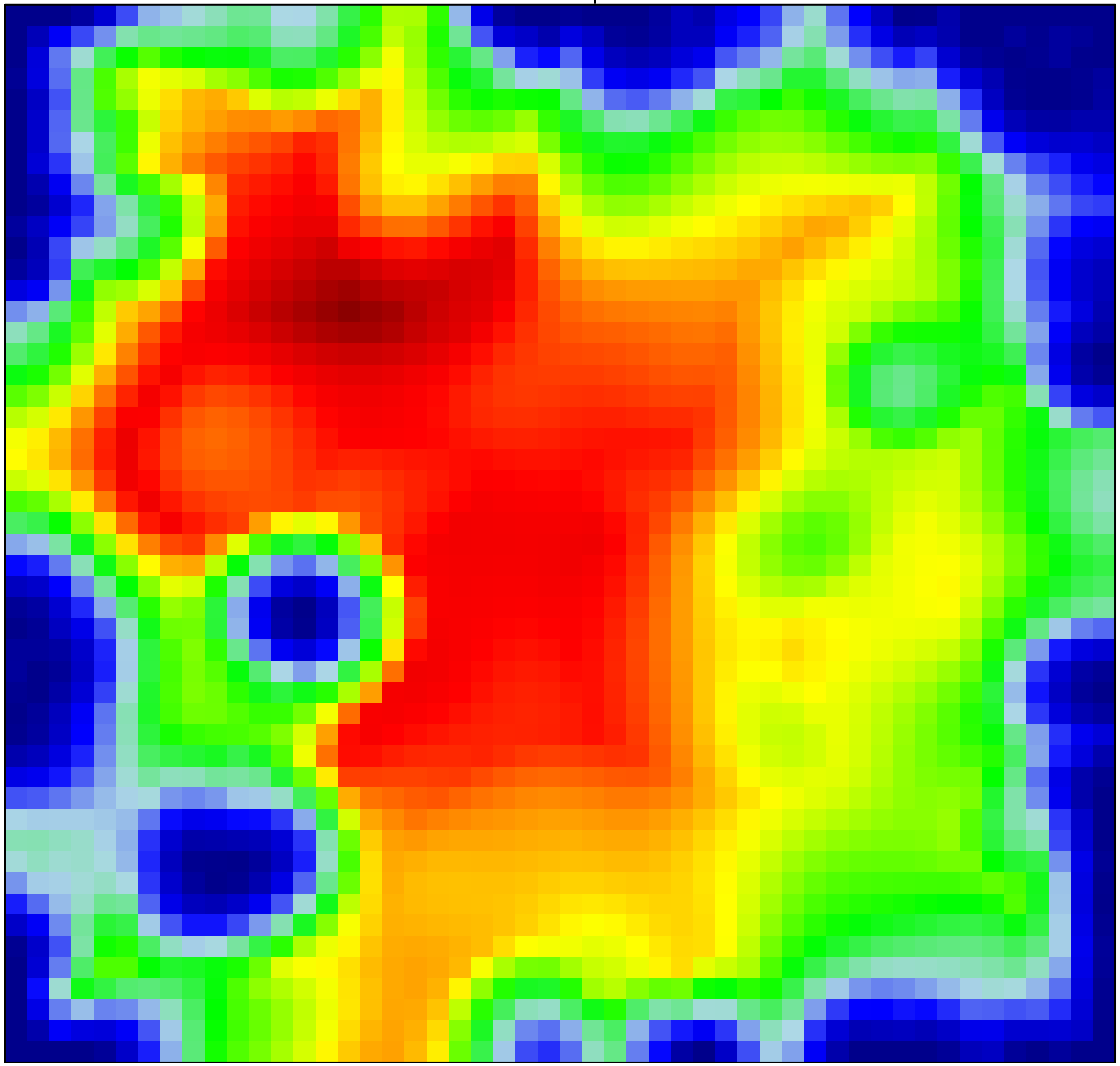
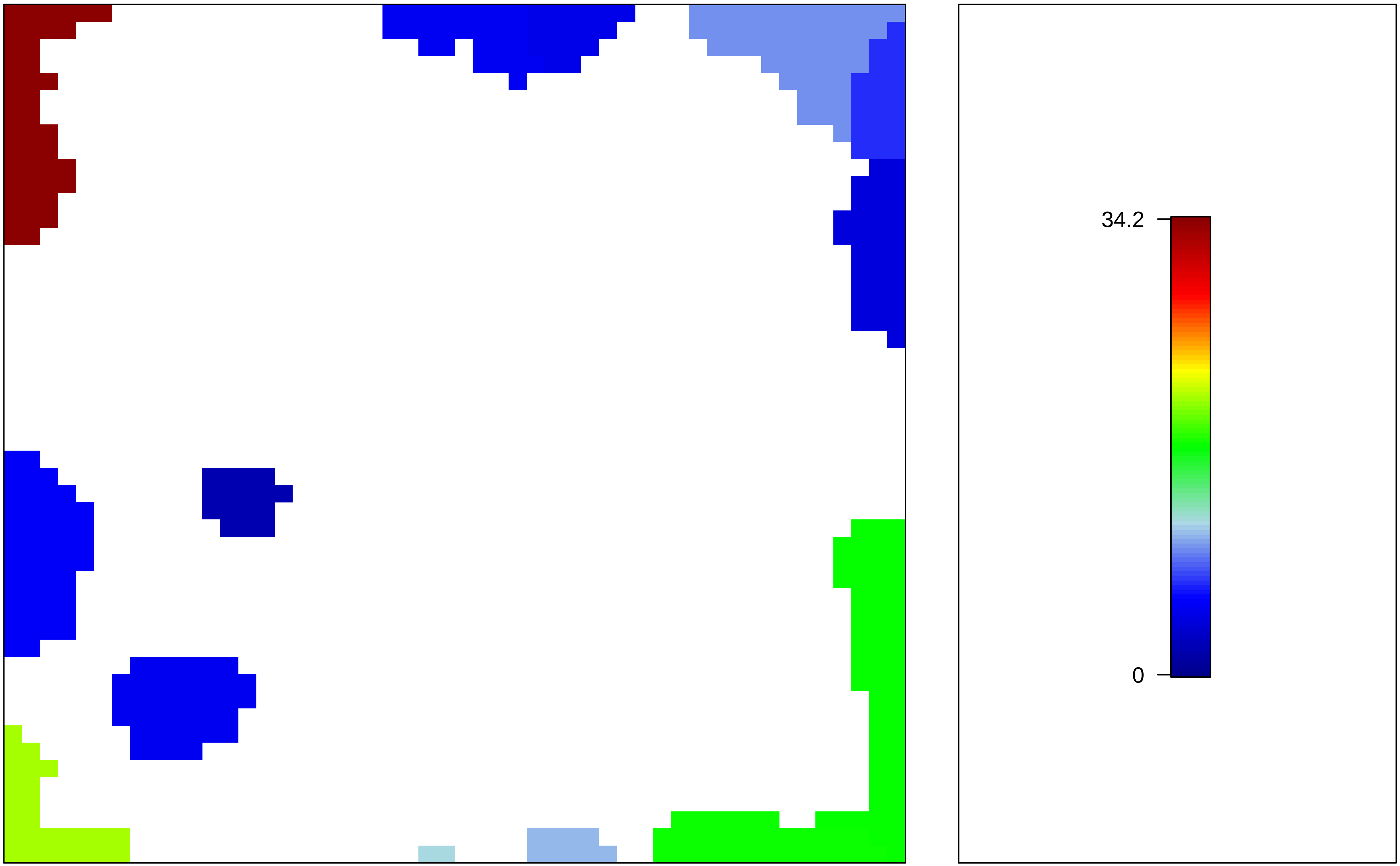
Sample−Underexpression

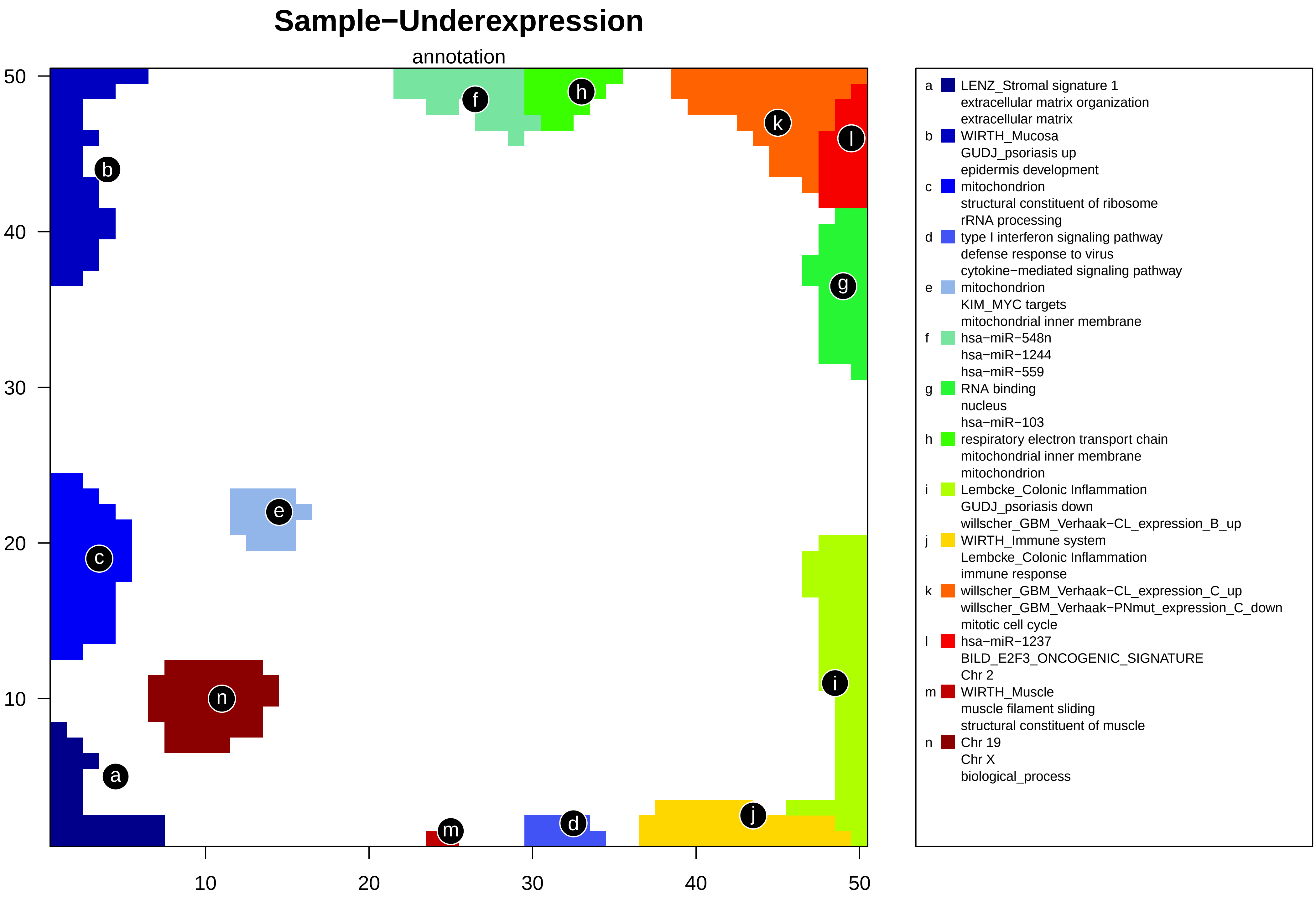
landscape



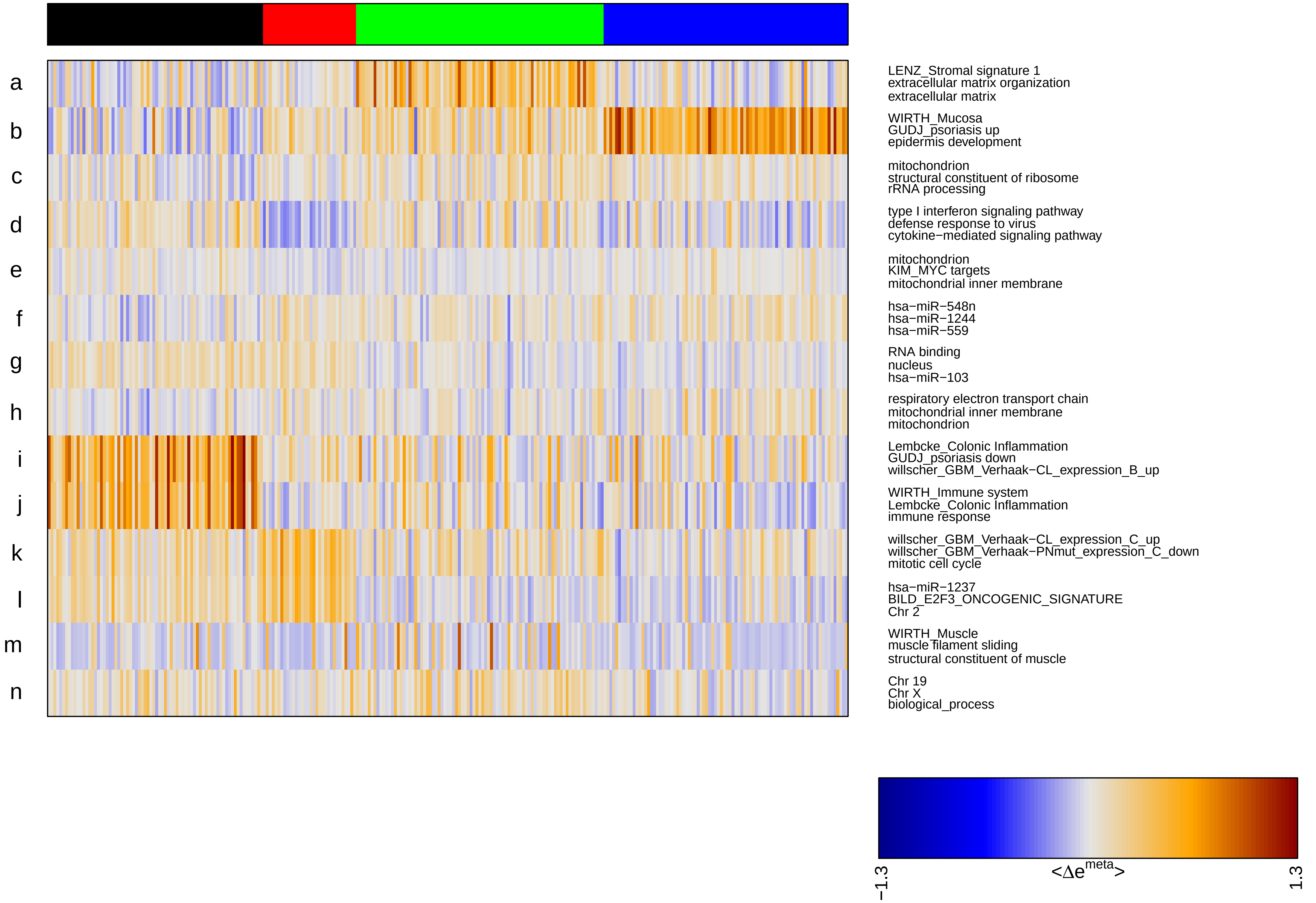
Sample−Underexpression

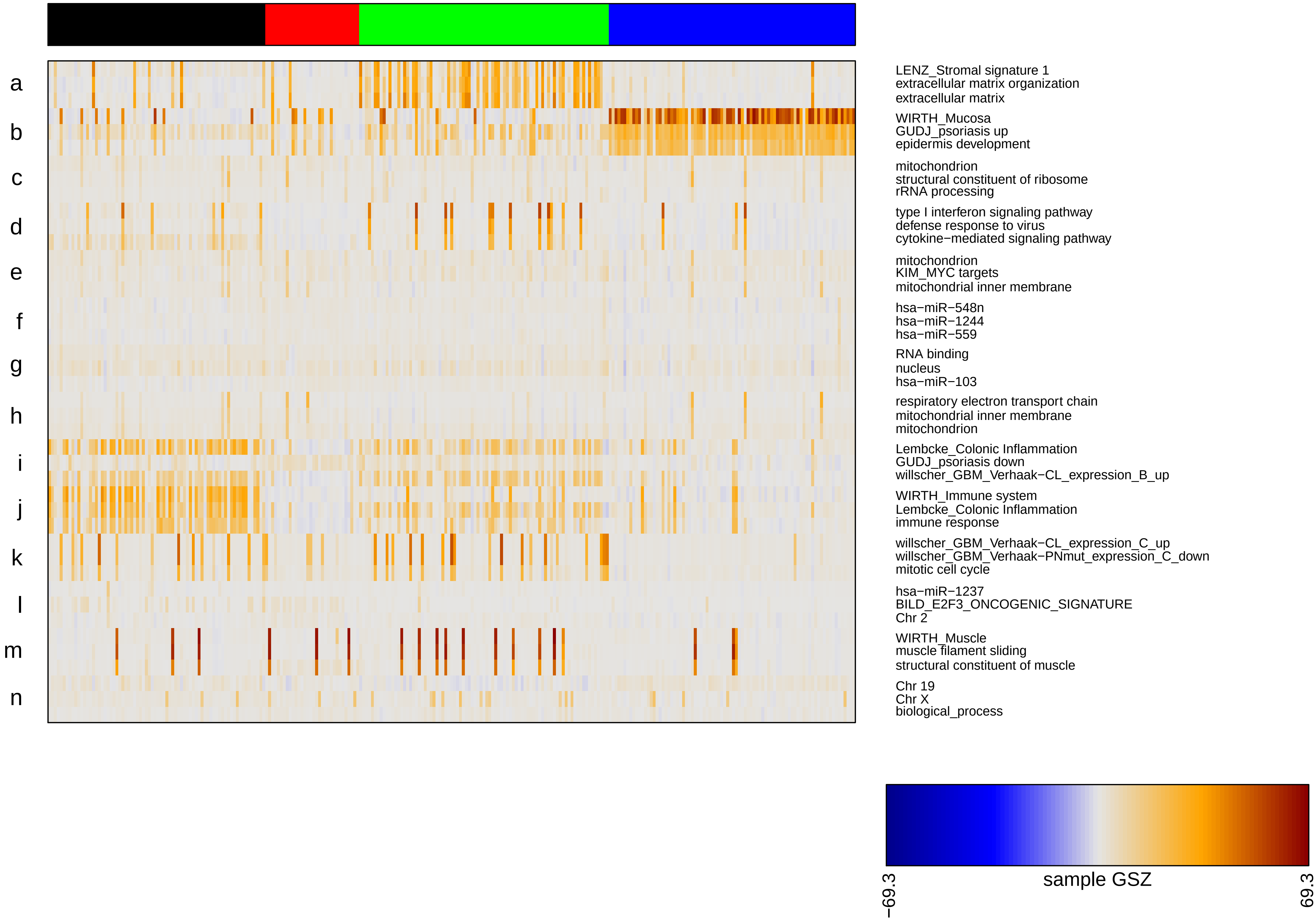
beta−scores




Sample−Underexpression

annotation


a
b
c
d
e
f
g
h
i
j
k
l
m
n
LENZ_Stromal signature 1
extracellular matrix organization
extracellular matrix
WIRTH_Mucosa
GUDJ_psoriasis up
epidermis development
mitochondrion
structural constituent of ribosome
rRNA processing
type I interferon signaling pathway
defense response to virus
cytokine−mediated signaling pathway
mitochondrion
KIM_MYC targets
mitochondrial inner membrane
hsa−miR−548n
hsa−miR−1244
hsa−miR−559
RNA binding
nucleus
hsa−miR−103
respiratory electron transport chain
mitochondrial inner membrane
mitochondrion
Lembcke_Colonic Inflammation
GUDJ_psoriasis down
willscher_GBM_Verhaak−CL_expression_B_up
WIRTH_Immune system
Lembcke_Colonic Inflammation
immune response
willscher_GBM_Verhaak−CL_expression_C_up
willscher_GBM_Verhaak−PNmut_expression_C_down
mitotic cell cycle
hsa−miR−1237
BILD_E2F3_ONCOGENIC_SIGNATURE
Chr 2
WIRTH_Muscle
muscle filament sliding
structural constituent of muscle
Chr 19
Chr X
biological_process
−1.3
<Δe^meta>
1.3


a
b
c
d
e
f
g
h
i
j
k
l
m
n
LENZ_Stromal signature 1
extracellular matrix organization
extracellular matrix
WIRTH_Mucosa
GUDJ_psoriasis up
epidermis development
mitochondrion
structural constituent of ribosome
rRNA processing
type I interferon signaling pathway
defense response to virus
cytokine−mediated signaling pathway
mitochondrion
KIM_MYC targets
mitochondrial inner membrane
hsa−miR−548n
hsa−miR−1244
hsa−miR−559
RNA binding
nucleus
hsa−miR−103
respiratory electron transport chain
mitochondrial inner membrane
mitochondrion
Lembcke_Colonic Inflammation
GUDJ_psoriasis down
willscher_GBM_Verhaak−CL_expression_B_up
WIRTH_Immune system
Lembcke_Colonic Inflammation
immune response
willscher_GBM_Verhaak−CL_expression_C_up
willscher_GBM_Verhaak−PNmut_expression_C_down
mitotic cell cycle
hsa−miR−1237
BILD_E2F3_ONCOGENIC_SIGNATURE
Chr 2
WIRTH_Muscle
muscle filament sliding
structural constituent of muscle
Chr 19
Chr X
biological_process
−69.3
sample GSZ
69.3

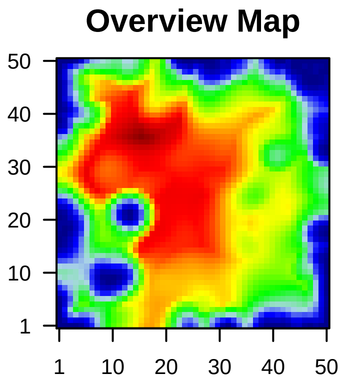
Sample−Underexpression

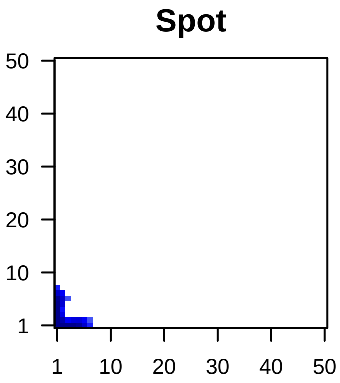
Spot Summary: a

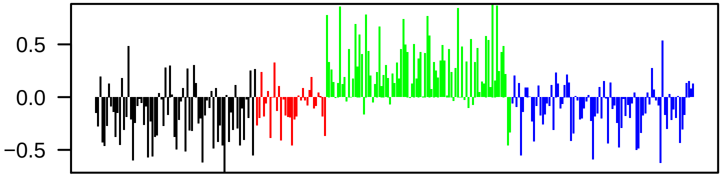
metagenes = 26
genes = 479

<r> metagenes = 0.87
<r> genes = 0.29
beta: r2= 20.85 / log p= −Inf

samples with spot = 54 (19.6 %)
Atypical : 31 (41.9 %)
Classical : 5 (15.6 %)
Mesenchymal : 2 (2.4 %)
Basal : 16 (19 %)





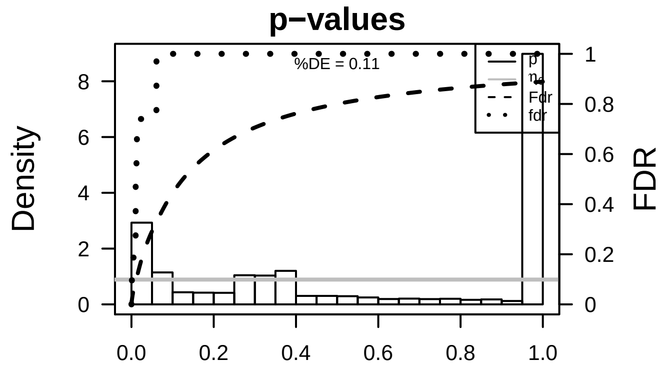


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3043	3.2	−3.29	0.32	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
2	1278	2.53	−3.03	0.81	COL1A2	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	2.17	−3.02	0.79	COL3A1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	4314	3.31	−3.02	0.71	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
5	3576	2.96	−2.98	0.58	IL8	interleukin 8 [Source:HGNC Symbol;Acc:6025]
6	4312	2.74	−2.96	0.78	MMP1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
7	3040	3.64	−2.76	0.32	HBA2	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	1277	2.83	−2.73	0.82	COL1A1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
9	4319	4.09	−2.68	0.57	MMP10	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
10	633	2.12	−2.52	0.8	BGN	biglycan [Source:HGNC Symbol;Acc:1044]
11	4060	2.14	−2.5	0.63	LUM	lumican [Source:HGNC Symbol;Acc:6724]
12	1294	1.73	−2.42	0.57	COL7A1	collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
13	1293	2.13	−2.42	0.84	COL6A3	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
14	1290	2.31	−2.39	0.86	COL5A2	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
15	4318	2.75	−2.38	0.51	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
16	3553	3.13	−2.37	0.54	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
17	12	3.84	−2.36	0.4	RP11−986E7.7	
18	3486	2.44	−2.35	0.27	IGFBP3	insulin−like growth factor binding protein 3 [Source:HGNC Sy
19	1289	2.82	−2.32	0.88	COL5A1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
20	3371	2.22	−2.3	0.68	TNC	tenascin C [Source:HGNC Symbol;Acc:5318]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−75	90 / 250	Lympl	LENZ_Stromal signature 1
2	7e−71	86 / 242	BP	extracellular matrix organization
3	9e−59	70 / 190	CC	extracellular matrix
4	3e−56	148 / 1182	CC	extracellular region
5	4e−42	99 / 683	CC	extracellular space
6	1e−34	70 / 403	BP	cell adhesion
7	9e−34	80 / 553	Canc	Lembcke_Colonic Inflammation
8	1e−32	33 / 69	BP	extracellular matrix disassembly
9	6e−28	29 / 64	BP	collagen catabolic process
10	5e−25	41 / 183	CC	proteinaceous extracellular matrix
11	1e−22	28 / 83	CC	basement membrane
12	1e−22	15 / 16	MMM	MACIEJ_MMML 1
13	2e−20	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	2e−20	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	2e−20	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	2e−20	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	1e−19	22 / 57	MF	extracellular matrix structural constituent
18	4e−18	45 / 330	CC	cell surface
19	2e−17	35 / 204	BP	angiogenesis
20	1e−16	12 / 15	GSEA	CROMER_TUMORIGENESIS_UP
21	5e−16	12 / 16	GSEA	FARMER_BREAST_CANCER_CLUSTER_5
22	5e−15	25 / 119	Lympl	ROSOLOWSKI_green total
23	1e−14	12 / 19	MF	extracellular matrix binding
24	1e−14	11 / 15	GSEA	ONDER_CDH1_TARGETS_2_UP
25	3e−14	21 / 85	MF	integrin binding
26	3e−14	18 / 59	Lympl	LENZ_Stromal signature 2
27	3e−13	23 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
28	5e−13	18 / 68	Glio	cultured astroglia vs. in vivo astrocytes
29	9e−13	138 / 2659	CC	plasma membrane
30	1e−12	10 / 15	GSEA	ONDER_CDH1_SIGNALING_VIA_CTNNB1
31	2e−12	18 / 72	CC	extracellular vesicular exosome
32	2e−12	39 / 364	BP	negative regulation of cell proliferation
33	2e−12	25 / 153	CC	endoplasmic reticulum lumen
34	5e−12	50 / 579	MF	calcium ion binding
35	6e−12	17 / 68	CC	collagen
36	7e−12	13 / 35	Glio	Colman_survival_associated
37	2e−11	13 / 37	BP	collagen fibril organization
38	2e−11	22 / 129	BP	cell migration
39	4e−11	17 / 76	BP	wound healing
40	5e−11	13 / 40	BP	cellular response to amino acid stimulus



BP

Rank	p−value	#in/all	Geneset
1	7e−71	86 / 242	extracellular matrix organization
2	1e−34	70 / 403	cell adhesion
3	1e−32	33 / 69	extracellular matrix disassembly
4	6e−28	29 / 64	collagen catabolic process
5	2e−17	35 / 204	angiogenesis
6	2e−12	39 / 364	negative regulation of cell proliferation
7	2e−11	13 / 37	collagen fibril organization
8	2e−11	22 / 129	cell migration
9	4e−11	17 / 76	wound healing
10	5e−11	13 / 40	cellular response to amino acid stimulus
11	8e−10	37 / 407	blood coagulation
12	1e−09	15 / 70	cell−matrix adhesion
13	1e−09	18 / 106	leukocyte migration
14	3e−09	11 / 36	embryo implantation
15	4e−09	12 / 45	chondroitin sulfate metabolic process
16	4e−09	19 / 126	skeletal system development
17	7e−09	17 / 104	glycosaminoglycan metabolic process
18	1e−08	14 / 70	cell junction assembly
19	1e−08	29 / 299	axon guidance
20	2e−08	20 / 151	response to hypoxia

Cancer

Rank	p−value	#in/all	Geneset
1	9e−34	80 / 553	Lembcke_Colonic Inflammation
2	4e−04	4 / 13	GENTLES_modul17
3	6e−03	3 / 13	GENTLES_modul16
4	9e−03	3 / 15	LIU_PROSTATE_CANCER_DN
5	1e−02	3 / 16	GENTLES_modul11
6	7e−02	2 / 15	RHODES_CANCER_META_SIGNATURE
7	2e−01	1 / 10	LIU_BREAST_CANCER
8	3e−01	1 / 10	GENTLES_modul3
9	3e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
10	3e−01	1 / 13	GENTLES_modul12
11	4e−01	1 / 15	BEN−PORATH_UP
12	4e−01	1 / 15	GENTLES_modul13
13	4e−01	1 / 16	GENTLES_modul10
14	5e−01	6 / 185	SPANG_LPS−index2
15	5e−01	16 / 530	Lembcke_Normal vs Adenoma
16	6e−01	9 / 316	SPANG_BCL6−index2
17	8e−01	1 / 48	KUIPER_MM poor survival
18	9e−01	1 / 68	SHAUGHNESSY_MM high risk
19	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
20	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	9e−59	70 / 190	extracellular matrix
2	3e−56	148 / 1182	extracellular region
3	4e−42	99 / 683	extracellular space
4	5e−25	41 / 183	proteinaceous extracellular matrix
5	1e−22	28 / 83	basement membrane
6	4e−18	45 / 330	cell surface
7	9e−13	138 / 2659	plasma membrane
8	2e−12	18 / 72	extracellular vesicular exosome
9	2e−12	25 / 153	endoplasmic reticulum lumen
10	6e−12	17 / 68	collagen
11	4e−08	17 / 115	cell−cell junction
12	2e−07	12 / 63	Golgi lumen
13	2e−07	16 / 116	lamellipodium
14	4e−07	90 / 1837	membrane
15	5e−07	10 / 45	stress fiber
16	7e−07	8 / 27	integrin complex
17	9e−07	16 / 128	focal adhesion
18	2e−06	11 / 65	lysosomal lumen
19	5e−06	6 / 17	basal lamina
20	2e−05	11 / 81	ruffle

Chr

Rank	p−value	#in/all	Geneset
1	0.03	31 / 743	Chr 7
2	0.05	37 / 957	Chr 11
3	0.05	28 / 699	Chr 5
4	0.06	25 / 618	Chr 4
5	0.11	37 / 1033	Chr 2
6	0.22	18 / 504	Chr 15
7	0.23	16 / 449	Chr 20
8	0.30	10 / 280	Chr 13
9	0.33	13 / 386	Chr 22
10	0.36	8 / 232	Chr 18
11	0.38	20 / 633	Chr 9
12	0.46	26 / 866	Chr 12
13	0.46	6 / 187	Chr 21
14	0.49	16 / 534	Chr 8
15	0.49	1 / 23	Chr HSCHR6_MHC_DBB
16	0.51	21 / 714	Chr 6
17	0.69	47 / 1720	Chr 1
18	0.73	24 / 914	Chr 3
19	0.84	17 / 717	Chr 16
20	0.88	14 / 630	Chr X

Disease

Rank	p−value	#in/all	Geneset
1	1e−09	35 / 375	GUDJ_psoriasis down
2	9e−01	13 / 572	GUDJ_psoriasis up
3	1e+00	0 / 17	BCHETNIA_EBM up
4	1e+00	0 / 2	BCHETNIA_EBM down
5	1e+00	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−20	43 / 265	willscher_GBM_Verhaak−CL_expression_B_up
2	2e−20	43 / 265	willscher_GBM_Verhaak−MES_expression_B_up
3	2e−20	43 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
4	2e−20	43 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
5	3e−13	23 / 117	GIEZELT_GBM_WT_up_VS_mut
6	5e−13	18 / 68	cultured astroglia vs. in vivo astrocytes
7	7e−12	13 / 35	Colman_survival_associated
8	7e−11	8 / 11	Phillips MES up vs Prolif & PN
9	3e−08	19 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	6e−06	10 / 58	OPC
11	1e−05	9 / 49	Christensen_hypomethylated_in_primary_glioblastoma
12	2e−05	13 / 112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
13	3e−05	14 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	3e−05	5 / 14	VERHAAK_CL subtype
15	4e−05	6 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
16	4e−05	9 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
17	5e−05	12 / 105	willscher_GBM_proteomics_wtOnly_SpotB
18	8e−05	7 / 37	Christensen_hypomethylated_in_ependymoma
19	4e−04	11 / 110	Christensen_hypermethylated_in_grade3_astrocytoma
20	4e−04	4 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−16	12 / 15	CROMER_TUMORIGENESIS_UP
2	5e−16	12 / 16	FARMER_BREAST_CANCER_CLUSTER_5
3	1e−14	11 / 15	ONDER_CDH1_TARGETS_2_UP
4	1e−12	10 / 15	ONDER_CDH1_SIGNALING_VIA_CTNNB1
5	5e−10	8 / 13	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
6	1e−09	8 / 14	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
7	3e−09	8 / 15	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
8	3e−09	8 / 15	LEE_LIVER_CANCER_HEPATOBLAST
9	5e−09	8 / 16	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
10	5e−09	8 / 16	ROZANOV_MMP14_TARGETS_SUBSET
11	1e−08	7 / 12	LY_AGING_MIDDLE_UP
12	9e−08	7 / 15	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_
13	9e−08	7 / 15	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
14	9e−08	7 / 15	DASU_IL6_SIGNALING_SCAR_DN
15	1e−07	6 / 10	JEON_SMAD6_TARGETS_UP
16	1e−07	6 / 10	VERRECCHIA_RESPONSE_TO_TGFB1_C4
17	1e−07	6 / 10	KEGG_ECM_RECEPTOR_INTERACTION
18	2e−07	7 / 16	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_
19	2e−07	7 / 16	LIEN_BREAST_CARCINOMA_METAPLASTIC
20	2e−07	7 / 16	AMIT_EGF_RESPONSE_60_HELA

H. Tiss

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 13	WIRTH_Sec. lymphoid organs
2	2e−02	4 / 36	WIRTH_Placenta
3	5e−02	2 / 13	WIRTH_Cortex cerebri
4	3e−01	1 / 12	WIRTH_Prim. lymphoid organs
5	3e−01	1 / 12	WIRTH_Lymphocytes
6	3e−01	1 / 13	WIRTH_Thymus
7	3e−01	1 / 13	WIRTH_Thyroid gland
8	4e−01	13 / 400	WIRTH_Nervous System
9	5e−01	4 / 127	WIRTH_Muscle
10	1e+00	1 / 417	WIRTH_Immune system
11	1e+00	0 / 5	WIRTH_Pituitary gland
12	1e+00	0 / 26	WIRTH_Pancreas
13	1e+00	0 / 10	WIRTH_B−cells
14	1e+00	0 / 13	WIRTH_Tonsil
15	1e+00	0 / 6	WIRTH_Bone marrow
16	1e+00	0 / 14	WIRTH_Globus pallidus
17	1e+00	0 / 15	WIRTH_Telencephalon
18	1e+00	0 / 16	WIRTH_Hippocampus
19	1e+00	0 / 13	WIRTH_Thalamus
20	1e+00	0 / 15	WIRTH_Cerebellum

Lymphoma

Rank	p−value	#in/all	Geneset
1	7e−75	90 / 250	LENZ_Stromal signature 1
2	5e−15	25 / 119	ROSOLOWSKI_green total
3	3e−14	18 / 59	LENZ_Stromal signature 2
4	2e−04	10 / 86	ROSOLOWSKI_green UP
5	5e−02	3 / 28	DAVE_Immune response 1
6	1e−01	2 / 20	DAVE_Immune response 2
7	2e−01	1 / 8	MASCQUE_GCB UP
8	3e−01	1 / 12	DAVE_BL UP
9	3e−01	2 / 38	ROSOLOWSKI_blue DOWN
10	3e−01	4 / 100	ROSOLOWSKI_blue total
11	3e−01	1 / 14	WRIGHT_GCB UP
12	4e−01	1 / 16	WRIGHT_ABC UP
13	4e−01	9 / 275	ZHANG_DLBCL mutated
14	4e−01	4 / 118	SPANG_LPS 6hrs UP
15	5e−01	1 / 22	DAVE_NFkB BL DN
16	6e−01	4 / 140	DAVE_BL−vs−DLBCL
17	6e−01	12 / 426	SPANG_CD40 6hrs DN
18	6e−01	9 / 327	SPANG_CD40 6hrs UP
19	6e−01	8 / 291	SPANG_IL21 UP
20	7e−01	2 / 86	ROSOLOWSKI_red total

MF

Rank	p−value	#in/all	Geneset
1	1e−19	22 / 57	extracellular matrix structural constituent
2	1e−14	12 / 19	extracellular matrix binding
3	3e−14	21 / 85	integrin binding
4	5e−12	50 / 579	calcium ion binding
5	7e−11	8 / 11	platelet−derived growth factor binding
6	1e−10	9 / 16	fibronectin binding
7	4e−09	18 / 112	heparin binding
8	1e−08	293 / 8023	protein binding
9	2e−08	18 / 124	growth factor activity
10	1e−07	8 / 22	insulin−like growth factor binding
11	4e−07	10 / 44	collagen binding
12	5e−07	6 / 12	transforming growth factor beta binding
13	6e−07	13 / 81	metalloendopeptidase activity
14	1e−06	12 / 73	metallopeptidase activity
15	1e−05	6 / 19	L−ascorbic acid binding
16	1e−05	5 / 12	activin binding
17	2e−05	8 / 41	SMAD binding
18	2e−05	6 / 21	glycosaminoglycan binding
19	2e−05	22 / 280	receptor binding
20	5e−05	5 / 15	platelet−derived growth factor receptor binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	2e−07	33 / 420	TGGT−29A−−29B−−29C
2	3e−07	40 / 577	GTGC−506
3	4e−05	20 / 247	GTGC−96
4	1e−04	29 / 467	TGTT−30A−5P−−30C−−30D−−30B−−30E−5P
5	1e−04	26 / 401	ACCA−9
6	1e−04	15 / 171	CTAT−153
7	8e−04	12 / 141	ATAC−202
8	9e−04	22 / 362	CAGT−200B−−200C−−429
9	1e−03	8 / 75	GGCA−324−3P
10	3e−03	14 / 205	GTAC−101
11	3e−03	13 / 184	GGCA−22
12	4e−03	10 / 125	ACAC−199A−−199B
13	4e−03	24 / 457	TGCC−124A
14	6e−03	14 / 225	TATT−374
15	7e−03	9 / 116	GACA−219
16	7e−03	12 / 182	TAGC−9
17	7e−03	5 / 42	CAGG−492
18	8e−03	12 / 185	AAAG−204−−211
19	8e−03	2 / 5	TCGA−213
20	8e−03	11 / 163	TAAT−126

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−10	8 / 12	miR−29c
2	8e−04	5 / 26	miR−21
3	5e−03	2 / 4	miR−195
4	1e−02	2 / 6	let−7b
5	1e−02	2 / 6	miR−200c
6	4e−02	2 / 11	miR−16
7	5e−02	2 / 12	miR−29b
8	5e−02	2 / 13	miR−34a
9	6e−02	1 / 2	miR−101b
10	6e−02	1 / 2	miR−124a
11	6e−02	1 / 2	miR−16−1
12	6e−02	1 / 2	miR−18
13	6e−02	1 / 2	miR−346
14	8e−02	1 / 3	miR−197
15	1e−01	1 / 4	let−7c
16	1e−01	1 / 4	let−7g
17	1e−01	1 / 4	miR−106b
18	1e−01	1 / 4	miR−133b
19	1e−01	1 / 4	miR−20a
20	1e−01	1 / 4	miR−29a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 12	hsa−miR−1249
2	9e−04	9 / 86	hsa−miR−220c
3	4e−03	8 / 89	hsa−miR−216b
4	4e−03	18 / 311	hsa−miR−98
5	5e−03	19 / 336	hsa−let−7e
6	5e−03	19 / 341	hsa−let−7a
7	7e−03	17 / 300	hsa−miR−548c−3p
8	7e−03	4 / 27	hsa−miR−483−3p
9	8e−03	6 / 60	hsa−miR−485−3p
10	9e−03	9 / 121	hsa−miR−646
11	1e−02	17 / 311	hsa−let−7f
12	1e−02	3 / 16	hsa−miR−891a
13	1e−02	17 / 318	hsa−miR−590−3p
14	1e−02	10 / 151	hsa−miR−429
15	1e−02	11 / 177	hsa−miR−300
16	1e−02	5 / 50	hsa−miR−1224−3p
17	2e−02	2 / 7	hsa−miR−566
18	2e−02	5 / 52	hsa−miR−487a
19	3e−02	16 / 321	hsa−let−7g
20	3e−02	4 / 39	hsa−miR−501−3p

MMML CGS

Rank	p−value	#in/all	Geneset
1	1e−22	15 / 16	MACIEJ_MMML 1
2	5e−09	7 / 11	MACIEJ_MMML 31
3	5e−03	2 / 4	MACIEJ_MMML 23
4	2e−02	2 / 7	MACIEJ_MMML 13
5	6e−02	1 / 2	MACIEJ_MMML 46
6	1e−01	1 / 4	MACIEJ_MMML 40
7	1e−01	1 / 4	MACIEJ_MMML 44
8	3e−01	1 / 11	MACIEJ_MMML 3
9	3e−01	1 / 13	MACIEJ_MMML 6
10	1e+00	0 / 13	MACIEJ_MMML 10
11	1e+00	0 / 9	MACIEJ_MMML 14
12	1e+00	0 / 11	MACIEJ_MMML 15
13	1e+00	0 / 15	MACIEJ_MMML 16
14	1e+00	0 / 2	MACIEJ_MMML 17
15	1e+00	0 / 14	MACIEJ_MMML 19
16	1e+00	0 / 4	MACIEJ_MMML 2
17	1e+00	0 / 5	MACIEJ_MMML 20
18	1e+00	0 / 15	MACIEJ_MMML 22
19	1e+00	0 / 12	MACIEJ_MMML 24
20	1e+00	0 / 14	MACIEJ_MMML 26

Patw Act

Rank	p−value	#in/all	Geneset
1	0.07	2 / 15	GUSTAFSON_PI3K_DN
2	0.28	1 / 11	BENTINK_e2f3.2
3	0.30	1 / 12	BENTINK_ras.1
4	0.32	1 / 13	BENTINK_src.10
5	0.34	1 / 14	BENTINK_myc.1
6	1.00	0 / 13	GUSTAFSON_PI3K_UP
7	1.00	0 / 12	BENTINK_e2f3.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−10	73 / 1146	HEBENSTREIT_low expression TF
2	6e−02	1 / 2	MYC_ECM cell adhesion DOWN
3	2e−01	1 / 9	MYC_Targets DOWN
4	4e−01	1 / 20	MYC_Metabolism UP
5	8e−01	1 / 63	MYC_Targets UP
6	9e−01	29 / 1233	KIM_MYC targets
7	1e+00	23 / 1095	HEBENSTREIT_high expression TF
8	1e+00	0 / 14	NOWICK_TF
9	1e+00	0 / 5	MYC_TFs
10	1e+00	0 / 4	MYC_Apoptosis UP
11	1e+00	0 / 8	MYC_Cell cycle UP
12	1e+00	0 / 2	MYC_Cell cycle DOWN
13	1e+00	0 / 4	MYC_Cell growth and proliferation UP
14	1e+00	0 / 2	MYC_Chromatin_modification UP
15	1e+00	0 / 7	MYC_DNA repair UP
16	1e+00	0 / 3	MYC_DNA replication UP
17	1e+00	0 / 16	MYC_Protein synthesis degradation UP
18	1e+00	0 / 8	MYC_RNA processing binding UP
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.008	5 / 43	VAQUERIZAS_Uterus
2	0.051	3 / 29	VAQUERIZAS_Smooth muscle
3	0.055	3 / 30	VAQUERIZAS_Fetal lung
4	0.077	2 / 16	VAQUERIZAS_Fetal thyroid
5	0.106	4 / 62	VAQUERIZAS_Lung
6	0.133	2 / 22	VAQUERIZAS_Spinal cord
7	0.135	3 / 44	VAQUERIZAS_Placenta
8	0.153	2 / 24	VAQUERIZAS_Trachea
9	0.292	2 / 37	VAQUERIZAS_Prostate
10	0.314	2 / 39	VAQUERIZAS_Thyroid
11	0.318	1 / 13	VAQUERIZAS_Skin
12	0.324	2 / 40	VAQUERIZAS_Fetal brain
13	0.376	1 / 16	VAQUERIZAS_Pancreas
14	0.376	1 / 16	VAQUERIZAS_Salivary gland
15	0.429	1 / 19	VAQUERIZAS_Pituitary
16	0.674	1 / 38	VAQUERIZAS_Testis
17	0.719	1 / 43	VAQUERIZAS_Whole brain
18	0.793	3 / 144	VAQUERIZAS_General
19	0.840	1 / 62	VAQUERIZAS_Whole blood
20	1.000	0 / 28	VAQUERIZAS_Liver

Sample−Underexpression

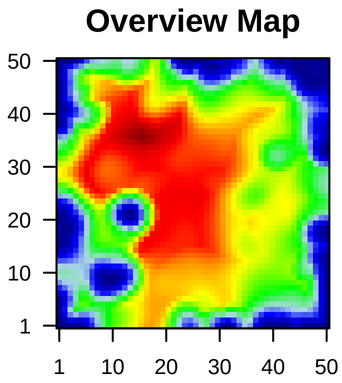
Spot Summary: b

metagenes = 43
genes = 584

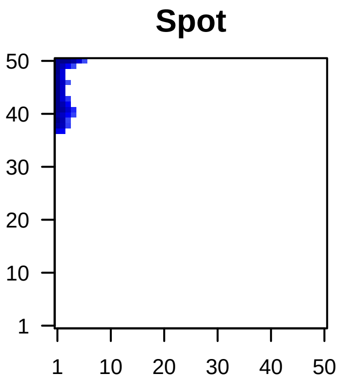
<r> metagenes = 0.79
<r> genes = 0.25
beta: r2= 34.22 / log p= −Inf

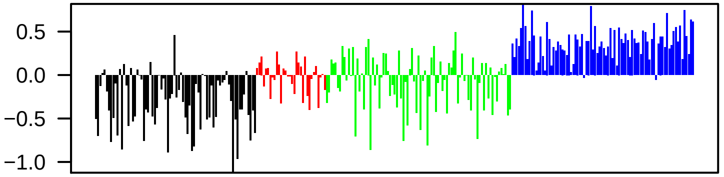
samples with spot = 69 (25.1 %)
Atypical : 40 (54.1 %)
Classical : 5 (15.6 %)
Mesenchymal : 24 (28.2 %)

Overview Map



Spot





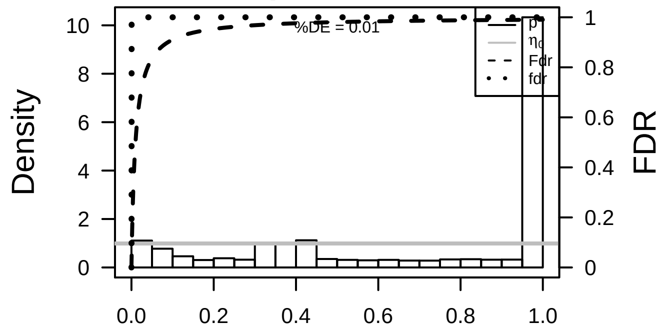
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3860	1.89	−5.51	0.54	KRT13	keratin 13 [Source:HGNC Symbol;Acc:6415]
2	6707	2.01	−5.26	0.74	SPRR3	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
3	286887	1.44	−5.11	0.65	KRT6C	keratin 6C [Source:HGNC Symbol;Acc:20406]
4	6278	2.17	−4.49	0.75	S100A7	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
5	5266	1.7	−4.44	0.68	PI3	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
6	388533	3.06	−4.41	0.79	KRTDAP	keratinocyte differentiation−associated protein [Source:HGNC
7	3861	1.7	−4.39	0.77	KRT14	keratin 14 [Source:HGNC Symbol;Acc:6416]
8	3963	2.29	−4.37	0.66	LGALS7	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
9	374897	2.69	−4.32	0.87	SBSN	suprabasin [Source:HGNC Symbol;Acc:24950]
10	6700	1.85	−4.32	0.86	SPRR2A	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
11	6698	1.26	−4.25	0.81	SPRR1A	small proline−rich protein 1A [Source:HGNC Symbol;Acc:112
12	6704	2.73	−4.24	0.85	SPRR2E	small proline−rich protein 2E [Source:HGNC Symbol;Acc:112
13	6705	1.9	−4.23	0.85	SPRR2F	small proline−rich protein 2F [Source:HGNC Symbol;Acc:112
14	84518	2.45	−3.78	0.9	CNFN	cornifelin [Source:HGNC Symbol;Acc:30183]
15	10804	2.26	−3.75	0.81	GJB6	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
16	57016	3.19	−3.72	0.69	AKR1B10	aldo−keto reductase family 1, member B10 (aldose reductase
17	4680	2.41	−3.7	0.71	CEACAM6	carcinoembryonic antigen−related cell adhesion molecule 6 (
18	9407	2.19	−3.69	0.74	TMPRSS11D	transmembrane protease, serine 11D [Source:HGNC Symbol
19	6699	2.74	−3.66	0.89	SPRR1B	small proline−rich protein 1B [Source:HGNC Symbol;Acc:112
20	218	2.79	−3.66	0.53	ALDH3A1	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	100 / 135	H.Tis	WIRTH_Mucosa
2	1e−92	151 / 572	Disea	GUDJ_psoriasis up
3	6e−31	35 / 76	BP	epidermis development
4	3e−24	26 / 53	BP	keratinocyte differentiation
5	6e−24	18 / 21	CC	cornified envelope
6	1e−18	20 / 42	BP	keratinization
7	7e−17	100 / 1182	CC	extracellular region
8	4e−16	24 / 82	CC	intermediate filament
9	7e−14	32 / 186	MF	structural molecule activity
10	3e−13	11 / 16	GSEA	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	7e−13	12 / 21	CC	desmosome
12	2e−10	10 / 19	BP	peptide cross−linking
13	2e−09	13 / 44	CC	keratin filament
14	4e−09	79 / 1146	TF	HEBENSTREIT_low expression TF
15	1e−08	8 / 15	GSEA	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
16	1e−08	8 / 15	GSEA	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	1e−08	16 / 79	MF	serine−type endopeptidase inhibitor activity
18	2e−08	144 / 2659	CC	plasma membrane
19	5e−08	11 / 38	BP	epithelial cell differentiation
20	2e−07	12 / 52	BP	negative regulation of endopeptidase activity
21	2e−07	46 / 579	MF	calcium ion binding
22	3e−07	7 / 15	GSEA	AIGNER_ZEB1_TARGETS
23	3e−07	7 / 15	GSEA	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
24	3e−07	7 / 15	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
25	5e−07	7 / 16	GSEA	ONDER_CDH1_TARGETS_3_DN
26	5e−07	7 / 16	GSEA	LEE_LIVER_CANCER_MYC_TGFA_UP
27	6e−07	23 / 201	CC	apical plasma membrane
28	9e−07	14 / 82	MF	structural constituent of cytoskeleton
29	1e−06	202 / 4310	CC	cytoplasm
30	1e−06	17 / 122	MF	serine−type endopeptidase activity
31	2e−06	49 / 683	CC	extracellular space
32	2e−06	10 / 44	BP	skin development
33	3e−06	6 / 13	BP	negative regulation of peptidase activity
34	3e−06	6 / 13	H.Tis	WIRTH_Tonsil
35	5e−06	8 / 29	BP	regulation of proteolysis
36	1e−05	6 / 16	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
37	1e−05	6 / 16	GSEA	JAEGER_METASTASIS_DN
38	1e−05	6 / 16	GSEA	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
39	1e−05	6 / 16	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
40	1e−05	6 / 16	GSEA	CROMER_TUMORIGENESIS_DN

p−values



BP

Rank	p−value	#in/all	Geneset
1	6e−31	35 / 76	epidermis development
2	3e−24	26 / 53	keratinocyte differentiation
3	1e−18	20 / 42	keratinization
4	2e−10	10 / 19	peptide cross−linking
5	5e−08	11 / 38	epithelial cell differentiation
6	2e−07	12 / 52	negative regulation of endopeptidase activity
7	2e−06	10 / 44	skin development
8	3e−06	6 / 13	negative regulation of peptidase activity
9	5e−06	8 / 29	regulation of proteolysis
10	3e−05	5 / 12	hemidesmosome assembly
11	6e−05	11 / 76	wound healing
12	2e−04	6 / 25	brown fat cell differentiation
13	2e−04	10 / 73	defense response to bacterium
14	5e−04	17 / 194	cell−cell signaling
15	7e−04	11 / 100	cell−cell adhesion
16	8e−04	4 / 13	intermediate filament cytoskeleton organization
17	8e−04	4 / 13	retinoic acid metabolic process
18	2e−03	5 / 26	positive regulation of reactive oxygen species metabolic process
19	2e−03	4 / 16	cellular response to extracellular stimulus
20	2e−03	4 / 16	ectoderm development

Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	36 / 530	Lembcke_Normal vs Adenoma
2	6e−02	11 / 185	SPANG_LPS−index2
3	8e−02	26 / 553	Lembcke_Colonic Inflammation
4	2e−01	1 / 7	ZHANG_MGUS up
5	2e−01	0 / 10	LIU_BREAST_CANCER
6	3e−01	1 / 9	WANG_ER_DN
7	3e−01	0 / 14	LIU_PROSTATE_CANCER_UP
8	4e−01	1 / 14	WANG_ER_UP
9	4e−01	1 / 15	LIU_PROSTATE_CANCER_DN
10	4e−01	1 / 16	GENTLES_modul4
11	4e−01	1 / 16	GENTLES_modul7
12	4e−01	1 / 16	GENTLES_modul11
13	7e−01	1 / 33	KUIPER_MM good survival
14	7e−01	2 / 68	SHAUGHNESSY_MM high risk
15	8e−01	1 / 39	ZHANG_MM up
16	8e−01	1 / 48	KUIPER_MM poor survival
17	9e−01	8 / 316	SPANG_BCL6−index2
18	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
19	1e+00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
20	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	6e−24	18 / 21	cornified envelope
2	7e−17	100 / 1182	extracellular region
3	4e−16	24 / 82	intermediate filament
4	7e−13	12 / 21	desmosome
5	2e−09	13 / 44	keratin filament
6	2e−08	144 / 2659	plasma membrane
7	6e−07	23 / 201	apical plasma membrane
8	1e−06	202 / 4310	cytoplasm
9	2e−06	49 / 683	extracellular space
10	5e−05	27 / 333	cytoskeleton
11	6e−05	6 / 21	gap junction
12	1e−04	7 / 32	cell−cell adherens junction
13	1e−04	5 / 15	connexon complex
14	1e−04	11 / 83	anchored to membrane
15	5e−04	48 / 835	integral to plasma membrane
16	7e−04	12 / 115	cell−cell junction
17	1e−03	13 / 137	basolateral plasma membrane
18	2e−03	4 / 16	microvillus membrane
19	2e−03	5 / 27	basal plasma membrane
20	3e−03	11 / 117	cytoplasmic vesicle

Chr

Rank	p−value	#in/all	Geneset
1	6e−05	90 / 1720	Chr 1
2	3e−03	17 / 232	Chr 18
3	2e−02	28 / 519	Chr 14
4	1e−01	37 / 866	Chr 12
5	2e−01	23 / 534	Chr 8
6	2e−01	2 / 23	Chr HSCHR6_MHC_DBB
7	2e−01	26 / 633	Chr 9
8	3e−01	24 / 602	Chr 10
9	3e−01	43 / 1135	Chr 19
10	3e−01	35 / 918	Chr 17
11	4e−01	19 / 504	Chr 15
12	4e−01	17 / 449	Chr 20
13	4e−01	23 / 618	Chr 4
14	4e−01	26 / 714	Chr 6
15	8e−01	22 / 717	Chr 16
16	8e−01	5 / 187	Chr 21
17	8e−01	1 / 52	Chr HSCHR6_MHC_QBL
18	9e−01	28 / 957	Chr 11
19	9e−01	6 / 280	Chr 13
20	9e−01	18 / 699	Chr 5

Disease

Rank	p−value	#in/all	Geneset
1	1e−92	151 / 572	GUDJ_psoriasis up
2	1e−01	2 / 17	BCHETNIA_EBM up
3	6e−01	1 / 26	BCHETNIA_EBM−DM up
4	7e−01	12 / 375	GUDJ_psoriasis down
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.001	7 / 48	Noushmehr_Pron_GCIMP_hypermeth_DN
2	0.002	11 / 110	Christensen_hypermethylated_in_grade3_astrocytoma
3	0.002	11 / 112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
4	0.002	12 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
5	0.003	11 / 117	GIEZELT_GBM_WT_up_VS_mut
6	0.003	9 / 85	laffaire_hypermeth_LGG_vs_control
7	0.007	6 / 49	Christensen_hypomethylated_in_primary_glioblastoma
8	0.011	11 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma
9	0.012	17 / 265	willscher_GBM_Verhaak−CL_expression_B_up
10	0.012	17 / 265	willscher_GBM_Verhaak−MES_expression_B_up
11	0.012	17 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
12	0.012	17 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
13	0.026	7 / 83	Christensen_hypermethylated_in_secondary_glioblastoma
14	0.027	4 / 33	willscher_GBM_proteomics_wtOnly_SpotC
15	0.032	6 / 68	cultured astroglia vs. in vivo astrocytes
16	0.033	4 / 35	Colman_survival_associated
17	0.037	5 / 53	Christensen_hypermethylated_in_primary_glioblastoma
18	0.040	4 / 37	Christensen_hypomethylated_in_ependymoma
19	0.052	5 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
20	0.055	2 / 11	VERHAAK_Brain

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−13	11 / 16	HUPER_BREAST_BASAL_VS_LUMINAL_UP
2	1e−08	8 / 15	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
3	1e−08	8 / 15	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
4	3e−07	7 / 15	AIGNER_ZEB1_TARGETS
5	3e−07	7 / 15	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
6	3e−07	7 / 15	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
7	5e−07	7 / 16	ONDER_CDH1_TARGETS_3_DN
8	5e−07	7 / 16	LEE_LIVER_CANCER_MYC_TGFA_UP
9	1e−05	6 / 16	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	1e−05	6 / 16	JAEGER_METASTASIS_DN
11	1e−05	6 / 16	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
12	1e−05	6 / 16	COLDREN_GEFITINIB_RESISTANCE_DN
13	1e−05	6 / 16	CROMER_TUMORIGENESIS_DN
14	1e−05	5 / 10	KEGG_LINOLEIC_ACID_METABOLISM
15	3e−05	5 / 12	REACTOME_GAP_JUNCTION_ASSEMBLY
16	8e−05	5 / 14	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
17	9e−05	4 / 8	LIU_CDX2_TARGETS_DN
18	1e−04	5 / 15	FARMER_BREAST_CANCER_CLUSTER_3
19	1e−04	5 / 15	LEE_LIVER_CANCER_MYC_E2F1_UP
20	1e−04	5 / 15	LEE_LIVER_CANCER_DENA_UP

H. Tiss

Rank	p−value	#in/all	Geneset
1	1e−99	100 / 135	WIRTH_Mucosa
2	3e−06	6 / 13	WIRTH_Tonsil
3	6e−04	4 / 12	WIRTH_Prim. lymphoid organs
4	9e−03	3 / 13	WIRTH_Thymus
5	2e−01	4 / 62	WIRTH_Liver
6	4e−01	1 / 13	WIRTH_Cortex cerebri
7	4e−01	1 / 13	WIRTH_Thalamus
8	4e−01	1 / 15	WIRTH_Cerebellum
9	6e−01	1 / 26	WIRTH_Pancreas
10	1e+00	8 / 400	WIRTH_Nervous System
11	1e+00	1 / 120	WIRTH_Testis
12	1e+00	0 / 5	WIRTH_Pituitary gland
13	1e+00	0 / 417	WIRTH_Immune system
14	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
15	1e+00	0 / 10	WIRTH_B−cells
16	1e+00	0 / 12	WIRTH_Lymphocytes
17	1e+00	0 / 6	WIRTH_Bone marrow
18	1e+00	0 / 14	WIRTH_Globus pallidus
19	1e+00	0 / 15	WIRTH_Telencephalon
20	1e+00	0 / 16	WIRTH_Hippocampus

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.007	17 / 250	LENZ_Stromal signature 1
2	0.008	18 / 275	ZHANG_DLBCL mutated
3	0.009	10 / 119	ROSOLOWSKI_green total
4	0.010	8 / 86	ROSOLOWSKI_green UP
5	0.152	4 / 59	LENZ_Stromal signature 2
6	0.205	2 / 24	SPANG_BAFF 9hrs UP
7	0.248	1 / 8	MASCQUE_GCB UP
8	0.348	1 / 12	DAVE_BL_DN
9	0.393	1 / 14	WRIGHT_GCB UP
10	0.597	4 / 118	SPANG_LPS 6hrs UP
11	0.742	1 / 38	ROSOLOWSKI_blue DOWN
12	0.748	8 / 274	SPANG_IL21 DN
13	0.795	26 / 852	SPANG_BCR DN
14	0.855	1 / 54	SPANG_BAFF 9hrs DN
15	0.873	3 / 140	DAVE_BL−vs−DLBCL
16	0.915	1 / 69	SPANG_LPS 6hrs DN
17	0.945	6 / 291	SPANG_IL21 UP
18	0.954	1 / 86	ROSOLOWSKI_red total
19	0.965	9 / 426	SPANG_CD40 6hrs DN
20	0.972	1 / 100	ROSOLOWSKI_blue total

MF

Rank	p−value	#in/all	Geneset
1	7e−14	32 / 186	structural molecule activity
2	1e−08	16 / 79	serine−type endopeptidase inhibitor activity
3	2e−07	46 / 579	calcium ion binding
4	9e−07	14 / 82	structural constituent of cytoskeleton
5	1e−06	17 / 122	serine−type endopeptidase activity
6	1e−04	5 / 15	retinol dehydrogenase activity
7	3e−04	4 / 10	gap junction channel activity
8	3e−04	4 / 10	RAGE receptor binding
9	4e−04	8 / 51	protein binding, bridging
10	4e−04	5 / 19	laminin binding
11	1e−03	5 / 23	peptidase inhibitor activity
12	1e−03	4 / 15	interleukin−1 receptor binding
13	2e−03	21 / 296	oxidoreductase activity
14	2e−03	7 / 53	serine−type peptidase activity
15	4e−03	31 / 531	catalytic activity
16	5e−03	4 / 20	scaffold protein binding
17	6e−03	7 / 62	protease binding
18	6e−03	5 / 34	endopeptidase inhibitor activity
19	7e−03	4 / 22	cysteine−type endopeptidase inhibitor activity
20	7e−03	3 / 12	retinol binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.005	28 / 470	GCAC−17−5P−−20A−−106A−−106B−−20B−−519D
2	0.017	13 / 190	CACT−520G−−520H
3	0.068	6 / 82	AAAC−140
4	0.072	20 / 401	ACCA−9
5	0.113	5 / 73	AGGC−515−3P
6	0.119	9 / 163	CTTG−381
7	0.138	12 / 240	CAGT−141−−200A
8	0.154	2 / 20	GTAG−189
9	0.162	12 / 248	TACT−26A−−26B
10	0.167	7 / 129	ACCA−522
11	0.193	4 / 65	TCTG−198
12	0.200	7 / 136	GCAT−105
13	0.206	12 / 261	TTGC−182
14	0.208	3 / 45	TATC−488
15	0.219	9 / 189	AAGC−520F
16	0.228	12 / 267	CACT−128A−−128B
17	0.238	11 / 244	GTGC−25−−32−−92−−363−−367
18	0.273	5 / 100	ACAG−10A−−10B
19	0.274	3 / 52	CCAC−147
20	0.275	1 / 9	TCCG−184

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 11	Melanoma, cutaneous malignant, 2
2	0.6	1 / 23	Stroke, susceptibility to
3	0.7	1 / 36	Lung cancer
4	1.0	0 / 3	Thyroid carcinoma, papillary
5	1.0	0 / 34	Pancreatic cancer
6	1.0	0 / 22	Glioblastoma multiforme, somatic
7	1.0	0 / 21	Gastrointestinal
8	1.0	0 / 2	Pituitary adenoma
9	1.0	0 / 36	Cancer
10	1.0	0 / 27	Colorectal cancer
11	1.0	0 / 2	Adenomas, multiple colorectal
12	1.0	0 / 35	Prostate cancer
13	1.0	0 / 11	Alzheimer disease, susceptibility to
14	1.0	0 / 3	Schizophrenia, susceptibility to
15	1.0	0 / 8	Parkinson disease
16	1.0	0 / 23	Hepatocellular carcinoma
17	1.0	0 / 29	Melanoma and neural system tumor syndrome
18	1.0	0 / 30	Ovarian cancer
19	1.0	0 / 38	Breast cancer
20	1.0	0 / 15	Gastric cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	2 / 2	miR−199a*
2	0.011	2 / 5	miR−196a
3	0.037	2 / 9	miR−125b
4	0.069	1 / 2	miR−346
5	0.074	2 / 13	miR−1
6	0.133	1 / 4	miR−122
7	0.133	1 / 4	miR−133b
8	0.133	1 / 4	miR−206
9	0.133	1 / 4	miR−20a
10	0.133	1 / 4	miR−29a
11	0.163	1 / 5	miR−126
12	0.193	1 / 6	miR−125a
13	0.221	1 / 7	miR−145
14	0.275	1 / 9	miR−17
15	0.348	1 / 12	miR−29b
16	0.348	1 / 12	miR−29c
17	0.605	1 / 26	miR−21
18	1.000	0 / 11	let−7a
19	1.000	0 / 6	let−7b
20	1.000	0 / 4	let−7c

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.01	2 / 5	hsa−miR−1268
2	0.01	4 / 27	hsa−miR−675
3	0.02	4 / 30	hsa−miR−631
4	0.03	8 / 102	hsa−miR−600
5	0.03	23 / 426	hsa−miR−519d
6	0.03	9 / 122	hsa−miR−105
7	0.03	30 / 603	hsa−miR−20a
8	0.04	28 / 565	hsa−miR−20b
9	0.06	4 / 43	hsa−miR−541
10	0.07	5 / 63	hsa−miR−455−3p
11	0.07	9 / 147	hsa−miR−143
12	0.08	10 / 172	hsa−miR−520h
13	0.08	2 / 14	hsa−miR−744
14	0.09	6 / 88	hsa−miR−1265
15	0.09	9 / 155	hsa−miR−31
16	0.10	3 / 32	hsa−miR−654−5p
17	0.11	2 / 16	hsa−miR−1298
18	0.11	3 / 33	hsa−miR−644
19	0.12	6 / 95	hsa−miR−888
20	0.12	5 / 75	hsa−miR−1290

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.001	3 / 7	MACIEJ_MMML 9
2	0.055	2 / 11	MACIEJ_MMML 3
3	0.069	1 / 2	MACIEJ_MMML 43
4	0.133	1 / 4	MACIEJ_MMML 47
5	0.221	1 / 7	MACIEJ_MMML 13
6	0.325	1 / 11	MACIEJ_MMML 31
7	0.393	1 / 14	MACIEJ_MMML 19
8	0.393	1 / 14	MACIEJ_MMML 30
9	0.435	1 / 16	MACIEJ_MMML 1
10	1.000	0 / 13	MACIEJ_MMML 10
11	1.000	0 / 9	MACIEJ_MMML 14
12	1.000	0 / 11	MACIEJ_MMML 15
13	1.000	0 / 15	MACIEJ_MMML 16
14	1.000	0 / 2	MACIEJ_MMML 17
15	1.000	0 / 4	MACIEJ_MMML 2
16	1.000	0 / 5	MACIEJ_MMML 20
17	1.000	0 / 15	MACIEJ_MMML 22
18	1.000	0 / 4	MACIEJ_MMML 23
19	1.000	0 / 12	MACIEJ_MMML 24
20	1.000	0 / 14	MACIEJ_MMML 26

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	3 / 15	GUSTAFSON_PI3K_DN
2	0.06	2 / 12	BENTINK_e2f3.1
3	0.35	1 / 12	BENTINK_ras.1
4	0.37	1 / 13	GUSTAFSON_PI3K_UP
5	1.00	0 / 11	BENTINK_e2f3.2
6	1.00	0 / 14	BENTINK_myc.1
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 15	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−09	79 / 1146	HEBENSTREIT_low expression TF
2	1e−01	2 / 16	MYC_Protein synthesis degradation UP
3	4e−01	3 / 63	MYC_Targets UP
4	5e−01	1 / 20	MYC_Metabolism UP
5	1e+00	29 / 1233	KIM_MYC targets
6	1e+00	20 / 1095	HEBENSTREIT_high expression TF
7	1e+00	0 / 14	NOWICK_TF
8	1e+00	0 / 5	MYC_TFs
9	1e+00	0 / 9	MYC_Targets DOWN
10	1e+00	0 / 4	MYC_Apoptosis UP
11	1e+00	0 / 8	MYC_Cell cycle UP
12	1e+00	0 / 2	MYC_Cell cycle DOWN
13	1e+00	0 / 4	MYC_Cell growth and proliferation UP
14	1e+00	0 / 2	MYC_Chromatin_modification UP
15	1e+00	0 / 7	MYC_DNA repair UP
16	1e+00	0 / 3	MYC_DNA replication UP
17	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
18	1e+00	0 / 8	MYC_RNA processing binding UP
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.001	5 / 24	VAQUERIZAS_Trachea
2	0.009	3 / 13	VAQUERIZAS_Skin
3	0.017	3 / 16	VAQUERIZAS_Pancreas
4	0.030	2 / 8	VAQUERIZAS_Tongue
5	0.067	4 / 44	VAQUERIZAS_Placenta
6	0.172	4 / 62	VAQUERIZAS_Lung
7	0.283	2 / 30	VAQUERIZAS_Fetal lung
8	0.348	1 / 12	VAQUERIZAS_Kidney
9	0.374	2 / 37	VAQUERIZAS_Prostate
10	0.399	2 / 39	VAQUERIZAS_Thyroid
11	0.435	1 / 16	VAQUERIZAS_Heart
12	0.448	2 / 43	VAQUERIZAS_Uterus
13	0.448	2 / 43	VAQUERIZAS_Whole brain
14	0.492	1 / 19	VAQUERIZAS_Pituitary
15	0.510	1 / 20	VAQUERIZAS_Adrenal cortex
16	0.527	1 / 21	VAQUERIZAS_Tonsil
17	0.544	1 / 22	VAQUERIZAS_Spinal cord
18	0.632	1 / 28	VAQUERIZAS_Liver
19	0.645	1 / 29	VAQUERIZAS_Smooth muscle
20	0.645	1 / 29	VAQUERIZAS_Lymph node

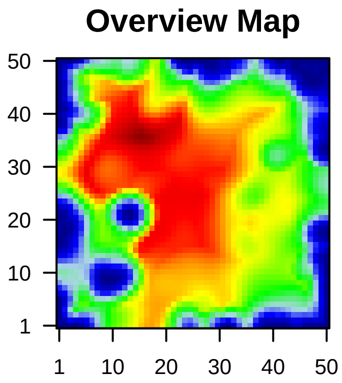
Sample−Underexpression

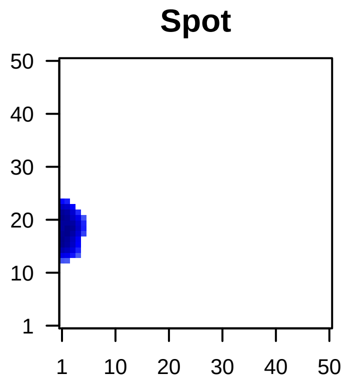
Spot Summary: c

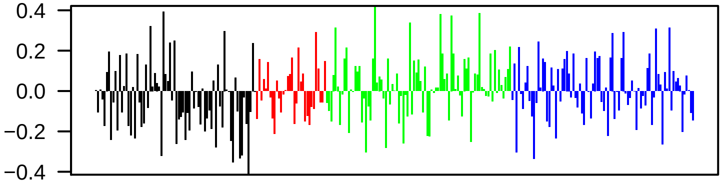
metagenes = 47
genes = 486

<r> metagenes = 0.91
<r> genes = 0.25
beta: r2= 5.41 / log p= −Inf

samples with spot = 12 (4.4 %)
Atypical : 7 (9.5 %)
Mesenchymal : 2 (2.4 %)
Basal : 3 (3.6 %)





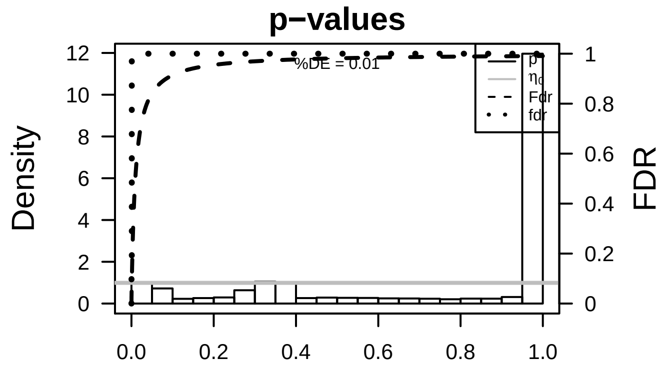


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	1152	2.07	−1.8	0.37	CKB	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
2	4495	2.82	−1.79	0.21	MT1G	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
3	10428	1.42	−1.7	0.53	CFDP1	craniofacial development protein 1 [Source:HGNC Symbol;Ac
4	991	1.49	−1.64	0.71	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
5	284085	2.29	−1.64	0.42	KRT18P55	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
6	5652	1.26	−1.57	0.49	PRSS8	protease, serine, 8 [Source:HGNC Symbol;Acc:9491]
7	2194	1.45	−1.54	0.52	FASN	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
8	131076	2.28	−1.53	0.33	CCDC58	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
9	283869	2.84	−1.53	0.53	NPW	neuropeptide W [Source:HGNC Symbol;Acc:30509]
10	26519	1.02	−1.5	0.27	TIMM10	translocase of inner mitochondrial membrane 10 homolog (ye
11	3006	2.13	−1.48	0.19	HIST1H1C	histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
12	27237	1.42	−1.48	0.44	ARHGEF16	Rho guanine nucleotide exchange factor (GEF) 16 [Source:H
13	79703	1.33	−1.36	0.37	C11orf80	chromosome 11 open reading frame 80 [Source:HGNC Symb
14	430	1.64	−1.34	0.32	ASCL2	achaete−scute family bHLH transcription factor 2 [Source:HG
15	230	1.64	−1.33	0.36	ALDOC	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A
16	8772	2.18	−1.29	0.52	FADD	Fas (TNFRSF6)−associated via death domain [Source:HGNC
17	80154	1.54	−1.25	0.45		
18	2017	1.86	−1.24	0.42	CTTN	cortactin [Source:HGNC Symbol;Acc:3338]
19	27341	1.09	−1.23	0.43	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae) [Sour
20	5639	0.92	−1.23	0.51	PRRG2	proline rich Gla (G−carboxyglutamic acid) 2 [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−20	102 / 1318	CC	mitochondrion
2	3e−12	25 / 153	MF	structural constituent of ribosome
3	4e−11	19 / 96	BP	rRNA processing
4	9e−11	48 / 579	CC	nucleolus
5	4e−10	29 / 253	BP	translation
6	7e−09	30 / 304	CC	mitochondrial inner membrane
7	1e−08	50 / 717	Chr	Chr 16
8	2e−08	21 / 167	CC	ribosome
9	1e−07	39 / 530	Canc	Lembcke_Normal vs Adenoma
10	4e−07	12 / 66	BP	positive regulation of ubiquitin−protein ligase activity involved in mitotic cell
11	8e−07	12 / 70	BP	regulation of ubiquitin−protein ligase activity involved in mitotic cell cycle
12	1e−06	25 / 287	BP	viral process
13	1e−06	42 / 649	BP	gene expression
14	2e−06	12 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−depende
15	2e−06	11 / 62	BP	negative regulation of ubiquitin−protein ligase activity involved in mitotic cel
16	4e−06	6 / 16	GSEA	BIOCARTA_PTDINS_PATHWAY
17	4e−06	10 / 55	CC	proteasome complex
18	5e−06	5 / 10	GSEA	REACTOME_HIV_LIFE_CYCLE
19	5e−06	12 / 83	BP	respiratory electron transport chain
20	9e−06	9 / 48	BP	regulation of cellular amino acid metabolic process
21	1e−05	21 / 242	BP	RNA metabolic process
22	1e−05	6 / 19	CC	mitochondrial small ribosomal subunit
23	2e−05	51 / 949	CC	nucleoplasm
24	2e−05	5 / 13	GSEA	REACTOME_GLYCOLYSIS
25	3e−05	5 / 14	GSEA	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
26	4e−05	61 / 1233	TF	KIM_MYC targets
27	4e−05	15 / 152	BP	cellular metabolic process
28	5e−05	5 / 15	CC	mitochondrial large ribosomal subunit
29	5e−05	5 / 15	Canc	GENTLES_modul1
30	5e−05	5 / 15	GSEA	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
31	7e−05	61 / 1253	BP	small molecule metabolic process
32	7e−05	12 / 106	BP	protein polyubiquitination
33	7e−05	5 / 16	GSEA	WONG_MITOCHONDRIA_GENE_MODULE
34	7e−05	5 / 16	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
35	7e−05	5 / 16	GSEA	MOOTHA_HUMAN_MITODB_6_2002
36	7e−05	22 / 298	BP	DNA repair
37	8e−05	4 / 9	GSEA	BIOCARTA_GLYCOLYSIS_PATHWAY
38	9e−05	18 / 219	BP	mRNA metabolic process
39	9e−05	9 / 63	BP	DNA damage response, signal transduction by p53 class mediator resulting
40	9e−05	9 / 63	TF	MYC_Targets UP



BP

Rank	p−value	#in/all	Geneset
1	4e−11	19 / 96	rRNA processing
2	4e−10	29 / 253	translation
3	4e−07	12 / 66	positive regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
4	8e−07	12 / 70	regulation of ubiquitin−protein ligase activity involved in mitotic cell cycle
5	1e−06	25 / 287	viral process
6	1e−06	42 / 649	gene expression
7	2e−06	12 / 74	anaphase−promoting complex−dependent proteasomal ubiquitin−dependent
8	2e−06	11 / 62	negative regulation of ubiquitin−protein ligase activity involved in mitotic cell cy
9	5e−06	12 / 83	respiratory electron transport chain
10	9e−06	9 / 48	regulation of cellular amino acid metabolic process
11	1e−05	21 / 242	RNA metabolic process
12	4e−05	15 / 152	cellular metabolic process
13	7e−05	61 / 1253	small molecule metabolic process
14	7e−05	12 / 106	protein polyubiquitination
15	7e−05	22 / 298	DNA repair
16	9e−05	18 / 219	mRNA metabolic process
17	9e−05	9 / 63	DNA damage response, signal transduction by p53 class mediator resulting in
18	2e−04	9 / 70	antigen processing and presentation of exogenous peptide antigen via MHC c
19	3e−04	9 / 74	antigen processing and presentation of exogenous peptide antigen via MHC c
20	3e−04	10 / 91	antigen processing and presentation of peptide antigen via MHC class I

Cancer

Rank	p−value	#in/all	Geneset
1	1e−07	39 / 530	Lembcke_Normal vs Adenoma
2	5e−05	5 / 15	GENTLES_modul1
3	8e−04	8 / 68	SHAUGHNESSY_MM high risk
4	1e−02	3 / 16	RHODES_UNDIFFERENTIATED_CANCER
5	1e−02	3 / 16	GENTLES_modul2
6	1e−02	3 / 16	GENTLES_modul7
7	5e−02	1 / 15	RHODES_CANCER_META_SIGNATURE
8	7e−02	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	7e−02	2 / 15	GENTLES_modul6
10	1e−01	3 / 39	ZHANG_MM up
11	2e−01	3 / 48	KUIPER_MM poor survival
12	3e−01	1 / 14	LIU_PROSTATE_CANCER_UP
13	3e−01	1 / 14	LIU_LIVER_CANCER
14	3e−01	1 / 14	WANG_ER_UP
15	4e−01	1 / 15	BEN−PORATH_UP
16	4e−01	1 / 16	GENTLES_modul4
17	4e−01	1 / 16	GENTLES_modul10
18	4e−01	1 / 16	GENTLES_modul11
19	1e+00	1 / 185	SPANG_LPS−index2
20	1e+00	1 / 553	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	4e−20	102 / 1318	mitochondrion
2	9e−11	48 / 579	nucleolus
3	7e−09	30 / 304	mitochondrial inner membrane
4	2e−08	21 / 167	ribosome
5	4e−06	10 / 55	proteasome complex
6	1e−05	6 / 19	mitochondrial small ribosomal subunit
7	2e−05	51 / 949	nucleoplasm
8	5e−05	5 / 15	mitochondrial large ribosomal subunit
9	1e−04	5 / 17	proteasome accessory complex
10	1e−04	100 / 2378	cytosol
11	6e−04	6 / 36	mitochondrial respiratory chain complex I
12	6e−04	4 / 14	exosome (RNase complex)
13	7e−04	6 / 37	mitochondrial nucleoid
14	1e−03	4 / 17	proteasome core complex
15	3e−03	10 / 118	ribonucleoprotein complex
16	3e−03	6 / 48	cell body
17	3e−03	164 / 4640	nucleus
18	4e−03	4 / 23	mitochondrial ribosome
19	7e−03	3 / 14	Ino80 complex
20	9e−03	3 / 15	DNA−directed RNA polymerase III complex

Chr

Rank	p−value	#in/all	Geneset
1	1e−08	50 / 717	Chr 16
2	4e−04	47 / 957	Chr 11
3	3e−02	3 / 23	Chr HSCHR6_MHC_DBB
4	3e−02	37 / 918	Chr 17
5	4e−02	23 / 534	Chr 8
6	5e−02	30 / 743	Chr 7
7	1e−01	18 / 449	Chr 20
8	1e−01	40 / 1135	Chr 19
9	2e−01	15 / 386	Chr 22
10	3e−01	54 / 1720	Chr 1
11	4e−01	17 / 519	Chr 14
12	4e−01	22 / 714	Chr 6
13	5e−01	2 / 52	Chr HSCHR6_MHC_QBL
14	9e−01	14 / 633	Chr 9
15	9e−01	3 / 187	Chr 21
16	1e+00	17 / 866	Chr 12
17	1e+00	21 / 1033	Chr 2
18	1e+00	17 / 914	Chr 3
19	1e+00	10 / 630	Chr X
20	1e+00	2 / 232	Chr 18

Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 17	BCHETNIA_EBM up
2	1.0	4 / 375	GUDJ_psoriasis down
3	1.0	6 / 572	GUDJ_psoriasis up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	7 / 62	Stuehler_Proteins_up_in_STS
2	0.007	8 / 95	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	0.025	9 / 142	willscher_GBM_Verhaak−CL_expression_C_up
4	0.025	9 / 142	willscher_GBM_Verhaak−PNmut_expression_C_down
5	0.028	10 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
6	0.083	3 / 35	Colman_survival_associated
7	0.094	3 / 37	willscher_GBM_proteomics_wtOnly_SpotH
8	0.113	1 / 4	willscher_GBM_STSwt_proteomics−L_UP
9	0.151	4 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
10	0.173	4 / 74	GIEZELT_GBM_STS_up_VS_LTS
11	0.212	3 / 54	willscher_GBM_proteomics_wtOnly_SpotG
12	0.260	12 / 328	Up
13	0.261	5 / 117	GIEZELT_GBM_WT_up_VS_mut
14	0.263	14 / 391	Down_b
15	0.280	1 / 11	KIM amplified & overexpressed in LTS
16	0.301	1 / 12	astrocytes_glio
17	0.301	1 / 12	willscher_GBM_LTSmut_proteomics−B_UP
18	0.301	1 / 12	willscher_GBM_STSwt_proteomics−B_DOWN
19	0.301	1 / 12	willscher_GBM_Verhaak−PNwt_expression_I_up
20	0.301	1 / 12	willscher_GBM_Verhaak−PNmut_expression_I_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−06	6 / 16	BIOCARTA_PTDINS_PATHWAY
2	5e−06	5 / 10	REACTOME_HIV_LIFE_CYCLE
3	2e−05	5 / 13	REACTOME_GLYCOLYSIS
4	3e−05	5 / 14	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
5	5e−05	5 / 15	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
6	7e−05	5 / 16	WONG_MITOCHONDRIA_GENE_MODULE
7	7e−05	5 / 16	WONG_EMBRYONIC_STEM_CELL_CORE
8	7e−05	5 / 16	MOOTHA_HUMAN_MITODB_6_2002
9	8e−05	4 / 9	BIOCARTA_GLYCOLYSIS_PATHWAY
10	2e−04	4 / 11	REACTOME_HIV_INFECTION
11	2e−04	3 / 5	NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
12	4e−04	4 / 13	MOOTHA_VOXPHOS
13	4e−04	4 / 13	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
14	6e−04	4 / 14	ELVIDGE_HYPOXIA_DN
15	6e−04	4 / 14	STEIN_ESRRA_TARGETS_UP
16	6e−04	4 / 14	CHANG_CORE_SERUM_RESPONSE_UP
17	6e−04	4 / 14	KEGG_COLORECTAL_CANCER
18	8e−04	4 / 15	BASAKI_YBX1_TARGETS_UP
19	8e−04	4 / 15	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
20	8e−04	4 / 15	MANALO_HYPOXIA_DN

H_Tiss

Rank	p−value	#in/all	Geneset
1	0.03	2 / 10	WIRTH_B−cells
2	0.30	1 / 12	WIRTH_Lymphocytes
3	0.32	1 / 13	WIRTH_Sec. lymphoid organs
4	0.32	1 / 13	WIRTH_Thalamus
5	0.36	1 / 15	WIRTH_Telencephalon
6	0.54	1 / 26	WIRTH_Pancreas
7	0.97	1 / 120	WIRTH_Testis
8	1.00	4 / 417	WIRTH_Immune system
9	1.00	1 / 400	WIRTH_Nervous System
10	1.00	0 / 5	WIRTH_Pituitary gland
11	1.00	0 / 12	WIRTH_Prim. lymphoid organs
12	1.00	0 / 13	WIRTH_Tonsil
13	1.00	0 / 13	WIRTH_Thymus
14	1.00	0 / 6	WIRTH_Bone marrow
15	1.00	0 / 14	WIRTH_Globus pallidus
16	1.00	0 / 13	WIRTH_Cortex cerebri
17	1.00	0 / 16	WIRTH_Hippocampus
18	1.00	0 / 15	WIRTH_Cerebellum
19	1.00	0 / 50	WIRTH_Homeostasis
20	1.00	0 / 62	WIRTH_Liver

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.002	37 / 755	SPANG_BCR UP
2	0.109	5 / 86	ROSOLOWSKI_green UP
3	0.116	2 / 20	ROSOLOWSKI_red UP
4	0.139	6 / 119	ROSOLOWSKI_green total
5	0.301	1 / 12	DAVE_BL UP
6	0.416	1 / 18	DAVE_c−myc BL UP
7	0.466	3 / 86	ROSOLOWSKI_red total
8	0.474	2 / 54	SPANG_BAFF 9hrs DN
9	0.486	13 / 426	SPANG_CD40 6hrs DN
10	0.512	1 / 24	SPANG_BAFF 9hrs UP
11	0.567	3 / 100	ROSOLOWSKI_blue total
12	0.593	4 / 140	DAVE_BL−vs−DLBCL
13	0.679	1 / 38	ROSOLOWSKI_blue DOWN
14	0.766	22 / 852	SPANG_BCR DN
15	0.861	6 / 291	SPANG_IL21 UP
16	0.910	5 / 275	ZHANG_DLBCL mutated
17	0.966	5 / 327	SPANG_CD40 6hrs UP
18	0.971	1 / 118	SPANG_LPS 6hrs UP
19	0.988	3 / 274	SPANG_IL21 DN
20	1.000	0 / 13	BENTINK_mBL UP

MF

Rank	p−value	#in/all	Geneset
1	3e−12	25 / 153	structural constituent of ribosome
2	1e−04	4 / 10	NADH dehydrogenase activity
3	4e−04	6 / 34	NADH dehydrogenase (ubiquinone) activity
4	6e−04	6 / 36	tRNA binding
5	6e−04	4 / 14	pseudouridine synthase activity
6	2e−03	4 / 18	ribonucleoprotein complex binding
7	2e−03	4 / 18	threonine−type endopeptidase activity
8	3e−03	3 / 10	monosaccharide binding
9	3e−03	30 / 595	RNA binding
10	3e−03	3 / 11	telomeric DNA binding
11	7e−03	3 / 14	snoRNA binding
12	8e−03	5 / 43	chaperone binding
13	9e−03	23 / 456	identical protein binding
14	9e−03	3 / 15	3'−5'−exoribonuclease activity
15	1e−02	3 / 16	enzyme regulator activity
16	1e−02	3 / 16	Hsp70 protein binding
17	1e−02	26 / 549	molecular_function
18	1e−02	7 / 88	unfolded protein binding
19	2e−02	8 / 112	methyltransferase activity
20	2e−02	4 / 35	aminoacyl−tRNA ligase activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.06	1 / 2	GGCG−371
2	0.15	11 / 261	CTCA−125B−−125A
3	0.16	3 / 47	CCAG−490
4	0.18	4 / 75	GGCA−324−3P
5	0.22	3 / 55	GGGG−296
6	0.23	3 / 56	GTGG−197
7	0.29	7 / 182	CTGA−24
8	0.30	2 / 37	TAGG−192−−215
9	0.33	5 / 129	CTCT−520A−−525
10	0.42	2 / 49	CTAG−384
11	0.42	2 / 49	AGGA−483
12	0.43	1 / 19	GTCA−380−5P
13	0.49	2 / 56	GTGT−342
14	0.50	1 / 23	CACG−302A
15	0.50	2 / 57	CTCA−526B
16	0.53	8 / 267	CACT−128A−−128B
17	0.57	2 / 64	ACAC−122A
18	0.57	2 / 65	TCTA−376A−−376B
19	0.61	2 / 69	AGCT−28
20	0.62	1 / 32	CTCT−368

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.06	1 / 2	miR−16−1
2	0.11	1 / 4	miR−27a
3	0.14	1 / 5	miR−15a
4	0.21	1 / 8	miR−155
5	0.24	1 / 9	miR−125b
6	0.54	1 / 26	miR−21
7	1.00	0 / 11	let−7a
8	1.00	0 / 6	let−7b
9	1.00	0 / 4	let−7c
10	1.00	0 / 6	let−7d
11	1.00	0 / 4	let−7g
12	1.00	0 / 13	miR−1
13	1.00	0 / 5	miR−101
14	1.00	0 / 2	miR−101b
15	1.00	0 / 4	miR−106b
16	1.00	0 / 2	miR−107
17	1.00	0 / 4	miR−122
18	1.00	0 / 2	miR−124a
19	1.00	0 / 6	miR−125a
20	1.00	0 / 5	miR−126

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.002	9 / 92	hsa−miR−378
2	0.003	8 / 83	hsa−miR−486−3p
3	0.005	5 / 39	hsa−miR−593
4	0.006	7 / 75	hsa−miR−939
5	0.007	7 / 77	hsa−miR−942
6	0.010	6 / 62	hsa−miR−637
7	0.015	7 / 88	hsa−miR−423−5p
8	0.015	7 / 88	hsa−miR−149
9	0.021	15 / 284	hsa−miR−503
10	0.028	5 / 58	hsa−miR−892a
11	0.029	4 / 40	hsa−miR−516a−3p
12	0.037	4 / 43	hsa−miR−658
13	0.040	2 / 11	hsa−miR−604
14	0.046	4 / 46	hsa−miR−874
15	0.049	4 / 47	hsa−miR−766
16	0.056	6 / 93	hsa−miR−125b
17	0.059	4 / 50	hsa−miR−940
18	0.062	3 / 31	hsa−miR−1296
19	0.069	7 / 122	hsa−miR−515−3p
20	0.070	5 / 75	hsa−miR−422a

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.003	3 / 11	MACIEJ_MMML 15
2	0.012	2 / 6	MACIEJ_MMML 29
3	0.016	2 / 7	MACIEJ_MMML 9
4	0.189	1 / 7	MACIEJ_MMML 13
5	0.236	1 / 9	MACIEJ_MMML 14
6	0.301	1 / 12	MACIEJ_MMML 24
7	0.342	1 / 14	MACIEJ_MMML 26
8	0.342	1 / 14	MACIEJ_MMML 4
9	1.000	0 / 16	MACIEJ_MMML 1
10	1.000	0 / 13	MACIEJ_MMML 10
11	1.000	0 / 15	MACIEJ_MMML 16
12	1.000	0 / 2	MACIEJ_MMML 17
13	1.000	0 / 14	MACIEJ_MMML 19
14	1.000	0 / 4	MACIEJ_MMML 2
15	1.000	0 / 5	MACIEJ_MMML 20
16	1.000	0 / 15	MACIEJ_MMML 22
17	1.000	0 / 4	MACIEJ_MMML 23
18	1.000	0 / 2	MACIEJ_MMML 27
19	1.000	0 / 5	MACIEJ_MMML 28
20	1.000	0 / 11	MACIEJ_MMML 3

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.007	3 / 14	BENTINK_myc.1
2	0.280	1 / 11	BENTINK_ras.4
3	0.301	1 / 12	BENTINK_ras.1
4	1.000	0 / 13	GUSTAFSON_PI3K_UP
5	1.000	0 / 15	GUSTAFSON_PI3K_DN
6	1.000	0 / 12	BENTINK_e2f3.1
7	1.000	0 / 11	BENTINK_e2f3.2
8	1.000	0 / 15	BENTINK_ras.6
9	1.000	0 / 13	BENTINK_src.10
10	1.000	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−05	61 / 1233	KIM_MYC targets
2	9e−05	9 / 63	MYC_Targets UP
3	5e−03	2 / 4	MYC_Cell growth and proliferation UP
4	2e−02	44 / 1095	HEBENSTREIT_high expression TF
5	6e−02	1 / 2	MYC_Chromatin_modification UP
6	9e−02	1 / 3	MYC_DNA replication UP
7	9e−02	1 / 3	MYC_Tumor supressor genes UP
8	1e−01	2 / 20	MYC_Metabolism UP
9	2e−01	1 / 7	MYC_DNA repair UP
10	2e−01	1 / 8	MYC_Cell cycle UP
11	2e−01	1 / 8	MYC_RNA processing binding UP
12	4e−01	1 / 16	MYC_Protein synthesis degradation UP
13	1e+00	5 / 1146	HEBENSTREIT_low expression TF
14	1e+00	0 / 14	NOWICK_TF
15	1e+00	0 / 5	MYC_TFs
16	1e+00	0 / 9	MYC_Targets DOWN
17	1e+00	0 / 4	MYC_Apoptosis UP
18	1e+00	0 / 2	MYC_Cell cycle DOWN
19	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
20	1e+00	0 / 2	MYC_Signal transduction UP

TF_Tissue

Rank	p−value	#in/all	Geneset
1	0.2	2 / 28	VAQUERIZAS_Liver
2	0.7	1 / 44	VAQUERIZAS_Placenta
3	0.8	3 / 144	VAQUERIZAS_General
4	1.0	0 / 40	VAQUERIZAS_Fetal brain
5	1.0	0 / 37	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 43	VAQUERIZAS_Uterus
8	1.0	0 / 12	VAQUERIZAS_Kidney
9	1.0	0 / 22	VAQUERIZAS_Spinal cord
10	1.0	0 / 43	VAQUERIZAS_Whole brain
11	1.0	0 / 41	VAQUERIZAS_Thymus
12	1.0	0 / 39	VAQUERIZAS_Thyroid
13	1.0	0 / 62	VAQUERIZAS_Whole blood
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 30	VAQUERIZAS_Fetal lung
16	1.0	0 / 62	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 24	VAQUERIZAS_Trachea
19	1.0	0 / 14	VAQUERIZAS_Fetal liver
20	1.0	0 / 21	VAQUERIZAS_Tonsil

Sample−Underexpression

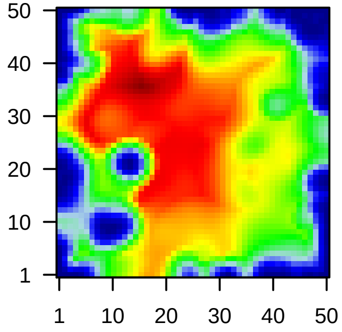
Spot Summary: d

metagenes = 9
genes = 129

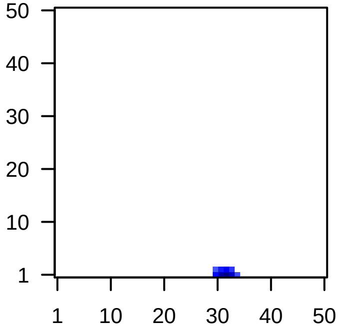
<r> metagenes = 0.98
<r> genes = 0.43
beta: r2= 10.61 / log p= −Inf

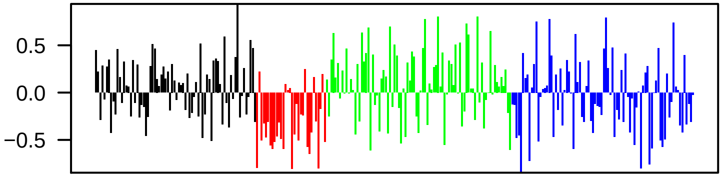
samples with spot = 73 (26.5 %)
Atypical : 11 (14.9 %)
Classical : 21 (65.6 %)
Mesenchymal : 14 (16.5 %)
Basal : 27 (32.1 %)

Overview Map



Spot





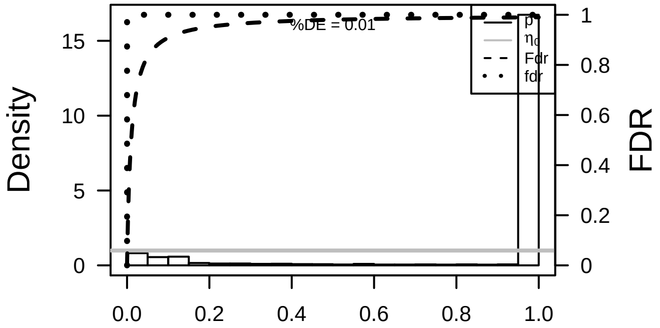
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	4599	1.79	−2.78	0.71	MX1	myxovirus (influenza virus) resistance 1, interferon−inducible
2	9636	2.47	−2.69	0.73	ISG15	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:40
3	3627	3.43	−2.5	0.75	CXCL10	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
4	2537	1.9	−2.48	0.69	IFI6	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
5	684	1.71	−2.44	0.79	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
6	10964	2.46	−2.33	0.78	IFI44L	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
7	8519	1.93	−2.3	0.81	IFITM1	interferon induced transmembrane protein 1 [Source:HGNC
8	629	2.42	−2.1	0.6	CFB	complement factor B [Source:HGNC Symbol;Acc:1037]
9	10410	1.47	−2.08	0.72	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC
10	3136	1.7	−2.07	0.69		
11	94240	2.04	−2.07	0.81	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
12	55008	1.98	−2.07	0.61	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase
13	8743	2.43	−2.05	0.38	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10 [Sourc
14	10581	1.63	−2	0.72	IFITM2	interferon induced transmembrane protein 2 [Source:HGNC
15	10561	1.95	−1.98	0.74	IFI44	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
16	51296	1.74	−1.96	0.83	SLC15A3	solute carrier family 15 (oligopeptide transporter), member 3 [
17	51191	1.79	−1.93	0.71	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase
18	115362	2.34	−1.91	0.73	GBP5	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
19	3106	1.27	−1.9	0.75	HLA−B	major histocompatibility complex, class I, B [Source:HGNC S
20	10866	1.55	−1.9	0.66	HCP5	HLA complex P5 (non−protein coding) [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−49	29 / 51	BP	type I interferon signaling pathway
2	5e−39	31 / 123	BP	defense response to virus
3	4e−36	34 / 204	BP	cytokine−mediated signaling pathway
4	1e−34	46 / 572	Disea	GUDJ_psoriasis up
5	1e−33	27 / 109	BP	response to virus
6	1e−27	31 / 274	Lymp	SPANG_IL21 DN
7	5e−23	12 / 16	GSE	MOSERLE_IFNA_RESPONSE
8	4e−22	28 / 312	BP	immune response
9	7e−21	16 / 60	BP	interferon−gamma−mediated signaling pathway
10	2e−20	11 / 16	GSE	EINAV_INTERFERON_SIGNATURE_IN_CANCER
11	2e−20	11 / 16	GSE	ZHANG_INTERFERON_RESPONSE
12	4e−20	13 / 31	BP	negative regulation of viral genome replication
13	2e−19	10 / 13	GSE	BOWIE_RESPONSE_TO_TAMOXIFEN
14	8e−19	9 / 10	GSE	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
15	4e−18	10 / 16	GSE	UROSEVIC_RESPONSE_TO_IMIQUIMOD
16	5e−16	8 / 10	GSE	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
17	2e−15	8 / 11	GSE	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
18	4e−14	26 / 530	BP	innate immune response
19	2e−13	7 / 10	CC	MHC class I protein complex
20	2e−13	6 / 6	Lymp	DAVE_MHCCII BL DN
21	2e−13	12 / 70	BP	antigen processing and presentation of exogenous peptide antigen via MH
22	4e−13	12 / 74	BP	antigen processing and presentation of exogenous peptide antigen via MH
23	4e−13	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
24	4e−13	20 / 316	Canc	SPANG_BCL6−index2
25	1e−12	16 / 185	Canc	SPANG_LPS−index2
26	4e−12	19 / 316	BP	modulation by virus of host morphology or physiology
27	5e−12	12 / 91	BP	antigen processing and presentation of peptide antigen via MHC class I
28	5e−12	6 / 8	GSE	ROETH_TERT_TARGETS_UP
29	1e−11	11 / 74	BP	regulation of immune response
30	2e−11	7 / 16	GSE	MAHADEVAN_RESPONSE_TO_MP470_UP
31	4e−11	7 / 18	MF	peptide antigen binding
32	8e−11	9 / 47	BP	antigen processing and presentation
33	2e−10	6 / 12	GSE	TSAI_DNAJB4_TARGETS_UP
34	2e−10	9 / 51	MF	double−stranded RNA binding
35	2e−10	9 / 52	Chr	Chr HSCHR6_MHC_QBL
36	6e−10	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
37	6e−10	6 / 14	GSE	XU_AKT1_TARGETS_6HR
38	6e−10	6 / 14	GSE	RADAEVA_RESPONSE_TO_IFNA1_UP
39	1e−09	6 / 16	GSE	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
40	1e−07	5 / 16	GSE	FARMER_BREAST_CANCER_CLUSTER_1

p−values



BP

Rank	p−value	#in/all	Geneset
1	3e−49	29 / 51	type I interferon signaling pathway
2	5e−39	31 / 123	defense response to virus
3	4e−36	34 / 204	cytokine−mediated signaling pathway
4	1e−33	27 / 109	response to virus
5	4e−22	28 / 312	immune response
6	7e−21	16 / 60	interferon−gamma−mediated signaling pathway
7	4e−20	13 / 31	negative regulation of viral genome replication
8	4e−14	26 / 530	innate immune response
9	2e−13	12 / 70	antigen processing and presentation of exogenous peptide antigen via MHC c
10	4e−13	12 / 74	antigen processing and presentation of exogenous peptide antigen via MHC c
11	4e−13	8 / 18	positive regulation of T cell mediated cytotoxicity
12	4e−12	19 / 316	modulation by virus of host morphology or physiology
13	5e−12	12 / 91	antigen processing and presentation of peptide antigen via MHC class I
14	1e−11	11 / 74	regulation of immune response
15	8e−11	9 / 47	antigen processing and presentation
16	1e−07	6 / 32	negative regulation of type I interferon production
17	2e−07	5 / 18	response to interferon−gamma
18	2e−05	4 / 21	positive regulation of interferon−beta production
19	2e−05	16 / 608	apoptotic process
20	5e−05	3 / 10	positive regulation of interferon−alpha production

Cancer

Rank	p−value	#in/all	Geneset
1	4e−13	20 / 316	SPANG_BCL6−index2
2	1e−12	16 / 185	SPANG_LPS−index2
3	6e−06	16 / 553	Lembcke_Colonic Inflammation
4	7e−02	1 / 9	WANG_ER_DN
5	8e−02	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
6	1e−01	1 / 14	LIU_COMMON_CANCER_GENES
7	4e−01	1 / 68	SHAUGHNESSY_MM high risk
8	1e+00	1 / 530	Lembcke_Normal vs Adenoma
9	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
10	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	1e+00	0 / 10	LIU_BREAST_CANCER
13	1e+00	0 / 14	LIU_LIVER_CANCER
14	1e+00	0 / 15	LIU_PROSTATE_CANCER_DN
15	1e+00	0 / 14	LIU_PROSTATE_CANCER_UP
16	1e+00	0 / 14	WANG_ER_UP
17	1e+00	0 / 16	WOLFER_overlap genes
18	1e+00	0 / 12	BEN−PORATH_DN
19	1e+00	0 / 15	BEN−PORATH_UP
20	1e+00	0 / 15	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	2e−13	7 / 10	MHC class I protein complex
2	1e−07	6 / 32	ER to Golgi transport vesicle membrane
3	3e−07	41 / 2378	cytosol
4	8e−07	5 / 23	integral to lumenal side of endoplasmic reticulum membrane
5	1e−06	6 / 45	phagocytic vesicle membrane
6	4e−05	6 / 80	early endosome membrane
7	3e−04	3 / 17	proteasome core complex
8	9e−04	14 / 683	extracellular space
9	9e−04	4 / 55	proteasome complex
10	4e−03	18 / 1182	extracellular region
11	1e−02	45 / 4310	cytoplasm
12	2e−02	2 / 27	SCF ubiquitin ligase complex
13	3e−02	5 / 215	lysosomal membrane
14	4e−02	4 / 162	external side of plasma membrane
15	5e−02	7 / 436	Golgi membrane
16	6e−02	4 / 184	lysosome
17	6e−02	2 / 51	cytoplasmic mRNA processing body
18	6e−02	7 / 455	perinuclear region of cytoplasm
19	7e−02	2 / 58	integral to endoplasmic reticulum membrane
20	8e−02	1 / 10	lateral element

Chr

Rank	p−value	#in/all	Geneset
1	2e−10	9 / 52	Chr HSCHR6_MHC_QBL
2	2e−02	14 / 957	Chr 11
3	1e−01	6 / 449	Chr 20
4	2e−01	1 / 23	Chr HSCHR6_MHC_DBB
5	2e−01	7 / 618	Chr 4
6	4e−01	4 / 386	Chr 22
7	4e−01	15 / 1720	Chr 1
8	4e−01	5 / 519	Chr 14
9	4e−01	9 / 1033	Chr 2
10	4e−01	2 / 187	Chr 21
11	5e−01	5 / 602	Chr 10
12	5e−01	7 / 866	Chr 12
13	6e−01	7 / 914	Chr 3
14	8e−01	7 / 1135	Chr 19
15	8e−01	4 / 714	Chr 6
16	8e−01	1 / 232	Chr 18
17	8e−01	5 / 918	Chr 17
18	9e−01	3 / 633	Chr 9
19	9e−01	1 / 280	Chr 13
20	9e−01	2 / 504	Chr 15

Disease

Rank	p−value	#in/all	Geneset
1	1e−34	46 / 572	GUDJ_psoriasis up
2	1e+00	0 / 375	GUDJ_psoriasis down
3	1e+00	0 / 17	BCHETNIA_EBM up
4	1e+00	0 / 2	BCHETNIA_EBM down
5	1e+00	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	6e−10	6 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
2	2e−04	5 / 72	GIEZELT_GBM_STSwt_down_VS_LTSwt
3	2e−04	10 / 328	Up
4	6e−04	4 / 49	Donson−innate immunity−associated with LTS in HGA
5	2e−02	3 / 68	cultured astroglia vs. in vivo astrocytes
6	3e−02	2 / 32	Donson−Misc immune function−associated with LTS in HGA
7	3e−02	2 / 33	willscher_GBM_proteomics_wtOnly_SpotC
8	5e−02	1 / 6	Martinez_Glio_hypometh
9	5e−02	1 / 7	willscher_GBM_LTSmut_proteomics−P_DOWN
10	6e−02	2 / 49	Christensen_hypomethylated_in_primary_glioblastoma
11	6e−02	5 / 265	willscher_GBM_Verhaak−CL_expression_B_up
12	6e−02	5 / 265	willscher_GBM_Verhaak−MES_expression_B_up
13	6e−02	5 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
14	6e−02	5 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
15	1e−01	1 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
16	2e−01	2 / 105	willscher_GBM_proteomics_wtOnly_SpotB
17	2e−01	2 / 117	GIEZELT_GBM_WT_up_VS_mut
18	2e−01	1 / 35	Colman_survival_associated
19	3e−01	1 / 37	Christensen_hypomethylated_in_ependymoma
20	3e−01	1 / 45	willscher_GBM_Verhaak−PNwt_expression_J_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−23	12 / 16	MOSERLE_IFNA_RESPONSE
2	2e−20	11 / 16	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	2e−20	11 / 16	ZHANG_INTERFERON_RESPONSE
4	2e−19	10 / 13	BOWIE_RESPONSE_TO_TAMOXIFEN
5	8e−19	9 / 10	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	4e−18	10 / 16	UROSEVIC_RESPONSE_TO_IMIQUIMOD
7	5e−16	8 / 10	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
8	2e−15	8 / 11	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	5e−12	6 / 8	ROETH_TERT_TARGETS_UP
10	2e−11	7 / 16	MAHADEVAN_RESPONSE_TO_MP470_UP
11	2e−10	6 / 12	TSAI_DNAJB4_TARGETS_UP
12	6e−10	6 / 14	XU_AKT1_TARGETS_6HR
13	6e−10	6 / 14	RADAEVA_RESPONSE_TO_IFNA1_UP
14	1e−09	6 / 16	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
15	1e−07	5 / 16	FARMER_BREAST_CANCER_CLUSTER_1
16	1e−07	5 / 16	ZHAN_MULTIPLE_MYELOMA_LB_DN
17	1e−07	5 / 16	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
18	7e−07	4 / 10	DAUER_STAT3_TARGETS_DN
19	7e−07	4 / 10	GRANDVAUX_IRF3_TARGETS_UP
20	2e−06	4 / 12	ZHU_CMV_8_HR_UP

H. Tiss

Rank	p−value	#in/all	Geneset
1	2e−05	13 / 417	WIRTH_Immune system
2	4e−03	2 / 12	WIRTH_Lymphocytes
3	1e−01	1 / 13	WIRTH_Sec. lymphoid organs
4	1e−01	1 / 13	WIRTH_Cortex cerebri
5	2e−01	1 / 36	WIRTH_Placenta
6	1e+00	0 / 5	WIRTH_Pituitary gland
7	1e+00	0 / 26	WIRTH_Pancreas
8	1e+00	0 / 12	WIRTH_Prim. lymphoid organs
9	1e+00	0 / 10	WIRTH_B−cells
10	1e+00	0 / 13	WIRTH_Tonsil
11	1e+00	0 / 13	WIRTH_Thymus
12	1e+00	0 / 6	WIRTH_Bone marrow
13	1e+00	0 / 400	WIRTH_Nervous System
14	1e+00	0 / 14	WIRTH_Globus pallidus
15	1e+00	0 / 15	WIRTH_Telencephalon
16	1e+00	0 / 16	WIRTH_Hippocampus
17	1e+00	0 / 13	WIRTH_Thalamus
18	1e+00	0 / 15	WIRTH_Cerebellum
19	1e+00	0 / 120	WIRTH_Testis
20	1e+00	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−27	31 / 274	SPANG_IL21 DN
2	2e−13	6 / 6	DAVE_MHCCII BL DN
3	2e−04	4 / 38	ROSOLOWSKI_blue DOWN
4	3e−04	6 / 119	ROSOLOWSKI_green total
5	1e−02	2 / 20	DAVE_Immune response 2
6	1e−02	4 / 118	SPANG_LPS 6hrs UP
7	1e−02	7 / 327	SPANG_CD40 6hrs UP
8	2e−02	3 / 69	SPANG_LPS 6hrs DN
9	2e−02	4 / 140	DAVE_BL−vs−DLBCL
10	3e−02	3 / 86	ROSOLOWSKI_green UP
11	9e−02	1 / 12	DAVE_BL_DN
12	2e−01	1 / 22	DAVE_NFkB BL DN
13	2e−01	1 / 28	DAVE_Immune response 1
14	2e−01	5 / 426	SPANG_CD40 6hrs DN
15	4e−01	1 / 59	LENZ_Stromal signature 2
16	5e−01	1 / 86	ROSOLOWSKI_red total
17	5e−01	7 / 852	SPANG_BCR DN
18	6e−01	2 / 275	ZHANG_DLBCL mutated
19	7e−01	2 / 291	SPANG_IL21 UP
20	8e−01	4 / 755	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	4e−11	7 / 18	peptide antigen binding
2	2e−10	9 / 51	double−stranded RNA binding
3	2e−05	4 / 22	NAD+ ADP−ribosyltransferase activity
4	3e−05	7 / 115	helicase activity
5	5e−05	4 / 27	single−stranded RNA binding
6	3e−04	82 / 8023	protein binding
7	3e−04	9 / 280	receptor binding
8	3e−04	4 / 43	chemokine activity
9	3e−04	3 / 18	threonine−type endopeptidase activity
10	4e−04	3 / 19	hydrolase activity, acting on acid anhydrides
11	7e−04	5 / 92	ATP−dependent helicase activity
12	1e−03	3 / 26	tumor necrosis factor receptor binding
13	1e−03	3 / 27	nucleotidyltransferase activity
14	2e−03	8 / 287	hydrolase activity
15	2e−03	4 / 72	transferase activity
16	3e−03	7 / 238	ubiquitin−protein ligase activity
17	3e−03	2 / 10	acid phosphatase activity
18	3e−03	2 / 11	regulatory region DNA binding
19	4e−03	2 / 12	MHC class I protein binding
20	7e−03	11 / 595	RNA binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.1	2 / 83	AGGA−516−3P
2	0.2	1 / 32	ACAA−453
3	0.2	1 / 33	TCTG−383
4	0.3	1 / 40	GTAA−200A
5	0.3	1 / 43	CCCA−299−3P
6	0.3	1 / 46	GGTG−412
7	0.4	1 / 75	ATGT−489
8	0.5	1 / 79	TCTC−185
9	0.5	1 / 80	TGAG−216
10	0.5	1 / 85	ATTA−380−3P
11	0.6	1 / 106	GGCA−519E
12	0.6	1 / 116	CAGC−370
13	0.6	2 / 261	CTCA−125B−−125A
14	0.6	1 / 125	ACAC−199A−−199B
15	0.7	1 / 139	GCAA−129
16	0.7	1 / 159	CACC−138
17	0.8	1 / 181	CCTG−214
18	0.8	1 / 182	TAGC−9
19	0.8	1 / 189	AACT−145
20	0.8	1 / 240	ACAT−1−−206

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	miR−152
2	0.02	1 / 3	miR−148a
3	0.07	1 / 9	miR−17
4	1.00	0 / 11	let−7a
5	1.00	0 / 6	let−7b
6	1.00	0 / 4	let−7c
7	1.00	0 / 6	let−7d
8	1.00	0 / 4	let−7g
9	1.00	0 / 13	miR−1
10	1.00	0 / 5	miR−101
11	1.00	0 / 2	miR−101b
12	1.00	0 / 4	miR−106b
13	1.00	0 / 2	miR−107
14	1.00	0 / 4	miR−122
15	1.00	0 / 2	miR−124a
16	1.00	0 / 6	miR−125a
17	1.00	0 / 9	miR−125b
18	1.00	0 / 5	miR−126
19	1.00	0 / 2	miR−127
20	1.00	0 / 3	miR−128

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.2	1 / 24	hsa−miR−519e*
2	0.3	1 / 38	hsa−miR−517*
3	0.3	1 / 41	hsa−miR−601
4	0.3	1 / 43	hsa−miR−129−3p
5	0.3	1 / 44	hsa−miR−636
6	0.3	1 / 47	hsa−miR−346
7	0.3	1 / 48	hsa−miR−549
8	0.3	1 / 53	hsa−miR−519b−5p
9	0.3	1 / 53	hsa−miR−519c−5p
10	0.3	1 / 53	hsa−miR−330−5p
11	0.4	1 / 58	hsa−miR−518d−5p
12	0.4	1 / 58	hsa−miR−520c−5p
13	0.4	1 / 59	hsa−miR−526b*
14	0.4	1 / 69	hsa−miR−578
15	0.4	1 / 72	hsa−miR−1262
16	0.4	1 / 73	hsa−miR−657
17	0.4	1 / 75	hsa−miR−375
18	0.4	1 / 75	hsa−miR−592
19	0.4	1 / 76	hsa−miR−1321
20	0.5	1 / 77	hsa−miR−620

MMML CGS

Rank	p−value	#in/all	Geneset
1	2e−06	3 / 4	MACIEJ_MMML 47
2	6e−05	2 / 2	MACIEJ_MMML 27
3	3e−02	1 / 4	MACIEJ_MMML 2
4	1e−01	1 / 13	MACIEJ_MMML 6
5	1e+00	0 / 16	MACIEJ_MMML 1
6	1e+00	0 / 13	MACIEJ_MMML 10
7	1e+00	0 / 7	MACIEJ_MMML 13
8	1e+00	0 / 9	MACIEJ_MMML 14
9	1e+00	0 / 11	MACIEJ_MMML 15
10	1e+00	0 / 15	MACIEJ_MMML 16
11	1e+00	0 / 2	MACIEJ_MMML 17
12	1e+00	0 / 14	MACIEJ_MMML 19
13	1e+00	0 / 5	MACIEJ_MMML 20
14	1e+00	0 / 15	MACIEJ_MMML 22
15	1e+00	0 / 4	MACIEJ_MMML 23
16	1e+00	0 / 12	MACIEJ_MMML 24
17	1e+00	0 / 14	MACIEJ_MMML 26
18	1e+00	0 / 5	MACIEJ_MMML 28
19	1e+00	0 / 6	MACIEJ_MMML 29
20	1e+00	0 / 11	MACIEJ_MMML 3

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	1 / 11	BENTINK_ras.4
2	0.10	1 / 13	BENTINK_src.10
3	1.00	0 / 13	GUSTAFSON_PI3K_UP
4	1.00	0 / 15	GUSTAFSON_PI3K_DN
5	1.00	0 / 12	BENTINK_e2f3.1
6	1.00	0 / 11	BENTINK_e2f3.2
7	1.00	0 / 14	BENTINK_myc.1
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	NOWICK_TF
2	0.5	9 / 1095	HEBENSTREIT_high expression TF
3	0.5	10 / 1233	KIM_MYC targets
4	0.9	5 / 1146	HEBENSTREIT_low expression TF
5	1.0	0 / 5	MYC_TFs
6	1.0	0 / 63	MYC_Targets UP
7	1.0	0 / 9	MYC_Targets DOWN
8	1.0	0 / 4	MYC_Apoptosis UP
9	1.0	0 / 8	MYC_Cell cycle UP
10	1.0	0 / 2	MYC_Cell cycle DOWN
11	1.0	0 / 4	MYC_Cell growth and proliferation UP
12	1.0	0 / 2	MYC_Chromatin_modification UP
13	1.0	0 / 7	MYC_DNA repair UP
14	1.0	0 / 3	MYC_DNA replication UP
15	1.0	0 / 2	MYC_ECM cell adhesion DOWN
16	1.0	0 / 20	MYC_Metabolism UP
17	1.0	0 / 16	MYC_Protein synthesis degradation UP
18	1.0	0 / 8	MYC_RNA processing binding UP
19	1.0	0 / 2	MYC_Signal transduction UP
20	1.0	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 29	VAQUERIZAS_Lymph node
2	5e−04	3 / 21	VAQUERIZAS_Tonsil
3	1e−03	4 / 62	VAQUERIZAS_Whole blood
4	4e−03	3 / 41	VAQUERIZAS_Thymus
5	8e−02	2 / 62	VAQUERIZAS_Lung
6	1e−01	1 / 16	VAQUERIZAS_Salivary gland
7	1e−01	1 / 16	VAQUERIZAS_Heart
8	2e−01	1 / 29	VAQUERIZAS_Smooth muscle
9	3e−01	1 / 44	VAQUERIZAS_Placenta
10	1e+00	0 / 40	VAQUERIZAS_Fetal brain
11	1e+00	0 / 28	VAQUERIZAS_Liver
12	1e+00	0 / 37	VAQUERIZAS_Prostate
13	1e+00	0 / 43	VAQUERIZAS_Uterus
14	1e+00	0 / 144	VAQUERIZAS_General
15	1e+00	0 / 12	VAQUERIZAS_Kidney
16	1e+00	0 / 22	VAQUERIZAS_Spinal cord
17	1e+00	0 / 43	VAQUERIZAS_Whole brain
18	1e+00	0 / 39	VAQUERIZAS_Thyroid
19	1e+00	0 / 7	VAQUERIZAS_Appendix
20	1e+00	0 / 30	VAQUERIZAS_Fetal lung

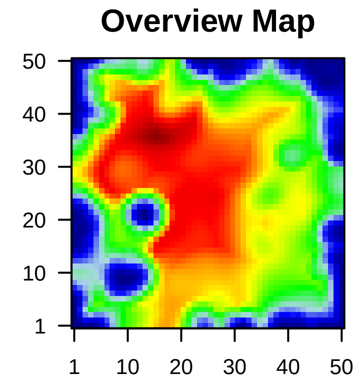
Sample−Underexpression

Spot Summary: e

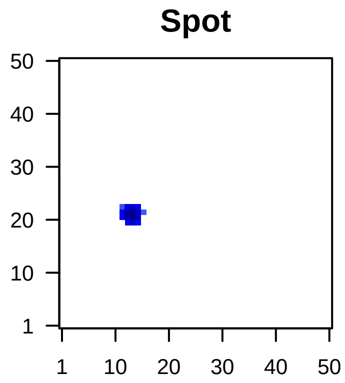
metagenes = 16
genes = 193

<r> metagenes = 0.98
<r> genes = 0.23
beta: r2= 1.91 / log p= −Inf

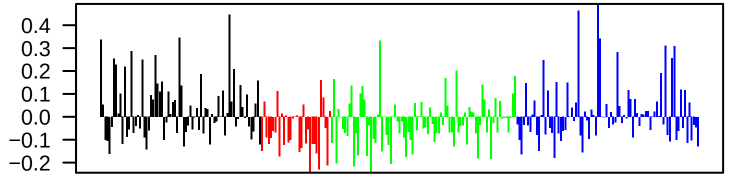
samples with spot = 0 (0 %)



Overview Map



Spot

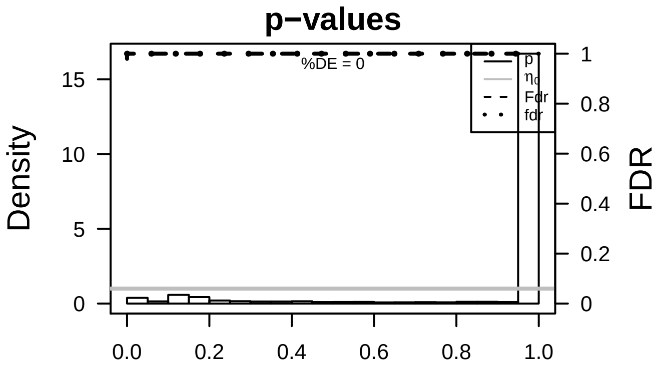


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	8673	1.03	−1.25	0.53	VAMP8	vesicle−associated membrane protein 8 [Source:HGNC Sym
2	3615	1.04	−1.16	0.41	IMPDH2	IMP (inosine 5'−monophosphate) dehydrogenase 2 [Source:
3	10217	1.09	−1.08	0.35	CTDSPL	CTD (carboxy−terminal domain, RNA polymerase II, polypept
4	8721	0.76	−1.03	0.47	EDF1	endothelial differentiation−related factor 1 [Source:HGNC Sy
5	27335	1.06	−1.02	0.52	EIF3K	eukaryotic translation initiation factor 3, subunit K [Source:HG
6	644	1.2	−0.96	0.3	BLVRA	biliverdin reductase A [Source:HGNC Symbol;Acc:1062]
7	7923	1.18	−0.96	0.45	HSD17B8	hydroxysteroid (17−beta) dehydrogenase 8 [Source:HGNC S
8	644928	1.21	−0.95	0.36		
9	54460	0.79	−0.95	0.38	MRPS21	mitochondrial ribosomal protein S21 [Source:HGNC Symbol;
10	254863	1.04	−0.95	0.53	TMEM256	transmembrane protein 256 [Source:HGNC Symbol;Acc:2861
11	140823	1.15	−0.93	0.52	ROMO1	reactive oxygen species modulator 1 [Source:HGNC Symbol;
12	327	0.73	−0.93	0.54	APEH	acylaminoacyl−peptide hydrolase [Source:HGNC Symbol;Acc
13	10591	1.1	−0.92	0.55	DNPH1	2'−deoxynucleoside 5'−phosphate N−hydrolase 1 [Source:HG
14	29082	0.79	−0.92	0.49	CHMP4A	charged multivesicular body protein 4A [Source:HGNC Symb
15	100128731	0.85	−0.91	0.45	OST4	oligosaccharyltransferase 4 homolog (S. cerevisiae) [Source:
16	25824	1.08	−0.89	0.39	PRDX5	peroxiredoxin 5 [Source:HGNC Symbol;Acc:9355]
17	9296	0.96	−0.89	0.52	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F [So
18	400156	1.2	−0.87	0.28		
19	100131187	1.05	−0.87	0.45	TSTD1	thiosulfate sulfurtransferase (rhodanese)−like domain contain
20	8574	0.76	−0.86	0.44	AKR7A2	aldo−keto reductase family 7, member A2 (aflatoxin aldehyde

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−16	52 / 1318	CC	mitochondrion
2	5e−08	37 / 1233	TF	KIM_MYC targets
3	4e−07	16 / 304	CC	mitochondrial inner membrane
4	3e−06	11 / 167	CC	ribosome
5	4e−05	12 / 253	BP	translation
6	5e−05	7 / 83	BP	respiratory electron transport chain
7	6e−05	9 / 152	BP	cellular metabolic process
8	7e−05	9 / 153	MF	structural constituent of ribosome
9	7e−05	5 / 38	MF	DNA−directed RNA polymerase activity
10	1e−04	3 / 9	GSE	KEGG_RNA_POLYMERASE
11	2e−04	3 / 10	MF	NADH dehydrogenase activity
12	2e−04	5 / 47	BP	protein targeting to mitochondrion
13	4e−04	3 / 13	CC	mitochondrial respiratory chain
14	4e−04	3 / 13	GSE	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
15	4e−04	3 / 13	GSE	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
16	4e−04	15 / 482	BP	cellular protein metabolic process
17	5e−04	18 / 649	BP	gene expression
18	5e−04	3 / 14	BP	mitochondrial ATP synthesis coupled proton transport
19	6e−04	4 / 34	MF	NADH dehydrogenase (ubiquinone) activity
20	6e−04	3 / 15	BP	ATP synthesis coupled proton transport
21	6e−04	3 / 15	GSE	REACTOME_MRNA_SPLICING_MINOR_PATHWAY
22	7e−04	7 / 128	BP	translational initiation
23	7e−04	5 / 62	Glio	Stuehler_Proteins_up_in_STS
24	7e−04	4 / 36	CC	mitochondrial respiratory chain complex I
25	7e−04	3 / 16	GSE	YANG_BREAST_CANCER_ESR1_LASER_UP
26	1e−03	9 / 220	CC	mitochondrial matrix
27	1e−03	25 / 1135	Chr	Chr 19
28	1e−03	3 / 19	CC	mitochondrial proton−transporting ATP synthase complex
29	1e−03	3 / 20	Lymp	ROSOLOWSKI_red UP
30	2e−03	3 / 21	CC	transcription factor TFIID complex
31	3e−03	2 / 7	MMM	MACIEJ_MMML 48
32	3e−03	15 / 579	CC	nucleolus
33	3e−03	3 / 25	MF	hydrogen ion transmembrane transporter activity
34	3e−03	23 / 1095	TF	HEBENSTREIT_high expression TF
35	4e−03	15 / 595	MF	RNA binding
36	4e−03	20 / 918	Chr	Chr 17
37	4e−03	2 / 9	GSE	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX
38	4e−03	2 / 9	GSE	REACTOME_HIV1_TRANSCRIPTION_ELONGATION
39	6e−03	2 / 10	BP	peroxisome fission
40	6e−03	2 / 10	GSE	LUI_TARGETS_OF_PAX8_PPARG_FUSION



p−values

BP

Rank	p−value	#in/all	Geneset
1	4e−05	12 / 253	translation
2	5e−05	7 / 83	respiratory electron transport chain
3	6e−05	9 / 152	cellular metabolic process
4	2e−04	5 / 47	protein targeting to mitochondrion
5	4e−04	15 / 482	cellular protein metabolic process
6	5e−04	18 / 649	gene expression
7	5e−04	3 / 14	mitochondrial ATP synthesis coupled proton transport
8	6e−04	3 / 15	ATP synthesis coupled proton transport
9	7e−04	7 / 128	translational initiation
10	6e−03	2 / 10	peroxisome fission
11	6e−03	9 / 287	viral process
12	7e−03	2 / 11	positive regulation of actin cytoskeleton reorganization
13	7e−03	2 / 11	positive regulation of protein targeting to membrane
14	7e−03	4 / 66	transcription elongation from RNA polymerase II promoter
15	7e−03	3 / 35	mitochondrial electron transport, NADH to ubiquinone
16	8e−03	2 / 12	cellular aldehyde metabolic process
17	9e−03	4 / 71	response to nutrient
18	9e−03	2 / 13	vesicle fusion
19	1e−02	3 / 40	histone H3 acetylation
20	1e−02	2 / 14	formation of translation preinitiation complex

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	2 / 11	GENTLES_modul5
2	0.014	2 / 16	GENTLES_modul7
3	0.129	0 / 14	LIU_PROSTATE_CANCER_UP
4	0.158	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.355	3 / 185	SPANG_LPS−index2
6	0.362	1 / 39	ZHANG_MM up
7	0.425	1 / 48	KUIPER_MM poor survival
8	0.879	2 / 316	SPANG_BCL6−index2
9	0.985	2 / 530	Lembcke_Normal vs Adenoma
10	0.998	1 / 553	Lembcke_Colonic Inflammation
11	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1.000	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
13	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1.000	0 / 10	LIU_BREAST_CANCER
15	1.000	0 / 14	LIU_COMMON_CANCER_GENES
16	1.000	0 / 14	LIU_LIVER_CANCER
17	1.000	0 / 15	LIU_PROSTATE_CANCER_DN
18	1.000	0 / 14	WANG_ER_UP
19	1.000	0 / 9	WANG_ER_DN
20	1.000	0 / 16	WOLFER_overlap genes

CC

Rank	p−value	#in/all	Geneset
1	8e−16	52 / 1318	mitochondrion
2	4e−07	16 / 304	mitochondrial inner membrane
3	3e−06	11 / 167	ribosome
4	4e−04	3 / 13	mitochondrial respiratory chain
5	7e−04	4 / 36	mitochondrial respiratory chain complex I
6	1e−03	9 / 220	mitochondrial matrix
7	1e−03	3 / 19	mitochondrial proton−transporting ATP synthase complex
8	2e−03	3 / 21	transcription factor TFIID complex
9	3e−03	15 / 579	nucleolus
10	9e−03	2 / 13	eukaryotic 48S preinitiation complex
11	9e−03	2 / 13	integral to peroxisomal membrane
12	9e−03	2 / 13	STAGA complex
13	1e−02	2 / 14	eukaryotic 43S preinitiation complex
14	1e−02	2 / 14	transcription factor TFTC complex
15	1e−02	2 / 15	DNA−directed RNA polymerase II, core complex
16	1e−02	2 / 15	eukaryotic translation initiation factor 3 complex
17	1e−02	2 / 15	mitochondrial large ribosomal subunit
18	1e−02	2 / 16	Ada2/Gcn5/Ada3 transcription activator complex
19	2e−02	3 / 46	intermediate filament cytoskeleton
20	2e−02	2 / 18	nuclear chromosome, telomeric region

Chr

Rank	p−value	#in/all	Geneset
1	0.001	25 / 1135	Chr 19
2	0.004	20 / 918	Chr 17
3	0.082	16 / 957	Chr 11
4	0.189	10 / 633	Chr 9
5	0.195	11 / 714	Chr 6
6	0.344	10 / 743	Chr 7
7	0.353	12 / 914	Chr 3
8	0.383	7 / 519	Chr 14
9	0.451	1 / 52	Chr HSCHR6_MHC_QBL
10	0.520	12 / 1033	Chr 2
11	0.536	7 / 602	Chr 10
12	0.550	8 / 699	Chr 5
13	0.586	5 / 449	Chr 20
14	0.647	4 / 386	Chr 22
15	0.833	2 / 280	Chr 13
16	0.841	16 / 1720	Chr 1
17	0.885	1 / 187	Chr 21
18	0.931	3 / 504	Chr 15
19	0.935	6 / 866	Chr 12
20	0.974	3 / 618	Chr 4

Disease

Rank	p−value	#in/all	Geneset
1	1	1 / 375	GUDJ_psoriasis down
2	1	0 / 572	GUDJ_psoriasis up
3	1	0 / 17	BCHETNIA_EBM up
4	1	0 / 2	BCHETNIA_EBM down
5	1	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	7e−04	5 / 62	Stuehler_Proteins_up_in_STS
2	1e−01	2 / 54	willscher_GBM_proteomics_wtOnly_SpotG
3	1e−01	4 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
4	1e−01	1 / 14	VERHAAK_CL subtype
5	1e−01	1 / 14	VERHAAK_NL subtype
6	2e−01	1 / 16	willscher_GBM_STSwt_proteomics−O_UP
7	3e−01	2 / 105	willscher_GBM_proteomics_wtOnly_SpotB
8	5e−01	1 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
9	6e−01	1 / 71	willscher_GBM_Verhaak−CL_expression_H_down
10	6e−01	1 / 71	willscher_GBM_Verhaak−MES_expression_H_up
11	6e−01	1 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
12	6e−01	1 / 73	GIEZELT_GBM_WT_down_VS_mut
13	6e−01	1 / 74	GIEZELT_GBM_STS_up_VS_LTS
14	7e−01	4 / 391	Down_b
15	7e−01	3 / 328	Up
16	7e−01	1 / 117	GIEZELT_GBM_WT_up_VS_mut
17	1e+00	1 / 265	willscher_GBM_Verhaak−CL_expression_B_up
18	1e+00	1 / 265	willscher_GBM_Verhaak−MES_expression_B_up
19	1e+00	1 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
20	1e+00	1 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	3 / 9	KEGG_RNA_POLYMERASE
2	4e−04	3 / 13	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
3	4e−04	3 / 13	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
4	6e−04	3 / 15	REACTOME_MRNA_SPLICING_MINOR_PATHWAY
5	7e−04	3 / 16	YANG_BREAST_CANCER_ESR1_LASER_UP
6	4e−03	2 / 9	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX
7	4e−03	2 / 9	REACTOME_HIV1_TRANSCRIPTION_ELONGATION
8	6e−03	2 / 10	LUI_TARGETS_OF_PAX8_PPARG_FUSION
9	6e−03	2 / 10	REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
10	6e−03	2 / 10	REACTOME_HIV1_TRANSCRIPTION_INITIATION
11	6e−03	2 / 10	REACTOME_MRNA_PROCESSING
12	6e−03	2 / 10	REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INTERACTIO
13	7e−03	2 / 11	REACTOME_TRANSCRIPTION_COUPLED_NER
14	8e−03	2 / 12	KEGG_PYRIMIDINE_METABOLISM
15	8e−03	2 / 12	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_THE_
16	8e−03	2 / 12	REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED_TRANSCR
17	8e−03	2 / 12	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEC
18	8e−03	2 / 12	REACTOME_NUCLEOTIDE_EXCISION_REPAIR
19	8e−03	2 / 12	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATION
20	9e−03	2 / 13	REACTOME_FORMATION_AND_MATURATION_OF_MRNA_TRANSCRIPT

H. Tiss

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	WIRTH_Globus pallidus
2	0.8	1 / 127	WIRTH_Muscle
3	1.0	1 / 400	WIRTH_Nervous System
4	1.0	0 / 5	WIRTH_Pituitary gland
5	1.0	0 / 26	WIRTH_Pancreas
6	1.0	0 / 417	WIRTH_Immune system
7	1.0	0 / 13	WIRTH_Sec. lymphoid organs
8	1.0	0 / 12	WIRTH_Prim. lymphoid organs
9	1.0	0 / 10	WIRTH_B−cells
10	1.0	0 / 13	WIRTH_Tonsil
11	1.0	0 / 13	WIRTH_Thymus
12	1.0	0 / 12	WIRTH_Lymphocytes
13	1.0	0 / 6	WIRTH_Bone marrow
14	1.0	0 / 15	WIRTH_Telencephalon
15	1.0	0 / 13	WIRTH_Cortex cerebri
16	1.0	0 / 16	WIRTH_Hippocampus
17	1.0	0 / 13	WIRTH_Thalamus
18	1.0	0 / 15	WIRTH_Cerebellum
19	1.0	0 / 120	WIRTH_Testis
20	1.0	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	3 / 20	ROSOLOWSKI_red UP
2	0.076	3 / 86	ROSOLOWSKI_red total
3	0.206	1 / 20	DAVE_Immune response 2
4	0.258	2 / 86	ROSOLOWSKI_green UP
5	0.396	2 / 119	ROSOLOWSKI_green total
6	0.497	9 / 755	SPANG_BCR UP
7	0.684	1 / 100	ROSOLOWSKI_blue total
8	0.801	1 / 140	DAVE_BL−vs−DLBCL
9	0.958	2 / 426	SPANG_CD40 6hrs DN
10	0.958	1 / 274	SPANG_IL21 DN
11	0.978	1 / 327	SPANG_CD40 6hrs UP
12	0.997	3 / 852	SPANG_BCR DN
13	1.000	0 / 13	BENTINK_mBL UP
14	1.000	0 / 13	BENTINK_mBL DOWN
15	1.000	0 / 12	DAVE_BL_DN
16	1.000	0 / 18	DAVE_BL Inter
17	1.000	0 / 12	DAVE_BL UP
18	1.000	0 / 18	DAVE_c−myc BL UP
19	1.000	0 / 6	DAVE_MHCCII BL DN
20	1.000	0 / 22	DAVE_NFkB BL DN

MF

Rank	p−value	#in/all	Geneset
1	7e−05	9 / 153	structural constituent of ribosome
2	7e−05	5 / 38	DNA−directed RNA polymerase activity
3	2e−04	3 / 10	NADH dehydrogenase activity
4	6e−04	4 / 34	NADH dehydrogenase (ubiquinone) activity
5	3e−03	3 / 25	hydrogen ion transmembrane transporter activity
6	4e−03	15 / 595	RNA binding
7	7e−03	3 / 35	aminoacyl−tRNA ligase activity
8	1e−02	4 / 79	electron carrier activity
9	1e−02	2 / 16	proton−transporting ATPase activity, rotational mechanism
10	2e−02	2 / 18	sialyltransferase activity
11	2e−02	2 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
12	2e−02	3 / 54	translation initiation factor activity
13	4e−02	2 / 26	cytochrome−c oxidase activity
14	4e−02	2 / 27	estrogen receptor binding
15	4e−02	2 / 27	protein disulfide oxidoreductase activity
16	4e−02	2 / 29	cofactor binding
17	5e−02	11 / 549	molecular_function
18	7e−02	2 / 39	histone acetyltransferase activity
19	7e−02	2 / 39	NAD binding
20	8e−02	2 / 41	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.06	1 / 5	AGTG−521
2	0.21	1 / 20	TACG−99A−−100−−99B
3	0.23	2 / 79	TCTC−185
4	0.34	3 / 181	CCTG−214
5	0.38	1 / 41	GCTG−512−5P
6	0.39	1 / 43	GACA−339
7	0.41	1 / 46	GGTG−412
8	0.42	2 / 124	GTCT−7
9	0.43	1 / 49	TCCC−491
10	0.44	2 / 129	CTCT−520A−−525
11	0.45	1 / 52	CCAC−147
12	0.47	1 / 55	GGGG−296
13	0.50	3 / 232	ACTT−142−5P
14	0.53	1 / 65	CAGG−504
15	0.53	1 / 65	TCTG−198
16	0.58	1 / 75	GTGT−505
17	0.58	1 / 75	CCAG−331
18	0.60	1 / 80	GAGC−484
19	0.62	2 / 181	ACTG−34B
20	0.62	1 / 83	GCAC−18A−−18B

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 5	Duchenne muscular dystrophy
2	0.06	1 / 5	Pigmented adrenocortical disease, primary isolated
3	0.07	1 / 6	Muscular dystrophy
4	0.07	1 / 6	Miyoshi myopathy
5	0.09	1 / 8	Parkinson disease
6	0.11	1 / 10	Myelofibrosis, idiopathic
7	0.17	1 / 16	Cervical cancer, somatic
8	0.17	1 / 16	Myopathy, nemaline, 3
9	0.18	1 / 17	Cardiomyopathy, dilated
10	0.20	1 / 19	Multiple myeloma
11	0.22	1 / 22	Glioblastoma multiforme, somatic
12	0.23	1 / 23	Hepatocellular carcinoma
13	0.23	1 / 23	Stroke, susceptibility to
14	0.24	1 / 24	Muscular
15	0.27	1 / 27	Colorectal cancer
16	0.28	1 / 29	Melanoma and neural system tumor syndrome
17	0.31	1 / 32	Leukemia
18	0.32	1 / 34	Pancreatic cancer
19	0.32	1 / 34	Squamous cell carcinoma, head and neck
20	0.32	1 / 34	Hematological

miRNA target

Rank	p−value	#in/all	Geneset
1	1	0 / 11	let−7a
2	1	0 / 6	let−7b
3	1	0 / 4	let−7c
4	1	0 / 6	let−7d
5	1	0 / 4	let−7g
6	1	0 / 13	miR−1
7	1	0 / 5	miR−101
8	1	0 / 2	miR−101b
9	1	0 / 4	miR−106b
10	1	0 / 2	miR−107
11	1	0 / 4	miR−122
12	1	0 / 2	miR−124a
13	1	0 / 6	miR−125a
14	1	0 / 9	miR−125b
15	1	0 / 5	miR−126
16	1	0 / 2	miR−127
17	1	0 / 3	miR−128
18	1	0 / 4	miR−128b
19	1	0 / 2	miR−129
20	1	0 / 6	miR−133a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.06	2 / 35	hsa−miR−1269
2	0.08	2 / 41	hsa−miR−423−3p
3	0.08	2 / 41	hsa−miR−532−3p
4	0.09	2 / 44	hsa−miR−769−3p
5	0.10	2 / 46	hsa−miR−874
6	0.11	3 / 101	hsa−miR−574−5p
7	0.11	2 / 50	hsa−miR−940
8	0.13	4 / 169	hsa−miR−183
9	0.14	2 / 58	hsa−miR−1260
10	0.15	1 / 14	hsa−miR−452*
11	0.16	2 / 62	hsa−miR−637
12	0.17	2 / 64	hsa−miR−550
13	0.19	2 / 71	hsa−miR−331−3p
14	0.20	1 / 19	hsa−miR−554
15	0.20	1 / 19	hsa−miR−542−5p
16	0.21	2 / 75	hsa−miR−513c
17	0.21	2 / 75	hsa−miR−708
18	0.21	1 / 21	hsa−miR−1288
19	0.22	3 / 141	hsa−miR−132
20	0.22	1 / 22	hsa−miR−1250

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.003	2 / 7	MACIEJ_MMML 48
2	0.045	1 / 4	MACIEJ_MMML 40
3	0.067	1 / 6	MACIEJ_MMML 29
4	0.119	1 / 11	MACIEJ_MMML 15
5	0.149	1 / 14	MACIEJ_MMML 26
6	1.000	0 / 16	MACIEJ_MMML 1
7	1.000	0 / 13	MACIEJ_MMML 10
8	1.000	0 / 7	MACIEJ_MMML 13
9	1.000	0 / 9	MACIEJ_MMML 14
10	1.000	0 / 15	MACIEJ_MMML 16
11	1.000	0 / 2	MACIEJ_MMML 17
12	1.000	0 / 14	MACIEJ_MMML 19
13	1.000	0 / 4	MACIEJ_MMML 2
14	1.000	0 / 5	MACIEJ_MMML 20
15	1.000	0 / 15	MACIEJ_MMML 22
16	1.000	0 / 4	MACIEJ_MMML 23
17	1.000	0 / 12	MACIEJ_MMML 24
18	1.000	0 / 2	MACIEJ_MMML 27
19	1.000	0 / 5	MACIEJ_MMML 28
20	1.000	0 / 11	MACIEJ_MMML 3

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	BENTINK_ras.4
2	1.0	0 / 13	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 12	BENTINK_e2f3.1
5	1.0	0 / 11	BENTINK_e2f3.2
6	1.0	0 / 14	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−08	37 / 1233	KIM_MYC targets
2	3e−03	23 / 1095	HEBENSTREIT_high expression TF
3	2e−01	1 / 16	MYC_Protein synthesis degradation UP
4	5e−01	1 / 63	MYC_Targets UP
5	1e+00	2 / 1146	HEBENSTREIT_low expression TF
6	1e+00	0 / 14	NOWICK_TF
7	1e+00	0 / 5	MYC_TFs
8	1e+00	0 / 9	MYC_Targets DOWN
9	1e+00	0 / 4	MYC_Apoptosis UP
10	1e+00	0 / 8	MYC_Cell cycle UP
11	1e+00	0 / 2	MYC_Cell cycle DOWN
12	1e+00	0 / 4	MYC_Cell growth and proliferation UP
13	1e+00	0 / 2	MYC_Chromatin_modification UP
14	1e+00	0 / 7	MYC_DNA repair UP
15	1e+00	0 / 3	MYC_DNA replication UP
16	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
17	1e+00	0 / 20	MYC_Metabolism UP
18	1e+00	0 / 8	MYC_RNA processing binding UP
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	1	0 / 40	VAQUERIZAS_Fetal brain
2	1	0 / 44	VAQUERIZAS_Placenta
3	1	0 / 28	VAQUERIZAS_Liver
4	1	0 / 37	VAQUERIZAS_Prostate
5	1	0 / 29	VAQUERIZAS_Smooth muscle
6	1	0 / 43	VAQUERIZAS_Uterus
7	1	0 / 144	VAQUERIZAS_General
8	1	0 / 12	VAQUERIZAS_Kidney
9	1	0 / 22	VAQUERIZAS_Spinal cord
10	1	0 / 43	VAQUERIZAS_Whole brain
11	1	0 / 41	VAQUERIZAS_Thymus
12	1	0 / 39	VAQUERIZAS_Thyroid
13	1	0 / 62	VAQUERIZAS_Whole blood
14	1	0 / 7	VAQUERIZAS_Appendix
15	1	0 / 30	VAQUERIZAS_Fetal lung
16	1	0 / 62	VAQUERIZAS_Lung
17	1	0 / 16	VAQUERIZAS_Pancreas
18	1	0 / 24	VAQUERIZAS_Trachea
19	1	0 / 14	VAQUERIZAS_Fetal liver
20	1	0 / 21	VAQUERIZAS_Tonsil

Sample−Underexpression

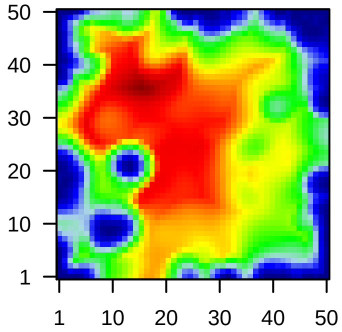
Spot Summary: f

metagenes = 26
genes = 387

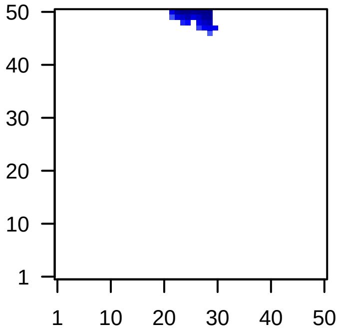
<r> metagenes = 0.91
<r> genes = 0.27
beta: r2= 5.13 / log p= −Inf

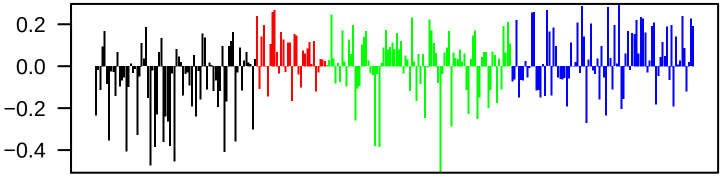
samples with spot = 17 (6.2 %)
Atypical : 12 (16.2 %)
Mesenchymal : 4 (4.7 %)
Basal : 1 (1.2 %)

Overview Map



Spot





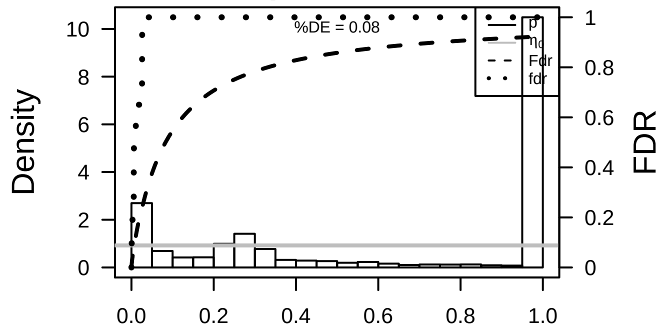
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	2353	1.43	−3.04	0.61	FOS	FBJ murine osteosarcoma viral oncogene homolog [Source:H
2	2354	2.13	−2.88	0.43	FOSB	FBJ murine osteosarcoma viral oncogene homolog B [Source
3	1843	1.8	−2.27	0.6	DUSP1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30
4	7538	1.53	−2.16	0.59	ZFP36	ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
5	1958	1.66	−2.12	0.48	EGR1	early growth response 1 [Source:HGNC Symbol;Acc:3238]
6	23645	1.71	−1.84	0.38	PPP1R15A	protein phosphatase 1, regulatory subunit 15A [Source:HGNC
7	3725	1.46	−1.81	0.53	JUN	jun proto−oncogene [Source:HGNC Symbol;Acc:6204]
8	5573	0.87	−1.75	0.34	PRKAR1A	protein kinase, cAMP−dependent, regulatory, type I, alpha [So
9	8553	1.05	−1.61	0.44	BHLHE40	basic helix−loop−helix family, member e40 [Source:HGNC Sy
10	4609	1.42	−1.59	0.59	MYC	v−myc avian myelocytomatosis viral oncogene homolog [Sou
11	10413	2.32	−1.54	0.46	YAP1	Yes−associated protein 1 [Source:HGNC Symbol;Acc:16262]
12	114908	1.77	−1.52	0.42	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:3013
13	100008589	1.84	−1.52	0.29	RNA28S5	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
14	3703	1.1	−1.5	0.41	STT3A	STT3A, subunit of the oligosaccharyltransferase complex (cat
15	150094	1.57	−1.48	0.38	SIK1	salt−inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
16	23022	1.18	−1.39	0.41	PALLD	palladin, cytoskeletal associated protein [Source:HGNC Symb
17	71	0.65	−1.37	0.45	ACTG1	actin, gamma 1 [Source:HGNC Symbol;Acc:144]
18	10950	1.54	−1.34	0.46	BTG3	BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
19	1316	1.02	−1.29	0.34	KLF6	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:2235]
20	10787	1.1	−1.28	0.77	NCKAP1	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−19	48 / 436	miRN	hsa−miR−548n
2	9e−16	34 / 269	miRN	hsa−miR−1244
3	9e−14	34 / 313	miRN	hsa−miR−559
4	2e−13	24 / 155	miRN	hsa−miR−802
5	6e−13	34 / 335	miRN	hsa−miR−142−5p
6	1e−12	27 / 217	miRN	hsa−miR−548m
7	2e−12	32 / 310	miRN	hsa−miR−340
8	4e−12	29 / 262	miRN	hsa−miR−548l
9	4e−12	31 / 300	miRN	hsa−miR−561
10	8e−12	31 / 307	miRN	hsa−miR−548c−5p
11	2e−11	22 / 157	miRN	hsa−miR−548o
12	2e−11	31 / 318	miRN	hsa−miR−590−3p
13	3e−11	31 / 324	miRN	hsa−miR−18a
14	5e−11	28 / 271	miRN	hsa−miR−548h
15	8e−11	26 / 240	miRN	hsa−miR−152
16	1e−10	39 / 517	miRN	hsa−miR−106a
17	3e−10	29 / 313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
18	3e−10	29 / 313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
19	3e−10	29 / 313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up
20	3e−10	38 / 511	miRN	hsa−miR−106b
21	4e−10	30 / 336	miRN	hsa−miR−548d−5p
22	4e−10	20 / 151	miRN	hsa−miR−429
23	6e−10	23 / 206	miRN	hsa−miR−148b
24	6e−10	22 / 189	miRN	hsa−miR−513a−3p
25	9e−10	41 / 603	miRN	hsa−miR−20a
26	9e−10	8 / 16	GSEA	NAGASHIMA_EGF_SIGNALING_UP
27	1e−09	24 / 232	miRN	ACTT−142−5P
28	1e−09	36 / 488	miRN	hsa−miR−16
29	1e−09	32 / 399	miRN	hsa−miR−519c−3p
30	1e−09	18 / 130	miRN	hsa−miR−155
31	2e−09	22 / 198	miRN	hsa−miR−33a
32	2e−09	39 / 565	miRN	hsa−miR−20b
33	2e−09	21 / 184	miRN	hsa−miR−586
34	2e−09	19 / 150	miRN	hsa−miR−200c
35	2e−09	20 / 167	miRN	hsa−miR−548g
36	3e−09	20 / 169	miRN	hsa−miR−374b
37	3e−09	30 / 368	miRN	hsa−miR−144
38	3e−09	26 / 284	miRN	hsa−miR−503
39	4e−09	28 / 328	Glio	Up
40	4e−09	19 / 155	miRN	hsa−miR−200b

p−values



BP

Rank	p−value	#in/all	Geneset
1	8e−09	21 / 198	vesicle−mediated transport
2	9e−08	24 / 290	intracellular protein transport
3	2e−06	9 / 49	ER to Golgi vesicle−mediated transport
4	2e−05	5 / 15	COPII vesicle coating
5	7e−05	11 / 113	transforming growth factor beta receptor signaling pathway
6	2e−04	4 / 13	COPI coating of Golgi vesicle
7	2e−04	13 / 170	post−translational protein modification
8	2e−04	25 / 485	negative regulation of apoptotic process
9	2e−04	4 / 14	response to light stimulus
10	3e−04	9 / 90	protein N−linked glycosylation via asparagine
11	3e−04	5 / 26	GPI anchor biosynthetic process
12	3e−04	4 / 15	long−term synaptic potentiation
13	4e−04	24 / 478	protein transport
14	4e−04	9 / 96	regulation of cell cycle
15	6e−04	4 / 17	intra−Golgi vesicle−mediated transport
16	1e−03	3 / 10	maternal placenta development
17	2e−03	3 / 11	regulation of proteasomal protein catabolic process
18	2e−03	5 / 39	response to cAMP
19	2e−03	6 / 57	endosomal transport
20	2e−03	3 / 12	regulation of acetyl−CoA biosynthetic process from pyruvate

Cancer

Rank	p−value	#in/all	Geneset
1	4e−07	18 / 185	SPANG_LPS−index2
2	2e−05	21 / 316	SPANG_BCL6−index2
3	2e−01	2 / 33	KUIPER_MM good survival
4	2e−01	0 / 15	LIU_PROSTATE_CANCER_DN
5	2e−01	1 / 10	GENTLES_modul3
6	3e−01	1 / 13	GENTLES_modul16
7	3e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	3e−01	1 / 15	GENTLES_modul1
9	3e−01	1 / 15	GENTLES_modul6
10	3e−01	1 / 15	GENTLES_modul13
11	3e−01	2 / 48	KUIPER_MM poor survival
12	3e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
13	3e−01	1 / 16	WOLFER_overlap genes
14	3e−01	1 / 16	GENTLES_modul4
15	3e−01	1 / 16	GENTLES_modul7
16	3e−01	1 / 16	GENTLES_modul10
17	8e−01	1 / 68	SHAUGHNESSY_MM high risk
18	1e+00	4 / 530	Lembcke_Normal vs Adenoma
19	1e+00	4 / 553	Lembcke_Colonic Inflammation
20	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	4e−09	43 / 686	Golgi apparatus
2	2e−06	90 / 2378	cytosol
3	3e−06	34 / 614	endoplasmic reticulum membrane
4	3e−05	26 / 455	perinuclear region of cytoplasm
5	2e−04	12 / 147	endosome
6	2e−04	5 / 24	endoplasmic reticulum−Golgi intermediate compartment membrane
7	2e−04	40 / 949	nucleoplasm
8	3e−04	23 / 436	Golgi membrane
9	3e−04	29 / 621	endoplasmic reticulum
10	1e−03	5 / 35	vesicle
11	1e−03	3 / 10	oligosaccharyltransferase complex
12	1e−03	6 / 53	endoplasmic reticulum−Golgi intermediate compartment
13	2e−03	6 / 55	proteasome complex
14	2e−03	6 / 58	ubiquitin ligase complex
15	2e−03	126 / 4310	cytoplasm
16	3e−03	134 / 4640	nucleus
17	3e−03	7 / 81	ruffle
18	3e−03	10 / 153	endosome membrane
19	4e−03	3 / 14	COPI vesicle coat
20	6e−03	8 / 116	lamellipodium

Chr

Rank	p−value	#in/all	Geneset
1	4e−05	19 / 280	Chr 13
2	3e−03	26 / 618	Chr 4
3	3e−03	36 / 957	Chr 11
4	8e−03	27 / 699	Chr 5
5	8e−03	24 / 602	Chr 10
6	5e−02	18 / 504	Chr 15
7	7e−02	8 / 187	Chr 21
8	9e−02	31 / 1033	Chr 2
9	1e−01	22 / 714	Chr 6
10	2e−01	26 / 914	Chr 3
11	3e−01	15 / 534	Chr 8
12	4e−01	16 / 630	Chr X
13	5e−01	6 / 232	Chr 18
14	8e−01	10 / 519	Chr 14
15	8e−01	36 / 1720	Chr 1
16	9e−01	16 / 866	Chr 12
17	9e−01	11 / 633	Chr 9
18	1e+00	10 / 743	Chr 7
19	1e+00	8 / 717	Chr 16
20	1e+00	3 / 449	Chr 20

Disease

Rank	p−value	#in/all	Geneset
1	0.5	1 / 26	BCHETNIA_EBM−DM up
2	0.9	10 / 572	GUDJ_psoriasis up
3	1.0	3 / 375	GUDJ_psoriasis down
4	1.0	0 / 17	BCHETNIA_EBM up
5	1.0	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−10	29 / 313	willscher_GBM_Verhaak−CL_expression_D_up
2	3e−10	29 / 313	willscher_GBM_Verhaak−MES_expression_D_down
3	3e−10	29 / 313	willscher_GBM_Verhaak−PNwt_expression_D_up
4	4e−09	28 / 328	Up
5	5e−05	9 / 73	GIEZELT_GBM_WT_down_VS_mut
6	2e−04	8 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
7	9e−04	6 / 49	Vishal_subnetwork signature of survival in GBM
8	6e−03	3 / 16	willscher_GBM_STSwt_proteomics−O_UP
9	7e−03	10 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
10	1e−02	4 / 37	willscher_GBM_proteomics_wtOnly_SpotH
11	3e−02	2 / 12	willscher_ GBM_LTSwt_proteomics−C_UP
12	6e−02	4 / 62	Stuehler_Proteins_up_in_STS
13	1e−01	5 / 105	willscher_GBM_proteomics_wtOnly_SpotB
14	1e−01	5 / 117	GIEZELT_GBM_WT_up_VS_mut
15	2e−01	1 / 7	Donson−adaptive−immunity−associated with LTS in HGA
16	2e−01	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expressio
17	2e−01	2 / 33	willscher_GBM_proteomics_wtOnly_SpotC
18	2e−01	1 / 11	willscher_GBM_Verhaak−CL_expression_M_down
19	2e−01	1 / 11	willscher_GBM_Verhaak−MES_expression_M_down
20	2e−01	1 / 11	willscher_GBM_Verhaak−PNmut_expression_M_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−10	8 / 16	NAGASHIMA_EGF_SIGNALING_UP
2	3e−08	7 / 16	AMIT_SERUM_RESPONSE_40_MCF10A
3	7e−07	6 / 15	AMIT_EGF_RESPONSE_40_HELA
4	1e−06	6 / 16	AMIT_DELAYED_EARLY_GENES
5	2e−06	5 / 10	CHASSOT_SKIN_WOUND
6	2e−05	5 / 15	SEIDEN_ONCOGENESIS_BY_MET
7	2e−05	5 / 16	CAFFAREL_RESPONSE_TO_THC_UP
8	2e−05	5 / 16	AMIT_EGF_RESPONSE_40_MCF10A
9	2e−05	5 / 16	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
10	2e−04	4 / 14	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
11	2e−04	4 / 14	BIOCARTA_IL2_PATHWAY
12	3e−04	4 / 15	DIRMEIER_LMP1_RESPONSE_EARLY
13	4e−04	4 / 16	AMIT_EGF_RESPONSE_60_MCF10A
14	4e−04	4 / 16	DORSAM_HOXA9_TARGETS_DN
15	4e−04	4 / 16	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
16	4e−04	4 / 16	JI_RESPONSE_TO_FSH_DN
17	4e−04	4 / 16	BIOCARTA_ETS_PATHWAY
18	1e−03	3 / 9	DISTECHE_ESCAPED_FROM_X_INACTIVATION
19	1e−03	3 / 10	BIOCARTA_CDMAC_PATHWAY
20	2e−03	3 / 11	AMIT_EGF_RESPONSE_20_HELA

H. Tiss

Rank	p−value	#in/all	Geneset
1	0.02	17 / 417	WIRTH_Immune system
2	0.04	2 / 13	WIRTH_Sec. lymphoid organs
3	0.21	1 / 10	WIRTH_B−cells
4	1.00	1 / 400	WIRTH_Nervous System
5	1.00	0 / 5	WIRTH_Pituitary gland
6	1.00	0 / 26	WIRTH_Pancreas
7	1.00	0 / 12	WIRTH_Prim. lymphoid organs
8	1.00	0 / 13	WIRTH_Tonsil
9	1.00	0 / 13	WIRTH_Thymus
10	1.00	0 / 12	WIRTH_Lymphocytes
11	1.00	0 / 6	WIRTH_Bone marrow
12	1.00	0 / 14	WIRTH_Globus pallidus
13	1.00	0 / 15	WIRTH_Telencephalon
14	1.00	0 / 13	WIRTH_Cortex cerebri
15	1.00	0 / 16	WIRTH_Hippocampus
16	1.00	0 / 13	WIRTH_Thalamus
17	1.00	0 / 15	WIRTH_Cerebellum
18	1.00	0 / 120	WIRTH_Testis
19	1.00	0 / 50	WIRTH_Homeostasis
20	1.00	0 / 62	WIRTH_Liver

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−08	48 / 852	SPANG_BCR DN
2	2e−03	8 / 100	ROSOLOWSKI_blue total
3	5e−03	14 / 274	SPANG_IL21 DN
4	1e−02	28 / 755	SPANG_BCR UP
5	4e−02	4 / 54	SPANG_BAFF 9hrs DN
6	4e−02	16 / 426	SPANG_CD40 6hrs DN
7	5e−02	5 / 86	ROSOLOWSKI_red total
8	8e−02	4 / 69	SPANG_LPS 6hrs DN
9	9e−02	1 / 4	MASCQUE_mBL DOWN
10	1e−01	10 / 291	SPANG_IL21 UP
11	2e−01	1 / 8	MASCQUE_GCB UP
12	2e−01	2 / 38	ROSOLOWSKI_blue DOWN
13	2e−01	5 / 140	DAVE_BL−vs−DLBCL
14	3e−01	1 / 13	BENTINK_mBL DOWN
15	3e−01	4 / 118	SPANG_LPS 6hrs UP
16	3e−01	1 / 18	DAVE_c−myc BL UP
17	4e−01	1 / 20	ROSOLOWSKI_red UP
18	4e−01	1 / 22	DAVE_NFkB BL DN
19	4e−01	1 / 24	SPANG_BAFF 9hrs UP
20	5e−01	1 / 28	DAVE_Immune response 1

MF

Rank	p−value	#in/all	Geneset
1	4e−08	240 / 8023	protein binding
2	5e−05	8 / 57	protein transporter activity
3	7e−04	5 / 31	RNA polymerase II activating transcription factor binding
4	8e−04	6 / 48	phosphoprotein phosphatase activity
5	1e−03	3 / 10	lamin binding
6	3e−03	14 / 252	transcription factor binding
7	3e−03	15 / 288	protein kinase binding
8	5e−03	17 / 361	binding
9	9e−03	4 / 35	guanyl nucleotide binding
10	9e−03	3 / 19	R−SMAD binding
11	1e−02	5 / 57	ubiquitin thiolesterase activity
12	1e−02	5 / 59	protein phosphatase binding
13	1e−02	11 / 216	transcription coactivator activity
14	1e−02	3 / 22	polyubiquitin binding
15	1e−02	44 / 1344	ATP binding
16	2e−02	4 / 41	kinase binding
17	2e−02	4 / 42	protein serine/threonine phosphatase activity
18	2e−02	3 / 24	repressing transcription factor binding
19	2e−02	5 / 66	flavin adenine dinucleotide binding
20	2e−02	9 / 172	magnesium ion binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	1e−09	24 / 232	ACTT−142−5P
2	3e−06	24 / 354	CTTT−524
3	6e−06	12 / 104	ACTG−139
4	4e−05	14 / 168	ATAC−144
5	8e−05	16 / 225	TATT−374
6	1e−04	9 / 81	AACT−223
7	1e−04	17 / 257	TTTG−520D
8	1e−04	13 / 165	TTTG−518A−2
9	1e−04	22 / 391	TGAA−181A−−181B−−181C−−181D
10	2e−04	16 / 240	ACAT−1−−206
11	2e−04	10 / 107	AACA−409−3P
12	4e−04	11 / 136	GCAT−105
13	5e−04	16 / 261	TTGC−182
14	5e−04	9 / 99	GTGC−507
15	6e−04	15 / 240	CAGT−141−−200A
16	7e−04	23 / 470	GCAC−17−5P−−20A−−106A−−106B−−20B−−519D
17	8e−04	10 / 126	ATGT−494
18	8e−04	5 / 32	CTCT−368
19	1e−03	6 / 52	CCAC−147
20	2e−03	22 / 467	TGTT−30A−5P−−30C−−30D−−30B−−30E−5P

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	Polycythemia vera
2	0.05	1 / 2	Cardiomyopathy, idiopathic dilated
3	0.07	1 / 3	Thyroid carcinoma, papillary
4	0.09	1 / 4	Thyroid carcinoma, follicular
5	0.11	1 / 5	Duchenne muscular dystrophy
6	0.11	1 / 5	Gastroesphageal reflux
7	0.13	1 / 6	Muscular dystrophy
8	0.13	1 / 6	Miyoshi myopathy
9	0.21	1 / 10	Esophageal cancer
10	0.23	1 / 11	Alzheimer disease, susceptibility to
11	0.23	1 / 11	Melanoma, cutaneous malignant, 2
12	0.25	1 / 12	Bladder cancer
13	0.25	1 / 12	Neuroblastoma
14	0.30	1 / 15	Gastric cancer
15	0.32	1 / 16	Myopathy, nemaline, 3
16	0.33	1 / 17	Cardiomyopathy, dilated
17	0.36	1 / 19	Multiple myeloma
18	0.39	1 / 21	Gastrointestinal
19	0.41	1 / 22	Glioblastoma multiforme, somatic
20	0.42	1 / 23	Hepatocellular carcinoma

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	2 / 3	miR−214
2	0.002	2 / 3	miR−373
3	0.005	2 / 5	miR−101
4	0.026	2 / 11	let−7a
5	0.046	1 / 2	miR−153
6	0.046	1 / 2	miR−328
7	0.046	1 / 2	miR−659
8	0.069	1 / 3	miR−19a
9	0.069	1 / 3	miR−223
10	0.090	1 / 4	miR−122
11	0.090	1 / 4	miR−133b
12	0.090	1 / 4	miR−195
13	0.090	1 / 4	miR−204
14	0.090	1 / 4	miR−34b
15	0.090	1 / 4	miR−34c
16	0.090	1 / 4	miR−7
17	0.112	1 / 5	miR−200a
18	0.112	1 / 5	miR−200b
19	0.112	1 / 5	miR−320
20	0.112	1 / 5	miR−372

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	3e−19	48 / 436	hsa−miR−548n
2	9e−16	34 / 269	hsa−miR−1244
3	9e−14	34 / 313	hsa−miR−559
4	2e−13	24 / 155	hsa−miR−802
5	6e−13	34 / 335	hsa−miR−142−5p
6	1e−12	27 / 217	hsa−miR−548m
7	2e−12	32 / 310	hsa−miR−340
8	4e−12	29 / 262	hsa−miR−548l
9	4e−12	31 / 300	hsa−miR−561
10	8e−12	31 / 307	hsa−miR−548c−5p
11	2e−11	22 / 157	hsa−miR−548o
12	2e−11	31 / 318	hsa−miR−590−3p
13	3e−11	31 / 324	hsa−miR−18a
14	5e−11	28 / 271	hsa−miR−548h
15	8e−11	26 / 240	hsa−miR−152
16	1e−10	39 / 517	hsa−miR−106a
17	3e−10	38 / 511	hsa−miR−106b
18	4e−10	30 / 336	hsa−miR−548d−5p
19	4e−10	20 / 151	hsa−miR−429
20	6e−10	23 / 206	hsa−miR−148b

MMML CGS

Rank	p−value	#in/all	Geneset
1	4e−07	5 / 8	MACIEJ_MMML 50
2	3e−03	3 / 13	MACIEJ_MMML 10
3	5e−03	2 / 5	MACIEJ_MMML 28
4	4e−02	2 / 14	MACIEJ_MMML 30
5	2e−01	1 / 7	MACIEJ_MMML 48
6	2e−01	1 / 11	MACIEJ_MMML 31
7	3e−01	1 / 15	MACIEJ_MMML 22
8	1e+00	0 / 16	MACIEJ_MMML 1
9	1e+00	0 / 7	MACIEJ_MMML 13
10	1e+00	0 / 9	MACIEJ_MMML 14
11	1e+00	0 / 11	MACIEJ_MMML 15
12	1e+00	0 / 15	MACIEJ_MMML 16
13	1e+00	0 / 2	MACIEJ_MMML 17
14	1e+00	0 / 14	MACIEJ_MMML 19
15	1e+00	0 / 4	MACIEJ_MMML 2
16	1e+00	0 / 5	MACIEJ_MMML 20
17	1e+00	0 / 4	MACIEJ_MMML 23
18	1e+00	0 / 12	MACIEJ_MMML 24
19	1e+00	0 / 14	MACIEJ_MMML 26
20	1e+00	0 / 2	MACIEJ_MMML 27

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	6e−04	43 / 1095	HEBENSTREIT_high expression TF
2	9e−03	42 / 1233	KIM_MYC targets
3	5e−02	1 / 2	MYC_Signal transduction UP
4	1e−01	1 / 5	MYC_TF and cofactors
5	2e−01	1 / 7	MYC_DNA repair UP
6	2e−01	3 / 63	MYC_Targets UP
7	2e−01	1 / 9	MYC_Targets DOWN
8	3e−01	1 / 14	NOWICK_TF
9	3e−01	1 / 16	MYC_Protein synthesis degradation UP
10	1e+00	4 / 1146	HEBENSTREIT_low expression TF
11	1e+00	0 / 5	MYC_TFs
12	1e+00	0 / 4	MYC_Apoptosis UP
13	1e+00	0 / 8	MYC_Cell cycle UP
14	1e+00	0 / 2	MYC_Cell cycle DOWN
15	1e+00	0 / 4	MYC_Cell growth and proliferation UP
16	1e+00	0 / 2	MYC_Chromatin_modification UP
17	1e+00	0 / 3	MYC_DNA replication UP
18	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
19	1e+00	0 / 20	MYC_Metabolism UP
20	1e+00	0 / 8	MYC_RNA processing binding UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	1e−06	6 / 16	VAQUERIZAS_Pancreas
2	2e−04	5 / 24	VAQUERIZAS_Trachea
3	6e−04	7 / 62	VAQUERIZAS_Lung
4	2e−03	5 / 39	VAQUERIZAS_Thyroid
5	3e−03	6 / 62	VAQUERIZAS_Whole blood
6	3e−02	2 / 12	VAQUERIZAS_Kidney
7	6e−02	3 / 37	VAQUERIZAS_Prostate
8	8e−02	2 / 20	VAQUERIZAS_Adrenal cortex
9	2e−01	1 / 7	VAQUERIZAS_Appendix
10	2e−01	2 / 30	VAQUERIZAS_Fetal lung
11	2e−01	2 / 41	VAQUERIZAS_Thymus
12	3e−01	1 / 13	VAQUERIZAS_Skin
13	3e−01	2 / 44	VAQUERIZAS_Placenta
14	3e−01	1 / 15	VAQUERIZAS_Adrenal gland
15	4e−01	1 / 19	VAQUERIZAS_Pituitary
16	4e−01	1 / 20	VAQUERIZAS_Bone marrow
17	5e−01	1 / 29	VAQUERIZAS_Lymph node
18	6e−01	1 / 38	VAQUERIZAS_Testis
19	6e−01	1 / 43	VAQUERIZAS_Uterus
20	6e−01	1 / 43	VAQUERIZAS_Whole brain

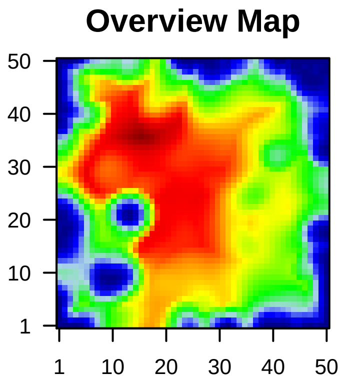
Sample−Underexpression

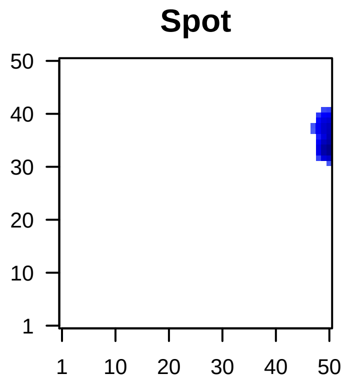
Spot Summary: g

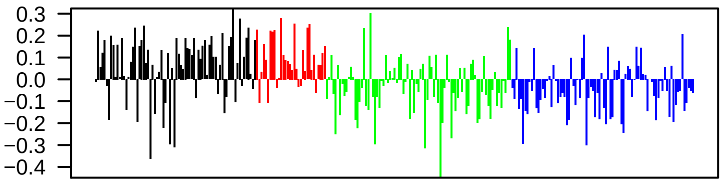
metagenes = 32
genes = 437

<r> metagenes = 0.9
<r> genes = 0.24
beta: r2= 4.09 / log p= −Inf

samples with spot = 9 (3.3 %)
Atypical : 3 (4.1 %)
Mesenchymal : 4 (4.7 %)
Basal : 2 (2.4 %)


Overview Map


Spot

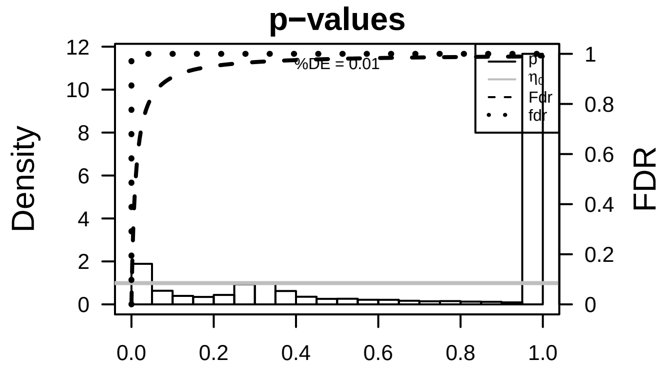


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	64207	1.94	−2.13	0.27	IRF2BPL	interferon regulatory factor 2 binding protein−like [Source:HG
2	4089	0.95	−1.52	0.69	SMAD4	SMAD family member 4 [Source:HGNC Symbol;Acc:6770]
3	27075	1.78	−1.45	0.37	TSPAN13	tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
4	3187	0.89	−1.41	0.53	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HG
5	23215	1.25	−1.4	0.57	PRRC2C	proline−rich coiled−coil 2C [Source:HGNC Symbol;Acc:2490
6	51765	1.13	−1.35	0.52	MST4	Serine/threonine−protein kinase MST4 [Source:UniProtKB/S
7	1429	1.26	−1.33	0.44	CRYZ	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
8	85460	1.13	−1.28	0.39	ZNF518B	zinc finger protein 518B [Source:HGNC Symbol;Acc:29365]
9	9908	1.07	−1.25	0.42	G3BP2	GTPase activating protein (SH3 domain) binding protein 2 [S
10	6146	1.05	−1.25	0.65	RPL22	ribosomal protein L22 [Source:HGNC Symbol;Acc:10315]
11	57088	1.41	−1.2	0.24	PLSCR4	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649
12	5612	1.08	−1.18	0.4	PRKRIR	protein−kinase, interferon−inducible double stranded RNA de
13	60481	1.39	−1.17	0.5	ELOVL5	ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213
14	51320	0.8	−1.15	0.61	MEX3C	mex−3 RNA binding family member C [Source:HGNC Symbo
15	4200	0.89	−1.12	0.48	ME2	malic enzyme 2, NAD(+)−dependent, mitochondrial [Source:
16	64083	0.73	−1.11	0.61	GOLPH3	golgi phosphoprotein 3 (coat−protein) [Source:HGNC Symbol
17	4254	1.49	−1.1	0.5	KITLG	KIT ligand [Source:HGNC Symbol;Acc:6343]
18	961	0.99	−1.1	0.31	CD47	CD47 molecule [Source:HGNC Symbol;Acc:1682]
19	55958	0.8	−1.09	0.47	KLHL9	kelch−like family member 9 [Source:HGNC Symbol;Acc:1873
20	64393	0.8	−1.08	0.44	ZMAT3	zinc finger, matrin−type 3 [Source:HGNC Symbol;Acc:29983]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−11	46 / 595	MF	RNA binding
2	3e−10	184 / 4640	CC	nucleus
3	4e−10	40 / 495	miRN	hsa−miR−103
4	7e−10	36 / 421	miRN	hsa−let−7b
5	7e−10	21 / 153	miRN	hsa−miR−450b−5p
6	2e−09	36 / 433	miRN	hsa−miR−19b
7	2e−09	21 / 163	BP	mRNA splicing, via spliceosome
8	3e−09	24 / 215	miRN	hsa−miR−203
9	5e−09	38 / 494	miRN	hsa−miR−107
10	8e−09	30 / 336	miRN	hsa−miR−548b−5p
11	9e−09	16 / 100	miRN	hsa−miR−544
12	9e−09	28 / 300	miRN	hsa−miR−548c−3p
13	1e−08	25 / 246	miRN	hsa−miR−524−5p
14	2e−08	26 / 271	miRN	hsa−miR−101
15	2e−08	33 / 412	miRN	hsa−miR−372
16	2e−08	17 / 121	miRN	hsa−miR−543
17	3e−08	20 / 169	miRN	hsa−miR−580
18	3e−08	28 / 315	miRN	hsa−miR−30e
19	3e−08	34 / 440	miRN	hsa−miR−19a
20	3e−08	35 / 463	miRN	hsa−miR−301a
21	3e−08	20 / 171	miRN	hsa−miR−369−3p
22	3e−08	55 / 940	MF	nucleic acid binding
23	3e−08	20 / 172	miRN	hsa−miR−607
24	3e−08	21 / 189	miRN	hsa−miR−1283
25	3e−08	26 / 280	miRN	hsa−miR−320a
26	4e−08	27 / 300	miRN	hsa−miR−561
27	4e−08	37 / 512	miRN	hsa−miR−15a
28	4e−08	27 / 303	miRN	hsa−miR−302b
29	5e−08	38 / 538	miRN	hsa−miR−17
30	5e−08	37 / 517	miRN	hsa−miR−106a
31	5e−08	16 / 113	miRN	hsa−miR−507
32	5e−08	23 / 229	BP	RNA splicing
33	5e−08	25 / 267	miRN	hsa−miR−577
34	7e−08	15 / 101	miRN	hsa−miR−410
35	7e−08	21 / 197	miRN	hsa−miR−568
36	8e−08	27 / 311	miRN	hsa−miR−98
37	9e−08	26 / 293	miRN	hsa−miR−186
38	9e−08	31 / 396	miRN	hsa−miR−301b
39	1e−07	28 / 336	miRN	hsa−miR−548d−5p
40	1e−07	16 / 119	miRN	hsa−miR−579


p−values

BP

Rank	p−value	#in/all	Geneset
1	2e−09	21 / 163	mRNA splicing, via spliceosome
2	5e−08	23 / 229	RNA splicing
3	2e−07	19 / 174	mRNA processing
4	1e−06	9 / 41	mRNA 3'−end processing
5	2e−06	9 / 44	termination of RNA polymerase II transcription
6	1e−04	66 / 1574	transcription, DNA−templated
7	1e−04	34 / 649	gene expression
8	4e−04	5 / 25	nuclear−transcribed mRNA poly(A) tail shortening
9	5e−04	4 / 15	mRNA splice site selection
10	1e−03	7 / 61	mRNA export from nucleus
11	2e−03	4 / 20	protein secretion
12	2e−03	16 / 262	protein ubiquitination
13	2e−03	6 / 50	BMP signaling pathway
14	2e−03	4 / 21	regulation of RNA splicing
15	3e−03	4 / 23	mRNA polyadenylation
16	4e−03	17 / 306	regulation of transcription from RNA polymerase II promoter
17	4e−03	3 / 13	vesicle organization
18	7e−03	10 / 149	ubiquitin−dependent protein catabolic process
19	7e−03	3 / 15	negative regulation of mRNA splicing, via spliceosome
20	7e−03	3 / 15	positive regulation of cell cycle arrest

Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	4 / 16	GENTLES_modul14
2	4e−02	4 / 48	KUIPER_MM poor survival
3	7e−02	2 / 16	WOLFER_overlap genes
4	7e−02	2 / 16	GENTLES_modul4
5	8e−02	3 / 39	ZHANG_MM up
6	1e−01	8 / 185	SPANG_LPS−index2
7	2e−01	1 / 9	WANG_ER_DN
8	2e−01	2 / 33	KUIPER_MM good survival
9	2e−01	1 / 10	LIU_BREAST_CANCER
10	3e−01	1 / 14	LIU_PROSTATE_CANCER_UP
11	3e−01	1 / 13	GENTLES_modul12
12	3e−01	1 / 13	GENTLES_modul16
13	3e−01	1 / 13	GENTLES_modul18
14	3e−01	1 / 14	WANG_ER_UP
15	3e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	3e−01	1 / 15	BEN−PORATH_UP
17	4e−01	1 / 16	GENTLES_modul7
18	4e−01	1 / 16	GENTLES_modul11
19	5e−01	9 / 316	SPANG_BCL6−index2
20	8e−01	1 / 68	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	3e−10	184 / 4640	nucleus
2	3e−05	10 / 76	catalytic step 2 spliceosome
3	4e−05	11 / 93	spliceosomal complex
4	3e−04	11 / 118	ribonucleoprotein complex
5	3e−04	13 / 159	nuclear speck
6	1e−03	21 / 380	intracellular membrane−bounded organelle
7	5e−03	39 / 949	nucleoplasm
8	5e−03	4 / 27	cytoplasmic stress granule
9	6e−03	7 / 81	nuclear matrix
10	7e−03	4 / 29	nuclear inner membrane
11	1e−02	25 / 579	nucleolus
12	1e−02	3 / 19	calcium channel complex
13	2e−02	135 / 4310	cytoplasm
14	2e−02	3 / 21	transcription factor TFIID complex
15	2e−02	6 / 80	chromatin
16	2e−02	7 / 104	midbody
17	3e−02	3 / 24	Cul3−RING ubiquitin ligase complex
18	3e−02	2 / 10	nBAF complex
19	3e−02	3 / 26	condensed chromosome
20	3e−02	2 / 11	npBAF complex

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	20 / 232	Chr 18
2	1e−03	33 / 699	Chr 5
3	4e−02	37 / 1033	Chr 2
4	7e−02	12 / 280	Chr 13
5	1e−01	31 / 914	Chr 3
6	1e−01	25 / 714	Chr 6
7	1e−01	25 / 743	Chr 7
8	1e−01	53 / 1720	Chr 1
9	2e−01	2 / 34	Chr Y
10	3e−01	19 / 618	Chr 4
11	5e−01	24 / 866	Chr 12
12	5e−01	11 / 386	Chr 22
13	5e−01	15 / 534	Chr 8
14	5e−01	14 / 504	Chr 15
15	6e−01	5 / 187	Chr 21
16	6e−01	15 / 602	Chr 10
17	7e−01	11 / 449	Chr 20
18	7e−01	15 / 630	Chr X
19	9e−01	19 / 918	Chr 17
20	9e−01	9 / 519	Chr 14

Disease

Rank	p−value	#in/all	Geneset
1	0.8	8 / 375	GUDJ_psoriasis down
2	1.0	3 / 572	GUDJ_psoriasis up
3	1.0	0 / 17	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1e−06	25 / 313	willscher_GBM_Verhaak−CL_expression_D_up
2	1e−06	25 / 313	willscher_GBM_Verhaak−MES_expression_D_down
3	1e−06	25 / 313	willscher_GBM_Verhaak−PNwt_expression_D_up
4	8e−06	24 / 328	Up
5	1e−02	6 / 71	willscher_GBM_Verhaak−CL_expression_H_down
6	1e−02	6 / 71	willscher_GBM_Verhaak−MES_expression_H_up
7	1e−02	6 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
8	6e−02	4 / 54	willscher_GBM_proteomics_wtOnly_SpotG
9	8e−02	8 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
10	2e−01	2 / 28	Barbus_GBM_STS_vs._LTS
11	2e−01	1 / 10	willscher_GBM_LTSmut_proteomics−A_UP
12	3e−01	1 / 11	neurons_glio
13	3e−01	3 / 71	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	3e−01	1 / 14	VERHAAK_NL subtype
15	3e−01	1 / 15	VERHAAK_PN subtype
16	6e−01	2 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
17	6e−01	1 / 32	Donson−Misc immune function−associated with LTS in HGA
18	6e−01	2 / 73	GIEZELT_GBM_WT_down_VS_mut
19	6e−01	1 / 33	willscher_GBM_proteomics_wtOnly_SpotC
20	6e−01	1 / 35	Colman_survival_associated

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	5 / 14	REACTOME_MRNA_3_END_PROCESSING
2	5e−04	4 / 15	OUILLETTE_CLL_13Q14_DELETION_UP
3	5e−04	4 / 15	GENTILE_UV_RESPONSE_CLUSTER_D2
4	1e−03	3 / 9	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_DN
5	3e−03	3 / 11	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELL
6	3e−03	3 / 12	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_MAGENTA_
7	3e−03	3 / 12	CHEOK_RESPONSE_TO_MERCAPTOPURINE_UP
8	4e−03	3 / 13	KEGG_O_GLYCAN_BIOSYNTHESIS
9	5e−03	3 / 14	BIOCARTA_TEL_PATHWAY
10	7e−03	3 / 15	SEIDEN_ONCOGENESIS_BY_MET
11	7e−03	3 / 15	ONDER_CDH1_TARGETS_1_DN
12	7e−03	3 / 15	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN
13	7e−03	3 / 15	DE_YY1_TARGETS_DN
14	7e−03	3 / 15	EHLERS_ANEUPLOIDY_UP
15	7e−03	3 / 15	BIOCARTA_CTCF_PATHWAY
16	8e−03	3 / 16	CHOI_ATL_CHRONIC_VS_ACUTE_DN
17	8e−03	3 / 16	YANG_BREAST_CANCER_ESR1_BULK_UP
18	8e−03	3 / 16	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_DN
19	8e−03	3 / 16	CROMER_METASTASIS_UP
20	8e−03	3 / 16	MOOTHA_GLYCOGEN_METABOLISM

H. Tiss

Rank	p−value	#in/all	Geneset
1	0.05	2 / 13	WIRTH_Thyroid gland
2	0.06	17 / 417	WIRTH_Immune system
3	0.24	1 / 10	WIRTH_B−cells
4	0.28	1 / 12	WIRTH_Lymphocytes
5	0.30	1 / 13	WIRTH_Cortex cerebri
6	0.33	1 / 15	WIRTH_Cerebellum
7	0.98	5 / 400	WIRTH_Nervous System
8	1.00	0 / 5	WIRTH_Pituitary gland
9	1.00	0 / 26	WIRTH_Pancreas
10	1.00	0 / 13	WIRTH_Sec. lymphoid organs
11	1.00	0 / 12	WIRTH_Prim. lymphoid organs
12	1.00	0 / 13	WIRTH_Tonsil
13	1.00	0 / 13	WIRTH_Thymus
14	1.00	0 / 6	WIRTH_Bone marrow
15	1.00	0 / 14	WIRTH_Globus pallidus
16	1.00	0 / 15	WIRTH_Telencephalon
17	1.00	0 / 16	WIRTH_Hippocampus
18	1.00	0 / 13	WIRTH_Thalamus
19	1.00	0 / 120	WIRTH_Testis
20	1.00	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.01	34 / 852	SPANG_BCR DN
2	0.02	14 / 291	SPANG_IL21 UP
3	0.03	13 / 275	ZHANG_DLBCL mutated
4	0.06	17 / 426	SPANG_CD40 6hrs DN
5	0.07	27 / 755	SPANG_BCR UP
6	0.08	2 / 18	DAVE_c−myc BL UP
7	0.10	6 / 118	SPANG_LPS 6hrs UP
8	0.10	2 / 20	ROSOLOWSKI_red UP
9	0.17	3 / 54	SPANG_BAFF 9hrs DN
10	0.19	1 / 8	MASCQUE_GCB UP
11	0.20	4 / 86	ROSOLOWSKI_green UP
12	0.21	5 / 119	ROSOLOWSKI_green total
13	0.26	11 / 327	SPANG_CD40 6hrs UP
14	0.28	1 / 12	DAVE_BL_DN
15	0.28	3 / 69	SPANG_LPS 6hrs DN
16	0.32	1 / 14	WRIGHT_GCB UP
17	0.32	5 / 140	DAVE_BL−vs−DLBCL
18	0.39	1 / 18	DAVE_BL Inter
19	0.40	3 / 86	ROSOLOWSKI_red total
20	0.48	1 / 24	SPANG_BAFF 9hrs UP

MF

Rank	p−value	#in/all	Geneset
1	9e−11	46 / 595	RNA binding
2	3e−08	55 / 940	nucleic acid binding
3	4e−05	74 / 1749	DNA binding
4	2e−04	73 / 1820	metal ion binding
5	5e−04	27 / 504	nucleotide binding
6	7e−04	5 / 27	nucleotidyltransferase activity
7	3e−03	3 / 11	AU−rich element binding
8	3e−03	3 / 11	telomeric DNA binding
9	4e−03	3 / 13	core promoter proximal region sequence−specific DNA binding
10	5e−03	14 / 238	ubiquitin−protein ligase activity
11	5e−03	17 / 318	chromatin binding
12	5e−03	13 / 216	transcription coactivator activity
13	7e−03	5 / 46	p53 binding
14	8e−03	4 / 30	RNA polymerase II transcription factor binding
15	1e−02	5 / 51	damaged DNA binding
16	2e−02	4 / 39	calcium−dependent protein binding
17	2e−02	5 / 62	single−stranded DNA binding
18	3e−02	2 / 10	co−SMAD binding
19	3e−02	2 / 10	NADPH binding
20	3e−02	2 / 10	poly(A) RNA binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	1e−06	25 / 314	TTGC−130A−−301−−130B
2	3e−06	16 / 151	GTAT−369−3P
3	1e−05	25 / 362	CAGT−200B−−200C−−429
4	2e−05	27 / 415	TTTG−19A−−19B
5	4e−05	8 / 49	GTAT−154−−487
6	5e−05	8 / 50	TACA−508
7	8e−05	23 / 354	CTTT−524
8	8e−05	16 / 198	ATGT−302C
9	9e−05	14 / 158	ATAT−448
10	1e−04	8 / 56	ATCT−31
11	1e−04	14 / 165	TTTG−518A−2
12	1e−04	24 / 391	TGAA−181A−−181B−−181C−−181D
13	1e−04	16 / 208	ATTC−186
14	1e−04	12 / 127	GACT−212−−132
15	2e−04	15 / 189	AACT−145
16	2e−04	10 / 95	GGGC−365
17	2e−04	11 / 114	TGTA−485−3P
18	3e−04	22 / 358	TGCA−519C−−519B−−519A
19	3e−04	9 / 80	TGAG−216
20	3e−04	10 / 99	GTGC−507

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	miR−98
2	0.08	1 / 3	miR−197
3	0.10	1 / 4	let−7c
4	0.10	1 / 4	let−7g
5	0.15	1 / 6	let−7b
6	0.15	1 / 6	let−7d
7	0.15	1 / 6	miR−26a
8	0.19	1 / 8	miR−9
9	0.22	1 / 9	miR−125b
10	0.22	1 / 9	miR−24
11	0.26	1 / 11	let−7a
12	0.30	1 / 13	miR−34a
13	0.50	1 / 26	miR−21
14	1.00	0 / 13	miR−1
15	1.00	0 / 5	miR−101
16	1.00	0 / 2	miR−101b
17	1.00	0 / 4	miR−106b
18	1.00	0 / 2	miR−107
19	1.00	0 / 4	miR−122
20	1.00	0 / 2	miR−124a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	4e−10	40 / 495	hsa−miR−103
2	7e−10	36 / 421	hsa−let−7b
3	7e−10	21 / 153	hsa−miR−450b−5p
4	2e−09	36 / 433	hsa−miR−19b
5	3e−09	24 / 215	hsa−miR−203
6	5e−09	38 / 494	hsa−miR−107
7	8e−09	30 / 336	hsa−miR−548b−5p
8	9e−09	16 / 100	hsa−miR−544
9	9e−09	28 / 300	hsa−miR−548c−3p
10	1e−08	25 / 246	hsa−miR−524−5p
11	2e−08	26 / 271	hsa−miR−101
12	2e−08	33 / 412	hsa−miR−372
13	2e−08	17 / 121	hsa−miR−543
14	3e−08	20 / 169	hsa−miR−580
15	3e−08	28 / 315	hsa−miR−30e
16	3e−08	34 / 440	hsa−miR−19a
17	3e−08	35 / 463	hsa−miR−301a
18	3e−08	20 / 171	hsa−miR−369−3p
19	3e−08	20 / 172	hsa−miR−607
20	3e−08	21 / 189	hsa−miR−1283

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.05	2 / 14	MACIEJ_MMML 19
2	0.05	1 / 2	MACIEJ_MMML 38
3	0.06	2 / 15	MACIEJ_MMML 16
4	0.06	2 / 15	MACIEJ_MMML 22
5	0.17	1 / 7	MACIEJ_MMML 48
6	0.17	1 / 7	MACIEJ_MMML 5
7	0.28	1 / 12	MACIEJ_MMML 24
8	0.32	1 / 14	MACIEJ_MMML 30
9	1.00	0 / 16	MACIEJ_MMML 1
10	1.00	0 / 13	MACIEJ_MMML 10
11	1.00	0 / 7	MACIEJ_MMML 13
12	1.00	0 / 9	MACIEJ_MMML 14
13	1.00	0 / 11	MACIEJ_MMML 15
14	1.00	0 / 2	MACIEJ_MMML 17
15	1.00	0 / 4	MACIEJ_MMML 2
16	1.00	0 / 5	MACIEJ_MMML 20
17	1.00	0 / 4	MACIEJ_MMML 23
18	1.00	0 / 14	MACIEJ_MMML 26
19	1.00	0 / 2	MACIEJ_MMML 27
20	1.00	0 / 5	MACIEJ_MMML 28

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.007	3 / 15	BENTINK_ras.6
2	0.039	2 / 12	BENTINK_e2f3.1
3	0.052	2 / 14	BENTINK_src.2
4	0.296	1 / 13	BENTINK_src.10
5	1.000	0 / 13	GUSTAFSON_PI3K_UP
6	1.000	0 / 15	GUSTAFSON_PI3K_DN
7	1.000	0 / 11	BENTINK_e2f3.2
8	1.000	0 / 14	BENTINK_myc.1
9	1.000	0 / 12	BENTINK_ras.1
10	1.000	0 / 11	BENTINK_ras.4
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−04	55 / 1233	KIM_MYC targets
2	1e−04	50 / 1095	HEBENSTREIT_high expression TF
3	8e−02	1 / 3	MYC_Tumor supressor genes UP
4	1e−01	1 / 4	MYC_Apoptosis UP
5	1e−01	1 / 5	MYC_TF and cofactors
6	2e−01	1 / 7	MYC_DNA repair UP
7	2e−01	1 / 8	MYC_Cell cycle UP
8	2e−01	1 / 8	MYC_RNA processing binding UP
9	2e−01	3 / 63	MYC_Targets UP
10	3e−01	1 / 14	NOWICK_TF
11	4e−01	1 / 16	MYC_Protein synthesis degradation UP
12	1e+00	8 / 1146	HEBENSTREIT_low expression TF
13	1e+00	0 / 5	MYC_TFs
14	1e+00	0 / 9	MYC_Targets DOWN
15	1e+00	0 / 2	MYC_Cell cycle DOWN
16	1e+00	0 / 4	MYC_Cell growth and proliferation UP
17	1e+00	0 / 2	MYC_Chromatin_modification UP
18	1e+00	0 / 3	MYC_DNA replication UP
19	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
20	1e+00	0 / 20	MYC_Metabolism UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.04	3 / 29	VAQUERIZAS_Smooth muscle
2	0.04	3 / 29	VAQUERIZAS_Lymph node
3	0.09	7 / 144	VAQUERIZAS_General
4	0.10	3 / 41	VAQUERIZAS_Thymus
5	0.11	3 / 43	VAQUERIZAS_Uterus
6	0.23	3 / 62	VAQUERIZAS_Whole blood
7	0.32	1 / 14	VAQUERIZAS_Fetal liver
8	0.53	1 / 28	VAQUERIZAS_Liver
9	0.65	1 / 39	VAQUERIZAS_Thyroid
10	0.66	1 / 40	VAQUERIZAS_Fetal brain
11	0.69	1 / 43	VAQUERIZAS_Whole brain
12	0.70	1 / 44	VAQUERIZAS_Placenta
13	1.00	0 / 37	VAQUERIZAS_Prostate
14	1.00	0 / 12	VAQUERIZAS_Kidney
15	1.00	0 / 22	VAQUERIZAS_Spinal cord
16	1.00	0 / 7	VAQUERIZAS_Appendix
17	1.00	0 / 30	VAQUERIZAS_Fetal lung
18	1.00	0 / 62	VAQUERIZAS_Lung
19	1.00	0 / 16	VAQUERIZAS_Pancreas
20	1.00	0 / 24	VAQUERIZAS_Trachea

Sample−Underexpression

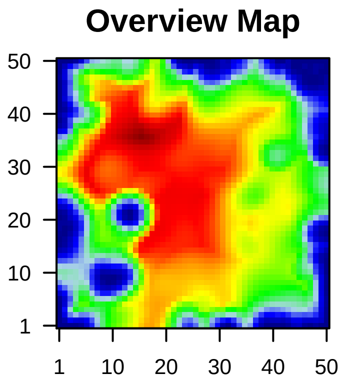
Spot Summary: h

metagenes = 17
genes = 235

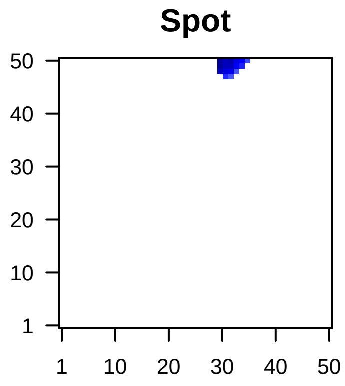
<r> metagenes = 0.96
<r> genes = 0.28
beta: r2= 4.68 / log p= −Inf

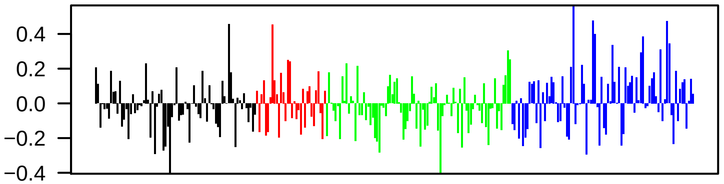
samples with spot = 6 (2.2 %)
Atypical : 3 (4.1 %)
Mesenchymal : 2 (2.4 %)
Basal : 1 (1.2 %)

Overview Map



Spot





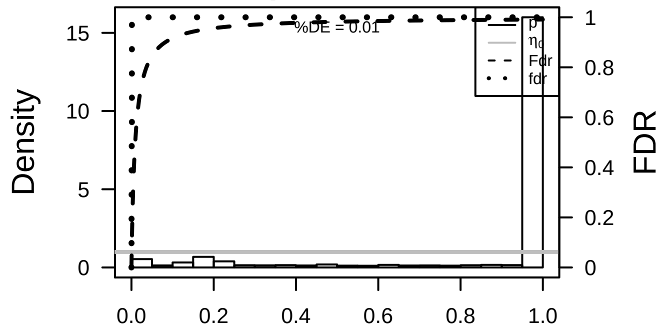
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	1207	1.52	−1.35	0.49	CLNS1A	chloride channel, nucleotide−sensitive, 1A [Source:HGNC Sy
2	100093630	1.47	−1.34	0.27	SNHG8	small nucleolar RNA host gene 8 (non−protein coding) [Sourc
3	8065	0.91	−1.32	0.47	CUL5	cullin 5 [Source:HGNC Symbol;Acc:2556]
4	139886	1.35	−1.31	0.32	SPIN4	spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
5	81853	1.07	−1.25	0.57	TMEM14B	transmembrane protein 14B [Source:HGNC Symbol;Acc:213
6	509	1.01	−1.14	0.68	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, ga
7	6175	1.19	−1.11	0.67	RPLP0	ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:1037
8	6392	1.06	−1.11	0.72	SDHD	succinate dehydrogenase complex, subunit D, integral memb
9	6166	0.96	−1.1	0.47	RPL36AL	ribosomal protein L36a−like [Source:HGNC Symbol;Acc:103
10	4259	0.93	−1.09	0.36	MGST3	microsomal glutathione S−transferase 3 [Source:HGNC Sym
11	4729	0.85	−1.09	0.45	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa [S
12	1349	1.11	−1.08	0.69	COX7B	cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;A
13	441951	0.93	−1.07	0.46	ZFAS1	ZNFX1 antisense RNA 1 [Source:HGNC Symbol;Acc:33101]
14	6129	1	−1.07	0.54	RPL7	ribosomal protein L7 [Source:HGNC Symbol;Acc:10363]
15	10799	0.99	−1.07	0.65	RPP40	ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;
16	84263	0.9	−1.05	0.39	HSDL2	hydroxysteroid dehydrogenase like 2 [Source:HGNC Symbol;
17	5423	1.39	−1.04	0.26	POLB	polymerase (DNA directed), beta [Source:HGNC Symbol;Acc
18	80227	1.1	−1.04	0.35	PAAF1	proteasomal ATPase−associated factor 1 [Source:HGNC Sy
19	27235	0.9	−1.03	0.53	COQ2	coenzyme Q2 4−hydroxybenzoate polyprenyltransferase [Sou
20	2271	0.92	−1.03	0.52	FH	fumarate hydratase [Source:HGNC Symbol;Acc:3700]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−28	26 / 83	BP	respiratory electron transport chain
2	3e−25	38 / 304	CC	mitochondrial inner membrane
3	6e−25	72 / 1318	CC	mitochondrion
4	3e−22	27 / 152	BP	cellular metabolic process
5	8e−20	25 / 153	MF	structural constituent of ribosome
6	2e−19	30 / 253	BP	translation
7	8e−18	19 / 87	BP	translational termination
8	3e−17	19 / 92	BP	translational elongation
9	4e−17	20 / 109	BP	SRP−dependent cotranslational protein targeting to membrane
10	5e−17	18 / 81	BP	viral transcription
11	8e−17	21 / 128	BP	translational initiation
12	5e−16	18 / 92	BP	viral life cycle
13	6e−16	28 / 287	BP	viral process
14	2e−15	22 / 167	CC	ribosome
15	3e−14	18 / 115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
16	2e−13	13 / 51	CC	cytosolic large ribosomal subunit
17	3e−13	37 / 649	BP	gene expression
18	1e−12	9 / 19	CC	mitochondrial proton−transporting ATP synthase complex
19	7e−12	30 / 482	BP	cellular protein metabolic process
20	3e−11	21 / 242	BP	RNA metabolic process
21	3e−11	20 / 219	BP	mRNA metabolic process
22	2e−10	47 / 1233	TF	KIM_MYC targets
23	6e−10	7 / 15	BP	ATP synthesis coupled proton transport
24	7e−10	9 / 34	MF	NADH dehydrogenase (ubiquinone) activity
25	1e−09	9 / 36	CC	mitochondrial respiratory chain complex I
26	1e−08	6 / 13	GSEA	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
27	2e−08	6 / 14	BP	mitochondrial ATP synthesis coupled proton transport
28	2e−08	8 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
29	1e−06	6 / 25	MF	hydrogen ion transmembrane transporter activity
30	1e−06	6 / 26	MF	cytochrome−c oxidase activity
31	3e−06	24 / 595	MF	RNA binding
32	5e−06	38 / 1253	BP	small molecule metabolic process
33	7e−06	4 / 10	CC	large ribosomal subunit
34	1e−05	4 / 11	Canc	GENTLES_modul5
35	1e−05	4 / 11	MMM	MACIEJ_MMML 49
36	2e−05	4 / 12	BP	oxidative phosphorylation
37	2e−05	7 / 62	Glio	Stuehler_Proteins_up_in_STS
38	3e−05	5 / 27	BP	DNA−dependent transcription, initiation
39	3e−05	5 / 27	MF	rRNA binding
40	5e−05	4 / 15	MMM	MACIEJ_MMML 22

p−values



BP

Rank	p−value	#in/all	Geneset
1	2e−28	26 / 83	respiratory electron transport chain
2	3e−22	27 / 152	cellular metabolic process
3	2e−19	30 / 253	translation
4	8e−18	19 / 87	translational termination
5	3e−17	19 / 92	translational elongation
6	4e−17	20 / 109	SRP−dependent cotranslational protein targeting to membrane
7	5e−17	18 / 81	viral transcription
8	8e−17	21 / 128	translational initiation
9	5e−16	18 / 92	viral life cycle
10	6e−16	28 / 287	viral process
11	3e−14	18 / 115	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
12	3e−13	37 / 649	gene expression
13	7e−12	30 / 482	cellular protein metabolic process
14	3e−11	21 / 242	RNA metabolic process
15	3e−11	20 / 219	mRNA metabolic process
16	6e−10	7 / 15	ATP synthesis coupled proton transport
17	2e−08	6 / 14	mitochondrial ATP synthesis coupled proton transport
18	2e−08	8 / 35	mitochondrial electron transport, NADH to ubiquinone
19	5e−06	38 / 1253	small molecule metabolic process
20	2e−05	4 / 12	oxidative phosphorylation

Cancer

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 11	GENTLES_modul5
2	6e−05	4 / 16	GENTLES_modul10
3	2e−02	2 / 15	GENTLES_modul1
4	1e−01	2 / 39	ZHANG_MM up
5	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
6	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	2e−01	1 / 15	GENTLES_modul6
8	2e−01	1 / 16	GENTLES_modul2
9	2e−01	1 / 16	GENTLES_modul7
10	9e−01	1 / 185	SPANG_LPS−index2
11	9e−01	2 / 316	SPANG_BCL6−index2
12	1e+00	2 / 530	Lembcke_Normal vs Adenoma
13	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
14	1e+00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
15	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
16	1e+00	0 / 10	LIU_BREAST_CANCER
17	1e+00	0 / 14	LIU_LIVER_CANCER
18	1e+00	0 / 15	LIU_PROSTATE_CANCER_DN
19	1e+00	0 / 14	LIU_PROSTATE_CANCER_UP
20	1e+00	0 / 14	WANG_ER_UP

CC

Rank	p−value	#in/all	Geneset
1	3e−25	38 / 304	mitochondrial inner membrane
2	6e−25	72 / 1318	mitochondrion
3	2e−15	22 / 167	ribosome
4	2e−13	13 / 51	cytosolic large ribosomal subunit
5	1e−12	9 / 19	mitochondrial proton−transporting ATP synthase complex
6	1e−09	9 / 36	mitochondrial respiratory chain complex I
7	7e−06	4 / 10	large ribosomal subunit
8	3e−04	4 / 23	mitochondrial ribosome
9	6e−04	5 / 49	mitochondrial intermembrane space
10	7e−04	3 / 13	mitochondrial respiratory chain
11	9e−04	3 / 14	transcription factor TFTC complex
12	1e−03	3 / 15	eukaryotic translation initiation factor 3 complex
13	2e−03	4 / 37	cytosolic small ribosomal subunit
14	2e−03	3 / 19	mitochondrial small ribosomal subunit
15	3e−03	3 / 21	transcription factor TFIID complex
16	4e−03	5 / 74	mitochondrial membrane
17	5e−03	48 / 2378	cytosol
18	6e−03	6 / 118	ribonucleoprotein complex
19	1e−02	2 / 11	WASH complex
20	1e−02	3 / 33	mediator complex

Chr

Rank	p−value	#in/all	Geneset
1	2e−04	28 / 957	Chr 11
2	1e−03	21 / 714	Chr 6
3	1e−03	19 / 618	Chr 4
4	8e−03	15 / 534	Chr 8
5	2e−02	17 / 699	Chr 5
6	1e−01	5 / 187	Chr 21
7	3e−01	11 / 630	Chr X
8	5e−01	15 / 1033	Chr 2
9	5e−01	1 / 52	Chr HSCHR6_MHC_QBL
10	6e−01	3 / 232	Chr 18
11	7e−01	11 / 866	Chr 12
12	7e−01	22 / 1720	Chr 1
13	7e−01	6 / 519	Chr 14
14	7e−01	7 / 602	Chr 10
15	8e−01	7 / 633	Chr 9
16	8e−01	10 / 918	Chr 17
17	9e−01	9 / 914	Chr 3
18	9e−01	2 / 280	Chr 13
19	9e−01	4 / 504	Chr 15
20	1e+00	2 / 386	Chr 22

Disease

Rank	p−value	#in/all	Geneset
1	0.9	5 / 572	GUDJ_psoriasis up
2	1.0	1 / 375	GUDJ_psoriasis down
3	1.0	0 / 17	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−05	7 / 62	Stuehler_Proteins_up_in_STS
2	1e−04	6 / 54	willscher_GBM_proteomics_wtOnly_SpotG
3	1e−04	10 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
4	7e−02	3 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
5	1e−01	1 / 10	willscher_GBM_LTSmut_proteomics−A_UP
6	2e−01	1 / 12	willscher_ GBM_LTSwt_proteomics−C_UP
7	2e−01	1 / 12	willscher_GBM_LTSmut_proteomics−B_UP
8	2e−01	1 / 12	willscher_GBM_STSwt_proteomics−B_DOWN
9	3e−01	2 / 74	GIEZELT_GBM_STS_up_VS_LTS
10	3e−01	1 / 28	Barbus_GBM_STS_vs._LTS
11	4e−01	1 / 33	willscher_GBM_proteomics_wtOnly_SpotC
12	4e−01	1 / 37	willscher_GBM_proteomics_wtOnly_SpotH
13	5e−01	1 / 49	Vishal_subnetwork signature of survival in GBM
14	6e−01	1 / 72	GIEZELT_GBM_STSwt_down_VS_LTSwt
15	6e−01	4 / 313	willscher_GBM_Verhaak−CL_expression_D_up
16	6e−01	4 / 313	willscher_GBM_Verhaak−MES_expression_D_down
17	6e−01	4 / 313	willscher_GBM_Verhaak−PNwt_expression_D_up
18	6e−01	5 / 391	Down_b
19	7e−01	4 / 328	Up
20	8e−01	1 / 117	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−08	6 / 13	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
2	1e−04	3 / 8	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS
3	2e−04	3 / 9	KEGG_RIBOSOME
4	2e−04	3 / 9	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBUNITS
5	2e−04	3 / 9	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_RIBOSOM
6	2e−04	3 / 9	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
7	2e−04	3 / 9	REACTOME_PEPTIDE_CHAIN_ELONGATION
8	2e−04	3 / 9	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
9	2e−04	3 / 9	REACTOME_VIRAL_MRNA_TRANSLATION
10	3e−04	3 / 10	REACTOME_TRANSLATION
11	4e−04	3 / 11	KEGG_BASAL_TRANSCRIPTION_FACTORS
12	4e−04	3 / 11	BIOCARTA_ETC_PATHWAY
13	7e−04	3 / 13	NAGY_TFTC_COMPONENTS_HUMAN
14	7e−04	3 / 13	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
15	7e−04	3 / 13	MOOTHA_VOXPHOS
16	1e−03	3 / 15	MOOTHA_TCA
17	1e−03	3 / 16	BARIS_THYROID_CANCER_UP
18	1e−03	3 / 16	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
19	2e−03	2 / 5	NAGY_PCAF_COMPONENTS_HUMAN
20	4e−03	2 / 7	YANAGISAWA_LUNG_CANCER_RECURRENCE

H. Tiss

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	WIRTH_Cerebellum
2	0.8	1 / 127	WIRTH_Muscle
3	0.8	4 / 417	WIRTH_Immune system
4	1.0	0 / 5	WIRTH_Pituitary gland
5	1.0	0 / 26	WIRTH_Pancreas
6	1.0	0 / 13	WIRTH_Sec. lymphoid organs
7	1.0	0 / 12	WIRTH_Prim. lymphoid organs
8	1.0	0 / 10	WIRTH_B−cells
9	1.0	0 / 13	WIRTH_Tonsil
10	1.0	0 / 13	WIRTH_Thymus
11	1.0	0 / 12	WIRTH_Lymphocytes
12	1.0	0 / 6	WIRTH_Bone marrow
13	1.0	0 / 400	WIRTH_Nervous System
14	1.0	0 / 14	WIRTH_Globus pallidus
15	1.0	0 / 15	WIRTH_Telencephalon
16	1.0	0 / 13	WIRTH_Cortex cerebri
17	1.0	0 / 16	WIRTH_Hippocampus
18	1.0	0 / 13	WIRTH_Thalamus
19	1.0	0 / 120	WIRTH_Testis
20	1.0	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	6 / 86	ROSOLOWSKI_red total
2	0.033	4 / 86	ROSOLOWSKI_green UP
3	0.086	4 / 119	ROSOLOWSKI_green total
4	0.110	15 / 755	SPANG_BCR UP
5	0.179	1 / 14	WRIGHT_GCB UP
6	0.224	1 / 18	DAVE_c−myc BL UP
7	0.246	1 / 20	ROSOLOWSKI_red UP
8	0.415	1 / 38	ROSOLOWSKI_blue DOWN
9	0.534	1 / 54	SPANG_BAFF 9hrs DN
10	0.623	1 / 69	SPANG_LPS 6hrs DN
11	0.715	5 / 426	SPANG_CD40 6hrs DN
12	0.757	1 / 100	ROSOLOWSKI_blue total
13	0.862	1 / 140	DAVE_BL−vs−DLBCL
14	0.900	2 / 275	ZHANG_DLBCL mutated
15	0.917	2 / 291	SPANG_IL21 UP
16	0.957	7 / 852	SPANG_BCR DN
17	0.991	1 / 327	SPANG_CD40 6hrs UP
18	1.000	0 / 13	BENTINK_mBL UP
19	1.000	0 / 13	BENTINK_mBL DOWN
20	1.000	0 / 12	DAVE_BL_DN

MF

Rank	p−value	#in/all	Geneset
1	8e−20	25 / 153	structural constituent of ribosome
2	7e−10	9 / 34	NADH dehydrogenase (ubiquinone) activity
3	1e−06	6 / 25	hydrogen ion transmembrane transporter activity
4	1e−06	6 / 26	cytochrome−c oxidase activity
5	3e−06	24 / 595	RNA binding
6	3e−05	5 / 27	rRNA binding
7	7e−05	6 / 50	transmembrane transporter activity
8	1e−04	4 / 18	2 iron, 2 sulfur cluster binding
9	1e−04	7 / 79	electron carrier activity
10	7e−03	7 / 158	protein complex binding
11	1e−02	2 / 12	lysophospholipase activity
12	1e−02	6 / 141	ATPase activity
13	3e−02	2 / 18	fatty−acyl−CoA binding
14	3e−02	2 / 18	TBP−class protein binding
15	4e−02	3 / 54	translation initiation factor activity
16	5e−02	13 / 549	molecular_function
17	5e−02	2 / 26	lyase activity
18	5e−02	2 / 26	thyroid hormone receptor binding
19	5e−02	2 / 27	protein disulfide oxidoreductase activity
20	6e−02	5 / 148	ubiquitin protein ligase binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.2	1 / 19	GTCA−380−5P
2	0.3	2 / 75	ATGT−489
3	0.3	2 / 76	GAGA−452
4	0.3	2 / 85	ATTA−380−3P
5	0.4	1 / 31	ACCA−509
6	0.4	2 / 91	CTGT−194
7	0.4	1 / 36	GGGA−324−5P
8	0.5	1 / 43	CCCA−299−3P
9	0.5	2 / 115	TTGG−515−5P−−519E
10	0.5	3 / 190	CACT−520G−−520H
11	0.5	1 / 49	CTAG−384
12	0.5	1 / 52	GTGT−514
13	0.5	2 / 125	ACAC−199A−−199B
14	0.5	1 / 53	GCAA−502
15	0.5	2 / 129	TAAT−323
16	0.6	3 / 208	ATTC−186
17	0.6	2 / 142	GTGC−183
18	0.6	1 / 64	TCTG−361
19	0.6	1 / 65	TCTA−376A−−376B
20	0.6	1 / 65	TCTG−198

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	1 / 2	miR−375
2	0.14	1 / 11	let−7a
3	1.00	0 / 6	let−7b
4	1.00	0 / 4	let−7c
5	1.00	0 / 6	let−7d
6	1.00	0 / 4	let−7g
7	1.00	0 / 13	miR−1
8	1.00	0 / 5	miR−101
9	1.00	0 / 2	miR−101b
10	1.00	0 / 4	miR−106b
11	1.00	0 / 2	miR−107
12	1.00	0 / 4	miR−122
13	1.00	0 / 2	miR−124a
14	1.00	0 / 6	miR−125a
15	1.00	0 / 9	miR−125b
16	1.00	0 / 5	miR−126
17	1.00	0 / 2	miR−127
18	1.00	0 / 3	miR−128
19	1.00	0 / 4	miR−128b
20	1.00	0 / 2	miR−129

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.02	8 / 241	hsa−miR−122
2	0.03	4 / 80	hsa−miR−562
3	0.03	6 / 166	hsa−miR−320b
4	0.03	3 / 48	hsa−miR−518e*
5	0.03	5 / 127	hsa−miR−1272
6	0.04	4 / 89	hsa−miR−496
7	0.04	4 / 91	hsa−miR−219−2−3p
8	0.04	6 / 178	hsa−miR−520f
9	0.04	5 / 134	hsa−miR−200a
10	0.04	8 / 280	hsa−miR−320a
11	0.06	3 / 62	hsa−miR−1243
12	0.07	3 / 69	hsa−miR−502−5p
13	0.07	3 / 69	hsa−miR−651
14	0.07	2 / 32	hsa−miR−17*
15	0.08	5 / 161	hsa−miR−511
16	0.08	1 / 6	hsa−miR−937
17	0.09	3 / 77	hsa−miR−584
18	0.11	2 / 40	hsa−miR−518f*
19	0.11	3 / 83	hsa−miR−433
20	0.11	2 / 41	hsa−miR−518b

MMML CGS

Rank	p−value	#in/all	Geneset
1	1e−05	4 / 11	MACIEJ_MMML 49
2	5e−05	4 / 15	MACIEJ_MMML 22
3	3e−02	1 / 2	MACIEJ_MMML 17
4	7e−02	1 / 5	MACIEJ_MMML 28
5	9e−02	1 / 7	MACIEJ_MMML 48
6	1e+00	0 / 16	MACIEJ_MMML 1
7	1e+00	0 / 13	MACIEJ_MMML 10
8	1e+00	0 / 7	MACIEJ_MMML 13
9	1e+00	0 / 9	MACIEJ_MMML 14
10	1e+00	0 / 11	MACIEJ_MMML 15
11	1e+00	0 / 15	MACIEJ_MMML 16
12	1e+00	0 / 14	MACIEJ_MMML 19
13	1e+00	0 / 4	MACIEJ_MMML 2
14	1e+00	0 / 5	MACIEJ_MMML 20
15	1e+00	0 / 4	MACIEJ_MMML 23
16	1e+00	0 / 12	MACIEJ_MMML 24
17	1e+00	0 / 14	MACIEJ_MMML 26
18	1e+00	0 / 2	MACIEJ_MMML 27
19	1e+00	0 / 6	MACIEJ_MMML 29
20	1e+00	0 / 11	MACIEJ_MMML 3

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	2e−10	47 / 1233	KIM_MYC targets
2	1e−01	20 / 1095	HEBENSTREIT_high expression TF
3	1e+00	2 / 1146	HEBENSTREIT_low expression TF
4	1e+00	0 / 14	NOWICK_TF
5	1e+00	0 / 5	MYC_TFs
6	1e+00	0 / 63	MYC_Targets UP
7	1e+00	0 / 9	MYC_Targets DOWN
8	1e+00	0 / 4	MYC_Apoptosis UP
9	1e+00	0 / 8	MYC_Cell cycle UP
10	1e+00	0 / 2	MYC_Cell cycle DOWN
11	1e+00	0 / 4	MYC_Cell growth and proliferation UP
12	1e+00	0 / 2	MYC_Chromatin_modification UP
13	1e+00	0 / 7	MYC_DNA repair UP
14	1e+00	0 / 3	MYC_DNA replication UP
15	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
16	1e+00	0 / 20	MYC_Metabolism UP
17	1e+00	0 / 16	MYC_Protein synthesis degradation UP
18	1e+00	0 / 8	MYC_RNA processing binding UP
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.6	2 / 144	VAQUERIZAS_General
2	1.0	0 / 40	VAQUERIZAS_Fetal brain
3	1.0	0 / 44	VAQUERIZAS_Placenta
4	1.0	0 / 28	VAQUERIZAS_Liver
5	1.0	0 / 37	VAQUERIZAS_Prostate
6	1.0	0 / 29	VAQUERIZAS_Smooth muscle
7	1.0	0 / 43	VAQUERIZAS_Uterus
8	1.0	0 / 12	VAQUERIZAS_Kidney
9	1.0	0 / 22	VAQUERIZAS_Spinal cord
10	1.0	0 / 43	VAQUERIZAS_Whole brain
11	1.0	0 / 41	VAQUERIZAS_Thymus
12	1.0	0 / 39	VAQUERIZAS_Thyroid
13	1.0	0 / 62	VAQUERIZAS_Whole blood
14	1.0	0 / 7	VAQUERIZAS_Appendix
15	1.0	0 / 30	VAQUERIZAS_Fetal lung
16	1.0	0 / 62	VAQUERIZAS_Lung
17	1.0	0 / 16	VAQUERIZAS_Pancreas
18	1.0	0 / 24	VAQUERIZAS_Trachea
19	1.0	0 / 14	VAQUERIZAS_Fetal liver
20	1.0	0 / 21	VAQUERIZAS_Tonsil

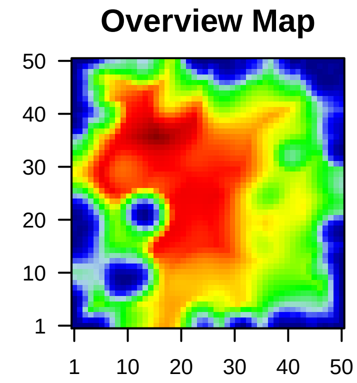
Sample−Underexpression

Spot Summary: i

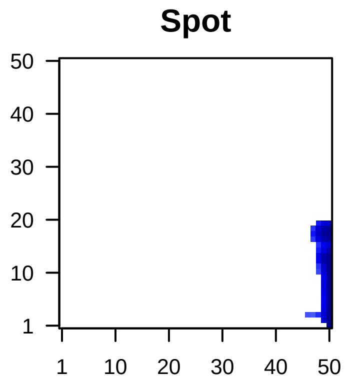
metagenes = 55
genes = 701

<r> metagenes = 0.75
<r> genes = 0.24
beta: r2= 17.23 / log p= −Inf

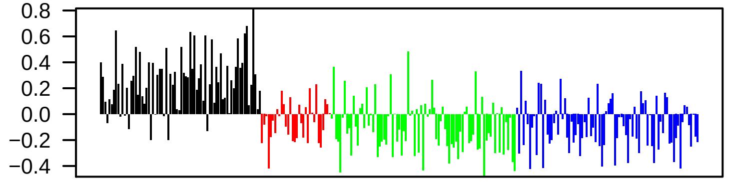
samples with spot = 35 (12.7 %)
Classical : 1 (3.1 %)
Mesenchymal : 20 (23.5 %)
Basal : 14 (16.7 %)



Overview Map



Spot

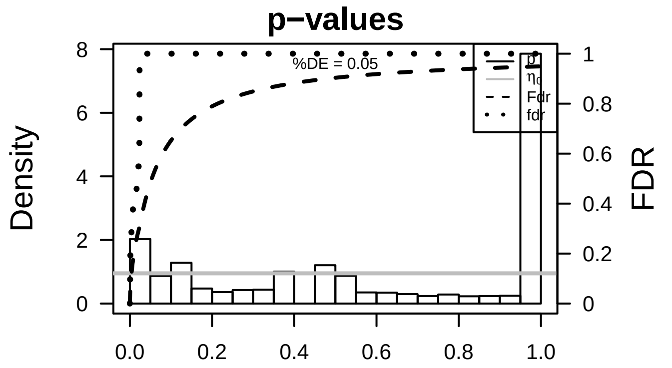


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	6192	2.37	−3.35	0.32	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
2	3122	2.02	−2.66	0.86	HLA−DRA	major histocompatibility complex, class II, DR alpha [Source:
3	3512	3.8	−2.52	0.56	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobu
4	8857	2.85	−2.38	0.49	FCGBP	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
5	3113	2.34	−2.37	0.89	HLA−DPA1	major histocompatibility complex, class II, DP alpha 1 [Source
6	3108	2.1	−2.36	0.86	HLA−DMA	major histocompatibility complex, class II, DM alpha [Source:
7	1396	1.78	−2.34	0.37	CRIP1	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
8	3109	2.27	−2.32	0.91	HLA−DMB	major histocompatibility complex, class II, DM beta [Source:H
9	3488	2.23	−2.24	0.64	IGFBP5	insulin−like growth factor binding protein 5 [Source:HGNC Sy
10	3128	2.53	−2.08	0.75	HLA−DRB6	major histocompatibility complex, class II, DR beta 6 (pseudo
11	3936	2.29	−2.07	0.89	LCP1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
12	972	1.95	−2.06	0.87	CD74	CD74 molecule, major histocompatibility complex, class II inv
13	713	2.72	−1.99	0.76	C1QB	complement component 1, q subcomponent, B chain [Source
14	5552	2.28	−1.97	0.78	SRGN	serglycin [Source:HGNC Symbol;Acc:9361]
15	6347	2.71	−1.97	0.63	CCL2	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
16	5880	2.14	−1.96	0.79	RAC2	ras−related C3 botulinum toxin substrate 2 (rho family, small
17	2878	2.16	−1.95	0.46	GPX3	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
18	894	2.15	−1.95	0.45	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:1583]
19	8404	2.29	−1.94	0.74	SPARCL1	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
20	3169	2.66	−1.9	0.65	FOXA1	forkhead box A1 [Source:HGNC Symbol;Acc:5021]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−19	74 / 553	Canc	Lembcke_Colonic Inflammation
2	1e−16	56 / 375	Disea	GUDJ_psoriasis down
3	3e−16	46 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	3e−16	46 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	3e−16	46 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	3e−16	46 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	7e−16	13 / 16	GSE	RICKMAN_HEAD_AND_NECK_CANCER_D
8	2e−12	71 / 683	CC	extracellular space
9	3e−12	102 / 1182	CC	extracellular region
10	1e−11	51 / 417	H.Tis	WIRTH_Immune system
11	3e−11	42 / 312	BP	immune response
12	4e−08	6 / 7	GSE	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
13	4e−08	6 / 7	GSE	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
14	5e−08	8 / 15	CC	MHC class II protein complex
15	2e−07	7 / 12	GSE	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN
16	4e−07	23 / 162	CC	external side of plasma membrane
17	8e−07	8 / 20	BP	complement activation
18	1e−06	18 / 112	MF	heparin binding
19	1e−06	7 / 15	GSE	NAKAJIMA_MAST_CELL
20	2e−06	7 / 16	GSE	CROMER_TUMORIGENESIS_DN
21	3e−06	5 / 7	GSE	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
22	3e−06	11 / 47	BP	antigen processing and presentation
23	4e−06	6 / 12	GSE	ZHAN_MULTIPLE_MYELOMA_DN
24	5e−06	11 / 49	Glio	Donson−innate immunity−associated with LTS in HGA
25	5e−06	32 / 316	Canc	SPANG_BCL6−index2
26	7e−06	5 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HGA
27	1e−05	28 / 269	BP	inflammatory response
28	1e−05	6 / 14	GSE	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
29	1e−05	6 / 14	GSE	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
30	2e−05	8 / 29	TF Ti	VAQUERIZAS_Lymph node
31	2e−05	6 / 15	GSE	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_D
32	2e−05	6 / 15	GSE	POOLA_INVASIVE_BREAST_CANCER_DN
33	3e−05	31 / 327	Lymp	SPANG_CD40 6hrs UP
34	3e−05	5 / 10	GSE	LU_TUMOR_VASCULATURE_DN
35	3e−05	5 / 10	GSE	FERRANDO_LYL1_NEIGHBORS
36	3e−05	5 / 10	GSE	BIOCARTA_MONOCYTE_PATHWAY
37	3e−05	6 / 16	Lymp	WRIGHT_ABC UP
38	3e−05	6 / 16	GSE	KORKOLA_TERATOMA_UP
39	3e−05	6 / 16	GSE	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
40	3e−05	6 / 16	GSE	BILBAN_B_CLL_LPL_DN



p−values

BP

Rank	p−value	#in/all	Geneset
1	3e−11	42 / 312	immune response
2	8e−07	8 / 20	complement activation
3	3e−06	11 / 47	antigen processing and presentation
4	1e−05	28 / 269	inflammatory response
5	1e−04	6 / 19	calcium−independent cell−cell adhesion
6	1e−04	16 / 129	response to lipopolysaccharide
7	1e−04	6 / 20	actin filament polymerization
8	2e−04	8 / 38	humoral immune response
9	2e−04	9 / 49	arachidonic acid metabolic process
10	2e−04	10 / 60	T cell costimulation
11	2e−04	7 / 30	positive regulation of B cell proliferation
12	2e−04	6 / 22	complement activation, classical pathway
13	3e−04	11 / 74	regulation of immune response
14	3e−04	33 / 407	blood coagulation
15	3e−04	8 / 42	B cell differentiation
16	3e−04	11 / 76	defense response
17	4e−04	8 / 43	cellular response to organic cyclic compound
18	5e−04	6 / 25	melanocyte differentiation
19	6e−04	5 / 17	positive regulation of neutrophil chemotaxis
20	6e−04	4 / 10	epoxygenase P450 pathway

Cancer

Rank	p−value	#in/all	Geneset
1	9e−19	74 / 553	Lembcke_Colonic Inflammation
2	5e−06	32 / 316	SPANG_BCL6−index2
3	3e−04	5 / 15	GENTLES_modul13
4	2e−03	4 / 13	GENTLES_modul17
5	4e−03	4 / 16	GENTLES_modul11
6	7e−03	3 / 10	LIU_BREAST_CANCER
7	7e−03	3 / 15	LIU_PROSTATE_CANCER_DN
8	2e−02	3 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	3e−02	2 / 7	ZHANG_MGUS up
10	1e−01	2 / 13	GENTLES_modul12
11	1e−01	2 / 13	GENTLES_modul18
12	1e−01	2 / 14	LIU_LIVER_CANCER
13	1e−01	2 / 16	GENTLES_modul14
14	3e−01	10 / 185	SPANG_LPS−index2
15	3e−01	1 / 9	WANG_ER_DN
16	4e−01	1 / 12	BEN−PORATH_DN
17	4e−01	2 / 33	KUIPER_MM good survival
18	5e−01	1 / 14	LIU_COMMON_CANCER_GENES
19	5e−01	1 / 14	LIU_PROSTATE_CANCER_UP
20	5e−01	1 / 15	RHODES_CANCER_META_SIGNATURE

CC

Rank	p−value	#in/all	Geneset
1	2e−12	71 / 683	extracellular space
2	3e−12	102 / 1182	extracellular region
3	5e−08	8 / 15	MHC class II protein complex
4	4e−07	23 / 162	external side of plasma membrane
5	1e−04	7 / 28	transport vesicle membrane
6	1e−04	8 / 37	actin filament
7	6e−04	7 / 35	trans−Golgi network membrane
8	6e−04	8 / 46	endocytic vesicle membrane
9	2e−03	5 / 21	clathrin−coated endocytic vesicle membrane
10	2e−03	141 / 2659	plasma membrane
11	2e−03	5 / 23	integral to lumenal side of endoplasmic reticulum membrane
12	4e−03	52 / 835	integral to plasma membrane
13	6e−03	10 / 92	tight junction
14	7e−03	3 / 10	nBAF complex
15	8e−03	24 / 330	cell surface
16	9e−03	6 / 43	platelet alpha granule lumen
17	1e−02	3 / 11	npBAF complex
18	1e−02	5 / 32	ER to Golgi transport vesicle membrane
19	1e−02	15 / 183	proteinaceous extracellular matrix
20	1e−02	3 / 12	phagocytic cup

Chr

Rank	p−value	#in/all	Geneset
1	0.02	6 / 52	Chr HSCHR6_MHC_QBL
2	0.05	40 / 714	Chr 6
3	0.05	39 / 699	Chr 5
4	0.08	33 / 602	Chr 10
5	0.10	33 / 618	Chr 4
6	0.15	51 / 1033	Chr 2
7	0.16	43 / 866	Chr 12
8	0.17	81 / 1720	Chr 1
9	0.20	27 / 534	Chr 8
10	0.21	15 / 280	Chr 13
11	0.27	10 / 187	Chr 21
12	0.29	35 / 743	Chr 7
13	0.38	41 / 914	Chr 3
14	0.43	2 / 34	Chr Y
15	0.52	27 / 633	Chr 9
16	0.66	9 / 232	Chr 18
17	0.89	17 / 519	Chr 14
18	0.90	12 / 386	Chr 22
19	0.90	32 / 918	Chr 17
20	0.90	21 / 630	Chr X

Disease

Rank	p−value	#in/all	Geneset
1	1e−16	56 / 375	GUDJ_psoriasis down
2	2e−02	4 / 26	BCHETNIA_EBM−DM up
3	2e−01	2 / 17	BCHETNIA_EBM up
4	6e−01	24 / 572	GUDJ_psoriasis up
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	3e−16	46 / 265	willscher_GBM_Verhaak−CL_expression_B_up
2	3e−16	46 / 265	willscher_GBM_Verhaak−MES_expression_B_up
3	3e−16	46 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
4	3e−16	46 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
5	5e−06	11 / 49	Donson−innate immunity−associated with LTS in HGA
6	7e−06	5 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
7	9e−05	10 / 55	OL vs. MOG− OL
8	6e−04	4 / 10	willscher_ GBM_LTSwt_proteomics−G_UP
9	4e−03	7 / 49	mature astrocytes
10	1e−02	9 / 85	laffaire_hypermeth_LGG_vs_control
11	1e−02	3 / 12	astrocytes_glio
12	1e−02	6 / 46	OL vs. OPC
13	1e−02	10 / 105	willscher_GBM_proteomics_wtOnly_SpotB
14	2e−02	3 / 14	VERHAAK_CL subtype
15	2e−02	10 / 112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	2e−02	3 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
17	3e−02	11 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
18	3e−02	2 / 7	oligodendrocytes_glio
19	3e−02	3 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
20	4e−02	5 / 44	in vivo astrocytes vs. cultured astroglia

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−16	13 / 16	RICKMAN_HEAD_AND_NECK_CANCER_D
2	4e−08	6 / 7	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
3	4e−08	6 / 7	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
4	2e−07	7 / 12	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN
5	1e−06	7 / 15	NAKAJIMA_MAST_CELL
6	2e−06	7 / 16	CROMER_TUMORIGENESIS_DN
7	3e−06	5 / 7	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
8	4e−06	6 / 12	ZHAN_MULTIPLE_MYELOMA_DN
9	1e−05	6 / 14	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
10	1e−05	6 / 14	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
11	2e−05	6 / 15	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN
12	2e−05	6 / 15	POOLA_INVASIVE_BREAST_CANCER_DN
13	3e−05	5 / 10	LU_TUMOR_VASCULATURE_DN
14	3e−05	5 / 10	FERRANDO_LYL1_NEIGHBORS
15	3e−05	5 / 10	BIOCARTA_MONOCYTE_PATHWAY
16	3e−05	6 / 16	KORKOLA_TERATOMA_UP
17	3e−05	6 / 16	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL
18	3e−05	6 / 16	BILBAN_B_CLL_LPL_DN
19	3e−05	6 / 16	RICKMAN_HEAD_AND_NECK_CANCER_A
20	3e−05	6 / 16	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN

H Tiss

Rank	p−value	#in/all	Geneset
1	1e−11	51 / 417	WIRTH_Immune system
2	2e−02	3 / 13	WIRTH_Sec. lymphoid organs
3	3e−01	2 / 26	WIRTH_Pancreas
4	4e−01	1 / 12	WIRTH_Prim. lymphoid organs
5	4e−01	1 / 12	WIRTH_Lymphocytes
6	4e−01	1 / 13	WIRTH_Thymus
7	4e−01	1 / 13	WIRTH_Thalamus
8	4e−01	1 / 13	WIRTH_Thyroid gland
9	5e−01	1 / 14	WIRTH_Globus pallidus
10	5e−01	1 / 15	WIRTH_Cerebellum
11	5e−01	3 / 62	WIRTH_Liver
12	5e−01	1 / 16	WIRTH_Hippocampus
13	5e−01	17 / 400	WIRTH_Nervous System
14	6e−01	5 / 120	WIRTH_Testis
15	9e−01	1 / 50	WIRTH_Homeostasis
16	1e+00	2 / 127	WIRTH_Muscle
17	1e+00	0 / 5	WIRTH_Pituitary gland
18	1e+00	0 / 10	WIRTH_B−cells
19	1e+00	0 / 13	WIRTH_Tonsil
20	1e+00	0 / 6	WIRTH_Bone marrow

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−05	31 / 327	SPANG_CD40 6hrs UP
2	3e−05	6 / 16	WRIGHT_ABC UP
3	1e−04	7 / 28	DAVE_Immune response 1
4	4e−04	23 / 250	LENZ_Stromal signature 1
5	4e−03	3 / 8	MASCQUE_ABC UP
6	1e−02	9 / 86	ROSOLOWSKI_red total
7	1e−02	11 / 118	SPANG_LPS 6hrs UP
8	2e−02	3 / 13	BENTINK_mBL UP
9	2e−02	2 / 5	MASCQUE_mBL UP
10	2e−02	3 / 14	WRIGHT_GCB UP
11	4e−02	11 / 140	DAVE_BL−vs−DLBCL
12	4e−02	6 / 59	LENZ_Stromal signature 2
13	5e−02	18 / 274	SPANG_IL21 DN
14	5e−02	3 / 20	DAVE_Immune response 2
15	6e−02	3 / 22	DAVE_NFkB BL DN
16	7e−02	18 / 291	SPANG_IL21 UP
17	8e−02	4 / 38	ROSOLOWSKI_blue DOWN
18	8e−02	17 / 275	ZHANG_DLBCL mutated
19	9e−02	2 / 12	DAVE_BL_DN
20	1e−01	24 / 426	SPANG_CD40 6hrs DN

MF

Rank	p−value	#in/all	Geneset
1	1e−06	18 / 112	heparin binding
2	2e−04	57 / 823	sequence−specific DNA binding transcription factor activity
3	2e−04	5 / 14	selenium binding
4	4e−04	8 / 43	chemokine activity
5	5e−04	23 / 252	transcription factor binding
6	8e−04	6 / 27	antigen binding
7	1e−03	4 / 12	Rac GTPase activator activity
8	2e−03	5 / 21	glycosaminoglycan binding
9	3e−03	6 / 34	endopeptidase inhibitor activity
10	4e−03	4 / 16	cytokine binding
11	5e−03	24 / 318	chromatin binding
12	5e−03	4 / 17	metallocarboxypeptidase activity
13	5e−03	4 / 17	RNA polymerase II distal enhancer sequence−specific DNA binding
14	5e−03	5 / 27	estrogen receptor binding
15	6e−03	4 / 18	aromatase activity
16	6e−03	9 / 79	electron carrier activity
17	9e−03	4 / 20	RNA polymerase II transcription coactivator activity
18	9e−03	6 / 43	scavenger receptor activity
19	1e−02	6 / 45	steroid hormone receptor activity
20	1e−02	4 / 22	coreceptor activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	7e−05	10 / 53	GCAA−502
2	4e−04	23 / 247	GTGC−96
3	7e−04	15 / 136	GCAT−105
4	9e−04	12 / 98	ATGT−221−−222
5	1e−03	34 / 457	TGCC−124A
6	1e−03	18 / 189	CTTT−527
7	4e−03	12 / 116	GACA−219
8	4e−03	20 / 244	GTGC−25−−32−−92−−363−−367
9	5e−03	9 / 76	GGCC−193A−−193B
10	5e−03	15 / 168	ATAC−144
11	6e−03	29 / 415	TTTG−19A−−19B
12	6e−03	11 / 108	AGCA−155
13	7e−03	9 / 81	AACT−223
14	9e−03	13 / 145	AAAG−511
15	1e−02	20 / 267	CACT−128A−−128B
16	1e−02	5 / 32	CCTG−510
17	1e−02	19 / 252	AGCA−93−−302A−−302B−−302C−−302D−−372−−373−−520E−−520A−−526
18	1e−02	6 / 45	GGCA−455
19	1e−02	36 / 577	GTGC−506
20	2e−02	8 / 77	GGTG−329

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 4	miR−204
2	2e−02	2 / 5	miR−15a
3	2e−02	4 / 26	miR−21
4	2e−02	2 / 6	miR−221
5	4e−02	2 / 8	miR−222
6	6e−02	2 / 10	miR−146a
7	8e−02	1 / 2	miR−153
8	1e−01	2 / 13	miR−34a
9	1e−01	1 / 3	miR−148a
10	1e−01	1 / 3	miR−223
11	2e−01	1 / 4	let−7c
12	2e−01	1 / 4	miR−34b
13	2e−01	1 / 4	miR−34c
14	2e−01	1 / 5	miR−101
15	2e−01	1 / 5	miR−205
16	2e−01	1 / 5	miR−320
17	2e−01	1 / 6	let−7d
18	2e−01	1 / 6	miR−133a
19	2e−01	1 / 6	miR−15b
20	2e−01	1 / 6	miR−26a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.002	13 / 122	hsa−miR−380
2	0.002	10 / 81	hsa−miR−188−5p
3	0.003	22 / 269	hsa−miR−1244
4	0.004	11 / 101	hsa−miR−410
5	0.004	9 / 75	hsa−miR−1305
6	0.007	13 / 141	hsa−miR−135b
7	0.008	21 / 278	hsa−miR−30c
8	0.008	7 / 55	hsa−miR−891b
9	0.009	16 / 194	hsa−miR−222
10	0.009	13 / 146	hsa−miR−494
11	0.014	15 / 187	hsa−miR−520d−5p
12	0.017	4 / 24	hsa−miR−1228
13	0.018	7 / 64	hsa−miR−324−5p
14	0.018	7 / 64	hsa−miR−371−5p
15	0.019	14 / 177	hsa−miR−1
16	0.021	19 / 268	hsa−miR−30b
17	0.023	11 / 130	hsa−miR−323−3p
18	0.026	5 / 40	hsa−miR−758
19	0.027	15 / 203	hsa−miR−221
20	0.028	28 / 449	hsa−miR−130b

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.002	4 / 13	MACIEJ_MMML 6
2	0.005	2 / 3	MACIEJ_MMML 7
3	0.083	1 / 2	MACIEJ_MMML 32
4	0.159	1 / 4	MACIEJ_MMML 2
5	0.159	1 / 4	MACIEJ_MMML 44
6	0.195	1 / 5	MACIEJ_MMML 20
7	0.262	1 / 7	MACIEJ_MMML 5
8	0.380	1 / 11	MACIEJ_MMML 3
9	0.380	1 / 11	MACIEJ_MMML 49
10	0.456	1 / 14	MACIEJ_MMML 26
11	0.456	1 / 14	MACIEJ_MMML 30
12	1.000	0 / 16	MACIEJ_MMML 1
13	1.000	0 / 13	MACIEJ_MMML 10
14	1.000	0 / 7	MACIEJ_MMML 13
15	1.000	0 / 9	MACIEJ_MMML 14
16	1.000	0 / 11	MACIEJ_MMML 15
17	1.000	0 / 15	MACIEJ_MMML 16
18	1.000	0 / 2	MACIEJ_MMML 17
19	1.000	0 / 14	MACIEJ_MMML 19
20	1.000	0 / 15	MACIEJ_MMML 22

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.08	2 / 11	BENTINK_e2f3.2
2	0.09	2 / 12	BENTINK_ras.1
3	0.38	1 / 11	BENTINK_ras.4
4	0.41	1 / 12	BENTINK_e2f3.1
5	0.43	1 / 13	BENTINK_src.10
6	0.46	1 / 14	BENTINK_myc.1
7	0.48	1 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	GUSTAFSON_PI3K_UP
9	1.00	0 / 15	BENTINK_ras.6
10	1.00	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−04	74 / 1146	HEBENSTREIT_low expression TF
2	8e−02	1 / 2	MYC_Cell cycle DOWN
3	8e−02	1 / 2	MYC_Chromatin_modification UP
4	2e−01	1 / 5	MYC_TFs
5	3e−01	1 / 8	MYC_Cell cycle UP
6	3e−01	1 / 9	MYC_Targets DOWN
7	5e−01	3 / 63	MYC_Targets UP
8	6e−01	1 / 20	MYC_Metabolism UP
9	1e+00	32 / 1095	HEBENSTREIT_high expression TF
10	1e+00	28 / 1233	KIM_MYC targets
11	1e+00	0 / 14	NOWICK_TF
12	1e+00	0 / 4	MYC_Apoptosis UP
13	1e+00	0 / 4	MYC_Cell growth and proliferation UP
14	1e+00	0 / 7	MYC_DNA repair UP
15	1e+00	0 / 3	MYC_DNA replication UP
16	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
17	1e+00	0 / 16	MYC_Protein synthesis degradation UP
18	1e+00	0 / 8	MYC_RNA processing binding UP
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	2e−05	8 / 29	VAQUERIZAS_Lymph node
2	3e−05	6 / 16	VAQUERIZAS_Salivary gland
3	2e−04	6 / 21	VAQUERIZAS_Tonsil
4	2e−04	8 / 40	VAQUERIZAS_Fetal brain
5	8e−04	7 / 37	VAQUERIZAS_Prostate
6	2e−03	3 / 7	VAQUERIZAS_Appendix
7	3e−03	5 / 24	VAQUERIZAS_Trachea
8	7e−03	6 / 41	VAQUERIZAS_Thymus
9	8e−03	4 / 19	VAQUERIZAS_Pituitary
10	8e−03	5 / 30	VAQUERIZAS_Fetal lung
11	9e−03	4 / 20	VAQUERIZAS_Bone marrow
12	9e−03	6 / 43	VAQUERIZAS_Uterus
13	9e−03	6 / 43	VAQUERIZAS_Whole brain
14	2e−02	7 / 62	VAQUERIZAS_Whole blood
15	2e−02	7 / 62	VAQUERIZAS_Lung
16	2e−02	5 / 39	VAQUERIZAS_Thyroid
17	3e−02	4 / 28	VAQUERIZAS_Liver
18	3e−02	4 / 29	VAQUERIZAS_Smooth muscle
19	5e−02	3 / 20	VAQUERIZAS_Adrenal cortex
20	1e−01	2 / 13	VAQUERIZAS_Ovary

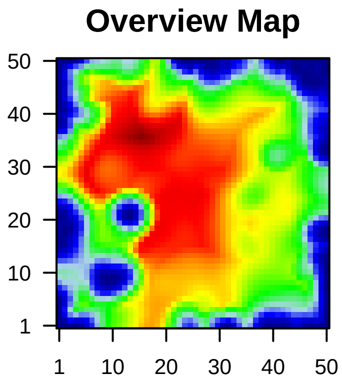
Sample−Underexpression

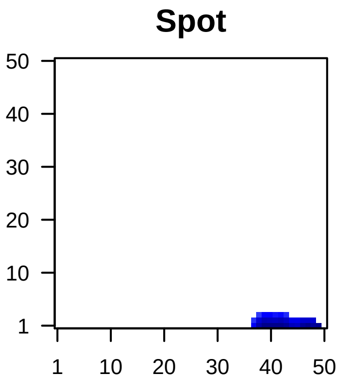
Spot Summary: j

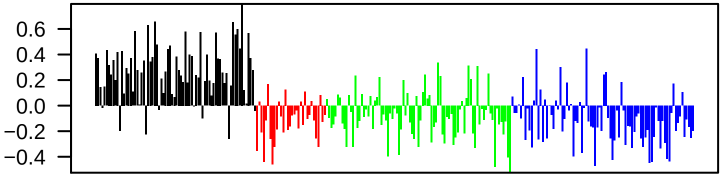
metagenes = 31
genes = 456

<r> metagenes = 0.85
<r> genes = 0.37
beta: r2= 17.38 / log p= −Inf

samples with spot = 36 (13.1 %)
Classical : 6 (18.8 %)
Mesenchymal : 12 (14.1 %)
Basal : 18 (21.4 %)





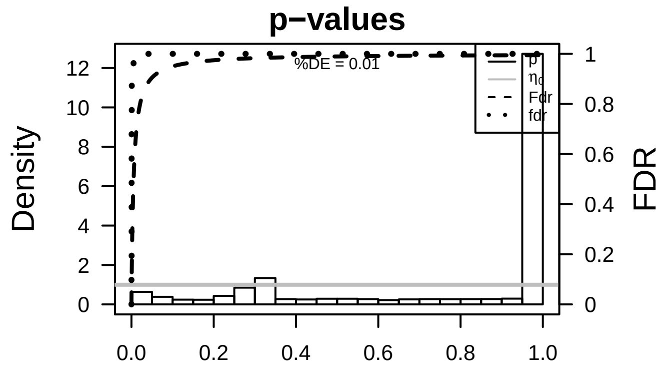


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3543	1.5	−4.05	0.53	IGLL1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
2	6364	3.07	−3.08	0.26	CCL20	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
3	57172	3.1	−2.31	0.69	CAMK1G	calcium/calmodulin−dependent protein kinase IG [Source:HG
4	54855	2.8	−2.28	0.76	FAM46C	family with sequence similarity 46, member C [Source:HGNC
5	5920	2.02	−2.17	0.59	RARRES3	retinoic acid receptor responder (tazarotene induced) 3 [Sour
6	51755	2.83	−2.17	0.66	CDK12	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:2422
7	400818	1.62	−1.99	0.69	AC239811.2	Neuroblastoma breakpoint family member 1 [Source:UniProt
8	23231	2.08	−1.93	0.63	SEL1L3	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
9	4283	2.98	−1.9	0.55	CXCL9	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
10	10628	1.61	−1.89	0.57	TXNIP	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
11	2634	1.44	−1.84	0.55	GBP2	guanylate binding protein 2, interferon−inducible [Source:HGN
12	3002	2.43	−1.84	0.71	GZMB	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
13	3123	3.58	−1.81	0.25	HLA−DRB1	major histocompatibility complex, class II, DR beta 1 [Source:
14	641737	1.2	−1.79	0.93		
15	3001	2.33	−1.74	0.65	GZMA	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
16	51466	1.65	−1.73	0.77	EVL	Enah/Vasp−like [Source:HGNC Symbol;Acc:20234]
17	3669	1.84	−1.71	0.71	ISG20	interferon stimulated exonuclease gene 20kDa [Source:HGNC
18	4067	1.56	−1.67	0.47	LYN	v−yes−1 Yamaguchi sarcoma viral related oncogene homolog
19	915	2.29	−1.66	0.91	CD3D	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
20	100132406	1.15	−1.64	0.64	NBPF10	neuroblastoma breakpoint family, member 10 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−31	64 / 417	H.Tiss	WIRTH_Immune system
2	5e−17	54 / 553	Cance	Lembcke_Colonic Inflammation
3	4e−13	35 / 312	BP	immune response
4	4e−08	12 / 60	BP	T cell costimulation
5	5e−07	6 / 13	Cance	GENTLES_modul18
6	1e−06	17 / 162	CC	external side of plasma membrane
7	1e−06	6 / 15	CC	MHC class II protein complex
8	2e−06	19 / 204	BP	cell surface receptor signaling pathway
9	2e−06	6 / 16	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
10	2e−06	6 / 16	GSEA	SU_THYMUS
11	5e−06	5 / 11	GSEA	BIOCARTA_TCYTOTOXIC_PATHWAY
12	6e−06	24 / 327	Lymph	SPANG_CD40 6hrs UP
13	1e−05	5 / 13	BP	negative regulation of B cell proliferation
14	1e−05	54 / 1135	Chr	Chr 19
15	2e−05	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
16	2e−05	5 / 14	GSEA	FINETTI_BREAST_CANCER_KINOME_GREEN
17	2e−05	10 / 74	BP	regulation of immune response
18	3e−05	8 / 47	BP	antigen processing and presentation
19	3e−05	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	6e−05	26 / 426	Lymph	SPANG_CD40 6hrs DN
21	7e−05	10 / 84	BP	T cell receptor signaling pathway
22	7e−05	6 / 28	BP	B cell receptor signaling pathway
23	1e−04	4 / 11	BP	positive regulation of B cell differentiation
24	1e−04	4 / 11	BP	positive regulation of natural killer cell mediated cytotoxicity
25	1e−04	4 / 11	GSEA	BIOCARTA_THELPER_PATHWAY
26	2e−04	7 / 45	BP	cellular defense response
27	2e−04	7 / 45	BP	T cell activation
28	2e−04	8 / 60	BP	interferon−gamma−mediated signaling pathway
29	2e−04	4 / 12	BP	negative regulation of T cell activation
30	2e−04	4 / 12	GSEA	BIOCARTA_CTL_PATHWAY
31	3e−04	4 / 13	Lymph	BENTINK_mBL DOWN
32	3e−04	4 / 13	GSEA	BIOCARTA_IL17_PATHWAY
33	3e−04	15 / 204	BP	cytokine−mediated signaling pathway
34	3e−04	5 / 24	BP	negative regulation of T cell proliferation
35	4e−04	4 / 14	GSEA	BIOCARTA_IL12_PATHWAY
36	4e−04	4 / 14	GSEA	BIOCARTA_NO2IL12_PATHWAY
37	4e−04	12 / 143	MF	transmembrane signaling receptor activity
38	5e−04	4 / 15	GSEA	HUMMEL_BURKITTS_LYMPHOMA_DN
39	7e−04	19 / 316	Cance	SPANG_BCL6−index2
40	7e−04	5 / 28	CC	transport vesicle membrane



BP

Rank	p−value	#in/all	Geneset
1	4e−13	35 / 312	immune response
2	4e−08	12 / 60	T cell costimulation
3	2e−06	19 / 204	cell surface receptor signaling pathway
4	1e−05	5 / 13	negative regulation of B cell proliferation
5	2e−05	10 / 74	regulation of immune response
6	3e−05	8 / 47	antigen processing and presentation
7	7e−05	10 / 84	T cell receptor signaling pathway
8	7e−05	6 / 28	B cell receptor signaling pathway
9	1e−04	4 / 11	positive regulation of B cell differentiation
10	1e−04	4 / 11	positive regulation of natural killer cell mediated cytotoxicity
11	2e−04	7 / 45	cellular defense response
12	2e−04	7 / 45	T cell activation
13	2e−04	8 / 60	interferon−gamma−mediated signaling pathway
14	2e−04	4 / 12	negative regulation of T cell activation
15	3e−04	15 / 204	cytokine−mediated signaling pathway
16	3e−04	5 / 24	negative regulation of T cell proliferation
17	1e−03	10 / 123	defense response to virus
18	4e−03	3 / 13	positive regulation of JAK−STAT cascade
19	5e−03	4 / 27	lipopolysaccharide−mediated signaling pathway
20	5e−03	3 / 14	defense response to protozoan

Cancer

Rank	p−value	#in/all	Geneset
1	5e−17	54 / 553	Lembcke_Colonic Inflammation
2	5e−07	6 / 13	GENTLES_modul18
3	7e−04	19 / 316	SPANG_BCL6−index2
4	1e−01	8 / 185	SPANG_LPS−index2
5	2e−01	1 / 7	ZHANG_MGUS up
6	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
7	3e−01	1 / 13	GENTLES_modul12
8	3e−01	1 / 14	LIU_LIVER_CANCER
9	3e−01	1 / 14	WANG_ER_UP
10	3e−01	1 / 15	LIU_PROSTATE_CANCER_DN
11	3e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
12	7e−01	1 / 48	KUIPER_MM poor survival
13	8e−01	1 / 68	SHAUGHNESSY_MM high risk
14	1e+00	5 / 530	Lembcke_Normal vs Adenoma
15	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
16	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1e+00	0 / 10	LIU_BREAST_CANCER
19	1e+00	0 / 14	LIU_PROSTATE_CANCER_UP
20	1e+00	0 / 9	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	1e−06	17 / 162	external side of plasma membrane
2	1e−06	6 / 15	MHC class II protein complex
3	7e−04	5 / 28	transport vesicle membrane
4	2e−03	4 / 21	clathrin−coated endocytic vesicle membrane
5	3e−03	4 / 23	integral to lumenal side of endoplasmic reticulum membrane
6	3e−03	4 / 24	immunological synapse
7	3e−03	3 / 12	T cell receptor complex
8	4e−03	30 / 686	Golgi apparatus
9	9e−03	11 / 184	lysosome
10	9e−03	4 / 32	ER to Golgi transport vesicle membrane
11	1e−02	4 / 35	trans−Golgi network membrane
12	2e−02	4 / 38	cytoplasmic side of plasma membrane
13	3e−02	5 / 65	lysosomal lumen
14	3e−02	4 / 46	endocytic vesicle membrane
15	4e−02	5 / 70	endomembrane system
16	4e−02	3 / 29	histone deacetylase complex
17	5e−02	5 / 78	PML body
18	6e−02	10 / 215	lysosomal membrane
19	9e−02	2 / 19	histone methyltransferase complex
20	9e−02	3 / 41	transport vesicle

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	54 / 1135	Chr 19
2	4e−03	38 / 918	Chr 17
3	6e−03	19 / 386	Chr 22
4	1e−01	8 / 187	Chr 21
5	1e−01	2 / 23	Chr HSCHR6_MHC_DBB
6	2e−01	3 / 52	Chr HSCHR6_MHC_QBL
7	3e−01	19 / 630	Chr X
8	3e−01	22 / 743	Chr 7
9	3e−01	21 / 717	Chr 16
10	3e−01	15 / 504	Chr 15
11	4e−01	15 / 519	Chr 14
12	6e−01	16 / 633	Chr 9
13	7e−01	17 / 699	Chr 5
14	7e−01	42 / 1720	Chr 1
15	8e−01	22 / 957	Chr 11
16	8e−01	13 / 602	Chr 10
17	8e−01	23 / 1033	Chr 2
18	8e−01	9 / 449	Chr 20
19	9e−01	4 / 232	Chr 18
20	9e−01	14 / 714	Chr 6

Disease

Rank	p−value	#in/all	Geneset
1	0.8	12 / 572	GUDJ_psoriasis up
2	1.0	4 / 375	GUDJ_psoriasis down
3	1.0	0 / 17	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
2	3e−05	5 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
3	9e−03	5 / 49	Donson−innate immunity−associated with LTS in HGA
4	9e−03	4 / 32	Donson−Misc immune function−associated with LTS in HGA
5	1e−02	2 / 7	Donson−adaptive−immunity−associated with LTS in HGA
6	2e−02	2 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
7	3e−02	4 / 45	willscher_GBM_Verhaak−PNwt_expression_J_up
8	7e−02	2 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
9	9e−02	11 / 265	willscher_GBM_Verhaak−CL_expression_B_up
10	9e−02	11 / 265	willscher_GBM_Verhaak−MES_expression_B_up
11	9e−02	11 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
12	9e−02	11 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
13	1e−01	1 / 4	willscher_GBM_STSwt_proteomics−L_UP
14	1e−01	4 / 71	willscher_GBM_Verhaak−CL_expression_H_down
15	1e−01	4 / 71	willscher_GBM_Verhaak−MES_expression_H_up
16	1e−01	4 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
17	1e−01	3 / 48	Noushmehr_Pron_GCIMP_hypermeth_DN
18	2e−01	3 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
19	2e−01	4 / 95	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
20	3e−01	1 / 12	Phillips PN up vs MES & Prolif

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	6 / 16	FARMER_BREAST_CANCER_CLUSTER_1
2	2e−06	6 / 16	SU_THYMUS
3	5e−06	5 / 11	BIOCARTA_TCYTOTOXIC_PATHWAY
4	2e−05	5 / 14	FINETTI_BREAST_CANCER_KINOME_GREEN
5	1e−04	4 / 11	BIOCARTA_THELPER_PATHWAY
6	2e−04	4 / 12	BIOCARTA_CTL_PATHWAY
7	3e−04	4 / 13	BIOCARTA_IL17_PATHWAY
8	4e−04	4 / 14	BIOCARTA_IL12_PATHWAY
9	4e−04	4 / 14	BIOCARTA_NO2IL12_PATHWAY
10	5e−04	4 / 15	HUMMEL_BURKITTS_LYMPHOMA_DN
11	9e−04	3 / 8	BOQUEST_STEM_CELL_DN
12	9e−04	3 / 8	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
13	2e−03	3 / 10	LEE_EARLY_T_LYMPHOCYTE_DN
14	3e−03	3 / 12	KLEIN_TARGETS_OF_BCR_ABL1_FUSION
15	3e−03	3 / 12	MCCABE_HOXC6_TARGETS_CANCER_UP
16	3e−03	3 / 12	ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN
17	3e−03	3 / 12	BIOCARTA_CTLA4_PATHWAY
18	4e−03	2 / 4	ROETH_TERT_TARGETS_DN
19	4e−03	2 / 4	BIOCARTA_CYTOKINE_PATHWAY
20	4e−03	3 / 13	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN

H. Tiss

Rank	p−value	#in/all	Geneset
1	4e−31	64 / 417	WIRTH_Immune system
2	1e−01	1 / 6	WIRTH_Bone marrow
3	3e−01	1 / 13	WIRTH_Cortex cerebri
4	3e−01	1 / 16	WIRTH_Hippocampus
5	6e−01	1 / 36	WIRTH_Placenta
6	1e+00	1 / 127	WIRTH_Muscle
7	1e+00	1 / 400	WIRTH_Nervous System
8	1e+00	0 / 5	WIRTH_Pituitary gland
9	1e+00	0 / 26	WIRTH_Pancreas
10	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
11	1e+00	0 / 12	WIRTH_Prim. lymphoid organs
12	1e+00	0 / 10	WIRTH_B−cells
13	1e+00	0 / 13	WIRTH_Tonsil
14	1e+00	0 / 13	WIRTH_Thymus
15	1e+00	0 / 12	WIRTH_Lymphocytes
16	1e+00	0 / 14	WIRTH_Globus pallidus
17	1e+00	0 / 15	WIRTH_Telencephalon
18	1e+00	0 / 13	WIRTH_Thalamus
19	1e+00	0 / 15	WIRTH_Cerebellum
20	1e+00	0 / 120	WIRTH_Testis

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−06	24 / 327	SPANG_CD40 6hrs UP
2	6e−05	26 / 426	SPANG_CD40 6hrs DN
3	3e−04	4 / 13	BENTINK_mBL DOWN
4	2e−03	7 / 69	SPANG_LPS 6hrs DN
5	2e−03	4 / 22	DAVE_NFkB BL DN
6	4e−03	10 / 140	DAVE_BL−vs−DLBCL
7	8e−03	3 / 16	WRIGHT_ABC UP
8	3e−02	6 / 86	ROSOLOWSKI_red total
9	4e−02	3 / 28	DAVE_Immune response 1
10	5e−02	4 / 54	SPANG_BAFF 9hrs DN
11	8e−02	3 / 38	ROSOLOWSKI_blue DOWN
12	1e−01	1 / 4	WRIGHT_custom GCB−DLBCL UP
13	1e−01	1 / 4	MASCQUE_mBL DOWN
14	1e−01	11 / 274	SPANG_IL21 DN
15	1e−01	5 / 100	ROSOLOWSKI_blue total
16	1e−01	1 / 5	WRIGHT_custom ABC−DLBCL UP
17	1e−01	28 / 852	SPANG_BCR DN
18	2e−01	1 / 8	MASCQUE_GCB UP
19	2e−01	1 / 8	MASCQUE_ABC UP
20	2e−01	5 / 118	SPANG_LPS 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	4e−04	12 / 143	transmembrane signaling receptor activity
2	4e−03	5 / 41	non−membrane spanning protein tyrosine kinase activity
3	5e−03	5 / 43	chemokine activity
4	1e−02	61 / 1749	DNA binding
5	2e−02	12 / 227	receptor activity
6	2e−02	3 / 22	Rab guanyl−nucleotide exchange factor activity
7	2e−02	22 / 529	protein homodimerization activity
8	3e−02	2 / 10	endodeoxyribonuclease activity
9	3e−02	2 / 10	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in cyclic
10	3e−02	2 / 10	small GTPase binding
11	3e−02	4 / 46	Rab GTPase activator activity
12	3e−02	2 / 11	regulatory region DNA binding
13	3e−02	4 / 47	transcription cofactor activity
14	4e−02	3 / 28	enzyme inhibitor activity
15	4e−02	4 / 48	cysteine−type endopeptidase activity
16	4e−02	2 / 12	MHC class I protein binding
17	4e−02	7 / 121	cytokine activity
18	4e−02	21 / 531	catalytic activity
19	4e−02	4 / 50	SH3/SH2 adaptor activity
20	5e−02	3 / 31	SH2 domain binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.02	7 / 99	CCTG−513
2	0.06	4 / 55	AATG−136
3	0.13	3 / 48	CCAT−432
4	0.15	5 / 108	AGCA−155
5	0.17	4 / 83	AGGA−516−3P
6	0.21	5 / 120	GAGC−149
7	0.25	2 / 37	TAGG−192−−215
8	0.31	4 / 107	TCCA−518C
9	0.31	3 / 75	CCAG−331
10	0.34	6 / 182	CTGA−24
11	0.36	1 / 17	AGTC−151
12	0.37	3 / 83	GCAC−18A−−18B
13	0.38	1 / 18	CGCT−503
14	0.39	2 / 51	ATAA−154
15	0.41	2 / 53	AAGT−422B−−422A
16	0.41	1 / 20	GTAG−189
17	0.42	6 / 199	CAGC−320
18	0.44	7 / 240	CAGT−141−−200A
19	0.46	1 / 23	CACG−302A
20	0.48	11 / 401	ACCA−9

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	2 / 13	miR−34a
2	0.05	1 / 2	miR−193a
3	0.50	1 / 26	miR−21
4	1.00	0 / 11	let−7a
5	1.00	0 / 6	let−7b
6	1.00	0 / 4	let−7c
7	1.00	0 / 6	let−7d
8	1.00	0 / 4	let−7g
9	1.00	0 / 13	miR−1
10	1.00	0 / 5	miR−101
11	1.00	0 / 2	miR−101b
12	1.00	0 / 4	miR−106b
13	1.00	0 / 2	miR−107
14	1.00	0 / 4	miR−122
15	1.00	0 / 2	miR−124a
16	1.00	0 / 6	miR−125a
17	1.00	0 / 9	miR−125b
18	1.00	0 / 5	miR−126
19	1.00	0 / 2	miR−127
20	1.00	0 / 3	miR−128

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.05	4 / 52	hsa−miR−513a−5p
2	0.05	6 / 101	hsa−miR−525−5p
3	0.07	5 / 86	hsa−miR−220c
4	0.08	2 / 18	hsa−miR−551a
5	0.09	3 / 41	hsa−miR−490−5p
6	0.10	3 / 43	hsa−miR−541
7	0.11	4 / 69	hsa−miR−578
8	0.11	6 / 125	hsa−miR−520a−5p
9	0.15	3 / 51	hsa−miR−370
10	0.18	2 / 29	hsa−miR−296−5p
11	0.19	3 / 58	hsa−miR−324−3p
12	0.19	2 / 31	hsa−miR−617
13	0.20	4 / 88	hsa−miR−423−5p
14	0.21	2 / 33	hsa−miR−934
15	0.22	2 / 34	hsa−miR−615−5p
16	0.22	2 / 34	hsa−miR−1226
17	0.23	2 / 35	hsa−miR−588
18	0.23	1 / 10	hsa−miR−933
19	0.27	3 / 69	hsa−miR−502−5p
20	0.27	2 / 39	hsa−miR−1258

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.005	3 / 14	MACIEJ_MMML 8
2	0.044	2 / 13	MACIEJ_MMML 6
3	0.052	1 / 2	MACIEJ_MMML 32
4	0.076	1 / 3	MACIEJ_MMML 7
5	0.101	1 / 4	MACIEJ_MMML 2
6	0.101	1 / 4	MACIEJ_MMML 44
7	0.169	1 / 7	MACIEJ_MMML 48
8	0.310	1 / 14	MACIEJ_MMML 30
9	0.328	1 / 15	MACIEJ_MMML 16
10	1.000	0 / 16	MACIEJ_MMML 1
11	1.000	0 / 13	MACIEJ_MMML 10
12	1.000	0 / 7	MACIEJ_MMML 13
13	1.000	0 / 9	MACIEJ_MMML 14
14	1.000	0 / 11	MACIEJ_MMML 15
15	1.000	0 / 2	MACIEJ_MMML 17
16	1.000	0 / 14	MACIEJ_MMML 19
17	1.000	0 / 5	MACIEJ_MMML 20
18	1.000	0 / 15	MACIEJ_MMML 22
19	1.000	0 / 4	MACIEJ_MMML 23
20	1.000	0 / 12	MACIEJ_MMML 24

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.05	2 / 14	NOWICK_TF
2	0.42	30 / 1095	HEBENSTREIT_high expression TF
3	0.99	20 / 1233	KIM_MYC targets
4	1.00	17 / 1146	HEBENSTREIT_low expression TF
5	1.00	0 / 5	MYC_TFs
6	1.00	0 / 63	MYC_Targets UP
7	1.00	0 / 9	MYC_Targets DOWN
8	1.00	0 / 4	MYC_Apoptosis UP
9	1.00	0 / 8	MYC_Cell cycle UP
10	1.00	0 / 2	MYC_Cell cycle DOWN
11	1.00	0 / 4	MYC_Cell growth and proliferation UP
12	1.00	0 / 2	MYC_Chromatin_modification UP
13	1.00	0 / 7	MYC_DNA repair UP
14	1.00	0 / 3	MYC_DNA replication UP
15	1.00	0 / 2	MYC_ECM cell adhesion DOWN
16	1.00	0 / 20	MYC_Metabolism UP
17	1.00	0 / 16	MYC_Protein synthesis degradation UP
18	1.00	0 / 8	MYC_RNA processing binding UP
19	1.00	0 / 2	MYC_Signal transduction UP
20	1.00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.007	4 / 29	VAQUERIZAS_Lymph node
2	0.036	3 / 28	VAQUERIZAS_Liver
3	0.064	2 / 16	VAQUERIZAS_Fetal thyroid
4	0.104	2 / 21	VAQUERIZAS_Tonsil
5	0.175	2 / 29	VAQUERIZAS_Smooth muscle
6	0.252	2 / 37	VAQUERIZAS_Prostate
7	0.272	2 / 39	VAQUERIZAS_Thyroid
8	0.310	1 / 14	VAQUERIZAS_Fetal liver
9	0.325	5 / 144	VAQUERIZAS_General
10	0.346	1 / 16	VAQUERIZAS_Salivary gland
11	0.412	1 / 20	VAQUERIZAS_Bone marrow
12	0.485	2 / 62	VAQUERIZAS_Whole blood
13	0.485	2 / 62	VAQUERIZAS_Lung
14	0.549	1 / 30	VAQUERIZAS_Fetal lung
15	0.635	1 / 38	VAQUERIZAS_Testis
16	0.663	1 / 41	VAQUERIZAS_Thymus
17	1.000	0 / 40	VAQUERIZAS_Fetal brain
18	1.000	0 / 44	VAQUERIZAS_Placenta
19	1.000	0 / 43	VAQUERIZAS_Uterus
20	1.000	0 / 12	VAQUERIZAS_Kidney

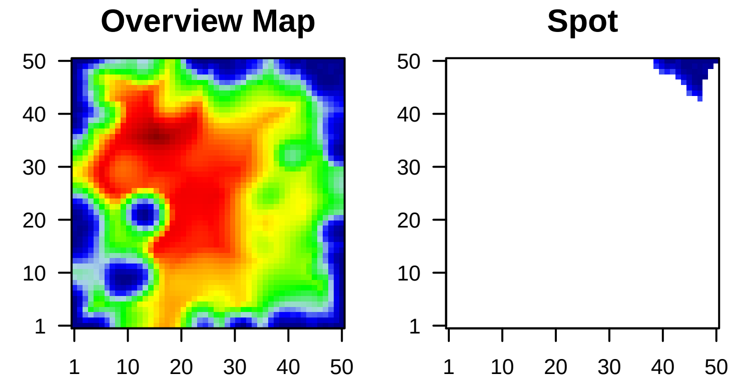
Sample−Underexpression

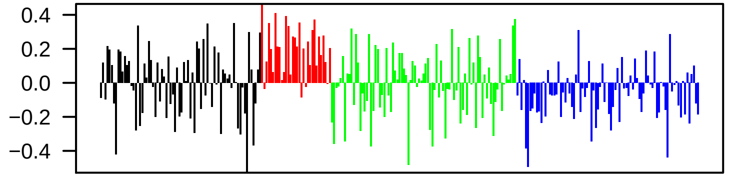
Spot Summary: k

metagenes = 49
genes = 685

<r> metagenes = 0.84
<r> genes = 0.25
beta: r2= 9.53 / log p= −Inf

samples with spot = 25 (9.1 %)
Atypical : 9 (12.2 %)
Mesenchymal : 10 (11.8 %)
Basal : 6 (7.1 %)



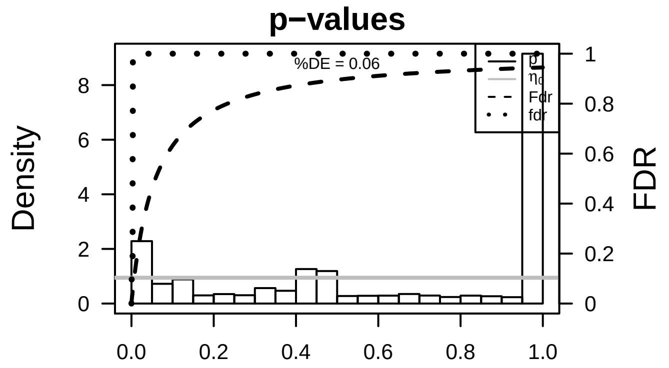


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3866	3.23	−3.16	0.46	KRT15	keratin 15 [Source:HGNC Symbol;Acc:6421]
2	9076	2.4	−3.14	0.37	CLDN1	claudin 1 [Source:HGNC Symbol;Acc:2032]
3	256764	2.31	−2.89	0.4	WDR72	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
4	94234	2.17	−2.63	0.35	FOXQ1	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
5	216	2.99	−2.41	0.63	ALDH1A1	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	4072	2.5	−2.3	0.71	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
7	3304	1.71	−2.26	0.26	HSPA1A	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
8	928	2.05	−2.1	0.65	CD9	CD9 molecule [Source:HGNC Symbol;Acc:1709]
9	11166	2.55	−1.98	0.68	SOX21	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
10	4953	2.24	−1.94	0.4	ODC1	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	7153	1.7	−1.84	0.83	TOP2A	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
12	655	1.77	−1.82	0.53	BMP7	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
13	116832	1.7	−1.8	0.61	RPL39L	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
14	55165	1.32	−1.76	0.81	CEP55	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
15	10643	2.03	−1.74	0.52	IGF2BP3	insulin−like growth factor 2 mRNA binding protein 3 [Source:
16	54443	1.46	−1.74	0.71	ANLN	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
17	3945	1.73	−1.73	0.38	LDHB	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
18	51659	1.45	−1.7	0.62	GINS2	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
19	6657	2.29	−1.7	0.85	SOX2	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
20	29968	1.51	−1.67	0.59	PSAT1	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−95	94 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	1e−95	94 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	2e−70	116 / 370	BP	mitotic cell cycle
4	1e−54	119 / 530	Canc	Lembcke_Normal vs Adenoma
5	8e−39	136 / 949	CC	nucleoplasm
6	6e−31	49 / 149	BP	DNA replication
7	2e−27	56 / 232	BP	mitosis
8	7e−23	16 / 16	GSEA	EGUCHI_CELL_CYCLE_RB1_TARGETS
9	3e−21	26 / 57	Glio	developing astrocytes
10	6e−21	39 / 148	BP	G1/S transition of mitotic cell cycle
11	3e−20	15 / 16	GSEA	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
12	3e−20	54 / 298	BP	DNA repair
13	6e−19	14 / 15	GSEA	FINETTI_BREAST_CANCER_KINOME_RED
14	2e−18	185 / 2378	CC	cytosol
15	4e−18	25 / 66	CC	condensed chromosome kinetochore
16	6e−18	18 / 30	BP	DNA strand elongation involved in DNA replication
17	8e−18	73 / 572	Disea	GUDJ_psoriasis up
18	1e−17	23 / 56	CC	chromosome, centromeric region
19	3e−16	12 / 13	GSEA	CROONQUIST_IL6_DEPRIVATION_DN
20	5e−16	13 / 16	GSEA	FARMER_BREAST_CANCER_CLUSTER_2
21	4e−14	12 / 16	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
22	4e−14	12 / 16	GSEA	KANG_DOXORUBICIN_RESISTANCE_UP
23	4e−14	89 / 914	Chr	Chr 3
24	1e−13	16 / 35	BP	mitotic nuclear envelope disassembly
25	2e−13	11 / 14	MMM	MACIEJ_MMML 4
26	2e−13	11 / 14	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	3e−13	113 / 1344	MF	ATP binding
28	4e−13	12 / 18	BP	spindle organization
29	4e−13	18 / 49	BP	telomere maintenance
30	5e−13	279 / 4640	CC	nucleus
31	7e−13	11 / 15	Canc	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
32	2e−12	13 / 24	BP	telomere maintenance via recombination
33	2e−12	11 / 16	Canc	WOLFER_overlap genes
34	2e−12	11 / 16	GSEA	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
35	2e−12	11 / 16	GSEA	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
36	2e−12	11 / 16	GSEA	CROONQUIST_NRAS_SIGNALING_DN
37	2e−12	11 / 16	GSEA	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
38	2e−12	11 / 16	GSEA	REACTOME_DNA_STRAND_ELONGATION
39	2e−12	11 / 16	GSEA	REACTOME_G2_M_CHECKPOINTS
40	3e−12	19 / 61	CC	kinetochore



BP

Rank	p−value	#in/all	Geneset
1	2e−70	116 / 370	mitotic cell cycle
2	6e−31	49 / 149	DNA replication
3	2e−27	56 / 232	mitosis
4	6e−21	39 / 148	G1/S transition of mitotic cell cycle
5	3e−20	54 / 298	DNA repair
6	6e−18	18 / 30	DNA strand elongation involved in DNA replication
7	1e−13	16 / 35	mitotic nuclear envelope disassembly
8	4e−13	12 / 18	spindle organization
9	4e−13	18 / 49	telomere maintenance
10	2e−12	13 / 24	telomere maintenance via recombination
11	5e−12	26 / 122	G2/M transition of mitotic cell cycle
12	5e−12	12 / 21	telomere maintenance via semi−conservative replication
13	1e−11	12 / 22	DNA replication initiation
14	7e−10	12 / 29	regulation of glucose transport
15	1e−09	8 / 11	mitotic metaphase plate congression
16	1e−09	17 / 67	chromosome segregation
17	2e−09	15 / 53	mRNA transport
18	5e−09	30 / 213	cell cycle
19	6e−09	10 / 22	CENP−A containing nucleosome assembly at centromere
20	6e−09	19 / 92	cell division

Cancer

Rank	p−value	#in/all	Geneset
1	1e−54	119 / 530	Lembcke_Normal vs Adenoma
2	7e−13	11 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	2e−12	11 / 16	WOLFER_overlap genes
4	1e−08	16 / 68	SHAUGHNESSY_MM high risk
5	8e−08	8 / 16	RHODES_UNDIFFERENTIATED_CANCER
6	1e−04	9 / 48	KUIPER_MM poor survival
7	3e−04	5 / 15	BEN−PORATH_UP
8	4e−04	7 / 33	KUIPER_MM good survival
9	5e−04	4 / 10	GENTLES_modul3
10	3e−03	4 / 15	RHODES_CANCER_META_SIGNATURE
11	3e−03	4 / 15	GENTLES_modul1
12	3e−03	4 / 15	GENTLES_modul6
13	4e−03	4 / 16	GENTLES_modul2
14	4e−03	4 / 16	GENTLES_modul4
15	5e−03	6 / 39	ZHANG_MM up
16	1e−01	2 / 16	GENTLES_modul7
17	3e−01	1 / 10	LIU_BREAST_CANCER
18	4e−01	1 / 11	GENTLES_modul5
19	4e−01	1 / 13	GENTLES_modul16
20	4e−01	1 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	8e−39	136 / 949	nucleoplasm
2	2e−18	185 / 2378	cytosol
3	4e−18	25 / 66	condensed chromosome kinetochore
4	1e−17	23 / 56	chromosome, centromeric region
5	5e−13	279 / 4640	nucleus
6	3e−12	19 / 61	kinetochore
7	2e−11	18 / 59	nuclear pore
8	1e−10	20 / 83	spindle pole
9	2e−10	59 / 579	nucleolus
10	6e−10	41 / 335	centrosome
11	6e−10	22 / 109	spindle
12	4e−09	22 / 120	nuclear envelope
13	2e−08	7 / 10	nuclear pore outer ring
14	4e−08	17 / 82	chromosome
15	9e−07	15 / 80	chromatin
16	6e−06	9 / 33	spindle microtubule
17	2e−05	227 / 4310	cytoplasm
18	3e−05	15 / 104	midbody
19	3e−05	5 / 10	lateral element
20	3e−05	8 / 31	condensed nuclear chromosome

Chr

Rank	p−value	#in/all	Geneset
1	4e−14	89 / 914	Chr 3
2	3e−05	43 / 534	Chr 8
3	2e−03	54 / 866	Chr 12
4	3e−02	56 / 1033	Chr 2
5	2e−01	13 / 232	Chr 18
6	2e−01	25 / 504	Chr 15
7	3e−01	77 / 1720	Chr 1
8	3e−01	29 / 630	Chr X
9	5e−01	26 / 618	Chr 4
10	5e−01	31 / 743	Chr 7
11	8e−01	26 / 714	Chr 6
12	8e−01	21 / 602	Chr 10
13	9e−01	21 / 633	Chr 9
14	9e−01	1 / 52	Chr HSCHR6_MHC_QBL
15	9e−01	14 / 449	Chr 20
16	9e−01	8 / 280	Chr 13
17	9e−01	16 / 519	Chr 14
18	9e−01	23 / 717	Chr 16
19	9e−01	11 / 386	Chr 22
20	9e−01	22 / 699	Chr 5

Disease

Rank	p−value	#in/all	Geneset
1	8e−18	73 / 572	GUDJ_psoriasis up
2	6e−01	15 / 375	GUDJ_psoriasis down
3	7e−01	1 / 26	BCHETNIA_EBM−DM up
4	1e+00	0 / 17	BCHETNIA_EBM up
5	1e+00	0 / 2	BCHETNIA_EBM down
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	1e−95	94 / 142	willscher_GBM_Verhaak−CL_expression_C_up
2	1e−95	94 / 142	willscher_GBM_Verhaak−PNmut_expression_C_down
3	3e−21	26 / 57	developing astrocytes
4	1e−04	11 / 68	cultured astroglia vs. in vivo astrocytes
5	7e−04	3 / 5	Phillips Prolif up vs PN & MES
6	2e−02	5 / 37	willscher_GBM_proteomics_wtOnly_SpotH
7	3e−02	21 / 328	Up
8	1e−01	2 / 13	Christensen_hypomethylated_in_grade2_astrocytoma
9	1e−01	2 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
10	1e−01	2 / 14	Christensen_hypomethylated_in_grade2_oligoastrocytoma
11	1e−01	2 / 14	Christensen_hypomethylated_in_grade3_oligoastrocytoma
12	1e−01	5 / 62	Stuehler_Proteins_up_in_STS
13	1e−01	2 / 15	VERHAAK_PN subtype
14	1e−01	3 / 31	KIM prognostic signature LTS vs. STS
15	1e−01	4 / 49	Vishal_subnetwork signature of survival in GBM
16	2e−01	1 / 4	willscher_GBM_STSwt_proteomics−L_UP
17	2e−01	1 / 4	willscher_GBM_Verhaak−CL_expression_E_up
18	2e−01	1 / 4	willscher_GBM_Verhaak−PNwt_expression_E_down
19	2e−01	1 / 4	willscher_GBM_Verhaak−PNmut_expression_E_down
20	2e−01	17 / 313	willscher_GBM_Verhaak−CL_expression_D_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−23	16 / 16	EGUCHI_CELL_CYCLE_RB1_TARGETS
2	3e−20	15 / 16	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
3	6e−19	14 / 15	FINETTI_BREAST_CANCER_KINOME_RED
4	3e−16	12 / 13	CROONQUIST_IL6_DEPRIVATION_DN
5	5e−16	13 / 16	FARMER_BREAST_CANCER_CLUSTER_2
6	4e−14	12 / 16	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	4e−14	12 / 16	KANG_DOXORUBICIN_RESISTANCE_UP
8	2e−13	11 / 14	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	7e−13	11 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	2e−12	11 / 16	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
11	2e−12	11 / 16	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
12	2e−12	11 / 16	CROONQUIST_NRAS_SIGNALING_DN
13	2e−12	11 / 16	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
14	2e−12	11 / 16	REACTOME_DNA_STRAND_ELONGATION
15	2e−12	11 / 16	REACTOME_G2_M_CHECKPOINTS
16	1e−11	10 / 14	ZHAN_MULTIPLE_MYELOMA_PR_UP
17	2e−11	9 / 11	KALMA_E2F1_TARGETS
18	4e−11	10 / 15	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
19	4e−11	10 / 15	LEE_EARLY_T_LYMPHOCYTE_UP
20	9e−11	10 / 16	FUJII_YBX1_TARGETS_DN

H Tiss

Rank	p−value	#in/all	Geneset
1	0.09	2 / 12	WIRTH_Lymphocytes
2	0.13	2 / 15	WIRTH_Telencephalon
3	0.13	2 / 15	WIRTH_Cerebellum
4	0.43	1 / 13	WIRTH_Thymus
5	0.43	1 / 13	WIRTH_Thalamus
6	0.45	1 / 14	WIRTH_Globus pallidus
7	0.74	4 / 120	WIRTH_Testis
8	0.78	1 / 36	WIRTH_Placenta
9	0.96	11 / 417	WIRTH_Immune system
10	0.99	9 / 400	WIRTH_Nervous System
11	1.00	1 / 135	WIRTH_Mucosa
12	1.00	0 / 5	WIRTH_Pituitary gland
13	1.00	0 / 26	WIRTH_Pancreas
14	1.00	0 / 13	WIRTH_Sec. lymphoid organs
15	1.00	0 / 12	WIRTH_Prim. lymphoid organs
16	1.00	0 / 10	WIRTH_B−cells
17	1.00	0 / 13	WIRTH_Tonsil
18	1.00	0 / 6	WIRTH_Bone marrow
19	1.00	0 / 13	WIRTH_Cortex cerebri
20	1.00	0 / 16	WIRTH_Hippocampus

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−09	24 / 140	DAVE_BL−vs−DLBCL
2	4e−06	16 / 100	ROSOLOWSKI_blue total
3	2e−05	56 / 755	SPANG_BCR UP
4	6e−05	6 / 18	DAVE_c−myc BL UP
5	9e−04	11 / 86	ROSOLOWSKI_green UP
6	1e−02	11 / 119	ROSOLOWSKI_green total
7	8e−02	44 / 852	SPANG_BCR DN
8	1e−01	2 / 13	BENTINK_mBL UP
9	2e−01	1 / 5	MASCQUE_mBL UP
10	3e−01	20 / 426	SPANG_CD40 6hrs DN
11	3e−01	14 / 291	SPANG_IL21 UP
12	4e−01	3 / 54	SPANG_BAFF 9hrs DN
13	4e−01	1 / 12	DAVE_BL_DN
14	4e−01	1 / 12	DAVE_BL_UP
15	4e−01	1 / 14	WRIGHT_GCB UP
16	5e−01	12 / 275	ZHANG_DLBCL mutated
17	5e−01	1 / 18	DAVE_BL Inter
18	6e−01	3 / 69	SPANG_LPS 6hrs DN
19	7e−01	3 / 86	ROSOLOWSKI_red total
20	7e−01	4 / 118	SPANG_LPS 6hrs UP

MF

Rank	p−value	#in/all	Geneset
1	3e−13	113 / 1344	ATP binding
2	1e−09	411 / 8023	protein binding
3	3e−07	7 / 13	nucleocytoplasmic transporter activity
4	3e−05	11 / 60	histone binding
5	3e−05	12 / 71	microtubule motor activity
6	4e−05	7 / 24	DNA helicase activity
7	7e−05	13 / 88	unfolded protein binding
8	2e−04	39 / 504	nucleotide binding
9	2e−04	10 / 62	single−stranded DNA binding
10	4e−04	7 / 33	DNA−dependent ATPase activity
11	4e−04	16 / 145	microtubule binding
12	4e−04	27 / 318	chromatin binding
13	4e−04	28 / 335	protein serine/threonine kinase activity
14	5e−04	6 / 25	Ran GTPase binding
15	8e−04	12 / 99	double−stranded DNA binding
16	9e−04	6 / 28	core promoter binding
17	1e−03	17 / 175	protein domain specific binding
18	1e−03	8 / 51	damaged DNA binding
19	1e−03	5 / 20	glutathione transferase activity
20	2e−03	11 / 92	ATP−dependent helicase activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.03	8 / 88	ATCA−433
2	0.04	14 / 198	ATGT−302C
3	0.05	5 / 47	AGTC−345
4	0.05	3 / 20	GTAG−189
5	0.05	6 / 64	TCTG−361
6	0.08	12 / 182	TAGC−9
7	0.09	9 / 129	ACCA−522
8	0.09	11 / 168	ATAC−144
9	0.10	5 / 60	AGGG−328
10	0.14	6 / 84	ATGC−217
11	0.14	11 / 182	TTTT−373
12	0.15	9 / 145	AAAG−511
13	0.16	1 / 4	CGGT−220
14	0.16	8 / 127	GACT−212−−132
15	0.19	2 / 19	GTCA−380−5P
16	0.20	4 / 56	GTGG−197
17	0.21	4 / 57	GTTA−302B
18	0.22	4 / 58	AGTC−499
19	0.24	3 / 41	GCTG−512−5P
20	0.25	11 / 208	ATTC−186

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−05	5 / 9	miR−24
2	2e−02	2 / 6	miR−26a
3	8e−02	1 / 2	miR−127
4	8e−02	1 / 2	miR−152
5	1e−01	1 / 3	miR−148a
6	2e−01	1 / 4	miR−195
7	2e−01	1 / 4	miR−34c
8	2e−01	1 / 5	miR−101
9	2e−01	1 / 5	miR−320
10	3e−01	1 / 7	miR−145
11	3e−01	1 / 8	miR−222
12	4e−01	1 / 11	miR−16
13	4e−01	1 / 13	miR−1
14	4e−01	1 / 13	miR−34a
15	7e−01	1 / 26	miR−21
16	1e+00	0 / 11	let−7a
17	1e+00	0 / 6	let−7b
18	1e+00	0 / 4	let−7c
19	1e+00	0 / 6	let−7d
20	1e+00	0 / 4	let−7g

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	7e−06	25 / 224	hsa−miR−181b
2	9e−06	21 / 171	hsa−miR−452
3	9e−06	18 / 132	hsa−miR−28−5p
4	1e−05	23 / 199	hsa−miR−181c
5	3e−05	31 / 336	hsa−miR−548d−5p
6	8e−05	27 / 288	hsa−miR−548j
7	1e−04	22 / 218	hsa−miR−181a
8	1e−04	22 / 219	hsa−miR−181d
9	2e−04	27 / 300	hsa−miR−548c−3p
10	2e−04	13 / 95	hsa−miR−888
11	2e−04	27 / 302	hsa−miR−548i
12	2e−04	19 / 181	hsa−miR−582−5p
13	2e−04	13 / 98	hsa−miR−210
14	2e−04	27 / 307	hsa−miR−548c−5p
15	3e−04	20 / 202	hsa−miR−196a
16	3e−04	18 / 172	hsa−miR−196b
17	4e−04	28 / 336	hsa−miR−548b−5p
18	4e−04	27 / 321	hsa−miR−548a−5p
19	6e−04	11 / 82	hsa−miR−1179
20	6e−04	17 / 166	hsa−miR−323b−5p

MMML CGS

Rank	p−value	#in/all	Geneset
1	2e−13	11 / 14	MACIEJ_MMML 4
2	6e−07	7 / 14	MACIEJ_MMML 19
3	9e−03	3 / 11	MACIEJ_MMML 15
4	1e−02	2 / 4	MACIEJ_MMML 41
5	2e−01	1 / 5	MACIEJ_MMML 20
6	2e−01	1 / 5	MACIEJ_MMML 28
7	3e−01	1 / 8	MACIEJ_MMML 50
8	4e−01	1 / 13	MACIEJ_MMML 10
9	4e−01	1 / 14	MACIEJ_MMML 8
10	5e−01	1 / 15	MACIEJ_MMML 16
11	5e−01	1 / 15	MACIEJ_MMML 22
12	1e+00	0 / 16	MACIEJ_MMML 1
13	1e+00	0 / 7	MACIEJ_MMML 13
14	1e+00	0 / 9	MACIEJ_MMML 14
15	1e+00	0 / 2	MACIEJ_MMML 17
16	1e+00	0 / 4	MACIEJ_MMML 2
17	1e+00	0 / 4	MACIEJ_MMML 23
18	1e+00	0 / 12	MACIEJ_MMML 24
19	1e+00	0 / 14	MACIEJ_MMML 26
20	1e+00	0 / 2	MACIEJ_MMML 27

Pathw Act

Rank	p−value	#in/all	Geneset
1	1e−04	5 / 13	GUSTAFSON_PI3K_UP
2	2e−03	4 / 14	BENTINK_myc.1
3	9e−03	3 / 11	BENTINK_e2f3.2
4	2e−02	3 / 15	BENTINK_ras.6
5	1e−01	2 / 14	BENTINK_src.2
6	4e−01	1 / 12	BENTINK_e2f3.1
7	4e−01	1 / 12	BENTINK_ras.1
8	4e−01	1 / 13	BENTINK_src.10
9	1e+00	0 / 15	GUSTAFSON_PI3K_DN
10	1e+00	0 / 11	BENTINK_ras.4
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−11	101 / 1233	KIM_MYC targets
2	3e−08	15 / 63	MYC_Targets UP
3	1e−05	7 / 20	MYC_Metabolism UP
4	6e−04	68 / 1095	HEBENSTREIT_high expression TF
5	3e−03	3 / 8	MYC_Cell cycle UP
6	3e−03	3 / 8	MYC_RNA processing binding UP
7	1e−02	2 / 4	MYC_Cell growth and proliferation UP
8	3e−02	2 / 7	MYC_DNA repair UP
9	1e−01	1 / 3	MYC_DNA replication UP
10	2e−01	1 / 4	MYC_Apoptosis UP
11	4e−01	1 / 14	NOWICK_TF
12	5e−01	1 / 16	MYC_Protein synthesis degradation UP
13	1e+00	19 / 1146	HEBENSTREIT_low expression TF
14	1e+00	0 / 5	MYC_TFs
15	1e+00	0 / 9	MYC_Targets DOWN
16	1e+00	0 / 2	MYC_Cell cycle DOWN
17	1e+00	0 / 2	MYC_Chromatin_modification UP
18	1e+00	0 / 2	MYC_ECM cell adhesion DOWN
19	1e+00	0 / 2	MYC_Signal transduction UP
20	1e+00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.007	3 / 10	VAQUERIZAS_Skeletal.muscle.psoas
2	0.210	3 / 38	VAQUERIZAS_Testis
3	0.233	2 / 22	VAQUERIZAS_Spinal cord
4	0.243	3 / 41	VAQUERIZAS_Thymus
5	0.400	1 / 12	VAQUERIZAS_Kidney
6	0.425	1 / 13	VAQUERIZAS_Ovary
7	0.449	1 / 14	VAQUERIZAS_Fetal liver
8	0.472	1 / 15	VAQUERIZAS_Adrenal gland
9	0.481	3 / 62	VAQUERIZAS_Whole blood
10	0.488	2 / 39	VAQUERIZAS_Thyroid
11	0.494	1 / 16	VAQUERIZAS_Fetal thyroid
12	0.540	2 / 43	VAQUERIZAS_Uterus
13	0.540	2 / 43	VAQUERIZAS_Whole brain
14	0.574	1 / 20	VAQUERIZAS_Bone marrow
15	0.591	1 / 21	VAQUERIZAS_Tonsil
16	0.697	1 / 28	VAQUERIZAS_Liver
17	0.710	1 / 29	VAQUERIZAS_Smooth muscle
18	0.710	1 / 29	VAQUERIZAS_Lymph node
19	0.722	1 / 30	VAQUERIZAS_Fetal lung
20	0.818	1 / 40	VAQUERIZAS_Fetal brain

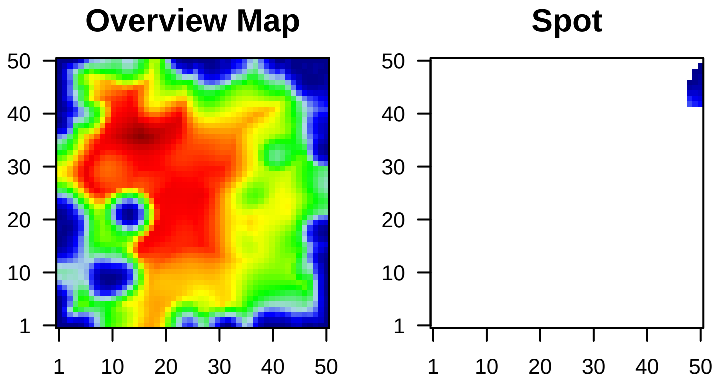
Sample−Underexpression

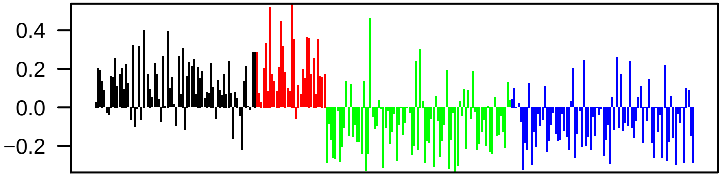
Spot Summary: I

metagenes = 20
genes = 185

<r> metagenes = 0.95
<r> genes = 0.24
beta: r2= 6.9 / log p= −Inf

samples with spot = 22 (8 %)
Mesenchymal : 12 (14.1 %)
Basal : 10 (11.9 %)



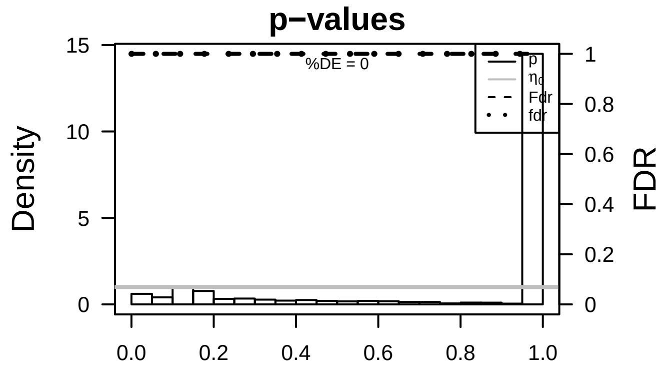


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3880	3.42	−4.05	0.56	KRT19	keratin 19 [Source:HGNC Symbol;Acc:6436]
2	3856	2.63	−2.21	0.46	KRT8P3	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
3	26227	1.93	−2.15	0.6	PHGDH	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
4	84707	2.04	−1.89	0.56	BEX2	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
5	445	2.19	−1.87	0.23	ASS1	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
6	59342	1.61	−1.74	0.57	SCPEP1	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
7	875	2.07	−1.61	0.59	CBS	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
8	57216	1.29	−1.54	0.46	VANGL2	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;
9	400916	1.6	−1.51	0.34	CHCHD10	coiled−coil−helix−coiled−coil−helix domain containing 10 [Sou
10	200634	1.51	−1.49	0.57	KRTCAP3	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
11	253782	1.46	−1.45	0.47	CERS6	ceramide synthase 6 [Source:HGNC Symbol;Acc:23826]
12	7345	3	−1.41	0.43	UCHL1	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
13	26053	1.29	−1.33	0.42	AUTS2	autism susceptibility candidate 2 [Source:HGNC Symbol;Acc:
14	5625	1.89	−1.32	0.4	PRODH	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
15	57549	1.98	−1.31	0.62	IGSF9	immunoglobulin superfamily, member 9 [Source:HGNC Symb
16	6647	0.97	−1.27	0.42	SOD1	superoxide dismutase 1, soluble [Source:HGNC Symbol;Acc:
17	286676	1.51	−1.2	0.62	ILDR1	immunoglobulin−like domain containing receptor 1 [Source:H
18	84171	2.55	−1.19	0.37	LOXL4	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
19	59271	1.36	−1.15	0.37	EVA1C	eva−1 homolog C (C. elegans) [Source:HGNC Symbol;Acc:1
20	56977	1.46	−1.14	0.48	STOX2	storkhead box 2 [Source:HGNC Symbol;Acc:25450]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−07	6 / 30	miRN	hsa−miR−1237
2	2e−05	4 / 16	GSEA	BILD_E2F3_ONCOGENIC_SIGNATURE
3	3e−05	27 / 1033	Chr	Chr 2
4	6e−04	3 / 15	GSEA	FARMER_BREAST_CANCER_CLUSTER_6
5	6e−04	3 / 15	GSEA	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
6	7e−04	3 / 16	GSEA	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
7	1e−03	3 / 19	BP	cellular amino acid biosynthetic process
8	1e−03	3 / 19	MF	Wnt−activated receptor activity
9	2e−03	5 / 75	miRN	hsa−miR−375
10	2e−03	3 / 21	Glio	Martinez_Glio_hypermeth
11	2e−03	2 / 6	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
12	2e−03	4 / 47	miRN	hsa−miR−346
13	2e−03	3 / 23	BP	gonad development
14	2e−03	3 / 23	miRN	hsa−miR−151−5p
15	3e−03	3 / 25	BP	cellular response to oxidative stress
16	3e−03	7 / 167	BP	cellular nitrogen compound metabolic process
17	3e−03	3 / 26	MF	Wnt−protein binding
18	3e−03	6 / 127	miRN	GACT−212−−132
19	3e−03	11 / 375	miRN	ACTG−27A−−27B
20	4e−03	2 / 9	GSEA	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
21	4e−03	6 / 136	miRN	hsa−miR−576−3p
22	4e−03	3 / 30	TF Ti	VAQUERIZAS_Fetal lung
23	5e−03	3 / 31	BP	regulation of actin cytoskeleton organization
24	5e−03	3 / 31	BP	response to nutrient levels
25	5e−03	2 / 10	CC	junctional sarcoplasmic reticulum membrane
26	5e−03	2 / 10	BP	negative regulation of cell−substrate adhesion
27	5e−03	2 / 10	MF	omega peptidase activity
28	5e−03	2 / 10	BP	oxaloacetate metabolic process
29	5e−03	2 / 10	BP	somatic stem cell division
30	5e−03	2 / 10	GSEA	AMUNDSON_RESPONSE_TO_ARSENITE
31	6e−03	3 / 33	miRN	hsa−miR−644
32	6e−03	4 / 66	miRN	GCTC−335
33	6e−03	2 / 11	BP	protein palmitoylation
34	6e−03	2 / 11	GSEA	CUI_GLUCOSE_DEPRIVATION
35	7e−03	3 / 35	miRN	hsa−miR−1274b
36	8e−03	2 / 12	GSEA	ONDER_CDH1_TARGETS_1_UP
37	8e−03	2 / 12	GSEA	HELLER_SILENCED_BY_METHYLATION_DN
38	8e−03	2 / 12	GSEA	KAYO_AGING_MUSCLE_UP
39	8e−03	2 / 12	GSEA	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION
40	8e−03	4 / 70	BP	canonical Wnt signaling pathway



BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 19	cellular amino acid biosynthetic process
2	0.002	3 / 23	gonad development
3	0.003	3 / 25	cellular response to oxidative stress
4	0.003	7 / 167	cellular nitrogen compound metabolic process
5	0.005	3 / 31	regulation of actin cytoskeleton organization
6	0.005	3 / 31	response to nutrient levels
7	0.005	2 / 10	negative regulation of cell−substrate adhesion
8	0.005	2 / 10	oxaloacetate metabolic process
9	0.005	2 / 10	somatic stem cell division
10	0.006	2 / 11	protein palmitoylation
11	0.008	4 / 70	canonical Wnt signaling pathway
12	0.009	3 / 38	placenta development
13	0.010	4 / 75	cilium assembly
14	0.010	2 / 14	neural tube formation
15	0.011	3 / 42	heart looping
16	0.012	2 / 15	positive regulation of branching involved in ureteric bud morphogenesis
17	0.012	2 / 15	spinal cord development
18	0.013	3 / 44	skin development
19	0.013	3 / 44	smoothened signaling pathway
20	0.013	2 / 16	positive regulation of cytokinesis

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	0 / 14	LIU_COMMON_CANCER_GENES
2	0.1	1 / 14	LIU_LIVER_CANCER
3	0.2	1 / 15	BEN−PORATH_UP
4	0.2	1 / 16	GENTLES_modul7
5	0.4	1 / 48	KUIPER_MM poor survival
6	0.6	2 / 185	SPANG_LPS−index2
7	0.7	5 / 530	Lembcke_Normal vs Adenoma
8	0.9	2 / 316	SPANG_BCL6−index2
9	1.0	0 / 15	RHODES_CANCER_META_SIGNATURE
10	1.0	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
11	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.0	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.0	0 / 10	LIU_BREAST_CANCER
14	1.0	0 / 15	LIU_PROSTATE_CANCER_DN
15	1.0	0 / 14	LIU_PROSTATE_CANCER_UP
16	1.0	0 / 14	WANG_ER_UP
17	1.0	0 / 9	WANG_ER_DN
18	1.0	0 / 16	WOLFER_overlap genes
19	1.0	0 / 12	BEN−PORATH_DN
20	1.0	0 / 15	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	0.005	2 / 10	junctional sarcoplasmic reticulum membrane
2	0.010	2 / 14	spindle midzone
3	0.021	8 / 304	mitochondrial inner membrane
4	0.022	23 / 1318	mitochondrion
5	0.023	2 / 21	photoreceptor connecting cilium
6	0.028	4 / 102	cilium
7	0.036	5 / 163	synapse
8	0.037	5 / 164	axon
9	0.043	59 / 4310	cytoplasm
10	0.050	2 / 32	peroxisomal matrix
11	0.061	2 / 36	sarcoplasmic reticulum
12	0.062	3 / 81	nuclear matrix
13	0.066	3 / 83	spindle pole
14	0.074	2 / 40	cleavage furrow
15	0.078	3 / 89	peroxisome
16	0.116	1 / 11	ciliary transition zone
17	0.116	1 / 11	dendrite cytoplasm
18	0.116	1 / 11	filopodium membrane
19	0.126	1 / 12	PRC1 complex
20	0.126	1 / 12	septin complex

Chr

Rank	p−value	#in/all	Geneset
1	3e−05	27 / 1033	Chr 2
2	3e−02	9 / 386	Chr 22
3	4e−02	14 / 743	Chr 7
4	5e−02	16 / 914	Chr 3
5	6e−02	5 / 187	Chr 21
6	1e−01	9 / 534	Chr 8
7	4e−01	8 / 602	Chr 10
8	4e−01	7 / 519	Chr 14
9	4e−01	21 / 1720	Chr 1
10	4e−01	6 / 449	Chr 20
11	5e−01	11 / 918	Chr 17
12	6e−01	7 / 630	Chr X
13	7e−01	7 / 714	Chr 6
14	7e−01	2 / 232	Chr 18
15	8e−01	5 / 618	Chr 4
16	9e−01	3 / 504	Chr 15
17	9e−01	6 / 866	Chr 12
18	1e+00	4 / 717	Chr 16
19	1e+00	3 / 633	Chr 9
20	1e+00	6 / 1135	Chr 19

Disease

Rank	p−value	#in/all	Geneset
1	0.4	5 / 375	GUDJ_psoriasis down
2	1.0	0 / 572	GUDJ_psoriasis up
3	1.0	0 / 17	BCHETNIA_EBM up
4	1.0	0 / 2	BCHETNIA_EBM down
5	1.0	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.002	3 / 21	Martinez_Glio_hypermeth
2	0.012	6 / 169	willscher_GBM_proteomics_wtOnly_Differencelist
3	0.014	4 / 83	Christensen_hypermethylated_in_secondary_glioblastoma
4	0.021	3 / 53	Christensen_hypermethylated_in_primary_glioblastoma
5	0.032	9 / 391	Down_b
6	0.032	3 / 62	Stuehler_Proteins_up_in_STS
7	0.036	2 / 27	WIRTH_PN subtype
8	0.044	3 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
9	0.045	3 / 71	willscher_GBM_Verhaak−CL_expression_H_down
10	0.045	3 / 71	willscher_GBM_Verhaak−MES_expression_H_up
11	0.045	3 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
12	0.070	3 / 85	GIEZELT_GBM_STS_down_VS_LTS
13	0.122	2 / 54	willscher_GBM_proteomics_wtOnly_SpotG
14	0.126	3 / 110	Christensen_hypermethylated_in_grade3_astrocytoma
15	0.126	1 / 12	VERHAAK_PN_Brain
16	0.126	1 / 12	Christensen_hypermethylated_in_ependymoma
17	0.137	2 / 58	OPC
18	0.161	2 / 64	Christensen_hypermethylated_in_grade2_astrocytoma
19	0.165	1 / 16	willscher_GBM_STSwt_proteomics−O_UP
20	0.189	2 / 71	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 16	BILD_E2F3_ONCOGENIC_SIGNATURE
2	6e−04	3 / 15	FARMER_BREAST_CANCER_CLUSTER_6
3	6e−04	3 / 15	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
4	7e−04	3 / 16	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
5	2e−03	2 / 6	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
6	4e−03	2 / 9	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
7	5e−03	2 / 10	AMUNDSON_RESPONSE_TO_ARSENITE
8	6e−03	2 / 11	CUI_GLUCOSE_DEPRIVATION
9	8e−03	2 / 12	ONDER_CDH1_TARGETS_1_UP
10	8e−03	2 / 12	HELLER_SILENCED_BY_METHYLATION_DN
11	8e−03	2 / 12	KAYO_AGING_MUSCLE_UP
12	8e−03	2 / 12	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION
13	9e−03	2 / 13	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP
14	9e−03	2 / 13	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
15	9e−03	2 / 13	LEE_LIVER_CANCER_MYC_E2F1_DN
16	9e−03	2 / 13	BLUM_RESPONSE_TO_SALIRASIB_UP
17	9e−03	2 / 13	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
18	9e−03	2 / 13	REACTOME_GLUCOSE_METABOLISM
19	9e−03	2 / 13	REACTOME_METABOLISM_OF_CARBOHYDRATES
20	1e−02	2 / 14	APPIERTO_RESPONSE_TO_FENRETINIDE_DN

H Tiss

Rank	p−value	#in/all	Geneset
1	0.05	1 / 5	WIRTH_Pituitary gland
2	0.16	7 / 400	WIRTH_Nervous System
3	0.76	1 / 127	WIRTH_Muscle
4	0.85	3 / 417	WIRTH_Immune system
5	1.00	0 / 26	WIRTH_Pancreas
6	1.00	0 / 13	WIRTH_Sec. lymphoid organs
7	1.00	0 / 12	WIRTH_Prim. lymphoid organs
8	1.00	0 / 10	WIRTH_B−cells
9	1.00	0 / 13	WIRTH_Tonsil
10	1.00	0 / 13	WIRTH_Thymus
11	1.00	0 / 12	WIRTH_Lymphocytes
12	1.00	0 / 6	WIRTH_Bone marrow
13	1.00	0 / 14	WIRTH_Globus pallidus
14	1.00	0 / 15	WIRTH_Telencephalon
15	1.00	0 / 13	WIRTH_Cortex cerebri
16	1.00	0 / 16	WIRTH_Hippocampus
17	1.00	0 / 13	WIRTH_Thalamus
18	1.00	0 / 15	WIRTH_Cerebellum
19	1.00	0 / 120	WIRTH_Testis
20	1.00	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	DAVE_BL UP
2	0.1	1 / 13	BENTINK_mBL UP
3	0.3	2 / 86	ROSOLOWSKI_red total
4	0.3	2 / 100	ROSOLOWSKI_blue total
5	0.3	1 / 38	ROSOLOWSKI_blue DOWN
6	0.5	1 / 54	SPANG_BAFF 9hrs DN
7	0.5	2 / 140	DAVE_BL−vs−DLBCL
8	0.5	9 / 755	SPANG_BCR UP
9	0.6	3 / 274	SPANG_IL21 DN
10	0.6	3 / 291	SPANG_IL21 UP
11	0.7	4 / 426	SPANG_CD40 6hrs DN
12	0.7	1 / 118	SPANG_LPS 6hrs UP
13	0.8	2 / 275	ZHANG_DLBCL mutated
14	0.8	7 / 852	SPANG_BCR DN
15	0.9	2 / 327	SPANG_CD40 6hrs UP
16	1.0	0 / 13	BENTINK_mBL DOWN
17	1.0	0 / 12	DAVE_BL_DN
18	1.0	0 / 18	DAVE_BL Inter
19	1.0	0 / 18	DAVE_c−myc BL UP
20	1.0	0 / 6	DAVE_MHCCII BL DN

MF

Rank	p−value	#in/all	Geneset
1	0.001	3 / 19	Wnt−activated receptor activity
2	0.003	3 / 26	Wnt−protein binding
3	0.005	2 / 10	omega peptidase activity
4	0.012	3 / 43	scavenger receptor activity
5	0.016	3 / 48	cysteine−type endopeptidase activity
6	0.026	3 / 57	ubiquitin thiolesterase activity
7	0.034	2 / 26	cytochrome−c oxidase activity
8	0.034	2 / 26	potassium channel regulator activity
9	0.036	2 / 27	antioxidant activity
10	0.041	2 / 29	cofactor binding
11	0.050	8 / 361	binding
12	0.052	3 / 75	PDZ domain binding
13	0.058	2 / 35	protein self−association
14	0.059	3 / 79	electron carrier activity
15	0.064	3 / 82	phosphotransferase activity, alcohol group as acceptor
16	0.067	2 / 38	ubiquitin binding
17	0.074	3 / 87	ligase activity
18	0.077	2 / 41	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
19	0.078	14 / 823	sequence−specific DNA binding transcription factor activity
20	0.084	3 / 92	ATP−dependent helicase activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.003	6 / 127	GACT−212−−132
2	0.003	11 / 375	ACTG−27A−−27B
3	0.006	4 / 66	GCTC−335
4	0.008	9 / 309	CTACLET−7A−LET−7B−LET−7C−LET−7D−LET−7E−LET−7F−−98−LET−7G-
5	0.009	5 / 115	TTGG−515−5P−−519E
6	0.010	8 / 267	CACT−128A−−128B
7	0.015	5 / 129	GTGA−224
8	0.015	5 / 129	TAAT−323
9	0.017	6 / 184	GGCA−22
10	0.018	6 / 185	AAAG−204−−211
11	0.018	5 / 136	GCAT−105
12	0.019	2 / 19	GTCA−380−5P
13	0.020	6 / 189	AACT−145
14	0.020	4 / 92	GCTT−498
15	0.029	2 / 24	TTCC−191
16	0.030	3 / 60	AGGG−328
17	0.032	4 / 107	TCCA−518C
18	0.036	3 / 65	CAGG−504
19	0.038	10 / 467	TGTT−30A−5P−−30C−−30D−−30B−−30E−5P
20	0.046	4 / 120	TCAT−143

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	miR−129
2	0.02	1 / 2	miR−193a
3	0.05	1 / 5	miR−126
4	0.10	1 / 9	miR−17
5	1.00	0 / 11	let−7a
6	1.00	0 / 6	let−7b
7	1.00	0 / 4	let−7c
8	1.00	0 / 6	let−7d
9	1.00	0 / 4	let−7g
10	1.00	0 / 13	miR−1
11	1.00	0 / 5	miR−101
12	1.00	0 / 2	miR−101b
13	1.00	0 / 4	miR−106b
14	1.00	0 / 2	miR−107
15	1.00	0 / 4	miR−122
16	1.00	0 / 2	miR−124a
17	1.00	0 / 6	miR−125a
18	1.00	0 / 9	miR−125b
19	1.00	0 / 2	miR−127
20	1.00	0 / 3	miR−128

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	9e−07	6 / 30	hsa−miR−1237
2	2e−03	5 / 75	hsa−miR−375
3	2e−03	4 / 47	hsa−miR−346
4	2e−03	3 / 23	hsa−miR−151−5p
5	4e−03	6 / 136	hsa−miR−576−3p
6	6e−03	3 / 33	hsa−miR−644
7	7e−03	3 / 35	hsa−miR−1274b
8	8e−03	9 / 311	hsa−miR−302c
9	9e−03	9 / 315	hsa−miR−30e
10	1e−02	8 / 264	hsa−miR−449a
11	1e−02	4 / 75	hsa−miR−509−3−5p
12	1e−02	6 / 163	hsa−miR−1297
13	1e−02	8 / 268	hsa−miR−30b
14	1e−02	6 / 166	hsa−miR−320b
15	1e−02	9 / 325	hsa−miR−302d
16	1e−02	5 / 120	hsa−miR−625
17	1e−02	4 / 78	hsa−miR−365
18	1e−02	8 / 278	hsa−miR−30c
19	1e−02	6 / 177	hsa−miR−29c
20	2e−02	7 / 234	hsa−miR−26a

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	MACIEJ_MMML 46
2	0.15	1 / 14	MACIEJ_MMML 30
3	0.15	1 / 14	MACIEJ_MMML 8
4	0.16	1 / 15	MACIEJ_MMML 16
5	1.00	0 / 16	MACIEJ_MMML 1
6	1.00	0 / 13	MACIEJ_MMML 10
7	1.00	0 / 7	MACIEJ_MMML 13
8	1.00	0 / 9	MACIEJ_MMML 14
9	1.00	0 / 11	MACIEJ_MMML 15
10	1.00	0 / 2	MACIEJ_MMML 17
11	1.00	0 / 14	MACIEJ_MMML 19
12	1.00	0 / 4	MACIEJ_MMML 2
13	1.00	0 / 5	MACIEJ_MMML 20
14	1.00	0 / 15	MACIEJ_MMML 22
15	1.00	0 / 4	MACIEJ_MMML 23
16	1.00	0 / 12	MACIEJ_MMML 24
17	1.00	0 / 14	MACIEJ_MMML 26
18	1.00	0 / 2	MACIEJ_MMML 27
19	1.00	0 / 5	MACIEJ_MMML 28
20	1.00	0 / 6	MACIEJ_MMML 29

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 11	BENTINK_e2f3.2
2	0.1	1 / 14	BENTINK_myc.1
3	1.0	0 / 13	GUSTAFSON_PI3K_UP
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 12	BENTINK_e2f3.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 15	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 14	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.02	22 / 1233	KIM_MYC targets
2	0.30	15 / 1146	HEBENSTREIT_low expression TF
3	0.69	11 / 1095	HEBENSTREIT_high expression TF
4	1.00	0 / 14	NOWICK_TF
5	1.00	0 / 5	MYC_TFs
6	1.00	0 / 63	MYC_Targets UP
7	1.00	0 / 9	MYC_Targets DOWN
8	1.00	0 / 4	MYC_Apoptosis UP
9	1.00	0 / 8	MYC_Cell cycle UP
10	1.00	0 / 2	MYC_Cell cycle DOWN
11	1.00	0 / 4	MYC_Cell growth and proliferation UP
12	1.00	0 / 2	MYC_Chromatin_modification UP
13	1.00	0 / 7	MYC_DNA repair UP
14	1.00	0 / 3	MYC_DNA replication UP
15	1.00	0 / 2	MYC_ECM cell adhesion DOWN
16	1.00	0 / 20	MYC_Metabolism UP
17	1.00	0 / 16	MYC_Protein synthesis degradation UP
18	1.00	0 / 8	MYC_RNA processing binding UP
19	1.00	0 / 2	MYC_Signal transduction UP
20	1.00	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.004	3 / 30	VAQUERIZAS_Fetal lung
2	0.032	3 / 62	VAQUERIZAS_Lung
3	0.064	2 / 37	VAQUERIZAS_Prostate
4	0.074	2 / 40	VAQUERIZAS_Fetal brain
5	0.083	2 / 43	VAQUERIZAS_Uterus
6	0.087	2 / 44	VAQUERIZAS_Placenta
7	0.126	1 / 12	VAQUERIZAS_Kidney
8	0.136	1 / 13	VAQUERIZAS_Skin
9	0.155	1 / 15	VAQUERIZAS_Adrenal gland
10	0.165	1 / 16	VAQUERIZAS_Pancreas
11	0.165	1 / 16	VAQUERIZAS_Fetal thyroid
12	0.202	1 / 20	VAQUERIZAS_Adrenal cortex
13	0.219	1 / 22	VAQUERIZAS_Spinal cord
14	0.237	1 / 24	VAQUERIZAS_Trachea
15	0.279	1 / 29	VAQUERIZAS_Smooth muscle
16	0.348	1 / 38	VAQUERIZAS_Testis
17	0.356	1 / 39	VAQUERIZAS_Thyroid
18	0.370	1 / 41	VAQUERIZAS_Thymus
19	0.384	1 / 43	VAQUERIZAS_Whole brain
20	0.804	1 / 144	VAQUERIZAS_General

Sample−Underexpression

Spot Summary: m

metagenes = 2
genes = 79

<r> metagenes = 1
<r> genes = 0.69
beta: r2= 11.57 / log p= −Inf

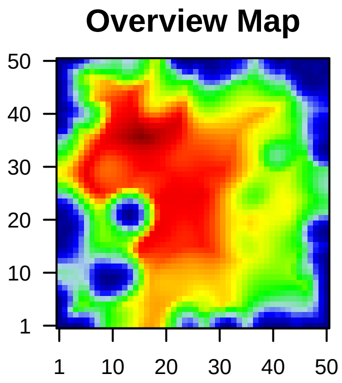
samples with spot = 65 (23.6 %)
Atypical : 24 (32.4 %)
Classical : 13 (40.6 %)
Mesenchymal : 15 (17.6 %)
Basal : 13 (15.5 %)

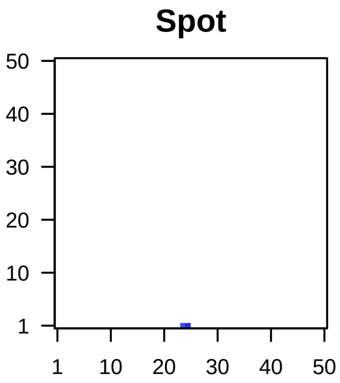
Spot Genelist

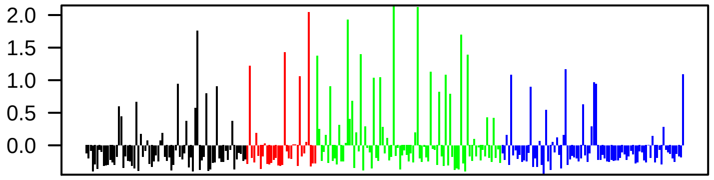
Rank	ID	max e	min e	r	Symbol	Description
1	283120	4.19	−2.42	0.34	H19	H19, imprinted maternally expressed transcript (non−protein
2	1410	2.48	−1.98	0.48	CRYAB	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
3	1917	3.04	−1.6	0.56	EEF1A2	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
4	2318	3	−1.57	0.81	FLNC	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
5	58	5.49	−1.44	0.9	ACTA1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
6	7060	3.17	−1.31	0.74	THBS4	thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
7	6588	4.37	−1.29	0.91	SLN	sarcolipin [Source:HGNC Symbol;Acc:11089]
8	2273	2.68	−1.28	0.79	FHL1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
9	22998	1.89	−1.24	0.46	LIMCH1	LIM and calponin homology domains 1 [Source:HGNC Symb
10	10486	1.85	−1.14	0.48	CAP2	CAP, adenylate cyclase−associated protein, 2 (yeast) [Source
11	1346	2.12	−1.14	0.7	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [Sc
12	27295	2.6	−1.04	0.7	PDLIM3	PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:20767]
13	70	3.94	−1.03	0.89	ACTC1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
14	84448	1.87	−1.03	0.43	ABLIM2	actin binding LIM protein family, member 2 [Source:HGNC Sy
15	4151	3.51	−0.93	0.9	MB	myoglobin [Source:HGNC Symbol;Acc:6915]
16	1158	4.27	−0.93	0.93	CKM	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
17	4703	3.13	−0.92	0.88	NEB	nebulin [Source:HGNC Symbol;Acc:7720]
18	222166	1.62	−0.9	0.51	MTURN	maturin, neural progenitor differentiation regulator homolog (X
19	7138	2.17	−0.89	0.58	TNNT1	troponin T type 1 (skeletal, slow) [Source:HGNC Symbol;Acc:
20	4608	3.11	−0.84	0.84	MYBPH	myosin binding protein H [Source:HGNC Symbol;Acc:7552]

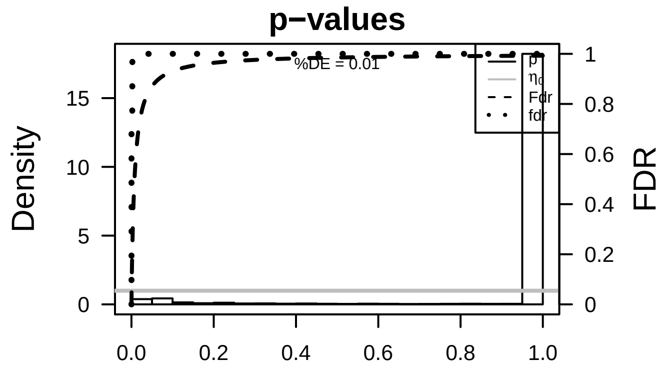
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−79	46 / 127	H.Tis	WIRTH_Muscle
2	7e−41	21 / 36	BP	muscle filament sliding
3	1e−33	19 / 44	MF	structural constituent of muscle
4	2e−27	19 / 84	BP	muscle contraction
5	3e−23	17 / 88	CC	Z disc
6	7e−23	11 / 16	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_F
7	4e−19	21 / 297	MF	actin binding
8	4e−18	11 / 34	CC	myofibril
9	1e−17	9 / 16	H.Tis	WIRTH_Hippocampus
10	1e−17	11 / 37	CC	sarcomere
11	1e−16	8 / 12	CC	myosin filament
12	1e−16	9 / 20	CC	I band
13	1e−13	9 / 37	BP	cardiac muscle contraction
14	2e−13	7 / 14	CC	contractile fiber
15	5e−13	7 / 16	CC	M band
16	9e−12	6 / 12	BP	skeletal muscle contraction
17	2e−11	6 / 13	CC	muscle myosin complex
18	2e−10	6 / 18	BP	regulation of muscle contraction
19	1e−09	5 / 11	BP	cardiac muscle tissue morphogenesis
20	2e−09	5 / 12	MF	titin binding
21	7e−09	5 / 15	GSEA	REACTOME_STRIATED_MUSCLE_CONTRACTION
22	2e−08	10 / 184	CC	actin cytoskeleton
23	5e−08	6 / 42	CC	myosin complex
24	2e−07	4 / 11	CC	A band
25	2e−07	6 / 53	MF	cytoskeletal protein binding
26	5e−07	4 / 14	MF	tropomyosin binding
27	6e−07	11 / 333	CC	cytoskeleton
28	7e−07	4 / 15	BP	striated muscle contraction
29	3e−06	4 / 21	BP	sarcomere organization
30	4e−06	6 / 88	BP	muscle organ development
31	5e−06	5 / 51	BP	skeletal muscle tissue development
32	7e−06	4 / 26	BP	ventricular cardiac muscle tissue morphogenesis
33	7e−06	5 / 56	MF	motor activity
34	1e−05	4 / 29	CC	sarcoplasmic reticulum membrane
35	1e−05	5 / 62	CC	sarcolemma
36	2e−05	12 / 579	MF	calcium ion binding
37	3e−05	4 / 36	CC	sarcoplasmic reticulum
38	3e−05	26 / 2378	CC	cytosol
39	3e−05	3 / 13	CC	pseudopodium
40	3e−05	5 / 77	MF	actin filament binding









BP

Rank	p−value	#in/all	Geneset
1	7e−41	21 / 36	muscle filament sliding
2	2e−27	19 / 84	muscle contraction
3	1e−13	9 / 37	cardiac muscle contraction
4	9e−12	6 / 12	skeletal muscle contraction
5	2e−10	6 / 18	regulation of muscle contraction
6	1e−09	5 / 11	cardiac muscle tissue morphogenesis
7	7e−07	4 / 15	striated muscle contraction
8	3e−06	4 / 21	sarcomere organization
9	4e−06	6 / 88	muscle organ development
10	5e−06	5 / 51	skeletal muscle tissue development
11	7e−06	4 / 26	ventricular cardiac muscle tissue morphogenesis
12	4e−05	3 / 14	adult heart development
13	8e−05	4 / 47	skeletal muscle cell differentiation
14	8e−05	3 / 18	regulation of the force of heart contraction
15	4e−04	3 / 29	regulation of heart contraction
16	1e−03	2 / 10	creatine metabolic process
17	1e−03	2 / 10	heart contraction
18	1e−03	2 / 10	skeletal muscle tissue regeneration
19	1e−03	2 / 12	muscle fiber development
20	2e−03	2 / 14	actomyosin structure organization

Cancer

Rank	p−value	#in/all	Geneset
1	5e−05	3 / 15	BEN−PORATH_UP
2	4e−02	1 / 9	WANG_ER_DN
3	6e−02	1 / 13	GENTLES_modul16
4	7e−02	1 / 14	LIU_LIVER_CANCER
5	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
6	1e+00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
7	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
9	1e+00	0 / 10	LIU_BREAST_CANCER
10	1e+00	0 / 14	LIU_COMMON_CANCER_GENES
11	1e+00	0 / 15	LIU_PROSTATE_CANCER_DN
12	1e+00	0 / 14	LIU_PROSTATE_CANCER_UP
13	1e+00	0 / 14	WANG_ER_UP
14	1e+00	0 / 16	WOLFER_overlap genes
15	1e+00	0 / 12	BEN−PORATH_DN
16	1e+00	0 / 15	GENTLES_modul1
17	1e+00	0 / 16	GENTLES_modul2
18	1e+00	0 / 10	GENTLES_modul3
19	1e+00	0 / 16	GENTLES_modul4
20	1e+00	0 / 11	GENTLES_modul5

CC

Rank	p−value	#in/all	Geneset
1	3e−23	17 / 88	Z disc
2	4e−18	11 / 34	myofibril
3	1e−17	11 / 37	sarcomere
4	1e−16	8 / 12	myosin filament
5	1e−16	9 / 20	I band
6	2e−13	7 / 14	contractile fiber
7	5e−13	7 / 16	M band
8	2e−11	6 / 13	muscle myosin complex
9	2e−08	10 / 184	actin cytoskeleton
10	5e−08	6 / 42	myosin complex
11	2e−07	4 / 11	A band
12	6e−07	11 / 333	cytoskeleton
13	1e−05	4 / 29	sarcoplasmic reticulum membrane
14	1e−05	5 / 62	sarcolemma
15	3e−05	4 / 36	sarcoplasmic reticulum
16	3e−05	26 / 2378	cytosol
17	3e−05	3 / 13	pseudopodium
18	8e−05	3 / 18	costamere
19	7e−04	3 / 37	actin filament
20	3e−03	4 / 128	focal adhesion

Chr

Rank	p−value	#in/all	Geneset
1	0.06	9 / 1033	Chr 2
2	0.15	7 / 918	Chr 17
3	0.18	5 / 618	Chr 4
4	0.20	11 / 1720	Chr 1
5	0.25	5 / 699	Chr 5
6	0.32	6 / 957	Chr 11
7	0.33	4 / 602	Chr 10
8	0.37	3 / 449	Chr 20
9	0.47	6 / 1135	Chr 19
10	0.61	4 / 866	Chr 12
11	0.65	4 / 914	Chr 3
12	0.68	1 / 232	Chr 18
13	0.81	2 / 630	Chr X
14	0.85	1 / 386	Chr 22
15	0.87	2 / 714	Chr 6
16	0.87	2 / 717	Chr 16
17	0.88	2 / 743	Chr 7
18	0.92	1 / 504	Chr 15
19	0.92	1 / 519	Chr 14
20	0.93	1 / 534	Chr 8

Disease

Rank	p−value	#in/all	Geneset
1	4e−04	8 / 375	GUDJ_psoriasis down
2	1e+00	0 / 572	GUDJ_psoriasis up
3	1e+00	0 / 17	BCHETNIA_EBM up
4	1e+00	0 / 2	BCHETNIA_EBM down
5	1e+00	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	0.05	2 / 74	GIEZELT_GBM_STS_up_VS_LTS
2	0.07	1 / 14	VERHAAK_NL subtype
3	0.10	1 / 22	KIM deleted & downregulated in LTS
4	0.11	2 / 118	willscher_GBM_Verhaak−CL_expression_K_down
5	0.11	2 / 118	willscher_GBM_Verhaak−MES_expression_K_down
6	0.11	2 / 118	willscher_GBM_Verhaak−PNwt_expression_K_up
7	0.11	2 / 118	willscher_GBM_Verhaak−PNmut_expression_K_up
8	0.12	1 / 27	WIRTH_PN subtype
9	0.13	1 / 28	Barbus_GBM_STS_vs._LTS
10	0.14	1 / 31	KIM prognostic signature LTS vs. STS
11	0.15	1 / 33	willscher_GBM_proteomics_wtOnly_SpotC
12	0.19	1 / 44	in vivo astrocytes vs. cultured astroglia
13	0.21	1 / 48	Noushmehr_Pron_GCIMP_hypermeth_DN
14	0.21	1 / 49	mature astrocytes
15	0.23	1 / 53	Christensen_hypermethylated_in_primary_glioblastoma
16	0.23	1 / 55	OL vs. MOG− OL
17	0.24	1 / 57	developing astrocytes
18	0.27	1 / 64	Christensen_hypermethylated_in_grade2_astrocytoma
19	0.28	3 / 379	Down_a
20	0.28	1 / 68	cultured astroglia vs. in vivo astrocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−23	11 / 16	RICKMAN_HEAD_AND_NECK_CANCER_F
2	7e−09	5 / 15	REACTOME_STRIATED_MUSCLE_CONTRACTION
3	5e−05	3 / 15	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
4	1e−03	2 / 12	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_DN
5	2e−03	2 / 13	LIU_TARGETS_OF_VMYB_VS_CMYB_UP
6	2e−03	2 / 14	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN
7	2e−03	2 / 14	LIANG_SILENCED_BY_METHYLATION_UP
8	2e−03	2 / 14	BIOCARTA_UCALPAIN_PATHWAY
9	2e−03	2 / 14	REACTOME_MUSCLE_CONTRACTION
10	2e−03	2 / 15	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
11	2e−03	2 / 15	BIOCARTA_INTEGRIN_PATHWAY
12	3e−03	2 / 16	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
13	3e−03	2 / 16	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
14	3e−03	2 / 16	SASSON_RESPONSE_TO_FORSKOLIN_DN
15	2e−02	1 / 5	LE_SKI_TARGETS_DN
16	2e−02	1 / 5	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
17	3e−02	1 / 6	LY_AGING_OLD_UP
18	3e−02	1 / 6	BIOCARTA_HSP27_PATHWAY
19	3e−02	1 / 7	OHASHI_AURKB_TARGETS
20	4e−02	1 / 8	XU_GH1_EXOGENOUS_TARGETS_UP

H. Tiss

Rank	p−value	#in/all	Geneset
1	1e−79	46 / 127	WIRTH_Muscle
2	1e−17	9 / 16	WIRTH_Hippocampus
3	6e−02	1 / 12	WIRTH_Prim. lymphoid organs
4	3e−01	3 / 400	WIRTH_Nervous System
5	1e+00	0 / 5	WIRTH_Pituitary gland
6	1e+00	0 / 26	WIRTH_Pancreas
7	1e+00	0 / 417	WIRTH_Immune system
8	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
9	1e+00	0 / 10	WIRTH_B−cells
10	1e+00	0 / 13	WIRTH_Tonsil
11	1e+00	0 / 13	WIRTH_Thymus
12	1e+00	0 / 12	WIRTH_Lymphocytes
13	1e+00	0 / 6	WIRTH_Bone marrow
14	1e+00	0 / 14	WIRTH_Globus pallidus
15	1e+00	0 / 15	WIRTH_Telencephalon
16	1e+00	0 / 13	WIRTH_Cortex cerebri
17	1e+00	0 / 13	WIRTH_Thalamus
18	1e+00	0 / 15	WIRTH_Cerebellum
19	1e+00	0 / 120	WIRTH_Testis
20	1e+00	0 / 50	WIRTH_Homeostasis

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.1	3 / 275	ZHANG_DLBCL mutated
2	0.3	1 / 69	SPANG_LPS 6hrs DN
3	0.3	2 / 250	LENZ_Stromal signature 1
4	0.5	1 / 140	DAVE_BL−vs−DLBCL
5	0.9	1 / 426	SPANG_CD40 6hrs DN
6	1.0	1 / 852	SPANG_BCR DN
7	1.0	0 / 13	BENTINK_mBL UP
8	1.0	0 / 13	BENTINK_mBL DOWN
9	1.0	0 / 12	DAVE_BL_DN
10	1.0	0 / 18	DAVE_BL Inter
11	1.0	0 / 12	DAVE_BL UP
12	1.0	0 / 18	DAVE_c−myc BL UP
13	1.0	0 / 6	DAVE_MHCCII BL DN
14	1.0	0 / 22	DAVE_NFkB BL DN
15	1.0	0 / 28	DAVE_Immune response 1
16	1.0	0 / 20	DAVE_Immune response 2
17	1.0	0 / 59	LENZ_Stromal signature 2
18	1.0	0 / 54	SPANG_BAFF 9hrs DN
19	1.0	0 / 24	SPANG_BAFF 9hrs UP
20	1.0	0 / 755	SPANG_BCR UP

MF

Rank	p−value	#in/all	Geneset
1	1e−33	19 / 44	structural constituent of muscle
2	4e−19	21 / 297	actin binding
3	2e−09	5 / 12	titin binding
4	2e−07	6 / 53	cytoskeletal protein binding
5	5e−07	4 / 14	tropomyosin binding
6	7e−06	5 / 56	motor activity
7	2e−05	12 / 579	calcium ion binding
8	3e−05	5 / 77	actin filament binding
9	6e−05	3 / 16	microfilament motor activity
10	3e−04	4 / 67	ion channel binding
11	8e−04	5 / 149	calmodulin binding
12	2e−03	52 / 8023	protein binding
13	2e−03	2 / 14	actin monomer binding
14	2e−03	2 / 14	structural constituent of eye lens
15	4e−03	2 / 20	myosin binding
16	7e−03	2 / 27	ATPase binding
17	1e−02	7 / 529	protein homodimerization activity
18	2e−02	2 / 39	calcium−dependent protein binding
19	2e−02	6 / 456	identical protein binding
20	5e−02	1 / 10	hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in cyclic

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.02	2 / 43	GACA−339
2	0.02	2 / 49	AGGA−483
3	0.03	1 / 6	CGTC−208
4	0.04	3 / 161	AAGC−137
5	0.05	1 / 10	CTAC−325
6	0.16	2 / 147	TGTG−377
7	0.16	1 / 37	CTCT−526C−−518F−−526A
8	0.17	1 / 39	GTAA−299−5P
9	0.21	3 / 329	AATG−23A−−23B
10	0.23	1 / 55	AATG−136
11	0.31	1 / 75	ATGT−489
12	0.35	1 / 88	ATCA−433
13	0.38	1 / 100	ACAG−10A−−10B
14	0.39	1 / 101	AAAG−501
15	0.41	1 / 108	AGCA−155
16	0.43	1 / 114	TGTA−485−3P
17	0.43	1 / 116	CAGC−370
18	0.47	1 / 129	ACCA−522
19	0.47	1 / 129	TAAT−323
20	0.49	1 / 140	CATG−496

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	1 / 5	miR−320
2	1.00	0 / 11	let−7a
3	1.00	0 / 6	let−7b
4	1.00	0 / 4	let−7c
5	1.00	0 / 6	let−7d
6	1.00	0 / 4	let−7g
7	1.00	0 / 13	miR−1
8	1.00	0 / 5	miR−101
9	1.00	0 / 2	miR−101b
10	1.00	0 / 4	miR−106b
11	1.00	0 / 2	miR−107
12	1.00	0 / 4	miR−122
13	1.00	0 / 2	miR−124a
14	1.00	0 / 6	miR−125a
15	1.00	0 / 9	miR−125b
16	1.00	0 / 5	miR−126
17	1.00	0 / 2	miR−127
18	1.00	0 / 3	miR−128
19	1.00	0 / 4	miR−128b
20	1.00	0 / 2	miR−129

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.03	1 / 7	hsa−miR−566
2	0.10	1 / 22	hsa−miR−596
3	0.11	1 / 25	hsa−miR−99a
4	0.12	1 / 27	hsa−miR−483−3p
5	0.15	1 / 34	hsa−miR−615−5p
6	0.16	1 / 36	hsa−miR−34c−3p
7	0.19	1 / 44	hsa−miR−636
8	0.21	1 / 48	hsa−miR−146b−3p
9	0.22	1 / 50	hsa−miR−504
10	0.23	1 / 53	hsa−miR−519b−5p
11	0.23	1 / 53	hsa−miR−519c−5p
12	0.23	1 / 55	hsa−miR−891b
13	0.24	2 / 192	hsa−miR−206
14	0.25	1 / 58	hsa−miR−518d−5p
15	0.25	1 / 58	hsa−miR−520c−5p
16	0.26	1 / 61	hsa−miR−1236
17	0.27	1 / 64	hsa−miR−873
18	0.27	1 / 66	hsa−miR−499−3p
19	0.30	1 / 73	hsa−miR−509−5p
20	0.31	1 / 75	hsa−miR−509−3−5p

MMML CGS

Rank	p−value	#in/all	Geneset
1	1	0 / 16	MACIEJ_MMML 1
2	1	0 / 13	MACIEJ_MMML 10
3	1	0 / 7	MACIEJ_MMML 13
4	1	0 / 9	MACIEJ_MMML 14
5	1	0 / 11	MACIEJ_MMML 15
6	1	0 / 15	MACIEJ_MMML 16
7	1	0 / 2	MACIEJ_MMML 17
8	1	0 / 14	MACIEJ_MMML 19
9	1	0 / 4	MACIEJ_MMML 2
10	1	0 / 5	MACIEJ_MMML 20
11	1	0 / 15	MACIEJ_MMML 22
12	1	0 / 4	MACIEJ_MMML 23
13	1	0 / 12	MACIEJ_MMML 24
14	1	0 / 14	MACIEJ_MMML 26
15	1	0 / 2	MACIEJ_MMML 27
16	1	0 / 5	MACIEJ_MMML 28
17	1	0 / 6	MACIEJ_MMML 29
18	1	0 / 11	MACIEJ_MMML 3
19	1	0 / 14	MACIEJ_MMML 30
20	1	0 / 11	MACIEJ_MMML 31

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.009	12 / 1146	HEBENSTREIT_low expression TF
2	0.906	3 / 1095	HEBENSTREIT_high expression TF
3	0.998	1 / 1233	KIM_MYC targets
4	1.000	0 / 14	NOWICK_TF
5	1.000	0 / 5	MYC_TFs
6	1.000	0 / 63	MYC_Targets UP
7	1.000	0 / 9	MYC_Targets DOWN
8	1.000	0 / 4	MYC_Apoptosis UP
9	1.000	0 / 8	MYC_Cell cycle UP
10	1.000	0 / 2	MYC_Cell cycle DOWN
11	1.000	0 / 4	MYC_Cell growth and proliferation UP
12	1.000	0 / 2	MYC_Chromatin_modification UP
13	1.000	0 / 7	MYC_DNA repair UP
14	1.000	0 / 3	MYC_DNA replication UP
15	1.000	0 / 2	MYC_ECM cell adhesion DOWN
16	1.000	0 / 20	MYC_Metabolism UP
17	1.000	0 / 16	MYC_Protein synthesis degradation UP
18	1.000	0 / 8	MYC_RNA processing binding UP
19	1.000	0 / 2	MYC_Signal transduction UP
20	1.000	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.05	1 / 10	VAQUERIZAS_Skeletal.muscle.psoas
2	1.00	0 / 40	VAQUERIZAS_Fetal brain
3	1.00	0 / 44	VAQUERIZAS_Placenta
4	1.00	0 / 28	VAQUERIZAS_Liver
5	1.00	0 / 37	VAQUERIZAS_Prostate
6	1.00	0 / 29	VAQUERIZAS_Smooth muscle
7	1.00	0 / 43	VAQUERIZAS_Uterus
8	1.00	0 / 144	VAQUERIZAS_General
9	1.00	0 / 12	VAQUERIZAS_Kidney
10	1.00	0 / 22	VAQUERIZAS_Spinal cord
11	1.00	0 / 43	VAQUERIZAS_Whole brain
12	1.00	0 / 41	VAQUERIZAS_Thymus
13	1.00	0 / 39	VAQUERIZAS_Thyroid
14	1.00	0 / 62	VAQUERIZAS_Whole blood
15	1.00	0 / 7	VAQUERIZAS_Appendix
16	1.00	0 / 30	VAQUERIZAS_Fetal lung
17	1.00	0 / 62	VAQUERIZAS_Lung
18	1.00	0 / 16	VAQUERIZAS_Pancreas
19	1.00	0 / 24	VAQUERIZAS_Trachea
20	1.00	0 / 14	VAQUERIZAS_Fetal liver

Sample−Underexpression

Spot Summary: n

metagenes = 39
genes = 341

<r> metagenes = 0.86
<r> genes = 0.22
beta: r2= 4.97 / log p= −Inf

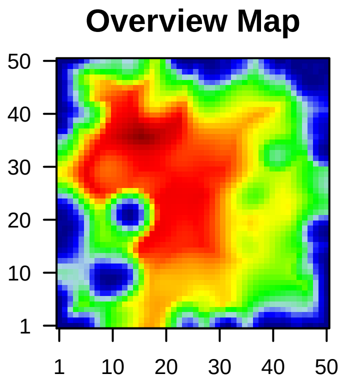
samples with spot = 10 (3.6 %)
Classical : 1 (3.1 %)
Mesenchymal : 1 (1.2 %)
Basal : 8 (9.5 %)

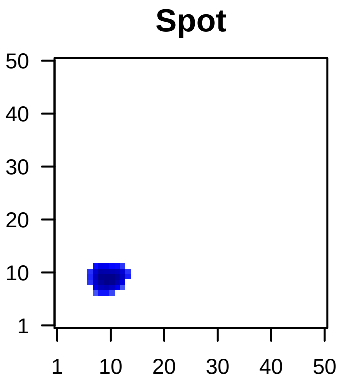
Spot Genelist

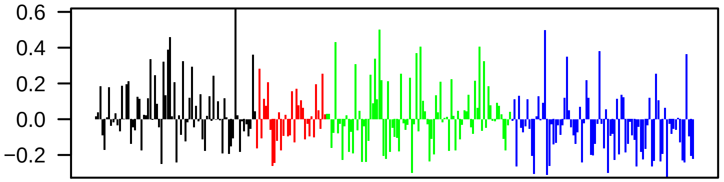
Rank	ID	max e	min e	r	Symbol	Description
1	3303	1.9	−2.49	0.33	HSPA1A	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
2	4037	1.65	−1.52	0.55	LRP3	low density lipoprotein receptor−related protein 3 [Source:HG
3	55506	1.09	−1.51	0.37	H2AFY2	H2A histone family, member Y2 [Source:HGNC Symbol;Acc:1
4	9627	2.05	−1.38	0.31	SNCAIP	synuclein, alpha interacting protein [Source:HGNC Symbol;A
5	9130	1.12	−1.34	0.63	FAM50A	family with sequence similarity 50, member A [Source:HGNC
6	3911	1.22	−1.33	0.52	LAMA5	laminin, alpha 5 [Source:HGNC Symbol;Acc:6485]
7	80728	1.6	−1.29	0.64	ARHGAP39	Rho GTPase activating protein 39 [Source:HGNC Symbol;Ac
8	2026	1.72	−1.27	0.54	ENO2	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
9	25894	1.36	−1.23	0.51	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGe
10	23753	1.72	−1.23	0.49	SDF2L1	stromal cell−derived factor 2−like 1 [Source:HGNC Symbol;A
11	128710	1.31	−1.16	0.42	SLX4IP	SLX4 interacting protein [Source:HGNC Symbol;Acc:16225]
12	5871	1.35	−1.14	0.46	MAP4K2	mitogen−activated protein kinase kinase kinase kinase 2 [Sou
13	29801	1.41	−1.14	0.39	ZDHHC8	zinc finger, DHHC−type containing 8 [Source:HGNC Symbol;
14	23338	1.78	−1.12	0.43	JADE2	jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
15	27161	1.33	−1.09	0.68	AGO2	argonaute RISC catalytic component 2 [Source:HGNC Symb
16	404217	1.59	−1.09	0.39	CTXN1	cortexin 1 [Source:HGNC Symbol;Acc:31108]
17	8408	1.06	−1.08	0.4	ULK1	unc−51 like autophagy activating kinase 1 [Source:HGNC Sy
18	64847	1.08	−1.06	0.59	SPATA20	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
19	55661	1.31	−1.06	0.68	DDX27	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
20	140465	1.15	−1.05	0.44	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non−muscl

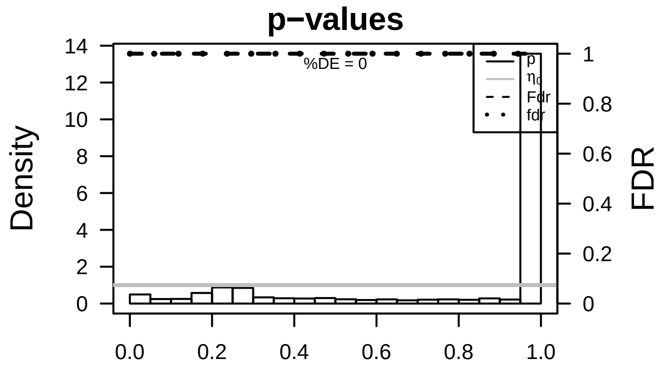
Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−07	49 / 1135	Chr	Chr 19
2	2e−05	29 / 630	Chr	Chr X
3	9e−05	23 / 481	BP	biological_process
4	2e−04	6 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
5	3e−04	21 / 449	Chr	Chr 20
6	3e−04	20 / 419	CC	cellular_component
7	6e−04	8 / 96	BP	chromatin modification
8	8e−04	3 / 10	CC	oligosaccharyltransferase complex
9	9e−04	118 / 4640	CC	nucleus
10	1e−03	4 / 24	BP	protein O−linked glycosylation
11	1e−03	4 / 24	BP	tissue development
12	2e−03	4 / 26	BP	histone acetylation
13	2e−03	32 / 940	MF	nucleic acid binding
14	2e−03	3 / 14	GSEA	RIZKI_TUMOR_INVASIVENESS_2D_DN
15	2e−03	4 / 29	miRN	hsa−miR−296−5p
16	3e−03	3 / 15	MF	acetylglucosaminyltransferase activity
17	3e−03	8 / 125	miRN	GAGC−337
18	4e−03	3 / 16	BP	intracellular steroid hormone receptor signaling pathway
19	4e−03	3 / 16	CC	NuRD complex
20	4e−03	3 / 16	CC	photoreceptor inner segment
21	4e−03	3 / 16	GSEA	BIOCARTA_ERK_PATHWAY
22	4e−03	3 / 16	GSEA	BIOCARTA_IGF1MTOR_PATHWAY
23	4e−03	2 / 5	GSEA	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
24	4e−03	3 / 17	BP	calcium ion homeostasis
25	5e−03	5 / 55	miRN	GGGG−296
26	6e−03	3 / 19	MF	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anh
27	6e−03	34 / 1095	TF	HEBENSTREIT_high expression TF
28	8e−03	45 / 1574	BP	transcription, DNA−templated
29	8e−03	3 / 21	BP	chromatin organization
30	8e−03	8 / 144	TF Ti	VAQUERIZAS_General
31	9e−03	4 / 41	miRN	hsa−miR−532−3p
32	9e−03	5 / 64	BP	neural tube closure
33	9e−03	3 / 22	MF	polyubiquitin binding
34	9e−03	4 / 42	BP	inositol phosphate metabolic process
35	9e−03	4 / 42	MF	ligand−dependent nuclear receptor transcription coactivator activity
36	1e−02	2 / 8	GSEA	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
37	1e−02	2 / 8	GSEA	WEBER_METHYLATED_ICP_IN_FIBROBLAST
38	1e−02	2 / 8	miRN	ACCG−423
39	1e−02	3 / 23	MF	RNA polymerase II repressing transcription factor binding
40	1e−02	4 / 44	CC	presynaptic membrane









BP

Rank	p−value	#in/all	Geneset
1	9e−05	23 / 481	biological_process
2	6e−04	8 / 96	chromatin modification
3	1e−03	4 / 24	protein O−linked glycosylation
4	1e−03	4 / 24	tissue development
5	2e−03	4 / 26	histone acetylation
6	4e−03	3 / 16	intracellular steroid hormone receptor signaling pathway
7	4e−03	3 / 17	calcium ion homeostasis
8	8e−03	45 / 1574	transcription, DNA−templated
9	8e−03	3 / 21	chromatin organization
10	9e−03	5 / 64	neural tube closure
11	9e−03	4 / 42	inositol phosphate metabolic process
12	1e−02	3 / 24	centrosome organization
13	2e−02	2 / 10	eyelid development in camera−type eye
14	2e−02	2 / 10	positive regulation of cyclin−dependent protein kinase activity
15	2e−02	2 / 10	positive regulation of macroautophagy
16	2e−02	2 / 11	bone remodeling
17	2e−02	2 / 11	cerebellar Purkinje cell layer development
18	2e−02	2 / 11	maintenance of protein location in nucleus
19	2e−02	2 / 11	positive regulation of synapse maturation
20	2e−02	3 / 29	ATP hydrolysis coupled proton transport

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	2 / 14	LIU_COMMON_CANCER_GENES
2	0.20	1 / 11	GENTLES_modul5
3	0.25	2 / 48	KUIPER_MM poor survival
4	0.25	13 / 530	Lembcke_Normal vs Adenoma
5	0.26	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.27	1 / 16	GENTLES_modul7
7	0.39	2 / 68	SHAUGHNESSY_MM high risk
8	0.75	5 / 316	SPANG_BCL6−index2
9	0.98	1 / 185	SPANG_LPS−index2
10	1.00	1 / 553	Lembcke_Colonic Inflammation
11	1.00	0 / 15	RHODES_CANCER_META_SIGNATURE
12	1.00	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
13	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1.00	0 / 10	LIU_BREAST_CANCER
15	1.00	0 / 14	LIU_LIVER_CANCER
16	1.00	0 / 15	LIU_PROSTATE_CANCER_DN
17	1.00	0 / 14	LIU_PROSTATE_CANCER_UP
18	1.00	0 / 14	WANG_ER_UP
19	1.00	0 / 9	WANG_ER_DN
20	1.00	0 / 16	WOLFER_overlap genes

CC

Rank	p−value	#in/all	Geneset
1	3e−04	20 / 419	cellular_component
2	8e−04	3 / 10	oligosaccharyltransferase complex
3	9e−04	118 / 4640	nucleus
4	4e−03	3 / 16	NuRD complex
5	4e−03	3 / 16	photoreceptor inner segment
6	1e−02	4 / 44	presynaptic membrane
7	2e−02	5 / 77	late endosome membrane
8	2e−02	20 / 614	endoplasmic reticulum membrane
9	2e−02	3 / 30	rough endoplasmic reticulum
10	2e−02	2 / 12	PRC1 complex
11	3e−02	2 / 13	STAGA complex
12	3e−02	3 / 33	mediator complex
13	3e−02	6 / 121	microtubule cytoskeleton
14	4e−02	19 / 621	endoplasmic reticulum
15	6e−02	8 / 215	lysosomal membrane
16	7e−02	3 / 48	cytoplasmic microtubule
17	7e−02	76 / 3274	integral to membrane
18	7e−02	2 / 22	heterochromatin
19	8e−02	3 / 51	cytoplasmic mRNA processing body
20	8e−02	2 / 24	endoplasmic reticulum−Golgi intermediate compartment membrane

Chr

Rank	p−value	#in/all	Geneset
1	2e−07	49 / 1135	Chr 19
2	2e−05	29 / 630	Chr X
3	3e−04	21 / 449	Chr 20
4	2e−02	23 / 743	Chr 7
5	3e−02	22 / 717	Chr 16
6	8e−02	2 / 23	Chr HSCHR6_MHC_DBB
7	9e−02	15 / 519	Chr 14
8	1e−01	24 / 918	Chr 17
9	3e−01	2 / 52	Chr HSCHR6_MHC_QBL
10	5e−01	18 / 866	Chr 12
11	8e−01	6 / 386	Chr 22
12	8e−01	9 / 602	Chr 10
13	9e−01	15 / 957	Chr 11
14	9e−01	2 / 187	Chr 21
15	9e−01	15 / 1033	Chr 2
16	9e−01	6 / 504	Chr 15
17	1e+00	12 / 914	Chr 3
18	1e+00	6 / 534	Chr 8
19	1e+00	25 / 1720	Chr 1
20	1e+00	5 / 633	Chr 9

Disease

Rank	p−value	#in/all	Geneset
1	1	1 / 572	GUDJ_psoriasis up
2	1	0 / 375	GUDJ_psoriasis down
3	1	0 / 17	BCHETNIA_EBM up
4	1	0 / 2	BCHETNIA_EBM down
5	1	0 / 26	BCHETNIA_EBM−DM up
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	
16	NA	0 / 0	
17	NA	0 / 0	
18	NA	0 / 0	
19	NA	0 / 0	
20	NA	0 / 0	

Glio

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 45	willscher_GBM_Verhaak−PNwt_expression_J_up
2	2e−02	3 / 27	WIRTH_PN subtype
3	4e−02	5 / 95	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
4	2e−01	2 / 37	willscher_GBM_proteomics_wtOnly_SpotH
5	2e−01	1 / 11	willscher_GBM_Verhaak−CL_expression_M_down
6	2e−01	1 / 11	willscher_GBM_Verhaak−MES_expression_M_down
7	2e−01	1 / 11	willscher_GBM_Verhaak−PNmut_expression_M_up
8	2e−01	1 / 11	KIM amplified & overexpressed in LTS
9	2e−01	4 / 117	GIEZELT_GBM_WT_up_VS_mut
10	2e−01	1 / 12	Phillips PN up vs MES & Prolif
11	2e−01	1 / 12	willscher_GBM_LTSmut_proteomics−B_UP
12	2e−01	1 / 12	willscher_GBM_STSwt_proteomics−B_DOWN
13	2e−01	10 / 379	Down_a
14	3e−01	2 / 54	willscher_GBM_proteomics_wtOnly_SpotG
15	3e−01	3 / 105	willscher_GBM_proteomics_wtOnly_SpotB
16	4e−01	9 / 391	Down_b
17	4e−01	2 / 71	willscher_GBM_Verhaak−CL_expression_H_down
18	4e−01	2 / 71	willscher_GBM_Verhaak−MES_expression_H_up
19	4e−01	2 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
20	4e−01	2 / 73	GIEZELT_GBM_WT_down_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	3 / 14	RIZKI_TUMOR_INVASIVENESS_2D_DN
2	0.004	3 / 16	BIOCARTA_ERK_PATHWAY
3	0.004	3 / 16	BIOCARTA_IGF1MTOR_PATHWAY
4	0.004	2 / 5	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
5	0.010	2 / 8	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
6	0.010	2 / 8	WEBER_METHYLATED_ICP_IN_FIBROBLAST
7	0.016	2 / 10	XU_GH1_AUTOCRINE_TARGETS_DN
8	0.019	2 / 11	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
9	0.019	2 / 11	BIOCARTA_AHSP_PATHWAY
10	0.019	2 / 11	BIOCARTA_TRKA_PATHWAY
11	0.023	2 / 12	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
12	0.023	2 / 12	KIM_WT1_TARGETS_12HR_UP
13	0.023	2 / 12	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
14	0.023	2 / 12	MITSIADES_RESPONSE_TO_APLIDIN_UP
15	0.023	2 / 12	BROWNE_HCMV_INFECTION_14HR_UP
16	0.023	2 / 12	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
17	0.026	2 / 13	COLDREN_GEFITINIB_RESISTANCE_UP
18	0.026	2 / 13	ENK_UV_RESPONSE_KERATINOCYTE_UP
19	0.026	2 / 13	DOUGLAS_BMI1_TARGETS_UP
20	0.026	2 / 13	WALLACE_JAK2_TARGETS_UP

H. Tiss

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	WIRTH_Lymphocytes
2	0.2	1 / 13	WIRTH_Thymus
3	0.2	1 / 13	WIRTH_Thyroid gland
4	0.4	3 / 120	WIRTH_Testis
5	0.5	1 / 36	WIRTH_Placenta
6	0.6	1 / 50	WIRTH_Homeostasis
7	0.8	6 / 400	WIRTH_Nervous System
8	0.9	1 / 127	WIRTH_Muscle
9	1.0	3 / 417	WIRTH_Immune system
10	1.0	0 / 5	WIRTH_Pituitary gland
11	1.0	0 / 26	WIRTH_Pancreas
12	1.0	0 / 13	WIRTH_Sec. lymphoid organs
13	1.0	0 / 12	WIRTH_Prim. lymphoid organs
14	1.0	0 / 10	WIRTH_B−cells
15	1.0	0 / 13	WIRTH_Tonsil
16	1.0	0 / 6	WIRTH_Bone marrow
17	1.0	0 / 14	WIRTH_Globus pallidus
18	1.0	0 / 15	WIRTH_Telencephalon
19	1.0	0 / 13	WIRTH_Cortex cerebri
20	1.0	0 / 16	WIRTH_Hippocampus

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.2	11 / 426	SPANG_CD40 6hrs DN
2	0.3	2 / 54	SPANG_BAFF 9hrs DN
3	0.3	1 / 20	DAVE_Immune response 2
4	0.4	1 / 28	DAVE_Immune response 1
5	0.5	1 / 38	ROSOLOWSKI_blue DOWN
6	0.7	1 / 59	LENZ_Stromal signature 2
7	0.7	1 / 69	SPANG_LPS 6hrs DN
8	0.8	1 / 86	ROSOLOWSKI_red total
9	0.9	11 / 755	SPANG_BCR UP
10	0.9	4 / 327	SPANG_CD40 6hrs UP
11	0.9	1 / 118	SPANG_LPS 6hrs UP
12	0.9	1 / 119	ROSOLOWSKI_green total
13	0.9	3 / 275	ZHANG_DLBCL mutated
14	0.9	12 / 852	SPANG_BCR DN
15	1.0	2 / 274	SPANG_IL21 DN
16	1.0	2 / 291	SPANG_IL21 UP
17	1.0	1 / 250	LENZ_Stromal signature 1
18	1.0	0 / 13	BENTINK_mBL UP
19	1.0	0 / 13	BENTINK_mBL DOWN
20	1.0	0 / 140	DAVE_BL−vs−DLBCL

MF

Rank	p−value	#in/all	Geneset
1	0.002	32 / 940	nucleic acid binding
2	0.003	3 / 15	acetylglucosaminyltransferase activity
3	0.006	3 / 19	hydrolase activity, acting on acid anhydrides, in phosphorus−containing anhyd
4	0.009	3 / 22	polyubiquitin binding
5	0.009	4 / 42	ligand−dependent nuclear receptor transcription coactivator activity
6	0.010	3 / 23	RNA polymerase II repressing transcription factor binding
7	0.013	3 / 25	phosphatidylinositol−3,4,5−trisphosphate binding
8	0.013	19 / 549	molecular_function
9	0.016	2 / 10	K63−linked polyubiquitin binding
10	0.017	3 / 28	ribosome binding
11	0.025	3 / 32	beta−tubulin binding
12	0.025	12 / 318	chromatin binding
13	0.036	17 / 531	catalytic activity
14	0.039	2 / 16	histone acetyl−lysine binding
15	0.039	2 / 16	vitamin D receptor binding
16	0.042	3 / 39	histone acetyltransferase activity
17	0.049	2 / 18	cation transmembrane transporter activity
18	0.054	2 / 19	mitogen−activated protein kinase kinase kinase binding
19	0.056	12 / 361	binding
20	0.064	2 / 21	translation elongation factor activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.003	8 / 125	GAGC−337
2	0.005	5 / 55	GGGG−296
3	0.010	2 / 8	ACCG−423
4	0.013	2 / 9	TCCG−184
5	0.045	9 / 235	CACT−34A−−34C−−449
6	0.069	3 / 48	CCAT−432
7	0.072	4 / 79	TCTC−185
8	0.076	9 / 261	CTCA−125B−−125A
9	0.095	1 / 5	GTCG−369−5P
10	0.099	3 / 56	ATCT−31
11	0.107	4 / 91	CTGT−194
12	0.134	3 / 64	TTGG−150
13	0.148	1 / 8	CGCA−450
14	0.191	3 / 76	GGCC−193A−−193B
15	0.191	3 / 76	GAGA−452
16	0.198	4 / 116	CAGC−370
17	0.202	2 / 42	GTAC−486
18	0.208	5 / 159	CACC−138
19	0.209	2 / 43	AGTT−146A−−146B
20	0.209	2 / 43	GACA−339

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 3	Thyroid carcinoma, papillary
2	1	0 / 34	Pancreatic cancer
3	1	0 / 22	Glioblastoma multiforme, somatic
4	1	0 / 21	Gastrointestinal
5	1	0 / 2	Pituitary adenoma
6	1	0 / 36	Cancer
7	1	0 / 27	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 35	Prostate cancer
10	1	0 / 11	Alzheimer disease, susceptibility to
11	1	0 / 3	Schizophrenia, susceptibility to
12	1	0 / 8	Parkinson disease
13	1	0 / 23	Hepatocellular carcinoma
14	1	0 / 29	Melanoma and neural system tumor syndrome
15	1	0 / 30	Ovarian cancer
16	1	0 / 38	Breast cancer
17	1	0 / 15	Gastric cancer
18	1	0 / 4	Thyroid carcinoma, follicular
19	1	0 / 36	Lung cancer
20	1	0 / 12	Bladder cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.04	1 / 2	miR−661
2	0.08	1 / 4	miR−122
3	0.10	1 / 5	miR−143
4	0.10	1 / 5	miR−196a
5	0.10	1 / 5	miR−205
6	0.11	1 / 6	miR−200c
7	0.13	1 / 7	miR−145
8	0.23	1 / 13	miR−1
9	0.41	1 / 26	miR−21
10	1.00	0 / 11	let−7a
11	1.00	0 / 6	let−7b
12	1.00	0 / 4	let−7c
13	1.00	0 / 6	let−7d
14	1.00	0 / 4	let−7g
15	1.00	0 / 5	miR−101
16	1.00	0 / 2	miR−101b
17	1.00	0 / 4	miR−106b
18	1.00	0 / 2	miR−107
19	1.00	0 / 2	miR−124a
20	1.00	0 / 6	miR−125a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.002	4 / 29	hsa−miR−296−5p
2	0.009	4 / 41	hsa−miR−532−3p
3	0.011	3 / 24	hsa−miR−602
4	0.017	8 / 164	hsa−miR−96
5	0.017	4 / 50	hsa−miR−571
6	0.023	2 / 12	hsa−miR−1249
7	0.026	7 / 145	hsa−miR−491−5p
8	0.029	3 / 34	hsa−miR−615−5p
9	0.032	3 / 35	hsa−miR−127−3p
10	0.033	4 / 61	hsa−miR−514
11	0.034	4 / 62	hsa−miR−637
12	0.037	5 / 93	hsa−miR−125a−5p
13	0.046	4 / 68	hsa−miR−193b
14	0.049	2 / 18	hsa−miR−564
15	0.052	4 / 71	hsa−miR−184
16	0.059	4 / 74	hsa−miR−877
17	0.091	3 / 54	hsa−miR−187
18	0.093	5 / 121	hsa−miR−493
19	0.099	3 / 56	hsa−miR−665
20	0.103	3 / 57	hsa−miR−193a−3p

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	MACIEJ_MMML 14
2	0.2	1 / 12	MACIEJ_MMML 24
3	1.0	0 / 16	MACIEJ_MMML 1
4	1.0	0 / 13	MACIEJ_MMML 10
5	1.0	0 / 7	MACIEJ_MMML 13
6	1.0	0 / 11	MACIEJ_MMML 15
7	1.0	0 / 15	MACIEJ_MMML 16
8	1.0	0 / 2	MACIEJ_MMML 17
9	1.0	0 / 14	MACIEJ_MMML 19
10	1.0	0 / 4	MACIEJ_MMML 2
11	1.0	0 / 5	MACIEJ_MMML 20
12	1.0	0 / 15	MACIEJ_MMML 22
13	1.0	0 / 4	MACIEJ_MMML 23
14	1.0	0 / 14	MACIEJ_MMML 26
15	1.0	0 / 2	MACIEJ_MMML 27
16	1.0	0 / 5	MACIEJ_MMML 28
17	1.0	0 / 6	MACIEJ_MMML 29
18	1.0	0 / 11	MACIEJ_MMML 3
19	1.0	0 / 14	MACIEJ_MMML 30
20	1.0	0 / 11	MACIEJ_MMML 31

Pathw Act

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

TF

Rank	p−value	#in/all	Geneset
1	0.006	34 / 1095	HEBENSTREIT_high expression TF
2	0.274	1 / 16	MYC_Protein synthesis degradation UP
3	0.330	1 / 20	MYC_Metabolism UP
4	0.567	24 / 1233	KIM_MYC targets
5	0.717	1 / 63	MYC_Targets UP
6	0.970	15 / 1146	HEBENSTREIT_low expression TF
7	1.000	0 / 14	NOWICK_TF
8	1.000	0 / 5	MYC_TFs
9	1.000	0 / 9	MYC_Targets DOWN
10	1.000	0 / 4	MYC_Apoptosis UP
11	1.000	0 / 8	MYC_Cell cycle UP
12	1.000	0 / 2	MYC_Cell cycle DOWN
13	1.000	0 / 4	MYC_Cell growth and proliferation UP
14	1.000	0 / 2	MYC_Chromatin_modification UP
15	1.000	0 / 7	MYC_DNA repair UP
16	1.000	0 / 3	MYC_DNA replication UP
17	1.000	0 / 2	MYC_ECM cell adhesion DOWN
18	1.000	0 / 8	MYC_RNA processing binding UP
19	1.000	0 / 2	MYC_Signal transduction UP
20	1.000	0 / 3	MYC_Tumor supressor genes UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.008	8 / 144	VAQUERIZAS_General
2	0.274	1 / 16	VAQUERIZAS_Heart
3	0.533	1 / 38	VAQUERIZAS_Testis
4	1.000	0 / 40	VAQUERIZAS_Fetal brain
5	1.000	0 / 44	VAQUERIZAS_Placenta
6	1.000	0 / 28	VAQUERIZAS_Liver
7	1.000	0 / 37	VAQUERIZAS_Prostate
8	1.000	0 / 29	VAQUERIZAS_Smooth muscle
9	1.000	0 / 43	VAQUERIZAS_Uterus
10	1.000	0 / 12	VAQUERIZAS_Kidney
11	1.000	0 / 22	VAQUERIZAS_Spinal cord
12	1.000	0 / 43	VAQUERIZAS_Whole brain
13	1.000	0 / 41	VAQUERIZAS_Thymus
14	1.000	0 / 39	VAQUERIZAS_Thyroid
15	1.000	0 / 62	VAQUERIZAS_Whole blood
16	1.000	0 / 7	VAQUERIZAS_Appendix
17	1.000	0 / 30	VAQUERIZAS_Fetal lung
18	1.000	0 / 62	VAQUERIZAS_Lung
19	1.000	0 / 16	VAQUERIZAS_Pancreas
20	1.000	0 / 24	VAQUERIZAS_Trachea