1.09	−2.16	0.67		
15	212589_at	1.17	−2.15	0.39	RRAS2	RAS related 2 [Source:HGNC Symbol;Acc:HGNC:17271]
16	202295_s_at	0.59	−2.12	0.8	CTSH	cathepsin H [Source:HGNC Symbol;Acc:HGNC:2535]
17	200628_s_at	0.87	−2.12	0.51	WARS	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:H
18	221658_s_at	0.94	−2.11	0.71	IL21R	interleukin 21 receptor [Source:HGNC Symbol;Acc:HGNC:60
19	202953_at	1.38	−2.11	0.46	C1QB	complement C1q B chain [Source:HGNC Symbol;Acc:HGNC
20	206337_at	1.72	−2.11	0.72	CCR7	C−C motif chemokine receptor 7 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−77	118 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−59	50 / 85	Lymp	Sha_DLBCL UP
3	2e−55	51 / 102	Refe	WIRTH_EBV B−cells
4	6e−45	78 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
5	2e−33	46 / 186	Canc	SPANG_LPS−index2
6	3e−32	56 / 317	Canc	SPANG_BCL6−index2
7	8e−30	41 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	9e−29	37 / 135	Lymp	DAVE_BL−vs−DLBCL
9	1e−27	31 / 90	GSE	BASSO_CD40_SIGNALING_UP
10	6e−27	61 / 480	Canc	Lembcke_Colonic Inflammation
11	6e−27	47 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
12	9e−27	39 / 173	Lymp	Victora_Light zone signature
13	3e−26	46 / 265	GSE	WALLACE_PROSTATE_CANCER_RACE_UP
14	4e−26	29 / 83	Mela	TCGA_melanoma_immune_high
15	5e−26	43 / 229	GSE	QI_PLASMACYTOMA_UP
16	8e−26	40 / 194	GSE	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
17	3e−25	41 / 213	Lymp	SPANG_IL21 DN
18	3e−24	37 / 176	HM	HALLMARK_ALLOGRAFT_REJECTION
19	2e−22	48 / 355	Refe	WIRTH_Immune system
20	5e−22	52 / 429	GSE	SMID_BREAST_CANCER_NORMAL_LIKE_UP
21	2e−20	50 / 431	BP	immune system process
22	5e−20	44 / 336	BP	immune response
23	1e−19	36 / 223	GSE	MCLACHLAN_DENTAL_CARIES_UP
24	2e−19	41 / 299	GSE	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
25	2e−19	17 / 33	Mela	Tirosh_T−cell specific genes−melanoma
26	2e−18	34 / 211	GSE	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
27	2e−18	37 / 255	GSE	HELLER_SILENCED_BY_METHYLATION_UP
28	4e−18	12 / 14	GSE	HUMMEL_BURKITTS_LYMPHOMA_DN
29	4e−18	37 / 261	GSE	POOLA_INVASIVE_BREAST_CANCER_UP
30	8e−18	22 / 78	GSE	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
31	9e−18	23 / 88	GSE	WIELAND_UP_BY_HBV_INFECTION
32	1e−17	20 / 62	GSE	BROWNE_INTERFERON_RESPONSIVE_GENES
33	2e−17	38 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
34	4e−17	33 / 219	GSE	MCLACHLAN_DENTAL_CARIES_DN
35	6e−17	29 / 166	GSE	VERHAAK_AML_WITH_NPM1_MUTATED_UP
36	2e−16	33 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
37	2e−16	62 / 795	GSE	NUYTTEN_EZH2_TARGETS_UP
38	3e−16	19 / 62	Lymp	Monti_Host_response_cluster
39	3e−16	20 / 71	Mela	Tirosh_Macrophage specific genes−melanoma
40	4e−16	13 / 22	Lymp	DAVE_NFkB BL DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.03	6 / 92	HORVATH_aging_genes meth DOWN
2	0.32	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.74	2 / 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	2e−20	50 / 431	immune system process
2	5e−20	44 / 336	immune response
3	8e−16	38 / 323	inflammatory response
4	9e−12	23 / 161	adaptive immune response
5	3e−11	19 / 113	regulation of immune response
6	3e−11	29 / 274	cytokine−mediated signaling pathway
7	2e−10	41 / 553	apoptotic process
8	2e−09	31 / 367	innate immune response
9	3e−09	18 / 131	chemotaxis
10	6e−09	13 / 66	interferon−gamma−mediated signaling pathway
11	6e−09	20 / 169	response to lipopolysaccharide
12	4e−08	12 / 63	chemokine−mediated signaling pathway
13	3e−07	7 / 20	positive regulation of interleukin−12 production
14	5e−07	15 / 127	positive regulation of NF−kappaB transcription factor activity
15	1e−06	20 / 232	cell surface receptor signaling pathway

Cancer

Rank	p−value	#in/all	Geneset
1	2e−33	46 / 186	SPANG_LPS−index2
2	3e−32	56 / 317	SPANG_BCL6−index2
3	6e−27	61 / 480	Lembcke_Colonic Inflammation
4	8e−09	7 / 13	GENTLES_modul18
5	2e−06	5 / 10	BENTINK_ras.4
6	4e−06	11 / 80	PanCan_JAK−ST_geneset_nanostring
7	2e−04	4 / 13	GENTLES_modul11
8	6e−04	9 / 96	PanCan_TXmisReg_geneset_nanostring
9	2e−03	2 / 14	LIU_PROSTATE_CANCER_DN
10	3e−03	3 / 12	HLA2_signature
11	3e−03	10 / 147	PanCan_MAPK_geneset_nanostring
12	4e−03	3 / 14	BENTINK_src.10
13	3e−02	1 / 16	LIU_LIVER_CANCER
14	4e−02	7 / 130	PanCan_CC+Apop_geneset_nanostring
15	5e−02	1 / 2	HLA1_signature

CC

Rank	p−value	#in/all	Geneset
1	3e−09	21 / 179	external side of plasma membrane
2	2e−08	75 / 1611	extracellular region
3	3e−08	123 / 3210	plasma membrane
4	2e−06	6 / 17	T cell receptor complex
5	1e−05	28 / 462	cell surface
6	1e−05	50 / 1090	extracellular space
7	1e−05	10 / 74	secretory granule membrane
8	6e−05	6 / 29	immunological synapse
9	1e−04	48 / 1128	integral component of plasma membrane
10	2e−04	28 / 537	perinuclear region of cytoplasm
11	4e−04	122 / 3805	cytosol
12	5e−04	161 / 5339	membrane
13	2e−03	3 / 10	amyloid−beta complex
14	2e−03	16 / 281	lysosome
15	3e−03	103 / 3270	integral component of membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.005	33 / 832	Chr 2
2	0.082	25 / 756	Chr 11
3	0.180	38 / 1325	Chr 1
4	0.211	17 / 556	Chr X
5	0.276	22 / 776	Chr 17
6	0.322	14 / 490	Chr 10
7	0.436	9 / 333	Chr 22
8	0.474	15 / 585	Chr 7
9	0.499	14 / 554	Chr 5
10	0.632	16 / 689	Chr 3
11	0.639	11 / 480	Chr 4
12	0.664	9 / 403	Chr 14
13	0.668	4 / 184	Chr 18
14	0.683	15 / 669	Chr 6
15	0.703	12 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−17	56 / 626	natural killer cells peripheral blood_3_TxFlnk
2	2e−12	39 / 432	monocytes peripheral blood_3_TxFlnk
3	8e−12	113 / 2507	Mid_Frontal_Lobe_ReprPC
4	5e−09	254 / 8370	natural killer cells peripheral blood_2_TssAFlnk
5	7e−09	53 / 932	Tcells peripheral blood_3_TxFlnk
6	1e−08	66 / 1308	Mid_Frontal_Lobe_K9K27me3
7	2e−08	24 / 258	T CD8+ naive cells peripheral blood_3_TxFlnk
8	3e−08	77 / 1676	Fetal_TxTrans
9	2e−07	39 / 642	Thelper cells peripheral blood_3_TxFlnk
10	3e−07	28 / 383	K9acLow_Colon
11	3e−07	54 / 1072	Mid_Frontal_Lobe_ReprPCWk
12	1e−06	45 / 867	Mid_Frontal_Lobe_Quies
13	4e−06	69 / 1639	Fetal_TssF
14	5e−06	43 / 847	Fetal_TssP
15	5e−06	115 / 3223	monocytes peripheral blood_6_EnhG

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−77	118 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−17	38 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	6e−14	34 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
4	2e−06	10 / 60	Marisa_CRC−cluster−g
5	6e−06	26 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
6	8e−06	8 / 43	Marisa_CRC−cluster−f
7	3e−05	10 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
8	3e−04	18 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
9	2e−03	5 / 35	Ang_CRC_Hypomethylated
10	2e−03	25 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	4e−03	3 / 13	Budinska_B_Lower crypt−like_DOWN
12	4e−03	41 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	5e−03	3 / 15	TCGA−CRC_less−agressive−disease−markers
14	8e−03	58 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
15	8e−03	37 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_

Glioma

Rank	p−value	#in/all	Geneset
1	6e−45	78 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	6e−27	47 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	2e−16	33 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
4	3e−10	26 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	5e−10	27 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
6	1e−09	15 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
7	2e−09	25 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
8	4e−07	14 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
9	5e−07	6 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
10	1e−06	9 / 45	Donson−innate immunity−associated with LTS in HGA
11	3e−06	7 / 27	Donson−Misc immune function−associated with LTS in HGA
12	1e−05	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
13	2e−04	4 / 12	Donson−immune cell intra signaling−associated with LTS in HGA
14	2e−04	63 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
15	3e−04	8 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−27	31 / 90	BASSO_CD40_SIGNALING_UP
2	3e−26	46 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
3	5e−26	43 / 229	QI_PLASMACYTOMA_UP
4	8e−26	40 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
5	5e−22	52 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	1e−19	36 / 223	MCLACHLAN_DENTAL_CARIES_UP
7	2e−19	41 / 299	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
8	2e−18	34 / 211	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
9	2e−18	37 / 255	HELLER_SILENCED_BY_METHYLATION_UP
10	4e−18	12 / 14	HUMMEL_BURKITTS_LYMPHOMA_DN
11	4e−18	37 / 261	POOLA_INVASIVE_BREAST_CANCER_UP
12	8e−18	22 / 78	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
13	9e−18	23 / 88	WIELAND_UP_BY_HBV_INFECTION
14	1e−17	20 / 62	BROWNE_INTERFERON_RESPONSIVE_GENES
15	4e−17	33 / 219	MCLACHLAN_DENTAL_CARIES_DN

HM

Rank	p−value	#in/all	Geneset
1	8e−30	41 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	3e−24	37 / 176	HALLMARK_ALLOGRAFT_REJECTION
3	3e−15	29 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	2e−13	19 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	6e−13	25 / 170	HALLMARK_IL2_STAT5_SIGNALING
6	7e−13	26 / 187	HALLMARK_INFLAMMATORY_RESPONSE
7	2e−08	20 / 178	HALLMARK_COMPLEMENT
8	2e−05	10 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
9	2e−05	14 / 150	HALLMARK_APOPTOSIS
10	2e−03	12 / 188	HALLMARK_HYPOXIA
11	3e−03	12 / 191	HALLMARK_P53_PATHWAY
12	9e−03	11 / 194	HALLMARK_KRAS_SIGNALING_UP
13	1e−02	10 / 174	HALLMARK_APICAL_JUNCTION
14	1e−02	5 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	4e−02	7 / 130	HALLMARK_COAGULATION

Immunome

Rank	p−value	#in/all	Geneset
1	6e−11	15 / 67	Angelova_immune−metagene−T−cells
2	8e−07	8 / 32	Angelova_immune−metagene−effector_memory_CD8
3	5e−06	7 / 29	Angelova_immune−metagene−Th1
4	5e−06	4 / 6	Immunity_immune−checkpoint−inhibitors
5	1e−05	4 / 7	Angelova_immune−metagene−cytotoxic_cells
6	7e−05	4 / 10	Angelova_immune−metagene−TFH
7	1e−04	7 / 45	Angelova_immune−metagene−MDSC
8	1e−04	5 / 21	Angelova_immune−metagene−central_memory_CD4
9	2e−04	4 / 13	Angelova_immune−metagene−activated_B−cells
10	5e−04	6 / 42	Angelova_immune−metagene−TGD
11	2e−03	4 / 23	Angelova_immune−metagene−Treg
12	8e−03	3 / 17	Angelova_immune−metagene−central_memory_CD8
13	9e−03	3 / 18	Angelova_CRC_immunostimulators
14	2e−02	2 / 10	Angelova_CRC_immonoinhibitors
15	8e−02	2 / 19	Angelova_immune−metagene−iDC

Lifestyle

Rank	p−value	#in/all	Geneset
1	6e−06	5 / 12	DUMEAUX_Women normal BMI literature genes up
2	1e−05	5 / 14	Huan_blood−pressure_SBP−signature
3	2e−03	2 / 3	Huan_blood−pressure_HTN−signature
4	2e−03	4 / 22	DUMEAUX_High bmi enriched genes
5	4e−03	3 / 13	Huan_blood−pressure_DBP−signature
6	2e−02	2 / 8	Marjolein_ageing−genes_UP
7	4e−02	3 / 32	Marjolein_ageing−genes_DN
8	1e−01	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	3e−01	7 / 210	Homuth_BMI−associated−genes_DN
10	3e−01	5 / 150	Homuth_BMI−associated−genes_UP
11	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
12	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
13	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
14	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
15	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−59	50 / 85	Sha_DLBCL UP
2	9e−29	37 / 135	DAVE_BL−vs−DLBCL
3	9e−27	39 / 173	Victora_Light zone signature
4	3e−25	41 / 213	SPANG_IL21 DN
5	3e−16	19 / 62	Monti_Host_response_cluster
6	4e−16	13 / 22	DAVE_NFkB BL DN
7	3e−15	39 / 353	SPANG_CD40 6hrs DN
8	5e−15	10 / 12	BENTINK_mBL DOWN
9	2e−13	198 / 5404	HOPP_Strong_enhancer
10	1e−11	9 / 15	Care_Polarized immune response
11	3e−10	55 / 906	SPANG_BCR DN
12	4e−09	10 / 33	Care_Extended T−cell
13	3e−08	14 / 88	ROSOLOWSKI_green UP
14	4e−07	4 / 4	MASCQUE_mBL DOWN
15	1e−06	10 / 57	SPANG_LPS 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	4e−26	29 / 83	TCGA_melanoma_immune_high
2	2e−19	17 / 33	Tirosh_T−cell specific genes−melanoma
3	3e−16	20 / 71	Tirosh_Macrophage specific genes−melanoma
4	9e−13	26 / 189	Tirosh_genes preferentially expressed by Tregs
5	5e−12	17 / 78	Tirosh_expression higher in CAFs than in T−cells
6	1e−10	18 / 107	Tirosh_Exhaustion program in Mel75
7	2e−06	4 / 5	Joensson_Melanoma Proliferative subtype
8	5e−06	16 / 171	Landsberg_dedifferentiation_up
9	2e−05	6 / 24	Tirosh_exhuastion−associated genes consitent across tumors
10	2e−04	15 / 204	Landsberg_dedifferentiation_down
11	1e−03	8 / 85	Tirosh_AXL−signature
12	2e−03	6 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
13	5e−03	13 / 230	Gerber_wt/wt_melanoma−cells−SpotC
14	4e−02	9 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
15	7e−02	3 / 38	Hugo_melanoma−BRAFmut−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	4e−06	8 / 39	chemokine activity
2	6e−06	16 / 173	cytokine activity
3	6e−06	7 / 30	tumor necrosis factor receptor binding
4	4e−05	5 / 17	MHC class I protein binding
5	3e−04	31 / 644	protein homodimerization activity
6	6e−04	5 / 29	coreceptor activity
7	1e−03	4 / 20	chemokine receptor activity
8	1e−03	220 / 7864	protein binding
9	1e−03	24 / 500	signal transducer activity
10	1e−03	11 / 154	serine−type endopeptidase activity
11	2e−03	4 / 22	phospholipase A2 activity
12	2e−03	5 / 38	cytokine receptor activity
13	3e−03	6 / 59	cell adhesion molecule binding
14	4e−03	5 / 44	antigen binding
15	5e−03	12 / 205	receptor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	8 / 122	hsa−miR−506
2	0.02	2 / 9	hsa−miR−604
3	0.02	5 / 64	hsa−miR−890
4	0.03	5 / 71	hsa−miR−188−3p
5	0.03	3 / 29	hsa−miR−647
6	0.05	8 / 165	hsa−miR−448
7	0.07	2 / 18	hsa−miR−1228
8	0.08	2 / 19	hsa−miR−554
9	0.10	2 / 22	hsa−miR−941
10	0.10	2 / 22	hsa−miR−24−1*
11	0.11	8 / 194	hsa−miR−124
12	0.11	4 / 74	hsa−miR−595
13	0.12	3 / 50	hsa−miR−892a
14	0.13	3 / 51	hsa−miR−648
15	0.16	2 / 29	hsa−miR−215

Pneumonia

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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−55	51 / 102	WIRTH_EBV B−cells
2	2e−22	48 / 355	WIRTH_Immune system
3	3e−14	18 / 68	Chaussabel_2,1_Cytotoxic cells
4	2e−08	20 / 182	WIRTH_post GC B−cells
5	9e−07	13 / 99	Chaussabel_1,5_Myeloid lineage
6	1e−06	11 / 72	Chaussabel_3,1_Interferon−inducible
7	2e−06	31 / 496	PROTEINATLAS_spleen
8	1e−05	9 / 59	Chaussabel_2,10_Immune related cell surface molecules
9	3e−05	17 / 219	WIRTH_GC B−cells
10	3e−05	16 / 198	Chaussabel_3,3_Inflammation II
11	9e−05	44 / 989	PROTEINATLAS_tonsil
12	2e−04	15 / 204	Chaussabel_3,2_Inflammation I
13	1e−03	30 / 678	PROTEINATLAS_lymph node
14	5e−03	8 / 109	Chaussabel_2,6_Myeloid lineage
15	1e−02	7 / 100	Chaussabel_2,8_T−cells

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	2e−06	70 / 1636	ICGC_Bcl11_targets
2	6e−06	87 / 2254	ICGC_BatfPcr1_targets
3	9e−06	77 / 1941	ICGC_Bcl3_targets
4	6e−05	61 / 1508	ICGC_Mef2_targets
5	6e−05	110 / 3213	ICGC_Pu1_targets
6	6e−05	116 / 3435	ICGC_Ebfsc137065_targets
7	5e−04	76 / 2150	ICGC_Irf4_targets
8	1e−03	119 / 3778	ICGC_Pol24_targets
9	1e−03	55 / 1494	ICGC_Cebpbsc150_targets
10	2e−03	117 / 3796	ICGC_Nficsc81335_targets
11	3e−03	77 / 2321	ICGC_Rad21_targets
12	4e−03	143 / 4851	ICGC_Runx3_targets
13	6e−03	91 / 2899	ICGC_Nfatc1_targets
14	1e−02	120 / 4072	ICGC_Mta3_targets
15	1e−02	103 / 3420	ICGC_Bclaf101388_targets

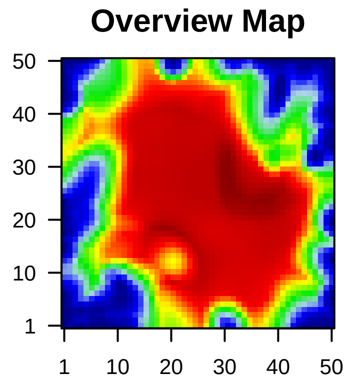
Underexpression Spots

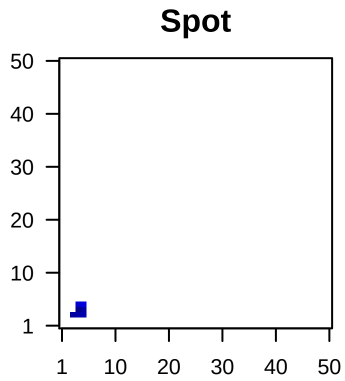
Spot Summary: b

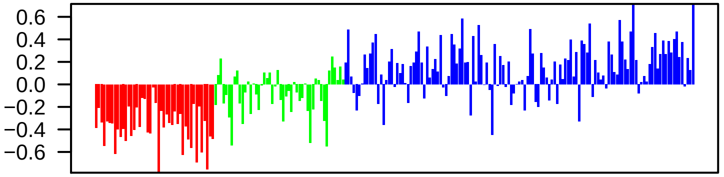
metagenes = 7
genes = 73

<r> metagenes = 0.99
<r> genes = 0.47
beta: r2= 19.05 / log p= −Inf

samples with spot = 56 (25.3 %)
mBL : 37 (84.1 %)
intermediate : 12 (25 %)
non−mBL : 7 (5.4 %)


Overview Map


Spot

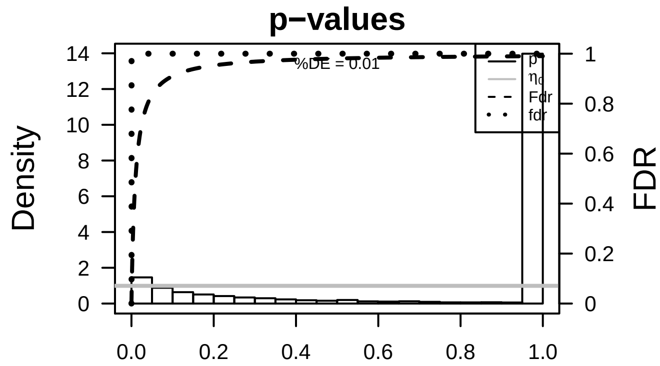


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212187_x_at	1.03	−3.04	0.72	PTGDS	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
2	205890_s_at	0.75	−2.75	0.68	UBD	ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
3	211748_x_at	1	−2.71	0.75	PTGDS	prostaglandin D2 synthase [Source:HGNC Symbol;Acc:HGN
4	203920_at	0.92	−2.04	0.76	NR1H3	nuclear receptor subfamily 1 group H member 3 [Source:HGN
5	219648_at	0.72	−1.96	0.64	MREG	melanoregulin [Source:HGNC Symbol;Acc:HGNC:25478]
6	209392_at	0.71	−1.91	0.68	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
7	212268_at	1.07	−1.81	0.65	SERPINB1	serpin family B member 1 [Source:HGNC Symbol;Acc:HGNC
8	201850_at	0.94	−1.78	0.77	CAPG	capping actin protein, gelsolin like [Source:HGNC Symbol;Ac
9	206134_at	0.93	−1.74	0.84	ADAMDEC1	ADAM like decysin 1 [Source:HGNC Symbol;Acc:HGNC:162
10	205844_at	1.42	−1.65	0.62	VNN1	vanin 1 [Source:HGNC Symbol;Acc:HGNC:12705]
11	201169_s_at	1.38	−1.64	0.6	BHLHE40	basic helix−loop−helix family member e40 [Source:HGNC Sy
12	210314_x_at	1.03	−1.63	0.8	TNFSF13	TNF superfamily member 13 [Source:HGNC Symbol;Acc:HG
13	209500_x_at	0.96	−1.62	0.81	TNFSF13	TNF superfamily member 13 [Source:HGNC Symbol;Acc:HG
14	203243_s_at	0.89	−1.58	0.56	PDLIM5	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:1
15	201302_at	0.87	−1.57	0.72	ANXA4	annexin A4 [Source:HGNC Symbol;Acc:HGNC:542]
16	211612_s_at	1.28	−1.57	0.79	IL13RA1	interleukin 13 receptor subunit alpha 1 [Source:HGNC Symb
17	210663_s_at	1.06	−1.55	0.64	KYNU	kynureninase [Source:HGNC Symbol;Acc:HGNC:6469]
18	212956_at	1.2	−1.52	0.59	TBC1D9	TBC1 domain family member 9 [Source:HGNC Symbol;Acc:
19	217388_s_at	1.08	−1.51	0.65	KYNU	kynureninase [Source:HGNC Symbol;Acc:HGNC:6469]
20	206295_at	1.23	−1.51	0.82	IL18	interleukin 18 [Source:HGNC Symbol;Acc:HGNC:5986]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−15	19 / 386	GSE	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	1e−14	19 / 404	GSE	RUTELLA_RESPONSE_TO_HGF_UP
3	6e−14	19 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
4	2e−12	14 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
5	8e−12	19 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
6	1e−11	15 / 317	Canc	SPANG_BCL6−index2
7	1e−11	13 / 214	Lymp	LENZ_Stromal signature 1
8	7e−10	13 / 297	GSE	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
9	1e−09	8 / 71	Mela	Tirosh_Macrophage specific genes−melanoma
10	3e−09	15 / 480	Canc	Lembcke_Colonic Inflammation
11	5e−09	11 / 223	GSE	MCLACHLAN_DENTAL_CARIES_UP
12	2e−08	13 / 386	GSE	MULLIGHAN_MLL_SIGNATURE_2_UP
13	2e−08	10 / 198	Refer	Chaussabel_3,3_Inflammation II
14	3e−08	8 / 109	Refer	Chaussabel_2,6_Myeloid lineage
15	3e−08	11 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
16	1e−07	9 / 176	GSE	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
17	1e−07	5 / 27	GSE	KAMIKUBO_MYELOID_CEBPA_NETWORK
18	2e−07	10 / 255	GSE	HELLER_SILENCED_BY_METHYLATION_UP
19	2e−07	5 / 30	GSE	APPEL_IMATINIB_RESPONSE
20	3e−07	11 / 327	GSE	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
21	5e−07	11 / 352	GSE	MULLIGHAN_MLL_SIGNATURE_1_UP
22	7e−07	9 / 219	GSE	MCLACHLAN_DENTAL_CARIES_DN
23	7e−07	6 / 69	GSE	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
24	1e−06	8 / 171	GSE	MARKEY_RB1_ACUTE_LOF_UP
25	1e−06	5 / 41	Lymp	ROSOLOWSKI_blue DOWN
26	2e−06	11 / 403	BP	neutrophil degranulation
27	2e−06	8 / 186	Canc	SPANG_LPS−index2
28	2e−06	16 / 902	GSE	CHEN_METABOLIC_SYNDROM_NETWORK
29	2e−06	7 / 131	GSE	BROWN_MYELOID_CELL_DEVELOPMENT_UP
30	2e−06	4 / 21	GSE	STEGER_ADIPOGENESIS_UP
31	2e−06	5 / 47	GSE	PARK_APL_PATHOGENESIS_DN
32	3e−06	9 / 265	GSE	WALLACE_PROSTATE_CANCER_RACE_UP
33	3e−06	5 / 50	GSE	ROSS_AML_WITH_CBFB_MYH11_FUSION
34	4e−06	8 / 202	GSE	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
35	5e−06	6 / 97	Lymp	ROSOLOWSKI_red total
36	6e−06	9 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
37	8e−06	6 / 104	GSE	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
38	9e−06	4 / 29	Immu	Angelova_immune−metagene−Th1
39	9e−06	4 / 29	GSE	STEARMAN_TUMOR_FIELD_EFFECT_UP
40	1e−05	8 / 229	GSE	QI_PLASMACYTOMA_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.009	3 / 92	HORVATH_aging_genes meth DOWN
2	0.392	1 / 107	HORVATH_aging_genes meth UP
3	1.000	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−06	11 / 403	neutrophil degranulation
2	2e−05	9 / 336	immune response
3	3e−05	3 / 13	toll−like receptor 4 signaling pathway
4	6e−05	6 / 150	leukocyte migration
5	3e−04	7 / 274	cytokine−mediated signaling pathway
6	9e−04	2 / 10	T−helper 1 type immune response
7	1e−03	2 / 11	amyloid−beta clearance
8	1e−03	2 / 11	interferon−gamma production
9	1e−03	4 / 100	activation of MAPK activity
10	1e−03	2 / 12	acute inflammatory response
11	2e−03	2 / 14	positive regulation of superoxide anion generation
12	2e−03	3 / 53	circadian regulation of gene expression
13	2e−03	11 / 885	positive regulation of transcription from RNA polymerase II promoter
14	2e−03	2 / 16	melanocyte differentiation
15	3e−03	2 / 18	heterotypic cell−cell adhesion

Cancer

Rank	p−value	#in/all	Geneset
1	1e−11	15 / 317	SPANG_BCL6−index2
2	3e−09	15 / 480	Lembcke_Colonic Inflammation
3	2e−06	8 / 186	SPANG_LPS−index2
4	4e−05	3 / 15	WANG_ER_UP
5	5e−02	1 / 10	BENTINK_ras.4
6	6e−02	1 / 13	GENTLES_modul18
7	6e−02	1 / 13	BENTINK_e2f3.1
8	6e−02	1 / 14	GUSTAFSON_PI3K_UP
9	7e−02	1 / 16	GENTLES_modul16
10	7e−02	2 / 96	PanCan_TXmisReg_geneset_nanostring
11	1e−01	1 / 32	KUIPER_MM good survival
12	2e−01	0 / 14	LIU_PROSTATE_CANCER_DN
13	3e−01	0 / 11	LIU_PROSTATE_CANCER_UP
14	4e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
15	5e−01	1 / 147	PanCan_MAPK_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 48	ficolin−1−rich granule membrane
2	2e−04	4 / 60	tertiary granule membrane
3	2e−04	3 / 26	integrin complex
4	3e−04	9 / 462	cell surface
5	4e−04	14 / 1090	extracellular space
6	5e−04	27 / 3210	plasma membrane
7	7e−04	27 / 3270	integral component of membrane
8	1e−03	5 / 179	external side of plasma membrane
9	1e−03	3 / 49	RNA polymerase II transcription factor complex
10	2e−03	4 / 113	receptor complex
11	2e−03	5 / 192	membrane raft
12	2e−03	16 / 1611	extracellular region
13	3e−03	36 / 5339	membrane
14	3e−03	2 / 19	plasma membrane raft
15	5e−03	19 / 2239	extracellular exosome

Chr

Rank	p−value	#in/all	Geneset
1	0.08	5 / 492	Chr 9
2	0.14	2 / 139	Chr 21
3	0.18	6 / 832	Chr 2
4	0.21	5 / 689	Chr 3
5	0.24	3 / 369	Chr 20
6	0.26	4 / 556	Chr X
7	0.33	3 / 437	Chr 8
8	0.37	4 / 669	Chr 6
9	0.38	3 / 480	Chr 4
10	0.40	3 / 490	Chr 10
11	0.41	4 / 700	Chr 12
12	0.53	2 / 382	Chr 15
13	0.58	1 / 184	Chr 18
14	0.69	3 / 756	Chr 11
15	0.73	2 / 548	Chr 16

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−09	14 / 432	monocytes peripheral blood_3_TxFlnk
2	2e−07	17 / 847	Fetal_TssP
3	6e−07	33 / 3223	monocytes peripheral blood_6_EnhG
4	4e−05	20 / 1676	Fetal_TxTrans
5	2e−04	51 / 8200	monocytes peripheral blood_2_TssAFlnk
6	3e−04	20 / 1930	Fetal_TssA
7	3e−04	27 / 3105	Tcells peripheral blood_15_Quies
8	9e−04	17 / 1633	monocytes peripheral blood_8_ZNF_Rpts
9	1e−03	45 / 7078	7_Enh_ESC_Mesoderm
10	2e−03	29 / 3838	15_Quies_ESC_Mesoderm
11	2e−03	47 / 7751	natural killer cells peripheral blood_1_TssA
12	2e−03	30 / 4079	15_Quies_ESC_Endoderm
13	2e−03	44 / 7078	Bcells peripheral blood_5_TxWk
14	3e−03	16 / 1639	Fetal_TssF
15	3e−03	46 / 7635	monocytes peripheral blood_1_TssA

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−12	19 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	6e−06	9 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	3e−05	6 / 132	Marisa_CRC−cluster−a
4	6e−05	8 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	1e−02	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
6	2e−02	12 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−02	14 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	5e−02	3 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	5e−02	8 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	6e−02	1 / 13	Budinska_B_Lower crypt−like_DOWN
11	9e−02	9 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	1e−01	5 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	1e−01	1 / 35	Ang_CRC_Hypomethylated
14	2e−01	4 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	2e−01	1 / 38	Marisa_CRC−cluster−e

Glioma

Rank	p−value	#in/all	Geneset
1	6e−14	19 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	2e−12	14 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	3e−08	11 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	3e−05	3 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
5	1e−04	7 / 242	ScoV_0.5_Sturm_C1_IDH_DN
6	9e−04	6 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
7	1e−03	6 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
8	1e−02	1 / 3	laffaire_hypometh_LGG_vs_control
9	3e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expression
10	4e−02	2 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
11	5e−02	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
12	5e−02	1 / 12	VERHAAK_Brain
13	6e−02	1 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
14	6e−02	1 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma
15	6e−02	1 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−15	19 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	1e−14	19 / 404	RUTELLA_RESPONSE_TO_HGF_UP
3	7e−10	13 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
4	5e−09	11 / 223	MCLACHLAN_DENTAL_CARIES_UP
5	2e−08	13 / 386	MULLIGHAN_MLL_SIGNATURE_2_UP
6	1e−07	9 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	1e−07	5 / 27	KAMIKUBO_MYELOID_CEBPA_NETWORK
8	2e−07	10 / 255	HELLER_SILENCED_BY_METHYLATION_UP
9	2e−07	5 / 30	APPEL_IMATINIB_RESPONSE
10	3e−07	11 / 327	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
11	5e−07	11 / 352	MULLIGHAN_MLL_SIGNATURE_1_UP
12	7e−07	9 / 219	MCLACHLAN_DENTAL_CARIES_DN
13	7e−07	6 / 69	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
14	1e−06	8 / 171	MARKEY_RB1_ACUTE_LOF_UP
15	2e−06	16 / 902	CHEN_METABOLIC_SYNDROM_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	3e−05	7 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	1e−04	6 / 170	HALLMARK_IL2_STAT5_SIGNALING
3	5e−04	5 / 141	HALLMARK_UV_RESPONSE_DN
4	1e−03	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
5	1e−03	5 / 178	HALLMARK_COMPLEMENT
6	1e−02	4 / 181	HALLMARK_XENOBIOTIC_METABOLISM
7	1e−02	4 / 187	HALLMARK_INFLAMMATORY_RESPONSE
8	1e−02	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
9	2e−02	2 / 51	HALLMARK_TGF_BETA_SIGNALING
10	6e−02	2 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	6e−02	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	6e−02	3 / 194	HALLMARK_KRAS_SIGNALING_UP
13	7e−02	2 / 96	HALLMARK_ANDROGEN_RESPONSE
14	7e−02	2 / 97	HALLMARK_BILE_ACID_METABOLISM
15	1e−01	2 / 130	HALLMARK_COAGULATION

Immunome

Rank	p−value	#in/all	Geneset
1	9e−06	4 / 29	Angelova_immune−metagene−Th1
2	2e−04	3 / 25	Angelova_immune−metagene−DC
3	3e−03	2 / 18	Angelova_CRC_immunostimulators
4	8e−02	1 / 18	Angelova_immune−metagene−pDC
5	1e−01	1 / 23	Angelova_immune−metagene−monocytes
6	1e−01	1 / 23	Angelova_immune−metagene−Th2
7	1e−01	1 / 32	Angelova_immune−metagene−effector_memory_CD8
8	2e−01	1 / 42	Angelova_immune−metagene−TGD
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 / 17	Angelova_immune−metagene−central_memory_CD8
14	1e+00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
15	1e+00	0 / 12	Angelova_immune−metagene−effector_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	5 / 210	Homuth_BMI−associated−genes_DN
2	0.023	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	0.041	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	0.054	1 / 12	DUMEAUX_Women normal BMI literature genes up
5	0.058	1 / 13	Huan_blood−pressure_DBP−signature
6	0.063	1 / 14	Huan_blood−pressure_SBP−signature
7	0.097	1 / 22	DUMEAUX_High bmi enriched genes
8	1.000	0 / 62	DUMEAUX_Smoking enriched genes
9	1.000	0 / 10	DUMEAUX_Smoking literature genes up
10	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1.000	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1.000	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.000	0 / 22	DUMEAUX_Fasting enriched genes
15	1.000	0 / 150	Homuth_BMI−associated−genes_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−11	13 / 214	LENZ_Stromal signature 1
2	1e−06	5 / 41	ROSOLOWSKI_blue DOWN
3	5e−06	6 / 97	ROSOLOWSKI_red total
4	4e−05	5 / 85	Sha_DLBCL UP
5	2e−04	4 / 62	Monti_Host_response_cluster
6	7e−04	4 / 88	ROSOLOWSKI_green UP
7	2e−03	4 / 121	ROSOLOWSKI_green total
8	3e−03	11 / 906	SPANG_BCR DN
9	6e−03	2 / 26	DAVE_Immune response 1
10	2e−02	15 / 1894	HOPP_Poised_promoter
11	2e−02	28 / 4357	HOPP_Weak_txn
12	2e−02	3 / 135	DAVE_BL−vs−DLBCL
13	3e−02	33 / 5404	HOPP_Strong_enhancer
14	3e−02	34 / 5682	HOPP_Weak_promoter
15	5e−02	3 / 173	Victora_Light zone signature

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−09	8 / 71	Tirosh_Macrophage specific genes−melanoma
2	3e−05	5 / 78	Tirosh_expression higher in CAFs than in T−cells
3	9e−05	7 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	7e−04	2 / 9	Joensson_Melanoma Pigmentation subtype
5	2e−03	5 / 204	Landsberg_dedifferentiation_down
6	1e−02	2 / 38	Hugo_melanoma−BRAFmut−MET_UP
7	2e−02	2 / 46	Tirosh_top50 correlated genes PC5
8	4e−02	3 / 171	Landsberg_dedifferentiation_up
9	5e−02	2 / 81	Tirosh_Genes in the MITF program
10	6e−02	3 / 189	Tirosh_genes preferentially expressed by Tregs
11	8e−02	1 / 17	Hugo_melanoma−all−MET_UP
12	9e−02	2 / 107	Tirosh_Exhaustion program in Mel75
13	1e−01	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
14	1e−01	3 / 276	Gerber_wt/wt_melanoma−cells−SpotB
15	2e−01	1 / 39	Tirosh_top50 correlated genes PC4

MF

Rank	p−value	#in/all	Geneset
1	2e−04	4 / 62	transcription factor activity, RNA polymerase II distal enhancer sequence−spe
2	5e−04	3 / 33	E−box binding
3	3e−03	5 / 205	receptor activity
4	4e−03	5 / 225	transcription coactivator activity
5	4e−03	5 / 234	transcriptional activator activity, RNA polymerase II proximal promoter seque
6	5e−03	2 / 23	bHLH transcription factor binding
7	5e−03	6 / 346	receptor binding
8	5e−03	4 / 153	protein dimerization activity
9	8e−03	4 / 172	transcription corepressor activity
10	8e−03	2 / 30	tumor necrosis factor receptor binding
11	1e−02	2 / 33	RNA polymerase II activating transcription factor binding
12	1e−02	6 / 408	protein heterodimerization activity
13	1e−02	2 / 38	cytokine receptor activity
14	1e−02	2 / 39	nuclear receptor activity
15	2e−02	2 / 41	protein kinase C binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	3 / 64	hsa−miR−562
2	0.007	2 / 28	hsa−miR−1274b
3	0.013	2 / 38	hsa−miR−769−3p
4	0.017	2 / 43	hsa−miR−328
5	0.018	2 / 44	hsa−miR−455−5p
6	0.020	4 / 224	hsa−miR−503
7	0.028	2 / 56	hsa−miR−193b
8	0.028	2 / 56	hsa−miR−592
9	0.044	2 / 72	hsa−miR−149
10	0.050	2 / 78	hsa−miR−216b
11	0.063	3 / 197	hsa−miR−152
12	0.069	3 / 205	hsa−miR−1252
13	0.071	1 / 16	hsa−miR−563
14	0.077	2 / 99	hsa−miR−664
15	0.080	1 / 18	hsa−miR−668

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.03	2 / 54	Burnham_timecourse
3	0.04	2 / 68	Burnham_sep_vs_con_UP
4	0.04	2 / 71	Burnham_cap_fp_vs_con_UP
5	0.14	1 / 33	Sweeney_viral_dn
6	0.20	1 / 48	Burnham_viral_DN
7	0.21	1 / 52	Burnham_day1_vs_5_DN
8	0.57	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
9	1.00	0 / 56	Burnham_sep_vs_con_DN
10	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
11	1.00	0 / 57	Burnham_viral_UP
12	1.00	0 / 57	Burnham_day1_vs_5_UP
13	1.00	0 / 18	Scicluna_UP
14	1.00	0 / 41	Scicluna_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−08	10 / 198	Chaussabel_3,3_Inflammation II
2	3e−08	8 / 109	Chaussabel_2,6_Myeloid lineage
3	2e−05	7 / 182	WIRTH_post GC B−cells
4	4e−05	7 / 204	Chaussabel_3,2_Inflammation I
5	1e−03	4 / 99	Chaussabel_1,5_Myeloid lineage
6	1e−02	2 / 32	VAQUERIZAS_Liver_TF
7	1e−02	3 / 102	WIRTH_EBV B−cells
8	3e−02	2 / 59	Chaussabel_2,10_Immune related cell surface molecules
9	4e−02	1 / 9	JONGENEEL_Colon
10	5e−02	1 / 12	VAQUERIZAS_Kidney_TF
11	6e−02	1 / 13	WIRTH_Prim. lymphoid organs
12	7e−02	1 / 15	JONGENEEL_Small Intestine
13	8e−02	6 / 642	PROTEINATLAS_lung
14	8e−02	6 / 645	PROTEINATLAS_bone marrow
15	8e−02	3 / 218	WIRTH_pre+post GC B−cells

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.005	19 / 2254	ICGC_BatfPcr1_targets
2	0.049	21 / 3213	ICGC_Pu1_targets
3	0.069	12 / 1636	ICGC_Bcl11_targets
4	0.203	7 / 1041	ICGC_P300_targets
5	0.205	26 / 4851	ICGC_Runx3_targets
6	0.278	7 / 1148	HEBENSTREIT_low expression TF
7	0.311	18 / 3435	ICGC_Ebfsc137065_targets
8	0.364	16 / 3121	ICGC_Egr1_targets
9	0.377	19 / 3778	ICGC_Pol24_targets
10	0.408	11 / 2150	ICGC_Irf4_targets
11	0.408	10 / 1941	ICGC_Bcl3_targets
12	0.415	21 / 4278	ICGC_Yy1_targets
13	0.436	3 / 522	ICGC_SrfPcr2_targets
14	0.463	7 / 1387	HEBENSTREIT_high expression TF
15	0.488	9 / 1848	ICGC_Pbx3_targets

Underexpression Spots

Spot Summary: c

metagenes = 57
genes = 564

<r> metagenes = 0.82
<r> genes = 0.17
beta: r2= 6.02 / log p= −Inf

samples with spot = 44 (19.9 %)
mBL : 36 (81.8 %)
intermediate : 6 (12.5 %)
non−mBL : 2 (1.6 %)

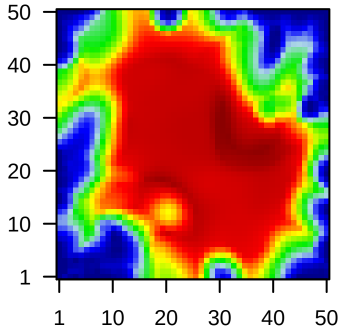
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	217418_x_at	0.78	−3.65	0.26	MS4A1	membrane spanning 4−domains A1 [Source:HGNC Symbol;A
2	205861_at	0.71	−3.47	0.32	SPIB	Spi−B transcription factor [Source:HGNC Symbol;Acc:HGNC:
3	210356_x_at	0.73	−3.31	0.27	MS4A1	membrane spanning 4−domains A1 [Source:HGNC Symbol;A
4	209374_s_at	1.26	−2.62	0.26		immunoglobulin heavy constant mu [Source:HGNC Symbol;A
5	203760_s_at	1.05	−2.45	0.65	SLA	Src like adaptor [Source:HGNC Symbol;Acc:HGNC:10902]
6	221601_s_at	1.4	−2.39	0.52	FCMR	Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGN
7	209829_at	0.72	−2.31	0.38	RIPOR2	RHO family interacting cell polarization regulator 2 [Source:H
8	207655_s_at	0.59	−2.24	0.42	BLNK	B cell linker [Source:HGNC Symbol;Acc:HGNC:14211]
9	216449_x_at	1.05	−2.22	0.38	HSP90B1	heat shock protein 90 beta family member 1 [Source:HGNC
10	203881_s_at	1.22	−2.22	0.22	DMD	dystrophin [Source:HGNC Symbol;Acc:HGNC:2928]
11	213888_s_at	0.88	−2.19	0.43	TRAF3IP3	TRAF3 interacting protein 3 [Source:HGNC Symbol;Acc:HGN
12	219563_at	0.73	−2.16	0.44	SYNE3	spectrin repeat containing nuclear envelope family member 3
13	213400_s_at	1.07	−2.12	0.15	TBL1X	transducin beta like 1 X−linked [Source:HGNC Symbol;Acc:H
14	210136_at	1.18	−2.09	0.38	MBP	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
15	221602_s_at	1.52	−2.03	0.5	FCMR	Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGN
16	203685_at	1.55	−2.03	0.67	BCL2	BCL2, apoptosis regulator [Source:HGNC Symbol;Acc:HGNC
17	222281_s_at	1.76	−1.97	0.73		
18	210448_s_at	0.88	−1.97	0.46	P2RX5	purinergic receptor P2X 5 [Source:HGNC Symbol;Acc:HGNC
19	206126_at	1.06	−1.96	0.38	CXCR5	C−X−C motif chemokine receptor 5 [Source:HGNC Symbol;A
20	219841_at	1.59	−1.96	0.19	AICDA	activation induced cytidine deaminase [Source:HGNC Symbo

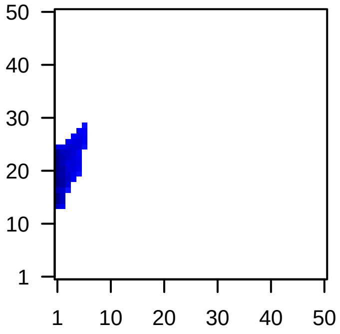
Geneset Overrepresentation

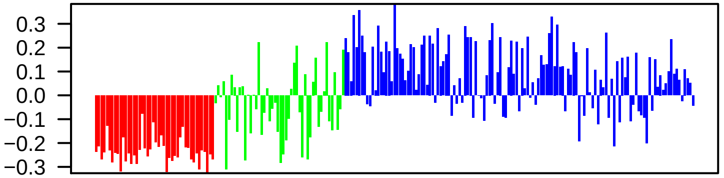
Rank	p−value	#in/all	Geneset	
1	6e−21	52 / 317	Cance	SPANG_BCL6−index2
2	2e−20	287 / 5404	Lympl	HOPP_Strong_enhancer
3	4e−19	27 / 85	Lympl	Aukema_BCL2 DN_BCL6 UP
4	2e−15	38 / 234	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_DN
5	2e−12	11 / 18	Lympl	WRIGHT_ABC UP
6	2e−11	31 / 213	Lympl	SPANG_IL21 DN
7	8e−11	19 / 85	Lympl	Sha_DLBCL UP
8	9e−11	8 / 10	Lympl	Care_ABC UP
9	2e−10	39 / 353	Lympl	SPANG_CD40 6hrs DN
10	1e−09	81 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
11	2e−09	25 / 173	Lympl	Victora_Light zone signature
12	4e−09	67 / 906	Lympl	SPANG_BCR DN
13	5e−09	25 / 182	Refer	WIRTH_post GC B−cells
14	7e−09	268 / 5908	Lympl	HOPP_Active_promoter
15	1e−08	27 / 218	Refer	WIRTH_pre+post GC B−cells
16	1e−08	12 / 42	Refer	Chaussabel_1,3_B−cells
17	3e−08	24 / 184	Chr	Chr 18
18	6e−08	14 / 67	Immu	Angelova_immune−metagene−T−cells
19	8e−08	16 / 90	GSEA	BASSO_CD40_SIGNALING_UP
20	1e−07	26 / 227	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP
21	1e−07	30 / 290	GSEA	ODONNELL_TFRC_TARGETS_UP
22	2e−07	38 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
23	4e−07	19 / 139	GSEA	BROCKE_APOPTOSIS_REVERSED_BY_IL6
24	4e−07	11 / 46	MF	SH3/SH2 adaptor activity
25	4e−07	108 / 1941	TF	ICGC_Bcl3_targets
26	4e−07	12 / 56	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
27	5e−07	44 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
28	5e−07	13 / 67	GSEA	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
29	6e−07	27 / 262	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
30	7e−07	94 / 1636	TF	ICGC_Bcl11_targets
31	8e−07	33 / 368	GSEA	ZHENG_BOUND_BY_FOXP3
32	1e−06	55 / 795	GSEA	NUYTTEN_EZH2_TARGETS_UP
33	1e−06	27 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
34	2e−06	4 / 4	Lympl	WRIGHT_custom ABC−DLBCL UP
35	2e−06	37 / 453	GSEA	ONDER_CDH1_TARGETS_2_DN
36	2e−06	197 / 4261	Lympl	HOPP_Txn_transition
37	2e−06	12 / 64	GSEA	GEORGANTAS_HSC_MARKERS
38	2e−06	118 / 2254	TF	ICGC_BatfPcr1_targets
39	2e−06	21 / 186	Cance	SPANG_LPS−index2
40	2e−06	38 / 480	Cance	Lembcke_Colonic Inflammation

Overview Map

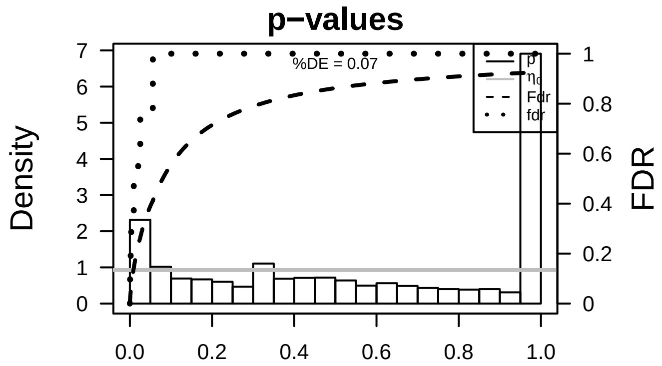


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	5 / 107	HORVATH_aging_genes meth UP
2	0.8	1 / 47	TESCHENDORFF_age_hypermethylated
3	0.8	2 / 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−06	58 / 885	positive regulation of transcription from RNA polymerase II promoter
2	1e−05	10 / 52	positive regulation of signal transduction
3	2e−05	38 / 520	positive regulation of transcription, DNA−templated
4	3e−05	5 / 12	leukocyte chemotaxis
5	4e−05	37 / 521	transcription from RNA polymerase II promoter
6	5e−05	92 / 1764	regulation of transcription, DNA−templated
7	1e−04	86 / 1655	transcription, DNA−templated
8	2e−04	5 / 16	N−glycan processing
9	2e−04	6 / 26	B cell activation
10	3e−04	12 / 106	regulation of small GTPase mediated signal transduction
11	4e−04	21 / 264	positive regulation of GTPase activity
12	2e−03	4 / 15	B cell homeostasis
13	2e−03	5 / 25	antibacterial humoral response
14	2e−03	6 / 38	positive regulation of fat cell differentiation
15	2e−03	4 / 16	negative regulation of B cell proliferation

Cancer

Rank	p−value	#in/all	Geneset
1	6e−21	52 / 317	SPANG_BCL6−index2
2	2e−06	21 / 186	SPANG_LPS−index2
3	2e−06	38 / 480	Lembcke_Colonic Inflammation
4	2e−03	9 / 80	PanCan_JAK−ST_geneset_nanostring
5	9e−03	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	2e−02	8 / 96	PanCan_TXmisReg_geneset_nanostring
7	6e−02	2 / 12	GENTLES_modul12
8	7e−02	2 / 13	BENTINK_e2f3.1
9	8e−02	1 / 14	LIU_COMMON_CANCER_GENES
10	8e−02	2 / 14	GUSTAFSON_PI3K_UP
11	8e−02	2 / 14	BENTINK_src.10
12	1e−01	10 / 187	PanCan_PI3K_geneset_nanostring
13	1e−01	0 / 11	LIU_PROSTATE_CANCER_UP
14	1e−01	3 / 36	ZHANG_MM up
15	2e−01	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−04	10 / 70	nucleosome
2	3e−03	14 / 171	nuclear chromatin
3	6e−03	5 / 34	peroxisomal matrix
4	6e−03	6 / 48	ficolin−1−rich granule membrane
5	9e−03	4 / 24	stereocilium
6	9e−03	157 / 3805	cytosol
7	2e−02	15 / 231	apical plasma membrane
8	2e−02	26 / 479	Golgi membrane
9	2e−02	6 / 62	extrinsic component of cytoplasmic side of plasma membrane
10	2e−02	6 / 62	filopodium
11	2e−02	3 / 18	phagocytic cup
12	3e−02	5 / 48	microvillus
13	3e−02	11 / 163	transcription factor complex
14	3e−02	44 / 938	Golgi apparatus
15	4e−02	7 / 88	bicellular tight junction

Chr

Rank	p−value	#in/all	Geneset
1	3e−08	24 / 184	Chr 18
2	4e−04	42 / 689	Chr 3
3	9e−03	23 / 382	Chr 15
4	2e−02	34 / 669	Chr 6
5	4e−02	28 / 556	Chr X
6	1e−01	26 / 585	Chr 7
7	2e−01	35 / 833	Chr 19
8	2e−01	18 / 403	Chr 14
9	5e−01	18 / 490	Chr 10
10	6e−01	45 / 1325	Chr 1
11	7e−01	4 / 139	Chr 21
12	8e−01	26 / 832	Chr 2
13	8e−01	23 / 756	Chr 11
14	8e−01	16 / 548	Chr 16
15	9e−01	13 / 492	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−18	380 / 8406	Bcells peripheral blood_2_TssAFlnk
2	4e−18	362 / 7833	Bcells peripheral blood_1_TssA
3	1e−16	408 / 9544	HSC_2_TssAFlnk
4	5e−15	210 / 3767	Bcells peripheral blood_6_EnhG
5	6e−14	348 / 7751	natural killer cells peripheral blood_1_TssA
6	1e−13	357 / 8068	Thelper cells peripheral blood_1_TssA
7	8e−13	364 / 8370	natural killer cells peripheral blood_2_TssAFlnk
8	9e−13	64 / 693	Bcells peripheral blood_3_TxFlnk
9	1e−12	275 / 5716	Bcells peripheral blood_4_Tx
10	2e−12	349 / 7930	Tregulatory cells peripheral blood_1_TssA
11	3e−12	376 / 8816	Thelper cells peripheral blood_2_TssAFlnk
12	6e−12	353 / 8102	TssWk_Colon
13	8e−12	344 / 7835	HSC_1_TssA
14	1e−11	359 / 8322	T CD8+ naive cells peripheral blood_1_TssA
15	2e−11	104 / 1535	Bcells peripheral blood_8_ZNF_Rpts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−09	81 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
2	1e−05	42 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	5e−04	86 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
4	5e−03	54 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
5	9e−03	3 / 13	Vilar_hypermutated−in−CRC
6	1e−02	2 / 5	Kaneda_CIMP−group1
7	2e−02	6 / 60	Marisa_CRC−cluster−g
8	3e−02	47 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	4e−02	15 / 255	Kosinski_top−crypt−long−list
10	4e−02	27 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
11	5e−02	39 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
12	7e−02	1 / 2	Hewish_dMMR−secondary−mutations_Cell−motility
13	7e−02	1 / 2	Budinska_D_Mesenchymal_DOWN
14	8e−02	22 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
15	9e−02	50 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

Glioma

Rank	p−value	#in/all	Geneset
1	5e−04	21 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	6e−04	10 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
3	1e−03	53 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
4	3e−03	18 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
5	8e−03	4 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
6	8e−03	26 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
7	9e−03	3 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
8	9e−03	3 / 13	Christensen_hypomethylated_in_grade2_oligoastrocytoma
9	9e−03	3 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
10	9e−03	3 / 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
11	1e−02	16 / 242	ScoV_0.5_Sturm_C1_IDH_DN
12	2e−02	6 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
13	3e−02	7 / 82	laffaire_hypermeth_LGG_vs_control
14	3e−02	6 / 67	Weller_LGG_1p19qDel−vs−intact_UP
15	3e−02	5 / 50	Christensen_hypomethylated_in_primary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−15	38 / 234	HOLLMANN_APOPTOSIS_VIA_CD40_DN
2	8e−08	16 / 90	BASSO_CD40_SIGNALING_UP
3	1e−07	26 / 227	JAATINEN_HEMATOPOIETIC_STEM_CELL_UP
4	1e−07	30 / 290	ODONNELL_TFRC_TARGETS_UP
5	2e−07	38 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	4e−07	19 / 139	BROCKE_APOPTOSIS_REVERSED_BY_IL6
7	4e−07	12 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
8	5e−07	44 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
9	5e−07	13 / 67	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
10	6e−07	27 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
11	8e−07	33 / 368	ZHENG_BOUND_BY_FOXP3
12	1e−06	55 / 795	NUYTTEN_EZH2_TARGETS_UP
13	1e−06	27 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
14	2e−06	37 / 453	ONDER_CDH1_TARGETS_2_DN
15	2e−06	12 / 64	GEORGANTAS_HSC_MARKERS

HM

Rank	p−value	#in/all	Geneset
1	0.001	16 / 191	HALLMARK_P53_PATHWAY
2	0.002	14 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.007	14 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	0.009	14 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.010	8 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.011	11 / 141	HALLMARK_UV_RESPONSE_DN
7	0.017	7 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	0.018	5 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
9	0.022	12 / 176	HALLMARK_ALLOGRAFT_REJECTION
10	0.023	12 / 178	HALLMARK_COMPLEMENT
11	0.040	12 / 193	HALLMARK_HEME_METABOLISM
12	0.066	11 / 187	HALLMARK_INFLAMMATORY_RESPONSE
13	0.077	10 / 170	HALLMARK_IL2_STAT5_SIGNALING
14	0.117	8 / 139	HALLMARK_FATTY_ACID_METABOLISM
15	0.159	8 / 150	HALLMARK_APOPTOSIS

Immunome

Rank	p−value	#in/all	Geneset
1	6e−08	14 / 67	Angelova_immune−metagene−T−cells
2	9e−03	3 / 13	Angelova_immune−metagene−activated_B−cells
3	9e−03	3 / 13	Angelova_immune−metagene−immature_B−cells
4	2e−02	5 / 45	Angelova_immune−metagene−MDSC
5	8e−02	3 / 29	Angelova_immune−metagene−Th1
6	8e−02	2 / 14	Angelova_immune−metagene−eosinophil
7	1e−01	2 / 15	Angelova_immune−metagene−NK
8	1e−01	2 / 16	Angelova_immune−metagene−Th17
9	1e−01	2 / 18	Angelova_immune−metagene−pDC
10	1e−01	1 / 4	Angelova_CRC_MSS−neoantigens
11	1e−01	2 / 19	Angelova_immune−metagene−iDC
12	2e−01	2 / 23	Angelova_immune−metagene−Treg
13	3e−01	1 / 10	Angelova_immune−metagene−TFH
14	3e−01	1 / 10	Angelova_CRC_immonoinhibitors
15	3e−01	1 / 11	Angelova_immune−metagene−macrophages

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	3 / 22	DUMEAUX_Fasting enriched genes
2	0.28	1 / 9	DUMEAUX_Monocytes in smokers literature genes up
3	0.30	1 / 10	DUMEAUX_Smoking literature genes up
4	0.46	8 / 210	Homuth_BMI−associated−genes_DN
5	0.55	1 / 22	DUMEAUX_High bmi enriched genes
6	0.68	1 / 32	Marjolein_ageing−genes_DN
7	0.78	4 / 150	Homuth_BMI−associated−genes_UP
8	0.89	1 / 62	DUMEAUX_Smoking enriched genes
9	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1.00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−20	287 / 5404	HOPP_Strong_enhancer
2	4e−19	27 / 85	Aukema_BCL2 DN_BCL6 UP
3	2e−12	11 / 18	WRIGHT_ABC UP
4	2e−11	31 / 213	SPANG_IL21 DN
5	8e−11	19 / 85	Sha_DLBCL UP
6	9e−11	8 / 10	Care_ABC UP
7	2e−10	39 / 353	SPANG_CD40 6hrs DN
8	2e−09	25 / 173	Victora_Light zone signature
9	4e−09	67 / 906	SPANG_BCR DN
10	7e−09	268 / 5908	HOPP_Active_promoter
11	2e−06	4 / 4	WRIGHT_custom ABC−DLBCL UP
12	2e−06	197 / 4261	HOPP_Txn_transition
13	1e−05	196 / 4357	HOPP_Weak_txn
14	3e−05	237 / 5529	HOPP_Txn_elongation
15	5e−05	241 / 5682	HOPP_Weak_promoter

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−05	7 / 24	Tirosh_B−cell specific genes−melanoma
2	5e−03	29 / 497	Gerber_wt/wt_melanoma−cells−SpotD
3	7e−03	8 / 81	Tirosh_Genes in the MITF program
4	9e−03	4 / 24	Tirosh_exhuastion−associated genes consitent across tumors
5	3e−02	7 / 83	TCGA_melanoma_immune_high
6	5e−02	4 / 39	Tirosh_top50 correlated genes PC4
7	6e−02	13 / 230	Gerber_wt/wt_melanoma−cells−SpotC
8	7e−02	1 / 2	Melanoma Epi−Enzyme Cluster 1
9	7e−02	11 / 189	Tirosh_genes preferentially expressed by Tregs
10	1e−01	2 / 16	Hugo_melanoma−all−LEF1_UP
11	1e−01	2 / 17	Hugo_melanoma−all−MET_UP
12	1e−01	9 / 171	Landsberg_dedifferentiation_up
13	2e−01	3 / 39	Tirosh_melanoma specific genes
14	2e−01	11 / 222	Gerber_wt/wt_melanoma−cells−SpotF
15	2e−01	1 / 5	Hugo_melanoma−BRAFmut−MET_DN

MF

Rank	p−value	#in/all	Geneset
1	4e−07	11 / 46	SH3/SH2 adaptor activity
2	4e−06	87 / 1541	DNA binding
3	7e−05	316 / 7864	protein binding
4	8e−05	10 / 65	protein phosphatase binding
5	9e−05	19 / 202	GTPase activator activity
6	2e−04	17 / 182	RNA polymerase II regulatory region sequence−specific DNA binding
7	5e−04	11 / 96	SH3 domain binding
8	8e−04	5 / 22	14−3−3 protein binding
9	1e−03	116 / 2529	metal ion binding
10	2e−03	5 / 26	transcriptional activator activity, RNA polymerase II distal enhancer sequence
11	3e−03	40 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindir
12	5e−03	40 / 741	DNA binding transcription factor activity
13	5e−03	11 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
14	5e−03	27 / 450	sequence−specific DNA binding
15	8e−03	13 / 172	transcription corepressor activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	11 / 88	hsa−miR−600
2	3e−04	27 / 369	hsa−miR−15b
3	3e−04	11 / 89	hsa−miR−1248
4	1e−03	6 / 34	hsa−miR−874
5	1e−03	12 / 124	hsa−miR−655
6	1e−03	19 / 251	hsa−let−7g
7	2e−03	26 / 397	hsa−miR−15a
8	2e−03	25 / 378	hsa−miR−16
9	3e−03	5 / 28	hsa−miR−654−5p
10	3e−03	23 / 350	hsa−miR−424
11	3e−03	8 / 71	hsa−miR−188−3p
12	4e−03	22 / 336	hsa−miR−519d
13	4e−03	18 / 257	hsa−let−7i
14	4e−03	23 / 361	hsa−miR−130b
15	5e−03	9 / 91	hsa−miR−211

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	3 / 33	Sweeney_viral_dn
2	0.1	4 / 52	Burnham_day1_vs_5_DN
3	0.1	2 / 18	Scicluna_UP
4	0.2	3 / 41	Scicluna_DN
5	0.2	7 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.2	4 / 68	Burnham_sep_vs_con_UP
7	0.3	3 / 57	Burnham_viral_UP
8	0.4	5 / 122	Terre_IMS_influenza_meta_signature
9	0.4	7 / 179	Terre_MSV_multiple_respiratory_viruses_dn
10	0.5	3 / 71	Burnham_cap_fp_vs_con_UP
11	0.5	2 / 48	Burnham_viral_DN
12	0.6	2 / 54	Burnham_timecourse
13	0.6	2 / 56	Burnham_sep_vs_con_DN
14	0.6	2 / 57	Burnham_day1_vs_5_UP
15	0.7	1 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−09	25 / 182	WIRTH_post GC B−cells
2	1e−08	27 / 218	WIRTH_pre+post GC B−cells
3	1e−08	12 / 42	Chaussabel_1,3_B−cells
4	3e−04	26 / 355	WIRTH_Immune system
5	7e−04	5 / 21	VAQUERIZAS_Tonsil_TF
6	2e−03	8 / 66	VAQUERIZAS_Whole blood_TF
7	3e−03	27 / 429	PROTEINATLAS_liver
8	6e−03	7 / 62	VAQUERIZAS_Lung_TF
9	7e−03	8 / 81	Chaussabel_1,2_Platelets
10	9e−03	28 / 496	PROTEINATLAS_spleen
11	1e−02	30 / 553	PROTEINATLAS_prostate
12	1e−02	14 / 204	Chaussabel_3,2_Inflammation I
13	2e−02	5 / 42	VAQUERIZAS_Fetal brain_TF
14	2e−02	3 / 16	VAQUERIZAS_Fetal liver_TF
15	2e−02	3 / 16	VAQUERIZAS_Salivary gland_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	4e−07	108 / 1941	ICGC_Bcl3_targets
2	7e−07	94 / 1636	ICGC_Bcl11_targets
3	2e−06	118 / 2254	ICGC_BatfPcr1_targets
4	2e−05	83 / 1508	ICGC_Mef2_targets
5	4e−05	142 / 2994	ICGC_Zeb1_targets
6	4e−05	138 / 2899	ICGC_Nfatc1_targets
7	5e−05	150 / 3213	ICGC_Pu1_targets
8	6e−05	158 / 3435	ICGC_Ebfsc137065_targets
9	1e−04	156 / 3420	ICGC_Bclaf101388_targets
10	3e−04	183 / 4212	ICGC_Pol2_targets
11	3e−04	166 / 3769	ICGC_Pmlsc71910_targets
12	4e−04	154 / 3451	ICGC_Atf2_targets
13	4e−04	103 / 2150	ICGC_Irf4_targets
14	6e−04	176 / 4072	ICGC_Mta3_targets
15	6e−04	157 / 3564	ICGC_Taf1_targets

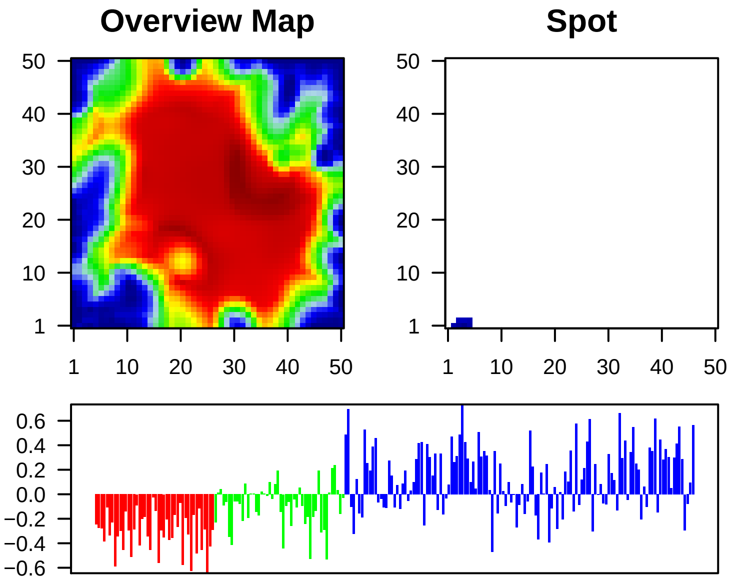
Underexpression Spots

Spot Summary: d

metagenes = 7
genes = 134

<r> metagenes = 0.98
<r> genes = 0.45
beta: r2= 22.18 / log p= −Inf

samples with spot = 55 (24.9 %)
mBL : 33 (75 %)
intermediate : 11 (22.9 %)
non−mBL : 11 (8.5 %)

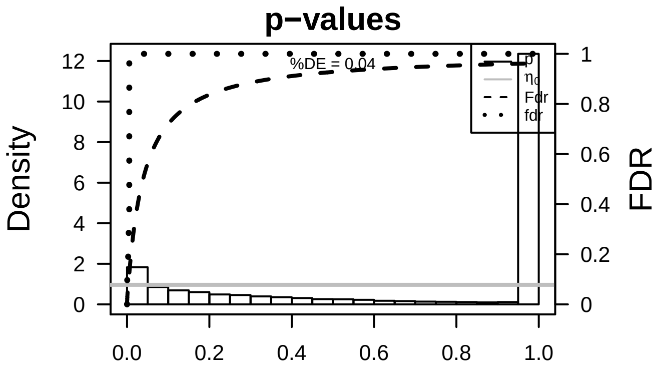


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209395_at	1.52	−2.3	0.69	CHI3L1	chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
2	209396_s_at	1.35	−2.29	0.67	CHI3L1	chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
3	216598_s_at	1.08	−2.24	0.51	CCL2	C−C motif chemokine ligand 2 [Source:HGNC Symbol;Acc:H
4	218345_at	0.91	−2.16	0.74	TMEM176A	transmembrane protein 176A [Source:HGNC Symbol;Acc:HG
5	204112_s_at	0.8	−1.76	0.66	HNMT	histamine N−methyltransferase [Source:HGNC Symbol;Acc:H
6	208581_x_at	1.37	−1.75	0.68	MT1X	metallothionein 1X [Source:HGNC Symbol;Acc:HGNC:7405]
7	209901_x_at	1.16	−1.71	0.57	AIF1	allograft inflammatory factor 1 [Source:HGNC Symbol;Acc:H
8	218035_s_at	1.08	−1.7	0.67	RBM47	RNA binding motif protein 47 [Source:HGNC Symbol;Acc:HG
9	1405_i_at	1.06	−1.7	0.77	CCL5	C−C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:H
10	203922_s_at	0.82	−1.7	0.66	CYBB	cytochrome b−245 beta chain [Source:HGNC Symbol;Acc:H
11	202497_x_at	1.54	−1.67	0.6	SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:
12	219385_at	1.19	−1.66	0.86	SLAMF8	SLAM family member 8 [Source:HGNC Symbol;Acc:HGNC:2
13	218559_s_at	0.74	−1.65	0.76	MAFB	MAF bZIP transcription factor B [Source:HGNC Symbol;Acc:H
14	207610_s_at	1.45	−1.62	0.76	ADGRE2	adhesion G protein−coupled receptor E2 [Source:HGNC Sym
15	200648_s_at	0.95	−1.62	0.57	GLUL	glutamate−ammonia ligase [Source:HGNC Symbol;Acc:HGN
16	202411_at	1.39	−1.59	0.6	IFI27	interferon alpha inducible protein 27 [Source:HGNC Symbol;
17	221477_s_at	0.97	−1.58	0.72	SOD2	superoxide dismutase 2 [Source:HGNC Symbol;Acc:HGNC:1
18	219386_s_at	0.83	−1.58	0.84	SLAMF8	SLAM family member 8 [Source:HGNC Symbol;Acc:HGNC:2
19	202855_s_at	1.2	−1.55	0.63	SLC16A3	solute carrier family 16 member 3 [Source:HGNC Symbol;Acc
20	202800_at	0.95	−1.54	0.76	SLC1A3	solute carrier family 1 member 3 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−25	33 / 386	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	2e−23	33 / 447	Gliom	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
3	5e−22	18 / 78	Melan	Tirosh_expression higher in CAFs than in T−cells
4	2e−19	27 / 354	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
5	5e−18	27 / 404	GSEA	RUTELLA_RESPONSE_TO_HGF_UP
6	6e−18	22 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
7	1e−17	31 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	3e−16	14 / 71	Melan	Tirosh_Macrophage specific genes−melanoma
9	1e−14	19 / 223	GSEA	MCLACHLAN_DENTAL_CARIES_UP
10	1e−14	21 / 297	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	7e−14	16 / 154	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
12	3e−13	19 / 269	Gliom	ScoV_0.5_Sturm_C3_Mesenchymal_DN
13	8e−13	13 / 99	Refer	Chaussabel_1,5_Myeloid lineage
14	1e−12	17 / 219	GSEA	MCLACHLAN_DENTAL_CARIES_DN
15	1e−12	16 / 187	HM	HALLMARK_INFLAMMATORY_RESPONSE
16	2e−12	13 / 104	GSEA	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
17	2e−11	22 / 480	Canc	Lembcke_Colonic Inflammation
18	5e−11	14 / 166	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
19	6e−11	15 / 202	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
20	6e−11	23 / 560	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
21	1e−10	14 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
22	1e−10	18 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
23	2e−10	28 / 902	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
24	3e−10	18 / 354	GSEA	RODWELL_AGING_KIDNEY_UP
25	5e−10	13 / 162	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
26	6e−10	17 / 323	BP	inflammatory response
27	9e−10	8 / 41	Lymp	ROSOLOWSKI_blue DOWN
28	2e−09	25 / 795	GSEA	NUYTTEN_EZH2_TARGETS_UP
29	2e−09	12 / 150	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_U
30	3e−09	18 / 403	BP	neutrophil degranulation
31	7e−09	12 / 166	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
32	8e−09	10 / 102	Refer	WIRTH_EBV B−cells
33	8e−09	16 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
34	1e−08	10 / 105	GSEA	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
35	2e−08	14 / 261	GSEA	POOLA_INVASIVE_BREAST_CANCER_UP
36	2e−08	8 / 60	CC	tertiary granule membrane
37	2e−08	9 / 85	GSEA	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP
38	3e−08	10 / 117	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_DN
39	3e−08	8 / 62	Lymp	Monti_Host_response_cluster
40	3e−08	17 / 422	GSEA	DELYS_THYROID_CANCER_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.6	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	6e−10	17 / 323	inflammatory response
2	3e−09	18 / 403	neutrophil degranulation
3	6e−08	15 / 336	immune response
4	2e−06	11 / 232	cell surface receptor signaling pathway
5	4e−06	4 / 14	cellular response to zinc ion
6	4e−06	4 / 14	negative regulation of growth
7	4e−06	4 / 14	positive regulation of monocyte chemotaxis
8	4e−06	9 / 156	positive regulation of ERK1 and ERK2 cascade
9	1e−05	6 / 63	chemokine−mediated signaling pathway
10	4e−05	13 / 431	immune system process
11	5e−05	5 / 50	positive regulation of protein kinase activity
12	8e−05	3 / 11	positive regulation of macrophage chemotaxis
13	8e−05	7 / 131	chemotaxis
14	1e−04	24 / 1361	signal transduction
15	2e−04	11 / 367	innate immune response

Cancer

Rank	p−value	#in/all	Geneset
1	2e−11	22 / 480	Lembcke_Colonic Inflammation
2	2e−06	10 / 186	SPANG_LPS−index2
3	4e−05	11 / 317	SPANG_BCL6−index2
4	6e−03	2 / 15	WANG_ER_UP
5	7e−02	1 / 9	WANG_ER_DN
6	7e−02	0 / 14	LIU_PROSTATE_CANCER_DN
7	1e−01	1 / 13	GENTLES_modul18
8	1e−01	1 / 13	BENTINK_e2f3.1
9	1e−01	1 / 14	BENTINK_src.10
10	1e−01	1 / 15	GENTLES_modul4
11	2e−01	2 / 96	PanCan_TXmisReg_geneset_nanostring
12	3e−01	2 / 130	PanCan_CC+Apop_geneset_nanostring
13	3e−01	2 / 147	PanCan_MAPK_geneset_nanostring
14	6e−01	1 / 113	PanCan_Driver_Gene_geneset_nanostring
15	6e−01	3 / 409	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	2e−08	8 / 60	tertiary granule membrane
2	3e−08	52 / 3270	integral component of membrane
3	3e−06	47 / 3210	plasma membrane
4	2e−05	64 / 5339	membrane
5	2e−05	23 / 1128	integral component of plasma membrane
6	2e−05	15 / 537	perinuclear region of cytoplasm
7	3e−05	6 / 74	secretory granule membrane
8	3e−05	6 / 77	specific granule membrane
9	4e−05	5 / 48	ficolin−1−rich granule membrane
10	4e−05	22 / 1090	extracellular space
11	2e−04	33 / 2239	extracellular exosome
12	7e−04	4 / 50	tertiary granule lumen
13	3e−03	4 / 77	cell
14	5e−03	6 / 196	nuclear membrane
15	1e−02	3 / 56	specific granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.08	9 / 669	Chr 6
2	0.17	5 / 369	Chr 20
3	0.20	6 / 490	Chr 10
4	0.28	8 / 776	Chr 17
5	0.32	7 / 700	Chr 12
6	0.34	8 / 833	Chr 19
7	0.40	4 / 403	Chr 14
8	0.49	11 / 1325	Chr 1
9	0.55	4 / 492	Chr 9
10	0.58	2 / 242	Chr 13
11	0.64	4 / 548	Chr 16
12	0.65	4 / 554	Chr 5
13	0.69	4 / 585	Chr 7
14	0.77	1 / 184	Chr 18
15	0.80	5 / 832	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−09	18 / 432	monocytes peripheral blood_3_TxFlnk
2	4e−06	47 / 3223	monocytes peripheral blood_6_EnhG
3	1e−05	39 / 2507	Mid_Frontal_Lobe_ReprPC
4	1e−05	30 / 1676	Fetal_TxTrans
5	3e−04	40 / 3001	Bcells peripheral blood_14_ReprPCWk
6	2e−03	15 / 827	Tcells peripheral blood_10_TssBiv
7	2e−03	71 / 7078	7_Enh_ESC_Mesoderm
8	3e−03	79 / 8200	monocytes peripheral blood_2_TssAFlnk
9	3e−03	34 / 2724	Tcells peripheral blood_11_BivFlnk
10	3e−03	21 / 1405	4_TxTrans_MSC_Adipocyte
11	3e−03	24 / 1700	Bcells peripheral blood_11_BivFlnk
12	4e−03	34 / 2747	Bcells peripheral blood_12_EnhBiv
13	4e−03	36 / 2972	13_ReprPC_ESC_Endoderm
14	4e−03	37 / 3110	14_ReprPCWk_ESC_Endoderm
15	6e−03	28 / 2203	EnhA_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−17	31 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	6e−08	14 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	1e−06	9 / 132	Marisa_CRC−cluster−a
4	2e−05	20 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
5	2e−05	11 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
6	6e−05	13 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
7	4e−04	4 / 43	Marisa_CRC−cluster−f
8	3e−03	2 / 10	Budinska_E_Mixed_UP
9	5e−03	2 / 13	Budinska_B_Lower crypt−like_DOWN
10	2e−02	1 / 2	Budinska_D_Mesenchymal_DOWN
11	2e−02	7 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
12	2e−02	15 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	3e−02	6 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	4e−02	2 / 38	Marisa_CRC−cluster−e
15	5e−02	4 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP

Glioma

Rank	p−value	#in/all	Geneset
1	2e−23	33 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	6e−18	22 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
3	3e−13	19 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	3e−06	11 / 242	ScoV_0.5_Sturm_C1_IDH_DN
5	4e−05	3 / 9	Colman_survival_robust
6	5e−05	10 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
7	2e−04	4 / 35	Colman_survival_associated
8	2e−04	3 / 14	Donson−chemokines/cytokines−associated with LTS in HGA
9	1e−03	5 / 99	GIEZELT_GBM_WT_up_VS_mut
10	2e−03	3 / 30	KIM prognostic signature LTS vs. STS
11	3e−03	2 / 11	KIM amplified & overexpressed in LTS
12	5e−03	2 / 13	Mukasa_UP_in_Astroglioma
13	5e−03	3 / 45	Donson−innate immunity−associated with LTS in HGA
14	1e−02	4 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
15	2e−02	3 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−25	33 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
2	2e−19	27 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
3	5e−18	27 / 404	RUTELLA_RESPONSE_TO_HGF_UP
4	1e−14	19 / 223	MCLACHLAN_DENTAL_CARIES_UP
5	1e−14	21 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
6	7e−14	16 / 154	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
7	1e−12	17 / 219	MCLACHLAN_DENTAL_CARIES_DN
8	2e−12	13 / 104	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
9	5e−11	14 / 166	VERHAAK_AML_WITH_NPM1_MUTATED_UP
10	6e−11	15 / 202	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
11	6e−11	23 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
12	1e−10	14 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
13	1e−10	18 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
14	2e−10	28 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
15	3e−10	18 / 354	RODWELL_AGING_KIDNEY_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−12	16 / 187	HALLMARK_INFLAMMATORY_RESPONSE
2	7e−09	12 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	3e−06	10 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
4	8e−06	9 / 170	HALLMARK_IL2_STAT5_SIGNALING
5	3e−05	8 / 150	HALLMARK_APOPTOSIS
6	3e−05	6 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
7	1e−04	8 / 188	HALLMARK_HYPOXIA
8	2e−04	8 / 194	HALLMARK_KRAS_SIGNALING_UP
9	5e−03	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	1e−02	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
11	1e−02	5 / 178	HALLMARK_COMPLEMENT
12	1e−02	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
13	2e−02	5 / 191	HALLMARK_P53_PATHWAY
14	4e−02	3 / 97	HALLMARK_PEROXISOME
15	5e−02	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Immunome

Rank	p−value	#in/all	Geneset
1	3e−07	5 / 19	Angelova_immune−metagene−iDC
2	1e−04	4 / 32	Angelova_immune−metagene−effector_memory_CD8
3	3e−04	4 / 42	Angelova_immune−metagene−TGD
4	5e−03	3 / 45	Angelova_immune−metagene−MDSC
5	2e−02	3 / 67	Angelova_immune−metagene−T−cells
6	8e−02	1 / 10	Angelova_immune−metagene−neutrophils
7	1e−01	1 / 13	Angelova_immune−metagene−immature_B−cells
8	1e−01	1 / 18	Angelova_immune−metagene−pDC
9	1e−01	1 / 18	Angelova_CRC_immunostimulators
10	2e−01	1 / 23	Angelova_immune−metagene−monocytes
11	2e−01	1 / 23	Angelova_immune−metagene−Treg
12	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
13	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
14	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
15	1e+00	0 / 21	Angelova_immune−metagene−central_memory_CD4

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	2 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	0.013	3 / 62	DUMEAUX_Smoking enriched genes
3	0.039	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	0.077	1 / 10	DUMEAUX_Smoking literature genes up
5	0.161	1 / 22	DUMEAUX_High bmi enriched genes
6	0.234	3 / 210	Homuth_BMI−associated−genes_DN
7	0.336	2 / 150	Homuth_BMI−associated−genes_UP
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
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 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.000	0 / 12	DUMEAUX_Women normal BMI literature genes up
13	1.000	0 / 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	9e−10	8 / 41	ROSOLOWSKI_blue DOWN
2	3e−08	8 / 62	Monti_Host_response_cluster
3	7e−08	9 / 97	ROSOLOWSKI_red total
4	1e−04	4 / 33	Care_Extended T−cell
5	8e−04	10 / 378	TARTE_Mature plasma cell signature
6	9e−03	4 / 102	ROSOLOWSKI_blue total
7	1e−02	36 / 3168	HOPP_Repressed
8	2e−02	2 / 26	DAVE_Immune response 1
9	3e−02	5 / 214	LENZ_Stromal signature 1
10	3e−02	53 / 5404	HOPP_Strong_enhancer
11	3e−02	3 / 85	Sha_DLBCL UP
12	4e−02	22 / 1894	HOPP_Poised_promoter
13	5e−02	1 / 7	CARO_OxPhos_vs_BCR_UP
14	6e−02	6 / 353	SPANG_CD40 6hrs DN
15	7e−02	2 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−22	18 / 78	Tirosh_expression higher in CAFs than in T−cells
2	3e−16	14 / 71	Tirosh_Macrophage specific genes−melanoma
3	1e−06	10 / 171	Landsberg_dedifferentiation_up
4	4e−05	14 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	6e−05	6 / 85	Tirosh_AXL−signature
6	1e−04	8 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
7	3e−02	3 / 83	TCGA_melanoma_immune_high
8	4e−02	2 / 38	Hugo_melanoma−BRAFmut−MET_UP
9	4e−02	1 / 5	Joensson_Melanoma Proliferative subtype
10	6e−02	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
11	8e−02	4 / 204	Landsberg_dedifferentiation_down
12	8e−02	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
13	9e−02	2 / 65	Harbst_melanoma_highgrade_up
14	1e−01	1 / 17	Hugo_melanoma−all−MET_UP
15	2e−01	3 / 189	Tirosh_genes preferentially expressed by Tregs

MF

Rank	p−value	#in/all	Geneset
1	5e−04	7 / 173	cytokine activity
2	5e−04	3 / 20	chemokine receptor activity
3	2e−03	11 / 500	signal transducer activity
4	3e−03	2 / 10	diacylglycerol binding
5	3e−03	2 / 10	glutamate binding
6	3e−03	4 / 77	peptidase inhibitor activity
7	3e−03	2 / 11	glucose transmembrane transporter activity
8	4e−03	3 / 39	chemokine activity
9	4e−03	6 / 191	transmembrane signaling receptor activity
10	6e−03	2 / 15	phosphatidic acid binding
11	6e−03	8 / 346	receptor binding
12	6e−03	7 / 276	GTP binding
13	7e−03	2 / 16	CCR chemokine receptor binding
14	7e−03	6 / 214	GTPase activity
15	8e−03	3 / 51	G−protein coupled receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	5 / 128	hsa−miR−200b
2	0.008	4 / 99	hsa−miR−543
3	0.017	4 / 123	hsa−miR−338−5p
4	0.017	4 / 123	hsa−miR−429
5	0.017	4 / 123	hsa−miR−200c
6	0.020	3 / 72	hsa−miR−339−5p
7	0.020	5 / 197	hsa−miR−122
8	0.024	3 / 78	hsa−miR−216b
9	0.031	2 / 35	hsa−miR−331−5p
10	0.033	2 / 36	hsa−miR−412
11	0.040	4 / 162	hsa−miR−641
12	0.048	2 / 44	hsa−miR−629
13	0.050	2 / 45	hsa−miR−891b
14	0.050	2 / 45	hsa−miR−431
15	0.055	3 / 108	hsa−miR−421

Pneumonia

Rank	p−value	#in/all	Geneset
1	5e−07	9 / 122	Terre_IMS_influenza_meta_signature
2	1e−06	9 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	9e−05	5 / 57	Burnham_viral_UP
4	8e−04	4 / 52	Burnham_day1_vs_5_DN
5	3e−02	2 / 37	Sweeney_viral_up
6	6e−02	2 / 48	Burnham_viral_DN
7	7e−02	2 / 56	Burnham_sep_vs_con_DN
8	8e−02	2 / 57	Burnham_day1_vs_5_UP
9	1e−01	2 / 71	Burnham_cap_fp_vs_con_UP
10	1e−01	1 / 18	Scicluna_UP
11	2e−01	1 / 33	Sweeney_viral_dn
12	3e−01	1 / 48	Burnham_cap_fp_vs_con_DN
13	4e−01	1 / 54	Burnham_timecourse
14	4e−01	1 / 68	Burnham_sep_vs_con_UP
15	1e+00	0 / 41	Scicluna_DN

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−13	13 / 99	Chaussabel_1,5_Myeloid lineage
2	8e−09	10 / 102	WIRTH_EBV B−cells
3	7e−08	12 / 204	Chaussabel_3,2_Inflammation I
4	2e−05	6 / 72	Chaussabel_3,1_Interferon−inducible
5	3e−05	7 / 109	Chaussabel_2,6_Myeloid lineage
6	3e−03	6 / 182	WIRTH_post GC B−cells
7	1e−02	3 / 59	Chaussabel_2,10_Immune related cell surface molecules
8	2e−02	5 / 198	Chaussabel_3,3_Inflammation II
9	5e−02	1 / 6	VAQUERIZAS_Appendix_TF
10	9e−02	2 / 62	VAQUERIZAS_Lung_TF
11	1e−01	1 / 13	WIRTH_Sec. lymphoid organs
12	1e−01	1 / 13	WIRTH_Prim. lymphoid organs
13	1e−01	1 / 17	VAQUERIZAS_Pancreas_TF
14	1e−01	1 / 18	JONGENEEL_Monocytes
15	2e−01	1 / 22	VAQUERIZAS_Trachea_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	0.04	36 / 3435	ICGC_Ebfsc137065_targets
2	0.04	15 / 1148	HEBENSTREIT_low expression TF
3	0.04	34 / 3213	ICGC_Pu1_targets
4	0.07	13 / 1041	ICGC_P300_targets
5	0.12	23 / 2254	ICGC_BatfPcr1_targets
6	0.19	37 / 4072	ICGC_Mta3_targets
7	0.21	43 / 4851	ICGC_Runx3_targets
8	0.21	22 / 2321	ICGC_Rad21_targets
9	0.22	15 / 1508	ICGC_Mef2_targets
10	0.28	32 / 3630	ICGC_Sp1_targets
11	0.29	37 / 4264	ICGC_Pax5_targets
12	0.34	31 / 3608	ICGC_Tcf12_targets
13	0.35	19 / 2150	ICGC_Irf4_targets
14	0.37	32 / 3769	ICGC_Pmlsc71910_targets
15	0.37	32 / 3778	ICGC_Pol24_targets

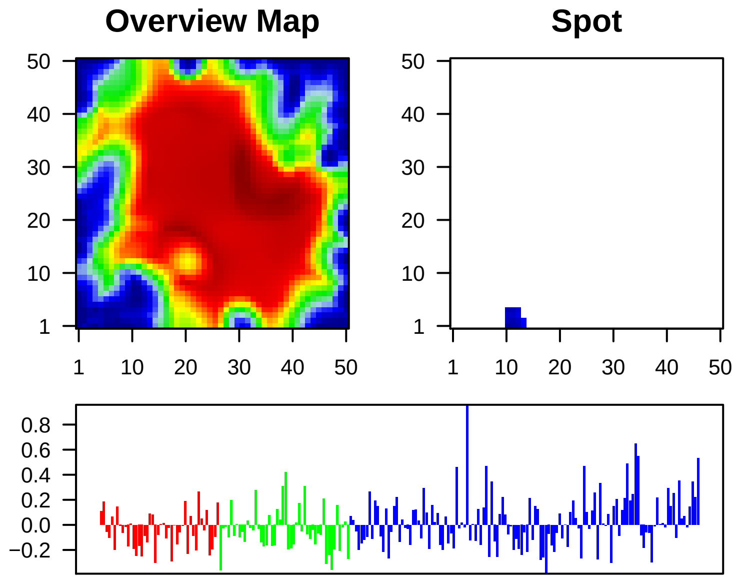
Underexpression Spots

Spot Summary: e

metagenes = 14
genes = 196

<r> metagenes = 0.97
<r> genes = 0.26
beta: r2= 8.07 / log p= −Inf

samples with spot = 27 (12.2 %)
mBL : 7 (15.9 %)
intermediate : 6 (12.5 %)
non−mBL : 14 (10.9 %)

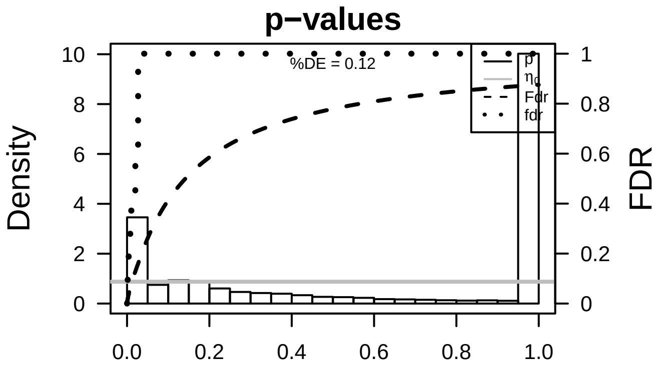


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	201162_at	0.97	−2.42	0.59	IGFBP7	insulin like growth factor binding protein 7 [Source:HGNC Sym
2	211964_at	0.99	−1.95	0.75	COL4A2	collagen type IV alpha 2 chain [Source:HGNC Symbol;Acc:H
3	201417_at	1.12	−1.92	0.34	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
4	211959_at	1.24	−1.84	0.47	IGFBP5	insulin like growth factor binding protein 5 [Source:HGNC Sym
5	211340_s_at	0.82	−1.74	0.48	MCAM	melanoma cell adhesion molecule [Source:HGNC Symbol;Ac
6	209070_s_at	1.53	−1.73	0.31	RGS5	regulator of G protein signaling 5 [Source:HGNC Symbol;Acc
7	210095_s_at	1	−1.72	0.48	IGFBP3	insulin like growth factor binding protein 3 [Source:HGNC Sym
8	212097_at	1.17	−1.71	0.54	CAV1	caveolin 1 [Source:HGNC Symbol;Acc:HGNC:1527]
9	202291_s_at	1.19	−1.55	0.46	MGP	matrix Gla protein [Source:HGNC Symbol;Acc:HGNC:7060]
10	200770_s_at	0.92	−1.52	0.42	LAMC1	laminin subunit gamma 1 [Source:HGNC Symbol;Acc:HGNC:
11	201508_at	1.26	−1.52	0.53	IGFBP4	insulin like growth factor binding protein 4 [Source:HGNC Sym
12	204396_s_at	1.01	−1.49	0.26	GRK5	G protein−coupled receptor kinase 5 [Source:HGNC Symbol;
13	212158_at	1.62	−1.46	0.53	SDC2	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
14	204168_at	1.11	−1.43	0.38	MGST2	microsomal glutathione S−transferase 2 [Source:HGNC Symb
15	214953_s_at	1.08	−1.42	0.37	APP	amyloid beta precursor protein [Source:HGNC Symbol;Acc:H
16	212012_at	1.4	−1.37	0.53	PXDN	peroxidasin [Source:HGNC Symbol;Acc:HGNC:14966]
17	204254_s_at	1.05	−1.36	0.36	VDR	vitamin D receptor [Source:HGNC Symbol;Acc:HGNC:12679]
18	217975_at	0.97	−1.36	0.45	TCEAL9	transcription elongation factor A like 9 [Source:HGNC Symbol
19	202771_at	1.11	−1.34	0.27	PIEZO1	piezo type mechanosensitive ion channel component 1 [Sour
20	201110_s_at	1.28	−1.34	0.66	THBS1	thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−36	39 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	4e−30	44 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
3	1e−29	56 / 747	GSEA	NABA_MATRISOME
4	1e−28	34 / 212	CC	extracellular matrix
5	1e−28	40 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
6	2e−28	33 / 197	GSEA	NABA_CORE_MATRISOME
7	8e−27	48 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
8	1e−25	61 / 1090	CC	extracellular space
9	6e−25	78 / 1894	Lymph	HOPP_Poised_promoter
10	1e−24	42 / 480	Cance	Lembcke_Colonic Inflammation
11	8e−24	37 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
12	1e−23	3 / 14	Cance	LIU_PROSTATE_CANCER_DN
13	1e−23	3 / 14	Cance	LIU_PROSTATE_CANCER_DN
14	2e−22	69 / 1611	CC	extracellular region
15	2e−22	36 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
16	6e−22	96 / 3168	Lymph	HOPP_Repressed
17	7e−21	30 / 262	GSEA	PASINI_SUZ12_TARGETS_DN
18	3e−20	29 / 253	CC	proteinaceous extracellular matrix
19	6e−20	27 / 214	Lymph	LENZ_Stromal signature 1
20	1e−19	25 / 178	GSEA	WU_CELL_MIGRATION
21	1e−19	38 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
22	4e−19	19 / 85	Gliom	ScoV_0.999_Sturm_E2_IDH_DN
23	8e−19	22 / 136	GSEA	NABA_ECM_GLYCOPROTEINS
24	1e−18	24 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
25	3e−18	29 / 297	Colon	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
26	4e−18	32 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
27	2e−17	31 / 374	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
28	5e−17	48 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
29	3e−16	31 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
30	3e−16	25 / 247	GSEA	BOQUEST_STEM_CELL_UP
31	3e−16	24 / 223	BP	angiogenesis
32	3e−16	20 / 138	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
33	6e−16	22 / 183	BP	extracellular matrix organization
34	1e−15	33 / 497	Melan	Gerber_wt/wt_melanoma−cells−SpotD
35	1e−15	26 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
36	1e−15	33 / 500	BP	cell adhesion
37	2e−15	14 / 53	Lymph	LENZ_Stromal signature 2
38	2e−15	24 / 241	CC	endoplasmic reticulum lumen
39	2e−15	14 / 54	GSEA	CROONQUIST_STROMAL_STIMULATION_UP
40	5e−15	24 / 251	GSEA	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.002	6 / 107	HORVATH_aging_genes meth UP
2	0.312	2 / 92	HORVATH_aging_genes meth DOWN
3	1.000	0 / 47	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

CC

Rank	p−value	#in/all	Geneset
1	1e−28	34 / 212	extracellular matrix
2	1e−25	61 / 1090	extracellular space
3	2e−22	69 / 1611	extracellular region
4	3e−20	29 / 253	proteinaceous extracellular matrix
5	2e−15	24 / 241	endoplasmic reticulum lumen
6	2e−12	28 / 462	cell surface
7	4e−10	11 / 66	basement membrane
8	1e−09	21 / 345	focal adhesion
9	2e−07	69 / 3210	plasma membrane
10	6e−07	53 / 2239	extracellular exosome
11	1e−06	8 / 65	collagen trimer
12	1e−05	7 / 63	platelet alpha granule lumen
13	4e−05	7 / 75	apical part of cell
14	8e−05	7 / 84	Golgi lumen
15	3e−04	6 / 74	secretory granule

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−18	29 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
2	5e−17	48 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	1e−15	26 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	5e−09	12 / 103	Marisa_CRC−cluster−b
5	8e−09	13 / 132	Marisa_CRC−cluster−a
6	2e−04	3 / 10	Budinska_E_Mixed_UP
7	3e−04	11 / 255	Kosinski_top−crypt−long−list
8	1e−03	8 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	2e−03	3 / 20	Kosinski_top−crypt−short−list
10	2e−03	11 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
11	6e−03	3 / 31	Kosinski_lower−crypt−short−list
12	8e−03	2 / 11	Kaneda_CIMP−group2
13	2e−02	7 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	3e−02	9 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
15	6e−02	7 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−36	39 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	2e−10	15 / 141	HALLMARK_UV_RESPONSE_DN
3	1e−09	16 / 188	HALLMARK_HYPOXIA
4	9e−08	14 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	1e−07	7 / 34	HALLMARK_ANGIOGENESIS
6	6e−07	11 / 130	HALLMARK_COAGULATION
7	2e−06	11 / 150	HALLMARK_APOPTOSIS
8	3e−05	11 / 194	HALLMARK_MYOGENESIS
9	8e−05	7 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
10	4e−04	5 / 51	HALLMARK_TGF_BETA_SIGNALING
11	4e−04	9 / 182	HALLMARK_GLYCOLYSIS
12	6e−04	9 / 194	HALLMARK_KRAS_SIGNALING_UP
13	2e−03	8 / 187	HALLMARK_INFLAMMATORY_RESPONSE
14	5e−03	3 / 29	HALLMARK_NOTCH_SIGNALING
15	6e−03	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−25	78 / 1894	HOPP_Poised_promoter
2	6e−22	96 / 3168	HOPP_Repressed
3	6e−20	27 / 214	LENZ_Stromal signature 1
4	2e−15	14 / 53	LENZ_Stromal signature 2
5	1e−06	9 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
6	2e−05	8 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
7	5e−05	6 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
8	6e−05	15 / 378	TARTE_Mature plasma cell signature
9	1e−04	8 / 118	Subero_INT_hyper_meth
10	1e−04	8 / 121	ROSOLOWSKI_green total
11	2e−04	8 / 132	Subero_DLBCL_hyper_meth
12	3e−04	45 / 2206	HOPP_Heterochrom
13	2e−03	5 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
14	5e−03	5 / 88	ROSOLOWSKI_green UP
15	8e−03	8 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	8 / 129	hsa−miR−29a
2	3e−04	8 / 135	hsa−miR−29c
3	6e−04	11 / 278	hsa−let−7d
4	1e−03	8 / 166	hsa−miR−29b
5	2e−03	9 / 235	hsa−let−7f
6	4e−03	9 / 251	hsa−let−7g
7	4e−03	9 / 257	hsa−let−7i
8	5e−03	9 / 261	hsa−let−7a
9	5e−03	4 / 57	hsa−miR−876−3p
10	7e−03	6 / 136	hsa−miR−511
11	7e−03	10 / 329	hsa−let−7b
12	8e−03	4 / 64	hsa−miR−562
13	1e−02	8 / 244	hsa−miR−98
14	1e−02	5 / 108	hsa−miR−421
15	1e−02	6 / 151	hsa−miR−1283

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−16	24 / 223	angiogenesis
2	6e−16	22 / 183	extracellular matrix organization
3	1e−15	33 / 500	cell adhesion
4	2e−11	24 / 368	negative regulation of cell proliferation
5	2e−10	14 / 121	positive regulation of angiogenesis
6	8e−09	15 / 185	cellular protein metabolic process
7	1e−08	7 / 25	endodermal cell differentiation
8	3e−08	9 / 58	collagen catabolic process
9	1e−06	12 / 169	response to lipopolysaccharide
10	6e−06	14 / 271	post−translational protein modification
11	6e−06	9 / 107	response to oxidative stress
12	7e−06	5 / 23	artery morphogenesis
13	8e−06	9 / 110	platelet degranulation
14	1e−05	4 / 12	positive regulation of peptidase activity
15	1e−05	7 / 62	extracellular matrix disassembly

Chr

Rank	p−value	#in/all	Geneset
1	0.007	6 / 139	Chr 21
2	0.015	12 / 480	Chr 4
3	0.046	9 / 382	Chr 15
4	0.056	12 / 585	Chr 7
5	0.078	6 / 242	Chr 13
6	0.090	9 / 437	Chr 8
7	0.194	20 / 1325	Chr 1
8	0.444	11 / 832	Chr 2
9	0.475	5 / 369	Chr 20
10	0.492	9 / 700	Chr 12
11	0.512	7 / 548	Chr 16
12	0.554	5 / 403	Chr 14
13	0.680	6 / 554	Chr 5
14	0.720	7 / 669	Chr 6
15	0.727	5 / 492	Chr 9

Glioma

Rank	p−value	#in/all	Geneset
1	4e−19	19 / 85	ScoV_0.999_Sturm_E2_IDH_DN
2	2e−12	22 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
3	3e−09	17 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
4	6e−09	23 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
5	2e−06	11 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	9e−06	13 / 242	ScoV_0.5_Sturm_C1_IDH_DN
7	1e−05	9 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
8	3e−05	8 / 99	GIEZELT_GBM_WT_up_VS_mut
9	4e−05	9 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
10	6e−05	7 / 82	laffaire_hypermeth_LGG_vs_control
11	7e−05	8 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
12	1e−04	6 / 64	cultured astroglia vs. in vivo astrocytes
13	2e−04	6 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
14	2e−04	3 / 10	Phillips MES up vs Prolif & PN
15	5e−04	3 / 13	Mukasa_UP_in_Astroglioma

Immunome

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 11	Angelova_immune−metagene−macrophages
2	2e−02	2 / 19	Angelova_immune−metagene−iDC
3	3e−02	2 / 21	Angelova_immune−metagene−central_memory_CD4
4	8e−02	2 / 38	Angelova_immune−metagene−mast−cells
5	2e−01	1 / 15	Angelova_immune−metagene−NK
6	2e−01	2 / 67	Angelova_immune−metagene−T−cells
7	2e−01	1 / 18	Angelova_CRC_immunostimulators
8	2e−01	1 / 23	Angelova_immune−metagene−Th2
9	3e−01	1 / 25	Angelova_immune−metagene−DC
10	4e−01	1 / 42	Angelova_immune−metagene−TGD
11	4e−01	1 / 45	Angelova_immune−metagene−MDSC
12	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells
13	1e+00	0 / 26	Angelova_immune−metagene−activated_CD4
14	1e+00	0 / 19	Angelova_immune−metagene−activated_CD8
15	1e+00	0 / 17	Angelova_immune−metagene−central_memory_CD8

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−15	33 / 497	Gerber_wt/wt_melanoma−cells−SpotD
2	3e−14	15 / 78	Tirosh_CAF−cell specific genes
3	3e−07	9 / 75	Tirosh_Endothelial−cell specific genes−melanoma
4	8e−05	7 / 85	Tirosh_AXL−signature
5	1e−04	5 / 41	Tirosh_top50 correlated genes PC3
6	1e−02	3 / 37	Hugo_melanoma−all−MET_DN
7	3e−02	6 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	2e−01	4 / 171	Landsberg_dedifferentiation_up
9	2e−01	5 / 236	Gerber_wt/wt_group3−specific
10	2e−01	3 / 119	TCGA_melanoma_MITF_low
11	2e−01	5 / 249	Gerber_wt/wt_melanoma−cells−SpotE
12	3e−01	1 / 24	Gerami_melanoma−metastatic−risk_DN
13	3e−01	2 / 81	Tirosh_Genes in the MITF program
14	4e−01	1 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	5e−01	3 / 204	Landsberg_dedifferentiation_down

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.08	4 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.12	2 / 48	Burnham_viral_DN
3	0.34	1 / 33	Sweeney_viral_dn
4	0.78	1 / 122	Terre_IMS_influenza_meta_signature
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 / 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 / 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

TF

Rank	p−value	#in/all	Geneset
1	1e−06	34 / 1148	HEBENSTREIT_low expression TF
2	1e−01	35 / 2321	ICGC_Rad21_targets
3	5e−01	13 / 1041	ICGC_P300_targets
4	6e−01	12 / 1032	ICGC_Usf1_targets
5	6e−01	19 / 1636	ICGC_Bcl11_targets
6	7e−01	15 / 1387	HEBENSTREIT_high expression TF
7	8e−01	4 / 415	ICGC_RxraPcr1_targets
8	8e−01	24 / 2254	ICGC_BatfPcr1_targets
9	8e−01	12 / 1241	KIM_MYC targets
10	9e−01	4 / 485	ICGC_NrsfPcr2_targets
11	9e−01	4 / 522	ICGC_SrfPcr2_targets
12	9e−01	14 / 1508	ICGC_Mef2_targets
13	9e−01	21 / 2150	ICGC_Irf4_targets
14	9e−01	34 / 3435	ICGC_Ebfsc137065_targets
15	1e+00	43 / 4264	ICGC_Pax5_targets

Cancer

Rank	p−value	#in/all	Geneset
1	1e−24	42 / 480	Lembcke_Colonic Inflammation
2	1e−23	3 / 14	LIU_PROSTATE_CANCER_DN
3	5e−04	3 / 13	GENTLES_modul17
4	1e−03	3 / 18	PanCan_Notch_geneset_nanostring
5	3e−03	4 / 47	PanCan_TGF−B_geneset_nanostring
6	1e−02	2 / 14	GENTLES_modul13
7	3e−02	6 / 187	PanCan_PI3K_geneset_nanostring
8	3e−02	4 / 96	PanCan_TXmisReg_geneset_nanostring
9	8e−02	4 / 134	PanCan_RAS_geneset_nanostring
10	1e−01	4 / 147	PanCan_MAPK_geneset_nanostring
11	1e−01	1 / 11	LIU_PROSTATE_CANCER_UP
12	1e−01	8 / 409	Lembcke_Normal vs Adenoma
13	1e−01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	2e−01	1 / 15	RHODES_CANCER_META_SIGNATURE
15	2e−01	1 / 14	GUSTAFSON_PI3K_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−34	105 / 2765	Tregulatory cells peripheral blood_13_ReprPC
2	4e−33	119 / 3724	Tcells peripheral blood_12_EnhBiv
3	4e−31	99 / 2602	natural killer cells peripheral blood_12_EnhBiv
4	1e−30	101 / 2747	Bcells peripheral blood_12_EnhBiv
5	6e−30	96 / 2515	natural killer cells peripheral blood_13_ReprPC
6	7e−30	94 / 2405	Bcells peripheral blood_13_ReprPC
7	8e−30	90 / 2194	Thelper cells peripheral blood_12_EnhBiv
8	1e−29	115 / 3734	Tcells peripheral blood_13_ReprPC
9	5e−29	79 / 1694	Thelper cells peripheral blood_11_BivFlnk
10	7e−28	97 / 2724	Tcells peripheral blood_11_BivFlnk
11	3e−27	86 / 2154	Tregulatory cells peripheral blood_11_BivFlnk
12	3e−25	83 / 2134	Tregulatory cells peripheral blood_12_EnhBiv
13	7e−25	74 / 1700	Bcells peripheral blood_11_BivFlnk
14	2e−24	97 / 3001	Bcells peripheral blood_14_ReprPCWk
15	2e−23	98 / 3150	monocytes peripheral blood_13_ReprPC

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−30	44 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
2	1e−29	56 / 747	NABA_MATRISOME
3	1e−28	40 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
4	2e−28	33 / 197	NABA_CORE_MATRISOME
5	8e−27	48 / 589	WONG_ADULT_TISSUE_STEM_MODULE
6	8e−24	37 / 366	LIM_MAMMARY_STEM_CELL_UP
7	1e−23	3 / 14	LIU_PROSTATE_CANCER_DN
8	2e−22	36 / 376	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
9	7e−21	30 / 262	PASINI_SUZ12_TARGETS_DN
10	1e−19	25 / 178	WU_CELL_MIGRATION
11	1e−19	38 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
12	8e−19	22 / 136	NABA_ECM_GLYCOPROTEINS
13	1e−18	24 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
14	4e−18	32 / 381	SWEET_LUNG_CANCER_KRAS_DN
15	2e−17	31 / 374	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	2 / 10	DUMEAUX_Smoking literature genes up
2	0.048	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
3	0.138	1 / 12	DUMEAUX_Women normal BMI literature genes up
4	0.159	1 / 14	Huan_blood−pressure_SBP−signature
5	0.327	1 / 32	Marjolein_ageing−genes_DN
6	0.478	3 / 210	Homuth_BMI−associated−genes_DN
7	0.536	1 / 62	DUMEAUX_Smoking enriched genes
8	0.845	1 / 150	Homuth_BMI−associated−genes_UP
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 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.000	0 / 22	DUMEAUX_High bmi enriched genes
15	1.000	0 / 22	DUMEAUX_Fasting enriched genes

MF

Rank	p−value	#in/all	Geneset
1	1e−08	9 / 53	extracellular matrix structural constituent
2	2e−08	24 / 517	calcium ion binding
3	1e−07	6 / 20	insulin−like growth factor binding
4	3e−07	7 / 37	growth factor binding
5	1e−06	12 / 173	cytokine activity
6	3e−06	5 / 19	fibronectin binding
7	7e−06	4 / 11	peptidase activator activity
8	9e−06	5 / 24	extracellular matrix binding
9	1e−05	4 / 12	insulin−like growth factor I binding
10	5e−05	8 / 106	integrin binding
11	6e−05	9 / 141	growth factor activity
12	1e−04	5 / 39	chemokine activity
13	2e−04	8 / 126	heparin binding
14	3e−04	3 / 11	platelet−derived growth factor binding
15	4e−04	3 / 12	proteoglycan binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−04	11 / 233	PROTEINATLAS_smooth muscle
2	5e−04	3 / 13	WIRTH_Sec. lymphoid organs
3	9e−04	9 / 204	Chaussabel_3,2_Inflammation I
4	1e−03	5 / 62	VAQUERIZAS_Lung_TF
5	1e−03	9 / 209	Chaussabel_2,5_Immune related molecules
6	3e−03	2 / 7	VAQUERIZAS_Tongue_TF
7	3e−03	5 / 81	Chaussabel_1,2_Platelets
8	6e−03	3 / 30	VAQUERIZAS_Fetal lung_TF
9	1e−02	3 / 36	VAQUERIZAS_Prostate_TF
10	1e−02	2 / 13	VAQUERIZAS_Skin_TF
11	1e−02	3 / 41	VAQUERIZAS_Thyroid_TF
12	1e−02	2 / 15	WIRTH_Telencephalon
13	2e−02	2 / 16	VAQUERIZAS_Fetal thyroid_TF
14	2e−02	3 / 45	VAQUERIZAS_Placenta_TF
15	3e−02	10 / 399	PROTEINATLAS_soft tissue

Underexpression Spots

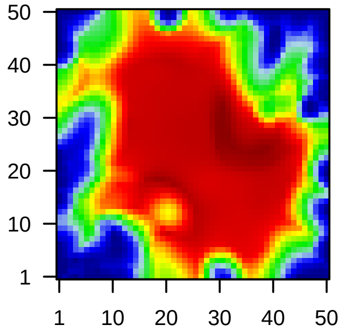
Spot Summary: f

metagenes = 34
genes = 642

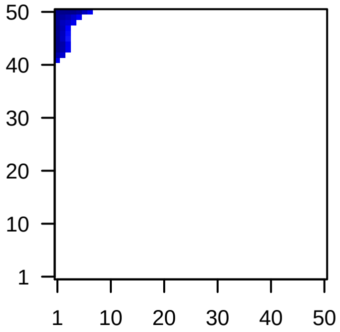
<r> metagenes = 0.86
<r> genes = 0.28
beta: r2= 9.99 / log p= −Inf

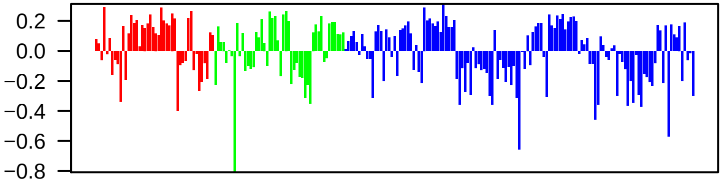
samples with spot = 36 (16.3 %)
mBL : 4 (9.1 %)
intermediate : 6 (12.5 %)
non−mBL : 26 (20.2 %)

Overview Map



Spot





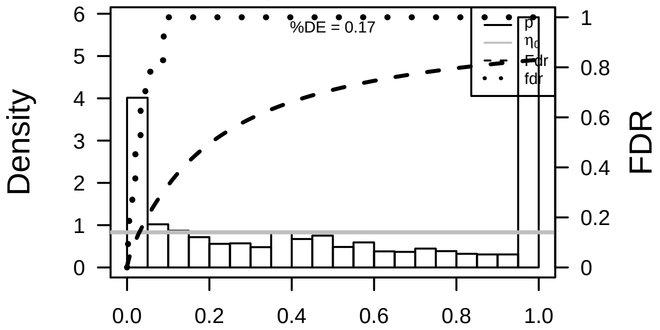
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	201123_s_at	0.97	−3.26	0.25	EIF5A	eukaryotic translation initiation factor 5A [Source:HGNC Syml
2	203028_s_at	0.55	−3.25	0.38	CYBA	cytochrome b−245 alpha chain [Source:HGNC Symbol;Acc:H
3	208621_s_at	0.88	−2.79	0.75	EZR	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
4	215780_s_at	0.45	−2.56	0.44		SET pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:4292
5	200796_s_at	1	−2.53	0.8	MCL1	MCL1, BCL2 family apoptosis regulator [Source:HGNC Symb
6	212574_x_at	0.78	−2.52	0.63	TMEM259	transmembrane protein 259 [Source:HGNC Symbol;Acc:HGN
7	205321_at	0.83	−2.48	0.55	EIF2S3B	eukaryotic translation initiation factor 2 subunit gamma B [Sou
8	212316_at	0.68	−2.48	0.49	NUP210	nucleoporin 210 [Source:HGNC Symbol;Acc:HGNC:30052]
9	203109_at	0.88	−2.48	0.52	UBE2M	ubiquitin conjugating enzyme E2 M [Source:HGNC Symbol;A
10	210978_s_at	0.57	−2.39	0.67	TAGLN2	transgelin 2 [Source:HGNC Symbol;Acc:HGNC:11554]
11	205049_s_at	0.63	−2.38	0.21	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
12	212107_s_at	0.51	−2.36	0.79	DHX9	DExH−box helicase 9 [Source:HGNC Symbol;Acc:HGNC:275
13	217211_at	0.85	−2.33	0.59		actin, beta pseudogene 9 [Source:HGNC Symbol;Acc:HGNC
14	201101_s_at	0.52	−2.3	0.77		BCL2 associated transcription factor 1 pseudogene 2 [Source
15	204152_s_at	0.83	−2.18	0.58	MFNG	MFNG O−fucosylpeptide 3−beta−N−acetylglucosaminyltransf
16	213887_s_at	0.37	−2.16	0.61	POLR2E	RNA polymerase II subunit E [Source:HGNC Symbol;Acc:HG
17	211090_s_at	0.39	−2.14	0.66	PRPF4B	pre−mRNA processing factor 4B [Source:HGNC Symbol;Acc:
18	208930_s_at	0.49	−2.12	0.67	ILF3	interleukin enhancer binding factor 3 [Source:HGNC Symbol;
19	213606_s_at	1	−2.09	0.69	ARHGDIA	Rho GDP dissociation inhibitor alpha [Source:HGNC Symbol;
20	200922_at	0.94	−2.04	0.49	KDELR1	KDEL endoplasmic reticulum protein retention receptor 1 [Sou

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−89	118 / 282	Gliom	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	3e−63	370 / 4261	Lympl	HOPP_Txn_transition
3	4e−61	422 / 5529	Lympl	HOPP_Txn_elongation
4	1e−58	69 / 136	Refer	Chaussabel_2,9_Cytosceleton
5	1e−45	92 / 372	GSEA	SENESE_HDAC1_TARGETS_UP
6	7e−39	88 / 405	GSEA	SENESE_HDAC3_TARGETS_UP
7	2e−37	81 / 355	Refer	WIRTH_Immune system
8	6e−33	366 / 5404	Lympl	HOPP_Strong_enhancer
9	8e−27	143 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	2e−26	372 / 5908	Lympl	HOPP_Active_promoter
11	1e−23	66 / 376	GSEA	GARY_CD5_TARGETS_UP
12	9e−23	62 / 344	GSEA	THUM_SYSTOLIC_HEART_FAILURE_UP
13	3e−22	80 / 564	GSEA	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
14	4e−21	264 / 3805	CC	cytosol
15	6e−21	144 / 1550	GSEA	PILON_KLF1_TARGETS_DN
16	1e−20	86 / 678	Refer	PROTEINATLAS_lymph node
17	8e−20	152 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
18	8e−18	368 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
19	2e−17	242 / 3564	TF	ICGC_Taf1_targets
20	3e−17	134 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
21	3e−16	99 / 989	Refer	PROTEINATLAS_tonsil
22	5e−16	27 / 92	GSEA	SENESE_HDAC2_TARGETS_UP
23	2e−15	117 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
24	1e−14	286 / 4701	CC	cytoplasm
25	1e−14	213 / 3150	TF	ICGC_Creb1_targets
26	1e−14	44 / 272	GSEA	LIU_SOX4_TARGETS_DN
27	4e−14	416 / 7864	MF	protein binding
28	5e−14	60 / 485	GSEA	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
29	1e−13	35 / 189	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
30	2e−13	63 / 539	GSEA	PARENT_MTOR_SIGNALING_UP
31	2e−13	325 / 5682	Lympl	HOPP_Weak_promoter
32	3e−13	64 / 560	GSEA	MARTINEZ_RB1_TARGETS_UP
33	5e−13	239 / 3804	TF	ICGC_Stat5_targets
34	6e−13	206 / 3121	TF	ICGC_Egr1_targets
35	6e−13	46 / 328	GSEA	OSMAN_BLADDER_CANCER_UP
36	7e−13	238 / 3796	TF	ICGC_Nficsc81335_targets
37	1e−12	82 / 848	Refer	PROTEINATLAS_adrenal gland
38	2e−12	29 / 146	GSEA	ELVIDGE_HYPOXIA_DN
39	4e−12	234 / 3769	TF	ICGC_Pmlsc71910_targets
40	5e−12	57 / 496	Refer	PROTEINATLAS_spleen

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 107	HORVATH_aging_genes meth UP
2	0.8	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	4e−21	264 / 3805	cytosol
2	1e−14	286 / 4701	cytoplasm
3	9e−12	270 / 4579	nucleus
4	4e−11	171 / 2541	nucleoplasm
5	2e−07	46 / 479	Golgi membrane
6	5e−07	72 / 938	Golgi apparatus
7	3e−06	39 / 416	macromolecular complex
8	3e−05	32 / 345	focal adhesion
9	3e−05	22 / 196	nuclear membrane
10	5e−05	10 / 51	endoplasmic reticulum−Golgi intermediate compartment
11	1e−04	27 / 292	microtubule organizing center
12	1e−04	29 / 326	nuclear speck
13	1e−04	10 / 58	phagocytic vesicle membrane
14	2e−04	41 / 537	perinuclear region of cytoplasm
15	2e−04	17 / 149	nuclear envelope

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−20	152 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
2	8e−18	368 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
3	7e−09	101 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	1e−08	85 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
5	8e−07	84 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
6	4e−06	64 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
7	2e−05	79 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
8	2e−04	58 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
9	2e−03	59 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
10	2e−03	4 / 14	TCGA_Mutated−in−CRC_hypermutated
11	1e−02	52 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	2e−02	33 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	3e−02	32 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	6e−02	2 / 10	KIM_CRC−MSI−regulated_DN
15	8e−02	2 / 11	KIM_MSI−in−CRC

HM

Rank	p−value	#in/all	Geneset
1	2e−08	26 / 173	HALLMARK_MITOTIC_SPINDLE
2	2e−06	16 / 94	HALLMARK_PROTEIN_SECRETION
3	7e−06	23 / 192	HALLMARK_MTORC1_SIGNALING
4	3e−05	22 / 195	HALLMARK_G2M_CHECKPOINT
5	2e−04	17 / 149	HALLMARK_UV_RESPONSE_UP
6	8e−04	9 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	2e−03	12 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	7e−03	10 / 96	HALLMARK_ANDROGEN_RESPONSE
9	2e−02	14 / 174	HALLMARK_APICAL_JUNCTION
10	2e−02	9 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	3e−02	12 / 150	HALLMARK_APOPTOSIS
12	4e−02	14 / 193	HALLMARK_HEME_METABOLISM
13	8e−02	10 / 141	HALLMARK_UV_RESPONSE_DN
14	1e−01	12 / 187	HALLMARK_E2F_TARGETS
15	1e−01	4 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY

Lympnoma

Rank	p−value	#in/all	Geneset
1	3e−63	370 / 4261	HOPP_Txn_transition
2	4e−61	422 / 5529	HOPP_Txn_elongation
3	6e−33	366 / 5404	HOPP_Strong_enhancer
4	2e−26	372 / 5908	HOPP_Active_promoter
5	2e−13	325 / 5682	HOPP_Weak_promoter
6	4e−08	39 / 353	SPANG_CD40 6hrs DN
7	1e−06	17 / 102	ROSOLOWSKI_blue total
8	2e−06	11 / 45	Monti_BCR_cluster
9	4e−06	70 / 955	SPANG_BCR UP
10	2e−05	65 / 906	SPANG_BCR DN
11	1e−04	22 / 213	SPANG_IL21 DN
12	5e−04	221 / 4357	HOPP_Weak_txn
13	6e−04	14 / 121	ROSOLOWSKI_green total
14	2e−03	4 / 14	YAMANE_AICDA_targets_recruited
15	5e−03	23 / 305	TARTE_Plasmablast signature

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−09	23 / 127	hsa−miR−1297
2	1e−08	25 / 157	hsa−miR−206
3	1e−08	41 / 364	hsa−miR−548n
4	2e−08	31 / 234	hsa−miR−570
5	3e−08	28 / 202	hsa−miR−26b
6	3e−08	33 / 267	hsa−miR−142−5p
7	4e−08	27 / 193	hsa−miR−26a
8	6e−08	38 / 344	hsa−miR−19a
9	6e−08	23 / 148	hsa−miR−1
10	9e−08	19 / 106	hsa−miR−223
11	1e−07	17 / 88	hsa−miR−613
12	2e−07	44 / 448	hsa−miR−20b
13	2e−07	23 / 157	hsa−miR−34b
14	3e−07	38 / 368	hsa−miR−301a
15	4e−07	27 / 216	hsa−miR−548l

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	7e−09	51 / 507	protein phosphorylation
2	4e−08	49 / 502	protein transport
3	2e−07	52 / 576	phosphorylation
4	1e−06	12 / 51	retrograde transport, endosome to Golgi
5	5e−06	9 / 32	regulation of cholesterol biosynthetic process
6	6e−06	15 / 91	mRNA transport
7	2e−05	18 / 136	ER to Golgi vesicle−mediated transport
8	2e−05	22 / 190	vesicle−mediated transport
9	2e−05	11 / 56	negative regulation of translation
10	3e−05	6 / 16	myeloid dendritic cell differentiation
11	3e−05	41 / 497	cell cycle
12	4e−05	26 / 260	chromatin organization
13	6e−05	12 / 74	regulation of mitotic cell cycle
14	6e−05	13 / 86	mRNA export from nucleus
15	9e−05	10 / 55	response to cytokine

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	55 / 833	Chr 19
2	1e−02	46 / 776	Chr 17
3	3e−02	43 / 756	Chr 11
4	2e−01	34 / 669	Chr 6
5	2e−01	8 / 139	Chr 21
6	3e−01	61 / 1325	Chr 1
7	3e−01	38 / 832	Chr 2
8	5e−01	16 / 369	Chr 20
9	5e−01	25 / 585	Chr 7
10	5e−01	17 / 403	Chr 14
11	6e−01	20 / 480	Chr 4
12	6e−01	23 / 554	Chr 5
13	7e−01	7 / 184	Chr 18
14	7e−01	21 / 548	Chr 16
15	7e−01	27 / 700	Chr 12

Glioma

Rank	p−value	#in/all	Geneset
1	8e−89	118 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−11	109 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	1e−11	15 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
4	5e−10	114 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−04	46 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
6	8e−04	15 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	7e−03	8 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	7e−03	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	2e−02	8 / 78	Weller_LGG_A_vs_O_UP
10	2e−02	6 / 50	Vishal_subnetwork signature of survival in GBM
11	2e−02	7 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
12	3e−02	6 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
13	3e−02	7 / 71	Weller_LGG_1p19qDel−vs−intact_DOWN
14	4e−02	18 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
15	6e−02	8 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB

Immunome

Rank	p−value	#in/all	Geneset
1	0.01	6 / 45	Angelova_immune−metagene−MDSC
2	0.06	6 / 67	Angelova_immune−metagene−T−cells
3	0.10	2 / 13	Angelova_immune−metagene−immature_B−cells
4	0.35	1 / 10	Angelova_immune−metagene−neutrophils
5	0.35	1 / 10	Angelova_immune−metagene−TFH
6	0.35	1 / 10	Angelova_CRC_immonoinhibitors
7	0.45	1 / 14	Angelova_immune−metagene−eosinophil
8	0.48	1 / 15	Angelova_immune−metagene−NK
9	0.52	1 / 17	Angelova_immune−metagene−central_memory_CD8
10	0.54	1 / 18	Angelova_immune−metagene−pDC
11	0.56	1 / 19	Angelova_immune−metagene−activated_CD8
12	0.56	1 / 19	Angelova_immune−metagene−iDC
13	0.63	1 / 23	Angelova_immune−metagene−Treg
14	0.68	1 / 26	Angelova_immune−metagene−activated_CD4
15	0.72	1 / 29	Angelova_immune−metagene−Th1

Melanoma

Rank	p−value	#in/all	Geneset
1	0.009	18 / 230	Gerber_wt/wt_melanoma−cells−SpotC
2	0.012	18 / 236	Gerber_wt/wt_group3−specific
3	0.012	15 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
4	0.015	4 / 23	Melanoma Epi−Enzyme Cluster 7
5	0.020	6 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	0.027	16 / 222	Gerber_wt/wt_melanoma−cells−SpotF
7	0.050	29 / 497	Gerber_wt/wt_melanoma−cells−SpotD
8	0.079	3 / 24	Tirosh_B−cell specific genes−melanoma
9	0.083	1 / 2	Melanoma Epi−Enzyme Cluster 1
10	0.094	4 / 41	Tirosh_top50 correlated genes PC3
11	0.129	4 / 46	Tirosh_top50 correlated genes PC5
12	0.137	4 / 47	Tirosh_G2/M phase specific genes
13	0.168	7 / 107	Tirosh_Exhaustion program in Mel75
14	0.172	14 / 249	Gerber_wt/wt_melanoma−cells−SpotE
15	0.217	3 / 38	Hugo_melanoma−BRAFmut−MET_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	14 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.06	10 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.40	3 / 54	Burnham_timecourse
4	0.44	3 / 57	Burnham_day1_vs_5_UP
5	0.59	5 / 122	Terre_IMS_influenza_meta_signature
6	0.61	2 / 48	Burnham_viral_DN
7	0.79	2 / 68	Burnham_sep_vs_con_UP
8	0.83	1 / 41	Scicluna_DN
9	0.95	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	2e−17	242 / 3564	ICGC_Taf1_targets
2	1e−14	213 / 3150	ICGC_Creb1_targets
3	5e−13	239 / 3804	ICGC_Stat5_targets
4	6e−13	206 / 3121	ICGC_Egr1_targets
5	7e−13	238 / 3796	ICGC_Nficsc81335_targets
6	4e−12	234 / 3769	ICGC_Pmlsc71910_targets
7	1e−11	217 / 3451	ICGC_Atf2_targets
8	6e−11	188 / 2899	ICGC_Nfatc1_targets
9	2e−10	242 / 4072	ICGC_Mta3_targets
10	3e−10	224 / 3703	ICGC_Foxm1_targets
11	4e−10	210 / 3420	ICGC_Bclaf101388_targets
12	6e−10	249 / 4278	ICGC_Yy1_targets
13	2e−09	89 / 1107	ICGC_Myc_targets
14	2e−09	217 / 3630	ICGC_Sp1_targets
15	5e−09	247 / 4319	ICGC_Pou2_targets

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	5 / 15	GENTLES_modul2
2	1e−03	15 / 147	PanCan_MAPK_geneset_nanostring
3	2e−03	2 / 2	GENTLES_modul8
4	3e−03	13 / 130	PanCan_CC+Apop_geneset_nanostring
5	4e−03	13 / 134	PanCan_RAS_geneset_nanostring
6	8e−03	11 / 113	PanCan_Driver_Gene_geneset_nanostring
7	1e−02	3 / 11	LIU_PROSTATE_CANCER_UP
8	2e−02	3 / 14	BENTINK_src.2
9	8e−02	19 / 317	SPANG_BCL6−index2
10	9e−02	2 / 12	GENTLES_modul12
11	1e−01	5 / 58	SHAUGHNESSY_MM high risk
12	1e−01	2 / 14	GENTLES_modul10
13	1e−01	2 / 15	GENTLES_modul4
14	1e−01	1 / 14	LIU_COMMON_CANCER_GENES
15	1e−01	2 / 16	GENTLES_modul16

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−80	456 / 5716	Bcells peripheral blood_4_Tx
2	8e−80	448 / 5527	Tregulatory cells peripheral blood_4_Tx
3	7e−74	462 / 6099	HSC_4_Tx
4	4e−73	448 / 5753	Tcells peripheral blood_4_Tx
5	4e−72	504 / 7420	Tcells peripheral blood_1_TssA
6	1e−70	444 / 5738	monocytes peripheral blood_4_Tx
7	2e−69	513 / 7833	Bcells peripheral blood_1_TssA
8	4e−69	443 / 5766	natural killer cells peripheral blood_4_Tx
9	5e−69	391 / 4528	T CD8+ naive cells peripheral blood_4_Tx
10	3e−67	434 / 5601	Thelper cells peripheral blood_4_Tx
11	1e−66	504 / 7635	monocytes peripheral blood_1_TssA
12	6e−63	354 / 3938	Thelper cells peripheral blood_6_EnhG
13	1e−62	512 / 8068	Thelper cells peripheral blood_1_TssA
14	1e−61	483 / 7165	Tx_Colon
15	2e−61	520 / 8406	Bcells peripheral blood_2_TssAFlnk

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−45	92 / 372	SENESE_HDAC1_TARGETS_UP
2	7e−39	88 / 405	SENESE_HDAC3_TARGETS_UP
3	8e−27	143 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	1e−23	66 / 376	GARY_CD5_TARGETS_UP
5	9e−23	62 / 344	THUM_SYSTOLIC_HEART_FAILURE_UP
6	3e−22	80 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
7	6e−21	144 / 1550	PILON_KLF1_TARGETS_DN
8	3e−17	134 / 1527	PUJANA_BRCA1_PCC_NETWORK
9	5e−16	27 / 92	SENESE_HDAC2_TARGETS_UP
10	2e−15	117 / 1312	PUJANA_ATM_PCC_NETWORK
11	1e−14	44 / 272	LIU_SOX4_TARGETS_DN
12	5e−14	60 / 485	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
13	1e−13	35 / 189	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
14	2e−13	63 / 539	PARENT_MTOR_SIGNALING_UP
15	3e−13	64 / 560	MARTINEZ_RB1_TARGETS_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−05	22 / 210	Homuth_BMI−associated−genes_DN
2	1e−02	4 / 22	DUMEAUX_Fasting enriched genes
3	1e−01	10 / 150	Homuth_BMI−associated−genes_UP
4	1e−01	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	5e−01	1 / 14	Huan_blood−pressure_SBP−signature
6	6e−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	4e−14	416 / 7864	protein binding
2	1e−11	112 / 1402	nucleotide binding
3	5e−09	39 / 328	chromatin binding
4	2e−08	38 / 331	protein serine/threonine kinase activity
5	4e−08	32 / 256	cadherin binding
6	5e−08	89 / 1185	ATP binding
7	2e−07	52 / 573	kinase activity
8	6e−07	42 / 437	protein kinase activity
9	1e−06	92 / 1329	transferase activity
10	4e−06	25 / 214	GTPase activity
11	6e−06	29 / 276	GTP binding
12	1e−05	25 / 225	transcription coactivator activity
13	2e−05	8 / 29	Rho GTPase binding
14	3e−05	78 / 1161	RNA binding
15	4e−05	11 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−58	69 / 136	Chaussabel_2,9_Cytosceleton
2	2e−37	81 / 355	WIRTH_Immune system
3	1e−20	86 / 678	PROTEINATLAS_lymph node
4	3e−16	99 / 989	PROTEINATLAS_tonsil
5	1e−12	82 / 848	PROTEINATLAS_adrenal gland
6	5e−12	57 / 496	PROTEINATLAS_spleen
7	5e−11	69 / 708	PROTEINATLAS_thyroid gland
8	7e−11	88 / 1022	PROTEINATLAS_placenta
9	8e−11	75 / 809	PROTEINATLAS_fallopian tube
10	9e−11	69 / 716	PROTEINATLAS_epididymis
11	2e−10	95 / 1161	PROTEINATLAS_colon
12	5e−10	89 / 1076	PROTEINATLAS_stomach
13	6e−10	87 / 1048	PROTEINATLAS_gallbladder
14	6e−10	87 / 1048	PROTEINATLAS_rectum
15	8e−10	70 / 770	PROTEINATLAS_endometrium

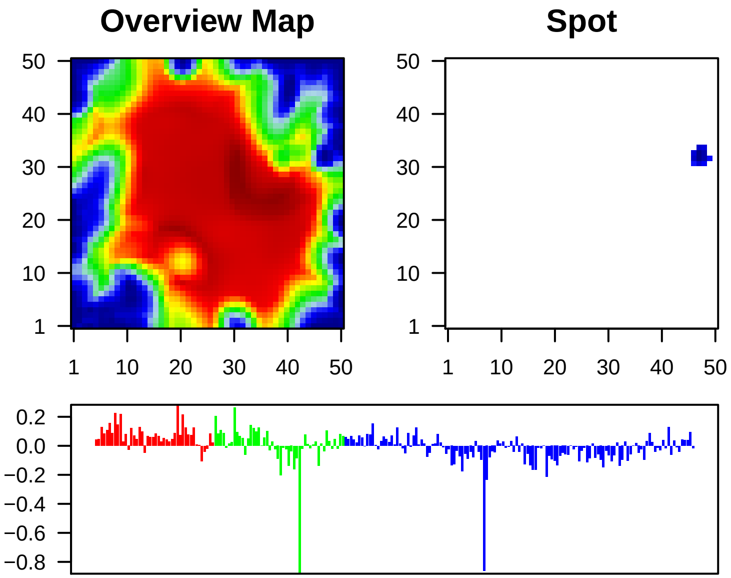
Underexpression Spots

Spot Summary: g

metagenes = 12
genes = 157

<r> metagenes = 0.98
<r> genes = 0.29
beta: r2= 2.63 / log p= −Inf

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

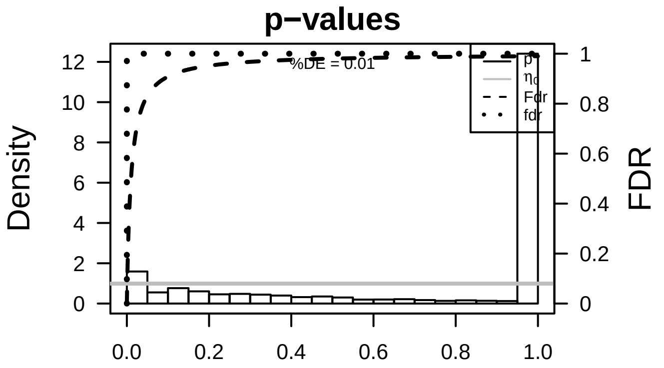


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202131_s_at	0.77	−2.26	0.47	RIOK3	RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]
2	218871_x_at	0.95	−2.17	0.56	CSGALNACT2	chondroitin sulfate N−acetylgalactosaminyltransferase 2 [Sou
3	203347_s_at	0.52	−2.02	0.66	MTF2	metal response element binding transcription factor 2 [Source
4	213000_at	0.73	−1.94	0.54	MORC3	MORC family CW−type zinc finger 3 [Source:HGNC Symbol;
5	212367_at	0.75	−1.84	0.52	FEM1B	fem−1 homolog B [Source:HGNC Symbol;Acc:HGNC:3649]
6	204314_s_at	0.45	−1.81	0.45	CREB1	cAMP responsive element binding protein 1 [Source:HGNC S
7	203132_at	0.45	−1.75	0.48	RB1	RB transcriptional corepressor 1 [Source:HGNC Symbol;Acc:
8	212476_at	0.43	−1.64	0.56	ACAP2	ArfGAP with coiled−coil, ankyrin repeat and PH domains 2 [S
9	203203_s_at	0.49	−1.61	0.74	KRR1	KRR1, small subunit processome component homolog [Sourc
10	218043_s_at	0.66	−1.56	0.58	AZI2	5−azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:
11	218172_s_at	0.61	−1.55	0.6	DERL1	derlin 1 [Source:HGNC Symbol;Acc:HGNC:28454]
12	205091_x_at	0.57	−1.53	0.64	RECQL	RecQ like helicase [Source:HGNC Symbol;Acc:HGNC:9948]
13	212920_at	0.43	−1.52	0.67	REST	RE1 silencing transcription factor [Source:HGNC Symbol;Acc
14	202314_at	0.96	−1.51	0.38	CYP51A1	cytochrome P450 family 51 subfamily A member 1 [Source:H
15	204299_at	0.6	−1.48	0.72	SRSF10	serine and arginine rich splicing factor 10 [Source:HGNC Syn
16	209023_s_at	0.52	−1.48	0.66	STAG2	stromal antigen 2 [Source:HGNC Symbol;Acc:HGNC:11355]
17	218538_s_at	0.64	−1.48	0.5	MRS2	MRS2, magnesium transporter [Source:HGNC Symbol;Acc:H
18	201409_s_at	0.39	−1.43	0.65	PPP1CB	protein phosphatase 1 catalytic subunit beta [Source:HGNC S
19	222182_s_at	0.59	−1.42	0.46	CNOT2	CCR4−NOT transcription complex subunit 2 [Source:HGNC S
20	201407_s_at	0.45	−1.4	0.77	PPP1CB	protein phosphatase 1 catalytic subunit beta [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−35	43 / 310	Refer	Chaussabel_3,4_Protein phosphatases
2	1e−28	129 / 5529	Lympl	HOPP_Txn_elongation
3	3e−26	130 / 5908	Lympl	HOPP_Active_promoter
4	1e−17	43 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	5e−17	34 / 516	GSEA	HAMAI_APOPTOSIS_VIA_TRAIL_UP
6	7e−17	38 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
7	6e−15	23 / 245	Refer	Chaussabel_3,9_Kinases
8	3e−13	109 / 5682	Lympl	HOPP_Weak_promoter
9	3e−13	92 / 4261	Lympl	HOPP_Txn_transition
10	8e−13	47 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	2e−11	31 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
12	5e−11	15 / 139	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
13	6e−11	24 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
14	1e−10	23 / 398	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
15	8e−10	89 / 4579	CC	nucleus
16	1e−09	23 / 442	GSEA	KIM_WT1_TARGETS_DN
17	1e−09	61 / 2541	CC	nucleoplasm
18	5e−09	13 / 137	GSEA	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
19	1e−08	17 / 269	GSEA	JOHNSTONE_PARVB_TARGETS_2_DN
20	2e−08	43 / 1550	GSEA	PILON_KLF1_TARGETS_DN
21	2e−08	34 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
22	3e−08	17 / 284	miRN	hsa−miR−548d−5p
23	4e−08	18 / 327	GSEA	ZHANG_BREAST_CANCER_PROGENITORS_UP
24	4e−08	39 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
25	5e−08	82 / 4357	Lympl	HOPP_Weak_txn
26	8e−08	13 / 172	GSEA	BROWNE_HCMV_INFECTION_18HR_UP
27	2e−07	8 / 54	miRN	hsa−miR−628−3p
28	5e−07	36 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
29	5e−07	32 / 1089	TF	ICGC_Ets1_targets
30	7e−07	8 / 65	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
31	8e−07	25 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
32	8e−07	17 / 361	GSEA	GARY_CD5_TARGETS_DN
33	9e−07	39 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
34	9e−07	15 / 285	miRN	hsa−miR−548b−5p
35	1e−06	29 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
36	2e−06	19 / 468	GSEA	ENK_UV_RESPONSE_KERATINOCYTE_DN
37	2e−06	19 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
38	2e−06	12 / 189	GSEA	BIDUS_METASTASIS_UP
39	2e−06	13 / 225	MF	transcription coactivator activity
40	2e−06	36 / 1390	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN



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	8e−10	89 / 4579	nucleus
2	1e−09	61 / 2541	nucleoplasm
3	1e−05	4 / 13	COPII vesicle coat
4	7e−05	77 / 4701	cytoplasm
5	4e−04	8 / 157	spindle
6	6e−04	6 / 90	nuclear matrix
7	2e−03	3 / 21	nuclear euchromatin
8	2e−03	60 / 3805	cytosol
9	3e−03	4 / 51	ER to Golgi transport vesicle membrane
10	3e−03	3 / 25	condensed chromosome
11	4e−03	3 / 27	mediator complex
12	6e−03	5 / 100	chromatin
13	7e−03	6 / 149	nuclear envelope
14	7e−03	7 / 196	nuclear membrane
15	7e−03	3 / 35	nuclear inner membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−08	39 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	8e−06	31 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	2e−04	24 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
4	4e−04	3 / 13	Vilar_hypermutated−in−CRC
5	5e−04	3 / 14	TCGA_Mutated−in−CRC_non−hypermutated
6	5e−04	15 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
7	7e−04	3 / 16	Vilar_mutated−in−CRC−CamP
8	7e−04	3 / 16	Vilar_non−hypermutated−in−CRC
9	1e−03	34 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
10	7e−03	23 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	8e−03	2 / 12	Juehling_HNPCC−mutated−in−4
12	1e−02	2 / 14	TCGA_Mutated−in−CRC_hypermutated
13	2e−02	13 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
14	2e−02	1 / 2	Juehling_HNPCC−mutated−in−6−to−8
15	3e−02	16 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_

HM

Rank	p−value	#in/all	Geneset
1	1e−05	11 / 195	HALLMARK_G2M_CHECKPOINT
2	1e−01	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	2e−01	3 / 122	HALLMARK_SPERMATOGENESIS
4	2e−01	4 / 193	HALLMARK_HEME_METABOLISM
5	3e−01	2 / 97	HALLMARK_PEROXISOME
6	3e−01	3 / 173	HALLMARK_MITOTIC_SPINDLE
7	3e−01	3 / 174	HALLMARK_ADIPOGENESIS
8	4e−01	3 / 194	HALLMARK_MYOGENESIS
9	4e−01	3 / 194	HALLMARK_KRAS_SIGNALING_UP
10	4e−01	1 / 51	HALLMARK_TGF_BETA_SIGNALING
11	5e−01	1 / 55	HALLMARK_MYC_TARGETS_V2
12	5e−01	2 / 139	HALLMARK_FATTY_ACID_METABOLISM
13	5e−01	2 / 141	HALLMARK_UV_RESPONSE_DN
14	5e−01	1 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
15	5e−01	2 / 149	HALLMARK_UV_RESPONSE_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−28	129 / 5529	HOPP_Txn_elongation
2	3e−26	130 / 5908	HOPP_Active_promoter
3	3e−13	109 / 5682	HOPP_Weak_promoter
4	3e−13	92 / 4261	HOPP_Txn_transition
5	5e−08	82 / 4357	HOPP_Weak_txn
6	5e−06	79 / 4559	HOPP_Weak_enhancer
7	2e−04	84 / 5404	HOPP_Strong_enhancer
8	9e−04	6 / 97	ROSOLOWSKI_red total
9	1e−02	3 / 41	ROSOLOWSKI_blue DOWN
10	2e−02	7 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
11	2e−02	4 / 88	ROSOLOWSKI_green UP
12	3e−02	4 / 102	ROSOLOWSKI_blue total
13	5e−02	4 / 121	ROSOLOWSKI_green total
14	6e−02	7 / 305	TARTE_Plasmablast signature
15	8e−02	16 / 955	SPANG_BCR UP

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−08	17 / 284	hsa−miR−548d−5p
2	2e−07	8 / 54	hsa−miR−628−3p
3	9e−07	15 / 285	hsa−miR−548b−5p
4	2e−06	14 / 269	hsa−miR−548a−5p
5	3e−06	13 / 235	hsa−miR−30e
6	5e−06	16 / 368	hsa−miR−301a
7	9e−06	10 / 151	hsa−miR−1283
8	1e−05	12 / 223	hsa−miR−1244
9	1e−05	12 / 226	hsa−miR−548h
10	1e−05	9 / 126	hsa−miR−548o
11	2e−05	13 / 275	hsa−miR−590−3p
12	2e−05	8 / 99	hsa−miR−543
13	2e−05	15 / 364	hsa−miR−548n
14	3e−05	10 / 171	hsa−miR−203
15	3e−05	12 / 251	hsa−miR−548i

Telomeres

Rank	p−value	#in/all	Geneset
1	0.04	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−05	18 / 497	cell cycle
2	7e−05	38 / 1764	regulation of transcription, DNA−templated
3	9e−05	36 / 1655	transcription, DNA−templated
4	9e−05	17 / 520	positive regulation of transcription, DNA−templated
5	1e−04	5 / 43	androgen receptor signaling pathway
6	1e−04	6 / 69	chromatin remodeling
7	2e−04	5 / 46	regulation of circadian rhythm
8	2e−04	14 / 407	viral process
9	3e−04	17 / 569	regulation of transcription from RNA polymerase II promoter
10	3e−04	7 / 113	rhythmic process
11	4e−04	3 / 13	striated muscle cell differentiation
12	5e−04	3 / 14	intracellular steroid hormone receptor signaling pathway
13	6e−04	13 / 391	protein ubiquitination
14	1e−03	9 / 233	RNA splicing
15	2e−03	7 / 148	transcription initiation from RNA polymerase II promoter

Chr

Rank	p−value	#in/all	Geneset
1	0.06	6 / 242	Chr 13
2	0.07	11 / 585	Chr 7
3	0.09	8 / 403	Chr 14
4	0.11	12 / 700	Chr 12
5	0.17	11 / 689	Chr 3
6	0.18	8 / 480	Chr 4
7	0.19	9 / 556	Chr X
8	0.21	3 / 139	Chr 21
9	0.23	7 / 437	Chr 8
10	0.35	17 / 1325	Chr 1
11	0.36	9 / 669	Chr 6
12	0.44	5 / 382	Chr 15
13	0.45	7 / 554	Chr 5
14	0.48	10 / 832	Chr 2
15	0.63	2 / 184	Chr 18

Glioma

Rank	p−value	#in/all	Geneset
1	4e−05	35 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	4e−05	32 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	1e−04	12 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	1e−03	11 / 330	Up
5	2e−02	5 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	2e−02	3 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	4e−02	3 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	8e−02	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
9	3e−01	1 / 32	WIRTH_PN subtype
10	4e−01	1 / 43	Patel_stemness signatures
11	4e−01	8 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
12	4e−01	1 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
13	4e−01	1 / 47	developing astrocytes
14	5e−01	1 / 53	Christensen_hypermethylated_in_primary_glioblastoma
15	5e−01	1 / 58	Stuehler_Proteins_up_in_STS

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	Angelova_immune−metagene−effector_memory_CD4
2	0.2	1 / 21	Angelova_immune−metagene−central_memory_CD4
3	0.4	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 / 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

Melanoma

Rank	p−value	#in/all	Geneset
1	0.004	8 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.011	9 / 319	Gerber_wt/wt_melanoma−cells−SpotA
3	0.045	1 / 4	Melanoma Epi−Enzyme Cluster 3
4	0.049	6 / 230	Gerber_wt/wt_melanoma−cells−SpotC
5	0.210	8 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	0.285	4 / 236	Gerber_wt/wt_group3−specific
7	0.347	2 / 107	Tirosh_Exhaustion program in Mel75
8	0.398	1 / 44	Tirosh_top50 correlated genes PC2
9	0.544	1 / 68	Tirosh_housekeeping_genes
10	0.598	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
11	0.628	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
12	0.782	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
13	0.828	2 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	0.862	1 / 171	Landsberg_dedifferentiation_up
15	0.888	1 / 189	Tirosh_genes preferentially expressed by Tregs

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 54	Burnham_timecourse
2	0.4	1 / 41	Scicluna_DN
3	0.4	2 / 122	Terre_IMS_influenza_meta_signature
4	0.5	2 / 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	5e−07	32 / 1089	ICGC_Ets1_targets
2	4e−04	30 / 1387	HEBENSTREIT_high expression TF
3	3e−03	22 / 1025	ICGC_NrsfPcr1_targets
4	7e−03	55 / 3564	ICGC_Taf1_targets
5	7e−03	24 / 1241	KIM_MYC targets
6	1e−02	28 / 1578	ICGC_GabpPcr2_targets
7	2e−02	20 / 1044	ICGC_Six5_targets
8	2e−02	46 / 2994	ICGC_Zeb1_targets
9	2e−02	12 / 522	ICGC_SrfPcr2_targets
10	2e−02	10 / 415	ICGC_RxraPcr1_targets
11	2e−02	1 / 2	MYC_Chromatin_modification UP
12	4e−02	49 / 3420	ICGC_Bclaf101388_targets
13	5e−02	49 / 3451	ICGC_Atf2_targets
14	5e−02	24 / 1494	ICGC_Cebpbsc150_targets
15	5e−02	45 / 3150	ICGC_Creb1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 16	GENTLES_modul6
2	2e−03	6 / 113	PanCan_Driver_Gene_geneset_nanostring
3	8e−03	2 / 12	GENTLES_modul12
4	2e−02	1 / 2	GENTLES_modul8
5	6e−02	2 / 36	ZHANG_MM up
6	1e−01	1 / 11	GENTLES_modul14
7	1e−01	1 / 12	LIU_BREAST_CANCER
8	1e−01	1 / 13	GENTLES_modul1
9	1e−01	2 / 58	SHAUGHNESSY_MM high risk
10	1e−01	1 / 14	BENTINK_src.2
11	2e−01	1 / 15	RHODES_CANCER_META_SIGNATURE
12	2e−01	1 / 15	WANG_ER_UP
13	2e−01	1 / 15	BEN−PORATH_UP
14	2e−01	1 / 16	WOLFER_overlap genes
15	2e−01	3 / 130	PanCan_CC+Apop_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−32	134 / 5716	Bcells peripheral blood_4_Tx
2	2e−29	119 / 4528	T CD8+ naive cells peripheral blood_4_Tx
3	2e−29	135 / 6099	HSC_4_Tx
4	1e−28	131 / 5753	Tcells peripheral blood_4_Tx
5	4e−28	129 / 5601	Thelper cells peripheral blood_4_Tx
6	9e−27	137 / 6637	Tcells peripheral blood_5_TxWk
7	4e−26	126 / 5527	Tregulatory cells peripheral blood_4_Tx
8	4e−25	127 / 5738	monocytes peripheral blood_4_Tx
9	6e−25	127 / 5766	natural killer cells peripheral blood_4_Tx
10	3e−24	143 / 7751	natural killer cells peripheral blood_1_TssA
11	4e−24	142 / 7635	monocytes peripheral blood_1_TssA
12	1e−23	143 / 7833	Bcells peripheral blood_1_TssA
13	1e−23	140 / 7420	Tcells peripheral blood_1_TssA
14	2e−23	137 / 7078	Bcells peripheral blood_5_TxWk
15	3e−23	135 / 6839	T CD8+ naive cells peripheral blood_5_TxWk

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−17	43 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	5e−17	34 / 516	HAMAI_APOPTOSIS_VIA_TRAIL_UP
3	7e−17	38 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
4	8e−13	47 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	2e−11	31 / 673	SCHLOSSER_SERUM_RESPONSE_DN
6	5e−11	15 / 139	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
7	6e−11	24 / 417	SHEN_SMARCA2_TARGETS_UP
8	1e−10	23 / 398	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
9	1e−09	23 / 442	KIM_WT1_TARGETS_DN
10	5e−09	13 / 137	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_UP
11	1e−08	17 / 269	JOHNSTONE_PARVB_TARGETS_2_DN
12	2e−08	43 / 1550	PILON_KLF1_TARGETS_DN
13	2e−08	34 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	4e−08	18 / 327	ZHANG_BREAST_CANCER_PROGENITORS_UP
15	8e−08	13 / 172	BROWNE_HCMV_INFECTION_18HR_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	2 / 22	DUMEAUX_Fasting enriched genes
2	0.03	6 / 210	Homuth_BMI−associated−genes_DN
3	1.00	0 / 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 / 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

MF

Rank	p−value	#in/all	Geneset
1	2e−06	13 / 225	transcription coactivator activity
2	1e−05	115 / 7864	protein binding
3	6e−05	12 / 267	binding
4	3e−04	4 / 28	RNA polymerase II transcription cofactor activity
5	3e−04	5 / 53	transcription cofactor activity
6	4e−04	3 / 13	vitamin D receptor binding
7	4e−04	5 / 55	core promoter binding
8	4e−03	15 / 601	zinc ion binding
9	4e−03	19 / 852	nucleic acid binding
10	4e−03	10 / 328	chromatin binding
11	5e−03	4 / 60	RNA polymerase II distal enhancer sequence−specific DNA binding
12	6e−03	8 / 237	ubiquitin−protein transferase activity
13	6e−03	3 / 33	RNA polymerase II activating transcription factor binding
14	7e−03	2 / 11	cAMP response element binding
15	7e−03	2 / 11	transcription factor activity, RNA polymerase II transcription factor binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−35	43 / 310	Chaussabel_3,4_Protein phosphatases
2	6e−15	23 / 245	Chaussabel_3,9_Kinases
3	8e−04	12 / 355	WIRTH_Immune system
4	9e−04	5 / 66	VAQUERIZAS_Whole blood_TF
5	1e−03	23 / 1022	PROTEINATLAS_placenta
6	2e−03	6 / 113	Chaussabel_1,8_Metabolism Biosynthesis
7	4e−03	5 / 93	Chaussabel_1,4_Replication
8	5e−03	6 / 136	Chaussabel_2,9_Cytosceleton
9	1e−02	3 / 40	VAQUERIZAS_Testis_TF
10	1e−02	15 / 677	PROTEINATLAS_esophagus
11	3e−02	5 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
12	3e−02	4 / 106	Chaussabel_2,11_Replication
13	4e−02	19 / 1076	PROTEINATLAS_stomach
14	4e−02	9 / 399	PROTEINATLAS_soft tissue
15	4e−02	13 / 671	PROTEINATLAS_cervix, uterine

Underexpression Spots

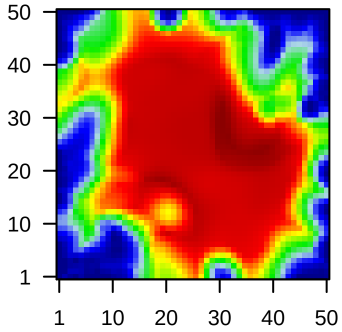
Spot Summary: h

metagenes = 9
genes = 169

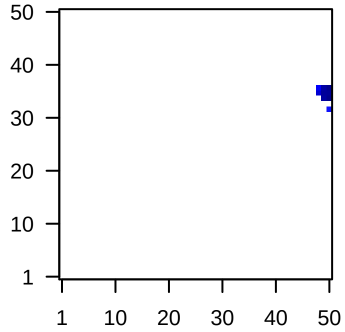
<r> metagenes = 0.97
<r> genes = 0.27
beta: r2= 4.06 / log p= −Inf

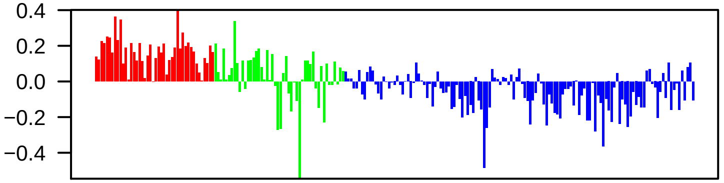
samples with spot = 18 (8.1 %)
intermediate : 4 (8.3 %)
non−mBL : 14 (10.9 %)

Overview Map



Spot





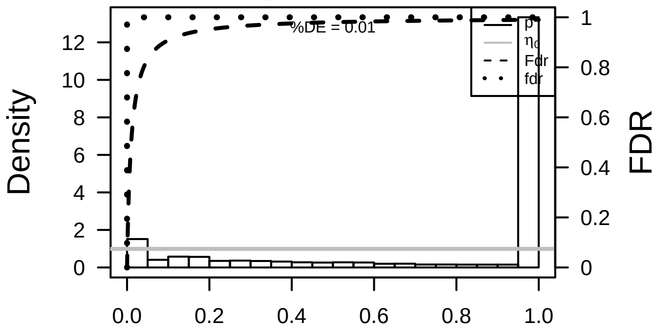
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202762_at	0.76	−1.8	0.44	ROCK2	Rho associated coiled−coil containing protein kinase 2 [Sourc
2	213489_at	1.67	−1.75	0.35	MAPRE2	microtubule associated protein RP/EB family member 2 [Sour
3	222119_s_at	0.67	−1.75	0.6	FBXO11	F−box protein 11 [Source:HGNC Symbol;Acc:HGNC:13590]
4	218230_at	0.56	−1.74	0.46	ARFIP1	ADP ribosylation factor interacting protein 1 [Source:HGNC S
5	212061_at	0.8	−1.69	0.7	U2SURP	U2 snRNP associated SURP domain containing [Source:HGN
6	218545_at	0.59	−1.64	0.43	CCDC91	coiled−coil domain containing 91 [Source:HGNC Symbol;Acc
7	219487_at	0.87	−1.58	0.64	BBS10	Bardet−Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGN
8	204061_at	0.9	−1.56	0.41	PRKX	protein kinase, X−linked [Source:HGNC Symbol;Acc:HGNC:
9	209884_s_at	0.69	−1.56	0.48	SLC4A7	solute carrier family 4 member 7 [Source:HGNC Symbol;Acc:
10	213416_at	1.01	−1.54	0.48		
11	212930_at	0.86	−1.51	0.45	ATP2B1	ATPase plasma membrane Ca2+ transporting 1 [Source:HGN
12	203992_s_at	0.98	−1.5	0.3	KDM6A	lysine demethylase 6A [Source:HGNC Symbol;Acc:HGNC:12
13	221193_s_at	0.65	−1.49	0.72	ZCCHC10	zinc finger CCHC−type containing 10 [Source:HGNC Symbol
14	213074_at	0.67	−1.47	0.5	PHIP	pleckstrin homology domain interacting protein [Source:HGN
15	218352_at	0.9	−1.45	0.62	RCBTB1	RCC1 and BTB domain containing protein 1 [Source:HGNC
16	218197_s_at	0.87	−1.44	0.46	OXR1	oxidation resistance 1 [Source:HGNC Symbol;Acc:HGNC:15
17	218568_at	0.79	−1.42	0.37	AGK	acylglycerol kinase [Source:HGNC Symbol;Acc:HGNC:2186
18	202969_at	0.95	−1.41	0.52	DYRK2	dual specificity tyrosine phosphorylation regulated kinase 2 [
19	203302_at	0.56	−1.4	0.67	DCK	deoxycytidine kinase [Source:HGNC Symbol;Acc:HGNC:270
20	212934_at	0.47	−1.39	0.55	UBXN2B	UBX domain protein 2B [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−27	37 / 310	Refer	Chaussabel_3,4_Protein phosphatases
2	5e−27	129 / 5529	Lympl	HOPP_Txn_elongation
3	1e−20	125 / 5908	Lympl	HOPP_Active_promoter
4	7e−17	117 / 5682	Lympl	HOPP_Weak_promoter
5	7e−16	30 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
6	1e−15	41 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
7	5e−13	93 / 4261	Lympl	HOPP_Txn_transition
8	5e−12	27 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
9	1e−11	26 / 448	miRN	hsa−miR−20b
10	1e−11	49 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
11	2e−11	91 / 4357	Lympl	HOPP_Weak_txn
12	3e−11	45 / 1343	Gliom	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
13	9e−11	48 / 1550	GSEA	PILON_KLF1_TARGETS_DN
14	1e−10	24 / 427	miRN	hsa−miR−17
15	1e−09	90 / 4559	Lympl	HOPP_Weak_enhancer
16	1e−09	24 / 474	miRN	hsa−miR−20a
17	4e−09	19 / 314	miRN	hsa−miR−372
18	9e−09	88 / 4579	CC	nucleus
19	1e−08	27 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
20	3e−08	16 / 245	Refer	Chaussabel_3,9_Kinases
21	5e−08	39 / 1338	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
22	5e−08	20 / 407	miRN	hsa−miR−106a
23	8e−08	27 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
24	1e−07	16 / 269	GSEA	JOHNSTONE_PARVB_TARGETS_2_DN
25	2e−07	15 / 248	miRN	hsa−miR−520c−3p
26	2e−07	16 / 285	miRN	hsa−miR−548b−5p
27	2e−07	19 / 403	miRN	hsa−miR−106b
28	2e−07	15 / 251	miRN	hsa−miR−548i
29	2e−07	11 / 126	miRN	hsa−miR−548o
30	4e−07	27 / 788	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
31	4e−07	17 / 336	miRN	hsa−miR−519d
32	4e−07	14 / 226	miRN	hsa−miR−302b
33	4e−07	14 / 226	miRN	hsa−miR−548h
34	4e−07	13 / 194	miRN	hsa−miR−520a−3p
35	5e−07	16 / 301	miRN	hsa−miR−519b−3p
36	6e−07	12 / 168	miRN	hsa−miR−33a
37	7e−07	19 / 435	miRN	hsa−miR−93
38	8e−07	15 / 275	miRN	hsa−miR−590−3p
39	1e−06	14 / 245	miRN	hsa−miR−302d
40	1e−06	15 / 284	miRN	hsa−miR−548d−5p

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	9e−09	88 / 4579	nucleus
2	6e−05	7 / 86	PML body
3	3e−04	48 / 2541	nucleoplasm
4	3e−04	4 / 29	histone deacetylase complex
5	4e−04	3 / 13	ESC/E(Z) complex
6	2e−03	11 / 326	nuclear speck
7	2e−03	5 / 73	ubiquitin ligase complex
8	8e−03	3 / 35	nuclear inner membrane
9	1e−02	2 / 15	phagophore assembly site membrane
10	2e−02	2 / 19	histone methyltransferase complex
11	2e−02	2 / 19	nuclear periphery
12	3e−02	6 / 196	nuclear membrane
13	3e−02	5 / 149	nuclear envelope
14	3e−02	2 / 24	heterochromatin
15	4e−02	2 / 27	mediator complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−06	41 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
2	5e−06	26 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
3	3e−05	33 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	3e−05	30 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
5	3e−04	5 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
6	5e−04	16 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
7	3e−03	20 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
8	9e−03	23 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	1e−02	14 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
10	1e−02	20 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
11	3e−02	18 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
12	4e−02	16 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	1e−01	9 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
14	2e−01	9 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
15	3e−01	2 / 83	Marisa_CRC−cluster−d

HM

Rank	p−value	#in/all	Geneset
1	0.02	6 / 190	HALLMARK_MYC_TARGETS_V1
2	0.03	6 / 195	HALLMARK_G2M_CHECKPOINT
3	0.07	5 / 187	HALLMARK_E2F_TARGETS
4	0.10	3 / 94	HALLMARK_PROTEIN_SECRETION
5	0.10	3 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.13	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.17	3 / 122	HALLMARK_SPERMATOGENESIS
8	0.37	3 / 187	HALLMARK_INFLAMMATORY_RESPONSE
9	0.40	3 / 194	HALLMARK_KRAS_SIGNALING_UP
10	0.49	2 / 141	HALLMARK_UV_RESPONSE_DN
11	0.60	2 / 173	HALLMARK_MITOTIC_SPINDLE
12	0.65	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
13	0.66	2 / 191	HALLMARK_P53_PATHWAY
14	0.66	2 / 192	HALLMARK_MTORC1_SIGNALING
15	0.68	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−27	129 / 5529	HOPP_Txn_elongation
2	1e−20	125 / 5908	HOPP_Active_promoter
3	7e−17	117 / 5682	HOPP_Weak_promoter
4	5e−13	93 / 4261	HOPP_Txn_transition
5	2e−11	91 / 4357	HOPP_Weak_txn
6	1e−09	90 / 4559	HOPP_Weak_enhancer
7	6e−05	87 / 5404	HOPP_Strong_enhancer
8	3e−04	23 / 906	SPANG_BCR DN
9	7e−04	23 / 955	SPANG_BCR UP
10	6e−03	33 / 1814	HOPP_Repetitive
11	2e−02	7 / 227	SPANG_IL21 UP
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	2e−01	1 / 14	WRIGHT_GCB UP

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−11	26 / 448	hsa−miR−20b
2	1e−10	24 / 427	hsa−miR−17
3	1e−09	24 / 474	hsa−miR−20a
4	4e−09	19 / 314	hsa−miR−372
5	5e−08	20 / 407	hsa−miR−106a
6	2e−07	15 / 248	hsa−miR−520c−3p
7	2e−07	16 / 285	hsa−miR−548b−5p
8	2e−07	19 / 403	hsa−miR−106b
9	2e−07	15 / 251	hsa−miR−548i
10	2e−07	11 / 126	hsa−miR−548o
11	4e−07	17 / 336	hsa−miR−519d
12	4e−07	14 / 226	hsa−miR−302b
13	4e−07	14 / 226	hsa−miR−548h
14	4e−07	13 / 194	hsa−miR−520a−3p
15	5e−07	16 / 301	hsa−miR−519b−3p

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	2e−06	14 / 260	chromatin organization
2	2e−04	37 / 1764	regulation of transcription, DNA−templated
3	3e−04	4 / 27	intrinsic apoptotic signaling pathway in response to DNA damage by p53 clas
4	3e−04	35 / 1655	transcription, DNA−templated
5	6e−04	4 / 33	autophagosome assembly
6	9e−04	4 / 37	negative regulation of gene expression, epigenetic
7	1e−03	5 / 68	protein sumoylation
8	3e−03	3 / 24	nuclear−transcribed mRNA poly(A) tail shortening
9	3e−03	5 / 87	cellular response to leukemia inhibitory factor
10	7e−03	4 / 64	Golgi organization
11	8e−03	2 / 12	regulation of cardiac muscle cell contraction
12	8e−03	3 / 36	chromatin silencing
13	1e−02	2 / 13	muscle cell differentiation
14	1e−02	2 / 13	regulation of interferon−gamma−mediated signaling pathway
15	1e−02	3 / 39	regulation of cell adhesion

Chr

Rank	p−value	#in/all	Geneset
1	0.001	14 / 480	Chr 4
2	0.011	15 / 669	Chr 6
3	0.060	11 / 554	Chr 5
4	0.064	6 / 242	Chr 13
5	0.066	13 / 700	Chr 12
6	0.120	9 / 490	Chr 10
7	0.168	4 / 184	Chr 18
8	0.265	12 / 832	Chr 2
9	0.284	10 / 689	Chr 3
10	0.374	8 / 585	Chr 7
11	0.402	6 / 437	Chr 8
12	0.589	15 / 1325	Chr 1
13	0.806	1 / 139	Chr 21
14	0.894	4 / 556	Chr X
15	0.896	6 / 776	Chr 17

Glioma

Rank	p−value	#in/all	Geneset
1	1e−11	49 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	3e−11	45 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	3e−04	5 / 52	GIEZELT_GBM_WT_down_VS_mut
4	2e−03	11 / 330	Up
5	5e−03	4 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	5e−03	15 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	2e−02	8 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	7e−02	1 / 6	Donson−adaptive−immunity−associated with LTS in HGA
9	1e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	2e−01	1 / 15	neurons_glio
11	2e−01	1 / 16	VERHAAK_NL subtype
12	2e−01	1 / 16	VERHAAK_PN subtype
13	2e−01	2 / 64	Weller_LGG_A_vs_O_DOWN
14	2e−01	1 / 21	Barbus_GBM_STS_vs._LTS
15	2e−01	1 / 21	WILLSCHER_GBM_Verhaak−PNmut_down (G)

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

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	2 / 23	Melanoma Epi−Enzyme Cluster 7
2	0.08	7 / 319	Gerber_wt/wt_melanoma−cells−SpotA
3	0.33	4 / 249	Gerber_wt/wt_melanoma−cells−SpotE
4	0.36	1 / 38	Tirosh_G1/S phase specific genes
5	0.52	6 / 497	Gerber_wt/wt_melanoma−cells−SpotD
6	0.53	1 / 65	Harbst_melanoma_highgrade_up
7	0.64	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.74	2 / 222	Gerber_wt/wt_melanoma−cells−SpotF
9	0.75	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
10	0.77	2 / 236	Gerber_wt/wt_group3−specific
11	0.89	1 / 189	Tirosh_genes preferentially expressed by Tregs
12	0.96	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
13	1.00	0 / 17	Hugo_melanoma−all−MET_UP
14	1.00	0 / 37	Hugo_melanoma−all−MET_DN
15	1.00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.06	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.38	1 / 41	Scicluna_DN
3	0.47	1 / 54	Burnham_timecourse
4	0.49	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

TF

Rank	p−value	#in/all	Geneset
1	0.004	23 / 1089	ICGC_Ets1_targets
2	0.004	31 / 1630	ICGC_SrfV0416101_targets
3	0.004	29 / 1494	ICGC_Cebpbsc150_targets
4	0.004	57 / 3564	ICGC_Taf1_targets
5	0.005	22 / 1044	ICGC_Six5_targets
6	0.005	27 / 1387	HEBENSTREIT_high expression TF
7	0.005	57 / 3608	ICGC_Tcf12_targets
8	0.005	59 / 3769	ICGC_Pmlsc71910_targets
9	0.006	59 / 3778	ICGC_Pol24_targets
10	0.008	47 / 2899	ICGC_Nfatc1_targets
11	0.008	29 / 1578	ICGC_GabpPcr2_targets
12	0.009	54 / 3451	ICGC_Atf2_targets
13	0.012	61 / 4072	ICGC_Mta3_targets
14	0.013	64 / 4319	ICGC_Pou2_targets
15	0.015	49 / 3150	ICGC_Creb1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	1 / 12	LIU_BREAST_CANCER
2	0.008	2 / 12	BENTINK_ras.1
3	0.042	2 / 28	PanCan_HK_geneset_nanostring
4	0.121	1 / 11	GENTLES_modul14
5	0.131	1 / 12	GENTLES_modul12
6	0.131	1 / 12	BENTINK_e2f3.2
7	0.145	3 / 113	PanCan_Driver_Gene_geneset_nanostring
8	0.152	1 / 14	GENTLES_modul10
9	0.152	1 / 14	BENTINK_myc.1
10	0.152	1 / 14	BENTINK_src.2
11	0.254	1 / 25	PanCan_HH_geneset_nanostring
12	0.309	2 / 96	PanCan_TXmisReg_geneset_nanostring
13	0.345	1 / 36	ZHANG_MM up
14	0.411	1 / 45	KUIPER_MM poor survival
15	0.424	0 / 14	LIU_COMMON_CANCER_GENES

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−29	120 / 4528	T CD8+ naive cells peripheral blood_4_Tx
2	3e−28	136 / 6099	HSC_4_Tx
3	7e−28	130 / 5527	Tregulatory cells peripheral blood_4_Tx
4	3e−26	130 / 5716	Bcells peripheral blood_4_Tx
5	5e−25	129 / 5753	Tcells peripheral blood_4_Tx
6	2e−23	142 / 7420	Tcells peripheral blood_1_TssA
7	8e−23	144 / 7751	natural killer cells peripheral blood_1_TssA
8	1e−22	143 / 7635	monocytes peripheral blood_1_TssA
9	1e−22	126 / 5766	natural killer cells peripheral blood_4_Tx
10	2e−22	124 / 5601	Thelper cells peripheral blood_4_Tx
11	3e−21	124 / 5738	monocytes peripheral blood_4_Tx
12	8e−21	130 / 6389	4_Tx_ESC_Mesoderm
13	1e−20	134 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
14	2e−20	142 / 7833	Bcells peripheral blood_1_TssA
15	9e−20	125 / 6034	5_Tx_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−16	30 / 417	SHEN_SMARCA2_TARGETS_UP
2	1e−15	41 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
3	5e−12	27 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
4	9e−11	48 / 1550	PILON_KLF1_TARGETS_DN
5	1e−08	27 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
6	5e−08	39 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	8e−08	27 / 730	ONKEN_UVEAL_MELANOMA_UP
8	1e−07	16 / 269	JOHNSTONE_PARVB_TARGETS_2_DN
9	4e−07	27 / 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
10	2e−06	15 / 298	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
11	3e−06	15 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
12	3e−06	20 / 528	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
13	4e−06	18 / 442	KIM_WT1_TARGETS_DN
14	4e−06	14 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
15	5e−06	16 / 361	GARY_CD5_TARGETS_DN

Lifestyle

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

MF

Rank	p−value	#in/all	Geneset
1	4e−04	112 / 7864	protein binding
2	5e−04	3 / 14	SUMO transferase activity
3	3e−03	25 / 1185	ATP binding
4	5e−03	5 / 93	histone deacetylase binding
5	5e−03	19 / 852	nucleic acid binding
6	5e−03	3 / 30	repressing transcription factor binding
7	6e−03	27 / 1402	nucleotide binding
8	7e−03	4 / 66	dioxygenase activity
9	8e−03	23 / 1161	RNA binding
10	8e−03	2 / 12	calcium−transporting ATPase activity
11	9e−03	42 / 2529	metal ion binding
12	9e−03	3 / 37	exonuclease activity
13	1e−02	2 / 13	GTP−Rho binding
14	1e−02	9 / 312	enzyme binding
15	1e−02	28 / 1541	DNA binding

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−27	37 / 310	Chaussabel_3,4_Protein phosphatases
2	3e−08	16 / 245	Chaussabel_3,9_Kinases
3	2e−04	7 / 106	Chaussabel_2,11_Replication
4	4e−04	7 / 113	Chaussabel_1,8_Metabolism Biosynthesis
5	9e−03	6 / 152	VAQUERIZAS_General_TF
6	2e−02	5 / 136	Chaussabel_2,9_Cytosceleton
7	2e−02	6 / 188	Chaussabel_3,8_Enzymes
8	4e−02	17 / 923	PROTEINATLAS_cerebral cortex
9	4e−02	3 / 66	VAQUERIZAS_Whole blood_TF
10	5e−02	12 / 604	PROTEINATLAS_hippocampus
11	6e−02	18 / 1032	PROTEINATLAS_small intestine
12	7e−02	15 / 840	PROTEINATLAS_urinary bladder
13	9e−02	2 / 42	VAQUERIZAS_Fetal brain_TF
14	9e−02	11 / 593	PROTEINATLAS_lateral ventricle
15	1e−01	2 / 45	VAQUERIZAS_Whole brain_TF

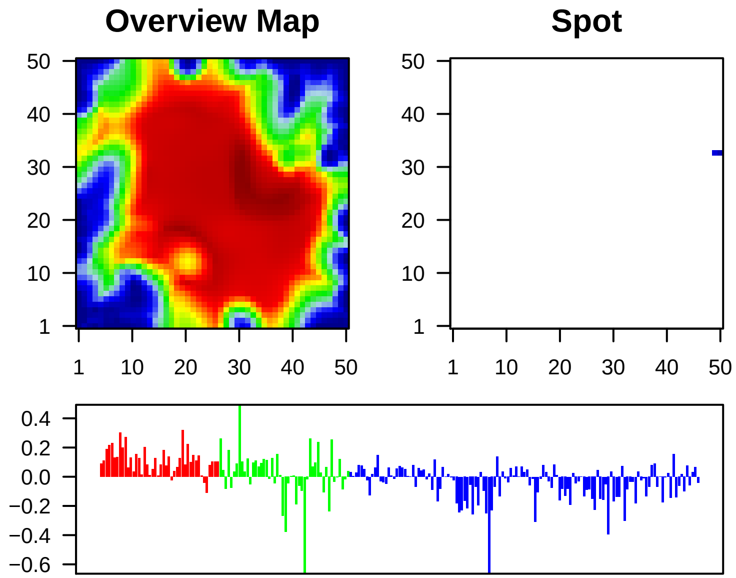
Underexpression Spots

Spot Summary: i

metagenes = 2
genes = 29

<r> metagenes = 1
<r> genes = 0.3
beta: r2= 3.47 / log p= −Inf

samples with spot = 15 (6.8 %)
intermediate : 4 (8.3 %)
non−mBL : 11 (8.5 %)

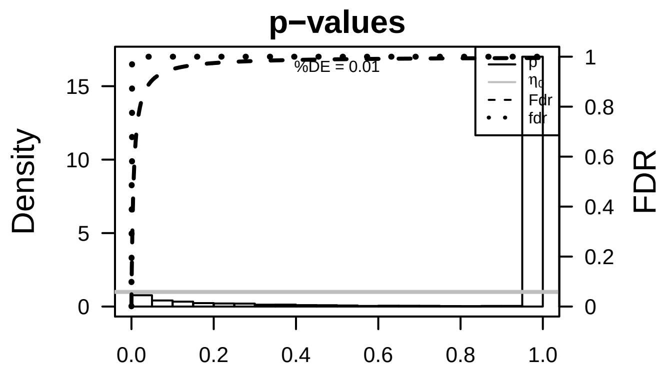


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212779_at	0.71	−1.92	0.6	KIAA1109	KIAA1109 [Source:HGNC Symbol;Acc:HGNC:26953]
2	216713_at	0.99	−1.62	0.62	KRIT1	KRIT1, ankyrin repeat containing [Source:HGNC Symbol;Acc
3	213140_s_at	0.69	−1.47	0.67	SS18L1	SS18L1, nBAF chromatin remodeling complex subunit [Sourc
4	214741_at	0.85	−1.41	0.32	ZNF131	zinc finger protein 131 [Source:HGNC Symbol;Acc:HGNC:12
5	204645_at	0.86	−1.29	0.64	CCNT2	cyclin T2 [Source:HGNC Symbol;Acc:HGNC:1600]
6	217028_at	0.72	−1.28	0.52	CXCR4	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
7	219378_at	0.75	−1.25	0.65	NAA16	N(alpha)−acetyltransferase 16, NatA auxiliary subunit [Source
8	204496_at	0.73	−1.24	0.66	STRN3	striatin 3 [Source:HGNC Symbol;Acc:HGNC:15720]
9	218158_s_at	0.67	−1.24	0.56	APPL1	adaptor protein, phosphotyrosine interacting with PH domain
10	203690_at	0.71	−1.17	0.61	TUBGCP3	tubulin gamma complex associated protein 3 [Source:HGNC
11	202661_at	1.39	−1.1	0.33		
12	215460_x_at	0.86	−1.1	0.61	BRD1	bromodomain containing 1 [Source:HGNC Symbol;Acc:HGN
13	205062_x_at	0.61	−1.05	0.43	ARID4A	AT−rich interaction domain 4A [Source:HGNC Symbol;Acc:H
14	204449_at	0.86	−1.03	0.53	PDCL	phosducin like [Source:HGNC Symbol;Acc:HGNC:8770]
15	219342_at	1.03	−1.01	0.52	CASD1	CAS1 domain containing 1 [Source:HGNC Symbol;Acc:HGN
16	221575_at	1.06	−0.97	0.36	SCLY	selenocysteine lyase [Source:HGNC Symbol;Acc:HGNC:181
17	213848_at	0.69	−0.95	0.41	DUSP7	dual specificity phosphatase 7 [Source:HGNC Symbol;Acc:H
18	201661_s_at	0.51	−0.88	0.46	ACSL3	acyl−CoA synthetase long chain family member 3 [Source:H
19	212927_at	0.8	−0.88	0.62	SMC5	structural maintenance of chromosomes 5 [Source:HGNC Sy
20	212579_at	0.77	−0.86	0.7	SMCHD1	structural maintenance of chromosomes flexible hinge domai

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−07	8 / 310	Refer	Chaussabel_3,4_Protein phosphatases
2	2e−07	7 / 216	miRN	hsa−miR−548l
3	3e−06	10 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
4	3e−06	8 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
5	3e−05	5 / 181	miRN	hsa−miR−520g
6	3e−05	22 / 5529	Lymp	HOPP_Txn_elongation
7	6e−05	19 / 4261	Lymp	HOPP_Txn_transition
8	6e−05	5 / 214	GSEA	CHEN_HOXA5_TARGETS_9HR_UP
9	2e−04	5 / 262	miRN	hsa−miR−32
10	3e−04	4 / 154	miRN	hsa−miR−944
11	3e−04	4 / 159	GSEA	JISON_SICKLE_CELL_DISEASE_DN
12	5e−04	4 / 183	GSEA	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN
13	5e−04	21 / 5908	Lymp	HOPP_Active_promoter
14	7e−04	2 / 19	GSEA	KONDO_COLON_CANCER_HCP_WITH_H3K27ME1
15	9e−04	5 / 377	GSEA	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP
16	9e−04	3 / 94	miRN	hsa−miR−875−3p
17	1e−03	3 / 99	miRN	hsa−miR−646
18	1e−03	3 / 99	miRN	hsa−miR−543
19	1e−03	2 / 25	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP
20	1e−03	3 / 105	miRN	hsa−miR−335
21	1e−03	4 / 236	miRN	hsa−miR−18b
22	1e−03	2 / 27	miRN	hsa−miR−621
23	1e−03	5 / 417	GSEA	SHEN_SMARCA2_TARGETS_UP
24	1e−03	3 / 111	miRN	hsa−miR−656
25	2e−03	4 / 251	CC	microtubule
26	2e−03	4 / 259	miRN	hsa−miR−18a
27	2e−03	2 / 32	GSEA	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
28	2e−03	3 / 124	miRN	hsa−miR−450b−5p
29	2e−03	9 / 1523	Gliom	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
30	3e−03	3 / 134	miRN	hsa−miR−520h
31	3e−03	4 / 305	GSEA	GENTILE_UV_HIGH_DOSE_DN
32	3e−03	4 / 307	GSEA	RATTENBACHER_BOUND_BY_CELF1
33	3e−03	4 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
34	3e−03	3 / 149	miRN	hsa−miR−23b
35	3e−03	2 / 43	GSEA	STREICHER_LSM1_TARGETS_UP
36	4e−03	3 / 153	miRN	hsa−miR−23a
37	4e−03	4 / 320	miRN	hsa−miR−519a
38	4e−03	3 / 157	miRN	hsa−miR−222
39	4e−03	4 / 324	CC	chromosome
40	4e−03	3 / 160	miRN	hsa−miR−545



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	0.009	2 / 70	microtubule cytoskeleton organization
2	0.015	2 / 91	sister chromatid cohesion
3	0.018	4 / 497	cell cycle
4	0.018	2 / 100	activation of MAPK activity
5	0.022	1 / 11	regulation of gene expression by genetic imprinting
6	0.024	1 / 12	negative regulation of intracellular estrogen receptor signaling pathway
7	0.026	1 / 13	histone H3−K4 trimethylation
8	0.028	1 / 14	dendritic cell chemotaxis
9	0.028	1 / 14	regulation of DNA replication
10	0.028	1 / 14	regulation of establishment of cell polarity
11	0.028	1 / 14	regulation of protein localization to plasma membrane
12	0.028	1 / 14	somite development
13	0.030	1 / 15	erythrocyte development
14	0.030	1 / 15	long−chain fatty−acyl−CoA biosynthetic process
15	0.030	1 / 15	microtubule nucleation

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 14	BENTINK_src.2
2	0.07	1 / 36	ZHANG_MM up
3	0.57	1 / 409	Lembcke_Normal vs Adenoma
4	0.63	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

CC

Rank	p−value	#in/all	Geneset
1	0.002	4 / 251	microtubule
2	0.004	4 / 324	chromosome
3	0.017	2 / 98	spindle pole
4	0.018	2 / 101	kinetochore
5	0.020	1 / 10	nuclear pore outer ring
6	0.022	1 / 11	condensed nuclear chromosome, centromeric region
7	0.022	1 / 11	nBAF complex
8	0.026	13 / 3805	cytosol
9	0.028	3 / 326	nuclear speck
10	0.030	1 / 15	NuRD complex
11	0.034	1 / 17	protein phosphatase type 2A complex
12	0.039	5 / 936	cytoskeleton
13	0.044	1 / 22	site of double−strand break
14	0.050	1 / 25	integral component of Golgi membrane
15	0.050	1 / 25	vesicle membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.02	5 / 832	Chr 2
2	0.08	3 / 492	Chr 9
3	0.09	2 / 242	Chr 13
4	0.12	3 / 585	Chr 7
5	0.20	2 / 403	Chr 14
6	0.26	2 / 480	Chr 4
7	0.32	1 / 184	Chr 18
8	0.42	2 / 689	Chr 3
9	0.50	1 / 333	Chr 22
10	0.54	1 / 369	Chr 20
11	0.68	1 / 548	Chr 16
12	0.69	1 / 554	Chr 5
13	0.77	1 / 700	Chr 12
14	0.80	1 / 756	Chr 11
15	1.00	0 / 1325	Chr 1

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−06	24 / 5716	Bcells peripheral blood_4_Tx
2	1e−06	24 / 5738	monocytes peripheral blood_4_Tx
3	1e−06	16 / 2325	HSC_8_ZNF_Rpts
4	4e−06	23 / 5527	Tregulatory cells peripheral blood_4_Tx
5	6e−06	23 / 5601	Thelper cells peripheral blood_4_Tx
6	1e−05	23 / 5753	Tcells peripheral blood_4_Tx
7	1e−05	23 / 5766	natural killer cells peripheral blood_4_Tx
8	2e−05	24 / 6466	5_Tx_MSC_Adipocyte
9	2e−05	18 / 3524	Tregulatory cells peripheral blood_6_EnhG
10	2e−05	25 / 7225	Overlap_fetal_midbrain_ReprPC
11	2e−05	22 / 5456	5_Tx_Neuronal_Progenitor
12	3e−05	20 / 4528	T CD8+ naive cells peripheral blood_4_Tx
13	3e−05	23 / 6068	4_Tx_ESC_Endoderm
14	3e−05	23 / 6099	HSC_4_Tx
15	4e−05	16 / 2946	6_EnhG_ESC_Endoderm

Colon Cancer

Rank	p−value	#in/all	Geneset
1	0.006	6 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
2	0.011	6 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
3	0.026	1 / 13	Budinska_B_Lower crypt−like_DOWN
4	0.028	5 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
5	0.086	5 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
6	0.093	3 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
7	0.116	1 / 60	Marisa_CRC−cluster−g
8	0.137	5 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
9	0.157	1 / 83	Marisa_CRC−cluster−d
10	0.212	4 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	0.238	1 / 132	Marisa_CRC−cluster−a
12	0.287	1 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
13	0.351	2 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
14	0.449	1 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
15	0.459	1 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	9 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.004	4 / 330	Up
3	0.016	7 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.081	1 / 41	mature astrocytes
5	0.083	1 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP
6	0.114	1 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	0.123	1 / 64	cultured astroglia vs. in vivo astrocytes
8	0.123	1 / 64	Weller_LGG_A_vs_O_DOWN
9	0.127	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
10	0.157	1 / 83	ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN
11	0.319	1 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
12	0.360	2 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
13	0.394	1 / 242	ScoV_0.5_Sturm_C1_IDH_DN
14	0.399	1 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
15	0.442	1 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−06	10 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	3e−06	8 / 469	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
3	6e−05	5 / 214	CHEN_HOXA5_TARGETS_9HR_UP
4	3e−04	4 / 159	JISON_SICKLE_CELL_DISEASE_DN
5	5e−04	4 / 183	ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN
6	7e−04	2 / 19	KONDO_COLON_CANCER_HCP_WITH_H3K27ME1
7	9e−04	5 / 377	BLALOCK_ALZHEIMERS_DISEASE_INCIPIENT_UP
8	1e−03	2 / 25	DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_UP
9	1e−03	5 / 417	SHEN_SMARCA2_TARGETS_UP
10	2e−03	2 / 32	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
11	3e−03	4 / 305	GENTILE_UV_HIGH_DOSE_DN
12	3e−03	4 / 307	RATTENBACHER_BOUND_BY_CELF1
13	3e−03	4 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
14	3e−03	2 / 43	STREICHER_LSM1_TARGETS_UP
15	4e−03	3 / 163	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.06	2 / 192	HALLMARK_MTORC1_SIGNALING
2	0.18	1 / 96	HALLMARK_ANDROGEN_RESPONSE
3	0.18	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
4	0.30	1 / 173	HALLMARK_MITOTIC_SPINDLE
5	0.30	1 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	0.31	1 / 182	HALLMARK_GLYCOLYSIS
7	0.32	1 / 188	HALLMARK_HYPOXIA
8	0.33	1 / 194	HALLMARK_KRAS_SIGNALING_UP
9	0.33	1 / 195	HALLMARK_G2M_CHECKPOINT
10	1.00	0 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
11	1.00	0 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	1.00	0 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	1.00	0 / 51	HALLMARK_TGF_BETA_SIGNALING
14	1.00	0 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
15	1.00	0 / 133	HALLMARK_DNA_REPAIR

Immunome

Rank	p−value	#in/all	Geneset
1	0.09	1 / 45	Angelova_immune−metagene−MDSC
2	0.13	1 / 67	Angelova_immune−metagene−T−cells
3	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
4	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
5	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
6	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
7	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
8	1.00	0 / 7	Angelova_immune−metagene−cytotoxic_cells
9	1.00	0 / 25	Angelova_immune−metagene−DC
10	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4
11	1.00	0 / 32	Angelova_immune−metagene−effector_memory_CD8
12	1.00	0 / 14	Angelova_immune−metagene−eosinophil
13	1.00	0 / 19	Angelova_immune−metagene−iDC
14	1.00	0 / 13	Angelova_immune−metagene−immature_B−cells
15	1.00	0 / 11	Angelova_immune−metagene−macrophages

Lifestyle

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

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−05	22 / 5529	HOPP_Txn_elongation
2	6e−05	19 / 4261	HOPP_Txn_transition
3	5e−04	21 / 5908	HOPP_Active_promoter
4	1e−02	15 / 4357	HOPP_Weak_txn
5	3e−02	17 / 5682	HOPP_Weak_promoter
6	4e−02	1 / 18	WRIGHT_ABC UP
7	6e−02	2 / 192	Victora_Dark zone signature
8	8e−02	2 / 227	SPANG_IL21 UP
9	9e−02	1 / 45	SPANG_BAFF 9hrs DN
10	9e−02	15 / 5404	HOPP_Strong_enhancer
11	1e−01	13 / 4559	HOPP_Weak_enhancer
12	1e−01	1 / 57	SPANG_LPS 6hrs DN
13	1e−01	1 / 77	TARTE_Plasma cell signature
14	2e−01	2 / 353	SPANG_CD40 6hrs DN
15	3e−01	3 / 906	SPANG_BCR DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.08	1 / 39	Tirosh_melanoma specific genes
2	0.08	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
3	0.09	1 / 46	Tirosh_top50 correlated genes PC5
4	0.09	1 / 47	Tirosh_G2/M phase specific genes
5	0.14	2 / 319	Gerber_wt/wt_melanoma−cells−SpotA
6	0.15	1 / 81	Tirosh_Genes in the MITF program
7	0.32	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.34	1 / 204	Landsberg_dedifferentiation_down
9	0.37	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
10	1.00	0 / 17	Hugo_melanoma−all−MET_UP
11	1.00	0 / 37	Hugo_melanoma−all−MET_DN
12	1.00	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
13	1.00	0 / 5	Hugo_melanoma−BRAFmut−MET_DN
14	1.00	0 / 16	Hugo_melanoma−all−LEF1_UP
15	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	0.02	1 / 10	armadillo repeat domain binding
2	0.02	1 / 11	long−chain fatty acid−CoA ligase activity
3	0.02	1 / 11	MAP kinase tyrosine/serine/threonine phosphatase activity
4	0.02	2 / 116	macromolecular complex binding
5	0.02	1 / 12	cyclin−dependent protein serine/threonine kinase regulator activity
6	0.02	1 / 12	protein kinase B binding
7	0.03	1 / 14	acetyltransferase activity
8	0.03	1 / 15	GTPase regulator activity
9	0.03	1 / 15	transcription coactivator binding
10	0.03	1 / 16	RNA polymerase binding
11	0.04	1 / 18	amino acid binding
12	0.04	1 / 18	cytokine binding
13	0.04	1 / 20	chemokine receptor activity
14	0.04	1 / 21	gamma−tubulin binding
15	0.04	1 / 22	protein phosphatase 2A binding

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−07	7 / 216	hsa−miR−548l
2	3e−05	5 / 181	hsa−miR−520g
3	2e−04	5 / 262	hsa−miR−32
4	3e−04	4 / 154	hsa−miR−944
5	9e−04	3 / 94	hsa−miR−875−3p
6	1e−03	3 / 99	hsa−miR−646
7	1e−03	3 / 99	hsa−miR−543
8	1e−03	3 / 105	hsa−miR−335
9	1e−03	4 / 236	hsa−miR−18b
10	1e−03	2 / 27	hsa−miR−621
11	1e−03	3 / 111	hsa−miR−656
12	2e−03	4 / 259	hsa−miR−18a
13	2e−03	3 / 124	hsa−miR−450b−5p
14	3e−03	3 / 134	hsa−miR−520h
15	3e−03	3 / 149	hsa−miR−23b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.3	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	1.0	0 / 68	Burnham_sep_vs_con_UP
3	1.0	0 / 56	Burnham_sep_vs_con_DN
4	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
5	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
6	1.0	0 / 48	Burnham_viral_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 / 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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−07	8 / 310	Chaussabel_3,4_Protein phosphatases
2	1e−02	3 / 245	Chaussabel_3,9_Kinases
3	3e−02	5 / 893	PROTEINATLAS_pancreas
4	4e−02	3 / 355	PROTEINATLAS_skeletal muscle
5	6e−02	2 / 188	Chaussabel_3,8_Enzymes
6	2e−01	3 / 671	PROTEINATLAS_cervix, uterine
7	2e−01	2 / 355	WIRTH_Immune system
8	2e−01	1 / 93	Chaussabel_1,4_Replication
9	2e−01	1 / 106	Chaussabel_2,11_Replication
10	2e−01	2 / 399	PROTEINATLAS_soft tissue
11	2e−01	2 / 455	PROTEINATLAS_heart muscle
12	2e−01	1 / 136	Chaussabel_2,9_Cytosceleton
13	2e−01	3 / 840	PROTEINATLAS_urinary bladder
14	2e−01	3 / 848	PROTEINATLAS_adrenal gland
15	3e−01	2 / 474	PROTEINATLAS_vagina

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	1 / 13	Alternative lengthening of telomeres
2	0.05	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	6 / 1041	ICGC_P300_targets
2	0.10	12 / 4131	ICGC_Tcf3_targets
3	0.12	11 / 3796	ICGC_Nficsc81335_targets
4	0.14	9 / 2994	ICGC_Zeb1_targets
5	0.15	5 / 1387	HEBENSTREIT_high expression TF
6	0.17	10 / 3564	ICGC_Taf1_targets
7	0.17	9 / 3150	ICGC_Creb1_targets
8	0.19	4 / 1107	ICGC_Myc_targets
9	0.19	5 / 1508	ICGC_Mef2_targets
10	0.20	12 / 4602	ICGC_Elf1_targets
11	0.22	10 / 3769	ICGC_Pmlsc71910_targets
12	0.22	10 / 3778	ICGC_Pol24_targets
13	0.23	10 / 3804	ICGC_Stat5_targets
14	0.23	11 / 4264	ICGC_Pax5_targets
15	0.25	9 / 3420	ICGC_Bclaf101388_targets

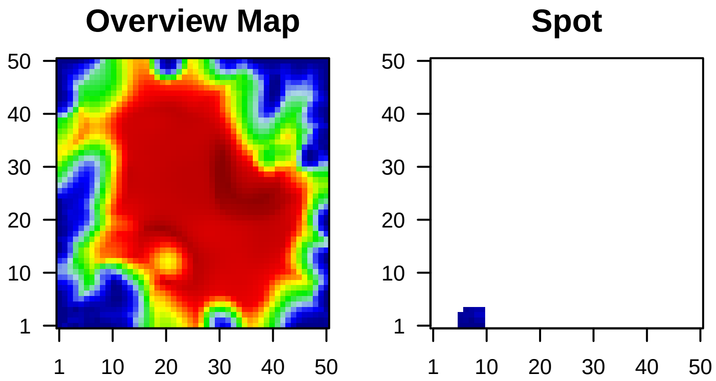
Underexpression Spots

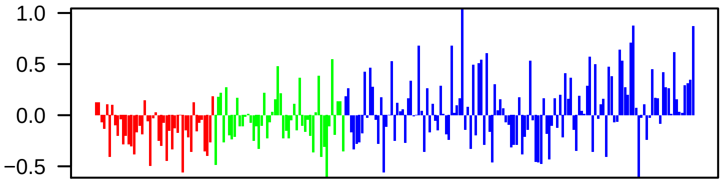
Spot Summary: j

metagenes = 19
genes = 280

<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 16.08 / log p= −Inf

samples with spot = 60 (27.1 %)
mBL : 18 (40.9 %)
intermediate : 15 (31.2 %)
non−mBL : 27 (20.9 %)



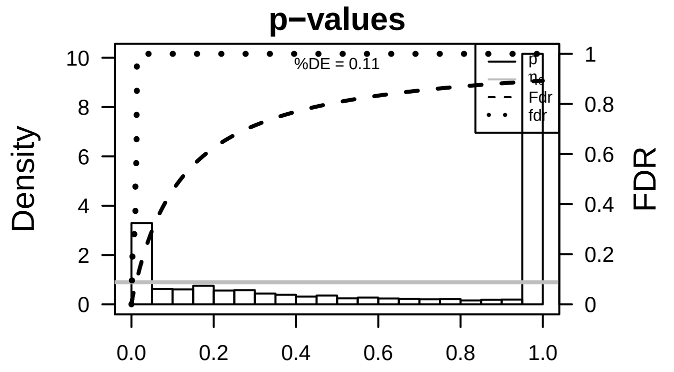


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	201438_at	0.92	−2.96	0.78	COL6A3	collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:H
2	211719_x_at	1.07	−2.87	0.81	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
3	212464_s_at	1.2	−2.76	0.8	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
4	210495_x_at	1.15	−2.53	0.81	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
5	201744_s_at	1.11	−2.42	0.81	LUM	lumican [Source:HGNC Symbol;Acc:HGNC:6724]
6	215076_s_at	1.26	−2.41	0.84	COL3A1	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
7	211161_s_at	1.1	−2.41	0.8	COL3A1	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
8	211981_at	1.02	−2.37	0.64	COL4A1	collagen type IV alpha 1 chain [Source:HGNC Symbol;Acc:H
9	202310_s_at	1.45	−2.36	0.77	COL1A1	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HG
10	201852_x_at	1.39	−2.32	0.84	COL3A1	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
11	221872_at	0.95	−2.28	0.51	RARRES1	retinoic acid receptor responder 1 [Source:HGNC Symbol;Ac
12	202404_s_at	1.28	−2.21	0.78	COL1A2	collagen type I alpha 2 chain [Source:HGNC Symbol;Acc:HG
13	216442_x_at	1.07	−2.18	0.8	FN1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
14	212077_at	0.81	−2.16	0.77	CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
15	201893_x_at	1.49	−2.12	0.78	DCN	decorin [Source:HGNC Symbol;Acc:HGNC:2705]
16	203477_at	0.95	−2.09	0.59	COL15A1	collagen type XV alpha 1 chain [Source:HGNC Symbol;Acc:H
17	219259_at	0.9	−2.08	0.32	SEMA4A	semaphorin 4A [Source:HGNC Symbol;Acc:HGNC:10729]
18	200665_s_at	0.92	−2.07	0.75	SPARC	secreted protein acidic and cysteine rich [Source:HGNC Sym
19	212667_at	0.83	−2.03	0.73	SPARC	secreted protein acidic and cysteine rich [Source:HGNC Sym
20	210809_s_at	1.41	−2.02	0.63	POSTN	periostin [Source:HGNC Symbol;Acc:HGNC:16953]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	87 / 214	Lymph	LENZ_Stromal signature 1
2	1e−98	94 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	1e−76	68 / 196	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	3e−56	39 / 63	GSEA	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
5	3e−55	53 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	6e−53	40 / 78	Melan	Tirosh_CAF−cell specific genes
7	7e−53	47 / 132	Colon	Marisa_CRC−cluster−a
8	2e−50	53 / 212	CC	extracellular matrix
9	8e−45	61 / 397	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
10	1e−43	47 / 197	GSEA	NABA_CORE_MATRISOME
11	2e−43	51 / 253	CC	proteinaceous extracellular matrix
12	3e−43	76 / 747	GSEA	NABA_MATRISOME
13	1e−42	50 / 247	GSEA	BOQUEST_STEM_CELL_UP
14	2e−39	43 / 183	BP	extracellular matrix organization
15	3e−39	39 / 138	GSEA	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
16	6e−36	45 / 249	GSEA	ONDER_CDH1_TARGETS_2_UP
17	2e−34	79 / 1090	CC	extracellular space
18	6e−33	53 / 443	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
19	1e−32	47 / 331	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
20	2e−32	59 / 589	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
21	1e−31	48 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
22	4e−31	40 / 231	Gliom	WILLSCHER_GBM_Verhaak−CL & MES_up
23	2e−29	88 / 1611	CC	extracellular region
24	3e−29	1 / 14	Cance	LIU_PROSTATE_CANCER_DN
25	3e−29	1 / 14	Cance	LIU_PROSTATE_CANCER_DN
26	5e−29	24 / 58	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
27	1e−28	24 / 60	GSEA	CROMER_TUMORIGENESIS_UP
28	7e−28	45 / 376	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
29	6e−27	23 / 60	GSEA	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
30	1e−26	30 / 136	GSEA	NABA_ECM_GLYCOPROTEINS
31	5e−26	28 / 117	GSEA	ZHU_CMV_ALL_DN
32	4e−25	38 / 288	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
33	8e−25	21 / 54	GSEA	CROONQUIST_STROMAL_STIMULATION_UP
34	2e−24	33 / 207	GSEA	WANG_SMARCE1_TARGETS_UP
35	3e−24	24 / 86	GSEA	ZHU_CMV_24_HR_DN
36	6e−24	28 / 138	GSEA	IGLESIAS_E2F_TARGETS_UP
37	7e−24	21 / 59	GSEA	PID_INTEGRIN1_PATHWAY
38	1e−23	22 / 70	GSEA	KIM_GLIS2_TARGETS_UP
39	1e−22	21 / 66	CC	basement membrane
40	1e−22	62 / 1001	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.03	3 / 47	TESCHENDORFF_age_hypermethylated
2	0.41	2 / 92	HORVATH_aging_genes meth DOWN
3	0.81	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	2e−39	43 / 183	extracellular matrix organization
2	7e−18	17 / 58	collagen catabolic process
3	2e−17	39 / 500	cell adhesion
4	2e−12	11 / 35	collagen fibril organization
5	5e−11	19 / 185	cellular protein metabolic process
6	2e−10	20 / 223	angiogenesis
7	2e−10	17 / 157	positive regulation of cell migration
8	5e−10	10 / 42	cellular response to amino acid stimulus
9	2e−09	11 / 62	extracellular matrix disassembly
10	2e−08	11 / 78	wound healing
11	4e−08	9 / 48	blood vessel development
12	7e−08	7 / 25	endodermal cell differentiation
13	7e−07	12 / 130	skeletal system development
14	9e−07	10 / 88	osteoblast differentiation
15	5e−06	8 / 64	response to mechanical stimulus

Cancer

Rank	p−value	#in/all	Geneset
1	3e−29	1 / 14	LIU_PROSTATE_CANCER_DN
2	6e−19	40 / 480	Lembcke_Colonic Inflammation
3	9e−07	5 / 13	GENTLES_modul17
4	6e−06	13 / 187	PanCan_PI3K_geneset_nanostring
5	2e−02	2 / 15	RHODES_CANCER_META_SIGNATURE
6	8e−02	2 / 32	KUIPER_MM good survival
7	1e−01	1 / 10	GENTLES_modul3
8	2e−01	3 / 96	PanCan_TXmisReg_geneset_nanostring
9	2e−01	1 / 13	GENTLES_modul1
10	2e−01	4 / 147	PanCan_MAPK_geneset_nanostring
11	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
12	2e−01	1 / 14	GUSTAFSON_PI3K_DN
13	2e−01	1 / 14	BENTINK_myc.1
14	2e−01	1 / 14	BENTINK_ras.6
15	2e−01	1 / 15	RHODES_UNDIFFERENTIATED_CANCER

CC

Rank	p−value	#in/all	Geneset
1	2e−50	53 / 212	extracellular matrix
2	2e−43	51 / 253	proteinaceous extracellular matrix
3	2e−34	79 / 1090	extracellular space
4	2e−29	88 / 1611	extracellular region
5	1e−22	21 / 66	basement membrane
6	3e−20	31 / 241	endoplasmic reticulum lumen
7	2e−18	18 / 65	collagen trimer
8	6e−17	84 / 2239	extracellular exosome
9	6e−07	23 / 462	cell surface
10	1e−06	19 / 345	focal adhesion
11	1e−05	5 / 20	lamellipodium membrane
12	1e−05	11 / 146	lamellipodium
13	3e−05	5 / 25	filamentous actin
14	5e−05	7 / 63	platelet alpha granule lumen
15	6e−05	6 / 45	stress fiber

Chr

Rank	p−value	#in/all	Geneset
1	0.05	19 / 832	Chr 2
2	0.10	15 / 689	Chr 3
3	0.12	11 / 480	Chr 4
4	0.13	11 / 492	Chr 9
5	0.14	12 / 554	Chr 5
6	0.18	14 / 700	Chr 12
7	0.23	8 / 382	Chr 15
8	0.36	3 / 139	Chr 21
9	0.50	7 / 437	Chr 8
10	0.53	3 / 184	Chr 18
11	0.54	9 / 585	Chr 7
12	0.58	5 / 333	Chr 22
13	0.61	11 / 756	Chr 11
14	0.62	8 / 556	Chr X
15	0.72	3 / 242	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−33	138 / 3724	Tcells peripheral blood_12_EnhBiv
2	2e−31	136 / 3734	Tcells peripheral blood_13_ReprPC
3	2e−29	107 / 2405	Bcells peripheral blood_13_ReprPC
4	4e−27	111 / 2747	Bcells peripheral blood_12_EnhBiv
5	3e−26	110 / 2765	Tregulatory cells peripheral blood_13_ReprPC
6	9e−25	98 / 2300	Thelper cells peripheral blood_13_ReprPC
7	1e−23	128 / 3918	Tcells peripheral blood_14_ReprPCWk
8	1e−23	94 / 2194	Thelper cells peripheral blood_12_EnhBiv
9	1e−23	101 / 2515	natural killer cells peripheral blood_13_ReprPC
10	9e−23	100 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
11	1e−22	80 / 1660	T CD8+ naive cells peripheral blood_12_EnhBiv
12	2e−22	109 / 3001	Bcells peripheral blood_14_ReprPCWk
13	5e−22	108 / 2984	natural killer cells peripheral blood_14_ReprPCWk
14	2e−21	109 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
15	3e−21	99 / 2602	natural killer cells peripheral blood_12_EnhBiv

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−53	47 / 132	Marisa_CRC−cluster−a
2	4e−25	38 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
3	1e−22	62 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	1e−16	30 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
5	5e−10	14 / 103	Marisa_CRC−cluster−b
6	2e−05	8 / 77	Ang_CRC_Hypermethylated
7	3e−05	16 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
8	4e−05	14 / 255	Kosinski_top−crypt−long−list
9	1e−04	7 / 72	Ang_CRC−CIMPH−vs−L_hyper
10	2e−04	2 / 2	Budinska_A_Surface crypt−like_DOWN
11	9e−04	14 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
12	1e−03	15 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
13	7e−03	15 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	2e−02	2 / 13	Budinska_B_Lower crypt−like_DOWN
15	3e−02	1 / 2	Juehling_HNPCC−mutated−in−6−to−8

Glioma

Rank	p−value	#in/all	Geneset
1	4e−31	40 / 231	WILLSCHER_GBM_Verhaak−CL & MES_up
2	4e−20	21 / 85	ScoV_0.999_Sturm_E2_IDH_DN
3	9e−19	31 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
4	5e−16	19 / 99	GIEZELT_GBM_WT_up_VS_mut
5	4e−14	33 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
6	7e−14	12 / 35	Colman_survival_associated
7	3e−11	15 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	2e−10	12 / 64	cultured astroglia vs. in vivo astrocytes
9	2e−09	6 / 10	Phillips MES up vs Prolif & PN
10	3e−08	18 / 242	ScoV_0.5_Sturm_C1_IDH_DN
11	4e−08	14 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
12	1e−07	13 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	2e−07	8 / 41	Gorovets_LGG_PG_subclass
14	2e−07	12 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	1e−05	5 / 21	KIM deleted & downregulated in LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−98	94 / 335	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	3e−56	39 / 63	ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
3	3e−55	53 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
4	8e−45	61 / 397	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
5	1e−43	47 / 197	NABA_CORE_MATRISOME
6	3e−43	76 / 747	NABA_MATRISOME
7	1e−42	50 / 247	BOQUEST_STEM_CELL_UP
8	3e−39	39 / 138	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
9	6e−36	45 / 249	ONDER_CDH1_TARGETS_2_UP
10	6e−33	53 / 443	CHICAS_RB1_TARGETS_CONFLUENT
11	1e−32	47 / 331	LINDGREN_BLADDER_CANCER_CLUSTER_2B
12	2e−32	59 / 589	WONG_ADULT_TISSUE_STEM_MODULE
13	1e−31	48 / 366	LIM_MAMMARY_STEM_CELL_UP
14	3e−29	1 / 14	LIU_PROSTATE_CANCER_DN
15	5e−29	24 / 58	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_

HM

Rank	p−value	#in/all	Geneset
1	1e−76	68 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	5e−16	21 / 130	HALLMARK_COAGULATION
3	1e−13	22 / 188	HALLMARK_HYPOXIA
4	2e−12	11 / 34	HALLMARK_ANGIOGENESIS
5	1e−11	20 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	3e−08	14 / 141	HALLMARK_UV_RESPONSE_DN
7	2e−06	14 / 194	HALLMARK_MYOGENESIS
8	3e−06	13 / 174	HALLMARK_APICAL_JUNCTION
9	2e−05	12 / 178	HALLMARK_COMPLEMENT
10	2e−05	11 / 150	HALLMARK_APOPTOSIS
11	4e−05	12 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	4e−05	12 / 194	HALLMARK_KRAS_SIGNALING_UP
13	1e−04	11 / 187	HALLMARK_INFLAMMATORY_RESPONSE
14	2e−04	11 / 191	HALLMARK_P53_PATHWAY
15	1e−03	9 / 170	HALLMARK_IL2_STAT5_SIGNALING

Immunome

Rank	p−value	#in/all	Geneset
1	3e−05	5 / 25	Angelova_immune−metagene−DC
2	2e−02	3 / 38	Angelova_immune−metagene−mast−cells
3	3e−02	2 / 17	Angelova_immune−metagene−central_memory_CD8
4	5e−02	2 / 23	Angelova_immune−metagene−Th2
5	7e−02	1 / 5	Angelova_immune−metagene−NK56_bright
6	1e−01	1 / 8	Immunity_HLA−class−II
7	1e−01	2 / 42	Angelova_immune−metagene−TGD
8	2e−01	1 / 11	Angelova_immune−metagene−macrophages
9	2e−01	1 / 12	Angelova_immune−metagene−NK56_dim
10	2e−01	1 / 18	Angelova_immune−metagene−pDC
11	3e−01	1 / 19	Angelova_immune−metagene−iDC
12	3e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
13	3e−01	1 / 23	Angelova_immune−metagene−Treg
14	4e−01	1 / 29	Angelova_immune−metagene−Th1
15	1e+00	0 / 13	Angelova_immune−metagene−activated_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	2 / 10	DUMEAUX_Smoking literature genes up
2	0.08	2 / 32	Marjolein_ageing−genes_DN
3	0.12	1 / 8	Marjolein_ageing−genes_UP
4	0.18	1 / 13	Huan_blood−pressure_DBP−signature
5	0.19	1 / 14	Huan_blood−pressure_SBP−signature
6	0.24	2 / 62	DUMEAUX_Smoking enriched genes
7	0.40	4 / 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 / 9	DUMEAUX_Monocytes in smokers literature genes up
13	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1.00	0 / 22	DUMEAUX_High bmi enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	87 / 214	LENZ_Stromal signature 1
2	1e−21	111 / 3168	HOPP_Repressed
3	1e−21	25 / 121	ROSOLOWSKI_green total
4	5e−15	73 / 1894	HOPP_Poised_promoter
5	3e−10	15 / 118	Subero_INT_hyper_meth
6	1e−09	15 / 132	Subero_DLBCL_hyper_meth
7	7e−08	22 / 378	TARTE_Mature plasma cell signature
8	1e−07	10 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
9	1e−07	11 / 91	Subero_T−ALL_hyper_meth
10	2e−06	60 / 2206	HOPP_Heterochrom
11	7e−06	9 / 88	ROSOLOWSKI_green UP
12	5e−05	8 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	6e−05	7 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	2e−03	5 / 56	Subero_mBL_hyper_meth
15	6e−03	3 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	6e−53	40 / 78	Tirosh_CAF−cell specific genes
2	1e−13	16 / 85	Tirosh_AXL−signature
3	4e−12	32 / 497	Gerber_wt/wt_melanoma−cells−SpotD
4	5e−06	13 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
5	1e−05	12 / 171	Landsberg_dedifferentiation_up
6	7e−03	5 / 78	Tirosh_expression higher in CAFs than in T−cells
7	2e−02	3 / 37	Hugo_melanoma−all−MET_DN
8	2e−02	4 / 71	Tirosh_Macrophage specific genes−melanoma
9	2e−02	3 / 41	Tirosh_top50 correlated genes PC3
10	3e−02	2 / 17	Hugo_melanoma−all−MET_UP
11	4e−02	1 / 3	Gerami_melanoma−metastatic−risk_UP
12	5e−02	2 / 24	Gerami_melanoma−metastatic−risk_DN
13	7e−02	7 / 236	Gerber_wt/wt_group3−specific
14	7e−02	3 / 64	Harbst_melanoma_lowgrade_up
15	1e−01	3 / 75	Tirosh_Endothelial−cell specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	4e−20	18 / 53	extracellular matrix structural constituent
2	9e−13	10 / 24	extracellular matrix binding
3	5e−11	7 / 11	platelet−derived growth factor binding
4	6e−11	15 / 106	integrin binding
5	8e−11	16 / 126	heparin binding
6	3e−10	11 / 52	collagen binding
7	2e−07	11 / 93	protease binding
8	3e−07	6 / 19	fibronectin binding
9	1e−06	24 / 517	calcium ion binding
10	1e−05	5 / 20	insulin−like growth factor binding
11	2e−05	4 / 11	peptidase activator activity
12	2e−05	11 / 154	serine−type endopeptidase activity
13	2e−04	5 / 37	growth factor binding
14	3e−04	4 / 21	glycosaminoglycan binding
15	3e−04	15 / 346	receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.006	4 / 47	hsa−miR−1279
2	0.014	6 / 128	hsa−miR−583
3	0.015	3 / 34	hsa−miR−581
4	0.026	4 / 74	hsa−miR−595
5	0.033	2 / 19	hsa−miR−596
6	0.045	3 / 52	hsa−miR−1246
7	0.045	4 / 88	hsa−miR−1271
8	0.047	3 / 53	hsa−miR−485−3p
9	0.047	8 / 262	hsa−miR−32
10	0.055	5 / 135	hsa−miR−7
11	0.072	2 / 29	hsa−miR−644
12	0.074	1 / 5	hsa−miR−937
13	0.074	1 / 5	hsa−miR−126
14	0.081	4 / 107	hsa−miR−198
15	0.085	3 / 68	hsa−miR−942

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.04	3 / 52	Burnham_day1_vs_5_DN
2	0.06	3 / 57	Burnham_day1_vs_5_UP
3	0.09	3 / 68	Burnham_sep_vs_con_UP
4	0.09	3 / 71	Burnham_cap_fp_vs_con_UP
5	0.17	2 / 48	Burnham_cap_fp_vs_con_DN
6	0.17	2 / 48	Burnham_viral_DN
7	0.24	1 / 18	Scicluna_UP
8	0.29	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
9	0.34	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
10	0.47	1 / 41	Scicluna_DN
11	0.56	2 / 122	Terre_IMS_influenza_meta_signature
12	0.56	1 / 54	Burnham_timecourse
13	0.58	1 / 56	Burnham_sep_vs_con_DN
14	0.58	1 / 57	Burnham_viral_UP
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 13	WIRTH_Sec. lymphoid organs
2	7e−05	12 / 204	Chaussabel_3,2_Inflammation I
3	4e−03	3 / 22	VAQUERIZAS_Trachea_TF
4	6e−03	6 / 109	Chaussabel_2,6_Myeloid lineage
5	8e−03	5 / 81	Chaussabel_1,2_Platelets
6	1e−02	3 / 30	VAQUERIZAS_Smooth muscle_TF
7	1e−02	4 / 62	VAQUERIZAS_Lung_TF
8	1e−02	8 / 209	Chaussabel_2,5_Immune related molecules
9	2e−02	5 / 99	Chaussabel_1,5_Myeloid lineage
10	2e−02	5 / 102	WIRTH_EBV B−cells
11	3e−02	2 / 18	JONGENEEL_Monocytes
12	3e−02	3 / 45	VAQUERIZAS_Placenta_TF
13	6e−02	2 / 25	VAQUERIZAS_Adrenal cortex_TF
14	6e−02	3 / 59	Chaussabel_2,10_Immune related cell surface molecules
15	8e−02	2 / 30	VAQUERIZAS_Fetal lung_TF

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	1e−04	34 / 1148	HEBENSTREIT_low expression TF
2	5e−02	45 / 2321	ICGC_Rad21_targets
3	5e−01	50 / 3213	ICGC_Pu1_targets
4	5e−01	33 / 2150	ICGC_Irf4_targets
5	5e−01	25 / 1636	ICGC_Bcl11_targets
6	6e−01	6 / 415	ICGC_RxraPcr1_targets
7	6e−01	15 / 1032	ICGC_Usf1_targets
8	6e−01	33 / 2254	ICGC_BatfPcr1_targets
9	7e−01	62 / 4264	ICGC_Pax5_targets
10	7e−01	19 / 1387	HEBENSTREIT_high expression TF
11	7e−01	49 / 3435	ICGC_Ebfsc137065_targets
12	8e−01	69 / 4851	ICGC_Runx3_targets
13	8e−01	26 / 1941	ICGC_Bcl3_targets
14	8e−01	13 / 1041	ICGC_P300_targets
15	9e−01	5 / 485	ICGC_NrsfPcr2_targets

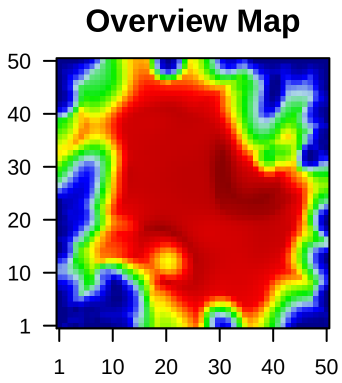
Underexpression Spots

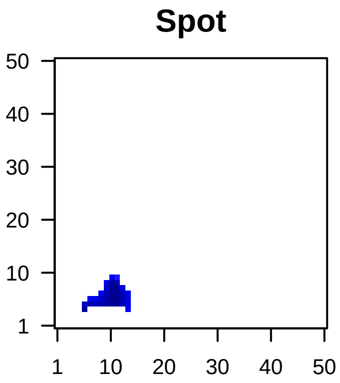
Spot Summary: k

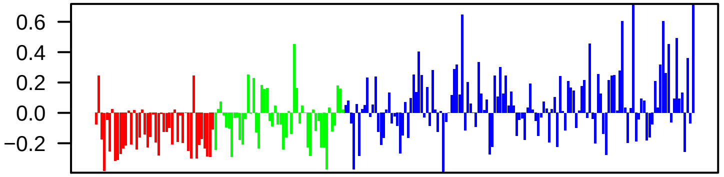
metagenes = 34
genes = 283

<r> metagenes = 0.88
<r> genes = 0.21
beta: r2= 6.93 / log p= −Inf

samples with spot = 40 (18.1 %)
mBL : 19 (43.2 %)
intermediate : 10 (20.8 %)
non−mBL : 11 (8.5 %)


Overview Map


Spot

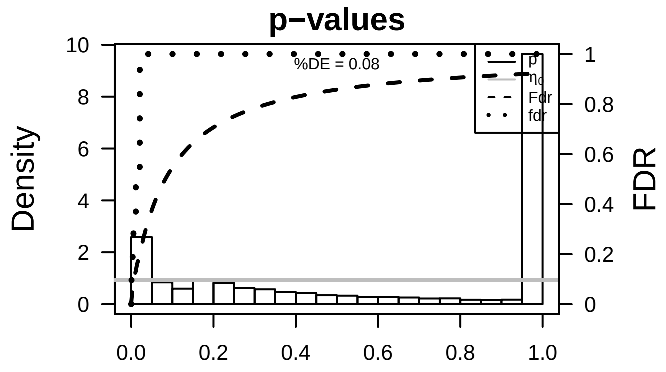


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	201141_at	0.67	−3.1	0.29	GPNMB	glycoprotein nmb [Source:HGNC Symbol;Acc:HGNC:4462]
2	217767_at	1.1	−2.67	0.56	C3	complement C3 [Source:HGNC Symbol;Acc:HGNC:1318]
3	204416_x_at	0.95	−2.3	0.44	APOC1	apolipoprotein C1 [Source:HGNC Symbol;Acc:HGNC:607]
4	215176_x_at	2.2	−2.27	0.54		immunoglobulin kappa variable 1−39 (gene/pseudogene) [So
5	206214_at	0.66	−2.26	0.49	PLA2G7	phospholipase A2 group VII [Source:HGNC Symbol;Acc:HGN
6	203936_s_at	1.04	−2.09	0.38	MMP9	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
7	211796_s_at	1.18	−1.95	0.39		T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:H
8	210915_x_at	1.39	−1.8	0.55		T cell receptor beta constant 1 [Source:HGNC Symbol;Acc:H
9	211902_x_at	0.89	−1.78	0.36		T cell receptor alpha constant [Source:HGNC Symbol;Acc:HG
10	217157_x_at	1.74	−1.77	0.59		
11	209671_x_at	1.12	−1.76	0.44		T cell receptor alpha constant [Source:HGNC Symbol;Acc:HG
12	214777_at	3.45	−1.71	0.45		immunoglobulin kappa variable 4−1 [Source:HGNC Symbol;A
13	211634_x_at	2.97	−1.71	0.51		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
14	211635_x_at	2.55	−1.67	0.49		immunoglobulin heavy variable 1−69 [Source:HGNC Symbol;
15	209670_at	1.08	−1.67	0.43		T cell receptor alpha constant [Source:HGNC Symbol;Acc:HG
16	209031_at	1.2	−1.67	0.22	CADM1	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:
17	201403_s_at	0.91	−1.67	0.31	MGST3	microsomal glutathione S−transferase 3 [Source:HGNC Symb
18	214916_x_at	1.69	−1.66	0.29		
19	209120_at	0.89	−1.66	0.55	NR2F2	nuclear receptor subfamily 2 group F member 2 [Source:HGN
20	216576_x_at	2.32	−1.65	0.57		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−22	42 / 412	GSEA	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
2	2e−21	42 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	7e−20	30 / 214	Lymph	LENZ_Stromal signature 1
4	3e−19	43 / 516	GSEA	SMID_BREAST_CANCER_LUMINAL_B_DN
5	4e−19	32 / 265	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
6	8e−17	25 / 176	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
7	8e−17	16 / 52	BP	complement activation, classical pathway
8	1e−16	15 / 44	MF	antigen binding
9	3e−16	36 / 431	BP	immune system process
10	6e−16	14 / 39	BP	complement activation
11	1e−14	36 / 480	Cance	Lembcke_Colonic Inflammation
12	1e−14	22 / 161	BP	adaptive immune response
13	2e−14	103 / 3210	CC	plasma membrane
14	6e−14	26 / 255	GSEA	HELLER_SILENCED_BY_METHYLATION_UP
15	8e−14	14 / 53	BP	regulation of complement activation
16	3e−13	18 / 113	BP	regulation of immune response
17	9e−13	65 / 1611	CC	extracellular region
18	1e−12	28 / 336	BP	immune response
19	1e−12	15 / 76	BP	Fc−gamma receptor signaling pathway involved in phagocytosis
20	2e−12	24 / 247	GSEA	BOQUEST_STEM_CELL_UP
21	4e−12	29 / 381	GSEA	SWEET_LUNG_CANCER_KRAS_DN
22	4e−12	10 / 26	GSEA	MOSERLE_IFNA_RESPONSE
23	7e−12	22 / 218	GSEA	DELYS_THYROID_CANCER_DN
24	8e−12	28 / 366	GSEA	LIM_MAMMARY_STEM_CELL_UP
25	1e−11	8 / 14	GSEA	ROETH_TERT_TARGETS_UP
26	3e−11	22 / 234	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_DN
27	4e−11	18 / 150	BP	leukocyte migration
28	9e−11	15 / 102	Refer	WIRTH_EBV B−cells
29	1e−10	16 / 122	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
30	6e−10	10 / 40	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
31	7e−10	18 / 180	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
32	1e−09	16 / 143	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
33	1e−09	9 / 32	Refer	Chaussabel_1,1_Plasma Cells
34	2e−09	17 / 169	GSEA	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
35	2e−09	31 / 565	GSEA	LEE_BMP2_TARGETS_UP
36	3e−09	16 / 150	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_U
37	4e−09	11 / 62	Lymph	Monti_Host_response_cluster
38	5e−09	23 / 335	GSEA	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
39	5e−09	9 / 37	Pneu	Sweeney_viral_up
40	6e−09	31 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 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	

BP

Rank	p−value	#in/all	Geneset
1	8e−17	16 / 52	complement activation, classical pathway
2	3e−16	36 / 431	immune system process
3	6e−16	14 / 39	complement activation
4	1e−14	22 / 161	adaptive immune response
5	8e−14	14 / 53	regulation of complement activation
6	3e−13	18 / 113	regulation of immune response
7	1e−12	28 / 336	immune response
8	1e−12	15 / 76	Fc−gamma receptor signaling pathway involved in phagocytosis
9	4e−11	18 / 150	leukocyte migration
10	7e−09	14 / 119	receptor−mediated endocytosis
11	5e−07	21 / 367	innate immune response
12	1e−06	12 / 129	Fc−epsilon receptor signaling pathway
13	3e−06	5 / 15	immunoglobulin production
14	4e−06	5 / 16	high−density lipoprotein particle remodeling
15	7e−06	10 / 104	response to virus

Cancer

Rank	p−value	#in/all	Geneset
1	1e−14	36 / 480	Lembcke_Colonic Inflammation
2	5e−08	6 / 14	GENTLES_modul13
3	6e−07	0 / 14	LIU_PROSTATE_CANCER_DN
4	2e−03	3 / 16	GENTLES_modul16
5	6e−03	12 / 317	SPANG_BCL6−index2
6	2e−02	2 / 13	GENTLES_modul11
7	2e−02	2 / 13	GENTLES_modul17
8	2e−02	2 / 13	GENTLES_modul18
9	4e−02	4 / 80	PanCan_JAK−ST_geneset_nanostring
10	7e−02	4 / 96	PanCan_TXmisReg_geneset_nanostring
11	1e−01	3 / 72	PanCan_Wnt_geneset_nanostring
12	1e−01	1 / 11	LIU_PROSTATE_CANCER_UP
13	2e−01	1 / 12	BEN−PORATH_DN
14	2e−01	5 / 186	SPANG_LPS−index2
15	2e−01	1 / 14	GUSTAFSON_PI3K_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−14	103 / 3210	plasma membrane
2	9e−13	65 / 1611	extracellular region
3	5e−08	13 / 116	blood microparticle
4	7e−07	40 / 1090	extracellular space
5	7e−06	13 / 179	external side of plasma membrane
6	2e−05	4 / 11	immunoglobulin complex, circulating
7	5e−05	115 / 5339	membrane
8	1e−04	35 / 1128	integral component of plasma membrane
9	3e−04	76 / 3270	integral component of membrane
10	5e−04	4 / 23	podosome
11	6e−04	9 / 146	cell−cell junction
12	8e−04	3 / 12	chylomicron
13	1e−03	54 / 2239	extracellular exosome
14	2e−03	3 / 16	very−low−density lipoprotein particle
15	2e−03	4 / 34	cortical actin cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.004	24 / 832	Chr 2
2	0.026	6 / 139	Chr 21
3	0.093	9 / 333	Chr 22
4	0.102	12 / 490	Chr 10
5	0.165	15 / 700	Chr 12
6	0.173	10 / 437	Chr 8
7	0.356	5 / 242	Chr 13
8	0.376	9 / 480	Chr 4
9	0.397	23 / 1325	Chr 1
10	0.404	9 / 492	Chr 9
11	0.414	10 / 556	Chr X
12	0.576	3 / 184	Chr 18
13	0.681	8 / 554	Chr 5
14	0.763	9 / 669	Chr 6
15	0.787	5 / 403	Chr 14

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−11	76 / 2197	monocytes peripheral blood_11_BivFlnk
2	3e−11	92 / 3001	Bcells peripheral blood_14_ReprPCWk
3	3e−10	93 / 3184	monocytes peripheral blood_12_EnhBiv
4	6e−10	103 / 3755	HSC_15_Quies
5	3e−09	92 / 3272	monocytes peripheral blood_14_ReprPCWk
6	6e−09	81 / 2747	Bcells peripheral blood_12_EnhBiv
7	1e−08	87 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
8	3e−08	50 / 1372	Tregulatory cells peripheral blood_10_TssBiv
9	8e−08	77 / 2700	Thelper cells peripheral blood_14_ReprPCWk
10	9e−08	100 / 3918	Tcells peripheral blood_14_ReprPCWk
11	2e−07	85 / 3150	monocytes peripheral blood_13_ReprPC
12	2e−07	68 / 2300	Thelper cells peripheral blood_13_ReprPC
13	2e−07	72 / 2515	natural killer cells peripheral blood_13_ReprPC
14	4e−07	65 / 2194	Thelper cells peripheral blood_12_EnhBiv
15	5e−07	69 / 2405	Bcells peripheral blood_13_ReprPC

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−09	31 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	3e−08	24 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
3	5e−08	20 / 288	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	2e−07	39 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
5	8e−07	11 / 103	Marisa_CRC−cluster−b
6	7e−06	9 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
7	3e−04	9 / 132	Marisa_CRC−cluster−a
8	1e−03	13 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
9	1e−03	3 / 14	TCGA_Mutated−in−CRC_non−hypermutated
10	2e−03	3 / 16	Vilar_non−hypermutated−in−CRC
11	3e−03	43 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	5e−03	2 / 7	Budinska_D_Mesenchymal_UP
13	1e−02	3 / 31	Kosinski_lower−crypt−short−list
14	3e−02	14 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
15	3e−02	11 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Glioma

Rank	p−value	#in/all	Geneset
1	4e−06	22 / 447	ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
2	8e−06	8 / 64	cultured astroglia vs. in vivo astrocytes
3	2e−04	13 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
4	5e−04	3 / 10	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
5	2e−03	3 / 15	Mukasa_UP_in_GBM
6	2e−03	7 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	2e−03	11 / 242	ScoV_0.5_Sturm_C1_IDH_DN
8	4e−03	11 / 269	ScoV_0.5_Sturm_C3_Mesenchymal_DN
9	6e−03	4 / 45	Donson−innate immunity−associated with LTS in HGA
10	9e−03	4 / 50	Vishal_subnetwork signature of survival in GBM
11	9e−03	2 / 9	Donson−migration tethering and rolling−associated with LTS in HGA
12	9e−03	2 / 9	Colman_survival_robust
13	1e−02	5 / 85	ScoV_0.999_Sturm_E2_IDH_DN
14	1e−02	3 / 30	Shaw_responders_down_in_oligo_glioma
15	2e−02	3 / 35	Colman_survival_associated

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−22	42 / 412	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
2	2e−21	42 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	3e−19	43 / 516	SMID_BREAST_CANCER_LUMINAL_B_DN
4	4e−19	32 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
5	8e−17	25 / 176	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
6	6e−14	26 / 255	HELLER_SILENCED_BY_METHYLATION_UP
7	2e−12	24 / 247	BOQUEST_STEM_CELL_UP
8	4e−12	29 / 381	SWEET_LUNG_CANCER_KRAS_DN
9	4e−12	10 / 26	MOSERLE_IFNA_RESPONSE
10	7e−12	22 / 218	DELYS_THYROID_CANCER_DN
11	8e−12	28 / 366	LIM_MAMMARY_STEM_CELL_UP
12	1e−11	8 / 14	ROETH_TERT_TARGETS_UP
13	3e−11	22 / 234	VERHAAK_AML_WITH_NPM1_MUTATED_DN
14	1e−10	16 / 122	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
15	6e−10	10 / 40	FARMER_BREAST_CANCER_CLUSTER_1

HM

Rank	p−value	#in/all	Geneset
1	4e−07	10 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
2	2e−05	13 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
3	2e−05	12 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
4	5e−05	10 / 130	HALLMARK_COAGULATION
5	8e−05	12 / 194	HALLMARK_KRAS_SIGNALING_UP
6	1e−04	11 / 174	HALLMARK_APICAL_JUNCTION
7	3e−04	11 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	1e−03	4 / 29	HALLMARK_NOTCH_SIGNALING
9	1e−03	10 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	2e−03	9 / 178	HALLMARK_COMPLEMENT
11	7e−03	8 / 170	HALLMARK_IL2_STAT5_SIGNALING
12	7e−03	8 / 174	HALLMARK_ADIPOGENESIS
13	1e−02	5 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	2e−02	3 / 34	HALLMARK_ANGIOGENESIS
15	3e−02	6 / 141	HALLMARK_UV_RESPONSE_DN

Immunome

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 23	Angelova_immune−metagene−Th2
2	2e−03	3 / 17	Angelova_immune−metagene−central_memory_CD8
3	3e−02	2 / 18	Angelova_CRC_immunostimulators
4	4e−02	2 / 21	Angelova_immune−metagene−central_memory_CD4
5	8e−02	1 / 5	Angelova_immune−metagene−NK56_bright
6	9e−02	3 / 67	Angelova_immune−metagene−T−cells
7	1e−01	1 / 7	Angelova_immune−metagene−cytotoxic_cells
8	1e−01	2 / 42	Angelova_immune−metagene−TGD
9	2e−01	1 / 11	Angelova_immune−metagene−macrophages
10	2e−01	2 / 45	Angelova_immune−metagene−MDSC
11	2e−01	1 / 13	Angelova_immune−metagene−immature_B−cells
12	2e−01	1 / 14	Angelova_immune−metagene−eosinophil
13	3e−01	1 / 18	Angelova_immune−metagene−pDC
14	3e−01	1 / 19	Angelova_immune−metagene−iDC
15	3e−01	1 / 25	Angelova_immune−metagene−DC

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 9	DUMEAUX_Monocytes in smokers literature genes up
2	9e−02	2 / 32	Marjolein_ageing−genes_DN
3	1e−01	1 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
4	2e−01	1 / 12	DUMEAUX_Women normal BMI literature genes up
5	2e−01	4 / 150	Homuth_BMI−associated−genes_UP
6	3e−01	1 / 22	DUMEAUX_High bmi enriched genes
7	9e−01	2 / 210	Homuth_BMI−associated−genes_DN
8	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
9	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
10	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1e+00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
14	1e+00	0 / 22	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−20	30 / 214	LENZ_Stromal signature 1
2	4e−09	11 / 62	Monti_Host_response_cluster
3	2e−08	88 / 3168	HOPP_Repressed
4	2e−08	62 / 1894	HOPP_Poised_promoter
5	8e−07	7 / 33	Care_Extended T−cell
6	3e−06	5 / 15	Care_Polarized immune response
7	2e−05	7 / 53	LENZ_Stromal signature 2
8	5e−05	6 / 41	ROSOLOWSKI_blue DOWN
9	1e−04	17 / 378	TARTE_Mature plasma cell signature
10	5e−04	7 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
11	7e−04	11 / 213	SPANG_IL21 DN
12	1e−03	12 / 263	SPANG_CD40 6hrs UP
13	2e−03	11 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
14	2e−02	48 / 2206	HOPP_Heterochrom
15	2e−02	6 / 132	Subero_DLBCL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	5e−07	10 / 78	Tirosh_CAF−cell specific genes
2	3e−06	9 / 75	Tirosh_Endothelial−cell specific genes−melanoma
3	1e−05	6 / 33	Tirosh_T−cell specific genes−melanoma
4	6e−05	21 / 497	Gerber_wt/wt_melanoma−cells−SpotD
5	3e−04	7 / 81	Tirosh_Genes in the MITF program
6	4e−03	5 / 64	Harbst_melanoma_lowgrade_up
7	5e−03	10 / 236	Gerber_wt/wt_group3−specific
8	2e−02	7 / 171	Landsberg_dedifferentiation_up
9	3e−02	2 / 17	Hugo_melanoma−all−MET_UP
10	4e−02	4 / 78	Tirosh_expression higher in CAFs than in T−cells
11	4e−02	3 / 46	Tirosh_top50 correlated genes PC5
12	5e−02	4 / 83	TCGA_melanoma_immune_high
13	6e−02	2 / 24	Tirosh_exhuastion−associated genes consitent across tumors
14	1e−01	4 / 107	Tirosh_Exhaustion program in Mel75
15	1e−01	3 / 71	Tirosh_Macrophage specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	1e−16	15 / 44	antigen binding
2	2e−07	14 / 154	serine−type endopeptidase activity
3	1e−04	4 / 16	immunoglobulin receptor binding
4	3e−04	8 / 106	integrin binding
5	5e−04	3 / 10	gamma−catenin binding
6	9e−04	6 / 70	beta−catenin binding
7	1e−03	8 / 126	heparin binding
8	1e−03	6 / 74	protein binding, bridging
9	2e−03	3 / 16	cholesterol transporter activity
10	3e−03	4 / 38	cytokine receptor activity
11	3e−03	4 / 38	signal transducer activity, downstream of receptor
12	4e−03	4 / 39	chemokine activity
13	4e−03	9 / 191	transmembrane signaling receptor activity
14	4e−03	13 / 346	receptor binding
15	5e−03	13 / 350	protein kinase binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	6 / 88	hsa−miR−1271
2	0.003	10 / 223	hsa−miR−1244
3	0.004	6 / 95	hsa−miR−376a
4	0.005	7 / 130	hsa−miR−96
5	0.005	6 / 99	hsa−miR−376b
6	0.010	3 / 28	hsa−miR−1237
7	0.011	8 / 185	hsa−miR−199a−3p
8	0.014	11 / 315	hsa−miR−144
9	0.015	5 / 90	hsa−miR−1301
10	0.018	9 / 244	hsa−miR−98
11	0.018	5 / 94	hsa−miR−875−3p
12	0.020	4 / 64	hsa−miR−562
13	0.020	3 / 36	hsa−miR−636
14	0.022	13 / 427	hsa−miR−17
15	0.022	14 / 474	hsa−miR−20a

Pneumonia

Rank	p−value	#in/all	Geneset
1	5e−09	9 / 37	Sweeney_viral_up
2	2e−08	10 / 57	Burnham_viral_UP
3	2e−05	7 / 52	Burnham_day1_vs_5_DN
4	3e−05	10 / 122	Terre_IMS_influenza_meta_signature
5	5e−04	5 / 41	Scicluna_DN
6	6e−02	3 / 57	Burnham_day1_vs_5_UP
7	1e−01	3 / 68	Burnham_sep_vs_con_UP
8	1e−01	2 / 33	Sweeney_viral_dn
9	1e−01	3 / 71	Burnham_cap_fp_vs_con_UP
10	2e−01	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
11	2e−01	2 / 48	Burnham_cap_fp_vs_con_DN
12	2e−01	2 / 48	Burnham_viral_DN
13	2e−01	2 / 56	Burnham_sep_vs_con_DN
14	9e−01	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
15	1e+00	0 / 54	Burnham_timecourse

Reference Signatures

Rank	p−value	#in/all	Geneset
1	9e−11	15 / 102	WIRTH_EBV B−cells
2	1e−09	9 / 32	Chaussabel_1,1_Plasma Cells
3	2e−07	10 / 72	Chaussabel_3,1_Interferon−inducible
4	6e−07	11 / 100	Chaussabel_2,8_T−cells
5	4e−05	4 / 13	WIRTH_Sec. lymphoid organs
6	3e−03	4 / 36	VAQUERIZAS_Prostate_TF
7	8e−03	4 / 49	VAQUERIZAS_Uterus_TF
8	1e−02	5 / 81	Chaussabel_1,2_Platelets
9	2e−02	2 / 12	WIRTH_Cortex cerebri
10	2e−02	2 / 12	VAQUERIZAS_Kidney_TF
11	2e−02	4 / 62	VAQUERIZAS_Lung_TF
12	2e−02	5 / 99	Chaussabel_1,5_Myeloid lineage
13	2e−02	4 / 68	Chaussabel_2,1_Cytotoxic cells
14	3e−02	3 / 41	VAQUERIZAS_Thymus_TF
15	6e−02	1 / 4	JONGENEEL_SpinalCord

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−04	33 / 1148	HEBENSTREIT_low expression TF
2	1e−01	44 / 2321	ICGC_Rad21_targets
3	2e−01	21 / 1041	ICGC_P300_targets
4	4e−01	9 / 485	ICGC_NrsfPcr2_targets
5	4e−01	28 / 1636	ICGC_Bcl11_targets
6	4e−01	38 / 2254	ICGC_BatfPcr1_targets
7	7e−01	15 / 1025	ICGC_NrsfPcr1_targets
8	7e−01	22 / 1494	ICGC_Cebpbsc150_targets
9	8e−01	31 / 2150	ICGC_Irf4_targets
10	8e−01	26 / 1848	ICGC_Pbx3_targets
11	9e−01	20 / 1508	ICGC_Mef2_targets
12	9e−01	48 / 3435	ICGC_Ebfsc137065_targets
13	9e−01	4 / 415	ICGC_RxraPcr1_targets
14	9e−01	17 / 1387	HEBENSTREIT_high expression TF
15	9e−01	25 / 1941	ICGC_Bcl3_targets

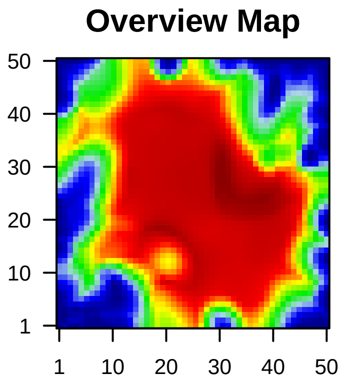
Underexpression Spots

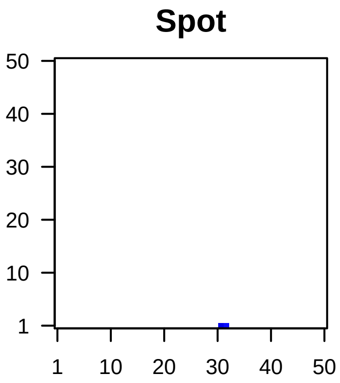
Spot Summary: l

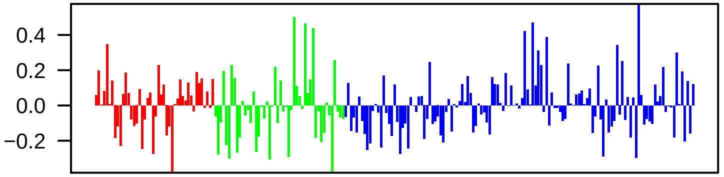
metagenes = 2
genes = 40

<r> metagenes = 1
<r> genes = 0.17
beta: r2= 2.11 / log p= −Inf

samples with spot = 22 (10 %)
mBL : 4 (9.1 %)
intermediate : 9 (18.8 %)
non−mBL : 9 (7 %)





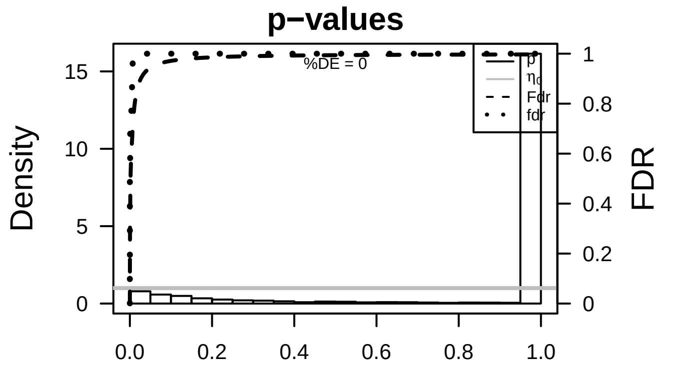


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	219014_at	1.76	−1.51	0.55	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254
2	202156_s_at	0.88	−1.43	0.57	CELF2	CUGBP Elav−like family member 2 [Source:HGNC Symbol;A
3	202158_s_at	0.83	−1.41	0.54	CELF2	CUGBP Elav−like family member 2 [Source:HGNC Symbol;A
4	221249_s_at	0.61	−1.41	0.4	FAM117A	family with sequence similarity 117 member A [Source:HGNC
5	209185_s_at	1.73	−1.38	0.42	IRS2	insulin receptor substrate 2 [Source:HGNC Symbol;Acc:HGN
6	219456_s_at	1.23	−1.33	0.35	RIN3	Ras and Rab interactor 3 [Source:HGNC Symbol;Acc:HGNC:
7	202178_at	1.19	−1.31	0.39	PRKCZ	protein kinase C zeta [Source:HGNC Symbol;Acc:HGNC:941
8	202364_at	1.02	−1.24	0.4	MXI1	MAX interactor 1, dimerization protein [Source:HGNC Symbo
9	202157_s_at	0.85	−1.18	0.6	CELF2	CUGBP Elav−like family member 2 [Source:HGNC Symbol;A
10	214032_at	1.27	−1.12	0.41	ZAP70	zeta chain of T cell receptor associated protein kinase 70 [So
11	201926_s_at	0.97	−1.12	0.4	CD55	CD55 molecule (Cromer blood group) [Source:HGNC Symbo
12	204131_s_at	0.92	−1.12	0.38	FOXO3	forkhead box O3 [Source:HGNC Symbol;Acc:HGNC:3821]
13	206057_x_at	1.22	−1.09	0.36	SPN	sialophorin [Source:HGNC Symbol;Acc:HGNC:11249]
14	203669_s_at	0.83	−1.08	0.21	DGAT1	diacylglycerol O−acyltransferase 1 [Source:HGNC Symbol;Ac
15	205926_at	1.01	−1.08	0.29	IL27RA	interleukin 27 receptor subunit alpha [Source:HGNC Symbol;
16	210749_x_at	1.42	−1.07	0.41	DDR1	discoidin domain receptor tyrosine kinase 1 [Source:HGNC S
17	208415_x_at	0.59	−1.07	0.35	ING1	inhibitor of growth family member 1 [Source:HGNC Symbol;A
18	207169_x_at	1.67	−1.05	0.42	DDR1	discoidin domain receptor tyrosine kinase 1 [Source:HGNC S
19	218033_s_at	1.17	−1	0.36	SNN	stannin [Source:HGNC Symbol;Acc:HGNC:11149]
20	221704_s_at	1.74	−0.99	0.53	VPS37B	VPS37B, ESCRT−I subunit [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−11	10 / 182	Refer	WIRTH_post GC B−cells
2	8e−08	8 / 218	Refer	WIRTH_pre+post GC B−cells
3	7e−07	6 / 121	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
4	3e−05	12 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
5	3e−05	4 / 66	GSEA	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
6	2e−04	6 / 329	GSEA	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
7	3e−04	4 / 121	GSEA	HUANG_GATA2_TARGETS_UP
8	3e−04	6 / 355	Refer	WIRTH_Immune system
9	4e−04	2 / 12	BP	positive regulation of endothelial cell apoptotic process
10	6e−04	3 / 64	GSEA	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES
11	7e−04	3 / 65	GSEA	AMIT_EGF_RESPONSE_120_HELA
12	7e−04	3 / 66	BP	insulin receptor signaling pathway
13	7e−04	19 / 3630	TF	ICGC_Sp1_targets
14	1e−03	4 / 170	miRN	hsa−miR−548m
15	1e−03	5 / 300	GSEA	OSMAN_BLADDER_CANCER_DN
16	1e−03	9 / 1029	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_UP
17	1e−03	5 / 306	GSEA	SANSOM_APC_TARGETS_DN
18	1e−03	2 / 20	Refer	VAQUERIZAS_Bone marrow_TF
19	1e−03	4 / 184	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
20	1e−03	4 / 188	HM	HALLMARK_HYPOXIA
21	2e−03	2 / 22	MF	14−3−3 protein binding
22	2e−03	8 / 863	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
23	2e−03	2 / 26	BP	positive regulation of glucose import
24	2e−03	2 / 27	GSEA	MARZEC_IL2_SIGNALING_DN
25	2e−03	3 / 100	Refer	Chaussabel_2,8_T−cells
26	2e−03	3 / 101	BP	defense response to bacterium
27	2e−03	2 / 28	GSEA	PID_IGF1_PATHWAY
28	2e−03	11 / 1636	TF	ICGC_Bcl11_targets
29	3e−03	4 / 220	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
30	3e−03	23 / 5404	Lymp	HOPP_Strong_enhancer
31	3e−03	2 / 31	GSEA	REACTOME_PI3K_AKT_ACTIVATION
32	3e−03	2 / 31	GSEA	REACTOME_GAB1_SIGNALOSOME
33	3e−03	12 / 1941	TF	ICGC_Bcl3_targets
34	3e−03	3 / 111	GSEA	QI_HYPOXIA
35	3e−03	2 / 32	GSEA	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES
36	3e−03	2 / 32	GSEA	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_15
37	3e−03	4 / 236	Mela	Gerber_wt/wt_group3−specific
38	3e−03	17 / 3435	TF	ICGC_Ebfsc137065_targets
39	3e−03	2 / 33	GSEA	PID_EPO_PATHWAY
40	4e−03	3 / 116	GSEA	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY



Aging

Rank	p−value	#in/all	Geneset
1	0.03	2 / 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	4e−04	2 / 12	positive regulation of endothelial cell apoptotic process
2	7e−04	3 / 66	insulin receptor signaling pathway
3	2e−03	2 / 26	positive regulation of glucose import
4	2e−03	3 / 101	defense response to bacterium
5	6e−03	2 / 45	phosphatidylinositol−3−phosphate biosynthetic process
6	7e−03	2 / 46	actin cytoskeleton reorganization
7	7e−03	2 / 46	peptidyl−tyrosine autophosphorylation
8	8e−03	2 / 50	cellular response to glucose stimulus
9	1e−02	4 / 336	immune response
10	1e−02	4 / 361	intracellular signal transduction
11	2e−02	2 / 72	cellular response to insulin stimulus
12	2e−02	2 / 85	phosphatidylinositol phosphorylation
13	3e−02	1 / 10	cytoplasmic sequestering of transcription factor
14	3e−02	1 / 10	interleukin−27−mediated signaling pathway
15	3e−02	1 / 10	negative regulation of peptidyl−tyrosine phosphorylation

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	1 / 13	GENTLES_modul11
2	0.04	1 / 14	GUSTAFSON_PI3K_DN
3	0.30	2 / 409	Lembcke_Normal vs Adenoma
4	0.37	2 / 480	Lembcke_Colonic Inflammation
5	0.63	0 / 14	LIU_PROSTATE_CANCER_DN
6	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
7	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
8	1.00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1.00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1.00	0 / 12	LIU_BREAST_CANCER
11	1.00	0 / 14	LIU_COMMON_CANCER_GENES
12	1.00	0 / 16	LIU_LIVER_CANCER
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

CC

Rank	p−value	#in/all	Geneset
1	0.01	3 / 192	membrane raft
2	0.03	1 / 10	AP−2 adaptor complex
3	0.03	1 / 10	neurofilament
4	0.03	14 / 3210	plasma membrane
5	0.03	1 / 12	uropod
6	0.04	1 / 17	T cell receptor complex
7	0.06	2 / 144	mitochondrial outer membrane
8	0.06	2 / 146	cell−cell junction
9	0.06	1 / 23	podosome
10	0.06	1 / 25	basal plasma membrane
11	0.06	1 / 25	filamentous actin
12	0.07	1 / 29	immunological synapse
13	0.10	1 / 39	cell leading edge
14	0.10	2 / 201	early endosome
15	0.10	6 / 1221	mitochondrion

Chr

Rank	p−value	#in/all	Geneset
1	0.1	2 / 242	Chr 13
2	0.1	3 / 490	Chr 10
3	0.3	2 / 403	Chr 14
4	0.4	2 / 480	Chr 4
5	0.4	2 / 492	Chr 9
6	0.4	3 / 833	Chr 19
7	0.4	2 / 548	Chr 16
8	0.5	4 / 1325	Chr 1
9	0.6	2 / 700	Chr 12
10	0.6	2 / 756	Chr 11
11	0.6	2 / 776	Chr 17
12	0.7	2 / 832	Chr 2
13	0.7	1 / 437	Chr 8
14	0.8	1 / 585	Chr 7
15	0.8	1 / 669	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−06	12 / 932	Tcells peripheral blood_3_TxFlnk
2	5e−05	6 / 258	T CD8+ naive cells peripheral blood_3_TxFlnk
3	7e−05	21 / 3682	natural killer cells peripheral blood_6_EnhG
4	2e−04	22 / 4208	Tcells peripheral blood_6_EnhG
5	5e−04	6 / 384	HSC_3_TxFlnk
6	5e−04	25 / 5620	TssF_Colon
7	6e−04	31 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
8	9e−04	31 / 8370	natural killer cells peripheral blood_2_TssAFlnk
9	1e−03	7 / 642	Thelper cells peripheral blood_3_TxFlnk
10	2e−03	20 / 4219	EnhWk1_Colon
11	2e−03	7 / 693	Bcells peripheral blood_3_TxFlnk
12	2e−03	27 / 6906	3_TssF_Fibroblasts
13	2e−03	13 / 2144	T CD8+ naive cells peripheral blood_6_EnhG
14	3e−03	12 / 1911	Mid_Frontal_Lobe_HetRpts
15	3e−03	28 / 7407	natural killer cells peripheral blood_5_TxWk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	12 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
2	4e−02	4 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
3	5e−02	1 / 20	Kosinski_top−crypt−short−list
4	5e−02	4 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
5	8e−02	1 / 31	Kosinski_lower−crypt−short−list
6	1e−01	1 / 38	Marisa_CRC−cluster−e
7	1e−01	1 / 43	Marisa_CRC−cluster−f
8	1e−01	3 / 452	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
9	1e−01	2 / 255	Kosinski_top−crypt−long−list
10	2e−01	5 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
11	2e−01	1 / 82	Pentrack_CRC_TCGA_group.over_A_normal_UP
12	2e−01	1 / 83	Marisa_CRC−cluster−d
13	2e−01	4 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	2e−01	1 / 92	Marisa_CRC−cluster−h
15	2e−01	2 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_

Glioma

Rank	p−value	#in/all	Geneset
1	0.005	4 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
2	0.040	3 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
3	0.041	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
4	0.042	1 / 16	VERHAAK_CL subtype
5	0.057	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
6	0.084	1 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	0.096	1 / 38	OL vs. OPC
8	0.113	1 / 45	Donson−innate immunity−associated with LTS in HGA
9	0.129	1 / 52	GIEZELT_GBM_WT_down_VS_mut
10	0.152	1 / 62	GIEZELT_GBM_STS_down_VS_LTS
11	0.155	2 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
12	0.163	1 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
13	0.194	1 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
14	0.218	2 / 330	Up
15	0.259	4 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−07	6 / 121	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
2	3e−05	4 / 66	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
3	2e−04	6 / 329	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
4	3e−04	4 / 121	HUANG_GATA2_TARGETS_UP
5	6e−04	3 / 64	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES
6	7e−04	3 / 65	AMIT_EGF_RESPONSE_120_HELA
7	1e−03	5 / 300	OSMAN_BLADDER_CANCER_DN
8	1e−03	9 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
9	1e−03	5 / 306	SANSOM_APC_TARGETS_DN
10	1e−03	4 / 184	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
11	2e−03	8 / 863	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
12	2e−03	2 / 27	MARZEC_IL2_SIGNALING_DN
13	2e−03	2 / 28	PID_IGF1_PATHWAY
14	3e−03	4 / 220	RUTELLA_RESPONSE_TO_HGF_DN
15	3e−03	2 / 31	REACTOME_PI3K_AKT_ACTIVATION

HM

Rank	p−value	#in/all	Geneset
1	0.001	4 / 188	HALLMARK_HYPOXIA
2	0.077	2 / 174	HALLMARK_ADIPOGENESIS
3	0.079	2 / 176	HALLMARK_ALLOGRAFT_REJECTION
4	0.084	2 / 182	HALLMARK_GLYCOLYSIS
5	0.090	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
6	0.091	2 / 191	HALLMARK_P53_PATHWAY
7	0.092	2 / 193	HALLMARK_HEME_METABOLISM
8	0.299	1 / 133	HALLMARK_DNA_REPAIR
9	0.314	1 / 141	HALLMARK_UV_RESPONSE_DN
10	0.328	1 / 149	HALLMARK_UV_RESPONSE_UP
11	0.330	1 / 150	HALLMARK_APOPTOSIS
12	0.372	1 / 174	HALLMARK_APICAL_JUNCTION
13	0.379	1 / 178	HALLMARK_COMPLEMENT
14	0.393	1 / 187	HALLMARK_INFLAMMATORY_RESPONSE
15	0.403	1 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE

Immunome

Rank	p−value	#in/all	Geneset
1	0.07	1 / 29	Angelova_immune−metagene−Th1
2	0.08	1 / 32	Angelova_immune−metagene−effector_memory_CD8
3	0.16	1 / 67	Angelova_immune−metagene−T−cells
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 / 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	0.01	2 / 62	DUMEAUX_Smoking enriched genes
2	0.02	3 / 210	Homuth_BMI−associated−genes_DN
3	0.06	1 / 22	DUMEAUX_High bmi enriched genes
4	0.08	1 / 32	Marjolein_ageing−genes_DN
5	0.33	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_Fasting enriched genes
15	1.00	0 / 14	Huan_blood−pressure_SBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	0.003	23 / 5404	HOPP_Strong_enhancer
2	0.005	4 / 263	SPANG_CD40 6hrs UP
3	0.010	23 / 5908	HOPP_Active_promoter
4	0.012	2 / 62	Monti_Host_response_cluster
5	0.037	1 / 14	Subero_B−ALL_hypo_meth
6	0.037	1 / 14	Subero_B−CLL_hypo_meth
7	0.038	6 / 955	SPANG_BCR UP
8	0.049	1 / 19	Subero_MCL_hypo_meth
9	0.059	1 / 23	Subero_mBL_hypo_meth
10	0.077	2 / 173	Victora_Light zone signature
11	0.084	1 / 33	Subero_T−PLL_hypo_meth
12	0.084	1 / 33	Care_Extended T−cell
13	0.113	1 / 45	Subero_INT_hypo_meth
14	0.115	1 / 46	Subero_DLBCL_hypo_meth
15	0.121	2 / 227	SPANG_IL21 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.003	4 / 236	Gerber_wt/wt_group3−specific
2	0.013	1 / 5	Hugo_melanoma−BRAFmut−MET_DN
3	0.084	1 / 33	Tirosh_T−cell specific genes−melanoma
4	0.102	2 / 204	Landsberg_dedifferentiation_down
5	0.127	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
6	0.194	1 / 81	Tirosh_Genes in the MITF program
7	0.198	1 / 83	TCGA_melanoma_immune_high
8	0.203	1 / 85	Tirosh_AXL−signature
9	0.448	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
10	0.487	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
11	0.739	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
12	1.000	0 / 17	Hugo_melanoma−all−MET_UP
13	1.000	0 / 37	Hugo_melanoma−all−MET_DN
14	1.000	0 / 38	Hugo_melanoma−BRAFmut−MET_UP
15	1.000	0 / 16	Hugo_melanoma−all−LEF1_UP

MF

Rank	p−value	#in/all	Geneset
1	0.002	2 / 22	14−3−3 protein binding
2	0.005	2 / 38	1−phosphatidylinositol−3−kinase activity
3	0.011	2 / 61	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
4	0.015	2 / 70	transcriptional repressor activity, RNA polymerase II transcription regulatory r
5	0.019	3 / 217	lipid binding
6	0.025	3 / 239	protein domain specific binding
7	0.026	1 / 10	clathrin adaptor activity
8	0.026	1 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
9	0.031	1 / 12	insulin receptor substrate binding
10	0.034	1 / 13	NAD+ kinase activity
11	0.037	1 / 14	phospholipase binding
12	0.037	1 / 14	pre−mRNA binding
13	0.037	1 / 14	protein kinase C activity
14	0.039	1 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
15	0.044	1 / 17	low−density lipoprotein particle receptor binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	4 / 170	hsa−miR−548m
2	0.010	2 / 57	hsa−miR−9*
3	0.011	2 / 60	hsa−miR−622
4	0.014	3 / 194	hsa−miR−124
5	0.031	1 / 12	hsa−miR−147b
6	0.038	2 / 117	hsa−miR−200a
7	0.040	2 / 119	hsa−miR−142−3p
8	0.049	2 / 134	hsa−miR−141
9	0.050	2 / 136	hsa−miR−302e
10	0.050	2 / 136	hsa−miR−153
11	0.052	1 / 20	hsa−miR−220b
12	0.054	1 / 21	hsa−miR−483−3p
13	0.054	1 / 21	hsa−miR−1273
14	0.059	1 / 23	hsa−miR−486−5p
15	0.062	1 / 24	hsa−miR−197

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.005	2 / 41	Scicluna_DN
2	0.120	1 / 48	Burnham_viral_DN
3	0.129	1 / 52	Burnham_day1_vs_5_DN
4	0.166	1 / 68	Burnham_sep_vs_con_UP
5	1.000	0 / 56	Burnham_sep_vs_con_DN
6	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.000	0 / 71	Burnham_cap_fp_vs_con_UP
8	1.000	0 / 57	Burnham_viral_UP
9	1.000	0 / 57	Burnham_day1_vs_5_UP
10	1.000	0 / 54	Burnham_timecourse
11	1.000	0 / 18	Scicluna_UP
12	1.000	0 / 37	Sweeney_viral_up
13	1.000	0 / 33	Sweeney_viral_dn
14	1.000	0 / 122	Terre_IMS_influenza_meta_signature
15	1.000	0 / 179	Terre_MSV_multiple_respiratory_viruses_dn

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−11	10 / 182	WIRTH_post GC B−cells
2	8e−08	8 / 218	WIRTH_pre+post GC B−cells
3	3e−04	6 / 355	WIRTH_Immune system
4	1e−03	2 / 20	VAQUERIZAS_Bone marrow_TF
5	2e−03	3 / 100	Chaussabel_2,8_T−cells
6	2e−02	3 / 204	Chaussabel_3,2_Inflammation I
7	2e−02	2 / 89	Chaussabel_2,3_Erythrocytes
8	4e−02	1 / 15	JONGENEEL_Lung
9	9e−02	2 / 188	Chaussabel_3,8_Enzymes
10	9e−02	4 / 645	PROTEINATLAS_bone marrow
11	9e−02	1 / 37	Chaussabel_2,2_Neutrophils
12	1e−01	4 / 678	PROTEINATLAS_lymph node
13	1e−01	5 / 989	PROTEINATLAS_tonsil
14	1e−01	5 / 1022	PROTEINATLAS_placenta
15	1e−01	3 / 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	7e−04	19 / 3630	ICGC_Sp1_targets
2	2e−03	11 / 1636	ICGC_Bcl11_targets
3	3e−03	12 / 1941	ICGC_Bcl3_targets
4	3e−03	17 / 3435	ICGC_Ebfsc137065_targets
5	4e−03	18 / 3778	ICGC_Pol24_targets
6	5e−03	10 / 1508	ICGC_Mef2_targets
7	5e−03	19 / 4212	ICGC_Pol2_targets
8	5e−03	8 / 1044	ICGC_Six5_targets
9	5e−03	17 / 3564	ICGC_Taf1_targets
10	6e−03	19 / 4264	ICGC_Pax5_targets
11	6e−03	17 / 3608	ICGC_Tcf12_targets
12	6e−03	11 / 1848	ICGC_Pbx3_targets
13	8e−03	17 / 3703	ICGC_Foxm1_targets
14	9e−03	16 / 3420	ICGC_Bclaf101388_targets
15	9e−03	17 / 3769	ICGC_Pmlsc71910_targets

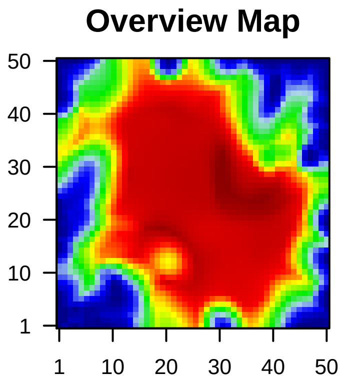
Underexpression Spots

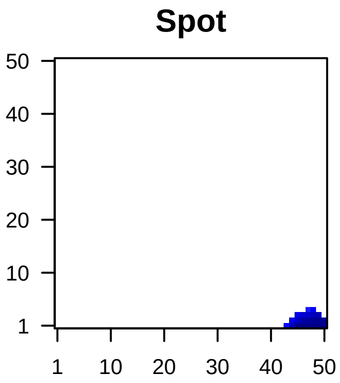
Spot Summary: m

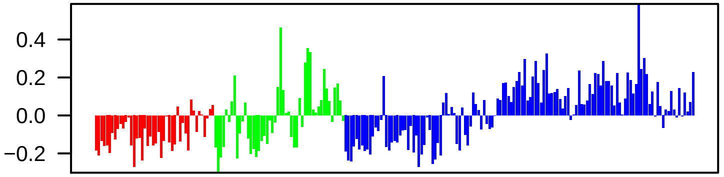
metagenes = 22
genes = 455

<r> metagenes = 0.94
<r> genes = 0.31
beta: r2= 6.87 / log p= −Inf

samples with spot = 17 (7.7 %)
mBL : 4 (9.1 %)
intermediate : 5 (10.4 %)
non−mBL : 8 (6.2 %)





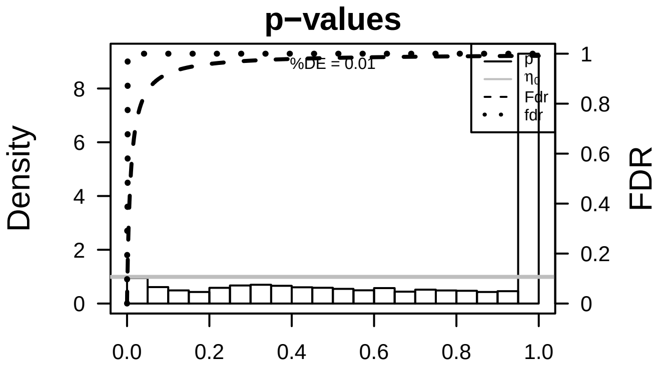


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	396_f_at	0.92	−2.24	0.52	EPOR	erythropoietin receptor [Source:HGNC Symbol;Acc:HGNC:34
2	215778_x_at	1.01	−2.04	0.55		
3	215383_x_at	0.76	−1.89	0.51		
4	220659_s_at	0.83	−1.5	0.46	C7orf43	chromosome 7 open reading frame 43 [Source:HGNC Symbo
5	209192_x_at	0.71	−1.43	0.44	KAT5	lysine acetyltransferase 5 [Source:HGNC Symbol;Acc:HGNC
6	215372_x_at	0.92	−1.36	0.82		
7	222023_at	0.8	−1.35	0.44		
8	214994_at	0.68	−1.34	0.5	APOBEC3F	apolipoprotein B mRNA editing enzyme catalytic subunit 3F [S
9	214368_at	1.14	−1.32	0.32	RASGRP2	RAS guanyl releasing protein 2 [Source:HGNC Symbol;Acc:H
10	218425_at	0.82	−1.3	0.51	RNF216	ring finger protein 216 [Source:HGNC Symbol;Acc:HGNC:21
11	209703_x_at	0.88	−1.3	0.39	METTL7A	methyltransferase like 7A [Source:HGNC Symbol;Acc:HGNC:
12	218833_at	0.65	−1.28	0.4	MAP3K20	mitogen−activated protein kinase kinase kinase 20 [Source:H
13	216434_at	0.97	−1.28	0.49		
14	210723_x_at	0.79	−1.27	0.45		
15	220193_at	1.13	−1.25	0.4	SH3D21	SH3 domain containing 21 [Source:HGNC Symbol;Acc:HGN
16	216715_at	0.93	−1.24	0.38		eukaryotic translation elongation factor 1 delta pseudogene 5
17	211909_x_at	0.87	−1.24	0.74	PTGER3	prostaglandin E receptor 3 [Source:HGNC Symbol;Acc:HGN
18	209241_x_at	0.68	−1.24	0.4	MINK1	misshapen like kinase 1 [Source:HGNC Symbol;Acc:HGNC:1
19	209979_at	0.92	−1.24	0.6	ADARB1	adenosine deaminase, RNA specific B1 [Source:HGNC Symb
20	222060_at	0.79	−1.22	0.35		keratin 8 pseudogene 12 [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−23	53 / 358	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	2e−17	22 / 72	GSEA	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	1e−07	230 / 6368	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
4	3e−07	35 / 483	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	3e−06	25 / 311	GSEA	SHEN_SMARCA2_TARGETS_DN
6	3e−06	76 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
7	4e−06	21 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
8	8e−06	27 / 373	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
9	4e−05	7 / 34	BP	regulation of synaptic plasticity
10	4e−05	7 / 34	BP	respiratory gaseous exchange
11	8e−05	23 / 333	Chr	Chr 22
12	1e−04	4 / 10	BP	cerebellar Purkinje cell differentiation
13	2e−04	10 / 88	GSEA	XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN
14	2e−04	10 / 88	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
15	2e−04	79 / 1894	Lymph	HOPP_Poised_promoter
16	2e−04	7 / 44	GSEA	PARENT_MTOR_SIGNALING_DN
17	3e−04	23 / 361	BP	intracellular signal transduction
18	3e−04	9 / 75	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_DN
19	3e−04	16 / 209	Refer	Chaussabel_2,5_Immune related molecules
20	3e−04	30 / 539	Colon	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
21	4e−04	15 / 194	HM	HALLMARK_MYOGENESIS
22	5e−04	5 / 24	GSEA	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLAC
23	7e−04	27 / 485	TF	ICGC_NrsfPcr2_targets
24	7e−04	117 / 3168	Lymph	HOPP_Repressed
25	7e−04	5 / 26	GSEA	CHO_NR4A1_TARGETS
26	7e−04	3 / 7	Gliom	Sturm_GBM_Meth_overexpression_C_G34_UP
27	8e−04	7 / 54	Lymph	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
28	8e−04	36 / 730	GSEA	BENPORATH_ES_WITH_H3K27ME3
29	9e−04	21 / 346	MF	receptor binding
30	9e−04	4 / 16	GSEA	STARK_HYPPOCAMPUS_22Q11_DELETION_DN
31	1e−03	5 / 28	miRN	hsa−miR−296−5p
32	1e−03	8 / 73	GSEA	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
33	1e−03	15 / 212	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
34	1e−03	4 / 17	GSEA	WU_ALZHEIMER_DISEASE_DN
35	1e−03	5 / 29	BP	long−term memory
36	1e−03	9 / 94	GSEA	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
37	1e−03	4 / 18	GSEA	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
38	2e−03	14 / 198	GSEA	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
39	2e−03	5 / 31	GSEA	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS
40	2e−03	17 / 268	MF	transcription factor binding



Aging

Rank	p−value	#in/all	Geneset
1	0.03	7 / 107	HORVATH_aging_genes meth UP
2	0.39	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.74	2 / 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 / 34	regulation of synaptic plasticity
2	4e−05	7 / 34	respiratory gaseous exchange
3	1e−04	4 / 10	cerebellar Purkinje cell differentiation
4	3e−04	23 / 361	intracellular signal transduction
5	1e−03	5 / 29	long−term memory
6	2e−03	5 / 33	cell death
7	2e−03	7 / 65	excitatory postsynaptic potential
8	2e−03	38 / 833	multicellular organism development
9	3e−03	3 / 11	regulation of filopodium assembly
10	3e−03	8 / 88	small GTPase mediated signal transduction
11	4e−03	3 / 12	acute inflammatory response
12	4e−03	3 / 12	regulation of embryonic development
13	5e−03	4 / 25	positive regulation of mitotic nuclear division
14	5e−03	9 / 114	calcium ion transport
15	5e−03	3 / 13	regulation of myelination

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	3 / 16	LIU_LIVER_CANCER
2	0.04	2 / 12	LIU_BREAST_CANCER
3	0.12	7 / 147	PanCan_MAPK_geneset_nanostring
4	0.14	5 / 96	PanCan_TXmisReg_geneset_nanostring
5	0.16	8 / 187	PanCan_PI3K_geneset_nanostring
6	0.18	6 / 134	PanCan_RAS_geneset_nanostring
7	0.18	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.22	5 / 113	PanCan_Driver_Gene_geneset_nanostring
9	0.23	1 / 9	WANG_ER_DN
10	0.31	1 / 13	GENTLES_modul18
11	0.33	1 / 14	LIU_COMMON_CANCER_GENES
12	0.33	1 / 14	LIU_PROSTATE_CANCER_DN
13	0.33	1 / 14	GUSTAFSON_PI3K_DN
14	0.33	1 / 14	BENTINK_ras.6
15	0.39	15 / 480	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	0.002	3 / 10	synaptic cleft
2	0.005	47 / 1128	integral component of plasma membrane
3	0.005	3 / 13	axolemma
4	0.006	29 / 623	cell projection
5	0.007	17 / 310	dendrite
6	0.008	11 / 168	postsynaptic density
7	0.009	111 / 3210	plasma membrane
8	0.010	3 / 16	dendrite membrane
9	0.010	6 / 65	collagen trimer
10	0.012	112 / 3270	integral component of membrane
11	0.012	8 / 109	dendritic spine
12	0.017	4 / 35	ciliary membrane
13	0.025	7 / 101	endomembrane system
14	0.025	37 / 938	Golgi apparatus
15	0.027	14 / 277	neuron projection

Chr

Rank	p−value	#in/all	Geneset
1	8e−05	23 / 333	Chr 22
2	2e−03	38 / 833	Chr 19
3	4e−03	27 / 548	Chr 16
4	2e−02	32 / 776	Chr 17
5	1e−01	7 / 139	Chr 21
6	1e−01	27 / 756	Chr 11
7	2e−01	18 / 492	Chr 9
8	2e−01	16 / 437	Chr 8
9	4e−01	18 / 585	Chr 7
10	4e−01	21 / 700	Chr 12
11	6e−01	10 / 369	Chr 20
12	7e−01	1 / 41	Chr Y
13	7e−01	10 / 403	Chr 14
14	7e−01	14 / 556	Chr X
15	8e−01	16 / 669	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−13	105 / 1813	8_EnhP_Fibroblasts
2	1e−13	82 / 1239	EnhP_Colon
3	3e−12	116 / 2203	EnhA_Colon
4	2e−11	103 / 1911	Mid_Frontal_Lobe_HetRpts
5	2e−10	117 / 2375	10_ReprPC_Fibroblasts
6	3e−10	161 / 3724	Tcells peripheral blood_12_EnhBiv
7	6e−10	120 / 2507	Mid_Frontal_Lobe_ReprPC
8	1e−09	99 / 1943	TssP_Colon
9	2e−09	109 / 2240	1_TssP_Fibroblasts
10	1e−08	119 / 2602	natural killer cells peripheral blood_12_EnhBiv
11	1e−08	138 / 3184	monocytes peripheral blood_12_EnhBiv
12	4e−08	87 / 1729	8_EnhP_Skeletal_Muscle
13	4e−08	122 / 2747	Bcells peripheral blood_12_EnhBiv
14	6e−08	120 / 2704	4_TxTrans_Fibroblasts
15	9e−08	96 / 2015	ReprPC_Colon

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−07	230 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
2	3e−07	35 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
3	3e−04	30 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
4	3e−03	38 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
5	7e−03	24 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
6	2e−02	2 / 8	Marisa_CRC−C3
7	4e−02	14 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
8	4e−02	16 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
9	5e−02	43 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	6e−02	12 / 255	Kosinski_top−crypt−long−list
11	6e−02	42 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	9e−02	18 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	9e−02	3 / 38	Marisa_CRC−cluster−e
14	1e−01	5 / 92	Marisa_CRC−cluster−h
15	2e−01	1 / 6	Hewish_dMMR−secondary−mutations_Transcriptional_regulation

Glioma

Rank	p−value	#in/all	Geneset
1	7e−04	3 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
2	8e−03	7 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	9e−03	21 / 421	Down_b
4	1e−02	7 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
5	3e−02	8 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	6e−02	2 / 14	astrocytes_glio
7	6e−02	4 / 53	Christensen_hypermethylated_in_primary_glioblastoma
8	6e−02	13 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
9	7e−02	3 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	8e−02	1 / 3	WILLSCHER_GBM_Verhaak−PNmut_up (N)
11	9e−02	3 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
12	1e−01	6 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
13	1e−01	5 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
14	1e−01	6 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	1e−01	4 / 64	Weller_LGG_gradeII−vs−III_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−23	53 / 358	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	2e−17	22 / 72	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	3e−06	25 / 311	SHEN_SMARCA2_TARGETS_DN
4	3e−06	76 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
5	4e−06	21 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
6	8e−06	27 / 373	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
7	2e−04	10 / 88	XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN
8	2e−04	10 / 88	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
9	2e−04	7 / 44	PARENT_MTOR_SIGNALING_DN
10	3e−04	9 / 75	LAIHO_COLORECTAL_CANCER_SERRATED_DN
11	5e−04	5 / 24	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO
12	7e−04	5 / 26	CHO_NR4A1_TARGETS
13	8e−04	36 / 730	BENPORATH_ES_WITH_H3K27ME3
14	9e−04	4 / 16	STARK_HYPPOCAMPUS_22Q11_DELETION_DN
15	1e−03	8 / 73	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON

HM

Rank	p−value	#in/all	Geneset
1	4e−04	15 / 194	HALLMARK_MYOGENESIS
2	2e−02	4 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	3e−02	10 / 174	HALLMARK_APICAL_JUNCTION
4	5e−02	10 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	2e−01	6 / 139	HALLMARK_FATTY_ACID_METABOLISM
6	2e−01	7 / 174	HALLMARK_ADIPOGENESIS
7	2e−01	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	3e−01	2 / 34	HALLMARK_APICAL_SURFACE
9	3e−01	4 / 96	HALLMARK_ANDROGEN_RESPONSE
10	3e−01	4 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	4e−01	6 / 170	HALLMARK_IL2_STAT5_SIGNALING
12	4e−01	6 / 182	HALLMARK_GLYCOLYSIS
13	4e−01	5 / 149	HALLMARK_UV_RESPONSE_UP
14	4e−01	2 / 51	HALLMARK_TGF_BETA_SIGNALING
15	4e−01	6 / 188	HALLMARK_HYPOXIA

Immunome

Rank	p−value	#in/all	Geneset
1	0.04	2 / 12	Angelova_immune−metagene−NK56_dim
2	0.16	1 / 6	Immunity_immune−checkpoint−inhibitors
3	0.20	2 / 29	Angelova_immune−metagene−Th1
4	0.21	1 / 8	Angelova_immune−metagene−mDC
5	0.25	1 / 10	Angelova_immune−metagene−TFH
6	0.25	1 / 10	Angelova_CRC_immonoinhibitors
7	0.33	1 / 14	Angelova_immune−metagene−eosinophil
8	0.37	1 / 16	Angelova_immune−metagene−Th17
9	0.39	1 / 17	Angelova_immune−metagene−central_memory_CD8
10	0.48	1 / 23	Angelova_immune−metagene−Treg
11	0.51	1 / 25	Angelova_immune−metagene−DC
12	0.73	1 / 45	Angelova_immune−metagene−MDSC
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 / 19	Angelova_immune−metagene−activated_CD8

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	2 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
2	0.13	2 / 22	DUMEAUX_Fasting enriched genes
3	0.33	1 / 14	Huan_blood−pressure_SBP−signature
4	0.47	1 / 22	DUMEAUX_High bmi enriched genes
5	0.55	6 / 210	Homuth_BMI−associated−genes_DN
6	0.80	3 / 150	Homuth_BMI−associated−genes_UP
7	0.83	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	2e−04	79 / 1894	HOPP_Poised_promoter
2	7e−04	117 / 3168	HOPP_Repressed
3	8e−04	7 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
4	9e−03	5 / 45	Subero_INT_hypo_meth
5	4e−02	6 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
6	7e−02	3 / 33	Subero_T−PLL_hypo_meth
7	7e−02	6 / 102	ROSOLOWSKI_blue total
8	7e−02	16 / 378	TARTE_Mature plasma cell signature
9	7e−02	4 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
10	8e−02	7 / 132	Subero_DLBCL_hyper_meth
11	1e−01	3 / 41	ROSOLOWSKI_blue DOWN
12	1e−01	3 / 46	Subero_DLBCL_hypo_meth
13	1e−01	2 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
14	2e−01	3 / 53	LENZ_Stromal signature 2
15	2e−01	3 / 56	Subero_mBL_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	11 / 204	Landsberg_dedifferentiation_down
2	0.03	2 / 10	Joensson_Melanoma Normal like subtype
3	0.07	5 / 78	Tirosh_CAF−cell specific genes
4	0.09	3 / 37	Hugo_melanoma−all−MET_DN
5	0.09	5 / 85	Tirosh_AXL−signature
6	0.10	3 / 39	Tirosh_melanoma specific genes
7	0.18	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	0.25	5 / 119	TCGA_melanoma_MITF_low
9	0.27	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
10	0.27	3 / 64	Harbst_melanoma_lowgrade_up
11	0.30	2 / 39	Tirosh_top50 correlated genes PC4
12	0.41	8 / 249	Gerber_wt/wt_melanoma−cells−SpotE
13	0.42	3 / 83	TCGA_melanoma_immune_high
14	0.50	1 / 24	Gerami_melanoma−metastatic−risk_DN
15	0.54	5 / 171	Landsberg_dedifferentiation_up

MF

Rank	p−value	#in/all	Geneset
1	9e−04	21 / 346	receptor binding
2	2e−03	17 / 268	transcription factor binding
3	3e−03	3 / 11	platelet−derived growth factor binding
4	4e−03	3 / 12	phospholipase C activity
5	5e−03	3 / 13	NAD+ binding
6	7e−03	3 / 14	C2H2 zinc finger domain binding
7	7e−03	11 / 163	transferase activity, transferring glycosyl groups
8	8e−03	3 / 15	GTPase regulator activity
9	8e−03	32 / 722	RNA polymerase II transcription factor activity, sequence−specific DNA bindin
10	1e−02	3 / 16	galactosyltransferase activity
11	2e−02	3 / 19	enhancer sequence−specific DNA binding
12	2e−02	3 / 19	receptor signaling complex scaffold activity
13	2e−02	4 / 35	scavenger receptor activity
14	2e−02	5 / 53	extracellular matrix structural constituent
15	2e−02	10 / 165	calmodulin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	5 / 28	hsa−miR−296−5p
2	0.006	4 / 26	hsa−miR−558
3	0.011	2 / 6	hsa−miR−886−5p
4	0.012	4 / 32	hsa−miR−615−5p
5	0.016	6 / 72	hsa−miR−339−5p
6	0.021	5 / 56	hsa−miR−1275
7	0.029	5 / 61	hsa−miR−939
8	0.033	4 / 43	hsa−miR−328
9	0.036	3 / 26	hsa−miR−555
10	0.040	3 / 27	hsa−miR−1296
11	0.082	4 / 58	hsa−miR−331−3p
12	0.082	2 / 17	hsa−miR−323−5p
13	0.082	2 / 17	hsa−miR−609
14	0.086	5 / 83	hsa−miR−147
15	0.112	5 / 90	hsa−miR−22

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	3 / 54	Burnham_timecourse
2	0.5	2 / 57	Burnham_day1_vs_5_UP
3	0.6	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	0.7	1 / 37	Sweeney_viral_up
5	0.7	1 / 41	Scicluna_DN
6	0.8	1 / 56	Burnham_sep_vs_con_DN
7	0.9	1 / 68	Burnham_sep_vs_con_UP
8	0.9	2 / 122	Terre_IMS_influenza_meta_signature
9	0.9	1 / 71	Burnham_cap_fp_vs_con_UP
10	1.0	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
11	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.0	0 / 48	Burnham_viral_DN
13	1.0	0 / 57	Burnham_viral_UP
14	1.0	0 / 52	Burnham_day1_vs_5_DN
15	1.0	0 / 18	Scicluna_UP

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−04	16 / 209	Chaussabel_2,5_Immune related molecules
2	1e−02	3 / 17	VAQUERIZAS_Heart_TF
3	3e−02	9 / 152	VAQUERIZAS_General_TF
4	4e−02	16 / 352	WIRTH_Nervous System
5	5e−02	11 / 218	WIRTH_pre+post GC B−cells
6	7e−02	2 / 16	VAQUERIZAS_Ovary_TF
7	8e−02	3 / 36	VAQUERIZAS_Prostate_TF
8	1e−01	1 / 4	JONGENEEL_Bladder
9	1e−01	4 / 66	VAQUERIZAS_Whole blood_TF
10	2e−01	2 / 25	VAQUERIZAS_Adrenal cortex_TF
11	2e−01	1 / 6	VAQUERIZAS_Appendix_TF
12	2e−01	1 / 7	VAQUERIZAS_Tongue_TF
13	2e−01	4 / 89	Chaussabel_2,3_Erythrocytes
14	3e−01	1 / 11	JONGENEEL_Peripheral Blood Lymphocytes
15	3e−01	1 / 11	JONGENEEL_Spleen

Telomeres

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

TF

Rank	p−value	#in/all	Geneset
1	7e−04	27 / 485	ICGC_NrsfPcr2_targets
2	9e−03	84 / 2321	ICGC_Rad21_targets
3	1e−02	46 / 1148	HEBENSTREIT_low expression TF
4	1e−02	108 / 3121	ICGC_Egr1_targets
5	1e−02	151 / 4602	ICGC_Elf1_targets
6	3e−02	135 / 4131	ICGC_Tcf3_targets
7	4e−02	154 / 4851	ICGC_Runx3_targets
8	6e−02	66 / 1941	ICGC_Bcl3_targets
9	1e−01	127 / 4072	ICGC_Mta3_targets
10	1e−01	108 / 3435	ICGC_Ebfsc137065_targets
11	1e−01	101 / 3213	ICGC_Pu1_targets
12	1e−01	118 / 3804	ICGC_Stat5_targets
13	2e−01	111 / 3630	ICGC_Sp1_targets
14	2e−01	52 / 1636	ICGC_Bcl11_targets
15	2e−01	129 / 4278	ICGC_Yy1_targets

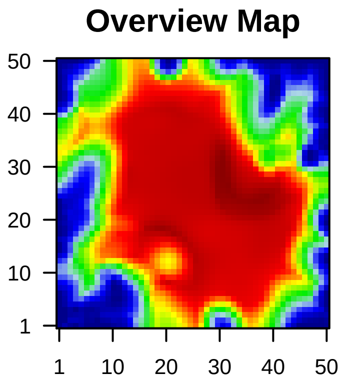
Underexpression Spots

Spot Summary: n

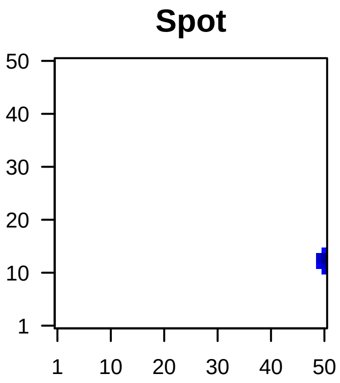
metagenes = 8
genes = 177

<r> metagenes = 0.94
<r> genes = 0.25
beta: r2= 3.54 / log p= −Inf

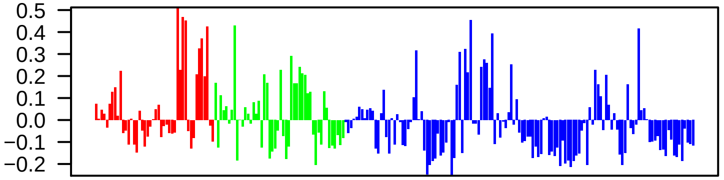
samples with spot = 8 (3.6 %)
intermediate : 1 (2.1 %)
non−mBL : 7 (5.4 %)



Overview Map



Spot

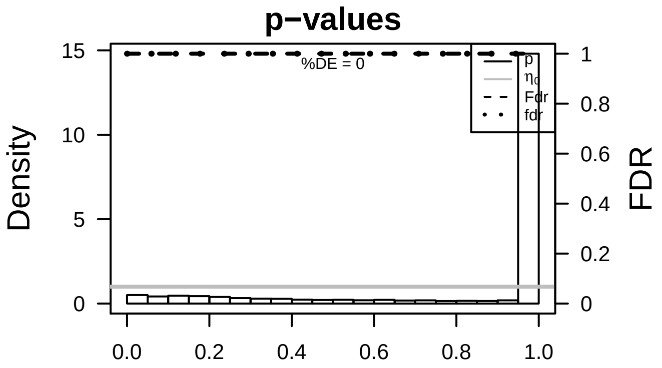


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	214001_x_at	1.11	−1.59	0.74		
2	219854_at	0.74	−1.54	0.31	ZNF14	zinc finger protein 14 [Source:HGNC Symbol;Acc:HGNC:129
3	217619_x_at	1.34	−1.37	0.43		
4	206551_x_at	1.04	−1.36	0.47	KLHL24	kelch like family member 24 [Source:HGNC Symbol;Acc:HGN
5	AFFX−r2−Ec−	0.87	−1.33	0.65		
6	213179_at	0.59	−1.25	0.55	CNOT9	CCR4−NOT transcription complex subunit 9 [Source:HGNC S
7	214056_at	1.34	−1.23	0.46		
8	214522_x_at	1.64	−1.21	0.44	HIST1H2AD	histone cluster 1 H2A family member d [Source:HGNC Symb
9	211172_x_at	1.19	−1.21	0.37	AKAP7	A−kinase anchoring protein 7 [Source:HGNC Symbol;Acc:HG
10	215587_x_at	1.6	−1.2	0.59		
11	222027_at	1.57	−1.19	0.66		
12	215182_x_at	1.77	−1.15	0.43		
13	206438_x_at	1.75	−1.15	0.31	TCTN2	tectonic family member 2 [Source:HGNC Symbol;Acc:HGNC:
14	221419_s_at	1.04	−1.14	0.33		
15	214041_x_at	1.22	−1.13	0.75		
16	219062_s_at	1.06	−1.13	0.32	ZCCHC2	zinc finger CCHC−type containing 2 [Source:HGNC Symbol;
17	214149_s_at	1.32	−1.11	0.63		
18	214372_x_at	0.94	−1.11	0.38	ERN2	endoplasmic reticulum to nucleus signaling 2 [Source:HGNC
19	208003_s_at	1.48	−1.09	0.56	NFAT5	nuclear factor of activated T cells 5 [Source:HGNC Symbol;A
20	207090_x_at	0.85	−1.06	0.26	ZFP30	ZFP30 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−12	11 / 70	CC	nucleosome
2	1e−09	8 / 42	GSEA	REACTOME_RNA_POL_I_PROMOTER_OPENING
3	1e−08	7 / 36	GSEA	REACTOME_PACKAGING_OF_TELOMERE_ENDS
4	2e−08	8 / 60	GSEA	REACTOME_AMYLOIDS
5	2e−08	8 / 62	GSEA	REACTOME_RNA_POL_I_TRANSCRIPTION
6	2e−08	8 / 62	GSEA	REACTOME_MEIOTIC_RECOMBINATION
7	4e−08	9 / 92	GSEA	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
8	5e−08	28 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
9	6e−08	7 / 46	GSEA	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOS
10	2e−07	8 / 78	BP	nucleosome assembly
11	3e−07	7 / 57	GSEA	REACTOME_MEIOTIC_SYNAPSIS
12	4e−07	8 / 88	GSEA	REACTOME_MEIOSIS
13	4e−07	7 / 61	GSEA	REACTOME_TELOMERE_MAINTENANCE
14	5e−07	8 / 91	GSEA	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRAN
15	1e−06	13 / 324	CC	chromosome
16	5e−06	9 / 164	GSEA	REACTOME_TRANSCRIPTION
17	9e−06	17 / 645	Refer	PROTEINATLAS_bone marrow
18	1e−05	7 / 98	GSEA	REACTOME_CHROMOSOME_MAINTENANCE
19	1e−05	19 / 809	Refer	PROTEINATLAS_fallopian tube
20	3e−05	17 / 708	Refer	PROTEINATLAS_thyroid gland
21	4e−05	7 / 118	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
22	7e−05	21 / 1076	Refer	PROTEINATLAS_stomach
23	8e−05	21 / 1081	Refer	PROTEINATLAS_testis
24	9e−05	4 / 31	CC	nuclear nucleosome
25	1e−04	26 / 1541	MF	DNA binding
26	2e−04	4 / 36	BP	chromatin silencing
27	2e−04	6 / 106	Refer	Chaussabel_2,11_Replication
28	2e−04	14 / 593	Refer	PROTEINATLAS_lateral ventricle
29	3e−04	4 / 42	BP	protein heterotetramerization
30	3e−04	5 / 76	GSEA	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN
31	4e−04	2 / 4	GSEA	NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON
32	4e−04	11 / 416	CC	macromolecular complex
33	5e−04	17 / 893	Refer	PROTEINATLAS_pancreas
34	6e−04	19 / 1072	Refer	PROTEINATLAS_duodenum
35	6e−04	3 / 22	BP	telomere organization
36	7e−04	16 / 833	Chr	Chr 19
37	7e−04	4 / 52	GSEA	KENNY_CTNNB1_TARGETS_DN
38	7e−04	17 / 923	Refer	PROTEINATLAS_cerebral cortex
39	1e−03	3 / 26	BP	DNA replication−dependent nucleosome assembly
40	1e−03	3 / 27	BP	chromatin silencing at rDNA



p−values

Aging

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

BP

Rank	p−value	#in/all	Geneset
1	2e−07	8 / 78	nucleosome assembly
2	2e−04	4 / 36	chromatin silencing
3	3e−04	4 / 42	protein heterotetramerization
4	6e−04	3 / 22	telomere organization
5	1e−03	3 / 26	DNA replication−dependent nucleosome assembly
6	1e−03	3 / 27	chromatin silencing at rDNA
7	2e−03	4 / 67	regulation of gene silencing by miRNA
8	3e−03	3 / 37	negative regulation of gene expression, epigenetic
9	4e−03	2 / 12	negative regulation of megakaryocyte differentiation
10	4e−03	2 / 13	histone H3−K4 trimethylation
11	5e−03	2 / 14	innate immune response in mucosa
12	6e−03	3 / 48	regulation of megakaryocyte differentiation
13	7e−03	3 / 49	positive regulation of gene expression, epigenetic
14	8e−03	3 / 52	double−strand break repair via nonhomologous end joining
15	9e−03	2 / 19	DNA replication−independent nucleosome assembly

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	BENTINK_src.2
2	0.1	1 / 20	PanCan_ChromMod_geneset_nanostring
3	0.3	2 / 134	PanCan_RAS_geneset_nanostring
4	0.3	1 / 47	PanCan_TGF−B_geneset_nanostring
5	0.5	1 / 96	PanCan_TXmisReg_geneset_nanostring
6	0.6	1 / 130	PanCan_CC+Apop_geneset_nanostring
7	0.8	1 / 186	SPANG_LPS−index2
8	0.8	1 / 187	PanCan_PI3K_geneset_nanostring
9	0.9	2 / 480	Lembcke_Colonic Inflammation
10	0.9	1 / 317	SPANG_BCL6−index2
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

CC

Rank	p−value	#in/all	Geneset
1	6e−12	11 / 70	nucleosome
2	1e−06	13 / 324	chromosome
3	9e−05	4 / 31	nuclear nucleosome
4	4e−04	11 / 416	macromolecular complex
5	5e−03	3 / 44	nuclear chromosome
6	1e−02	5 / 171	nuclear chromatin
7	1e−02	2 / 23	desmosome
8	1e−02	3 / 65	voltage−gated potassium channel complex
9	4e−02	2 / 42	azurophil granule membrane
10	5e−02	3 / 103	nuclear chromosome, telomeric region
11	5e−02	44 / 4579	nucleus
12	8e−02	1 / 10	catenin complex
13	8e−02	1 / 10	intrinsic component of the cytoplasmic side of the plasma membrane
14	8e−02	1 / 11	axon initial segment
15	8e−02	1 / 11	CCR4−NOT complex

Chr

Rank	p−value	#in/all	Geneset
1	7e−04	16 / 833	Chr 19
2	2e−03	13 / 669	Chr 6
3	3e−01	6 / 548	Chr 16
4	3e−01	7 / 689	Chr 3
5	3e−01	4 / 369	Chr 20
6	4e−01	4 / 403	Chr 14
7	4e−01	7 / 776	Chr 17
8	6e−01	3 / 382	Chr 15
9	6e−01	5 / 700	Chr 12
10	7e−01	1 / 139	Chr 21
11	7e−01	4 / 585	Chr 7
12	7e−01	3 / 480	Chr 4
13	7e−01	3 / 492	Chr 9
14	8e−01	1 / 184	Chr 18
15	8e−01	3 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−04	10 / 383	14_ZNF_Fibroblasts
2	8e−04	44 / 3682	natural killer cells peripheral blood_6_EnhG
3	1e−03	77 / 7957	Tcells peripheral blood_2_TssAFlnk
4	3e−03	78 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
5	4e−03	13 / 713	ZNF_Colon
6	4e−03	44 / 3938	Thelper cells peripheral blood_6_EnhG
7	4e−03	69 / 7078	Bcells peripheral blood_5_TxWk
8	5e−03	75 / 7930	Tregulatory cells peripheral blood_1_TssA
9	5e−03	65 / 6590	Tregulatory cells peripheral blood_5_TxWk
10	5e−03	42 / 3767	Bcells peripheral blood_6_EnhG
11	7e−03	13 / 778	T CD8+ naive cells peripheral blood_8_ZNF_Rpts
12	9e−03	60 / 6099	HSC_4_Tx
13	9e−03	56 / 5601	Thelper cells peripheral blood_4_Tx
14	1e−02	57 / 5753	Tcells peripheral blood_4_Tx
15	1e−02	77 / 8406	Bcells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−08	28 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	1e−02	3 / 60	Marisa_CRC−cluster−g
3	1e−02	9 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
4	6e−02	1 / 8	KIM_MSI−in−EC
5	8e−02	1 / 10	KIM_CRC−MSI−regulated_DN
6	2e−01	6 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
7	3e−01	1 / 38	Marisa_CRC−cluster−e
8	4e−01	52 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9	4e−01	12 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	4e−01	2 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
11	4e−01	9 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	5e−01	7 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	5e−01	2 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	5e−01	6 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
15	6e−01	7 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_

Glioma

Rank	p−value	#in/all	Geneset
1	0.04	6 / 330	Up
2	0.04	3 / 101	Hopp_Sturm_GBM_Epi3_E_G34_UP
3	0.06	2 / 50	Vishal_subnetwork signature of survival in GBM
4	0.08	2 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	0.08	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
6	0.10	15 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	0.12	1 / 16	VERHAAK_CL subtype
8	0.13	16 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
9	0.15	1 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
10	0.18	4 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
11	0.23	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
12	0.28	1 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP
13	0.30	1 / 45	OL vs. MOG− OL
14	0.34	3 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
15	0.39	1 / 64	Weller_LGG_A_vs_O_DOWN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−09	8 / 42	REACTOME_RNA_POL_I_PROMOTER_OPENING
2	1e−08	7 / 36	REACTOME_PACKAGING_OF_TELOMERE_ENDS
3	2e−08	8 / 60	REACTOME_AMYLOIDS
4	2e−08	8 / 62	REACTOME_RNA_POL_I_TRANSCRIPTION
5	2e−08	8 / 62	REACTOME_MEIOTIC_RECOMBINATION
6	4e−08	9 / 92	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
7	6e−08	7 / 46	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSO
8	3e−07	7 / 57	REACTOME_MEIOTIC_SYNAPSIS
9	4e−07	8 / 88	REACTOME_MEIOSIS
10	4e−07	7 / 61	REACTOME_TELOMERE_MAINTENANCE
11	5e−07	8 / 91	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSC
12	5e−06	9 / 164	REACTOME_TRANSCRIPTION
13	1e−05	7 / 98	REACTOME_CHROMOSOME_MAINTENANCE
14	4e−05	7 / 118	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
15	3e−04	5 / 76	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN

HM

Rank	p−value	#in/all	Geneset
1	0.03	2 / 34	HALLMARK_APICAL_SURFACE
2	0.25	2 / 122	HALLMARK_SPERMATOGENESIS
3	0.39	2 / 174	HALLMARK_APICAL_JUNCTION
4	0.41	2 / 181	HALLMARK_XENOBIOTIC_METABOLISM
5	0.42	2 / 182	HALLMARK_GLYCOLYSIS
6	0.43	2 / 188	HALLMARK_HYPOXIA
7	0.44	2 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	0.45	2 / 193	HALLMARK_HEME_METABOLISM
9	0.45	2 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.53	1 / 96	HALLMARK_ANDROGEN_RESPONSE
11	0.53	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	0.53	1 / 97	HALLMARK_PEROXISOME
13	0.65	1 / 133	HALLMARK_DNA_REPAIR
14	0.67	1 / 141	HALLMARK_UV_RESPONSE_DN
15	0.69	1 / 149	HALLMARK_UV_RESPONSE_UP

Immunome

Rank	p−value	#in/all	Geneset
1	0.09	1 / 12	Angelova_immune−metagene−NK56_dim
2	0.10	1 / 13	Angelova_immune−metagene−immature_B−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 / 11	Angelova_immune−metagene−macrophages
15	1.00	0 / 38	Angelova_immune−metagene−mast−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	3 / 210	Homuth_BMI−associated−genes_DN
2	0.4	1 / 62	DUMEAUX_Smoking enriched genes
3	0.7	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 / 14	Huan_blood−pressure_SBP−signature
15	1.0	0 / 13	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	45 / 4261	HOPP_Txn_transition
2	0.05	3 / 102	ROSOLOWSKI_blue total
3	0.07	1 / 9	YAMANE_AICDA_targets_nonrecruited
4	0.09	4 / 213	SPANG_IL21 DN
5	0.11	4 / 237	ZHANG_DLBCL mutated
6	0.23	1 / 33	Subero_T−PLL_hypo_meth
7	0.25	47 / 5529	HOPP_Txn_elongation
8	0.27	9 / 906	SPANG_BCR DN
9	0.28	3 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
10	0.32	45 / 5404	HOPP_Strong_enhancer
11	0.35	1 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
12	0.39	48 / 5908	HOPP_Active_promoter
13	0.42	1 / 70	Subero_FL_hyper_meth
14	0.45	1 / 77	TARTE_Plasma cell signature
15	0.50	1 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.003	4 / 75	Tirosh_Endothelial−cell specific genes−melanoma
2	0.060	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
3	0.083	1 / 11	Tirosh_genes shared by CD8 T−cells and malign cells in Mel79−melanoma
4	0.165	1 / 23	Melanoma Epi−Enzyme Cluster 7
5	0.250	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
6	0.308	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
7	0.425	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
8	0.553	2 / 236	Gerber_wt/wt_group3−specific
9	0.715	2 / 319	Gerber_wt/wt_melanoma−cells−SpotA
10	0.750	3 / 497	Gerber_wt/wt_melanoma−cells−SpotD
11	0.775	1 / 189	Tirosh_genes preferentially expressed by Tregs
12	0.838	1 / 230	Gerber_wt/wt_melanoma−cells−SpotC
13	0.888	1 / 276	Gerber_wt/wt_melanoma−cells−SpotB
14	1.000	0 / 17	Hugo_melanoma−all−MET_UP
15	1.000	0 / 37	Hugo_melanoma−all−MET_DN

MF

Rank	p−value	#in/all	Geneset
1	1e−04	26 / 1541	DNA binding
2	5e−03	9 / 408	protein heterodimerization activity
3	5e−03	2 / 14	retinoic acid receptor binding
4	7e−03	2 / 16	retinoid X receptor binding
5	8e−03	4 / 100	cysteine−type peptidase activity
6	2e−02	2 / 25	nuclear localization sequence binding
7	3e−02	3 / 88	histone binding
8	4e−02	2 / 39	SNARE binding
9	4e−02	5 / 239	protein domain specific binding
10	5e−02	2 / 44	protein serine/threonine phosphatase activity
11	5e−02	2 / 47	voltage−gated potassium channel activity
12	6e−02	2 / 50	cysteine−type endopeptidase activity
13	6e−02	2 / 52	chromatin DNA binding
14	7e−02	2 / 57	thiol−dependent ubiquitin−specific protease activity
15	8e−02	2 / 58	cytoskeletal protein binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 34	hsa−miR−760
2	0.010	3 / 57	hsa−miR−518c*
3	0.017	4 / 126	hsa−miR−338−3p
4	0.021	3 / 75	hsa−miR−425
5	0.022	3 / 77	hsa−miR−526a
6	0.023	3 / 78	hsa−miR−224
7	0.023	4 / 139	hsa−miR−548e
8	0.029	4 / 149	hsa−miR−548a−3p
9	0.032	2 / 36	hsa−miR−518f*
10	0.032	2 / 36	hsa−miR−129−3p
11	0.037	2 / 39	hsa−miR−623
12	0.040	7 / 407	hsa−miR−106a
13	0.041	2 / 41	hsa−miR−518e*
14	0.046	2 / 44	hsa−miR−455−5p
15	0.048	6 / 336	hsa−miR−519d

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.3	1 / 54	Burnham_timecourse
2	0.4	2 / 179	Terre_MSV_multiple_respiratory_viruses_dn
3	0.6	1 / 122	Terre_IMS_influenza_meta_signature
4	1.0	0 / 68	Burnham_sep_vs_con_UP
5	1.0	0 / 56	Burnham_sep_vs_con_DN
6	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
7	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
8	1.0	0 / 48	Burnham_viral_DN
9	1.0	0 / 57	Burnham_viral_UP
10	1.0	0 / 57	Burnham_day1_vs_5_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 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−06	17 / 645	PROTEINATLAS_bone marrow
2	1e−05	19 / 809	PROTEINATLAS_fallopian tube
3	3e−05	17 / 708	PROTEINATLAS_thyroid gland
4	7e−05	21 / 1076	PROTEINATLAS_stomach
5	8e−05	21 / 1081	PROTEINATLAS_testis
6	2e−04	6 / 106	Chaussabel_2,11_Replication
7	2e−04	14 / 593	PROTEINATLAS_lateral ventricle
8	5e−04	17 / 893	PROTEINATLAS_pancreas
9	6e−04	19 / 1072	PROTEINATLAS_duodenum
10	7e−04	17 / 923	PROTEINATLAS_cerebral cortex
11	1e−03	13 / 642	PROTEINATLAS_lung
12	2e−03	13 / 671	PROTEINATLAS_cervix, uterine
13	2e−03	17 / 1022	PROTEINATLAS_placenta
14	2e−03	15 / 848	PROTEINATLAS_adrenal gland
15	7e−03	13 / 770	PROTEINATLAS_endometrium

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	38 / 3564	ICGC_Taf1_targets
2	0.02	32 / 2899	ICGC_Nfatc1_targets
3	0.02	25 / 2150	ICGC_Irf4_targets
4	0.03	20 / 1630	ICGC_SrfV0416101_targets
5	0.03	36 / 3420	ICGC_Bclaf101388_targets
6	0.03	36 / 3451	ICGC_Atf2_targets
7	0.04	37 / 3630	ICGC_Sp1_targets
8	0.04	38 / 3769	ICGC_Pmlsc71910_targets
9	0.04	18 / 1508	ICGC_Mef2_targets
10	0.04	38 / 3796	ICGC_Nficsc81335_targets
11	0.05	38 / 3804	ICGC_Stat5_targets
12	0.05	37 / 3703	ICGC_Foxm1_targets
13	0.05	40 / 4072	ICGC_Mta3_targets
14	0.06	18 / 1578	ICGC_GabpPcr2_targets
15	0.07	41 / 4278	ICGC_Yy1_targets

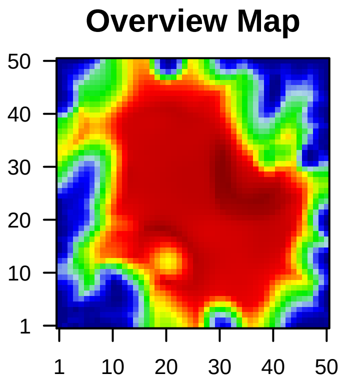
Underexpression Spots

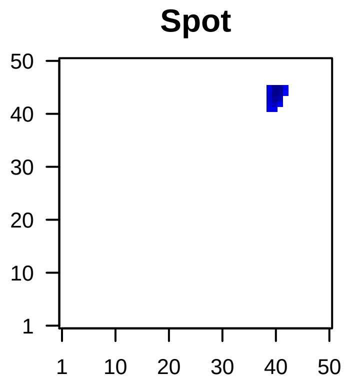
Spot Summary: o

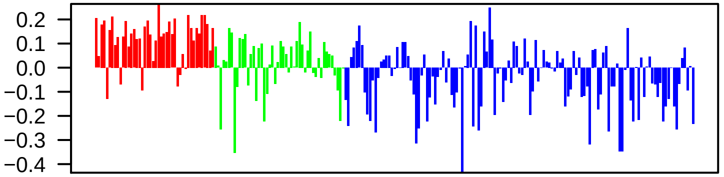
metagenes = 16
genes = 176

<r> metagenes = 0.97
<r> genes = 0.26
beta: r2= 3.56 / log p= −Inf

samples with spot = 22 (10 %)
intermediate : 4 (8.3 %)
non−mBL : 18 (14 %)


Overview Map


Spot

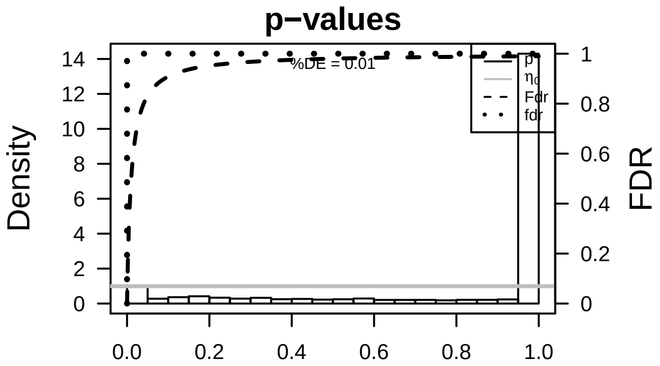


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212827_at	1.05	−2.46	0.38		immunoglobulin heavy constant mu [Source:HGNC Symbol;A
2	221239_s_at	1.35	−1.87	0.4	FCRL2	Fc receptor like 2 [Source:HGNC Symbol;Acc:HGNC:14875]
3	219419_at	1.03	−1.57	0.57	RBFA	ribosome binding factor A [Source:HGNC Symbol;Acc:HGNC
4	204372_s_at	0.36	−1.56	0.54	KHSRP	KH−type splicing regulatory protein [Source:HGNC Symbol;A
5	204305_at	0.81	−1.48	0.32	MIPEP	mitochondrial intermediate peptidase [Source:HGNC Symbol
6	203229_s_at	0.48	−1.39	0.5	CLK2	CDC like kinase 2 [Source:HGNC Symbol;Acc:HGNC:2069]
7	218951_s_at	0.68	−1.37	0.35	PLCXD1	phosphatidylinositol specific phospholipase C X domain conta
8	201802_at	1.13	−1.37	0.38	SLC29A1	solute carrier family 29 member 1 (Augustine blood group) [S
9	204824_at	0.83	−1.33	0.44	ENDOG	endonuclease G [Source:HGNC Symbol;Acc:HGNC:3346]
10	204432_at	0.88	−1.32	0.51	SOX12	SRY−box 12 [Source:HGNC Symbol;Acc:HGNC:11198]
11	204610_s_at	0.49	−1.32	0.53	CCDC85B	coiled−coil domain containing 85B [Source:HGNC Symbol;Ac
12	204411_at	0.91	−1.32	0.24	KIF21B	kinesin family member 21B [Source:HGNC Symbol;Acc:HGN
13	218524_at	0.6	−1.3	0.5	E4F1	E4F transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:
14	213947_s_at	0.7	−1.28	0.54	NUP210	nucleoporin 210 [Source:HGNC Symbol;Acc:HGNC:30052]
15	212303_x_at	0.6	−1.28	0.51		
16	210062_s_at	0.92	−1.26	0.45	ZNF589	zinc finger protein 589 [Source:HGNC Symbol;Acc:HGNC:16
17	209832_s_at	0.51	−1.24	0.58	CDT1	chromatin licensing and DNA replication factor 1 [Source:HG
18	218555_at	0.58	−1.24	0.51	ANAPC2	anaphase promoting complex subunit 2 [Source:HGNC Symb
19	220007_at	1.01	−1.24	0.37	METTL8	methyltransferase like 8 [Source:HGNC Symbol;Acc:HGNC:2
20	204993_at	1.61	−1.23	0.31	GNAZ	G protein subunit alpha z [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−18	43 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	2e−12	21 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
3	2e−12	44 / 1107	TF	ICGC_Myc_targets
4	2e−11	32 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	6e−11	11 / 55	HM	HALLMARK_MYC_TARGETS_V2
6	6e−11	9 / 30	GSEA	SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY
7	1e−10	16 / 159	GSEA	SANSOM_APC_TARGETS_REQUIRE_MYC
8	3e−10	20 / 280	GSEA	MANALO_HYPOXIA_DN
9	2e−09	27 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
10	6e−09	39 / 1161	MF	RNA binding
11	1e−08	14 / 158	GSEA	BILD_MYC_ONCOGENIC_SIGNATURE
12	1e−08	78 / 3564	TF	ICGC_Taf1_targets
13	5e−08	61 / 2541	CC	nucleoplasm
14	1e−07	44 / 1578	TF	ICGC_GabpPcr2_targets
15	2e−07	69 / 3150	TF	ICGC_Creb1_targets
16	4e−07	7 / 38	Gliom	WILLSCHER_GBM_Verhaak−PNwt_up
17	6e−07	77 / 3804	TF	ICGC_Stat5_targets
18	6e−07	14 / 220	GSEA	BHAT_ESR1_TARGETS_VIA_AKT1_UP
19	7e−07	9 / 81	Gliom	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
20	9e−07	87 / 4579	CC	nucleus
21	1e−06	41 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
22	1e−06	22 / 549	TF	ICGC_Atf3_targets
23	1e−06	83 / 4319	TF	ICGC_Pou2_targets
24	2e−06	25 / 703	GSEA	LEE_BMP2_TARGETS_DN
25	2e−06	80 / 4131	TF	ICGC_Tcf3_targets
26	2e−06	73 / 3630	TF	ICGC_Sp1_targets
27	2e−06	8 / 70	GSEA	JAIN_NFKB_SIGNALING
28	3e−06	65 / 3121	TF	ICGC_Egr1_targets
29	3e−06	72 / 3608	TF	ICGC_Tcf12_targets
30	3e−06	12 / 186	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
31	4e−06	63 / 2994	TF	ICGC_Zeb1_targets
32	4e−06	27 / 833	Chr	Chr 19
33	4e−06	74 / 3769	TF	ICGC_Pmlsc71910_targets
34	4e−06	12 / 190	HM	HALLMARK_MYC_TARGETS_V1
35	7e−06	80 / 4261	Lymp	HOPP_Txn_transition
36	8e−06	6 / 39	GSEA	IRITANI_MAD1_TARGETS_DN
37	9e−06	15 / 314	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
38	9e−06	80 / 4278	TF	ICGC_Yy1_targets
39	1e−05	4 / 12	GSEA	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
40	1e−05	11 / 174	BP	rRNA processing


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	5e−08	61 / 2541	nucleoplasm
2	9e−07	87 / 4579	nucleus
3	3e−05	5 / 30	small−subunit processome
4	2e−04	20 / 653	nucleolus
5	5e−04	29 / 1221	mitochondrion
6	2e−03	3 / 19	nuclear periphery
7	2e−03	3 / 20	preribosome, large subunit precursor
8	2e−03	6 / 107	fibrillar center
9	3e−03	5 / 77	catalytic step 2 spliceosome
10	7e−03	9 / 270	cellular_component
11	7e−03	10 / 324	chromosome
12	1e−02	2 / 13	exosome (RNase complex)
13	1e−02	2 / 15	small nuclear ribonucleoprotein complex
14	2e−02	3 / 43	Cajal body
15	2e−02	5 / 128	spliceosomal complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−04	18 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	6e−04	28 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	2e−03	16 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	6e−02	29 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
5	8e−02	1 / 7	TCGA_Mutated−in−CRC_mismatch−repair−genes
6	1e−01	1 / 12	Juehling_HNPCC−mutated−in−4
7	2e−01	1 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
8	2e−01	18 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
9	3e−01	1 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
10	3e−01	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
11	4e−01	18 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
12	5e−01	7 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	5e−01	1 / 60	Marisa_CRC−cluster−g
14	6e−01	2 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
15	6e−01	10 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_

HM

Rank	p−value	#in/all	Geneset
1	6e−11	11 / 55	HALLMARK_MYC_TARGETS_V2
2	4e−06	12 / 190	HALLMARK_MYC_TARGETS_V1
3	7e−04	9 / 195	HALLMARK_G2M_CHECKPOINT
4	3e−02	6 / 187	HALLMARK_E2F_TARGETS
5	4e−02	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	4e−02	5 / 149	HALLMARK_UV_RESPONSE_UP
7	9e−02	5 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
8	1e−01	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	2e−01	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	3e−01	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	4e−01	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
12	6e−01	2 / 173	HALLMARK_MITOTIC_SPINDLE
13	7e−01	2 / 182	HALLMARK_GLYCOLYSIS
14	7e−01	2 / 191	HALLMARK_P53_PATHWAY
15	7e−01	1 / 97	HALLMARK_BILE_ACID_METABOLISM

Lymphnoma

Rank	p−value	#in/all	Geneset
1	7e−06	80 / 4261	HOPP_Txn_transition
2	3e−04	91 / 5529	HOPP_Txn_elongation
3	1e−03	8 / 173	Victora_Light zone signature
4	6e−03	90 / 5908	HOPP_Active_promoter
5	2e−02	19 / 906	SPANG_BCR DN
6	2e−02	2 / 18	WRIGHT_ABC UP
7	2e−02	4 / 88	ROSOLOWSKI_green UP
8	5e−02	18 / 955	SPANG_BCR UP
9	6e−02	4 / 121	ROSOLOWSKI_green total
10	7e−02	8 / 353	SPANG_CD40 6hrs DN
11	1e−01	1 / 10	MASCQUE_ABC UP
12	1e−01	1 / 12	Subero_MM_hypo_meth
13	2e−01	74 / 5404	HOPP_Strong_enhancer
14	2e−01	2 / 57	SPANG_LPS 6hrs DN
15	2e−01	1 / 17	DAVE_c−myc BL UP

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−04	5 / 55	hsa−miR−637
2	2e−03	5 / 72	hsa−miR−149
3	2e−03	5 / 73	hsa−miR−423−5p
4	5e−03	3 / 28	hsa−miR−654−5p
5	8e−03	4 / 64	hsa−miR−486−3p
6	1e−02	3 / 36	hsa−miR−541
7	1e−02	5 / 109	hsa−miR−485−5p
8	1e−02	2 / 15	hsa−miR−598
9	2e−02	2 / 19	hsa−miR−943
10	2e−02	3 / 49	hsa−miR−671−5p
11	2e−02	3 / 49	hsa−miR−330−5p
12	2e−02	4 / 89	hsa−miR−526b
13	3e−02	3 / 52	hsa−miR−1278
14	3e−02	2 / 22	hsa−miR−1225−3p
15	4e−02	3 / 58	hsa−miR−433

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	1e−05	11 / 174	rRNA processing
2	1e−04	4 / 20	tRNA modification
3	4e−04	8 / 144	methylation
4	1e−03	5 / 67	tRNA processing
5	2e−03	3 / 20	ribosomal large subunit biogenesis
6	3e−03	9 / 233	RNA splicing
7	3e−03	10 / 281	mRNA processing
8	4e−03	11 / 351	cellular response to DNA damage stimulus
9	5e−03	5 / 90	RNA processing
10	6e−03	3 / 30	histone acetylation
11	6e−03	4 / 59	positive regulation of protein targeting to mitochondrion
12	6e−03	2 / 10	intra−S DNA damage checkpoint
13	6e−03	2 / 10	regulation of DNA methylation
14	7e−03	6 / 137	DNA replication
15	8e−03	2 / 11	phosphatidylethanolamine biosynthetic process

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	27 / 833	Chr 19
2	2e−02	13 / 548	Chr 16
3	3e−02	16 / 756	Chr 11
4	9e−02	8 / 369	Chr 20
5	1e−01	7 / 333	Chr 22
6	2e−01	12 / 700	Chr 12
7	4e−01	4 / 242	Chr 13
8	5e−01	2 / 139	Chr 21
9	6e−01	5 / 403	Chr 14
10	6e−01	8 / 689	Chr 3
11	6e−01	9 / 776	Chr 17
12	7e−01	2 / 184	Chr 18
13	7e−01	5 / 492	Chr 9
14	9e−01	3 / 382	Chr 15
15	9e−01	4 / 490	Chr 10

Glioma

Rank	p−value	#in/all	Geneset
1	4e−07	7 / 38	WILLSCHER_GBM_Verhaak−PNwt_up
2	7e−07	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	8e−03	27 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−02	14 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
5	6e−02	26 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	1e−01	1 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
7	1e−01	1 / 11	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
8	1e−01	1 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
9	3e−01	1 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	3e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
11	4e−01	1 / 35	Gorovets_LGG_EPL_subclass
12	4e−01	3 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
13	4e−01	1 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	5e−01	1 / 50	Vishal_subnetwork signature of survival in GBM
15	5e−01	1 / 52	GIEZELT_GBM_WT_down_VS_mut

Immunome

Rank	p−value	#in/all	Geneset
1	0.06	1 / 5	Angelova_immune−metagene−NKT
2	0.15	1 / 13	Angelova_immune−metagene−immature_B−cells
3	0.28	1 / 26	Angelova_immune−metagene−activated_CD4
4	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
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 / 11	Angelova_immune−metagene−macrophages
15	1.00	0 / 38	Angelova_immune−metagene−mast−cells

Melanoma

Rank	p−value	#in/all	Geneset
1	0.02	8 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	0.25	1 / 23	Melanoma Epi−Enzyme Cluster 7
3	0.26	1 / 24	Gerami_melanoma−metastatic−risk_DN
4	0.34	4 / 236	Gerber_wt/wt_group3−specific
5	0.42	1 / 44	Tirosh_top50 correlated genes PC2
6	0.63	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
7	0.76	3 / 319	Gerber_wt/wt_melanoma−cells−SpotA
8	0.78	2 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	0.82	2 / 249	Gerber_wt/wt_melanoma−cells−SpotE
10	0.88	1 / 171	Landsberg_dedifferentiation_up
11	0.90	1 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
12	0.91	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	0.94	1 / 222	Gerber_wt/wt_melanoma−cells−SpotF
14	1.00	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD
15	1.00	0 / 17	Hugo_melanoma−all−MET_UP

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.07	5 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.49	1 / 54	Burnham_timecourse
3	0.82	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
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

TF

Rank	p−value	#in/all	Geneset
1	2e−12	44 / 1107	ICGC_Myc_targets
2	1e−08	78 / 3564	ICGC_Taf1_targets
3	1e−07	44 / 1578	ICGC_GabpPcr2_targets
4	2e−07	69 / 3150	ICGC_Creb1_targets
5	6e−07	77 / 3804	ICGC_Stat5_targets
6	1e−06	22 / 549	ICGC_Atf3_targets
7	1e−06	83 / 4319	ICGC_Pou2_targets
8	2e−06	80 / 4131	ICGC_Tcf3_targets
9	2e−06	73 / 3630	ICGC_Sp1_targets
10	3e−06	65 / 3121	ICGC_Egr1_targets
11	3e−06	72 / 3608	ICGC_Tcf12_targets
12	4e−06	63 / 2994	ICGC_Zeb1_targets
13	4e−06	74 / 3769	ICGC_Pmlsc71910_targets
14	9e−06	80 / 4278	ICGC_Yy1_targets
15	1e−05	84 / 4602	ICGC_Elf1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 14	BENTINK_myc.1
2	2e−03	13 / 409	Lembcke_Normal vs Adenoma
3	1e−02	2 / 15	GENTLES_modul2
4	4e−02	3 / 58	SHAUGHNESSY_MM high risk
5	9e−02	2 / 41	PanCan_DNARepair_geneset_nanostring
6	1e−01	2 / 45	KUIPER_MM poor survival
7	1e−01	1 / 10	GENTLES_modul3
8	2e−01	1 / 13	GENTLES_modul1
9	2e−01	1 / 15	GENTLES_modul4
10	2e−01	1 / 16	LIU_LIVER_CANCER
11	2e−01	1 / 16	WOLFER_overlap genes
12	2e−01	1 / 16	GENTLES_modul6
13	2e−01	3 / 130	PanCan_CC+Apop_geneset_nanostring
14	2e−01	1 / 20	PanCan_ChromMod_geneset_nanostring
15	4e−01	0 / 14	LIU_COMMON_CANCER_GENES

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−16	81 / 2704	4_TxTrans_Fibroblasts
2	1e−15	120 / 5620	TssF_Colon
3	1e−15	107 / 4595	6_EnhG_Melanocytes
4	4e−15	143 / 7833	Bcells peripheral blood_1_TssA
5	5e−15	144 / 7957	Tcells peripheral blood_2_TssAFlnk
6	1e−14	100 / 4208	Tcells peripheral blood_6_EnhG
7	2e−14	147 / 8370	natural killer cells peripheral blood_2_TssAFlnk
8	3e−14	147 / 8406	Bcells peripheral blood_2_TssAFlnk
9	1e−13	144 / 8200	monocytes peripheral blood_2_TssAFlnk
10	3e−13	144 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
11	2e−12	71 / 2563	Mid_Frontal_Lobe_ZNF
12	2e−12	90 / 3803	6_EnhG_Fibroblasts
13	1e−11	142 / 8322	T CD8+ naive cells peripheral blood_1_TssA
14	2e−11	136 / 7751	natural killer cells peripheral blood_1_TssA
15	3e−11	146 / 8816	Thelper cells peripheral blood_2_TssAFlnk

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−18	43 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	2e−12	21 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
3	2e−11	32 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
4	6e−11	9 / 30	SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY
5	1e−10	16 / 159	SANSOM_APC_TARGETS_REQUIRE_MYC
6	3e−10	20 / 280	MANALO_HYPOXIA_DN
7	2e−09	27 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	1e−08	14 / 158	BILD_MYC_ONCOGENIC_SIGNATURE
9	6e−07	14 / 220	BHAT_ESR1_TARGETS_VIA_AKT1_UP
10	1e−06	41 / 1527	PUJANA_BRCA1_PCC_NETWORK
11	2e−06	25 / 703	LEE_BMP2_TARGETS_DN
12	2e−06	8 / 70	JAIN_NFKB_SIGNALING
13	3e−06	12 / 186	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
14	8e−06	6 / 39	IRITANI_MAD1_TARGETS_DN
15	9e−06	15 / 314	PENG_GLUTAMINE_DEPRIVATION_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.2	1 / 22	DUMEAUX_High bmi enriched genes
3	0.2	1 / 22	DUMEAUX_Fasting enriched genes
4	0.9	1 / 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 / 12	DUMEAUX_Women normal BMI literature genes up
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

MF

Rank	p−value	#in/all	Geneset
1	6e−09	39 / 1161	RNA binding
2	1e−04	24 / 852	nucleic acid binding
3	2e−04	8 / 132	methyltransferase activity
4	1e−03	4 / 38	4 iron, 4 sulfur cluster binding
5	2e−03	10 / 267	binding
6	4e−03	3 / 25	nuclear localization sequence binding
7	4e−03	4 / 53	iron−sulfur cluster binding
8	9e−03	2 / 12	GTPase inhibitor activity
9	9e−03	2 / 12	methyl−CpG binding
10	1e−02	3 / 36	ligand−dependent nuclear receptor transcription coactivator activity
11	2e−02	2 / 16	3'−5' exonuclease activity
12	2e−02	2 / 16	snoRNA binding
13	2e−02	4 / 81	single−stranded DNA binding
14	3e−02	2 / 23	oxidoreductase activity, acting on the CH−CH group of donors
15	4e−02	24 / 1329	transferase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−05	25 / 866	PROTEINATLAS_cerebellum
2	1e−04	10 / 188	Chaussabel_3,8_Enzymes
3	5e−04	26 / 1048	PROTEINATLAS_rectum
4	6e−04	21 / 776	PROTEINATLAS_skin
5	8e−04	26 / 1076	PROTEINATLAS_stomach
6	1e−03	27 / 1161	PROTEINATLAS_colon
7	1e−03	13 / 399	PROTEINATLAS_soft tissue
8	2e−03	25 / 1081	PROTEINATLAS_testis
9	3e−03	24 / 1048	PROTEINATLAS_gallbladder
10	3e−03	16 / 594	PROTEINATLAS_parathyroid gland
11	4e−03	23 / 1022	PROTEINATLAS_placenta
12	7e−03	16 / 645	PROTEINATLAS_bone marrow
13	7e−03	23 / 1072	PROTEINATLAS_duodenum
14	7e−03	15 / 593	PROTEINATLAS_lateral ventricle
15	8e−03	15 / 604	PROTEINATLAS_hippocampus

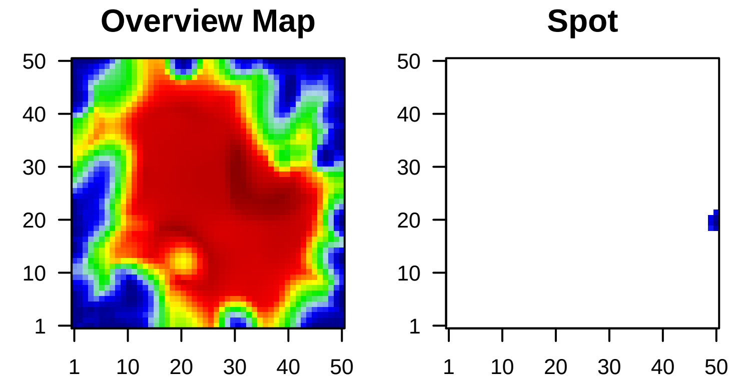
Underexpression Spots

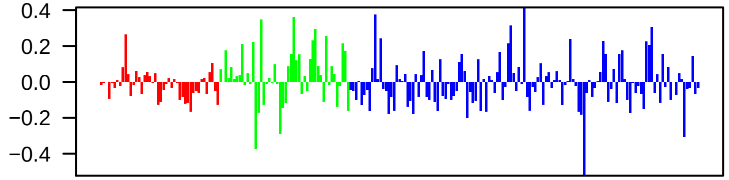
Spot Summary: p

metagenes = 7
genes = 153

<r> metagenes = 0.97
<r> genes = 0.16
beta: r2= 1.83 / log p= −Inf

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



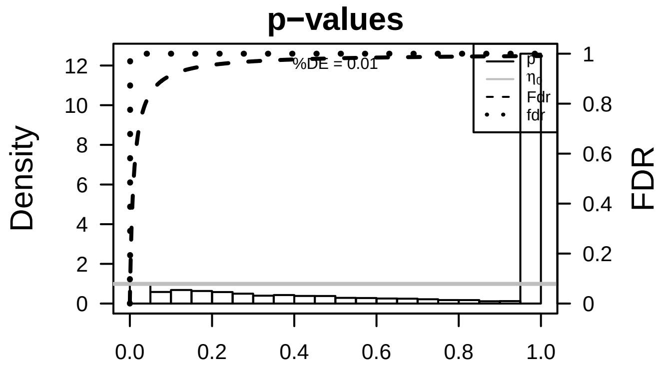


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	206398_s_at	0.54	−2.74	0.36	CD19	CD19 molecule [Source:HGNC Symbol;Acc:HGNC:1633]
2	221969_at	0.56	−2.69	0.39	PAX5	paired box 5 [Source:HGNC Symbol;Acc:HGNC:8619]
3	207339_s_at	0.9	−2.49	0.34	LTB	lymphotoxin beta [Source:HGNC Symbol;Acc:HGNC:6711]
4	34210_at	0.49	−2.36	0.39	CD52	CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
5	219497_s_at	0.65	−2.34	0.47	BCL11A	B cell CLL/lymphoma 11A [Source:HGNC Symbol;Acc:HGNC
6	207540_s_at	0.59	−2.29	0.29	SYK	spleen associated tyrosine kinase [Source:HGNC Symbol;Ac
7	217422_s_at	0.82	−2.27	0.49	CD22	CD22 molecule [Source:HGNC Symbol;Acc:HGNC:1643]
8	203233_at	0.65	−2.11	0.4	IL4R	interleukin 4 receptor [Source:HGNC Symbol;Acc:HGNC:601
9	218303_x_at	0.58	−2.06	0.46	KRCC1	lysine rich coiled−coil 1 [Source:HGNC Symbol;Acc:HGNC:2
10	210279_at	1.15	−2.01	0.42	GPR18	G protein−coupled receptor 18 [Source:HGNC Symbol;Acc:H
11	205671_s_at	1.08	−2	0.53	HLA−DOB	major histocompatibility complex, class II, DO beta [Source:H
12	203569_s_at	0.61	−1.92	0.47	OFD1	OFD1, centriole and centriolar satellite protein [Source:HGNC
13	215836_s_at	0.87	−1.8	0.49	PCDHGA5	protocadherin gamma subfamily A, 5 [Source:HGNC Symbol;
14	206206_at	0.62	−1.76	0.29	CD180	CD180 molecule [Source:HGNC Symbol;Acc:HGNC:6726]
15	204352_at	0.85	−1.73	0.55	TRAF5	TNF receptor associated factor 5 [Source:HGNC Symbol;Acc
16	207677_s_at	0.55	−1.68	0.3	NCF4	neutrophil cytosolic factor 4 [Source:HGNC Symbol;Acc:HGN
17	214084_x_at	0.65	−1.66	0.5	NCF1	neutrophil cytosolic factor 1 [Source:HGNC Symbol;Acc:HGN
18	209306_s_at	0.65	−1.65	0.55	SWAP70	switching B cell complex subunit SWAP70 [Source:HGNC Sy
19	204057_at	0.62	−1.64	0.47	IRF8	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:HG
20	209539_at	0.7	−1.64	0.16	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor 6 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−14	98 / 5404	Lympl	HOPP_Strong_enhancer
2	9e−08	8 / 56	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
3	1e−07	6 / 24	Melar	Tirosh_B−cell specific genes−melanoma
4	2e−07	90 / 5908	Lympl	HOPP_Active_promoter
5	3e−07	7 / 45	Lympl	Monti_BCR_cluster
6	8e−07	7 / 51	GSEA	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
7	8e−07	72 / 4357	Lympl	HOPP_Weak_txn
8	1e−06	5 / 19	GSEA	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
9	1e−06	6 / 34	Lympl	TARTE_B−cell signature
10	1e−06	6 / 35	GSEA	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
11	2e−06	17 / 429	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
12	3e−06	83 / 5529	Lympl	HOPP_Txn_elongation
13	4e−06	6 / 42	Refer	Chaussabel_1,3_B−cells
14	1e−05	83 / 5682	Lympl	HOPP_Weak_promoter
15	2e−05	12 / 263	Lympl	SPANG_CD40 6hrs UP
16	4e−05	66 / 4261	Lympl	HOPP_Txn_transition
17	4e−05	9 / 163	GSEA	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
18	6e−05	18 / 621	BP	negative regulation of transcription from RNA polymerase II promoter
19	8e−05	33 / 1636	TF	ICGC_Bcl11_targets
20	1e−04	13 / 368	GSEA	ZHENG_BOUND_BY_FOXP3
21	1e−04	10 / 227	Lympl	SPANG_IL21 UP
22	1e−04	26 / 1166	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
23	1e−04	3 / 10	BP	respiratory burst
24	1e−04	10 / 229	GSEA	QI_PLASMACYTOMA_UP
25	2e−04	9 / 195	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
26	2e−04	5 / 52	GSEA	SMIRNOV_RESPONSE_TO_IR_2HR_DN
27	2e−04	7 / 121	GSEA	PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
28	2e−04	30 / 1508	TF	ICGC_Mef2_targets
29	3e−04	5 / 59	GSEA	PID_BCR_5PATHWAY
30	3e−04	16 / 589	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
31	3e−04	4 / 33	GSEA	ZHAN_MULTIPLE_MYELOMA_PR_DN
32	4e−04	30 / 1550	GSEA	PILON_KLF1_TARGETS_DN
33	4e−04	5 / 61	GSEA	BASSO_CD40_SIGNALING_DN
34	4e−04	3 / 15	GSEA	XU_RESPONSE_TO_TRETINOIN_UP
35	4e−04	6 / 96	Lympl	SPANG_LPS 6hrs UP
36	5e−04	4 / 36	GSEA	NAKAYAMA_FRA2_TARGETS
37	5e−04	10 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
38	5e−04	3 / 16	Gliom	VERHAAK_MES subtype
39	6e−04	4 / 38	GSEA	GENTILE_UV_RESPONSE_CLUSTER_D7
40	6e−04	4 / 38	GSEA	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_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	

CC

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 17	T cell receptor complex
2	2e−03	55 / 3805	cytosol
3	6e−03	2 / 12	HOPS complex
4	2e−02	3 / 51	clathrin−coated vesicle
5	2e−02	3 / 51	endoplasmic reticulum−Golgi intermediate compartment
6	2e−02	2 / 20	COPII−coated ER to Golgi transport vesicle
7	2e−02	3 / 56	lipid droplet
8	3e−02	2 / 25	basal plasma membrane
9	3e−02	17 / 1016	intracellular
10	3e−02	10 / 494	endosome
11	5e−02	5 / 196	nuclear membrane
12	6e−02	15 / 938	Golgi apparatus
13	6e−02	4 / 146	lamellipodium
14	7e−02	2 / 42	Cul3−RING ubiquitin ligase complex
15	7e−02	2 / 42	sarcoplasmic reticulum

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	26 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
2	3e−04	16 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	4e−03	29 / 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	13 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
6	5e−02	6 / 255	Kosinski_top−crypt−long−list
7	5e−02	2 / 35	Ang_CRC_Hypomethylated
8	9e−02	15 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	9e−02	13 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
10	1e−01	1 / 15	TCGA−CRC_less−agressive−disease−markers
11	2e−01	12 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
12	2e−01	71 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
13	2e−01	5 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	2e−01	5 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
15	2e−01	3 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

HM

Rank	p−value	#in/all	Geneset
1	0.03	5 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.09	4 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.18	3 / 141	HALLMARK_UV_RESPONSE_DN
4	0.26	2 / 97	HALLMARK_PEROXISOME
5	0.26	3 / 174	HALLMARK_APICAL_JUNCTION
6	0.28	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
7	0.30	1 / 34	HALLMARK_APICAL_SURFACE
8	0.30	1 / 34	HALLMARK_ANGIOGENESIS
9	0.30	3 / 188	HALLMARK_HYPOXIA
10	0.30	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
11	0.31	3 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.31	3 / 191	HALLMARK_P53_PATHWAY
13	0.31	3 / 192	HALLMARK_MTORC1_SIGNALING
14	0.32	3 / 193	HALLMARK_HEME_METABOLISM
15	0.32	3 / 194	HALLMARK_KRAS_SIGNALING_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−14	98 / 5404	HOPP_Strong_enhancer
2	2e−07	90 / 5908	HOPP_Active_promoter
3	3e−07	7 / 45	Monti_BCR_cluster
4	8e−07	72 / 4357	HOPP_Weak_txn
5	1e−06	6 / 34	TARTE_B−cell signature
6	3e−06	83 / 5529	HOPP_Txn_elongation
7	1e−05	83 / 5682	HOPP_Weak_promoter
8	2e−05	12 / 263	SPANG_CD40 6hrs UP
9	4e−05	66 / 4261	HOPP_Txn_transition
10	1e−04	10 / 227	SPANG_IL21 UP
11	4e−04	6 / 96	SPANG_LPS 6hrs UP
12	6e−04	3 / 17	Aukema_BCL2 UP_BCL6 DN
13	7e−04	21 / 955	SPANG_BCR UP
14	9e−04	20 / 906	SPANG_BCR DN
15	2e−02	9 / 378	TARTE_Mature plasma cell signature

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	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	0.011	3 / 45	hsa−miR−891b
6	0.018	5 / 148	hsa−miR−1
7	0.019	6 / 205	hsa−miR−548p
8	0.020	3 / 56	hsa−miR−618
9	0.020	4 / 101	hsa−miR−155
10	0.022	3 / 59	hsa−miR−643
11	0.024	5 / 160	hsa−miR−545
12	0.025	8 / 344	hsa−miR−19b
13	0.026	3 / 62	hsa−miR−578
14	0.029	4 / 114	hsa−miR−494
15	0.032	3 / 68	hsa−miR−767−5p

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	6e−05	18 / 621	negative regulation of transcription from RNA polymerase II promoter
2	1e−04	3 / 10	respiratory burst
3	8e−04	6 / 106	regulation of small GTPase mediated signal transduction
4	2e−03	3 / 26	cellular response to dexamethasone stimulus
5	3e−03	4 / 56	regulation of Rho protein signal transduction
6	3e−03	9 / 288	positive regulation of apoptotic process
7	5e−03	4 / 66	interferon−gamma−mediated signaling pathway
8	5e−03	2 / 11	leukotriene biosynthetic process
9	6e−03	2 / 12	actin polymerization or depolymerization
10	6e−03	2 / 12	negative regulation of fatty acid biosynthetic process
11	6e−03	5 / 115	actin cytoskeleton organization
12	7e−03	3 / 39	B cell receptor signaling pathway
13	9e−03	2 / 14	motor neuron axon guidance
14	1e−02	2 / 15	negative regulation of cell−matrix adhesion
15	1e−02	2 / 15	oogenesis

Chr

Rank	p−value	#in/all	Geneset
1	0.005	13 / 556	Chr X
2	0.017	12 / 585	Chr 7
3	0.231	6 / 403	Chr 14
4	0.231	11 / 832	Chr 2
5	0.235	4 / 242	Chr 13
6	0.329	7 / 548	Chr 16
7	0.386	6 / 490	Chr 10
8	0.417	2 / 139	Chr 21
9	0.464	5 / 437	Chr 8
10	0.502	6 / 554	Chr 5
11	0.552	4 / 382	Chr 15
12	0.562	7 / 689	Chr 3
13	0.569	5 / 492	Chr 9
14	0.666	3 / 333	Chr 22
15	0.728	4 / 480	Chr 4

Glioma

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 16	VERHAAK_MES subtype
2	6e−04	5 / 67	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
3	2e−03	9 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
4	6e−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	2e−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	9 / 423	Down_a
11	4e−02	6 / 239	ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN
12	4e−02	2 / 30	Shaw_responders_down_in_oligo_glioma
13	5e−02	5 / 191	ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN
14	5e−02	6 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
15	5e−02	4 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

Immunome

Rank	p−value	#in/all	Geneset
1	0.004	2 / 10	Angelova_immune−metagene−TFH
2	0.008	2 / 13	Angelova_immune−metagene−activated_B−cells
3	0.008	2 / 13	Angelova_immune−metagene−immature_B−cells
4	0.040	1 / 4	Angelova_CRC_MHC_class_II
5	0.079	1 / 8	Immunity_HLA−class−II
6	0.169	1 / 18	Angelova_immune−metagene−pDC
7	0.211	1 / 23	Angelova_immune−metagene−Treg
8	0.258	1 / 29	Angelova_immune−metagene−Th1
9	0.281	1 / 32	Angelova_immune−metagene−effector_memory_CD8
10	0.499	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

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	1e−01	2 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
4	1e−01	3 / 107	Tirosh_Exhaustion program in Mel75
5	1e−01	4 / 171	Landsberg_dedifferentiation_up
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	1 / 81	Tirosh_Genes in the MITF program
14	6e−01	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
15	6e−01	2 / 189	Tirosh_genes preferentially expressed by Tregs

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.002	7 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.344	1 / 41	Scicluna_DN
3	0.390	1 / 48	Burnham_cap_fp_vs_con_DN
4	0.390	1 / 48	Burnham_viral_DN
5	0.403	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
6	0.415	1 / 52	Burnham_day1_vs_5_DN
7	0.427	1 / 54	Burnham_timecourse
8	0.438	1 / 56	Burnham_sep_vs_con_DN
9	0.504	1 / 68	Burnham_sep_vs_con_UP
10	0.519	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

TF

Rank	p−value	#in/all	Geneset
1	8e−05	33 / 1636	ICGC_Bcl11_targets
2	2e−04	30 / 1508	ICGC_Mef2_targets
3	1e−03	36 / 2150	ICGC_Irf4_targets
4	2e−03	38 / 2321	ICGC_Rad21_targets
5	2e−03	37 / 2254	ICGC_BatfPcr1_targets
6	2e−03	33 / 1941	ICGC_Bcl3_targets
7	2e−03	48 / 3213	ICGC_Pu1_targets
8	2e−03	27 / 1494	ICGC_Cebpbsc150_targets
9	6e−03	30 / 1848	ICGC_Pbx3_targets
10	7e−03	45 / 3121	ICGC_Egr1_targets
11	9e−03	19 / 1032	ICGC_Usf1_targets
12	9e−03	48 / 3435	ICGC_Ebfsc137065_targets
13	1e−02	47 / 3420	ICGC_Bclaf101388_targets
14	1e−02	51 / 3796	ICGC_Nficsc81335_targets
15	2e−02	49 / 3630	ICGC_Sp1_targets

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	2 / 6	ZHANG_MGUS up
2	0.025	10 / 480	Lembcke_Colonic Inflammation
3	0.116	1 / 12	GENTLES_modul12
4	0.116	1 / 12	HLA2_signature
5	0.125	1 / 13	GENTLES_modul11
6	0.125	1 / 13	GENTLES_modul18
7	0.125	1 / 13	BENTINK_e2f3.1
8	0.152	1 / 16	LIU_LIVER_CANCER
9	0.227	1 / 25	PanCan_HH_geneset_nanostring
10	0.371	1 / 45	KUIPER_MM poor survival
11	0.450	1 / 58	SHAUGHNESSY_MM high risk
12	0.524	1 / 72	PanCan_Wnt_geneset_nanostring
13	0.538	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.573	2 / 187	PanCan_PI3K_geneset_nanostring
15	0.606	4 / 409	Lembcke_Normal vs Adenoma

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−15	82 / 3767	Bcells peripheral blood_6_EnhG
2	2e−10	95 / 5716	Bcells peripheral blood_4_Tx
3	1e−08	89 / 5527	Tregulatory cells peripheral blood_4_Tx
4	4e−08	106 / 7407	natural killer cells peripheral blood_5_TxWk
5	1e−07	24 / 693	Bcells peripheral blood_3_TxFlnk
6	2e−07	87 / 5601	Thelper cells peripheral blood_4_Tx
7	2e−07	113 / 8406	Bcells peripheral blood_2_TssAFlnk
8	6e−07	104 / 7489	monocytes peripheral blood_5_TxWk
9	6e−07	96 / 6637	Tcells peripheral blood_5_TxWk
10	6e−07	107 / 7833	Bcells peripheral blood_1_TssA
11	2e−06	86 / 5738	monocytes peripheral blood_4_Tx
12	2e−06	105 / 7751	natural killer cells peripheral blood_1_TssA
13	2e−06	63 / 3682	natural killer cells peripheral blood_6_EnhG
14	4e−06	94 / 6651	Thelper cells peripheral blood_5_TxWk
15	5e−06	85 / 5766	natural killer cells peripheral blood_4_Tx

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−08	8 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
2	8e−07	7 / 51	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
3	1e−06	5 / 19	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
4	1e−06	6 / 35	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
5	2e−06	17 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	4e−05	9 / 163	ZHENG_FOXP3_TARGETS_IN_THYMUS_UP
7	1e−04	13 / 368	ZHENG_BOUND_BY_FOXP3
8	1e−04	10 / 229	QI_PLASMACYTOMA_UP
9	2e−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	3e−04	5 / 59	PID_BCR_5PATHWAY
13	3e−04	4 / 33	ZHAN_MULTIPLE_MYELOMA_PR_DN
14	4e−04	30 / 1550	PILON_KLF1_TARGETS_DN
15	4e−04	5 / 61	BASSO_CD40_SIGNALING_DN

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	0.116	1 / 12	DUMEAUX_Women normal BMI literature genes up
4	0.152	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.472	1 / 62	DUMEAUX_Smoking enriched genes
6	0.788	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

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	0.007	3 / 38	signal transducer activity, downstream of receptor
6	0.007	9 / 331	protein serine/threonine kinase activity
7	0.008	2 / 13	triglyceride lipase activity
8	0.011	5 / 130	guanyl−nucleotide exchange factor activity
9	0.011	2 / 16	phospholipid transporter activity
10	0.016	2 / 19	steroid binding
11	0.017	2 / 20	phosphatidylinositol−3,4−bisphosphate binding
12	0.018	6 / 202	GTPase activator activity
13	0.021	2 / 22	protein phosphatase 2A binding
14	0.024	92 / 7864	protein binding
15	0.028	3 / 64	phosphatidylinositol binding

Reference Signatures

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

Underexpression Spots

Spot Summary: q

metagenes = 6
genes = 101

<r> metagenes = 0.99
<r> genes = 0.23
beta: r2= 1.32 / log p= −Inf

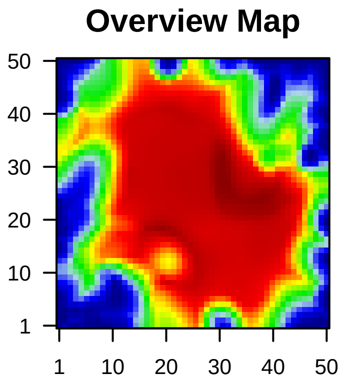
samples with spot = 3 (1.4 %)
intermediate : 1 (2.1 %)
non−mBL : 2 (1.6 %)

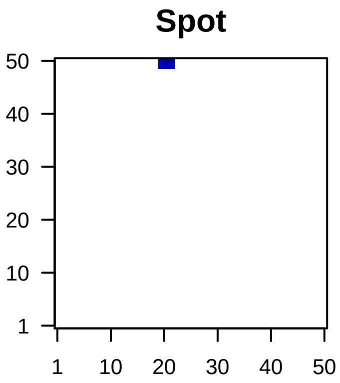
Spot Genelist

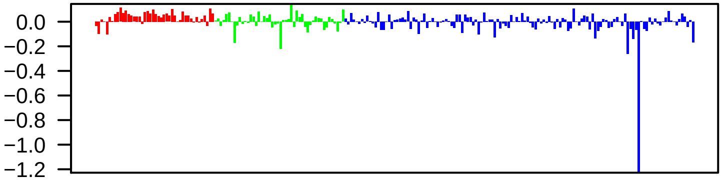
Rank	ID	max e	min e	r	Symbol	Description
1	209924_at	1.04	−2.14	0.39	CCL18	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:
2	202349_at	0.58	−1.99	0.53	TOR1A	torsin family 1 member A [Source:HGNC Symbol;Acc:HGNC:
3	201434_at	0.32	−1.96	0.65	TTC1	tetratricopeptide repeat domain 1 [Source:HGNC Symbol;Acc
4	217757_at	0.56	−1.95	0.42	A2M	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
5	221620_s_at	0.52	−1.93	0.6	APOO	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
6	218477_at	0.47	−1.79	0.53	TMEM14A	transmembrane protein 14A [Source:HGNC Symbol;Acc:HGN
7	32128_at	1.12	−1.78	0.33	CCL18	C−C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:
8	219083_at	0.49	−1.73	0.7	SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor [Source:HG
9	219547_at	0.45	−1.72	0.56	COX15	COX15, cytochrome c oxidase assembly homolog [Source:H
10	201937_s_at	0.84	−1.7	0.43	DNPEP	aspartyl aminopeptidase [Source:HGNC Symbol;Acc:HGNC:
11	204366_s_at	0.43	−1.68	0.71	GTF3C2	general transcription factor IIIC subunit 2 [Source:HGNC Sym
12	218493_at	0.58	−1.66	0.62	SNRNP25	small nuclear ribonucleoprotein U11/U12 subunit 25 [Source:
13	209796_s_at	0.5	−1.64	0.58		
14	201440_at	0.37	−1.64	0.55	DDX23	DEAD−box helicase 23 [Source:HGNC Symbol;Acc:HGNC:1
15	215165_x_at	0.54	−1.63	0.67	UMPS	uridine monophosphate synthetase [Source:HGNC Symbol;A
16	212405_s_at	0.5	−1.61	0.65	METTL13	methyltransferase like 13 [Source:HGNC Symbol;Acc:HGNC:
17	218361_at	0.75	−1.59	0.43	GOLPH3L	golgi phosphoprotein 3 like [Source:HGNC Symbol;Acc:HGN
18	222216_s_at	0.43	−1.57	0.65	MRPL17	mitochondrial ribosomal protein L17 [Source:HGNC Symbol;
19	218561_s_at	0.68	−1.55	0.48	LYRM4	LYR motif containing 4 [Source:HGNC Symbol;Acc:HGNC:21
20	201523_x_at	0.75	−1.53	0.61	UBE2N	ubiquitin conjugating enzyme E2 N [Source:HGNC Symbol;A

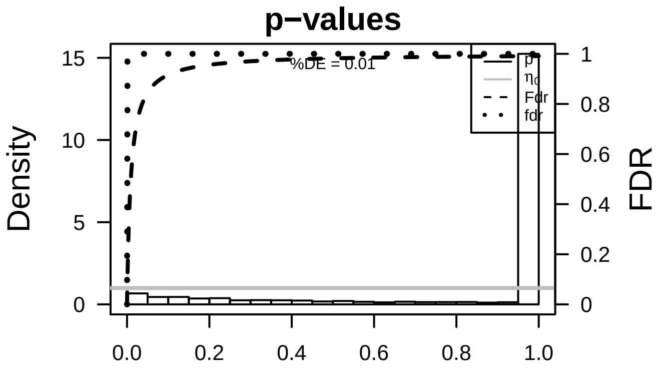
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−13	77 / 5908	Lymp	HOPP_Active_promoter
2	3e−11	71 / 5529	Lymp	HOPP_Txn_elongation
3	3e−08	67 / 5682	Lymp	HOPP_Weak_promoter
4	4e−08	18 / 540	GSE	TIEN_INTESTINE_PROBIOTICS_24HR_UP
5	5e−07	27 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
6	1e−06	9 / 152	Refer	Chaussabel_3,6_Mitochondrial ribosomal proteins
7	3e−06	22 / 1044	TF	ICGC_Six5_targets
8	8e−06	13 / 417	GSE	SHEN_SMARCA2_TARGETS_UP
9	1e−05	4 / 21	CC	mitochondrial small ribosomal subunit
10	1e−05	4 / 21	BP	mitochondrial translation
11	1e−05	8 / 156	GSE	TIEN_INTESTINE_PROBIOTICS_6HR_DN
12	3e−05	12 / 406	GSE	MOOTHA_HUMAN_MITODB_6_2002
13	4e−05	22 / 1221	CC	mitochondrion
14	5e−05	11 / 361	GSE	GARY_CD5_TARGETS_DN
15	5e−05	49 / 4261	Lymp	HOPP_Txn_transition
16	6e−05	25 / 1550	GSE	PILON_KLF1_TARGETS_DN
17	6e−05	20 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tra
18	1e−04	21 / 1241	TF	KIM_MYC targets
19	2e−04	9 / 277	CC	mitochondrial matrix
20	2e−04	8 / 219	Refer	WIRTH_GC B−cells
21	2e−04	9 / 280	GSE	MANALO_HYPOXIA_DN
22	2e−04	3 / 16	GSE	MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA
23	2e−04	18 / 1007	Refer	PROTEINATLAS_kidney
24	2e−04	22 / 1387	TF	HEBENSTREIT_high expression TF
25	3e−04	10 / 366	GSE	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
26	3e−04	4 / 46	CC	peroxisomal membrane
27	4e−04	6 / 133	HM	HALLMARK_DNA_REPAIR
28	5e−04	4 / 53	BP	mitochondrial translational termination
29	6e−04	23 / 1578	TF	ICGC_GabpPcr2_targets
30	6e−04	9 / 330	CC	mitochondrial inner membrane
31	6e−04	4 / 54	BP	mitochondrial translational elongation
32	6e−04	19 / 1190	GSE	BLALOCK_ALZHEIMERS_DISEASE_DN
33	6e−04	15 / 819	Refer	PROTEINATLAS_bronchus
34	8e−04	4 / 58	Gliom	Stuehler_Proteins_up_in_STS
35	8e−04	10 / 422	GSE	MOOTHA_MITOCHONDRIA
36	9e−04	22 / 1527	GSE	PUJANA_BRCA1_PCC_NETWORK
37	9e−04	9 / 352	GSE	MULLIGHAN_MLL_SIGNATURE_1_UP
38	9e−04	5 / 106	MF	ligase activity
39	1e−03	20 / 1338	GSE	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
40	1e−03	12 / 595	Refer	PROTEINATLAS_breast









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	4 / 21	mitochondrial translation
2	5e−04	4 / 53	mitochondrial translational termination
3	6e−04	4 / 54	mitochondrial translational elongation
4	1e−03	7 / 232	translation
5	2e−03	2 / 10	mitochondrial genome maintenance
6	2e−03	2 / 10	negative regulation of viral transcription
7	4e−03	2 / 13	organelle organization
8	6e−03	2 / 17	branched−chain amino acid catabolic process
9	6e−03	2 / 17	positive regulation of ubiquitin−protein transferase activity
10	9e−03	2 / 20	peroxisome organization
11	1e−02	2 / 22	mRNA polyadenylation
12	1e−02	3 / 64	transcription−coupled nucleotide−excision repair
13	1e−02	5 / 198	mRNA splicing, via spliceosome
14	1e−02	2 / 26	transcription elongation from RNA polymerase I promoter
15	2e−02	2 / 27	termination of RNA polymerase I transcription

Cancer

Rank	p−value	#in/all	Geneset
1	0.06	2 / 58	SHAUGHNESSY_MM high risk
2	0.07	1 / 10	GENTLES_modul5
3	0.10	1 / 15	GENTLES_modul7
4	0.18	1 / 28	PanCan_HK_geneset_nanostring
5	0.31	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.56	3 / 409	Lembcke_Normal vs Adenoma
7	0.65	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.66	2 / 317	SPANG_BCL6−index2
9	0.74	1 / 186	SPANG_LPS−index2
10	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
11	1.00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	1.00	0 / 12	LIU_BREAST_CANCER
13	1.00	0 / 14	LIU_COMMON_CANCER_GENES
14	1.00	0 / 16	LIU_LIVER_CANCER
15	1.00	0 / 14	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 21	mitochondrial small ribosomal subunit
2	4e−05	22 / 1221	mitochondrion
3	2e−04	9 / 277	mitochondrial matrix
4	3e−04	4 / 46	peroxisomal membrane
5	6e−04	9 / 330	mitochondrial inner membrane
6	3e−03	5 / 139	ribosome
7	4e−03	2 / 14	integral component of peroxisomal membrane
8	6e−03	39 / 3805	cytosol
9	6e−03	2 / 17	retromer complex
10	9e−03	2 / 20	integral component of mitochondrial inner membrane
11	2e−02	3 / 73	ubiquitin ligase complex
12	2e−02	2 / 30	small−subunit processome
13	2e−02	8 / 479	Golgi membrane
14	3e−02	3 / 92	peroxisome
15	3e−02	26 / 2541	nucleoplasm

Chr

Rank	p−value	#in/all	Geneset
1	0.01	12 / 832	Chr 2
2	0.06	9 / 700	Chr 12
3	0.12	8 / 689	Chr 3
4	0.20	6 / 548	Chr 16
5	0.25	3 / 242	Chr 13
6	0.29	7 / 756	Chr 11
7	0.34	11 / 1325	Chr 1
8	0.46	4 / 490	Chr 10
9	0.47	4 / 492	Chr 9
10	0.55	3 / 403	Chr 14
11	0.69	2 / 333	Chr 22
12	0.76	2 / 382	Chr 15
13	0.76	3 / 554	Chr 5
14	0.79	3 / 585	Chr 7
15	0.86	2 / 480	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−10	84 / 7833	Bcells peripheral blood_1_TssA
2	3e−10	62 / 4528	T CD8+ naive cells peripheral blood_4_Tx
3	8e−10	84 / 8068	Thelper cells peripheral blood_1_TssA
4	1e−09	83 / 7930	Tregulatory cells peripheral blood_1_TssA
5	2e−09	72 / 6099	HSC_4_Tx
6	2e−09	78 / 7078	Bcells peripheral blood_5_TxWk
7	1e−08	74 / 6637	Tcells peripheral blood_5_TxWk
8	2e−08	75 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
9	3e−08	80 / 7751	natural killer cells peripheral blood_1_TssA
10	3e−08	78 / 7420	Tcells peripheral blood_1_TssA
11	3e−08	83 / 8322	T CD8+ naive cells peripheral blood_1_TssA
12	4e−08	66 / 5601	Thelper cells peripheral blood_4_Tx
13	4e−08	79 / 7635	monocytes peripheral blood_1_TssA
14	4e−08	73 / 6651	Thelper cells peripheral blood_5_TxWk
15	5e−08	67 / 5753	Tcells peripheral blood_4_Tx

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−07	27 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
2	6e−05	20 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
3	1e−03	12 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	7e−03	10 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
5	1e−01	10 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
6	2e−01	11 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	3e−01	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
8	3e−01	2 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
9	4e−01	2 / 184	Kosinski_lower−crypt−long−list
10	4e−01	8 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
11	4e−01	1 / 83	Marisa_CRC−cluster−d
12	5e−01	2 / 255	Kosinski_top−crypt−long−list
13	6e−01	6 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
14	6e−01	8 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	7e−01	3 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv

Glioma

Rank	p−value	#in/all	Geneset
1	8e−04	4 / 58	Stuehler_Proteins_up_in_STS
2	4e−02	2 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
3	7e−02	2 / 59	GIEZELT_GBM_STS_up_VS_LTS
4	7e−02	16 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−01	4 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	1e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
7	2e−01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
8	2e−01	12 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	3e−01	2 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
10	3e−01	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
11	4e−01	4 / 421	Down_b
12	4e−01	1 / 66	Weller_LGG_gradeII−vs−III_DOWN
13	4e−01	1 / 78	Weller_LGG_A_vs_O_UP
14	4e−01	5 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
15	5e−01	1 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−08	18 / 540	TIEN_INTESTINE_PROBIOTICS_24HR_UP
2	8e−06	13 / 417	SHEN_SMARCA2_TARGETS_UP
3	1e−05	8 / 156	TIEN_INTESTINE_PROBIOTICS_6HR_DN
4	3e−05	12 / 406	MOOTHA_HUMAN_MITODB_6_2002
5	5e−05	11 / 361	GARY_CD5_TARGETS_DN
6	6e−05	25 / 1550	PILON_KLF1_TARGETS_DN
7	2e−04	9 / 280	MANALO_HYPOXIA_DN
8	2e−04	3 / 16	MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA
9	3e−04	10 / 366	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
10	6e−04	19 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
11	8e−04	10 / 422	MOOTHA_MITOCHONDRIA
12	9e−04	22 / 1527	PUJANA_BRCA1_PCC_NETWORK
13	9e−04	9 / 352	MULLIGHAN_MLL_SIGNATURE_1_UP
14	1e−03	20 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
15	1e−03	3 / 30	REACTOME_RNA_POL_III_TRANSCRIPTION

HM

Rank	p−value	#in/all	Geneset
1	4e−04	6 / 133	HALLMARK_DNA_REPAIR
2	1e−02	5 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	1e−02	5 / 192	HALLMARK_MTORC1_SIGNALING
4	2e−01	3 / 190	HALLMARK_MYC_TARGETS_V1
5	2e−01	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	2e−01	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
7	3e−01	2 / 139	HALLMARK_FATTY_ACID_METABOLISM
8	3e−01	1 / 55	HALLMARK_MYC_TARGETS_V2
9	4e−01	2 / 174	HALLMARK_ADIPOGENESIS
10	5e−01	1 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	5e−01	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	5e−01	1 / 97	HALLMARK_BILE_ACID_METABOLISM
13	5e−01	1 / 97	HALLMARK_PEROXISOME
14	6e−01	1 / 122	HALLMARK_SPERMATOGENESIS
15	6e−01	1 / 130	HALLMARK_COAGULATION

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 19	Angelova_immune−metagene−activated_CD8
2	0.3	1 / 42	Angelova_immune−metagene−TGD
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 / 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	0.7	1 / 150	Homuth_BMI−associated−genes_UP
2	0.8	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−13	77 / 5908	HOPP_Active_promoter
2	3e−11	71 / 5529	HOPP_Txn_elongation
3	3e−08	67 / 5682	HOPP_Weak_promoter
4	5e−05	49 / 4261	HOPP_Txn_transition
5	4e−03	44 / 4357	HOPP_Weak_txn
6	2e−02	43 / 4559	HOPP_Weak_enhancer
7	2e−02	13 / 955	SPANG_BCR UP
8	3e−02	23 / 2206	HOPP_Heterochrom
9	1e−01	5 / 353	SPANG_CD40 6hrs DN
10	1e−01	1 / 17	DAVE_c−myc BL UP
11	2e−01	43 / 5404	HOPP_Strong_enhancer
12	2e−01	1 / 40	CARO_OxPhos_in_DLBCL_UP
13	3e−01	1 / 42	Monti_OxPhos_cluster
14	3e−01	1 / 57	SPANG_LPS 6hrs DN
15	5e−01	1 / 85	Aukema_BCL2 DN_BCL6 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	1 / 4	Melanoma Epi−Enzyme Cluster 5
2	0.11	2 / 81	Tirosh_Genes in the MITF program
3	0.13	4 / 276	Gerber_wt/wt_melanoma−cells−SpotB
4	0.21	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
5	0.23	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
6	0.24	3 / 236	Gerber_wt/wt_group3−specific
7	0.24	1 / 38	Tirosh_top50 correlated genes PC1
8	0.25	1 / 41	Tirosh_top50 correlated genes PC3
9	0.26	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
10	0.31	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
11	0.38	2 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
12	0.43	2 / 204	Landsberg_dedifferentiation_down
13	0.43	1 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
14	0.74	1 / 189	Tirosh_genes preferentially expressed by Tregs
15	0.97	1 / 497	Gerber_wt/wt_melanoma−cells−SpotD

MF

Rank	p−value	#in/all	Geneset
1	9e−04	5 / 106	ligase activity
2	1e−03	5 / 109	structural constituent of ribosome
3	4e−03	4 / 90	unfolded protein binding
4	4e−03	5 / 148	ubiquitin protein ligase activity
5	2e−02	2 / 32	aminoacyl−tRNA ligase activity
6	2e−02	2 / 32	DNA−directed 5'−3' RNA polymerase activity
7	2e−02	16 / 1329	transferase activity
8	3e−02	5 / 237	ubiquitin−protein transferase activity
9	3e−02	14 / 1161	RNA binding
10	4e−02	2 / 42	pyridoxal phosphate binding
11	4e−02	14 / 1185	ATP binding
12	5e−02	2 / 51	ubiquitin binding
13	5e−02	2 / 53	ATP−dependent RNA helicase activity
14	7e−02	3 / 132	methyltransferase activity
15	7e−02	1 / 10	cyclosporin A binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	5 / 145	hsa−miR−607
2	0.007	6 / 236	hsa−miR−34a
3	0.026	5 / 234	hsa−miR−570
4	0.033	3 / 98	hsa−miR−520a−5p
5	0.042	1 / 6	hsa−miR−373*
6	0.044	2 / 47	hsa−miR−665
7	0.058	2 / 55	hsa−miR−637
8	0.062	1 / 9	hsa−miR−604
9	0.063	3 / 128	hsa−miR−518a−5p
10	0.064	2 / 58	hsa−miR−331−3p
11	0.068	3 / 132	hsa−miR−527
12	0.072	2 / 62	hsa−miR−578
13	0.074	2 / 63	hsa−miR−657
14	0.086	3 / 146	hsa−miR−548k
15	0.089	3 / 148	hsa−miR−196b

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.04	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.25	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	1.00	0 / 68	Burnham_sep_vs_con_UP
4	1.00	0 / 56	Burnham_sep_vs_con_DN
5	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
6	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
7	1.00	0 / 48	Burnham_viral_DN
8	1.00	0 / 57	Burnham_viral_UP
9	1.00	0 / 57	Burnham_day1_vs_5_UP
10	1.00	0 / 52	Burnham_day1_vs_5_DN
11	1.00	0 / 54	Burnham_timecourse
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	1e−06	9 / 152	Chaussabel_3,6_Mitochondrial ribosomal proteins
2	2e−04	8 / 219	WIRTH_GC B−cells
3	2e−04	18 / 1007	PROTEINATLAS_kidney
4	6e−04	15 / 819	PROTEINATLAS_bronchus
5	1e−03	12 / 595	PROTEINATLAS_breast
6	1e−03	5 / 113	Chaussabel_1,8_Metabolism Biosynthesis
7	3e−03	14 / 861	PROTEINATLAS_nasopharynx
8	3e−03	11 / 594	PROTEINATLAS_parathyroid gland
9	4e−03	16 / 1076	PROTEINATLAS_stomach
10	6e−03	15 / 1032	PROTEINATLAS_small intestine
11	6e−03	13 / 840	PROTEINATLAS_urinary bladder
12	7e−03	15 / 1048	PROTEINATLAS_gallbladder
13	7e−03	10 / 569	PROTEINATLAS_salivary gland
14	8e−03	6 / 245	Chaussabel_3,9_Kinases
15	8e−03	12 / 770	PROTEINATLAS_endometrium

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	22 / 1044	ICGC_Six5_targets
2	1e−04	21 / 1241	KIM_MYC targets
3	2e−04	22 / 1387	HEBENSTREIT_high expression TF
4	6e−04	23 / 1578	ICGC_GabpPcr2_targets
5	3e−02	34 / 3564	ICGC_Taf1_targets
6	4e−02	34 / 3630	ICGC_Sp1_targets
7	4e−02	35 / 3769	ICGC_Pmlsc71910_targets
8	4e−02	35 / 3778	ICGC_Pol24_targets
9	4e−02	13 / 1089	ICGC_Ets1_targets
10	5e−02	35 / 3796	ICGC_Nficsc81335_targets
11	5e−02	32 / 3420	ICGC_Bclaf101388_targets
12	5e−02	34 / 3703	ICGC_Foxm1_targets
13	6e−02	19 / 1848	ICGC_Pbx3_targets
14	7e−02	17 / 1630	ICGC_SrfV0416101_targets
15	7e−02	36 / 4072	ICGC_Mta3_targets

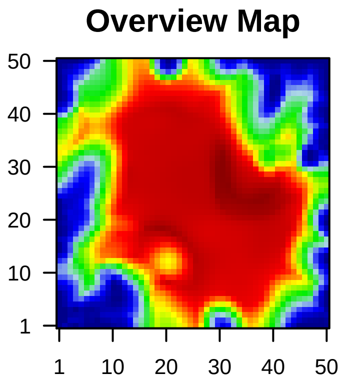
Underexpression Spots

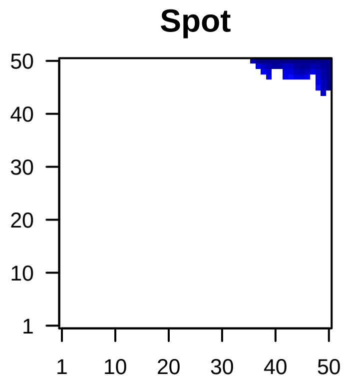
Spot Summary: r

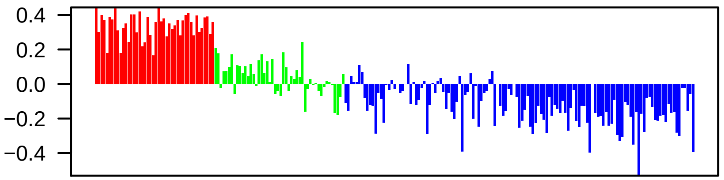
metagenes = 56
genes = 953

<r> metagenes = 0.86
<r> genes = 0.26
beta: r2= 11.93 / log p= −Inf

samples with spot = 35 (15.8 %)
non−mBL : 35 (27.1 %)


Overview Map


Spot

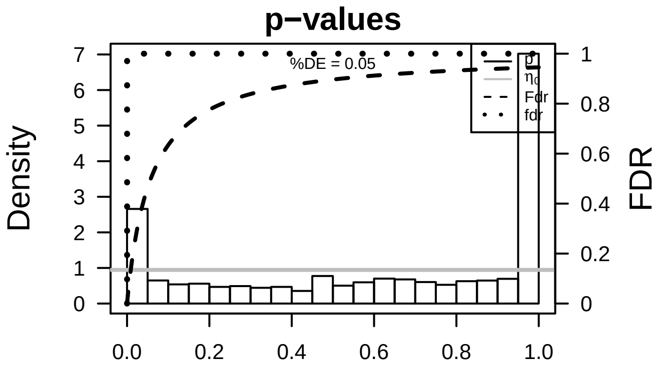


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209995_s_at	1.43	−2.94	0.56	TCL1A	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
2	203795_s_at	0.8	−2.54	0.41	BCL7A	BCL tumor suppressor 7A [Source:HGNC Symbol;Acc:HGNC
3	203819_s_at	1.01	−2.54	0.4	IGF2BP3	insulin like growth factor 2 mRNA binding protein 3 [Source:H
4	205780_at	0.94	−2.54	0.29	BIK	BCL2 interacting killer [Source:HGNC Symbol;Acc:HGNC:10
5	208650_s_at	1.04	−2.44	0.37	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
6	221234_s_at	1.09	−2.4	0.55	BACH2	BTB domain and CNC homolog 2 [Source:HGNC Symbol;Ac
7	209771_x_at	1	−2.38	0.33	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
8	212592_at	1.04	−2.37	0.33	JCHAIN	joining chain of multimeric IgA and IgM [Source:HGNC Symb
9	216379_x_at	1.05	−2.31	0.35	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
10	206255_at	1.05	−2.29	0.36	BLK	BLK proto−oncogene, Src family tyrosine kinase [Source:HG
11	208651_x_at	1.08	−2.28	0.36	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
12	266_s_at	1.08	−2.22	0.38	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
13	201764_at	0.71	−2.22	0.42	TMEM106C	transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
14	219471_at	0.93	−2.21	0.39	RUBCNL	RUN and cysteine rich domain containing beclin 1 interacting
15	205229_s_at	1.84	−2.18	0.33	COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
16	39318_at	1.22	−2.16	0.56	TCL1A	T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HG
17	212094_at	1.35	−2.12	0.57	PEG10	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:1
18	209772_s_at	1.14	−2.11	0.34	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
19	220085_at	1.22	−2.09	0.56	HELLS	helicase, lymphoid specific [Source:HGNC Symbol;Acc:HGN
20	44790_s_at	0.89	−2.07	0.38	RUBCNL	RUN and cysteine rich domain containing beclin 1 interacting

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−96	148 / 319	Melar	Gerber_wt/wt_melanoma−cells−SpotA
2	6e−86	235 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	3e−81	155 / 431	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	3e−79	85 / 115	Gliom	WILLSCHER_GBM_Verhaak−CL_up (C)
5	2e−73	102 / 192	Lymp	Victora_Dark zone signature
6	4e−67	108 / 244	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
7	9e−65	82 / 137	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
8	1e−64	152 / 526	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	2e−63	138 / 439	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
10	4e−63	133 / 409	Canc	Lembcke_Normal vs Adenoma
11	1e−60	129 / 400	GSEA	PUJANA_BRCA2_PCC_NETWORK
12	2e−59	103 / 254	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
13	1e−55	171 / 758	GSEA	NUYTTEN_EZH2_TARGETS_DN
14	2e−53	201 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
15	7e−48	9 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	7e−48	9 / 14	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	9e−47	155 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
18	2e−46	80 / 195	HM	HALLMARK_G2M_CHECKPOINT
19	2e−45	135 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
20	3e−45	100 / 321	GSEA	BLUM_RESPONSE_TO_SALIRASIB_DN
21	7e−44	76 / 187	HM	HALLMARK_E2F_TARGETS
22	8e−44	92 / 280	GSEA	MANALO_HYPOXIA_DN
23	2e−43	85 / 240	GSEA	MITSIADES_RESPONSE_TO_APLIDIN_DN
24	5e−43	81 / 219	Refer	WIRTH_GC B−cells
25	2e−42	142 / 669	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
26	8e−42	54 / 93	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
27	8e−41	226 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
28	4e−40	70 / 174	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
29	8e−40	54 / 99	Lymp	Sha_BL UP
30	8e−40	53 / 95	GSEA	ODONNELL_TFRC_TARGETS_DN
31	3e−39	64 / 147	GSEA	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
32	6e−39	78 / 226	GSEA	ZHANG_TLX_TARGETS_60HR_DN
33	2e−38	306 / 2541	CC	nucleoplasm
34	2e−38	36 / 42	GSEA	HUMMEL_BURKITTS_LYMPHOMA_UP
35	5e−37	120 / 548	GSEA	BENPORATH_CYCLING_GENES
36	7e−37	447 / 4579	CC	nucleus
37	4e−36	93 / 347	GSEA	REACTOME_CELL_CYCLE
38	3e−35	51 / 102	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
39	5e−35	111 / 497	BP	cell cycle
40	8e−35	64 / 169	GSEA	FUJII_YBX1_TARGETS_DN


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	10 / 107	HORVATH_aging_genes meth UP
2	0.5	6 / 92	HORVATH_aging_genes meth DOWN
3	0.9	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	5e−35	111 / 497	cell cycle
2	1e−28	78 / 307	cell division
3	9e−23	46 / 137	DNA replication
4	1e−21	65 / 281	DNA repair
5	1e−15	64 / 351	cellular response to DNA damage stimulus
6	4e−14	29 / 91	sister chromatid cohesion
7	1e−13	30 / 101	mitotic cell cycle
8	1e−13	25 / 70	chromosome segregation
9	2e−13	25 / 71	regulation of G2/M transition of mitotic cell cycle
10	4e−13	17 / 32	centrosome cycle
11	1e−11	30 / 119	G2/M transition of mitotic cell cycle
12	1e−09	26 / 110	regulation of cell cycle
13	1e−08	25 / 113	regulation of signal transduction by p53 class mediator
14	2e−08	22 / 91	G1/S transition of mitotic cell cycle
15	7e−08	12 / 30	mitotic spindle organization

Cancer

Rank	p−value	#in/all	Geneset
1	4e−63	133 / 409	Lembcke_Normal vs Adenoma
2	7e−48	9 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	9e−12	8 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	4e−11	10 / 12	BENTINK_e2f3.2
5	7e−09	15 / 41	PanCan_DNARepair_geneset_nanostring
6	7e−08	8 / 12	BENTINK_ras.1
7	2e−07	25 / 130	PanCan_CC+Apop_geneset_nanostring
8	6e−05	11 / 45	KUIPER_MM poor survival
9	2e−04	5 / 10	GENTLES_modul3
10	1e−03	5 / 14	BENTINK_myc.1
11	2e−03	5 / 16	WOLFER_overlap genes
12	2e−03	2 / 15	RHODES_CANCER_META_SIGNATURE
13	8e−03	4 / 14	LIU_COMMON_CANCER_GENES
14	8e−03	4 / 14	BENTINK_src.10
15	1e−02	6 / 32	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	2e−38	306 / 2541	nucleoplasm
2	7e−37	447 / 4579	nucleus
3	9e−19	66 / 324	chromosome
4	1e−16	66 / 354	centrosome
5	5e−14	33 / 118	chromosome, centromeric region
6	5e−14	30 / 98	spindle pole
7	9e−14	38 / 157	spindle
8	5e−12	51 / 292	microtubule organizing center
9	1e−11	109 / 936	cytoskeleton
10	8e−10	80 / 653	nucleolus
11	1e−09	25 / 101	kinetochore
12	2e−09	27 / 121	midbody
13	2e−08	40 / 251	microtubule
14	2e−08	20 / 77	condensed chromosome kinetochore
15	3e−08	300 / 3805	cytosol

Chr

Rank	p−value	#in/all	Geneset
1	1e−04	55 / 548	Chr 16
2	2e−03	34 / 333	Chr 22
3	6e−03	25 / 242	Chr 13
4	6e−02	94 / 1325	Chr 1
5	8e−02	37 / 480	Chr 4
6	9e−02	30 / 382	Chr 15
7	1e−01	33 / 437	Chr 8
8	4e−01	45 / 700	Chr 12
9	4e−01	31 / 492	Chr 9
10	5e−01	3 / 41	Chr Y
11	5e−01	25 / 403	Chr 14
12	5e−01	51 / 833	Chr 19
13	6e−01	22 / 369	Chr 20
14	6e−01	45 / 776	Chr 17
15	7e−01	28 / 490	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−60	708 / 8406	Bcells peripheral blood_2_TssAFlnk
2	1e−59	680 / 7833	Bcells peripheral blood_1_TssA
3	5e−56	697 / 8322	T CD8+ naive cells peripheral blood_1_TssA
4	1e−51	678 / 8068	Thelper cells peripheral blood_1_TssA
5	3e−49	667 / 7930	Tregulatory cells peripheral blood_1_TssA
6	3e−49	688 / 8370	natural killer cells peripheral blood_2_TssAFlnk
7	4e−49	682 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
8	4e−49	706 / 8766	2_TssA_Melanocytes
9	5e−49	708 / 8816	Thelper cells peripheral blood_2_TssAFlnk
10	2e−48	529 / 5456	5_Tx_Neuronal_Progenitor
11	2e−48	722 / 9160	2_TssA_Neuronal_Progenitor
12	1e−46	580 / 6389	4_Tx_ESC_Mesoderm
13	5e−46	652 / 7751	natural killer cells peripheral blood_1_TssA
14	7e−46	674 / 8200	monocytes peripheral blood_2_TssAFlnk
15	8e−46	662 / 7957	Tcells peripheral blood_2_TssAFlnk

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−14	42 / 184	Kosinski_lower−crypt−long−list
2	7e−11	126 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
3	1e−10	74 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
4	8e−09	73 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
5	4e−07	153 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
6	2e−04	85 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
7	3e−04	76 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	2e−03	7 / 31	Kosinski_lower−crypt−short−list
9	2e−02	41 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
10	5e−02	3 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
11	6e−02	63 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
12	7e−02	41 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
13	7e−02	3 / 16	Budinska_B_Lower crypt−like_UP
14	8e−02	2 / 8	KIM_MSI−in−EC
15	8e−02	2 / 8	Boland_CRC−MMR−system

Glioma

Rank	p−value	#in/all	Geneset
1	3e−79	85 / 115	WILLSCHER_GBM_Verhaak−CL_up (C)
2	6e−14	21 / 47	developing astrocytes
3	7e−09	19 / 66	Weller_LGG_gradeII−vs−III_DOWN
4	5e−08	129 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	9e−08	141 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	4e−03	2 / 2	Phillips Prolif up vs PN & MES
7	1e−02	9 / 64	Weller_LGG_A_vs_O_DOWN
8	3e−02	3 / 12	Mukasa_UP_in_Oligodendroglioma_with_1intact
9	6e−02	47 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	7e−02	3 / 16	VERHAAK_PN subtype
11	7e−02	6 / 49	OPC
12	8e−02	2 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
13	9e−02	7 / 64	cultured astroglia vs. in vivo astrocytes
14	1e−01	6 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
15	2e−01	3 / 23	Christensen_hypomethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−86	235 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	3e−81	155 / 431	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	4e−67	108 / 244	KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	9e−65	82 / 137	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e−64	152 / 526	MARSON_BOUND_BY_E2F4_UNSTIMULATED
6	2e−63	138 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
7	1e−60	129 / 400	PUJANA_BRCA2_PCC_NETWORK
8	2e−59	103 / 254	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	1e−55	171 / 758	NUYTTEN_EZH2_TARGETS_DN
10	2e−53	201 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	7e−48	9 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	9e−47	155 / 726	PUJANA_CHEK2_PCC_NETWORK
13	2e−45	135 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
14	3e−45	100 / 321	BLUM_RESPONSE_TO_SALIRASIB_DN
15	8e−44	92 / 280	MANALO_HYPOXIA_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−46	80 / 195	HALLMARK_G2M_CHECKPOINT
2	7e−44	76 / 187	HALLMARK_E2F_TARGETS
3	2e−14	41 / 173	HALLMARK_MITOTIC_SPINDLE
4	9e−05	12 / 55	HALLMARK_MYC_TARGETS_V2
5	6e−04	24 / 192	HALLMARK_MTORC1_SIGNALING
6	5e−03	21 / 190	HALLMARK_MYC_TARGETS_V1
7	7e−02	12 / 122	HALLMARK_SPERMATOGENESIS
8	8e−02	17 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
9	1e−01	12 / 133	HALLMARK_DNA_REPAIR
10	2e−01	5 / 51	HALLMARK_TGF_BETA_SIGNALING
11	4e−01	7 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	4e−01	13 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	4e−01	3 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	4e−01	12 / 182	HALLMARK_GLYCOLYSIS
15	5e−01	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Immunome

Rank	p−value	#in/all	Geneset
1	3e−18	19 / 26	Angelova_immune−metagene−activated_CD4
2	3e−02	3 / 12	Angelova_immune−metagene−memory_B−cells
3	1e−01	3 / 19	Angelova_immune−metagene−activated_CD8
4	2e−01	1 / 4	Angelova_CRC_MSS−neoantigens
5	3e−01	2 / 18	Angelova_immune−metagene−pDC
6	4e−01	1 / 7	Angelova_CRC_MSI−neoantigens
7	5e−01	2 / 25	Angelova_immune−metagene−DC
8	5e−01	1 / 10	Angelova_immune−metagene−neutrophils
9	6e−01	1 / 13	Angelova_immune−metagene−activated_B−cells
10	6e−01	1 / 13	Angelova_immune−metagene−immature_B−cells
11	6e−01	1 / 13	Angelova_CRC_MSS^−neoantigens
12	7e−01	1 / 17	Angelova_immune−metagene−central_memory_CD8
13	7e−01	1 / 18	Angelova_CRC_immunostimulators
14	7e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
15	8e−01	1 / 23	Angelova_immune−metagene−Th2

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	4 / 32	Marjolein_ageing−genes_DN
2	0.3	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	0.4	10 / 150	Homuth_BMI−associated−genes_UP
4	0.5	13 / 210	Homuth_BMI−associated−genes_DN
5	0.7	1 / 22	DUMEAUX_Fasting enriched genes
6	0.9	2 / 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_High bmi enriched genes
15	1.0	0 / 14	Huan_blood−pressure_SBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−73	102 / 192	Victora_Dark zone signature
2	8e−40	54 / 99	Sha_BL UP
3	8e−35	502 / 5529	HOPP_Txn_elongation
4	1e−32	157 / 955	SPANG_BCR UP
5	8e−30	512 / 5908	HOPP_Active_promoter
6	4e−17	368 / 4261	HOPP_Txn_transition
7	1e−16	14 / 15	BENTINK_mBL UP
8	1e−14	57 / 305	TARTE_Plasmablast signature
9	2e−14	36 / 135	DAVE_BL−vs−DLBCL
10	7e−11	432 / 5682	HOPP_Weak_promoter
11	2e−10	26 / 102	ROSOLOWSKI_blue total
12	3e−08	37 / 227	SPANG_IL21 UP
13	5e−08	6 / 6	MASCQUE_mBL UP
14	4e−06	388 / 5404	HOPP_Strong_enhancer
15	5e−05	33 / 263	SPANG_CD40 6hrs UP

Melanoma

Rank	p−value	#in/all	Geneset
1	2e−96	148 / 319	Gerber_wt/wt_melanoma−cells−SpotA
2	5e−30	33 / 47	Tirosh_G2/M phase specific genes
3	6e−30	32 / 44	Tirosh_top50 correlated genes PC2
4	2e−29	41 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
5	4e−15	20 / 38	Tirosh_G1/S phase specific genes
6	1e−11	22 / 65	Harbst_melanoma_highgrade_up
7	6e−03	8 / 46	Tirosh_top50 correlated genes PC5
8	2e−02	2 / 4	Melanoma Epi−Enzyme Cluster 5
9	1e−01	1 / 2	Melanoma Epi−Enzyme Cluster 6
10	2e−01	21 / 276	Gerber_wt/wt_melanoma−cells−SpotB
11	2e−01	1 / 4	Melanoma Epi−Enzyme Cluster 3
12	2e−01	6 / 68	Tirosh_housekeeping_genes
13	4e−01	2 / 23	Melanoma Epi−Enzyme Cluster 7
14	4e−01	15 / 230	Gerber_wt/wt_melanoma−cells−SpotC
15	4e−01	2 / 24	Tirosh_B−cell specific genes−melanoma

MF

Rank	p−value	#in/all	Geneset
1	4e−14	165 / 1541	DNA binding
2	1e−10	560 / 7864	protein binding
3	3e−10	123 / 1161	RNA binding
4	2e−07	19 / 81	single−stranded DNA binding
5	5e−07	44 / 328	chromatin binding
6	8e−06	108 / 1185	ATP binding
7	2e−05	28 / 196	microtubule binding
8	6e−05	17 / 97	double−stranded DNA binding
9	8e−05	79 / 852	nucleic acid binding
10	1e−04	118 / 1402	nucleotide binding
11	1e−04	9 / 33	DNA−dependent ATPase activity
12	1e−04	7 / 20	DNA−directed DNA polymerase activity
13	2e−04	18 / 116	helicase activity
14	4e−04	14 / 83	microtubule motor activity
15	7e−04	6 / 19	DNA helicase activity

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	23 / 171	hsa−miR−196a
2	4e−04	8 / 31	hsa−miR−661
3	6e−04	20 / 148	hsa−miR−196b
4	6e−04	11 / 58	hsa−miR−331−3p
5	7e−04	14 / 87	hsa−miR−449b
6	9e−04	8 / 35	hsa−miR−1224−5p
7	1e−03	14 / 92	hsa−miR−199a−5p
8	2e−03	19 / 148	hsa−miR−539
9	2e−03	20 / 160	hsa−miR−330−3p
10	2e−03	14 / 98	hsa−miR−520a−5p
11	2e−03	26 / 236	hsa−miR−34a
12	3e−03	5 / 17	hsa−miR−151−5p
13	3e−03	14 / 101	hsa−miR−515−3p
14	3e−03	7 / 33	hsa−miR−502−3p
15	3e−03	10 / 61	hsa−miR−619

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	8 / 57	Burnham_day1_vs_5_UP
2	0.07	13 / 135	Terre_MSV_multiple_respiratory_viruses_up
3	0.10	5 / 41	Scicluna_DN
4	0.23	5 / 54	Burnham_timecourse
5	0.26	5 / 57	Burnham_viral_UP
6	0.40	12 / 179	Terre_MSV_multiple_respiratory_viruses_dn
7	0.68	1 / 18	Scicluna_UP
8	0.79	3 / 68	Burnham_sep_vs_con_UP
9	0.81	3 / 71	Burnham_cap_fp_vs_con_UP
10	0.86	2 / 56	Burnham_sep_vs_con_DN
11	0.87	5 / 122	Terre_IMS_influenza_meta_signature
12	0.95	1 / 48	Burnham_cap_fp_vs_con_DN
13	0.96	1 / 52	Burnham_day1_vs_5_DN
14	1.00	0 / 48	Burnham_viral_DN
15	1.00	0 / 37	Sweeney_viral_up

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−43	81 / 219	WIRTH_GC B−cells
2	3e−09	25 / 106	Chaussabel_2,11_Replication
3	5e−08	77 / 677	PROTEINATLAS_esophagus
4	5e−08	77 / 678	PROTEINATLAS_lymph node
5	3e−07	106 / 1081	PROTEINATLAS_testis
6	4e−07	82 / 776	PROTEINATLAS_skin
7	4e−07	103 / 1048	PROTEINATLAS_rectum
8	7e−07	104 / 1072	PROTEINATLAS_duodenum
9	1e−06	97 / 989	PROTEINATLAS_tonsil
10	1e−06	103 / 1076	PROTEINATLAS_stomach
11	3e−06	108 / 1161	PROTEINATLAS_colon
12	5e−06	64 / 595	PROTEINATLAS_breast
13	6e−06	58 / 527	PROTEINATLAS_oral mucosa
14	9e−06	67 / 645	PROTEINATLAS_bone marrow
15	2e−05	86 / 905	PROTEINATLAS_appendix

Telomeres

Rank	p−value	#in/all	Geneset
1	6e−05	6 / 13	Alternative lengthening of telomeres
2	2e−02	5 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−13	306 / 3564	ICGC_Taf1_targets
2	4e−12	274 / 3150	ICGC_Creb1_targets
3	1e−09	127 / 1241	KIM_MYC targets
4	1e−09	306 / 3796	ICGC_Nficsc81335_targets
5	3e−08	288 / 3630	ICGC_Sp1_targets
6	5e−08	292 / 3703	ICGC_Foxm1_targets
7	5e−08	296 / 3769	ICGC_Pmlsc71910_targets
8	2e−07	295 / 3804	ICGC_Stat5_targets
9	2e−07	346 / 4602	ICGC_Elf1_targets
10	2e−07	328 / 4319	ICGC_Pou2_targets
11	6e−07	107 / 1107	ICGC_Myc_targets
12	7e−07	102 / 1044	ICGC_Six5_targets
13	8e−07	105 / 1089	ICGC_Ets1_targets
14	2e−06	277 / 3608	ICGC_Tcf12_targets
15	2e−06	306 / 4072	ICGC_Mta3_targets

Underexpression Spots

Spot Summary: s

metagenes = 6
genes = 152

<r> metagenes = 0.99
<r> genes = 0.21
beta: r2= 3.52 / log p= −Inf

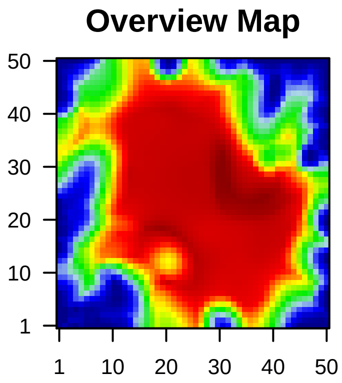
samples with spot = 24 (10.9 %)
intermediate : 7 (14.6 %)
non−mBL : 17 (13.2 %)

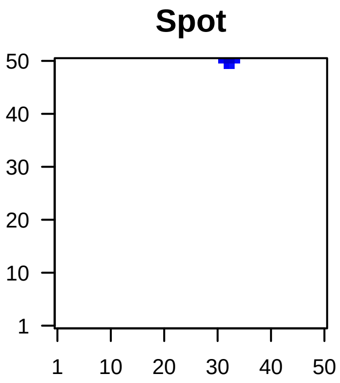
Spot Genelist

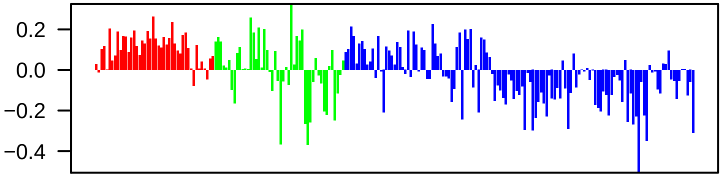
Rank	ID	max e	min e	r	Symbol	Description
1	202417_at	0.69	−2.17	0.46	KEAP1	kelch like ECH associated protein 1 [Source:HGNC Symbol;
2	209132_s_at	0.43	−1.95	0.63	COMMD4	COMM domain containing 4 [Source:HGNC Symbol;Acc:HG
3	218567_x_at	0.61	−1.93	0.61	DPP3	dipeptidyl peptidase 3 [Source:HGNC Symbol;Acc:HGNC:30
4	202958_at	0.59	−1.92	0.43	PTPN9	protein tyrosine phosphatase, non−receptor type 9 [Source:H
5	214531_s_at	0.49	−1.79	0.56	SNX1	sorting nexin 1 [Source:HGNC Symbol;Acc:HGNC:11172]
6	203465_at	0.45	−1.73	0.56	MRPL19	mitochondrial ribosomal protein L19 [Source:HGNC Symbol;
7	215343_at	0.88	−1.71	0.38	CCDC88C	coiled−coil domain containing 88C [Source:HGNC Symbol;Ac
8	207513_s_at	0.58	−1.67	0.43	ZNF189	zinc finger protein 189 [Source:HGNC Symbol;Acc:HGNC:12
9	218890_x_at	0.6	−1.63	0.62	MRPL35	mitochondrial ribosomal protein L35 [Source:HGNC Symbol;
10	217968_at	0.48	−1.63	0.5	EIPR1	EARP complex and GARP complex interacting protein 1 [Sou
11	203447_at	0.58	−1.62	0.39	PSMD5	proteasome 26S subunit, non−ATPase 5 [Source:HGNC Sym
12	201618_x_at	1.16	−1.59	0.49	GPAA1	glycosylphosphatidylinositol anchor attachment 1 [Source:HG
13	202818_s_at	0.9	−1.58	0.62	ELOA	elongin A [Source:HGNC Symbol;Acc:HGNC:11620]
14	205037_at	0.72	−1.57	0.5	IFT27	intraflagellar transport 27 [Source:HGNC Symbol;Acc:HGNC:
15	202201_at	0.86	−1.52	0.37	BLVRB	biliverdin reductase B [Source:HGNC Symbol;Acc:HGNC:10
16	219553_at	0.79	−1.49	0.55	NME7	NME/NM23 family member 7 [Source:HGNC Symbol;Acc:HG
17	219819_s_at	0.45	−1.47	0.6	MRPS28	mitochondrial ribosomal protein S28 [Source:HGNC Symbol;
18	202793_at	0.92	−1.45	0.57	LPCAT3	lysophosphatidylcholine acyltransferase 3 [Source:HGNC Sy
19	212003_at	0.6	−1.43	0.43	SZRD1	SUZ RNA binding domain containing 1 [Source:HGNC Symb
20	218703_at	0.8	−1.41	0.36	SEC22A	SEC22 homolog A, vesicle trafficking protein [Source:HGNC

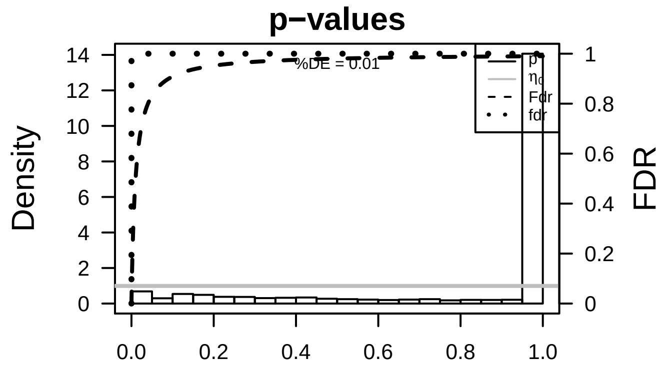
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−14	106 / 5529	Lymp	HOPP_Txn_elongation
2	2e−10	103 / 5908	Lymp	HOPP_Active_promoter
3	7e−10	83 / 4261	Lymp	HOPP_Txn_transition
4	3e−09	44 / 1578	TF	ICGC_GabpPcr2_targets
5	3e−08	33 / 1044	TF	ICGC_Six5_targets
6	5e−07	62 / 3150	TF	ICGC_Creb1_targets
7	8e−07	31 / 1089	TF	ICGC_Ets1_targets
8	2e−06	30 / 1083	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tra
9	2e−05	63 / 3564	TF	ICGC_Taf1_targets
10	2e−05	61 / 3420	TF	ICGC_Bclaf101388_targets
11	2e−05	6 / 53	BP	mitochondrial translational termination
12	3e−05	65 / 3769	TF	ICGC_Pmlsc71910_targets
13	3e−05	61 / 3451	TF	ICGC_Atf2_targets
14	3e−05	6 / 54	BP	mitochondrial translational elongation
15	3e−05	36 / 1630	TF	ICGC_SrfV0416101_targets
16	3e−05	63 / 3630	TF	ICGC_Sp1_targets
17	5e−05	17 / 510	GSE	STEIN_ESRRA_TARGETS
18	6e−05	6 / 61	BP	snRNA transcription from RNA polymerase II promoter
19	6e−05	48 / 2541	CC	nucleoplasm
20	7e−05	4 / 21	CC	mitochondrial small ribosomal subunit
21	8e−05	86 / 5682	Lymp	HOPP_Weak_promoter
22	9e−05	6 / 67	BP	tRNA processing
23	1e−04	8 / 130	GSE	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
24	1e−04	36 / 1729	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
25	1e−04	3 / 9	GSE	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
26	2e−04	18 / 615	GSE	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
27	2e−04	13 / 361	GSE	GARY_CD5_TARGETS_DN
28	2e−04	28 / 1241	TF	KIM_MYC targets
29	2e−04	41 / 2150	TF	ICGC_Irf4_targets
30	2e−04	61 / 3703	TF	ICGC_Foxm1_targets
31	2e−04	52 / 2994	TF	ICGC_Zeb1_targets
32	3e−04	62 / 3804	TF	ICGC_Stat5_targets
33	3e−04	3 / 13	GSE	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTH
34	4e−04	29 / 1354	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
35	4e−04	15 / 502	BP	protein transport
36	5e−04	5 / 59	miRN	hsa−miR−651
37	5e−04	61 / 3796	TF	ICGC_Nficsc81335_targets
38	6e−04	64 / 4072	TF	ICGC_Mta3_targets
39	8e−04	8 / 178	GSE	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
40	9e−04	12 / 371	GSE	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	

BP

Rank	p−value	#in/all	Geneset
1	2e−05	6 / 53	mitochondrial translational termination
2	3e−05	6 / 54	mitochondrial translational elongation
3	6e−05	6 / 61	snRNA transcription from RNA polymerase II promoter
4	9e−05	6 / 67	tRNA processing
5	4e−04	15 / 502	protein transport
6	2e−03	3 / 21	mitochondrial translation
7	3e−03	4 / 55	negative regulation of DNA binding transcription factor activity
8	4e−03	8 / 232	translation
9	4e−03	3 / 30	biosynthetic process
10	5e−03	2 / 10	snRNA processing
11	6e−03	2 / 11	regulation of mRNA splicing, via spliceosome
12	7e−03	3 / 35	cellular amino acid metabolic process
13	7e−03	2 / 12	layer formation in cerebral cortex
14	1e−02	10 / 391	protein ubiquitination
15	1e−02	6 / 173	proteasome−mediated ubiquitin−dependent protein catabolic process

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	2 / 10	GENTLES_modul5
2	0.026	3 / 58	SHAUGHNESSY_MM high risk
3	0.131	0 / 15	RHODES_CANCER_META_SIGNATURE
4	0.144	1 / 14	BENTINK_myc.1
5	0.154	1 / 15	GENTLES_modul2
6	0.154	1 / 15	GENTLES_modul4
7	0.154	1 / 15	GENTLES_modul7
8	0.268	1 / 28	PanCan_HK_geneset_nanostring
9	0.408	0 / 14	LIU_COMMON_CANCER_GENES
10	0.440	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0.478	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	0.766	1 / 130	PanCan_CC+Apop_geneset_nanostring
13	0.776	1 / 134	PanCan_RAS_geneset_nanostring
14	0.807	1 / 147	PanCan_MAPK_geneset_nanostring
15	0.835	3 / 409	Lembcke_Normal vs Adenoma

CC

Rank	p−value	#in/all	Geneset
1	6e−05	48 / 2541	nucleoplasm
2	7e−05	4 / 21	mitochondrial small ribosomal subunit
3	1e−03	11 / 330	mitochondrial inner membrane
4	2e−03	8 / 196	nuclear membrane
5	4e−03	3 / 29	mitochondrial large ribosomal subunit
6	4e−03	6 / 139	ribosome
7	7e−03	2 / 12	integrator complex
8	8e−03	23 / 1221	mitochondrion
9	1e−02	8 / 268	intracellular ribonucleoprotein complex
10	1e−02	2 / 16	neuron projection terminus
11	1e−02	14 / 653	nucleolus
12	2e−02	2 / 19	transcriptionally active chromatin
13	2e−02	54 / 3805	cytosol
14	2e−02	2 / 20	mitochondrial ribosome
15	2e−02	3 / 56	proteasome complex

Chr

Rank	p−value	#in/all	Geneset
1	0.002	18 / 756	Chr 11
2	0.012	16 / 776	Chr 17
3	0.022	16 / 832	Chr 2
4	0.062	8 / 382	Chr 15
5	0.079	8 / 403	Chr 14
6	0.179	8 / 492	Chr 9
7	0.232	10 / 689	Chr 3
8	0.354	6 / 437	Chr 8
9	0.442	10 / 833	Chr 19
10	0.633	6 / 585	Chr 7
11	0.717	13 / 1325	Chr 1
12	0.717	3 / 333	Chr 22
13	0.730	5 / 548	Chr 16
14	0.779	3 / 369	Chr 20
15	0.789	1 / 139	Chr 21

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−23	135 / 7331	TssA_Colon
2	3e−22	140 / 8200	monocytes peripheral blood_2_TssAFlnk
3	5e−22	141 / 8406	Bcells peripheral blood_2_TssAFlnk
4	8e−22	141 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
5	1e−21	143 / 8816	Thelper cells peripheral blood_2_TssAFlnk
6	5e−21	135 / 7635	monocytes peripheral blood_1_TssA
7	9e−21	137 / 7957	Tcells peripheral blood_2_TssAFlnk
8	2e−20	139 / 8322	T CD8+ naive cells peripheral blood_1_TssA
9	8e−20	138 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
10	1e−19	139 / 8430	3_TssF_Melanocytes
11	2e−19	143 / 9146	3_TssF_Skeletal_Muscle
12	5e−19	138 / 8370	natural killer cells peripheral blood_2_TssAFlnk
13	9e−19	134 / 7833	Bcells peripheral blood_1_TssA
14	1e−18	141 / 8918	1_TssA_ESC_Mesoderm
15	2e−18	140 / 8766	2_TssA_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	30 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
2	1e−04	36 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
3	4e−04	29 / 1354	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	3e−02	12 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
5	7e−02	10 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
6	1e−01	14 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	2e−01	8 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
8	3e−01	1 / 31	Marisa_CRC−cluster−c
9	3e−01	15 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	4e−01	12 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
11	4e−01	1 / 43	Marisa_CRC−cluster−f
12	4e−01	7 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	4e−01	1 / 49	Pentrack_CRC_TCGA_corr_N_msi−h_DN
14	5e−01	1 / 60	Marisa_CRC−cluster−g
15	6e−01	8 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN

Glioma

Rank	p−value	#in/all	Geneset
1	0.002	29 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.027	3 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.039	22 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.106	2 / 50	Vishal_subnetwork signature of survival in GBM
5	0.203	5 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	0.226	2 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.369	8 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.388	2 / 121	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	0.394	1 / 45	Donson−innate immunity−associated with LTS in HGA
10	0.458	1 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	0.476	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.482	1 / 59	GIEZELT_GBM_STS_up_VS_LTS
13	0.510	1 / 64	Weller_LGG_A_vs_O_DOWN
14	0.521	1 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
15	0.526	1 / 67	Weller_LGG_1p19qDel−vs−intact_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−05	17 / 510	STEIN_ESRRA_TARGETS
2	1e−04	8 / 130	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP
3	1e−04	3 / 9	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
4	2e−04	18 / 615	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
5	2e−04	13 / 361	GARY_CD5_TARGETS_DN
6	3e−04	3 / 13	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHES
7	8e−04	8 / 178	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
8	9e−04	12 / 371	STEIN_ESRRA_TARGETS_UP
9	9e−04	7 / 139	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
10	1e−03	13 / 439	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	1e−03	7 / 147	WANG_CLIM2_TARGETS_DN
12	1e−03	13 / 442	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
13	1e−03	3 / 20	REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLIC
14	2e−03	7 / 156	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_
15	2e−03	3 / 22	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN

HM

Rank	p−value	#in/all	Geneset
1	0.09	3 / 97	HALLMARK_PEROXISOME
2	0.14	4 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	0.15	4 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	0.18	3 / 133	HALLMARK_DNA_REPAIR
5	0.29	2 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.29	2 / 97	HALLMARK_BILE_ACID_METABOLISM
7	0.30	3 / 174	HALLMARK_ADIPOGENESIS
8	0.33	3 / 182	HALLMARK_GLYCOLYSIS
9	0.33	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
10	0.43	1 / 51	HALLMARK_TGF_BETA_SIGNALING
11	0.49	2 / 149	HALLMARK_UV_RESPONSE_UP
12	0.55	2 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	0.57	2 / 173	HALLMARK_MITOTIC_SPINDLE
14	0.59	2 / 178	HALLMARK_COMPLEMENT
15	0.62	2 / 190	HALLMARK_MYC_TARGETS_V1

Immunome

Rank	p−value	#in/all	Geneset
1	0.1	1 / 10	Angelova_immune−metagene−neutrophils
2	0.2	1 / 19	Angelova_immune−metagene−activated_CD8
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 / 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	0.3	1 / 32	Marjolein_ageing−genes_DN
2	0.5	1 / 62	DUMEAUX_Smoking enriched genes
3	0.7	2 / 210	Homuth_BMI−associated−genes_DN
4	0.8	1 / 150	Homuth_BMI−associated−genes_UP
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 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	4e−14	106 / 5529	HOPP_Txn_elongation
2	2e−10	103 / 5908	HOPP_Active_promoter
3	7e−10	83 / 4261	HOPP_Txn_transition
4	8e−05	86 / 5682	HOPP_Weak_promoter
5	7e−03	75 / 5404	HOPP_Strong_enhancer
6	8e−03	31 / 1814	HOPP_Repetitive
7	8e−02	59 / 4559	HOPP_Weak_enhancer
8	1e−01	1 / 9	YAMANE_AICDA_targets_nonrecruited
9	1e−01	5 / 227	SPANG_IL21 UP
10	1e−01	2 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
11	1e−01	55 / 4357	HOPP_Weak_txn
12	2e−01	14 / 955	SPANG_BCR UP
13	3e−01	12 / 906	SPANG_BCR DN
14	4e−01	1 / 40	CARO_OxPhos_in_DLBCL_UP
15	6e−01	1 / 77	TARTE_Plasma cell signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.003	8 / 222	Gerber_wt/wt_melanoma−cells−SpotF
2	0.034	7 / 276	Gerber_wt/wt_melanoma−cells−SpotB
3	0.112	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC
4	0.149	4 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
5	0.226	2 / 81	Tirosh_Genes in the MITF program
6	0.234	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
7	0.522	3 / 249	Gerber_wt/wt_melanoma−cells−SpotE
8	0.531	1 / 68	Tirosh_housekeeping_genes
9	0.613	1 / 85	Tirosh_AXL−signature
10	0.663	2 / 204	Landsberg_dedifferentiation_down
11	0.739	2 / 236	Gerber_wt/wt_group3−specific
12	0.880	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	0.917	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

MF

Rank	p−value	#in/all	Geneset
1	0.006	5 / 106	ligase activity
2	0.007	5 / 109	structural constituent of ribosome
3	0.016	100 / 7864	protein binding
4	0.016	7 / 237	ubiquitin−protein transferase activity
5	0.021	4 / 95	isomerase activity
6	0.024	2 / 22	phospholipase A2 activity
7	0.034	4 / 110	transferase activity, transferring acyl groups
8	0.035	22 / 1329	transferase activity
9	0.038	2 / 28	aminopeptidase activity
10	0.038	2 / 28	ephrin receptor binding
11	0.046	2 / 31	SNAP receptor activity
12	0.049	2 / 32	Hsp70 protein binding
13	0.054	2 / 34	tRNA binding
14	0.063	2 / 37	single−stranded RNA binding
15	0.069	2 / 39	SNARE binding

miRNA target

Rank	p−value	#in/all	Geneset
1	5e−04	5 / 59	hsa−miR−651
2	5e−03	4 / 61	hsa−miR−1290
3	2e−02	3 / 54	hsa−miR−628−3p
4	3e−02	2 / 25	hsa−miR−892b
5	3e−02	4 / 107	hsa−miR−24
6	3e−02	5 / 160	hsa−miR−545
7	3e−02	2 / 26	hsa−miR−1226
8	4e−02	3 / 66	hsa−miR−567
9	5e−02	3 / 72	hsa−miR−378
10	5e−02	1 / 5	hsa−miR−126
11	6e−02	3 / 78	hsa−miR−224
12	6e−02	2 / 35	hsa−miR−640
13	6e−02	4 / 131	hsa−miR−137
14	6e−02	3 / 82	hsa−miR−516b
15	6e−02	3 / 83	hsa−miR−325

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.1	2 / 54	Burnham_timecourse
2	0.3	1 / 33	Sweeney_viral_dn
3	0.4	1 / 52	Burnham_day1_vs_5_DN
4	0.4	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
5	0.7	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

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.04	4 / 113	Chaussabel_1,8_Metabolism Biosynthesis
2	0.05	4 / 123	Chaussabel_3,7_Spliceosome
3	0.06	1 / 6	JONGENEEL_Uterus
4	0.13	1 / 13	WIRTH_Prim. lymphoid organs
5	0.14	5 / 245	Chaussabel_3,9_Kinases
6	0.15	1 / 15	JONGENEEL_Lung
7	0.19	4 / 204	Chaussabel_3,2_Inflammation I
8	0.19	1 / 19	JONGENEEL_Adrenal Gland
9	0.23	12 / 848	PROTEINATLAS_adrenal gland
10	0.26	2 / 89	Chaussabel_2,3_Erythrocytes
11	0.33	3 / 182	WIRTH_post GC B−cells
12	0.33	8 / 592	PROTEINATLAS_seminal vesicle
13	0.34	8 / 594	PROTEINATLAS_parathyroid gland
14	0.44	3 / 219	WIRTH_GC B−cells
15	0.44	12 / 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−09	44 / 1578	ICGC_GabpPcr2_targets
2	3e−08	33 / 1044	ICGC_Six5_targets
3	5e−07	62 / 3150	ICGC_Creb1_targets
4	8e−07	31 / 1089	ICGC_Ets1_targets
5	2e−05	63 / 3564	ICGC_Taf1_targets
6	2e−05	61 / 3420	ICGC_Bclaf101388_targets
7	3e−05	65 / 3769	ICGC_Pmlsc71910_targets
8	3e−05	61 / 3451	ICGC_Atf2_targets
9	3e−05	36 / 1630	ICGC_SrfV0416101_targets
10	3e−05	63 / 3630	ICGC_Sp1_targets
11	2e−04	28 / 1241	KIM_MYC targets
12	2e−04	41 / 2150	ICGC_Irf4_targets
13	2e−04	61 / 3703	ICGC_Foxm1_targets
14	2e−04	52 / 2994	ICGC_Zeb1_targets
15	3e−04	62 / 3804	ICGC_Stat5_targets

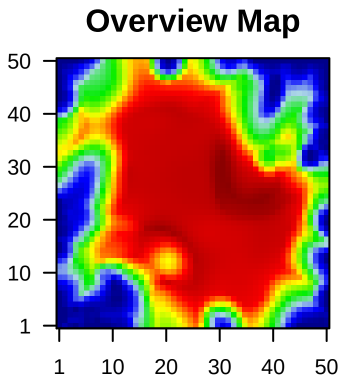
Underexpression Spots

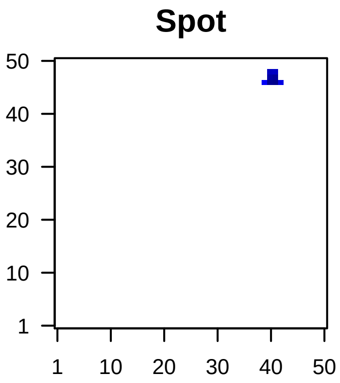
Spot Summary: t

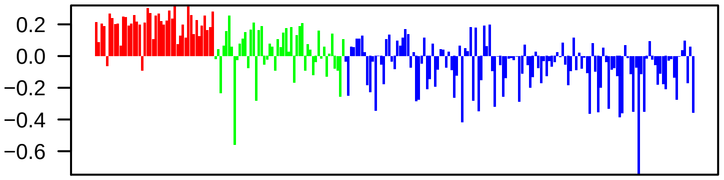
metagenes = 8
genes = 109

<r> metagenes = 0.99
<r> genes = 0.36
beta: r2= 6.59 / log p= −Inf

samples with spot = 28 (12.7 %)
intermediate : 4 (8.3 %)
non−mBL : 24 (18.6 %)


Overview Map


Spot

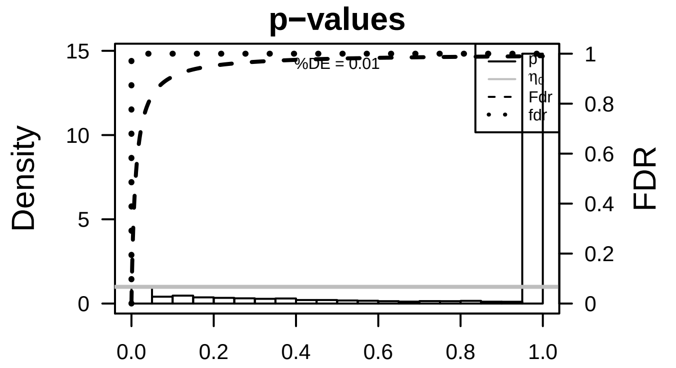


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212563_at	0.53	−2.26	0.73	BOP1	block of proliferation 1 [Source:HGNC Symbol;Acc:HGNC:15
2	212653_s_at	0.61	−2.07	0.5	EHBP1	EH domain binding protein 1 [Source:HGNC Symbol;Acc:HG
3	218051_s_at	0.94	−2.05	0.64	NT5DC2	5'−nucleotidase domain containing 2 [Source:HGNC Symbol;
4	201614_s_at	0.47	−2.03	0.7	RUVBL1	RuvB like AAA ATPase 1 [Source:HGNC Symbol;Acc:HGNC:
5	209825_s_at	0.7	−1.98	0.64	UCK2	uridine−cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
6	203219_s_at	0.55	−1.83	0.6	APRT	adenine phosphoribosyltransferase [Source:HGNC Symbol;A
7	202070_s_at	0.58	−1.8	0.56	IDH3A	isocitrate dehydrogenase 3 (NAD(+)) alpha [Source:HGNC S
8	218481_at	0.59	−1.8	0.74	EXOSC5	exosome component 5 [Source:HGNC Symbol;Acc:HGNC:24
9	218984_at	0.69	−1.68	0.67	PUS7	pseudouridylate synthase 7 (putative) [Source:HGNC Symbol
10	216212_s_at	0.5	−1.66	0.62	DKC1	dyskerin pseudouridine synthase 1 [Source:HGNC Symbol;A
11	205129_at	0.54	−1.66	0.67	NPM3	nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:
12	203277_at	0.61	−1.65	0.48	DFFA	DNA fragmentation factor subunit alpha [Source:HGNC Sym
13	203931_s_at	0.42	−1.65	0.71		
14	215293_s_at	0.67	−1.59	0.53	PGAP2	post−GPI attachment to proteins 2 [Source:HGNC Symbol;A
15	213427_at	0.7	−1.58	0.58	RPP40	ribonuclease P/MRP subunit p40 [Source:HGNC Symbol;Acc
16	203550_s_at	0.58	−1.57	0.46	FAM189B	family with sequence similarity 189 member B [Source:HGNC
17	218296_x_at	1.2	−1.56	0.62	MSTO1	misato 1, mitochondrial distribution and morphology regulator
18	208502_s_at	1.64	−1.55	0.45	PITX1	paired like homeodomain 1 [Source:HGNC Symbol;Acc:HGN
19	212279_at	0.61	−1.53	0.62	TMEM97	transmembrane protein 97 [Source:HGNC Symbol;Acc:HGN
20	209336_at	0.7	−1.51	0.53	LOC102724159	

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−28	44 / 728	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	8e−25	29 / 280	GSEA	MANALO_HYPOXIA_DN
3	2e−19	35 / 703	GSEA	LEE_BMP2_TARGETS_DN
4	6e−19	20 / 158	GSEA	BILD_MYC_ONCOGENIC_SIGNATURE
5	2e−18	33 / 651	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
6	3e−16	14 / 72	GSEA	SCHUHMACHER_MYC_TARGETS_UP
7	4e−16	29 / 575	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	1e−14	12 / 55	HM	HALLMARK_MYC_TARGETS_V2
9	2e−14	30 / 726	GSEA	PUJANA_CHEK2_PCC_NETWORK
10	7e−13	22 / 409	Canc	Lembcke_Normal vs Adenoma
11	1e−12	32 / 966	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	1e−12	26 / 616	GSEA	WEI_MYCN_TARGETS_WITH_E_BOX
13	2e−11	18 / 305	Lymp	TARTE_Plasmablast signature
14	3e−11	38 / 1527	GSEA	PUJANA_BRCA1_PCC_NETWORK
15	1e−10	17 / 290	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
16	1e−10	17 / 295	GSEA	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
17	2e−10	23 / 602	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
18	2e−09	21 / 561	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
19	2e−09	13 / 186	GSEA	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
20	3e−09	16 / 314	GSEA	PENG_GLUTAMINE_DEPRIVATION_DN
21	5e−09	11 / 129	GSEA	WELCSH_BRCA1_TARGETS_DN
22	6e−09	22 / 653	CC	nucleolus
23	7e−09	16 / 335	GSEA	BENPORATH_ES_1
24	1e−08	10 / 107	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_DN
25	1e−08	12 / 174	BP	rRNA processing
26	1e−08	11 / 140	GSEA	RUIZ_TNC_TARGETS_DN
27	1e−08	19 / 509	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
28	2e−08	21 / 641	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
29	3e−08	20 / 590	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
30	3e−08	13 / 233	GSEA	PENG_RAPAMYCIN_RESPONSE_DN
31	4e−08	12 / 193	GSEA	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP
32	5e−08	7 / 44	GSEA	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
33	5e−08	11 / 159	GSEA	SANSOM_APC_TARGETS_REQUIRE_MYC
34	1e−07	26 / 1052	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
35	2e−07	11 / 179	GSEA	CHANG_CORE_SERUM_RESPONSE_UP
36	2e−07	27 / 1161	MF	RNA binding
37	2e−07	12 / 226	GSEA	ZHANG_TLX_TARGETS_60HR_DN
38	2e−07	9 / 113	GSEA	KATSANOU_ELAVL1_TARGETS_DN
39	4e−07	17 / 510	GSEA	STEIN_ESRRA_TARGETS
40	5e−07	11 / 202	GSEA	BENPORATH_MYC_TARGETS_WITH_EBOX


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	1e−08	12 / 174	rRNA processing
2	1e−04	3 / 12	ubiquinone biosynthetic process
3	2e−04	3 / 14	folic acid metabolic process
4	3e−04	5 / 76	ribosome biogenesis
5	1e−03	3 / 26	one−carbon metabolic process
6	1e−03	3 / 27	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
7	3e−03	2 / 10	CTP biosynthetic process
8	3e−03	2 / 10	positive regulation of cilium assembly
9	3e−03	2 / 10	rRNA transcription
10	5e−03	2 / 13	ribosomal small subunit assembly
11	5e−03	2 / 14	centrosome duplication
12	5e−03	2 / 14	positive regulation of telomerase RNA localization to Cajal body
13	5e−03	2 / 14	purine nucleotide biosynthetic process
14	5e−03	2 / 14	purine ribonucleoside monophosphate biosynthetic process
15	6e−03	2 / 15	microtubule nucleation

Cancer

Rank	p−value	#in/all	Geneset
1	7e−13	22 / 409	Lembcke_Normal vs Adenoma
2	9e−06	5 / 36	ZHANG_MM up
3	2e−04	3 / 14	BENTINK_myc.1
4	2e−04	3 / 15	GENTLES_modul2
5	3e−03	1 / 11	LIU_PROSTATE_CANCER_UP
6	7e−03	2 / 16	WOLFER_overlap genes
7	7e−03	2 / 16	GENTLES_modul6
8	1e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
9	1e−02	3 / 58	SHAUGHNESSY_MM high risk
10	1e−02	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
11	3e−02	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	8e−02	1 / 10	GENTLES_modul3
13	8e−02	1 / 10	GENTLES_modul5
14	1e−01	1 / 13	GENTLES_modul1
15	1e−01	1 / 15	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	6e−09	22 / 653	nucleolus
2	2e−06	12 / 277	mitochondrial matrix
3	6e−06	25 / 1221	mitochondrion
4	9e−05	4 / 30	small−subunit processome
5	5e−03	2 / 13	exosome (RNase complex)
6	6e−03	49 / 4579	nucleus
7	1e−02	49 / 4701	cytoplasm
8	1e−02	3 / 57	mitochondrial intermembrane space
9	1e−02	30 / 2541	nucleoplasm
10	1e−02	41 / 3805	cytosol
11	2e−02	5 / 196	nuclear membrane
12	3e−02	2 / 35	nuclear inner membrane
13	4e−02	2 / 38	mitochondrial nucleoid
14	5e−02	2 / 43	Cajal body
15	5e−02	3 / 107	fibrillar center

Chr

Rank	p−value	#in/all	Geneset
1	0.06	11 / 833	Chr 19
2	0.12	5 / 333	Chr 22
3	0.16	14 / 1325	Chr 1
4	0.16	9 / 776	Chr 17
5	0.25	8 / 756	Chr 11
6	0.26	6 / 548	Chr 16
7	0.30	2 / 139	Chr 21
8	0.34	5 / 490	Chr 10
9	0.55	4 / 492	Chr 9
10	0.58	3 / 382	Chr 15
11	0.64	5 / 689	Chr 3
12	0.67	3 / 437	Chr 8
13	0.73	3 / 480	Chr 4
14	0.77	1 / 184	Chr 18
15	0.79	2 / 369	Chr 20

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−12	94 / 7957	Tcells peripheral blood_2_TssAFlnk
2	1e−11	95 / 8200	monocytes peripheral blood_2_TssAFlnk
3	5e−11	95 / 8370	natural killer cells peripheral blood_2_TssAFlnk
4	9e−11	94 / 8245	Tregulatory cells peripheral blood_2_TssAFlnk
5	4e−10	94 / 8406	Bcells peripheral blood_2_TssAFlnk
6	6e−10	96 / 8816	Thelper cells peripheral blood_2_TssAFlnk
7	9e−10	86 / 7165	Tx_Colon
8	7e−09	82 / 6798	TxWk_Colon
9	1e−08	90 / 8068	Thelper cells peripheral blood_1_TssA
10	1e−08	83 / 6997	Overlap_fetal_midbrain_K9K27me3
11	1e−08	92 / 8430	3_TssF_Melanocytes
12	1e−08	80 / 6590	Tregulatory cells peripheral blood_5_TxWk
13	1e−08	91 / 8275	2_TssA_Fibroblasts
14	4e−08	94 / 8918	1_TssA_ESC_Mesoderm
15	5e−08	93 / 8766	2_TssA_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−10	23 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	2e−09	21 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	6e−04	7 / 184	Kosinski_lower−crypt−long−list
4	5e−02	1 / 6	Marisa_CRC−C6
5	1e−01	18 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
6	1e−01	7 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
7	4e−01	7 / 738	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
8	4e−01	10 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	5e−01	1 / 83	Marisa_CRC−cluster−d
10	6e−01	4 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
11	6e−01	8 / 1083	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	8e−01	2 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	9e−01	2 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	9e−01	1 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
15	9e−01	2 / 483	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN

Glioma

Rank	p−value	#in/all	Geneset
1	0.003	12 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
2	0.007	21 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	0.008	19 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	0.011	3 / 58	Stuehler_Proteins_up_in_STS
5	0.063	2 / 52	GIEZELT_GBM_WT_down_VS_mut
6	0.098	1 / 13	WILLSCHER_GBM_STSwt_proteomics−O_UP
7	0.134	2 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	0.153	1 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN
9	0.218	1 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
10	0.236	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
11	0.311	1 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
12	0.327	1 / 50	Vishal_subnetwork signature of survival in GBM
13	0.366	9 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
14	0.369	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt
15	0.392	3 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−28	44 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	8e−25	29 / 280	MANALO_HYPOXIA_DN
3	2e−19	35 / 703	LEE_BMP2_TARGETS_DN
4	6e−19	20 / 158	BILD_MYC_ONCOGENIC_SIGNATURE
5	2e−18	33 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
6	3e−16	14 / 72	SCHUHMACHER_MYC_TARGETS_UP
7	4e−16	29 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
8	2e−14	30 / 726	PUJANA_CHEK2_PCC_NETWORK
9	1e−12	32 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	1e−12	26 / 616	WEI_MYCN_TARGETS_WITH_E_BOX
11	3e−11	38 / 1527	PUJANA_BRCA1_PCC_NETWORK
12	1e−10	17 / 290	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
13	1e−10	17 / 295	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
14	2e−09	13 / 186	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
15	3e−09	16 / 314	PENG_GLUTAMINE_DEPRIVATION_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−14	12 / 55	HALLMARK_MYC_TARGETS_V2
2	2e−06	8 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	2e−06	10 / 190	HALLMARK_MYC_TARGETS_V1
4	1e−04	8 / 187	HALLMARK_E2F_TARGETS
5	1e−04	8 / 192	HALLMARK_MTORC1_SIGNALING
6	2e−02	5 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	2e−02	5 / 195	HALLMARK_G2M_CHECKPOINT
8	5e−02	4 / 174	HALLMARK_ADIPOGENESIS
9	8e−02	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	9e−02	3 / 133	HALLMARK_DNA_REPAIR
11	2e−01	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
12	2e−01	2 / 97	HALLMARK_BILE_ACID_METABOLISM
13	2e−01	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
14	4e−01	2 / 170	HALLMARK_IL2_STAT5_SIGNALING
15	4e−01	2 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION

Immunome

Rank	p−value	#in/all	Geneset
1	0.04	1 / 5	Angelova_immune−metagene−NK56_bright
2	0.13	1 / 18	Angelova_immune−metagene−pDC
3	0.14	1 / 19	Angelova_immune−metagene−activated_CD8
4	0.26	1 / 38	Angelova_immune−metagene−mast−cells
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 / 13	Angelova_immune−metagene−immature_B−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 32	Marjolein_ageing−genes_DN
2	0.5	2 / 210	Homuth_BMI−associated−genes_DN
3	0.7	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

Lympnoma

Rank	p−value	#in/all	Geneset
1	2e−11	18 / 305	TARTE_Plasmablast signature
2	9e−06	9 / 173	Victora_Light zone signature
3	1e−05	7 / 99	Sha_BL UP
4	9e−05	63 / 5529	HOPP_Txn_elongation
5	1e−04	52 / 4261	HOPP_Txn_transition
6	3e−04	3 / 17	DAVE_c−myc BL UP
7	7e−04	6 / 135	DAVE_BL−vs−DLBCL
8	8e−04	59 / 5404	HOPP_Strong_enhancer
9	8e−04	63 / 5908	HOPP_Active_promoter
10	5e−03	4 / 88	ROSOLOWSKI_green UP
11	2e−02	4 / 121	ROSOLOWSKI_green total
12	3e−02	55 / 5682	HOPP_Weak_promoter
13	4e−02	2 / 40	CARO_OxPhos_in_DLBCL_UP
14	4e−02	3 / 97	ROSOLOWSKI_red total
15	7e−02	1 / 9	YAMANE_AICDA_targets_nonrecruited

Melanoma

Rank	p−value	#in/all	Geneset
1	1e−05	11 / 276	Gerber_wt/wt_melanoma−cells−SpotB
2	9e−04	9 / 319	Gerber_wt/wt_melanoma−cells−SpotA
3	4e−02	2 / 38	Tirosh_top50 correlated genes PC1
4	1e−01	2 / 79	Tirosh_core cycling genes in low− and high−proliferation melanoma
5	1e−01	2 / 81	Tirosh_Genes in the MITF program
6	3e−01	3 / 222	Gerber_wt/wt_melanoma−cells−SpotF
7	3e−01	1 / 39	Tirosh_melanoma specific genes
8	3e−01	3 / 230	Gerber_wt/wt_melanoma−cells−SpotC
9	4e−01	1 / 59	TCGA_melanoma_keratin_high
10	4e−01	1 / 65	Harbst_melanoma_highgrade_up
11	6e−01	2 / 236	Gerber_wt/wt_group3−specific
12	8e−01	1 / 189	Tirosh_genes preferentially expressed by Tregs
13	9e−01	1 / 249	Gerber_wt/wt_melanoma−cells−SpotE
14	9e−01	2 / 497	Gerber_wt/wt_melanoma−cells−SpotD
15	1e+00	0 / 17	Hugo_melanoma−all−MET_UP

MF

Rank	p−value	#in/all	Geneset
1	2e−07	27 / 1161	RNA binding
2	2e−05	7 / 106	ligase activity
3	3e−03	2 / 10	neutral amino acid transmembrane transporter activity
4	5e−03	2 / 14	NADPH binding
5	7e−03	2 / 16	3'−5'−exoribonuclease activity
6	7e−03	2 / 16	snoRNA binding
7	1e−02	2 / 20	DNA−directed DNA polymerase activity
8	1e−02	2 / 21	gamma−tubulin binding
9	2e−02	2 / 25	nuclear localization sequence binding
10	2e−02	2 / 28	Ran GTPase binding
11	2e−02	2 / 29	amino acid transmembrane transporter activity
12	3e−02	2 / 32	aminoacyl−tRNA ligase activity
13	3e−02	2 / 32	DNA−directed 5'−3' RNA polymerase activity
14	3e−02	17 / 1329	transferase activity
15	3e−02	2 / 35	NAD binding

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	2 / 16	hsa−miR−380*
2	0.018	2 / 26	hsa−miR−934
3	0.023	2 / 30	hsa−miR−518e
4	0.033	2 / 36	hsa−miR−766
5	0.036	3 / 92	hsa−miR−199a−5p
6	0.039	1 / 5	hsa−miR−126
7	0.045	3 / 101	hsa−miR−199b−5p
8	0.050	5 / 254	hsa−miR−520d−3p
9	0.052	3 / 107	hsa−miR−204
10	0.055	3 / 109	hsa−miR−194
11	0.059	2 / 50	hsa−miR−187
12	0.061	2 / 51	hsa−miR−502−5p
13	0.067	4 / 194	hsa−miR−520a−3p
14	0.070	2 / 55	hsa−miR−637
15	0.074	2 / 57	hsa−miR−935

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.2	1 / 33	Sweeney_viral_dn
2	0.3	1 / 48	Burnham_viral_DN
3	0.3	1 / 54	Burnham_timecourse
4	0.8	1 / 179	Terre_MSV_multiple_respiratory_viruses_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 / 57	Burnham_viral_UP
10	1.0	0 / 57	Burnham_day1_vs_5_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 18	Scicluna_UP
13	1.0	0 / 41	Scicluna_DN
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	0.003	15 / 866	PROTEINATLAS_cerebellum
2	0.008	6 / 219	WIRTH_GC B−cells
3	0.010	16 / 1076	PROTEINATLAS_stomach
4	0.019	16 / 1161	PROTEINATLAS_colon
5	0.020	8 / 429	PROTEINATLAS_liver
6	0.031	1 / 4	JONGENEEL_SpinalCord
7	0.031	14 / 1032	PROTEINATLAS_small intestine
8	0.035	14 / 1048	PROTEINATLAS_rectum
9	0.039	2 / 40	VAQUERIZAS_Testis_TF
10	0.041	10 / 678	PROTEINATLAS_lymph node
11	0.041	14 / 1072	PROTEINATLAS_duodenum
12	0.044	9 / 594	PROTEINATLAS_parathyroid gland
13	0.049	9 / 604	PROTEINATLAS_hippocampus
14	0.054	1 / 7	VAQUERIZAS_Tongue_TF
15	0.060	3 / 113	Chaussabel_1,8_Metabolism Biosynthesis

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	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−05	23 / 1107	ICGC_Myc_targets
2	3e−05	24 / 1241	KIM_MYC targets
3	1e−04	5 / 62	MYC_Targets UP
4	1e−03	22 / 1387	HEBENSTREIT_high expression TF
5	3e−03	2 / 10	MYC_RNA processing binding UP
6	1e−02	2 / 19	MYC_Metabolism UP
7	2e−02	9 / 522	ICGC_SrfPcr2_targets
8	2e−02	1 / 3	MYC_DNA replication UP
9	4e−02	33 / 3150	ICGC_Creb1_targets
10	5e−02	19 / 1630	ICGC_SrfV0416101_targets
11	7e−02	8 / 549	ICGC_Atf3_targets
12	7e−02	40 / 4131	ICGC_Tcf3_targets
13	8e−02	35 / 3564	ICGC_Taf1_targets
14	1e−01	6 / 415	ICGC_RxraPcr1_targets
15	1e−01	12 / 1032	ICGC_Usf1_targets

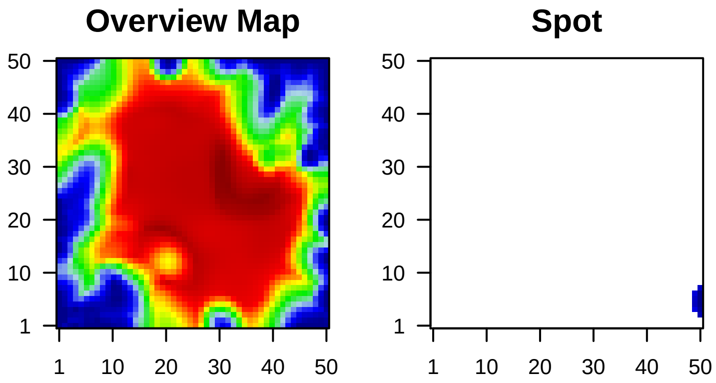
Underexpression Spots

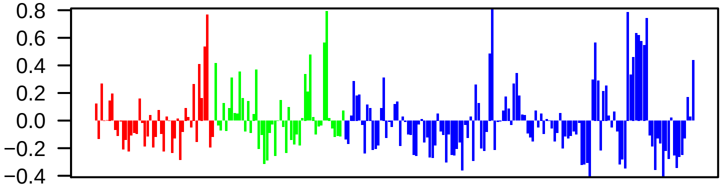
Spot Summary: u

metagenes = 10
genes = 268

<r> metagenes = 0.95
<r> genes = 0.41
beta: r2= 8.98 / log p= −Inf

samples with spot = 43 (19.5 %)
mBL : 5 (11.4 %)
intermediate : 5 (10.4 %)
non−mBL : 33 (25.6 %)



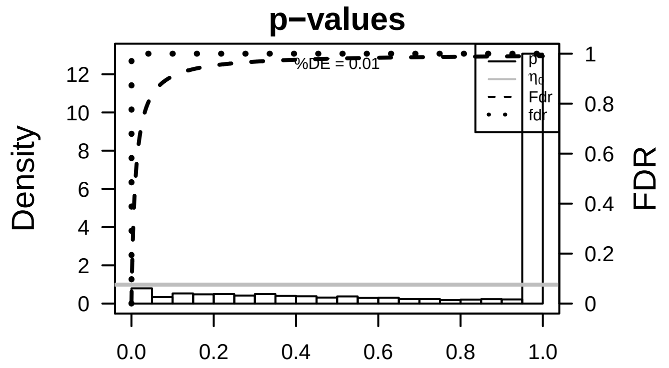


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	214870_x_at	0.97	−2.06	0.58	NPIPA5	nuclear pore complex−interacting protein family member A5 is
2	204538_x_at	0.81	−1.88	0.6	NPIPA5	nuclear pore complex−interacting protein family member A5 is
3	202379_s_at	1.1	−1.86	0.65	NKTR	natural killer cell triggering receptor [Source:HGNC Symbol;A
4	221501_x_at	1	−1.77	0.6	NPIPA5	nuclear pore complex−interacting protein family member A5 is
5	219269_at	0.96	−1.73	0.31	HMBOX1	homeobox containing 1 [Source:HGNC Symbol;Acc:HGNC:2
6	220035_at	1.22	−1.62	0.62	NUP210	nucleoporin 210 [Source:HGNC Symbol;Acc:HGNC:30052]
7	213359_at	1.25	−1.57	0.6	HNRNPD	heterogeneous nuclear ribonucleoprotein D [Source:HGNC S
8	217713_x_at	0.8	−1.52	0.72		
9	210425_x_at	1.04	−1.46	0.5	GOLGA8A	golgin A8 family member A [Source:HGNC Symbol;Acc:HGN
10	213593_s_at	1.44	−1.45	0.81		
11	216908_x_at	0.87	−1.44	0.47		RRN3 homolog, RNA polymerase I transcription factor pseud
12	217586_x_at	1.1	−1.43	0.72		
13	208433_s_at	1.18	−1.41	0.44	LRP8	LDL receptor related protein 8 [Source:HGNC Symbol;Acc:H
14	214722_at	1.22	−1.38	0.66		
15	213326_at	1.04	−1.38	0.35	VAMP1	vesicle associated membrane protein 1 [Source:HGNC Symb
16	207953_at	1.18	−1.38	0.68		
17	213089_at	1.75	−1.37	0.89		
18	212177_at	1.23	−1.36	0.69	PNISR	PNN interacting serine and arginine rich protein [Source:HGN
19	217591_at	1.02	−1.36	0.47		
20	213517_at	1.25	−1.36	0.7		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−27	33 / 218	Refer	WIRTH_pre+post GC B−cells
2	1e−18	53 / 1174	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
3	3e−17	23 / 188	Refer	Chaussabel_3,8_Enzymes
4	3e−12	12 / 59	Gliom	WILLSCHER_GBM_Verhaak−PNwt & MES_up
5	5e−12	5 / 14	Canc	LIU_COMMON_CANCER_GENES
6	5e−12	5 / 14	Canc	LIU_COMMON_CANCER_GENES
7	1e−11	16 / 143	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
8	2e−11	27 / 492	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
9	4e−11	8 / 20	Refer	Chaussabel_2,7_Unknown function
10	5e−10	7 / 17	GSEA	SPIRA_SMOKERS_LUNG_CANCER_DN
11	3e−09	12 / 102	Lympl	ROSOLOWSKI_blue total
12	5e−08	83 / 4261	Lympl	HOPP_Txn_transition
13	2e−07	21 / 477	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
14	3e−07	11 / 127	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
15	4e−06	12 / 198	BP	mRNA splicing, via spliceosome
16	5e−06	10 / 136	GSEA	REACTOME_MRNA_PROCESSING
17	5e−06	5 / 22	Refer	Chaussabel_1,6_Signaling molecules
18	7e−06	26 / 852	MF	nucleic acid binding
19	8e−06	21 / 600	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
20	9e−06	11 / 179	Pneu	Terre_MSV_multiple_respiratory_viruses_dn
21	1e−05	9 / 120	GSEA	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
22	2e−05	23 / 730	GSEA	ONKEN_UVEAL_MELANOMA_UP
23	2e−05	26 / 906	Lympl	SPANG_BCR DN
24	3e−05	12 / 239	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
25	3e−05	7 / 75	GSEA	LAIHO_COLORECTAL_CANCER_SERRATED_DN
26	3e−05	13 / 281	BP	mRNA processing
27	4e−05	13 / 289	GSEA	LU_EZH2_TARGETS_DN
28	5e−05	90 / 5529	Lympl	HOPP_Txn_elongation
29	5e−05	13 / 297	GSEA	BASAKI_YBX1_TARGETS_DN
30	7e−05	16 / 445	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
31	9e−05	3 / 8	Gliom	WILLSCHER_GBM_LTSmut_proteomics−A_UP
32	9e−05	5 / 39	GSEA	BILBAN_B_CLL_LPL_DN
33	9e−05	36 / 1602	GSEA	BLALOCK_ALZHEIMERS_DISEASE_UP
34	1e−04	7 / 92	GSEA	REACTOME_MRNA_SPLICING
35	1e−04	31 / 1312	GSEA	PUJANA_ATM_PCC_NETWORK
36	2e−04	4 / 24	GSEA	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
37	2e−04	28 / 1161	MF	RNA binding
38	2e−04	18 / 592	GSEA	BENPORATH_SOX2_TARGETS
39	3e−04	7 / 110	GSEA	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
40	4e−04	4 / 29	GSEA	REACTOME_MRNA_3_END_PROCESSING



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	0.005	9 / 268	intracellular ribonucleoprotein complex
2	0.005	70 / 4579	nucleus
3	0.007	43 / 2541	nucleoplasm
4	0.007	2 / 11	holo TFIIH complex
5	0.012	3 / 41	cytosolic large ribosomal subunit
6	0.013	2 / 15	phagophore assembly site membrane
7	0.013	3 / 42	cleavage furrow
8	0.015	9 / 326	nuclear speck
9	0.018	5 / 128	spliceosomal complex
10	0.023	2 / 20	nuclear outer membrane
11	0.025	5 / 139	ribosome
12	0.026	3 / 54	axoneme
13	0.027	2 / 22	smooth endoplasmic reticulum
14	0.031	4 / 100	chromatin
15	0.032	2 / 24	stereocilium

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−18	53 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
2	2e−11	27 / 492	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
3	1e−02	18 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
4	1e−02	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
5	1e−02	18 / 854	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
6	2e−02	30 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
7	2e−02	12 / 532	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
8	5e−02	11 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
9	7e−02	11 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	9e−02	1 / 8	KIM_MSI−in−EC
11	1e−01	1 / 10	KIM_CRC−MSI−regulated_DN
12	1e−01	1 / 12	Juehling_HNPCC−mutated−in−4
13	2e−01	2 / 60	Marisa_CRC−cluster−g
14	2e−01	1 / 16	Vilar_mutated−in−CRC−CamP
15	2e−01	2 / 72	Ang_CRC−CIMPH−vs−L_hyper

HM

Rank	p−value	#in/all	Geneset
1	0.07	5 / 190	HALLMARK_MYC_TARGETS_V1
2	0.10	2 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	0.19	4 / 193	HALLMARK_HEME_METABOLISM
4	0.20	4 / 195	HALLMARK_G2M_CHECKPOINT
5	0.33	1 / 34	HALLMARK_APICAL_SURFACE
6	0.33	1 / 34	HALLMARK_ANGIOGENESIS
7	0.36	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.38	3 / 187	HALLMARK_E2F_TARGETS
9	0.40	3 / 194	HALLMARK_MYOGENESIS
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	0.64	2 / 182	HALLMARK_GLYCOLYSIS
14	0.65	2 / 188	HALLMARK_HYPOXIA
15	0.66	2 / 191	HALLMARK_P53_PATHWAY

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−09	12 / 102	ROSOLOWSKI_blue total
2	5e−08	83 / 4261	HOPP_Txn_transition
3	2e−05	26 / 906	SPANG_BCR DN
4	5e−05	90 / 5529	HOPP_Txn_elongation
5	3e−03	2 / 7	Shaknovich_ABC_hypo_meth
6	4e−03	87 / 5908	HOPP_Active_promoter
7	2e−02	3 / 45	Monti_BCR_cluster
8	2e−02	2 / 19	Subero_MCL_hypo_meth
9	3e−02	76 / 5404	HOPP_Strong_enhancer
10	7e−02	1 / 6	MASCQUE_mBL UP
11	1e−01	2 / 45	SPANG_BAFF 9hrs DN
12	1e−01	3 / 99	Sha_BL UP
13	1e−01	1 / 12	BENTINK_mBL DOWN
14	1e−01	5 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	2e−01	1 / 14	Subero_B−ALL_hypo_meth

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	5 / 72	hsa−miR−339−5p
2	0.002	9 / 234	hsa−miR−101
3	0.002	6 / 111	hsa−miR−656
4	0.003	10 / 301	hsa−miR−519b−3p
5	0.005	4 / 59	hsa−miR−499−3p
6	0.006	6 / 136	hsa−miR−511
7	0.006	10 / 333	hsa−miR−519c−3p
8	0.007	3 / 33	hsa−miR−654−3p
9	0.011	5 / 114	hsa−miR−494
10	0.015	3 / 44	hsa−miR−455−5p
11	0.016	5 / 124	hsa−miR−655
12	0.016	4 / 82	hsa−miR−210
13	0.017	3 / 46	hsa−miR−1260
14	0.019	2 / 18	hsa−miR−668
15	0.020	3 / 49	hsa−miR−330−5p

Telomeres

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

BP

Rank	p−value	#in/all	Geneset
1	4e−06	12 / 198	mRNA splicing, via spliceosome
2	3e−05	13 / 281	mRNA processing
3	4e−04	10 / 233	RNA splicing
4	8e−04	3 / 16	programmed cell death
5	1e−03	4 / 42	RNA metabolic process
6	5e−03	3 / 30	positive regulation of telomere maintenance via telomerase
7	6e−03	3 / 32	activation of JUN kinase activity
8	6e−03	8 / 232	translation
9	1e−02	5 / 110	translational initiation
10	1e−02	4 / 71	regulation of G2/M transition of mitotic cell cycle
11	1e−02	5 / 113	rhythmic process
12	1e−02	2 / 14	regulation of establishment of cell polarity
13	1e−02	2 / 15	positive regulation of telomere capping
14	1e−02	2 / 15	response to peptide
15	1e−02	2 / 16	positive regulation of dendritic spine morphogenesis

Chr

Rank	p−value	#in/all	Geneset
1	0.01	13 / 548	Chr 16
2	0.04	12 / 585	Chr 7
3	0.07	9 / 437	Chr 8
4	0.12	14 / 833	Chr 19
5	0.21	12 / 776	Chr 17
6	0.34	6 / 403	Chr 14
7	0.37	3 / 184	Chr 18
8	0.45	9 / 700	Chr 12
9	0.47	5 / 382	Chr 15
10	0.49	2 / 139	Chr 21
11	0.52	10 / 832	Chr 2
12	0.55	3 / 242	Chr 13
13	0.56	4 / 333	Chr 22
14	0.57	8 / 689	Chr 3
15	0.64	6 / 554	Chr 5

Glioma

Rank	p−value	#in/all	Geneset
1	3e−12	12 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
2	9e−05	3 / 8	WILLSCHER_GBM_LTSmut_proteomics−A_UP
3	1e−02	2 / 15	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	2e−02	1 / 2	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
5	6e−02	25 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	6e−02	12 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	6e−02	3 / 78	Weller_LGG_A_vs_O_UP
8	1e−01	21 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	1e−01	1 / 10	Phillips PN up vs MES & Prolif
10	1e−01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
11	1e−01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	2e−01	1 / 16	VERHAAK_PN subtype
13	2e−01	2 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
14	2e−01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_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	0.15	1 / 14	Angelova_immune−metagene−eosinophil
7	0.19	1 / 18	Angelova_CRC_immunostimulators
8	0.24	1 / 23	Angelova_immune−metagene−monocytes
9	1.00	0 / 13	Angelova_immune−metagene−activated_B−cells
10	1.00	0 / 26	Angelova_immune−metagene−activated_CD4
11	1.00	0 / 19	Angelova_immune−metagene−activated_CD8
12	1.00	0 / 21	Angelova_immune−metagene−central_memory_CD4
13	1.00	0 / 17	Angelova_immune−metagene−central_memory_CD8
14	1.00	0 / 25	Angelova_immune−metagene−DC
15	1.00	0 / 12	Angelova_immune−metagene−effector_memory_CD4

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	0.11	6 / 276	Gerber_wt/wt_melanoma−cells−SpotB
4	0.17	5 / 249	Gerber_wt/wt_melanoma−cells−SpotE
5	0.17	1 / 16	Hugo_melanoma−all−LEF1_UP
6	0.19	2 / 68	Tirosh_housekeeping_genes
7	0.24	1 / 23	Melanoma Epi−Enzyme Cluster 7
8	0.27	4 / 222	Gerber_wt/wt_melanoma−cells−SpotF
9	0.33	3 / 171	Landsberg_dedifferentiation_up
10	0.36	1 / 37	Hugo_melanoma−all−MET_DN
11	0.36	1 / 38	Tirosh_top50 correlated genes PC1
12	0.37	1 / 39	Tirosh_top50 correlated genes PC4
13	0.37	3 / 185	Tirosh_genes from malignant cells in Mel79−melanoma
14	0.39	1 / 41	Tirosh_top50 correlated genes PC3
15	0.46	1 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma

Pneumonia

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

TF

Rank	p−value	#in/all	Geneset
1	0.05	26 / 1578	ICGC_GabpPcr2_targets
2	0.07	51 / 3564	ICGC_Taf1_targets
3	0.09	45 / 3150	ICGC_Creb1_targets
4	0.10	25 / 1630	ICGC_SrfV0416101_targets
5	0.11	1 / 10	MYC_RNA processing binding UP
6	0.11	51 / 3703	ICGC_Foxm1_targets
7	0.12	52 / 3796	ICGC_Nficsc81335_targets
8	0.12	9 / 485	ICGC_NrsfPcr2_targets
9	0.13	58 / 4319	ICGC_Pou2_targets
10	0.14	51 / 3769	ICGC_Pmlsc71910_targets
11	0.15	61 / 4602	ICGC_Elf1_targets
12	0.17	2 / 62	MYC_Targets UP
13	0.17	1 / 16	MYC_Protein synthesis degradation UP
14	0.20	9 / 549	ICGC_Atf3_targets
15	0.21	50 / 3804	ICGC_Stat5_targets

Cancer

Rank	p−value	#in/all	Geneset
1	5e−12	5 / 14	LIU_COMMON_CANCER_GENES
2	5e−04	3 / 14	GUSTAFSON_PI3K_DN
3	1e−01	1 / 12	LIU_BREAST_CANCER
4	2e−01	1 / 14	GENTLES_modul10
5	2e−01	1 / 14	BENTINK_myc.1
6	4e−01	1 / 41	PanCan_DNARepair_geneset_nanostring
7	4e−01	1 / 45	KUIPER_MM poor survival
8	4e−01	0 / 14	LIU_PROSTATE_CANCER_DN
9	5e−01	2 / 134	PanCan_RAS_geneset_nanostring
10	5e−01	6 / 480	Lembcke_Colonic Inflammation
11	6e−01	0 / 11	LIU_PROSTATE_CANCER_UP
12	7e−01	2 / 187	PanCan_PI3K_geneset_nanostring
13	7e−01	1 / 96	PanCan_TXmisReg_geneset_nanostring
14	7e−01	4 / 409	Lembcke_Normal vs Adenoma
15	8e−01	1 / 147	PanCan_MAPK_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−10	105 / 5601	Thelper cells peripheral blood_4_Tx
2	1e−09	77 / 3524	Tregulatory cells peripheral blood_6_EnhG
3	1e−09	79 / 3682	natural killer cells peripheral blood_6_EnhG
4	2e−09	105 / 5753	Tcells peripheral blood_4_Tx
5	2e−09	105 / 5766	natural killer cells peripheral blood_4_Tx
6	2e−09	29 / 693	Bcells peripheral blood_3_TxFlnk
7	3e−09	127 / 7833	Bcells peripheral blood_1_TssA
8	3e−09	104 / 5716	Bcells peripheral blood_4_Tx
9	4e−09	85 / 4208	Tcells peripheral blood_6_EnhG
10	6e−09	101 / 5527	Tregulatory cells peripheral blood_4_Tx
11	1e−08	78 / 3767	Bcells peripheral blood_6_EnhG
12	2e−08	112 / 6590	Tregulatory cells peripheral blood_5_TxWk
13	5e−08	105 / 6068	4_Tx_ESC_Endoderm
14	6e−08	117 / 7165	Tx_Colon
15	1e−07	97 / 5456	5_Tx_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−12	5 / 14	LIU_COMMON_CANCER_GENES
2	1e−11	16 / 143	LEE_DIFFERENTIATING_T_LYMPHOCYTE
3	5e−10	7 / 17	SPIRA_SMOKERS_LUNG_CANCER_DN
4	2e−07	21 / 477	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
5	3e−07	11 / 127	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
6	5e−06	10 / 136	REACTOME_MRNA_PROCESSING
7	8e−06	21 / 600	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
8	1e−05	9 / 120	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
9	2e−05	23 / 730	ONKEN_UVEAL_MELANOMA_UP
10	3e−05	12 / 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
11	3e−05	7 / 75	LAIHO_COLORECTAL_CANCER_SERRATED_DN
12	4e−05	13 / 289	LU_EZH2_TARGETS_DN
13	5e−05	13 / 297	BASAKI_YBX1_TARGETS_DN
14	7e−05	16 / 445	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
15	9e−05	5 / 39	BILBAN_B_CLL_LPL_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	3 / 210	Homuth_BMI−associated−genes_DN
4	0.5	2 / 150	Homuth_BMI−associated−genes_UP
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	7e−06	26 / 852	nucleic acid binding
2	2e−04	28 / 1161	RNA binding
3	1e−02	2 / 14	endodeoxyribonuclease activity
4	2e−02	2 / 19	miRNA binding
5	2e−02	2 / 20	RNA polymerase II transcription corepressor activity
6	3e−02	2 / 22	translation factor activity, RNA binding
7	3e−02	2 / 23	telomeric DNA binding
8	4e−02	3 / 65	protein phosphatase binding
9	5e−02	2 / 29	SH2 domain binding
10	5e−02	2 / 30	histone−lysine N−methyltransferase activity
11	5e−02	3 / 70	transcriptional repressor activity, RNA polymerase II transcription regulatory r
12	6e−02	2 / 33	DNA−dependent ATPase activity
13	6e−02	2 / 34	kinesin binding
14	7e−02	2 / 37	ribosome binding
15	7e−02	4 / 132	methyltransferase activity

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−27	33 / 218	WIRTH_pre+post GC B−cells
2	3e−17	23 / 188	Chaussabel_3,8_Enzymes
3	4e−11	8 / 20	Chaussabel_2,7_Unknown function
4	5e−06	5 / 22	Chaussabel_1,6_Signaling molecules
5	1e−03	23 / 989	PROTEINATLAS_tonsil
6	2e−03	6 / 106	Chaussabel_2,11_Replication
7	2e−03	14 / 496	PROTEINATLAS_spleen
8	3e−03	17 / 678	PROTEINATLAS_lymph node
9	1e−02	14 / 593	PROTEINATLAS_lateral ventricle
10	1e−02	18 / 866	PROTEINATLAS_cerebellum
11	2e−02	4 / 83	Chaussabel_1,7_MHC Ribosomal proteins
12	2e−02	14 / 642	PROTEINATLAS_lung
13	2e−02	7 / 233	PROTEINATLAS_smooth muscle
14	2e−02	17 / 840	PROTEINATLAS_urinary bladder
15	2e−02	6 / 182	WIRTH_post GC B−cells

Underexpression Spots

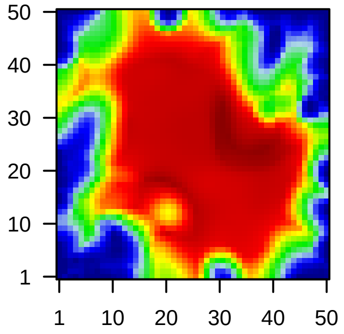
Spot Summary: v

metagenes = 20
genes = 310

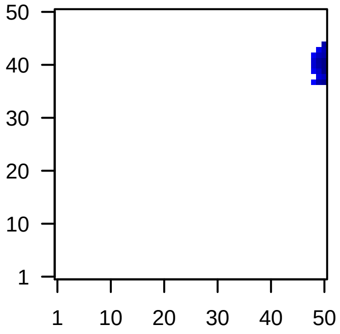
<r> metagenes = 0.91
<r> genes = 0.2
beta: r2= 6.2 / log p= −Inf

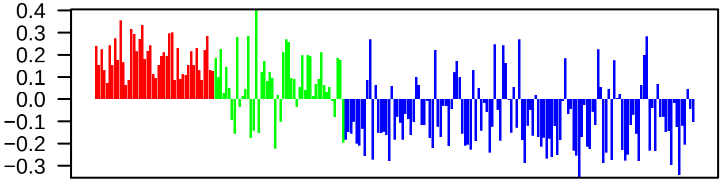
samples with spot = 33 (14.9 %)
intermediate : 1 (2.1 %)
non−mBL : 32 (24.8 %)

Overview Map



Spot





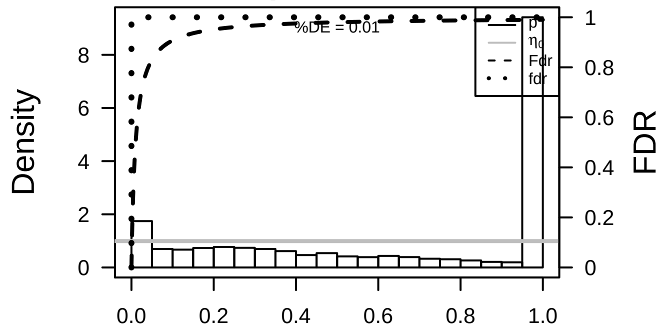
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	210258_at	0.95	−2.84	0.27	RGS13	regulator of G protein signaling 13 [Source:HGNC Symbol;Ac
2	204581_at	0.8	−2.63	0.35	CD22	CD22 molecule [Source:HGNC Symbol;Acc:HGNC:1643]
3	212560_at	0.82	−2.57	0.41	SORL1	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
4	220588_at	0.74	−2.54	0.49	BCAS4	breast carcinoma amplified sequence 4 [Source:HGNC Symb
5	219517_at	0.92	−2.5	0.49		
6	220059_at	0.79	−2.46	0.74	STAP1	signal transducing adaptor family member 1 [Source:HGNC S
7	219518_s_at	0.95	−2.37	0.48		
8	204961_s_at	0.91	−2.35	0.45	NCF1	neutrophil cytosolic factor 1 [Source:HGNC Symbol;Acc:HGN
9	204891_s_at	0.85	−2.23	0.58	LCK	LCK proto−oncogene, Src family tyrosine kinase [Source:HGI
10	205922_at	1.09	−2.13	0.44	VNN2	vanin 2 [Source:HGNC Symbol;Acc:HGNC:12706]
11	204004_at	0.91	−2	0.48	PAWR	pro−apoptotic WT1 regulator [Source:HGNC Symbol;Acc:HG
12	204890_s_at	0.95	−1.97	0.54	LCK	LCK proto−oncogene, Src family tyrosine kinase [Source:HGI
13	212715_s_at	0.71	−1.94	0.4	MICAL3	microtubule associated monooxygenase, calponin and LIM do
14	219109_at	0.7	−1.91	0.41	SPAG16	sperm associated antigen 16 [Source:HGNC Symbol;Acc:HG
15	200702_s_at	0.71	−1.88	0.27	DDX24	DEAD−box helicase 24 [Source:HGNC Symbol;Acc:HGNC:1
16	201560_at	0.61	−1.88	0.41	CLIC4	chloride intracellular channel 4 [Source:HGNC Symbol;Acc:H
17	212411_at	0.57	−1.87	0.51	IMP4	IMP4, U3 small nucleolar ribonucleoprotein [Source:HGNC S
18	212314_at	0.67	−1.86	0.64	SEL1L3	SEL1L family member 3 [Source:HGNC Symbol;Acc:HGNC:2
19	203509_at	0.92	−1.86	0.35	SORL1	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
20	219812_at	0.63	−1.82	0.49	STAG3	stromal antigen 3 [Source:HGNC Symbol;Acc:HGNC:11356]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−21	37 / 263	Lympl	SPANG_CD40 6hrs UP
2	1e−19	185 / 5908	Lympl	HOPP_Active_promoter
3	6e−19	174 / 5404	Lympl	HOPP_Strong_enhancer
4	8e−18	29 / 195	GSEA	HOLLMANN_APOPTOSIS_VIA_CD40_UP
5	7e−16	173 / 5682	Lympl	HOPP_Weak_promoter
6	2e−12	162 / 5529	Lympl	HOPP_Txn_elongation
7	5e−12	137 / 4357	Lympl	HOPP_Weak_txn
8	6e−12	52 / 955	Lympl	SPANG_BCR UP
9	7e−12	14 / 61	GSEA	BASSO_CD40_SIGNALING_DN
10	2e−11	26 / 275	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
11	5e−10	20 / 186	GSEA	PENG_RAPAMYCIN_RESPONSE_UP
12	9e−10	135 / 4559	Lympl	HOPP_Weak_enhancer
13	1e−09	6 / 8	Lympl	MASCQUE_GCB UP
14	1e−09	10 / 37	GSEA	ZHAN_MULTIPLE_MYELOMA_CD2_UP
15	2e−09	128 / 4261	Lympl	HOPP_Txn_transition
16	4e−09	14 / 96	Lympl	SPANG_LPS 6hrs UP
17	6e−09	16 / 133	GSEA	PENG_LEUCINE_DEPRIVATION_UP
18	1e−08	11 / 59	GSEA	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
19	1e−07	22 / 309	GSEA	DAZARD_RESPONSE_TO_UV_NHEK_DN
20	2e−07	39 / 830	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
21	2e−07	18 / 219	Refer	WIRTH_GC B−cells
22	3e−07	6 / 16	GSEA	ZHAN_LATE_DIFFERENTIATION_GENES_DN
23	5e−07	6 / 17	Lympl	Aukema_BCL2 UP_BCL6 DN
24	1e−06	9 / 56	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
25	1e−06	8 / 42	Refer	Chaussabel_1,3_B−cells
26	2e−06	32 / 673	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
27	7e−06	5 / 15	Lympl	DAVE_BL Inter
28	7e−06	11 / 107	GSEA	SMIRNOV_RESPONSE_TO_IR_6HR_DN
29	9e−06	21 / 368	GSEA	ZHENG_BOUND_BY_FOXP3
30	2e−05	35 / 848	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
31	2e−05	7 / 43	GSEA	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN
32	2e−05	5 / 18	Lympl	SPANG_BAFF 9hrs UP
33	3e−05	36 / 906	Lympl	SPANG_BCR DN
34	3e−05	3 / 4	Lympl	WRIGHT_custom GCB−DLBCL UP
35	3e−05	59 / 1814	Lympl	HOPP_Repetitive
36	4e−05	23 / 469	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
37	4e−05	8 / 67	GSEA	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM
38	4e−05	52 / 1550	GSEA	PILON_KLF1_TARGETS_DN
39	6e−05	16 / 266	GSEA	MULLIGHAN_MLL_SIGNATURE_2_DN
40	7e−05	16 / 268	miRN	hsa−miR−367

p−values



Aging

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

BP

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 17	T cell proliferation
2	8e−04	21 / 507	protein phosphorylation
3	9e−04	10 / 157	positive regulation of cell migration
4	2e−03	16 / 361	intracellular signal transduction
5	2e−03	9 / 146	cytoskeleton organization
6	2e−03	3 / 14	activation of MAPKKK activity
7	2e−03	3 / 14	regulation of establishment of cell polarity
8	3e−03	4 / 30	cognition
9	3e−03	3 / 15	positive regulation of histone H3−K4 methylation
10	3e−03	3 / 16	negative regulation of Rho protein signal transduction
11	3e−03	3 / 16	negative regulation of T cell receptor signaling pathway
12	4e−03	4 / 33	T cell differentiation
13	4e−03	3 / 17	positive regulation of receptor−mediated endocytosis
14	4e−03	21 / 576	phosphorylation
15	4e−03	4 / 34	negative regulation of phosphoprotein phosphatase activity

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	19 / 480	Lembcke_Colonic Inflammation
2	0.013	5 / 72	PanCan_Wnt_geneset_nanostring
3	0.013	7 / 130	PanCan_CC+Apop_geneset_nanostring
4	0.056	2 / 20	PanCan_ChromMod_geneset_nanostring
5	0.110	1 / 6	ZHANG_MGUS up
6	0.177	1 / 10	GENTLES_modul3
7	0.193	1 / 11	LIU_PROSTATE_CANCER_UP
8	0.193	1 / 11	GENTLES_modul14
9	0.209	1 / 12	GENTLES_modul12
10	0.224	1 / 13	GENTLES_modul17
11	0.230	2 / 47	PanCan_TGF−B_geneset_nanostring
12	0.239	1 / 14	GUSTAFSON_PI3K_DN
13	0.239	1 / 14	BENTINK_ras.6
14	0.239	1 / 14	BENTINK_src.2
15	0.254	1 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	3e−04	99 / 3805	cytosol
2	9e−04	8 / 104	trans−Golgi network
3	1e−03	112 / 4579	nucleus
4	5e−03	10 / 196	nuclear membrane
5	5e−03	111 / 4701	cytoplasm
6	5e−03	66 / 2541	nucleoplasm
7	6e−03	3 / 20	nuclear outer membrane
8	1e−02	28 / 936	cytoskeleton
9	2e−02	4 / 51	clathrin−coated vesicle
10	2e−02	12 / 310	dendrite
11	2e−02	3 / 29	immunological synapse
12	2e−02	2 / 11	SAGA complex
13	2e−02	12 / 315	neuronal cell body
14	2e−02	3 / 30	aggresome
15	2e−02	4 / 55	brush border

Chr

Rank	p−value	#in/all	Geneset
1	0.001	25 / 669	Chr 6
2	0.017	22 / 700	Chr 12
3	0.023	15 / 437	Chr 8
4	0.029	16 / 490	Chr 10
5	0.102	16 / 585	Chr 7
6	0.126	21 / 832	Chr 2
7	0.132	5 / 139	Chr 21
8	0.203	30 / 1325	Chr 1
9	0.576	13 / 689	Chr 3
10	0.584	9 / 480	Chr 4
11	0.610	7 / 382	Chr 15
12	0.626	6 / 333	Chr 22
13	0.694	3 / 184	Chr 18
14	0.739	8 / 492	Chr 9
15	0.749	9 / 554	Chr 5

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−27	194 / 5716	Bcells peripheral blood_4_Tx
2	6e−24	190 / 5766	natural killer cells peripheral blood_4_Tx
3	9e−24	149 / 3767	Bcells peripheral blood_6_EnhG
4	1e−22	222 / 7833	Bcells peripheral blood_1_TssA
5	1e−22	230 / 8406	Bcells peripheral blood_2_TssAFlnk
6	3e−22	215 / 7407	natural killer cells peripheral blood_5_TxWk
7	3e−22	229 / 8370	natural killer cells peripheral blood_2_TssAFlnk
8	4e−22	223 / 7957	Tcells peripheral blood_2_TssAFlnk
9	2e−21	219 / 7751	natural killer cells peripheral blood_1_TssA
10	3e−21	208 / 7078	Bcells peripheral blood_5_TxWk
11	4e−21	234 / 8865	Thelper cells peripheral blood_7_Enh
12	7e−21	213 / 7420	Tcells peripheral blood_1_TssA
13	8e−21	200 / 6637	Tcells peripheral blood_5_TxWk
14	4e−20	232 / 8816	Thelper cells peripheral blood_2_TssAFlnk
15	4e−19	181 / 5753	Tcells peripheral blood_4_Tx

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	35 / 848	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
2	1e−04	37 / 1001	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
3	2e−03	37 / 1174	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
4	3e−03	49 / 1729	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
5	2e−02	8 / 172	Pentrack_CRC_TCGA_corr_U_msi−h_UP
6	2e−02	139 / 6368	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
7	6e−02	24 / 883	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
8	6e−02	9 / 255	Kosinski_top−crypt−long−list
9	6e−02	30 / 1166	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	6e−02	17 / 589	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
11	1e−01	9 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
12	1e−01	24 / 958	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
13	1e−01	9 / 297	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
14	1e−01	1 / 7	TCGA−CRC_agressive−disease−markers
15	1e−01	1 / 8	Marisa_CRC−C1

Glioma

Rank	p−value	#in/all	Geneset
1	0.001	42 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.003	13 / 282	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	0.005	14 / 330	Up
4	0.008	16 / 421	Down_b
5	0.011	42 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
6	0.016	20 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	0.027	4 / 59	WILLSCHER_GBM_Verhaak−PNwt & MES_up
8	0.036	10 / 268	ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN
9	0.051	10 / 286	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
10	0.075	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_down (A)
11	0.095	2 / 27	Donson−Misc immune function−associated with LTS in HGA
12	0.105	8 / 246	ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN
13	0.110	1 / 6	Shaw_responders_up_in_oligo_glioma
14	0.110	1 / 6	WILLSCHER_GBM_Verhaak−PNmut_up (M)
15	0.128	1 / 7	oligodendrocytes_glio

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−18	29 / 195	HOLLMANN_APOPTOSIS_VIA_CD40_UP
2	7e−12	14 / 61	BASSO_CD40_SIGNALING_DN
3	2e−11	26 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
4	5e−10	20 / 186	PENG_RAPAMYCIN_RESPONSE_UP
5	1e−09	10 / 37	ZHAN_MULTIPLE_MYELOMA_CD2_UP
6	6e−09	16 / 133	PENG_LEUCINE_DEPRIVATION_UP
7	1e−08	11 / 59	HUTTMANN_B_CLL_POOR_SURVIVAL_DN
8	1e−07	22 / 309	DAZARD_RESPONSE_TO_UV_NHEK_DN
9	2e−07	39 / 830	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
10	3e−07	6 / 16	ZHAN_LATE_DIFFERENTIATION_GENES_DN
11	1e−06	9 / 56	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
12	2e−06	32 / 673	SCHLOSSER_SERUM_RESPONSE_DN
13	7e−06	11 / 107	SMIRNOV_RESPONSE_TO_IR_6HR_DN
14	9e−06	21 / 368	ZHENG_BOUND_BY_FOXP3
15	2e−05	7 / 43	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	8 / 170	HALLMARK_IL2_STAT5_SIGNALING
2	0.05	7 / 173	HALLMARK_MITOTIC_SPINDLE
3	0.06	6 / 141	HALLMARK_UV_RESPONSE_DN
4	0.08	7 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.11	2 / 29	HALLMARK_NOTCH_SIGNALING
6	0.12	4 / 96	HALLMARK_ANDROGEN_RESPONSE
7	0.17	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
8	0.17	6 / 192	HALLMARK_MTORC1_SIGNALING
9	0.25	5 / 176	HALLMARK_ALLOGRAFT_REJECTION
10	0.26	2 / 51	HALLMARK_TGF_BETA_SIGNALING
11	0.26	5 / 178	HALLMARK_COMPLEMENT
12	0.27	3 / 94	HALLMARK_PROTEIN_SECRETION
13	0.29	2 / 55	HALLMARK_MYC_TARGETS_V2
14	0.31	5 / 191	HALLMARK_P53_PATHWAY
15	0.34	3 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Immunome

Rank	p−value	#in/all	Geneset
1	8e−05	4 / 13	Angelova_immune−metagene−immature_B−cells
2	3e−02	2 / 13	Angelova_immune−metagene−activated_B−cells
3	4e−02	2 / 16	Angelova_immune−metagene−Th17
4	1e−01	1 / 8	Angelova_immune−metagene−mDC
5	2e−01	1 / 10	Angelova_immune−metagene−neutrophils
6	2e−01	1 / 10	Angelova_immune−metagene−TFH
7	2e−01	1 / 11	Angelova_immune−metagene−macrophages
8	2e−01	1 / 12	Angelova_immune−metagene−memory_B−cells
9	3e−01	1 / 15	Angelova_immune−metagene−NK
10	3e−01	1 / 18	Angelova_CRC_immunostimulators
11	3e−01	1 / 21	Angelova_immune−metagene−central_memory_CD4
12	5e−01	1 / 32	Angelova_immune−metagene−effector_memory_CD8
13	5e−01	1 / 38	Angelova_immune−metagene−mast−cells
14	6e−01	1 / 42	Angelova_immune−metagene−TGD
15	7e−01	1 / 67	Angelova_immune−metagene−T−cells

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
2	0.11	7 / 210	Homuth_BMI−associated−genes_DN
3	0.13	2 / 32	Marjolein_ageing−genes_DN
4	0.14	1 / 8	Marjolein_ageing−genes_UP
5	0.35	1 / 22	DUMEAUX_High bmi enriched genes
6	0.35	1 / 22	DUMEAUX_Fasting enriched genes
7	0.79	2 / 150	Homuth_BMI−associated−genes_UP
8	1.00	0 / 62	DUMEAUX_Smoking enriched genes
9	1.00	0 / 10	DUMEAUX_Smoking literature genes up
10	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
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 / 12	DUMEAUX_Women normal BMI literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−21	37 / 263	SPANG_CD40 6hrs UP
2	1e−19	185 / 5908	HOPP_Active_promoter
3	6e−19	174 / 5404	HOPP_Strong_enhancer
4	7e−16	173 / 5682	HOPP_Weak_promoter
5	2e−12	162 / 5529	HOPP_Txn_elongation
6	5e−12	137 / 4357	HOPP_Weak_txn
7	6e−12	52 / 955	SPANG_BCR UP
8	9e−10	135 / 4559	HOPP_Weak_enhancer
9	1e−09	6 / 8	MASCQUE_GCB UP
10	2e−09	128 / 4261	HOPP_Txn_transition
11	4e−09	14 / 96	SPANG_LPS 6hrs UP
12	5e−07	6 / 17	Aukema_BCL2 UP_BCL6 DN
13	7e−06	5 / 15	DAVE_BL Inter
14	2e−05	5 / 18	SPANG_BAFF 9hrs UP
15	3e−05	36 / 906	SPANG_BCR DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.005	7 / 107	Tirosh_Exhaustion program in Mel75
2	0.011	3 / 24	Tirosh_B−cell specific genes−melanoma
3	0.037	3 / 38	Hugo_melanoma−BRAFmut−MET_UP
4	0.038	1 / 2	Melanoma Epi−Enzyme Cluster 2
5	0.072	2 / 23	Melanoma Epi−Enzyme Cluster 7
6	0.075	1 / 4	Melanoma Epi−Enzyme Cluster 3
7	0.075	3 / 51	Tirosh_genes from CD8 T−cells in Mel79−melanoma
8	0.077	4 / 83	TCGA_melanoma_immune_high
9	0.101	7 / 204	Landsberg_dedifferentiation_down
10	0.139	7 / 222	Gerber_wt/wt_melanoma−cells−SpotF
11	0.366	11 / 497	Gerber_wt/wt_melanoma−cells−SpotD
12	0.374	1 / 24	Tirosh_exhuastion−associated genes consitent across tumors
13	0.420	7 / 319	Gerber_wt/wt_melanoma−cells−SpotA
14	0.443	6 / 276	Gerber_wt/wt_melanoma−cells−SpotB
15	0.459	5 / 230	Gerber_wt/wt_melanoma−cells−SpotC

MF

Rank	p−value	#in/all	Geneset
1	5e−04	43 / 1329	transferase activity
2	5e−04	15 / 291	actin binding
3	8e−04	3 / 10	MAP kinase kinase kinase kinase activity
4	1e−03	176 / 7864	protein binding
5	1e−03	4 / 25	protein phosphatase inhibitor activity
6	1e−03	10 / 165	calmodulin binding
7	1e−03	6 / 64	phosphatidylinositol binding
8	2e−03	18 / 437	protein kinase activity
9	4e−03	21 / 573	kinase activity
10	5e−03	14 / 331	protein serine/threonine kinase activity
11	6e−03	10 / 202	GTPase activator activity
12	6e−03	3 / 20	phosphatidylinositol−3,4−bisphosphate binding
13	1e−02	4 / 44	methylated histone binding
14	1e−02	64 / 2529	metal ion binding
15	1e−02	3 / 25	cyclin binding

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−05	16 / 268	hsa−miR−367
2	1e−04	6 / 41	hsa−miR−504
3	1e−04	17 / 315	hsa−miR−144
4	1e−04	9 / 101	hsa−miR−199b−5p
5	3e−04	13 / 217	hsa−miR−92a
6	4e−04	8 / 92	hsa−miR−199a−5p
7	4e−04	11 / 167	hsa−miR−432
8	7e−04	8 / 99	hsa−miR−376b
9	7e−04	12 / 207	hsa−miR−92b
10	7e−04	6 / 56	hsa−miR−193b
11	8e−04	17 / 369	hsa−miR−130a
12	9e−04	12 / 213	hsa−miR−363
13	1e−03	12 / 216	hsa−miR−548l
14	1e−03	15 / 312	hsa−miR−301b
15	1e−03	8 / 109	hsa−miR−194

Pneumonia

Rank	p−value	#in/all	Geneset
1	0.02	8 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.19	2 / 41	Scicluna_DN
3	0.48	1 / 33	Sweeney_viral_dn
4	0.51	1 / 37	Sweeney_viral_up
5	0.61	1 / 48	Burnham_viral_DN
6	0.67	1 / 56	Burnham_sep_vs_con_DN
7	0.67	1 / 57	Burnham_viral_UP
8	0.67	1 / 57	Burnham_day1_vs_5_UP
9	0.69	2 / 122	Terre_IMS_influenza_meta_signature
10	0.93	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
11	1.00	0 / 68	Burnham_sep_vs_con_UP
12	1.00	0 / 48	Burnham_cap_fp_vs_con_DN
13	1.00	0 / 71	Burnham_cap_fp_vs_con_UP
14	1.00	0 / 52	Burnham_day1_vs_5_DN
15	1.00	0 / 54	Burnham_timecourse

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−07	18 / 219	WIRTH_GC B−cells
2	1e−06	8 / 42	Chaussabel_1,3_B−cells
3	3e−04	27 / 678	PROTEINATLAS_lymph node
4	4e−04	16 / 310	Chaussabel_3,4_Protein phosphatases
5	1e−03	33 / 989	PROTEINATLAS_tonsil
6	3e−03	7 / 100	Chaussabel_2,8_T−cells
7	1e−02	9 / 188	Chaussabel_3,8_Enzymes
8	2e−02	13 / 355	WIRTH_Immune system
9	2e−02	10 / 245	Chaussabel_3,9_Kinases
10	2e−02	3 / 32	Chaussabel_1,1_Plasma Cells
11	3e−02	2 / 13	WIRTH_B−cells
12	3e−02	20 / 645	PROTEINATLAS_bone marrow
13	3e−02	28 / 1007	PROTEINATLAS_kidney
14	3e−02	2 / 15	WIRTH_Cerebellum
15	3e−02	5 / 93	Chaussabel_1,4_Replication

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	67 / 2254	ICGC_BatfPcr1_targets
2	2e−04	52 / 1636	ICGC_Bcl11_targets
3	1e−03	46 / 1508	ICGC_Mef2_targets
4	1e−03	89 / 3451	ICGC_Atf2_targets
5	2e−03	53 / 1848	ICGC_Pbx3_targets
6	3e−03	59 / 2150	ICGC_Irf4_targets
7	3e−03	44 / 1494	ICGC_Cebpbsc150_targets
8	3e−03	94 / 3796	ICGC_Nficsc81335_targets
9	3e−03	33 / 1041	ICGC_P300_targets
10	5e−03	88 / 3564	ICGC_Taf1_targets
11	5e−03	74 / 2899	ICGC_Nfatc1_targets
12	7e−03	92 / 3804	ICGC_Stat5_targets
13	9e−03	77 / 3121	ICGC_Egr1_targets
14	9e−03	31 / 1032	ICGC_Usf1_targets
15	1e−02	97 / 4131	ICGC_Tcf3_targets