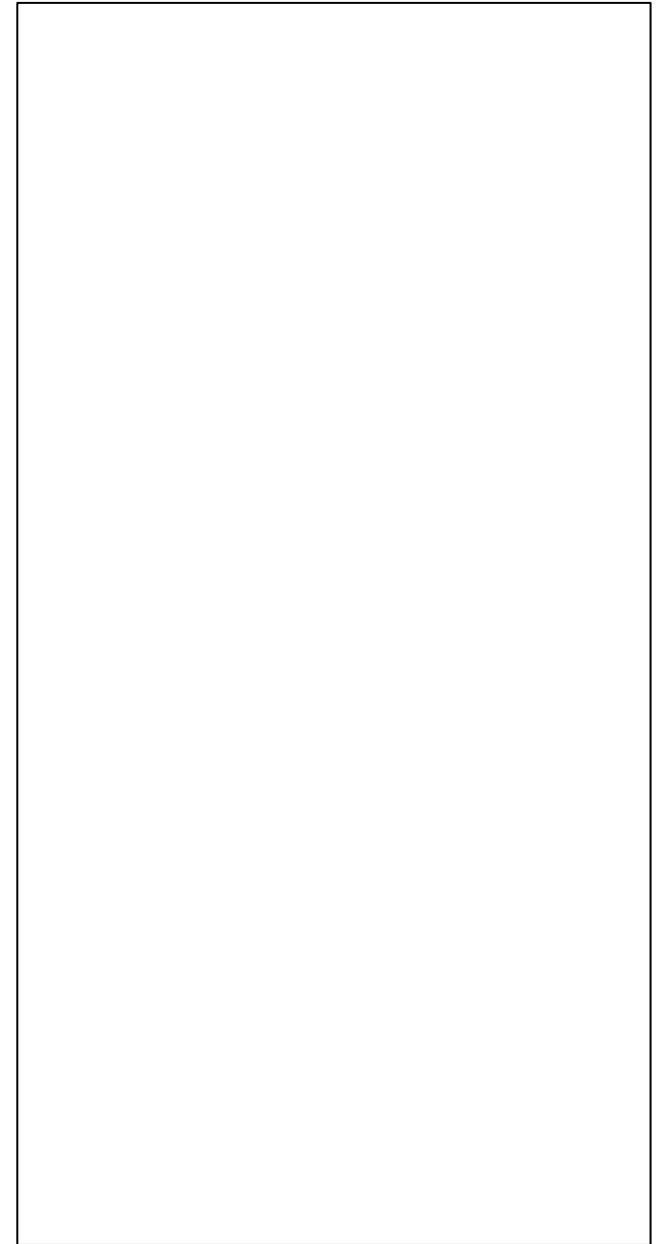
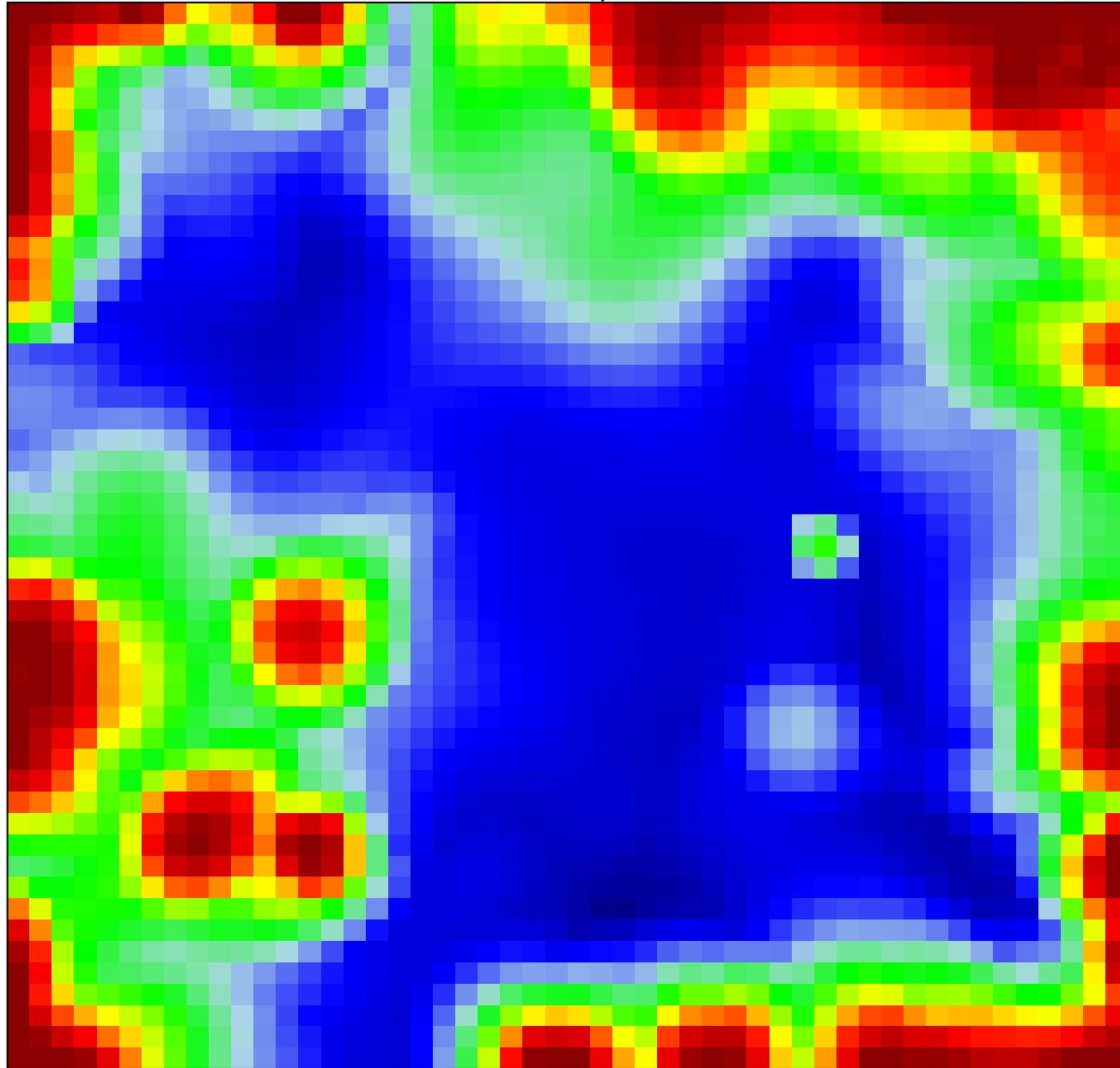


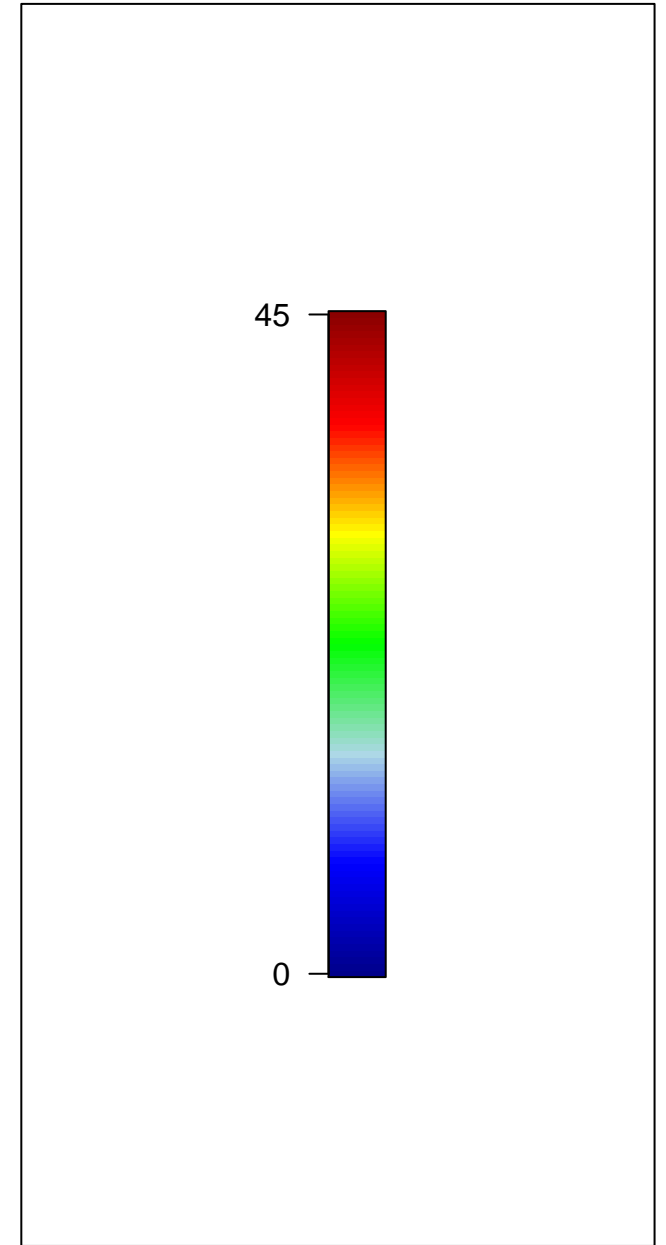
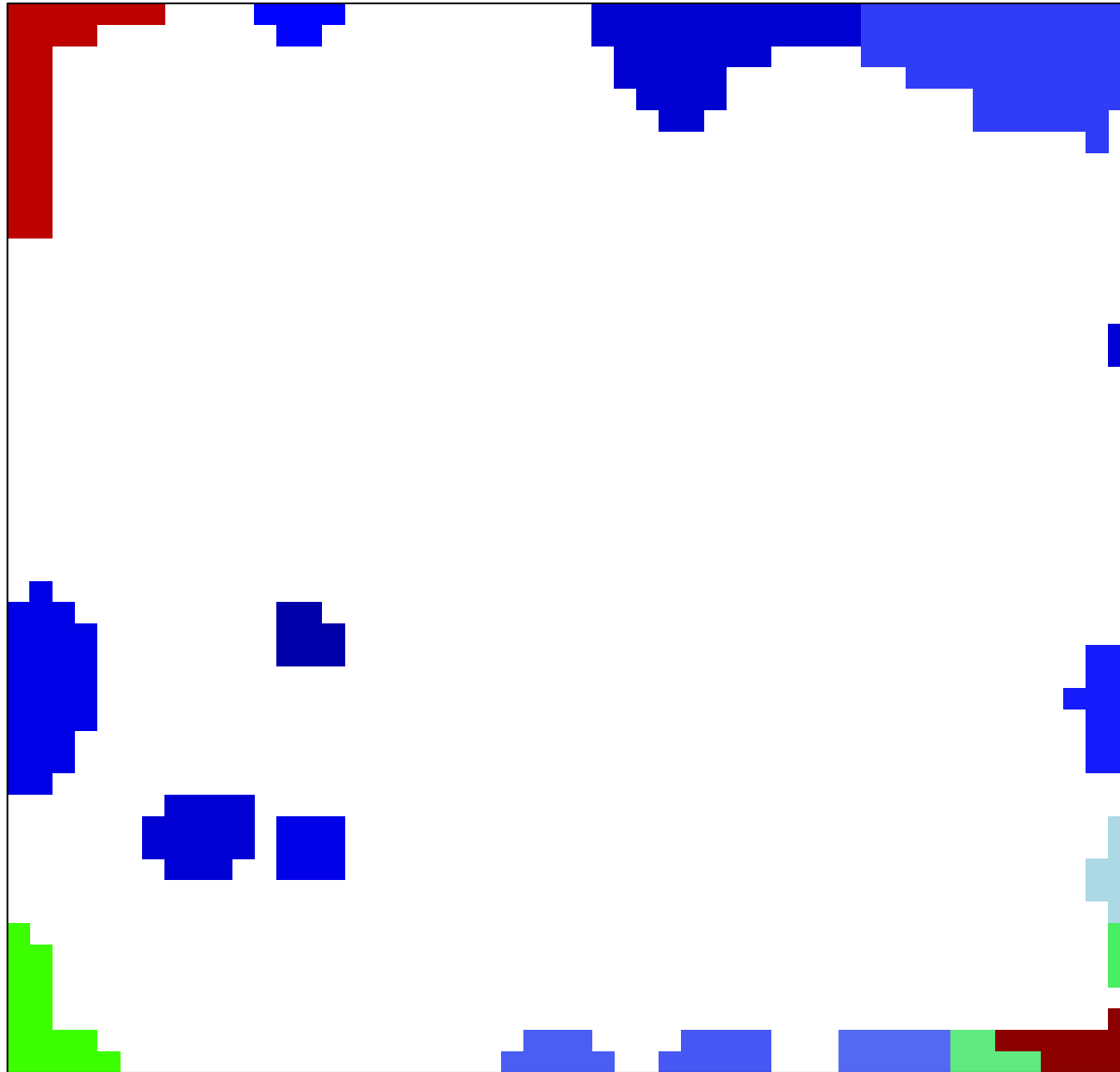
# Sample-Overexpression

landscape



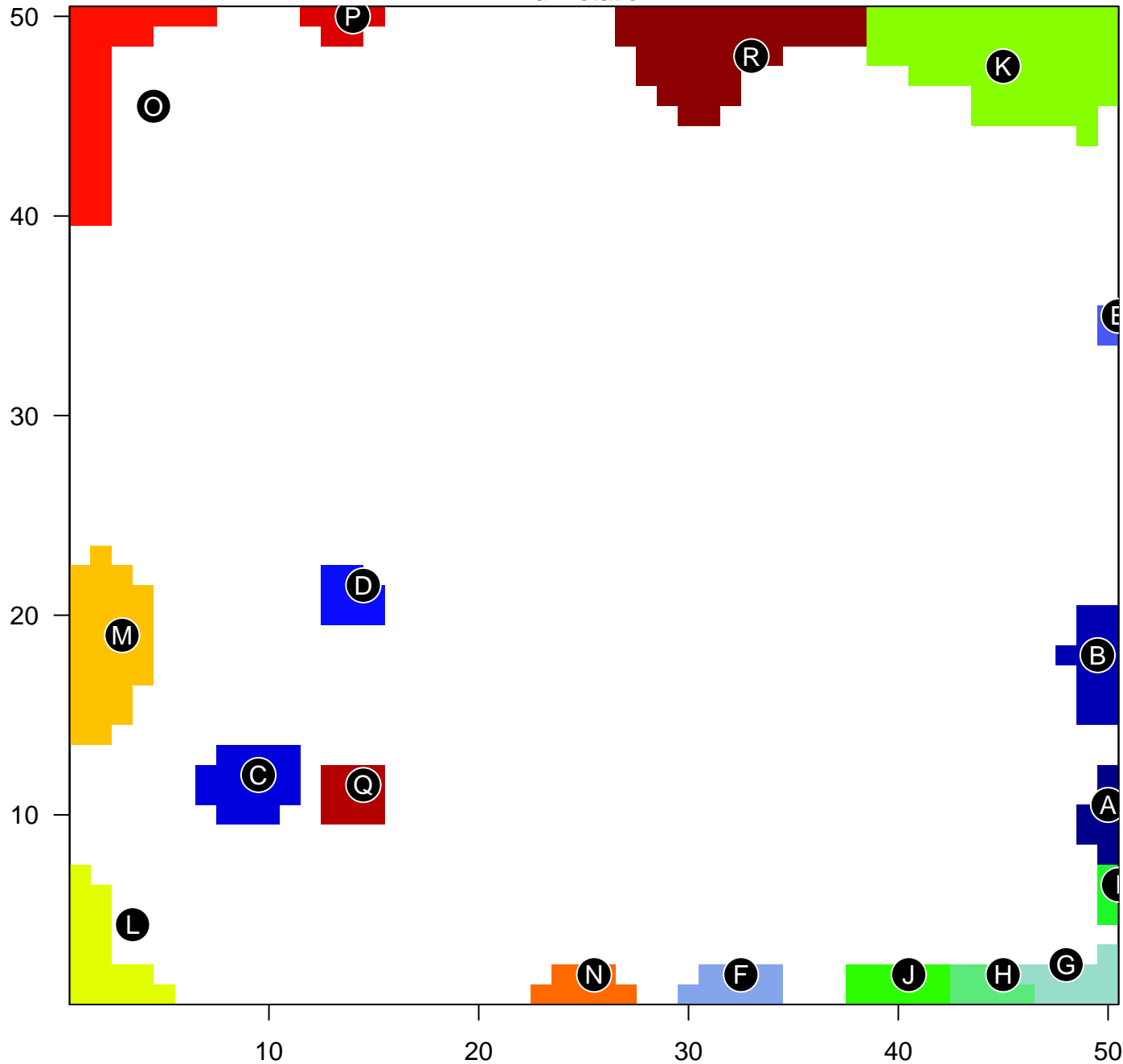
# Sample-Overexpression

beta-scores



# Sample-Overexpression

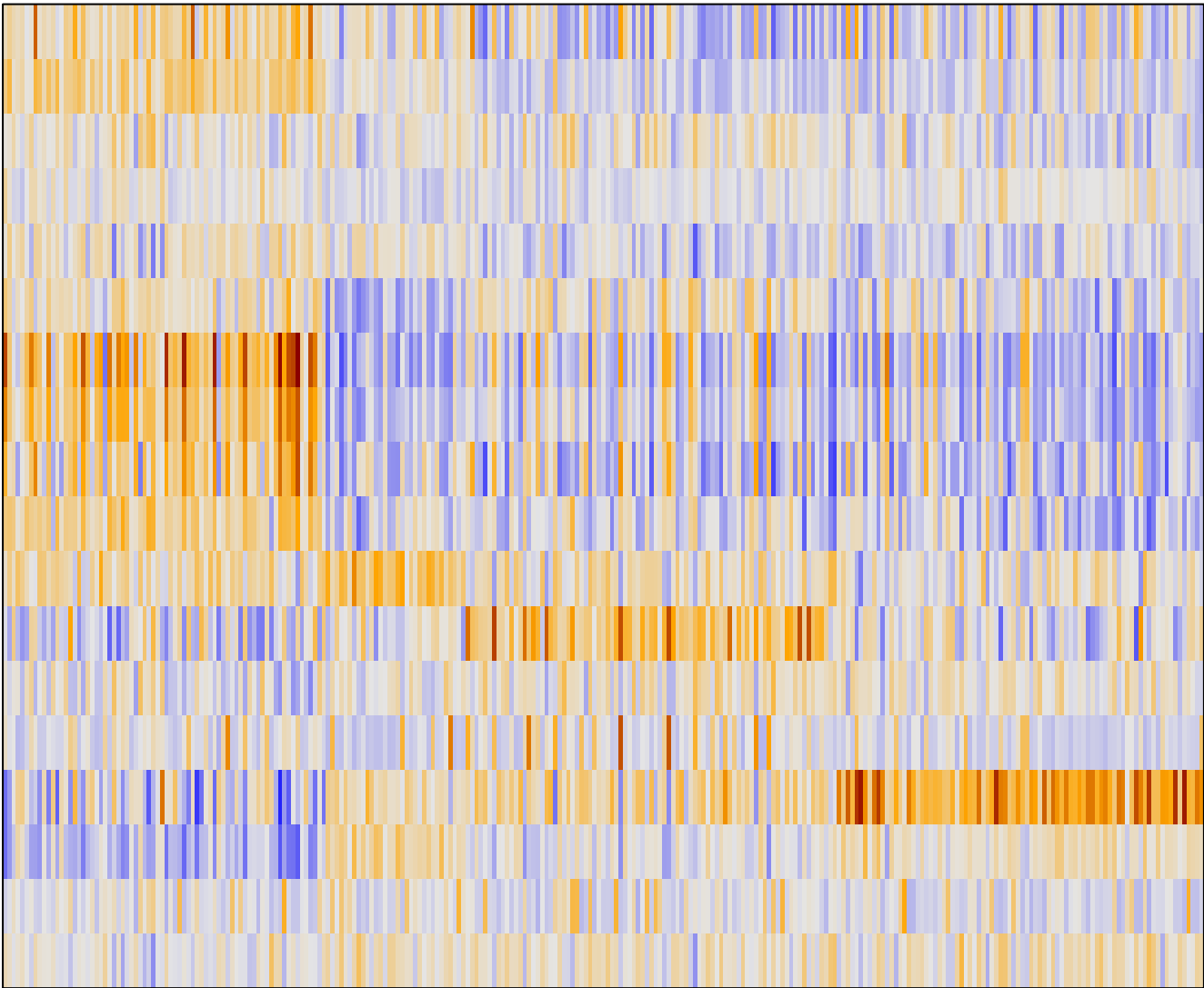
annotation



- A ■ RICKMAN\_HEAD\_AND\_NECK\_CANCER\_D  
GUDJ\_psoriasis down  
extracellular region
- B ■ hsa-miR-188-5p  
RICKMAN\_HEAD\_AND\_NECK\_CANCER\_A  
DNA binding
- C ■ nucleic acid binding  
Chr 19  
willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up
- D ■ mitochondrion  
mitochondrial inner membrane  
KIM\_MYC targets
- E ■ hsa-miR-301b  
hsa-miR-411  
hsa-miR-10b
- F ■ type I interferon signaling pathway  
defense response to virus  
cytokine-mediated signaling pathway
- G ■ WIRTH\_Immune system  
Lembcke\_Colonic Inflammation  
immune response
- H ■ SPANG\_CD40 6hrs DN  
immune response  
cytokine-mediated signaling pathway
- I ■ extracellular matrix  
extracellular space  
extracellular region
- J ■ Chr 19  
SPIRA\_SMOKERS\_LUNG\_CANCER\_DN  
MACIEJ\_MMML 8
- K ■ willscher\_GBM\_Verhaak-CL\_expression\_C\_up  
willscher\_GBM\_Verhaak-PNmut\_expression\_C\_down  
mitotic cell cycle
- L ■ extracellular matrix organization  
LENZ\_Stromal signature 1  
extracellular matrix
- M ■ mitochondrion  
structural constituent of ribosome  
translation
- N ■ WIRTH\_Muscle  
muscle filament sliding  
structural constituent of muscle
- O ■ WIRTH\_Mucosa  
GUDJ\_psoriasis up  
epidermis development
- P ■ integral to membrane



A  
B  
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D  
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R



RICKMAN\_HEAD\_AND\_NECK\_CANCER\_D  
GUDJ\_psoriasis\_down  
extracellular region

hsa-miR-188-5p  
RICKMAN\_HEAD\_AND\_NECK\_CANCER\_A  
DNA binding

nucleic acid binding  
Chr\_19  
Willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up

mitochondrion  
mitochondrial inner membrane  
KIM\_MYC targets

hsa-miR-301b  
hsa-miR-411  
hsa-miR-10b

type I interferon signaling pathway  
defense response to virus  
cytokine-mediated signaling pathway

WIRTH\_Immune system  
Lembcke\_Colonic Inflammation  
immune response

SPANG\_CD40 6hrs DN  
immune response  
cytokine-mediated signaling pathway

extracellular matrix  
extracellular space  
extracellular region

Chr\_19  
SBRA\_SMOKERS\_LUNG\_CANCER\_DN  
MACIEJ\_MMML 8

willscher\_GBM\_Verhaak-CL\_expression\_C\_up  
willscher\_GBM\_Verhaak-PNmut\_expression\_C\_down  
mitotic cell cycle

extracellular matrix organization  
LENZ\_Stromal signature 1  
extracellular matrix

mitochondrion  
structural constituent of ribosome  
translation

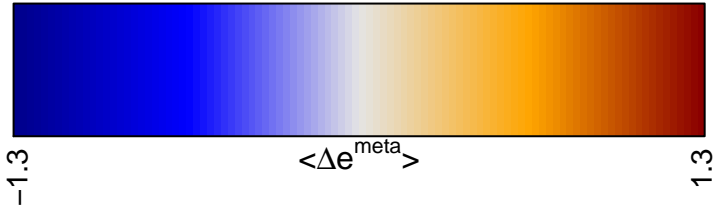
WIRTH\_Muscle  
muscle filament sliding  
structural constituent of muscle

WIRTH\_Mucosa  
GUDJ\_psoriasis\_up  
epidermis development

integral to membrane  
oxidation-reduction process  
modulation by virus of host morphology or physiology

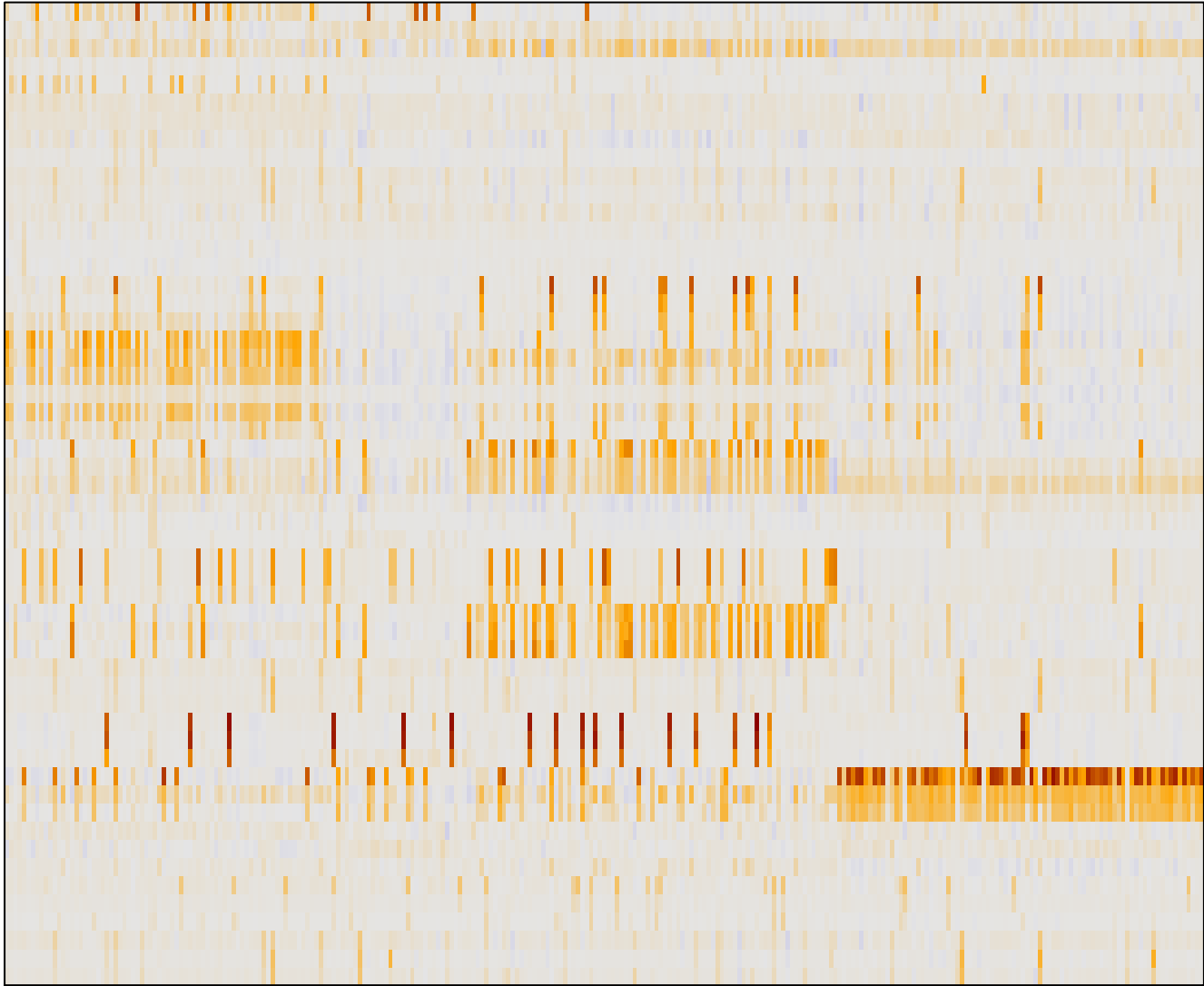
Chr\_X  
WIRTH\_Testis  
MATTIOLI\_MULTIPLE\_MYELOMA\_SUBGROUPS

mitochondrion  
respiratory electron transport chain  
translation

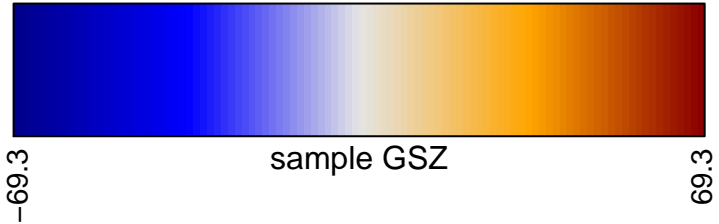




A  
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P  
Q  
R



RICKMAN\_HEAD\_AND\_NECK\_CANCER\_D  
GUDJ\_psoriasis down  
extracellular region  
hsa-miR-188-5p  
RICKMAN\_HEAD\_AND\_NECK\_CANCER\_A  
DNA binding  
nucleic acid binding  
Chr 19  
willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up  
mitochondrion  
mitochondrial inner membrane  
KIM\_MYC targets  
hsa-miR-301b  
hsa-miR-411  
hsa-miR-10b  
type I interferon signaling pathway  
defense response to virus  
cytokine-mediated signaling pathway  
WIRTH\_Immune system  
Lembcke\_Colonc Inflammation  
immune response  
SPANG\_CD40 6hrs DN  
immune response  
cytokine-mediated signaling pathway  
extracellular matrix  
extracellular space  
extracellular region  
Chr 19  
SPIRA\_SMOKERS\_LUNG\_CANCER\_DN  
MACIEJ\_MMML 8  
willscher\_GBM\_Verhaak-CL\_expression\_C\_up  
willscher\_GBM\_Verhaak-PNmut\_expression\_C\_down  
mitotic cell cycle  
extracellular matrix organization  
LENZ\_Stromal signature 1  
extracellular matrix  
mitochondrion  
structural constituent of ribosome  
translation  
WIRTH\_Muscle  
muscle filament sliding  
structural constituent of muscle  
WIRTH\_Mucosa  
GUDJ\_psoriasis up  
epidermis development  
integral to membrane  
oxidation-reduction process  
modulation by virus of host morphology or physiology  
Chr X  
WIRTH\_Testis  
MATTIOLI\_MULTIPLE\_MYELOMA\_SUBGROUPS  
mitochondrion  
respiratory electron transport chain  
translation



# Sample-Overexpression

## Spot Summary: A

# metagenes = 7  
# genes = 126

<r> metagenes = 0.96  
<r> genes = 0.32  
beta: r2= 15.03 / log p= -Inf

# samples with spot = 35 ( 12.7 % )  
Atypical : 10 ( 13.5 % )  
Classical : 6 ( 18.8 % )  
Mesenchymal : 8 ( 9.4 % )  
Basal : 11 ( 13.1 % )

## Spot Genelist

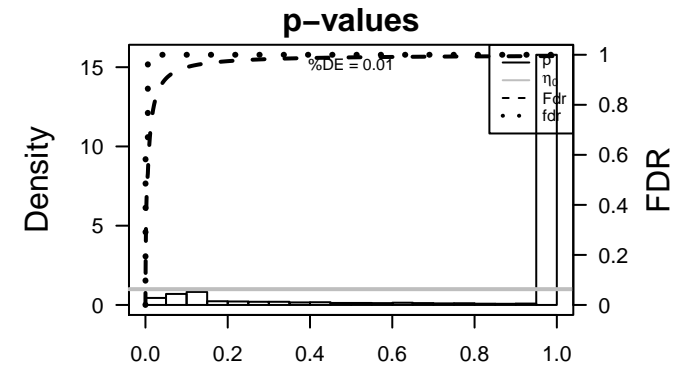
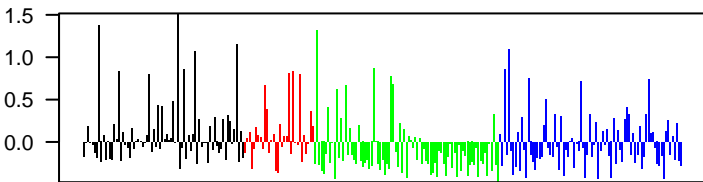
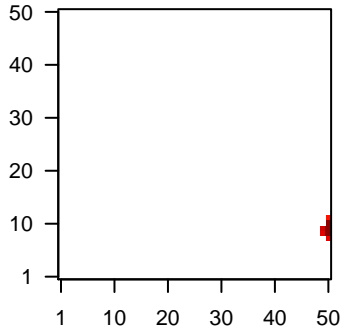
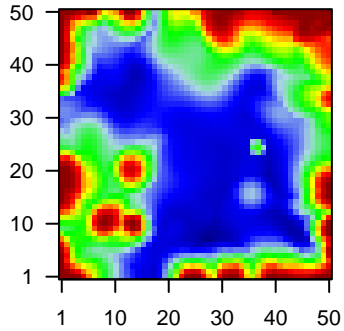
Rank	ID	max e	r	min e	Description
					Symbol
1	92747	5.31	-1.24	0.64	BPIFB1 BPI fold containing family B, member 1 [Source:HGNC Symb
2	11272	4.99	-1.08	0.67	PRR4 proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
3	7033	4.95	-1.78	0.72	TFF3 trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
4	92304	4.22	-1.04	0.65	SCGB3A secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
5	5304	4.06	-0.71	0.68	PIP prolactin-induced protein [Source:HGNC Symbol;Acc:8993]
6	124220	3.67	-0.81	0.69	ZG16B zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
7	51297	3.63	-0.56	0.51	BPIFA1 BPI fold containing family A, member 1 [Source:HGNC Symb
8	10232	3.46	-1.55	0.3	MSLN mesothelin [Source:HGNC Symbol;Acc:7371]
9	4477	3.44	-0.83	0.46	MSMB microseminoprotein, beta- [Source:HGNC Symbol;Acc:7372]
10	6422	3.44	-1.55	0.28	SFRP1 secreted frizzled-related protein 1 [Source:HGNC Symbol;Ac
11	10551	3.21	-1.32	0.59	AGR2 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
12	80341	3.15	-0.53	0.63	BPIFB2 BPI fold containing family B, member 2 [Source:HGNC Symb
13	352999	3.14	-0.47	0.51	C6orf58 chromosome 6 open reading frame 58 [Source:HGNC Symbc
14	7018	3.1	-1.18	0.68	TF transferrin [Source:HGNC Symbol;Acc:11740]
15	8842	3.09	-1	0.64	PROM1 prominin 1 [Source:HGNC Symbol;Acc:9454]
16	389816	3.08	-1.05	0.77	LRRC26 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
17	5284	3.04	-0.77	0.69	PIGR polymeric immunoglobulin receptor [Source:HGNC Symbol;A
18	124	3.01	-0.85	0.47	ADH1A alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
19	9071	2.87	-1.22	0.64	CLDN10 claudin 10 [Source:HGNC Symbol;Acc:2033]
20	7103	2.85	-0.83	0.75	TSPAN8 tetraspanin 8 [Source:HGNC Symbol;Acc:11855]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-20	11 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_D
2	9e-12	20 / 375	Disea GUDJ_psooriasis down
3	4e-09	30 / 1182	CC extracellular region
4	1e-08	22 / 683	CC extracellular space
5	1e-07	27 / 1146	TF HEBENSTREIT_low expression TF
6	4e-06	4 / 15	GSE/ POOLA_INVASIVE_BREAST_CANCER_DN
7	2e-05	3 / 7	GSE/ LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
8	2e-05	12 / 364	BP negative regulation of cell proliferation
9	1e-04	5 / 61	CC secretory granule
10	1e-04	3 / 13	GSE/ WONG_ENDOMETRIUM_CANCER_UP
11	2e-04	3 / 14	BP negative regulation of epithelial to mesenchymal transition
12	2e-04	3 / 14	MF selenium binding
13	2e-04	3 / 14	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
14	2e-04	3 / 16	GSE/ TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMA
15	2e-04	3 / 16	GSE/ TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
16	2e-04	3 / 16	GSE/ HWANG_PROSTATE_CANCER_MARKERS
17	2e-04	3 / 16	GSE/ CROMER_TUMORIGENESIS_DN
18	2e-04	3 / 16	TF Ti VAQUERIZAS_Salivary gland
19	5e-04	3 / 20	BP actin filament polymerization
20	8e-04	3 / 24	TF Ti VAQUERIZAS_Trachea
21	9e-04	7 / 201	CC apical plasma membrane
22	1e-03	5 / 100	BP regulation of cell shape
23	1e-03	2 / 7	GSE/ LOPEZ_MESOTELIOMA_SURVIVAL_WORST_VS_BEST_DN
24	1e-03	2 / 7	GSE/ LOPEZ_MESOTELIOMA_SURVIVAL_OVERALL_UP
25	1e-03	2 / 7	TF Ti VAQUERIZAS_Appendix
26	1e-03	3 / 28	BP branching morphogenesis of an epithelial tube
27	2e-03	2 / 8	GSE/ LEE_SP4_THYMOCYTE
28	2e-03	5 / 112	MF heparin binding
29	2e-03	3 / 32	BP metanephros development
30	2e-03	2 / 9	GSE/ REACTOME_ETHANOL_OXIDATION
31	3e-03	2 / 10	BP hormone biosynthetic process
32	3e-03	2 / 10	BP negative regulation of vascular permeability
33	3e-03	2 / 10	Glio willscher_GBM_LTSwt_proteomics-G_UP
34	3e-03	1 / 15	Canc LIU_PROSTATE_CANCER_DN
35	3e-03	2 / 10	GSE/ LUI_THYROID_CANCER_CLUSTER_5
36	3e-03	2 / 10	GSE/ YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
37	3e-03	3 / 37	CC actin filament
38	3e-03	3 / 37	TF Ti VAQUERIZAS_Prostate
39	3e-03	2 / 11	BP cellular response to stress
40	3e-03	2 / 11	BP dorsal/ventral axis specification

## Overview Map

## Spot



Rank	p-value	#in/all	Geneset
1	0.000	1/364	negative regulation of cell proliferation
2	0.004	3/14	negative regulation of epithelial to mesenchymal transition
3	0.005	1/10	actin filament polymerization
4	0.005	5/100	regulation of cell shape
5	0.006	1/28	branching morphogenesis of an epithelial tube
6	0.007	3/32	metanephros development
7	0.007	2/10	hormone biosynthetic process
8	0.008	2/10	negative regulation of vascular permeability
9	0.008	2/11	cellular response to stress
10	0.009	2/11	dorsal/ventral axis specification
11	0.009	2/12	urogenital system development
12	0.009	3/42	ureteric bud development
13	0.009	3/43	somitogenesis
14	0.009	3/44	neuron projection morphogenesis
15	0.009	3/45	negative regulation of epithelial cell proliferation
16	0.009	3/45	cellular protein localization
17	0.009	2/15	digestive tract morphogenesis
18	0.009	2/17	iron ion transport
19	0.009	2/19	positive regulation of protein serine/threonine kinase activity
20	0.009	2/19	positive regulation of smoothened signaling pathway

Rank	p-value	#in/all	Geneset
1	0.002	10/618	Chr Y
2	0.03	2/34	Chr 21
3	0.06	4/187	Chr 20
4	0.09	4/449	Chr 20
5	0.22	9/866	Chr 12
6	0.36	6/633	Chr 9
7	0.41	6/914	Chr 7
8	0.51	6/743	Chr 9
9	0.54	2/232	Chr 18
10	0.54	5/630	Chr X
11	0.58	10/33	Chr 2
12	0.59	4/534	Chr 8
13	0.64	2/280	Chr 13
14	0.65	2/74	Chr 6
15	0.72	6/918	Chr 6
16	0.75	6/957	Chr 17
17	0.77	3/519	Chr 14
18	0.78	1/1720	Chr 1
19	0.81	4/1720	Chr 16
20	0.85	3/602	Chr 10

Rank	p-value	#in/all	Geneset
1	2e-20	11/16	RICKMAN HEAD AND NECK CANCER_D
2	2e-05	4/15	HELA INVASIVE BREAST CANCER_DN
3	2e-05	4/15	LOPEZ_MESOTHELIOMA_SURVIVAL_TIME_DN
4	1e-04	3/13	WONG_ENDOMETRIUM_CANCER_UP
5	2e-04	3/14	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
6	2e-04	1/1	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_I
7	2e-04	3/16	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_I
8	2e-04	3/16	HWANG_PROSTATE_CANCER_MARKERS
9	2e-04	3/16	CRUMER_TUMORIGENESIS_DN
10	1e-03	2/16	LOPEZ_MESOHELIOMA_SURVIVAL_WORST_VS_BEST_DN
11	1e-03	2/7	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
12	2e-03	2/8	LEE_SP4_THYMOCYTE
13	2e-03	1/9	REACTION_ETHANOL_OXIDATION
14	3e-03	1/15	LIU_PROSTATE_CANCER_DN
15	3e-03	2/10	LJI_THYROID_CANCER_CLUSTER_5
16	3e-03	2/10	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
17	4e-03	2/10	BELICIO_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN
18	4e-03	2/13	WIKMAN_HIBBOSTOS_LUNG_CANCER_UP
19	4e-03	2/13	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
20	4e-03	2/13	HUANG_DASATINIB_RESISTANCE_DN

Rank	p-value	#in/all	Geneset
1	2e-03	5/112	heparin binding
2	4e-03	2/12	calcium-dependent cysteine-type endopeptidase activity
3	6e-03	7/297	actin binding
4	1e-02	2/21	glycosaminoglycan binding
5	1e-02	2/122	serine-type endopeptidase activity
6	2e-02	2/27	estrogen receptor binding
7	2e-02	3/75	RNA polymerase II distal enhancer sequence-specific DNA binding transcript
8	2e-02	3/77	actin filament binding
9	4e-02	2/41	transferase activity, transferring acyl groups other than aminoacyl groups
10	4e-02	2/43	scavenger receptor activity
11	5e-02	2/44	structural constituent of muscle
12	6e-02	2/46	GDP binding
13	6e-02	2/50	Rab GTPase binding
14	6e-02	3/115	lipid binding
15	6e-02	8/549	molecular function
16	7e-02	3/121	cytokine activity
17	7e-02	2/56	motor activity
18	7e-02	1/10	armadillo repeat domain binding

Rank	p-value	#in/all	Geneset
1	0.03	1/1	miR-20
2	0.05	1/6	miR-133a
3	0.18	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	0/4	let-7d
8	1.00	0/4	let-7e
9	1.00	0/13	miR-1
10	1.00	0/5	miR-101
11	1.00	0/4	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	0/6	miR-124a
16	1.00	0/6	miR-125a
17	1.00	0/9	miR-125b
18	1.00	0/3	miR-129
19	1.00	0/3	miR-128

Rank	p-value	#in/all	Geneset
1	0.09	1/13	BENTINK_e2f3.1
2	1.00	0/15	GUSTAFSON_Pi3K_UP
3	1.00	0/15	GUSTAFSON_Pi3K_DN
4	1.00	0/11	BENTINK_e2f3.2
5	1.00	0/14	BENTINK_myc.1
6	1.00	0/15	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	

Rank	p-value	#in/all	Geneset
1	0.000	2/15	LIU_PROSTATE_CANCER_DN
2	0.005	2/14	LIU_BREAST_CANCER
3	0.074	1/10	GENTLES_modul13
4	0.110	1/15	Lembcke_Normal_vs_Adenoma
5	0.388	5/30	Lembcke_Colonc_Inflammation
6	0.620	4/553	SPANG_BCL6-index
7	0.915	1/316	RHODES_CANCER_META_SIGNATURE
8	1.000	0/15	RHODES_UNDIFFERENTIATED_CANCER
9	1.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.000	0/14	LIU_COMMON_CANCER_GENES
12	1.000	0/14	LIU_PROSTATE_CANCER_UP
13	1.000	0/14	WANG_ER_UP
14	1.000	0/9	WANG_ER_DN
15	1.000	0/16	WOLF_FETAL_overlap_genes
16	1.000	0/12	BEN-PORATH_DN
17	1.000	0/15	BEN-PORATH_UP
18	1.000	0/15	GENTLES_modul1
19	1.000	0/15	GENTLES_modul2

Rank	p-value	#in/all	Geneset
1	6e-12	20/378	GUDJ_psooriasis_down
2	7e-03	2/17	BCHETNIA_EBM_up
3	2e-01	1/26	BCHETNIA_EBM_DN_up
4	6e-01	2/22	GUDJ_psooriasis_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	

Rank	p-value	#in/all	Geneset
1	0.08	2/62	WIRTH_Liver
2	0.08	1/13	WIRTH_Prim_lymphoid_organs
3	0.10	1/13	WIRTH_Sec_lymphoid_organs
4	0.20	5/400	WIRTH_Nervous_System
5	0.61	1/120	WIRTH_Testis
6	1.00	0/2	WIRTH_Pituitary_gland
7	1.00	0/26	WIRTH_Pancreas
8	1.00	0/417	WIRTH_Immune_system
9	1.00	0/10	WIRTH_B-cells
10	1.00	0/13	WIRTH_Tonsil
11	1.00	0/13	WIRTH_Thymus
12	1.00	0/12	WIRTH_Lymphocytes
13	1.00	0/6	WIRTH_Bone_marrow
14	1.00	0/14	WIRTH_Glioxys_pallidus
15	1.00	0/15	WIRTH_Telencephalon
16	1.00	0/13	WIRTH_Cortex_cerebri
17	1.00	0/16	WIRTH_Hippocampus
18	1.00	0/13	WIRTH_Thalamus
19	1.00	0/15	WIRTH_Cerebellum
20	1.00	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.02	3/10	ATAA-210
2	0.04	3/84	TCCA-518C
3	0.05	3/107	GCAA-502
4	0.06	2/53	GCG-296
5	0.07	3/85	AACG-451
6	0.10	4/225	TATT-374
7	0.10	4/232	CATT-142-5P
8	0.12	2/81	AACT-223
9	0.13	2/84	ATGC-217
10	0.14	3/187	AAGC-103--107
11	0.18	3/189	AAGC-520F
12	0.18	2/101	ACTA-196A--196B
13	0.20	2/106	GGCA-519E
14	0.20	2/106	AAGC-408-3P
15	0.22	1/32	CTCT-368
16	0.22	2/116	GACA-219
17	0.22	2/220	CATT-203
18	0.28	2/220	CACT-12--132

Rank	p-value	#in/all	Geneset
1	0.008	2/18	hsa-miR564
2	0.043	2/43	hsa-miR-412
3	0.054	3/111	hsa-miR-491-3p
4	0.083	3/113	hsa-miR-509-3p
5	0.096	1/13	hsa-miR-614
6	0.107	4/234	hsa-miR-26a
7	0.117	4/245	hsa-miR-26b
8	0.118	4/245	hsa-miR-26c
9	0.131	3/163	hsa-miR-1297
10	0.142	3/169	hsa-miR-183
11	0.163	1/10	hsa-miR-1225-5p
12	0.166	2/95	hsa-miR-1259
13	0.172	4/281	hsa-miR-570
14	0.174	2/98	hsa-miR-526a
15	0.180	2/100	hsa-miR-1616b
16	0.183	2/101	hsa-miR-410
17	0.195	1/28	hsa-miR-597
18	0.207	1/30	hsa-miR-1237
19	0.207	1/30	hsa-miR-626
20	0.211	2/111	hsa-miR-376c

Rank	p-value	#in/all	Geneset
1	1e-07	2/128	HEBESTREIT_low_expression_TF
2	1e+00	5/1033	KIM_MYC_targets
3	1e+00	1/1095	NOWICK_TF
4	1e+00	0/14	MYC_TFs
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_suppressor_genes_UP

Rank	p-value	#in/all	Geneset
1	1e-08	22/683	actin cytoskeleton
2	1e-04	5/61	extracellular space
3	9e-04	7/201	secretory granule
4	3e-03	3/207	apical plasma membrane
5	4e-03	4/81	actin filament
6	4e-03	3/40	ruffle
7	4e-03	3/40	extrinsic to membrane
8	4e-03	3/42	apical junction complex
9	6e-03	3/45	stress fiber
10	6e-03	4/92	tight junction
11	7e-03	24/1837	membrane
12	7e-03	7/330	cell surface
13	1e-02	16/1142	intracellular cytoskeleton
14	1e-02	7/333	cytoskeleton
15	3e-02	3/88	melanosome
16	4e-02	2/3	adocyte vesicle
17	4e-02	2/42	myosin complex
18	5e-02	4/183	proteinaceous extracellular matrix
19	5e-02	4/184	actin cytoskeleton
20	5e-02	3/116	cell cortex

Rank	p-value	#in/all	Geneset
1	0.003	2/10	willscher_GBM_LTSwt_proteomics-G_UP
2	0.004	2/12	astrocytes_glio
3	0.006	3/33	Christensen_hypermethylated_in_primary_glioblastoma
4	0.024	2/11	KIM_prognostic_signature_LTS_vs_STS
5	0.028	3/85	laffaire_hypermeth_LGG_vs_control
6	0.053	2/48	Noushmehr_Pron_GCIMP_hypermeth_DN
7	0.054	3/265	willscher_GBM_Verhaak_GL_expression_B_up
8	0.054	3/265	willscher_GBM_Verhaak-MES_expression_B_up
9	0.054	5/265	willscher_GBM_Verhaak-PNwt_expression_B_down
10	0.054	5/265	willscher_GBM_Verhaak-PNmwt_expression_B_down
11	0.082	1/11	KIM_amplified_and_overexpressed_in_LTS
12	0.087	2/64	Christensen_hypermethylated_in_grade2_astrocytoma
13	0.089	1/12	VERHAAK_PN_Brain
14	0.088	1/17	willscher_GBM_LTSwt_proteomics-C_UP
15	0.123	1/17	Danson_chemok

# Sample-Overexpression

## Spot Summary: B

# metagenes = 13  
# genes = 198

<r> metagenes = 0.97  
<r> genes = 0.34  
beta: r2= 8.48 / log p= -Inf

# samples with spot = 38 ( 13.8 % )  
Atypical : 36 ( 48.6 % )  
Mesenchymal : 1 ( 1.2 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

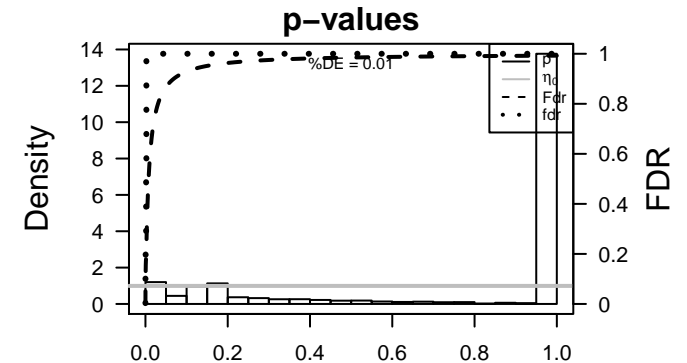
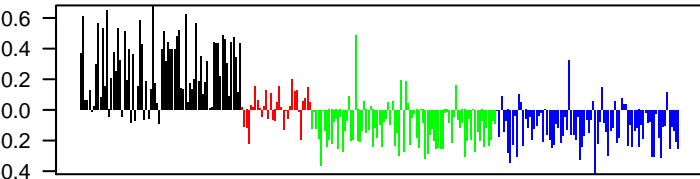
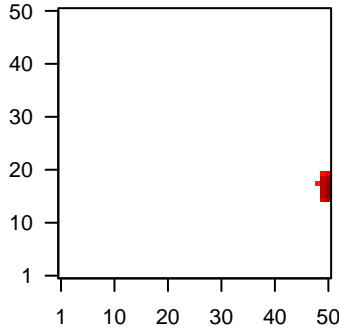
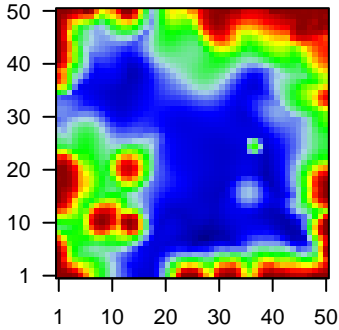
Rank	ID	max e	r	min e	Description
					Symbol
1	54959	2.94	-0.58	0.36	ODAM odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:21187]
2	4602	2.8	-1.04	0.76	MYB v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:21187]
3	728715	2.6	-1.25	0.5	RP11-726G1.1
4	83988	2.43	-1.29	0.53	NCALD neurocalcin delta [Source:HGNC Symbol;Acc:7655]
5	26002	2.42	-1.28	0.41	MOXD1 monooxygenase, DBH-like 1 [Source:HGNC Symbol;Acc:21187]
6	1298	2.41	-1.14	0.55	COL9A2 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
7	6263	2.31	-0.72	0.41	RYR3 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
8	10439	2.3	-1.77	0.44	OLFM1 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
9	399948	2.29	-0.65	0.68	COLCA1 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:31696]
10	2248	2.21	-0.33	0.4	FGF3 fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
11	6542	2.15	-1.11	0.53	SLC7A2 solute carrier family 7 (cationic amino acid transporter, y+ sys
12	21	2.13	-0.7	0.74	ABCA3 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
13	9603	2.1	-1.75	0.49	NFE2L3 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:2045]
14	1365	2.05	-0.55	0.63	CLDN3 claudin 3 [Source:HGNC Symbol;Acc:2045]
15	494470	2.04	-1.37	0.6	RNF165 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
16	1959	2.02	-1.28	0.36	EGR2 early growth response 2 [Source:HGNC Symbol;Acc:3239]
17	909	1.99	-1.12	0.34	CD1A CD1a molecule [Source:HGNC Symbol;Acc:1634]
18	3670	1.98	-0.84	0.35	ISL1 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
19	9915	1.9	-0.54	0.7	ARNT2 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
20	63917	1.86	-1.59	0.42	GALNT1UDP-N-acetyl-alpha-D-galactosamine;polypeptide N-acetyl

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-07	9 / 81	miRN hsa-miR-188-5p
2	9e-07	5 / 16	GSE# RICKMAN_HEAD_AND_NECK_CANCER_A
3	2e-05	41 / 1749	MF DNA binding
4	2e-05	4 / 15	GSE# GOLUB_ALL_VS_AML_UP
5	7e-05	10 / 182	miRN TTTT-373
6	8e-05	4 / 20	MF RNA polymerase II transcription coactivator activity
7	1e-04	10 / 189	miRN CTTT-527
8	1e-04	22 / 755	Lymp SPANG_BCR_UP
9	1e-04	13 / 318	MF chromatin binding
10	2e-04	11 / 247	miRN GTGC-96
11	3e-04	35 / 1581	BP regulation of transcription, DNA-dependent
12	3e-04	5 / 48	BP cilium morphogenesis
13	3e-04	10 / 215	miRN hsa-miR-199a-3p
14	3e-04	9 / 179	miRN hsa-miR-34b
15	3e-04	15 / 449	miRN hsa-miR-130b
16	3e-04	6 / 78	BP positive regulation of angiogenesis
17	3e-04	78 / 4640	CC nucleus
18	4e-04	8 / 146	miRN hsa-miR-494
19	4e-04	11 / 267	miRN CACT-128A--128B
20	4e-04	15 / 456	miRN hsa-miR-130a
21	4e-04	5 / 53	miRN GCAA-502
22	4e-04	4 / 30	BP response to steroid hormone
23	4e-04	9 / 187	miRN hsa-miR-520d-5p
24	4e-04	12 / 316	miRN hsa-miR-302a
25	4e-04	3 / 13	Lymp BENTINK_mBL UP
26	5e-04	14 / 415	miRN TTTG-19A--19B
27	5e-04	9 / 193	miRN hsa-miR-330-3p
28	7e-04	7 / 122	miRN hsa-miR-380
29	7e-04	3 / 15	GSE# DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMES_DN
30	7e-04	3 / 15	GSE# MASSARWEH_RESPONSE_TO ESTRADIOL
31	7e-04	4 / 34	BP thymus development
32	8e-04	10 / 246	miRN TGCT-330
33	8e-04	3 / 16	GSE# BILBAN_B CLL_LPL_DN
34	8e-04	3 / 16	GSE# RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
35	9e-04	16 / 545	miRN hsa-miR-93
36	9e-04	21 / 823	MF sequence-specific DNA binding transcription factor activity
37	1e-03	5 / 64	miRN hsa-miR-324-5p
38	1e-03	11 / 301	miRN hsa-miR-18b
39	1e-03	33 / 1574	BP transcription, DNA-templated
40	1e-03	8 / 171	miRN CTAT-153

## Overview Map

## Spot





Rank	p-value	#in/all	Geneset
3e-04	5/48	1581	transcription, DNA-dependent
3e-04	6/78		cilium morphogenesis
4e-04	4/30		positive regulation of angiogenesis
7e-04	1/34		response to steroid hormone
1e-03	33/1574		thymus development
1e-03	18/676		transcription, DNA-templated
2e-03	5/12		positive regulation of transcription from RNA polymerase II promoter
2e-03	4/42		B cell differentiation
3e-03	6/104		regulation of gene expression
2e-03	3/22		histone H4 acetylation
3e-03	4/48		negative regulation of neuron differentiation
5e-03	2/10		extrinsic apoptotic signaling pathway in absence of ligand
6e-03	2/10		positive regulation of histone H3-K4 methylation
9e-03	2/12		histone H2A acetylation
1e-02	2/13		cellular response to lithium ion
1e-02	2/13		developmental pigmentation
1e-02	2/13		histone H4-K16 acetylation
1e-02	2/13		mRNA catabolic process
1e-02	2/13		N-acetylglucosamine metabolic process
1e-02	2/13		natural killer cell differentiation

Rank	p-value	#in/all	Geneset
0.01	41/602		Chromosome 10
0.05	14/714		Chr 6
0.06	11/534		Chr 3
0.10	15/663		Chr 12
0.18	12/743		Chr 7
0.25	15/280		Chr 13
0.33	13/918		Chr 17
0.33	10/699		Chr 5
0.47	13/1033		Chr 2
0.49	8/633		Chr 9
0.54	21/1720		Chr 1
0.54	11/914		Chr 3
0.66	2/187		Chr 21
0.75	6/619		Chr 4
0.77	3/62		Chr 18
0.84	3/386		Chr 22
0.86	4/504		Chr 15
0.87	3/419		Chr 14
0.91	3/449		Chr 20
0.93	5/717		Chr 16

Rank	p-value	#in/all	Geneset
9e-07	5/16		RICKMAN HEAD AND NECK_CANCER_A
2e-04	4/15		OVARY VS ANL UP
7e-04	4/15		DAVICIONI_PAX_FOXP0_SIGNATURE_IN_ARMS_DN
7e-04	3/15		MASSARWEH_RESPONSE_TO_ESTRADIOL
9e-04	3/16		BILBAN_B_CELL_LPL_DN
9e-04	2/7		RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
3e-03	6/27		LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
4e-03	2/28		BERTUCCIO_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
4e-03	2/28		HOEGERKORP_CD44_TARGETS_TEMPORAL_UP
5e-03	2/9		GOLD_ESR1_TARGETS_DN
5e-03	2/9		REACTIONOME_ETHANOL_OXIDATION
6e-03	2/10		GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYEEL
6e-03	2/10		LIFERANTIC_CANCER
6e-03	2/10		BASSO_CD40_SIGNALING_DN
6e-03	2/10		LOPEZ_MESOTHELIOMA_SURVIVAL_UP
9e-03	2/12		KIM_WT1_TARGETS_12HR_UP
9e-03	2/12		PROVENZANI_METASTASIS_UP
9e-03	2/12		BLALOCK_ALZHEIMERS_DISEASE_UP
9e-03	2/12		WANG_SMARCE1_TARGETS_DN
1e-02	2/13		CHENG_IMPRINTED_BY_ESTRADIOL

Rank	p-value	#in/all	Geneset
8e-05	4/20	749	RNA polymerase II transcription coactivator activity
1e-04	13/318		chromatin binding
9e-04	21/823		sequence-specific DNA binding transcription factor activity
3e-04	3/252		transcription factor binding
7e-03	2/11		enhancer sequence-specific DNA binding
7e-03	2/11		poly(A)-specific ribonuclease activity
1e-02	2/15		acetylglucosaminyltransferase activity
2e-02	2/15		histone acetyl-lysine binding
2e-02	7/216		transcription coactivator activity
2e-02	19/940		nucleic acid binding
2e-02	2/19		hydrolase activity, acting on acid anhydrides
2e-02	2/19		hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydride
3e-02	2/21		bHLH transcription factor binding
3e-02	2/24		mRNA 3'-UTR binding
3e-02	3/62		protein phosphatase binding
4e-02	3/62		single-stranded DNA binding
4e-02	11/504		nucleotide binding
4e-02	30/1820		metal ion binding
4e-02	2/31		RNA polymerase II activating transcription factor binding

Rank	p-value	#in/all	Geneset
0.01	1/2	34	miR-34
0.02	1/2	153	miR-153
0.04	1/3	148a	miR-148a
0.05	1/4	7c	let-7c
0.05	1/4	204	miR-204
0.05	1/4	34b	miR-34b
0.05	1/4	34c	miR-34c
0.06	1/5	101	miR-101
0.06	1/5	15a	miR-15a
0.06	1/5	320	miR-320
0.07	1/6	7	let-7
0.07	1/6	15b	miR-15b
0.07	1/6	221	miR-221
0.09	1/8	222	miR-222
0.12	1/11	3	let-3
0.12	1/11	16	miR-16
0.15	1/13	21	miR-21
0.27	1/26	7b	let-7b
1.00	0/4	7g	let-7g

Rank	p-value	#in/all	Geneset
0.1	1/13		BENTINK_823.2
0.2	1/14		BENTINK_src.10
0.2	1/14		BENTINK_mvc.1
0.2	1/15		GUSTAFSON_Pi3K_DN
1.0	0/13		GUSTAFSON_Pi3K_UP
1.0	0/12		BENTINK_e203.1
1.0	0/12		BENTINK_ras.1
1.0	0/11		BENTINK_ras.4
1.0	0/15		BENTINK_ras.6
1.0	0/14		BENTINK_src.2
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		

Rank	p-value	#in/all	Geneset
0.001	2/10		LITHE PROSTATE_CANCER
0.010	2/13		GENTLES_modul12
0.081	1/7		ZHANG_MGUS UP
0.103	1/9		WANG_ER_UP
0.103	1/14		LIU_COMMON_CANCER_GENES
0.165	1/15		RHODES_CANCER_META_SIGNATURE
0.165	1/15		SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
0.165	1/15		LIT PROSTATE_CANCER_DN
0.165	1/15		GENTLES_modul11
0.176	1/16		SPANG_BCL6-index2
0.329	5/316		KUIPER_MM_poor_survival
0.440	1/48		SHALICHNESSY_MM_high_risk
0.560	1/68		SPANG_LPS-index2
0.894	1/185		Lembcke_Normal vs Adenoma
0.955	3/530		Lembcke_Colonie_Inflammation
0.964	3/553		RHODES_LINDIFFERENTIATED_CANCER
1.000	0/15		SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
1.000	0/14		LIU_LIVER_CANCER
1.000	0/14		LIU_PROSTATE_CANCER_UP
1.000	0/14		WANG_ER_UP

Rank	p-value	#in/all	Geneset
0.02	10/376		GUDDI_psoarosis_down
0.99	2/572		GUDDI_psoarosis_up
1.00	0/17		ECHETNIA_EBM_up
1.00	0/26		ECHETNIA_EBM_down
1.00	0/26		ECHETNIA_EBM-DM_up
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
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NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		
NA	0/0		

Rank	p-value	#in/all	Geneset
0.1	1/12		WIRTH_Lymphocytes
0.1	1/12		WIRTH_Thyroid_gland
0.2	1/15		WIRTH_Cerebellum
0.2	3/120		WIRTH_Testis
0.3	1/26		WIRTH_Pancreas
0.3	6/140		WIRTH_Nervous_System
0.5	1/50		WIRTH_Homeostasis
0.5	1/62		WIRTH_Liver
0.6	5/417		WIRTH_Immune_system
0.6	1/5		WIRTH_Pituitary_gland
1.0	0/13		WIRTH_Sec_lymphoid_organs
1.0	0/12		WIRTH_Prim_lymphoid_organs
1.0	0/13		WIRTH_B-cells
1.0	0/13		WIRTH_Tonsils
1.0	0/13		WIRTH_Thymus
1.0	0/6		WIRTH_Bone_marrow
1.0	0/14		WIRTH_Globus_pallidus
1.0	0/15		WIRTH_Telencephalon
1.0	0/13		WIRTH_Cortex_cerebri
1.0	0/16		WIRTH_Hippocampus

Rank	p-value	#in/all	Geneset
9e-05	9/82		CTTT-527
1e-04	10/189		GTGC-96
2e-04	11/247		CACT-128A---128B
4e-04	11/267		ACA-502
4e-04	5/63		TTTG-19A---19B
5e-04	14/415		TGCT-330
8e-04	10/246		CTAT-153
1e-03	8/173		CTAT-153
1e-03	6/139		AGCT-28
1e-03	5/69		AGGG-18A
1e-03	6/102		AGC-123
1e-03	7/129		TTTG-130A---301---130B
2e-03	8/190		GTTC-495
3e-03	9/243		ATGT-493
3e-03	9/243		AGCA-33---302A---302B---302C---302D---372---373---520E---520A---526I
4e-03	13/457		TGCC-124A
4e-03	11/358		TGCA-519C---519B---519A
4e-03	6/267		GACT-242---132
4e-03	6/267		

Rank	p-value	#in/all	Geneset
5e-07	9/181		hsa-miR-18b-5p
3e-04	10/215		hsa-miR-199a-3p
3e-04	9/179		hsa-miR-34b
3e-04	15/449		hsa-miR-130b
4e-04	8/146		hsa-miR-494
4e-04	15/456		hsa-miR-130a
4e-04	9/147		hsa-miR-302a
4e-04	12/316		hsa-miR-302a
5e-04	9/193		hsa-miR-330-3p
7e-04	7/122		hsa-miR-380
8e-04	16/545		hsa-miR-324
1e-03	5/64		hsa-miR-324-5p
1e-03	11/301		hsa-miR-18b
1e-03	11/303		hsa-miR-302b
1e-03	8/140		hsa-miR-15b
1e-03	8/177		hsa-miR-1
1e-03	14/463		hsa-miR-301a
1e-03	10/267		hsa-miR-177
1e-03	8/180		hsa-miR-199b-3p
1e-03	7/140		hsa-miR-138

Rank	p-value	#in/all	Geneset
0.02	1/2		MYC_Cell_cycle_DOWN
0.06	1/5		MYC_Chromatin_modification_UP
0.06	1/5		MYC_TFS
0.10	1/9		MYC_Targets_DOWN
0.17	2/63		MYC_Targets_UP
0.21	1/20		MYC_Metabolism_UP
0.40	15/1146		HEBENSTREIT_low_expression_TF
0.67	12/1095		HEBENSTREIT_high_expression_TF
0.96	9/1233		KIM_MYC_targets
1.00	0/14		NOWICK_TF
1.00	0/4		MYC_Apoptosis_UP
1.00	0/8		MYC_Cell_cycle_UP
1.00	0/4		MYC_Cell_growth_and_proliferation_UP
1.00	0/7		MYC_DNA_repair_UP
1.00	0/3		MYC_DNA_replication_UP
1.00	0/7		MYC_ECM_cell_adhesion_DOWN
1.00	0/8		MYC_Protein_synthesis_degradation_UP
1.00	0/8		MYC_RNA_processing_binding_UP
1.00	0/2		MYC_Signal_transduction_UP
1.00	0/3		MYC_Tumor_suppressor_genes_UP

Rank	p-value	#in/all	Geneset
2e-03	3/22		nucleus
6e-03	2/10		nuclear heterochromatin
7e-03	2/11		nsBAF_complex
9e-03	2/12		PC1_complex
9e-03	2/12		SWI/SNF_complex
1e-03	2/12		TCTIN-3BD_complex
1e-03	2/18		NuA4_histone_acetyltransferase_complex
2e-02	2/18		histone acetyltransferase complex
2e-02	3/50		microtubule basal body
2e-02	3/51		cytoplasmic mRNA processing body
3e-02	2/18		photoreceptor connecting cilium
4e-02	2/25		PCG_protein_complex
4e-02	2/25		primary cilium
5e-02	2/30		photoreceptor outer segment
5e-02	2/30		reticular chromatin
1e-01	3/93		spliceosomal complex
1e-01	16/949		nucleoplasm
1e-01	7/335		centrosome
1e-01	2/47		nucleosome

Rank	p-value	#in/all	Geneset
0.04	3/12		Su(Hw)er_Proteins_up_in_STS
0.04	2/27		WIRTH_PN_subtype
0.04	8/328		Up
0.07	4/332		Up
0.08	1/7		Christensen_hypermethylated_in_grade3_oligoastrocytoma
0.09	4/142		Christensen_hypermethylated_in_grade2_oligodendroglioma
0.11	1/10		wilscher_GBM_LTSmut_proteomics-A_UP
0.12	2/49		mature astrocytes
0.13	1/12		Phillips_PN_up_vs_MES & Prolif
0.13	1/12		wilscher_GBM_LTSmut_proteomics-B_UP
0.13	1/12		wilscher_GBM_STSwt_proteomics-B_DOWN
0.15	3/110		Christensen_hypermethylated_in_grade3_astrocytoma
0.15	2/57		developing astrocytes
0.16	3/112		Christensen_hypermethylated_in_grade2_oligoastrocytoma
0.18	1/14		VERHAAK_CL_subtype
0.17	1/15		VERHAAK_PN_subtype
0.17	7/379		Down_a
0.17	6/313		wilscher_GBM_Verhaak-MES_expression_D_down
0.17	6/313		wilscher_GBM_Verhaak-P

# Sample-Overexpression

## Spot Summary: C

# metagenes = 17  
# genes = 185

<r> metagenes = 0.96  
<r> genes = 0.32  
beta: r2= 4.79 / log p= -Inf

# samples with spot = 14 ( 5.1 % )  
Atypical : 8 ( 10.8 % )  
Mesenchymal : 5 ( 5.9 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	3303	1.9	-2.49	0.33	HSPA1A heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52212]
2	23338	1.78	-1.12	0.43	JADE2 jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
3	2026	1.72	-1.27	0.54	ENO2 enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33022]
4	51477	1.71	-0.85	0.61	ISYNA1 inositol-3-phosphate synthase 1 [Source:HGNC Symbol;Acc:22984]
5	93109	1.63	-0.99	0.41	TMEM44transmembrane protein 44 [Source:HGNC Symbol;Acc:25120]
6	80728	1.6	-1.29	0.64	ARHGAP8 GTPase activating protein 39 [Source:HGNC Symbol;Acc:22984]
7	729021	1.52	-0.97	0.41	
8	401357	1.51	-0.94	0.45	
9	55653	1.45	-0.87	0.53	BCAS4 breast carcinoma amplified sequence 4 [Source:HGNC Symbol;Acc:22984]
10	1951	1.4	-1.06	0.45	CELSR3 cadherin, EGF LAG seven-pass G-type receptor 3 [Source:HGNC Symbol;Acc:22984]
11	100170841	1.36	-0.75	0.58	C17orf96chromosome 17 open reading frame 96 [Source:HGNC Symbol;Acc:22984]
12	5871	1.35	-1.14	0.46	MAP4K2 mitogen-activated protein kinase kinase kinase 2 [Source:HGNC Symbol;Acc:22984]
13	9862	1.33	-0.73	0.48	MED24 mediator complex subunit 24 [Source:HGNC Symbol;Acc:22984]
14	27161	1.33	-1.09	0.68	AGO2 argonaute RISC catalytic component 2 [Source:HGNC Symbol;Acc:22984]
15	128710	1.31	-1.16	0.42	SLX4IP SLX4 interacting protein [Source:HGNC Symbol;Acc:16225]
16	22913	1.26	-0.67	0.57	RALY RALY heterogeneous nuclear ribonucleoprotein [Source:HGNC Symbol;Acc:22984]
17	64710	1.25	-0.99	0.67	NUCKS1 nuclear casein kinase and cyclin-dependent kinase substrate [Source:HGNC Symbol;Acc:22984]
18	6526	1.24	-0.84	0.57	SLC5A3 sodium/myo-inositol cotransporter [Source:RefSeq peptide;Acc:22984]
19	10948	1.24	-0.47	0.61	STARD3 STAR-related lipid transfer (START) domain containing 3 [Source:HGNC Symbol;Acc:22984]
20	149473	1.22	-0.99	0.47	CCDC24 coiled-coil domain containing 24 [Source:HGNC Symbol;Acc:22984]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-08	31 / 940	MF nucleic acid binding
2	3e-07	33 / 1135	Chr Chr 19
3	1e-04	5 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
4	1e-04	20 / 717	Chr Chr 16
5	6e-04	6 / 93	miRN hsa-miR-125a-5p
6	9e-04	22 / 949	CC nucleoplasm
7	9e-04	17 / 649	BP gene expression
8	1e-03	4 / 41	miRN hsa-miR-532-3p
9	1e-03	2 / 5	GSE/ DASU_IL6_SIGNALING_UP
10	2e-03	70 / 4640	CC nucleus
11	2e-03	3 / 23	Chr Chr HSCR6_MHC_DBB
12	2e-03	3 / 24	BP tissue development
13	2e-03	7 / 163	BP mRNA splicing, via spliceosome
14	3e-03	3 / 25	BP RNA splicing, via transesterification reactions
15	3e-03	3 / 26	BP histone acetylation
16	3e-03	2 / 8	GSE/ BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
17	4e-03	3 / 28	MF ribosome binding
18	4e-03	5 / 96	BP chromatin modification
19	5e-03	12 / 449	Chr Chr 20
20	5e-03	2 / 10	BP positive regulation of macroautophagy
21	5e-03	2 / 10	GSE/ BORCZUK_MALIGNANT_MESOTHELIOMA_DN
22	5e-03	2 / 10	GSE/ XU_GH1_AUTOCRINE_TARGETS_DN
23	7e-03	10 / 361	MF binding
24	8e-03	2 / 12	BP long term synaptic depression
25	8e-03	2 / 12	BP mRNA cleavage
26	8e-03	2 / 12	MMM MACIEJ_MMML 24
27	8e-03	2 / 12	GSE/ TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
28	8e-03	2 / 12	GSE/ KIM_WT1_TARGETS_12HR_UP
29	8e-03	2 / 12	GSE/ CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
30	8e-03	2 / 12	GSE/ BROWNE_HCMV_INFECTION_14HR_UP
31	8e-03	4 / 71	miRN hsa-miR-331-3p
32	9e-03	28 / 1574	BP transcription, DNA-templated
33	9e-03	6 / 159	CC nuclear speck
34	9e-03	2 / 13	CC STAGA complex
35	9e-03	2 / 13	GSE/ COLDREN_GEFITINIB_RESISTANCE_UP
36	9e-03	2 / 13	GSE/ REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
37	9e-03	3 / 39	MF histone acetyltransferase activity
38	1e-02	3 / 40	BP histone H3 acetylation
39	1e-02	4 / 76	CC catalytic step 2 spliceosome
40	1e-02	2 / 14	BP muscle cell cellular homeostasis

## Overview Map

## Spot

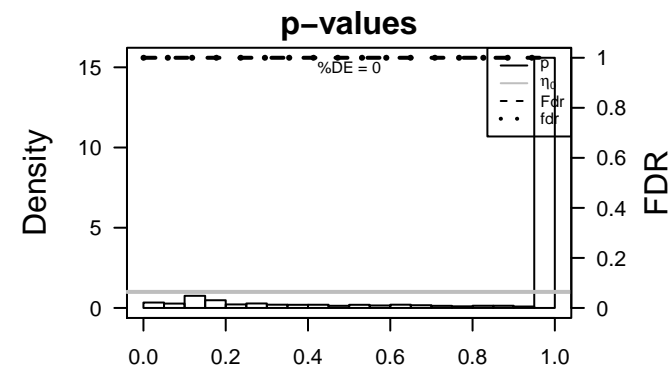
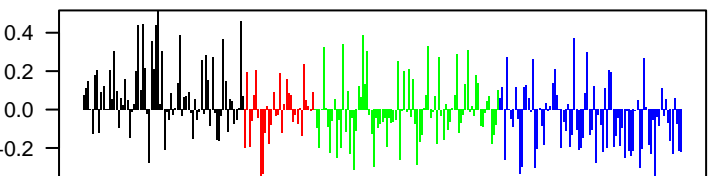
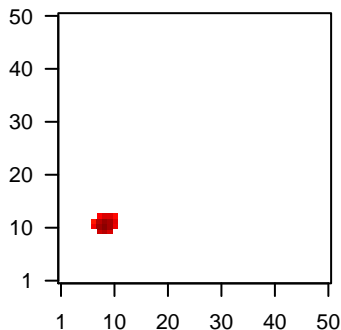
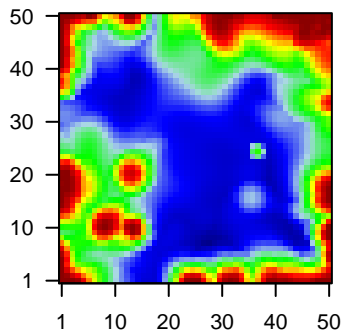


Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes like transcription, tissue development, RNA splicing, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists chromosomes from Chr 1 to Chr 5.

Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes like signaling, cancer, growth, stress, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists molecular functions like binding, enzyme activity, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists miRNAs like miR-1, miR-7a, miR-7b, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists pathways like BENTINK\_ras.2, GUSTAFSON\_Pi3K\_UP, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists cancer-related genes like GENTLES\_modul5, GENTLES\_modul1, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists disease-related genes like GUDJ\_psoiriasis up, WIRTH\_Sec. lymphoid organs, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists tissue-related genes like WIRTH\_Lymphocytes, WIRTH\_Tonsil, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists miRNAs like hsa-miR-525a-5p, hsa-miR-532-3p, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists pathways like HEBENSTREIT\_high expression TF, MYC\_Targets UP, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists pathways like HEBENSTREIT\_low expression TF, MYC\_Targets DOWN, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes like nucleus, nuclear speck, STAGA complex, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists genes like wilscher\_GBM\_Verhaak-PNwt\_expression\_J\_up, GIEZELT\_GBM\_MGMTmethyl\_up, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes like lymphocytes, muscle, immune system, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists diseases like Myxoid liposarcoma, papillary, Pancreatic cancer, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists miRNAs like MAC1EJ\_MMML 24, MAC1EJ\_MMML 1, etc.

Table with 3 columns: p-value, #in/all, Geneset. Lists tissues like VAQUERIZAS\_General, VAQUERIZAS\_Testis, etc.

# Sample-Overexpression

## Spot Summary: D

# metagenes = 8  
# genes = 139

<r> metagenes = 0.99  
<r> genes = 0.26  
beta: r2= 2.03 / log p= -Inf

# samples with spot = 11 ( 4 % )  
Atypical : 5 ( 6.8 % )  
Mesenchymal : 1 ( 1.2 % )  
Basal : 5 ( 6 % )

## Spot Genelist

Rank	ID	max e	r	min e	Description
1	10430	1.22	-0.82	0.35	TMEM147 transmembrane protein 147 [Source:HGNC Symbol;Acc:3041
2	644928	1.21	-0.95	0.36	
3	400156	1.2	-0.87	0.28	
4	5438	1.19	-0.78	0.54	POLR2I polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [S
5	7923	1.18	-0.96	0.45	HSD17B8 hydroxysteroid (17-beta) dehydrogenase 8 [Source:HGNC Sy
6	4713	1.15	-0.75	0.71	NDUFB7 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 1E
7	140823	1.15	-0.93	0.52	ROMO1 reactive oxygen species modulator 1 [Source:HGNC Symbol;
8	51647	1.12	-0.73	0.49	FAM96B family with sequence similarity 96, member B [Source:HGNC
9	84681	1.11	-0.82	0.43	HINT2 histidine triad nucleotide binding protein 2 [Source:HGNC Syr
10	10591	1.1	-0.92	0.55	DNPH1 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 [Source:HG
11	10217	1.09	-1.08	0.35	CTDSPL CTD (carboxy-terminal domain, RNA polymerase II, polypept
12	60386	1.07	-0.67	0.57	SLC25A10olute carrier family 25 (mitochondrial thiamine pyrophosphat
13	27335	1.06	-1.02	0.52	EIF3K eukaryotic translation initiation factor 3, subunit K [Source:HG
14	100131187	1.05	-0.87	0.45	TSTD1 thiosulfate sulfurtransferase (rhodanese)-like domain contain
15	254863	1.04	-0.95	0.53	TMEM256 transmembrane protein 256 [Source:HGNC Symbol;Acc:2861
16	51024	1.04	-0.79	0.44	FIS1 fission 1 (mitochondrial outer membrane) homolog (S. cerevis
17	3615	1.04	-1.16	0.41	IMPDH2 IMP (inosine 5'-monophosphate) dehydrogenase 2 [Source:HG
18	26001	1.04	-0.76	0.35	RNF167 ring finger protein 167 [Source:HGNC Symbol;Acc:24544]
19	8673	1.03	-1.25	0.53	VAMP8 vesicle-associated membrane protein 8 [Source:HGNC Sym]
20	4201	0.99	-0.63	0.6	MEA1 male-enhanced antigen 1 [Source:HGNC Symbol;Acc:6986]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-14	41 / 1318	CC mitochondrion
2	4e-09	16 / 304	CC mitochondrial inner membrane
3	2e-05	25 / 1233	TF KIM_MYC targets
4	4e-05	5 / 47	BP protein targeting to mitochondrion
5	4e-05	3 / 9	GSE/ KEGG_RNA_POLYMERASE
6	6e-05	6 / 83	BP respiratory electron transport chain
7	6e-05	3 / 10	MF NADH dehydrogenase activity
8	7e-05	8 / 167	CC ribosome
9	1e-04	3 / 13	CC mitochondrial respiratory chain
10	1e-04	3 / 13	GSE/ CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
11	2e-04	4 / 34	MF NADH dehydrogenase (ubiquinone) activity
12	2e-04	4 / 36	CC mitochondrial respiratory chain complex I
13	2e-04	3 / 15	GSE/ REACTOME_MRNA_SPLICING_MINOR_PATHWAY
14	3e-04	7 / 152	BP cellular metabolic process
15	3e-04	4 / 38	MF DNA-directed RNA polymerase activity
16	4e-04	21 / 1135	Chr Chr 19
17	6e-04	3 / 20	Lymp ROSOLOWSKI_red UP
18	6e-04	6 / 128	BP translational initiation
19	1e-03	3 / 25	MF hydrogen ion transmembrane transporter activity
20	1e-03	8 / 253	BP translation
21	1e-03	2 / 7	MMM MACIEJ_MMML 48
22	2e-03	6 / 153	MF structural constituent of ribosome
23	2e-03	11 / 482	BP cellular protein metabolic process
24	2e-03	2 / 9	GSE/ REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX
25	2e-03	2 / 9	GSE/ REACTOME_HIV1_TRANSCRIPTION_ELONGATION
26	3e-03	2 / 10	BP peroxisome fission
27	3e-03	2 / 10	GSE/ REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
28	3e-03	2 / 10	GSE/ REACTOME_HIV1_TRANSCRIPTION_INITIATION
29	3e-03	2 / 10	GSE/ REACTOME_MRNA_PROCESSING
30	3e-03	2 / 10	GSE/ REACTOME_RNA_POL_I_CTD_PHOSPHORYLATION_AND_INTERACT
31	3e-03	12 / 579	CC nucleolus
32	3e-03	3 / 35	BP mitochondrial electron transport, NADH to ubiquinone
33	3e-03	2 / 11	Canc GENTLES_modul5
34	3e-03	2 / 11	GSE/ REACTOME_TRANSCRIPTION_COUPLED_NER
35	4e-03	2 / 12	BP cellular aldehyde metabolic process
36	4e-03	2 / 12	GSE/ KEGG_PYRIMIDINE_METABOLISM
37	4e-03	2 / 12	GSE/ REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIPT_IN_TH
38	4e-03	2 / 12	GSE/ REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED_TRANS
39	4e-03	2 / 12	GSE/ REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
40	4e-03	2 / 12	GSE/ REACTOME_NUCLEOTIDE_EXCISION_REPAIR

## Overview Map

## Spot

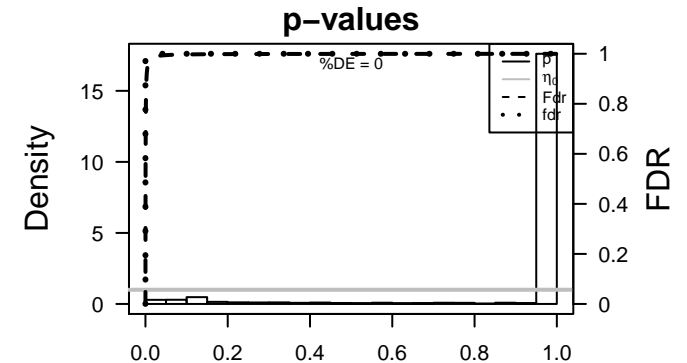
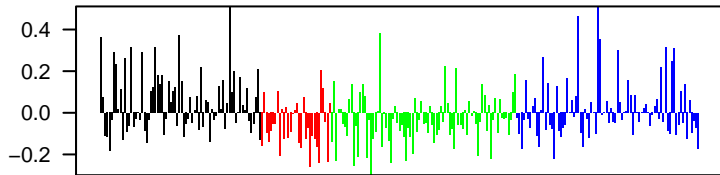
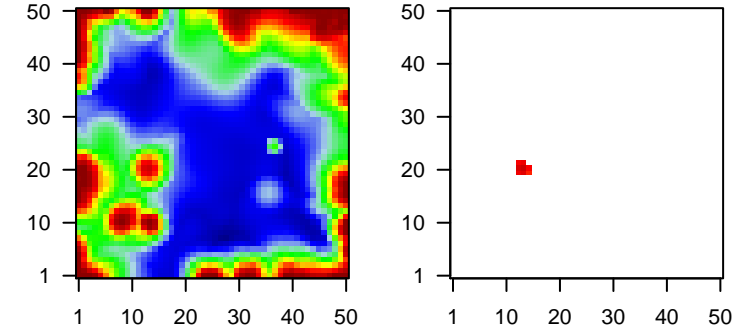


Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes such as 'respiration leading to mitochondrion', 'cellular metabolic process', and 'ATP synthesis coupled proton transport'.

Table with 3 columns: Rank, p-value, #in/all. Lists cancer-related terms like 'Lymph node metastasis' and 'Solid tumor metastasis'.

Table with 3 columns: Geneset, #in/all. Lists cancer-related genesets such as 'LIU\_PROSTATE\_CANCER\_UP', 'LIU\_BREAST\_CANCER', and 'LIU\_LIVER\_CANCER'.

Table with 3 columns: p-value, #in/all. Lists biological processes like 'mitochondrion', 'mitochondrial respiratory chain', and 'nucleolus'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to mitochondrial and cellular processes, such as 'mitochondrial inner membrane' and 'eukaryotic 48S preinitiation complex'.

Table with 3 columns: Chr, p-value, #in/all, Geneset. Lists chromosomes and associated genesets like 'Chr 19', 'Chr 22', and 'Chr 1'.

Table with 3 columns: Rank, p-value, #in/all. Lists disease-related terms like 'Ductal carcinoma in situ', 'GUDJ psoriasis down', and 'Echthyma'.

Table with 3 columns: Geneset, #in/all. Lists disease-related genesets such as 'Ductal carcinoma in situ', 'GUDJ psoriasis down', and 'Echthyma'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'Stamen', 'Protein synthesis', and 'Protein transport'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to protein synthesis and transport, such as 'Stamen Proteins up\_in\_STS' and 'willscher\_GBM\_proteomics\_wtOnly\_SpotG'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'KEGG RNA POLYMERASE', 'CHUNK MULTIPLE MYELOMA HYPERPLOID UP', and 'REACTOME MRNA SPLICING MINOR PATHWAY'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'WIRTH\_Globus pallidus', 'WIRTH\_Muscle', and 'WIRTH\_Pituitary gland'.

Table with 3 columns: Geneset, #in/all. Lists biological processes like 'WIRTH\_Globus pallidus', 'WIRTH\_Muscle', and 'WIRTH\_Pituitary gland'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'ROSOLOWSKI\_red UP', 'ROSOLOWSKI\_red total', and 'ROSOLOWSKI\_green UP'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to ROSOLOWSKI and SPANG, such as 'ROSOLOWSKI\_red UP' and 'SPANG\_IL21 DN'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'DNA dependent RNA polymerase activity', 'DNA-directed RNA polymerase activity', and 'RNA binding'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'TACG-99A--100-99B', 'CTCT-520A--525', and 'GCTC-512-5P'.

Table with 3 columns: Geneset, #in/all. Lists biological processes like 'TACG-99A--100-99B', 'CTCT-520A--525', and 'GCTC-512-5P'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'MikRNASis papillary', 'Pancreatic cancer', and 'Glioblastoma multiforme, somatic'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to MikRNASis and cancer, such as 'MikRNASis papillary' and 'Pancreatic cancer'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists miRNAs like 'let-7a', 'let-7b', 'let-7c', and 'let-7d'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'hsa-miR-574', 'hsa-miR-940', and 'hsa-miR-1260'.

Table with 3 columns: Geneset, #in/all. Lists biological processes like 'hsa-miR-574', 'hsa-miR-940', and 'hsa-miR-1260'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'MACEJ-MMML 48', 'MACEJ-MMML 40', and 'MACEJ-MMML 29'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to MACEJ-MMML, such as 'MACEJ-MMML 48' and 'MACEJ-MMML 40'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'GUSTAFSSON\_Pi3K UP', 'GUSTAFSSON\_Pi3K\_DN', and 'BENTINK\_e2f3.2'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'HEBENSTREIT\_high expression TF', 'HEBENSTREIT\_low expression TF', and 'NOWICK\_TF'.

Table with 3 columns: Geneset, #in/all. Lists biological processes like 'HEBENSTREIT\_high expression TF', 'HEBENSTREIT\_low expression TF', and 'NOWICK\_TF'.

Table with 3 columns: Rank, p-value, #in/all. Lists biological processes like 'VAQUERIZAS\_Fetal brain', 'VAQUERIZAS\_Placenta', and 'VAQUERIZAS\_Liver'.

Table with 3 columns: Geneset, #in/all. Lists genesets related to VAQUERIZAS, such as 'VAQUERIZAS\_Fetal brain' and 'VAQUERIZAS\_Placenta'.

# Sample-Overexpression

## Spot Summary: E

# metagenes = 2  
# genes = 66

<r> metagenes = 1  
<r> genes = 0.36  
beta: r2= 4.93 / log p= -Inf

# samples with spot = 14 ( 5.1 % )  
Atypical : 10 ( 13.5 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 1 ( 1.2 % )  
Basal : 2 ( 2.4 % )

## Spot Genelist

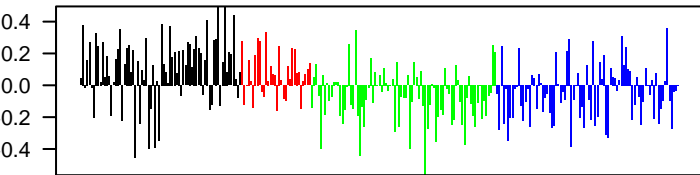
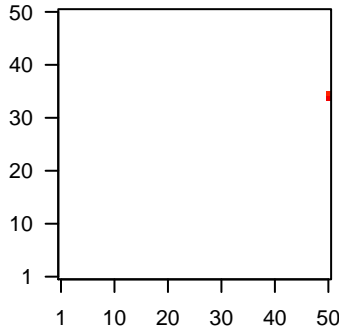
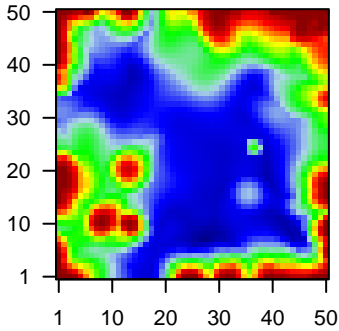
Rank	ID	max e	r	min e	Description
1	1429	1.26	-1.33	0.44	CRYZ crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
2	64747	1.18	-0.88	0.33	MFSD1 major facilitator superfamily domain containing 1 [Source:HGI
3	57763	1.1	-0.72	0.75	ANKRA2 ankyrin repeat, family A (RFXANK-like), 2 [Source:HGNC Sy
4	26996	1.1	-0.52	0.5	GPR160 G protein-coupled receptor 160 [Source:HGNC Symbol;Acc:1
5	4942	1.09	-1.01	0.51	OAT ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
6	25874	1.08	-1	0.48	MPC2 mitochondrial pyruvate carrier 2 [Source:HGNC Symbol;Acc:2
7	5612	1.08	-1.18	0.4	PRKRIR protein-kinase, interferon-inducible double stranded RNA de
8	11064	1.08	-0.65	0.62	CNTRL centriolin [Source:HGNC Symbol;Acc:1858]
9	1195	1.06	-0.86	0.55	CLK1 CDC-like kinase 1 [Source:HGNC Symbol;Acc:2068]
10	9061	1.05	-0.88	0.59	PAPSS1 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Source
11	8287	1.05	-0.57	0.37	USP9Y ubiquitin specific peptidase 9, Y-linked [Source:HGNC Symb
12	6146	1.05	-1.25	0.65	RPL22 ribosomal protein L22 [Source:HGNC Symbol;Acc:10315]
13	1975	1.02	-0.96	0.6	EIF4B eukaryotic translation initiation factor 4B [Source:HGNC Symb
14	22862	1.01	-0.87	0.5	FNDC3A fibronectin type III domain containing 3A [Source:HGNC Sym
15	10289	1	-0.73	0.45	EIF1B eukaryotic translation initiation factor 1B [Source:HGNC Symb
16	10015	1	-0.95	0.6	PDCD6IP programmed cell death 6 interacting protein [Source:HGNC S
17	3150	0.99	-0.94	0.64	HMGN1 high mobility group nucleosome binding domain 1 [Source:HC
18	51124	0.99	-0.96	0.52	IER3IP1 immediate early response 3-interacting protein 1 [Source:Ur
19	34	0.98	-1	0.69	ACADM acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Sourc
20	54495	0.97	-1	0.62	TMX3 thioredoxin-related transmembrane protein 3 [Source:HGNC

## Geneset Overrepresentation

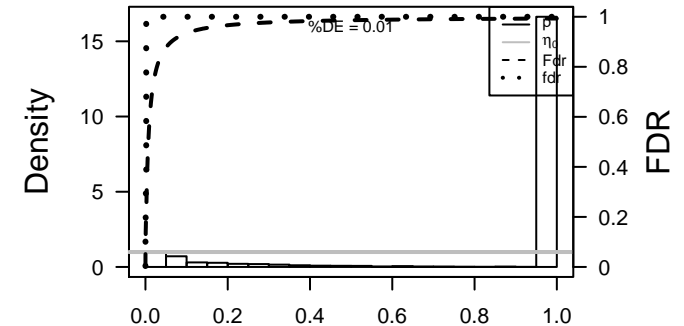
Rank	p-value	#in/all	Geneset
1	5e-07	11 / 396	miRN hsa-miR-301b
2	1e-06	5 / 45	miRN hsa-miR-411
3	2e-06	6 / 93	miRN hsa-miR-10b
4	6e-06	7 / 172	miRN hsa-miR-607
5	2e-05	10 / 463	miRN hsa-miR-301a
6	2e-05	6 / 142	miRN hsa-miR-522
7	3e-05	5 / 90	miRN hsa-miR-10a
8	3e-05	5 / 90	miRN hsa-miR-362-5p
9	4e-05	4 / 49	miRN GTAT-154-487
10	5e-05	5 / 100	miRN hsa-miR-544
11	5e-05	10 / 538	miRN hsa-miR-17
12	7e-05	5 / 107	miRN AACAA-409-3P
13	1e-04	5 / 114	miRN TGTA-485-3P
14	1e-04	10 / 603	miRN hsa-miR-20a
15	2e-04	33 / 4640	CC nucleus
16	2e-04	7 / 300	miRN hsa-miR-561
17	2e-04	7 / 303	miRN hsa-miR-302b
18	3e-04	7 / 318	miRN hsa-miR-590-3p
19	3e-04	6 / 229	miRN hsa-miR-520g
20	3e-04	4 / 82	miRN hsa-miR-567
21	4e-04	8 / 440	miRN hsa-miR-19a
22	4e-04	5 / 153	miRN hsa-miR-450b-5p
23	4e-04	6 / 240	miRN ACAT-1-206
24	4e-04	9 / 565	miRN hsa-miR-20b
25	4e-04	8 / 449	miRN hsa-miR-130b
26	5e-04	8 / 456	miRN hsa-miR-130a
27	5e-04	3 / 38	miRN hsa-miR-1277
28	5e-04	4 / 93	CC spliceosomal complex
29	6e-04	5 / 169	miRN hsa-miR-374b
30	6e-04	5 / 172	miRN hsa-miR-520h
31	7e-04	8 / 479	miRN hsa-miR-15b
32	7e-04	6 / 264	miRN hsa-miR-449a
33	7e-04	2 / 10	MF NADPH binding
34	7e-04	2 / 10	BP negative regulation of DNA damage response, signal transduction by p53 c
35	7e-04	8 / 488	miRN hsa-miR-16
36	8e-04	5 / 180	miRN hsa-miR-374a
37	9e-04	7 / 382	miRN hsa-miR-454
38	9e-04	3 / 47	miRN hsa-miR-302b*
39	9e-04	6 / 280	miRN hsa-miR-320a
40	9e-04	5 / 186	miRN hsa-miR-382

## Overview Map

## Spot



## p-values



Rank	p-value	#in/all	Geneset
1	2e-03	2/15	Regulation of DNA damage response, signal transduction by p53 class 3'-phosphoadenosine 5'-phosphosulfate metabolic process
2	2e-03	2/21	regulation of RNA splicing
3	4e-03	4/163	mRNA splicing, via spliceosome
4	7e-03	7/131	peptidyl-threonine phosphorylation
5	7e-03	6/423	negative regulation of transcription, DNA-dependent
6	1e-02	2/37	regulation of translational initiation
7	1e-02	2/44	mRNA 3'-end processing
8	1e-02	4/229	termination of RNA polymerase II transcription
9	1e-02	4/122	RNA splicing
10	2e-02	7/649	translational initiation
11	2e-02	7/50	gene expression
12	2e-02	2/50	BMP signaling pathway
13	2e-02	2/50	protein homotrimerization
14	2e-02	2/59	peptidyl-serine phosphorylation
15	3e-02	2/59	mRNA export from nucleus
16	3e-02	2/72	proteasome-mediated ubiquitin-dependent protein catabolic process
17	4e-02	2/74	peptidyl-tyrosine phosphorylation
18	4e-02	1/10	cellular glucose homeostasis
19	4e-02	1/10	fatty acid homeostasis

Rank	p-value	#in/all	Geneset
1	0.002	8/124	Chr 18
2	0.040	3/187	Chr 21
3	0.055	9/1033	Chr 3
4	0.074	1/19	Chr 3
5	0.095	5/602	Chr 10
6	0.129	1/34	Chr Y
7	0.171	5/699	Chr 5
8	0.151	10/9720	Chr 1
9	0.161	5/714	Chr 6
10	0.312	2/280	Chr 13
11	0.345	1/957	Chr 11
12	0.608	4/2504	Chr 15
13	0.718	2/2618	Chr 4
14	0.871	2/866	Chr 12
15	0.881	2/649	Chr 4
16	0.926	1/633	Chr 9
17	0.978	1/918	Chr 17
18	0.991	1/135	Chr 19
19	1.000	0/715	Chr 16
20	1.000	0/449	Chr 20

Rank	p-value	#in/all	Geneset
1	0.001	2/14	REACTION_MRNA_3_END_PROCESSING
2	0.011	2/15	REACTOME_MRNA_SPLICING
3	0.002	2/15	TIEN_INTESTINE_PROBIOTICS_6HR_UP
4	0.002	2/15	ONDER_CDH1_TARGETS_1_DN
5	0.002	2/15	DE_VY_TARGETS_DN
6	0.002	2/16	GENTILE_UV_RESPONSE_CLUSTER_D6
7	0.002	2/16	SESTO_RESPONSE_TO_UV_C5
8	0.020	1/5	KIM_LRRC3B_TARGETS
9	0.024	1/6	MYC_KANGAS_AMPLIFICATION_HOT_SPOT_7
10	0.024	1/6	BLOC4_FML_PATHWAY
11	0.028	1/7	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN
12	0.032	1/8	RUNNIE_GENDER_EFFECT_UP
13	0.040	1/10	YAGI_4ML_WITH_T_8_21_TRANSLOCATION
14	0.040	1/10	LIJ_THYROID_CANCER_CLUSTER_5
15	0.040	1/10	WHITE_NEUROBLASTOMA_WITH_TP36_3_DELETION
16	0.040	1/10	LIJ_BREAST_CANCER
17	0.040	1/10	LITHIOPHARYNGEAL_CARINOMA
18	0.040	1/10	LEE_LIVER_CANCER_MYC_TGFA_DN
19	0.040	1/10	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
20	0.040	1/10	JISON_SICKLE_CELL_DISEASE_DN

Rank	p-value	#in/all	Geneset
1	3e-03	2/20	protein serine/threonine/tyrosine kinase activity
2	5e-03	2/27	nucleotidyltransferase activity
3	7e-03	7/595	RNA binding
4	1e-02	2/38	calcium-dependent protein binding
5	1e-02	2/41	non-membrane spanning protein tyrosine kinase activity
6	1e-02	9/940	nucleic acid binding
7	2e-02	5/361	binding
8	2e-02	2/54	damaged DNA binding
9	4e-02	1/10	translational initiation factor activity
10	4e-02	1/10	co-SMAD binding
11	4e-02	1/10	quinone binding
12	4e-02	1/10	RNA polymerase II transcription factor binding transcription factor activity
13	4e-02	1/11	glutathione binding
14	4e-02	1/11	I-SMAD binding
15	4e-02	1/12	telomeric DNA binding
16	5e-02	1/12	low-density lipoprotein particle receptor binding
17	5e-02	1/12	NAD+ binding
18	5e-02	1/12	phospholipase binding
19	5e-02	1/13	core promoter proximal region sequence-specific DNA binding

Rank	p-value	#in/all	Geneset
1	0.008	1/13	miR-36
2	0.016	1/4	let-7c
3	0.016	1/4	let-7g
4	0.024	1/6	let-7f
5	0.024	1/6	let-7d
6	0.024	1/6	miR-26a
7	0.036	1/9	miR-125b
8	0.044	1/9	let-7a
9	0.051	1/13	miR-34a
10	1.000	0/13	miR-1
11	1.000	0/2	miR-101
12	1.000	0/2	miR-101b
13	1.000	0/4	miR-106b
14	1.000	0/2	miR-107
15	1.000	0/2	miR-122
16	1.000	0/2	miR-124a
17	1.000	0/6	miR-125a
18	1.000	0/2	miR-129
19	1.000	0/3	miR-129
20	1.000	0/3	miR-128

Rank	p-value	#in/all	Geneset
1	0.013	0/13	GUSTAFSSON_PI3K_UP
2	0.013	0/13	GUSTAFSSON_PI3K_DN
3	0.12	0/12	BENTINK_e2f3
4	0.11	0/11	BENTINK_e2f3.2
5	0.14	0/14	BENTINK_myc.1
6	0.11	0/11	BENTINK_ras.1
7	0.11	0/11	BENTINK_ras.4
8	0.15	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	

Rank	p-value	#in/all	Geneset
1	0.040	1/10	LIU_BREAST_CANCER
2	0.171	2/185	SPANG_LPS-index2
3	0.365	2/316	SPANG_BCL6-index2
4	1.000	0/16	RHODES_LANCER_META_SIGNATURE
5	1.000	0/16	RHODES_UNDIFFERENTIATED_CANCER
6	1.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	1.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	1.000	0/14	LIJ_COMMON_CANCER_GENES
9	1.000	0/14	LIJ_LIVER_CANCER
10	1.000	0/15	LIJ_PROSTATE_CANCER_DN
11	1.000	0/14	LIJ_PROSTATE_CANCER_UP
12	1.000	0/9	WANG_ER_UP
13	1.000	0/9	WANG_ER_DN
14	1.000	0/16	WOLFE_overlap_genes
15	1.000	0/12	BEN-PORATH_DN
16	1.000	0/15	BEN-PORATH_UP
17	1.000	0/15	GENTLES_modul1
18	1.000	0/16	GENTLES_modul2
19	1.000	0/16	GENTLES_modul3

Rank	p-value	#in/all	Geneset
1	0.000	5/113	UDU_pсорosisis up
2	0.009	5/313	UDU_pсорosisis down
3	0.009	5/313	UDU_EBM up
4	0.033	2/71	BCHETNIA_EBM down
5	0.043	4/328	BCHETNIA_EBM-DM up
6	0.125	1/33	
7	0.149	2/69	
8	0.196	2/54	
9	0.222	1/62	
10	0.250	1/71	
11	0.250	1/71	
12	0.250	1/71	
13	0.256	1/73	
14	0.265	1/76	
15	0.470	2/81	
16	1.000	0/14	
17	1.000	0/16	
18	1.000	0/14	
19	1.000	0/15	
20	1.000	0/27	

Rank	p-value	#in/all	Geneset
1	0.5	2/41	WIRTH_Timline system
2	0.7	5/1	WIRTH_Pituitary gland
3	1.0	0/26	WIRTH_Pancreas
4	1.0	0/13	WIRTH_Sec. lymphoid organs
5	1.0	0/12	WIRTH_PrIm. lymphoid organs
6	1.0	0/10	WIRTH_B-cell
7	1.0	0/13	WIRTH_Tonsil
8	1.0	0/13	WIRTH_Thymus
9	1.0	0/12	WIRTH_Lymphocytes
10	1.0	0/6	WIRTH_Bone marrow
11	1.0	0/400	WIRTH_Nervous System
12	1.0	0/14	WIRTH_Globus pallidus
13	1.0	0/15	WIRTH_Telencephalon
14	1.0	0/16	WIRTH_Cortex cerebri
15	1.0	0/16	WIRTH_Hippocampus
16	1.0	0/13	WIRTH_Thalamus
17	1.0	0/15	WIRTH_Cerebellum
18	1.0	0/120	WIRTH_Testis
19	1.0	0/50	WIRTH_Homeostasis
20	1.0	0/62	WIRTH_Liver

Rank	p-value	#in/all	Geneset
1	7e-05	5/107	AACA-409-3P
2	7e-05	5/114	TGTA-485-3P
3	1e-04	6/240	ACAT-1--206
4	4e-04	4/127	GAC-212--132
5	2e-03	3/73	AGGC-515-3P
6	5e-03	4/168	ATAC-144
7	5e-03	6/381	GTAA-181A--181B--181C--181D
8	7e-03	5/95	GTC-383
9	7e-03	4/189	AACT-145
10	8e-03	3/101	AAAG-501
11	8e-03	1/192	CACT-302C
12	9e-03	3/107	ACAC-442-3P
13	1e-02	2/37	CTCT-526C--518F--526A
14	1e-02	2/40	GTAA-200A
15	1e-02	4/46	BENTINK_DN
16	1e-02	3/126	ATGT-494
17	2e-02	3/129	GTGA-224
18	2e-02	5/362	CACT-200B--200C--429
19	2e-02	1/0	
20	2e-02	1/0	

Rank	p-value	#in/all	Geneset
1	5e-07	7/336	hsa-miR-501b
2	1e-06	5/45	hsa-miR-411
3	2e-06	6/93	hsa-miR-10b
4	2e-06	7/172	hsa-miR-507
5	2e-05	10/463	hsa-miR-301a
6	2e-05	6/142	hsa-miR-522
7	3e-05	5/90	hsa-miR-369-5p
8	5e-05	5/100	hsa-miR-544
9	5e-05	10/538	hsa-miR-17
10	1e-04	10/603	hsa-miR-20a
11	2e-04	7/300	hsa-miR-561
12	2e-04	7/303	hsa-miR-302b
13	3e-04	7/318	hsa-miR-393-3p
14	3e-04	5/229	hsa-miR-520g
15	3e-04	4/82	hsa-miR-567
16	4e-04	8/440	hsa-miR-19a
17	4e-04	5/153	hsa-miR-150b-5p
18	4e-04	5/65	hsa-miR-20b
19	4e-04	8/449	hsa-miR-130b

Rank	p-value	#in/all	Geneset
1	0.003	12/1293	MYC_targets
2	0.012	11/1093	HEBENSTREIT_high expression TF
3	0.063	1/6	MYC_Protein synthesis degradation UP
4	0.225	1/63	MYC_targets UP
5	0.951	2/1146	HEBENSTREIT_low expression TF
6	1.000	0/5	NOWICK_TF
7	1.000	0/5	MYC_TFs
8	1.000	0/9	MYC_targets DOWN
9	1.000	0/4	MYC_Apoptosis UP
10	1.000	0/8	MYC_Cell cycle UP
11	1.000	0/2	MYC_Cell cycle DOWN
12	1.000	0/4	MYC_Cell growth and proliferation UP
13	1.000	0/2	MYC_Chromatin_modification UP
14	1.000	0/3	MYC_DNA repair
15	1.000	0/3	MYC_DNA replication UP
16	1.000	0/2	MYC_ECM_cell adhesion DOWN
17	1.000	0/20	MYC_Metabolism 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 suppressor genes UP

Rank	p-value	#in/all	Geneset
1	5e-04	4/93	nucleus
2	1e-03	4/120	spliceosomal complex
3	4e-03	3/76	nuclear envelope
4	4e-03	4/159	catalytic step 2 spliceosome
5	5e-03	18/238	nuclear speck
6	6e-03	2/29	cytosol
7	1e-03	7/35	nuclear inner membrane
8	1e-02	4/220	vesicle
9	1e-02	3/110	mitochondrial matrix
10	3e-02	26/431	ribonucleoprotein complex
11	4e-02	8/949	cytoplasm
12	4e-02	2/80	nucleoplasm
13	4e-02	2/81	chromatin
14	5e-02	1/12	nuclear matrix
15	5e-02	1/12	ESC/E2 complex
16	6e-02	1/13	nuclear chromatin
17	6e-02	1/15	vesicle membrane
18	6e-02	1/16	viral nucleocapsid
19	7e-02	1/17	nuclear heterochromatin
20	7e-02	1/17	nuclear chromosome, telomeric region

Rank	p-value	#in/all	Geneset
1	0.009	5/113	willscher_GBM_Verhaak-CL_expression_D_up
2	0.009	5/313	willscher_GBM_Verhaak-MES_expression_D_down
3	0.009	5/313	willscher_GBM_Verhaak-PNwt_expression_D_up
4	0.043	4/328	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl Up
5	0.125	1/33	willscher_GBM_proteomics_wtOnly_SpotC
6	0.149	2/69	willscher_GBM_proteomics_wtOnly_Differencelst
7	0.196	2/54	willscher_GBM_proteomics_wtOnly_SpotG
8	0.222	1/62	Stuehler_Proteins_up_in_STS
9	0.250	1/71	willscher_GBM_Verhaak-CL_expression_H_down
10	0.250	1/71	willscher_GBM_Verhaak-MES_expression_H_up
11	0.250	1/71	

# Sample-Overexpression

## Spot Summary: F

# metagenes = 9  
# genes = 130

<r> metagenes = 0.98  
<r> genes = 0.43  
beta: r2= 10.55 / log p= -Inf

# samples with spot = 58 ( 21.1 % )  
Atypical : 16 ( 21.6 % )  
Mesenchymal : 27 ( 31.8 % )  
Basal : 15 ( 17.9 % )

## Spot Genelist

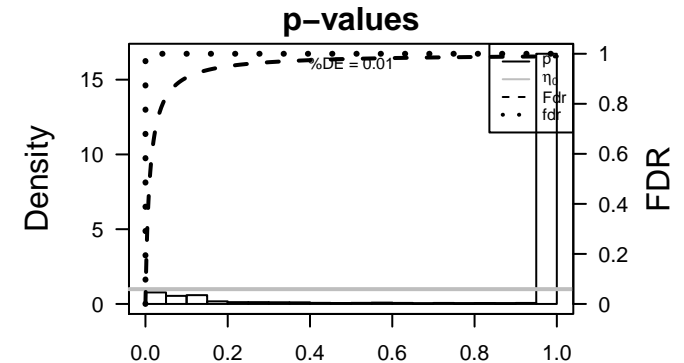
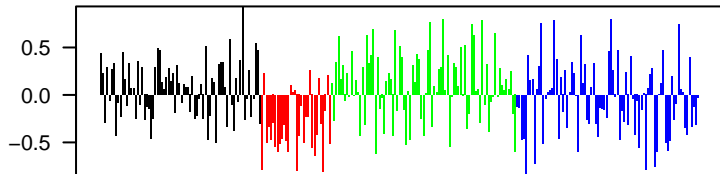
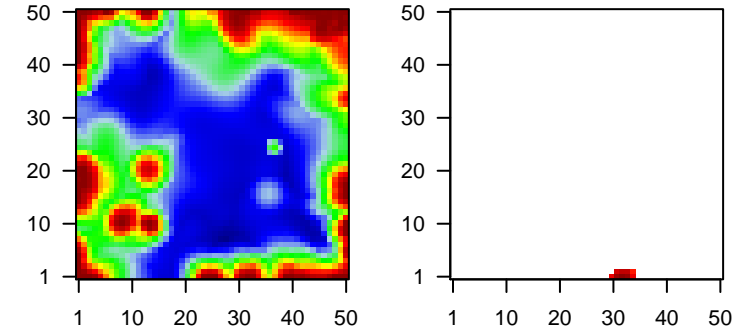
Rank	ID	max e	r	min e	Description
					Symbol
1	3627	3.43	-2.5	0.75	CXCL10 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:3627]
2	6373	2.89	-1.08	0.54	CXCL11 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:6373]
3	9560	2.65	-1.76	0.49	CCL4L1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:9560]
4	9636	2.47	-2.69	0.73	ISG15 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:40596]
5	10964	2.46	-2.33	0.78	IFI44L interferon-induced protein 44-like [Source:HGNC Symbol;Acc:10964]
6	8743	2.43	-2.05	0.38	TNFSF10 tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:8743]
7	629	2.42	-2.1	0.6	CFB complement factor B [Source:HGNC Symbol;Acc:1037]
8	7453	2.35	-1.7	0.73	WARS tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:11937]
9	115362	2.34	-1.91	0.73	GBP5 guanylate binding protein 5 [Source:HGNC Symbol;Acc:115362]
10	388372	2.33	-1.11	0.62	CCL4L1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:388372]
11	6355	2.3	-1.49	0.54	CCL8 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:6355]
12	9536	2.23	-1.43	0.33	PTGES prostaglandin E synthase [Source:HGNC Symbol;Acc:9599]
13	4321	2.23	-1.74	0.44	MMP12 matrix metalloproteinase 12 (macrophage elastase) [Source:HGNC Symbol;Acc:4321]
14	970	2.2	-0.71	0.41	CD70 CD70 molecule [Source:HGNC Symbol;Acc:11937]
15	3433	2.19	-1.63	0.69	IFIT2 interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:3433]
16	1591	2.19	-1.48	0.24	CYP24A1 cytochrome P450, family 24, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:1591]
17	94240	2.04	-2.07	0.81	EPST11 epithelial stromal interaction 1 (breast) [Source:HGNC Symbol;Acc:94240]
18	3135	1.98	-1.39	0.66	HLA-G major histocompatibility complex, class I, G [Source:HGNC Symbol;Acc:3135]
19	55008	1.98	-2.07	0.61	HERC6 HECT and RLD domain containing E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:55008]
20	10561	1.95	-1.98	0.74	IFI44 interferon-induced protein 44 [Source:HGNC Symbol;Acc:10561]

## Geneset Overrepresentation

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

## Overview Map

## Spot





Rank	p-value	#in/all	Geneset
1	1e-05	31/123	antigen presentation signaling pathway
2	7e-36	34/204	defense response to virus
3	5e-36	27/109	cytokine-mediated signaling pathway
4	1e-33	28/112	response to virus
5	8e-21	16/60	immune response
6	4e-20	13/31	interferon-gamma-mediated signaling pathway
7	2e-13	15/530	negative regulation of viral genome replication
8	4e-13	25/530	antigen processing and presentation of exogenous peptide antigen via MHC class II
9	5e-13	12/74	innate immune response
10	5e-13	8/18	antigen processing and presentation of exogenous peptide antigen via MHC class I
11	1e-11	19/116	positive regulation of T cell mediated cytotoxicity
12	6e-12	12/91	modulation by virus of host morphology or physiology
13	1e-11	11/74	antigen processing and presentation of peptide antigen via MHC class I
14	9e-07	9/47	regulation of immune response
15	2e-07	9/47	antigen processing and presentation
16	2e-07	5/18	negative regulation of type I interferon production
17	2e-05	4/21	response to interferon-gamma
18	2e-05	16/608	positive regulation of interferon-beta production
19	2e-05	3/10	apoptotic process
20	2e-05	3/10	positive regulation of interferon-alpha production

Rank	p-value	#in/all	Geneset
1	6e-09	8/32	CH15HSCHR6_MHC_OBL
2	1e-02	2/23	CH15HSCHR6_MHC_DBB
3	6/4497	1/1	Chr 1
4	1e-01	6/4497	Chr 20
5	2e-01	5/386	Chr 22
6	2e-01	7/618	Chr 4
7	4e-01	5/1720	Chr 4
8	4e-01	5/519	Chr 14
9	4e-01	9/1033	Chr 2
10	4e-01	2/187	Chr 21
11	5e-02	2/187	Chr 10
12	5e-01	7/866	Chr 10
13	6e-01	7/914	Chr 3
14	6e-01	7/1135	Chr 19
15	6e-01	4/7	Chr 19
16	8e-01	1/232	Chr 18
17	9e-01	5/918	Chr 17
18	9e-01	3/143	Chr 9
19	9e-01	2/280	Chr 13
20	9e-01	2/504	Chr 15

Rank	p-value	#in/all	Geneset
1	6e-23	12/146	MUSELERNA_RESPONSE
2	2e-20	11/18	INTERFERON_SIGNATURE_INTERFERON_IN_CANCER
3	2e-19	10/13	ZHANG_INTERFERON_RESPONSE
4	5e-19	9/10	BOWIE_RESPONSE_TO_TAMOXIFEN
5	5e-16	10/13	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	2e-15	8/11	PROGVIC_RESPONSE_TO_IMQUIMOD
7	2e-15	8/11	GRANDVAUX_IIN_RESPONSE_NOT_VIA_IRF3
8	2e-12	6/14	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	2e-10	6/14	ROTH_TERT_TARGETS_UP
10	2e-09	6/16	MAHADEVAN_RESPONSE_TO_MP470_UP
11	2e-09	6/16	TSAI_DNAJB4_TARGETS_UP
12	2e-09	6/16	XU_AKT1_TARGETS_6HR
13	2e-09	6/16	RADAVIA_RESPONSE_TO_IFNA1_UP
14	2e-09	6/16	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
15	1e-07	5/16	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
16	1e-07	5/16	FARMER_BREAST_CANCER_CLUSTER_1
17	7e-07	4/10	ZHANG_MULTIPLE_MYELOMA_LB_DN
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

Rank	p-value	#in/all	Geneset
1	2e-10	9/51	double-stranded RNA binding
2	2e-06	4/22	NAD+ ADP-ribosyltransferase activity
3	2e-05	86/8023	protein binding
4	2e-05	7/115	helicase activity
5	3e-04	4/27	single-stranded RNA binding
6	3e-04	4/43	chemokine activity
7	4e-04	3/280	threonine-type endopeptidase activity
8	4e-04	3/19	receptor binding
9	4e-04	5/92	hydrolase activity, acting on acid anhydrides
10	1e-03	3/27	ATP-dependent helicase activity
11	1e-03	3/27	tumor necrosis factor receptor binding
12	2e-03	8/287	nucleotidyltransferase activity
13	2e-03	4/72	hydrolase activity
14	3e-03	7/238	transferase activity
15	3e-03	2/11	ubiquitin-protein ligase activity
16	4e-03	2/12	regulatory region DNA binding
17	7e-03	11/595	MHC class I protein binding
18	7e-03	16/1043	RNA binding
19	7e-03	16/1043	zinc ion binding

Rank	p-value	#in/all	Geneset
1	0.02	1/3	miR-15
2	0.02	1/3	miR-148a
3	0.07	0/11	miR-17
4	1.00	0/6	let-7a
5	1.00	0/6	let-7b
6	1.00	0/4	let-7c
7	1.00	0/4	let-7d
8	1.00	0/4	let-7e
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	0/3	miR-129
19	1.00	0/3	miR-128

Rank	p-value	#in/all	Geneset
1	0.08	1/13	BENTINK_ras.4
2	0.00	0/13	BENTINK_src.10
3	1.00	0/13	GUSTAFSON_P13K_UP
4	1.00	0/15	GUSTAFSON_P13K_DN
5	1.00	0/12	BENTINK_e23.1
6	1.00	0/12	BENTINK_e23.2
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	

Rank	p-value	#in/all	Geneset
1	1e-05	19/316	SPANG_BCL6-index2
2	1e-06	17/553	Lemboke_Colonc Inflammation
3	7e-02	0/16	WANG_ER
4	6e-02	1/14	LIU_COMMON_CANCER_GENES
5	1e-01	1/14	SHAUGHNESSY_MM_high_risk
6	1e+00	1/68	LIU_Normal_vs_Adenoma
7	1e+00	0/530	RHODES_CANCER_META_SIGNATURE
8	1e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1e+00	0/15	LIU_BREAST_CANCER
11	1e+00	0/14	LIU_LIVER_CANCER
12	1e+00	0/15	LIU_PROSTATE_CANCER_DN
13	1e+00	0/14	LIU_PROSTATE_CANCER_UP
14	1e+00	0/14	WANG_UP
15	1e+00	0/16	WOLFER_overlap_genes
16	1e+00	0/12	BEN-PORATH_DN
17	1e+00	0/15	BEN-PORATH_UP
18	1e+00	0/15	GENTLES_modul1

Rank	p-value	#in/all	Geneset
1	1e-35	17/572	GOO_psooriasis_up
2	1e+00	0/375	GUJJI_psooriasis_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	

Rank	p-value	#in/all	Geneset
1	2e-05	13/147	WIRTH_Immune system
2	4e-01	2/13	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_Placentia
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-cell
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	0/16	WIRTH_Globus pallidus
15	1e+00	0/15	WIRTH_Telencephalon
16	1e+00	0/16	WIRTH_Hippocampus
17	1e+00	0/13	WIRTH_Triaxium
18	1e+00	0/15	WIRTH_Cerebellum
19	1e+00	0/120	WIRTH_Testis
20	1e+00	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.1	2/32	hsa-miR-519e-3p
2	0.2	1/33	ACAA-453
3	0.2	1/33	TCG-383
4	0.3	1/40	GTA-200A
5	0.3	1/43	CCCA-295-3P
6	0.3	1/46	CGTC-412
7	0.4	1/73	AGGC-515-3P
8	0.4	1/75	ATGT-185
9	0.5	1/80	TGAG-216
10	0.5	1/85	ATTA-380-3P
11	0.6	1/86	hsc-miR-519f
12	0.6	1/107	TCCA-518C
13	0.6	1/116	CAGC-370
14	0.6	2/261	CTCA-125B-125A
15	0.6	1/135	CTCA-198A-199B
16	0.7	1/139	GCAA-129
17	0.7	1/159	CACC-138
18	0.8	1/182	CCTC-214
19	0.8	1/82	CCTC-9

Rank	p-value	#in/all	Geneset
1	0.2	1/124	hsa-miR-519e*
2	0.3	1/38	hsa-miR-517-3p
3	0.3	1/41	hsa-miR-123-3p
4	0.3	1/41	let-7a
5	0.3	1/43	hsa-miR-129-3p
6	0.3	1/44	hsa-miR-636
7	0.3	1/47	hsa-miR-346
8	0.3	1/48	hsa-miR-519b-5p
9	0.3	1/53	hsa-miR-519b-3p
10	0.3	1/53	hsa-miR-519c-5p
11	0.4	1/59	hsa-miR-330-5p
12	0.4	1/58	hsa-miR-518d-5p
13	0.4	1/58	hsa-miR-520c-5p
14	0.4	1/59	hsa-miR-526b
15	0.4	1/63	hsa-miR-1212
16	0.4	1/63	hsa-miR-1285
17	0.4	1/69	hsa-miR-578
18	0.4	1/75	hsa-miR-1292
19	0.4	1/75	hsa-miR-659
20	0.4	1/75	hsa-miR-375

Rank	p-value	#in/all	Geneset
1	0.1	10/1095	HEBENSTREIT_high expression TF
2	0.6	9/1233	KIM_MYC_targets
3	0.9	6/1146	HEBENSTREIT_low expression TF
4	1.0	0/5	MYC_TFs
5	1.0	0/63	MYC_Targets UP
6	1.0	0/9	MYC_Targets DOWN
7	1.0	0/4	MYC_Apoptosis UP
8	1.0	0/8	MYC_Cell cycle UP
9	1.0	0/2	MYC_Cell cycle DOWN
10	1.0	0/4	MYC_Cell growth and proliferation UP
11	1.0	0/2	MYC_Chromatin_modification UP
12	1.0	0/5	MYC_DNA repair UP
13	1.0	0/3	MYC_DNA replication UP
14	1.0	0/2	MYC_ECM cell adhesion DOWN
15	1.0	0/20	MYC_Metabolism UP
16	1.0	0/16	MYC_Protein synthesis degradation UP
17	1.0	0/8	MYC_RNA processing binding UP
18	1.0	0/2	MYC_Signal transduction UP
19	1.0	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	1e-07	42/2378	proteasome protein complex
2	2e-07	6/32	cytosol
3	6e-07	5/23	ER to Golgi transport vesicle membrane
4	1e-06	6/46	integral to luminal side of endoplasmic reticulum membrane
5	4e-05	6/80	phagocytic vesicle membrane
6	3e-04	15/1683	early endosome membrane
7	3e-04	3/55	extracellular space
8	3e-04	4/55	proteasome core complex
9	3e-04	18/1182	proteasome complex
10	6e-03	2/15	extracellular region
11	2e-02	4/54310	high-density lipoprotein particle
12	2e-02	2/27	cytoplasm
13	4e-02	4/162	SCF ubiquitin ligase complex
14	6e-02	7/436	external side of plasma membrane
15	6e-02	7/436	Golgi membrane
16	7e-02	7/455	cytoplasmic mRNA processing body
17	8e-02	1/10	perinuclear region of cytoplasm
18	8e-02	3/59	lateral element
19	8e-02	3/129	integral to endoplasmic reticulum membrane
20	8e-02	3/129	membrane raft

Rank	p-value	#in/all	Geneset
1	5e-12	5/49	Donson-immune cell intra signaling-associated with LTS in HGA
2	4e-05	5/49	Donson-innate immunity-associated with LTS in HGA
3	2e-04	5/27	GIEZELT_GBM_S1Swt_down_VS_L1Swt UP
4	3e-04	10/7328	cultured astroglia vs. in vivo astrocytes
5	3e-02	2/32	Donson-Misc immune function-associated with LTS in HGA
6	3e-02	1/20	Martinson_Glio_hypomet
7	6e-02	2/49	Christensen_hypomethylated_in_primary_glioblastoma
8	1e-01	1/15	Donson-chemokines/cytokines-associated with LTS in HGA
9	2e-01	4/265	willscher_GBM_Verhaak-CL_expression_B_up
10	2e-01	4/265	willscher_GBM_Verhaak-MES_expression_B_up
11	2e-01	4/265	willscher_GBM_Verhaak-PNwt_expression_B_down
12	2e-01	4/265	willscher_GBM_Verhaak-PNwt_expression_B_down
13	2e-01	1/33	willscher_GBM_proteomics_wtOnly_SpotC
14	2e-01	2/117	GIEZELT_GBM_WT_up_VS_mut UP
15			

# Sample-Overexpression

## Spot Summary: G

# metagenes = 11  
# genes = 229

<r> metagenes = 0.99  
<r> genes = 0.62  
beta: r2= 44.95 / log p= -Inf

# samples with spot = 63 ( 22.9 % )  
Atypical : 48 ( 64.9 % )  
Mesenchymal : 9 ( 10.6 % )  
Basal : 6 ( 7.1 % )

## Spot Genelist

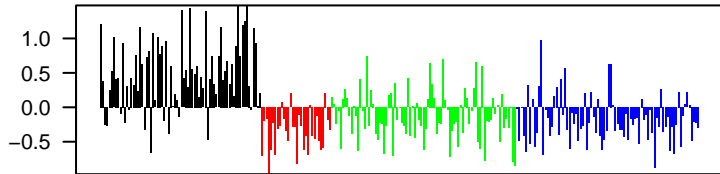
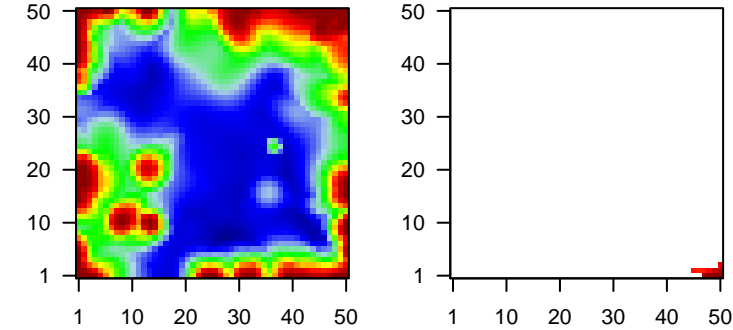
Rank	ID	max e	r	min e	Description
					Symbol
1	260436	4.41	-1.73	0.46	FDCSP follicular dendritic cell secreted protein [Source:HGNC Symbc
2	6363	3.84	-1.64	0.79	CCL19 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
3	3512	3.8	-2.52	0.56	IGJ immunoglobulin J polypeptide, linker protein for immunoglobu
4	3620	3.29	-1.36	0.5	IDO1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:1
5	10537	3.29	-1.89	0.78	UBD ubiquitin D [Source:HGNC Symbol;Acc:18795]
6	930	3.28	-1.12	0.82	CD19 CD19 molecule [Source:HGNC Symbol;Acc:1633]
7	5730	3.15	-1.43	0.71	PTGDS prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
8	6366	3.15	-1.26	0.57	CCL21 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
9	57172	3.1	-2.31	0.69	CAMK1Gcalcium/calmodulin-dependent protein kinase IG [Source:HG
10	4069	3.05	-1.52	0.62	LYZ lysozyme [Source:HGNC Symbol;Acc:6740]
11	9806	3.05	-1.59	0.84	SPOCK2sparc/osteonectin, cwcv and kazal-like domains proteoglycar
12	4283	2.98	-1.9	0.55	CXCL9 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
13	962	2.92	-1.66	0.95	CD48 CD48 molecule [Source:HGNC Symbol;Acc:1683]
14	25849	2.86	-1.41	0.61	PARM1 prostate androgen-regulated mucin-like protein 1 [Source:H
15	3120	2.85	-1.57	0.37	HLA-DQB1major histocompatibility complex, class II, DQ beta 2 [Source:
16	51755	2.83	-2.17	0.66	CDK12 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
17	54855	2.8	-2.28	0.76	FAM46C family with sequence similarity 46, member C [Source:HGNC
18	4050	2.8	-1.39	0.9	LTB lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
19	1236	2.76	-1.33	0.86	CCR7 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
20	713	2.72	-1.99	0.76	C1QB complement component 1, q subcomponent, B chain [Source

## Geneset Overrepresentation

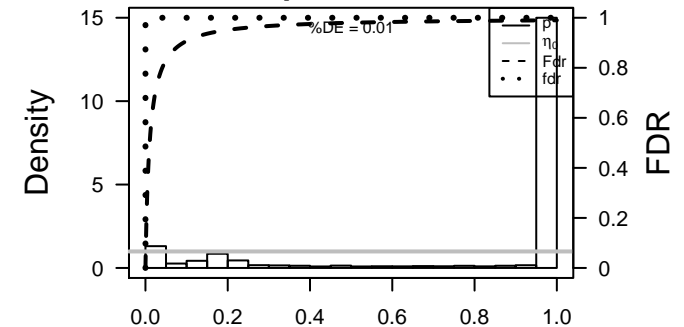
Rank	p-value	#in/all	Geneset
1	8e-82	88 / 417	H.Tis: WIRTH_Immune system
2	8e-59	79 / 553	Canci: Lembecke_Colonic Inflammation
3	3e-35	47 / 312	BP: immune response
4	4e-22	33 / 265	Glio: willscher_GBM_Verhaak-CL_expression_B_up
5	4e-22	33 / 265	Glio: willscher_GBM_Verhaak-MES_expression_B_up
6	4e-22	33 / 265	Glio: willscher_GBM_Verhaak-PNwt_expression_B_down
7	4e-22	33 / 265	Glio: willscher_GBM_Verhaak-PNmut_expression_B_down
8	2e-20	12 / 15	CC: MHC class II protein complex
9	6e-17	23 / 162	CC: external side of plasma membrane
10	2e-16	17 / 74	BP: regulation of immune response
11	1e-15	14 / 47	BP: antigen processing and presentation
12	3e-15	15 / 60	BP: T cell costimulation
13	5e-15	28 / 316	Canci: SPANG_BCL6-index2
14	1e-14	23 / 204	BP: cell surface receptor signaling pathway
15	2e-13	9 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_1
16	6e-13	81 / 2659	CC: plasma membrane
17	1e-11	8 / 16	GSE/ SU_THYMUS
18	3e-11	22 / 269	BP: inflammatory response
19	3e-11	7 / 11	GSE/ BIOCARTA_TCYTOTOXIC_PATHWAY
20	3e-10	37 / 835	CC: integral to plasma membrane
21	2e-09	12 / 84	BP: T cell receptor signaling pathway
22	3e-09	12 / 87	BP: antigen processing and presentation of exogenous peptide antigen via MH
23	3e-09	6 / 11	GSE/ BIOCARTA_THELPER_PATHWAY
24	6e-09	6 / 12	GSE/ BIOCARTA_CTL_PATHWAY
25	6e-09	9 / 43	BP: positive regulation of T cell proliferation
26	9e-09	7 / 21	CC: clathrin-coated endocytic vesicle membrane
27	9e-09	10 / 60	BP: interferon-gamma-mediated signaling pathway
28	9e-09	9 / 45	BP: T cell activation
29	1e-08	6 / 13	Canci: GENTLES_modul18
30	2e-08	7 / 23	CC: integral to luminal side of endoplasmic reticulum membrane
31	2e-08	26 / 530	BP: innate immune response
32	3e-08	6 / 15	GSE/ FINAK_BREAST_CANCER_SDPP_SIGNATURE
33	8e-08	13 / 140	Lymp: DAVE_BL-vs-DLBCL
34	8e-08	7 / 28	CC: transport vesicle membrane
35	9e-08	40 / 1167	BP: signal transduction
36	2e-07	15 / 204	BP: cytokine-mediated signaling pathway
37	2e-07	5 / 11	BP: positive regulation of B cell differentiation
38	2e-07	7 / 32	CC: ER to Golgi transport vesicle membrane
39	3e-07	11 / 106	BP: leukocyte migration
40	3e-07	8 / 49	Glio: Donson-innate immunity-associated with LTS in HGA

## Overview Map

## Spot



## p-values



Rank	p-value	#in/all	Geneset
1	0.000	1/1	immune response
2	1e-16	17/74	regulation of immune response
3	1e-15	14/47	antigen processing and presentation
4	3e-15	15/60	T cell costimulation
5	1e-14	23/204	cell surface receptor signaling pathway
6	3e-11	22/269	inflammatory response
7	2e-09	12/84	T cell receptor signaling pathway
8	3e-09	12/84	antigen processing and presentation of exogenous peptide antigen via MHC class II
9	3/43	9/43	positive regulation of T cell proliferation
10	9/60	10/60	interferon-gamma-mediated signaling pathway
11	9e-09	10/45	T cell activation
12	2e-08	26/630	innate immune response
13	9e-08	40/1167	signal transduction
14	2e-07	15/204	cytokine-mediated signaling pathway
15	2e-07	5/11	positive regulation of B cell differentiation
16	2e-07	5/11	leukocyte migration
17	4e-07	11/106	immunoglobulin mediated immune response
18	2e-06	6/28	B cell receptor signaling pathway
19	3e-06	7/45	cellular defense response
20	3e-06	5/17	positive regulation of neutrophil chemotaxis

Rank	p-value	#in/all	Geneset
1	8e-02	8/32	CHR15_PINK_MHC_QBL
2	2/23	2/23	CHR_HSCHR6_MHC_DBB
3	10/386	10/386	Chr 22
4	15/633	15/633	Chr 19
5	20/1135	20/1135	Chr 19
6	17/957	17/957	Chr 11
7	10/1720	10/1720	Chr 1
8	10/630	10/630	Chr X
9	4/280	4/280	Chr 13
10	7/534	7/534	Chr 8
11	26/1918	26/1918	Chr 17
12	8/633	8/633	Chr 9
13	11/866	11/866	Chr 12
14	9/743	9/743	Chr 7
15	15/187	15/187	Chr 21
16	7/618	7/618	Chr 4
17	12/1033	12/1033	Chr 20
18	6/1802	6/1802	Chr 10
19	6/1449	6/1449	Chr 20
20	9/914	9/914	Chr 3

Rank	p-value	#in/all	Geneset
1	8e-13	9/16	FARMER_BREAST_CANCER_CLUSTER_1
2	9/16	9/16	WIRTH_Bone marrow
3	3e-11	6/11	BIOCARTA_TCYTOTOXIC_PATHWAY
4	6/11	6/11	BIOCARTA_THELPER_PATHWAY
5	6e-09	6/12	BIOCARTA_CTL_PATHWAY
6	6/12	6/12	FINAK_BREAST_CANCER_SDDP_SIGNATURE
7	4e-07	6/12	ZHAN_MULTIPLE_MYELOMA_DN
8	6e-07	5/13	HAHTOLA_CTL_PATHOGENESIS
9	2/13	2/13	BIOCARTA_IL7_PATHWAY
10	2e-06	5/16	FINER_BREAST_CANCER_KINOME_GREEN
11	2e-06	4/8	FERRANDO_TAL1_NEIGHBORS
12	2e-06	4/8	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
13	2e-06	4/10	CHRISCHENSEN_IMMUNOREGULATORY_INTERACTION_BETWEEN_A_LYMPHOCYTE_AND_T_CELL
14	7e-06	4/10	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
15	7e-06	4/10	LEE_DIFFERENTIATING_T_LYMPHOCYTE
16	7e-06	4/10	BIOCARTA_LYM_PATHWAY
17	4/12	4/12	LOCKART_CTL4_PATHWAY
18	3e-05	3/5	WONG_ENDOMETRIAL_CANCER_LATE
19	4/14	4/14	BIOCARTA_NOZIL12_PATHWAY
20	3e-05	4/14	BIOCARTA_STATHMIN_PATHWAY

Rank	p-value	#in/all	Geneset
1	3e-05	142/8023	cytokine signaling receptor activity
2	3e-05	6/43	protein binding
3	3e-05	6/43	chemokine activity
4	3e-04	11/227	receptor activity
5	3e-04	4/12	antigen binding
6	1e-03	6/86	Rac GTPase activator activity
7	2e-03	4/39	guanylyl-nucleotide exchange factor activity
8	3e-03	3/12	cell adhesion molecule binding
9	4e-03	6/107	coreceptor activity
10	4e-03	3/24	SH3 domain binding
11	5e-03	3/24	cytokine receptor activity
12	5e-03	1/2	electron carrier activity
13	5e-03	4/50	SH3/SH2 adaptor activity
14	7e-03	5/85	integrin binding
15	7e-03	15/529	protein homodimerization activity
16	8e-03	6/124	GTPase activator activity
17	8e-03	2/10	small GTPase binding
18	1e-02	2/11	regulatory region DNA binding
19	1e-02	2/12	fatty acid binding
20	1e-02	4/66	Rho guanylyl-nucleotide exchange factor activity

Rank	p-value	#in/all	Geneset
1	0.2	1/13	miR-15b
2	1.0	0/16	miR-34a
3	1.0	0/16	let-7a
4	1.0	0/4	let-7b
5	1.0	0/4	let-7c
6	1.0	0/6	let-7d
7	1.0	0/13	let-7g
8	1.0	0/3	miR-1
9	1.0	0/5	miR-101
10	1.0	0/2	miR-101b
11	1.0	0/2	miR-106b
12	1.0	0/2	miR-107
13	1.0	0/4	miR-122
14	1.0	0/2	miR-124a
15	1.0	0/2	miR-125a
16	1.0	0/9	miR-125b
17	1.0	0/5	miR-126
18	1.0	0/7	miR-127
19	1.0	0/3	miR-128
20	1.0	0/4	miR-128b

Rank	p-value	#in/all	Geneset
1	0.1	0/13	BENTINK_ras.4
2	1.0	0/15	GUSTAFSON_P13K_UP
3	1.0	0/12	GUSTAFSON_P13K_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	

Rank	p-value	#in/all	Geneset
1	1e-05	28/316	Leukocyte adhesion molecule 1
2	1e-08	6/13	SPANG_BCL6-index2
3	3e-04	10/185	GENTLES_LPS_modul18
4	4e-03	2/7	ZHANG_IL6_IL8_IL10
5	2e-02	2/16	GENTLES_modul11
6	2e-01	1/16	RHODES_UNDIFFERENTIATED_CANCER
7	4e-01	1/33	Leukocyte adhesion molecule 1
8	1e+00	1/530	Lembocke_Normal_vs_Adenoma
9	0e+00	0/15	RHODES_CANCER_META_SIGNATURE
10	0e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	0e+00	0/15	LIU_BREAST_CANCER_GRADE_1_VS_3_UP
12	0e+00	0/10	LIU_BREAST_CANCER
13	0e+00	0/14	LIU_COMMON_CANCER_GENES
14	0e+00	0/14	LIU_LIVER_CANCER
15	0e+00	0/15	LIU_PROSTATE_CANCER_DN
16	0e+00	0/14	LIU_PROSTATE_CANCER_UP
17	0e+00	0/14	WANG_ER_UP
18	0e+00	0/9	WANG_ER_DN
19	0e+00	0/16	WOLFER_overlap genes

Rank	p-value	#in/all	Geneset
1	6e-05	1/752	IL6/IL6R2/IL6ST
2	3e-01	1/26	BCHETNIA_EBM-DM up
3	1e+00	2/375	IL6/IL6R2/IL6ST down
4	1e+00	1/7	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	

Rank	p-value	#in/all	Geneset
1	8e-82	88/417	WIRTH_Immune system
2	9e-02	1/6	WIRTH_Bone marrow
3	2e-01	1/6	WIRTH_Hippocampus
4	8e-01	1/127	WIRTH_Muscle
5	1e+00	1/400	WIRTH_Nervous system
6	1e+00	0/6	WIRTH_Pituitary gland
7	1e+00	0/26	WIRTH_Pancreas
8	1e+00	0/13	WIRTH_Sec. lymphoid organs
9	1e+00	0/12	WIRTH_Prim. lymphoid organs
10	1e+00	0/10	WIRTH_B-cells
11	1e+00	0/13	WIRTH_Tonsil
12	1e+00	0/13	WIRTH_Thymus
13	1e+00	0/12	WIRTH_Lymphocytes
14	1e+00	0/12	WIRTH_Globus pallidus
15	1e+00	0/15	WIRTH_Telencephalon
16	1e+00	0/13	WIRTH_Cortex cerebri
17	0e+00	0/13	WIRTH_Triolamus
18	1e+00	0/15	WIRTH_Cerebellum
19	1e+00	0/120	WIRTH_Testis
20	1e+00	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.003	6/105	CTGC-208
2	0.080	1/6	CTGC-208
3	0.110	5/182	CTGA-24
4	0.233	2/66	GCTC-335
5	0.233	1/19	GTC-480-5P
6	0.252	5/244	GTGC-25-32-92-363-367
7	0.295	2/78	GTA-410
8	0.305	1/26	TAGA-182
9	0.306	1/80	GAG-484
10	0.310	2/81	AACT-223
11	0.324	1/28	GATA-409-5P
12	0.338	2/89	ATG-338
13	0.352	1/31	ACCA-509
14	0.400	2/99	CCTC-513
15	0.424	3/171	CTAT-153
16	0.452	1/45	ACT-146A-146B
17	0.467	1/45	IATC-488
18	0.467	1/45	GGCA-455
19	0.480	2/116	CAGC-370
20	0.486	1/66	CTC-388

Rank	p-value	#in/all	Geneset
1	0.03	1/18	hsa-miR-551a
2	0.15	1/12	hsa-miR-671-3p
3	0.15	2/51	hsa-miR-628-5p
4	0.16	1/9	hsa-miR-296-3p
5	0.21	1/17	hsa-miR-551b
6	0.28	1/23	hsa-miR-1225-5p
7	0.29	1/27	hsa-miR-129b
8	0.31	1/29	hsa-miR-1293
9	0.33	1/29	hsa-miR-296-5p
10	0.34	1/30	hsa-miR-486-5p
11	0.35	1/31	hsa-miR-617
12	0.36	1/32	hsa-miR-1229
13	0.37	1/33	hsa-miR-634
14	0.38	1/34	hsa-miR-615-5p
15	0.41	2/100	hsa-miR-33b
16	0.41	1/38	hsa-miR-517*
17	0.43	2/106	hsa-miR-526b
18	0.44	2/11	hsa-miR-390-5p
19	0.45	1/43	hsa-miR-541

Rank	p-value	#in/all	Geneset
1	0.2	13/1095	HEBENSTREIT_high expression TF
2	0.2	10/1146	HEBENSTREIT_low expression TF
3	1.0	3/1233	KIM_MYC targets
4	1.0	0/5	MYC_TFs
5	1.0	0/63	MYC_Targets UP
6	1.0	0/9	MYC_Targets DOWN
7	1.0	0/4	MYC_Apoptosis UP
8	1.0	0/8	MYC_Cell cycle UP
9	1.0	0/2	MYC_Cell cycle DOWN
10	1.0	0/4	MYC_Cell growth and proliferation UP
11	1.0	0/2	MYC_Chromatin_modification UP
12	1.0	0/3	MYC_DNA repair UP
13	1.0	0/3	MYC_DNA replication UP
14	1.0	0/2	MYC_ECM cell adhesion DOWN
15	1.0	0/20	MYC_Metabolism UP
16	1.0	0/16	MYC_Protein synthesis degradation UP
17	1.0	0/8	MYC_RNA processing binding UP
18	1.0	0/2	MYC_Signal transduction UP
19	1.0	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	6e-17	23/162	plasma membrane
2	6e-13	81/2659	external side of plasma membrane
3	3e-10	37/835	integral to plasma membrane
4	3e-09	7/23	clathrin-coated endocytic vesicle membrane
5	2e-08	7/23	integral to luminal side of endoplasmic reticulum membrane
6	8e-08	7/28	transport vesicle membrane
7	2e-07	7/30	ER to Golgi transport vesicle membrane
8	4e-07	7/30	trans-Golgi network membrane
9	7e-07	6/24	immunological synapse
10	3e-06	7/46	endocytic vesicle membrane
11	2e-04	4/12	cell receptor complex
12	2e-05	47/1837	membrane
13	5e-05	12/215	lysosomal membrane
14	9e-05	33/1182	extracellular region
15	2e-04	9/153	lamellipodium
16	3e-04	9/153	endosome membrane
17	4e-04	8/129	membrane raft
18	5e-04	3/9	phagocytic cup
19	7e-04	6/3274	integral to membrane

Rank	p-value	#in/all	Geneset
1	4e-22	33/268	willscher_GBM_Verhaak-CL_expression_B_up
2	4e-22	33/265	willscher_GBM_Verhaak-MES_expression_B_up
3	4e-22	33/265	willscher_GBM_Verhaak-PNwt_expression_B_down
4	3e-07	8/49	Donson-innate immunity-associated with LTS in HGA
5	1e-06	4/7	Donson-cytotoxic effectors-associated with LTS in HGA
6	2e-06	7/8	Donson-migration tethering and rolling-associated with LTS in HGA
7	4e-05	4/5	Donson-chemokines/cytokines-associated with LTS in HGA
8	7e-05	5/32	Donson-Misc immune function-associated with LTS in HGA
9	4e-07	4/17	Donson-chemokine/cytokine-receptors-associated with LTS in HGA
10	4e-03	2/7	Donson-adaptive-immunity-associated with LTS in HGA
11	2e-02	2/14	Donson-immune cell intra signaling-associated with LTS in HGA
12	4e-02	3/55	OL vs MCG-OL
13	5e-02	3/58	Christensen_hypomethylated_in_secondary_glioblastoma

# Sample-Overexpression

## Spot Summary: H

# metagenes = 6  
# genes = 68

<r> metagenes = 0.98

<r> genes = 0.42

beta: r2= 18.38 / log p= -Inf

# samples with spot = 50 ( 18.2 % )

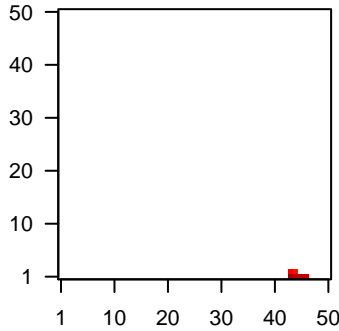
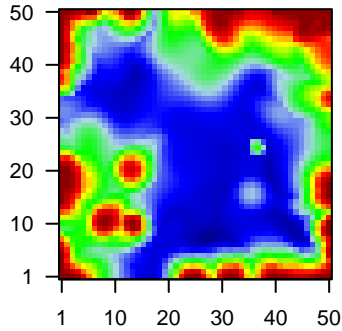
Atypical : 41 ( 55.4 % )

Mesenchymal : 6 ( 7.1 % )

Basal : 3 ( 3.6 % )

Overview Map

Spot

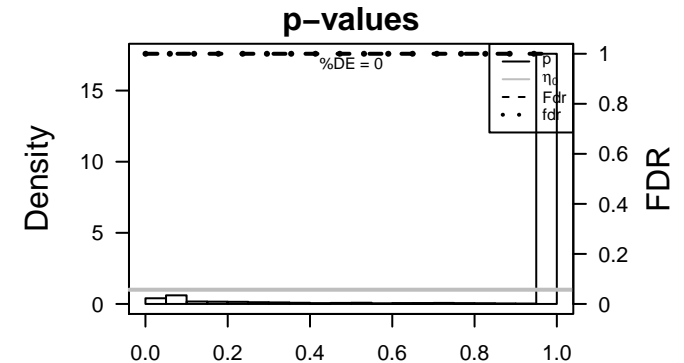
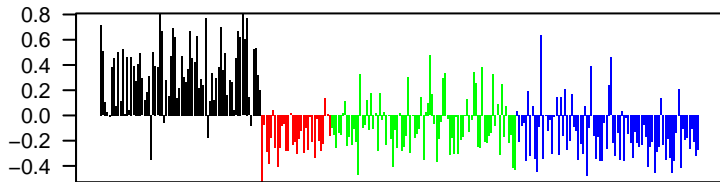


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	3127	4.47	-1.24	0.19	HLA-DRB1 major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:10242]
2	3123	3.58	-1.81	0.25	HLA-DRB1 major histocompatibility complex, class II, DR beta 1 [Source:HGNC Symbol;Acc:10241]
3	6364	3.07	-3.08	0.26	CCL20 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:10242]
4	169044	2.78	-1.11	0.36	COL22A1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:22986]
5	22809	2.1	-1.19	0.63	ATF5 activating transcription factor 5 [Source:HGNC Symbol;Acc:7122]
6	6376	2.05	-1.53	0.43	CX3CL1 chemokine (C-X3-C motif) ligand 1 [Source:HGNC Symbol;Acc:10242]
7	4248	2	-0.96	0.65	MGAT3 mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase III [Source:HGNC Symbol;Acc:10242]
8	3902	1.91	-0.73	0.72	LAG3 lymphocyte-activation gene 3 [Source:HGNC Symbol;Acc:6422]
9	80307	1.89	-0.84	0.64	
10	10062	1.87	-0.99	0.68	NR1H3 nuclear receptor subfamily 1, group H, member 3 [Source:HGNC Symbol;Acc:10242]
11	9235	1.87	-1.47	0.61	IL32 interleukin 32 [Source:HGNC Symbol;Acc:16830]
12	11067	1.82	-1.18	0.53	C10orf10 chromosome 10 open reading frame 10 [Source:HGNC Symbol;Acc:10242]
13	80162	1.79	-0.97	0.67	ATHL1 ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;Acc:10242]
14	864	1.76	-1.54	0.69	RUNX3 runt-related transcription factor 3 [Source:HGNC Symbol;Acc:10242]
15	84446	1.74	-1.13	0.68	BRSK1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18522]
16	441168	1.72	-0.96	0.64	FAM26F family with sequence similarity 26, member F [Source:HGNC Symbol;Acc:10242]
17	2120	1.7	-1.04	0.72	ETV6 ets variant 6 [Source:HGNC Symbol;Acc:3495]
18	7127	1.66	-0.92	0.42	TNFAIP2 tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:10242]
19	64780	1.54	-0.81	0.72	MICAL1 microtubule associated monoxygenase, calponin and LIM domain containing 1 [Source:HGNC Symbol;Acc:10242]
20	65108	1.52	-1.44	0.52	MARCKS MARCKS-like 1 [Source:HGNC Symbol;Acc:7142]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-06	10 / 426	Lymph SPANG_CD40 6hrs DN
2	4e-05	8 / 312	BP immune response
3	2e-04	6 / 204	BP cytokine-mediated signaling pathway
4	4e-04	9 / 553	Cancer Lemcke_Colonc Inflammation
5	5e-04	2 / 8	GSE/ OSAWA_TNF_TARGETS
6	7e-04	2 / 10	GSE/ LEE_EARLY_T_LYMPHOCYTE_DN
7	9e-04	6 / 274	Lymph SPANG_IL21 DN
8	9e-04	2 / 11	GSE/ PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP
9	9e-04	5 / 184	CC lysosome
10	1e-03	2 / 13	MMM MACIEJ_MMML 6
11	1e-03	3 / 52	miRN hsa-miR-513a-5p
12	2e-03	7 / 417	H.Tis: WIRTH_Immune system
13	2e-03	2 / 15	CC MHC class II protein complex
14	2e-03	2 / 15	GSE/ SABATES_COLORECTAL_ADENOMA_SIZE_UP
15	2e-03	2 / 15	GSE/ BASSO_B_LYMPHOCYTE_NETWORK
16	2e-03	2 / 15	GSE/ ZHAN_MULTIPLE_MYELOMA_CD1_UP
17	2e-03	9 / 686	CC Golgi apparatus
18	2e-03	3 / 60	BP interferon-gamma-mediated signaling pathway
19	2e-03	3 / 60	BP T cell costimulation
20	2e-03	2 / 16	BP negative regulation of neurogenesis
21	2e-03	2 / 16	GSE/ PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
22	2e-03	3 / 65	CC lysosomal lumen
23	3e-03	2 / 19	BP negative regulation of extrinsic apoptotic signaling pathway via death domain receptors
24	3e-03	4 / 143	MF transmembrane signaling receptor activity
25	3e-03	2 / 21	CC clathrin-coated endocytic vesicle membrane
26	4e-03	2 / 22	MF Rab guanyl-nucleotide exchange factor activity
27	4e-03	3 / 76	BP defense response
28	4e-03	2 / 23	CC integral to luminal side of endoplasmic reticulum membrane
29	5e-03	3 / 84	BP T cell receptor signaling pathway
30	5e-03	3 / 86	Lymph ROSOLOWSKI_red total
31	5e-03	3 / 87	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
32	6e-03	2 / 28	CC transport vesicle membrane
33	6e-03	2 / 28	TF Ti: VAQUERIZAS_Liver
34	6e-03	2 / 29	TF Ti: VAQUERIZAS_Lymph node
35	8e-03	2 / 32	CC ER to Golgi transport vesicle membrane
36	8e-03	2 / 33	BP defense response to Gram-positive bacterium
37	8e-03	1 / 2	miRN miR-193a
38	9e-03	2 / 34	BP positive regulation of tumor necrosis factor production
39	9e-03	2 / 35	CC trans-Golgi network membrane
40	9e-03	5 / 316	Cancer SPANG_BCL6-index2



Rank	p-value	#in/all	Geneset
1	2e-04	6/204	interferon response
2	2e-03	3/60	cytokine-mediated signaling pathway
3	2e-03	3/60	interferon-gamma-mediated signaling pathway
4	2e-03	3/60	T cell costimulation
5	1e-03	1/6	negative regulation of neurogenesis
6	3e-03	2/19	negative regulation of extrinsic apoptotic signaling pathway via death domain 1
7	4e-03	3/76	defense response
8	1e-03	1/6	TNFR receptor signaling pathway
9	3e-03	3/87	antigen processing and presentation of exogenous peptide antigen via MHC c
10	8e-03	2/33	defense response to Gram-positive bacterium
11	9e-03	2/34	positive regulation of tumor necrosis factor production
12	1e-02	2/47	positive regulation of interleukin-6 production
13	1e-02	3/123	defense response to virus
14	1e-02	2/45	positive regulation of catalytic activity
15	2e-02	2/47	antigen processing and presentation
16	2e-02	2/41	positive regulation of I-kappaB kinase/NF-kappaB signaling
17	3e-02	2/66	lipid catabolic process
18	3e-02	3/174	cellular response to DNA damage stimulus
19	4e-02	2/73	cellular response to lipopolysaccharide
20	4e-02	1/10	biotin metabolic process

Rank	p-value	#in/all	Geneset
1	0.02	1/10	CD19
2	0.03	7/714	Chr 6
3	0.19	1/52	Chr 22
4	0.21	3/156	Chr 22
5	0.23	4/602	Chr 10
6	0.34	4/717	Chr 16
7	0.34	3/84	Chr 14
8	0.36	3/519	Chr 14
9	0.52	4/918	Chr 17
10	0.54	1/187	Chr 21
11	0.56	1/957	Chr 11
12	0.62	1/232	Chr 18
13	0.65	2/534	Chr 8
14	0.70	3/866	Chr 12
15	0.74	3/143	Chr 3
16	0.80	3/1033	Chr 2
17	0.81	2/743	Chr 7
18	0.85	2/1720	Chr 7
19	0.90	2/1120	Chr 3
20	0.93	1/630	Chr X

Rank	p-value	#in/all	Geneset
1	9e-04	2/8	OSAWA_T1_TARGETS
2	7e-04	2/10	LEBARYL_T_LYMPHOCYTE_DN
3	9e-04	2/10	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP
4	2e-03	2/15	SABATES_COLORECTAL_ADENOMA_SIZE_UP
5	2e-03	2/15	BASSO_B_LYMPHOCYTE_NETWORK
6	2e-03	2/15	ZHANG_MULTIPLE_MYELOMA_CD1_UP
7	2e-03	2/16	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
8	2e-02	1/6	PENG GLUTAMINE DEPRIVATION_UP
9	2e-02	1/6	ST_INTERLEUKIN_T3_PATHWAY
10	2e-02	1/6	ST_IL13_PATHWAY
11	2e-02	1/6	SA_FAS_SIGNALING
12	3e-02	1/8	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
13	3e-02	1/8	KANGAS_AMPLIFICATION_HOT_SPOT_15
14	3e-02	1/8	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
15	3e-02	1/8	BOQUEST_STEM_CELL_DN
16	3e-02	1/8	ZEMBUTSD_SENSITIVITY_TO_MITOMYCIN
17	3e-02	1/8	FELSEN_LIPOSARCOMA_UP
18	3e-02	1/8	KEGG_TASTE_TRANSDUCTION
19	3e-02	1/8	ST_TYPE_1_INTERFERON_PATHWAY
20	4e-02	1/9	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS

Rank	p-value	#in/all	Geneset
1	0.003	2/23	interleukin-1 receptor signaling receptor activity
2	0.004	2/22	Rab guanyl-nucleotide exchange factor activity
3	0.011	2/39	enzyme activator activity
4	0.013	2/43	chemokine activity
5	0.030	1/298	protein kinase binding
6	0.040	1/10	endonucleolytic ribonuclease activity
7	0.040	1/10	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic
8	0.040	1/10	hydrolase activity, acting on glycosyl bonds
9	0.044	1/11	phospholipase C activity
10	0.044	1/11	tau-protein kinase activity
11	0.048	1/12	histone methyltransferase activity (H3-K4 specific)
12	0.049	1/12	ligase activity
13	0.054	5/500	sequence-specific DNA binding
14	0.064	1/16	ribonuclease activity
15	0.071	2/107	SH3 domain binding
16	0.071	1/18	gamma-tubulin binding
17	0.079	1/20	WW domain binding
18	0.083	1/21	Rac GTPase binding
19	0.088	1/21	cytokine activity
20	0.094	2/24	cytokine receptor activity

Rank	p-value	#in/all	Geneset
1	0.008	0/11	miR-133a
2	1.000	0/6	let-7a
3	1.000	0/6	let-7b
4	1.000	0/6	let-7c
5	1.000	0/6	let-7d
6	1.000	0/4	let-7g
7	1.000	1/3	miR-1
8	1.000	0/2	miR-101
9	1.000	0/2	miR-101b
10	1.000	0/4	miR-106b
11	1.000	0/107	miR-107
12	1.000	0/4	miR-122
13	1.000	0/2	miR-124a
14	1.000	0/69	miR-125a
15	1.000	0/5	miR-125b
16	1.000	0/5	miR-126
17	1.000	0/2	miR-127
18	1.000	0/4	miR-128
19	1.000	0/4	miR-128b
20	1.000	0/2	miR-129

Rank	p-value	#in/all	Geneset
1	0.013	0/13	GUSTAFSSON_Pi3K_UP
2	0.013	0/12	GUSTAFSSON_Pi3K_DN
3	0.011	0/11	BENTINK_e2f3
4	0.011	0/14	BENTINK_e2f3.2
5	0.011	0/14	BENTINK_myc.1
6	0.011	0/13	BENTINK_ras.1
7	0.011	0/11	BENTINK_ras.4
8	0.011	0/15	BENTINK_ras.6
9	0.013	0/13	BENTINK_src.10
10	0.013	0/4	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	

Rank	p-value	#in/all	Geneset
1	1e-04	1/4	IL12A
2	9e-03	5/316	IL12A
3	5e-02	1/13	SPANG_BCL6-index2
4	6e-02	1/15	LIU_PROSTATE_CANCER_DN
5	2e-01	2/185	SPANG_IL6-index2
6	9e-01	1/530	Lembcke_Normal vs Adenoma
7	1e+00	0/15	RHODES_CANCER_META_SIGNATURE
8	1e+00	0/16	PHOTOGENIA_EBM_up
9	1e+00	0/16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1e+00	0/10	LIU_BREAST_CANCER
12	1e+00	0/14	LIU_COMMON_CANCER_GENES
13	1e+00	0/14	LIU_LIVER_CANCER
14	1e+00	0/14	LIU_PROSTATE_CANCER_UP
15	1e+00	0/14	WANG_ER_UP
16	1e+00	0/9	WANG_DN
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

Rank	p-value	#in/all	Geneset
1	0.4	0/0	CD19
2	0.8	1/375	CD19
3	1.0	0/17	CD19
4	1.0	0/0	CD19
5	1.0	0/0	CD19
6	1.0	0/0	CD19
7	1.0	0/0	CD19
8	1.0	0/0	CD19
9	1.0	0/0	CD19
10	1.0	0/0	CD19
11	1.0	0/0	CD19
12	1.0	0/0	CD19
13	1.0	0/0	CD19
14	1.0	0/0	CD19
15	1.0	0/0	CD19
16	1.0	0/0	CD19
17	1.0	0/0	CD19
18	1.0	0/0	CD19
19	1.0	0/0	CD19
20	1.0	0/0	CD19

Rank	p-value	#in/all	Geneset
1	0.002	7/41	WIRTH_Immune system
2	0.002	5/21	WIRTH_Pituitary gland
3	0.006	0/26	WIRTH_Pancreas
4	0.006	0/13	WIRTH_Sec_lymphoid organs
5	0.006	0/12	WIRTH_PrIm_lymphoid organs
6	0.006	0/10	WIRTH_B-cells
7	0.006	0/13	WIRTH_Tonsil
8	0.006	0/13	WIRTH_Thymus
9	0.006	0/12	WIRTH_Lymphocytes
10	0.006	0/16	WIRTH_Bone marrow
11	0.006	0/400	WIRTH_Nervous System
12	0.006	0/14	WIRTH_Globus pallidus
13	0.006	0/15	WIRTH_Telencephalon
14	0.006	0/15	WIRTH_Cortex cerebri
15	0.006	0/16	WIRTH_Hippocampus
16	0.006	0/13	WIRTH_Thalamus
17	0.006	0/15	WIRTH_Cerebellum
18	0.006	0/120	WIRTH_Testis
19	0.006	0/50	WIRTH_Homeostasis
20	0.006	0/62	WIRTH_Liver

Rank	p-value	#in/all	Geneset
1	0.04	3/182	CGCT-503
2	0.07	1/18	GTAG-189
3	0.08	1/20	GAGC-149
4	0.089	2/120	GTAG-125B-125A
5	0.091	3/314	TTGC-130A-301-130B
6	0.14	1/41	GTCA-378
7	0.16	1/48	CGA-432
8	0.18	1/49	CGGA-483
9	0.20	1/55	GGGG-296
10	0.21	1/56	GTGG-197
11	0.22	4/57	GGGG-328
12	0.22	1/60	AGGG-328
13	0.24	3/415	TTTG-19A-19B
14	0.26	2/240	ACAT-1-206
15	0.26	1/231	GTAG-331
16	0.27	2/246	TGCT-330
17	0.27	1/76	GGCC-193A-193B
18	0.28	1/83	CG-184-18B
19	0.29	1/83	CGGA-316-3P
20	0.29	1/83	CGGA-316-3P

Rank	p-value	#in/all	Geneset
1	0.001	2/192	hsa-miR-5913a-5p
2	0.039	2/76	hsa-miR-1321
3	0.052	1/13	hsa-miR-1741-3p
4	0.056	1/14	hsa-miR-638
5	0.058	2/95	hsa-miR-133b
6	0.059	2/96	hsa-miR-133a
7	0.070	2/106	hsa-miR-1361-5p
8	0.072	2/108	hsa-miR-449b
9	0.086	2/119	hsa-miR-421
10	0.090	1/23	hsa-miR-608
11	0.094	2/264	hsa-miR-149a
12	0.102	2/132	hsa-miR-485-5p
13	0.112	3/285	hsa-miR-34a
14	0.120	1/31	hsa-miR-617
15	0.123	1/32	hsa-miR-899
16	0.130	1/34	hsa-miR-615-5p
17	0.130	1/34	hsa-miR-1226
18	0.134	1/35	hsa-miR-502-3p
19	0.148	1/39	hsa-miR-502-3p
20	0.148	1/39	hsa-miR-501-3p

Rank	p-value	#in/all	Geneset
1	0.3	6/1095	HEBESTREIT_high expression TF
2	0.6	4/1233	HEBESTREIT_high expression TF
3	0.9	3/146	HEBESTREIT_low expression TF
4	0.14	0/14	NOVICK_TF
5	0/5	0/5	MYC_TFs
6	0/63	0/63	MYC_TF_targets UP
7	0/9	0/9	MYC_TF_targets DOWN
8	0/4	0/4	MYC_Apoptosis UP
9	0/8	0/8	MYC_Cell cycle UP
10	0/2	0/2	MYC_Cell cycle DOWN
11	0/4	0/4	MYC_Cell growth and proliferation UP
12	0/2	0/2	MYC_Chromatin_modification UP
13	0/7	0/7	MYC_DNA repair UP
14	0/3	0/3	MYC_DNA replication UP
15	0/2	0/2	MYC_ECM cell adhesion DOWN
16	0/20	0/20	MYC_Metabolism UP
17	0/16	0/16	MYC_Protein synthesis degradation UP
18	0/8	0/8	MYC_RNA processing binding UP
19	0/2	0/2	MYC_Signal transduction UP
20	0/3	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	2e-03	2/15	MHC class II protein complex
2	2e-03	9/686	Golgi apparatus
3	2e-03	3/65	lysosomal lumen
4	3e-03	2/23	clathrin-coated endocytic vesicle membrane
5	4e-03	2/23	integral to luminal side of endoplasmic reticulum membrane
6	6e-03	2/28	transport vesicle membrane
7	6e-03	2/35	ER to Golgi transport vesicle membrane
8	6e-03	2/35	trans-Golgi network membrane
9	1e-02	4/215	lysosomal membrane
10	2e-02	2/46	endocytic vesicle membrane
11	2e-02	7/283	extracellular space
12	4e-02	2/77	late endosome membrane
13	4e-02	2/78	PML body
14	5e-02	1/12	exocyst
15	5e-02	2/380	nuclear chromatin
16	7e-02	4/380	intracellular membrane-bounded organelle
17	8e-02	1/19	histone methyltransferase complex
18	9e-02	1/29	clathrin adaptor complex
19	9e-02	1/29	dendritic shaft

Rank	p-value	#in/all	Geneset
1	0.02	1/15	willscher_GBM_STSwt_proteomics-L_UP
2	0.06	1/15	Donson-chemokines/cytokines-associated with LTS in HGA
3	0.09	3/265	willscher_GBM_Verhaak-CL_expression_B_up
4	0.09	3/265	willscher_GBM_Verhaak-MES_expression_B_up
5	0.09	3/265	willscher_GBM_Verhaak-PNwt_expression_B_down
6	0.09	3/265	willscher_GBM_Verhaak-PNmut_expression_B_down
7	0.12	1/32	Barbus_GBM_STS_vs_LTS
8	0.12	1/32	Donson-Misc immune function-associated with LTS in HGA
9	0.18	1	

# Sample-Overexpression

## Spot Summary: I

# metagenes = 3  
# genes = 89

<r> metagenes = 0.98  
<r> genes = 0.44  
beta: r2= 19.35 / log p= -Inf

# samples with spot = 46 ( 16.7 % )  
Atypical : 21 ( 28.4 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 18 ( 21.2 % )  
Basal : 5 ( 6 % )

## Spot Genelist

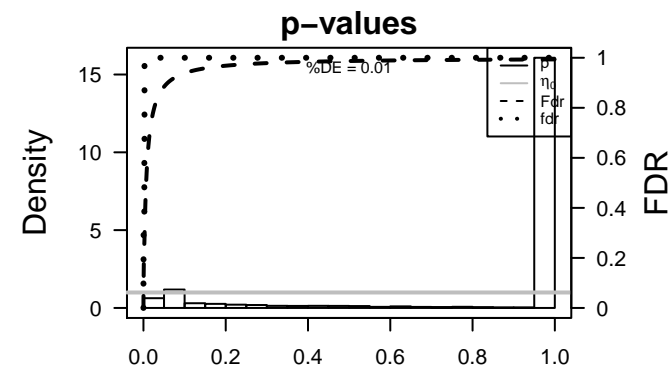
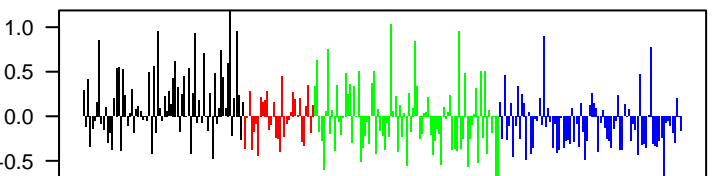
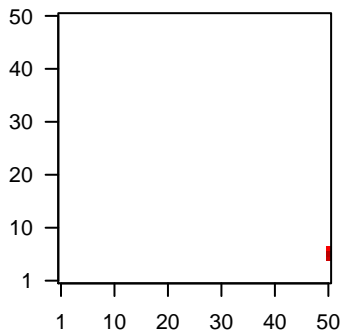
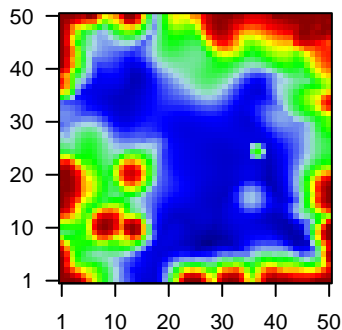
Rank	ID	max e	r	min e	Description
					Symbol
1	347733	3.34	-1.41	0.47	TUBB2B tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
2	347	3.19	-1.49	0.74	APOD apolipoprotein D [Source:HGNC Symbol;Acc:612]
3	2532	2.7	-1.57	0.74	DARC Duffy blood group, atypical chemokine receptor [Source:HGNC]
4	6358	2.45	-0.92	0.78	CCL14 chemokine (C-C motif) ligand 14 [Source:HGNC Symbol;Acc:
5	4256	2.36	-1.6	0.8	MGP matrix Gla protein [Source:HGNC Symbol;Acc:7060]
6	4239	2.35	-1.37	0.78	MFAP4 microfibrillar-associated protein 4 [Source:HGNC Symbol;Acc:
7	8404	2.29	-1.94	0.74	SPARCL1 SPARC-like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
8	1805	2.24	-1.01	0.74	DPT dermatopontin [Source:HGNC Symbol;Acc:3011]
9	3488	2.23	-2.24	0.64	IGFBP5 insulin-like growth factor binding protein 5 [Source:HGNC Sy
10	338773	2.2	-1.21	0.67	TMEM119 transmembrane protein 119 [Source:HGNC Symbol;Acc:2786
11	56892	2.2	-1.29	0.37	C8orf4 chromosome 8 open reading frame 4 [Source:HGNC Symbol
12	51176	2.16	-1.27	0.55	LEF1 lymphoid enhancer-binding factor 1 [Source:HGNC Symbol;A
13	5166	2.14	-0.7	0.7	PDK4 pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S
14	1359	2.14	-1.67	0.54	CPA3 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
15	90865	2.07	-0.95	0.57	IL33 interleukin 33 [Source:HGNC Symbol;Acc:16028]
16	23705	2.03	-1.02	0.46	CADM1 cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
17	7122	1.96	-0.98	0.51	CLDN5 claudin 5 [Source:HGNC Symbol;Acc:2047]
18	2219	1.91	-0.89	0.58	FCN1 ficolin (collagen/fibrinogen domain containing) 1 [Source:HG
19	6387	1.9	-0.76	0.81	CXCL12 chemokine (C-X-C motif) ligand 12 [Source:HGNC Symbol;A
20	1511	1.88	-1.23	0.64	CTSG cathepsin G [Source:HGNC Symbol;Acc:2532]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-10	12 / 190	CC extracellular matrix
2	5e-10	20 / 683	CC extracellular space
3	1e-08	24 / 1182	CC extracellular region
4	1e-08	14 / 375	Disea GUDJ_psooriasis down
5	3e-07	13 / 403	BP cell adhesion
6	4e-07	4 / 12	GSE/ BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN
7	6e-07	4 / 13	Cancr GENTLES_modul17
8	5e-06	5 / 46	Glio OL vs. OPC
9	7e-06	8 / 183	CC proteinaceous extracellular matrix
10	2e-05	5 / 59	Lymph LENZ_Stromal signature 2
11	2e-05	3 / 10	BP germ cell migration
12	5e-05	3 / 14	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
13	7e-05	3 / 15	GSE/ TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
14	8e-05	3 / 16	CC dystrophin-associated glycoprotein complex
15	1e-04	3 / 17	MF metalloproteinase activity
16	1e-04	3 / 19	BP calcium-independent cell-cell adhesion
17	1e-04	3 / 19	BP positive regulation of epithelial to mesenchymal transition
18	1e-04	3 / 19	TF Tr VAQUERIZAS_Pituitary
19	2e-04	3 / 20	BP complement activation
20	2e-04	2 / 4	GSE/ LU_TUMOR_ENDOTHELIAL_MARKERS_DN
21	2e-04	11 / 553	Cancr Lembcke_Colonc Inflammation
22	2e-04	4 / 55	Glio OL vs. MOG-OL
23	3e-04	3 / 23	MF peptidase inhibitor activity
24	3e-04	2 / 5	GSE/ SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_DN
25	4e-04	9 / 407	BP blood coagulation
26	4e-04	3 / 27	BP negative regulation of smooth muscle cell proliferation
27	5e-04	4 / 68	Glio cultured astroglia vs. in vivo astrocytes
28	6e-04	3 / 31	BP vasculature development
29	8e-04	3 / 34	MF endopeptidase inhibitor activity
30	9e-04	4 / 79	MF serine-type endopeptidase inhibitor activity
31	1e-03	2 / 9	GSE/ LEE_LIVER_CANCER
32	1e-03	2 / 9	GSE/ LEE_LIVER_CANCER_TOP50
33	1e-03	5 / 142	MF carbohydrate binding
34	1e-03	4 / 85	MF integrin binding
35	1e-03	2 / 10	BP angiotensin maturation
36	1e-03	2 / 10	BP cellular response to thyroid hormone stimulus
37	1e-03	2 / 10	GSE/ LU_TUMOR_VASCULATURE_DN
38	1e-03	2 / 10	GSE/ FERRANDO_LYL1_NEIGHBORS
39	1e-03	2 / 10	GSE/ EHRlich_ICF_SYNDROM_UP
40	1e-03	2 / 10	GSE/ REACTOME_INTRINSIC_PATHWAY

## Overview Map

## Spot



Rank	p-value	#in/all	Geneset
1	2e-05	3/10	cell adhesion
2	1e-04	3/19	calcium-independent cell-cell adhesion
3	1e-04	3/19	positive regulation of epithelial to mesenchymal transition
4	2e-04	3/19	complement activation
5	4e-04	9/407	blood coagulation
6	4e-04	3/27	negative regulation of smooth muscle cell proliferation
7	5e-04	3/11	vascular development
8	1e-03	3/10	angiostensin maturation
9	1e-03	2/10	cellular response to thyroid hormone stimulus
10	2e-03	2/11	blood coagulation, intrinsic pathway
11	2e-03	2/12	miRNA transcription from RNA polymerase II promoter
12	2e-03	2/12	regulation of glucose metabolic process
13	2e-03	3/45	negative regulation of angiogenesis
14	2e-03	6/242	extracellular matrix organization
15	2e-03	3/11	glucose metabolic process
16	3e-03	4/214	regulation of Wnt signaling pathway
17	3e-03	3/51	osteoblast differentiation
18	4e-03	4/114	positive regulation of cell migration
19	4e-03	5/188	brain development

Rank	p-value	#in/all	Geneset
1	0.06	8/316	Chr 4
2	0.12	6/618	Chr 4
3	0.14	13/1720	Chr 3
4	0.23	7/914	Chr 3
5	0.23	5/602	Chr 10
6	0.33	4/4534	Chr 8
7	0.33	5/698	Chr 6
8	0.35	5/924	Chr 6
9	0.45	4/633	Chr 9
10	0.50	6/1033	Chr 9
11	0.51	5/866	Chr 12
12	0.58	4/743	Chr 7
13	0.62	1/187	Chr 21
14	0.74	2/504	Chr 18
15	0.76	2/504	Chr 18
16	0.79	1/280	Chr 13
17	0.86	2/630	Chr X
18	0.88	1/386	Chr 22
19	0.88	1/918	Chr 17
20	0.90	3/957	Chr 11

Rank	p-value	#in/all	Geneset
1	8e-07	4/12	BERTUCCEAN INVASIVE CARCINOMA DUCTAL VS LOBULAR_DN
2	3e-05	3/15	SHIBUKAWA CANCER RELAPSE IN LUNGS_DN
3	7e-05	3/15	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
4	2e-04	2/4	LU TUMOR ENDOTHELIAL MARKERS_DN
5	3e-04	2/5	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_DN
6	1e-03	2/9	LEE_LIVER_CANCER
7	1e-03	2/9	LEE_LIVER_CANCER_TOP50
8	1e-03	2/10	LU TUMOR VASCULATURE_DN
9	1e-03	2/10	GRANDI_LY1_NEIGHBORS
10	1e-03	2/10	EHRLICH_ICF_SYNDROM_UP
11	1e-03	2/10	REACTOME_INTRINSIC_PATHWAY
12	2e-03	2/11	MASSARWEH_TAMOXIFEN_RESISTANCE_UP
13	2e-03	2/12	RIGBY_EWING_SARCOMA_PROGENITOR_DN
14	2e-03	2/12	SHI_SPARC_TARGETS_DN
15	2e-03	2/12	LEE_LIVER_CANCER_E2F1_DN
16	2e-03	2/12	ZHANG_MULTIPLE_MYELOMA_DN
17	2e-03	2/12	ZHANG_VI_LATE_DIFFERENTIATION_GENES_UP
18	2e-03	2/13	KAYO_CALORIE_RESTRICTION_MUSCLE_UP
19	2e-03	2/13	KEGG_RENIN_ANGIOTENSIN_SYSTEM
20	3e-03	2/14	KEGG_GASTRIC_CANCER_EARLY_DN

Rank	p-value	#in/all	Geneset
1	3e-04	3/23	metallopeptidase activity
2	3e-04	3/34	peptidase inhibitor activity
3	9e-04	4/79	endopeptidase inhibitor activity
4	1e-03	5/142	serine-type endopeptidase inhibitor activity
5	1e-03	4/85	carbohydrate binding
6	2e-03	2/13	integrin binding
7	3e-03	4/112	RNA polymerase II transcription regulatory region sequence-specific DNA binding
8	4e-03	4/112	heparin binding
9	5e-03	9/579	carboxypeptidase activity
10	5e-03	3/62	calcium ion binding
11	5e-03	3/62	protease binding
12	9e-03	2/26	PDZ domain binding
13	9e-03	2/26	E-box binding
14	9e-03	2/27	RNA polymerase II regulatory region sequence-specific DNA binding
15	1e-02	4/156	protein C-terminus binding
16	2e-02	2/36	cell adhesion molecule binding
17	2e-02	2/37	RNA polymerase II core promoter proximal region sequence-specific DNA binding
18	2e-02	4/186	structural molecule activity
19	2e-02	2/42	DNA binding, bending
20	2e-02	2/42	chemokine activity

Rank	p-value	#in/all	Geneset
1	0.001	1/1	miR-146b
2	0.027	1/5	miR-205
3	0.032	1/8	miR-221
4	0.043	1/8	miR-221
5	0.132	1/26	miR-21
6	1.000	0/11	let-7a
7	1.000	0/4	let-7b
8	1.000	0/4	let-7c
9	1.000	0/6	let-7d
10	1.000	0/4	let-7g
11	1.000	0/13	miR-1
12	1.000	0/5	miR-101
13	1.000	0/2	miR-101b
14	1.000	0/4	miR-106b
15	1.000	0/10	miR-107
16	1.000	0/4	miR-122
17	1.000	0/2	miR-124a
18	1.000	0/9	miR-125b
19	1.000	0/5	miR-126

Rank	p-value	#in/all	Geneset
1	0.06	2/13	BENTINK_e2f3.2
2	1.00	0/15	GUSTAFSON_Pi3K_UP
3	1.00	0/15	GUSTAFSON_Pi3K_DN
4	1.00	0/12	BENTINK_e2f3.1
5	1.00	0/14	BENTINK_myc.1
6	1.00	0/14	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	0/4	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	

Rank	p-value	#in/all	Geneset
1	2e-04	11/553	GENESET_modul17
2	3e-03	2/15	Lembcke_Colonc Inflammation
3	5e-02	1/15	GENTLES_modul13
4	5e-02	1/12	LIU_PROSTATE_CANCER_DN
5	7e-02	1/14	BEN-PORATH_DN
6	8e-02	1/15	LIU_PROSTATE_CANCER_UP
7	2e-01	3/316	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	2e-01	1/16	SPANG_BCL6-index2
9	4e-01	1/16	SPANG_LPS-index2
10	4e-01	2/530	Lembcke_Normal vs Adenoma
11	1e+00	0/15	RHODES_CANCER_META_SIGNATURE
12	1e+00	0/12	RHODES_UNDIFFERENTIATED_CANCER
13	1e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	1e+00	0/10	LIU_BREAST_CANCER
15	1e+00	0/14	LIU_COMMON_CANCER_GENES
16	1e+00	0/14	LIU_LIVER_CANCER
17	1e+00	0/14	WANG_ER_UP
18	1e+00	0/9	WANG_ER_DN
19	1e+00	0/16	WOLFET_overlap_genes
20	1e+00	0/15	BEN-PORATH_UP

Rank	p-value	#in/all	Geneset
1	1e-08	17/378	GUDDI_proliferas down
2	8e-01	2/572	GUDDI_proliferas 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	

Rank	p-value	#in/all	Geneset
1	0.002	2/13	WIRTH_Sec_lymphoid organs
2	0.008	1/13	WIRTH_Thalamus
3	0.074	1/16	WIRTH_Globus pallidus
4	0.084	1/16	WIRTH_Hippocampus
5	0.132	1/26	WIRTH_Pancreas
6	0.372	3/30	WIRTH_Nervous System
7	0.501	1/127	WIRTH_Muscle
8	0/5	0/5	WIRTH_Pituitary gland
9	0/417	0/417	WIRTH_Immune system
10	0/12	0/12	WIRTH_Prim_lymphoid organs
11	0/10	0/10	WIRTH_B-cells
12	0/13	0/13	WIRTH_Tonsil
13	0/13	0/13	WIRTH_Thymus
14	0/6	0/6	WIRTH_Lymphocytes
15	0/15	0/15	WIRTH_Bone marrow
16	0/13	0/13	WIRTH_Telencephalon
17	0/13	0/13	WIRTH_Cortex cerebri
18	0/15	0/15	WIRTH_Cerebellum
19	0/120	0/120	WIRTH_Testis
20	0/50	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.01	6/363	GAGC-200C-200C-429
2	0.03	3/120	GAGC-149
3	0.03	2/53	GCAA-502
4	0.04	2/96	ATCT-31
5	0.04	3/16	GATC-105
6	0.05	4/247	GTGC-96
7	0.06	3/165	TTTG-518A-2
8	0.06	2/26	GCCC-193A-193B
9	0.12	2/110	CAGC-512-3P
10	0.13	2/116	GACA-219
11	0.16	3/252	AGCA-302A-302B-302C-302D-372-373-520E-520A-520E
12	0.17	1/35	GCAA-431
13	0.19	2/145	AAAG-511
14	0.19	2/145	TTTTC19A-19B
15	0.20	1/40	GTA-200A
16	0.21	1/43	CCCA-299-3P
17	0.23	1/48	TATC-488
18	0.23	1/48	ACAT-90

Rank	p-value	#in/all	Geneset
1	0.002	3/64	hsa-miR-5639
2	0.005	3/64	hsa-miR-618
3	0.007	2/24	hsa-miR-1228
4	0.036	2/56	hsa-miR-831b
5	0.048	5/364	hsa-miR-519b-3p
6	0.059	4/269	hsa-miR-1244
7	0.060	5/387	hsa-miR-1519a
8	0.061	5/387	hsa-miR-1827
9	0.063	6/517	hsa-miR-106a
10	0.065	3/169	hsa-miR-374b
11	0.066	5/399	hsa-miR-519c-3p
12	0.068	1/13	hsa-miR-1234
13	0.074	5/412	hsa-miR-372
14	0.077	6/545	hsa-miR-93
15	0.087	6/567	hsa-miR-20b
16	0.095	3/199	hsa-miR-181c
17	0.103	1/20	hsa-miR-380*
18	0.110	6/603	hsa-miR-20a
19	0.116	7/28	hsa-miR-181a
20	0.128	1/25	hsa-miR-1273

Rank	p-value	#in/all	Geneset
1	0.05	11/126	HEBENSTREIT_low expression TF
2	0.935	2/1235	HEBENSTREIT_high expression TF
3	1.00	12/33	KIM_MYC targets
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 suppressor genes UP

Rank	p-value	#in/all	Geneset
1	5e-10	20/683	extracellular matrix
2	1e-08	24/1182	extracellular space
3	7e-06	8/183	extracellular region
4	3e-06	3/16	proteaceous extracellular matrix
5	1e-03	3/41	glycophorin-associated glycoprotein complex
6	2e-03	3/43	transport vesicle
7	3e-03	3/43	platelet alpha granule lumen
8	3e-03	3/43	coated pit
9	3e-03	3/82	sarcolemma
10	1e-02	4/162	external side of plasma membrane
11	1e-02	3/92	tight junction
12	2e-02	2/88	cytoplasmic side of plasma membrane
13	2e-02	4/198	transcription factor complex
14	3e-02	4/207	dendrite
15	4e-02	2/61	secretory granule
16	5e-02	2/2859	plasma membrane
17	5e-02	2/66	synaptic vesicle
18	5e-02	1/10	paranode region of axon
19	6e-02	1/11	Schmidt-Lanterman incisure
20	6e-02	1/11	platelet alpha granule

Rank	p-value	#in/all	Geneset
1	5e-06	5/46	OL vs. MCG-OL
2	2e-04	4/55	cultured astroglia vs. in vivo astrocytes
3	5e-04	4/68	GIEZELT_GBM_STSwt_down_VS_LTSwt
4	7e-03	3/27	laffaire_hypermeth_LGG_vs_CTRL
5	1e-02	3/85	willscher_GBM_proteomics_wtOnly_SpotB
6	2e-02	3/105	willscher_GBM_Verhaak_PNmwt_expression_A_down
7	2e-02	1/28	Christensen_hypermethylated_in_grade3_astrocytoma
8	2e-02	3/110	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	3e-02	2/49	Donson-innate immunity-associated with LTS in HGA
10	4e-02	3/32	Christensen_hypermethylated_in_grade3_oligoastrocytoma
11	4e-02	1/7	oligodendrocytes_glio
12	4e-02	3/142	

# Sample-Overexpression

## Spot Summary: J

# metagenes = 10  
# genes = 211

<r> metagenes = 0.98  
<r> genes = 0.51  
beta: r2= 11.17 / log p= -Inf

# samples with spot = 30 ( 10.9 % )  
Atypical : 22 ( 29.7 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 3 ( 3.6 % )

## Spot Genelist

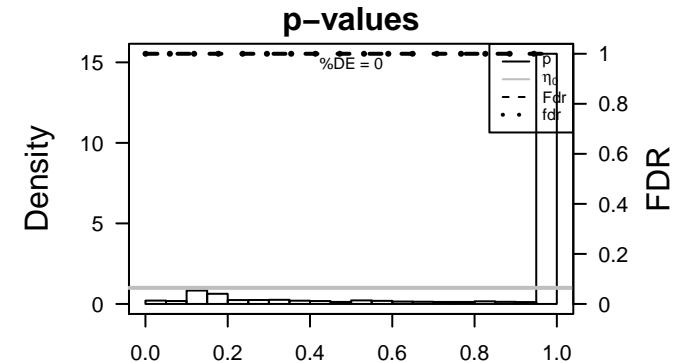
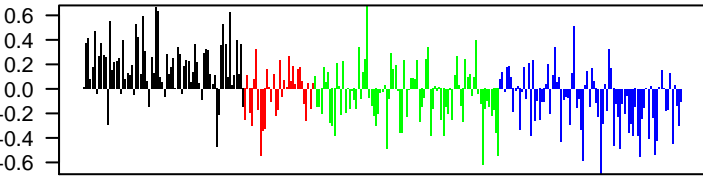
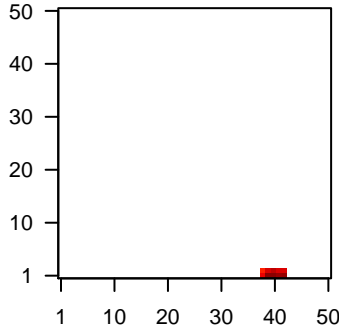
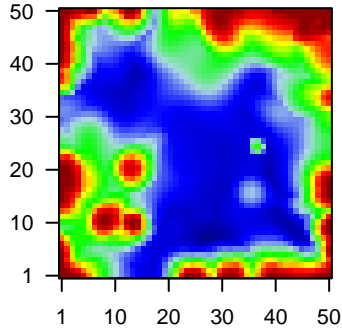
Rank	ID	max e	r	min e	Description
					Symbol
1	125050	2.79	-0.87	0.28	RN7SK RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
2	84061	1.78	-1.53	0.84	MAGT1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
3	126205	1.77	-1.63	0.93	NLRP8 NLR family, pyrin domain containing 8 [Source:HGNC Symbol;Acc:10037]
4	51326	1.73	-1.07	0.41	ARL17B ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc:10037]
5	401261	1.68	-0.87	0.83	
6	79058	1.66	-1.01	0.63	ASPSCR1 alveolar soft part sarcoma chromosome region, candidate 1 [Source:HGNC Symbol;Acc:10037]
7	618	1.64	-1.41	0.41	BCYRN1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
8	400818	1.62	-1.99	0.69	AC23981 neuroblastoma breakpoint family member 1 [Source:UniProtKB/Swiss-Prot]
9	29944	1.58	-0.69	0.61	PNMA3 paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187]
10	4851	1.57	-1.35	0.44	NOTCH1 notch 1 [Source:HGNC Symbol;Acc:7881]
11	25862	1.53	-1.56	0.93	USP49 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20037]
12	136051	1.51	-1.26	0.92	ZNF786 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
13	23466	1.49	-1.42	0.45	CBX6 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
14	85452	1.49	-1.23	0.78	C1orf222 chromosome 1 open reading frame 222 [Source:HGNC Symbol;Acc:10037]
15	55876	1.48	-0.91	0.71	GSDMB gasdermin B [Source:HGNC Symbol;Acc:23690]
16	80224	1.47	-1.22	0.9	NUBPL nucleotide binding protein-like [Source:HGNC Symbol;Acc:20037]
17	375775	1.46	-0.65	0.63	PNPLA7 patatin-like phospholipase domain containing 7 [Source:HGNC Symbol;Acc:10037]
18	728903	1.45	-1.04	0.66	
19	399761	1.43	-1.23	0.72	BMS1P5 BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653]
20	286257	1.42	-0.82	0.51	C9orf142 chromosome 9 open reading frame 142 [Source:HGNC Symbol;Acc:10037]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-06	31 / 1135	Chr Chr 19
2	4e-04	3 / 13	GSE# SPIRA_SMOKERS_LUNG_CANCER_DN
3	5e-04	3 / 14	MMM MACIEJ_MMML 8
4	7e-04	3 / 16	GSE# HAMAL_APOPTOSIS_VIA_TRAIL_UP
5	8e-04	2 / 4	GSE# BIOCARTA_CYTOKINE_PATHWAY
6	1e-03	3 / 19	BP sprouting angiogenesis
7	2e-03	34 / 1749	MF DNA binding
8	2e-03	4 / 44	BP meiosis
9	2e-03	21 / 918	Chr Chr 17
10	3e-03	3 / 24	BP negative regulation of T cell proliferation
11	5e-03	5 / 96	BP chromatin modification
12	6e-03	5 / 99	miRN CCTG-513
13	6e-03	3 / 33	MF DNA-dependent ATPase activity
14	7e-03	2 / 11	GSE# STEIN_ESRRA_TARGETS_DN
15	8e-03	2 / 12	GSE# BARRIER_COLON_CANCER_RECURRENCE_DN
16	8e-03	4 / 69	miRN hsa-miR-578
17	9e-03	3 / 38	MF methylated histone residue binding
18	9e-03	2 / 13	BP positive regulation of JAK-STAT cascade
19	9e-03	2 / 13	GSE# BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
20	9e-03	2 / 13	GSE# REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
21	9e-03	2 / 13	GSE# ST_GAQ_PATHWAY
22	9e-03	2 / 13	GSE# ST_GA13_PATHWAY
23	9e-03	4 / 72	BP forebrain development
24	1e-02	2 / 14	BP cellular response to estradiol stimulus
25	1e-02	2 / 14	BP mitochondrion morphogenesis
26	1e-02	2 / 15	BP female gamete generation
27	1e-02	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
28	1e-02	2 / 15	GSE# ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN
29	1e-02	2 / 15	GSE# THUM_SYSTOLIC_HEART_FAILURE_DN
30	1e-02	2 / 15	GSE# WANG_CLIM2_TARGETS_UP
31	1e-02	2 / 15	GSE# ZHOU_INFLAMMATORY_RESPONSE_LPS_DN
32	1e-02	2 / 15	GSE# FIRESTEIN_PROLIFERATION
33	1e-02	2 / 15	GSE# CAIRO_HEPATOBLASTOMA_UP
34	1e-02	2 / 15	GSE# JI_RESPONSE_TO_FSH_UP
35	1e-02	2 / 15	GSE# REACTOME_DARPP32_EVENTS
36	1e-02	2 / 15	GSE# REACTOME_SPHINGOLIPID_METABOLISM
37	1e-02	3 / 44	BP regulation of Rab GTPase activity
38	1e-02	2 / 16	BP cognition
39	1e-02	2 / 16	GSE# LUI_THYROID_CANCER_CLUSTER_1
40	1e-02	2 / 16	GSE# SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC

## Overview Map

## Spot







# Sample-Overexpression

## Spot Summary: K

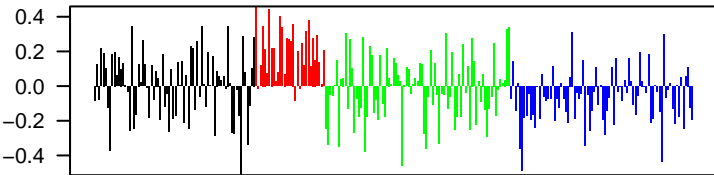
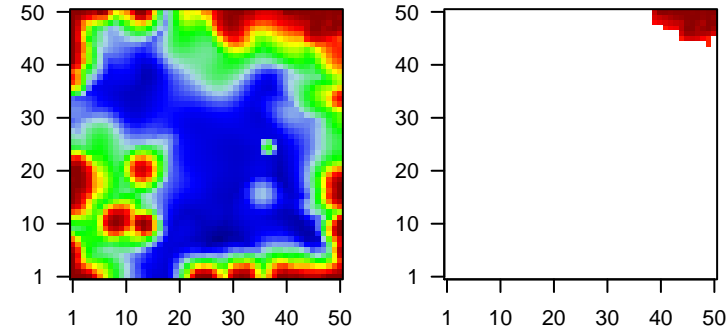
# metagenes = 60  
# genes = 766

<r> metagenes = 0.81  
<r> genes = 0.24  
beta: r2= 9.62 / log p= -Inf

# samples with spot = 14 ( 5.1 % )  
Atypical : 3 ( 4.1 % )  
Classical : 8 ( 25 % )  
Mesenchymal : 2 ( 2.4 % )  
Basal : 1 ( 1.2 % )

### Overview Map

### Spot

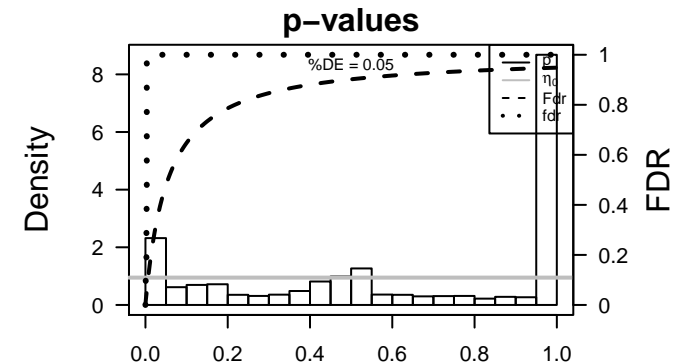


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
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;Acc:10000]
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 thiolesterase) [Source:HGNC Symbol;Acc:10000]
7	216	2.99	-2.41	0.63	ALDH1A1 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:10000]
8	83888	2.98	-0.56	0.37	FGFBP2 fibroblast growth factor binding protein 2 [Source:HGNC Symbol;Acc:10000]
9	154664	2.78	-1.49	0.67	ABCA13 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:10000]
10	2944	2.69	-1.57	0.43	GSTM1 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:10000]
11	339512	2.68	-1.34	0.5	C1orf110 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:10000]
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;Acc:10000]
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 Symbol;Acc:10000]
17	4072	2.5	-2.3	0.71	EPCAM epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:10000]
18	139728	2.48	-1.61	0.51	PNCK pregnancy up-regulated nonubiquitous CaM kinase [Source:HGNC Symbol;Acc:10000]
19	4915	2.4	-1.19	0.75	NTRK2 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC Symbol;Acc:10000]
20	2947	2.4	-0.99	0.43	GSTM3 glutathione S-transferase mu 3 (brain) [Source:HGNC Symbol;Acc:10000]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-92	95 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	1e-92	95 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	4e-67	118 / 370	BP mitotic cell cycle
4	3e-56	127 / 530	Cancer_Lembcke_Normal vs Adenoma
5	3e-35	139 / 949	CC nucleoplasm
6	8e-31	51 / 149	BP DNA replication
7	1e-27	59 / 232	BP mitosis
8	4e-22	16 / 16	GSE/ EGUCHI_CELL_CYCLE_RB1_TARGETS
9	5e-21	41 / 148	BP G1/S transition of mitotic cell cycle
10	5e-20	26 / 57	Glio developing astrocytes
11	1e-19	15 / 16	GSE/ FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
12	6e-19	202 / 2378	CC cytosol
13	9e-19	55 / 298	BP DNA repair
14	1e-18	19 / 30	BP DNA strand elongation involved in DNA replication
15	3e-18	14 / 15	GSE/ FINETTI_BREAST_CANCER_KINOME_RED
16	8e-18	24 / 56	CC chromosome, centromeric region
17	6e-17	25 / 66	CC condensed chromosome kinetochore
18	6e-17	13 / 14	MMM MACIEJ_MMML4
19	3e-16	75 / 572	Disease_GUDJ_psooriasis_up
20	1e-15	12 / 13	GSE/ CROONQUIST_IL6_DEPRIVATION_DN
21	2e-15	13 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_2
22	1e-14	97 / 914	Chr Chr3
23	4e-14	12 / 15	GSE/ CHANG_CYCLING_GENES
24	1e-13	12 / 16	GSE/ KANG_DOXORUBICIN_RESISTANCE_UP
25	1e-13	12 / 16	GSE/ CROONQUIST_NRAS_SIGNALING_DN
26	1e-13	12 / 16	GSE/ REACTOME_DNA_STRAND_ELONGATION
27	2e-13	19 / 49	BP telomere maintenance
28	3e-13	14 / 24	BP telomere maintenance via recombination
29	6e-13	13 / 21	BP telomere maintenance via semi-conservative replication
30	7e-13	11 / 14	GSE/ ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
31	7e-13	11 / 14	GSE/ ZHAN_MULTIPLE_MYELOMA_PR_UP
32	1e-12	12 / 18	BP spindle organization
33	1e-12	13 / 22	BP DNA replication initiation
34	2e-12	20 / 61	CC kinetochore
35	2e-12	303 / 4640	CC nucleus
36	2e-12	11 / 15	Cancer_SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
37	7e-12	11 / 16	Cancer_WOLFER_overlap genes
38	7e-12	11 / 16	GSE/ GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
39	7e-12	11 / 16	GSE/ SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
40	7e-12	11 / 16	GSE/ FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN



Rank	p-value	#in/all	Geneset
1	0	1	Gene ontology
2	8e-31	18 / 1371	DNA replication
3	8e-31	51 / 149	mitosis
4	8e-31	59 / 232	G2/M transition of mitotic cell cycle
5	2e-27	41 / 148	DNA repair
6	3e-28	53 / 238	DNA strand elongation involved in DNA replication
7	1e-18	19 / 30	telomere maintenance
8	2e-13	19 / 49	telomere maintenance via recombination
9	3e-13	14 / 24	telomere maintenance via semi-conservative replication
10	8e-33	13 / 21	spindle organization
11	1e-12	12 / 18	DNA replication initiation
12	1e-12	13 / 22	mitotic nuclear envelope disassembly
13	1e-12	13 / 22	mitotic nuclear envelope disassembly
14	1e-11	20 / 67	chromosome segregation
15	1e-11	12 / 22	CENP-A containing nucleosome assembly at centromere
16	1e-09	21 / 92	cell division
17	1e-09	18 / 18	nucleotide-excision repair, DNA gap filling
18	2e-09	24 / 122	G2/M transition of mitotic cell cycle
19	3e-09	8 / 11	mitotic metaphase plate congression
20	2e-08	32 / 213	cell cycle
21	1e-08	14 / 48	transcription-coupled nucleotide-excision repair

### Cancer

Rank	p-value	#in/all	Geneset
1	1e-14	76 / 523	Uterine leiomyomas
2	6e-11	17 / 375	Uterine leiomyomas
3	7e-11	1 / 26	BCHETNIA_EBM up
4	1e+00	0 / 17	BCHETNIA_EBM down
5	1e+00	0 / 2	
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	
21	NA	0 / 0	
22	NA	0 / 0	
23	NA	0 / 0	
24	NA	0 / 0	
25	NA	0 / 0	
26	NA	0 / 0	
27	NA	0 / 0	
28	NA	0 / 0	
29	NA	0 / 0	
30	NA	0 / 0	

### Disease

Rank	p-value	#in/all	Geneset
1	0.1	2 / 12	WIRTH_Lymphocytes
2	0.2	2 / 15	WIRTH_Telecephalon
3	0.2	1 / 13	WIRTH_Cerebellum
4	0.5	1 / 13	WIRTH_Thymus
5	0.5	1 / 13	WIRTH_Thalamus
6	0.8	3 / 120	WIRTH_Testis
7	1.0	11 / 400	WIRTH_Nervous System
8	1.0	11 / 417	WIRTH_Immune system
9	1.0	1 / 35	WIRTH_Mucosa
10	0.5	0 / 6	WIRTH_Pituitary gland
11	0.26	0 / 26	WIRTH_Pancreas
12	0.13	0 / 13	WIRTH_Sec. lymphoid organs
13	0.13	0 / 13	WIRTH_Prim. lymphoid organs
14	0.10	0 / 10	WIRTH_B-cells
15	0.13	0 / 13	WIRTH_Tonsils
16	0.16	0 / 16	WIRTH_Bone marrow
17	0.14	0 / 14	WIRTH_Globus pallidus
18	0.13	0 / 13	WIRTH_Cortex cerebri
19	0.16	0 / 16	WIRTH_Hippocampus

### Lymphoma

Rank	p-value	#in/all	Geneset
1	1e-09	26 / 140	DAVE_BCRs-DLBCL
2	1e-07	19 / 100	ROSOLOWSKI_plus total
3	9e-06	7 / 80	DAVE_c-myc BL UP
4	1e-04	58 / 755	SPANG_BCR UP
5	2e-03	11 / 86	ROSOLOWSKI_green UP
6	2e-02	11 / 119	BENTINK_mBL UP
7	1e-01	47 / 852	SPANG_BCR DN
8	2e-01	1 / 5	MASCOQUE_mBL UP
9	1e-01	4 / 24	Stuehr_Proteins up in STS
10	4e-01	14 / 275	ZHANG_DLBCL mutated
11	4e-01	21 / 426	SPANG_CD40 6hrs DN
12	4e-01	1 / 12	DAVE_BL UP
13	4e-01	1 / 14	WRIGHT_GCB UP
14	6e-01	1 / 18	DAVE_BL Inter
15	1e-01	13 / 291	SPANG_IL2 UP
16	6e-01	3 / 69	SPANG_LPS 6hrs DN
17	6e-01	5 / 118	SPANG_LPS 6hrs UP
18	8e-01	10 / 274	SPANG_IL21 DN

### MikRNA Disease

Rank	p-value	#in/all	Geneset
1	0.34	0 / 34	MicroRNA expression, papillary
2	0.22	0 / 22	Pancreatic cancer
3	0.21	0 / 21	Glioblastoma multiforme, somatic
4	0.36	0 / 36	Gastrointestinal
5	0.27	0 / 27	Hepatic adenoma
6	0.2	0 / 20	Colorectal cancer
7	0.35	0 / 35	Adenomas, multiple colorectal
8	0.11	0 / 11	Prostate cancer
9	0.3	0 / 30	Alzheimer disease, susceptibility to
10	0.5	0 / 5	Schizophrenia, susceptibility to
11	0.23	0 / 23	Parkinson disease
12	0.29	0 / 29	Hepatocellular carcinoma
13	0.30	0 / 30	Melanoma and neural system tumor syndrome
14	0.30	0 / 30	Ovarian cancer
15	0.28	0 / 28	Breast cancer
16	0.15	0 / 15	Gastric cancer
17	0.4	0 / 4	Thyroid carcinoma, follicular
18	0.36	0 / 36	Lung cancer
19	0.22	0 / 22	Bladder cancer

### Chromosome

Rank	p-value	#in/all	Geneset
1	1e-14	48 / 534	Chr 8
2	5e-10	65 / 1033	Chr 2
3	2e-02	54 / 127	Chr 12
4	1e-01	29 / 504	Chr 15
5	2e-01	14 / 232	Chr 18
6	2e-01	87 / 1720	Chr 7
7	3e-01	36 / 745	Chr 7
8	3e-01	32 / 630	Chr X
9	5e-01	29 / 618	Chr 21
10	6e-01	8 / 187	Chr 21
11	7e-01	12 / 280	Chr 13
12	8e-01	15 / 386	Chr 22
13	9e-01	29 / 714	Chr 6
14	9e-01	23 / 62	Chr 10
15	9e-01	24 / 633	Chr 9
16	9e-01	19 / 519	Chr 14
17	1e+00	1 / 52	Chr HSCR6_MHC_QBL
18	1e+00	14 / 249	Chr 20
19	1e+00	24 / 717	Chr 16

### HLISS

Rank	p-value	#in/all	Geneset
1	0.1	2 / 12	WIRTH_Lymphocytes
2	0.2	2 / 15	WIRTH_Telecephalon
3	0.2	1 / 13	WIRTH_Cerebellum
4	0.5	1 / 13	WIRTH_Thymus
5	0.5	1 / 13	WIRTH_Thalamus
6	0.8	3 / 120	WIRTH_Testis
7	1.0	11 / 400	WIRTH_Nervous System
8	1.0	11 / 417	WIRTH_Immune system
9	1.0	1 / 35	WIRTH_Mucosa
10	0.5	0 / 6	WIRTH_Pituitary gland
11	0.26	0 / 26	WIRTH_Pancreas
12	0.13	0 / 13	WIRTH_Sec. lymphoid organs
13	0.13	0 / 13	WIRTH_Prim. lymphoid organs
14	0.10	0 / 10	WIRTH_B-cells
15	0.13	0 / 13	WIRTH_Tonsils
16	0.16	0 / 16	WIRTH_Bone marrow
17	0.14	0 / 14	WIRTH_Globus pallidus
18	0.13	0 / 13	WIRTH_Cortex cerebri
19	0.16	0 / 16	WIRTH_Hippocampus

### MikRNA Target

Rank	p-value	#in/all	Geneset
1	0.03	7 / 58	hsa-miR-186
2	0.03	7 / 64	TCTG-361
3	0.04	15 / 198	ATGT-302C
4	0.06	3 / 19	GTCA-380-5P
5	0.07	6 / 60	AGCG-329
6	0.07	10 / 127	GACF-212-132
7	0.08	10 / 129	ACCA-522
8	0.10	7 / 84	ATGC-217
9	0.12	14 / 208	ATTC-186
10	0.12	7 / 88	ATCA-433
11	0.12	5 / 57	GTAA-302B
12	0.13	13 / 145	AAAG-111
13	0.17	10 / 4	CGGT-220
14	0.19	2 / 17	AGTC-151
15	0.19	5 / 66	GCTC-335
16	0.22	4 / 49	TCGC-191
17	0.22	3 / 35	CAGT-134
18	0.23	11 / 182	TAGC-9
19	0.23	11 / 182	TATT-873
20	0.23	10 / 85	TATC-126

### MikRNA Target

Rank	p-value	#in/all	Geneset
1	0.03	7 / 58	hsa-miR-186
2	0.03	7 / 64	TCTG-361
3	0.04	15 / 198	ATGT-302C
4	0.06	3 / 19	GTCA-380-5P
5	0.07	6 / 60	AGCG-329
6	0.07	10 / 127	GACF-212-132
7	0.08	10 / 129	ACCA-522
8	0.10	7 / 84	ATGC-217
9	0.12	14 / 208	ATTC-186
10	0.12	7 / 88	ATCA-433
11	0.12	5 / 57	GTAA-302B
12	0.13	13 / 145	AAAG-111
13	0.17	10 / 4	CGGT-220
14	0.19	2 / 17	AGTC-151
15	0.19	5 / 66	GCTC-335
16	0.22	4 / 49	TCGC-191
17	0.22	3 / 35	CAGT-134
18	0.23	11 / 182	TAGC-9
19	0.23	11 / 182	TATT-873
20	0.23	10 / 85	TATC-126

### MikRNA Target

Rank	p-value	#in/all	Geneset
1	0.03	7 / 58	hsa-miR-186
2	0.03	7 / 64	TCTG-361
3	0.04	15 / 198	ATGT-302C
4	0.06	3 / 19	GTCA-380-5P
5	0.07	6 / 60	AGCG-329
6	0.07	10 / 127	GACF-212-132
7	0.08	10 / 129	ACCA-522
8	0.10	7 / 84	ATGC-217
9	0.12	14 / 208	ATTC-186
10	0.12	7 / 88	ATCA-433
11	0.12	5 / 57	GTAA-302B
12	0.13	13 / 145	AAAG-111
13	0.17	10 / 4	CGGT-220
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18	0.23	11 / 182	TAGC-9
19	0.23	11 / 182	TATT-873
20	0.23	10 / 85	TATC-126

### HLISS

Rank	p-value	#in/all	Geneset
1	1e-29	16 / 146	EGUCHI_CELL_CYCLE_RB1_TARGETS
2	1e-29	13 / 199	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
3	1e-15	13 / 169	FINETTI_BREAST_CANCER_KINOME_RED
4	1e-15	12 / 13	CROONQUIST_IL6_DEPRIVATION_DN
5	1e-15	13 / 16	FARMER_BREAST_CANCER_CLUSTER_2
6	1e-13	48 / 25	KANG_CYCLE_CYCLING_GENES
7	1e-13	12 / 16	KANG_DOXORUBICIN_RESISTANCE_UP
8	1e-13	12 / 16	CROONQUIST_NRAS_SIGNALING_DN
9	1e-13	12 / 16	REACTIONE_DNA_STRAND_ELONGATION
10	1e-13	12 / 16	ROGATY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
11	7e-13	11 / 14	ZHAN_MULTIPLE_MYELOMA_PR_UP
12	7e-12	11 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	7e-12	11 / 18	GHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	7e-12	11 / 16	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP23_DN
15	7e-12	11 / 16	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
16	7e-12	11 / 16	REACTIONE_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
17	7e-12	11 / 16	REACTIONE_G2_M_CHECKPOINTS
18	9e-10	9 / 10	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
19	9e-11	9 / 11	KALMA_E2F1_TARGETS
20	9e-11	9 / 11	LIANG_SILENCED_BY_METHYLATION_DN

### MikRNA Target

Rank	p-value	#in/all	Geneset
1	0.03	7 / 58	hsa-miR-186
2	0.03	7 / 64	TCTG-361
3	0.04	15 / 198	ATGT-302C
4	0.06	3 / 19	GTCA-380-5P
5	0.07	6 / 60	AGCG-329
6	0.07	10 / 127	GACF-212-132
7	0.08	10 / 129	ACCA-522
8	0.10	7 / 84	ATGC-217
9	0.12	14 / 208	ATTC-186
10	0.12	7 / 88	ATCA-433
11	0.12	5 / 57	GTAA-302B
12	0.13	13 / 145	AAAG-111
13	0.17	10 / 4	CGGT-220
14	0.19	2 / 17	AGTC-151
15	0.19	5 / 66	GCTC-335
16	0.22	4 / 49	TCGC-191
17	0.22	3 / 35	CAGT-134
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### MikRNA Target

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4	0.06	3 / 19	GTCA-380-5P
5	0.07	6 / 60	AGCG-329
6	0.07	10 / 127	GACF-212-132
7	0.08	10 / 129	ACCA-522
8	0.10	7 / 84	ATGC-217
9	0.12	14 / 208	ATTC-186
10	0.12	7 / 88	ATCA-433
11	0.12	5 / 57	GTAA-302B
12	0.13	13 / 145	AAAG-111
13	0.17	10 / 4	CGGT-220
14	0.19	2 / 17	AGTC-151
15	0.19	5 / 66	GCTC-335
16	0.22	4 / 49	TCGC-191
17	0.22	3 / 35	CAGT-134
18	0.23	11 / 182	TAGC-9
19	0.23	11 / 182	TATT-873
20	0.23	10 / 85	TATC-126

# Sample-Overexpression

## Spot Summary: L

# metagenes = 18  
# genes = 348

<r> metagenes = 0.92  
<r> genes = 0.32  
beta: r2= 24.27 / log p= -Inf

# samples with spot = 48 ( 17.5 % )  
Atypical : 3 ( 4.1 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 43 ( 50.6 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

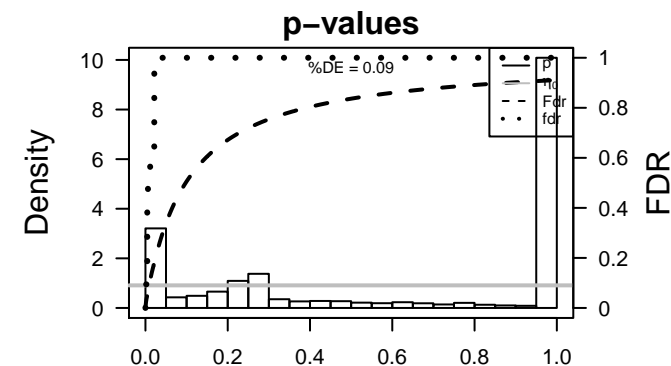
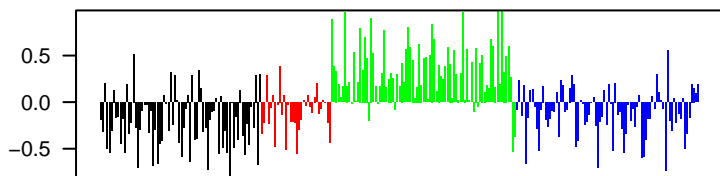
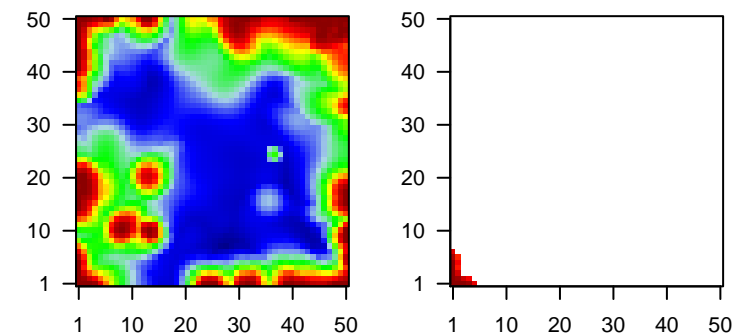
Rank	ID	max e	r	min e	Description
					Symbol
1	4319	4.09	-2.68	0.57	MMP10 matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
2	12	3.84	-2.36	0.4	RP11-986E7.7
3	3040	3.64	-2.76	0.32	HBA2 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	401138	3.58	-1.16	0.28	AMTN amelotin [Source:HGNC Symbol;Acc:33188]
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:f
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;Ac
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 Symbc
15	6372	3.07	-1.65	0.49	CXCL6 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Ac
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:524E

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-67	75 / 242	BP extracellular matrix organization
2	4e-62	72 / 250	LympL LENZ_Stromal signature 1
3	4e-57	62 / 190	CC extracellular matrix
4	4e-53	122 / 1182	CC extracellular region
5	3e-40	83 / 683	CC extracellular space
6	6e-34	31 / 69	BP extracellular matrix disassembly
7	8e-34	60 / 403	BP cell adhesion
8	2e-30	28 / 64	BP collagen catabolic process
9	2e-29	64 / 553	Cancer Lembecke_Colonc Inflammation
10	8e-25	15 / 16	MMM MACIEJ_MMM1
11	8e-24	26 / 83	CC basement membrane
12	1e-23	35 / 183	CC proteinaceous extracellular matrix
13	7e-23	40 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
14	7e-23	40 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
15	7e-23	40 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
16	7e-23	40 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
17	1e-19	20 / 57	MF extracellular matrix structural constituent
18	3e-18	12 / 15	GSE/ CROMER_TUMORIGENESIS_UP
19	1e-17	12 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_5
20	4e-17	24 / 119	Lymp ROSOLOWSKI_green total
21	3e-16	12 / 19	MF extracellular matrix binding
22	1e-14	19 / 85	MF integrin binding
23	2e-14	34 / 330	CC cell surface
24	4e-14	17 / 68	CC collagen
25	4e-14	17 / 68	Glio cultured astroglia vs. in vivo astrocytes
26	4e-14	10 / 15	GSE/ ONDER_CDH1_TARGETS_2_UP
27	1e-13	13 / 35	Glio Colman_survival_associated
28	1e-13	23 / 153	CC endoplasmic reticulum lumen
29	2e-13	26 / 204	BP angiogenesis
30	3e-13	13 / 37	BP collagen fibril organization
31	5e-13	20 / 117	Glio GIEZELT_GBM_WT_up_VS_mut
32	3e-12	9 / 15	GSE/ ONDER_CDH1_SIGNALING_VIA_CTNNB1
33	6e-12	8 / 11	MF platelet-derived growth factor binding
34	2e-11	8 / 12	miRN miR-29c
35	2e-11	15 / 72	CC extracellular vesicular exosome
36	2e-11	12 / 40	BP cellular response to amino acid stimulus
37	4e-11	8 / 13	GSE/ MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
38	1e-10	39 / 579	MF calcium ion binding
39	2e-10	32 / 407	BP blood coagulation
40	2e-10	8 / 15	GSE/ LEE_LIVER_CANCER_HEPATOBLAST

## Overview Map

## Spot





# Sample-Overexpression

## Spot Summary: M

# metagenes = 32  
# genes = 354

<r> metagenes = 0.93  
<r> genes = 0.27  
beta: r2= 5.97 / log p= -Inf

# samples with spot = 13 ( 4.7 % )

Atypical : 3 ( 4.1 % )

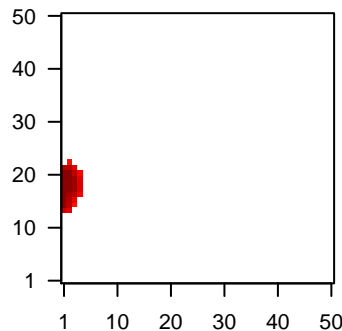
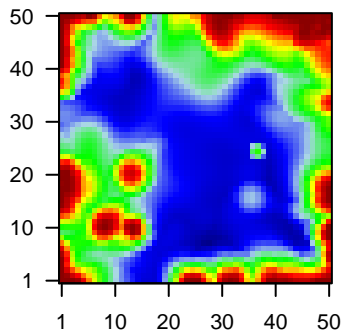
Classical : 1 ( 3.1 % )

Mesenchymal : 6 ( 7.1 % )

Basal : 3 ( 3.6 % )

Overview Map

Spot

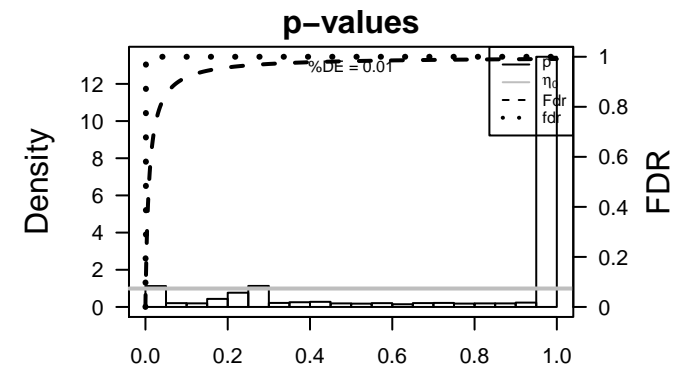
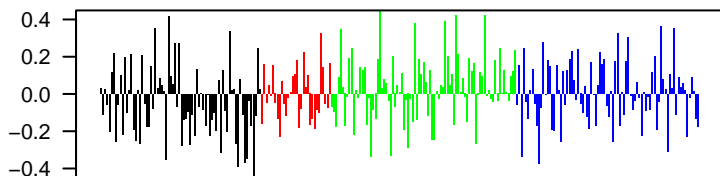


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	283869	2.84	-1.53	0.53	NPW neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	4495	2.82	-1.79	0.21	MT1G metallothionein 1G [Source:HGNC Symbol;Acc:7399]
3	220064	2.61	-1.08	0.48	ORAOV1 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175]
4	10202	2.48	-0.58	0.41	DHRS2 dehydrogenase/reductase (SDR family) member 2 [Source:HGNC Symbol;Acc:26874]
5	284085	2.29	-1.64	0.42	KRT18P5 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]
6	131076	2.28	-1.53	0.33	CCDC58 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:131076]
7	51083	2.28	-0.81	0.5	GAL galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:417]
8	8772	2.18	-1.29	0.52	FADD Fas (TNFRSF6)-associated via death domain [Source:HGNC Symbol;Acc:8772]
9	51702	2.13	-1.03	0.26	PADI3 peptidyl arginine deiminase, type III [Source:HGNC Symbol;Acc:51702]
10	1152	2.07	-1.8	0.37	CKB creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
11	219931	2.01	-0.93	0.56	TPCN2 two pore segment channel 2 [Source:HGNC Symbol;Acc:208]
12	51373	1.97	-1.11	0.64	MRPS1728S ribosomal protein S17, mitochondrial; HCG1984214, isoform 2 [Source:HGNC Symbol;Acc:51373]
13	2017	1.86	-1.24	0.42	CTTN cortactin [Source:HGNC Symbol;Acc:3338]
14	219927	1.84	-0.94	0.54	MRPL21 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;Acc:219927]
15	2821	1.69	-0.94	0.44	GPI glucose-6-phosphate isomerase [Source:HGNC Symbol;Acc:2821]
16	23246	1.68	-1.14	0.75	BOP1 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
17	93273	1.67	-0.94	0.31	LEMD1 LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
18	230	1.64	-1.33	0.36	ALDOC aldolase C, fructose-bisphosphate [Source:HGNC Symbol;Acc:230]
19	430	1.64	-1.34	0.32	ASCL2 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:430]
20	6884	1.58	-1	0.52	TAF13 TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor 13 [Source:HGNC Symbol;Acc:6884]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-19	82 / 1318	CC mitochondrion
2	2e-14	24 / 153	MF structural constituent of ribosome
3	1e-12	28 / 253	BP translation
4	7e-11	21 / 167	CC ribosome
5	2e-10	16 / 96	BP rRNA processing
6	1e-08	36 / 579	CC nucleolus
7	9e-08	39 / 717	Chr Chr 16
8	2e-07	23 / 304	CC mitochondrial inner membrane
9	2e-06	21 / 298	BP DNA repair
10	2e-06	6 / 19	CC mitochondrial small ribosomal subunit
11	4e-06	20 / 287	BP viral process
12	4e-06	51 / 1233	TF KIM_MYC targets
13	1e-05	9 / 66	BP positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
14	1e-05	5 / 15	GSE/ ZHANG_RESPONSE_TO_CANTHARIDIN_DN
15	2e-05	9 / 70	BP regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
16	2e-05	8 / 55	CC proteasome complex
17	2e-05	4 / 9	GSE/ BIOCARTA_GLYCOLYSIS_PATHWAY
18	3e-05	31 / 649	BP gene expression
19	3e-05	9 / 74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-dependent proteolysis
20	3e-05	27 / 530	Canco/ Lembcke_Normal vs Adenoma
21	4e-05	4 / 10	MF NADH dehydrogenase activity
22	4e-05	4 / 10	GSE/ REACTOME_HIV_LIFE_CYCLE
23	5e-05	8 / 62	BP negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
24	6e-05	4 / 11	GSE/ REACTOME_HIV_INFECTION
25	7e-05	7 / 48	BP regulation of cellular amino acid metabolic process
26	7e-05	9 / 83	BP respiratory electron transport chain
27	8e-05	6 / 34	MF NADH dehydrogenase (ubiquinone) activity
28	8e-05	8 / 66	BP transcription elongation from RNA polymerase II promoter
29	9e-05	10 / 106	BP protein polyubiquitination
30	9e-05	3 / 5	GSE/ NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
31	1e-04	6 / 36	CC mitochondrial respiratory chain complex I
32	1e-04	4 / 13	BP ribosomal small subunit biogenesis
33	1e-04	4 / 13	GSE/ XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
34	1e-04	4 / 13	GSE/ REACTOME_GLYCOLYSIS
35	2e-04	4 / 14	GSE/ LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
36	2e-04	4 / 14	GSE/ CHANG_CORE_SERUM_RESPONSE_UP
37	2e-04	4 / 15	CC mitochondrial large ribosomal subunit
38	2e-04	4 / 15	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
39	2e-04	4 / 15	GSE/ VANTVEER_BREAST_CANCER_BRCA1_UP
40	2e-04	46 / 1253	BP small molecule metabolic process



Rank	p-value	#in/all	Geneset
1	0.000	7/253	translational
2	2e-10	16/96	rRNA processing
3	2e-06	21/298	DNA repair
4	4e-06	20/287	viral process
5	1e-05	9/66	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
6	2e-05	9/70	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
7	3e-05	31/649	gene expression
8	3e-05	8/162	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent t
9	5e-05	6/62	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
10	7e-05	7/48	regulation of cellular amino acid metabolic process
11	7e-05	9/83	respiratory electron transport chain
12	8e-05	8/136	transcription elongation from RNA polymerase II promoter
13	9e-05	10/106	protein polyubiquitination
14	4/13	4/13	ribosomal small subunit biogenesis
15	2e-04	46/1253	small molecule metabolic process
16	2e-04	15/242	RNA metabolic process
17	3e-04	6/44	positive regulation of viral transcription
18	4e-04	7/63	DNA damage response, signal transduction by p53 class mediator resulting in protein targeting to mitochondrion
19	7e-04	6/47	antigen processing and presentation of exogenous peptide antigen via MHC c

Rank	p-value	#in/all	Geneset
1	8e-08	26/117	Chr16
2	9e-04	36/957	Chr11
3	9e-04	9/29	Chr HSCHR6_MHC_DBB
4	4e-02	18/534	Chr17
5	9e-02	23/743	Chr7
6	6e-02	27/918	Chr17
7	2e-01	15/174	Chr14
8	2e-01	13/449	Chr20
9	2e-01	11/386	Chr22
10	2e-01	28/1135	Chr18
11	3e-01	2/52	Chr HSCHR6_MHC_QBL
12	7e-01	14/714	Chr6
13	7e-01	34/1720	Chr1
14	9e-01	15/814	Chr3
15	9e-01	2/21	Chr21
16	9e-01	9/630	ChrX
17	9e-01	9/633	Chr9
18	9e-01	13/866	Chr12
19	1e+00	13/866	Chr18
20	1e+00	12/1033	Chr2

Rank	p-value	#in/all	Geneset
1	1e-05	5/15	ZNRING_RESPONSE_TO_CANTHARIDIN_DN
2	2e-05	28/874	BIOARTA_GLYCOLYSIS_PATHWAY
3	4e-05	4/10	REACTOME_HIV_LIFE_CYCLE
4	9e-05	4/11	REACTOME_HIV_INFECTION
5	9e-05	3/5	NIKOLSKY_BREAST_CANCER_1021_AMPLICON
6	1e-04	18/128	XU_RESPONSE_TO_TRETINOIN_AND_NS682994_DN
7	1e-04	4/13	REACTOME_GLYCOLYSIS
8	2e-04	4/14	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
9	4/14	4/14	CHIANG_CORE_SERUM_RESPONSE_UP
10	2e-04	4/14	WILUARYKOKU_OVARIAN_CANCER_LMP_UP
11	2e-04	4/15	VANTVEER_BREAST_CANCER_BRCA1_UP
12	3e-04	4/16	KORKOLA_EMBRYONAL_CARCINOMA_UP
13	3e-04	4/16	WONG_MITOCHONDRIA_GENE_MODULE
14	3e-04	4/16	MOOTHA_HUMAN_MITODB_6_2002
15	3e-04	4/16	MOOTHA_MITOCHONDRIA
16	3/7	3/7	PARK_HSC_MARKERS
17	3/9	3/9	MUELLER_PLURINET
18	7e-04	3/9	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
19	7e-04	3/9	MOREIRA_RESPONSE_TO_TSA_UP
20	7e-04	3/9	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE

Rank	p-value	#in/all	Geneset
1	4e-05	4/10	structural constituent of ribosome
2	6e-05	6/34	NADH dehydrogenase activity
3	7e-03	3/10	NADH dehydrogenase (ubiquinone) activity
4	3e-03	3/10	monosaccharide binding
5	3e-03	3/14	chaperone binding
6	3e-03	3/14	snoRNA binding
7	3e-03	23/595	RNA binding
8	3e-03	3/18	ribonucleoprotein complex binding
9	3e-03	3/18	threonine-type endopeptidase activity
10	7e-03	4/36	tRNA binding
11	9e-03	4/38	DNA-directed RNA polymerase activity
12	9e-03	4/38	unfolded protein binding
13	1e-02	3/24	DNA helicase activity
14	2e-02	3/25	Ran GTPase binding
15	2e-02	3/26	virus receptor activity
16	2e-02	3/26	four-way junction helicase activity
17	2e-02	3/27	tRNA binding
18	2e-02	3/28	ATP-dependent DNA helicase activity
19	2e-02	3/28	ribosome binding
20	2e-02	3/28	glutathione binding

Rank	p-value	#in/all	Geneset
1	0.08	2/7	miR-27
2	0.16	1/8	miR-155
3	0.48	1/9	miR-125b
4	1.00	0/26	miR-21
5	1.00	0/11	let-7a
6	1.00	0/6	let-7b
7	1.00	0/6	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	0/10	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-127
16	1.00	0/2	miR-124a
17	1.00	0/6	miR-125a
18	1.00	0/3	miR-129
19	1.00	0/3	miR-128

Rank	p-value	#in/all	Geneset
1	0.003	3/14	BENTINK_myc.1
2	1.000	0/13	BENTINK_ras
3	1.000	0/13	GUSTAFSON_P13K_UP
4	1.000	0/15	GUSTAFSON_P13K_DN
5	1.000	0/12	BENTINK_e2f3.1
6	1.000	0/11	BENTINK_e2f3.2
7	1.000	0/11	BENTINK_ras.4
8	1.000	0/15	BENTINK_ras.6
9	1.000	0/13	BENTINK_ras.10
10	1.000	0/14	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	

Rank	p-value	#in/all	Geneset
1	1e-300	6e-300	LU_C1orf113_vs_Adenoma
2	4e-03	3/15	GENTLES_modul1
3	4e-03	3/16	RHODES_UNDIFFERENTIATED_CANCER
4	4e-03	3/16	GENTLES_modul2
5	4e-03	3/16	GENTLES_modul7
6	2e-02	5/68	SHAUGHNESSY_MM_high_risk
7	3e-02	0/15	RHODES_CANCER_META_SIGNATURE
8	4e-02	2/15	SOTIROU_BREAST_CANCER_GRADE_1_VS_3_UP
9	4e-02	2/15	GENTLES_modul6
10	8e-02	3/48	KUiper_MM_poor_survival
11	2e-01	2/39	ZHANG_MM_up
12	3e-01	1/14	LIU_PROSTATE_CANCER_UP
13	3e-01	1/14	LIU_LIVER_CANCER
14	3e-01	1/15	BEN-PORATH_UP
15	3e-01	1/16	GENTLES_modul4
16	3e-01	1/16	SPANG_LPS-index2
17	1e+00	1/185	SOTIROU_BREAST_CANCER_GRADE_1_VS_3_DN
18	1e+00	0/15	LIU_COMMON_CANCER_GENES
19	1e+00	0/14	LIU_COMMON_CANCER_GENES

Rank	p-value	#in/all	Geneset
1	0.3	0/1	BCHETNIA_EBM_up
2	1.0	4/375	GUDJ_psooriasis_down
3	1.0	5/572	GUDJ_psooriasis_up
4	1.0	0/26	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	

Rank	p-value	#in/all	Geneset
1	0.02	2/10	WIRTH_F-cells
2	0.23	1/13	WIRTH_Lymphocytes
3	0.25	1/13	WIRTH_Sec_lymphoid_organs
4	0.25	1/13	WIRTH_Thalamus
5	0.28	1/15	WIRTH_Telencephalon
6	0.92	3/920	WIRTH_Testis
7	0.99	3/417	WIRTH_Immune_system
8	1.00	1/400	WIRTH_Nervous_System
9	1.00	0/26	WIRTH_Pituitary_gland
10	1.00	0/26	WIRTH_Pancreas
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	0/13	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

Rank	p-value	#in/all	Geneset
1	0.04	4/75	CGCA-324-3P
2	0.08	3/47	CCAG-490
3	0.28	2/49	CTAG-384
4	0.33	1/241	CTCA-125B-125A
5	0.34	1/19	GTCA-380-5P
6	0.34	2/66	GTGG-497
7	0.35	5/162	CTCA-302A
8	0.39	2/69	AGCT-28
9	0.44	3/120	GAGC-149
10	0.48	1/56	CTCA-302A
11	0.51	6/267	CACT-128A-128B
12	0.53	3/129	CTCT-520A-525
13	0.55	4/181	CCTG-214
14	0.56	1/52	TAG-592-215
15	0.60	1/42	CAGG-492
16	0.61	1/43	AGTT-146A-146B
17	0.61	1/43	CGCA-298-3P
18	0.61	1/43	CGCA-298-3P
19	0.61	1/43	CGCA-298-3P
20	0.61	1/43	CGCA-298-3P

Rank	p-value	#in/all	Geneset
1	6e-04	8/102	hsa-miR-27b
2	3e-03	7/88	hsa-miR-2423-5p
3	9e-03	6/83	hsa-miR-486-3p
4	1e-02	4/40	hsa-miR-516a-3p
5	1e-02	5/62	hsa-miR-637
6	1e-02	6/88	hsa-miR-149
7	2e-02	4/46	hsa-miR-174
8	2e-02	12/284	hsa-miR-503
9	2e-02	2/11	hsa-miR-604
10	2e-02	5/75	hsa-miR-422a
11	2e-02	5/75	hsa-miR-939
12	2e-02	5/77	hsa-miR-942
13	4e-02	4/58	hsa-miR-324-3p
14	4e-02	4/58	hsa-miR-592a
15	4e-02	5/83	hsa-miR-125b
16	5e-02	3/39	hsa-miR-647
17	5e-02	3/39	hsa-miR-593
18	6e-02	4/18	hsa-miR-664
19	7e-02	4/72	hsa-miR-857
20	7e-02	4/74	hsa-miR-1304

Rank	p-value	#in/all	Geneset
1	4e-06	51/233	MYC_targets
2	2e-03	6/63	MYC_Targets_UP
3	2e-03	6/63	MYC_Cell_growth_and_proliferation_UP
4	7e-03	36/1095	HEBENSTREIT_high_expression_TF
5	6e-02	1/3	MYC_DNA_replication_UP
6	6e-02	1/3	MYC_tumor_suppressor_genes_UP
7	9e-02	2/20	MYC_Metabolism_UP
8	1e-01	1/7	MYC_DNA_repair_UP
9	2e-01	1/8	MYC_Cell_cycle_UP
10	1e+00	3/1146	HEBENSTREIT_low_expression_TF
11	1e+00	0/14	NOWICK_TF
12	1e+00	0/5	MYC_TFs
13	1e+00	0/9	MYC_Targets_DOWN
14	1e+00	0/9	MYC_Apoptosis_UP
15	1e+00	0/2	MYC_Cell_cycle_DOWN
16	1e+00	0/2	MYC_Chromatin_modification_UP
17	1e+00	0/16	MYC_ECM_cell_adhesion_DOWN
18	1e+00	0/8	MYC_Protein_synthesis_degradation_UP
19	1e+00	0/8	MYC_RNA_processing_binding_UP
20	1e+00	0/2	MYC_Signal_transduction_UP

Rank	p-value	#in/all	Geneset
1	7e-11	21/167	nucleolus
2	1e-08	36/579	ribosome
3	2e-07	23/304	mitochondrial inner membrane
4	2e-06	6/19	mitochondrial small ribosomal subunit
5	2e-05	8/55	proteasome complex
6	1e-04	6/36	mitochondrial respiratory chain complex I
7	3e-04	4/23	mitochondrial large ribosomal subunit
8	3e-04	37/949	nucleoplasm
9	4e-04	4/17	proteasome accessory complex
10	5e-04	17/2378	cytosol
11	9/118	9/118	ribonucleoprotein complex
12	1e-03	5/37	mitochondrial nucleoid
13	1e-03	126/4640	nucleus
14	1e-03	4/23	mitochondrial ribosome
15	1e-03	3e0	3e0 complex
16	4e-03	5/48	cell body
17	4e-03	3/15	DNA-directed RNA polymerase III complex
18	5e-03	8/121	microtubule cytoskeleton
19	5e-03	3/121	proteasome core complex

Rank	p-value	#in/all	Geneset
1	0.002	6/12	StuB_mR_proteins_up_in_STS
2	0.004	9/142	wilscher_GBM_Verhaak-Cl_expression_C_up
3	0.004	9/142	wilscher_GBM_Verhaak-PNmut_expression_C_down
4	0.004	7/95	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
5	0.044	3/37	wilscher_GBM_proteomics_wOnly_SpotH
6	0.072	7/169	wilscher_GBM_proteomics_wOnly_Differencelist
7	0.073	4/24	GIEZELT_GBM_STS_up_VS_LTS
8	0.137	12/391	Down_b
9	0.169	10/328	Up
10	0.190	3/70	wilscher_GBM_proteomics_wOnly_SpotJ
11	0.201	3/72	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.229	1/1	

# Sample-Overexpression

## Spot Summary: N

# metagenes = 8  
# genes = 101

<r> metagenes = 0.99  
<r> genes = 0.65  
beta: r2= 10.8 / log p= -Inf

# samples with spot = 39 ( 14.2 % )  
Atypical : 9 ( 12.2 % )  
Classical : 4 ( 12.5 % )  
Mesenchymal : 18 ( 21.2 % )  
Basal : 8 ( 9.5 % )

## Spot Genelist

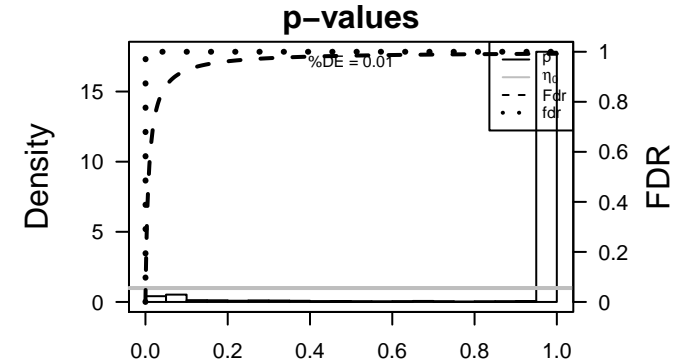
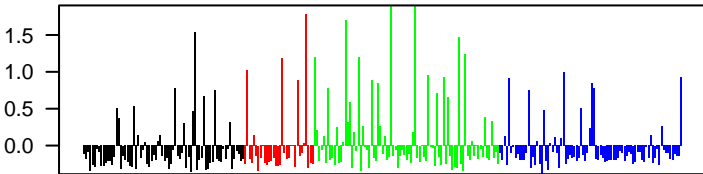
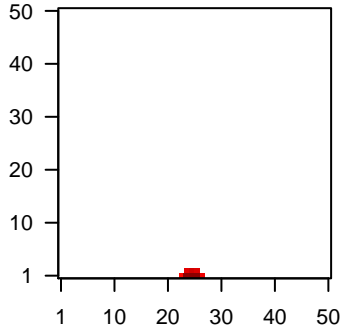
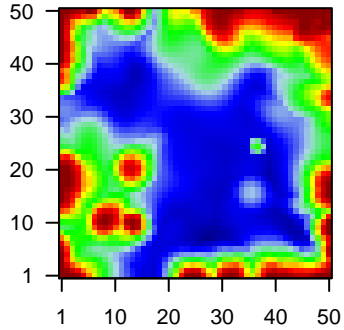
Rank	ID	max e	r	min e	Description
					Symbol
1	58	5.49	-1.44	0.9	ACTA1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	6588	4.37	-1.29	0.91	SLN sarcolipin [Source:HGNC Symbol;Acc:11089]
3	1158	4.27	-0.93	0.93	CKM creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	283120	4.19	-2.42	0.34	H19 H19, imprinted maternally expressed transcript (non-protein c
5	4620	3.96	-0.75	0.92	MYH2 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
6	70	3.94	-1.03	0.89	ACTC1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
7	4151	3.51	-0.93	0.9	MB myoglobin [Source:HGNC Symbol;Acc:6915]
8	10324	3.47	-0.7	0.95	KLHL41 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
9	4625	3.27	-0.73	0.88	MYH7 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
10	4633	3.2	-0.7	0.91	MYL2 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
11	7134	3.18	-0.66	0.93	TNNC1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
12	7060	3.17	-1.31	0.74	THBS4 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
13	8557	3.15	-0.57	0.95	TCAP titin-cap [Source:HGNC Symbol;Acc:11610]
14	4703	3.13	-0.92	0.88	NEB nebulin [Source:HGNC Symbol;Acc:7720]
15	4608	3.11	-0.84	0.84	MYBPH myosin binding protein H [Source:HGNC Symbol;Acc:7552]
16	1917	3.04	-1.6	0.56	EEF1A2 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
17	9499	3.03	-0.66	0.93	MYOT myotilin [Source:HGNC Symbol;Acc:12399]
18	2318	3	-1.57	0.81	FLNC filamin C, gamma [Source:HGNC Symbol;Acc:3756]
19	4619	2.82	-0.5	0.88	MYH1 myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC
20	4606	2.79	-0.54	0.92	MYBPC2 myosin binding protein C, fast type [Source:HGNC Symbol;Ac

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-93	55 / 127	H.Tis: WIRTH_Muscle
2	2e-43	23 / 36	BP muscle filament sliding
3	4e-38	22 / 44	MF structural constituent of muscle
4	2e-32	23 / 84	BP muscle contraction
5	3e-28	21 / 88	CC Z disc
6	4e-25	15 / 34	CC myofibril
7	1e-21	25 / 297	MF actin binding
8	1e-21	11 / 16	H.Tis: WIRTH_Hippocampus
9	1e-21	11 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_F
10	3e-21	10 / 12	CC myosin filament
11	3e-18	12 / 37	CC sarcomere
12	1e-15	9 / 20	CC I band
13	2e-15	8 / 13	CC muscle myosin complex
14	5e-15	8 / 14	CC contractile fiber
15	2e-14	8 / 16	CC M band
16	2e-13	7 / 12	MF titin binding
17	1e-12	9 / 37	BP cardiac muscle contraction
18	2e-12	7 / 15	BP striated muscle contraction
19	2e-12	7 / 15	GSE/ REACTOME_STRIATED_MUSCLE_CONTRACTION
20	3e-11	7 / 21	BP sarcomere organization
21	4e-11	6 / 12	BP skeletal muscle contraction
22	2e-10	10 / 88	BP muscle organ development
23	2e-10	8 / 42	CC myosin complex
24	8e-10	6 / 18	BP regulation of muscle contraction
25	4e-09	5 / 11	BP cardiac muscle tissue morphogenesis
26	2e-08	11 / 184	CC actin cytoskeleton
27	5e-08	7 / 56	MF motor activity
28	9e-08	17 / 579	MF calcium ion binding
29	1e-07	7 / 62	CC sarcolemma
30	4e-07	4 / 11	CC A band
31	5e-07	5 / 26	BP ventricular cardiac muscle tissue morphogenesis
32	7e-07	6 / 51	BP skeletal muscle tissue development
33	9e-07	6 / 53	MF cytoskeletal protein binding
34	1e-06	12 / 333	CC cytoskeleton
35	1e-06	4 / 14	BP adult heart development
36	1e-06	4 / 14	MF tropomyosin binding
37	2e-06	4 / 16	MF microfilament motor activity
38	4e-06	8 / 149	MF calmodulin binding
39	4e-06	4 / 18	BP regulation of the force of heart contraction
40	3e-05	31 / 2378	CC cytosol

## Overview Map

## Spot





Rank	p-value	#in/all	Geneset
1	0.06	10/318	muscle cell sliding
2	0.10	10/1033	muscle contraction
3	0.26	13/1720	cardiac muscle contraction
4	0.31	5/602	striated muscle contraction
5	0.33	5/618	sarcomere organization
6	0.44	4/504	skeletal muscle contraction
7	0.38	4/111	muscle organ development
8	0.42	7/232	regiation of muscle contraction
9	0.43	5/699	cardiac muscle tissue morphogenesis
10	0.46	7/717	ventricular cardiac muscle tissue morphogenesis
11	0.53	3/449	skeletal muscle tissue development
12	0.63	3/519	adult heart development
13	0.71	6/914	regulation of the force of heart contraction
14	0.75	6/1335	regulation of heart contraction
15	0.79	4/866	muscle cell differentiation
16	0.82	3/714	actin filament-based movement
17	0.84	3/743	skeletal muscle cell differentiation
18	0.91	2/1630	regulation of heart rate
19	0.91	1/386	positive regulation of muscle cell differentiation
20	0.91	1/386	creatine metabolic process

Rank	p-value	#in/all	Geneset
1	0.06	10/318	Chr 2
2	0.10	10/1033	Chr 1
3	0.26	13/1720	Chr 10
4	0.31	5/602	Chr 4
5	0.33	5/618	Chr 15
6	0.44	4/504	Chr 11
7	0.38	4/111	Chr 18
8	0.42	7/232	Chr 5
9	0.43	5/699	Chr 16
10	0.46	7/717	Chr 23
11	0.53	3/449	Chr 14
12	0.63	3/519	Chr 3
13	0.71	6/914	Chr 19
14	0.75	6/1335	Chr 7
15	0.79	4/866	Chr 6
16	0.82	3/714	Chr 7
17	0.84	3/743	Chr X
18	0.91	2/1630	Chr Y
19	0.91	1/386	Chr 22

Rank	p-value	#in/all	Geneset
1	1e-21	11/16	RICKMAN HEAD AND NECK CANCER F
2	9e-05	7/14	SARCOMER STRIATED MUSCLE CONTRACTION
3	8e-05	3/14	RORIE TARGETS OF EWSR1 FLT3 FUSION DN
4	8e-05	3/14	DAIRKEE CANCER PRONE RESPONSE BPA
5	1e-04	3/15	EBALIER MYOGENIC TARGETS OF PAX3 FOXO1 FUSION
6	1e-04	3/15	DAVICION TARGETS OF PAX_FOXO1_FUSIONS_DN
7	6e-04	2/26	BIOCARTA_HSP27_PATHWAY
8	2e-03	2/12	MOROSSETTI FACIOSCAPULOHUMERAL MUSCULAR_DISTROPHY_DN
9	2e-03	2/12	KEGG_GLYCOLYSIS_GLIUCONEGENESIS
10	3e-03	2/13	LIG SILENCED BY METHYLATION_UP
11	3e-03	2/13	REACTOME_GLUCOSE_METABOLISM
12	3e-03	2/13	REACTOME_GLYCOLYSIS
13	3e-03	2/14	LIG SILENCED BY METHYLATION_UP
14	3e-03	2/14	BIOCARTA_UCALPAIN_PATHWAY
15	4e-03	2/14	REACTOME_MUSCLE_CONTRACTION
16	4e-03	2/15	DAVICION_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
17	4e-03	2/15	METABO_GLYCOLYSIS
18	4e-03	2/15	BIOCARTA_INTEGRIN_PATHWAY
19	4e-03	2/15	REACTOME_GLYUCONEGENESIS
20	4e-03	2/15	REACTOME_MYOGENESIS

Rank	p-value	#in/all	Geneset
1	1e-21	25/297	structural constituent of muscle
2	2e-13	7/12	actin binding
3	5e-08	7/12	titin binding
4	9e-08	7/56	motor activity
5	1e-06	17/579	calcium ion binding
6	1e-06	6/53	cytoskeletal protein binding
7	1e-06	4/14	tropomyosin binding
8	4e-06	4/16	microfilament motor activity
9	4e-06	8/149	calmodulin binding
10	1e-04	5/77	actin filament binding
11	8e-04	66/8023	protein binding
12	2e-04	4/81	ion channel binding
13	2e-03	2/14	actin-dependent ATPase activity
14	3e-03	2/14	actin monomer binding
15	3e-03	2/14	structural constituent of eye lens
16	7e-03	2/20	myosin binding
17	1e-02	2/26	cytochrome-c oxidase activity
18	1e-02	2/26	E-box binding
19	2e-02	2/39	ATPase binding
20	2e-02	2/39	calcium-dependent protein binding

Rank	p-value	#in/all	Geneset
1	0.03	1/10	miR-320
2	1.00	0/11	let-7a
3	1.00	0/6	let-7b
4	1.00	0/6	let-7c
5	1.00	0/6	let-7d
6	1.00	0/4	let-7g
7	1.00	0/5	miR-1
8	1.00	0/2	miR-101
9	1.00	0/4	miR-101b
10	1.00	0/4	miR-106b
11	1.00	0/107	miR-107
12	1.00	0/4	miR-122
13	1.00	0/2	miR-124a
14	1.00	0/69	miR-125a
15	1.00	0/5	miR-125b
16	1.00	0/5	miR-126
17	1.00	0/2	miR-127
18	1.00	0/8	miR-128
19	1.00	0/4	miR-128b
20	1.00	0/2	miR-129

Rank	p-value	#in/all	Geneset
1	0/13	0/13	GUSTAFSON_P13K_UP
2	0/12	0/12	GUSTAFSON_P13K_DN
3	0/11	0/11	BENTINK_e2i3
4	0/14	0/14	BENTINK_e2i3.2
5	0/11	0/11	BENTINK_myc.1
6	0/13	0/13	BENTINK_ras.1
7	0/11	0/11	BENTINK_ras.4
8	0/15	0/15	BENTINK_ras.6
9	0/13	0/13	BENTINK_src.10
10	0/14	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	

Rank	p-value	#in/all	Geneset
1	1e-04	3/15	BENTINK_ORATH_UP
2	1e-02	3/9	WANG_ER_DN
3	8e-02	1/13	GENTLES_modul16
4	8e-02	1/14	LIU_LIVER_CANCER
5	1e+00	1/630	Leukemia_Normal_vs_Adenoma
6	1e+00	0/15	RHODES_CANCER_META_SIGNATURE
7	1e+00	0/16	RHODES_UNDIFFERENTIATED_CANCER
8	1e+00	0/15	SCITIROU_BREAST_CANCER_GRADE_1_VS_3_DN
9	1e+00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	1e+00	0/10	LIU_BREAST_CANCER
11	1e+00	0/14	LIU_COMMON_CANCER_GENES
12	1e+00	0/15	LIU_PROSTATE_CANCER_DN
13	1e+00	0/14	LIU_PROSTATE_CANCER_UP
14	1e+00	0/14	WANG_ER_UP
15	1e+00	0/16	WOLF_overlap_genes
16	1e+00	0/12	BEN_PORATH_DN
17	1e+00	0/15	GENTLES_modul1
18	1e+00	0/16	GENTLES_modul2
19	1e+00	0/10	GENTLES_modul3
20	1e+00	0/16	GENTLES_modul4

Rank	p-value	#in/all	Geneset
1	1e-04	10/378	GUO1_psoarosis_down
2	1e+00	0/572	GUO1_psoarosis_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	

Rank	p-value	#in/all	Geneset
1	1e-93	55/127	WIRTH_Muscle
2	1e-16	11/16	WIRTH_Hippocampus
3	7e-02	11/12	WIRTH Prim. lymphoid organs
4	2e-01	4/400	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	0/19	WIRTH_Hypothalamus
18	1e+00	0/15	WIRTH_Cerebellum
19	1e+00	0/120	WIRTH_Testis
20	1e+00	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.02	3/0	hsa-miR-518F--518F--526A
2	0.03	2/43	GACA-333
3	0.04	1/6	CCTC-208
4	0.04	2/49	AGGA-483
5	0.07	1/10	CTAC-023
6	0.08	3/161	AAGC-137
7	0.09	1/15	AGCG-518F--518E--518A
8	0.13	4/329	AATC-285--23B
9	0.18	1/114	TGT-146A--146B
10	0.18	1/32	CTCT-368
11	0.19	2/129	CTCT-520A--525
12	0.19	2/39	AGCA-522
13	0.21	1/39	GTAA-299-5P
14	0.22	1/41	GTCA-378
15	0.23	2/147	TGT-377
16	0.23	1/23	ATAT-46A--146B
17	0.26	2/158	ATAT-448
18	0.27	1/50	CAAG-362
19	0.28	1/53	GCAA-502
20	0.28	1/53	AATC-136

Rank	p-value	#in/all	Geneset
1	0.04	1/10	hsa-miR-566
2	0.07	1/12	hsa-miR-652
3	0.13	1/22	hsa-miR-596
4	0.15	1/23	hsa-miR-484
5	0.15	1/27	hsa-miR-483-3p
6	0.19	1/34	hsa-miR-615-5p
7	0.20	1/36	hsa-miR-54c-3p
8	0.24	1/44	hsa-miR-636
9	0.26	1/48	hsa-miR-146b-3p
10	0.27	1/50	hsa-miR-504
11	0.28	1/53	hsa-miR-519b-5p
12	0.28	1/53	hsa-miR-519c-5p
13	0.29	1/55	hsa-miR-891b
14	0.30	1/58	hsa-miR-184-5p
15	0.30	1/58	hsa-miR-520c-3p
16	0.32	1/61	hsa-miR-1236
17	0.33	1/64	hsa-miR-873
18	0.33	2/106	hsa-miR-299-3p
19	0.34	2/66	hsa-miR-499-3p
20	0.36	1/73	hsa-miR-509-5p

Rank	p-value	#in/all	Geneset
1	6e-04	17/146	HEBESTREIT_low expression TF
2	1e+00	3/1335	HEBESTREIT_high expression TF
3	1e+00	1233	KIM_MYC targets
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 suppressor genes UP

Rank	p-value	#in/all	Geneset
1	4e-25	15/34	myofibril
2	3e-21	10/12	myosin filament
3	3e-18	12/37	sarcomere
4	1e-19	9/10	band
5	2e-15	8/13	muscle myosin complex
6	5e-15	8/14	contractile fiber
7	2e-14	8/46	M band
8	2e-10	10/42	myosin complex
9	1e-08	11/184	actin cytoskeleton
10	1e-07	7/62	sarcolemma
11	4e-07	4/11	A band
12	1e-06	12/333	cytoskeleton
13	3e-05	31/2378	cytosolic reticulum membrane
14	3e-05	4/29	sarcolemmal adherens junction
15	3e-05	3/17	cell adhesion
16	6e-05	3/13	pseudopodium
17	7e-05	4/36	sarcoplasmic reticulum
18	1e-04	6/128	focal adhesion
19	3e-04	3/18	costamere

Rank	p-value	#in/all	Geneset
1	0.08	2/4	SHRIMP2_EBM_STS_up_VS_LTS
2	0.08	1/14	VERHAAK_NL_subtype
3	0.10	1/22	KIM deleted & downregulated in LTS
4	0.13	1/27	WIRTH_PN_subtype
5	0.16	1/28	Barbus_GBM_STS_vs_LTS
6	0.17	2/118	wilscher_GBM_Verhaak-CL_expression_K_down
7	0.17	2/118	wilscher_GBM_Verhaak-MES_expression_K_down
8	0.17	2/118	wilscher_GBM_Verhaak-PNwt_expression_K_up
9	0.17	2/118	wilscher_GBM_Verhaak-PNmut_expression_K_up
10	0.17	1/31	KIM prognostic signature LTS vs_STS
11	0.19	1/49	wilscher_GBM_proteomics_wOnly_SpotC
12	0.24	1/44	in vivo astrocytes vs. cultured astroglia
13	0.26	1/48	Noushmehr_Pron_GCIMP_hypermeth_DN
14			

# Sample-Overexpression

## Spot Summary: O

# metagenes = 29  
# genes = 488

<r> metagenes = 0.79  
<r> genes = 0.27  
beta: r2= 41.74 / log p= -Inf

# samples with spot = 70 ( 25.5 % )

Atypical : 1 ( 1.4 % )

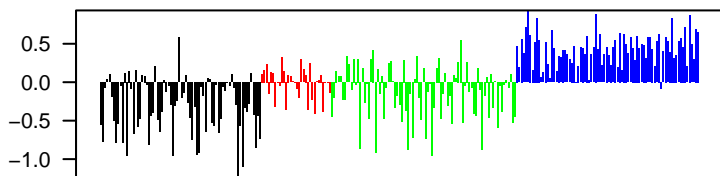
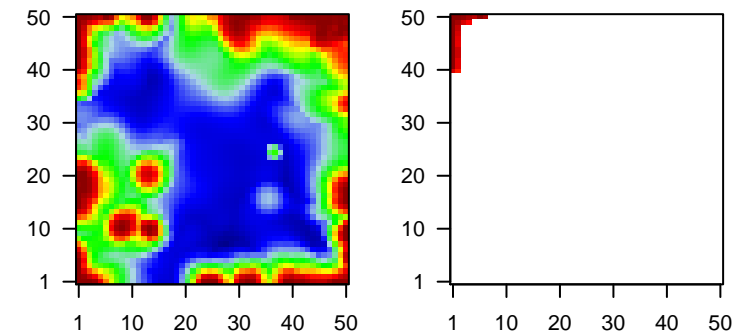
Classical : 1 ( 3.1 % )

Mesenchymal : 5 ( 5.9 % )

Basal : 63 ( 75 % )

Overview Map

Spot

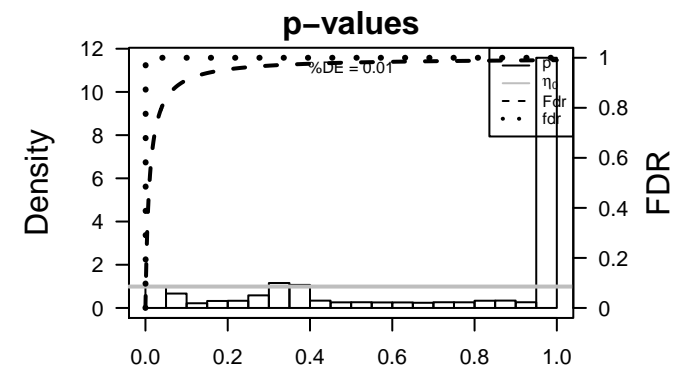


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	2167	5.04	-2.11	0.33	FABP4 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
2	3848	4.75	-1.88	0.67	KRT1 keratin 1 [Source:HGNC Symbol;Acc:6412]
3	3851	4.24	-3.19	0.57	KRT4 keratin 4 [Source:HGNC Symbol;Acc:6441]
4	49860	4.24	-3.23	0.72	CRNN cornulin [Source:HGNC Symbol;Acc:1230]
5	4118	3.95	-3.23	0.61	MAL mal, T-cell differentiation protein [Source:HGNC Symbol;Acc:
6	4014	3.86	-0.97	0.38	LOR lorocrin [Source:HGNC Symbol;Acc:6663]
7	1673	3.84	-3.54	0.67	DEFB4B defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	6701	3.84	-2.1	0.75	SPRR2B small proline-rich protein 2B [Source:HGNC Symbol;Acc:112
9	374918	3.79	-1.25	0.43	IGFL1 IGF-like family member 1 [Source:HGNC Symbol;Acc:24093]
10	6947	3.77	-1.96	0.46	TCN1 transcobalamin 1 (vitamin B12 binding protein, R binder family
11	414325	3.77	-2.67	0.71	DEFB103B defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	6706	3.74	-3.05	0.71	SPRR2G small proline-rich protein 2G [Source:HGNC Symbol;Acc:112
13	57152	3.69	-1.77	0.81	SLURP1 secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
14	2877	3.69	-3.11	0.44	GPX2 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
15	338324	3.66	-2.9	0.68	S100A7AS100 calcium binding protein A7A [Source:HGNC Symbol;Ac
16	7053	3.52	-3.39	0.81	TGM3 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
17	1828	3.51	-1.97	0.78	DSG1 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	55894	3.4	-1.83	0.73	DEFB103B defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	8644	3.37	-2.96	0.4	AKR1C3 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
20	84651	3.36	-1.82	0.74	SPINK7 serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	100 / 135	H.Tis: WIRTH_Mucosa
2	8e-91	139 / 572	Disea: GUDJ_psooriasis up
3	3e-29	32 / 76	BP epidermis development
4	2e-25	18 / 21	CC cornified envelope
5	1e-24	25 / 53	BP keratinocyte differentiation
6	4e-20	20 / 42	BP keratinization
7	8e-17	89 / 1182	CC extracellular region
8	1e-15	22 / 82	CC intermediate filament
9	2e-14	30 / 186	MF structural molecule activity
10	8e-14	12 / 21	CC desmosome
11	3e-12	10 / 16	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	3e-11	10 / 19	BP peptide cross-linking
13	2e-10	13 / 44	CC keratin filament
14	5e-10	12 / 38	BP epithelial cell differentiation
15	6e-10	72 / 1146	TF HEBENSTREIT_low expression TF
16	9e-10	16 / 79	MF serine-type endopeptidase inhibitor activity
17	2e-09	13 / 52	BP negative regulation of endopeptidase activity
18	3e-09	8 / 15	GSE/ WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
19	3e-09	8 / 15	GSE/ AIGNER_ZEB1_TARGETS
20	3e-09	8 / 15	GSE/ HINATA_NFKB_TARGETS_KERATINOCYTE_DN
21	5e-09	8 / 16	GSE/ ONDER_CDH1_TARGETS_3_DN
22	3e-08	7 / 13	H.Tis: WIRTH_Tonsil
23	9e-08	7 / 15	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
24	9e-08	7 / 15	GSE/ LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
25	1e-07	22 / 201	CC apical plasma membrane
26	2e-07	7 / 16	GSE/ CROMER_TUMORIGENESIS_DN
27	4e-07	120 / 2659	CC plasma membrane
28	5e-07	40 / 579	MF calcium ion binding
29	9e-07	6 / 13	BP negative regulation of peptidase activity
30	1e-06	8 / 29	BP regulation of proteolysis
31	2e-06	43 / 683	CC extracellular space
32	2e-06	6 / 15	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_E
33	3e-06	15 / 122	MF serine-type endopeptidase activity
34	4e-06	6 / 16	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
35	4e-06	6 / 16	GSE/ JAEGER_METASTASIS_DN
36	4e-06	6 / 16	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
37	4e-06	6 / 16	GSE/ LEE_LIVER_CANCER_MYC_TGFA_UP
38	5e-06	5 / 10	GSE/ KEGG_LINOLEIC_ACID_METABOLISM
39	5e-06	12 / 83	CC anchored to membrane
40	3e-05	11 / 82	MF structural constituent of cytoskeleton



Rank	p-value	#in/all	Geneset
1	0.00	76/200	Geneset
2	0.00	18/232	Chromosome development
3	0.01	24/534	keratinocyte differentiation
4	0.01	12/348	keratinization
5	0.01	10/119	peptide cross-linking
6	0.02	12/348	epithelial cell differentiation
7	0.09	13/52	negative regulation of endopeptidase activity
8	0.07	6/13	negative regulation of peptidase activity
9	0.07	8/44	regulation of proteolysis
10	0.05	8/44	skin development
11	0.05	6/25	brown fat cell differentiation
12	0.04	11/100	cell-cell adhesion
13	0.04	4/12	hemidesmosome assembly
14	0.04	9/76	wound healing
15	0.04	4/13	retinoic acid metabolic process
16	0.04	10/39	homophilic cell adhesion
17	0.04	6/20	retinoid metabolic process
18	0.03	4/16	ectoderm development
19	0.03	4/17	morphogenesis of an epithelium
20	0.03	8/73	disease response to bacterium
21	0.03	4/18	retinoid metabolic process

Rank	p-value	#in/all	Geneset
1	0.00	76/200	Geneset
2	0.00	18/232	Chr 18
3	0.01	24/534	Chr 8
4	0.01	12/348	Chr 10
5	0.01	2/23	Chr HSCHR6_MHC_DBB
6	0.01	30/866	Chr 12
7	0.01	19/519	Chr 19
8	0.01	5/1135	Chr 19
9	0.01	21/618	Chr 4
10	0.01	16/504	Chr 15
11	0.01	22/714	Chr 3
12	0.01	13/449	Chr 20
13	0.01	25/918	Chr 17
14	0.01	7/280	Chr 13
15	0.01	4/187	Chr HSCHR6_MHC_QBL
16	0.01	15/633	Chr 9
17	0.01	17/717	Chr 16
18	0.01	25/1033	Chr 2
19	0.01	15/699	Chr 5

Rank	p-value	#in/all	Geneset
1	0.00	10/16	HUPPER_BREAST_BASAL_VS_LUMINAL_UP
2	0.00	8/15	RICKMAN_TARGETS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
3	0.00	8/15	AIGNER_ZEB1_TARGETS
4	0.00	8/15	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
5	0.00	8/16	ONDER_CDH1_TARGETS_3_DN
6	0.00	7/15	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
7	0.00	7/15	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
8	0.00	7/16	CROMER_TUMORIGENESIS_DN
9	0.00	6/15	RICKMAN_HEAD_AND_NECK_CANCER_E
10	0.00	4e-06	SENPLATA_NASOPHARYNGEAL_CARCIOMA_DN
11	0.00	6/16	JAEGER_METASTASIS_DN
12	0.00	6/16	COLDREN_GEFITINIB_RESISTANCE_DN
13	0.00	6/10	KEGG_LIVER_CANCER_MYC_TGFA_UP
14	0.00	5/10	KEGG_LINOLEIC_ACID_METABOLISM
15	0.00	5/14	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
16	0.00	4/8	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
17	0.00	5/16	FARMER_BREAST_CANCER_CLUSTER_3
18	0.00	5/16	ELVIDGE_HIF1A_TARGETS_DN
19	0.00	5/16	WANG_BARRETTES_ESOPHAGUS_DN
20	0.00	5/16	FARMER_BREAST_CANCER_CLUSTER_4

Rank	p-value	#in/all	Geneset
1	0.00	16/89	serine-type endopeptidase activity
2	0.00	16/79	calcium ion binding
3	0.00	40/579	serine-type endopeptidase activity
4	0.00	15/122	structural constituent of cytoskeleton
5	0.00	11/42	protein binding, bridging
6	0.00	4/10	RAGE receptor binding
7	0.00	8/53	serine-type peptidase activity
8	0.00	8/34	endopeptidase inhibitor activity
9	0.00	5/23	peptidase inhibitor activity
10	0.00	7/50	Rab GTPase binding
11	0.00	4/15	interleukin-1 receptor binding
12	0.00	4/15	retinol dehydrogenase activity
13	0.00	4/19	laminin binding
14	0.00	4/22	cysteine-type endopeptidase inhibitor activity
15	0.00	10/125	iron ion binding
16	0.00	3/12	retinol binding
17	0.00	3/12	sodium channel activity
18	0.00	17/296	oxidoreductase activity
19	0.00	26/531	catalytic activity

Rank	p-value	#in/all	Geneset
1	0.00	2/5	miR-199a
2	0.00	2/5	miR-196a
3	0.00	2/13	miR-1
4	0.00	1/4	miR-206
5	0.00	1/6	miR-125a
6	0.00	0/69	miR-145
7	0.00	1/9	miR-125b
8	0.00	1/26	miR-21
9	0.00	0/11	let-7a
10	0.00	0/6	let-7b
11	0.00	0/4	let-7d
12	0.00	0/6	let-7d
13	0.00	0/4	let-7g
14	0.00	0/5	miR-101
15	0.00	0/5	miR-101b
16	0.00	0/4	miR-106b
17	0.00	0/2	miR-107
18	0.00	0/2	miR-122
19	0.00	0/2	miR-124a
20	0.00	0/5	miR-126

Rank	p-value	#in/all	Geneset
1	0.05	2/12	BENTINK_e23.1
2	0.07	1/12	GUSTAFSON_Pi3K_DN
3	0.07	1/12	BENTINK_ras
4	1.00	0/13	GUSTAFSON_Pi3K_UP
5	1.00	0/11	BENTINK_e23.2
6	1.00	0/4	BENTINK_myc
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	0/4	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	

Rank	p-value	#in/all	Geneset
1	0.00	25/533	Lembecke_Colonic_Inflammation
2	0.00	1/2	GENTLES_modul8
3	0.00	1/9	ZHANG_ILGS_up
4	0.00	1/7	WANG_ER_DN
5	0.00	0/14	LIU_PROSTATE_CANCER_UP
6	0.00	1/14	WANG_ER_UP
7	0.00	1/16	LIU_PROSTATE_CANCER_DN
8	0.00	1/16	GENTLES_modul4
9	0.00	1/16	GENTLES_modul1
10	0.00	1/33	KUIPER_MM_god11
11	0.00	5/85	SPANG_LP-index2
12	0.00	1/68	SHAUGHNESSY_MM_high_risk
13	0.00	4/316	SPANG_BCL6-index2
14	0.00	0/15	RHODES_CANCER_META_SIGNATURE
15	0.00	0/16	RHODES_INDIFFERENTIATED_CANCER
16	0.00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
17	0.00	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
18	0.00	0/14	LIU_BREAST_CANCER
19	0.00	0/14	LIU_COMMON_CANCER_GENES

Rank	p-value	#in/all	Geneset
1	0.00	138/592	Geneset
2	0.00	3/17	GDJL_psooriasis_up
3	0.00	3/26	BCHETNIA_EBM_up
4	0.00	3/26	BCHETNIA_EBM_DM_up
5	0.00	0/2	GDJL_psooriasis_down
6	0.00	0/2	BCHETNIA_EBM_down
7	0.00	0/0	
8	0.00	0/0	
9	0.00	0/0	
10	0.00	0/0	
11	0.00	0/0	
12	0.00	0/0	
13	0.00	0/0	
14	0.00	0/0	
15	0.00	0/0	
16	0.00	0/0	
17	0.00	0/0	
18	0.00	0/0	
19	0.00	0/0	
20	0.00	0/0	

Rank	p-value	#in/all	Geneset
1	0.00	100/135	WIRTH_Mucosa
2	0.00	7/13	WIRTH_Tonsil
3	0.00	2/13	WIRTH_Prim_lymphoid_organ
4	0.00	2/13	WIRTH_Thymus
5	0.00	1/13	WIRTH_Thalamus
6	0.00	1/15	WIRTH_Cerebellum
7	0.00	1/26	WIRTH_Pancreas
8	0.00	2/62	WIRTH_Liver
9	0.00	7/400	WIRTH_Nervous_System
10	0.00	1/20	WIRTH_Testis
11	0.00	0/5	WIRTH_Pituitary_gland
12	0.00	0/417	WIRTH_Immune_system
13	0.00	0/10	WIRTH_Sec_lymphoid_organ
14	0.00	0/12	WIRTH_B_cells
15	0.00	0/12	WIRTH_Lymphocytes
16	0.00	0/6	WIRTH_Bone_marrow
17	0.00	0/14	WIRTH_Globus_pallidus
18	0.00	0/15	WIRTH_Telencephalon
19	0.00	0/13	WIRTH_Cortex_cerebri
20	0.00	0/16	WIRTH_Hippocampus

Rank	p-value	#in/all	Geneset
1	0.00	3/190	hsa-miR-520H
2	0.00	2/20	GTAG-189
3	0.00	18/470	GCAC-17-5P-20A-106A-106B-20B-519D
4	0.00	4/73	AGGC-515-3P
5	0.00	5/10	AGC-104-10B
6	0.00	10/244	GTGC-25-32-92-363-367
7	0.00	7/163	CTTG-381
8	0.00	4/87	TCCT-128A-128B
9	0.00	4/89	TCCT-516-5P
10	0.00	9/239	TGCA-148A-152-148B
11	0.00	6/151	GTAT-369-3P
12	0.00	3/64	AAGG-188
13	0.00	3/65	CAGG-504
14	0.00	5/125	ACAC-199A-199B
15	0.00	9/248	TACT-26A-26B
16	0.00	1/13	TGCA-517A-517C
17	0.00	5/139	ATGC-517B
18	0.00	5/139	CTGC-520-525

Rank	p-value	#in/all	Geneset
1	0.001	4/27	hsa-miR-528
2	0.008	4/27	hsa-miR-675
3	0.011	4/30	hsa-miR-631
4	0.081	7/95	hsa-miR-988
5	0.068	7/122	hsa-miR-105
6	0.069	5/75	hsa-miR-1290
7	0.106	3/30	hsa-miR-35
8	0.106	3/39	hsa-miR-484
9	0.112	3/40	hsa-miR-450a
10	0.113	4/63	hsa-miR-1285
11	0.121	5/89	hsa-miR-505
12	0.125	17/426	hsa-miR-519d
13	0.134	8/172	hsa-miR-520h
14	0.135	2/22	hsa-miR-596
15	0.138	1/5	hsa-miR-1268
16	0.156	2/24	hsa-miR-632
17	0.164	1/6	hsa-miR-1281
18	0.164	1/6	hsa-miR-126
19	0.164	8/181	hsa-miR-381
20	0.166	2/25	hsa-miR-517c

Rank	p-value	#in/all	Geneset
1	0.00	72/146	HEBENSTREIT_low_expression_TF
2	0.00	1/20	MYC_Protein_synthesis_degradation_UP
3	0.00	1/20	MYC_Metabolism_UP
4	0.00	2/63	MYC_Targets_UP
5	0.00	19/1233	KIM_MYC_targets
6	0.00	0/14	HEBENSTREIT_high_expression_TF
7	0.00	0/14	NOWICK_TF
8	0.00	0/5	MYC_Tfs
9	0.00	0/9	MYC_Targets_DOWN
10	0.00	0/9	MYC_Apoptosis_UP
11	0.00	0/8	MYC_Cell_cycle_UP
12	0.00	0/2	MYC_Cell_cycle_DOWN
13	0.00	0/4	MYC_growth_and_proliferation_UP
14	0.00	0/2	MYC_Chromatin_modification_UP
15	0.00	0/7	MYC_DNA_repair_UP
16	0.00	0/3	MYC_DNA_replication_UP
17	0.00	0/8	MYC_ECM_cell_adhesion_DOWN
18	0.00	0/8	MYC_RNA_processing_binding_UP
19	0.00	0/2	MYC_Signal_transduction_UP
20	0.00	0/3	MYC_Tumor_suppressor_genes_UP

Rank	p-value	#in/all	Geneset
1	0.00	89/1182	Cell envelope
2	0.00	22/82	extracellular region
3	0.00	12/21	intermediate filament
4	0.00	12/21	desmosome
5	0.00	13/44	keratin filament
6	0.00	22/201	apical plasma membrane
7	0.00	120/2659	plasma membrane
8	0.00	12/683	extracellular space
9	0.00	7/32	anchored to membrane
10	0.00	165/4310	cell-cell adherens junction
11	0.00	13/137	cytoplasm
12	0.00	8/63	basolateral plasma membrane
13	0.00	11/117	Golgi lumen
14	0.00	6/37	cytoplasmic vesicle
15	0.00	7/44	lateral plasma membrane
16	0.00	4/15	annexin complex
17	0.00	41/835	integral to plasma membrane
18	0.00	4/16	microvillus membrane
19	0.00	5/27	basal plasma membrane
20	0.00	4/21	gap junction

Rank	p-value	#in/all	Geneset
1	0.00	12/132	Christensen_hypermethylated_in_grade2_oligoastrocytoma
2	0.00	7/49	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	0.00	9/35	Christensen_hypermethylated_in_primary_glioblastoma
4	0.00	10/110	Christensen_hypermethylated_in_grade3_astrocytoma
5	0.00	11/142	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	0.00	5/57	Christensen_hypermethylated_in_ependymoma
7	0.00	6/58	Christensen_hypermethylated_in_secondary_glioblastoma
8	0.00	7/83	Christensen_hypermethylated_in_secondary_glioblastoma
9	0.00	2/6	Martinez_Glio_hypermeth
10	0.00	5/48	Moushahar_Fron_GCIMP_hypermeth_DN
11	0.00	5/53	Christensen_hypermethylated_in_primary_glioblastoma
12	0.00	5/64	Christensen_hypermethylated_in_grade2_astrocytoma
13	0		

# Sample-Overexpression

## Spot Summary: P

# metagenes = 6  
# genes = 110

<r> metagenes = 0.99  
<r> genes = 0.28  
beta: r2= 7.64 / log p= -Inf

# samples with spot = 31 ( 11.3 % )  
Classical : 13 ( 40.6 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 14 ( 16.7 % )

## Spot Genelist

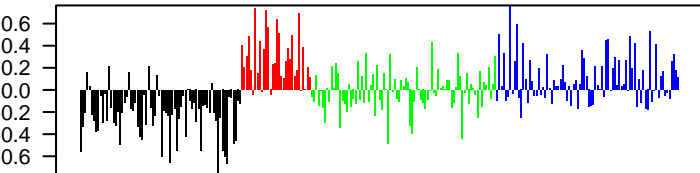
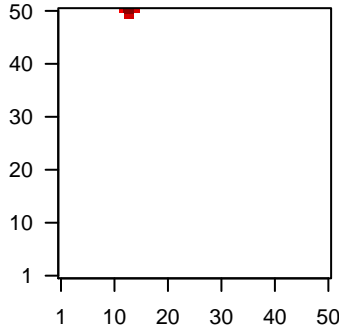
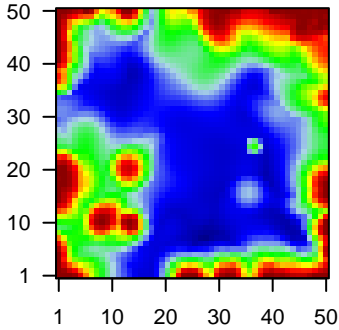
Rank	ID	max e	r	min e	Description
					Symbol
1	1109	3.73	-2.74	0.69	AKR1C4 aldo-keto reductase family 1, member C4 [Source:HGNC Sym]
2	57834	2.91	-1.53	0.7	CYP4F1 cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
3	1749	2.89	-1.7	0.51	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:2918]
4	1066	2.8	-0.72	0.47	CES1 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
5	1717	2.74	-1.44	0.42	DHCR7 7-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
6	140809	2.51	-1.38	0.73	SRXN1 sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
7	7102	2.39	-1.41	0.4	TSPAN7 tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
8	5217	2.22	-2.55	0.59	PFN2 profilin 2 [Source:HGNC Symbol;Acc:8882]
9	7062	2.14	-0.7	0.4	TCHH trichohyalin [Source:HGNC Symbol;Acc:11791]
10	7296	2.07	-0.96	0.54	TXNRD1 thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
11	493861	2.06	-0.82	0.49	EID3 EP300 interacting inhibitor of differentiation 3 [Source:HGNC
12	10457	2.06	-2.32	0.42	GNPMB glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
13	57007	2.05	-2.01	0.49	ACKR3 atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
14	1646	2.04	-1.84	0.67	AKR1C2 aldo-keto reductase family 1, member C2 [Source:HGNC Sym]
15	56666	1.9	-1.37	0.58	PANX2 pannexin 2 [Source:HGNC Symbol;Acc:8600]
16	406988	1.9	-1.65	0.3	MIR205HG MIR205 host gene (non-protein coding) [Source:HGNC Sym]
17	4741	1.88	-0.55	0.38	NEFM neurofilament, medium polypeptide [Source:HGNC Symbol;A
18	84002	1.88	-1.31	0.7	B3GNT5 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransf
19	2539	1.87	-1.09	0.61	G6PD glucose-6-phosphate dehydrogenase [Source:HGNC Symb
20	100288413	1.84	-0.96	0.49	ERVMSR endogenous retrovirus group MER34, member 1 [Source:HG

## Geneset Overrepresentation

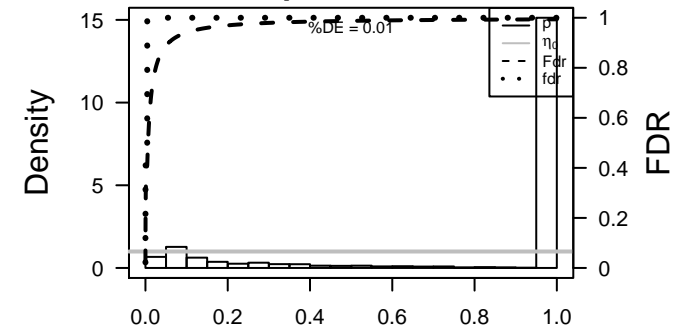
Rank	p-value	#in/all	Geneset
1	6e-06	42 / 3274	CC integral to membrane
2	6e-06	13 / 434	BP oxidation-reduction process
3	5e-05	10 / 316	BP modulation by virus of host morphology or physiology
4	7e-05	21 / 1253	BP small molecule metabolic process
5	8e-05	3 / 13	GSE/ SINGH_NFE2L2_TARGETS
6	1e-04	5 / 69	BP response to toxic substance
7	1e-04	3 / 15	GSE/ PODAR_RESPONSE_TO_ADAPHOSTIN_DN
8	2e-04	9 / 299	BP axon guidance
9	3e-04	3 / 19	BP anatomical structure formation involved in morphogenesis
10	4e-04	16 / 914	Chr Chr 3
11	4e-04	12 / 565	BP transmembrane transport
12	4e-04	15 / 835	CC integral to plasma membrane
13	5e-04	6 / 147	CC endosome
14	7e-04	3 / 26	MF virus receptor activity
15	7e-04	5 / 106	BP leukocyte migration
16	8e-04	8 / 296	MF oxidoreductase activity
17	8e-04	4 / 63	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
18	9e-04	31 / 2659	CC plasma membrane
19	1e-03	3 / 31	BP positive regulation of actin filament polymerization
20	1e-03	5 / 118	miRN hsa-miR-509-3p
21	1e-03	5 / 119	BP xenobiotic metabolic process
22	1e-03	3 / 32	MF ATPase activity, coupled to transmembrane movement of substances
23	1e-03	3 / 32	MF NADP binding
24	1e-03	4 / 71	BP pattern specification process
25	1e-03	3 / 33	BP cholesterol biosynthetic process
26	1e-03	3 / 33	BP tight junction assembly
27	1e-03	3 / 34	BP glutathione metabolic process
28	2e-03	5 / 126	miRN hsa-miR-145
29	2e-03	3 / 35	BP hair follicle development
30	2e-03	2 / 10	BP response to food
31	2e-03	2 / 10	GSE/ BIOCARTA_EGFR_SMRTE_PATHWAY
32	2e-03	2 / 10	GSE/ REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOLESTER
33	2e-03	2 / 10	GSE/ REACTOME_RNA_POLYMERASE_I_PROMOTER_OPENING
34	2e-03	23 / 1837	CC membrane
35	2e-03	3 / 38	BP epithelial cell differentiation
36	2e-03	3 / 39	BP retinoid metabolic process
37	2e-03	5 / 137	CC basolateral plasma membrane
38	2e-03	2 / 11	MF guanylate kinase activity
39	2e-03	2 / 11	GSE/ REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION
40	3e-03	2 / 12	BP head development

## Overview Map

## Spot



## p-values





# Sample-Overexpression

## Spot Summary: Q

# metagenes = 9  
# genes = 61

<r> metagenes = 0.99  
<r> genes = 0.38  
beta: r2= 6.15 / log p= -Inf

# samples with spot = 34 ( 12.4 % )  
Atypical : 5 ( 6.8 % )  
Classical : 5 ( 15.6 % )  
Mesenchymal : 12 ( 14.1 % )  
Basal : 12 ( 14.3 % )

## Spot Genelist

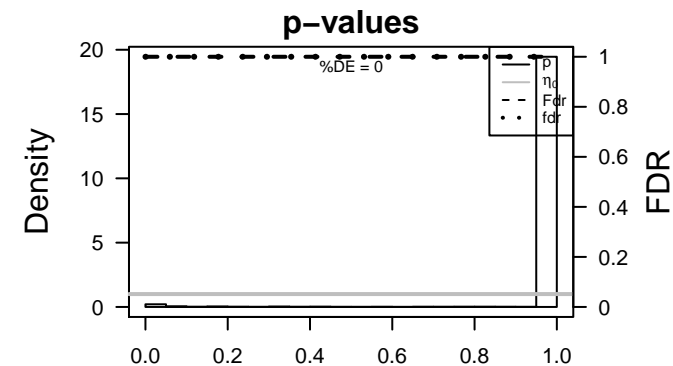
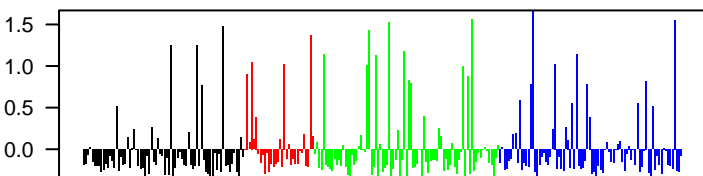
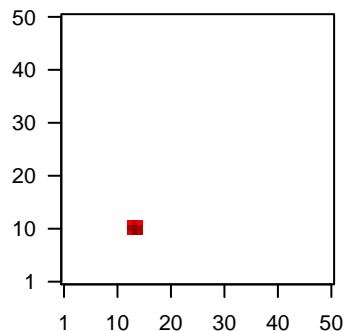
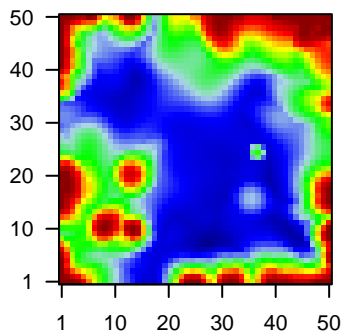
Rank	ID	max e	r	min e	Description
					Symbol
1	645037	4.91	-0.85	0.85	GAGE2CG antigen 2C [Source:HGNC Symbol;Acc:31958]
2	729422	4.91	-0.82	0.86	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	729442	4.7	-0.77	0.85	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	2577	4.65	-0.69	0.85	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	729428	4.58	-0.7	0.86	GAGE12G antigen 12C [Source:HGNC Symbol;Acc:28402]
6	2576	4.56	-0.69	0.85	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	4.55	-0.68	0.85	GAGE12G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	645073	4.39	-0.7	0.85	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	100008586	4.37	-0.71	0.84	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	2579	3.8	-0.56	0.8	GAGE12G antigen 12I [Source:HGNC Symbol;Acc:4105]
11	26749	3.77	-0.6	0.85	GAGE2EG antigen 2E [Source:HGNC Symbol;Acc:31960]
12	729447	3.7	-0.56	0.85	GAGE2AG antigen 2A [Source:HGNC Symbol;Acc:4099]
13	8277	3.56	-0.39	0.29	TKTL1 transketolase-like 1 [Source:HGNC Symbol;Acc:11835]
14	729396	3.52	-0.52	0.85	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	441520	3.26	-0.75	0.6	CT45A2 cancer/testis antigen family 45, member A2 [Source:HGNC S
16	4109	3.25	-0.86	0.6	MAGEA1melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
17	653219	3.18	-0.46	0.69	XAGE1B X antigen family, member 1B [Source:HGNC Symbol;Acc:254
18	100101629	3.04	-0.52	0.84	GAGE2EG antigen 2E [Source:HGNC Symbol;Acc:31960]
19	4103	2.69	-0.85	0.47	MAGEA4melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
20	4100	2.59	-0.76	0.67	MAGEA1melanoma antigen family A, 1 (directs expression of antigen I

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-25	26 / 630	Chr Chr X
2	3e-08	7 / 120	H.Tis: WIRTH_Testis
3	9e-06	3 / 15	GSE# MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
4	7e-04	2 / 14	GSE# MAHADEVAN_IMATINIB_RESISTANCE_UP
5	7e-04	7 / 549	MF molecular_function
6	7e-04	5 / 259	BP spermatogenesis
7	1e-03	6 / 419	CC cellular_component
8	2e-03	2 / 23	BP calcium-dependent cell-cell adhesion
9	2e-03	6 / 481	BP biological_process
10	5e-03	2 / 37	BP synapse assembly
11	8e-03	2 / 48	Cancr KUIPER_MM poor survival
12	1e-02	1 / 4	GSE# WEBER_METHYLATED_ICP_IN_SPERM_DN
13	1e-02	1 / 5	GSE# CHOI_ATL_ACUTE_STAGE
14	1e-02	4 / 346	BP cell differentiation
15	2e-02	1 / 6	GSE# NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
16	2e-02	1 / 6	GSE# NIELSEN_LEIOMYOSARCOMA_UP
17	2e-02	1 / 7	GSE# NIELSEN_SYNOVIAL_SARCOMA_UP
18	2e-02	1 / 7	GSE# REACTOME_AMINE_LIGAND_BINDING_RECEPTORS
19	2e-02	1 / 8	GSE# WEBER_METHYLATED_ICP_IN_FIBROBLAST
20	2e-02	1 / 9	GSE# ABE_VEGFA_TARGETS_30MIN
21	3e-02	1 / 10	BP piRNA metabolic process
22	3e-02	1 / 10	CC XY body
23	3e-02	1 / 10	GSE# NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
24	3e-02	1 / 10	GSE# TSUNODA_CISPLATIN_RESISTANCE_DN
25	3e-02	1 / 10	GSE# XU_RESPONSE_TO_TRETINOIN_DN
26	3e-02	1 / 10	GSE# CONRAD_GERMLINE_STEM_CELL
27	3e-02	1 / 11	BP regulation of organ growth
28	3e-02	1 / 11	Glio willscher_GBM_Verhaak-CL_expression_M_down
29	3e-02	1 / 11	Glio willscher_GBM_Verhaak-MES_expression_M_down
30	3e-02	1 / 11	Glio willscher_GBM_Verhaak-PNmut_expression_M_up
31	3e-02	1 / 11	GSE# NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
32	3e-02	1 / 11	GSE# SU_PLACENTA
33	3e-02	1 / 11	GSE# ABE_VEGFA_TARGETS_2HR
34	3e-02	2 / 99	BP homophilic cell adhesion
35	3e-02	1 / 12	GSE# HSIAO_LIVER_SPECIFIC_GENES
36	3e-02	1 / 12	GSE# ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
37	3e-02	1 / 12	GSE# RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
38	3e-02	1 / 12	GSE# HO_LIVER_CANCER_VASCULAR_INVASION
39	4e-02	1 / 13	CC axonemal dynein complex
40	4e-02	1 / 13	CC mitochondrial respiratory chain

### Overview Map

### Spot



Rank	p-value	#in/all	Geneset
1	6e-02	2/73	synaptogenesis
2	2e-03	2/23	calcium-dependent cell-cell adhesion
3	6/481	6/481	biological_process
4	2/37	2/37	synapse assembly
5	1e-02	1/346	cell differentiation
6	3e-02	1/10	piRNA metabolic process
7	3e-02	1/11	regulation of organ growth
8	1/11	1/11	hemophilic cell adhesion
9	2/39	2/39	positive regulation of smooth muscle contraction
10	4e-02	1/3	synapsis
11	1/13	1/13	DNA methylation involved in gamete generation
12	4e-02	1/14	negative regulation of retinoic acid receptor signaling pathway
13	1/4	1/4	ciliary or bacterial-type flagellar motility
14	4e-02	1/16	positive regulation of interleukin-1 beta secretion
15	5e-02	1/17	smooth muscle contraction
16	5e-02	1/18	congestion
17	5e-02	1/19	regulation of vasoconstriction
18	6e-02	1/21	chromatin organization
19	6e-02	1/22	negative regulation of Notch signaling pathway
20	6e-02	1/22	male meiosis

Rank	p-value	#in/all	Geneset
1	1e-20	26/630	Chr 2
2	9e-02	1/34	Chr Y
3	9e-01	3/749	Chr 1
4	9e-01	3/749	Chr 14
5	9e-01	2/699	Chr 5
6	7e-01	1/386	Chr 22
7	7e-01	2/1033	Chr 2
8	7e-01	2/618	Chr 4
9	9e-01	1/633	Chr 9
10	9e-01	1/71	Chr 16
11	9e-01	1/866	Chr 12
12	9e-01	1/918	Chr 17
13	1e+00	2/1720	Chr 1
14	1e+00	1/1135	Chr 19
15	1e+00	0/602	Chr 12
16	1e+00	0/957	Chr 11
17	1e+00	0/280	Chr 13
18	1e+00	0/504	Chr 15
19	1e+00	0/232	Chr 18
20	1e+00	0/449	Chr 20

Rank	p-value	#in/all	Geneset
1	9e-06	3/15	MATPLOL_MULTIPLE MYELOMA SUBGROUPS
2	1e-02	2/14	METFORMIN_IMATINIB_RESISTANCE_UP
3	1e-02	1/5	WEBER METHYLATED_ICP_IN_SPERM_DN
4	2e-02	1/6	WELLS LIOMYOSARCOMA_UP
5	2e-02	1/6	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
6	2e-02	1/9	NIELSEN_SYNOVIAL_SARCOMA_UP
7	2e-02	1/7	REACTOME_AMINE_LIGAND_BINDING_RECEPTORS
8	2e-02	1/8	WEBER METHYLATED_ICP_IN_FIBROBLAST
9	3e-02	1/10	ABC_VICFA_TARGETS_50MIN
10	3e-02	1/10	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
11	3e-02	1/10	TSUNODA_CISPLATIN_RESISTANCE_DN
12	3e-02	1/10	RESPONSE_TO_TRETINOIN_DN
13	3e-02	1/10	CONRAD_GERMLINE_STEM_CELL
14	3e-02	1/11	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
15	3e-02	1/11	SU_PLACENTA
16	3e-02	1/11	ABC_VICFA_TARGETS_2HR
17	3e-02	1/12	HSIAO_LIVER_SPECIFIC_GENES
18	3e-02	1/12	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
19	3e-02	1/12	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP

Rank	p-value	#in/all	Geneset
1	5e-02	1/19	metabolic function
2	5e-02	1/26	retinoic acid receptor binding
3	7e-02	1/26	cytochrome-c oxidase activity
4	7e-02	1/26	phosphatidylinositol phospholipase C activity
5	1e-01	1/55	drug binding
6	2e-01	1/68	histone deacetylase binding
7	2e-01	1/69	microtubule motor activity
8	2e-01	1/73	serine-type endopeptidase inhibitor activity
9	2e-01	2/321	G-protein coupled receptor activity
10	3e-01	1/331	nucleoside-triphosphatase activity
11	3e-01	1/141	ATase activity
12	3e-01	1/143	transmembrane signaling receptor activity
13	4e-01	1/156	protein dimerization activity
14	4e-01	2/504	nucleotide binding
15	5e-01	1/27	receptor activity
16	5e-01	2/579	calcium ion binding
17	6e-01	1/318	chromatin binding
18	7e-01	1/335	protein serine/threonine kinase activity
19	7e-01	1/335	protein tyrosine kinase activity

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

Rank	p-value	#in/all	Geneset
1	0/13	0/13	GUSTAFSON_Pi3K_UP
2	0/12	0/12	GUSTAFSON_Pi3K_DN
3	0/11	0/11	BENTINK_e2f3
4	0/11	0/11	BENTINK_e2f3.2
5	0/14	0/14	BENTINK_myc.1
6	0/11	0/11	BENTINK_ras.1
7	0/11	0/11	BENTINK_ras.4
8	0/15	0/15	BENTINK_ras.6
9	0/13	0/13	BENTINK_src.10
10	0/4	0/4	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	

Rank	p-value	#in/all	Geneset
1	0.000000	1/48	BRAC1A1_poor survival
2	0.000000	1/68	SHAUGHNESSY_MM_high risk
3	0.000000	0.773	Lembocke_Normal_vs_Adenoma
4	0.000000	0/15	RHODES_CANCER_META_SIGNATURE
5	0.000000	0/16	LIN_LINDIFFERENTIATED_CANCER
6	0.000000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.000000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
8	0.000000	0/10	BREAST_CANCER
9	0.000000	0/14	LIU_COMMON_CANCER_GENES
10	0.000000	0/14	LIU_LIVER_CANCER
11	0.000000	0/15	LIU_PROSTATE_CANCER_DN
12	0.000000	0/14	LIU_PROSTATE_CANCER_UP
13	0.000000	0/9	WANG_ER_UP
14	0.000000	0/9	WANG_ER_DN
15	0.000000	0/16	WOLFER_overlap_genes
16	0.000000	0/12	BEN-PORATH_DN
17	0.000000	0/15	BEN-PORATH_UP
18	0.000000	0/15	GENTLES_modul1
19	0.000000	0/16	GENTLES_modul2
20	0.000000	0/10	GENTLES_modul3

Rank	p-value	#in/all	Geneset
1	0.8	0/0	CDU12_breastis up
2	1.0	0/375	GUDDJ_poriasis down
3	1.0	0/17	WILSON_EBM up
4	1.0	0/2	ECHEPNIA_EBM down
5	1.0	0/26	ECHEPNIA_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	

Rank	p-value	#in/all	Geneset
1	5e-08	7/120	WIRTH_testis
2	1e+00	0/26	WIRTH_Pituitary gland
3	1e+00	0/417	WIRTH_Pancreas
4	1e+00	0/13	WIRTH_Immune system
5	1e+00	0/13	WIRTH_Sec_lymphoid organs
6	1e+00	0/12	WIRTH_Prim_lymphoid organs
7	1e+00	0/10	WIRTH_B-cells
8	1e+00	0/13	WIRTH_Tonsil
9	1e+00	0/13	WIRTH_Thymus
10	1e+00	0/12	WIRTH_Lymphocytes
11	1e+00	0/6	WIRTH_Bone marrow
12	1e+00	0/400	WIRTH_Nervous System
13	1e+00	0/14	WIRTH_Globus pallidus
14	1e+00	0/14	WIRTH_Telencephalon
15	1e+00	0/13	WIRTH_Cortex cerebri
16	1e+00	0/16	WIRTH_Hippocampus
17	1e+00	0/13	WIRTH_Hypothalamus
18	1e+00	0/15	WIRTH_Cerebellum
19	1e+00	0/50	WIRTH_Homeostasis
20	1e+00	0/62	WIRTH_Liver

Rank	p-value	#in/all	Geneset
1	0.2	0/0	TGGC-515-5P-519E
2	0.3	1/115	ACTG-30A-3P-30E-3P
3	0.3	1/146	ATTC-186
4	0.4	1/208	TGCG-48A-152-148B
5	0.5	1/457	TGCC-124A
6	1.0	0/252	AGCA-93-302A-302B-302C-302D-372-373-520E-520A-526I
7	1.0	0/306	CTACLET-7A-LET-7B-LET-7C-LET-7D-LET-7E-LET-7F-98-LET-7G-
8	1.0	0/200	GC-17-20A-106A-106B-20B-51D
9	1.0	0/481	TGCT-15A-16-15B-195-424-497
10	1.0	0/467	TGTT-30A-5P-30C-30D-30B-30E-5P
11	1.0	0/141	TGTC-32-32-92-363-367
12	1.0	0/391	TGAA-181A-181B-181C-181D
13	1.0	0/17	CGCC-518B-518C-518D
14	1.0	0/420	TGCT-29A-29B-29C
15	1.0	0/285	CAG-34A-34C-449
16	1.0	0/20	TACG-99A-100-99B
17	1.0	0/37	CTCT-526C-518F-526A
18	1.0	0/314	TGGC-130A-301-130B
19	1.0	0/588	TGCT-131C-131B-519A

Rank	p-value	#in/all	Geneset
1	0/295	0/295	hsa-miR-34c-5p
2	0/306	0/306	hsa-miR-548c-3p
3	0/378	0/378	hsa-miR-373
4	0/178	0/178	hsa-miR-520f
5	0/314	0/314	hsa-miR-520c-3p
6	0/31	0/31	hsa-miR-149b
7	0/32	0/32	hsa-miR-429
8	0/271	0/271	hsa-miR-520b
9	0/155	0/155	hsa-miR-31
10	0/170	0/170	hsa-miR-302e
11	0/181	0/181	hsa-miR-582-5p
12	0/325	0/325	hsa-miR-302d
13	0/316	0/316	hsa-miR-302a
14	0/423	0/423	hsa-miR-1319d
15	0/545	0/545	hsa-miR-93
16	0/157	0/157	hsa-miR-139-5p
17	0/567	0/567	hsa-miR-20b
18	0/57	0/57	hsa-miR-105a
19	0/538	0/538	hsa-miR-17

Rank	p-value	#in/all	Geneset
1	0.6	3/146	HEBENSTREIT_low expression TF
2	1.0	0/14	HEBENSTREIT_high expression TF
3	1.0	1095	KIM_MYC targets
4	1.0	0/1233	MYC Targets
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 suppressor genes UP

Rank	p-value	#in/all	Geneset
1	0.00	1/0	centriole component
2	0.027	1/10	XY body
3	0.035	1/13	axonal dynein complex
4	0.035	1/13	mitochondrial respiratory chain
5	0.045	1/20	dynein complex
6	0.082	1/31	axon terminus
7	0.171	1/68	collagen
8	1/83	1/83	chromatin
9	0.209	1/83	basement membrane
10	0.213	3/579	nucleolus
11	0.281	2/380	intracellular membrane-bounded organelle
12	0.315	1/137	basolateral plasma membrane
13	0.323	1/141	postsynaptic membrane
14	0.345	1/153	endoplasmic reticulum lumen
15	0.395	14/4640	nucleus
16	0.398	1/84	actin cytoskeleton
17	0.405	3/835	integral to plasma membrane
18	0.437	1/207	dendrite
19	0.520	1/284	microtubule
20	0.538	12/4310	cytoplasm

Rank	p-value	#in/all	Geneset
1	0.03	1/118	willscher_GBM_Verhaak-CL_expression_M_down
2	0.03	1/11	willscher_GBM_Verhaak-MES_expression_M_down
3	0.03	1/11	willscher_GBM_Verhaak-PNmut_expression_M_up
4	0.13	1/13	GIEBEL_GBM_WT_down_VS_mut
5	1.00	0/14	VERHAAK_CL subtype
6	1.00	0/16	VERHAAK_MES subtype
7	1.00	0/14	VERHAAK_NL subtype
8	1.00	0/15	VERHAAK_PN subtype
9	1.00	0/27	WIRTH_PN subtype
10	1.00	0/89	WIRTH_Normal Brain
11	1.00	0/11	

# Sample-Overexpression

## Spot Summary: R

# metagenes = 42  
# genes = 547

<r> metagenes = 0.87  
<r> genes = 0.24  
beta: r2= 4.56 / log p= -Inf

# samples with spot = 5 ( 1.8 % )  
Atypical : 1 ( 1.4 % )  
Classical : 1 ( 3.1 % )  
Basal : 3 ( 3.6 % )

## Spot Genelist

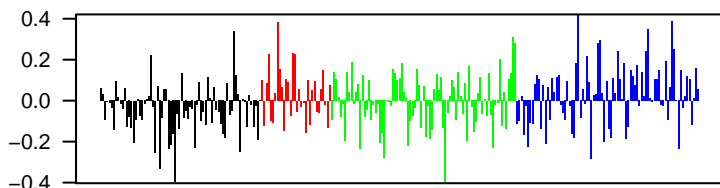
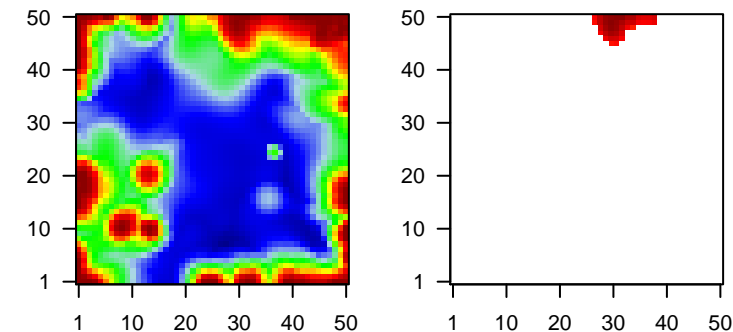
Rank	ID	max e	r	min e	Description
					Symbol
1	55915	1.8	-0.75	0.34	LANCL2 LanC lantibiotic synthetase component C-like 2 (bacterial) [S
2	5321	1.65	-0.85	0.46	PLA2G4A phospholipase A2, group IVA (cytosolic, calcium-dependent)
3	10950	1.54	-1.34	0.46	BTG3 BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
4	1207	1.52	-1.35	0.49	CLNS1A chloride channel, nucleotide-sensitive, 1A [Source:HGNC Sy
5	54802	1.51	-0.79	0.47	TRIT1 tRNA isopentenyltransferase 1 [Source:HGNC Symbol;Acc:2f
6	144363	1.49	-0.94	0.49	LYRM5 LYR motif containing 5 [Source:HGNC Symbol;Acc:27052]
7	100093630	1.47	-1.34	0.27	SNHG8 small nucleolar RNA host gene 8 (non-protein coding) [Sourc
8	653566	1.46	-1.06	0.54	
9	6622	1.44	-0.92	0.28	SNCA synuclein, alpha (non A4 component of amyloid precursor) [S
10	84833	1.42	-0.97	0.4	USMG5 up-regulated during skeletal muscle growth 5 homolog (mous
11	5723	1.39	-0.48	0.53	PSPH phosphoserine phosphatase [Source:HGNC Symbol;Acc:957
12	5423	1.39	-1.04	0.26	POLB polymerase (DNA directed), beta [Source:HGNC Symbol;Acc
13	401505	1.36	-0.87	0.59	TOMM5 translocase of outer mitochondrial membrane 5 homolog (yea
14	51142	1.36	-0.79	0.45	CHCHD2 coiled-coil-helix-coiled-coil-helix domain containing 2 [Sour
15	139886	1.35	-1.31	0.32	SPIN4 spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
16	8560	1.35	-1.12	0.52	DEGS1 delta(4)-desaturase, sphingolipid 1 [Source:HGNC Symbol;A
17	55848	1.34	-0.94	0.45	PLGRKT plasminogen receptor, C-terminal lysine transmembrane prot
18	388722	1.27	-0.85	0.53	C1orf53 chromosome 1 open reading frame 53 [Source:HGNC Symbc
19	8803	1.25	-1.1	0.65	SUCLA2 succinate-CoA ligase, ADP-forming, beta subunit [Source:Hi
20	51504	1.25	-0.91	0.45	TRMT112 RNA methyltransferase 11-2 homolog (S. cerevisiae) [Sourc

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-35	136 / 1318	CC mitochondrion
2	8e-24	30 / 83	BP respiratory electron transport chain
3	1e-22	47 / 253	BP translation
4	2e-21	50 / 304	CC mitochondrial inner membrane
5	4e-21	36 / 153	MF structural constituent of ribosome
6	3e-20	35 / 152	BP cellular metabolic process
7	9e-19	102 / 1233	TF KIM_MYC targets
8	6e-18	34 / 167	CC ribosome
9	8e-14	24 / 109	BP SRP-dependent cotranslational protein targeting to membrane
10	8e-14	61 / 649	BP gene expression
11	9e-13	37 / 287	BP viral process
12	3e-12	24 / 128	BP translational initiation
13	4e-12	20 / 87	BP translational termination
14	1e-11	19 / 81	BP viral transcription
15	1e-11	20 / 92	BP translational elongation
16	7e-11	46 / 482	BP cellular protein metabolic process
17	1e-10	19 / 92	BP viral life cycle
18	1e-10	21 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
19	3e-10	30 / 242	BP RNA metabolic process
20	7e-10	28 / 219	BP mRNA metabolic process
21	3e-09	9 / 19	CC mitochondrial proton-transporting ATP synthase complex
22	6e-09	11 / 34	MF NADH dehydrogenase (ubiquinone) activity
23	6e-09	13 / 51	CC cytosolic large ribosomal subunit
24	8e-09	11 / 35	BP mitochondrial electron transport, NADH to ubiquinone
25	1e-08	11 / 36	CC mitochondrial respiratory chain complex I
26	2e-08	9 / 23	CC mitochondrial ribosome
27	1e-07	76 / 1253	BP small molecule metabolic process
28	2e-07	7 / 15	BP ATP synthesis coupled proton transport
29	2e-07	6 / 10	CC large ribosomal subunit
30	5e-07	6 / 11	Canc GENTLES_modul5
31	6e-07	12 / 62	Glio Stuehler_Proteins_up_in_STS
32	9e-07	60 / 957	Chr Chr 11
33	9e-07	43 / 595	MF RNA binding
34	1e-06	8 / 26	MF cytochrome-c oxidase activity
35	2e-06	6 / 13	GSE/ REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
36	3e-06	6 / 14	BP mitochondrial ATP synthesis coupled proton transport
37	3e-06	22 / 220	CC mitochondrial matrix
38	6e-06	42 / 618	Chr Chr 4
39	7e-06	6 / 16	Canc GENTLES_modul10
40	7e-06	6 / 16	GSE/ MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN

Overview Map

Spot



p-values

