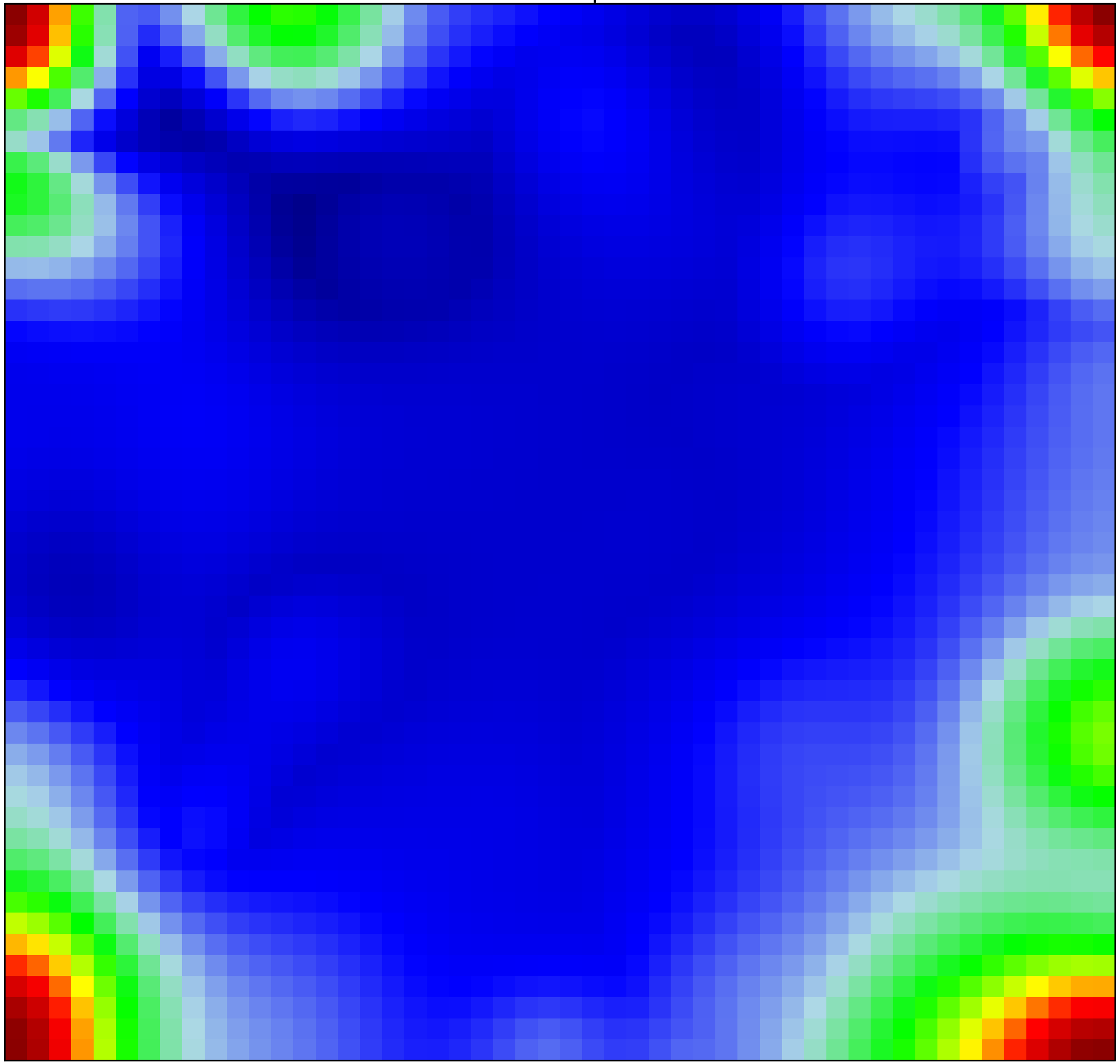
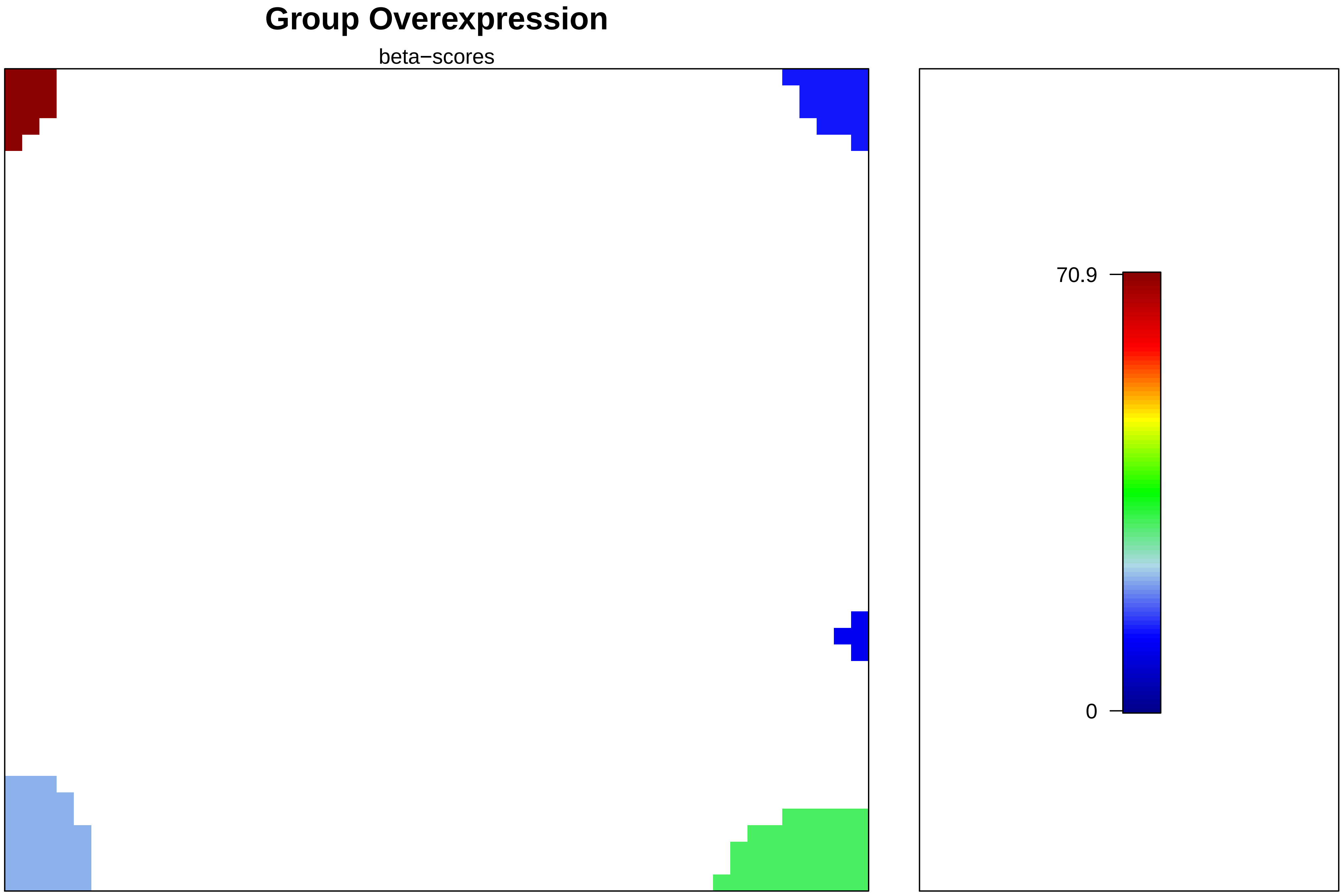
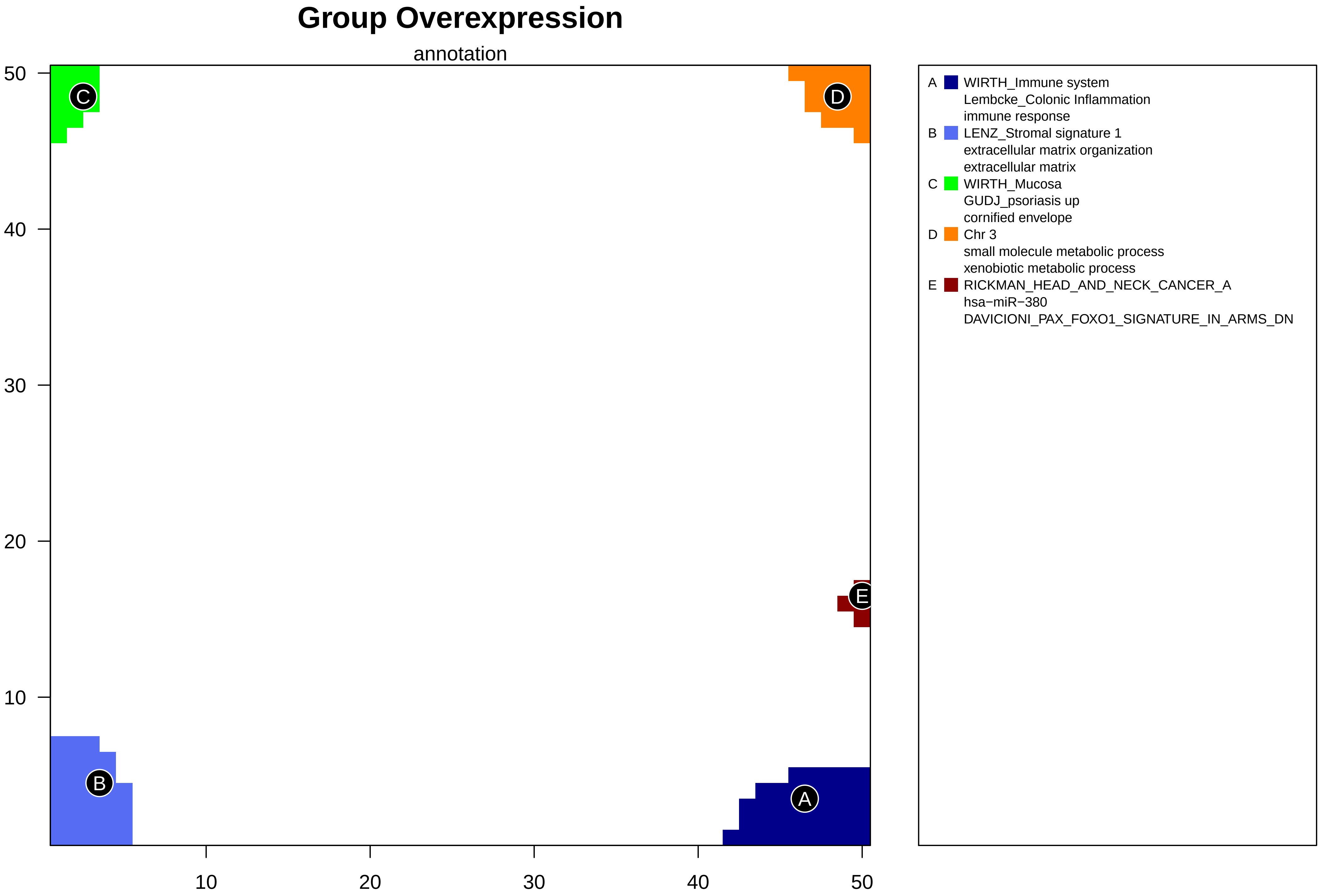
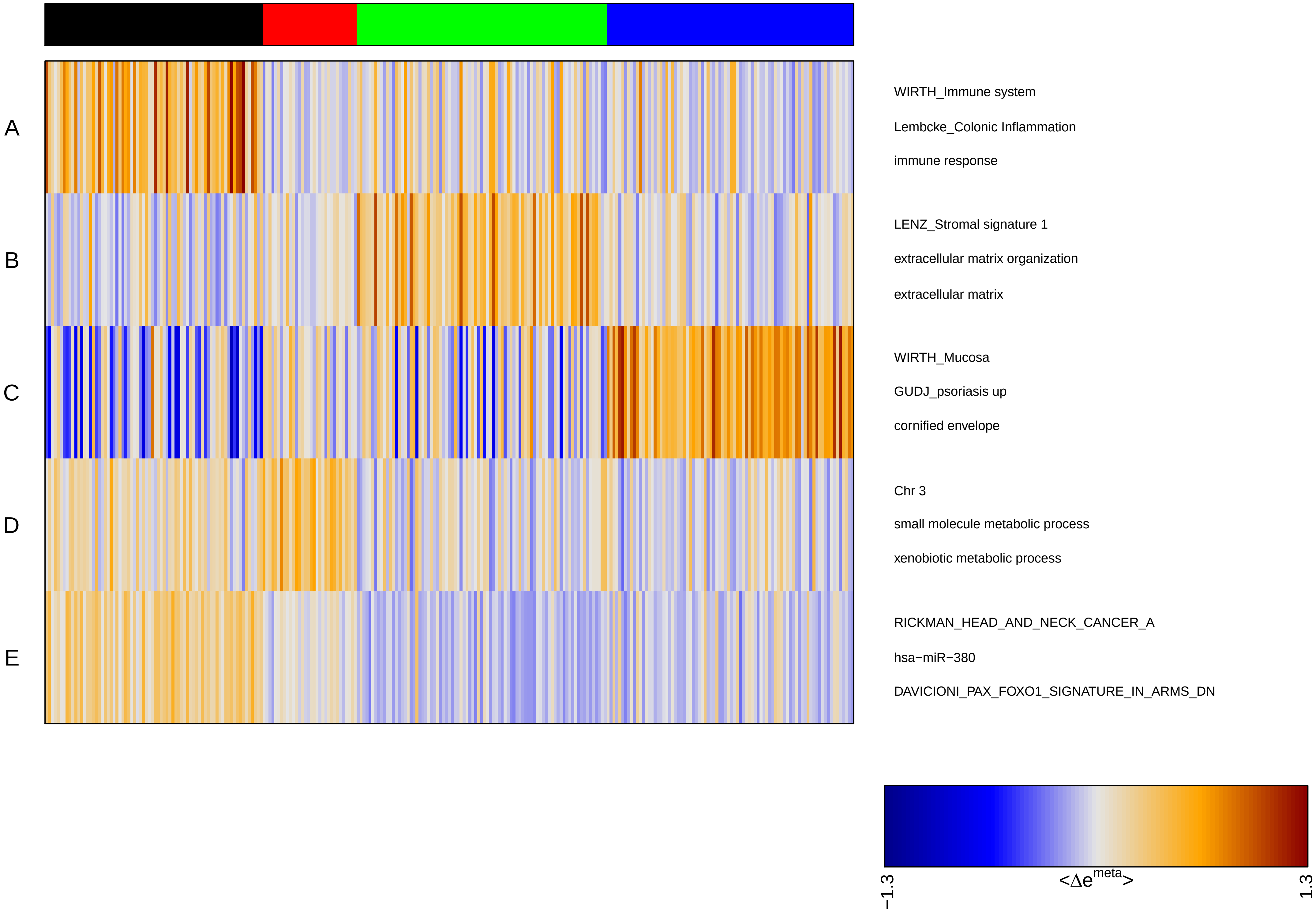
Group Overexpression

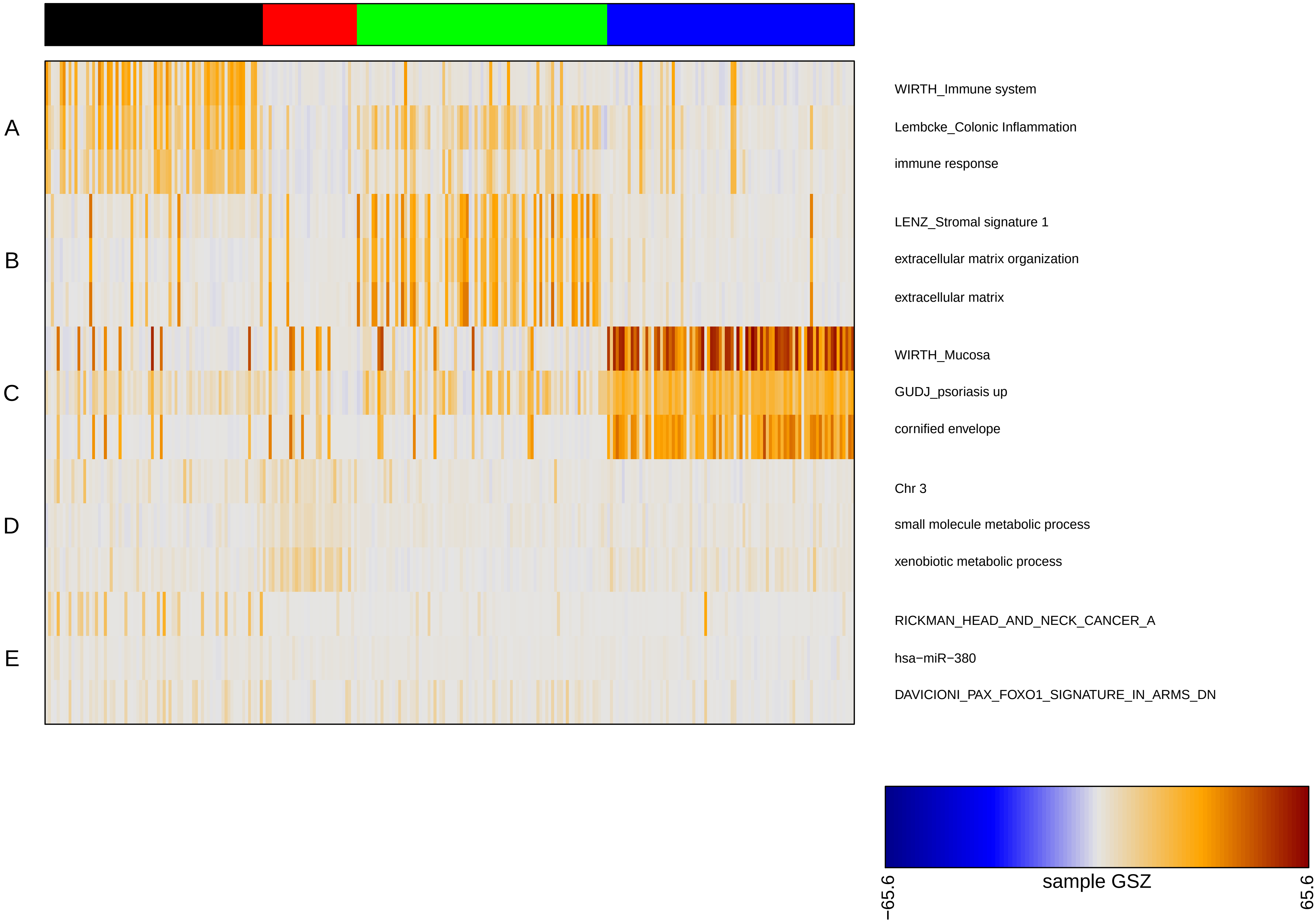
landscape




Group Overexpression
beta−scores
70.9
0


Group Overexpression
annotation
50
40
30
20
10
10
20
30
40
50
C
D
E
B
A
A WIRTH_Immune system
Lembcke_Colonic Inflammation
immune response
B LENZ_Stromal signature 1
extracellular matrix organization
extracellular matrix
C WIRTH_Mucosa
GUDJ_psoriasis up
cornified envelope
D Chr 3
small molecule metabolic process
xenobiotic metabolic process
E RICKMAN_HEAD_AND_NECK_CANCER_A
hsa−miR−380
DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN


A
B
C
D
E
WIRTH_Immune system
Lembcke_Colonic Inflammation
immune response
LENZ_Stromal signature 1
extracellular matrix organization
extracellular matrix
WIRTH_Mucosa
GUDJ_psoriasis up
cornified envelope
Chr 3
small molecule metabolic process
xenobiotic metabolic process
RICKMAN_HEAD_AND_NECK_CANCER_A
hsa−miR−380
DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
−1.3
<Δe^meta>
1.3


A
B
C
D
E
WIRTH_Immune system
Lembcke_Colonic Inflammation
immune response
LENZ_Stromal signature 1
extracellular matrix organization
extracellular matrix
WIRTH_Mucosa
GUDJ_psoriasis up
cornified envelope
Chr 3
small molecule metabolic process
xenobiotic metabolic process
RICKMAN_HEAD_AND_NECK_CANCER_A
hsa−miR−380
DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
−65.6
sample GSZ
65.6

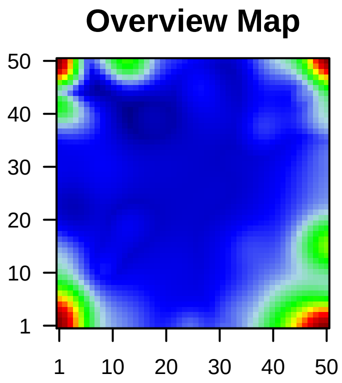
Group Overexpression

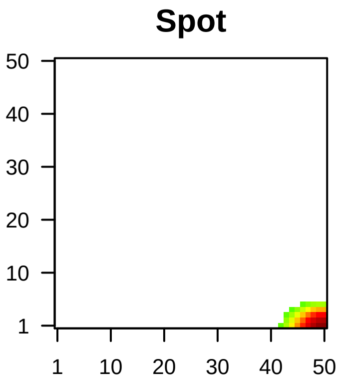
Spot Summary: A

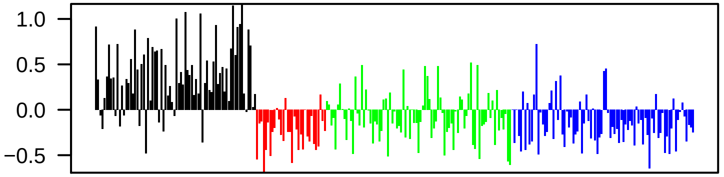
metagenes = 37
genes = 492

<r> metagenes = 0.95
<r> genes = 0.49
beta: r2= 30.5 / log p= −Inf

samples with spot = 41 (14.9 %)
Atypical : 32 (43.2 %)
Mesenchymal : 6 (7.1 %)
Basal : 3 (3.6 %)


Overview Map


Spot

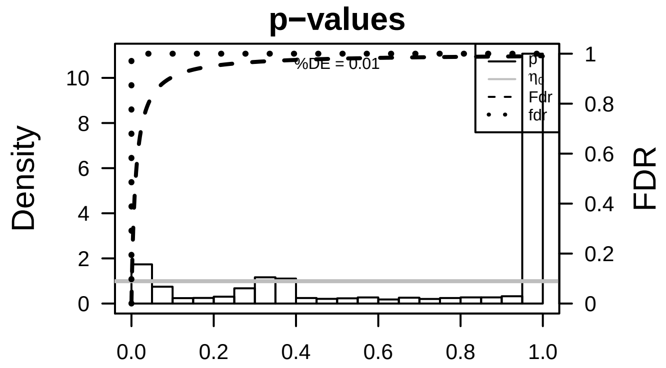


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3127	4.47	−1.24	0.19	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	260436	4.41	−1.73	0.46	FDCSP	follicular dendritic cell secreted protein [Source:HGNC Symbo
3	6363	3.84	−1.64	0.79	CCL19	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
4	3512	3.8	−2.52	0.56	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobu
5	3123	3.58	−1.81	0.25	HLA−DRB1	major histocompatibility complex, class II, DR beta 1 [Source:
6	347733	3.34	−1.41	0.47	TUBB2B	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
7	3620	3.29	−1.36	0.5	IDO1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
8	10537	3.29	−1.89	0.78	UBD	ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	930	3.28	−1.12	0.82	CD19	CD19 molecule [Source:HGNC Symbol;Acc:1633]
10	5730	3.15	−1.43	0.71	PTGDS	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
11	6366	3.15	−1.26	0.57	CCL21	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
12	57172	3.1	−2.31	0.69	CAMK1G	calcium/calmodulin−dependent protein kinase IG [Source:HG
13	6364	3.07	−3.08	0.26	CCL20	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
14	4069	3.05	−1.52	0.62	LYZ	lysozyme [Source:HGNC Symbol;Acc:6740]
15	9806	3.05	−1.59	0.84	SPOCK2	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
16	4283	2.98	−1.9	0.55	CXCL9	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
17	962	2.92	−1.66	0.95	CD48	CD48 molecule [Source:HGNC Symbol;Acc:1683]
18	1545	2.91	−1.15	0.48	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
19	25849	2.86	−1.41	0.61	PARM1	prostate androgen−regulated mucin−like protein 1 [Source:H
20	3120	2.85	−1.57	0.37	HLA−DQB2	major histocompatibility complex, class II, DQ beta 2 [Source:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−97	129 / 417	H.Tiss	WIRTH_Immune system
2	1e−81	130 / 553	Cance	Lembcke_Colonic Inflammation
3	8e−47	75 / 312	BP	immune response
4	7e−37	61 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	7e−37	61 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	7e−37	61 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	7e−37	61 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	5e−21	14 / 15	CC	MHC class II protein complex
9	4e−20	23 / 60	BP	T cell costimulation
10	1e−18	25 / 84	BP	T cell receptor signaling pathway
11	1e−17	44 / 316	Cance	SPANG_BCL6−index2
12	1e−17	154 / 2659	CC	plasma membrane
13	1e−16	31 / 162	CC	external side of plasma membrane
14	2e−16	43 / 327	Lymp	SPANG_CD40 6hrs UP
15	3e−16	34 / 204	BP	cell surface receptor signaling pathway
16	5e−16	18 / 47	BP	antigen processing and presentation
17	7e−15	37 / 269	BP	inflammatory response
18	1e−14	14 / 28	BP	B cell receptor signaling pathway
19	1e−13	10 / 13	Cance	GENTLES_modul18
20	3e−13	19 / 74	BP	regulation of immune response
21	5e−13	10 / 14	GSEA	BIOCARTA_NO2IL12_PATHWAY
22	7e−12	15 / 49	Glio	Donson−innate immunity−associated with LTS in HGA
23	9e−12	63 / 835	CC	integral to plasma membrane
24	1e−11	16 / 60	BP	interferon−gamma−mediated signaling pathway
25	2e−11	28 / 204	BP	cytokine−mediated signaling pathway
26	6e−11	12 / 32	Glio	Donson−Misc immune function−associated with LTS in HGA
27	7e−11	18 / 87	BP	antigen processing and presentation of exogenous peptide antigen via MH
28	9e−11	8 / 11	GSEA	BIOCARTA_TCYTOTOXIC_PATHWAY
29	9e−11	8 / 11	GSEA	BIOCARTA_THELPER_PATHWAY
30	1e−10	40 / 426	Lymp	SPANG_CD40 6hrs DN
31	2e−10	9 / 16	GSEA	FARMER_BREAST_CANCER_CLUSTER_1
32	2e−10	9 / 16	GSEA	SU_THYMUS
33	2e−10	22 / 140	Lymp	DAVE_BL−vs−DLBCL
34	2e−10	75 / 1167	BP	signal transduction
35	2e−10	11 / 28	Lymp	DAVE_Immune response 1
36	3e−10	22 / 143	MF	transmembrane signaling receptor activity
37	3e−10	45 / 530	BP	innate immune response
38	4e−10	13 / 45	BP	T cell activation
39	2e−09	8 / 14	GSEA	FINETTI_BREAST_CANCER_KINOME_GREEN
40	3e−09	11 / 35	CC	trans−Golgi network membrane


p−values

BP

Rank	p−value	#in/all	Geneset
1	8e−47	75 / 312	immune response
2	4e−20	23 / 60	T cell costimulation
3	1e−18	25 / 84	T cell receptor signaling pathway
4	3e−16	34 / 204	cell surface receptor signaling pathway
5	5e−16	18 / 47	antigen processing and presentation
6	7e−15	37 / 269	inflammatory response
7	1e−14	14 / 28	B cell receptor signaling pathway
8	3e−13	19 / 74	regulation of immune response
9	1e−11	16 / 60	interferon−gamma−mediated signaling pathway
10	2e−11	28 / 204	cytokine−mediated signaling pathway
11	7e−11	18 / 87	antigen processing and presentation of exogenous peptide antigen via MHC c
12	2e−10	75 / 1167	signal transduction
13	3e−10	45 / 530	innate immune response
14	4e−10	13 / 45	T cell activation
15	2e−08	35 / 407	blood coagulation
16	4e−08	11 / 43	positive regulation of T cell proliferation
17	9e−08	30 / 336	intracellular signal transduction
18	1e−07	16 / 106	leukocyte migration
19	2e−07	16 / 111	chemotaxis
20	3e−07	13 / 76	defense response

Cancer

Rank	p−value	#in/all	Geneset
1	1e−81	130 / 553	Lembcke_Colonic Inflammation
2	1e−17	44 / 316	SPANG_BCL6−index2
3	1e−13	10 / 13	GENTLES_modul18
4	2e−07	21 / 185	SPANG_LPS−index2
5	1e−03	4 / 16	GENTLES_modul11
6	2e−02	2 / 7	ZHANG_MGUS up
7	3e−01	2 / 33	KUIPER_MM good survival
8	3e−01	1 / 13	GENTLES_modul12
9	3e−01	1 / 13	GENTLES_modul17
10	3e−01	1 / 14	WANG_ER_UP
11	4e−01	1 / 15	LIU_PROSTATE_CANCER_DN
12	4e−01	1 / 15	GENTLES_modul13
13	4e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
14	9e−01	1 / 68	SHAUGHNESSY_MM high risk
15	1e+00	5 / 530	Lembcke_Normal vs Adenoma
16	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
17	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
18	1e+00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	1e+00	0 / 10	LIU_BREAST_CANCER
20	1e+00	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	5e−21	14 / 15	MHC class II protein complex
2	1e−17	154 / 2659	plasma membrane
3	1e−16	31 / 162	external side of plasma membrane
4	9e−12	63 / 835	integral to plasma membrane
5	3e−09	11 / 35	trans−Golgi network membrane
6	4e−09	9 / 21	clathrin−coated endocytic vesicle membrane
7	1e−08	9 / 23	integral to lumenal side of endoplasmic reticulum membrane
8	2e−08	9 / 24	immunological synapse
9	3e−08	22 / 184	lysosome
10	7e−08	9 / 28	transport vesicle membrane
11	8e−08	11 / 46	endocytic vesicle membrane
12	9e−08	94 / 1837	membrane
13	2e−07	46 / 683	extracellular space
14	3e−07	9 / 32	ER to Golgi transport vesicle membrane
15	5e−07	6 / 12	T cell receptor complex
16	2e−06	21 / 215	lysosomal membrane
17	7e−06	15 / 129	membrane raft
18	1e−04	131 / 3274	integral to membrane
19	2e−04	57 / 1182	extracellular region
20	2e−04	9 / 70	endomembrane system

Chr

Rank	p−value	#in/all	Geneset
1	2e−05	9 / 52	Chr HSCHR6_MHC_QBL
2	4e−03	50 / 1135	Chr 19
3	6e−03	21 / 386	Chr 22
4	1e−01	2 / 23	Chr HSCHR6_MHC_DBB
5	3e−01	22 / 630	Chr X
6	3e−01	31 / 957	Chr 11
7	4e−01	29 / 918	Chr 17
8	4e−01	27 / 866	Chr 12
9	5e−01	16 / 534	Chr 8
10	5e−01	18 / 602	Chr 10
11	6e−01	15 / 519	Chr 14
12	6e−01	30 / 1033	Chr 2
13	6e−01	50 / 1720	Chr 1
14	7e−01	5 / 187	Chr 21
15	7e−01	19 / 699	Chr 5
16	7e−01	20 / 743	Chr 7
17	7e−01	19 / 714	Chr 6
18	8e−01	18 / 717	Chr 16
19	8e−01	23 / 914	Chr 3
20	8e−01	6 / 280	Chr 13

Disease

Rank	p−value	#in/all	Geneset
1	0.001	31 / 572	GUDJ_psoriasis up
2	0.181	2 / 26	BCHETNIA_EBM−DM up
3	0.934	7 / 375	GUDJ_psoriasis down
4	1.000	0 / 17	BCHETNIA_EBM up
5	1.000	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	7e−37	61 / 265	willscher_GBM_Verhaak−CL_expression_B_up
2	7e−37	61 / 265	willscher_GBM_Verhaak−MES_expression_B_up
3	7e−37	61 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
4	7e−37	61 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
5	7e−12	15 / 49	Donson−innate immunity−associated with LTS in HGA
6	6e−11	12 / 32	Donson−Misc immune function−associated with LTS in HGA
7	2e−08	6 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
8	1e−07	7 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
9	3e−05	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
10	4e−05	5 / 14	Donson−immune cell intra signaling−associated with LTS in HGA
11	1e−04	5 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
12	8e−04	3 / 7	Donson−adaptive−immunity−associated with LTS in HGA
13	4e−03	9 / 105	willscher_GBM_proteomics_wtOnly_SpotB
14	3e−02	5 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
15	3e−02	2 / 10	willscher_ GBM_LTSwt_proteomics−G_UP
16	4e−02	6 / 85	laffaire_hypermeth_LGG_vs_control
17	8e−02	4 / 55	OL vs. MOG− OL
18	1e−01	5 / 83	Christensen_hypermethylated_in_secondary_glioblastoma
19	1e−01	1 / 4	willscher_GBM_STSwt_proteomics−L_UP
20	1e−01	1 / 4	willscher_GBM_Verhaak−PNmut_expression_A_down

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−13	10 / 14	BIOCARTA_NO2IL12_PATHWAY
2	9e−11	8 / 11	BIOCARTA_TCYTOTOXIC_PATHWAY
3	9e−11	8 / 11	BIOCARTA_THELPER_PATHWAY
4	2e−10	9 / 16	FARMER_BREAST_CANCER_CLUSTER_1
5	2e−10	9 / 16	SU_THYMUS
6	2e−09	8 / 14	FINETTI_BREAST_CANCER_KINOME_GREEN
7	1e−08	7 / 12	BIOCARTA_CTL_PATHWAY
8	2e−08	6 / 8	BIOCARTA_TCRA_PATHWAY
9	3e−08	7 / 13	BIOCARTA_IL17_PATHWAY
10	6e−08	7 / 14	BIOCARTA_IL12_PATHWAY
11	1e−07	7 / 15	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	1e−07	7 / 15	BIOCARTA_TCR_PATHWAY
13	1e−07	6 / 10	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
14	2e−07	7 / 16	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
15	3e−07	6 / 11	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP
16	3e−07	6 / 11	WILENSKY_RESPONSE_TO_DARAPLADIB
17	5e−07	6 / 12	ZHAN_MULTIPLE_MYELOMA_DN
18	1e−06	6 / 13	HAHTOLA_CTCL_PATHOGENESIS
19	1e−06	5 / 8	NIELSEN_SYNOVIAL_SARCOMA_DN
20	1e−06	5 / 8	BIOCARTA_TCAPOPTOSIS_PATHWAY

H. Tiss

Rank	p−value	#in/all	Geneset
1	2e−97	129 / 417	WIRTH_Immune system
2	2e−01	1 / 6	WIRTH_Bone marrow
3	3e−01	1 / 13	WIRTH_Thalamus
4	4e−01	1 / 16	WIRTH_Hippocampus
5	1e+00	1 / 127	WIRTH_Muscle
6	1e+00	6 / 400	WIRTH_Nervous System
7	1e+00	0 / 5	WIRTH_Pituitary gland
8	1e+00	0 / 26	WIRTH_Pancreas
9	1e+00	0 / 13	WIRTH_Sec. lymphoid organs
10	1e+00	0 / 12	WIRTH_Prim. lymphoid organs
11	1e+00	0 / 10	WIRTH_B−cells
12	1e+00	0 / 13	WIRTH_Tonsil
13	1e+00	0 / 13	WIRTH_Thymus
14	1e+00	0 / 12	WIRTH_Lymphocytes
15	1e+00	0 / 14	WIRTH_Globus pallidus
16	1e+00	0 / 15	WIRTH_Telencephalon
17	1e+00	0 / 13	WIRTH_Cortex cerebri
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	2e−16	43 / 327	SPANG_CD40 6hrs UP
2	1e−10	40 / 426	SPANG_CD40 6hrs DN
3	2e−10	22 / 140	DAVE_BL−vs−DLBCL
4	2e−10	11 / 28	DAVE_Immune response 1
5	2e−07	7 / 16	WRIGHT_ABC UP
6	2e−07	26 / 274	SPANG_IL21 DN
7	4e−07	16 / 118	SPANG_LPS 6hrs UP
8	2e−06	7 / 22	DAVE_NFkB BL DN
9	9e−06	12 / 86	ROSOLOWSKI_red total
10	1e−05	8 / 38	ROSOLOWSKI_blue DOWN
11	2e−05	5 / 13	BENTINK_mBL DOWN
12	4e−05	10 / 69	SPANG_LPS 6hrs DN
13	5e−05	4 / 8	MASCQUE_ABC UP
14	5e−04	18 / 250	LENZ_Stromal signature 1
15	5e−04	43 / 852	SPANG_BCR DN
16	1e−03	7 / 54	SPANG_BAFF 9hrs DN
17	7e−03	17 / 291	SPANG_IL21 UP
18	8e−03	3 / 14	WRIGHT_GCB UP
19	8e−03	2 / 5	WRIGHT_custom ABC−DLBCL UP
20	1e−01	1 / 4	WRIGHT_custom GCB−DLBCL UP

MF

Rank	p−value	#in/all	Geneset
1	3e−10	22 / 143	transmembrane signaling receptor activity
2	4e−07	10 / 43	chemokine activity
3	3e−06	9 / 41	non−membrane spanning protein tyrosine kinase activity
4	3e−06	289 / 8023	protein binding
5	5e−06	21 / 227	receptor activity
6	1e−05	7 / 27	antigen binding
7	2e−05	13 / 107	SH3 domain binding
8	1e−04	8 / 50	SH3/SH2 adaptor activity
9	4e−04	5 / 22	coreceptor activity
10	6e−04	5 / 24	cytokine receptor activity
11	2e−03	5 / 31	SH2 domain binding
12	3e−03	4 / 20	phosphatidylinositol 3−kinase binding
13	3e−03	17 / 270	signal transducer activity
14	4e−03	4 / 22	Rab guanyl−nucleotide exchange factor activity
15	4e−03	8 / 86	guanyl−nucleotide exchange factor activity
16	5e−03	3 / 12	Rac GTPase activator activity
17	5e−03	27 / 529	protein homodimerization activity
18	6e−03	9 / 110	heme binding
19	6e−03	17 / 288	protein kinase binding
20	6e−03	3 / 13	phosphotyrosine binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.02	8 / 108	AGCA−155
2	0.10	9 / 182	CTGA−24
3	0.10	2 / 18	CGCT−503
4	0.17	1 / 6	CGTC−208
5	0.18	2 / 26	TAGA−182
6	0.22	4 / 81	AACT−223
7	0.24	2 / 31	ACCA−509
8	0.24	1 / 9	GGAT−127
9	0.25	10 / 261	CTCA−125B−−125A
10	0.34	4 / 98	ATGT−221−−222
11	0.34	4 / 99	CCTG−513
12	0.37	1 / 15	GTCT−379
13	0.41	3 / 78	GTTA−410
14	0.42	4 / 110	CAGC−512−3P
15	0.43	3 / 80	GAGC−484
16	0.44	1 / 19	GTCA−380−5P
17	0.45	3 / 83	GCAC−18A−−18B
18	0.45	3 / 83	AGGA−516−3P
19	0.45	1 / 20	GTAG−189
20	0.46	8 / 247	GTGC−96

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	2 / 8	miR−155
2	0.06	2 / 13	miR−34a
3	0.06	1 / 2	miR−193a
4	0.14	1 / 5	miR−15a
5	0.14	1 / 5	miR−205
6	0.14	1 / 5	miR−93
7	0.17	1 / 6	miR−26a
8	1.00	0 / 11	let−7a
9	1.00	0 / 6	let−7b
10	1.00	0 / 4	let−7c
11	1.00	0 / 6	let−7d
12	1.00	0 / 4	let−7g
13	1.00	0 / 13	miR−1
14	1.00	0 / 5	miR−101
15	1.00	0 / 2	miR−101b
16	1.00	0 / 4	miR−106b
17	1.00	0 / 2	miR−107
18	1.00	0 / 4	miR−122
19	1.00	0 / 2	miR−124a
20	1.00	0 / 6	miR−125a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.02	3 / 18	hsa−miR−551a
2	0.05	2 / 12	hsa−miR−639
3	0.07	4 / 52	hsa−miR−513a−5p
4	0.08	3 / 34	hsa−miR−1226
5	0.09	2 / 17	hsa−miR−551b
6	0.14	4 / 68	hsa−miR−193b
7	0.19	4 / 75	hsa−miR−939
8	0.19	2 / 27	hsa−miR−1292
9	0.24	2 / 31	hsa−miR−617
10	0.24	3 / 57	hsa−miR−193a−3p
11	0.25	3 / 58	hsa−miR−324−3p
12	0.25	4 / 86	hsa−miR−220c
13	0.26	3 / 59	hsa−miR−296−3p
14	0.26	2 / 33	hsa−miR−1231
15	0.26	1 / 10	hsa−miR−1306
16	0.27	2 / 34	hsa−miR−615−5p
17	0.27	3 / 61	hsa−miR−1200
18	0.27	4 / 89	hsa−miR−608
19	0.28	2 / 35	hsa−miR−1269
20	0.28	1 / 11	hsa−miR−604

MMML CGS

Rank	p−value	#in/all	Geneset
1	3e−08	7 / 13	MACIEJ_MMML 6
2	3e−05	3 / 3	MACIEJ_MMML 7
3	5e−03	2 / 4	MACIEJ_MMML 2
4	4e−02	2 / 11	MACIEJ_MMML 3
5	6e−02	1 / 2	MACIEJ_MMML 32
6	6e−02	1 / 2	MACIEJ_MMML 38
7	1e−01	1 / 4	MACIEJ_MMML 44
8	1e−01	1 / 5	MACIEJ_MMML 20
9	3e−01	1 / 14	MACIEJ_MMML 30
10	1e+00	0 / 16	MACIEJ_MMML 1
11	1e+00	0 / 13	MACIEJ_MMML 10
12	1e+00	0 / 7	MACIEJ_MMML 13
13	1e+00	0 / 9	MACIEJ_MMML 14
14	1e+00	0 / 11	MACIEJ_MMML 15
15	1e+00	0 / 15	MACIEJ_MMML 16
16	1e+00	0 / 2	MACIEJ_MMML 17
17	1e+00	0 / 14	MACIEJ_MMML 19
18	1e+00	0 / 15	MACIEJ_MMML 22
19	1e+00	0 / 4	MACIEJ_MMML 23
20	1e+00	0 / 12	MACIEJ_MMML 24

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 11	BENTINK_e2f3.2
2	0.3	1 / 11	BENTINK_ras.4
3	0.3	1 / 13	BENTINK_src.10
4	1.0	0 / 13	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 12	BENTINK_e2f3.1
7	1.0	0 / 14	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 15	BENTINK_ras.6
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	0.2	1 / 8	MYC_Cell cycle UP
2	0.3	36 / 1095	HEBENSTREIT_high expression TF
3	0.3	1 / 14	NOWICK_TF
4	0.9	1 / 63	MYC_Targets UP
5	0.9	26 / 1146	HEBENSTREIT_low expression TF
6	1.0	13 / 1233	KIM_MYC targets
7	1.0	0 / 5	MYC_TFs
8	1.0	0 / 9	MYC_Targets DOWN
9	1.0	0 / 4	MYC_Apoptosis 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	2e−05	7 / 29	VAQUERIZAS_Lymph node
2	2e−03	7 / 62	VAQUERIZAS_Whole blood
3	3e−03	4 / 20	VAQUERIZAS_Bone marrow
4	3e−03	4 / 21	VAQUERIZAS_Tonsil
5	9e−03	4 / 28	VAQUERIZAS_Liver
6	1e−02	3 / 16	VAQUERIZAS_Salivary gland
7	4e−02	5 / 62	VAQUERIZAS_Lung
8	6e−02	2 / 14	VAQUERIZAS_Fetal liver
9	1e−01	3 / 37	VAQUERIZAS_Prostate
10	1e−01	3 / 41	VAQUERIZAS_Thymus
11	2e−01	2 / 30	VAQUERIZAS_Fetal lung
12	3e−01	2 / 38	VAQUERIZAS_Testis
13	4e−01	1 / 16	VAQUERIZAS_Fetal thyroid
14	4e−01	1 / 19	VAQUERIZAS_Pituitary
15	5e−01	1 / 20	VAQUERIZAS_Adrenal cortex
16	5e−01	1 / 24	VAQUERIZAS_Trachea
17	6e−01	1 / 29	VAQUERIZAS_Smooth muscle
18	7e−01	1 / 39	VAQUERIZAS_Thyroid
19	8e−01	3 / 144	VAQUERIZAS_General
20	1e+00	0 / 40	VAQUERIZAS_Fetal brain

Group Overexpression

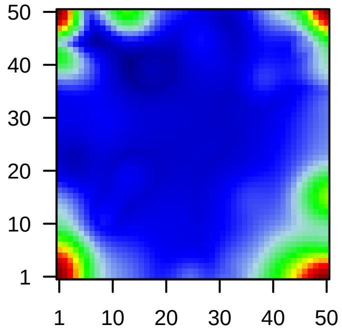
Spot Summary: B

metagenes = 31
genes = 446

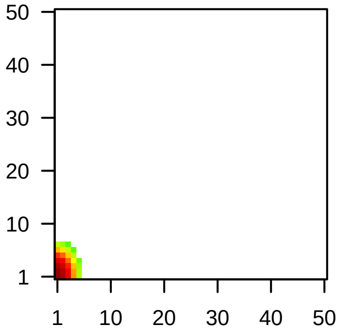
<r> metagenes = 0.92
<r> genes = 0.32
beta: r2= 21.52 / log p= −Inf

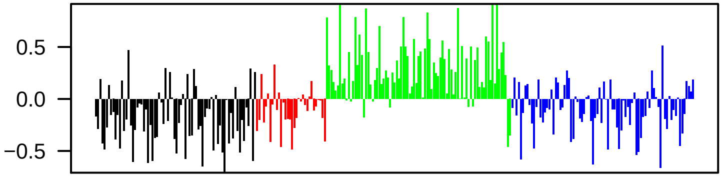
samples with spot = 30 (10.9 %)
Atypical : 1 (1.4 %)
Mesenchymal : 28 (32.9 %)
Basal : 1 (1.2 %)

Overview Map



Spot





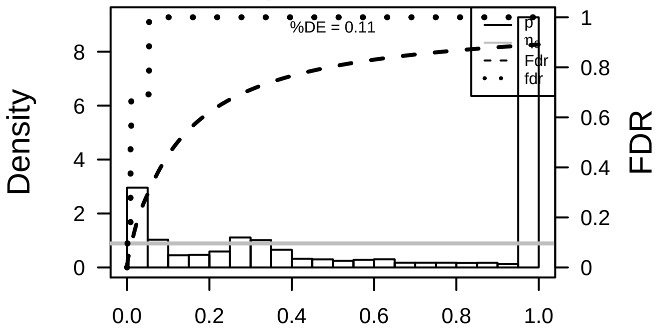
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	4319	4.09	−2.68	0.57	MMP10	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
2	12	3.84	−2.36	0.4	RP11−986E7.7	
3	3040	3.64	−2.76	0.32	HBA2	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	401138	3.58	−1.16	0.28	AMTN	amelotin [Source:HGNC Symbol;Acc:33188]
5	6696	3.4	−1.67	0.39	SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
6	4316	3.39	−2.29	0.41	MMP7	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
7	4322	3.32	−1.16	0.59	MMP13	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
8	4314	3.31	−3.02	0.71	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
9	3569	3.28	−1.5	0.62	IL6	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
10	3043	3.2	−3.29	0.32	HBB	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
11	3039	3.15	−1.75	0.3	HBA2	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
12	6374	3.14	−0.9	0.59	CXCL5	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;A
13	3553	3.13	−2.37	0.54	IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
14	414062	3.13	−2.13	0.52	CCL3L3	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
15	6372	3.07	−1.65	0.49	CXCL6	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
16	55107	3.05	−2.27	0.44	ANO1	anoctamin 1, calcium activated chloride channel [Source:HG
17	2201	2.99	−1.35	0.29	FBN2	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
18	3576	2.96	−2.98	0.58	IL8	interleukin 8 [Source:HGNC Symbol;Acc:6025]
19	4320	2.88	−1.94	0.49	MMP11	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
20	8988	2.87	−1.41	0.38	HSPB3	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:524

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−69	84 / 250	Lymp	LENZ_Stromal signature 1
2	1e−65	80 / 242	BP	extracellular matrix organization
3	6e−57	67 / 190	CC	extracellular matrix
4	1e−56	143 / 1182	CC	extracellular region
5	2e−42	96 / 683	CC	extracellular space
6	4e−36	80 / 553	Canc	Lembcke_Colonic Inflammation
7	7e−35	68 / 403	BP	cell adhesion
8	1e−33	33 / 69	BP	extracellular matrix disassembly
9	5e−30	52 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	5e−30	52 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	5e−30	52 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	5e−30	52 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	8e−29	29 / 64	BP	collagen catabolic process
14	3e−27	42 / 183	CC	proteinaceous extracellular matrix
15	4e−23	15 / 16	MMM	MACIEJ_MMML 1
16	3e−22	27 / 83	CC	basement membrane
17	1e−21	23 / 57	MF	extracellular matrix structural constituent
18	6e−17	12 / 15	GSE	CROMER_TUMORIGENESIS_UP
19	1e−16	33 / 204	BP	angiogenesis
20	2e−16	12 / 16	GSE	FARMER_BREAST_CANCER_CLUSTER_5
21	5e−16	16 / 37	BP	collagen fibril organization
22	8e−16	28 / 153	CC	endoplasmic reticulum lumen
23	1e−15	25 / 119	Lymp	ROSOLOWSKI_green total
24	6e−15	12 / 19	MF	extracellular matrix binding
25	6e−15	21 / 85	MF	integrin binding
26	4e−14	38 / 330	CC	cell surface
27	7e−14	23 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
28	2e−13	18 / 68	CC	collagen
29	4e−13	9 / 11	Glio	Phillips MES up vs Prolif & PN
30	5e−13	18 / 72	CC	extracellular vesicular exosome
31	5e−13	10 / 15	GSE	ONDER_CDH1_TARGETS_2_UP
32	2e−12	17 / 68	Glio	cultured astroglia vs. in vivo astrocytes
33	3e−12	13 / 35	Glio	Colman_survival_associated
34	5e−12	9 / 13	GSE	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
35	3e−11	38 / 407	BP	blood coagulation
36	3e−11	9 / 15	GSE	ONDER_CDH1_SIGNALING_VIA_CTNNB1
37	3e−11	9 / 15	GSE	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITOR
38	4e−11	8 / 11	MF	platelet−derived growth factor binding
39	5e−11	30 / 269	BP	inflammatory response
40	7e−11	9 / 16	MF	fibronectin binding

p−values



BP

Rank	p−value	#in/all	Geneset
1	1e−65	80 / 242	extracellular matrix organization
2	7e−35	68 / 403	cell adhesion
3	1e−33	33 / 69	extracellular matrix disassembly
4	8e−29	29 / 64	collagen catabolic process
5	1e−16	33 / 204	angiogenesis
6	5e−16	16 / 37	collagen fibril organization
7	3e−11	38 / 407	blood coagulation
8	5e−11	30 / 269	inflammatory response
9	2e−10	16 / 76	wound healing
10	4e−10	12 / 40	cellular response to amino acid stimulus
11	1e−09	33 / 364	negative regulation of cell proliferation
12	2e−09	18 / 114	positive regulation of cell migration
13	2e−09	19 / 129	cell migration
14	3e−09	29 / 299	axon guidance
15	3e−09	16 / 93	cellular component movement
16	4e−09	14 / 70	cell−matrix adhesion
17	5e−09	20 / 151	response to hypoxia
18	1e−08	9 / 25	chondroitin sulfate biosynthetic process
19	2e−08	11 / 45	chondroitin sulfate metabolic process
20	2e−08	16 / 106	leukocyte migration

Cancer

Rank	p−value	#in/all	Geneset
1	4e−36	80 / 553	Lembcke_Colonic Inflammation
2	3e−04	4 / 13	GENTLES_modul17
3	7e−03	3 / 15	RHODES_CANCER_META_SIGNATURE
4	7e−03	3 / 15	LIU_PROSTATE_CANCER_DN
5	8e−03	3 / 16	GENTLES_modul11
6	5e−02	2 / 13	GENTLES_modul16
7	8e−02	20 / 530	Lembcke_Normal vs Adenoma
8	2e−01	1 / 10	LIU_BREAST_CANCER
9	2e−01	1 / 10	GENTLES_modul3
10	3e−01	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
11	3e−01	1 / 13	GENTLES_modul12
12	3e−01	1 / 14	LIU_PROSTATE_CANCER_UP
13	3e−01	1 / 15	GENTLES_modul13
14	4e−01	1 / 16	GENTLES_modul10
15	5e−01	9 / 316	SPANG_BCL6−index2
16	6e−01	5 / 185	SPANG_LPS−index2
17	6e−01	1 / 33	KUIPER_MM good survival
18	8e−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	6e−57	67 / 190	extracellular matrix
2	1e−56	143 / 1182	extracellular region
3	2e−42	96 / 683	extracellular space
4	3e−27	42 / 183	proteinaceous extracellular matrix
5	3e−22	27 / 83	basement membrane
6	8e−16	28 / 153	endoplasmic reticulum lumen
7	4e−14	38 / 330	cell surface
8	2e−13	18 / 68	collagen
9	5e−13	18 / 72	extracellular vesicular exosome
10	1e−07	114 / 2659	plasma membrane
11	3e−07	10 / 45	stress fiber
12	4e−07	8 / 27	integrin complex
13	2e−06	9 / 43	platelet alpha granule lumen
14	2e−06	15 / 128	focal adhesion
15	3e−06	14 / 116	cell cortex
16	4e−06	6 / 17	basal lamina
17	5e−06	10 / 61	secretory granule
18	5e−05	9 / 63	Golgi lumen
19	6e−05	77 / 1837	membrane
20	6e−05	9 / 65	lysosomal lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.005	31 / 699	Chr 5
2	0.011	31 / 743	Chr 7
3	0.076	23 / 618	Chr 4
4	0.125	32 / 957	Chr 11
5	0.180	33 / 1033	Chr 2
6	0.235	15 / 449	Chr 20
7	0.267	20 / 633	Chr 9
8	0.376	21 / 714	Chr 6
9	0.438	7 / 232	Chr 18
10	0.468	1 / 23	Chr HSCHR6_MHC_DBB
11	0.472	11 / 386	Chr 22
12	0.541	14 / 519	Chr 14
13	0.608	13 / 504	Chr 15
14	0.615	45 / 1720	Chr 1
15	0.636	7 / 280	Chr 13
16	0.649	22 / 866	Chr 12
17	0.748	4 / 187	Chr 21
18	0.782	12 / 534	Chr 8
19	0.832	13 / 602	Chr 10
20	0.874	13 / 630	Chr X

Disease

Rank	p−value	#in/all	Geneset
1	3e−05	25 / 375	GUDJ_psoriasis down
2	7e−01	14 / 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	5e−30	52 / 265	willscher_GBM_Verhaak−CL_expression_B_up
2	5e−30	52 / 265	willscher_GBM_Verhaak−MES_expression_B_up
3	5e−30	52 / 265	willscher_GBM_Verhaak−PNwt_expression_B_down
4	5e−30	52 / 265	willscher_GBM_Verhaak−PNmut_expression_B_down
5	7e−14	23 / 117	GIEZELT_GBM_WT_up_VS_mut
6	4e−13	9 / 11	Phillips MES up vs Prolif & PN
7	2e−12	17 / 68	cultured astroglia vs. in vivo astrocytes
8	3e−12	13 / 35	Colman_survival_associated
9	6e−07	10 / 49	Christensen_hypomethylated_in_primary_glioblastoma
10	1e−06	16 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	2e−06	7 / 23	Christensen_hypomethylated_in_grade3_astrocytoma
12	1e−05	14 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	2e−05	9 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
14	3e−05	12 / 105	willscher_GBM_proteomics_wtOnly_SpotB
15	5e−05	12 / 112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
16	2e−04	8 / 58	OPC
17	2e−04	11 / 110	Christensen_hypermethylated_in_grade3_astrocytoma
18	2e−04	6 / 33	willscher_GBM_proteomics_wtOnly_SpotC
19	3e−04	4 / 13	Christensen_hypomethylated_in_grade2_oligodendroglioma
20	4e−04	3 / 6	Martinez_Glio_hypometh

GSEA C2

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

H Tiss

Rank	p−value	#in/all	Geneset
1	2e−05	5 / 13	WIRTH_Sec. lymphoid organs
2	2e−02	4 / 36	WIRTH_Placenta
3	4e−02	2 / 12	WIRTH_Prim. lymphoid organs
4	5e−02	2 / 13	WIRTH_Cortex cerebri
5	3e−01	1 / 12	WIRTH_Lymphocytes
6	3e−01	1 / 15	WIRTH_Telencephalon
7	5e−01	4 / 127	WIRTH_Muscle
8	8e−01	1 / 62	WIRTH_Liver
9	9e−01	8 / 400	WIRTH_Nervous System
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 / 13	WIRTH_Thymus
16	1e+00	0 / 6	WIRTH_Bone marrow
17	1e+00	0 / 14	WIRTH_Globus pallidus
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	1e−69	84 / 250	LENZ_Stromal signature 1
2	1e−15	25 / 119	ROSOLOWSKI_green total
3	4e−07	11 / 59	LENZ_Stromal signature 2
4	1e−04	10 / 86	ROSOLOWSKI_green UP
5	1e−02	8 / 118	SPANG_LPS 6hrs UP
6	4e−02	3 / 28	DAVE_Immune response 1
7	1e−01	13 / 327	SPANG_CD40 6hrs UP
8	1e−01	2 / 24	SPANG_BAFF 9hrs UP
9	2e−01	1 / 8	MASCQUE_GCB UP
10	3e−01	1 / 12	DAVE_BL UP
11	3e−01	4 / 100	ROSOLOWSKI_blue total
12	3e−01	1 / 13	BENTINK_mBL UP
13	3e−01	1 / 14	WRIGHT_GCB UP
14	3e−01	5 / 140	DAVE_BL−vs−DLBCL
15	4e−01	1 / 16	WRIGHT_ABC UP
16	4e−01	1 / 20	DAVE_Immune response 2
17	5e−01	1 / 22	DAVE_NFkB BL DN
18	5e−01	8 / 275	ZHANG_DLBCL mutated
19	6e−01	11 / 426	SPANG_CD40 6hrs DN
20	6e−01	1 / 38	ROSOLOWSKI_blue DOWN

MF

Rank	p−value	#in/all	Geneset
1	1e−21	23 / 57	extracellular matrix structural constituent
2	6e−15	12 / 19	extracellular matrix binding
3	6e−15	21 / 85	integrin binding
4	4e−11	8 / 11	platelet−derived growth factor binding
5	7e−11	9 / 16	fibronectin binding
6	2e−10	45 / 579	calcium ion binding
7	8e−09	17 / 112	heparin binding
8	2e−08	11 / 44	collagen binding
9	4e−08	17 / 124	growth factor activity
10	4e−07	7 / 19	L−ascorbic acid binding
11	5e−07	268 / 8023	protein binding
12	1e−06	7 / 22	insulin−like growth factor binding
13	6e−06	23 / 297	actin binding
14	8e−06	6 / 19	laminin binding
15	8e−06	22 / 280	receptor binding
16	3e−05	10 / 73	metallopeptidase activity
17	3e−05	5 / 15	platelet−derived growth factor receptor binding
18	6e−05	10 / 81	metalloendopeptidase activity
19	1e−04	6 / 29	oxidoreductase activity, acting on paired donors, with incorporation or reductio
20	1e−04	5 / 19	peroxidase activity

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	4e−06	29 / 420	TGGT−29A−−29B−−29C
2	7e−06	35 / 577	GTGC−506
3	6e−04	14 / 189	AACT−145
4	8e−04	13 / 171	CTAT−153
5	9e−04	21 / 362	CAGT−200B−−200C−−429
6	1e−03	22 / 401	ACCA−9
7	3e−03	15 / 247	GTGC−96
8	3e−03	23 / 457	TGCC−124A
9	4e−03	13 / 205	GTAC−101
10	7e−03	14 / 244	GTGC−25−−32−−92−−363−−367
11	7e−03	2 / 5	TCGA−213
12	8e−03	10 / 152	GGGA−133A−−133B
13	1e−02	4 / 32	CCTG−510
14	1e−02	11 / 189	CTTT−527
15	1e−02	11 / 190	CACT−520G−−520H
16	1e−02	9 / 141	ATAC−202
17	2e−02	21 / 467	TGTT−30A−5P−−30C−−30D−−30B−−30E−5P
18	2e−02	9 / 145	AAAG−511
19	2e−02	13 / 248	TACT−26A−−26B
20	2e−02	12 / 225	TATT−374

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 6	Miyoshi myopathy
2	0.2	1 / 8	Hodgkin lymphoma
3	0.2	1 / 9	Non−Hodgkin lymphoma, somatic
4	0.4	1 / 17	Cardiomyopathy, dilated
5	0.5	1 / 29	Melanoma and neural system tumor syndrome
6	0.6	1 / 30	Ovarian cancer
7	0.6	1 / 32	Leukemia
8	0.6	1 / 34	Pancreatic cancer
9	0.6	1 / 34	Squamous cell carcinoma, head and neck
10	0.6	1 / 34	Hematological
11	0.6	1 / 35	Prostate cancer
12	0.6	1 / 36	Cancer
13	0.6	1 / 36	Lung cancer
14	0.6	1 / 38	Breast cancer
15	1.0	0 / 3	Thyroid carcinoma, papillary
16	1.0	0 / 22	Glioblastoma multiforme, somatic
17	1.0	0 / 21	Gastrointestinal
18	1.0	0 / 2	Pituitary adenoma
19	1.0	0 / 27	Colorectal cancer
20	1.0	0 / 2	Adenomas, multiple colorectal

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−10	8 / 12	miR−29c
2	6e−04	5 / 26	miR−21
3	4e−03	3 / 12	miR−29b
4	4e−03	2 / 4	miR−195
5	7e−03	2 / 5	miR−143
6	1e−02	2 / 6	let−7b
7	2e−02	2 / 8	miR−222
8	3e−02	2 / 11	miR−16
9	5e−02	2 / 13	miR−34a
10	5e−02	1 / 2	miR−101b
11	5e−02	1 / 2	miR−124a
12	5e−02	1 / 2	miR−16−1
13	5e−02	1 / 2	miR−18
14	5e−02	1 / 2	miR−346
15	8e−02	1 / 3	miR−197
16	1e−01	1 / 4	let−7c
17	1e−01	1 / 4	let−7g
18	1e−01	1 / 4	miR−106b
19	1e−01	1 / 4	miR−20a
20	1e−01	1 / 4	miR−29a

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.002	6 / 50	hsa−miR−1224−3p
2	0.004	3 / 12	hsa−miR−1249
3	0.004	4 / 24	hsa−miR−663b
4	0.005	6 / 60	hsa−miR−485−3p
5	0.006	9 / 121	hsa−miR−646
6	0.006	4 / 27	hsa−miR−483−3p
7	0.006	3 / 14	hsa−miR−452*
8	0.009	7 / 86	hsa−miR−220c
9	0.011	16 / 311	hsa−miR−98
10	0.013	5 / 52	hsa−miR−487a
11	0.015	10 / 167	hsa−miR−7
12	0.019	6 / 78	hsa−miR−205
13	0.021	4 / 39	hsa−miR−501−3p
14	0.021	16 / 336	hsa−let−7e
15	0.022	9 / 151	hsa−miR−429
16	0.022	15 / 311	hsa−let−7f
17	0.023	16 / 341	hsa−let−7a
18	0.033	6 / 89	hsa−miR−216b
19	0.039	9 / 168	hsa−miR−190
20	0.040	9 / 169	hsa−miR−183

MMML CGS

Rank	p−value	#in/all	Geneset
1	4e−23	15 / 16	MACIEJ_MMML 1
2	2e−07	6 / 11	MACIEJ_MMML 31
3	4e−03	2 / 4	MACIEJ_MMML 23
4	1e−02	2 / 7	MACIEJ_MMML 13
5	3e−02	2 / 11	MACIEJ_MMML 3
6	1e−01	1 / 4	MACIEJ_MMML 40
7	1e−01	1 / 4	MACIEJ_MMML 44
8	3e−01	1 / 13	MACIEJ_MMML 6
9	1e+00	0 / 13	MACIEJ_MMML 10
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 / 15	MACIEJ_MMML 22
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	0.004	3 / 12	BENTINK_ras.1
2	0.061	2 / 15	GUSTAFSON_PI3K_DN
3	0.260	1 / 11	BENTINK_e2f3.2
4	0.300	1 / 13	BENTINK_src.10
5	0.319	1 / 14	BENTINK_myc.1
6	1.000	0 / 13	GUSTAFSON_PI3K_UP
7	1.000	0 / 12	BENTINK_e2f3.1
8	1.000	0 / 11	BENTINK_ras.4
9	1.000	0 / 15	BENTINK_ras.6
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	2e−10	69 / 1146	HEBENSTREIT_low expression TF
2	2e−02	2 / 9	MYC_Targets DOWN
3	5e−02	1 / 2	MYC_ECM cell adhesion DOWN
4	1e−01	1 / 5	MYC_TF and cofactors
5	8e−01	30 / 1233	KIM_MYC targets
6	8e−01	26 / 1095	HEBENSTREIT_high expression TF
7	1e+00	0 / 14	NOWICK_TF
8	1e+00	0 / 5	MYC_TFs
9	1e+00	0 / 63	MYC_Targets UP
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 / 20	MYC_Metabolism UP
18	1e+00	0 / 16	MYC_Protein synthesis degradation UP
19	1e+00	0 / 8	MYC_RNA processing binding UP
20	1e+00	0 / 2	MYC_Signal transduction UP

TF Tissue

Rank	p−value	#in/all	Geneset
1	0.03	4 / 44	VAQUERIZAS_Placenta
2	0.05	3 / 30	VAQUERIZAS_Fetal lung
3	0.08	3 / 37	VAQUERIZAS_Prostate
4	0.09	4 / 62	VAQUERIZAS_Lung
5	0.11	3 / 43	VAQUERIZAS_Uterus
6	0.18	2 / 29	VAQUERIZAS_Smooth muscle
7	0.28	2 / 39	VAQUERIZAS_Thyroid
8	0.30	1 / 13	VAQUERIZAS_Skin
9	0.30	1 / 13	VAQUERIZAS_Ovary
10	0.36	1 / 16	VAQUERIZAS_Pancreas
11	0.36	1 / 16	VAQUERIZAS_Fetal thyroid
12	0.36	1 / 16	VAQUERIZAS_Salivary gland
13	0.36	1 / 16	VAQUERIZAS_Heart
14	0.41	1 / 19	VAQUERIZAS_Pituitary
15	0.42	1 / 20	VAQUERIZAS_Adrenal cortex
16	0.45	1 / 22	VAQUERIZAS_Spinal cord
17	0.48	1 / 24	VAQUERIZAS_Trachea
18	0.65	1 / 38	VAQUERIZAS_Testis
19	0.67	1 / 40	VAQUERIZAS_Fetal brain
20	0.69	1 / 43	VAQUERIZAS_Whole brain

Group Overexpression

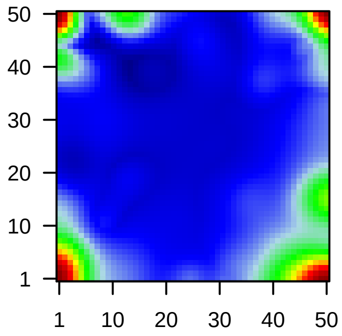
Spot Summary: C

metagenes = 12
genes = 187

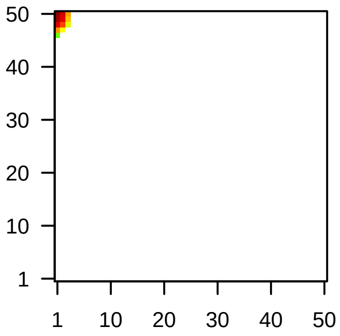
<r> metagenes = 0.97
<r> genes = 0.47
beta: r2= 70.9 / log p= −Inf

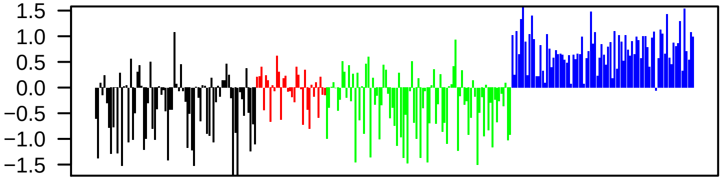
samples with spot = 83 (30.2 %)
Atypical : 6 (8.1 %)
Classical : 1 (3.1 %)
Mesenchymal : 7 (8.2 %)
Basal : 69 (82.1 %)

Overview Map



Spot





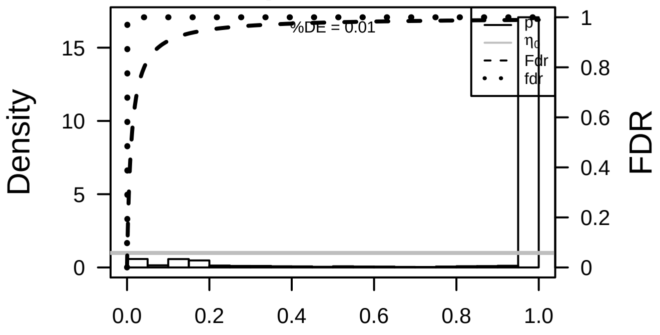
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	3848	4.75	−1.88	0.67	KRT1	keratin 1 [Source:HGNC Symbol;Acc:6412]
2	3851	4.24	−3.19	0.57	KRT4	keratin 4 [Source:HGNC Symbol;Acc:6441]
3	49860	4.24	−3.23	0.72	CRNN	cornulin [Source:HGNC Symbol;Acc:1230]
4	4118	3.95	−3.23	0.61	MAL	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
5	4014	3.86	−0.97	0.38	LOR	loricrin [Source:HGNC Symbol;Acc:6663]
6	1673	3.84	−3.54	0.67	DEFB4B	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
7	6701	3.84	−2.1	0.75	SPRR2B	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
8	6947	3.77	−1.96	0.46	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family
9	414325	3.77	−2.67	0.71	DEFB103B	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	6706	3.74	−3.05	0.71	SPRR2G	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
11	57152	3.69	−1.77	0.81	SLURP1	secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
12	2877	3.69	−3.11	0.44	GPX2	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
13	338324	3.66	−2.9	0.68	S100A7A	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
14	7053	3.52	−3.39	0.81	TGM3	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	1828	3.51	−1.97	0.78	DSG1	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
16	55894	3.4	−1.83	0.73	DEFB103B	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	8644	3.37	−2.96	0.4	AKR1C3	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
18	84651	3.36	−1.82	0.74	SPINK7	serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
19	84648	3.36	−2.37	0.72	LCE3D	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
20	29113	3.29	−1.18	0.39	C6orf15	chromosome 6 open reading frame 15 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	77 / 135	H.Tiss	WIRTH_Mucosa
2	7e−75	85 / 572	Disea	GUDJ_psoriasis up
3	4e−33	18 / 21	CC	cornified envelope
4	1e−31	23 / 53	BP	keratinocyte differentiation
5	1e−26	19 / 42	BP	keratinization
6	1e−25	22 / 76	BP	epidermis development
7	7e−17	50 / 1182	CC	extracellular region
8	2e−15	10 / 19	BP	peptide cross−linking
9	2e−14	20 / 186	MF	structural molecule activity
10	6e−12	13 / 82	CC	intermediate filament
11	4e−11	8 / 21	CC	desmosome
12	7e−11	12 / 79	MF	serine−type endopeptidase inhibitor activity
13	1e−10	7 / 15	GSEA	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
14	3e−10	10 / 52	BP	negative regulation of endopeptidase activity
15	3e−10	39 / 1146	TF	HEBENSTREIT_low expression TF
16	1e−09	9 / 44	CC	keratin filament
17	3e−09	6 / 13	BP	negative regulation of peptidase activity
18	8e−09	6 / 15	GSEA	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	1e−08	12 / 122	MF	serine−type endopeptidase activity
20	1e−08	6 / 16	GSEA	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
21	1e−08	6 / 16	GSEA	WANG_BARRETTS_ESOPHAGUS_DN
22	1e−08	6 / 16	GSEA	ONDER_CDH1_TARGETS_3_DN
23	1e−08	6 / 16	GSEA	HUPER_BREAST_BASAL_VS_LUMINAL_UP
24	1e−08	6 / 16	GSEA	CROMER_TUMORIGENESIS_DN
25	2e−08	7 / 29	BP	regulation of proteolysis
26	4e−08	5 / 10	MF	RAGE receptor binding
27	7e−07	24 / 683	CC	extracellular space
28	1e−06	7 / 51	MF	protein binding, bridging
29	3e−06	4 / 10	GSEA	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_PROTEIN
30	4e−06	6 / 38	BP	epithelial cell differentiation
31	2e−05	7 / 73	BP	defense response to bacterium
32	2e−05	4 / 15	MF	retinol dehydrogenase activity
33	2e−05	4 / 15	GSEA	AIGNER_ZEB1_TARGETS
34	2e−05	4 / 15	GSEA	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
35	2e−05	4 / 15	GSEA	LEE_LIVER_CANCER_MYC_E2F1_UP
36	2e−05	4 / 15	GSEA	CHANG_IMMORTALIZED_BY_HPV31_DN
37	2e−05	4 / 16	GSEA	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
38	2e−05	4 / 16	GSEA	COLDREN_GEFITINIB_RESISTANCE_DN
39	2e−05	4 / 16	GSEA	LEE_LIVER_CANCER_MYC_TGFA_UP
40	3e−05	6 / 53	MF	serine−type peptidase activity

p−values



BP

Rank	p−value	#in/all	Geneset
1	1e−31	23 / 53	keratinocyte differentiation
2	1e−26	19 / 42	keratinization
3	1e−25	22 / 76	epidermis development
4	2e−15	10 / 19	peptide cross−linking
5	3e−10	10 / 52	negative regulation of endopeptidase activity
6	3e−09	6 / 13	negative regulation of peptidase activity
7	2e−08	7 / 29	regulation of proteolysis
8	4e−06	6 / 38	epithelial cell differentiation
9	2e−05	7 / 73	defense response to bacterium
10	1e−04	7 / 100	cell−cell adhesion
11	2e−04	4 / 27	response to bacterium
12	3e−04	3 / 12	cellular aldehyde metabolic process
13	5e−04	3 / 14	defense response to fungus
14	7e−04	13 / 405	proteolysis
15	9e−04	4 / 39	retinoid metabolic process
16	1e−03	3 / 18	retinol metabolic process
17	2e−03	4 / 46	cellular component disassembly involved in execution phase of apoptosis
18	3e−03	3 / 25	response to zinc ion
19	5e−03	2 / 10	chronic inflammatory response
20	7e−03	3 / 36	neutrophil chemotaxis

Cancer

Rank	p−value	#in/all	Geneset
1	0.007	13 / 530	Lembcke_Normal vs Adenoma
2	0.022	12 / 553	Lembcke_Colonic Inflammation
3	0.096	1 / 9	WANG_ER_DN
4	0.165	1 / 16	GENTLES_modul11
5	0.535	1 / 68	SHAUGHNESSY_MM high risk
6	0.877	1 / 185	SPANG_LPS−index2
7	0.972	1 / 316	SPANG_BCL6−index2
8	1.000	0 / 15	RHODES_CANCER_META_SIGNATURE
9	1.000	0 / 16	RHODES_UNDIFFERENTIATED_CANCER
10	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	1.000	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	1.000	0 / 10	LIU_BREAST_CANCER
13	1.000	0 / 14	LIU_COMMON_CANCER_GENES
14	1.000	0 / 14	LIU_LIVER_CANCER
15	1.000	0 / 15	LIU_PROSTATE_CANCER_DN
16	1.000	0 / 14	LIU_PROSTATE_CANCER_UP
17	1.000	0 / 14	WANG_ER_UP
18	1.000	0 / 16	WOLFER_overlap genes
19	1.000	0 / 12	BEN−PORATH_DN
20	1.000	0 / 15	BEN−PORATH_UP

CC

Rank	p−value	#in/all	Geneset
1	4e−33	18 / 21	cornified envelope
2	7e−17	50 / 1182	extracellular region
3	6e−12	13 / 82	intermediate filament
4	4e−11	8 / 21	desmosome
5	1e−09	9 / 44	keratin filament
6	7e−07	24 / 683	extracellular space
7	4e−05	7 / 83	anchored to membrane
8	2e−03	8 / 201	apical plasma membrane
9	9e−03	5 / 115	cell−cell junction
10	1e−02	2 / 15	connexon complex
11	1e−02	9 / 333	cytoskeleton
12	1e−02	62 / 4310	cytoplasm
13	2e−02	2 / 21	gap junction
14	3e−02	3 / 63	Golgi lumen
15	4e−02	4 / 116	cytoplasmic membrane−bounded vesicle
16	4e−02	39 / 2659	plasma membrane
17	5e−02	2 / 32	cell−cell adherens junction
18	6e−02	2 / 37	lateral plasma membrane
19	7e−02	4 / 137	basolateral plasma membrane
20	1e−01	1 / 12	fascia adherens

Chr

Rank	p−value	#in/all	Geneset
1	7e−05	37 / 1720	Chr 1
2	3e−04	10 / 232	Chr 18
3	8e−03	22 / 1135	Chr 19
4	3e−02	2 / 23	Chr HSCHR6_MHC_DBB
5	1e−01	9 / 534	Chr 8
6	2e−01	10 / 618	Chr 4
7	4e−01	11 / 866	Chr 12
8	4e−01	1 / 52	Chr HSCHR6_MHC_QBL
9	5e−01	6 / 519	Chr 14
10	6e−01	5 / 449	Chr 20
11	6e−01	3 / 280	Chr 13
12	7e−01	9 / 918	Chr 17
13	8e−01	6 / 699	Chr 5
14	8e−01	4 / 504	Chr 15
15	8e−01	5 / 633	Chr 9
16	8e−01	8 / 957	Chr 11
17	9e−01	1 / 187	Chr 21
18	9e−01	8 / 1033	Chr 2
19	9e−01	5 / 717	Chr 16
20	9e−01	4 / 602	Chr 10

Disease

Rank	p−value	#in/all	Geneset
1	7e−75	85 / 572	GUDJ_psoriasis up
2	2e−02	2 / 17	BCHETNIA_EBM up
3	3e−01	1 / 26	BCHETNIA_EBM−DM up
4	8e−01	3 / 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	5e−04	5 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
2	2e−03	4 / 49	Christensen_hypomethylated_in_primary_glioblastoma
3	8e−02	1 / 7	KIM_epithelial−mesenchymal−transition related genes_decreased expressio
4	1e−01	2 / 48	Noushmehr_Pron_GCIMP_hypermeth_DN
5	1e−01	1 / 10	willscher_ GBM_LTSwt_proteomics−G_UP
6	1e−01	1 / 11	VERHAAK_Brain
7	1e−01	2 / 53	Christensen_hypermethylated_in_primary_glioblastoma
8	1e−01	2 / 55	OL vs. MOG− OL
9	1e−01	1 / 12	Christensen_hypermethylated_in_ependymoma
10	1e−01	3 / 112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	1e−01	7 / 391	Down_b
12	2e−01	1 / 17	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
13	2e−01	2 / 68	cultured astroglia vs. in vivo astrocytes
14	2e−01	3 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	2e−01	1 / 21	Martinez_Glio_hypermeth
16	2e−01	3 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma
17	2e−01	2 / 83	Christensen_hypermethylated_in_secondary_glioblastoma
18	2e−01	2 / 85	laffaire_hypermeth_LGG_vs_control
19	3e−01	1 / 28	Barbus_GBM_STS_vs._LTS
20	3e−01	1 / 33	willscher_GBM_proteomics_wtOnly_SpotC

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−10	7 / 15	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
2	8e−09	6 / 15	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
3	1e−08	6 / 16	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
4	1e−08	6 / 16	WANG_BARRETTS_ESOPHAGUS_DN
5	1e−08	6 / 16	ONDER_CDH1_TARGETS_3_DN
6	1e−08	6 / 16	HUPER_BREAST_BASAL_VS_LUMINAL_UP
7	1e−08	6 / 16	CROMER_TUMORIGENESIS_DN
8	3e−06	4 / 10	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_PROTEINS
9	2e−05	4 / 15	AIGNER_ZEB1_TARGETS
10	2e−05	4 / 15	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
11	2e−05	4 / 15	LEE_LIVER_CANCER_MYC_E2F1_UP
12	2e−05	4 / 15	CHANG_IMMORTALIZED_BY_HPV31_DN
13	2e−05	4 / 16	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
14	2e−05	4 / 16	COLDREN_GEFITINIB_RESISTANCE_DN
15	2e−05	4 / 16	LEE_LIVER_CANCER_MYC_TGFA_UP
16	2e−04	3 / 10	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
17	2e−04	3 / 10	SMID_BREAST_CANCER_ERBB2_UP
18	2e−04	3 / 10	AUJLA_IL22_AND_IL17A_SIGNALING
19	2e−04	3 / 10	MURAKAMI_UV_RESPONSE_1HR_UP
20	2e−04	3 / 11	MURAKAMI_UV_RESPONSE_24HR

H.Tiss

Rank	p−value	#in/all	Geneset
1	1e−99	77 / 135	WIRTH_Mucosa
2	3e−04	3 / 12	WIRTH_Prim. lymphoid organs
3	4e−04	3 / 13	WIRTH_Tonsil
4	9e−01	2 / 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_Thymus
11	1e+00	0 / 12	WIRTH_Lymphocytes
12	1e+00	0 / 6	WIRTH_Bone marrow
13	1e+00	0 / 14	WIRTH_Globus pallidus
14	1e+00	0 / 15	WIRTH_Telencephalon
15	1e+00	0 / 13	WIRTH_Cortex cerebri
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	0.1	1 / 14	WRIGHT_GCB UP
2	0.2	5 / 275	ZHANG_DLBCL mutated
3	0.2	1 / 20	DAVE_Immune response 2
4	0.2	1 / 24	SPANG_BAFF 9hrs UP
5	0.5	3 / 250	LENZ_Stromal signature 1
6	0.7	1 / 119	ROSOLOWSKI_green total
7	0.9	2 / 327	SPANG_CD40 6hrs UP
8	1.0	3 / 755	SPANG_BCR UP
9	1.0	2 / 852	SPANG_BCR DN
10	1.0	0 / 13	BENTINK_mBL UP
11	1.0	0 / 13	BENTINK_mBL DOWN
12	1.0	0 / 140	DAVE_BL−vs−DLBCL
13	1.0	0 / 12	DAVE_BL_DN
14	1.0	0 / 18	DAVE_BL Inter
15	1.0	0 / 12	DAVE_BL UP
16	1.0	0 / 18	DAVE_c−myc BL UP
17	1.0	0 / 6	DAVE_MHCCII BL DN
18	1.0	0 / 22	DAVE_NFkB BL DN
19	1.0	0 / 28	DAVE_Immune response 1
20	1.0	0 / 59	LENZ_Stromal signature 2

MF

Rank	p−value	#in/all	Geneset
1	2e−14	20 / 186	structural molecule activity
2	7e−11	12 / 79	serine−type endopeptidase inhibitor activity
3	1e−08	12 / 122	serine−type endopeptidase activity
4	4e−08	5 / 10	RAGE receptor binding
5	1e−06	7 / 51	protein binding, bridging
6	2e−05	4 / 15	retinol dehydrogenase activity
7	3e−05	6 / 53	serine−type peptidase activity
8	9e−05	18 / 579	calcium ion binding
9	1e−04	4 / 23	peptidase inhibitor activity
10	3e−04	16 / 531	catalytic activity
11	5e−04	4 / 34	endopeptidase inhibitor activity
12	1e−03	3 / 19	laminin binding
13	2e−03	3 / 22	cysteine−type endopeptidase inhibitor activity
14	2e−03	5 / 82	structural constituent of cytoskeleton
15	5e−03	4 / 62	protease binding
16	6e−03	9 / 296	oxidoreductase activity
17	8e−03	2 / 12	retinol binding
18	1e−02	3 / 40	chloride channel activity
19	1e−02	2 / 15	interleukin−1 receptor binding
20	1e−02	5 / 125	iron ion binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.1	2 / 57	GTTA−302B
2	0.2	1 / 20	GTAG−189
3	0.2	2 / 83	AGGA−516−3P
4	0.3	2 / 89	TCCA−516−5P
5	0.4	1 / 43	CCCA−299−3P
6	0.5	1 / 55	AATG−136
7	0.5	1 / 56	GTGT−342
8	0.6	1 / 73	AGGT−500
9	0.6	1 / 75	CCAG−331
10	0.6	1 / 79	TCTC−185
11	0.6	1 / 89	ATGC−338
12	0.7	1 / 100	ACAG−10A−−10B
13	0.7	1 / 108	AGCA−155
14	0.8	2 / 240	CAGT−141−−200A
15	0.8	1 / 129	CTCT−520A−−525
16	0.8	1 / 136	GCAT−105
17	0.8	1 / 140	CATG−496
18	0.8	1 / 146	ACTG−30A−3P−−30E−3P
19	0.8	1 / 147	TGTG−377
20	0.8	1 / 165	TTTG−518A−2

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 / 5	miR−196a
2	0.25	1 / 26	miR−21
3	1.00	0 / 11	let−7a
4	1.00	0 / 6	let−7b
5	1.00	0 / 4	let−7c
6	1.00	0 / 6	let−7d
7	1.00	0 / 4	let−7g
8	1.00	0 / 13	miR−1
9	1.00	0 / 5	miR−101
10	1.00	0 / 2	miR−101b
11	1.00	0 / 4	miR−106b
12	1.00	0 / 2	miR−107
13	1.00	0 / 4	miR−122
14	1.00	0 / 2	miR−124a
15	1.00	0 / 6	miR−125a
16	1.00	0 / 9	miR−125b
17	1.00	0 / 5	miR−126
18	1.00	0 / 2	miR−127
19	1.00	0 / 3	miR−128
20	1.00	0 / 4	miR−128b

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.2	1 / 18	hsa−miR−564
2	0.2	1 / 23	hsa−miR−151−5p
3	0.2	1 / 24	hsa−miR−220b
4	0.3	2 / 106	hsa−miR−526b
5	0.4	1 / 43	hsa−miR−483−5p
6	0.4	1 / 48	hsa−miR−610
7	0.4	2 / 130	hsa−miR−218
8	0.5	1 / 59	hsa−miR−556−5p
9	0.5	1 / 66	hsa−miR−628−3p
10	0.5	1 / 69	hsa−miR−502−5p
11	0.5	1 / 70	hsa−miR−622
12	0.6	1 / 75	hsa−miR−1290
13	0.6	1 / 75	hsa−miR−939
14	0.6	1 / 75	hsa−miR−513c
15	0.6	1 / 75	hsa−miR−708
16	0.6	1 / 77	hsa−miR−620
17	0.6	1 / 80	hsa−miR−339−5p
18	0.6	1 / 83	hsa−miR−433
19	0.6	1 / 90	hsa−miR−10a
20	0.6	1 / 92	hsa−miR−378

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.2	1 / 16	MACIEJ_MMML 1
2	1.0	0 / 13	MACIEJ_MMML 10
3	1.0	0 / 7	MACIEJ_MMML 13
4	1.0	0 / 9	MACIEJ_MMML 14
5	1.0	0 / 11	MACIEJ_MMML 15
6	1.0	0 / 15	MACIEJ_MMML 16
7	1.0	0 / 2	MACIEJ_MMML 17
8	1.0	0 / 14	MACIEJ_MMML 19
9	1.0	0 / 4	MACIEJ_MMML 2
10	1.0	0 / 5	MACIEJ_MMML 20
11	1.0	0 / 15	MACIEJ_MMML 22
12	1.0	0 / 4	MACIEJ_MMML 23
13	1.0	0 / 12	MACIEJ_MMML 24
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	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	3e−10	39 / 1146	HEBENSTREIT_low expression TF
2	2e−01	1 / 16	MYC_Protein synthesis degradation UP
3	5e−01	1 / 63	MYC_Targets UP
4	1e+00	4 / 1233	KIM_MYC targets
5	1e+00	0 / 14	NOWICK_TF
6	1e+00	0 / 1095	HEBENSTREIT_high expression 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	0.09	1 / 8	VAQUERIZAS_Tongue
2	0.19	1 / 19	VAQUERIZAS_Pituitary
3	0.80	1 / 144	VAQUERIZAS_General
4	1.00	0 / 40	VAQUERIZAS_Fetal brain
5	1.00	0 / 44	VAQUERIZAS_Placenta
6	1.00	0 / 28	VAQUERIZAS_Liver
7	1.00	0 / 37	VAQUERIZAS_Prostate
8	1.00	0 / 29	VAQUERIZAS_Smooth muscle
9	1.00	0 / 43	VAQUERIZAS_Uterus
10	1.00	0 / 12	VAQUERIZAS_Kidney
11	1.00	0 / 22	VAQUERIZAS_Spinal cord
12	1.00	0 / 43	VAQUERIZAS_Whole brain
13	1.00	0 / 41	VAQUERIZAS_Thymus
14	1.00	0 / 39	VAQUERIZAS_Thyroid
15	1.00	0 / 62	VAQUERIZAS_Whole blood
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

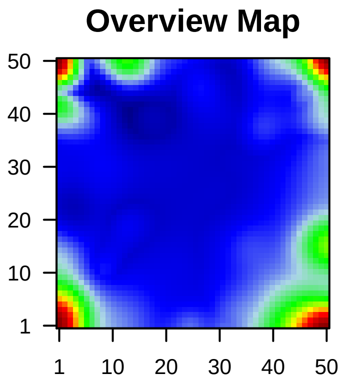
Group Overexpression

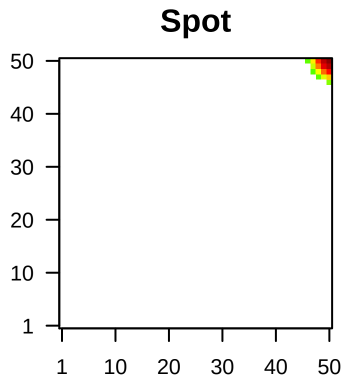
Spot Summary: D

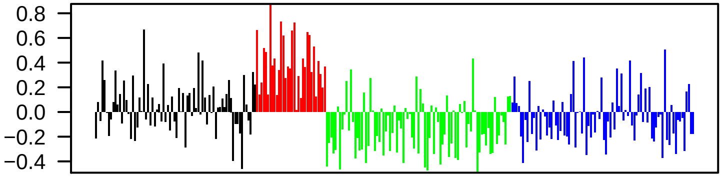
metagenes = 17
genes = 242

<r> metagenes = 0.95
<r> genes = 0.27
beta: r2= 13.09 / log p= −Inf

samples with spot = 18 (6.5 %)
Atypical : 2 (2.7 %)
Classical : 13 (40.6 %)
Mesenchymal : 1 (1.2 %)
Basal : 2 (2.4 %)





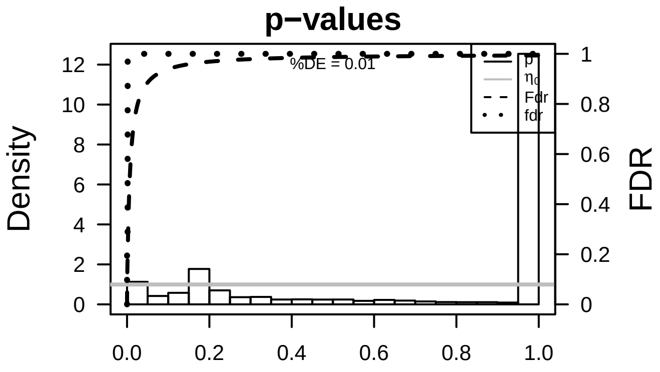


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	4922	5.09	−1.67	0.69	NTS	neurotensin [Source:HGNC Symbol;Acc:8038]
2	2938	3.6	−1.05	0.56	GSTA2	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
3	3880	3.42	−4.05	0.56	KRT19	keratin 19 [Source:HGNC Symbol;Acc:6436]
4	3866	3.23	−3.16	0.46	KRT15	keratin 15 [Source:HGNC Symbol;Acc:6421]
5	1056	3.22	−1.53	0.5	CEL	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	7345	3	−1.41	0.43	UCHL1	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
7	216	2.99	−2.41	0.63	ALDH1A1	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	83888	2.98	−0.56	0.37	FGFBP2	fibroblast growth factor binding protein 2 [Source:HGNC Sym
9	154664	2.78	−1.49	0.67	ABCA13	ATP−binding cassette, sub−family A (ABC1), member 13 [So
10	2944	2.69	−1.57	0.43	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
11	339512	2.68	−1.34	0.5	C1orf110	chromosome 1 open reading frame 110 [Source:HGNC Sym
12	3856	2.63	−2.21	0.46	KRT8P3	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
13	26047	2.62	−1.61	0.31	CNTNAP2	contactin associated protein−like 2 [Source:HGNC Symbol;A
14	2719	2.58	−0.74	0.53	GPC3	glypican 3 [Source:HGNC Symbol;Acc:4451]
15	84171	2.55	−1.19	0.37	LOXL4	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
16	11166	2.55	−1.98	0.68	SOX21	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
17	4072	2.5	−2.3	0.71	EPCAM	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
18	139728	2.48	−1.61	0.51	PNCK	pregnancy up−regulated nonubiquitous CaM kinase [Source:
19	4915	2.4	−1.19	0.75	NTRK2	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
20	2947	2.4	−0.99	0.43	GSTM3	glutathione S−transferase mu 3 (brain) [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−28	66 / 914	Chr	Chr 3
2	6e−09	46 / 1253	BP	small molecule metabolic process
3	2e−08	13 / 119	BP	xenobiotic metabolic process
4	2e−08	8 / 34	BP	glutathione metabolic process
5	1e−06	5 / 14	GSEA	PUJANA_BRCA_CENTERED_NETWORK
6	1e−06	6 / 25	BP	glutathione derivative biosynthetic process
7	2e−06	5 / 15	GSEA	KEGG_GLUTATHIONE_METABOLISM
8	8e−06	5 / 20	MF	glutathione transferase activity
9	3e−05	4 / 13	BP	regulation of blood vessel size
10	3e−05	4 / 13	GSEA	PUJANA_XPRSS_INT_NETWORK
11	3e−05	4 / 13	GSEA	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
12	4e−05	11 / 167	BP	cellular nitrogen compound metabolic process
13	4e−05	4 / 14	GSEA	VANTVEER_BREAST_CANCER_METASTASIS_DN
14	5e−05	4 / 15	GSEA	UDAYAKUMAR_MED1_TARGETS_UP
15	5e−05	4 / 15	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_E
16	5e−05	4 / 15	GSEA	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
17	5e−05	4 / 15	GSEA	REACTOME_GLUTATHIONE_CONJUGATION
18	6e−05	3 / 6	GSEA	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
19	7e−05	4 / 16	GSEA	RODWELL_AGING_KIDNEY_DN
20	1e−04	4 / 19	BP	cellular amino acid biosynthetic process
21	2e−04	3 / 8	GSEA	LIU_CDX2_TARGETS_DN
22	2e−04	14 / 304	CC	mitochondrial inner membrane
23	2e−04	3 / 9	GSEA	BROWNE_HCMV_INFECTION_8HR_UP
24	2e−04	3 / 9	GSEA	REACTOME_METABOLISM_OF_AMINO_ACIDS
25	3e−04	5 / 41	MF	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NA
26	3e−04	4 / 23	BP	apoptotic mitochondrial changes
27	5e−04	3 / 11	MF	glutathione binding
28	5e−04	3 / 11	GSEA	ODONNELL_TFRC_TARGETS_DN
29	5e−04	3 / 11	GSEA	ITO_PTTG1_TARGETS_UP
30	5e−04	3 / 11	GSEA	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
31	5e−04	4 / 26	BP	sulfur amino acid metabolic process
32	6e−04	3 / 12	GSEA	BROCKE_APOPTOSIS_REVERSED_BY_IL6
33	6e−04	3 / 12	GSEA	HELLER_SILENCED_BY_METHYLATION_DN
34	6e−04	3 / 12	GSEA	KAYO_AGING_MUSCLE_UP
35	8e−04	3 / 13	GSEA	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
36	8e−04	3 / 13	GSEA	COLLER_MYC_TARGETS_UP
37	1e−03	3 / 14	GSEA	TIEN_INTESTINE_PROBIOTICS_6HR_DN
38	1e−03	3 / 14	GSEA	KORKOLA_YOLK_SAC_TUMOR
39	1e−03	3 / 14	GSEA	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY
40	1e−03	53 / 2378	CC	cytosol



BP

Rank	p−value	#in/all	Geneset
1	6e−09	46 / 1253	small molecule metabolic process
2	2e−08	13 / 119	xenobiotic metabolic process
3	2e−08	8 / 34	glutathione metabolic process
4	1e−06	6 / 25	glutathione derivative biosynthetic process
5	3e−05	4 / 13	regulation of blood vessel size
6	4e−05	11 / 167	cellular nitrogen compound metabolic process
7	1e−04	4 / 19	cellular amino acid biosynthetic process
8	3e−04	4 / 23	apoptotic mitochondrial changes
9	5e−04	4 / 26	sulfur amino acid metabolic process
10	1e−03	4 / 32	glycosaminoglycan biosynthetic process
11	1e−03	3 / 15	lipid glycosylation
12	2e−03	15 / 434	oxidation−reduction process
13	5e−03	6 / 107	negative regulation of neuron apoptotic process
14	5e−03	3 / 24	telomere maintenance via recombination
15	5e−03	13 / 390	metabolic process
16	6e−03	5 / 79	vitamin metabolic process
17	9e−03	2 / 10	biotin metabolic process
18	9e−03	3 / 30	negative regulation of cell death
19	1e−02	2 / 11	planar cell polarity pathway involved in neural tube closure
20	1e−02	5 / 93	anatomical structure morphogenesis

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 15	RHODES_CANCER_META_SIGNATURE
2	0.14	0 / 14	LIU_COMMON_CANCER_GENES
3	0.15	1 / 16	RHODES_UNDIFFERENTIATED_CANCER
4	0.17	1 / 13	GENTLES_modul16
5	0.20	1 / 15	BEN−PORATH_UP
6	0.20	1 / 15	GENTLES_modul6
7	0.21	1 / 16	WOLFER_overlap genes
8	0.21	1 / 16	GENTLES_modul4
9	0.38	9 / 530	Lembcke_Normal vs Adenoma
10	0.44	1 / 39	ZHANG_MM up
11	0.51	1 / 48	KUIPER_MM poor survival
12	0.63	1 / 68	SHAUGHNESSY_MM high risk
13	0.76	2 / 185	SPANG_LPS−index2
14	0.85	3 / 316	SPANG_BCL6−index2
15	0.91	5 / 553	Lembcke_Colonic Inflammation
16	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	1.00	0 / 10	LIU_BREAST_CANCER
19	1.00	0 / 14	LIU_LIVER_CANCER
20	1.00	0 / 15	LIU_PROSTATE_CANCER_DN

CC

Rank	p−value	#in/all	Geneset
1	2e−04	14 / 304	mitochondrial inner membrane
2	1e−03	53 / 2378	cytosol
3	2e−03	3 / 17	mitochondrial envelope
4	5e−03	6 / 109	mitochondrial outer membrane
5	6e−03	5 / 78	PML body
6	6e−03	31 / 1318	mitochondrion
7	1e−02	3 / 31	condensed nuclear chromosome
8	1e−02	63 / 3274	integral to membrane
9	2e−02	2 / 13	NuA4 histone acetyltransferase complex
10	2e−02	3 / 37	lateral plasma membrane
11	2e−02	2 / 14	membrane−bounded vesicle
12	2e−02	16 / 614	endoplasmic reticulum membrane
13	2e−02	16 / 621	endoplasmic reticulum
14	2e−02	2 / 16	male germ cell nucleus
15	3e−02	2 / 18	costamere
16	3e−02	7 / 201	apical plasma membrane
17	3e−02	4 / 82	chromosome
18	3e−02	3 / 48	voltage−gated potassium channel complex
19	3e−02	6 / 164	axon
20	6e−02	9 / 335	centrosome

Chr

Rank	p−value	#in/all	Geneset
1	3e−28	66 / 914	Chr 3
2	1e−02	17 / 630	Chr X
3	2e−02	24 / 1033	Chr 2
4	3e−01	4 / 187	Chr 21
5	3e−01	9 / 504	Chr 15
6	5e−01	10 / 633	Chr 9
7	5e−01	11 / 714	Chr 6
8	6e−01	9 / 618	Chr 4
9	7e−01	10 / 743	Chr 7
10	7e−01	3 / 232	Chr 18
11	7e−01	7 / 534	Chr 8
12	7e−01	11 / 866	Chr 12
13	8e−01	4 / 386	Chr 22
14	8e−01	21 / 1720	Chr 1
15	9e−01	6 / 602	Chr 10
16	9e−01	2 / 280	Chr 13
17	9e−01	9 / 918	Chr 17
18	1e+00	3 / 449	Chr 20
19	1e+00	3 / 519	Chr 14
20	1e+00	4 / 717	Chr 16

Disease

Rank	p−value	#in/all	Geneset
1	0.004	13 / 375	GUDJ_psoriasis down
2	0.971	4 / 572	GUDJ_psoriasis up
3	1.000	0 / 17	BCHETNIA_EBM up
4	1.000	0 / 2	BCHETNIA_EBM down
5	1.000	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	0.01	7 / 169	willscher_GBM_proteomics_wtOnly_Differencelist_
2	0.01	4 / 62	Stuehler_Proteins_up_in_STS
3	0.01	12 / 391	Down_b
4	0.02	3 / 37	willscher_GBM_proteomics_wtOnly_SpotH
5	0.04	3 / 49	Vishal_subnetwork signature of survival in GBM
6	0.04	2 / 22	KIM deleted & downregulated in LTS
7	0.04	3 / 53	Christensen_hypermethylated_in_primary_glioblastoma
8	0.06	1 / 4	willscher_GBM_STSwt_proteomics−L_UP
9	0.08	2 / 31	KIM prognostic signature LTS vs. STS
10	0.09	3 / 71	willscher_GBM_Verhaak−CL_expression_H_down
11	0.09	3 / 71	willscher_GBM_Verhaak−MES_expression_H_up
12	0.09	3 / 71	willscher_GBM_Verhaak−PNwt_expression_H_up
13	0.11	8 / 328	Up
14	0.12	3 / 83	Christensen_hypermethylated_in_secondary_glioblastoma
15	0.13	3 / 85	laffaire_hypermeth_LGG_vs_control
16	0.15	1 / 11	neurons_glio
17	0.15	1 / 11	willscher_GBM_Verhaak−CL_expression_M_down
18	0.15	1 / 11	willscher_GBM_Verhaak−MES_expression_M_down
19	0.15	1 / 11	willscher_GBM_Verhaak−PNmut_expression_M_up
20	0.16	4 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−06	5 / 14	PUJANA_BRCA_CENTERED_NETWORK
2	2e−06	5 / 15	KEGG_GLUTATHIONE_METABOLISM
3	3e−05	4 / 13	PUJANA_XPRSS_INT_NETWORK
4	3e−05	4 / 13	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
5	4e−05	4 / 14	VANTVEER_BREAST_CANCER_METASTASIS_DN
6	5e−05	4 / 15	UDAYAKUMAR_MED1_TARGETS_UP
7	5e−05	4 / 15	RICKMAN_HEAD_AND_NECK_CANCER_E
8	5e−05	4 / 15	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
9	5e−05	4 / 15	REACTOME_GLUTATHIONE_CONJUGATION
10	6e−05	3 / 6	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
11	7e−05	4 / 16	RODWELL_AGING_KIDNEY_DN
12	2e−04	3 / 8	LIU_CDX2_TARGETS_DN
13	2e−04	3 / 9	BROWNE_HCMV_INFECTION_8HR_UP
14	2e−04	3 / 9	REACTOME_METABOLISM_OF_AMINO_ACIDS
15	5e−04	3 / 11	ODONNELL_TFRC_TARGETS_DN
16	5e−04	3 / 11	ITO_PTTG1_TARGETS_UP
17	5e−04	3 / 11	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
18	6e−04	3 / 12	BROCKE_APOPTOSIS_REVERSED_BY_IL6
19	6e−04	3 / 12	HELLER_SILENCED_BY_METHYLATION_DN
20	6e−04	3 / 12	KAYO_AGING_MUSCLE_UP

H Tiss

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	WIRTH_Lymphocytes
2	0.2	1 / 13	WIRTH_Thalamus
3	0.2	1 / 15	WIRTH_Telencephalon
4	0.2	1 / 15	WIRTH_Cerebellum
5	0.4	7 / 400	WIRTH_Nervous System
6	0.4	1 / 36	WIRTH_Placenta
7	0.8	1 / 120	WIRTH_Testis
8	0.9	1 / 135	WIRTH_Mucosa
9	1.0	2 / 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 / 13	WIRTH_Thymus
17	1.0	0 / 6	WIRTH_Bone marrow
18	1.0	0 / 14	WIRTH_Globus pallidus
19	1.0	0 / 13	WIRTH_Cortex cerebri
20	1.0	0 / 16	WIRTH_Hippocampus

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.02	2 / 13	BENTINK_mBL UP
2	0.03	18 / 755	SPANG_BCR UP
3	0.05	9 / 327	SPANG_CD40 6hrs UP
4	0.06	5 / 140	DAVE_BL−vs−DLBCL
5	0.14	7 / 291	SPANG_IL21 UP
6	0.16	1 / 12	DAVE_BL UP
7	0.23	1 / 18	DAVE_BL Inter
8	0.25	3 / 118	SPANG_LPS 6hrs UP
9	0.27	2 / 69	SPANG_LPS 6hrs DN
10	0.29	8 / 426	SPANG_CD40 6hrs DN
11	0.36	2 / 86	ROSOLOWSKI_green UP
12	0.37	14 / 852	SPANG_BCR DN
13	0.38	5 / 275	ZHANG_DLBCL mutated
14	0.43	2 / 100	ROSOLOWSKI_blue total
15	0.52	2 / 119	ROSOLOWSKI_green total
16	0.72	1 / 86	ROSOLOWSKI_red total
17	0.91	2 / 274	SPANG_IL21 DN
18	1.00	0 / 13	BENTINK_mBL DOWN
19	1.00	0 / 12	DAVE_BL_DN
20	1.00	0 / 18	DAVE_c−myc BL UP

MF

Rank	p−value	#in/all	Geneset
1	8e−06	5 / 20	glutathione transferase activity
2	3e−04	5 / 41	oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP
3	5e−04	3 / 11	glutathione binding
4	2e−03	4 / 39	NAD binding
5	4e−03	8 / 175	protein domain specific binding
6	6e−03	3 / 26	cytochrome−c oxidase activity
7	6e−03	3 / 26	potassium channel regulator activity
8	7e−03	5 / 82	structural constituent of cytoskeleton
9	8e−03	9 / 237	enzyme binding
10	9e−03	3 / 29	cofactor binding
11	9e−03	5 / 87	ligase activity
12	1e−02	2 / 12	phosphate ion binding
13	1e−02	7 / 172	magnesium ion binding
14	2e−02	2 / 13	magnesium ion transmembrane transporter activity
15	2e−02	5 / 99	double−stranded DNA binding
16	2e−02	14 / 500	sequence−specific DNA binding
17	2e−02	3 / 37	transferase activity, transferring hexosyl groups
18	2e−02	2 / 14	calmodulin−dependent protein kinase activity
19	2e−02	2 / 15	glucuronosyltransferase activity
20	2e−02	5 / 110	heme binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	0.003	3 / 19	GTCA−380−5P
2	0.003	8 / 168	ATAC−144
3	0.006	7 / 145	AAAG−511
4	0.009	8 / 198	ATGT−302C
5	0.010	4 / 57	GTTA−302B
6	0.012	4 / 60	AGGG−328
7	0.016	5 / 100	ACAG−10A−−10B
8	0.016	4 / 66	GCTC−335
9	0.018	7 / 181	ACTG−34B
10	0.018	13 / 457	TGCC−124A
11	0.018	6 / 141	ATAC−202
12	0.018	7 / 182	TAGC−9
13	0.020	7 / 185	AAAG−204−−211
14	0.021	8 / 232	ACTT−142−5P
15	0.022	7 / 189	AACT−145
16	0.022	3 / 41	GCTG−512−5P
17	0.025	8 / 239	TGCA−148A−−152−−148B
18	0.027	8 / 243	ATGT−493
19	0.030	8 / 247	GTGC−96
20	0.032	5 / 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	0.03	1 / 2	miR−127
2	0.07	1 / 5	miR−320
3	0.10	1 / 7	miR−145
4	0.11	1 / 8	miR−222
5	0.17	1 / 13	miR−1
6	1.00	0 / 11	let−7a
7	1.00	0 / 6	let−7b
8	1.00	0 / 4	let−7c
9	1.00	0 / 6	let−7d
10	1.00	0 / 4	let−7g
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 / 5	miR−126
20	1.00	0 / 3	miR−128

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	0.003	6 / 95	hsa−miR−888
2	0.003	8 / 163	hsa−miR−1297
3	0.007	5 / 82	hsa−miR−1179
4	0.007	7 / 153	hsa−miR−506
5	0.008	9 / 234	hsa−miR−26a
6	0.008	7 / 155	hsa−miR−298
7	0.009	8 / 199	hsa−miR−181c
8	0.010	9 / 242	hsa−miR−26b
9	0.011	8 / 206	hsa−miR−148b
10	0.012	6 / 130	hsa−miR−508−3p
11	0.013	9 / 253	hsa−miR−548p
12	0.015	8 / 218	hsa−miR−181a
13	0.016	4 / 66	hsa−miR−499−3p
14	0.017	9 / 267	hsa−miR−577
15	0.018	7 / 181	hsa−miR−582−5p
16	0.018	8 / 224	hsa−miR−181b
17	0.018	10 / 315	hsa−miR−30e
18	0.018	6 / 142	hsa−miR−409−3p
19	0.019	13 / 463	hsa−miR−301a
20	0.020	5 / 106	hsa−miR−361−5p

MMML CGS

Rank	p−value	#in/all	Geneset
1	0.02	2 / 14	MACIEJ_MMML 19
2	0.06	1 / 4	MACIEJ_MMML 41
3	0.11	1 / 8	MACIEJ_MMML 50
4	0.19	1 / 14	MACIEJ_MMML 8
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 / 15	MACIEJ_MMML 16
11	1.00	0 / 2	MACIEJ_MMML 17
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	0.01	2 / 11	BENTINK_e2f3.2
2	0.16	1 / 12	BENTINK_e2f3.1
3	0.17	1 / 13	GUSTAFSON_PI3K_UP
4	0.17	1 / 13	BENTINK_src.10
5	0.19	1 / 14	BENTINK_myc.1
6	0.20	1 / 15	BENTINK_ras.6
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 11	BENTINK_ras.4
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	0.03	2 / 20	MYC_Metabolism UP
2	0.05	24 / 1146	HEBENSTREIT_low expression TF
3	0.26	19 / 1095	HEBENSTREIT_high expression TF
4	0.27	21 / 1233	KIM_MYC targets
5	0.61	1 / 63	MYC_Targets UP
6	1.00	0 / 14	NOWICK_TF
7	1.00	0 / 5	MYC_TFs
8	1.00	0 / 9	MYC_Targets DOWN
9	1.00	0 / 4	MYC_Apoptosis UP
10	1.00	0 / 8	MYC_Cell cycle UP
11	1.00	0 / 2	MYC_Cell cycle DOWN
12	1.00	0 / 4	MYC_Cell growth and proliferation UP
13	1.00	0 / 2	MYC_Chromatin_modification UP
14	1.00	0 / 7	MYC_DNA repair UP
15	1.00	0 / 3	MYC_DNA replication UP
16	1.00	0 / 2	MYC_ECM cell adhesion DOWN
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	0.009	2 / 10	VAQUERIZAS_Skeletal.muscle.psoas
2	0.175	1 / 13	VAQUERIZAS_Ovary
3	0.199	1 / 15	VAQUERIZAS_Adrenal gland
4	0.211	1 / 16	VAQUERIZAS_Fetal thyroid
5	0.256	1 / 20	VAQUERIZAS_Adrenal cortex
6	0.358	1 / 30	VAQUERIZAS_Fetal lung
7	0.439	1 / 39	VAQUERIZAS_Thyroid
8	0.479	1 / 44	VAQUERIZAS_Placenta
9	0.601	1 / 62	VAQUERIZAS_Whole blood
10	0.601	1 / 62	VAQUERIZAS_Lung
11	0.627	2 / 144	VAQUERIZAS_General
12	1.000	0 / 40	VAQUERIZAS_Fetal brain
13	1.000	0 / 28	VAQUERIZAS_Liver
14	1.000	0 / 37	VAQUERIZAS_Prostate
15	1.000	0 / 29	VAQUERIZAS_Smooth muscle
16	1.000	0 / 43	VAQUERIZAS_Uterus
17	1.000	0 / 12	VAQUERIZAS_Kidney
18	1.000	0 / 22	VAQUERIZAS_Spinal cord
19	1.000	0 / 43	VAQUERIZAS_Whole brain
20	1.000	0 / 41	VAQUERIZAS_Thymus

Group Overexpression

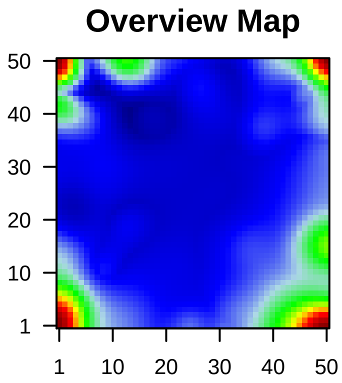
Spot Summary: E

metagenes = 4
genes = 94

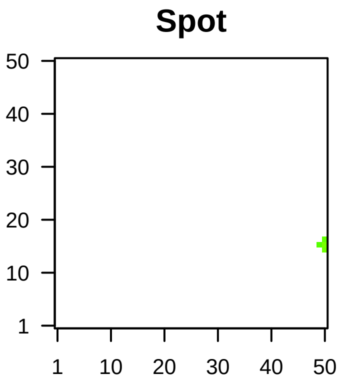
<r> metagenes = 0.99
<r> genes = 0.39
beta: r2= 10.3 / log p= −Inf

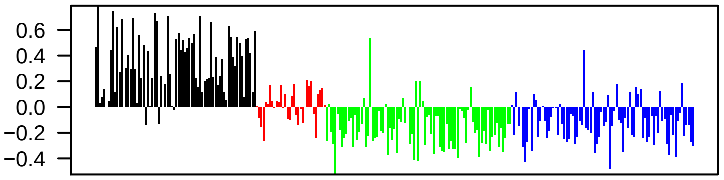
samples with spot = 33 (12 %)
Atypical : 31 (41.9 %)
Mesenchymal : 1 (1.2 %)
Basal : 1 (1.2 %)

Overview Map



Spot





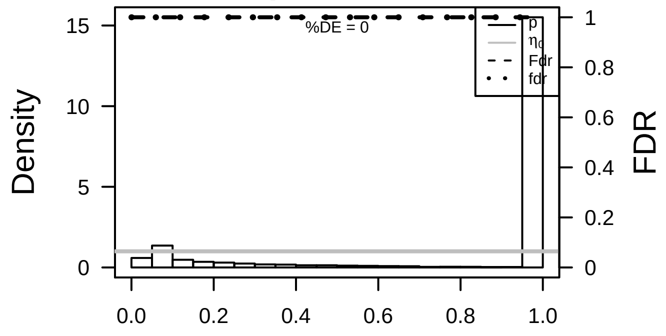
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	54959	2.94	−0.58	0.36	ODAM	odontogenic, ameloblast asssociated [Source:HGNC Symbol
2	4602	2.8	−1.04	0.76	MYB	v−myb avian myeloblastosis viral oncogene homolog [Source
3	83988	2.43	−1.29	0.53	NCALD	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
4	26002	2.42	−1.28	0.41	MOXD1	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
5	1298	2.41	−1.14	0.55	COL9A2	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
6	10439	2.3	−1.77	0.44	OLFM1	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
7	399948	2.29	−0.65	0.68	COLCA1	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
8	6542	2.15	−1.11	0.53	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ sys
9	21	2.13	−0.7	0.74	ABCA3	ATP−binding cassette, sub−family A (ABC1), member 3 [Sou
10	1365	2.05	−0.55	0.63	CLDN3	claudin 3 [Source:HGNC Symbol;Acc:2045]
11	494470	2.04	−1.37	0.6	RNF165	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
12	909	1.99	−1.12	0.34	CD1A	CD1a molecule [Source:HGNC Symbol;Acc:1634]
13	3670	1.98	−0.84	0.35	ISL1	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
14	9915	1.9	−0.54	0.7	ARNT2	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
15	63917	1.86	−1.59	0.42	GALNT11	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acet
16	8543	1.83	−1.35	0.76	LMO4	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
17	57556	1.76	−1.15	0.57	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmi
18	221061	1.75	−1.13	0.72	FAM171A1	family with sequence similarity 171, member A1 [Source:HG
19	26018	1.73	−1.25	0.69	LRIG1	leucine−rich repeats and immunoglobulin−like domains 1 [So
20	56994	1.71	−1.21	0.75	CHPT1	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−06	4 / 16	GSE	RICKMAN_HEAD_AND_NECK_CANCER_A
2	7e−05	6 / 122	miRN	hsa−miR−380
3	8e−05	3 / 15	GSE	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
4	8e−05	9 / 318	MF	chromatin binding
5	1e−04	7 / 189	miRN	CTTT−527
6	1e−04	10 / 415	miRN	TTTG−19A−−19B
7	2e−04	3 / 20	MF	RNA polymerase II transcription coactivator activity
8	9e−04	3 / 34	BP	thymus development
9	1e−03	2 / 9	GSE	GOZGIT_ESR1_TARGETS_DN
10	1e−03	2 / 9	GSE	REACTOME_ETHANOL_OXIDATION
11	1e−03	12 / 755	Lymp	SPANG_BCR UP
12	1e−03	5 / 144	miRN	hsa−miR−24
13	2e−03	3 / 40	TF Ti	VAQUERIZAS_Fetal brain
14	2e−03	11 / 676	BP	positive regulation of transcription from RNA polymerase II promoter
15	2e−03	8 / 387	BP	positive regulation of cell proliferation
16	2e−03	5 / 150	miRN	hsa−miR−633
17	2e−03	2 / 11	MF	enhancer sequence−specific DNA binding
18	2e−03	3 / 42	BP	B cell differentiation
19	2e−03	2 / 12	CC	PRC1 complex
20	2e−03	2 / 12	GSE	KIM_WT1_TARGETS_12HR_UP
21	2e−03	2 / 13	BP	developmental pigmentation
22	2e−03	2 / 13	miRN	miR−34a
23	3e−03	4 / 101	miRN	hsa−miR−525−5p
24	3e−03	2 / 14	GSE	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
25	3e−03	2 / 14	GSE	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL
26	3e−03	4 / 104	BP	regulation of gene expression
27	3e−03	2 / 15	BP	embryonic digestive tract development
28	3e−03	2 / 15	BP	positive regulation vascular endothelial growth factor production
29	3e−03	2 / 15	GSE	DOANE_BREAST_CANCER_CLASSES_UP
30	3e−03	2 / 15	GSE	GEORGES_TARGETS_OF_MIR192_AND_MIR215
31	3e−03	2 / 15	GSE	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON
32	3e−03	2 / 15	GSE	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
33	3e−03	2 / 15	GSE	MASSARWEH_RESPONSE_TO_ESTRADIOL
34	4e−03	5 / 179	miRN	hsa−miR−34b
35	4e−03	5 / 180	miRN	hsa−miR−199b−3p
36	4e−03	2 / 16	BP	negative regulation of mitotic cell cycle
37	4e−03	2 / 16	GSE	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
38	4e−03	2 / 16	GSE	HOEBEKE_LYMPHOID_STEM_CELL_UP
39	4e−03	2 / 16	GSE	MANN_RESPONSE_TO_AMIFOSTINE_UP
40	4e−03	2 / 16	GSE	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP

p−values



BP

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 34	thymus development
2	2e−03	11 / 676	positive regulation of transcription from RNA polymerase II promoter
3	2e−03	8 / 387	positive regulation of cell proliferation
4	2e−03	3 / 42	B cell differentiation
5	2e−03	2 / 13	developmental pigmentation
6	3e−03	4 / 104	regulation of gene expression
7	3e−03	2 / 15	embryonic digestive tract development
8	3e−03	2 / 15	positive regulation vascular endothelial growth factor production
9	4e−03	2 / 16	negative regulation of mitotic cell cycle
10	5e−03	2 / 19	spinal cord motor neuron differentiation
11	6e−03	2 / 21	DNA−dependent DNA replication
12	6e−03	2 / 21	nucleotide−excision repair, DNA damage removal
13	9e−03	2 / 25	melanocyte differentiation
14	1e−02	3 / 77	hemopoiesis
15	1e−02	3 / 77	post−embryonic development
16	1e−02	4 / 148	G1/S transition of mitotic cell cycle
17	1e−02	2 / 28	face morphogenesis
18	1e−02	2 / 28	T cell differentiation
19	1e−02	2 / 29	positive regulation of cell death
20	1e−02	2 / 30	response to steroid hormone

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	1 / 7	ZHANG_MGUS up
2	0.07	1 / 13	GENTLES_modul12
3	0.08	1 / 15	RHODES_CANCER_META_SIGNATURE
4	0.08	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
5	0.08	1 / 15	LIU_PROSTATE_CANCER_DN
6	0.09	1 / 16	GENTLES_modul11
7	0.24	1 / 48	KUIPER_MM poor survival
8	0.32	1 / 68	SHAUGHNESSY_MM high risk
9	0.83	2 / 553	Lembcke_Colonic Inflammation
10	0.84	1 / 316	SPANG_BCL6−index2
11	0.95	1 / 530	Lembcke_Normal vs Adenoma
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_COMMON_CANCER_GENES
16	1.00	0 / 14	LIU_LIVER_CANCER
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	0.002	2 / 12	PRC1 complex
2	0.007	2 / 22	heterochromatin
3	0.009	2 / 25	PcG protein complex
4	0.019	11 / 949	nucleoplasm
5	0.055	1 / 10	nBAF complex
6	0.055	1 / 10	transcriptionally active chromatin
7	0.057	3 / 153	endosome membrane
8	0.060	3 / 157	nuclear membrane
9	0.061	1 / 11	axolemma
10	0.061	1 / 11	npBAF complex
11	0.061	1 / 11	nuclear periphery
12	0.066	1 / 12	ESC/E(Z) complex
13	0.066	1 / 12	SWI/SNF complex
14	0.073	2 / 78	PML body
15	0.077	1 / 14	myelin sheath
16	0.081	33 / 4640	nucleus
17	0.089	2 / 88	nuclear chromatin
18	0.092	1 / 17	alpha−amino−3−hydroxy−5−methyl−4−isoxazolepropionic acid selective gluta
19	0.092	1 / 17	nuclear heterochromatin
20	0.092	1 / 17	pericentriolar material

Chr

Rank	p−value	#in/all	Geneset
1	0.03	7 / 534	Chr 8
2	0.06	8 / 743	Chr 7
3	0.10	7 / 699	Chr 5
4	0.15	6 / 633	Chr 9
5	0.22	6 / 714	Chr 6
6	0.23	8 / 1033	Chr 2
7	0.26	5 / 602	Chr 10
8	0.37	6 / 866	Chr 12
9	0.38	2 / 232	Chr 18
10	0.42	6 / 914	Chr 3
11	0.47	2 / 280	Chr 13
12	0.52	10 / 1720	Chr 1
13	0.60	5 / 918	Chr 17
14	0.79	2 / 504	Chr 15
15	0.80	2 / 519	Chr 14
16	0.87	2 / 618	Chr 4
17	0.89	1 / 386	Chr 22
18	0.92	2 / 717	Chr 16
19	0.93	1 / 449	Chr 20
20	0.97	1 / 630	Chr X

Disease

Rank	p−value	#in/all	Geneset
1	0.02	6 / 375	GUDJ_psoriasis down
2	0.96	1 / 572	GUDJ_psoriasis up
3	1.00	0 / 17	BCHETNIA_EBM up
4	1.00	0 / 2	BCHETNIA_EBM down
5	1.00	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	0.03	2 / 49	mature astrocytes
2	0.05	2 / 62	Stuehler_Proteins_up_in_STS
3	0.06	1 / 10	willscher_GBM_LTSmut_proteomics−A_UP
4	0.08	1 / 15	VERHAAK_PN subtype
5	0.13	2 / 110	Christensen_hypermethylated_in_grade3_astrocytoma
6	0.14	1 / 27	WIRTH_PN subtype
7	0.15	1 / 28	Barbus_GBM_STS_vs._LTS
8	0.17	2 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
9	0.19	2 / 142	Christensen_hypermethylated_in_grade2_oligodendroglioma
10	0.24	1 / 49	Donson−innate immunity−associated with LTS in HGA
11	0.25	1 / 51	willscher_GBM_Verhaak−PNmut_expression_G_down
12	0.26	1 / 53	Christensen_hypermethylated_in_primary_glioblastoma
13	0.27	1 / 55	OL vs. MOG− OL
14	0.28	1 / 58	Christensen_hypomethylated_in_secondary_glioblastoma
15	0.33	1 / 70	willscher_GBM_proteomics_wtOnly_SpotJ
16	0.33	1 / 71	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
17	0.34	1 / 73	GIEZELT_GBM_WT_down_VS_mut
18	0.34	1 / 74	GIEZELT_GBM_STS_up_VS_LTS
19	0.37	3 / 379	Down_a
20	0.38	1 / 85	GIEZELT_GBM_STS_down_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−06	4 / 16	RICKMAN_HEAD_AND_NECK_CANCER_A
2	8e−05	3 / 15	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
3	1e−03	2 / 9	GOZGIT_ESR1_TARGETS_DN
4	1e−03	2 / 9	REACTOME_ETHANOL_OXIDATION
5	2e−03	2 / 12	KIM_WT1_TARGETS_12HR_UP
6	3e−03	2 / 14	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
7	3e−03	2 / 14	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL
8	3e−03	2 / 15	DOANE_BREAST_CANCER_CLASSES_UP
9	3e−03	2 / 15	GEORGES_TARGETS_OF_MIR192_AND_MIR215
10	3e−03	2 / 15	NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON
11	3e−03	2 / 15	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
12	3e−03	2 / 15	MASSARWEH_RESPONSE_TO_ESTRADIOL
13	4e−03	2 / 16	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
14	4e−03	2 / 16	HOEBEKE_LYMPHOID_STEM_CELL_UP
15	4e−03	2 / 16	MANN_RESPONSE_TO_AMIFOSTINE_UP
16	4e−03	2 / 16	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
17	4e−03	2 / 16	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
18	4e−03	2 / 16	SASAKI_ADULT_T_CELL_LEUKEMIA
19	4e−03	2 / 16	TOOKER_GEMCITABINE_RESISTANCE_UP
20	4e−03	2 / 16	TOOKER_RESPONSE_TO_BEXAROTENE_DN

H_Tiss

Rank	p−value	#in/all	Geneset
1	0.1	1 / 26	WIRTH_Pancreas
2	0.4	3 / 400	WIRTH_Nervous System
3	0.5	1 / 120	WIRTH_Testis
4	0.7	2 / 417	WIRTH_Immune system
5	1.0	0 / 5	WIRTH_Pituitary gland
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 / 14	WIRTH_Globus pallidus
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 / 50	WIRTH_Homeostasis
20	1.0	0 / 62	WIRTH_Liver

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	12 / 755	SPANG_BCR UP
2	0.025	5 / 291	SPANG_IL21 UP
3	0.053	9 / 852	SPANG_BCR DN
4	0.071	1 / 13	BENTINK_mBL UP
5	0.087	1 / 16	WRIGHT_ABC UP
6	0.118	1 / 22	DAVE_NFkB BL DN
7	0.145	2 / 118	SPANG_LPS 6hrs UP
8	0.205	3 / 274	SPANG_IL21 DN
9	0.206	3 / 275	ZHANG_DLBCL mutated
10	0.285	3 / 327	SPANG_CD40 6hrs UP
11	0.417	2 / 250	LENZ_Stromal signature 1
12	0.438	3 / 426	SPANG_CD40 6hrs DN
13	1.000	0 / 13	BENTINK_mBL DOWN
14	1.000	0 / 140	DAVE_BL−vs−DLBCL
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 / 28	DAVE_Immune response 1

MF

Rank	p−value	#in/all	Geneset
1	8e−05	9 / 318	chromatin binding
2	2e−04	3 / 20	RNA polymerase II transcription coactivator activity
3	2e−03	2 / 11	enhancer sequence−specific DNA binding
4	5e−03	3 / 59	protein phosphatase binding
5	1e−02	5 / 252	transcription factor binding
6	2e−02	17 / 1749	DNA binding
7	2e−02	2 / 38	methylated histone residue binding
8	3e−02	2 / 45	steroid hormone receptor activity
9	5e−02	5 / 342	protein heterodimerization activity
10	5e−02	2 / 62	single−stranded DNA binding
11	6e−02	1 / 10	acetyltransferase activity
12	6e−02	1 / 10	diacylglycerol binding
13	6e−02	1 / 11	AMP binding
14	6e−02	1 / 11	histone methyltransferase activity
15	6e−02	1 / 11	protein kinase A catalytic subunit binding
16	7e−02	1 / 12	channel activity
17	7e−02	1 / 12	cyclin−dependent protein serine/threonine kinase inhibitor activity
18	8e−02	1 / 15	Notch binding
19	9e−02	1 / 16	histone acetyl−lysine binding
20	9e−02	1 / 16	Hsp70 protein binding

miRNA 3UTR

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 189	CTTT−527
2	1e−04	10 / 415	TTTG−19A−−19B
3	4e−03	5 / 182	TTTT−373
4	6e−03	4 / 127	GACT−212−−132
5	8e−03	4 / 140	CATG−496
6	9e−03	3 / 76	CAAT−33
7	1e−02	5 / 247	GTGC−96
8	2e−02	4 / 168	ATAC−144
9	2e−02	3 / 92	GCTT−498
10	2e−02	5 / 267	CACT−128A−−128B
11	2e−02	3 / 107	ACAC−142−3P
12	2e−02	3 / 108	AGCA−155
13	2e−02	6 / 391	TGAA−181A−−181B−−181C−−181D
14	3e−02	3 / 116	GACA−219
15	3e−02	2 / 48	ACAT−190
16	3e−02	6 / 420	TGGT−29A−−29B−−29C
17	3e−02	2 / 50	CAAG−362
18	3e−02	5 / 314	TTGC−130A−−301−−130B
19	3e−02	2 / 51	ATAA−154
20	3e−02	3 / 125	GAGC−337

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	0.002	2 / 13	miR−34a
2	0.011	1 / 2	miR−153
3	0.023	1 / 4	let−7c
4	0.023	1 / 4	miR−204
5	0.023	1 / 4	miR−34b
6	0.023	1 / 4	miR−34c
7	0.028	1 / 5	miR−101
8	0.028	1 / 5	miR−15a
9	0.028	1 / 5	miR−320
10	0.034	1 / 6	let−7d
11	0.034	1 / 6	miR−15b
12	0.034	1 / 6	miR−221
13	0.045	1 / 8	miR−222
14	0.061	1 / 11	let−7a
15	0.061	1 / 11	miR−16
16	0.071	1 / 13	miR−1
17	0.138	1 / 26	miR−21
18	1.000	0 / 6	let−7b
19	1.000	0 / 4	let−7g
20	1.000	0 / 2	miR−101b

miRNA target starBase

Rank	p−value	#in/all	Geneset
1	7e−05	6 / 122	hsa−miR−380
2	1e−03	5 / 144	hsa−miR−24
3	2e−03	5 / 150	hsa−miR−633
4	3e−03	4 / 101	hsa−miR−525−5p
5	4e−03	5 / 179	hsa−miR−34b
6	4e−03	5 / 180	hsa−miR−199b−3p
7	6e−03	7 / 382	hsa−miR−454
8	6e−03	4 / 130	hsa−miR−155
9	7e−03	7 / 396	hsa−miR−301b
10	7e−03	3 / 70	hsa−miR−548b−3p
11	8e−03	3 / 73	hsa−miR−518c
12	9e−03	3 / 75	hsa−miR−422a
13	9e−03	3 / 76	hsa−miR−569
14	1e−02	4 / 149	hsa−miR−655
15	1e−02	3 / 80	hsa−miR−339−5p
16	1e−02	4 / 157	hsa−miR−139−5p
17	1e−02	3 / 88	hsa−miR−1265
18	2e−02	4 / 169	hsa−miR−580
19	2e−02	4 / 171	hsa−miR−369−3p
20	2e−02	4 / 171	hsa−miR−452

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	0.06	1 / 11	BENTINK_e2f3.2
2	0.08	1 / 14	BENTINK_myc.1
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 / 12	BENTINK_ras.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	0.01	1 / 2	MYC_Cell cycle DOWN
2	0.03	1 / 5	MYC_TFs
3	0.05	1 / 9	MYC_Targets DOWN
4	0.20	9 / 1146	HEBENSTREIT_low expression TF
5	0.43	7 / 1095	HEBENSTREIT_high expression TF
6	0.97	3 / 1233	KIM_MYC targets
7	1.00	0 / 14	NOWICK_TF
8	1.00	0 / 63	MYC_Targets UP
9	1.00	0 / 4	MYC_Apoptosis UP
10	1.00	0 / 8	MYC_Cell cycle UP
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	0.002	3 / 40	VAQUERIZAS_Fetal brain
2	0.023	2 / 41	VAQUERIZAS_Thymus
3	0.025	2 / 43	VAQUERIZAS_Uterus
4	0.025	2 / 43	VAQUERIZAS_Whole brain
5	0.066	1 / 12	VAQUERIZAS_Kidney
6	0.071	1 / 13	VAQUERIZAS_Skin
7	0.108	1 / 20	VAQUERIZAS_Bone marrow
8	0.113	1 / 21	VAQUERIZAS_Tonsil
9	0.118	1 / 22	VAQUERIZAS_Spinal cord
10	0.153	1 / 29	VAQUERIZAS_Smooth muscle
11	0.190	1 / 37	VAQUERIZAS_Prostate
12	0.200	1 / 39	VAQUERIZAS_Thyroid
13	0.298	1 / 62	VAQUERIZAS_Whole blood
14	0.562	1 / 144	VAQUERIZAS_General
15	1.000	0 / 44	VAQUERIZAS_Placenta
16	1.000	0 / 28	VAQUERIZAS_Liver
17	1.000	0 / 7	VAQUERIZAS_Appendix
18	1.000	0 / 30	VAQUERIZAS_Fetal lung
19	1.000	0 / 62	VAQUERIZAS_Lung
20	1.000	0 / 16	VAQUERIZAS_Pancreas