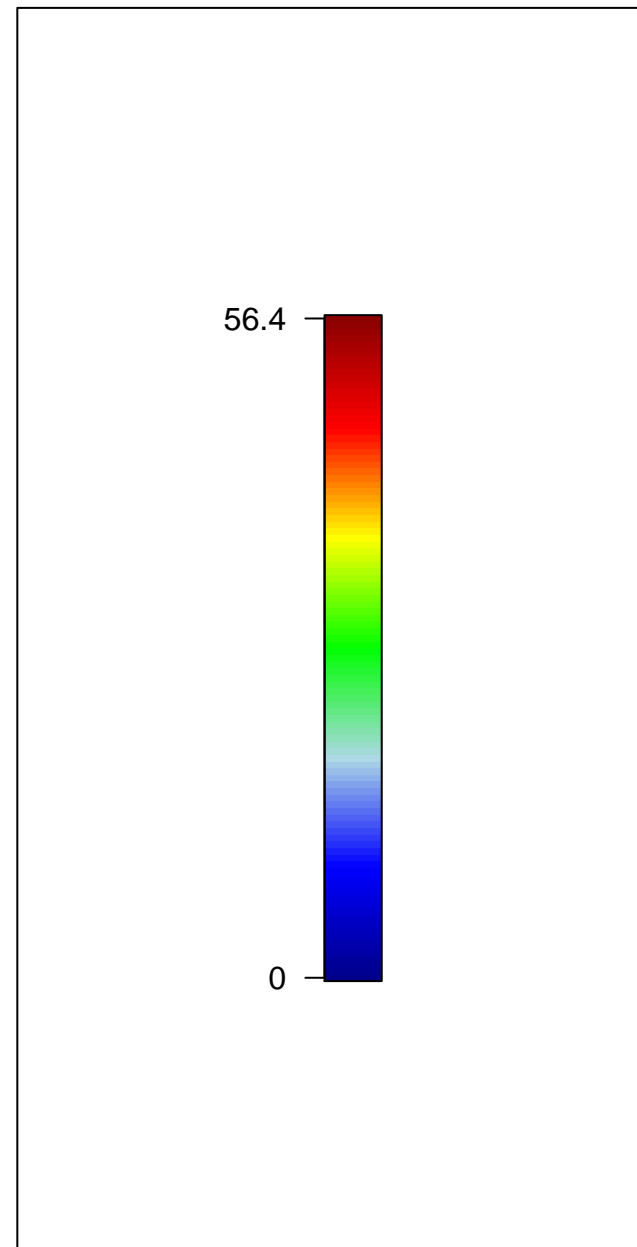
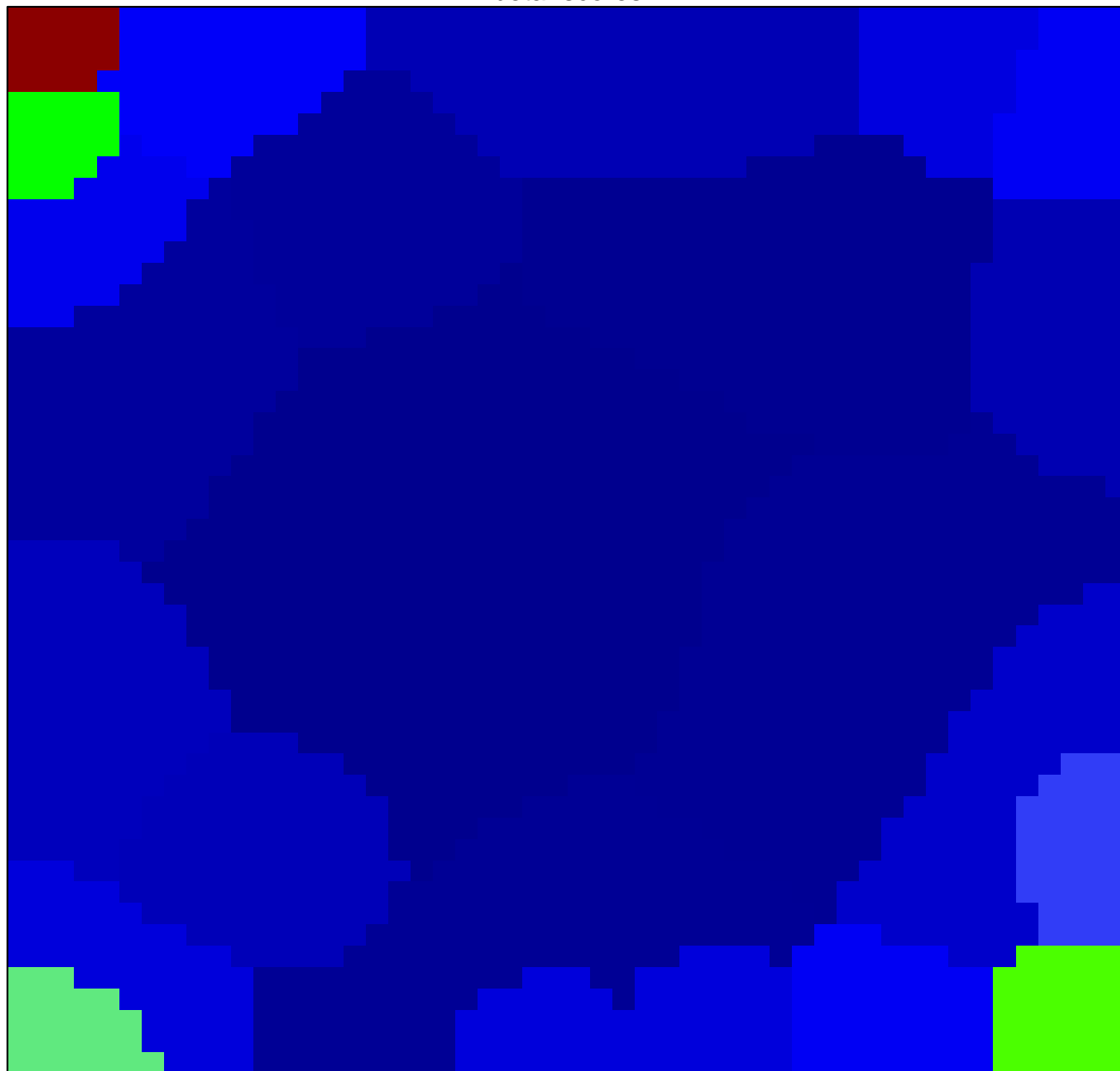


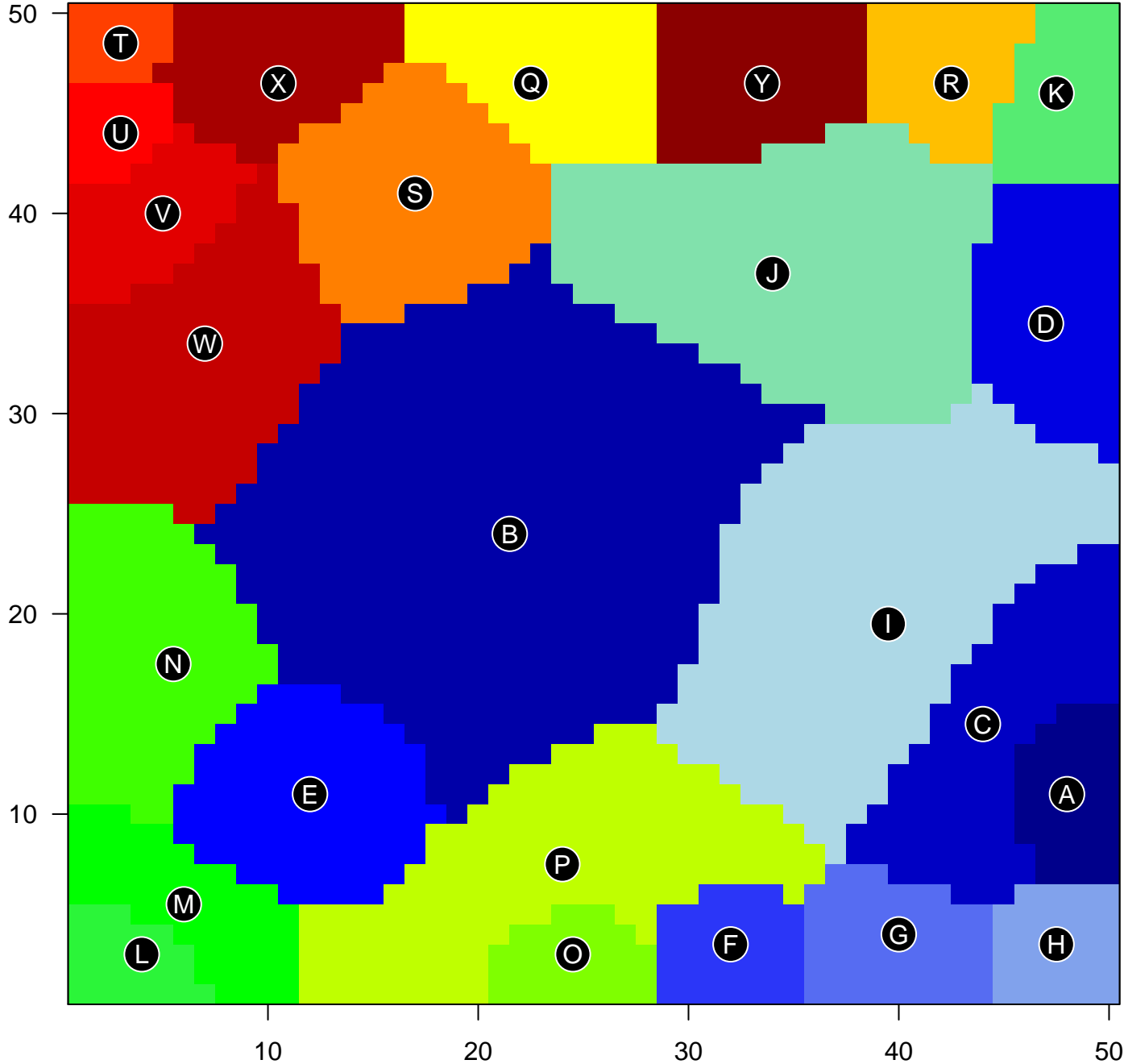
# K-Means Cluster

beta-scores



# K-Means Cluster

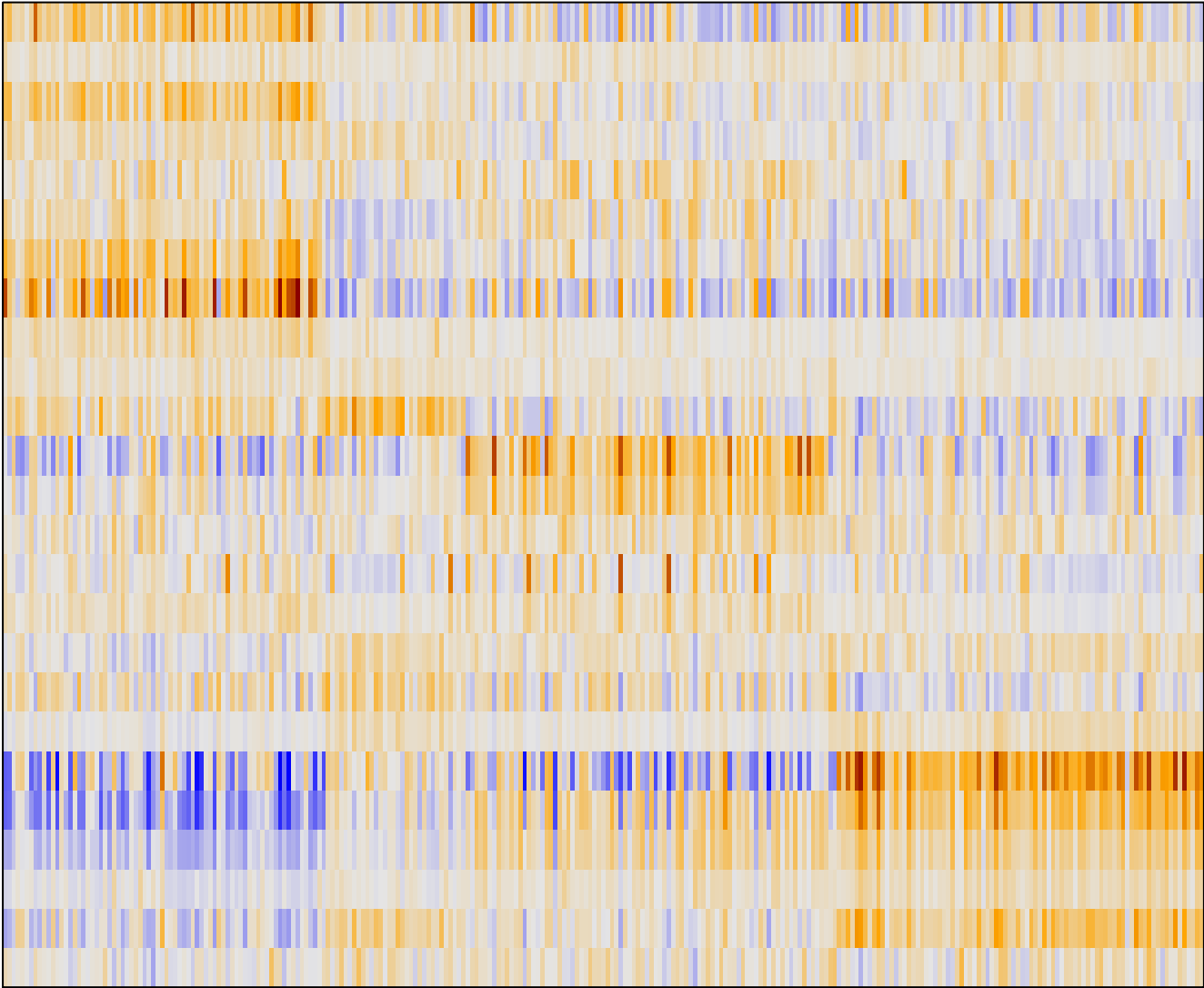
annotation



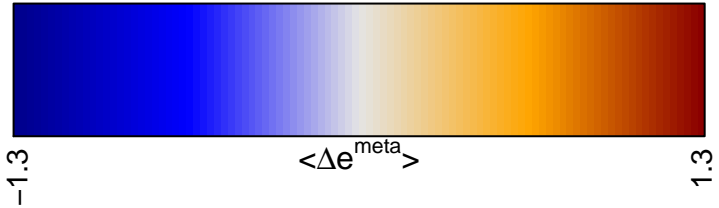
- A ■ GUDJ\_psoriasis down  
RICKMAN\_HEAD\_AND\_NECK\_CANCER\_D  
CROMER\_TUMORIGENESIS\_DN
- B ■ olfactory receptor activity  
G-protein coupled receptor activity  
G-protein coupled receptor signaling pathway
- C ■ Chr 3  
WIRTH\_Immune system  
transcription, DNA-templated
- D ■ nucleus  
nucleic acid binding  
RNA binding
- E ■ Chr 19  
Chr X  
anterior/posterior pattern specification
- F ■ type I interferon signaling pathway  
defense response to virus  
SPANG\_IL21 DN
- G ■ Chr 19  
hydrolase activity, hydrolyzing O-glycosyl compounds  
DNA binding
- H ■ Lembcke\_Colonic Inflammation  
WIRTH\_Immune system  
immune response
- I ■ willscher\_GBM\_Verhaak-PNmut\_expression\_G\_down  
viral transcription  
translational elongation
- J ■ regulation of transcription, DNA-dependent  
DNA binding  
nucleic acid binding
- K ■ Chr 3  
DNA replication  
mitotic cell cycle
- L ■ LENZ\_Stromal signature 1  
extracellular matrix  
extracellular matrix organization
- M ■ extracellular matrix organization  
LENZ\_Stromal signature 1  
cell adhesion
- N ■ mitochondrion  
Chr 16  
Lembcke\_Normal vs Adenoma
- O ■ WIRTH\_Muscle  
muscle filament sliding  
muscle contraction
- P ■ integral to membrane



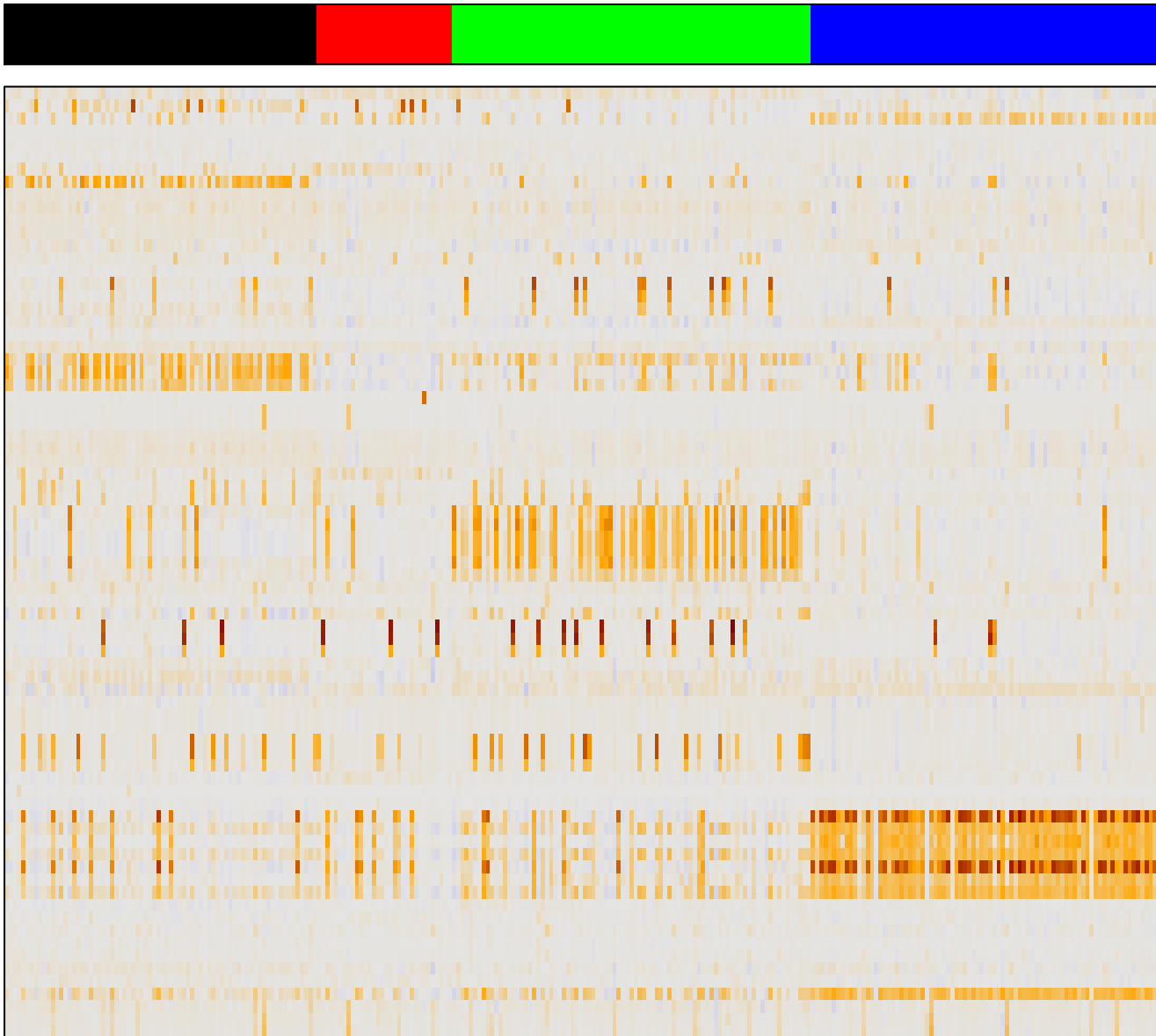
A  
B  
C  
D  
E  
F  
G  
H  
I  
J  
K  
L  
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O  
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Q  
R  
S  
T  
U  
V  
W  
X  
Y



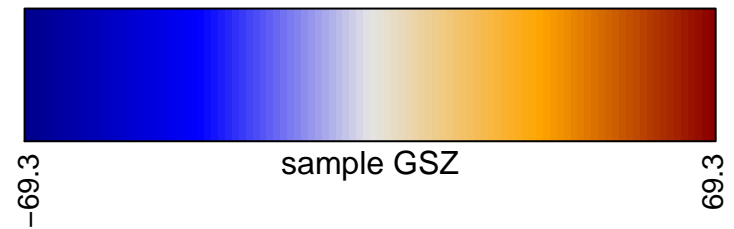
GLUD1\_pсориаз down  
 CROMER\_HEAD\_AND\_NECK\_CANCER\_D  
 CROMER\_TUMORIGENESIS\_DN  
 olfactory receptor activity  
 G-protein coupled receptor signaling pathway  
 WIRTH\_Immune system  
 transcription, DNA-templated  
 nucleus  
 RNA binding  
 Chr 19  
 anterior/posterior pattern specification  
 type I interferon signaling pathway  
 SPRING\_IL21\_DN  
 Chr 19  
 hydrolase activity, hydrolyzing O-glycosyl compounds  
 DNA binding  
 Lembcke\_Colonial Inflammation  
 WIRTH\_Immune system  
 immune response  
 wilscher\_GBM\_Verhaak-PNmut\_expression\_G\_down  
 translational elongation  
 regulation of transcription, DNA-dependent  
 nucleic acid binding  
 Chr 3  
 DNA replication  
 mitotic cell cycle  
 LENZ\_Stromal signature 1  
 extracellular matrix organization  
 extracellular matrix organization  
 LENZ\_Stromal signature 1  
 cell adhesion  
 mitochondrion  
 Lembcke\_Normal vs Adenoma  
 WIRTH\_Muscle  
 muscle filament sliding  
 muscle contraction  
 integral to membrane  
 plasma membrane  
 HEBENSTREIT\_low expression TF  
 hsa-miR-548a  
 wilscher\_GBM\_Verhaak-CL\_expression\_D\_up  
 wilscher\_GBM\_Verhaak-MES\_expression\_D\_down  
 wilscher\_GBM\_Verhaak-CL\_expression\_C\_up  
 mitotic cell cycle  
 vitamin metabolic process  
 fatty acid beta-oxidation using acyl-CoA oxidase  
 sphingolipid metabolic process  
 WIRTH\_Mucosa  
 GLUD1\_pсориаз up  
 keratinocyte differentiation  
 GLUD1\_pсориаз up  
 epidermis development  
 GLUD1\_pсориаз up  
 Chr 14  
 hsa-miR-1265  
 Chr 16\_p-331-3p  
 hsa-miR-423-3p  
 integral to membrane  
 GLUD1\_pсориаз up  
 mitochondrion  
 structural constituent of ribosome



A  
B  
C  
D  
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F  
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L  
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R  
S  
T  
U  
V  
W  
X  
Y



GUDJ\_psoriasis down  
 RICKMAN\_HEAD\_AND\_NECK\_CANCER\_D  
 CROMER\_TUMORIGENESIS\_DN  
 olfactory receptor activity  
 G-protein coupled receptor activity  
 G-protein coupled receptor signaling pathway  
 Chr3  
 WIRTH\_Immune system  
 transcription, DNA-templated  
 nucleus  
 nucleic acid binding  
 RNA binding  
 Chr19  
 anterior/posterior pattern specification  
 type I interferon signaling pathway  
 defense response to virus  
 SPRNG\_IL21 DN  
 Chr19  
 hydrolase activity, hydrolyzing O-glycosyl compounds  
 DNA binding  
 Lembcke\_Colonc Inflammation  
 WIRTH\_Immune system  
 immune response  
 wilscher\_GBM\_Verhaak-PNmut\_expression\_G\_down  
 viral transcription  
 translational elongation  
 regulation of transcription, DNA-dependent  
 nucleic acid binding  
 Chr3  
 DNA replication  
 mitotic cell cycle  
 LENZ\_Stromal signature 1  
 extracellular matrix organization  
 extracellular matrix organization  
 LENZ\_Stromal signature 1  
 cell adhesion  
 mitochondrion  
 mitochondrion  
 Lembcke\_Normal vs Adenoma  
 WIRTH\_Muscle  
 muscle filament sliding  
 muscle contraction  
 integral to membrane  
 plasma membrane  
 HEBENSTREIT\_low expression TF  
 hsa-miR-548b  
 wilscher\_GBM\_Verhaak-CL\_expression\_D\_up  
 wilscher\_GBM\_Verhaak-MES\_expression\_D\_down  
 wilscher\_GBM\_Verhaak-CL\_expression\_C\_up  
 wilscher\_GBM\_Verhaak-PNmut\_expression\_C\_down  
 mitotic cell cycle  
 vitamin metabolic process  
 fatty acid beta-oxidation using acyl-CoA oxidase  
 sphingolipid metabolic process  
 WIRTH\_Mucosa  
 GUDJ\_psoriasis up  
 keratinocyte differentiation  
 GUDJ\_psoriasis up  
 epidermis development  
 GUDJ\_psoriasis up  
 Chr14  
 hsa-miR-1265  
 Chr16  
 hsa-miR-331-3p  
 hsa-miR-423-3p  
 integral to membrane  
 cell junction  
 GUDJ\_psoriasis up  
 mitochondrion  
 structural constituent of ribosome



# K-Means Cluster

## Spot Summary: A

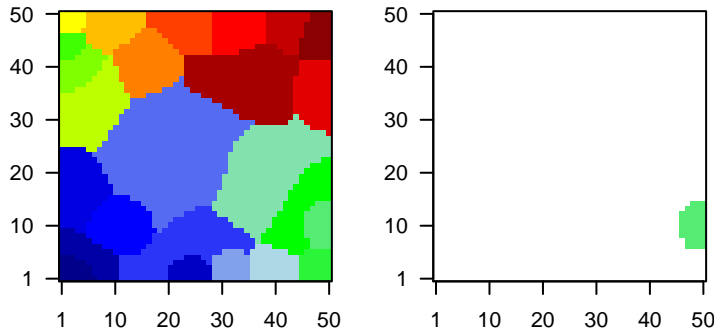
# metagenes = 40  
# genes = 394

<r> metagenes = 0.88  
<r> genes = 0.24  
beta: r2= 12.14 / log p= -Inf

# samples with spot = 42 ( 15.3 % )  
Atypical : 19 ( 25.7 % )  
Classical : 4 ( 12.5 % )  
Mesenchymal : 5 ( 5.9 % )  
Basal : 14 ( 16.7 % )

Overview Map

Spot

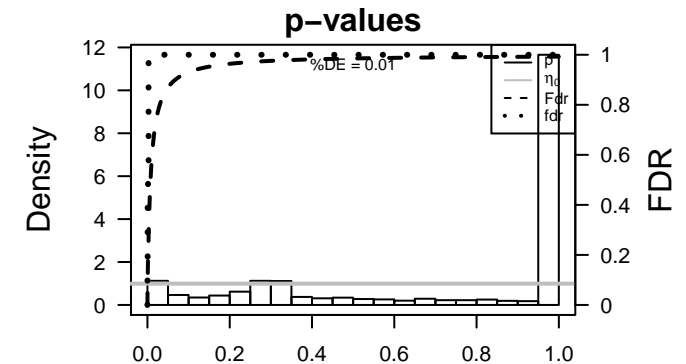
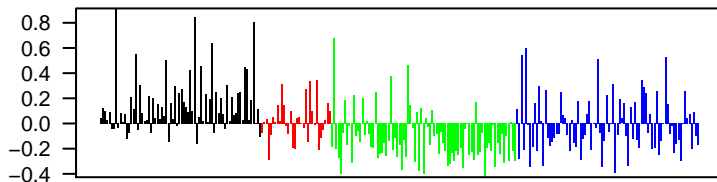


## Spot Genelist

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	SCGB3A3 secretoglobulin, 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	347	3.19	-1.49	0.74	APOD apolipoprotein D [Source:HGNC Symbol;Acc:612]
13	80341	3.15	-0.53	0.63	BPIFB2 BPI fold containing family B, member 2 [Source:HGNC Symb
14	352999	3.14	-0.47	0.51	C6orf58 chromosome 6 open reading frame 58 [Source:HGNC Symb
15	7018	3.1	-1.18	0.68	TF transferrin [Source:HGNC Symbol;Acc:11740]
16	8842	3.09	-1	0.64	PROM1 prominin 1 [Source:HGNC Symbol;Acc:9454]
17	389816	3.08	-1.05	0.77	LRRC26 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
18	5284	3.04	-0.77	0.69	PIGR polymeric immunoglobulin receptor [Source:HGNC Symbol;A
19	2568	3.03	-1.68	0.74	GABRP gamma-aminobutyric acid (GABA) A receptor, pi [Source:HG
20	124	3.01	-0.85	0.47	ADH1A alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-19	45 / 375	Disea GUDJ_pсориазis down
2	5e-15	11 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_D
3	4e-08	7 / 16	GSE/ CROMER_TUMORIGENESIS_DN
4	1e-07	40 / 683	CC extracellular space
5	5e-07	56 / 1182	CC extracellular region
6	3e-06	13 / 112	MF heparin binding
7	6e-06	27 / 434	BP oxidation-reduction process
8	1e-05	4 / 7	MMM MACIEJ_MMM5
9	1e-05	4 / 7	GSE/ LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
10	2e-05	5 / 15	GSE/ NAKAJIMA_MAST_CELL
11	2e-05	5 / 15	GSE/ POOLA_INVASIVE_BREAST_CANCER_DN
12	2e-05	4 / 8	GSE/ RUNNE_GENDER_EFFECT_UP
13	3e-05	5 / 16	GSE/ TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMA
14	3e-05	5 / 16	GSE/ TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORM
15	3e-05	12 / 119	BP xenobiotic metabolic process
16	7e-05	5 / 19	BP calcium-independent cell-cell adhesion
17	1e-04	5 / 21	BP drug metabolic process
18	2e-04	8 / 66	MF flavin adenine dinucleotide binding
19	2e-04	47 / 1146	TF HEBENSTREIT_low expression TF
20	2e-04	4 / 13	GSE/ HUANG_DASATINIB_RESISTANCE_DN
21	3e-04	4 / 14	MF selenium binding
22	3e-04	4 / 14	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
23	3e-04	4 / 14	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
24	3e-04	18 / 296	MF oxidoreductase activity
25	3e-04	4 / 15	GSE/ TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL
26	3e-04	4 / 15	GSE/ DOANE_BREAST_CANCER_CLASSES_UP
27	3e-04	4 / 15	GSE/ IZADPANAHA_STEM_CELL_ADIPOSE_VS_BONE_DN
28	3e-04	4 / 15	GSE/ CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
29	3e-04	4 / 15	GSE/ PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	3e-04	4 / 15	GSE/ KEGG_PROPANOATE_METABOLISM
31	4e-04	26 / 531	MF catalytic activity
32	4e-04	3 / 7	GSE/ LOPEZ_MESOTELIOMA_SURVIVAL_WORST_VS_BEST_DN
33	4e-04	3 / 7	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_DN
34	4e-04	3 / 7	TF Ti: VAQUERIZAS_Appendix
35	4e-04	8 / 76	BP male gonad development
36	5e-04	4 / 16	GSE/ TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMA
37	5e-04	4 / 16	GSE/ ROY_WOUND_BLOOD_VESSEL_DN
38	5e-04	4 / 16	GSE/ WANG_BARRETTS_ESOPHAGUS_DN
39	5e-04	4 / 16	TF Ti: VAQUERIZAS_Salivary gland
40	6e-04	4 / 17	MF metallocarboxypeptidase activity



Rank	p-value	#in/all	Geneset
1	3e-05	12/119	cellular reduction process
2	7e-05	5/19	xenobiotic metabolic process
3	1e-04	5/21	calcium-independent cell-cell adhesion
4	4e-04	5/76	drug metabolic process
5	1e-03	10/128	male gonad development
6	1e-03	47/1253	translational initiation
7	1e-03	3/10	small molecule metabolic process
8	1e-03	3/10	cellular response to thyroid hormone stimulus
9	1e-03	3/10	epoxygenase P450 pathway
10	1e-03	3/10	leukocyte tethering or rolling
11	2e-03	3/11	DNA integration
12	3e-03	4/123	stem cell differentiation
13	3e-03	4/12	cellular aldehyde metabolic process
14	3e-03	19/390	metabolic process
15	3e-03	4/25	brown fat cell differentiation
16	3e-03	3/267	cellular response to oxidative stress
17	3e-03	18/364	negative regulation of cell proliferation
18	4e-03	4/27	negative regulation of smooth muscle cell proliferation
19	4e-03	3/144	proliferation
20	4e-03	3/14	negative regulation of epithelial to mesenchymal transition

Rank	p-value	#in/all	Geneset
1	0.001	8/34	Chr 3
2	0.002	36/914	Chr 3
3	0.023	23/618	Chr 21
4	0.079	8/167	Chr 6
5	0.087	23/714	Chr 13
6	0.132	10/280	Chr 9
7	0.137	17/234	Chr 5
8	0.307	19/699	Chr 2
9	0.411	26/1033	Chr 16
10	0.438	16/633	Chr 15
11	0.540	12/504	Chr 10
12	0.573	14/602	Chr 7
13	0.601	17/743	Chr 18
14	0.650	5/259	Chr 9
15	0.684	11/319	Chr 1
16	0.711	38/1720	Chr 12
17	0.756	18/866	Chr 11
18	0.817	8/267	Chr 20
19	0.842	8/449	Chr X
20	0.888	11/630	Chr X

Rank	p-value	#in/all	Geneset
1	5e-15	11/16	RICKMAN HEAD AND NECK CANCER_D
2	4e-05	7/16	CHURCH TUMORIGENESIS DN
3	1e-05	2/16	LOPEZ MESOTHELIOMA SURVIVAL_TIME_DN
4	2e-05	5/15	NAKAJIMA MAST CELL
5	3e-05	5/15	POOLA INVASIVE BREAST CANCER_DN
6	2e-05	18/19	RUNGE GENDER_EFFECT_UP
7	2e-05	4/16	TURASHVILI BREAST DUCTAL CARCINOMA VS LOBULAR_NORMAL_I
8	3e-05	5/16	TURASHVILI BREAST LOBULAR CARCINOMA VS LOBULAR_NORMAL_I
9	3e-05	4/13	HUANG BASALINB_RESISTANCE DN
10	2e-04	1/16	SEGIPTA NASOPHARYNGEAL CARCINOMA_WITH_LMP1_DN
11	3e-04	4/14	SMID BREAST CANCER RELAPSE_IN LUNG_DN
12	3e-04	4/15	TURASHVILI BREAST DUCTAL CARCINOMA VS DUCTAL_NORMAL_DI
13	3e-04	4/15	DOAN BREAST CANCER CLASSES UP
14	3e-04	4/15	IZADPANAH STEM CELL ADIPOSE VS BONE DN
15	3e-04	4/15	CHIANG LIVER CANCER SUBCLASS PROLIFERATION_DN
16	3e-04	4/15	PYEON CANCER HEAD AND NECK VS CERVICAL_DN
17	3e-04	4/15	KIG PROPANOATE METABOLISM
18	4e-04	3/7	LOPEZ MESOTHELIOMA SURVIVAL_WORST_VS_BEST_DN
19	4e-04	3/7	HUPER BREAST BASAL VS LUMINAL_DN
20	4e-04	4/16	TURASHVILI BREAST LOBULAR CARCINOMA VS DUCTAL_NORMAL_I

Rank	p-value	#in/all	Geneset
1	2e-04	13/12	metal ion binding
2	2e-04	8/66	flavin adenine dinucleotide binding
3	3e-04	4/14	selenium binding
4	3e-04	18/296	oxidoreductase activity
5	3e-04	26/531	catalytic activity
6	4e-04	4/17	metallocarboxypeptidase activity
7	1e-03	4/21	glycosaminoglycan binding
8	2e-03	5/79	NAD binding
9	3e-03	5/79	electron carrier activity
10	4e-03	5/45	steroid hormone receptor activity
11	7e-03	4/32	NADP binding
12	7e-03	7/17	carboxypeptidase activity
13	8e-03	3/18	amino acid binding
14	8e-03	3/18	aromatase activity
15	8e-03	3/18	transforming growth factor beta-activated receptor activity
16	9e-03	8/122	serine-type endopeptidase activity
17	9e-03	4/35	ligand-activated sequence-specific DNA binding RNA polymerase II transcrip
18	1e-02	8/125	iron ion binding
19	2e-02	3/23	peptidase inhibitor activity
20	2e-02	3/23	phosphatidate phosphatase activity

Rank	p-value	#in/all	Geneset
1	0.003	2/10	miR-20a
2	0.022	2/10	miR-146a
3	0.023	3/26	miR-21
4	0.070	1/3	miR-223
5	0.070	1/3	miR-25
6	0.092	1/4	miR-106b
7	0.113	1/6	miR-93a
8	0.113	1/6	miR-93
9	0.134	1/6	miR-133a
10	0.134	1/6	miR-181b
11	0.134	1/6	miR-134
12	0.175	1/8	miR-222
13	0.251	1/12	miR-29b
14	1.000	0/11	let-7a
15	1.000	0/16	let-7b
16	1.000	0/4	let-7c
17	1.000	0/6	let-7d
18	1.000	0/4	let-7g
19	1.000	0/13	miR-1
20	1.000	0/5	miR-101

Rank	p-value	#in/all	Geneset
1	0.03	2/12	BENTINK_ras.1
2	0.25	0/13	BENTINK_e23.1
3	1.00	0/13	GUSTAFSON_P13K_UP
4	1.00	0/15	GUSTAFSON_P13K_DN
5	1.00	0/11	BENTINK_e23.2
6	1.00	0/14	BENTINK_myc.3
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	0.001	3/15	UPPER AIRWAY CANCER_DN
2	0.005	3/15	SOTIRIOU BREAST CANCER_GRADE_1_VS_3_DN
3	0.037	2/13	GENTLES_modul17
4	0.043	2/14	LIU LIVER CANCER
5	0.043	2/14	LIU PROSTATE CANCER_UP
6	0.048	2/15	GENTLES_modul13
7	0.134	11/316	SPANG_BCL6-index2
8	0.195	2/5	WIRTH_Bone survival
9	0.214	10	LIU BREAST CANCER
10	0.251	1/12	BEN-PORATH_DN
11	0.320	1/16	GENTLES_modul11
12	12/688	12/583	Lembcke Colonic Inflammation
13	0.814	10/530	Lembcke_Normal vs Adenoma
14	0.820	3/185	SPANG_LPS-index2
15	1.000	0/15	RHODES CANCER META SIGNATURE
16	1.000	0/16	LODES_LINDIFFERENTIATED CANCER
17	1.000	0/15	SOTIRIOU BREAST CANCER_GRADE_1_VS_3_UP
18	1.000	0/14	LIU COMMON CANCER_GENES
19	1.000	0/14	WANG_ER_UP
20	1.000	0/9	WANG_ER_DN

Rank	p-value	#in/all	Geneset
1	6e-19	46/378	GUDJ_proliferation down
2	6e-02	2/17	BCHETNIA_EBM up
3	1e-01	8/26	BCHETNIA_EBM_DM up
4	1e+00	8/22	GUDJ_proliferation 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	0.04	2/13	WIRTH_Sec. lymphoid organs
2	0.23	1/13	WIRTH_Prim. lymphoid organs
3	0.27	1/13	WIRTH_Thymus
4	0.29	1/14	WIRTH_Globus pallidus
5	0.32	1/16	WIRTH_Hippocampus
6	0.32	2/26	WIRTH_Liver
7	0.47	1/26	WIRTH_Pancreas
8	0.61	9/400	WIRTH_Nervous System
9	0.70	1/90	WIRTH_Homeostasis
10	0.90	0/120	WIRTH_Testis
11	0.95	1/127	WIRTH_Muscle
12	0.97	5/417	WIRTH_Immune system
13	1.00	0/5	WIRTH_Pituitary gland
14	1.00	0/10	WIRTH_B-cells
15	1.00	0/13	WIRTH_Tonsil
16	1.00	0/12	WIRTH_Lymphocytes
17	1.00	0/6	WIRTH_Bone marrow
18	1.00	0/15	WIRTH_Telencephalon
19	1.00	0/13	WIRTH_Cortex cerebri
20	1.00	0/13	WIRTH_Thalamus

Rank	p-value	#in/all	Geneset
1	0.01	8/0	ATAA-223
2	0.02	6/84	ATAA-21
3	0.03	6/98	ATGT-221-222
4	0.03	11/244	GTGC-25-32-92-363-367
5	0.05	5/162	GAGA-142
6	0.05	5/82	AAAC-140
7	0.05	5/84	ATGC-217
8	0.05	6/116	GACA-219
9	0.06	6/88	ATCA-433
10	0.07	4/65	TCTA-376A-376B
11	0.07	1/3	ACGC-210
12	0.08	16/457	TTCG-124A
13	0.09	9/225	TAT-374
14	0.09	3/45	GGCA-455
15	0.10	2/23	CACG-302A
16	0.10	2/12	TT-142-5P
17	0.11	6/136	GCAT-105
18	0.11	7/168	ATAC-144
19	0.11	5/107	AACA-408-3P
20	0.11	5/107	AACA-181B

Rank	p-value	#in/all	Geneset
1	0.03	1/48	hsa-miR-5624-3p
2	0.03	5/75	hsa-miR-1305
3	0.06	5/76	hsa-miR-1261
4	0.06	5/87	hsa-miR-134
5	0.06	19/538	hsa-miR-17
6	0.07	3/39	hsa-miR-484
7	0.07	2/18	hsa-miR-664
8	0.07	1/14	hsa-miR-429
9	0.07	18/517	hsa-miR-106a
10	0.08	6/124	hsa-miR-212
11	0.08	8/187	hsa-miR-520d-5p
12	0.08	5/98	hsa-miR-526a
13	0.09	5/101	hsa-miR-410
14	0.09	5/101	hsa-miR-525-5p
15	0.10	3/46	hsa-miR-1322
16	0.10	7/164	hsa-miR-96
17	0.10	8/198	hsa-miR-33a
18	0.10	13/368	hsa-miR-144
19	0.10	2/23	hsa-miR-943
20	0.11	3/48	hsa-miR-610

Rank	p-value	#in/all	Geneset
1	2e-04	47/146	HEBENSTREIT_low expression TF
2	8e-01	1/63	MYC_Metabolism UP
3	8e-01	1/63	MYC_targets UP
4	8e-01	25/1233	KIM_MYC targets
5	1e+00	17/1095	HEBENSTREIT_high expression TF
6	1e+00	0/4	NOVICK_TF
7	1e+00	0/5	MYC_TFs
8	1e+00	0/9	MYC_targets DOWN
9	1e+00	0/4	MYC_Apoptosis UP
10	1e+00	0/8	MYC_Cell cycle UP
11	1e+00	0/2	MYC_Cell cycle DOWN
12	1e+00	0/4	MYC_Cell growth and proliferation UP
13	1e+00	0/2	MYC_Chromatin_modification UP
14	1e+00	0/3	MYC_DNA repair UP
15	1e+00	0/3	MYC_DNA replication UP
16	1e+00	0/7	MYC_ECM cell adhesion DOWN
17	1e+00	0/16	MYC_Protein synthesis degradation UP
18	1e+00	0/8	MYC_RNA processing binding UP
19	1e+00	0/2	MYC_Signal transduction UP
20	1e+00	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	5e-07	56/1182	cytosolic space
2	6e-04	7/61	extracellular region
3	2e-03	8/92	secretory granule
4	2e-03	3/220	tight junction
5	2e-03	5/40	mitochondrial matrix
6	9e-03	11/201	extrinsic to membrane
7	1e-02	4/47	apical plasma membrane
8	1e-02	14/304	cytosolic small ribosomal subunit
9	2e-02	3/25	mitochondrial inner membrane
10	2e-02	4/45	small ribosomal subunit
11	2e-02	39/1142	stress fiber
12	3e-02	2/11	intracellular
13	3e-02	2/11	A band
14	3e-02	14/333	photoreceptor outer segment membrane
15	3e-02	2/12	cytoskeleton
16	4e-02	2/13	integral to peroxisomal membrane
17	5e-02	2/15	interstitial matrix
18	5e-02	3/19	dystrochin-associated glycoprotein complex
19	5e-02	3/37	actin filament

Rank	p-value	#in/all	Geneset
1	0.006	5/9	mature astrocytes
2	0.010	5/55	OL vs. MCG_OL
3	0.022	2/10	willscher_GemLTSwt_proteomics-G_UP
4	0.032	2/12	astrocytes_glio
5	0.037	4/53	Christensen_hypermethylated_in_primary_glioblastoma
6	0.049	4/58	OPC
7	0.052	5/87	isletaire_hypermeth_LGG_vs_control
8	0.061	3/48	Donson-chemokine/cytokine-receptors-associated with LTS in HGA
9	0.087	3/44	in vivo astrocytes vs. cultured astroglia
10	0.096	3/46	OL vs. OPC

# K-Means Cluster

## Spot Summary: B

# metagenes = 468  
# genes = 3085

<r> metagenes = 0.4

beta: r2= 0.29 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

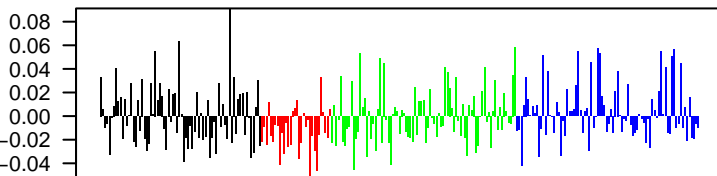
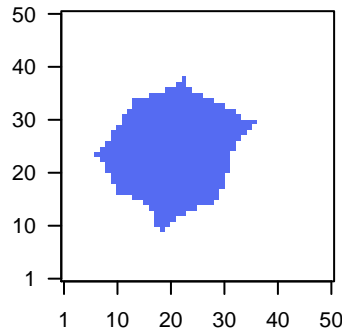
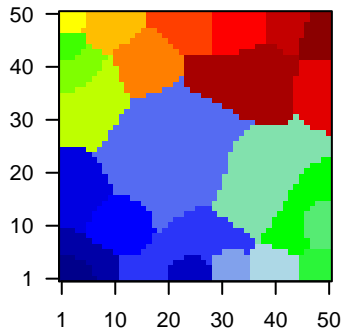
Rank	ID	max e	r	min e	Description
					Symbol
1	3047	1.69	-0.36	0.26	HBG1 hemoglobin, gamma A [Source:HGNC Symbol;Acc:4831]
2	3048	1.65	-0.34	0.26	HBG2 hemoglobin, gamma G [Source:HGNC Symbol;Acc:4832]
3	140690	1.62	-0.28	0.24	CTCF1 CCCTC-binding factor (zinc finger protein)-like [Source:HGNC]
4	5179	1.58	-0.43	0.23	PENK proenkephalin [Source:HGNC Symbol;Acc:8831]
5	55857	1.44	-0.75	0.21	
6	6086	1.37	-0.58	0.44	RNY4 RNA, Ro-associated Y4 [Source:HGNC Symbol;Acc:10244]
7	337959	1.32	-0.23	0.15	KRTAP13 keratin associated protein 13-2 [Source:HGNC Symbol;Acc:13432]
8	100169760	1.3	-0.65	0.21	RNA5S9 RNA, 5S ribosomal 9 [Source:HGNC Symbol;Acc:34370]
9	84873	1.3	-0.23	0.16	GPR128 G protein-coupled receptor 128 [Source:HGNC Symbol;Acc:10244]
10	4496	1.27	-0.44	0.27	MT1H metallothionein 1H [Source:HGNC Symbol;Acc:7400]
11	10430	1.22	-0.82	0.35	TMEM147 transmembrane protein 147 [Source:HGNC Symbol;Acc:3041]
12	644928	1.21	-0.95	0.36	
13	84299	1.21	-0.52	0.35	MIEN1 migration and invasion enhancer 1 [Source:HGNC Symbol;Acc:10244]
14	400156	1.2	-0.87	0.28	
15	644	1.2	-0.96	0.3	BLVRA biliverdin reductase A [Source:HGNC Symbol;Acc:1062]
16	5438	1.19	-0.78	0.54	POLR2I polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [Source:HGNC Symbol;Acc:10244]
17	26871	1.18	-0.77	0.32	RNU1-1 RNA, U1 small nuclear 1 [Source:HGNC Symbol;Acc:10120]
18	7923	1.18	-0.96	0.45	HSD17B8 hydroxysteroid (17-beta) dehydrogenase 8 [Source:HGNC Symbol;Acc:10244]
19	2172	1.16	-0.47	0.27	FABP6 fatty acid binding protein 6, ileal [Source:HGNC Symbol;Acc:10244]
20	4713	1.15	-0.75	0.71	NDUFB7 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 15kDa [Source:HGNC Symbol;Acc:10244]

## Geneset Overrepresentation

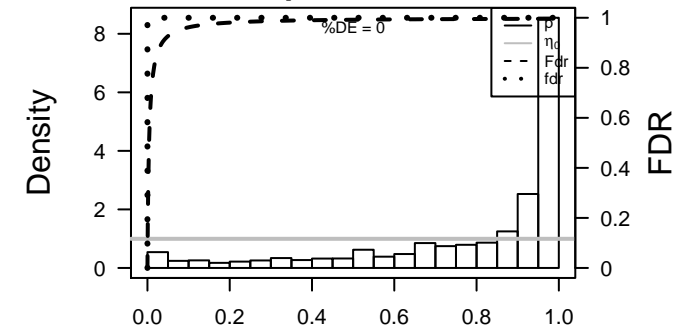
Rank	p-value	#in/all	Geneset
1	1e-34	59 / 69	MF olfactory receptor activity
2	6e-24	133 / 321	MF G-protein coupled receptor activity
3	9e-18	150 / 435	BP G-protein coupled receptor signaling pathway
4	8e-15	303 / 1146	TF HEBENSTREIT_low expression TF
5	1e-14	58 / 120	H.Tis: WIRTH_Testis
6	3e-12	31 / 50	H.Tis: WIRTH_Homeostasis
7	7e-12	35 / 62	H.Tis: WIRTH_Liver
8	1e-11	25 / 36	miRN Cancer
9	7e-11	25 / 38	miRN Breast cancer
10	4e-10	23 / 35	miRN Prostate cancer
11	6e-10	120 / 400	H.Tis: WIRTH_Nervous System
12	9e-10	23 / 36	miRN Lung cancer
13	2e-09	22 / 34	miRN Pancreatic cancer
14	2e-09	22 / 34	miRN Squamous cell carcinoma, head and neck
15	2e-09	22 / 34	miRN Hematological
16	2e-09	21 / 32	miRN Leukemia
17	1e-08	17 / 24	miRN Muscular
18	2e-08	18 / 27	miRN Colorectal cancer
19	3e-08	19 / 30	miRN Ovarian cancer
20	1e-07	45 / 118	Glio willscher_GBM_Verhaak-CL_expression_K_down
21	1e-07	45 / 118	Glio willscher_GBM_Verhaak-MES_expression_K_down
22	1e-07	45 / 118	Glio willscher_GBM_Verhaak-PNwt_expression_K_up
23	1e-07	45 / 118	Glio willscher_GBM_Verhaak-PNmut_expression_K_up
24	1e-07	88 / 293	BP synaptic transmission
25	1e-07	18 / 29	miRN Melanoma and neural system tumor syndrome
26	1e-06	35 / 89	Glio WIRTH_Normal Brain
27	3e-06	46 / 135	BP visual perception
28	3e-06	18 / 34	Chr Chr Y
29	5e-06	14 / 23	miRN Hepatocellular carcinoma
30	5e-06	14 / 23	miRN Stroke, susceptibility to
31	8e-06	13 / 21	miRN Gastrointestinal
32	9e-06	26 / 63	MF hormone activity
33	9e-06	24 / 56	BP regulation of membrane potential
34	1e-05	12 / 19	miRN Multiple myeloma
35	2e-05	13 / 22	miRN Glioblastoma multiforme, somatic
36	3e-05	8 / 10	GSE/ WEBER_METHYLATED_HCP_IN_SPERM_DN
37	3e-05	8 / 10	miRN Myelofibrosis, idiopathic
38	6e-05	654 / 3274	CC integral to membrane
39	8e-05	10 / 16	miRN Cervical cancer, somatic
40	2e-04	10 / 17	miRN Cardiomyopathy, dilated

Overview Map

Spot



p-values







# K-Means Cluster

## Spot Summary: C

# metagenes = 108  
# genes = 715

<r> metagenes = 0.85  
<r> genes = 0.24  
beta: r2= 5.18 / log p= -Inf

# samples with spot = 23 ( 8.4 % )  
Atypical : 23 ( 31.1 % )

## Spot Genelist

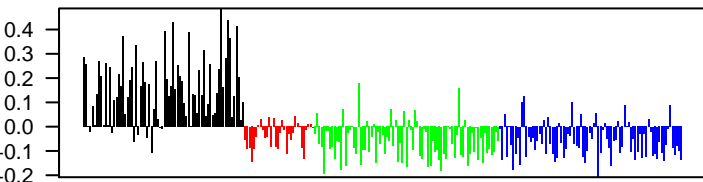
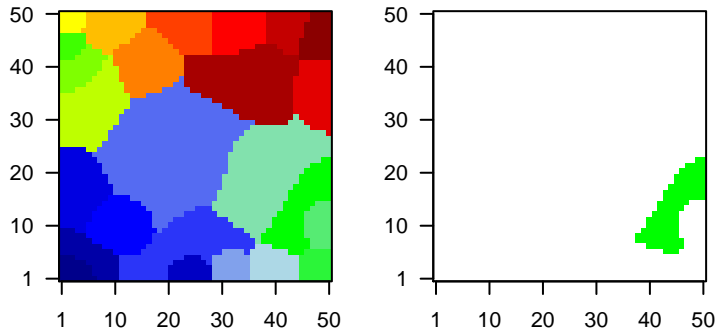
Rank	ID	max e	r	min e	Description
					Symbol
1	54959	2.94	-0.58	0.36	ODAM odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:10485]
2	4602	2.8	-1.04	0.76	MYB v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:10485]
3	728715	2.6	-1.25	0.5	RP11-726G1.1
4	83988	2.43	-1.29	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:21000]
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	2248	2.21	-0.33	0.4	FGF3 fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
10	10562	2.2	-0.61	0.19	OLFM4 olfactomedin 4 [Source:HGNC Symbol;Acc:17190]
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:10485]
14	494470	2.04	-1.37	0.6	RNF165 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
15	1959	2.02	-1.28	0.36	EGR2 early growth response 2 [Source:HGNC Symbol;Acc:3239]
16	909	1.99	-1.12	0.34	CD1A CD1a molecule [Source:HGNC Symbol;Acc:1634]
17	3670	1.98	-0.84	0.35	ISL1 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
18	26824	1.91	-0.97	0.28	RNU11 RNA, U11 small nuclear [Source:HGNC Symbol;Acc:10108]
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

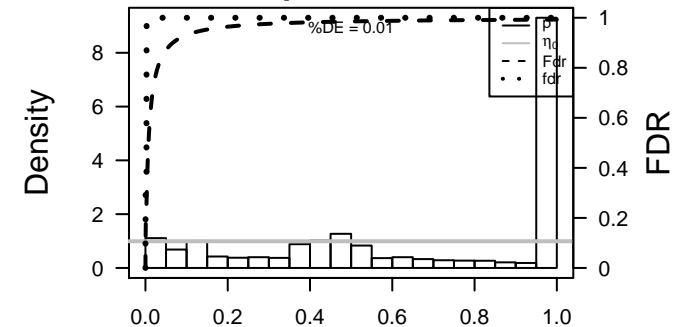
Rank	p-value	#in/all	Geneset
1	8e-09	77 / 914	Chr Chr 3
2	1e-08	45 / 417	H.Tiss: WIRTH_Immune system
3	1e-07	110 / 1574	BP transcription, DNA-templated
4	1e-07	33 / 280	Chr Chr 13
5	3e-07	16 / 81	miRN hsa-miR-188-5p
6	3e-07	109 / 1581	BP regulation of transcription, DNA-dependent
7	8e-06	80 / 1142	CC intracellular
8	1e-05	115 / 1820	MF metal ion binding
9	3e-05	16 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
10	3e-05	109 / 1749	MF DNA binding
11	3e-05	6 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_A
12	1e-04	13 / 92	BP translational elongation
13	2e-04	12 / 81	BP viral transcription
14	2e-04	20 / 189	miRN CTTT-527
15	2e-04	16 / 134	miRN hsa-miR-200a
16	2e-04	37 / 463	miRN hsa-miR-301a
17	2e-04	28 / 314	miRN TTGC-130A--301--130B
18	2e-04	27 / 300	miRN hsa-miR-548c-3p
19	2e-04	8 / 40	BP androgen receptor signaling pathway
20	3e-04	63 / 940	MF nucleic acid binding
21	3e-04	5 / 15	GSE/ ZHAN_MULTIPLE_MYELOMA_CD2_UP
22	3e-04	12 / 87	BP translational termination
23	4e-04	14 / 116	miRN GACA-219
24	5e-04	12 / 92	BP viral life cycle
25	6e-04	4 / 10	GSE/ BASSO_CD40_SIGNALING_DN
26	7e-04	10 / 69	miRN AGCT-28
27	7e-04	3 / 5	Lymp MASCQUE_mBL UP
28	8e-04	13 / 109	BP SRP-dependent cotranslational protein targeting to membrane
29	8e-04	18 / 182	miRN TTTT-373
30	9e-04	7 / 37	CC cytosolic small ribosomal subunit
31	9e-04	4 / 11	GSE/ KEGG_CALCIIUM_SIGNALING_PATHWAY
32	9e-04	31 / 396	miRN hsa-miR-301b
33	1e-03	6 / 28	BP B cell activation
34	1e-03	6 / 28	BP T cell differentiation
35	1e-03	14 / 128	BP translational initiation
36	1e-03	54 / 823	MF sequence-specific DNA binding transcription factor activity
37	1e-03	235 / 4640	CC nucleus
38	1e-03	34 / 456	miRN hsa-miR-130a
39	1e-03	26 / 318	MF chromatin binding
40	1e-03	5 / 20	MF RNA polymerase II transcription coactivator activity

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: D

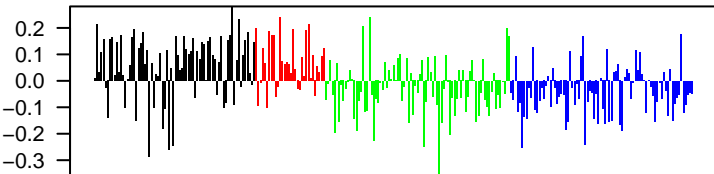
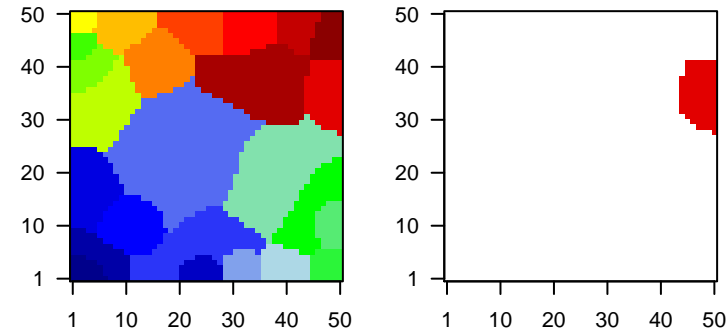
# metagenes = 83  
# genes = 699

<r> metagenes = 0.87  
<r> genes = 0.21  
beta: r2= 3.21 / log p= -Inf

# samples with spot = 4 ( 1.5 % )  
Atypical : 2 ( 2.7 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 1 ( 1.2 % )

Overview Map

Spot



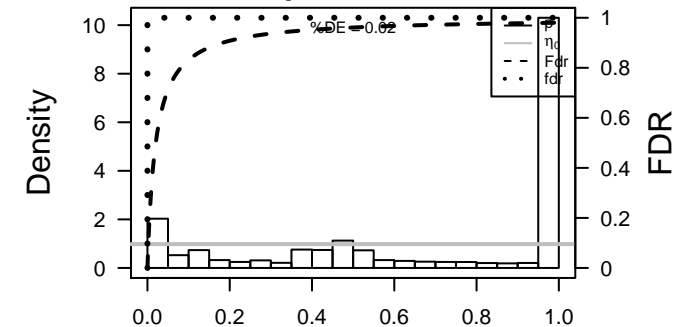
## Spot Genelist

Rank	ID	max e	r	min e	Description Symbol
1	64207	1.94	-2.13	0.27	IRF2BPL interferon regulatory factor 2 binding protein-like [Source:HGNC Symbol;Acc:21643]
2	27075	1.78	-1.45	0.37	TSPAN13 tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
3	5274	1.74	-0.65	0.41	SERPIN1 serpin peptidase inhibitor, clade I (neuroserpin), member 1 [Source:HGNC Symbol;Acc:21643]
4	2059	1.62	-0.67	0.48	EPS8 epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:21643]
5	4254	1.49	-1.1	0.5	KITLG KIT ligand [Source:HGNC Symbol;Acc:6343]
6	10257	1.47	-0.85	0.54	ABCC4 ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:HGNC Symbol;Acc:21643]
7	81552	1.46	-0.72	0.3	VOPP1 vesicular, overexpressed in cancer, pro-survival protein 1 [Source:HGNC Symbol;Acc:21643]
8	11212	1.46	-1.05	0.35	PROSC proline synthetase co-transcribed homolog (bacterial) [Source:HGNC Symbol;Acc:21643]
9	4856	1.43	-0.77	0.25	NOV nephroblastoma overexpressed [Source:HGNC Symbol;Acc:21643]
10	132430	1.42	-0.8	0.39	PABPC4 poly(A) binding protein, cytoplasmic 4-like [Source:HGNC Symbol;Acc:21643]
11	57088	1.41	-1.2	0.24	PLSCR4 phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649]
12	1953	1.4	-0.87	0.37	MEGF6 multiple EGF-like-domains 6 [Source:HGNC Symbol;Acc:32]
13	60481	1.39	-1.17	0.5	ELOVL5 ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213]
14	4982	1.39	-0.58	0.28	TNFRSF11B tumor necrosis factor receptor superfamily, member 11b [Source:HGNC Symbol;Acc:213]
15	151613	1.34	-0.72	0.47	TTC14 tetratricopeptide repeat domain 14 [Source:HGNC Symbol;Acc:213]
16	54467	1.32	-0.78	0.42	ANKIB1 ankyrin repeat and IBR domain containing 1 [Source:HGNC Symbol;Acc:213]
17	7095	1.32	-0.69	0.46	SEC62 SEC62 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1]
18	171586	1.32	-0.85	0.49	ABHD3 abhydrolase domain containing 3 [Source:HGNC Symbol;Acc:213]
19	3730	1.32	-0.6	0.36	KAL1 Kallmann syndrome 1 sequence [Source:HGNC Symbol;Acc:213]
20	56243	1.28	-1.1	0.22	KIAA1217 KIAA1217 [Source:HGNC Symbol;Acc:25428]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-16	295 / 4640	CC nucleus
2	1e-14	93 / 940	MF nucleic acid binding
3	8e-14	68 / 595	MF RNA binding
4	2e-12	30 / 153	miRN hsa-miR-450b-5p
5	8e-12	25 / 113	miRN hsa-miR-507
6	2e-11	43 / 318	miRN hsa-miR-590-3p
7	2e-11	32 / 189	miRN hsa-miR-1283
8	2e-11	56 / 495	miRN hsa-miR-103
9	4e-11	25 / 121	miRN hsa-miR-543
10	4e-11	51 / 433	miRN hsa-miR-19b
11	5e-11	53 / 463	miRN hsa-miR-301a
12	5e-11	30 / 174	BP mRNA processing
13	5e-11	48 / 396	miRN hsa-miR-301b
14	1e-10	33 / 215	miRN hsa-miR-203
15	2e-10	29 / 172	miRN hsa-miR-607
16	2e-10	37 / 267	miRN hsa-miR-577
17	2e-10	50 / 440	miRN hsa-miR-19a
18	3e-10	42 / 335	miRN hsa-miR-142-5p
19	7e-10	47 / 412	miRN hsa-miR-372
20	8e-10	28 / 171	miRN hsa-miR-452
21	1e-09	41 / 336	miRN hsa-miR-548b-5p
22	1e-09	34 / 246	miRN hsa-miR-524-5p
23	2e-09	29 / 188	miRN hsa-miR-548d-3p
24	2e-09	44 / 382	miRN hsa-miR-454
25	2e-09	39 / 314	miRN TTGC-130A---301---130B
26	2e-09	59 / 603	miRN hsa-miR-20a
27	2e-09	24 / 134	miRN hsa-miR-656
28	3e-09	27 / 169	miRN hsa-miR-580
29	3e-09	32 / 229	BP RNA splicing
30	4e-09	27 / 171	miRN hsa-miR-369-3p
31	4e-09	115 / 1574	BP transcription, DNA-templated
32	4e-09	54 / 538	miRN hsa-miR-17
33	4e-09	51 / 494	miRN hsa-miR-107
34	4e-09	46 / 421	miRN hsa-let-7b
35	4e-09	47 / 436	miRN hsa-miR-548n
36	6e-09	26 / 163	BP mRNA splicing, via spliceosome
37	6e-09	37 / 300	miRN hsa-miR-561
38	6e-09	20 / 100	miRN hsa-miR-544
39	7e-09	52 / 517	miRN hsa-miR-106a
40	7e-09	20 / 101	miRN hsa-miR-410

p-values





# K-Means Cluster

## Spot Summary: E

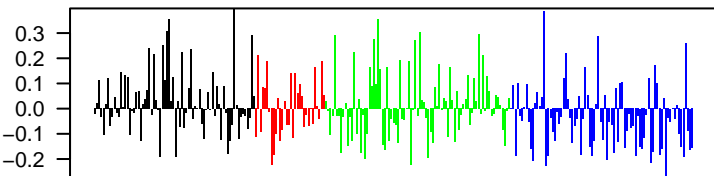
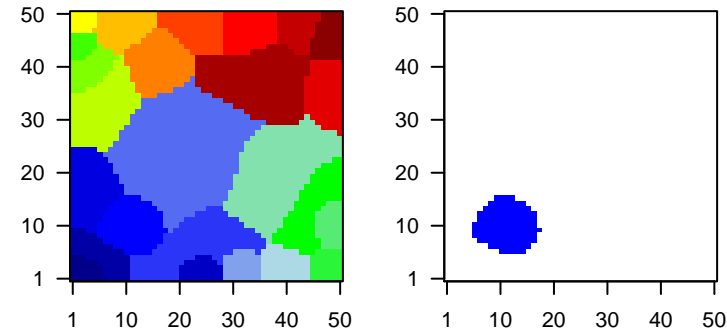
# metagenes = 103  
# genes = 682

<r> metagenes = 0.79  
<r> genes = 0.17  
beta: r2= 3.77 / log p= -Inf

# samples with spot = 19 ( 6.9 % )  
Atypical : 8 ( 10.8 % )  
Mesenchymal : 7 ( 8.2 % )  
Basal : 4 ( 4.8 % )

### Overview Map

### Spot

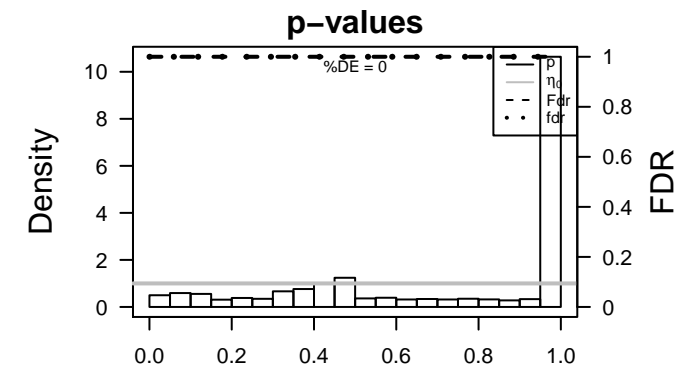


## Spot Genelist

Rank	ID	max e	r	min e	Description
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	MAGEA10melanoma 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	547	2.87	-0.5	0.45	KIF1A kinesin family member 1A [Source:HGNC Symbol;Acc:888]
20	4103	2.69	-0.85	0.47	MAGEA4melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-10	90 / 1135	Chr Chr 19
2	5e-09	57 / 630	Chr Chr X
3	6e-07	16 / 92	BP anterior/posterior pattern specification
4	1e-06	11 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
5	3e-05	231 / 4640	CC nucleus
6	2e-04	60 / 940	MF nucleic acid binding
7	2e-04	5 / 15	BP associative learning
8	2e-04	5 / 15	BP semaphorin-plexin signaling pathway
9	2e-04	90 / 1574	BP transcription, DNA-templated
10	3e-04	34 / 449	Chr Chr 20
11	3e-04	6 / 24	BP tissue development
12	3e-04	5 / 16	GSE/ SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
13	3e-04	23 / 261	miRN CTCA-125B--125A
14	4e-04	12 / 96	BP chromatin modification
15	9e-04	46 / 717	Chr Chr 16
16	1e-03	5 / 21	BP chromatin organization
17	1e-03	12 / 109	CC spindle
18	2e-03	5 / 23	Chr Chr HSCHR6_MHC_DBB
19	2e-03	93 / 1749	MF DNA binding
20	2e-03	85 / 1581	BP regulation of transcription, DNA-dependent
21	2e-03	4 / 15	GSE/ JIANG_TIP30_TARGETS_DN
22	2e-03	4 / 15	GSE/ KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULF
23	2e-03	7 / 47	BP embryonic skeletal system morphogenesis
24	3e-03	3 / 8	GSE/ BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
25	3e-03	3 / 8	miRN ACCG-423
26	3e-03	4 / 16	MF histone acetyl-lysine binding
27	4e-03	8 / 64	BP neural tube closure
28	4e-03	4 / 17	BP calcium ion homeostasis
29	4e-03	12 / 125	miRN GAGC-337
30	4e-03	20 / 264	CC microtubule
31	5e-03	5 / 29	BP lysosome organization
32	5e-03	5 / 29	miRN hsa-miR-296-5p
33	6e-03	31 / 481	BP biological_process
34	6e-03	7 / 55	miRN GGGG-296
35	6e-03	10 / 99	MF double-stranded DNA binding
36	6e-03	4 / 19	MF hydrolase activity, acting on acid anhydrides, in phosphorus-containing an
37	6e-03	3 / 10	CC oligosaccharyltransferase complex
38	6e-03	3 / 10	BP positive regulation of excitatory postsynaptic membrane potential
39	6e-03	3 / 10	GSE/ BORCZUK_MALIGNANT_MESOTHELIOMA_DN
40	6e-03	3 / 10	GSE/ RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP





# K-Means Cluster

## Spot Summary: F

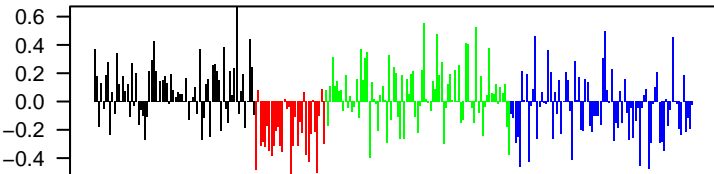
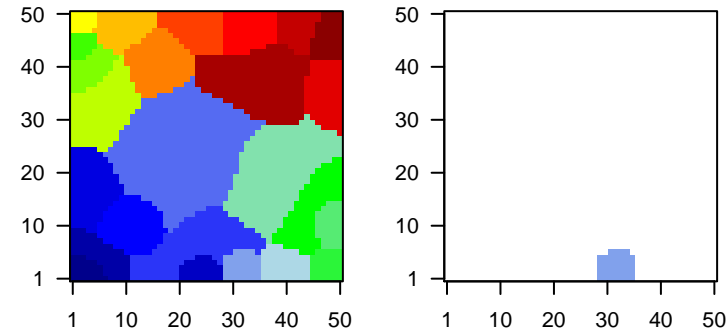
# metagenes = 39  
# genes = 300

<r> metagenes = 0.92  
<r> genes = 0.27  
beta: r2= 6.54 / log p= -Inf

# samples with spot = 37 ( 13.5 % )  
Atypical : 14 ( 18.9 % )  
Mesenchymal : 16 ( 18.8 % )  
Basal : 7 ( 8.3 % )

Overview Map

Spot

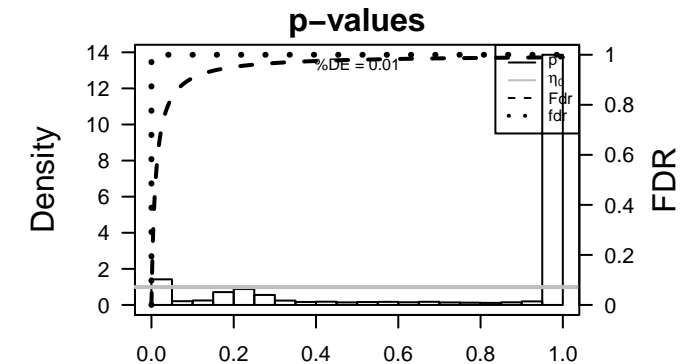


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	3627	3.43	-2.5	0.75	CXCL10 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;Acc:10514]
2	7503	2.98	-0.78	0.16	XIST X inactive specific transcript (non-protein coding) [Source:HGNC Symbol;Acc:10514]
3	6373	2.89	-1.08	0.54	CXCL11 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:10514]
4	9560	2.65	-1.76	0.49	CCL4L1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:10514]
5	9636	2.47	-2.69	0.73	ISG15 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:40610]
6	10964	2.46	-2.33	0.78	IFI44L interferon-induced protein 44-like [Source:HGNC Symbol;Acc:10514]
7	8743	2.43	-2.05	0.38	TNFSF10 tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:10514]
8	629	2.42	-2.1	0.6	CFB complement factor B [Source:HGNC Symbol;Acc:1037]
9	7453	2.35	-1.7	0.73	WARS tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:10514]
10	115362	2.34	-1.91	0.73	GBP5 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989]
11	388372	2.33	-1.11	0.62	CCL4L1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbol;Acc:10514]
12	6355	2.3	-1.49	0.54	CCL8 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:10514]
13	6289	2.26	-0.91	0.39	SAA2 serum amyloid A2 [Source:HGNC Symbol;Acc:10514]
14	9536	2.23	-1.43	0.33	PTGES prostaglandin E synthase [Source:HGNC Symbol;Acc:9599]
15	4321	2.23	-1.74	0.44	MMP12 matrix metalloproteinase 12 (macrophage elastase) [Source:HGNC Symbol;Acc:10514]
16	970	2.2	-0.71	0.41	CD70 CD70 molecule [Source:HGNC Symbol;Acc:11937]
17	3433	2.19	-1.63	0.69	IFIT2 interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:10514]
18	1591	2.19	-1.48	0.24	CYP24A cytochrome P450, family 24, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:10514]
19	7124	2.18	-1.07	0.36	TNF tumor necrosis factor [Source:HGNC Symbol;Acc:11892]
20	79931	2.06	-0.8	0.4	TNIP3 TNFAIP3 interacting protein 3 [Source:HGNC Symbol;Acc:1989]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-39	30 / 51	BP type I interferon signaling pathway
2	2e-36	38 / 123	BP defense response to virus
3	2e-33	48 / 274	LympI SPANG_IL21 DN
4	1e-28	39 / 204	BP cytokine-mediated signaling pathway
5	1e-27	45 / 312	BP immune response
6	3e-27	30 / 109	BP response to virus
7	5e-23	53 / 572	Disea GUDJ_psooriasis up
8	3e-21	49 / 530	BP innate immune response
9	1e-20	13 / 16	GSE/ MOSERLE_IFNA_RESPONSE
10	2e-20	16 / 31	BP negative regulation of viral genome replication
11	5e-19	19 / 60	BP interferon-gamma-mediated signaling pathway
12	2e-18	12 / 16	GSE/ EINAV_INTERFERON_SIGNATURE_IN_CANCER
13	8e-18	35 / 316	Canci SPANG_BCL6-index2
14	2e-16	11 / 16	GSE/ ZHANG_INTERFERON_RESPONSE
15	2e-16	11 / 16	GSE/ UROSEVIC_RESPONSE_TO_IMIQIMOD
16	9e-16	10 / 13	GSE/ BOWIE_RESPONSE_TO_TAMOXIFEN
17	2e-15	9 / 10	GSE/ BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
18	5e-13	8 / 10	GSE/ GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
19	2e-12	15 / 70	BP antigen processing and presentation of exogenous peptide antigen via MHC class I protein complex
20	2e-12	8 / 11	GSE/ BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
21	3e-12	22 / 185	Canci SPANG_LPS-index2
22	4e-12	15 / 74	BP antigen processing and presentation of exogenous peptide antigen via MHC class I protein complex
23	4e-12	15 / 74	BP regulation of immune response
24	8e-12	16 / 91	BP antigen processing and presentation of peptide antigen via MHC class I protein complex
25	3e-11	6 / 6	Lymp DAVE_MHCCII BL DN
26	7e-11	7 / 10	CC MHC class I protein complex
27	4e-10	8 / 18	MF peptide antigen binding
28	4e-10	8 / 18	BP positive regulation of T cell mediated cytotoxicity
29	7e-10	29 / 417	H.Tis: WIRTH_Immune system
30	9e-10	6 / 8	GSE/ ROETH_TERT_TARGETS_UP
31	2e-09	7 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
32	2e-09	33 / 553	Canci Lembcke_Colonin Inflammation
33	4e-09	9 / 32	BP negative regulation of type I interferon production
34	4e-09	24 / 316	BP modulation by virus of host morphology or physiology
35	6e-09	7 / 16	GSE/ MAHADEVAN_RESPONSE_TO_MP470_UP
36	7e-09	17 / 162	CC external side of plasma membrane
37	7e-09	6 / 10	GSE/ GILMORE_CORE_NFKB_PATHWAY
38	1e-08	10 / 47	BP antigen processing and presentation
39	2e-08	7 / 18	BP response to interferon-gamma
40	3e-08	10 / 52	Chr Chr HSCHR6_MHC_QBL







# K-Means Cluster

## Spot Summary: G

# metagenes = 55  
# genes = 537

<r> metagenes = 0.92  
<r> genes = 0.34  
beta: r2= 8.57 / log p= -Inf

# samples with spot = 35 ( 12.7 % )  
Atypical : 27 ( 36.5 % )  
Mesenchymal : 6 ( 7.1 % )  
Basal : 2 ( 2.4 % )

## Spot Genelist

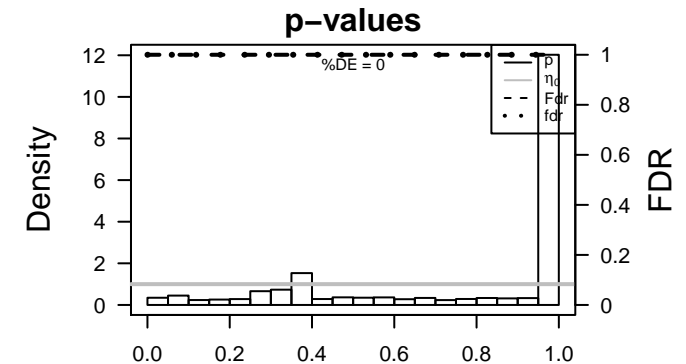
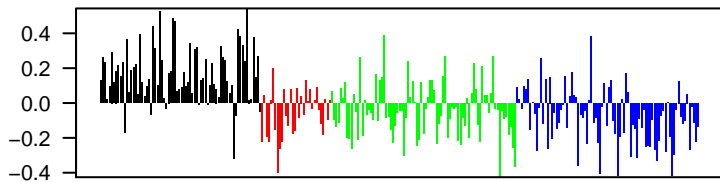
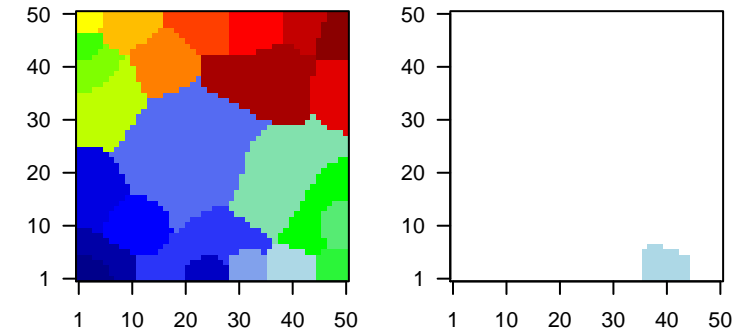
Rank	ID	max e	r	min e	Description
					Symbol
1	3127	4.47	-1.24	0.19	HLA-DRB3 major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:10037]
2	125050	2.79	-0.87	0.28	RN7SK RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
3	22809	2.1	-1.19	0.63	ATF5 activating transcription factor 5 [Source:HGNC Symbol;Acc:7151]
4	6376	2.05	-1.53	0.43	CX3CL1 chemokine (C-X3-C motif) ligand 1 [Source:HGNC Symbol;Acc:10037]
5	11067	1.82	-1.18	0.53	C10orf10 chromosome 10 open reading frame 10 [Source:HGNC Symbol;Acc:10037]
6	80162	1.79	-0.97	0.67	ATHL1 ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;Acc:10037]
7	84061	1.78	-1.53	0.84	MAGT1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
8	126205	1.77	-1.63	0.93	NLRP8 NLR family, pyrin domain containing 8 [Source:HGNC Symbol;Acc:10037]
9	84446	1.74	-1.13	0.68	BRSK1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18510]
10	51326	1.73	-1.07	0.41	ARL17B ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc:10037]
11	23475	1.73	-0.82	0.44	QPRT quinolate phosphoribosyltransferase [Source:HGNC Symbol;Acc:10037]
12	2120	1.7	-1.04	0.72	ETV6 ets variant 6 [Source:HGNC Symbol;Acc:3495]
13	401261	1.68	-0.87	0.83	USP49 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20000]
14	7127	1.66	-0.92	0.42	TNFAIP2 tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:10037]
15	79058	1.66	-1.01	0.63	ASPSCR1 alveolar soft part sarcoma chromosome region, candidate 1 [Source:HGNC Symbol;Acc:10037]
16	618	1.64	-1.41	0.41	BCYRN1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
17	400818	1.62	-1.99	0.69	AC23981 Neuroblastoma breakpoint family member 1 [Source:UniProt]
18	29944	1.58	-0.69	0.61	PNMA3 paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187]
19	4851	1.57	-1.35	0.44	NOTCH1 notch 1 [Source:HGNC Symbol;Acc:7881]
20	25862	1.53	-1.56	0.93	USP49 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20000]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-09	73 / 1135	Chr Chr 19
2	7e-05	7 / 34	MF hydrolase activity, hydrolyzing O-glycosyl compounds
3	2e-04	80 / 1749	MF DNA binding
4	5e-04	4 / 13	GSE# SPIRA_SMOKERS_LUNG_CANCER_DN
5	5e-04	4 / 13	GSE# ST_GAQ_PATHWAY
6	7e-04	4 / 14	MMM MACIEJ_MMML 8
7	9e-04	26 / 426	Lymph SPANG_CD40 6hrs DN
8	1e-03	4 / 15	GSE# NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON
9	1e-03	4 / 16	BP regulation of type I interferon-mediated signaling pathway
10	1e-03	4 / 16	GSE# PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
11	1e-03	8 / 70	CC endomembrane system
12	3e-03	24 / 417	H.Tis: WIRTH_Immune system
13	3e-03	3 / 10	GSE# MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
14	4e-03	7 / 64	BP activation of signaling protein activity involved in unfolded protein response
15	4e-03	8 / 82	BP endoplasmic reticulum unfolded protein response
16	5e-03	43 / 918	Chr Chr 17
17	5e-03	3 / 12	MF diacylglycerol kinase activity
18	5e-03	3 / 12	GSE# CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
19	5e-03	3 / 12	GSE# KEGG_SULFUR_METABOLISM
20	5e-03	3 / 12	GSE# BIOCARTA_HDAC_PATHWAY
21	6e-03	2 / 4	GSE# BIOCARTA_CYTOKINE_PATHWAY
22	6e-03	13 / 187	Chr Chr 21
23	6e-03	4 / 24	BP negative regulation of T cell proliferation
24	7e-03	3 / 13	GSE# BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
25	7e-03	3 / 13	GSE# BIOCARTA_MEF2D_PATHWAY
26	7e-03	8 / 90	BP RNA processing
27	7e-03	4 / 25	BP positive regulation of cytokine secretion
28	8e-03	11 / 152	BP regulation of small GTPase mediated signal transduction
29	8e-03	3 / 14	MF NAD+ kinase activity
30	8e-03	3 / 14	GSE# ST_ADRENERGIC
31	1e-02	8 / 96	BP chromatin modification
32	1e-02	9 / 116	CC cytoplasmic membrane-bound vesicle
33	1e-02	3 / 15	GSE# PRAMOONJAGO_SOX4_TARGETS_UP
34	1e-02	3 / 15	GSE# WANG_CLIM2_TARGETS_UP
35	1e-02	3 / 15	GSE# MUELLER_METHYLATED_IN_GLIOMASTOMA
36	1e-02	3 / 15	GSE# DACOSTA_UV_RESPONSE_VIA_ERCC3_XPCS_DN
37	1e-02	3 / 15	GSE# CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
38	1e-02	3 / 15	GSE# SAGIV_CD24_TARGETS_UP
39	1e-02	3 / 15	GSE# BIOCARTA_NKCELLS_PATHWAY
40	1e-02	6 / 60	BP T cell costimulation

## Overview Map

## Spot





# K-Means Cluster

## Spot Summary: H

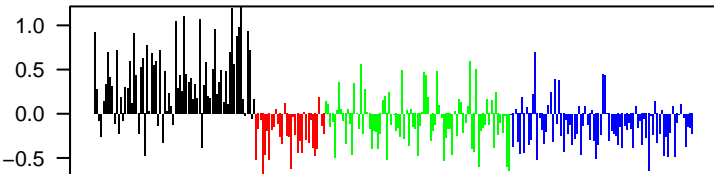
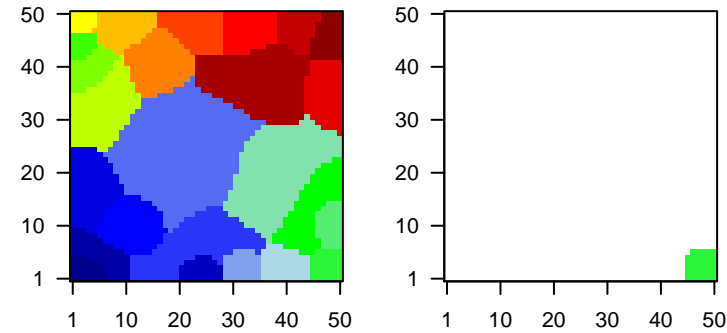
# metagenes = 35  
# genes = 482

<r> metagenes = 0.96  
<r> genes = 0.51  
beta: r2= 31.06 / log p= -Inf

# samples with spot = 66 ( 24 % )  
Atypical : 47 ( 63.5 % )  
Mesenchymal : 12 ( 14.1 % )  
Basal : 7 ( 8.3 % )

### Overview Map

### Spot

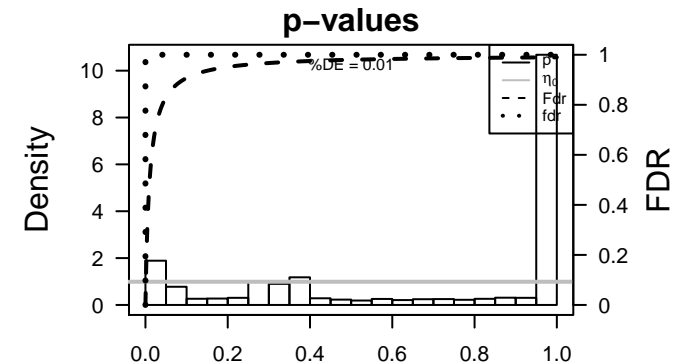


## Spot Genelist

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	3123	3.58	-1.81	0.25	HLA-DRB1 major histocompatibility complex, class II, DR beta 1 [Source:
5	347733	3.34	-1.41	0.47	TUBB2B tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
6	3620	3.29	-1.36	0.5	IDO1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:f
7	10537	3.29	-1.89	0.78	UBD ubiquitin D [Source:HGNC Symbol;Acc:18795]
8	930	3.28	-1.12	0.82	CD19 CD19 molecule [Source:HGNC Symbol;Acc:1633]
9	5730	3.15	-1.43	0.71	PTGDS prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
10	6366	3.15	-1.26	0.57	CCL21 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
11	57172	3.1	-2.31	0.69	CAMK1G calcium/calmodulin-dependent protein kinase IG [Source:HG
12	6364	3.07	-3.08	0.26	CCL20 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
13	4069	3.05	-1.52	0.62	LYZ lysozyme [Source:HGNC Symbol;Acc:6740]
14	9806	3.05	-1.59	0.84	SPOCK2 Sparc/osteonectin, cwcv and kazal-like domains proteoglycar
15	4283	2.98	-1.9	0.55	CXCL9 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
16	962	2.92	-1.66	0.95	CD48 CD48 molecule [Source:HGNC Symbol;Acc:1683]
17	1545	2.91	-1.15	0.48	CYP1B1 cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
18	25849	2.86	-1.41	0.61	PARM1 prostate androgen-regulated mucin-like protein 1 [Source:HK
19	3120	2.85	-1.57	0.37	HLA-DQB1 major histocompatibility complex, class II, DQ beta 2 [Source:
20	51755	2.83	-2.17	0.66	CDK12 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	151 / 553	Cancor Lembcke_Colonc Inflammation
2	4e-91	123 / 417	H.Tiss: WIRTH_Immune system
3	2e-47	75 / 312	BP immune response
4	1e-41	65 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
5	1e-41	65 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
6	1e-41	65 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
7	1e-41	65 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
8	7e-24	38 / 162	CC external side of plasma membrane
9	3e-23	165 / 2659	CC plasma membrane
10	5e-23	51 / 327	Lymph SPANG_CD40 6hrs UP
11	6e-19	22 / 60	BP T cell costimulation
12	1e-18	13 / 15	CC MHC class II protein complex
13	5e-18	44 / 316	Cancor SPANG_BCL6-index2
14	1e-16	22 / 74	BP regulation of immune response
15	1e-16	34 / 204	BP cell surface receptor signaling pathway
16	1e-16	23 / 84	BP T cell receptor signaling pathway
17	4e-16	18 / 47	BP antigen processing and presentation
18	4e-15	37 / 269	BP inflammatory response
19	8e-15	14 / 28	BP B cell receptor signaling pathway
20	6e-14	82 / 1167	BP signal transduction
21	2e-13	50 / 530	BP innate immune response
22	5e-13	25 / 143	MF transmembrane signaling receptor activity
23	1e-12	64 / 835	CC integral to plasma membrane
24	5e-12	15 / 49	Glio Donson-innate immunity-associated with LTS in HGA
25	7e-12	12 / 28	Lymph DAVE_Immune response 1
26	9e-12	9 / 13	Cancor GENTLES_modul18
27	2e-11	14 / 45	BP T cell activation
28	3e-11	9 / 14	GSE/ BIOCARTEA_NO2IL12_PATHWAY
29	4e-11	12 / 32	Glio Donson-Misc immune function-associated with LTS in HGA
30	8e-11	8 / 11	GSE/ BIOCARTEA_TCYTOTOXIC_PATHWAY
31	8e-11	8 / 11	GSE/ BIOCARTEA_THELPER_PATHWAY
32	1e-10	9 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_1
33	2e-10	20 / 118	Lymph SPANG_LPS 6hrs UP
34	3e-10	38 / 407	BP blood coagulation
35	5e-10	19 / 111	BP chemotaxis
36	6e-10	8 / 13	GSE/ BIOCARTEA_IL17_PATHWAY
37	7e-10	21 / 140	Lymph DAVE_BL-vs-DLBCL
38	1e-09	8 / 14	GSE/ FINETTI_BREAST_CANCER_KINOME_GREEN
39	1e-09	14 / 60	BP interferon-gamma-mediated signaling pathway
40	2e-09	12 / 43	BP positive regulation of T cell proliferation





# K-Means Cluster

## Spot Summary: I

# metagenes = 274  
# genes = 977

<r> metagenes = 0.67  
<r> genes = 0.09  
beta: r2= 0.78 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

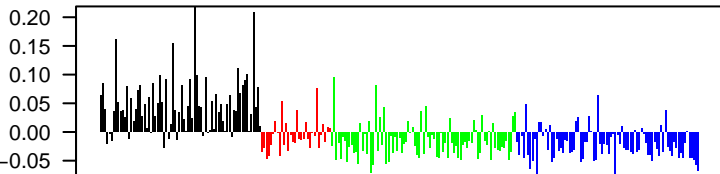
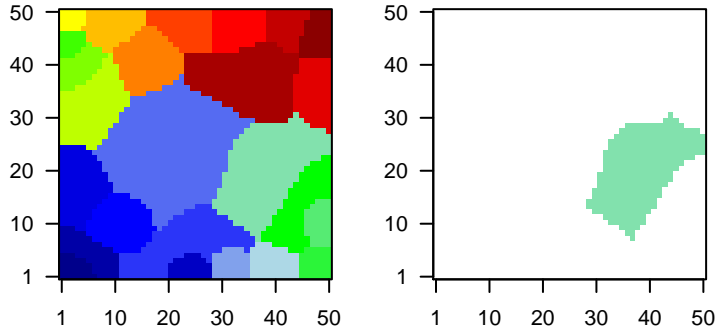
Rank	ID	max e	min e	Description	
				Symbol	
1	85415	2.15	-1.21	0.31	RHPN2 rhophilin, Rho GTPase binding protein 2 [Source:HGNC Sym
2	8190	1.95	-0.45	0.38	MIA melanoma inhibitory activity [Source:HGNC Symbol;Acc:7076
3	149563	1.76	-0.33	0.37	C1orf64 chromosome 1 open reading frame 64 [Source:HGNC Symb
4	1448	1.61	-0.19	0.3	CSN3 casein kappa [Source:HGNC Symbol;Acc:2446]
5	4250	1.58	-0.36	0.4	SCGB2A2secretoglobin, family 2A, member 2 [Source:HGNC Symbol;A
6	9518	1.58	-0.65	0.3	GDF15 growth differentiation factor 15 [Source:HGNC Symbol;Acc:30
7	2813	1.57	-0.26	0.53	GP2 glycoprotein 2 (zymogen granule membrane) [Source:HGNC
8	127003	1.5	-0.31	0.82	C1orf194chromosome 1 open reading frame 194 [Source:HGNC Symt
9	84688	1.47	-0.34	0.73	C9orf24 chromosome 9 open reading frame 24 [Source:HGNC Symb
10	3212	1.46	-0.74	0.32	HOXB2 homeobox B2 [Source:HGNC Symbol;Acc:5113]
11	399949	1.4	-0.3	0.62	C11orf88chromosome 11 open reading frame 88 [Source:HGNC Symt
12	83657	1.39	-0.51	0.69	DYNLRB2dynein, light chain, roadblock-type 2 [Source:HGNC Symbol;
13	222256	1.37	-0.27	0.7	CDHR3 cadherin-related family member 3 [Source:HGNC Symbol;Ac
14	5542	1.36	-0.21	0.44	PRB1 proline-rich protein BstNI subfamily 1 [Source:HGNC Symbol
15	283	1.34	-0.66	0.52	ANG angiogenin, ribonuclease, RNase A family, 5 [Source:HGNC S
16	55861	1.33	-1.37	0.3	DBNDD2dysbindin (dystrobrein binding protein 1) domain containi
17	89765	1.31	-0.28	0.81	RSPH1 radial spoke head 1 homolog (Chlamydomonas) [Source:HG
18	85016	1.31	-0.41	0.35	C11orf70chromosome 11 open reading frame 70 [Source:HGNC Symt
19	65987	1.28	-0.62	0.26	KCTD14 potassium channel tetramerization domain containing 14 [So
20	116151	1.28	-0.93	0.43	FAM210Bfamily with sequence similarity 210, member B [Source:HGNC

## Geneset Overrepresentation

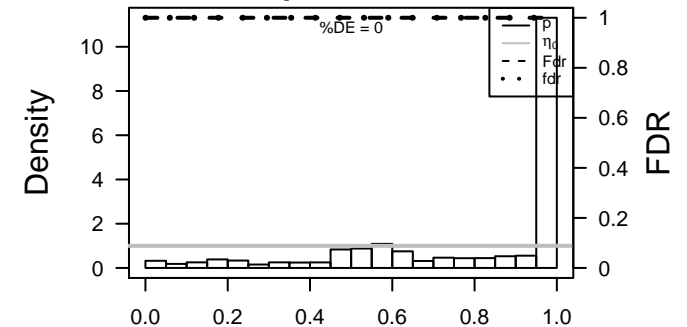
Rank	p-value	#in/all	Geneset
1	1e-31	35 / 51	Glio willscher_GBM_Verhaak-PNmut_expression_G_down
2	1e-10	23 / 81	BP viral transcription
3	3e-10	24 / 92	BP translational elongation
4	6e-10	23 / 87	BP translational termination
5	2e-09	23 / 92	BP viral life cycle
6	3e-09	25 / 109	BP SRP-dependent cotranslational protein targeting to membrane
7	9e-09	20 / 76	Glio GIEZELT_GBM_STSwt_up_VS_LTSwt
8	4e-08	24 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
9	5e-08	12 / 30	CC axoneme
10	3e-07	24 / 128	BP translational initiation
11	7e-07	12 / 37	CC cytosolic small ribosomal subunit
12	9e-06	24 / 153	MF structural constituent of ribosome
13	3e-05	16 / 85	Glio GIEZELT_GBM_STS_down_VS_LTS
14	6e-05	8 / 25	CC small ribosomal subunit
15	6e-05	9 / 32	CC motile cilium
16	8e-05	17 / 102	CC cilium
17	9e-05	7 / 20	CC dynein complex
18	1e-04	6 / 15	GSE/ FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP
19	1e-04	11 / 51	CC cytosolic large ribosomal subunit
20	2e-04	30 / 253	BP translation
21	2e-04	27 / 219	BP mRNA metabolic process
22	3e-04	22 / 167	CC ribosome
23	3e-04	32 / 287	BP viral process
24	4e-04	13 / 75	BP cilium assembly
25	6e-04	5 / 13	CC axonemal dynein complex
26	1e-03	4 / 9	GSE/ REACTOME_PEPTIDE_CHAIN_ELONGATION
27	1e-03	4 / 9	GSE/ REACTOME_VIRAL_MRNA_TRANSLATION
28	2e-03	4 / 10	GSE/ DIRMEIER_LMP1_RESPONSE_LATE_DN
29	2e-03	4 / 10	GSE/ SU_SALIVARY_GLAND
30	2e-03	26 / 242	BP RNA metabolic process
31	2e-03	38 / 400	H.Tis: WIRTH_Nervous System
32	3e-03	11 / 71	MF microtubule motor activity
33	4e-03	15 / 118	Glio willscher_GBM_Verhaak-CL_expression_K_down
34	4e-03	15 / 118	Glio willscher_GBM_Verhaak-MES_expression_K_down
35	4e-03	15 / 118	Glio willscher_GBM_Verhaak-PNwt_expression_K_up
36	4e-03	15 / 118	Glio willscher_GBM_Verhaak-PNmut_expression_K_up
37	4e-03	4 / 12	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP
38	4e-03	4 / 12	GSE/ REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
39	4e-03	4 / 12	GSE/ REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATION
40	4e-03	6 / 27	MF rRNA binding

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: J

# metagenes = 227  
# genes = 1175

<r> metagenes = 0.66

beta: r2= 0.52 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

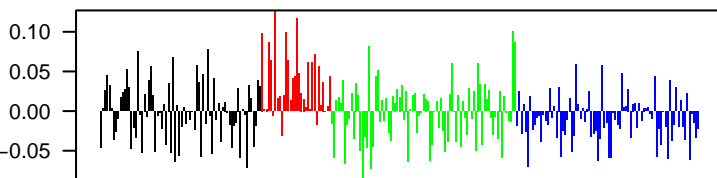
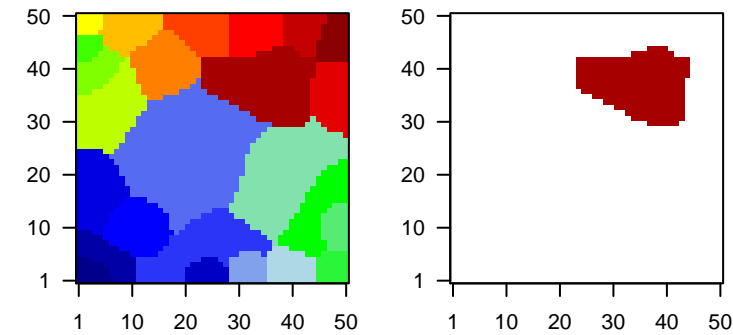
Rank	ID	max e	r	min e	Description
					Symbol
1	441317	1.61	-0.46	0.31	FAM90A2 family with sequence similarity 90, member A21, pseudogene
2	11197	1.42	-0.29	0.35	WIF1 WNT inhibitory factor 1 [Source:HGNC Symbol;Acc:18081]
3	2258	1.31	-0.36	0.33	FGF13 fibroblast growth factor 13 [Source:HGNC Symbol;Acc:3670]
4	4848	1.25	-0.86	0.29	CNOT2 CCR4-NOT transcription complex, subunit 2 [Source:HGNC Symbol;Acc:10000]
5	341640	1.23	-0.32	0.39	FREM2 FRAS1 related extracellular matrix protein 2 [Source:HGNC Symbol;Acc:10000]
6	100130889	1.2	-0.35	0.2	PSORS1C psoriasis susceptibility 1 candidate 3 (non-protein coding) [Source:HGNC Symbol;Acc:10000]
7	2516	1.17	-0.2	0.25	NR5A1 nuclear receptor subfamily 5, group A, member 1 [Source:HGNC Symbol;Acc:10000]
8	55916	1.11	-0.87	0.38	NXT2 nuclear transport factor 2-like export factor 2 [Source:HGNC Symbol;Acc:10000]
9	200916	1.08	-0.33	0.16	RPL22L1 ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:276]
10	63908	1.07	-0.63	0.31	NAPB N-ethylmaleimide-sensitive factor attachment protein, beta [Source:HGNC Symbol;Acc:10000]
11	95681	1.05	-0.58	0.34	CEP41 centrosomal protein 41kDa [Source:HGNC Symbol;Acc:1237]
12	8445	1.04	-0.52	0.19	DYRK2 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase [Source:HGNC Symbol;Acc:10000]
13	4074	1.04	-0.92	0.29	M6PR mannose-6-phosphate receptor (cation dependent) [Source:HGNC Symbol;Acc:10000]
14	126859	1.03	-0.33	0.34	AXDND1 axonemal dynein light chain domain containing 1 [Source:HGNC Symbol;Acc:10000]
15	2918	1.01	-0.29	0.3	GRM8 glutamate receptor, metabotropic 8 [Source:HGNC Symbol;Acc:10000]
16	728655	1.01	-0.28	0.3	HULC hepatocellular carcinoma up-regulated long non-coding RNA [Source:HGNC Symbol;Acc:10000]
17	55283	1	-0.53	0.32	MCOLN3 mucopolipin 3 [Source:HGNC Symbol;Acc:13358]
18	55508	0.99	-0.83	0.31	SLC35E3 solute carrier family 35, member E3 [Source:HGNC Symbol;Acc:10000]
19	8995	0.99	-0.27	0.35	TNFSF18 tumor necrosis factor (ligand) superfamily, member 18 [Source:HGNC Symbol;Acc:10000]
20	51196	0.98	-0.44	0.36	PLCE1 phospholipase C, epsilon 1 [Source:HGNC Symbol;Acc:1717]

## Geneset Overrepresentation

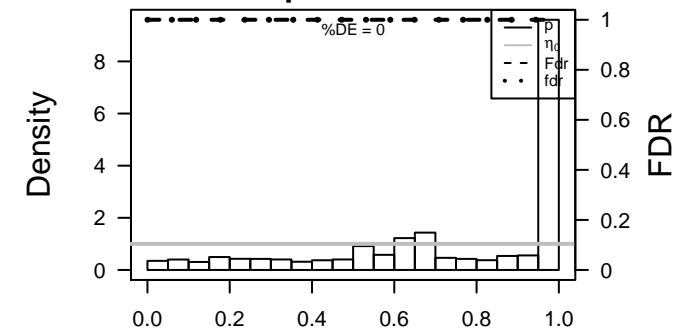
Rank	p-value	#in/all	Geneset
1	3e-10	172 / 1581	BP regulation of transcription, DNA-dependent
2	9e-10	184 / 1749	MF DNA binding
3	1e-09	114 / 940	MF nucleic acid binding
4	2e-08	164 / 1574	BP transcription, DNA-templated
5	9e-07	176 / 1820	MF metal ion binding
6	5e-05	376 / 4640	CC nucleus
7	6e-05	12 / 47	CC nucleosome
8	3e-04	55 / 500	MF sequence-specific DNA binding
9	6e-04	81 / 823	MF sequence-specific DNA binding transcription factor activity
10	9e-04	8 / 31	MF RNA polymerase II transcription cofactor activity
11	1e-03	18 / 119	miRN hsa-miR-515-5p
12	1e-03	9 / 40	BP histone H3 acetylation
13	2e-03	5 / 14	MMM MACIEJ_MMLL 8
14	2e-03	5 / 14	GSE/ SMID_BREAST_CANCER_LUMINAL_B_UP
15	2e-03	14 / 86	BP nucleosome assembly
16	2e-03	10 / 52	miRN hsa-miR-552
17	3e-03	5 / 15	miRN Medulloblastoma
18	3e-03	5 / 16	miRN Myopathy, nemaline, 3
19	4e-03	8 / 39	MF histone acetyltransferase activity
20	5e-03	14 / 94	miRN hsa-miR-125a-3p
21	6e-03	19 / 147	miRN hsa-miR-143
22	6e-03	30 / 271	miRN hsa-miR-548h
23	7e-03	4 / 12	BP cellular response to cholesterol
24	7e-03	4 / 12	BP nucleotide biosynthetic process
25	7e-03	4 / 12	GSE/ GEISS_RESPONSE_TO_DSRNA_DN
26	8e-03	34 / 321	miRN hsa-miR-548a-5p
27	8e-03	11 / 70	miRN hsa-miR-1266
28	8e-03	5 / 19	MF sodium channel regulator activity
29	8e-03	15 / 110	miRN hsa-miR-22
30	9e-03	11 / 71	BP pattern specification process
31	9e-03	3 / 7	GSE/ PALOMERO_GSL_SENSITIVITY_UP
32	9e-03	32 / 302	miRN hsa-miR-548i
33	1e-02	4 / 13	BP regulation of smoothened signaling pathway
34	1e-02	4 / 13	GSE/ REACTOME_PACKAGING_OF_TELOMERE_ENDS
35	1e-02	59 / 633	Chr Chr 9
36	1e-02	7 / 37	miRN hsa-miR-635
37	1e-02	18 / 147	miRN hsa-miR-142-3p
38	1e-02	9 / 55	miRN hsa-miR-28-3p
39	1e-02	6 / 29	miRN Melanoma and neural system tumor syndrome
40	1e-02	4 / 14	BP pharyngeal system development

Overview Map

Spot



p-values







# K-Means Cluster

## Spot Summary: K

# metagenes = 47  
# genes = 513

<r> metagenes = 0.91  
<r> genes = 0.22  
beta: r2= 8.62 / log p= -Inf

# samples with spot = 36 ( 13.1 % )  
Atypical : 14 ( 18.9 % )  
Classical : 14 ( 43.8 % )  
Mesenchymal : 3 ( 3.5 % )  
Basal : 5 ( 6 % )

## Spot Genelist

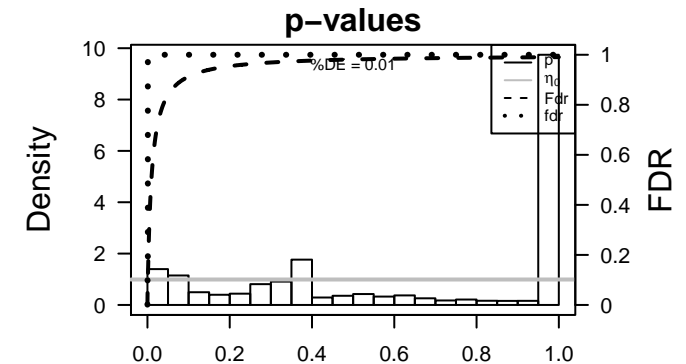
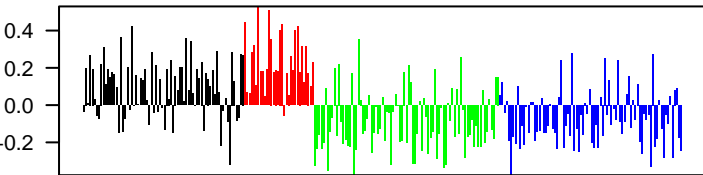
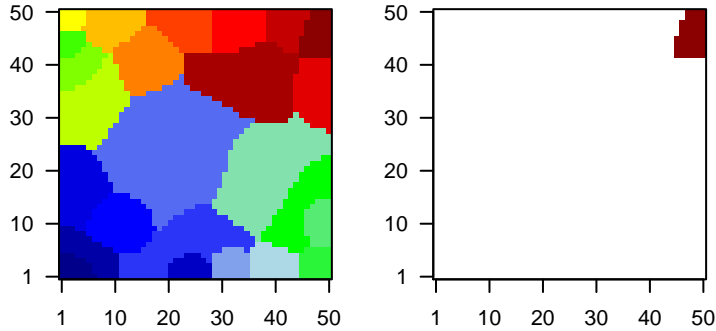
Rank	ID	max e	r	min e	Description
					Symbol
1	4922	5.09	-1.67	0.69	NTS neurotensin [Source:HGNC Symbol;Acc:8038]
2	2938	3.6	-1.05	0.56	GSTA2 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc:1848]
3	3880	3.42	-4.05	0.56	KRT19 keratin 19 [Source:HGNC Symbol;Acc:6436]
4	3866	3.23	-3.16	0.46	KRT15 keratin 15 [Source:HGNC Symbol;Acc:6421]
5	1056	3.22	-1.53	0.5	CEL carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	7345	3	-1.41	0.43	UCHL1 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
7	216	2.99	-2.41	0.63	ALDH1A1 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
8	83888	2.98	-0.56	0.37	FGFBP2 fibroblast growth factor binding protein 2 [Source:HGNC Sym
9	154664	2.78	-1.49	0.67	ABCA13 ATP-binding cassette, sub-family A (ABC1), member 13 [So
10	2944	2.69	-1.57	0.43	GSTM1 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
11	339512	2.68	-1.34	0.5	C1orf110 chromosome 1 open reading frame 110 [Source:HGNC Symt
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;Ac
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 Symt
17	4072	2.5	-2.3	0.71	EPCAM epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
18	139728	2.48	-1.61	0.51	PNCK pregnancy up-regulated nonubiquitous CaM kinase [Source:l
19	4915	2.4	-1.19	0.75	NTRK2 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
20	2947	2.4	-0.99	0.43	GSTM3 glutathione S-transferase mu 3 (brain) [Source:HGNC Symb

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-13	72 / 914	Chr Chr 3
2	2e-07	19 / 149	BP DNA replication
3	6e-07	31 / 370	BP mitotic cell cycle
4	7e-07	9 / 34	BP glutathione metabolic process
5	1e-06	6 / 13	GSE/ SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
6	2e-06	6 / 14	GSE/ PUJANA_BRCA_CENTERED_NETWORK
7	3e-06	8 / 30	BP DNA strand elongation involved in DNA replication
8	3e-06	6 / 15	GSE/ KEGG_Glutathione_Metabolism
9	5e-06	6 / 16	GSE/ BILD_E2F3_ONCOGENIC_SIGNATURE
10	1e-05	4 / 6	GSE/ MYLYKANGAS_AMPLIFICATION_HOT_SPOT_7
11	1e-05	22 / 253	miRN hsa-miR-548p
12	2e-05	6 / 19	BP cellular amino acid biosynthetic process
13	2e-05	35 / 530	Cancr Lembecke_Normal vs Adenoma
14	3e-05	53 / 949	CC nucleoplasm
15	3e-05	5 / 13	GSE/ PUJANA_XPRSS_INT_NETWORK
16	3e-05	6 / 21	BP chromatin organization
17	5e-05	5 / 14	GSE/ VANTVEER_BREAST_CANCER_METASTASIS_DN
18	6e-05	6 / 23	BP apoptotic mitochondrial changes
19	7e-05	5 / 15	GSE/ UDAYAKUMAR_MED1_TARGETS_UP
20	7e-05	5 / 15	GSE/ O'DONNELL_TARGETS_OF_MYC_AND_TFRC_DN
21	7e-05	5 / 15	GSE/ KIM_MYCN_AMPLIFICATION_TARGETS_DN
22	7e-05	5 / 15	GSE/ KEGG_DNA_REPLICATION
23	7e-05	6 / 24	BP telomere maintenance via recombination
24	8e-05	23 / 304	CC mitochondrial inner membrane
25	8e-05	13 / 119	BP xenobiotic metabolic process
26	9e-05	9 / 60	miRN AGGG-328
27	9e-05	5 / 16	GSE/ MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
28	9e-05	5 / 16	GSE/ SONG_TARGETS_OF_IE86_CMV_PROTEIN
29	9e-05	5 / 16	GSE/ KEGG_BASE_EXCISION_REPAIR
30	9e-05	6 / 25	BP glutathione derivative biosynthetic process
31	1e-04	54 / 1033	Chr Chr 2
32	2e-04	4 / 10	GSE/ REACTOME_GLOBAL_GENOMIC_NER
33	2e-04	22 / 298	BP DNA repair
34	2e-04	5 / 18	BP nucleotide-excision repair, DNA gap filling
35	2e-04	62 / 1253	BP small molecule metabolic process
36	2e-04	15 / 167	BP cellular nitrogen compound metabolic process
37	2e-04	5 / 19	miRN GTCA-380-5P
38	2e-04	64 / 1318	CC mitochondrion
39	3e-04	4 / 11	GSE/ KALMA_E2F1_TARGETS
40	3e-04	4 / 11	GSE/ SMID_BREAST_CANCER_BASAL_UP

### Overview Map

### Spot





# K-Means Cluster

## Spot Summary: L

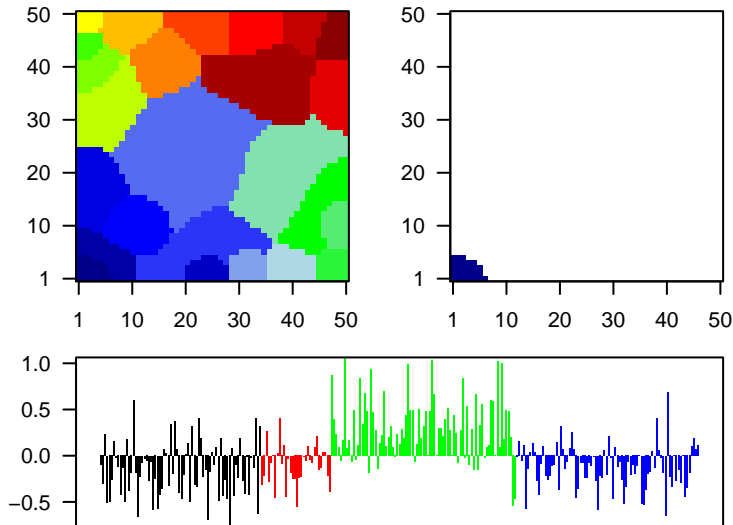
# metagenes = 27  
# genes = 418

<r> metagenes = 0.93  
<r> genes = 0.34  
beta: r2= 23.03 / log p= -Inf

# samples with spot = 60 ( 21.8 % )  
Atypical : 8 ( 10.8 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 46 ( 54.1 % )  
Basal : 4 ( 4.8 % )

Overview Map

Spot

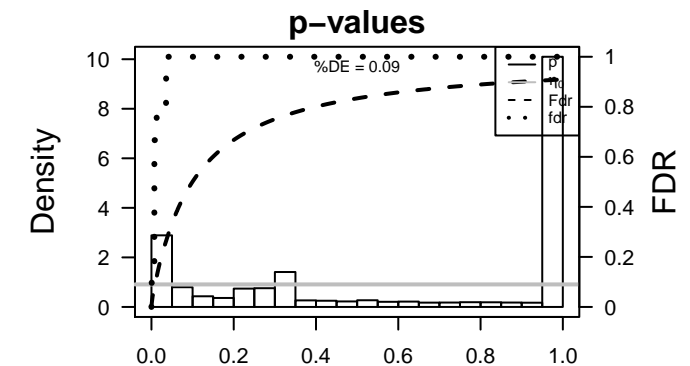


## Spot Genelist

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	387914	3.32	-1.5	0.35	SHISA2 shisa family member 2 [Source:HGNC Symbol;Acc:20366]
8	4322	3.32	-1.16	0.59	MMP13 matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
9	4314	3.31	-3.02	0.71	MMP3 matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
10	3569	3.28	-1.5	0.62	IL6 interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:f
11	3043	3.2	-3.29	0.32	HBB hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
12	3039	3.15	-1.75	0.3	HBA2 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
13	6374	3.14	-0.9	0.59	CXCL5 chemokine (C-X-C motif) ligand 5 [Source:HGNC Symbol;Ar
14	3553	3.13	-2.37	0.54	IL1B interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
15	414062	3.13	-2.13	0.52	CCL3L3 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
16	6372	3.07	-1.65	0.49	CXCL6 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Ar
17	55107	3.05	-2.27	0.44	ANO1 anoctamin 1, calcium activated chloride channel [Source:HGf
18	2201	2.99	-1.35	0.29	FBN2 fibrillin 2 [Source:HGNC Symbol;Acc:3604]
19	3576	2.96	-2.98	0.58	IL8 interleukin 8 [Source:HGNC Symbol;Acc:6025]
20	4320	2.88	-1.94	0.49	MMP11 matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-86	94 / 250	LympL LENZ_Stromal signature 1
2	6e-66	72 / 190	CC extracellular matrix
3	4e-65	78 / 242	BP extracellular matrix organization
4	2e-56	138 / 1182	CC extracellular region
5	7e-46	97 / 683	CC extracellular space
6	1e-42	85 / 553	Cancer Lembecke_Colonc Inflammation
7	4e-36	34 / 69	BP extracellular matrix disassembly
8	4e-34	47 / 183	CC proteinaceous extracellular matrix
9	2e-32	53 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
10	2e-32	53 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
11	2e-32	53 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
12	2e-32	53 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
13	6e-32	63 / 403	BP cell adhesion
14	1e-29	29 / 64	BP collagen catabolic process
15	9e-24	24 / 57	MF extracellular matrix structural constituent
16	1e-23	15 / 16	MMM MACIEJ_MMLL 1
17	5e-23	27 / 83	CC basement membrane
18	8e-19	13 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_5
19	1e-17	33 / 204	BP angiogenesis
20	3e-17	12 / 15	GSE/ CROMER_TUMORIGENESIS_UP
21	2e-16	28 / 153	CC endoplasmic reticulum lumen
22	2e-16	40 / 330	CC cell surface
23	2e-16	16 / 37	BP collagen fibril organization
24	2e-16	25 / 119	Lymp ROSOLOWSKI_green total
25	3e-15	12 / 19	MF extracellular matrix binding
26	3e-15	11 / 15	GSE/ ONDER_CDH1_TARGETS_2_UP
27	5e-14	18 / 68	CC collagen
28	6e-14	17 / 59	Lymp LENZ_Stromal signature 2
29	2e-13	22 / 117	Glio GIEZELT_GBM_WT_up_VS_mut
30	3e-13	19 / 85	MF integrin binding
31	5e-12	17 / 76	BP wound healing
32	6e-12	46 / 579	MF calcium ion binding
33	1e-11	30 / 269	BP inflammatory response
34	1e-11	69 / 1146	TF HEBENSTREIT_low expression TF
35	1e-11	35 / 364	BP negative regulation of cell proliferation
36	2e-11	9 / 15	GSE/ ONDER_CDH1_SIGNALING_VIA_CTNNB1
37	2e-11	8 / 11	MF platelet-derived growth factor binding
38	2e-11	8 / 11	Glio Phillips MES up vs Prolif & PN
39	2e-11	16 / 72	CC extracellular vesicular exosome
40	3e-11	12 / 35	Glio Colman_survival_associated



Rank	p-value	#in/all	Geneset
1	0.22	2/22	extracellular matrix organization
2	4e-36	54/69	extracellular matrix disassembly
3	6e-32	63/403	cell adhesion
4	1e-29	29/64	collagen catabolic process
5	1e-24	33/53	angiogenesis
6	2e-16	16/37	collagen fibril organization
7	5e-12	17/76	wound healing
8	1e-11	30/269	inflammatory response
9	1e-11	30/269	negative regulation of cell proliferation
10	20/129	20/129	cell migration
11	2e-10	12/40	cellular response to amino acid stimulus
12	3e-10	35/407	blood coagulation
13	6e-10	18/114	positive regulation of cell migration
14	6e-10	11/36	embryo implantation
15	3e-09	18/126	skeletal system development
16	3e-09	8/25	chondroitin sulfate biosynthetic process
17	1e-08	16/106	leukocyte migration
18	1e-08	11/45	chondroitin sulfate metabolic process
19	6e-08	26/299	axon guidance
20	6e-08	13/77	negative regulation of canonical Wnt signaling pathway

Rank	p-value	#in/all	Geneset
1	0.02	26/43	Chromosome 1
2	0.03	24/618	Chr 4
3	0.05	25/899	Chr 5
4	0.05	23/633	Chr 6
5	0.14	9/232	Chr 18
6	0.18	29/957	Chr 11
7	0.18	9/13	Chr 13
8	0.30	15/504	Chr 15
9	0.45	1/23	Chr HSCHR6_MHC_DBB
10	0.47	27/1033	Chr 1
11	0.52	5/187	Chr 21
12	0.52	10/386	Chr 22
13	0.53	22/866	Chr 12
14	0.56	18/714	Chr 2
15	0.56	13/19	Chr 14
16	0.59	11/449	Chr 20
17	0.60	13/534	Chr 8
18	0.69	20/770	Chr 1
19	0.78	20/914	Chr 8
20	0.84	12/602	Chr 10

Rank	p-value	#in/all	Geneset
1	6e-19	13/146	FARMER_BREAST_CANCER_CLUSTER_5
2	3e-15	11/115	CHROMATID_ORGANIZATION
3	2e-11	9/15	ONDER_CDH1_SIGNALING_VIA_CTNNB1
4	9e-10	8/15	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_1
5	9e-10	8/15	LEU_LIVER_CANCER_HEPATOBLAST
6	8e-10	8/15	LEU_IL6_SIGNALING_SCAR_DN
7	8e-09	8/16	ROZANOV_MMP14_TARGETS_SUBSET
8	5e-09	7/12	LY_AGING_MIDDLE_UP
9	3e-08	7/12	MISHA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
10	5e-08	6/10	JEON_SMAD6_TARGETS_UP
11	6e-08	6/10	VERRECCHIA_RESPONSE_TO_TGFB1_C4
12	6e-08	7/16	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_1
13	6e-08	7/16	LIEN_BREAST_CARCINOMA_METAPLASTIC
14	6e-08	7/16	GU_PDEF_TARGETS_UP
15	6e-08	7/16	CRONQUIST_STROMAL_STIMULATION_UP
16	6e-08	7/16	ZHU_CMV_ALL_DN
17	2e-07	5/7	TSUNODA_CISPLATIN_RESISTANCE_UP
18	4e-07	6/13	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL
19	4e-07	6/13	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH

Rank	p-value	#in/all	Geneset
1	3e-15	12/19	extracellular matrix structural constituent
2	3e-13	19/85	integrin binding
3	6e-12	46/579	calcium ion binding
4	2e-11	11/11	platelet-derived growth factor binding
5	4e-10	18/112	heparin binding
6	9e-09	11/44	collagen binding
7	2e-07	6/19	transforming growth factor beta binding
8	2e-07	6/19	L-ascorbic acid binding
9	3e-07	12/73	metallopeptidase activity
10	3e-07	254/8023	protein binding
11	9e-07	12/81	metalloendopeptidase activity
12	7e-06	5/12	actinin binding
13	1e-05	21/280	receptor binding
14	1e-05	6/21	glycosaminoglycan binding
15	1e-05	13/13	chemokine activity
16	2e-05	5/15	platelet-derived growth factor receptor binding
17	4e-05	5/16	fibronectin binding
18	7e-05	6/29	SMAD binding
19	7e-05	6/29	oxidoreductase activity, acting on paired donors, with incorporation or reduction

Rank	p-value	#in/all	Geneset
1	7e-11	8/11	miR-28
2	3e-03	3/12	miR-29b
3	4e-03	4/26	miR-21
4	6e-03	2/6	miR-143
5	9e-03	2/6	miR-200c
6	5e-02	1/2	miR-101b
7	6e-02	1/2	miR-18
8	9e-02	1/2	miR-146
9	7e-02	1/3	miR-197
10	1e-01	1/4	miR-429
11	1e-01	1/5	miR-126
12	1e-01	1/5	miR-141
13	1e-01	1/5	miR-200a
14	1e-01	1/5	miR-200b
15	1e-01	1/5	miR-205
16	2e-01	1/7	miR-145
17	2e-01	1/8	miR-222
18	2e-01	1/8	miR-9
19	1e+00	0/8	let-7a
20	1e+00	0/6	let-7b

Rank	p-value	#in/all	Geneset
1	0.04	2/12	BENTINK_ras.1
2	0.05	2/11	GUSTAFSON_P13K_DN
3	0.25	1/11	BENTINK_e2f3.2
4	0.28	1/13	GUSTAFSON_P13K_UP
5	0.28	1/13	BENTINK_src.10
6	0.30	1/14	BENTINK_myc.6
7	1.00	0/12	BENTINK_e2f3.1
8	1.00	0/11	BENTINK_ras.4
9	1.00	0/15	BENTINK_ras.6
10	1.00	0/14	BENTINK_src.2
11	NA	0/0	
12	NA	0/0	
13	NA	0/0	
14	NA	0/0	
15	NA	0/0	
16	NA	0/0	
17	NA	0/0	
18	NA	0/0	
19	NA	0/0	
20	NA	0/0	

Rank	p-value	#in/all	Geneset
1	1e-33	35/333	IL12R1B1_ectonic Inflammation
2	6e-03	6/13	GENTLES_modul17
3	3e-03	3/15	RHODES_CANCER_META_SIGNATURE
4	3e-03	3/15	LIU_PROSTATE_CANCER_DN
5	4e-02	2/13	GENTLES_modul16
6	6e-02	2/16	GENTLES_modul11
7	1e-01	1/10	LIU_BREAST_CANCER
8	2e-01	1/10	GENTLES_modul3
9	2e-01	1/16	RHODES_UNDIFFERENTIATED_CANCER
10	2e-01	1/14	LIU_PROSTATE_CANCER_UP
11	3e-01	1/15	BEN-PORATH_UP
12	3e-01	1/15	GENTLES_modul13
13	3e-01	1/16	GENTLES_modul10
14	4e-01	15/530	Lembcke_Normal_vs Adenoma
15	5e-01	5/185	SPANG_LPS-index2
16	5e-01	1/16	KAUFER_MM_good survival
17	6e-01	1/68	SHAUGHNESSY_MM_high risk
18	9e-01	5/316	SPANG_BCL6-index2
19	1e+00	0/15	GENTRIUO_BREAST_CANCER_GRADE_1_VS_3_DN
20	1e+00	0/15	SOTRIURO_BREAST_CANCER_GRADE_1_VS_3_UP

Rank	p-value	#in/all	Geneset
1	6e-09	21/378	GUDJ_poriasis down
2	7e-01	13/572	GUDJ_poriasis up
3	1e+00	0/17	WIRTH_IL23A_EBM up
4	1e+00	0/2	ECHEMIA_EBM-down
5	1e+00	0/26	ECHEMIA_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-04	4/13	WIRTH_Sec_lymphoid organs
2	2e-02	2/13	WIRTH_Prim_lymphoid organs
3	4e-02	2/13	WIRTH_Cortex cerebri
4	6e-02	3/36	WIRTH_Placenta
5	3e-01	1/12	WIRTH_Lymphocytes
6	3e-01	1/13	WIRTH_Thymus
7	3e-01	1/13	WIRTH_Thyroid gland
8	6e-01	10/400	WIRTH_Nervous System
9	6e-01	3/127	WIRTH_Muscle
10	1e+00	0/5	WIRTH_Liver
11	1e+00	0/6	WIRTH_Pituitary gland
12	1e+00	0/26	WIRTH_Pancreas
13	1e+00	0/417	WIRTH_Immune system
14	1e+00	0/13	WIRTH_B-cells
15	1e+00	0/13	WIRTH_Tonsil
16	1e+00	0/6	WIRTH_Bone marrow
17	1e+00	0/14	WIRTH_Globus pallidus
18	1e+00	0/15	WIRTH_Telencephalon
19	1e+00	0/16	WIRTH_Hippocampus
20	1e+00	0/13	WIRTH_Thalamus

Rank	p-value	#in/all	Geneset
1	3e-05	28/411	TCGT-5P-30C-30D-30E-5P
2	3e-05	26/420	TGCT-29A-29B-29C
3	5e-05	23/362	CAGT-200B-200C-429
4	6e-04	8/75	GGCA-324-3P
5	6e-04	11/141	ATC-202
6	1e-03	21/401	ACCA-9
7	2e-03	27/577	GTGC-506
8	4e-03	14/243	ATGT-493
9	1e-03	12/247	GTGC-506
10	4e-03	9/124	ATGA-205
11	5e-03	13/225	TAT-374
12	6e-03	12/205	GTGC-101
13	7e-03	11/182	TAGC-9
14	1e-02	13/244	GTGC-25-32-92-363-367
15	1e-02	4/35	GCAA-431
16	1e-02	9/145	ACTG-27A-27B
17	2e-02	17/375	GGCA-22
18	2e-02	10/184	GGCA-22
19	2e-02	4/7	TAGC-492
20	2e-02	17/391	GGCA-187A-181B-181C-181D

Rank	p-value	#in/all	Geneset
1	0.004	6/80	hsa-miR-515-3p
2	0.005	3/14	hsa-miR-452*
3	0.006	16/311	hsa-let-7f
4	0.009	5/50	hsa-miR-1224-3p
5	0.012	16/336	hsa-let-7e
6	0.013	15/311	hsa-miR-98
7	0.014	16/341	hsa-let-7a
8	0.015	9/151	hsa-miR-429
9	0.022	5/63	hsa-miR-306*
10	0.031	9/171	hsa-miR-369-3p
11	0.035	14/321	hsa-let-7d
12	0.035	6/96	hsa-miR-1303
13	0.038	8/150	hsa-miR-200c
14	0.038	4/50	hsa-miR-571
15	0.039	15/356	hsa-let-7d
16	0.043	4/52	hsa-miR-487a
17	0.044	8/155	hsa-miR-200b
18	0.049	6/80	hsa-miR-539-5p
19	0.053	8/80	hsa-miR-629
20	0.056	4/57	

Rank	p-value	#in/all	Geneset
1	1e-11	69/146	HEBENSTREIT_low expression TF
2	2e-02	2/9	MYC_targets DOWN
3	1e-02	1/2	MYC_ECM cell adhesion DOWN
4	1e-01	1/5	MYC_TF and cofactors
5	4e-01	1/20	MYC_Metabolism UP
6	4e-01	1/6	MYC_targets UP
7	1e+00	19/1095	HEBENSTREIT_high expression TF
8	1e+00	18/1233	KIM_MYC targets
9	1e+00	0/14	NOVICIK_TF
10	1e+00	0/5	MYC_TF
11	1e+00	0/4	MYC_Apoptosis UP
12	1e+00	0/8	MYC_Cell cycle UP
13	1e+00	0/4	MYC_Cell cycle DOWN
14	1e+00	0/4	MYC_Cell growth and proliferation UP
15	1e+00	0/2	MYC_Chromatin_modification UP
16	1e+00	0/7	MYC_DNA repair UP
17	1e+00	0/3	MYC_DNA replication UP
18	1e+00	0/16	MYC_Protein synthesis degradation UP
19	1e+00	0/8	MYC_RNA processing binding UP
20	1e+00	0/2	MYC_Signal transduction UP

Rank	p-value	#in/all	Geneset
1	2e-56	138/1182	extracellular matrix
2	7e-46	97/683	extracellular region
3	4e-34	47/183	extracellular space
4	5e-24	27/83	proteinaceous extracellular matrix
5	2e-16	28/153	basement membrane
6	2e-16	40/330	endoplasmic reticulum lumen
7	2e-16	18/69	cell surface
8	5e-14	18/69	collagen
9	5e-14	18/69	extracellular vesicular exosome
10	7e-09	113/2659	plasma membrane
11	5e-07	11/63	Golgi lumen
12	1e-05	14/115	cell-cell junction
13	5e-06	10/65	lysosomal lumen
14	6e-06	77/1837	membrane
15	8e-06	13/116	lamellipodium
16	8e-06	8/48	platelet alpha granule lumen
17	5e-05	5/17	basal lamina
18	7e-05	14/162	external side of plasma membrane
19	1e-04	8/61	secretory granule
20	8e-04	8/62	sarcolemma

Rank	p-value	#in/all	Geneset
1	2e-32	59/268	willscher_GBM_Verhaak-CL_expression_B_up
2	2e-32	53/265	willscher_GBM_Verhaak-MES_expression_B_up
3	2e-32	53/265	willscher_GBM_Verhaak-PNwt_expression_B_down
4	2e-32	53/265	willscher_GBM_Verhaak-PNmut_expression_B_down
5	2e-13	22/117	GIEZELT_GBM_WT_up_VS_mut
6	2e-11	8/11	Phillips_MES_up_vs_Prolif&PN
7	3e-11	12/35	Colman_survival_associated
8	1e-10	15/68	cultured astroglia vs. in vivo astrocytes
9	3e		

# K-Means Cluster

## Spot Summary: M

# metagenes = 60  
# genes = 619

<r> metagenes = 0.77  
<r> genes = 0.18  
beta: r2= 6.55 / log p= -Inf

# samples with spot = 18 ( 6.5 % )  
Mesenchymal : 18 ( 21.2 % )

## Spot Genelist

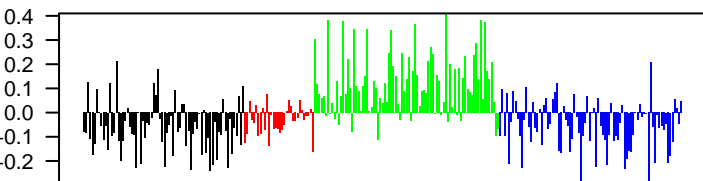
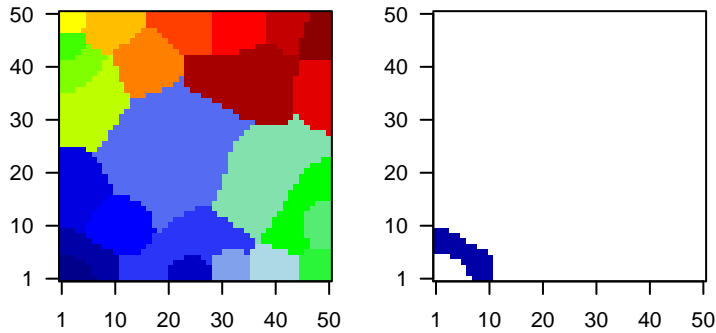
Rank	ID	max e	r	min e	Description
1	25805	2.63	-1.74	0.29	BAMBI BMP and activin membrane-bound inhibitor [Source:HGNC S
2	1469	2.51	-0.85	0.22	CST1 cystatin SN [Source:HGNC Symbol;Acc:2473]
3	3486	2.44	-2.35	0.27	IGFBP3 insulin-like growth factor binding protein 3 [Source:HGNC Sy
4	768	2.41	-1.33	0.42	CA9 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
5	2239	2.29	-0.94	0.43	GPC4 glypican 4 [Source:HGNC Symbol;Acc:4452]
6	595	2.23	-2.16	0.34	CCND1 cyclin D1 [Source:HGNC Symbol;Acc:1582]
7	8614	2.16	-1.3	0.48	STC2 stanniocalcin 2 [Source:HGNC Symbol;Acc:11374]
8	1021	2.11	-1.65	0.56	CDK6 cyclin-dependent kinase 6 [Source:HGNC Symbol;Acc:1777]
9	55603	2.11	-1.76	0.38	FAM46A family with sequence similarity 46, member A [Source:HGNC
10	3310	2.09	-0.79	0.36	HSPA6 heat shock 70kDa protein 6 (HSP70B) [Source:HGNC Symb
11	284111	2.07	-0.78	0.35	SLC13A5olute carrier family 13 (sodium-dependent citrate transporte
12	85409	2.06	-1.76	0.28	NKD2 naked cuticle homolog 2 (Drosophila) [Source:HGNC Symbol
13	3311	2	-0.73	0.37	HSPA7 heat shock 70kDa protein 7 (HSP70B) [Source:HGNC Symbc
14	10644	1.94	-2.12	0.48	IGF2BP2insulin-like growth factor 2 mRNA binding protein 2 [Source:l
15	6349	1.91	-0.69	0.55	CCL3L3 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
16	5473	1.9	-0.61	0.39	PPBP pro-platelet basic protein (chemokine (C-X-C motif) ligand 7
17	22943	1.89	-0.93	0.45	DKK1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
18	8632	1.83	-0.73	0.35	DNAH17 dynein, axonemal, heavy chain 17 [Source:HGNC Symbol;Ac
19	2296	1.83	-1.35	0.35	FOXC1 forkhead box C1 [Source:HGNC Symbol;Acc:3800]
20	114335	1.82	-0.83	0.64	CGB chorionic gonadotropin, beta polypeptide [Source:HGNC Syrr

## Geneset Overrepresentation

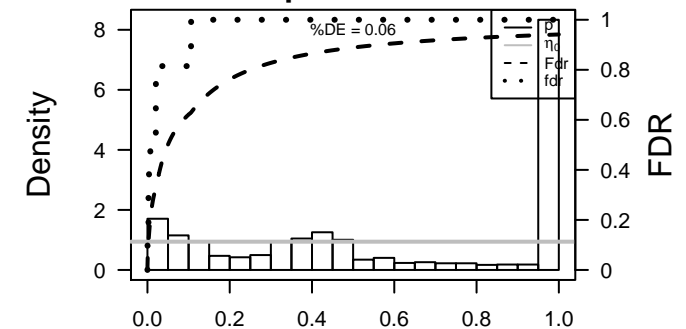
Rank	p-value	#in/all	Geneset
1	3e-11	34 / 242	BP extracellular matrix organization
2	3e-10	33 / 250	LympL LENZ_Stromal signature 1
3	6e-10	43 / 403	BP cell adhesion
4	5e-09	154 / 2659	CC plasma membrane
5	5e-08	18 / 104	BP glycosaminoglycan metabolic process
6	6e-08	20 / 128	CC focal adhesion
7	8e-08	32 / 297	MF actin binding
8	8e-07	21 / 163	CC synapse
9	8e-07	30 / 297	CC cell junction
10	9e-07	358 / 8023	MF protein binding
11	1e-06	22 / 184	CC actin cytoskeleton
12	2e-06	31 / 330	CC cell surface
13	3e-06	19 / 149	BP actin cytoskeleton organization
14	4e-06	58 / 835	CC integral to plasma membrane
15	4e-06	75 / 1182	CC extracellular region
16	5e-06	74 / 1167	BP signal transduction
17	5e-06	105 / 1837	CC membrane
18	6e-06	167 / 3274	CC integral to membrane
19	8e-06	30 / 333	CC cytoskeleton
20	1e-05	12 / 70	BP cell junction assembly
21	1e-05	7 / 22	BP positive regulation of BMP signaling pathway
22	2e-05	8 / 33	MF Rho GTPase binding
23	2e-05	27 / 299	BP axon guidance
24	3e-05	5 / 11	CC filopodium membrane
25	3e-05	5 / 11	GSE/ REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE
26	3e-05	20 / 190	CC extracellular matrix
27	3e-05	12 / 78	BP ossification
28	4e-05	9 / 45	CC stress fiber
29	4e-05	47 / 683	CC extracellular space
30	5e-05	5 / 12	BP heparan sulfate proteoglycan biosynthetic process
31	5e-05	5 / 12	GSE/ NUTT_GBM_VS_AO_GLIOMA_UP
32	5e-05	12 / 82	BP endoplasmic reticulum unfolded protein response
33	5e-05	40 / 553	CancL Lembecke_Colonc Inflammation
34	5e-05	11 / 70	BP cell-matrix adhesion
35	5e-05	8 / 37	MF transferase activity, transferring hexosyl groups
36	7e-05	5 / 13	GSE/ MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
37	7e-05	7 / 29	CC dendritic shaft
38	8e-05	16 / 142	Glio Christensen_hypermethylated_in_grade2_oligodendroglioma
39	9e-05	11 / 74	BP integrin-mediated signaling pathway
40	9e-05	10 / 62	MF transferase activity, transferring glycosyl groups

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: N

# metagenes = 115  
# genes = 908

<r> metagenes = 0.85  
<r> genes = 0.2  
beta: r2= 4.03 / log p= -Inf

# samples with spot = 9 ( 3.3 % )  
Atypical : 2 ( 2.7 % )  
Mesenchymal : 6 ( 7.1 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

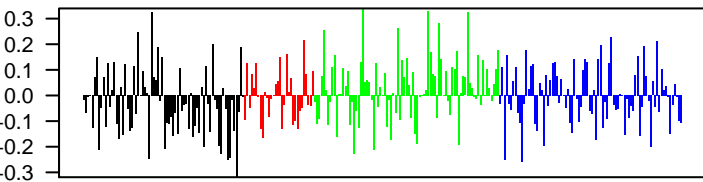
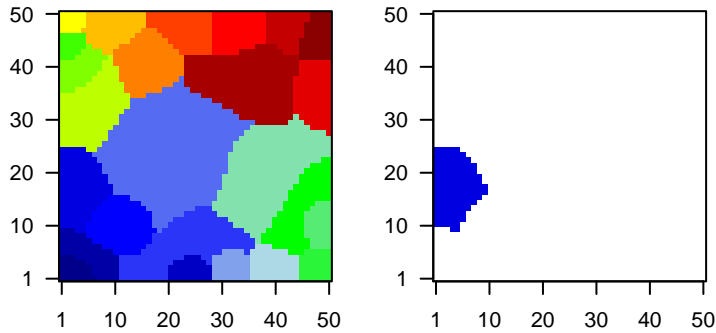
Rank	ID	max e	r	min e	Description
1	283869	2.84	-1.53	0.53	NPW neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	4495	2.82	-1.79	0.21	MT1G metallothionein 1G [Source:HGNC Symbol;Acc:7399]
3	220064	2.61	-1.08	0.48	ORAOV1 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175]
4	10202	2.48	-0.58	0.41	DHRS2 dehydrogenase/reductase (SDR family) member 2 [Source:H]
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:
7	51083	2.28	-0.81	0.5	GAL galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
8	8772	2.18	-1.29	0.52	FADD Fas (TNFRSF6)-associated via death domain [Source:HGNC
9	51702	2.13	-1.03	0.26	PADI3 peptidyl arginine deiminase, type III [Source:HGNC Symbol;A
10	3006	2.13	-1.48	0.19	HIST1H1 histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
11	1152	2.07	-1.8	0.37	CKB creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
12	219931	2.01	-0.93	0.56	TPCN2 two pore segment channel 2 [Source:HGNC Symbol;Acc:208
13	51373	1.97	-1.11	0.64	MRPS1728S ribosomal protein S17, mitochondrial; HCG1984214, isof
14	2017	1.86	-1.24	0.42	CTTN cortactin [Source:HGNC Symbol;Acc:3338]
15	219927	1.84	-0.94	0.54	MRPL21 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;A
16	26579	1.7	-0.65	0.22	MYEOV myeloma overexpressed [Source:HGNC Symbol;Acc:7563]
17	2821	1.69	-0.94	0.44	GPI glucose-6-phosphate isomerase [Source:HGNC Symbol;Acc
18	23246	1.68	-1.14	0.75	BOP1 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
19	93273	1.67	-0.94	0.31	LEMD1 LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
20	230	1.64	-1.33	0.36	ALDOC aldolase C, fructose-bisphosphate [Source:HGNC Symbol;A

## Geneset Overrepresentation

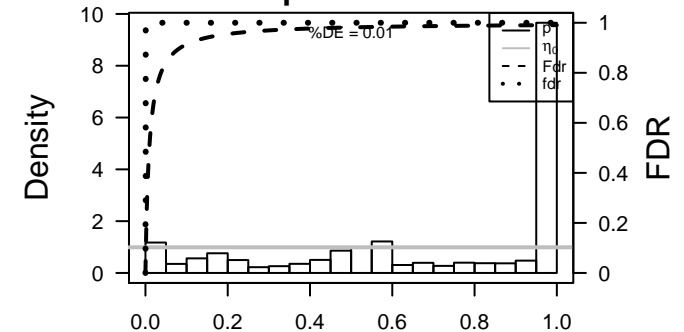
Rank	p-value	#in/all	Geneset
1	8e-17	146 / 1318	CC mitochondrion
2	9e-17	97 / 717	Chr Chr 16
3	1e-10	67 / 530	Cancer_Lembcke_Normal vs Adenoma
4	2e-10	71 / 579	CC nucleolus
5	8e-10	75 / 649	BP gene expression
6	1e-09	111 / 1135	Chr Chr 19
7	3e-09	16 / 48	BP regulation of cellular amino acid metabolic process
8	3e-09	17 / 55	CC proteasome complex
9	7e-09	9 / 14	GSE/ LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
10	8e-09	22 / 96	BP rRNA processing
11	1e-08	18 / 66	BP positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
12	2e-08	17 / 62	BP negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
13	3e-08	18 / 70	BP regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
14	7e-08	18 / 74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
15	7e-08	9 / 17	CC proteasome accessory complex
16	1e-07	41 / 304	CC mitochondrial inner membrane
17	1e-07	91 / 949	CC nucleoplasm
18	2e-07	324 / 4640	CC nucleus
19	2e-07	20 / 96	BP DNA recombination
20	3e-07	26 / 153	MF structural constituent of ribosome
21	5e-07	38 / 287	BP viral process
22	8e-07	108 / 1233	TF KIM_MYC targets
23	1e-06	20 / 106	BP protein polyubiquitination
24	1e-06	15 / 63	BP DNA damage response, signal transduction by p53 class mediator resulting
25	1e-06	33 / 242	BP RNA metabolic process
26	3e-06	11 / 37	CC mitochondrial nucleoid
27	5e-06	6 / 10	GSE/ REACTOME_HIV_LIFE_CYCLE
28	5e-06	15 / 70	BP antigen processing and presentation of exogenous peptide antigen via MHC
29	8e-06	14 / 64	BP tRNA processing
30	1e-05	32 / 253	BP translation
31	1e-05	15 / 74	BP antigen processing and presentation of exogenous peptide antigen via MHC
32	1e-05	6 / 11	GSE/ REACTOME_HIV_INFECTION
33	1e-05	16 / 83	BP respiratory electron transport chain
34	1e-05	29 / 219	BP mRNA metabolic process
35	1e-05	7 / 16	GSE/ BIOCARTE_PTDINS_PATHWAY
36	2e-05	24 / 167	BP cellular nitrogen compound metabolic process
37	2e-05	24 / 167	CC ribosome
38	2e-05	41 / 370	BP mitotic cell cycle
39	2e-05	7 / 17	BP RNA modification
40	2e-05	35 / 298	BP DNA repair

Overview Map

Spot



p-values









# K-Means Cluster

## Spot Summary: O

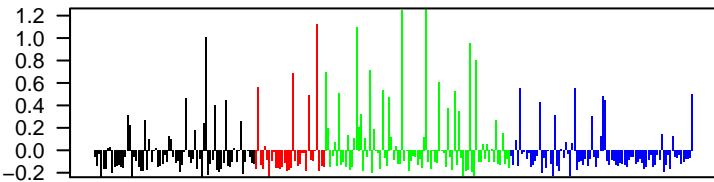
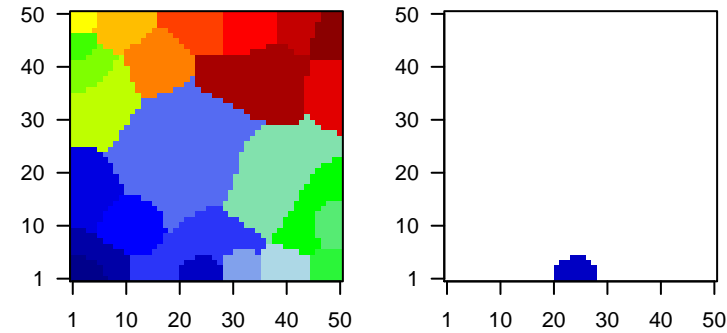
# metagenes = 33  
# genes = 203

<r> metagenes = 0.94  
<r> genes = 0.44  
beta: r2= 6.52 / log p= -Inf

# samples with spot = 37 ( 13.5 % )  
Atypical : 9 ( 12.2 % )  
Classical : 4 ( 12.5 % )  
Mesenchymal : 16 ( 18.8 % )  
Basal : 8 ( 9.5 % )

### Overview Map

### Spot

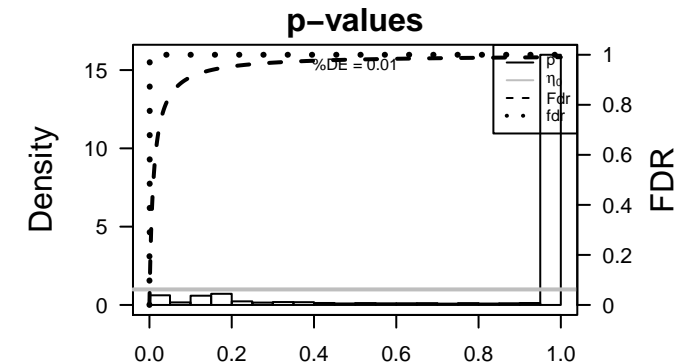


## Spot Genelist

Rank	ID	max e	r	min e	Description
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-99	82 / 127	H.Tis: WIRTH_Muscle
2	4e-38	24 / 36	BP muscle filament sliding
3	4e-33	28 / 84	BP muscle contraction
4	5e-33	23 / 44	MF structural constituent of muscle
5	4e-26	24 / 88	CC Z disc
6	5e-23	13 / 16	H.Tis: WIRTH_Hippocampus
7	3e-22	16 / 34	CC myofibril
8	4e-20	31 / 297	MF actin binding
9	1e-18	12 / 20	CC I band
10	3e-18	11 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_F
11	4e-18	10 / 12	CC myosin filament
12	3e-16	13 / 37	CC sarcomere
13	3e-14	9 / 15	BP striated muscle contraction
14	6e-14	9 / 16	CC M band
15	6e-13	8 / 13	CC muscle myosin complex
16	1e-12	8 / 14	CC contractile fiber
17	3e-12	8 / 15	GSE/ REACTOME_STRIATED_MUSCLE_CONTRACTION
18	2e-11	10 / 37	BP cardiac muscle contraction
19	3e-11	7 / 12	MF titin binding
20	4e-11	9 / 29	CC sarcoplasmic reticulum membrane
21	5e-11	13 / 88	BP muscle organ development
22	8e-11	8 / 21	BP sarcomere organization
23	4e-10	9 / 36	CC sarcoplasmic reticulum
24	1e-09	7 / 18	BP regulation of muscle contraction
25	1e-09	6 / 11	BP cardiac muscle tissue morphogenesis
26	3e-09	6 / 12	BP skeletal muscle contraction
27	4e-09	10 / 62	CC sarcolemma
28	1e-08	9 / 53	MF cytoskeletal protein binding
29	3e-08	19 / 333	CC cytoskeleton
30	4e-08	8 / 42	CC myosin complex
31	5e-08	7 / 29	BP regulation of heart contraction
32	1e-07	5 / 11	CC A band
33	2e-07	8 / 51	BP skeletal muscle tissue development
34	3e-07	12 / 149	MF calmodulin binding
35	5e-07	5 / 14	MF tropomyosin binding
36	7e-07	5 / 15	GSE/ EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
37	9e-07	18 / 375	Disea GUDJ_psoriasis down
38	1e-06	6 / 28	CC T-tubule
39	1e-06	5 / 16	GSE/ KEGG_DILATED_CARDIOMYOPATHY
40	2e-06	5 / 18	BP regulation of the force of heart contraction



Rank	p-value	#in/all	Geneset
1	0.000	11/116	muscle filament sliding
2	4e-33	28/84	muscle contraction
3	3e-14	9/15	striated muscle contraction
4	2e-11	10/37	cardiac muscle contraction
5	6e-11	13/68	muscle organ development
6	8e-11	8/21	sarcomere organization
7	1e-09	7/18	regulation of muscle contraction
8	1e-09	6/17	cardiac muscle tissue morphogenesis
9	3e-09	6/12	skeletal muscle contraction
10	5e-08	7/29	regulation of heart contraction
11	2e-07	8/51	skeletal muscle tissue development
12	2e-06	5/18	regulation of the force of heart contraction
13	1e-05	5/26	ventricular cardiac muscle tissue morphogenesis
14	1e-05	8/90	calcium ion transport
15	2e-05	4/14	adult heart development
16	2e-05	6/18	neuromuscular synaptic transmission
17	3e-05	4/15	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic
18	2e-04	4/24	regulation of calcium ion transport
19	2e-04	3/10	heart contraction
20	3e-04	5/47	skeletal muscle cell differentiation

Rank	p-value	#in/all	Geneset
1	0.005	29/1720	Chr 1
2	0.049	10/449	Chr 20
3	0.051	11/602	Chr 10
4	0.124	9/618	Chr 4
5	0.350	7/504	Chr 15
6	0.425	12/514	Chr 4
7	0.475	12/521	Chr HSCHR6_MHC_QBL
8	0.618	6/519	Chr 14
9	0.622	12/1033	Chr 1
10	0.660	8/717	Chr 16
11	0.665	8/763	Chr 9
12	0.672	3/280	Chr 13
13	0.687	10/957	Chr 11
14	0.761	7/699	Chr 3
15	0.780	7/714	Chr 6
16	0.781	2/232	Chr 18
17	0.791	6/630	Chr X
18	0.813	6/743	Chr 7
19	0.841	8/866	Chr 12

Rank	p-value	#in/all	Geneset
1	9e-18	11/16	RICKMAN HEAD AND NECK CANCER F
2	1e-07	8/15	REACTOME STRIATED MUSCLE CONTRACTION
3	7e-07	5/16	EBAUER MYOGENIC TARGETS OF PAX3_FOXP01_FUSION
4	1e-06	5/16	KEGG DILATED CARDIOMYOPATHY
5	2e-05	4/14	KEGG ARRYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY
6	4e-04	3/13	KEGG HYPERTROPHIC CARDIOMYOPATHY HOM
7	5e-04	3/13	FONTAINE FOLLICULAR THYROID ADENOMA_UP
8	5e-04	3/13	REACTOME GLUCOSE METABOLISM
9	5e-04	3/13	REACTOME CREB PHOSPHORYLATION THROUGH THE ACTIVATION C
10	5e-04	3/13	REACTOME ACTIVATION OF NMDA RECEPTOR UPON GLUTAMATE_E
11	6e-04	3/14	RORIE TARGETS OF EWSRT FLI1_FUSION_DN
12	6e-04	3/14	DAIRKEE CANCER PRONE_RESPONSE_BPA
13	6e-04	3/14	REACTOME POST NMDA RECEPTOR ACTIVATION_EVENTS
14	7e-04	3/15	DAVICIONI PAX_FOXP01_SIGNATURE_IN_ARM5_DN
15	7e-04	3/15	DAIRKEE CANCER PRONE_RESPONSE_E2
16	7e-04	3/15	MOOTHA_GLYCOLYSIS
17	9e-04	3/16	DAVICIONI TARGETS OF PAX_FOXP01_FUSIONS_DN
18	9e-04	3/16	MOOTHA_GLUONEOGENESIS
19	1e-03	2/5	PASTURAL_RIZ1_TARGETS_DN
20	2e-03	2/6	BUSA_SAM68_TARGETS_DN

Rank	p-value	#in/all	Geneset
1	4e-20	31/297	structural constituent of muscle
2	3e-11	7/12	actin binding
3	1e-09	9/53	titin binding
4	3e-08	12/149	cytoskeletal protein binding
5	5e-07	5/14	calmodulin binding
6	5e-06	7/56	tropomyosin binding
7	3e-05	20/879	motor activity
8	4e-05	4/16	calcium ion binding
9	3e-04	4/27	microfilament motor activity
10	4e-04	4/28	ATPase binding
11	6e-04	12/8023	voltage-gated calcium channel activity
12	3e-03	5/77	protein binding
13	5e-03	3/28	actin monomer binding
14	5e-03	3/28	actin filament binding
15	5e-03	3/28	enzyme inhibitor activity
16	7e-03	4/63	cofactor binding
17	8e-03	27/1344	hormone activity
18	8e-03	2/11	ATP binding
19	8e-03	2/11	acetylcholine-activated cation-selective channel activity
20	8e-03	2/11	actin-dependent ATPase activity

Rank	p-value	#in/all	Geneset
1	0.06	0/11	miR-32
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	0/5	miR-101
9	1.00	0/2	miR-101b
10	1.00	0/4	miR-106b
11	1.00	0/7	miR-107
12	1.00	0/4	miR-122
13	1.00	0/2	miR-124a
14	1.00	0/6	miR-125a
15	1.00	0/5	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	0.1	0/13	BENTINK_e2/3.1
2	1.0	0/15	GUSTAFSON_P13K_UP
3	1.0	0/15	GUSTAFSON_P13K_DN
4	1.0	0/11	BENTINK_e2/3.2
5	1.0	0/14	BENTINK_myc.1
6	1.0	0/14	BENTINK_ras.1
7	1.0	0/11	BENTINK_ras.4
8	1.0	0/15	BENTINK_ras.6
9	1.0	0/13	BENTINK_src.10
10	1.0	0/14	BENTINK_src.2
11	NA	0/0	
12	NA	0/0	
13	NA	0/0	
14	NA	0/0	
15	NA	0/0	
16	NA	0/0	
17	NA	0/0	
18	NA	0/0	
19	NA	0/0	
20	NA	0/0	

Rank	p-value	#in/all	Geneset
1	1e-04	3/15	BEN-PORATH_UP
2	1e-01	1/9	WANG_ER_DN
3	1e-01	1/13	GENTLES_modul16
4	2e-01	1/14	LIU_LIVER_CANCER
5	3e-01	1/185	SPANG_BCL6-index2
6	9e-01	2/316	SPANG_BCL6-index2
7	1e+00	2/530	Lembcke_Normal vs Adenoma
8	1e+00	2/553	Lembcke_Colonc Inflammation
9	1e+00	0/16	RHODES_CANCER_META_SIGNATURE
10	1e+00	0/16	RHODES_UNDIFFERENTIATED_CANCER
11	1e+00	0/15	ROTIRIQUO_BREAST_CANCER_GRADE_1_VS_3_DN
12	1e+00	0/15	WIRTH_BREAST_CANCER_GRADE_1_VS_3_UP
13	1e+00	0/10	LIU_BREAST_CANCER
14	1e+00	0/14	LIU_COMMON_CANCER_GENES
15	1e+00	0/15	LIU_POSTSTATE_CANCER_DN
16	1e+00	0/14	LIU_PROSTATE_CANCER_UP
17	1e+00	0/14	WANG_ER_UP
18	1e+00	0/16	WOLFER_overlap_genes
19	1e+00	0/12	BEN-PORATH_DN
20	1e+00	0/15	GENTLES_modul1

Rank	p-value	#in/all	Geneset
1	9e-07	18/378	GUO_Psoriasis_down
2	1e+00	1/572	GUO_Psoriasis_up
3	1e+00	0/17	BCHETNIA_EBM_up
4	1e+00	0/2	BCHETNIA_EBM_down
5	1e+00	0/26	BCHETNIA_EBM-DM_up
6	NA	0/0	
7	NA	0/0	
8	NA	0/0	
9	NA	0/0	
10	NA	0/0	
11	NA	0/0	
12	NA	0/0	
13	NA	0/0	
14	NA	0/0	
15	NA	0/0	
16	NA	0/0	
17	NA	0/0	
18	NA	0/0	
19	NA	0/0	
20	NA	0/0	

Rank	p-value	#in/all	Geneset
1	1e-99	82/126	WIRTH_Muscle
2	5e-09	13/16	WIRTH_Hippocampus
3	1e-01	1/6	WIRTH_B-cells
4	1e-01	8/400	WIRTH_Nervous System
5	1e-01	1/12	WIRTH_Prim. lymphoid organs
6	1e-01	1/15	WIRTH_Cerebellum
7	5e-01	1/120	WIRTH_Testis
8	1e+00	0/5	WIRTH_Pituitary gland
9	1e+00	0/26	WIRTH_Pancreas
10	1e+00	0/417	WIRTH_Immune system
11	1e+00	0/13	WIRTH_Sec. lymphoid organs
12	1e+00	0/13	WIRTH_Tonsil
13	1e+00	0/13	WIRTH_Thymus
14	1e+00	0/6	WIRTH_Lymphocytes
15	1e+00	0/14	WIRTH_Bone marrow
16	1e+00	0/14	WIRTH_Globus pallidus
17	1e+00	0/15	WIRTH_Telencephalon
18	1e+00	0/13	WIRTH_Cortex cerebri
19	1e+00	0/13	WIRTH_Thalamus
20	1e+00	0/50	WIRTH_Homeostasis

Rank	p-value	#in/all	Geneset
1	0.002	3/49	AGGA-483
2	0.022	3/49	GGGG-296
3	0.030	3/65	ATCT-3
4	0.031	3/56	AGCG-137
5	0.049	4/120	TCAT-143
6	0.061	3/75	CCAG-331
7	0.065	2/35	GCCT-208
8	0.072	6	CTCT-526C---518F---526A
9	0.076	2/37	GCAT-105
10	0.087	4/136	TCAC-325
11	0.116	2/49	TCCC-491
12	0.122	1/11	AGCG-191
13	0.127	2/53	GCAA-502
14	0.138	1/36	ATGC-517B
15	0.149	1/13	ATAC-144
16	0.153	4/168	ATCA-226B
17	0.155	3/57	TCAT-166-3P
18	0.163	1/14	TCAT-166-3P

Rank	p-value	#in/all	Geneset
1	0.009	1/7	hsa-miR-562
2	0.083	1/7	hsa-miR-566
3	0.102	2/44	hsa-miR-536
4	0.138	2/53	hsa-miR-519b-5p
5	0.138	2/53	hsa-miR-519c-5p
6	0.147	2/55	hsa-miR-891b
7	0.159	2/88	hsa-miR-186d-5p
8	0.159	2/88	hsa-miR-520c-5p
9	0.172	2/61	hsa-miR-1236
10	0.209	1/19	hsa-miR-554
11	0.217	2/71	hsa-miR-531-3p
12	0.238	1/22	hsa-miR-596
13	0.248	1/23	hsa-miR-24-1*
14	0.266	1/25	hsa-miR-39a
15	0.284	1/27	hsa-miR-283-3p
16	0.284	1/27	hsa-miR-521
17	0.284	1/27	hsa-miR-1292
18	0.308	1/29	hsa-miR-293
19	0.327	3/164	hsa-miR-96
20	0.331	2/96	hsa-miR-1303

Rank	p-value	#in/all	Geneset
1	8e-04	27/146	HEBESTREIT_low expression TF
2	1e+00	3/1235	HEBESTREIT_high expression TF
3	1e+00	0/14	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	1e-25	16/34	Zeb1
2	3e-25	16/34	myotubulin
3	1e-18	12/20	I band
4	4e-18	10/12	myosin filament
5	3e-16	13/37	sarcomere
6	6e-14	9/16	M band
7	6e-13	8/13	muscle myosin complex
8	1e-12	8/29	contractile fiber
9	8e-12	8/29	sarcoplasmic reticulum membrane
10	4e-10	9/36	sarcoplasmic reticulum
11	4e-09	10/62	sarcolemma
12	3e-08	19/333	cytoskeleton
13	4e-08	8/42	myosin complex
14	1e-07	5/11	A band
15	1e-06	6/28	T-tubule
16	3e-06	13/184	actin cytoskeleton
17	3e-06	54/2378	cytosol
18	9e-06	5/24	voltage-gated calcium channel complex
19	1e-05	4/18	pseudopodium
20	6e-05	4/18	costamere

Rank	p-value	#in/all	Geneset
1	0.02	3/4	in vivo astrocytes vs. cultured astroglia
2	0.02	3/49	mature astrocytes
3	0.02	3/64	Christensen_hypermethylated_in_grade2_astrocytoma
4	0.05	9/391	Down_b
5	0.12	2/48	Noushimehr_Pron_GCIMP_hypermeth_DN
6	0.16	1/14	VERHAAK_CL subtype
7	0.16	1/14	VERHAAK_NL subtype
8	0.16	3/122	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	0.17	1/15	VERHAAK_PN subtype
10	0.18	3/118	willscher_GBM_Verhaak-CL_expression_K_down
11	0.18	3/118	willscher_GBM_Verhaak-MES_expression_K_down
12	0.18	3/118	willscher_GBM_Verhaak-PNwt_expression_K_up
13	0.18	3/118</	

# K-Means Cluster

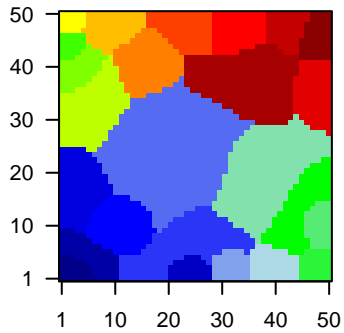
## Spot Summary: P

# metagenes = 171  
# genes = 651

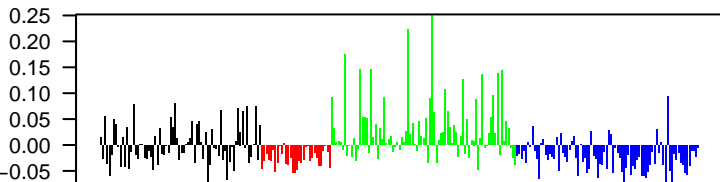
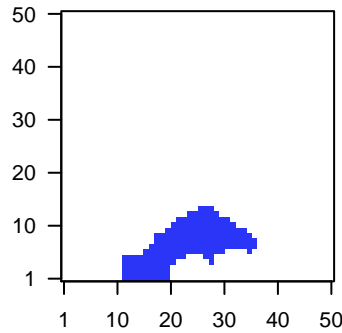
<r> metagenes = 0.71  
<r> genes = 0.1  
beta: r2= 0.9 / log p= -Inf

# samples with spot = 2 ( 0.7 % )  
Mesenchymal : 2 ( 2.4 % )

Overview Map



Spot

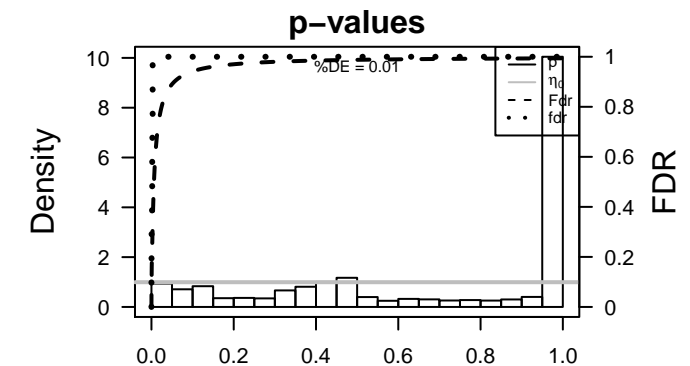


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	3598	1.82	-0.55	0.25	IL13RA2 interleukin 13 receptor, alpha 2 [Source:HGNC Symbol;Acc:5
2	2710	1.79	-0.85	0.28	GK glycerol kinase [Source:HGNC Symbol;Acc:4289]
3	3162	1.52	-0.96	0.35	HMOX1 heme oxygenase (decycling) 1 [Source:HGNC Symbol;Acc:5
4	84830	1.43	-0.67	0.26	ADTRP androgen-dependent TFPI-regulating protein [Source:HGNC
5	4852	1.39	-0.2	0.39	NPY neuropeptide Y [Source:HGNC Symbol;Acc:7955]
6	11026	1.33	-0.38	0.45	LILRA3 leukocyte immunoglobulin-like receptor, subfamily A (without
7	2081	1.29	-0.88	0.35	ERN1 endoplasmic reticulum to nucleus signaling 1 [Source:HGNC
8	1028	1.27	-0.56	0.28	CDKN1C cyclin-dependent kinase inhibitor 1C (p57, Kip2) [Source:HG
9	51561	1.25	-0.57	0.25	IL23A interleukin 23, alpha subunit p19 [Source:HGNC Symbol;Acc:
10	2254	1.25	-0.33	0.35	FGF9 fibroblast growth factor 9 [Source:HGNC Symbol;Acc:3687]
11	6653	1.23	-0.96	0.23	SORL1 sortilin-related receptor, L(DLR class) A repeats containing [
12	597	1.22	-0.43	0.54	BCL2A1 BCL2-related protein A1 [Source:HGNC Symbol;Acc:991]
13	22941	1.22	-0.42	0.35	SHANK2 SH3 and multiple ankyrin repeat domains 2 [Source:HGNC S
14	116372	1.19	-0.45	0.24	LYPD1 LY6/PLAUR domain containing 1 [Source:HGNC Symbol;Acc
15	168544	1.18	-0.78	0.47	ZNF467 zinc finger protein 467 [Source:HGNC Symbol;Acc:23154]
16	7850	1.16	-0.64	0.28	IL1R2 interleukin 1 receptor, type II [Source:HGNC Symbol;Acc:599
17	1803	1.14	-0.53	0.38	DPP4 dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:3009]
18	4884	1.14	-0.31	0.26	NPTX1 neuronal pentraxin I [Source:HGNC Symbol;Acc:7952]
19	4124	1.13	-0.89	0.18	MAN2A1 mannosidase, alpha, class 2A, member 1 [Source:HGNC Syr
20	3976	1.11	-0.3	0.52	LIF leukemia inhibitory factor [Source:HGNC Symbol;Acc:6596]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-12	199 / 3274	CC integral to membrane
2	1e-09	162 / 2659	CC plasma membrane
3	3e-08	83 / 1146	TF HEBENSTREIT_low expression TF
4	2e-07	48 / 553	Cancer Lembecke_Colonial Inflammation
5	9e-07	112 / 1837	CC membrane
6	2e-06	79 / 1182	CC extracellular region
7	4e-06	60 / 835	CC integral to plasma membrane
8	3e-05	4 / 6	H.Tis: WIRTH_Bone marrow
9	7e-05	72 / 1167	BP signal transduction
10	8e-05	23 / 242	BP extracellular matrix organization
11	1e-04	34 / 435	BP G-protein coupled receptor signaling pathway
12	1e-04	6 / 21	BP osteoclast differentiation
13	1e-04	32 / 403	BP cell adhesion
14	1e-04	7 / 30	BP blood vessel remodeling
15	1e-04	10 / 62	CC sarcolemma
16	1e-04	24 / 269	BP inflammatory response
17	1e-04	20 / 204	BP angiogenesis
18	2e-04	21 / 227	MF receptor activity
19	2e-04	4 / 9	GSE/ SA_MMP_CYTOKINE_CONNECTION
20	3e-04	8 / 44	CC presynaptic membrane
21	3e-04	7 / 35	BP glycosphingolipid metabolic process
22	4e-04	21 / 234	CC neuronal cell body
23	4e-04	12 / 96	BP central nervous system development
24	6e-04	11 / 88	BP muscle organ development
25	7e-04	24 / 299	BP axon guidance
26	7e-04	22 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
27	7e-04	22 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
28	7e-04	22 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
29	7e-04	22 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
30	8e-04	6 / 29	BP negative regulation of BMP signaling pathway
31	9e-04	25 / 321	MF G-protein coupled receptor activity
32	9e-04	4 / 12	BP cAMP catabolic process
33	9e-04	4 / 12	CC presynaptic active zone
34	9e-04	4 / 12	GSE/ KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES
35	1e-03	28 / 379	Glio Down_a
36	1e-03	29 / 400	H.Tis: WIRTH_Nervous System
37	1e-03	4 / 13	CC anchored to external side of plasma membrane
38	1e-03	4 / 13	BP cGMP biosynthetic process
39	1e-03	4 / 13	BP positive regulation of ossification
40	1e-03	9 / 68	BP positive regulation of MAPK cascade





# K-Means Cluster

## Spot Summary: Q

# metagenes = 76  
# genes = 710

<r> metagenes = 0.85  
<r> genes = 0.21  
beta: r2= 3.42 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

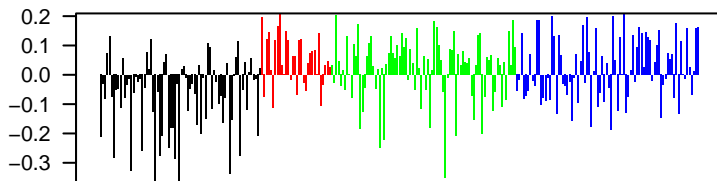
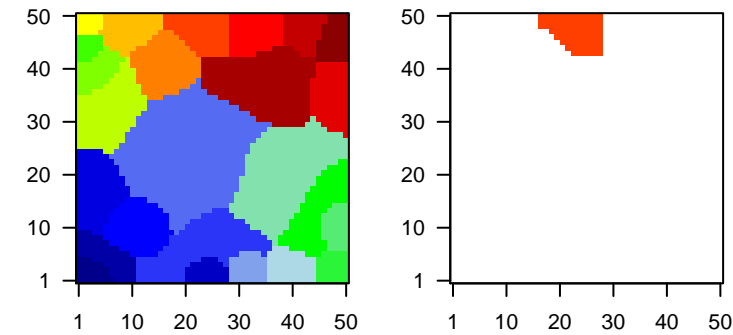
Rank	ID	max e	r	min e	Description
1	10413	2.32	-1.54	0.46	YAP1 Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
2	2354	2.13	-2.88	0.43	FOSB FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:100000000]
3	8349	2.04	-1.67	0.46	HIST2H2BE histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760]
4	91612	2	-1.22	0.2	CHURC1 Churchill domain containing 1 [Source:HGNC Symbol;Acc:200000000]
5	329	1.92	-0.97	0.34	BIRC2 baculoviral IAP repeat containing 2 [Source:HGNC Symbol;Acc:100000000]
6	147463	1.9	-1.14	0.36	ANKRD29 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
7	100008589	1.84	-1.52	0.29	RNA28S rRNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
8	1843	1.8	-2.27	0.6	DUSP1 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:300000000]
9	114908	1.77	-1.52	0.42	TMEM129 transmembrane protein 123 [Source:HGNC Symbol;Acc:301000000]
10	1647	1.77	-1.07	0.3	GADD45 growth arrest and DNA-damage-inducible, alpha [Source:HGNC Symbol;Acc:100000000]
11	25800	1.74	-1.25	0.54	SLC39A6 solute carrier family 39 (zinc transporter), member 6 [Source:HGNC Symbol;Acc:100000000]
12	23645	1.71	-1.84	0.38	PPP1R15A protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:100000000]
13	1958	1.66	-2.12	0.48	EGR1 early growth response 1 [Source:HGNC Symbol;Acc:3238]
14	79659	1.63	-0.75	0.28	DYNC2H1 dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:100000000]
15	57214	1.61	-1.51	0.27	KIAA1199 KIAA1199 [Source:HGNC Symbol;Acc:29213]
16	150094	1.57	-1.48	0.38	SIK1 salt-inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
17	10972	1.55	-1.23	0.61	TMED10 transmembrane emp24-like trafficking protein 10 (yeast) [Source:HGNC Symbol;Acc:100000000]
18	10950	1.54	-1.34	0.46	BTG3 BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
19	7538	1.53	-2.16	0.59	ZFP36 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
20	5366	1.49	-1.15	0.43	PMAIP1 phorbol-12-myristate-13-acetate-induced protein 1 [Source:HGNC Symbol;Acc:100000000]

## Geneset Overrepresentation

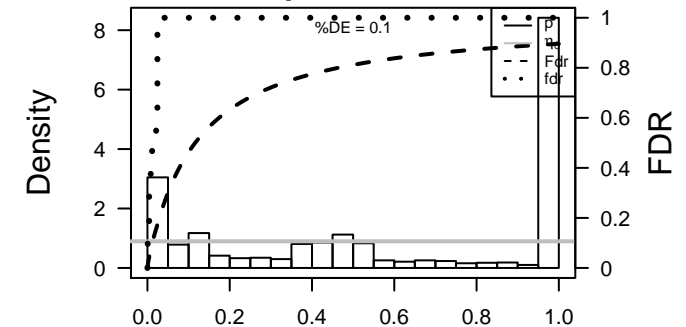
Rank	p-value	#in/all	Geneset
1	1e-30	82 / 436	miRN hsa-miR-548n
2	1e-24	62 / 313	Glio willscher_GBM_Verhaak-CL_expression_D_up
3	1e-24	62 / 313	Glio willscher_GBM_Verhaak-MES_expression_D_down
4	1e-24	62 / 313	Glio willscher_GBM_Verhaak-PNwt_expression_D_up
5	2e-23	79 / 517	miRN hsa-miR-106a
6	1e-22	55 / 269	miRN hsa-miR-1244
7	2e-22	59 / 310	miRN hsa-miR-340
8	8e-22	76 / 511	miRN hsa-miR-106b
9	6e-21	79 / 565	miRN hsa-miR-20b
10	8e-21	52 / 262	miRN hsa-miR-548l
11	9e-21	62 / 368	miRN hsa-miR-144
12	1e-20	77 / 545	miRN hsa-miR-93
13	2e-20	76 / 538	miRN hsa-miR-17
14	2e-20	81 / 603	miRN hsa-miR-20a
15	2e-19	38 / 150	miRN hsa-miR-200c
16	6e-19	45 / 217	miRN hsa-miR-548m
17	1e-18	54 / 313	miRN hsa-miR-559
18	9e-18	68 / 494	miRN hsa-miR-107
19	1e-17	60 / 399	miRN hsa-miR-519c-3p
20	3e-17	48 / 271	miRN hsa-miR-548h
21	4e-17	36 / 155	miRN hsa-miR-200b
22	5e-17	58 / 387	miRN hsa-miR-519a
23	5e-17	51 / 307	miRN hsa-miR-548c-5p
24	6e-17	56 / 364	miRN hsa-miR-519b-3p
25	7e-17	64 / 463	miRN hsa-miR-301a
26	1e-16	53 / 335	miRN hsa-miR-142-5p
27	1e-16	53 / 336	miRN hsa-miR-548d-5p
28	1e-16	66 / 495	miRN hsa-miR-103
29	2e-16	39 / 189	miRN hsa-miR-513a-3p
30	2e-16	38 / 180	miRN hsa-miR-374a
31	8e-16	50 / 315	miRN hsa-miR-30e
32	9e-16	34 / 151	miRN hsa-miR-429
33	1e-15	59 / 426	miRN hsa-miR-519d
34	2e-15	61 / 456	miRN hsa-miR-130a
35	2e-15	42 / 234	miRN hsa-miR-26a
36	2e-15	48 / 300	miRN hsa-miR-561
37	2e-15	50 / 324	miRN hsa-miR-18a
38	4e-15	57 / 412	miRN hsa-miR-372
39	4e-15	54 / 376	miRN hsa-miR-373
40	5e-15	35 / 169	miRN hsa-miR-374b

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: R

# metagenes = 50  
# genes = 596

<r> metagenes = 0.92  
<r> genes = 0.32  
beta: r2= 6.9 / log p= -Inf

# samples with spot = 25 ( 9.1 % )  
Atypical : 5 ( 6.8 % )  
Classical : 6 ( 18.8 % )  
Mesenchymal : 13 ( 15.3 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

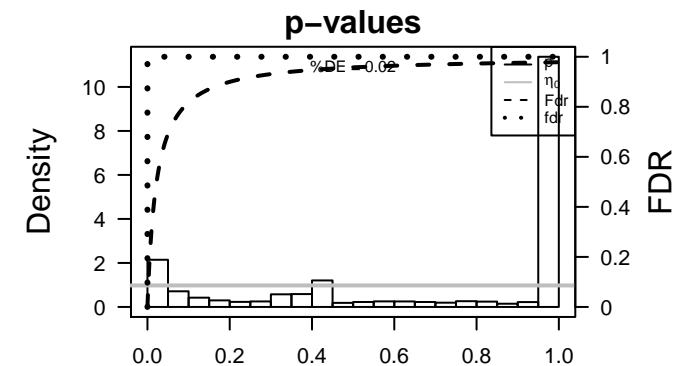
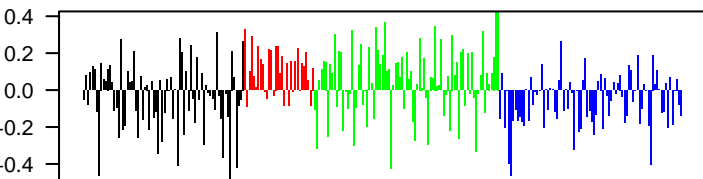
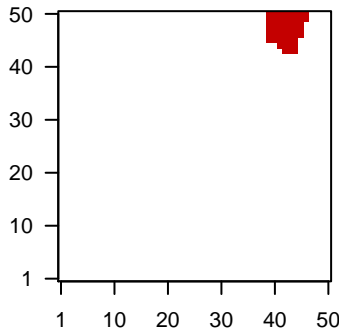
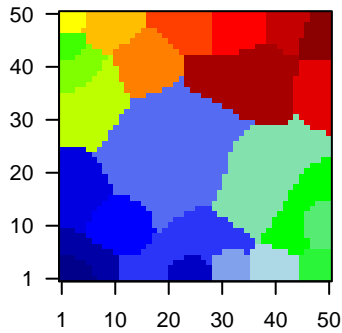
Rank	ID	max e	r	min e	Description
					Symbol
1	100008588	2.37	-0.91	0.23	RNA18S <small>r</small> RNA, 18S ribosomal 5 [Source:HGNC Symbol;Acc:37657]
2	908	1.96	-0.89	0.63	CCT6A chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
3	8500	1.93	-1.22	0.43	PPFIA1 protein tyrosine phosphatase, receptor type, f polypeptide (P1
4	9918	1.93	-1.18	0.52	NCAPD2non-SMC condensin I complex, subunit D2 [Source:HGNC S
5	793	1.83	-0.42	0.29	CALB1 calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
6	23480	1.83	-1.04	0.49	SEC61G Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
7	8836	1.83	-1.06	0.52	GGH gamma-glutamyl hydrolase (conjugase, folylpolyglamagluta
8	387103	1.83	-1.44	0.62	CENPW centromere protein W [Source:HGNC Symbol;Acc:21488]
9	2631	1.79	-0.97	0.4	GBAS glioblastoma amplified sequence [Source:HGNC Symbol;Acc
10	26872	1.76	-1.29	0.41	STEAP1 six transmembrane epithelial antigen of the prostate 1 [Sourc
11	81831	1.76	-1.65	0.52	NETO2 neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Sym
12	86	1.75	-1.06	0.84	ACTL6A actin-like 6A [Source:HGNC Symbol;Acc:24124]
13	3992	1.73	-1.29	0.47	FADS1 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
14	3945	1.73	-1.73	0.38	LDHB lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
15	5984	1.72	-1.26	0.89	RFC4 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn
16	116832	1.7	-1.8	0.61	RPL39L ribosomal protein L39-like [Source:HGNC Symbol;Acc:17094]
17	7153	1.7	-1.84	0.83	TOP2A topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
18	1894	1.64	-1.47	0.85	ECT2 epithelial cell transforming sequence 2 oncogene [Source:HG
19	10635	1.63	-1.2	0.84	RAD51AP1RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
20	3191	1.62	-1.54	0.22	HNRNPLheterogeneous nuclear ribonucleoprotein L [Source:HGNC S

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	98 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	1e-99	98 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	6e-78	116 / 370	BP mitotic cell cycle
4	5e-60	117 / 530	Cancr Lembcke_Normal vs Adenoma
5	1e-51	143 / 949	CC nucleoplasm
6	9e-37	62 / 232	BP mitosis
7	3e-27	43 / 149	BP DNA replication
8	2e-22	276 / 4640	CC nucleus
9	3e-21	15 / 16	GSE/ FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
10	9e-21	172 / 2378	CC cytosol
11	2e-20	24 / 56	CC chromosome, centromeric region
12	5e-20	50 / 298	BP DNA repair
13	8e-20	14 / 15	GSE/ FINETTI_BREAST_CANCER_KINOME_RED
14	1e-19	25 / 66	CC condensed chromosome kinetochore
15	1e-19	70 / 572	Disea GUDJ_psooriasis up
16	3e-19	35 / 148	BP G1/S transition of mitotic cell cycle
17	6e-19	14 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_2
18	2e-18	13 / 14	MMM MACIEJ_MMMML 4
19	3e-18	24 / 67	BP chromosome segregation
20	1e-17	14 / 18	BP spindle organization
21	4e-17	105 / 1233	TF KIM_MYC targets
22	2e-16	21 / 57	Glio developing astrocytes
23	9e-16	64 / 579	CC nucleolus
24	2e-15	107 / 1344	MF ATP binding
25	7e-15	12 / 16	GSE/ EGUCHI_CELL_CYCLE_RB1_TARGETS
26	7e-15	12 / 16	GSE/ CROONQUIST_NRAS_SIGNALING_DN
27	9e-15	11 / 13	GSE/ CROONQUIST_IL6_DEPRIVATION_DN
28	1e-14	16 / 35	BP mitotic nuclear envelope disassembly
29	2e-14	20 / 61	CC kinetochore
30	2e-14	15 / 30	BP DNA strand elongation involved in DNA replication
31	4e-14	11 / 14	GSE/ ZHAN_MULTIPLE_MYELOMA_PR_UP
32	6e-14	13 / 22	BP CENP-A containing nucleosome assembly at centromere
33	1e-13	19 / 59	CC nuclear pore
34	1e-13	11 / 15	Cancr SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
35	2e-13	20 / 68	Cancr SHAUGHNESSY_MM high risk
36	2e-13	26 / 122	BP G2/M transition of mitotic cell cycle
37	4e-13	11 / 16	GSE/ SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
38	4e-13	11 / 16	GSE/ REACTOME_G2_M_CHECKPOINTS
39	5e-13	17 / 49	BP telomere maintenance
40	9e-13	10 / 13	GSE/ REN_BOUND_BY_E2F

### Overview Map

### Spot







# K-Means Cluster

## Spot Summary: S

# metagenes = 117  
# genes = 517

<r> metagenes = 0.81  
<r> genes = 0.14  
beta: r2= 1.25 / log p= -Inf

# samples with spot = 2 ( 0.7 % )  
Basal : 2 ( 2.4 % )

## Spot Genelist

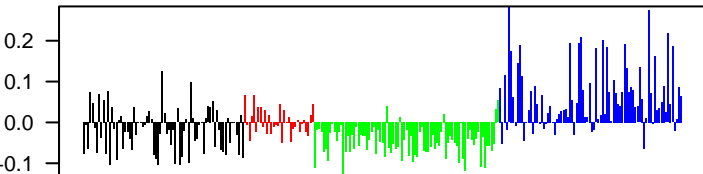
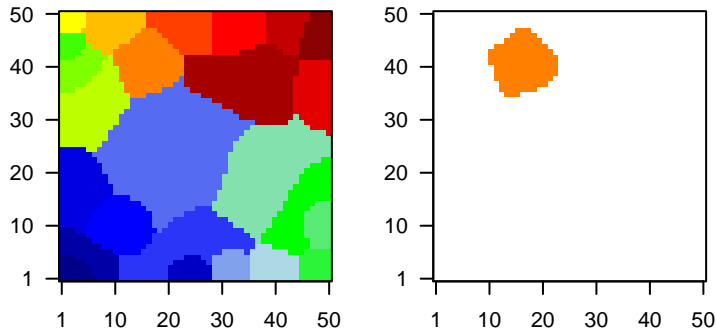
Rank	ID	max e	r	min e	Description Symbol
1	3933	2.9	-0.29	0.26	LCN1 lipocalin 1 [Source:HGNC Symbol;Acc:6525]
2	140683	1.96	-0.22	0.23	BPIFA2 BPI fold containing family A, member 2 [Source:HGNC Symb
3	3849	1.85	-0.46	0.31	KRT2 keratin 2 [Source:HGNC Symbol;Acc:6439]
4	10913	1.63	-0.56	0.38	EDAR ectodysplasin A receptor [Source:HGNC Symbol;Acc:2895]
5	79746	1.63	-1.28	0.23	ECHDC3enoyl CoA hydratase domain containing 3 [Source:HGNC Syr
6	3656	1.46	-0.91	0.33	IRAK2 interleukin-1 receptor-associated kinase 2 [Source:HGNC S
7	10331	1.44	-0.51	0.42	B3GNT3 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransf
8	3359	1.44	-0.35	0.36	HTR3A 5-hydroxytryptamine (serotonin) receptor 3A, ionotropic [Sou
9	10451	1.43	-1.18	0.34	VAV3 vav 3 guanine nucleotide exchange factor [Source:HGNC Syr
10	55344	1.42	-0.83	0.29	PLCXD1 phosphatidylinositol-specific phospholipase C, X domain con
11	3850	1.41	-0.4	0.54	KRT3 keratin 3 [Source:HGNC Symbol;Acc:6440]
12	51350	1.4	-0.21	0.33	KRT76 keratin 76 [Source:HGNC Symbol;Acc:24430]
13	29949	1.4	-0.4	0.25	IL19 interleukin 19 [Source:HGNC Symbol;Acc:5990]
14	2952	1.38	-1.77	0.21	GSTT1 glutathione S-transferase theta 1 [Source:HGNC Symbol;Acc
15	4217	1.33	-0.95	0.18	MAP3K5 mitogen-activated protein kinase kinase kinase 5 [Source:HC
16	1373	1.32	-0.55	0.24	CPS1 carbamoyl-phosphate synthase 1, mitochondrial [Source:HG
17	55277	1.29	-0.64	0.32	FGGY FGGY carbohydrate kinase domain containing [Source:HGNC
18	158158	1.29	-0.96	0.3	RASEF RAS and EF-hand domain containing [Source:HGNC Symbo
19	55640	1.26	-0.72	0.41	FLVCR2 feline leukemia virus subgroup C cellular receptor family, men
20	116362	1.25	-0.68	0.41	RBP7 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:.

## Geneset Overrepresentation

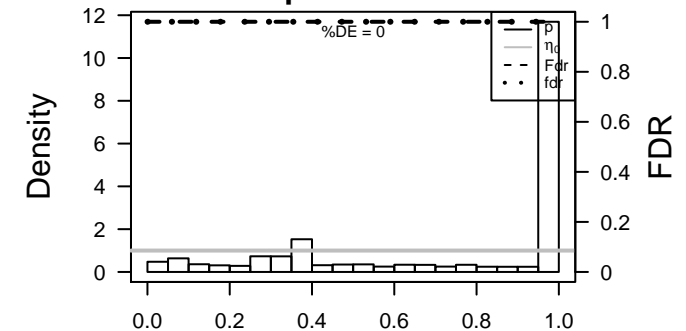
Rank	p-value	#in/all	Geneset
1	2e-04	10 / 79	BP vitamin metabolic process
2	3e-04	4 / 11	BP fatty acid beta-oxidation using acyl-CoA oxidase
3	3e-04	9 / 69	BP sphingolipid metabolic process
4	4e-04	9 / 73	BP water-soluble vitamin metabolic process
5	9e-04	6 / 37	BP fatty acid beta-oxidation
6	1e-03	4 / 15	GSE/ GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_DN
7	1e-03	4 / 16	BP very long-chain fatty acid metabolic process
8	2e-03	6 / 44	CC keratin filament
9	2e-03	57 / 1253	BP small molecule metabolic process
10	2e-03	4 / 19	BP ceramide biosynthetic process
11	3e-03	20 / 320	BP small GTPase mediated signal transduction
12	3e-03	33 / 633	Chr Chr 9
13	3e-03	5 / 32	CC peroxisomal matrix
14	3e-03	4 / 20	BP histone deacetylation
15	3e-03	4 / 20	BP nitrogen compound metabolic process
16	3e-03	3 / 10	BP epoxygenase P450 pathway
17	3e-03	3 / 10	BP pantothenate metabolic process
18	3e-03	3 / 10	GSE/ REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7A
19	3e-03	5 / 33	BP sphingolipid biosynthetic process
20	4e-03	4 / 21	BP drug metabolic process
21	4e-03	30 / 572	Disea GUDJ_psooriasis up
22	4e-03	3 / 11	BP alpha-linolenic acid metabolic process
23	4e-03	3 / 11	BP unsaturated fatty acid metabolic process
24	4e-03	3 / 11	GSE/ RICKMAN_METASTASIS_DN
25	4e-03	26 / 478	BP protein transport
26	4e-03	5 / 35	MF monoxygenase activity
27	5e-03	26 / 481	miRN TGCT-15A-16-15B-195-424-497
28	5e-03	3 / 12	MF hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in line
29	5e-03	3 / 12	CC Sin3 complex
30	5e-03	3 / 12	GSE/ MANALO_HYPOXIA_UP
31	5e-03	3 / 12	GSE/ KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS
32	5e-03	3 / 12	GSE/ REACTOME_JNK_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED
33	6e-03	7 / 69	BP response to toxic substance
34	6e-03	7 / 69	miRN hsa-miR-578
35	6e-03	13 / 186	MF structural molecule activity
36	6e-03	2 / 4	GSE/ GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
37	6e-03	6 / 54	BP JNK cascade
38	6e-03	8 / 89	CC peroxisome
39	7e-03	3 / 13	GSE/ BLALOCK_ALZHEIMERS_DISEASE_INCIPENT_DN
40	7e-03	3 / 13	GSE/ KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLAC

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: T

# metagenes = 19  
# genes = 260

<r> metagenes = 0.97  
<r> genes = 0.46  
beta: r2= 56.45 / log p= -Inf

# samples with spot = 101 ( 36.7 % )  
Atypical : 11 ( 14.9 % )  
Classical : 7 ( 21.9 % )  
Mesenchymal : 10 ( 11.8 % )  
Basal : 73 ( 86.9 % )

## Spot Genelist

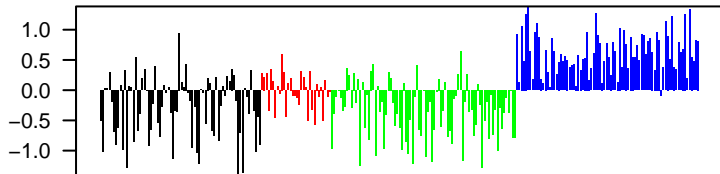
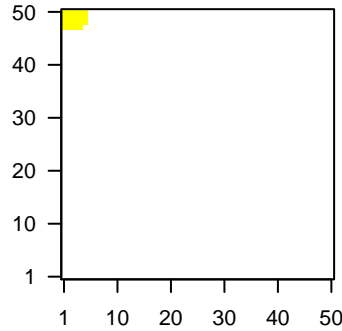
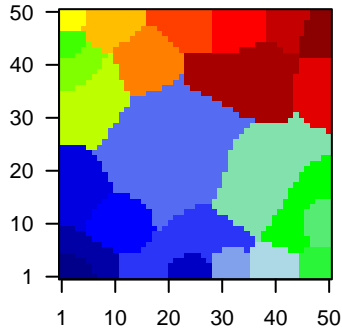
Rank	ID	max e	r	min e	Description
					Symbol
1	3848	4.75	-1.88	0.67	KRT1 keratin 1 [Source:HGNC Symbol;Acc:6412]
2	3851	4.24	-3.19	0.57	KRT4 keratin 4 [Source:HGNC Symbol;Acc:6441]
3	49860	4.24	-3.23	0.72	CRNN cornulin [Source:HGNC Symbol;Acc:1230]
4	4118	3.95	-3.23	0.61	MAL mal, T-cell differentiation protein [Source:HGNC Symbol;Acc:1230]
5	4014	3.86	-0.97	0.38	LOR lorricrin [Source:HGNC Symbol;Acc:6663]
6	1673	3.84	-3.54	0.67	DEFB4B defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
7	6701	3.84	-2.1	0.75	SPRR2B small proline-rich protein 2B [Source:HGNC Symbol;Acc:112]
8	6947	3.77	-1.96	0.46	TCN1 transcobalamin I (vitamin B12 binding protein, R binder family)
9	414325	3.77	-2.67	0.71	DEFB103B defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	6706	3.74	-3.05	0.71	SPRR2G small proline-rich protein 2G [Source:HGNC Symbol;Acc:112]
11	57152	3.69	-1.77	0.81	SLURP1 secreted LY6/PLAUR domain containing 1 [Source:HGNC Symbol;Acc:112]
12	2877	3.69	-3.11	0.44	GPX2 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Symbol;Acc:112]
13	338324	3.66	-2.9	0.68	S100A7AS100 calcium binding protein A7A [Source:HGNC Symbol;Acc:112]
14	7053	3.52	-3.39	0.81	TGM3 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	1828	3.51	-1.97	0.78	DSG1 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
16	55894	3.4	-1.83	0.73	DEFB103B defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	8644	3.37	-2.96	0.4	AKR1C3 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:112]
18	84651	3.36	-1.82	0.74	SPINK7 serine peptidase inhibitor, Kazal type 7 (putative) [Source:HGNC Symbol;Acc:112]
19	84648	3.36	-2.37	0.72	LCE3D late cornified envelope 3D [Source:HGNC Symbol;Acc:16615]
20	29113	3.29	-1.18	0.39	C6orf15 chromosome 6 open reading frame 15 [Source:HGNC Symbol;Acc:112]

## Geneset Overrepresentation

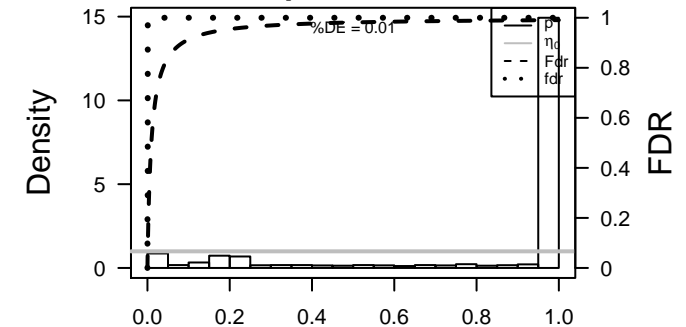
Rank	p-value	#in/all	Geneset
1	1e-99	87 / 135	H.Tis: WIRTH_Mucosa
2	2e-74	96 / 572	Disea GUDJ_psooriasis up
3	3e-28	23 / 53	BP keratinocyte differentiation
4	5e-28	17 / 21	CC cornified envelope
5	7e-24	19 / 42	BP keratinization
6	7e-24	23 / 76	BP epidermis development
7	7e-16	11 / 19	BP peptide cross-linking
8	2e-15	10 / 15	GSE/ WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
9	2e-14	56 / 1182	CC extracellular region
10	1e-12	21 / 186	MF structural molecule activity
11	5e-12	51 / 1146	TF HEBENSTREIT_low expression TF
12	6e-10	15 / 122	MF serine-type endopeptidase activity
13	1e-09	7 / 15	GSE/ HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	2e-09	7 / 16	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	2e-09	7 / 16	GSE/ WANG_BARRETTES_ESOPHAGUS_DN
16	2e-09	7 / 16	GSE/ ONDER_CDH1_TARGETS_3_DN
17	2e-08	6 / 13	BP negative regulation of peptidase activity
18	3e-08	11 / 79	MF serine-type endopeptidase inhibitor activity
19	5e-08	11 / 82	CC intermediate filament
20	9e-08	9 / 52	BP negative regulation of endopeptidase activity
21	9e-08	6 / 16	GSE/ JAEGER_METASTASIS_DN
22	9e-08	6 / 16	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
23	9e-08	6 / 16	GSE/ CROMER_TUMORIGENESIS_DN
24	1e-07	8 / 38	BP epithelial cell differentiation
25	2e-07	5 / 10	MF RAGE receptor binding
26	2e-07	5 / 10	GSE/ KEGG_LINOLEIC_ACID_METABOLISM
27	3e-07	8 / 44	CC keratin filament
28	6e-07	10 / 83	CC anchored to membrane
29	1e-06	5 / 13	H.Tis: WIRTH_Tonsil
30	1e-06	8 / 53	MF serine-type peptidase activity
31	2e-06	5 / 14	GSE/ CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
32	2e-06	5 / 15	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_E
33	2e-06	5 / 15	GSE/ LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
34	3e-06	5 / 16	GSE/ LEE_LIVER_CANCER_MYC_TGFA_UP
35	3e-06	5 / 16	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
36	4e-06	25 / 579	MF calcium ion binding
37	5e-06	6 / 29	BP regulation of proteolysis
38	1e-05	4 / 10	GSE/ SMID_BREAST_CANCER_ERBB2_UP
39	1e-05	7 / 51	MF protein binding, bridging
40	1e-05	5 / 21	CC desmosome

### Overview Map

### Spot



### p-values



Rank	p-value	#in/all	Geneset
1	0.001	7/33	antigen differentiation
2	7e-24	19/42	keratinization
3	7e-24	23/76	epidermis development
4	7e-16	11/19	peptide cross-linking
5	9e-08	6/13	negative regulation of peptidase activity
6	9e-08	9/52	negative regulation of endopeptidase activity
7	1e-07	8/38	epithelial cell differentiation
8	8e-05	8/73	regulation of proteolysis
9	2e-05	8/73	defense response to bacterium
10	1e-04	18/434	oxidation-reduction process
11	2e-04	4/19	phosphatidylethanolamine acyl-chain remodeling
12	2e-04	8/19	phosphatidylcholine acyl-chain remodeling
13	5e-04	8/119	xenobiotic metabolic process
14	6e-04	5/44	steroid metabolic process
15	6e-04	16/405	proteolysis
16	7e-04	3/12	cellular aldehyde metabolic process
17	7e-04	4/27	response to bacterium
18	9e-04	5/49	arachidonic acid metabolic process
19	1e-03	5/14	excretion
20	1e-03	5/14	defense response to fungus

Rank	p-value	#in/all	Geneset
1	0.001	23/20	Chr 18
2	0.010	9/232	Chr 18
3	0.023	26/345	Chr 19
4	0.13	13/1818	Chr 18
5	0.192	2/52	Chr HSCHR6_MHC_QBL
6	0.223	12/602	Chr 10
7	0.24	10/64	Chr 15
8	0.284	10/519	Chr 14
9	0.301	1/23	Chr HSCHR6_MHC_DBB
10	0.363	15/866	Chr 12
11	0.373	1/633	Chr 9
12	0.545	7/449	Chr 20
13	0.555	3/187	Chr 21
14	0.687	8/534	Chr 8
15	0.6247	14/11	Chr 11
16	0.632	4/280	Chr 11
17	0.766	12/918	Chr 17
18	0.734	9/717	Chr 16
19	0.882	12/1033	Chr 2
20	0.929	7/714	Chr 6

Rank	p-value	#in/all	Geneset
1	2e-15	10/15	WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
2	1e-09	7/16	HINSHAW_TARGETS_KERATINOCYTE_DN
3	2e-09	7/16	SENGUPTA_NASOPHARYNGEAL_CARCIOMA_DN
4	2e-09	7/16	WANG_BARRETTES_ESOPHAGUS_DN
5	2e-09	7/16	ONDER_CDH1_TARGETS_3_DN
6	9e-08	6/16	JAEGER_METASTASIS_DN
7	9e-08	6/16	CHILDREN_GEFITINIB_RESISTANCE_DN
8	9e-08	6/16	CROMER_TUMORIGENESIS_DN
9	2e-07	5/10	KEGG_LINOLEIC_ACID_METABOLISM
10	2e-06	5/15	KEGG_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
11	2e-06	5/15	RICKMAN_HEAD_AND_NECK_CANCER_E
12	3e-06	5/15	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
13	3e-06	5/16	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	1e-05	4/10	SMID_BREAST_CANCER_ERBB2_UP
15	9e-05	4/14	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
16	7e-05	4/12	ALIGNE_ZEB1_TARGETS
17	7e-05	4/15	LEE_LIVER_CANCER_MYC_E2F1_UP
18	7e-05	4/15	CHANG_IMMORTALIZED_BY_HP31_DN
19	9e-05	4/16	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN

Rank	p-value	#in/all	Geneset
1	6e-10	15/122	serine-type endopeptidase activity
2	3e-08	11/79	serine-type endopeptidase inhibitor activity
3	2e-07	5/10	RAGE_receptor_binding
4	1e-07	1/3	serine-type peptidase activity
5	4e-06	25/579	calcium ion binding
6	1e-05	7/51	protein binding, bridging
7	2e-05	16/296	oxidoreductase activity
8	7e-05	4/15	retinol dehydrogenase activity
9	1e-04	9/125	iron ion binding
10	4e-04	4/23	peptidase inhibitor activity
11	6e-04	19/531	catalytic activity
12	7e-04	3/12	lysophospholipase activity
13	1e-03	3/15	interleukin-1 receptor binding
14	2e-03	4/34	endopeptidase inhibitor activity
15	2e-03	3/19	monooxygenase activity
16	3e-03	3/19	laminin binding
17	5e-03	3/22	cysteine-type endopeptidase inhibitor activity
18	7e-03	3/25	oxygen binding
19	8e-03	3/25	calcium-dependent phospholipid binding

Rank	p-value	#in/all	Geneset
1	0.002	1/6	miR-136a
2	0.089	1/6	miR-200c
3	0.103	1/7	miR-145
4	0.103	1/7	miR-210
5	0.117	1/8	miR-9
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	miR-1
11	1.000	0/3	miR-101
12	1.000	0/2	miR-101b
13	1.000	0/4	miR-106b
14	1.000	0/10	miR-107
15	1.000	0/4	miR-122
16	1.000	0/2	miR-124a
17	1.000	0/6	miR-125b
18	1.000	0/9	miR-125b
19	1.000	0/5	miR-126

Rank	p-value	#in/all	Geneset
1	0.2	1/13	BENTINK_ras.6
2	1.0	0/15	BENTINK_pi3k_UP
3	1.0	0/15	GUSTAFSON_pi3k_DN
4	1.0	0/12	BENTINK_e2f3.1
5	1.0	0/11	BENTINK_e2f3.2
6	1.0	0/14	BENTINK_myc.4
7	1.0	0/12	BENTINK_ras.1
8	1.0	0/11	BENTINK_ras.4
9	1.0	0/13	BENTINK_src.10
10	1.0	0/14	BENTINK_src.2
11	NA	0/0	
12	NA	0/0	
13	NA	0/0	
14	NA	0/0	
15	NA	0/0	
16	NA	0/0	
17	NA	0/0	
18	NA	0/0	
19	NA	0/0	
20	NA	0/0	

Rank	p-value	#in/all	Geneset
1	0.001	18/300	epidermal vs Adenoma
2	0.010	0/15	LIU_PROSTATE_CANCER_DN
3	0.049	14/553	Lemcke_Colonc Inflammation
4	0.131	1/4	WANG_ER_DN
5	0.196	1/14	WANG_ER_DN
6	0.221	1/16	GENTLES_modul11
7	0.527	1/48	KUIPER_MM_poor_survival
8	0.945	2/185	SPANG_BCL6_index2
9	1.000	0/15	RHODES_CANCER_META_SIGNATURE
10	1.000	0/16	RHODES_UNDIFFERENTIATED_CANCER
11	1.000	0/15	WIRTH_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.000	0/10	LIU_BREAST_CANCER
14	1.000	0/14	LIU_COMMON_CANCER_GENES
15	1.000	0/14	LIU_LIVER_CANCER
16	1.000	0/14	LIU_PROSTATE_CANCER_UP
17	1.000	0/16	WOLFNER_overlap_genes
18	1.000	0/12	BEN-PORATH_DN
19	1.000	0/12	BEN-PORATH_UP

Rank	p-value	#in/all	Geneset
1	6e-74	86/572	GUDDI_psoiasis up
2	3e-02	2/17	BCHEITNIA_EBM up
3	3e-01	4/26	BCHEITNIA_EBM_DM up
4	1e-01	1/35	GUDDI_psoiasis down
5	1e+00	0/2	BCHEITNIA_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	1e-99	87/135	WIRTH_Mucosa
2	5e-13	5/13	WIRTH_Tonsil
3	1e-02	5/13	WIRTH_Prim. lymphoid organs
4	1e-01	1/13	WIRTH_Thymus
5	2e-01	1/13	WIRTH_Cerebellum
6	2e-01	1/15	WIRTH_Pituitary gland
7	6e-01	1/120	WIRTH_Testis
8	9e-01	1/127	WIRTH_Muscle
9	1e+00	2/400	WIRTH_Nervous System
10	1e+00	5	TACT_25A
11	1e+00	0/26	WIRTH_Pancreas
12	1e+00	0/417	WIRTH_Immune system
13	1e+00	0/10	WIRTH_Sec. lymphoid organs
14	1e+00	0/10	WIRTH_B-cells
15	1e+00	0/12	WIRTH_Lymphocytes
16	1e+00	0/6	WIRTH_Bone marrow
17	1e+00	0/14	WIRTH_Globus pallidus
18	1e+00	0/15	WIRTH_Telencephalon
19	1e+00	0/13	WIRTH_Cortex cerebri
20	1e+00	0/16	WIRTH_Hippocampus

Rank	p-value	#in/all	Geneset
1	0.2	1/20	CTCT-17A--517C
2	0.3	1/20	GTAG-189
3	0.3	2/73	AGAG-500
4	0.3	3/129	CTCT-520A--525
5	0.3	3/129	TACT-26A--26B
6	0.3	3/142	GTGC-183
7	0.4	2/89	ATCG-338
8	0.4	1/33	TCTG-383
9	0.4	1/34	WITA-517
10	0.4	1/36	GGGA-324-5P
11	0.4	1/37	TAGG-192--215
12	0.5	1/42	hsa-miR-508
13	0.5	1/43	CCCA-299-3P
14	0.5	1/43	GACA-339
15	0.5	2/107	ACAC-142-3P
16	0.5	2/110	GGCG-512-3P
17	0.5	5/309	CTACLET-7A-LET-7B-LET-7C-LET-7D-LET-7E-LET-7F--98-LET-7G
18	0.5	1/50	TACA-508
19	0.5	4/252	CCCA-93--302A--302B--302C--302D--372--373--520E--520A--526I
20	0.6	0/0	

Rank	p-value	#in/all	Geneset
1	0.02	1/39	hsa-miR-508
2	0.11	3/75	hsa-miR-1290
3	0.11	3/75	hsa-miR-1305
4	0.16	2/43	hsa-miR-518d-3p
5	0.16	5/186	hsa-miR-382
6	0.17	7/294	hsa-miR-202
7	0.20	3/99	hsa-miR-590-5p
8	0.20	2/54	hsa-miR-409-5p
9	0.21	4/151	hsa-miR-583
10	0.21	4/153	hsa-miR-508
11	0.22	2/57	hsa-miR-532-5p
12	0.22	1/16	hsa-miR-1298
13	0.24	1/18	hsa-miR-564
14	0.24	3/21	hsa-miR-376c
15	0.26	2/64	hsa-miR-873
16	0.29	2/69	hsa-miR-1184
17	0.30	4/129	hsa-miR-302a
18	0.30	1/23	hsa-miR-518a
19	0.30	1/23	hsa-miR-668

Rank	p-value	#in/all	Geneset
1	5e-12	51/146	HEBESTREIT_low expression TF
2	3e-2	1/2	MYC_cycle DOWN
3	1e-01	1/9	MYC_targets DOWN
4	2e-01	1/16	MYC_Protein synthesis degradation UP
5	6e-01	1/63	MYC_targets UP
6	1e+00	5/195	HEBESTREIT_high expression TF
7	1e+00	5/1233	KIM_MYC targets
8	1e+00	0/14	NOWICK_TF
9	1e+00	0/5	MYC_TFs
10	1e+00	0/4	MYC_Apoptosis UP
11	1e+00	0/8	MYC_Cell cycle UP
12	1e+00	0/4	MYC_Cell growth and proliferation UP
13	1e+00	0/2	MYC_Chromatin_modification UP
14	1e+00	0/3	MYC_DNA repair UP
15	1e+00	0/3	MYC_DNA replication UP
16	1e+00	0/2	MYC_ECM_cell adhesion DOWN
17	1e+00	0/20	MYC_Metabolism UP
18	1e+00	0/8	MYC_RNA processing binding UP
19	1e+00	0/2	MYC_Signal transduction UP
20	1e+00	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	2e-14	56/1182	extracellular region
2	5e-08	11/82	intermediate filament
3	3e-07	8/44	keratin filament
4	6e-07	10/83	anchored to membrane
5	1e-05	5/21	desmosome
6	2e-05	13/201	apical plasma membrane
7	6e-05	25/683	extracellular space
8	3e-03	55/599	plasma membrane
9	9e-03	84/430	cytoplasm
10	1e-02	47/58	ruffle membrane
11	1e-02	3/32	cell-cell adhesion junction
12	2e-02	3/36	brush border membrane
13	2e-02	3/37	lateral plasma membrane
14	2e-02	3/38	clathrin-coated vesicle
15	2e-02	2/16	connexon complex
16	3e-02	4/77	apical part of cell
17	3e-02	2/21	gap junction
18	3e-02	2/23	brush border

Rank	p-value	#in/all	Geneset
1	0.002	5/8	Christensen_hypermethylated_in_secondary_glioblastoma
2	0.007	4/49	Christensen_hypermethylated_in_primary_glioblastoma
3	0.010	3/37	Christensen_hypermethylated_in_ependymoma
4	0.028	5/10	Christensen_hypermethylated_in_grade3_astrocytoma
5	0.030	5/112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
6	0.040	4/83	Christensen_hypermethylated_in_secondary_glioblastoma
7	0.047	3/53	Christensen_hypermethylated_in_primary_glioblastoma
8	0.054	3/32	Christensen_hypermethylated_in_grade3_oligoastrocytoma
9	0.070	5/142	Christensen_hypermethylated_in_grade2_oligoastrocytoma
10	0.077	3/64	Christensen_hypermethylated_in_grade2_astrocytoma
11	0.088	3/68	cultured_astroglia_vs_in_vivo_astrocytes
12	0.103	1/7	wilscher_GBM_LTSmut_protomics-P_DOWN
13	0.103	1/7	KIM_epithelial-mesenchymal-transition related genes_decreased expression</

# K-Means Cluster

## Spot Summary: U

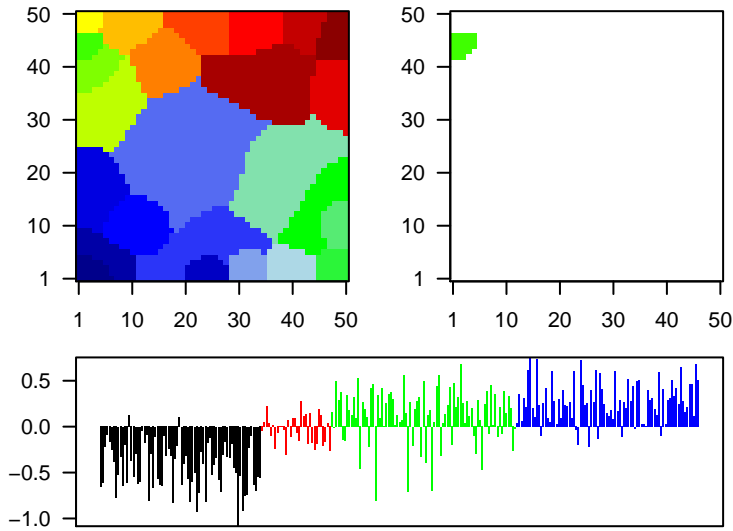
# metagenes = 22  
# genes = 241

<r> metagenes = 0.95  
<r> genes = 0.38  
beta: r2= 28.45 / log p= -Inf

# samples with spot = 89 ( 32.4 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 36 ( 42.4 % )  
Basal : 51 ( 60.7 % )

Overview Map

Spot

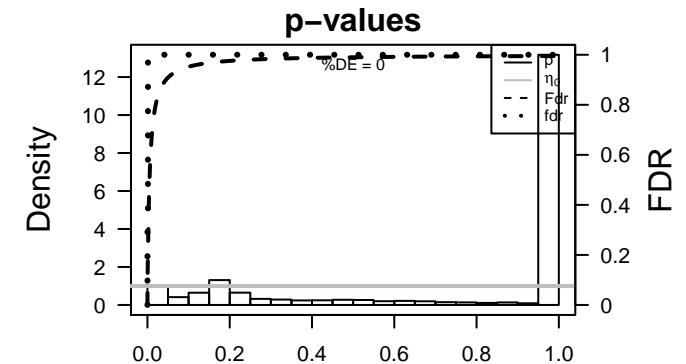


## Spot Genelist

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	374918	3.79	-1.25	0.43	IGFL1 IGF-like family member 1 [Source:HGNC Symbol;Acc:24093]
3	404203	3.3	-0.91	0.51	SPINK6 serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb]
4	118430	3.17	-0.81	0.37	MUCL1 mucin-like 1 [Source:HGNC Symbol;Acc:30588]
5	1041	3.12	-1.1	0.66	CDSN corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	151516	2.97	-1.01	0.52	ASPRV1 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
7	3489	2.81	-2.42	0.59	IGFBP6 insulin-like growth factor binding protein 6 [Source:HGNC Sy
8	760	2.81	-2.26	0.69	CA2 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	51200	2.78	-1.85	0.64	CPA4 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
10	9119	2.63	-0.92	0.55	KRT75 keratin 75 [Source:HGNC Symbol;Acc:24431]
11	8710	2.62	-1.39	0.5	SERPINF1 serpin peptidase inhibitor, clade B (ovalbumin), member 7 [Sc
12	5947	2.61	-2.47	0.45	RBP1 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:1
13	5744	2.59	-2.33	0.7	PTH1H parathyroid hormone-like hormone [Source:HGNC Symbol;A
14	1823	2.59	-0.82	0.61	DSC1 desmocollin 1 [Source:HGNC Symbol;Acc:3035]
15	4753	2.56	-1.8	0.39	NELL2 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
16	55214	2.54	-2.24	0.56	LEPREL1 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
17	1308	2.51	-2.89	0.64	COL17A1 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	6273	2.51	-2.5	0.7	S100A2 S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
19	2352	2.48	-0.81	0.52	FOLR3 folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
20	147495	2.48	-1.6	0.49	APCDD1 adenomatosis polyposis coli down-regulated 1 [Source:HGNC

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-32	57 / 572	Disea GUDJ_pсориазис up
2	1e-19	24 / 135	H.Tiss WIRTH_Mucosa
3	6e-11	13 / 76	BP epidermis development
4	2e-10	13 / 82	CC intermediate filament
5	3e-10	8 / 21	CC desmosome
6	6e-08	6 / 16	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
7	9e-08	15 / 186	MF structural molecule activity
8	3e-07	10 / 82	MF structural constituent of cytoskeleton
9	2e-06	67 / 2659	CC plasma membrane
10	2e-05	4 / 12	BP hemidesmosome assembly
11	4e-05	6 / 44	BP skin development
12	5e-05	4 / 15	GSE/ AIGNER_ZEB1_TARGETS
13	5e-05	4 / 15	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
14	5e-05	4 / 15	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
15	5e-05	9 / 117	Glio GIEZELT_GBM_WT_up_VS_mut
16	6e-05	3 / 6	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
17	7e-05	4 / 16	GSE/ ELVIDGE_HIF1A_TARGETS_DN
18	2e-04	4 / 21	BP filopodium assembly
19	3e-04	4 / 22	MF cadherin binding
20	3e-04	18 / 488	miRN hsa-miR-16
21	3e-04	3 / 10	BP negative regulation of interleukin-2 production
22	3e-04	3 / 10	GSE/ DAZARD_UV_RESPONSE_CLUSTER_G3
23	4e-04	5 / 44	CC keratin filament
24	5e-04	3 / 11	GSE/ GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
25	5e-04	6 / 70	BP cell junction assembly
26	6e-04	3 / 12	CC fascia adherens
27	6e-04	3 / 12	BP keratinocyte proliferation
28	6e-04	7 / 100	BP cell-cell adhesion
29	8e-04	5 / 50	MF Rab GTPase binding
30	8e-04	3 / 13	BP intermediate filament cytoskeleton organization
31	8e-04	3 / 13	GSE/ KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_DN
32	8e-04	85 / 4310	CC cytoplasm
33	9e-04	5 / 51	CC lipid particle
34	9e-04	9 / 170	miRN hsa-miR-29a
35	9e-04	8 / 137	CC basolateral plasma membrane
36	1e-03	3 / 14	GSE/ BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
37	1e-03	10 / 210	miRN hsa-miR-29b
38	1e-03	4 / 32	CC cell-cell adherens junction
39	1e-03	9 / 177	miRN hsa-miR-29c
40	1e-03	3 / 15	BP response to osmotic stress



Rank	p-value	#in/all	Geneset
1	0.000	4/176	positive regulation of development
2	0.000	4/112	hemidesmosome assembly
3	0.000	6/44	skin development
4	0.000	4/21	filopodium assembly
5	0.000	3/10	negative regulation of interleukin-2 production
6	0.000	6/70	cell junction assembly
7	0.000	3/12	keratinocyte proliferation
8	0.000	7/100	cell-cell adhesion
9	0.000	7/13	intermediate filament cytoskeleton organization
10	0.000	3/15	response to osmotic stress
11	0.000	3/17	morphogenesis of an epithelium
12	0.000	3/12	negative regulation of interferon-gamma production
13	0.000	3/25	brown fat cell differentiation
14	0.000	3/25	response to zinc ion
15	0.000	3/26	positive regulation of vasodilation
16	0.000	13/403	cell adhesion
17	0.000	3/27	protein polymerization
18	0.000	4/53	keratinocyte differentiation
19	0.000	4/53	positive regulation of epithelial cell proliferation
20	0.000	4/55	odontogenesis of dentin-containing tooth

Rank	p-value	#in/all	Geneset
1	0.001	1/24	Chr 18
2	0.041	13/519	Chr 14
3	0.061	15/534	Chr 8
4	0.089	15/714	Chr 6
5	0.119	11/504	Chr 15
6	0.124	31/1720	Chr 9
7	0.249	1/23	Chr 20
8	0.286	1/23	Chr HSCHR6_MHC_DBB
9	0.320	12/699	Chr 5
10	0.359	15/918	Chr 17
11	0.461	4/3	Chr 3
12	0.542	15/1033	Chr 2
13	0.584	4/280	Chr 13
14	0.611	12/866	Chr 12
15	0.777	7/103	Chr 1
16	0.817	4/386	Chr 22
17	0.819	7/633	Chr 9
18	0.827	11/957	Chr 11
19	0.852	8/743	Chr 7
20	0.902	7/717	Chr 16

Rank	p-value	#in/all	Geneset
1	0.000	6/16	HIGHER_BREAST_BASAL_VS_LUMINAL_UP
2	0.000	1/1	ALKBH1_TARGETS
3	0.000	4/15	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
4	0.000	4/15	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
5	0.000	3/6	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
6	0.000	4/16	ELVIDGE_HIF1A_TARGETS_DN
7	0.000	3/10	DAZARD_UV_RESPONSE_CLUSTER_G3
8	0.000	3/11	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
9	0.000	3/13	KUROKAWA_LIVER_CANCER_CHEMOTHERAPY_DN
10	0.000	1/1	BERTHOLO_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
11	0.000	3/15	PRAMONJAGO_SOX4_TARGETS_UP
12	0.000	3/15	SENSE_HDAC1_AND_HDAC2_TARGETS_DN
13	0.000	3/15	WILLIAMS_KUHLI_OVARIAN_CANCER_GRADES_1_2_UP
14	0.000	3/15	FRIDMAN_IMMORTALIZATION_DN
15	0.000	3/15	CROMER_METASTASIS_DN
16	0.000	3/15	GHO_ATF5_TARGETS_DN
17	0.000	3/16	JAEGER_METASTASIS_DN
18	0.000	3/16	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
19	0.000	3/16	COLDREN_GEFITINIB_RESISTANCE_DN
20	0.000	3/16	YANG_BREAST_CANCER_ESR1_DN

Rank	p-value	#in/all	Geneset
1	0.000	10/82	ribosome biogenesis
2	0.000	4/22	structural constituent of cytoskeleton
3	0.000	5/50	cadherin binding
4	0.000	3/20	Rab GTPase binding
5	0.000	17/579	scaffold protein binding
6	0.000	5/79	calcium ion binding
7	0.000	3/32	serine-type endopeptidase inhibitor activity
8	0.000	2/12	G-protein coupled purinergic nucleotide receptor activity
9	0.000	2/12	potassium channel activity
10	0.000	2/12	fatty acid binding
11	0.000	9/256	GTPase activity
12	0.000	2/13	inward rectifier potassium channel activity
13	0.000	2/13	magnesium ion transmembrane transporter activity
14	0.000	2/15	cytoskeletal adaptor activity
15	0.000	2/17	amino acid transmembrane transporter activity
16	0.000	10/339	GTP binding
17	0.000	2/21	epidermal growth factor receptor binding
18	0.000	9/321	G-protein coupled receptor activity
19	0.000	13/529	protein homodimerization activity
20	0.000	2/2	antigen binding

Rank	p-value	#in/all	Geneset
1	0.03	1/1	miR-346
2	0.06	1/4	miR-122
3	0.06	1/4	miR-133b
4	0.07	1/5	miR-126
5	0.07	1/5	miR-196a
6	0.32	1/26	miR-21
7	1.00	0/6	let-7a
8	1.00	0/6	let-7b
9	1.00	0/4	let-7c
10	1.00	0/6	let-7d
11	1.00	0/4	let-7f
12	1.00	0/13	miR-1
13	1.00	0/5	miR-101
14	1.00	0/2	miR-101b
15	1.00	0/2	miR-106b
16	1.00	0/2	miR-107
17	1.00	0/2	miR-124a
18	1.00	0/9	miR-125b
19	1.00	0/2	miR-127

Rank	p-value	#in/all	Geneset
1	0.02	2/13	GUSTAFSON_Pi3K_DN
2	0.16	0/13	BENTINK_ras
3	0.16	0/13	GUSTAFSON_Pi3K_UP
4	0.00	0/12	BENTINK_e2f3.1
5	0.00	0/11	BENTINK_e2f3.2
6	0.00	0/11	BENTINK_myc
7	0.00	0/11	BENTINK_ras.4
8	0.00	0/13	BENTINK_ras.6
9	0.00	0/13	BENTINK_src.10
10	0.00	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	0.000	12/553	ZNF616_MODS_up
2	0.000	0/10	Lembcke_Colonc Inflammation
3	0.000	1/14	LIU_BREAST_CANCER_UP
4	0.000	1/16	LIU_PROSTATE_CANCER_UP
5	0.000	1/16	LIU_PROSTATE_CANCER_DN
6	0.000	1/16	GENTLES_modul4
7	0.000	10/530	Lembcke_Normal vs Adenoma
8	0.000	6/316	SPANG_BCL6-index2
9	0.000	4/4	KUIPER_MM_good survival
10	0.000	3/185	SPANG_LPS-index2
11	0.000	1/68	SHAUGHNESSY_MM_high risk
12	0.000	0/16	RHODES_CANCER_MET_A_SIGNATURE
13	0.000	0/16	RHODES_UNDIFFERENTIATED_CANCER
14	0.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	0.000	0/15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	0.000	0/14	LIU_COLOMION_CANCER_GENES
17	0.000	0/14	LIU_LIVER_CANCER
18	0.000	0/14	WANG_ER_UP
19	0.000	0/9	WANG_ER_DN
20	0.000	0/16	WOLFER_overlap genes

Rank	p-value	#in/all	Geneset
1	0.000	6e-32	GUDJ_psooriasis_up
2	0.000	1/17	UCHETNIA_EBM_up
3	0.000	1/26	UCHETNIA_EBM_DM_up
4	0.000	6/265	GUDJ_psooriasis_down
5	0.000	0/2	UCHETNIA_EBM_down
6	0.000	0/0	
7	0.000	0/0	
8	0.000	0/0	
9	0.000	0/0	
10	0.000	0/0	
11	0.000	0/0	
12	0.000	0/0	
13	0.000	0/0	
14	0.000	0/0	
15	0.000	0/0	
16	0.000	0/0	
17	0.000	0/0	
18	0.000	0/0	
19	0.000	0/0	
20	0.000	0/0	

Rank	p-value	#in/all	Geneset
1	1e-19	24/135	WIRTH_Mucosa
2	2e-01	2/13	WIRTH_Prim_lymphoid organs
3	2e-01	1/13	WIRTH_Tonsil
4	2e-01	1/13	WIRTH_Thymus
5	2e-01	1/13	WIRTH_Cortex cerebri
6	2e-01	1/13	WIRTH_Glioblastoma
7	2e-01	1/14	WIRTH_Globus pallidus
8	3e-01	1/26	WIRTH_Pancreas
9	4e-01	7/400	WIRTH_Nervous System
10	4e-01	1/36	WIRTH_Placenta
11	6e-01	1/62	WIRTH_Liver
12	8e-01	1/120	WIRTH_Testis
13	1e+00	0/417	WIRTH_Pituitary gland
14	1e+00	0/13	WIRTH_Immune system
15	1e+00	0/13	WIRTH_Sec_lymphoid organs
16	1e+00	0/10	WIRTH_B-cells
17	1e+00	0/12	WIRTH_Lymphocytes
18	1e+00	0/6	WIRTH_Bone marrow
19	1e+00	0/15	WIRTH_Telencephalon
20	1e+00	0/16	WIRTH_Hippocampus

Rank	p-value	#in/all	Geneset
1	0.003	11/48	hsa-miR-26B
2	0.015	12/401	ACCA-3
3	0.017	11/362	CAGT-200B-200C-429
4	0.019	12/415	TTTG-19A-19B
5	0.020	13/467	TCG-30A-5P-30C-30D-30B-30E-5P
6	0.020	12/420	TGGT-29A-29B-29C
7	0.026	4/77	GGTG-329
8	0.032	6/163	CTTG-381
9	0.034	4/84	ATG-202
10	0.045	4/92	GCTT-498
11	0.050	4/95	GGGC-365
12	0.057	5/97	hsa-miR-92B
13	0.050	6/182	CTGA-24
14	0.052	9/329	AATG-23A-23B
15	0.062	7/240	CAGT-141-200A
16	0.066	7/240	hsa-miR-25-32-92-363-367
17	0.069	3/65	TCIG-198
18	0.070	6/198	ATGT-302C
19	0.070	5/151	GTAT-369-3P
20	0.079	5/168	TCG-138C-519B-519A

Rank	p-value	#in/all	Geneset
1	9e-04	18/188	hsa-miR516
2	9e-04	9/170	hsa-miR-29a
3	1e-03	10/210	hsa-miR-29b
4	1e-03	9/172	hsa-miR-29c
5	2e-03	15/438	hsa-miR-424
6	2e-03	7/122	hsa-miR-105
7	3e-03	6/96	hsa-miR-133a
8	3e-03	15/464	hsa-miR-195
9	6e-03	15/494	hsa-miR-107
10	6e-03	6/114	hsa-miR-675-3p
11	1e-03	5/93	hsa-miR-433
12	1e-03	13/414	hsa-miR-497
13	1e-02	14/479	hsa-miR-15b
14	1e-02	5/95	hsa-miR-133b
15	1e-02	14/495	hsa-miR-103
16	2e-02	9/267	hsa-miR-577
17	2e-02	14/512	hsa-miR-15a
18	2e-02	3/40	hsa-miR-450b
19	2e-02	7/5	hsa-miR-1420
20	2e-02	4/76	hsa-miR-1261

Rank	p-value	#in/all	Geneset
1	0.009	27/1146	HEBENSTREIT_low expression TF
2	0.604	1/63	MYC_Metabolism UP
3	0.604	1/63	MYC_targets UP
4	0.720	16/1233	KIM_MYC targets
5	0.961	10/1095	HEBENSTREIT_high expression TF
6	1.000	0/4	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 UP
15	1.000	0/3	MYC_DNA replication UP
16	1.000	0/2	MYC_ECM cell adhesion DOWN
17	1.000	0/16	MYC_Protein synthesis degradation UP
18	1.000	0/8	MYC_RNA processing binding UP
19	1.000	0/2	MYC_Signal transduction UP
20	1.000	0/3	MYC_Tumor suppressor genes UP

Rank	p-value	#in/all	Geneset
1	3e-10	8/21	intermediate filament
2	2e-06	67/2659	desmosome
3	4e-04	5/44	plasma membrane
4	3e-04	5/44	keratin filament
5	8e-04	85/4310	casia adherens
6	9e-04	5/51	cytoplasm
7	9e-04	8/137	lipid particle
8	1e-03	4/37	basolateral plasma membrane
9	1e-03	6/83	cell-cell adherens junction
10	1e-03	7/115	basement membrane
11	1e-03	4/35	cell-cell junction
12	2e-03	20/683	vesicle
13	7e-03	3/27	extracellular space
14	7e-03	6/117	basal plasma membrane
15	7e-03	6/117	cytoplasmic vesicle
16	8e-03	6/121	microtubule cytoskeleton
17	1e-02	21/835	integral to plasma membrane
18	1e-02	3/33	intercalated disc
19	1e-02	37/182	EXTRACELLULAR region
20	3e-02	3/35	cell periphery

Rank	p-value	#in/all	Geneset
1	3e-05	8/11	GIEZELT_GBM_WT_vs_UP_mut
2	3e-03	7/132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	6e-03	4/48	Noushahrif_Pron_GCIMP_hypermeth DN
4	6e-03	6/112	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	8e-03	5/85	laffaire_hypermeth_LGG_vs_control
6	2e-02	6/142	Christensen_hypermethylated_in_grade2_olig

# K-Means Cluster

## Spot Summary: V

# metagenes = 48  
# genes = 395

<r> metagenes = 0.93  
<r> genes = 0.25  
beta: r2= 7.98 / log p= -Inf

# samples with spot = 25 ( 9.1 % )  
Mesenchymal : 12 ( 14.1 % )  
Basal : 13 ( 15.5 % )

## Spot Genelist

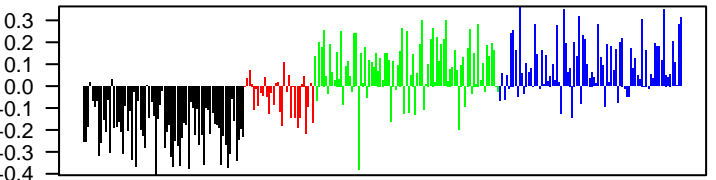
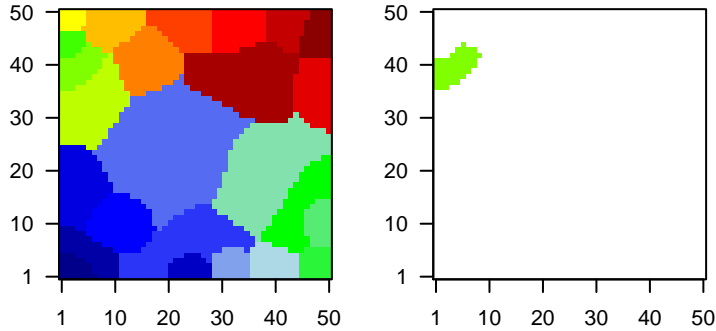
Rank	ID	max e	r	min e	Description
1	780854	3.58	-1.9	0.24	SNORD33 small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc:6664]
2	780851	3.23	-1.91	0.23	SNORD33 small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc:6664]
3	780853	3.15	-1.74	0.25	SNORD33 small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc:6664]
4	2731	2.65	-0.96	0.22	GLDC glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:6664]
5	4015	2.63	-1.39	0.41	LOX lysyl oxidase [Source:HGNC Symbol;Acc:6664]
6	948	2.41	-0.99	0.34	CD36 CD36 molecule (thrombospondin receptor) [Source:HGNC Symbol;Acc:6664]
7	387882	2.28	-1.59	0.37	C12orf75 chromosome 12 open reading frame 75 [Source:HGNC Symbol;Acc:6664]
8	84259	2.28	-1.19	0.4	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 5 [Source:HGNC Symbol;Acc:6664]
9	135398	2.22	-1	0.39	C6orf141 chromosome 6 open reading frame 141 [Source:HGNC Symbol;Acc:6664]
10	8339	2.1	-1.01	0.37	HIST1H2BC histone cluster 1, H2bc [Source:HGNC Symbol;Acc:4757]
11	200315	2.02	-0.86	0.45	APOBEC3B apolipoprotein B mRNA editing enzyme, catalytic polypeptide [Source:HGNC Symbol;Acc:6664]
12	353141	1.96	-0.38	0.43	LCE2D late cornified envelope 2D [Source:HGNC Symbol;Acc:16518]
13	723790	1.91	-1.5	0.35	HIST2H2AB histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
14	1466	1.9	-1.81	0.32	CSRP2 cysteine and glycine-rich protein 2 [Source:HGNC Symbol;Acc:6664]
15	8942	1.87	-1.87	0.32	KYNU kynureninase [Source:HGNC Symbol;Acc:6469]
16	1984	1.86	-1.04	0.35	EIF5A eukaryotic translation initiation factor 5A [Source:HGNC Symbol;Acc:6664]
17	80117	1.84	-0.9	0.38	ARL14 ADP-ribosylation factor-like 14 [Source:HGNC Symbol;Acc:29469]
18	148304	1.78	-1.23	0.51	C1orf74 chromosome 1 open reading frame 74 [Source:HGNC Symbol;Acc:6664]
19	5091	1.78	-0.99	0.55	PC pyruvate carboxylase [Source:HGNC Symbol;Acc:8636]
20	353139	1.76	-0.36	0.48	LCE2A late cornified envelope 2A [Source:HGNC Symbol;Acc:29469]

## Geneset Overrepresentation

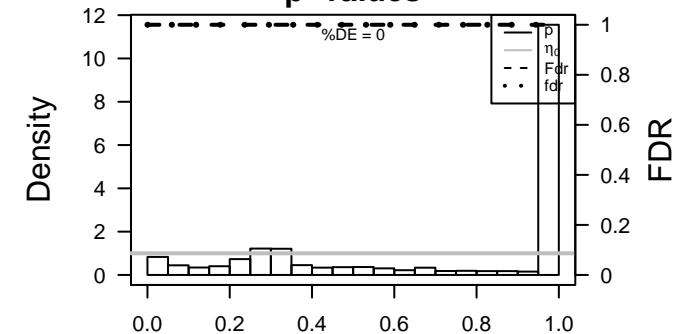
Rank	p-value	#in/all	Geneset
1	2e-11	43 / 572	Disea GUDJ_psooriasis up
2	2e-05	29 / 519	Chr Chr 14
3	4e-05	10 / 88	miRN hsa-miR-1265
4	7e-05	39 / 852	Lymph SPANG_BCR DN
5	1e-04	4 / 12	GSEF SESTO_RESPONSE_TO_UV_C3
6	3e-04	4 / 15	GSEF NAGASHIMA_NRG1_SIGNALING_UP
7	4e-04	24 / 470	miRN GCAC-17-5P--20A--106A--106B--20B--519D
8	4e-04	5 / 27	miRN hsa-miR-675
9	4e-04	3 / 7	MMM MACIEJ_MMML 9
10	5e-04	4 / 16	GSEF AMIT_EGF_RESPONSE_120_MCF10A
11	5e-04	11 / 140	miRN hsa-miR-138
12	6e-04	2 / 2	miRN miR-199a*
13	6e-04	131 / 4310	CC cytoplasm
14	7e-04	7 / 63	miRN hsa-miR-455-3p
15	8e-04	20 / 380	CC intracellular membrane-bounded organelle
16	8e-04	6 / 47	CC nucleosome
17	1e-03	13 / 204	BP cell surface receptor signaling pathway
18	1e-03	8 / 89	miRN hsa-miR-608
19	1e-03	86 / 2659	CC plasma membrane
20	2e-03	12 / 185	Canc SPANG_LPS-index2
21	2e-03	9 / 115	MF lipid binding
22	2e-03	3 / 11	GSEF HOFMANN_CELL_LYMPHOMA_DN
23	2e-03	3 / 11	GSEF DANG_MYC_TARGETS_UP
24	3e-03	10 / 147	miRN hsa-miR-143
25	3e-03	7 / 80	miRN hsa-miR-339-5p
26	3e-03	33 / 835	CC integral to plasma membrane
27	3e-03	8 / 102	miRN hsa-miR-600
28	3e-03	5 / 42	MF acid-amino acid ligase activity
29	3e-03	3 / 13	MF phosphatidylinositol-3,4-bisphosphate binding
30	3e-03	5 / 43	miRN hsa-miR-661
31	3e-03	17 / 342	MF protein heterodimerization activity
32	4e-03	13 / 234	miRN hsa-miR-26a
33	4e-03	11 / 181	miRN ACTG-34B
34	4e-03	4 / 28	BP neurotransmitter transport
35	4e-03	4 / 28	MF small GTPase regulator activity
36	4e-03	16 / 320	BP small GTPase mediated signal transduction
37	4e-03	9 / 132	miRN hsa-miR-485-5p
38	4e-03	7 / 86	Lymph ROSLOWSKI_green UP
39	5e-03	13 / 238	miRN hsa-miR-214
40	5e-03	3 / 15	MF retinol dehydrogenase activity

Overview Map

Spot



p-values







# K-Means Cluster

## Spot Summary: W

# metagenes = 142  
# genes = 556

<r> metagenes = 0.86  
<r> genes = 0.15  
beta: r2= 1.55 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

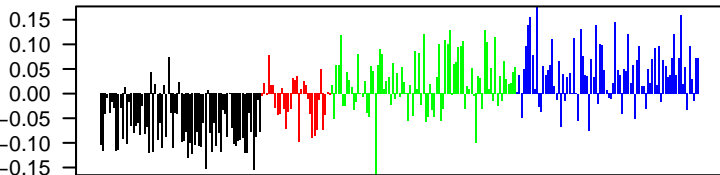
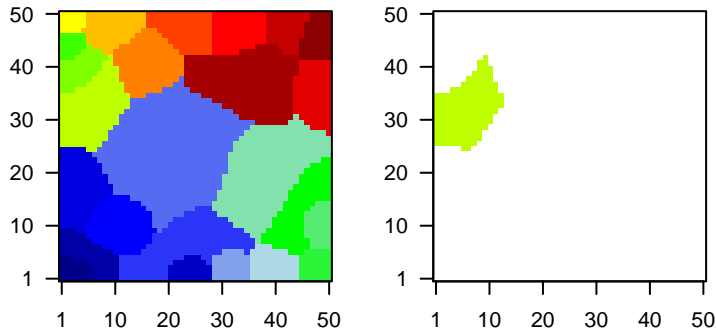
Rank	ID	max e	r	min e	Description
1	1907	1.81	-0.7	0.26	EDN2 endothelin 2 [Source:HGNC Symbol;Acc:3177]
2	170680	1.71	-0.44	0.43	PSORS1C psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;Acc:32930]
3	10809	1.35	-0.99	0.37	STARD1 START-related lipid transfer (START) domain containing 10 [Source:HGNC Symbol;Acc:32930]
4	159686	1.31	-0.36	0.27	CCDC14 coiled-coil domain containing 147 [Source:HGNC Symbol;Acc:32930]
5	55004	1.29	-0.83	0.32	LAMTOR1 late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [Source:HGNC Symbol;Acc:32930]
6	388555	1.27	-0.5	0.3	IGFL3 IGF-like family member 3 [Source:HGNC Symbol;Acc:32930]
7	83648	1.26	-0.67	0.22	FAM167A family with sequence similarity 167, member A [Source:HGNC Symbol;Acc:32930]
8	8689	1.24	-0.35	0.55	KRT36 keratin 36 [Source:HGNC Symbol;Acc:6454]
9	118663	1.24	-0.39	0.34	BTBD16 BTB (POZ) domain containing 16 [Source:HGNC Symbol;Acc:32930]
10	7172	1.22	-1.1	0.21	TPMT thiopurine S-methyltransferase [Source:HGNC Symbol;Acc:1907]
11	9914	1.19	-0.65	0.41	ATP2C2 ATPase, Ca++ transporting, type 2C, member 2 [Source:HGNC Symbol;Acc:32930]
12	4821	1.17	-0.26	0.28	NKX2-2 NK2 homeobox 2 [Source:HGNC Symbol;Acc:7835]
13	389084	1.16	-0.41	0.35	C2orf82 chromosome 2 open reading frame 82 [Source:HGNC Symbol;Acc:32930]
14	6326	1.15	-0.34	0.3	SCN2A sodium channel, voltage-gated, type II, alpha subunit [Source:HGNC Symbol;Acc:32930]
15	9764	1.12	-0.63	0.32	KIAA0513 KIAA0513 [Source:HGNC Symbol;Acc:29058]
16	9322	1.11	-0.83	0.48	TRIP10 thyroid hormone receptor interactor 10 [Source:HGNC Symbol;Acc:32930]
17	1606	1.11	-0.91	0.34	DGKA diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Acc:32930]
18	23085	1.1	-0.81	0.32	ERC1 ELKS/RAB6-interacting/CAST family member 1 [Source:HGNC Symbol;Acc:32930]
19	2582	1.08	-0.82	0.53	GALE UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:41]
20	448835	1.08	-0.23	0.42	LCE6A late cornified envelope 6A [Source:HGNC Symbol;Acc:31824]

## Geneset Overrepresentation

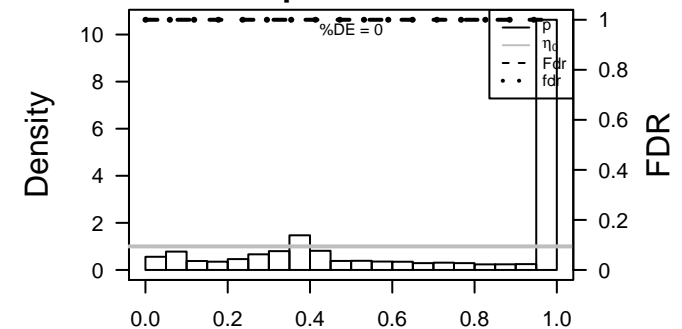
Rank	p-value	#in/all	Geneset
1	6e-07	50 / 717	Chr Chr 16
2	1e-04	10 / 71	miRN hsa-miR-331-3p
3	2e-04	11 / 88	miRN hsa-miR-423-5p
4	3e-04	6 / 28	CC Golgi stack
5	4e-04	6 / 30	miRN hsa-miR-631
6	8e-04	30 / 481	miRN TGCT-15A-16-15B-195-424-497
7	8e-04	9 / 75	miRN CCAG-331
8	2e-03	4 / 16	GSE/ BIOCARTE_RHO_PATHWAY
9	2e-03	9 / 83	miRN hsa-miR-486-3p
10	2e-03	22 / 336	BP intracellular signal transduction
11	2e-03	6 / 41	MF kinase binding
12	2e-03	6 / 42	BP keratinization
13	3e-03	14 / 181	miRN CCTG-214
14	3e-03	4 / 19	BP protein peptidyl-prolyl isomerization
15	3e-03	4 / 19	MF SNARE binding
16	4e-03	3 / 10	CC paranode region of axon
17	4e-03	3 / 10	GSE/ REACTOME_ADENYLATE_CYCLASE_ACTIVATING_PATHWAY
18	4e-03	22 / 354	miRN CTTT-524
19	4e-03	4 / 20	BP carbohydrate transport
20	5e-03	4 / 21	BP filopodium assembly
21	5e-03	7 / 63	BP positive regulation of type I interferon production
22	5e-03	12 / 152	miRN GGGA-133A-133B
23	5e-03	3 / 11	BP activation of innate immune response
24	5e-03	3 / 11	GSE/ GALE_APL_WITH_FLT3_MUTATED_DN
25	5e-03	4 / 22	BP methylation
26	6e-03	15 / 215	CC lysosomal membrane
27	6e-03	296 / 8023	MF protein binding
28	6e-03	3 / 12	BP long term synaptic depression
29	6e-03	3 / 12	BP peptidyl-proline modification
30	6e-03	3 / 12	BP rRNA transcription
31	6e-03	3 / 12	Glio wilscher_GBM_Verhaak-PNwt_expression_l_up
32	6e-03	3 / 12	Glio wilscher_GBM_Verhaak-PNmut_expression_l_up
33	6e-03	3 / 12	miRN hsa-miR-671-3p
34	6e-03	4 / 23	BP endosome organization
35	7e-03	7 / 68	BP positive regulation of MAPK cascade
36	8e-03	4 / 24	BP photoreceptor cell maintenance
37	8e-03	9 / 104	miRN ACTG-139
38	8e-03	10 / 123	BP defense response to virus
39	8e-03	5 / 38	BP post-Golgi vesicle-mediated transport
40	8e-03	3 / 13	MF FK506 binding

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: X

# metagenes = 68  
# genes = 585

<r> metagenes = 0.83  
<r> genes = 0.2  
beta: r2= 8.97 / log p= -Inf

# samples with spot = 25 ( 9.1 % )  
Classical : 5 ( 15.6 % )  
Basal : 20 ( 23.8 % )

## Spot Genelist

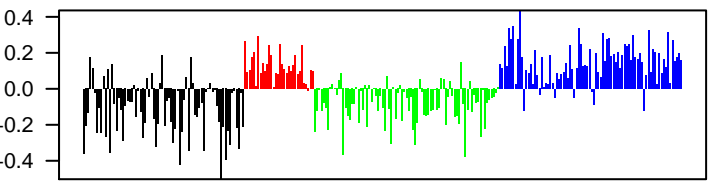
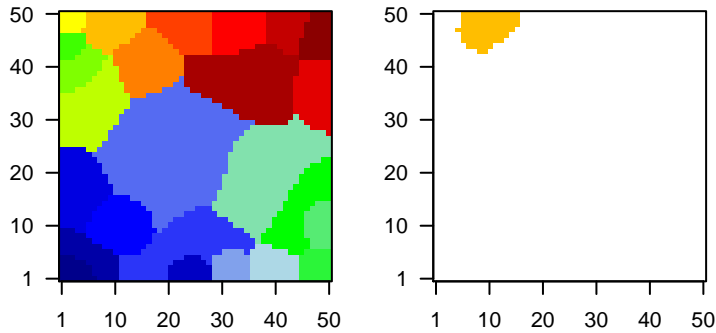
Rank	ID	max e	r	min e	Description
					Symbol
1	1109	3.73	-2.74	0.69	AKR1C4 aldo-keto reductase family 1, member C4 [Source:HGNC Sym]
2	57834	2.91	-1.53	0.7	CYP4F1 cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
3	1749	2.89	-1.7	0.51	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:2918]
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	5327	2.56	-1.74	0.35	PLAT plasminogen activator, tissue [Source:HGNC Symbol;Acc:90f
7	140809	2.51	-1.38	0.73	SRXN1 sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
8	9073	2.47	-0.88	0.44	CLDN8 claudin 8 [Source:HGNC Symbol;Acc:2050]
9	5413	2.39	-1.75	0.34	SEPT5 septin 5 [Source:HGNC Symbol;Acc:9164]
10	7102	2.39	-1.41	0.4	TSPAN7 tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
11	3485	2.34	-2.39	0.36	IGFBP2 insulin-like growth factor binding protein 2, 36kDa [Source:H
12	5217	2.22	-2.55	0.59	PFN2 profilin 2 [Source:HGNC Symbol;Acc:8882]
13	479	2.22	-0.66	0.39	ATP12A ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
14	10135	2.15	-1.34	0.38	NAMPT nicotinamide phosphoribosyltransferase [Source:HGNC Synt
15	7062	2.14	-0.7	0.4	TCHH trichohyalin [Source:HGNC Symbol;Acc:11791]
16	200958	2.1	-1.52	0.57	MUC20 mucin 20, cell surface associated [Source:HGNC Symbol;Acc
17	7296	2.07	-0.96	0.54	TXNRD1 thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
18	493861	2.06	-0.82	0.49	EID3 EP300 interacting inhibitor of differentiation 3 [Source:HGNC
19	10457	2.06	-2.32	0.42	GPNUMB glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
20	2064	2.05	-1.36	0.52	ERBB2 v-erb-b2 avian erythroblastic leukemia viral oncogene homol

## Geneset Overrepresentation

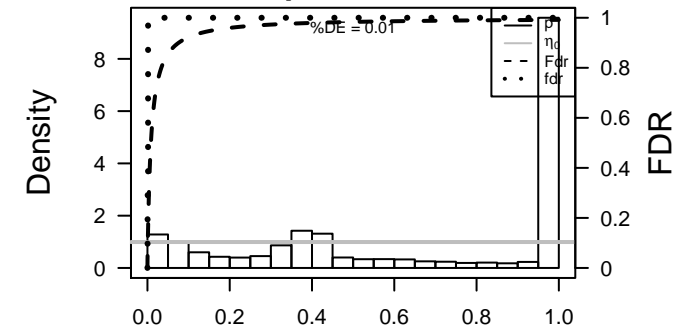
Rank	p-value	#in/all	Geneset
1	2e-11	183 / 3274	CC integral to membrane
2	3e-09	18 / 92	CC tight junction
3	3e-08	48 / 572	Disea GUDJ_psoriasis up
4	7e-08	31 / 296	MF oxidoreductase activity
5	2e-07	141 / 2659	CC plasma membrane
6	3e-07	79 / 1253	BP small molecule metabolic process
7	6e-07	47 / 614	CC endoplasmic reticulum membrane
8	8e-07	104 / 1837	CC membrane
9	8e-07	37 / 434	BP oxidation-reduction process
10	1e-06	34 / 390	BP metabolic process
11	1e-06	9 / 33	BP tight junction assembly
12	3e-06	6 / 13	GSE/ SINGH_NFE2L2_TARGETS
13	4e-06	11 / 57	BP cell-cell junction organization
14	6e-06	18 / 149	BP cellular lipid metabolic process
15	7e-06	6 / 15	GSE/ REACTOME_CHOLESTEROL_BIOSYNTHESIS
16	1e-05	5 / 10	BP response to food
17	1e-05	5 / 10	GSE/ REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOLESTER
18	3e-05	31 / 395	BP transport
19	5e-05	9 / 49	BP fatty acid metabolic process
20	6e-05	5 / 13	H.Tis: WIRTH_Tonsil
21	8e-05	19 / 198	miRN ATGT-302C
22	8e-05	5 / 14	GSE/ KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
23	9e-05	6 / 22	BP response to axon injury
24	1e-04	41 / 621	CC endoplasmic reticulum
25	1e-04	5 / 15	BP pentose-phosphate shunt
26	1e-04	5 / 15	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
27	1e-04	5 / 15	GSE/ WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN
28	1e-04	5 / 15	GSE/ AIGNER_ZEB1_TARGETS
29	1e-04	5 / 15	GSE/ REACTOME_TIGHT_JUNCTION_INTERACTIONS
30	1e-04	7 / 33	BP cholesterol biosynthetic process
31	2e-04	5 / 16	GSE/ KEGG_STEROID_BIOSYNTHESIS
32	2e-04	10 / 71	BP response to nutrient
33	2e-04	7 / 35	miRN hsa-miR-127-3p
34	2e-04	24 / 303	miRN AAGC-218
35	2e-04	8 / 47	miRN hsa-miR-302b*
36	2e-04	15 / 147	CC endosome
37	2e-04	33 / 481	miRN TGCT-15A-16-15B-195-424-497
38	2e-04	5 / 17	BP long-chain fatty-acyl-CoA biosynthetic process
39	2e-04	6 / 26	MF virus receptor activity
40	3e-04	37 / 565	BP transmembrane transport

Overview Map

Spot



p-values





# K-Means Cluster

## Spot Summary: Y

# metagenes = 73  
# genes = 734

<r> metagenes = 0.88  
<r> genes = 0.2  
beta: r2= 3.43 / log p= -Inf

# samples with spot = 10 ( 3.6 % )  
Atypical : 1 ( 1.4 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 2 ( 2.4 % )  
Basal : 6 ( 7.1 % )

## Spot Genelist

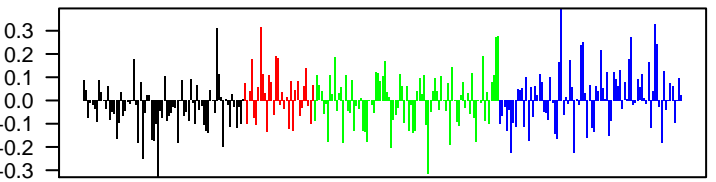
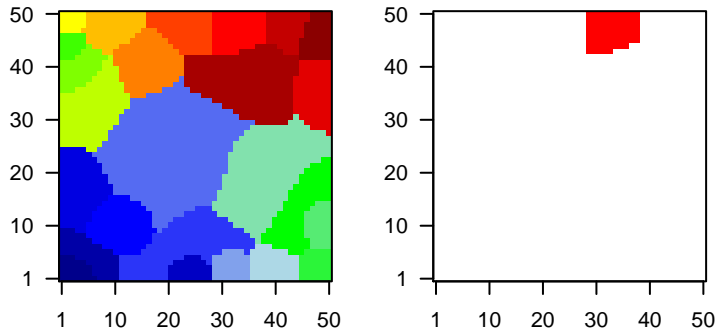
Rank	ID	max e	r	min e	Description
					Symbol
1	55915	1.8	-0.75	0.34	LANCL2 LanC lantibiotic synthetase component C-like 2 (bacterial) [S
2	5321	1.65	-0.85	0.46	PLA2G4A phospholipase A2, group IVA (cytosolic, calcium-dependent)
3	1207	1.52	-1.35	0.49	CLNS1A chloride channel, nucleotide-sensitive, 1A [Source:HGNC Sy
4	54802	1.51	-0.79	0.47	TRIT1 tRNA isopentenyltransferase 1 [Source:HGNC Symbol;Acc:21
5	144363	1.49	-0.94	0.49	LYRM5 LYR motif containing 5 [Source:HGNC Symbol;Acc:27052]
6	100093630	1.47	-1.34	0.27	SNHG8 small nucleolar RNA host gene 8 (non-protein coding) [Sour
7	84833	1.42	-0.97	0.4	USMG5 up-regulated during skeletal muscle growth 5 homolog (mous
8	5723	1.39	-0.48	0.53	PSPH phosphoserine phosphatase [Source:HGNC Symbol;Acc:957
9	5423	1.39	-1.04	0.26	POLB polymerase (DNA directed), beta [Source:HGNC Symbol;Acc
10	401505	1.36	-0.87	0.59	TOMM5 translocase of outer mitochondrial membrane 5 homolog (yea
11	51142	1.36	-0.79	0.45	CHCHD2coiled-coil-helix-coiled-coil-helix domain containing 2 [Sour
12	139886	1.35	-1.31	0.32	SPIN4 spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
13	55848	1.34	-0.94	0.45	PLGRKT plasminogen receptor, C-terminal lysine transmembrane prot
14	388722	1.27	-0.85	0.53	C1orf53 chromosome 1 open reading frame 53 [Source:HGNC Symbc
15	51504	1.25	-0.91	0.45	TRMT112RNA methyltransferase 11-2 homolog (S. cerevisiae) [Sourc
16	3301	1.23	-1.12	0.29	DNAJA1 DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGNC
17	6154	1.21	-0.73	0.6	RPL26 ribosomal protein L26 [Source:HGNC Symbol;Acc:10327]
18	57001	1.21	-0.8	0.6	ACN9 ACN9 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:21
19	27257	1.21	-0.84	0.36	LSM1 LSM1 homolog, U6 small nuclear RNA associated (S. cerevis
20	6160	1.2	-0.91	0.56	RPL31 ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-37	165 / 1318	CC mitochondrion
2	5e-26	58 / 253	BP translation
3	2e-24	44 / 153	MF structural constituent of ribosome
4	1e-23	33 / 83	BP respiratory electron transport chain
5	9e-22	58 / 304	CC mitochondrial inner membrane
6	6e-20	41 / 167	CC ribosome
7	5e-19	124 / 1233	TF KIM_MYC targets
8	7e-19	38 / 152	BP cellular metabolic process
9	2e-18	82 / 649	BP gene expression
10	8e-16	48 / 287	BP viral process
11	2e-15	29 / 109	BP SRP-dependent cotranslational protein targeting to membrane
12	2e-13	24 / 87	BP translational termination
13	3e-13	40 / 242	BP RNA metabolic process
14	3e-13	23 / 81	BP viral transcription
15	8e-13	24 / 92	BP translational elongation
16	1e-12	28 / 128	BP translational initiation
17	3e-12	26 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
18	6e-12	36 / 219	BP mRNA metabolic process
19	6e-12	23 / 92	BP viral life cycle
20	6e-11	63 / 595	MF RNA binding
21	7e-11	55 / 482	BP cellular protein metabolic process
22	1e-10	14 / 36	CC mitochondrial respiratory chain complex I
23	8e-10	13 / 34	MF NADH dehydrogenase (ubiquinone) activity
24	9e-10	11 / 23	CC mitochondrial ribosome
25	1e-09	13 / 35	BP mitochondrial electron transport, NADH to ubiquinone
26	3e-09	15 / 51	CC cytosolic large ribosomal subunit
27	3e-08	7 / 10	CC large ribosomal subunit
28	3e-08	9 / 19	CC mitochondrial proton-transporting ATP synthase complex
29	7e-07	23 / 163	BP mRNA splicing, via spliceosome
30	9e-07	9 / 26	MF cytochrome-c oxidase activity
31	1e-06	7 / 15	BP ATP synthesis coupled proton transport
32	2e-06	51 / 579	CC nucleolus
33	2e-06	7 / 16	Canc GENTLES_modul10
34	3e-06	6 / 11	Canc GENTLES_modul5
35	3e-06	6 / 11	MMM MACIEJ_MMML_49
36	4e-06	16 / 96	BP rRNA processing
37	9e-06	6 / 13	GSE/ REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
38	2e-05	6 / 14	BP mitochondrial ATP synthesis coupled proton transport
39	2e-05	5 / 9	GSE/ REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBUNITS
40	2e-05	5 / 9	GSE/ REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_RIBOS

Overview Map

Spot



p-values

