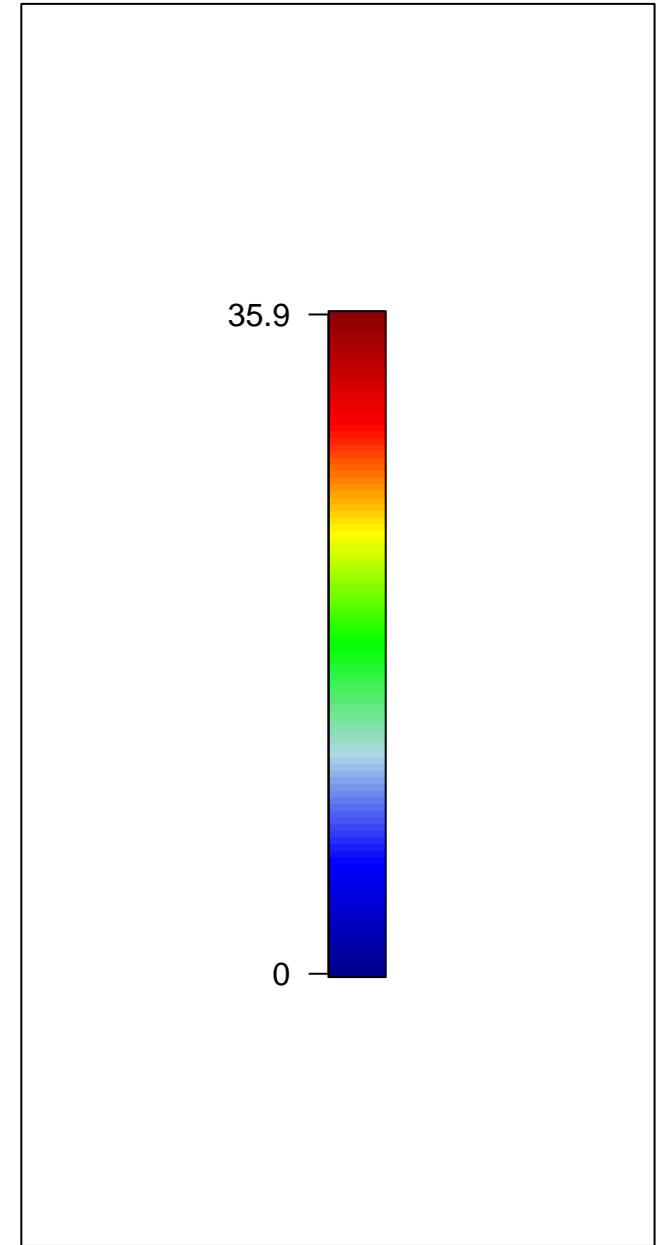
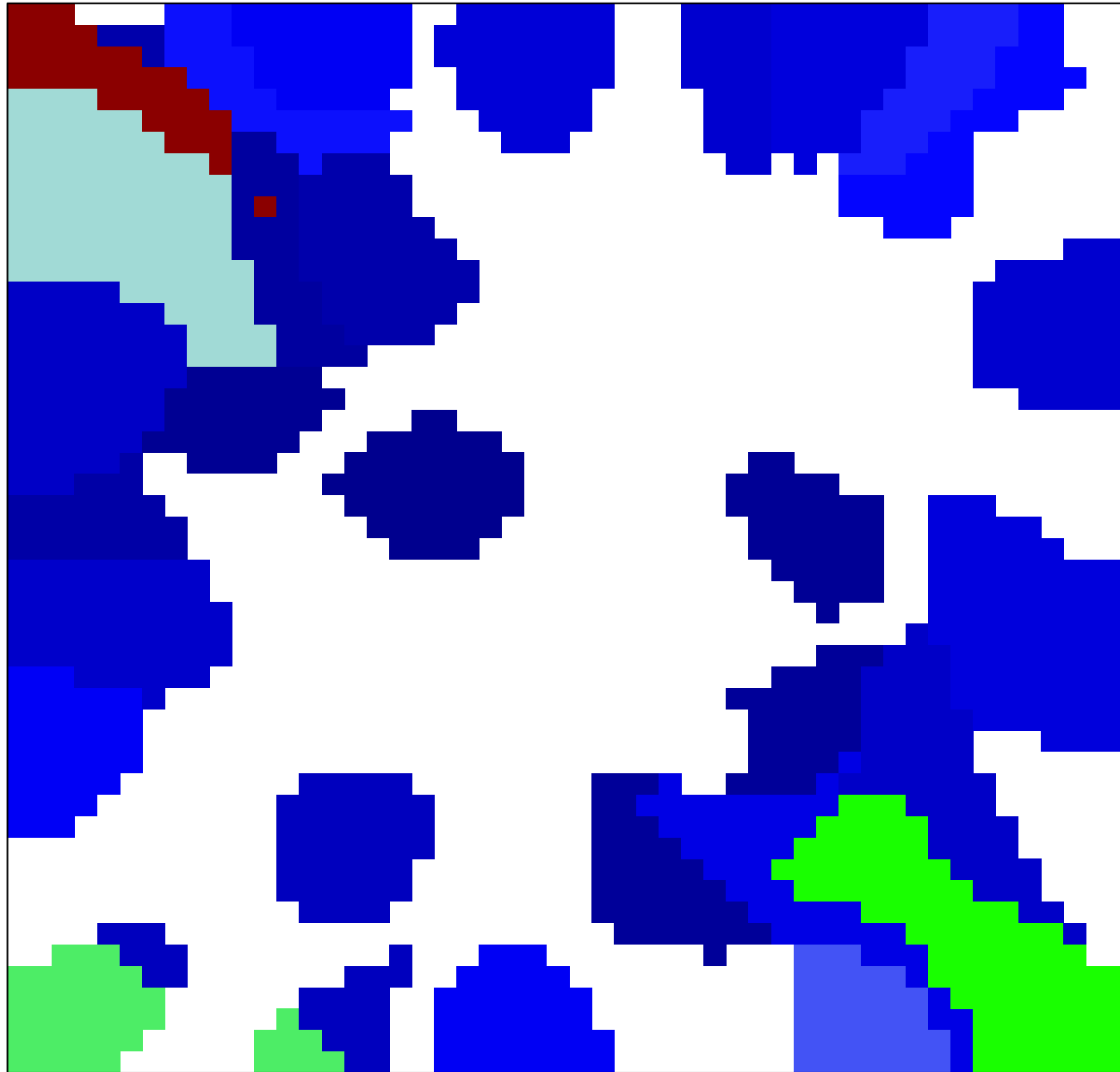


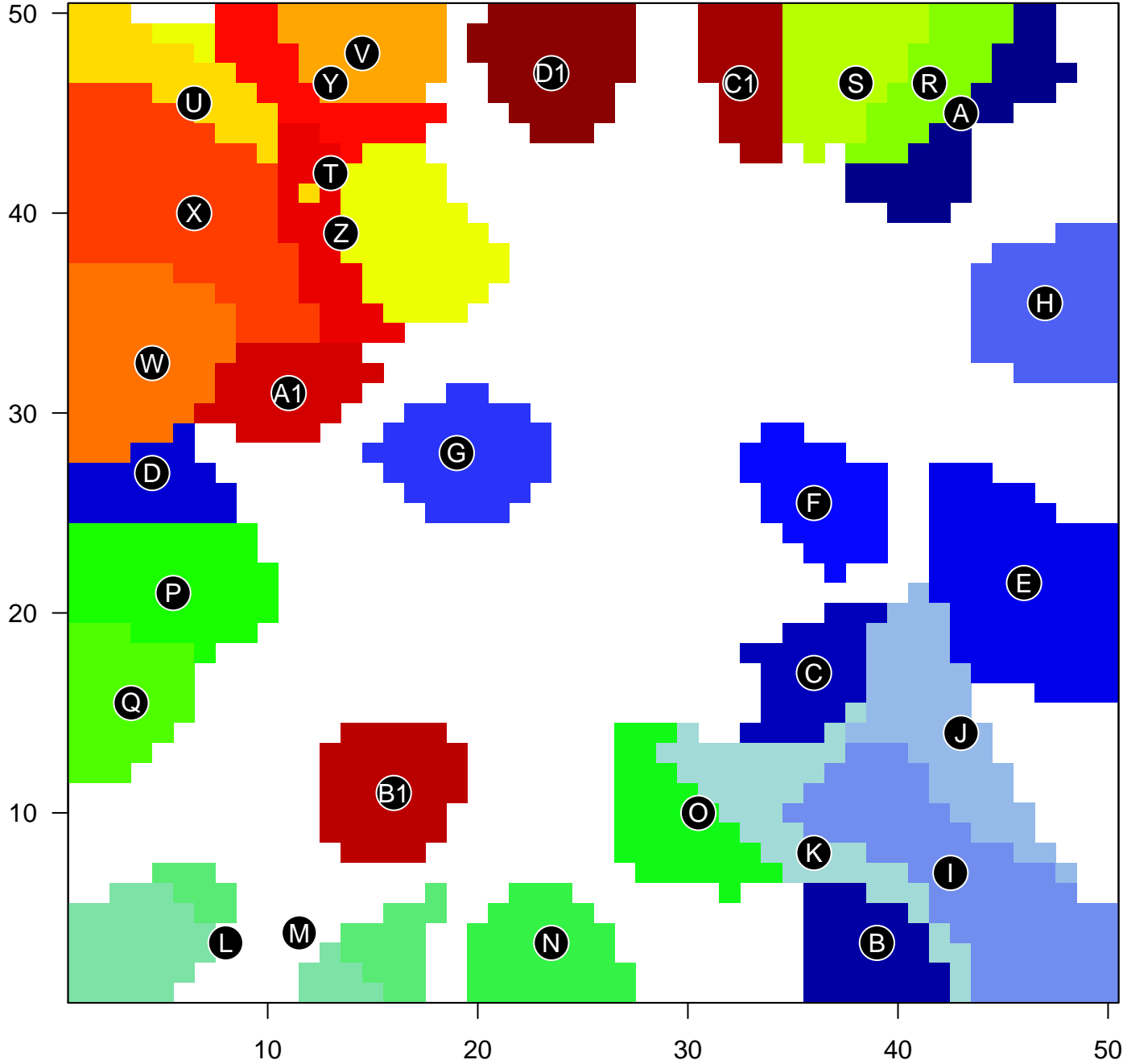
# Correlation Cluster

beta-scores



# Correlation Cluster

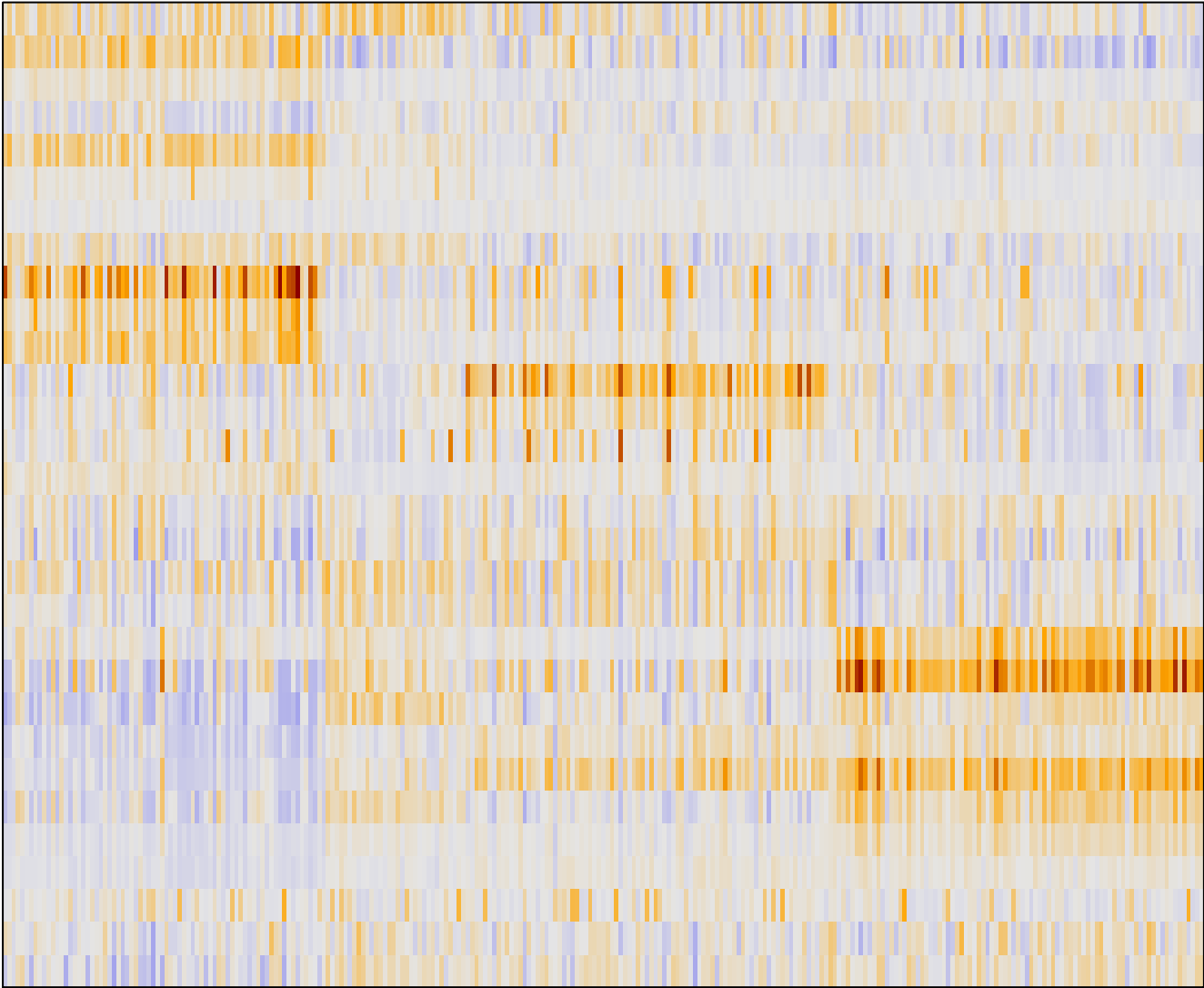
annotation



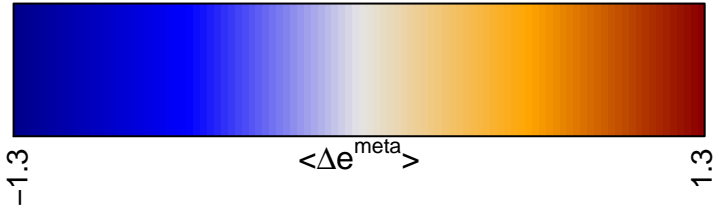
- A ■ DNA replication  
mitotic cell cycle  
Lembcke\_Normal vs Adenoma
- B ■ Chr 19  
DNA binding  
SPIRA\_SMOKERS\_LUNG\_CANCER\_DN
- C ■ Chr 19  
nucleic acid binding  
NIKOLSKY\_BREAST\_CANCER\_19Q13.1\_AMPLICON
- D ■ hsa-miR-631  
hsa-miR-331-3p  
willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up
- E ■ DNA binding  
transcription, DNA-templated  
regulation of transcription, DNA-dependent
- F ■ willscher\_GBM\_Verhaak-PNmut\_expression\_G\_down  
cilium  
axoneme
- G ■ G-protein coupled receptor activity  
G-protein coupled receptor signaling pathway  
olfactory receptor activity
- H ■ RNA binding  
hsa-miR-543  
nucleus
- I ■ WIRTH\_Immune system  
Lembcke\_Colonc Inflammation  
immune response
- J ■ Chr 3  
translational termination  
translational initiation
- K ■ activation of signaling protein activity involved in unfolded pr  
endoplasmic reticulum unfolded protein response  
SPANG\_CD40 6hrs DN
- L ■ LENZ\_Stromal signature 1  
extracellular matrix organization  
extracellular matrix
- M ■ camera-type eye morphogenesis  
Christensen\_hypermethylated\_in\_primary\_glioblastoma  
dendrite
- N ■ WIRTH\_Muscle  
muscle filament sliding  
structural constituent of muscle
- O ■ plasma membrane  
inflammatory response  
signal transduction
- P ■ Chr 19



A  
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R  
S  
T  
U  
V  
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Z  
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B1  
C1  
D1

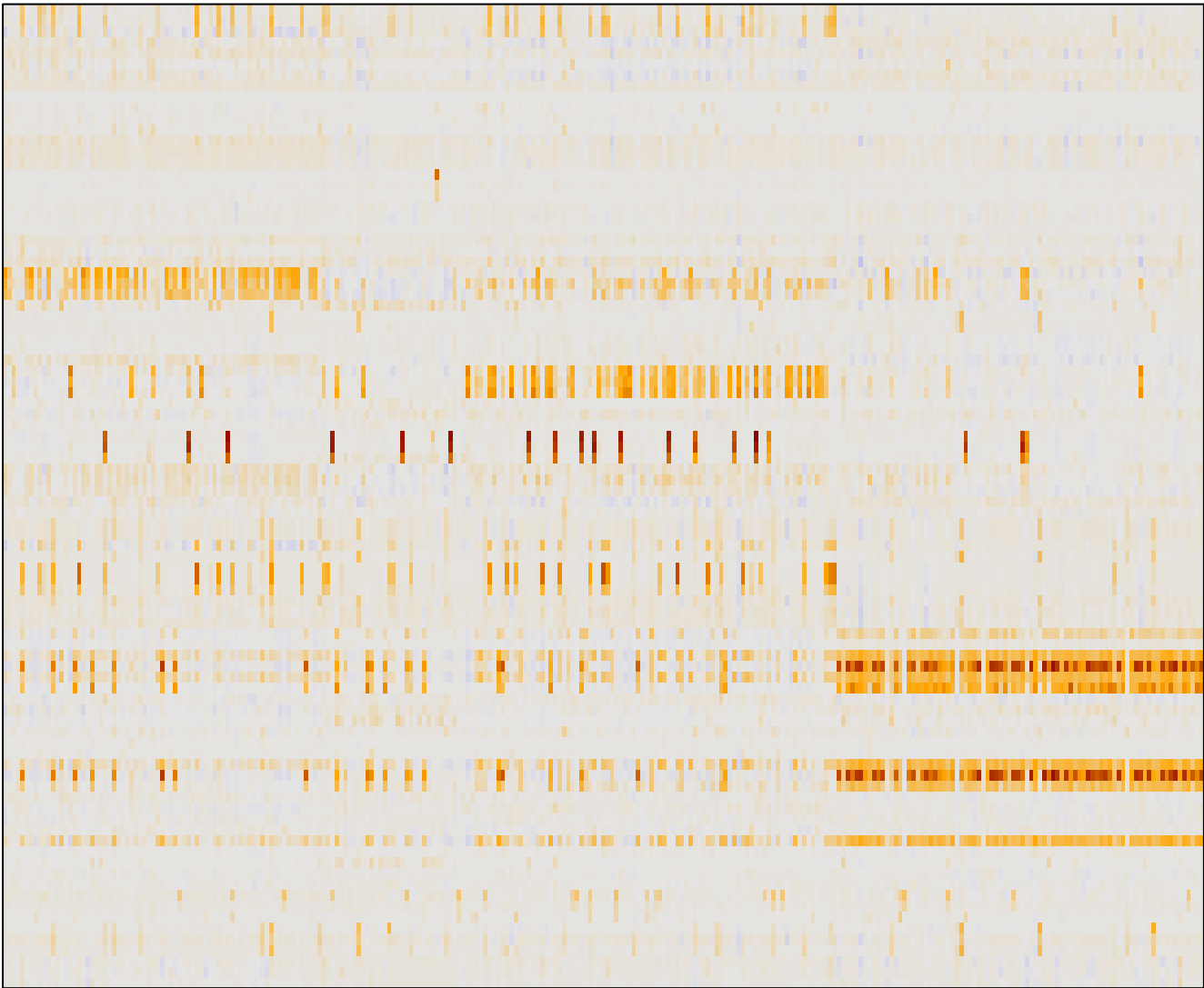


- DNA replication
- Lamblocke\_Normal vs Adenoma
- Chr19
- SPRA\_SMOKERS\_LUNG\_CANCER\_DN
- middle acid binding
- NIKOLSKY\_BREAST\_CANCER\_19Q13.1\_AMPLICON
- hsa-miR-631-3p
- willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up
- DNA binding DNA templated
- regulation of transcription, DNA-dependent
- willscher\_GBM\_Verhaak-PNmut\_expression\_G\_down
- axlme
- G-protein coupled receptor activity
- olfactory receptor activity
- RNA binding
- hsa-miR-543
- WIRTF\_Immune system
- immune response
- inflammation
- Chr3
- translational termination
- activation of signaling protein activity involved in unfolded protein response
- SPANIS\_CD47\_815\_DN
- LENZ\_Stromal signature 1
- extracellular matrix organization
- camera-type eye morphogenesis
- primary\_glioblastoma
- hypermethylated
- dentrite
- muscle fiber sliding
- muscle fiber
- structural constituent of muscle
- plasma membrane
- signal transduction
- Chr19
- mitochondrion
- mitochondrion
- Lamblocke\_Normal vs Adenoma
- structural constituent of ribosome
- willscher\_GBM\_Verhaak-PN\_expression\_C\_up
- mitotic cell cycle
- mitochondrion
- gene expression
- keratin filament
- epithelial cell metabolic process
- WIRTF\_Mucosa
- epithelial cell
- cornified envelope
- Chr4
- reductase activity
- SINCH1\_NFE2L2\_TARGETS
- Chr16
- some organization
- ribosome
- GLD1\_pсориаз up
- epidermis development
- hair function
- hair function organization
- Chr15
- lipid catabolic process
- hydrolase activity, acting on ester bonds
- anterior/posterior axis specification
- Wnt signaling pathway
- ChrX
- ChrY
- Testis
- respiratory electron transport chain
- structural constituent of ribosome
- hsa-miR-648p
- hsa-miR-348

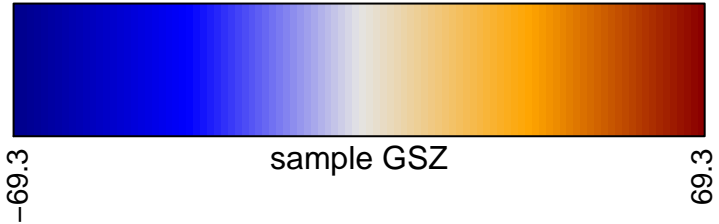




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V  
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X  
Y  
Z  
A1  
B1  
C1  
D1



- DNA replication
- Lam Locke\_Normal vs Adenoma
- Chr 19
- SPRINGER SMOKERS\_LUNG\_CANCER\_DN
- nucleic acid binding
- NIKOLSKY\_BREAST\_CANCER\_19Q13.1\_AMPLICON
- hsa-miR-631
- Willscher\_GBM\_Verhaak-PNwt\_expression\_J\_up
- DNA binding DNA templated
- regulation of transcription, DNA-dependent
- Willscher\_GBM\_Verhaak-PNmut\_expression\_G\_down
- axillim
- G-protein coupled receptor activity
- translational elongation of signaling pathway
- translational elongation
- RNA binding
- hsa-miR-543
- WIRTF\_Immune system
- Lam Locke\_Coloring inflammation
- immune response
- Chr 3
- translational termination
- activation of signaling protein activity involved in unfolded protein response
- SPANG\_CD40\_8hrs\_DN
- LENY\_Stromal signature 1
- extracellular matrix organization
- camera-type eye morphogenesis
- Carnstensen\_hypermethylated\_1h\_glioblastoma
- genome
- muscle filament sliding
- structural constituent of muscle
- plasma membrane
- signal transduction
- Chr 19
- mitochondrion
- Lam Locke\_Normal vs Adenoma
- structural constituent of ribosome
- Willscher\_GBM\_Verhaak-PN\_expression\_C\_up
- mitotic cell cycle
- mitochondrion
- gene expression
- keratin filament
- skin\_diloid metabolic process
- WIRTF\_purpura up
- cornified envelope
- Chr 6 reductase activity
- SINGH\_NFE2L2\_TARGETS
- Chr 16
- endosome organization
- endosome
- GLD1\_poriasis up
- WIRTF\_Mucosa
- epidermis development
- light refraction organization
- Chr 15
- lipid catabolic process
- hydrolase activity, acting on ester bonds
- anterior/posterior axis specification
- Wnt signaling pathway
- Chr X
- WIRTF\_Testis
- Chr Y
- respiratory electron transport chain
- structural constituent of ribosome
- hsa-miR-548p
- hsa-miR-348



# Correlation Cluster

## Spot Summary: A

# metagenes = 38  
# genes = 284

<r> metagenes = 0.93  
<r> genes = 0.29  
beta: r2= 6.15 / log p= -Inf

# samples with spot = 44 ( 16 % )  
Atypical : 21 ( 28.4 % )  
Classical : 8 ( 25 % )  
Mesenchymal : 14 ( 16.5 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

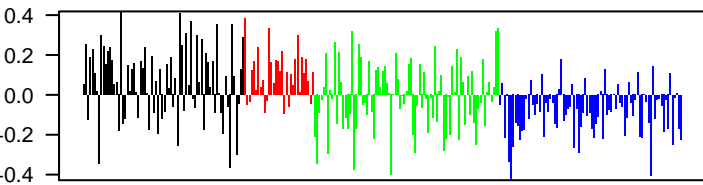
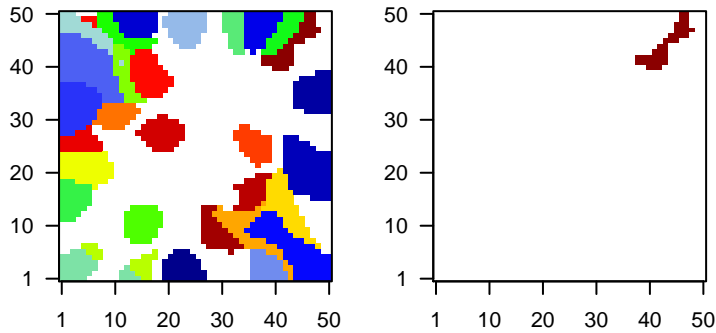
Rank	ID	max e	r	min e	Description
					Symbol
1	84223	2.16	-1.59	0.38	IQCG IQ motif containing G [Source:HGNC Symbol;Acc:25251]
2	10388	1.89	-0.59	0.6	SYCP2 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
3	9355	1.77	-0.89	0.57	LHX2 LIM homeobox 2 [Source:HGNC Symbol;Acc:6594]
4	86	1.75	-1.06	0.84	ACTL6A actin-like 6A [Source:HGNC Symbol;Acc:24124]
5	5984	1.72	-1.26	0.89	RFC4 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syr
6	116832	1.7	-1.8	0.61	RPL39L ribosomal protein L39-like [Source:HGNC Symbol;Acc:17094
7	55190	1.67	-1.07	0.39	NUDT11 nudix (nucleoside diphosphate linked moiety X)-type motif 11
8	4171	1.63	-1.4	0.8	MCM2 minichromosome maintenance complex component 2 [Source
9	3191	1.62	-1.54	0.22	HNRNPLheterogeneous nuclear ribonucleoprotein L [Source:HGNC S;
10	51087	1.62	-0.89	0.61	YBX2 Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
11	55832	1.61	-0.79	0.45	CAND1 cullin-associated and neddylation-dissociated 1 [Source:HGI
12	113802	1.6	-1.54	0.47	HENMT1HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:HC
13	7037	1.59	-1.54	0.65	TFRC transferrin receptor [Source:HGNC Symbol;Acc:11763]
14	494514	1.59	-1.17	0.51	C18orf56chromosome 18 open reading frame 56 [Source:HGNC Synt
15	7298	1.58	-1.36	0.71	TYMS thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
16	3148	1.55	-1.13	0.7	HMGB2 high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
17	9070	1.51	-0.85	0.32	ASH2L ash2 (absent, small, or homeotic)-like (Drosophila) [Source:+
18	79682	1.5	-1.27	0.57	CENPU centromere protein U [Source:HGNC Symbol;Acc:21348]
19	116028	1.49	-1.31	0.68	RM12 RecQ mediated genome instability 2 [Source:HGNC Symbol;
20	11073	1.45	-0.94	0.77	TOPBP1 topoisomerase (DNA) II binding protein 1 [Source:HGNC Syr

## Geneset Overrepresentation

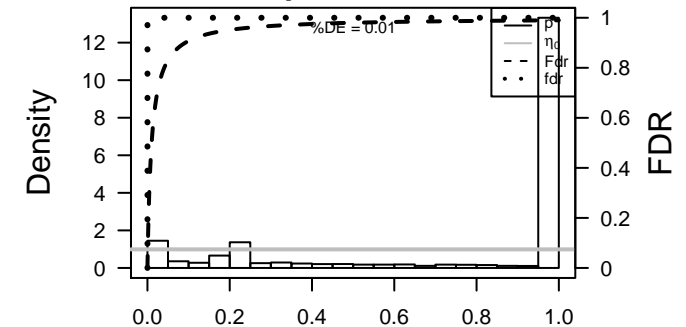
Rank	p-value	#in/all	Geneset
1	2e-35	39 / 149	BP DNA replication
2	1e-23	43 / 370	BP mitotic cell cycle
3	2e-22	49 / 530	Cancer_Lembcke_Normal vs Adenoma
4	6e-22	28 / 142	Glio_willscher_GBM_Verhaak-CL_expression_C_up
5	6e-22	28 / 142	Glio_willscher_GBM_Verhaak-PNmut_expression_C_down
6	5e-21	63 / 949	CC nucleoplasm
7	2e-17	14 / 30	BP DNA strand elongation involved in DNA replication
8	1e-16	32 / 298	BP DNA repair
9	2e-14	140 / 4640	CC nucleus
10	1e-12	8 / 11	GSE/ KALMA_E2F1_TARGETS
11	1e-12	13 / 49	BP telomere maintenance
12	3e-11	9 / 21	BP telomere maintenance via semi-conservative replication
13	4e-11	8 / 15	GSE/ KEGG_DNA_REPLICATION
14	5e-11	9 / 22	BP DNA replication initiation
15	8e-11	8 / 16	GSE/ EGUCHI_CELL_CYCLE_RB1_TARGETS
16	8e-11	8 / 16	GSE/ SONG_TARGETS_OF_IE86_CMV_PROTEIN
17	8e-11	8 / 16	GSE/ REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
18	1e-10	9 / 24	BP telomere maintenance via recombination
19	5e-10	66 / 1749	MF DNA binding
20	7e-10	17 / 148	BP G1/S transition of mitotic cell cycle
21	4e-09	7 / 16	GSE/ VERNELL_RETINOBLASTOMA_PATHWAY_UP
22	4e-09	7 / 16	GSE/ FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
23	4e-09	7 / 16	GSE/ BIOCARTA_MCM_PATHWAY
24	4e-09	7 / 16	GSE/ REACTOME_DNA_STRAND_ELONGATION
25	1e-08	6 / 11	GSE/ REACTOME_UNWINDING_OF_DNA
26	7e-08	6 / 14	GSE/ REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE
27	8e-08	5 / 8	GSE/ REACTOME_DNA_REPLICATION_PRE_INITIATION
28	1e-07	6 / 15	GSE/ REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION
29	1e-07	6 / 15	GSE/ REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES_LONG_E
30	1e-07	7 / 24	MF DNA helicase activity
31	2e-07	6 / 16	GSE/ REACTOME_G2_M_CHECKPOINTS
32	2e-07	6 / 16	GSE/ REACTOME_LAGGING_STRAND_SYNTHESIS
33	3e-07	5 / 10	GSE/ REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE_FROM_THE_E
34	4e-07	6 / 18	BP nucleotide-excision repair, DNA gap filling
35	6e-07	17 / 232	BP mitosis
36	8e-07	11 / 96	BP DNA recombination
37	8e-07	28 / 579	CC nucleolus
38	1e-06	37 / 914	Chr Chr 3
39	1e-06	10 / 82	CC chromosome
40	1e-06	177 / 8023	MF protein binding

Overview Map

Spot



p-values





# Correlation Cluster

## Spot Summary: B

# metagenes = 34  
# genes = 397

<r> metagenes = 0.96  
<r> genes = 0.39  
beta: r2= 8.32 / log p= -Inf

# samples with spot = 49 ( 17.8 % )  
Atypical : 33 ( 44.6 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 9 ( 10.6 % )  
Basal : 5 ( 6 % )

## Spot Genelist

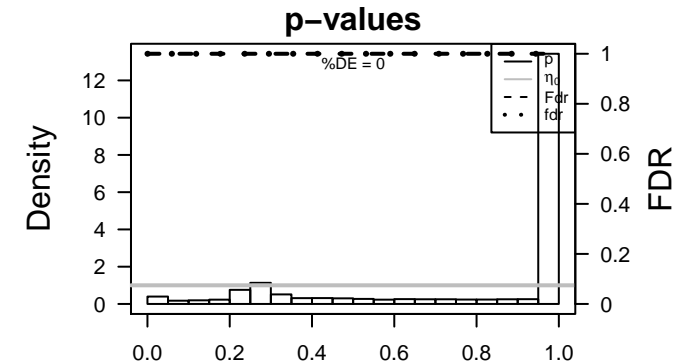
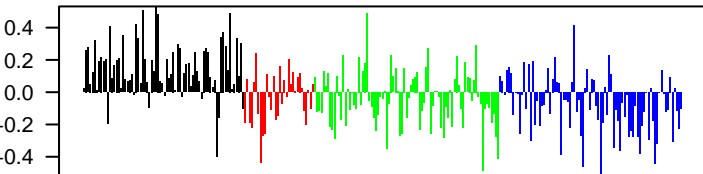
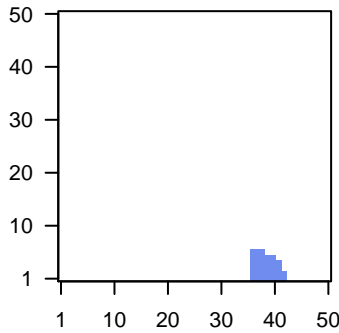
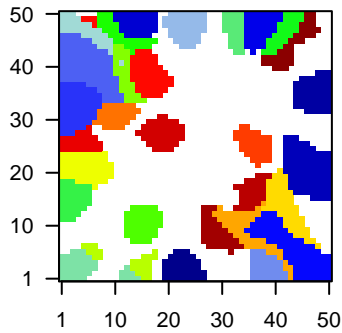
Rank	ID	max e	r	min e	Description
1	125050	2.79	-0.87	0.28	RN7SK RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
2	84061	1.78	-1.53	0.84	MAGT1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
3	126205	1.77	-1.63	0.93	NLRP8 NLR family, pyrin domain containing 8 [Source:HGNC Symbo
4	51326	1.73	-1.07	0.41	ARL17B ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc
5	401261	1.68	-0.87	0.83	
6	79058	1.66	-1.01	0.63	ASPSCR1alveolar soft part sarcoma chromosome region, candidate 1 [
7	618	1.64	-1.41	0.41	BCYRN1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
8	400818	1.62	-1.99	0.69	AC23981Nuroblastoma breakpoint family member 1 [Source:UniProt
9	29944	1.58	-0.69	0.61	PNMA3 paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187
10	4851	1.57	-1.35	0.44	NOTCH1 notch 1 [Source:HGNC Symbol;Acc:7881]
11	25862	1.53	-1.56	0.93	USP49 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
12	136051	1.51	-1.26	0.92	ZNF786 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
13	23466	1.49	-1.42	0.45	CBX6 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
14	85452	1.49	-1.23	0.78	C1orf222chromosome 1 open reading frame 222 [Source:HGNC Synt
15	9647	1.49	-0.85	0.5	PPM1F protein phosphatase, Mg2+/Mn2+ dependent, 1F [Source:HG
16	55876	1.48	-0.91	0.71	GSDMB gasdermin B [Source:HGNC Symbol;Acc:23690]
17	80224	1.47	-1.22	0.9	NUBPL nucleotide binding protein-like [Source:HGNC Symbol;Acc:20
18	375775	1.46	-0.65	0.63	PNPLA7 patatin-like phospholipase domain containing 7 [Source:HG
19	4249	1.45	-1.15	0.53	MGAT5 mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glu
20	728903	1.45	-1.04	0.66	

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-08	56 / 1135	Chr Chr 19
2	3e-06	69 / 1749	MF DNA binding
3	2e-04	4 / 13	GSE/ SPIRA_SMOKERS_LUNG_CANCER_DN
4	2e-04	4 / 13	GSE/ ST_GAQ_PATHWAY
5	2e-04	4 / 14	MMM MACIEJ_MMML 8
6	7e-04	37 / 940	MF nucleic acid binding
7	9e-04	5 / 34	MF hydrolase activity, hydrolyzing O-glycosyl compounds
8	2e-03	3 / 12	GSE/ CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
9	2e-03	3 / 12	GSE/ KEGG_SULFUR_METABOLISM
10	2e-03	3 / 12	GSE/ BIOCARTA_HDAC_PATHWAY
11	2e-03	130 / 4640	CC nucleus
12	3e-03	3 / 13	GSE/ BIOCARTA_MEF2D_PATHWAY
13	3e-03	2 / 4	GSE/ BIOCARTA_CYTOKINE_PATHWAY
14	3e-03	52 / 1574	BP transcription, DNA-templated
15	4e-03	3 / 15	GSE/ WANG_CLIM2_TARGETS_UP
16	4e-03	3 / 15	GSE/ NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON
17	5e-03	3 / 16	GSE/ HAMAL_APOPTOSIS_VIA_TRAIL_UP
18	5e-03	3 / 16	GSE/ REACTOME_SIGNALLING_BY_NGF
19	5e-03	3 / 16	GSE/ REACTOME_TRKA_SIGNALLING_FROM_THE_PLASMA_MEMBRANE
20	6e-03	28 / 743	Chr Chr 7
21	7e-03	2 / 6	GSE/ KAUFFMANN_MELANOMA_RELAPSE_DN
22	8e-03	3 / 19	BP sprouting angiogenesis
23	1e-02	2 / 7	GSE/ KEGG_STEROID_HORMONE_BIOSYNTHESIS
24	1e-02	4 / 38	MF methylated histone residue binding
25	1e-02	2 / 8	GSE/ BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
26	1e-02	2 / 8	GSE/ REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
27	1e-02	6 / 88	miRN hsa-miR-423-5p
28	2e-02	3 / 24	CC Cui3-RING ubiquitin ligase complex
29	2e-02	3 / 24	BP negative regulation of T cell proliferation
30	2e-02	31 / 918	Chr Chr 17
31	2e-02	4 / 44	BP meiosis
32	2e-02	4 / 44	BP response to ionizing radiation
33	2e-02	5 / 67	BP glucose homeostasis
34	2e-02	5 / 67	miRN hsa-miR-326
35	2e-02	3 / 25	MF ARF GTPase activator activity
36	2e-02	4 / 45	BP circadian rhythm
37	2e-02	11 / 238	miRN hsa-miR-214
38	2e-02	3 / 26	BP regulation of ARF GTPase activity
39	2e-02	2 / 10	BP negative regulation of cell-substrate adhesion
40	2e-02	2 / 10	MF RNA polymerase II core binding

## Overview Map

## Spot



Chr1 p-value #in/all Geneset #in/all description

Chr2 p-value #in/all Geneset #in/all description

Chr3 p-value #in/all Geneset #in/all description

Chr4 p-value #in/all Geneset #in/all description

Chr5 p-value #in/all Geneset #in/all description

Chr6 p-value #in/all Geneset #in/all description

Cancer p-value #in/all Geneset #in/all description

Disease p-value #in/all Geneset #in/all description

TISS p-value #in/all Geneset #in/all description

MIRNA TARGET p-value #in/all Geneset #in/all description

MIRNA TARGET STABLE p-value #in/all Geneset #in/all description

Pathw Act p-value #in/all Geneset #in/all description

Chk p-value #in/all Geneset #in/all description

Chlo p-value #in/all Geneset #in/all description

Lymphoma p-value #in/all Geneset #in/all description

MIRNA LIASEASE p-value #in/all Geneset #in/all description

MIRNA LIASEASE STABLE p-value #in/all Geneset #in/all description

LISSUE p-value #in/all Geneset #in/all description



# Correlation Cluster

## Spot Summary: C

# metagenes = 31  
# genes = 124

<r> metagenes = 0.94  
<r> genes = 0.19  
beta: r2= 0.79 / log p= -Inf

# samples with spot = 6 ( 2.2 % )  
Atypical : 6 ( 8.1 % )

## Spot Genelist

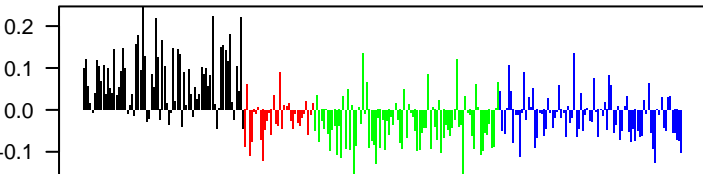
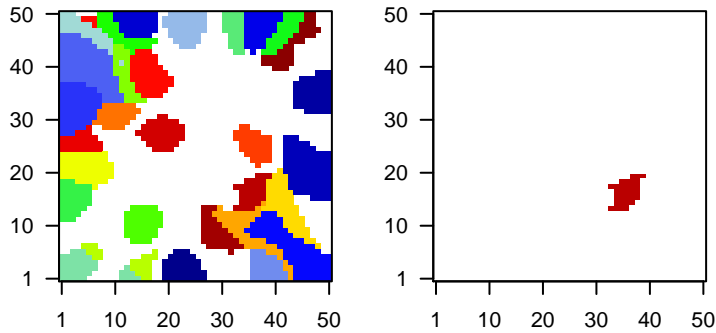
Rank	ID	max e	r	min e	Description
					Symbol
1	126668	1.06	-0.34	0.39	TDRD10 tudor domain containing 10 [Source:HGNC Symbol;Acc:2531
2	128866	1.06	-0.62	0.22	CHMP4Bcharged multivesicular body protein 4B [Source:HGNC Symb
3	3275	1.01	-0.8	0.45	PRMT2 protein arginine methyltransferase 2 [Source:HGNC Symbol;f
4	115399	0.98	-0.49	0.5	LRRCS6 leucine rich repeat containing 56 [Source:HGNC Symbol;Acc:
5	57185	0.85	-0.71	0.49	NIPAL3 NIPA-like domain containing 3 [Source:HGNC Symbol;Acc:2f
6	374977	0.84	-0.33	0.32	MROH7 maestro heat-like repeat family member 7 [Source:HGNC Sy
7	125875	0.81	-0.52	0.42	CLDND2 claudin domain containing 2 [Source:HGNC Symbol;Acc:285
8	55756	0.81	-0.58	0.45	INTS9 integrator complex subunit 9 [Source:HGNC Symbol;Acc:255
9	7920	0.8	-0.58	0.29	ABHD16Abhydrolase domain containing 16A [Source:HGNC Symbol;f
10	338440	0.8	-0.42	0.46	ANO9 anoctamin 9 [Source:HGNC Symbol;Acc:20679]
11	649446	0.79	-0.47	0.32	DLGAP1-DL3AP1 antisense RNA 1 [Source:HGNC Symbol;Acc:3167f
12	645644	0.77	-0.56	0.38	RP11-20I23.13
13	100287569	0.76	-0.23	0.51	LINC00170 long intergenic non-protein coding RNA 173 [Source:HGNC :
14	55049	0.75	-0.42	0.55	C19orf60 chromosome 19 open reading frame 60 [Source:HGNC Synt
15	9798	0.74	-0.76	0.26	IST1 increased sodium tolerance 1 homolog (yeast) [Source:HGNC
16	9501	0.74	-0.33	0.25	RPH3AL rabphilin 3A-like (without C2 domains) [Source:HGNC Symb
17	197258	0.73	-0.55	0.56	FUK fucokinase [Source:HGNC Symbol;Acc:29500]
18	148413	0.73	-0.78	0.5	
19	79159	0.71	-0.69	0.44	NOL12 nucleolar protein 12 [Source:HGNC Symbol;Acc:28585]
20	6667	0.71	-0.57	0.5	SP1 Sp1 transcription factor [Source:HGNC Symbol;Acc:11205]

## Geneset Overrepresentation

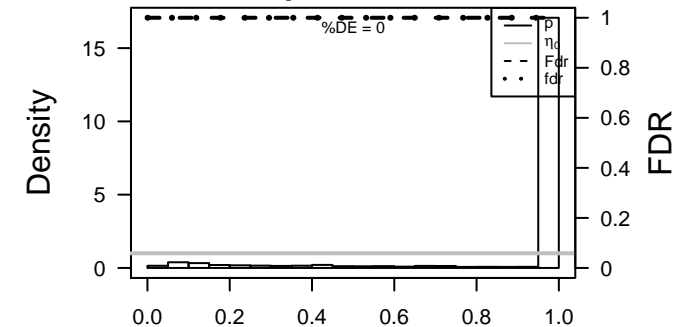
Rank	p-value	#in/all	Geneset
1	2e-04	20 / 1135	Chr Chr 19
2	2e-03	16 / 940	MF nucleic acid binding
3	3e-03	2 / 12	GSE# NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON
4	3e-03	2 / 12	GSE# SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
5	3e-03	24 / 1820	MF metal ion binding
6	5e-03	2 / 15	BP histone H4-K5 acetylation
7	5e-03	2 / 15	BP histone H4-K8 acetylation
8	5e-03	2 / 15	GSE# O'DONNELL_METASTASIS_UP
9	6e-03	3 / 50	MF Rab GTPase binding
10	6e-03	2 / 16	GSE# RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
11	6e-03	2 / 16	GSE# WILLERT_WNT_SIGNALING
12	8e-03	2 / 18	CC histone acetyltransferase complex
13	8e-03	2 / 18	MF protein methyltransferase activity
14	9e-03	2 / 19	BP maternal process involved in female pregnancy
15	9e-03	2 / 19	BP negative regulation of G1/S transition of mitotic cell cycle
16	1e-02	4 / 113	BP transforming growth factor beta receptor signaling pathway
17	1e-02	2 / 21	miRN hsa-miR-1288
18	1e-02	2 / 22	MF N-acetyltransferase activity
19	1e-02	3 / 65	miRN hsa-miR-1275
20	1e-02	2 / 24	BP protein methylation
21	2e-02	2 / 26	MF thyroid hormone receptor binding
22	2e-02	2 / 26	miRN miR-21
23	2e-02	2 / 28	miRN hsa-miR-597
24	2e-02	3 / 76	miRN hsa-miR-1321
25	2e-02	2 / 29	miRN hsa-miR-1225-3p
26	2e-02	2 / 29	miRN hsa-miR-296-5p
27	2e-02	5 / 216	MF transcription coactivator activity
28	2e-02	7 / 386	Chr Chr 22
29	3e-02	4 / 151	miRN hsa-miR-518a-5p
30	3e-02	2 / 34	BP extrinsic apoptotic signaling pathway
31	3e-02	2 / 34	miRN hsa-miR-555
32	3e-02	3 / 88	miRN hsa-miR-1265
33	3e-02	4 / 155	miRN hsa-miR-527
34	3e-02	2 / 37	MF androgen receptor binding
35	3e-02	2 / 38	Lymp ROSOLOWSKI_blue DOWN
36	3e-02	5 / 241	miRN hsa-miR-122
37	3e-02	2 / 39	MF histone acetyltransferase activity
38	4e-02	2 / 40	BP histone H3 acetylation
39	4e-02	2 / 40	MF phosphatase binding
40	4e-02	3 / 99	miRN hsa-miR-147

Overview Map

Spot



p-values





# Correlation Cluster

## Spot Summary: D

# metagenes = 27  
# genes = 118

<r> metagenes = 0.95  
<r> genes = 0.19  
beta: r2= 1.41 / log p= -Inf

# samples with spot = 6 ( 2.2 % )  
Atypical : 1 ( 1.4 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

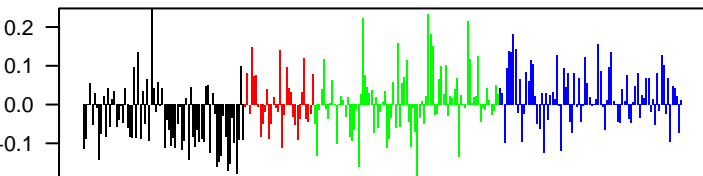
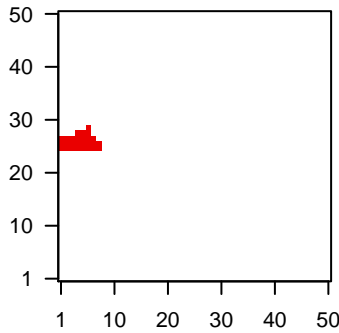
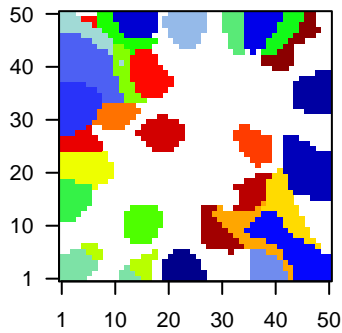
Rank	ID	max e	r	min e	Description
1	26579	1.7	-0.65	0.22	MYEOV myeloma overexpressed [Source:HGNC Symbol;Acc:7563]
2	4821	1.17	-0.26	0.28	NKX2-2 NK2 homeobox 2 [Source:HGNC Symbol;Acc:7835]
3	389084	1.16	-0.41	0.35	C2orf82 chromosome 2 open reading frame 82 [Source:HGNC Symbc
4	6326	1.15	-0.34	0.3	SCN2A sodium channel, voltage-gated, type II, alpha subunit [Source
5	9993	1.15	-0.79	0.5	DGCR2 DiGeorge syndrome critical region gene 2 [Source:HGNC Syr
6	5190	1.14	-0.92	0.21	PEX6 peroxisomal biogenesis factor 6 [Source:HGNC Symbol;Acc:f
7	29800	1.12	-1.05	0.33	ZDHHC1 zinc finger, DHHC-type containing 1 [Source:HGNC Symbol;
8	53947	1.05	-1.02	0.23	A4GALT alpha 1,4-galactosyltransferase [Source:HGNC Symbol;Acc:
9	529	1.04	-0.77	0.32	ATP6V1EATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1 [S
10	6813	1.04	-0.93	0.4	STXBP2 syntaxin binding protein 2 [Source:HGNC Symbol;Acc:11445]
11	23616	1.02	-0.99	0.39	SH3BP1 SH3-domain binding protein 1 [Source:HGNC Symbol;Acc:1f
12	784	0.99	-1	0.28	CACNB3 calcium channel, voltage-dependent, beta 3 subunit [Source:
13	90007	0.97	-0.99	0.38	MIDN midnolin [Source:HGNC Symbol;Acc:16298]
14	9258	0.94	-0.58	0.38	MFHAS1 malignant fibrous histiocytoma amplified sequence 1 [Source:
15	10489	0.86	-0.71	0.43	LRRC41 leucine rich repeat containing 41 [Source:HGNC Symbol;Acc:
16	24139	0.86	-0.69	0.4	EML2 echinoderm microtubule associated protein like 2 [Source:HG
17	7692	0.83	-0.48	0.43	ZNF133 zinc finger protein 133 [Source:HGNC Symbol;Acc:12917]
18	80853	0.78	-0.57	0.3	KDM7A lysine (K)-specific demethylase 7A [Source:HGNC Symbol;A
19	2801	0.76	-0.41	0.47	GOLGA2 golgin A2 [Source:HGNC Symbol;Acc:4425]
20	24144	0.76	-0.46	0.46	TFIP11 tuftelin interacting protein 11 [Source:HGNC Symbol;Acc:171

## Geneset Overrepresentation

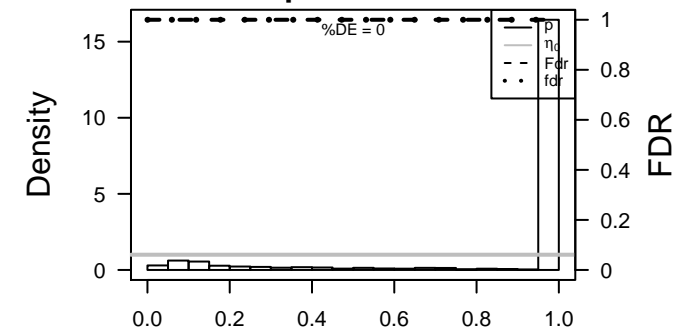
Rank	p-value	#in/all	Geneset
1	6e-05	4 / 30	miRN hsa-miR-631
2	1e-04	5 / 71	miRN hsa-miR-331-3p
3	3e-04	4 / 45	Glio willscher_GBM_Verhaak-PNwt_expression_J_up
4	4e-04	19 / 1135	Chr Chr 19
5	5e-04	3 / 22	BP negative regulation of intrinsic apoptotic signaling pathway
6	2e-03	2 / 10	GSE/ REACTOME_COPI_MEDIATED_TRANSPORT
7	2e-03	3 / 38	BP post-Golgi vesicle-mediated transport
8	3e-03	2 / 11	MF palmitoyltransferase activity
9	3e-03	2 / 12	miRN hsa-miR-671-3p
10	3e-03	3 / 42	MF ligand-dependent nuclear receptor transcription coactivator activity
11	3e-03	4 / 87	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
12	4e-03	2 / 13	BP COPI coating of Golgi vesicle
13	4e-03	2 / 14	BP negative regulation of release of cytochrome c from mitochondria
14	4e-03	2 / 14	GSE/ NOUZOVA_METHYLATED_IN_APL
15	4e-03	3 / 47	miRN AGTC-345
16	4e-03	3 / 47	miRN hsa-miR-346
17	5e-03	2 / 15	BP negative regulation of anoikis
18	5e-03	2 / 15	GSE/ MATTIOLI_MGUS_VS_MULTIPLE_MYELOMA
19	5e-03	2 / 15	GSE/ BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN
20	5e-03	2 / 15	GSE/ REACTOME_CLATHRIN_DERIVED_VESICLE_BUDDING
21	5e-03	2 / 15	GSE/ REACTOME_LYSOSOME_VESICLE_BIOGENESIS
22	5e-03	2 / 15	GSE/ REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_RECEPTORS
23	6e-03	2 / 16	GSE/ BIOCARTA_ARAP_PATHWAY
24	6e-03	2 / 16	GSE/ BIOCARTA_PTDINS_PATHWAY
25	6e-03	2 / 16	GSE/ REACTOME_MEMBRANE_TRAFFICKING
26	6e-03	2 / 16	GSE/ REACTOME_THE_ROLE_OF_NEF_IN_HIV1_REPLICATION_AND_DISEASE
27	6e-03	12 / 743	Chr Chr 7
28	7e-03	5 / 171	miRN CTAT-153
29	8e-03	3 / 57	BP phosphatidylinositol biosynthetic process
30	8e-03	2 / 19	CC exon-exon junction complex
31	8e-03	2 / 19	BP peroxisome organization
32	9e-03	70 / 8023	MF protein binding
33	1e-02	2 / 21	BP anterograde axon cargo transport
34	1e-02	2 / 21	BP positive regulation of axonogenesis
35	1e-02	2 / 21	miRN hsa-miR-99b
36	1e-02	2 / 22	TF Tf: VAQUERIZAS_Spinal cord
37	1e-02	8 / 426	Lymp SPANG_CD40 6hrs DN
38	1e-02	2 / 23	MF galactosyltransferase activity
39	1e-02	2 / 23	MF protein-cysteine S-palmitoyltransferase activity
40	1e-02	2 / 23	BP protein N-linked glycosylation

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: E

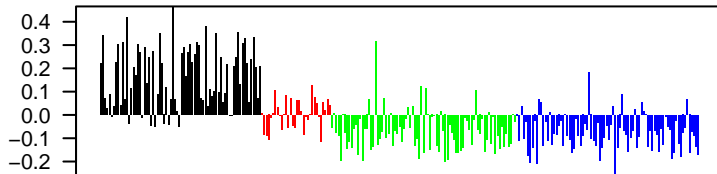
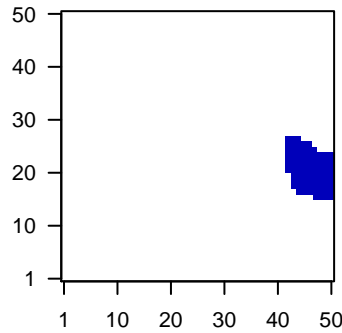
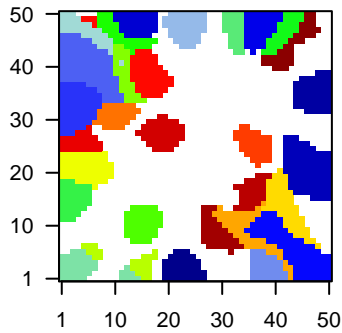
# metagenes = 85  
# genes = 431

<r> metagenes = 0.95  
<r> genes = 0.25  
beta: r2= 4.23 / log p= -Inf

# samples with spot = 39 ( 14.2 % )  
Atypical : 37 ( 50 % )  
Mesenchymal : 1 ( 1.2 % )  
Basal : 1 ( 1.2 % )

Overview Map

Spot

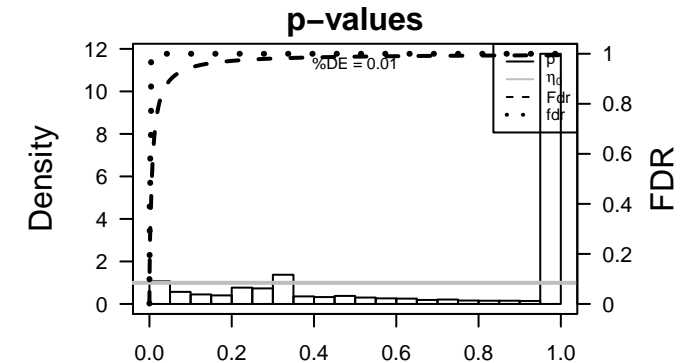


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	54959	2.94	-0.58	0.36	ODAM odontogenic, ameloblast associated [Source:HGNC Symbol]
2	4602	2.8	-1.04	0.76	MYB v-myb avian myeloblastosis viral oncogene homolog [Source
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:210
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	6542	2.15	-1.11	0.53	SLC7A2 solute carrier family 7 (cationic amino acid transporter, y+ sys
11	21	2.13	-0.7	0.74	ABCA3 ATP-binding cassette, sub-family A (ABC1), member 3 [Sou
12	9603	2.1	-1.75	0.49	NFE2L3 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:
13	494470	2.04	-1.37	0.6	RNF165 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
14	1959	2.02	-1.28	0.36	EGR2 early growth response 2 [Source:HGNC Symbol;Acc:3239]
15	909	1.99	-1.12	0.34	CD1A CD1a molecule [Source:HGNC Symbol;Acc:1634]
16	3670	1.98	-0.84	0.35	ISL1 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
17	8190	1.95	-0.45	0.38	MIA melanoma inhibitory activity [Source:HGNC Symbol;Acc:7076]
18	9915	1.9	-0.54	0.7	ARNT2 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HG
19	63917	1.86	-1.59	0.42	GALNT1UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl
20	30812	1.84	-0.44	0.63	SOX8 SRY (sex determining region Y)-box 8 [Source:HGNC Symb

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-09	85 / 1749	MF DNA binding
2	2e-07	74 / 1574	BP transcription, DNA-templated
3	5e-07	73 / 1581	BP regulation of transcription, DNA-dependent
4	2e-06	6 / 16	GSE# RICKMAN_HEAD_AND_NECK_CANCER_A
5	7e-06	11 / 81	miRN hsa-miR-188-5p
6	3e-05	10 / 77	miRN GGTG-329
7	4e-05	157 / 4640	CC nucleus
8	4e-05	45 / 940	MF nucleic acid binding
9	8e-05	18 / 247	miRN GTGC-96
10	1e-04	72 / 1820	MF metal ion binding
11	2e-04	3 / 5	Lymp MASCQUE_mBL UP
12	2e-04	39 / 823	MF sequence-specific DNA binding transcription factor activity
13	2e-04	11 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
14	2e-04	17 / 246	miRN TGCT-330
15	3e-04	4 / 13	BP histone H4-K16 acetylation
16	3e-04	4 / 13	Lymp BENTINK_mBL UP
17	3e-04	10 / 102	miRN AGGG-18A
18	3e-04	10 / 104	miRN hsa-miR-605
19	4e-04	5 / 25	CC PcG protein complex
20	4e-04	7 / 53	miRN GCAA-502
21	4e-04	12 / 146	miRN hsa-miR-494
22	4e-04	13 / 168	miRN hsa-miR-190
23	5e-04	15 / 215	miRN hsa-miR-199a-3p
24	5e-04	4 / 15	GSE# THUM_SYSTOLIC_HEART_FAILURE_DN
25	5e-04	6 / 40	TF Tf: VAQUERIZAS_Fetal brain
26	6e-04	9 / 92	BP translational elongation
27	7e-04	8 / 75	miRN ATGT-489
28	7e-04	11 / 134	miRN hsa-miR-200a
29	9e-04	9 / 98	miRN ATGT-221-222
30	1e-03	47 / 1142	CC intracellular
31	1e-03	18 / 306	BP regulation of transcription from RNA polymerase II promoter
32	1e-03	10 / 122	miRN hsa-miR-380
33	1e-03	13 / 189	miRN CTTT-527
34	1e-03	6 / 48	BP cilium morphogenesis
35	1e-03	16 / 264	miRN hsa-miR-30a
36	2e-03	4 / 20	MF RNA polymerase II transcription coactivator activity
37	2e-03	18 / 318	MF chromatin binding
38	2e-03	16 / 267	miRN CACT-128A-128B
39	2e-03	14 / 219	BP mRNA metabolic process
40	2e-03	14 / 220	miRN hsa-miR-185





# Correlation Cluster

## Spot Summary: F

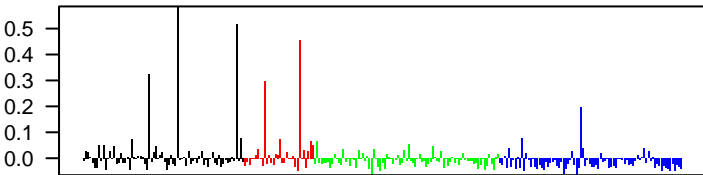
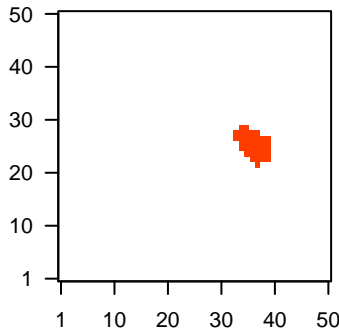
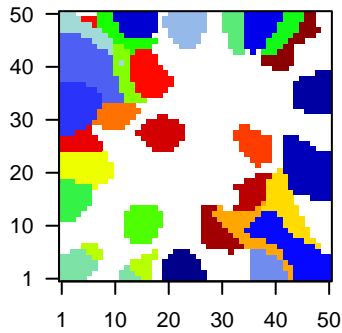
# metagenes = 36  
# genes = 193

<r> metagenes = 0.94  
<r> genes = 0.25  
beta: r2= 0.56 / log p= -Inf

# samples with spot = 6 ( 2.2 % )  
Atypical : 3 ( 4.1 % )  
Classical : 2 ( 6.2 % )  
Basal : 1 ( 1.2 % )

Overview Map

Spot

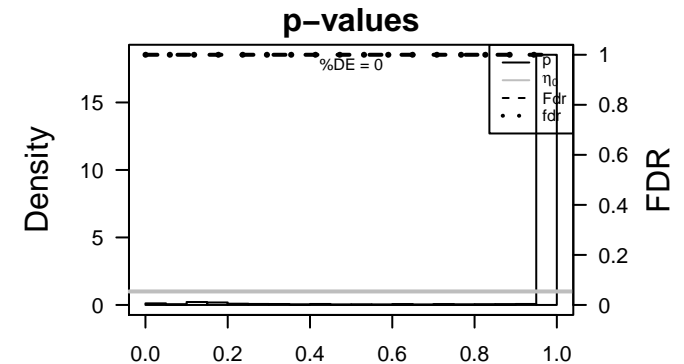


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	9518	1.58	-0.65	0.3	GDF15 growth differentiation factor 15 [Source:HGNC Symbol;Acc:30
2	2813	1.57	-0.26	0.53	GP2 glycoprotein 2 (zymogen granule membrane) [Source:HGNC
3	127003	1.5	-0.31	0.82	C1orf194chromosome 1 open reading frame 194 [Source:HGNC Synt
4	84688	1.47	-0.34	0.73	C9orf24 chromosome 9 open reading frame 24 [Source:HGNC Symbc
5	3212	1.46	-0.74	0.32	HOXB2 homeobox B2 [Source:HGNC Symbol;Acc:5113]
6	399949	1.4	-0.3	0.62	C11orf88chromosome 11 open reading frame 88 [Source:HGNC Synt
7	83657	1.39	-0.51	0.69	DYNLRB2dynein, light chain, roadblock-type 2 [Source:HGNC Symbol;
8	222256	1.37	-0.27	0.7	CDHR3 cadherin-related family member 3 [Source:HGNC Symbol;Ac
9	5542	1.36	-0.21	0.44	PRB1 proline-rich protein BstNI subfamily 1 [Source:HGNC Symbol
10	89765	1.31	-0.28	0.81	RSPH1 radial spoke head 1 homolog (Chlamydomonas) [Source:HG
11	2302	1.25	-0.39	0.54	FOXJ1 forkhead box J1 [Source:HGNC Symbol;Acc:3816]
12	284434	1.2	-0.32	0.76	NWD1 NACHT and WD repeat domain containing 1 [Source:HGNC :
13	345895	1.18	-0.27	0.8	RSPH4A radial spoke head 4 homolog A (Chlamydomonas) [Source:Hi
14	83853	1.14	-0.28	0.71	ROPN1Lropophilin associated tail protein 1-like [Source:HGNC Symb
15	8399	1.14	-0.5	0.45	PLA2G1Pphospholipase A2, group X [Source:HGNC Symbol;Acc:9029
16	400566	1.14	-0.74	0.33	C17orf97chromosome 17 open reading frame 97 [Source:HGNC Synt
17	1356	1.13	-0.33	0.47	CP ceruloplasmin (ferroxidase) [Source:HGNC Symbol;Acc:2295
18	128602	1.13	-0.23	0.79	C20orf85chromosome 20 open reading frame 85 [Source:HGNC Synt
19	83659	1.12	-0.27	0.74	TEKT1 tektin 1 [Source:HGNC Symbol;Acc:15534]
20	80217	1.12	-0.32	0.72	WDR96 WD repeat domain 96 [Source:HGNC Symbol;Acc:26684]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-62	37 / 51	Glio wilscher_GBM_Verhaak-PNmut_expression_G_down
2	1e-11	14 / 102	CC cilium
3	4e-11	9 / 30	CC axoneme
4	7e-11	12 / 76	Glio GIEZELT_GBM_STSwt_up_VS_LTSwt
5	5e-08	10 / 85	Glio GIEZELT_GBM_STS_down_VS_LTS
6	7e-08	7 / 32	BP cell projection organization
7	8e-08	6 / 20	CC dynein complex
8	2e-07	5 / 13	CC axonemal dynein complex
9	8e-07	5 / 16	BP ciliary or bacterial-type flagellar motility
10	2e-05	7 / 71	MF microtubule motor activity
11	2e-05	6 / 48	BP cilium morphogenesis
12	3e-05	5 / 32	CC motile cilium
13	5e-05	3 / 7	GSE/ NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
14	7e-05	12 / 264	CC microtubule
15	1e-04	6 / 68	BP microtubule-based movement
16	1e-03	4 / 42	BP heart looping
17	2e-03	5 / 75	BP cilium assembly
18	2e-03	4 / 48	Glio Noushmehr_Pron_GCIMP_hypermeth_DN
19	3e-03	9 / 259	BP spermatogenesis
20	4e-03	2 / 8	GSE/ NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
21	5e-03	2 / 9	GSE/ KORKOLA_CHORIOCARCINOMA_DN
22	6e-03	2 / 10	GSE/ KORKOLA_EMBRYONAL_CARCINOMA_DN
23	6e-03	2 / 10	GSE/ KORKOLA_SEMINOMA_DN
24	7e-03	2 / 11	CC ciliary transition zone
25	7e-03	2 / 11	GSE/ KORKOLA_YOLK_SAC_TUMOR_DN
26	8e-03	23 / 1146	TF HEBENSTREIT_low expression TF
27	8e-03	14 / 579	MF calcium ion binding
28	8e-03	2 / 12	CC TCTN-B9D complex
29	1e-02	2 / 13	BP copper ion transport
30	1e-02	2 / 16	MF ribonuclease activity
31	2e-02	5 / 131	MF nucleoside-triphosphatase activity
32	2e-02	3 / 49	BP spermatid development
33	2e-02	2 / 20	BP sperm motility
34	2e-02	1 / 2	miRN miR-433
35	2e-02	2 / 21	BP digestive tract development
36	2e-02	5 / 141	MF ATPase activity
37	3e-02	29 / 1720	Chr Chr 1
38	3e-02	4 / 99	BP homophilic cell adhesion
39	4e-02	2 / 26	H.Tis: WIRTH_Pancreas
40	4e-02	14 / 717	Chr Chr 16







# Correlation Cluster

## Spot Summary: G

# metagenes = 43  
# genes = 385

<r> metagenes = 0.94  
<r> genes = 0.12  
beta: r2= 0.19 / log p= -13.21

# samples with spot = 0 ( 0 % )

## Spot Genelist

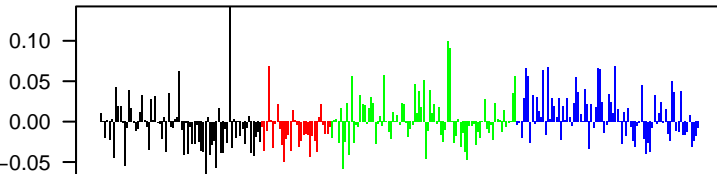
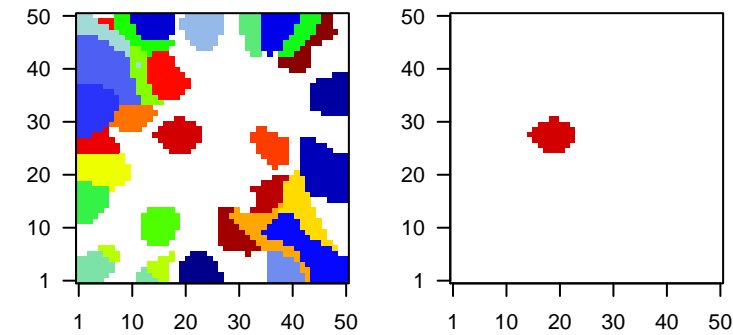
Rank	ID	max e	r	min e	Description
					Symbol
1	25963	0.84	-0.7	0.25	TMEM87 transmembrane protein 87A [Source:HGNC Symbol;Acc:245178]
2	3588	0.77	-0.54	0.24	IL10RB interleukin 10 receptor, beta [Source:HGNC Symbol;Acc:59672]
3	4543	0.7	-0.22	0.11	MTNR1A melatonin receptor 1A [Source:HGNC Symbol;Acc:7463]
4	1543	0.64	-0.23	0.26	CYP1A1 cytochrome P450, family 1, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:1034]
5	55421	0.62	-0.46	0.21	C17orf85 chromosome 17 open reading frame 85 [Source:HGNC Synt
6	8303	0.58	-0.43	0.21	SNN stannin [Source:HGNC Symbol;Acc:11149]
7	23057	0.56	-0.27	0.36	NMNAT2 nicotinamide nucleotide adenyltransferase 2 [Source:HGNC
8	1178	0.56	-0.19	0.26	CLC Charcot-Leyden crystal galectin [Source:HGNC Symbol;Acc:1034]
9	5068	0.52	-0.18	0.23	REG3A regenerating islet-derived 3 alpha [Source:HGNC Symbol;Ac
10	91056	0.52	-0.32	0.22	AP5B1 adaptor-related protein complex 5, beta 1 subunit [Source:HK
11	387836	0.51	-0.26	0.27	CLEC2A C-type lectin domain family 2, member A [Source:HGNC Syn
12	4935	0.48	-0.27	0.28	GPR143 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:1034]
13	84649	0.47	-0.34	0.45	DGAT2 diacylglycerol O-acyltransferase 2 [Source:HGNC Symbol;Ac
14	5101	0.46	-0.22	0.31	PCDH9 protocadherin 9 [Source:HGNC Symbol;Acc:8661]
15	57449	0.46	-0.24	0.5	PLEKHG7 pleckstrin homology domain containing, family G (with RhoGe
16	238	0.45	-0.28	0.44	ALK anaplastic lymphoma receptor tyrosine kinase [Source:HGNC
17	7812	0.45	-0.29	0.33	CSDE1 cold shock domain containing E1, RNA-binding [Source:HGNC
18	55336	0.44	-0.23	0.26	FBXL8 F-box and leucine-rich repeat protein 8 [Source:HGNC Syml
19	8501	0.44	-0.27	0.51	SLC43A1 solute carrier family 43 (amino acid system L transporter), me
20	4150	0.42	-0.27	0.29	MAZ MYC-associated zinc finger protein (purine-binding transcrip

## Geneset Overrepresentation

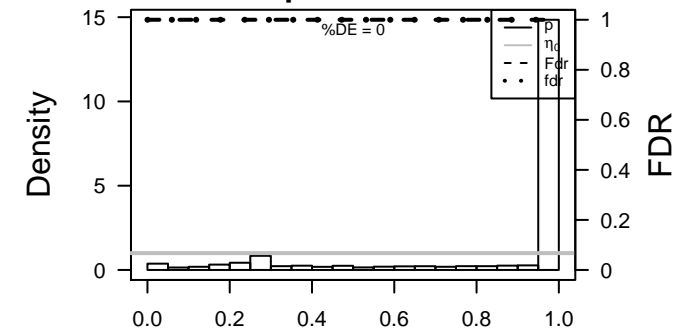
Rank	p-value	#in/all	Geneset
1	6e-10	28 / 321	MF G-protein coupled receptor activity
2	1e-07	29 / 435	BP G-protein coupled receptor signaling pathway
3	3e-07	11 / 69	MF olfactory receptor activity
4	8e-05	5 / 21	BP G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide
5	1e-04	7 / 50	H.Tis: WIRTH_Homeostasis
6	1e-04	6 / 36	miRN Cancer
7	2e-04	4 / 14	GSE/ JAZAG_TGFB1_SIGNALING_DN
8	3e-04	7 / 58	BP cellular response to insulin stimulus
9	6e-04	5 / 32	miRN Leukemia
10	1e-03	5 / 36	miRN Lung cancer
11	1e-03	9 / 118	Glio wilscher_GBM_Verhaak-CL_expression_K_down
12	1e-03	9 / 118	Glio wilscher_GBM_Verhaak-MES_expression_K_down
13	1e-03	9 / 118	Glio wilscher_GBM_Verhaak-PNwt_expression_K_up
14	1e-03	9 / 118	Glio wilscher_GBM_Verhaak-PNmut_expression_K_up
15	2e-03	3 / 11	MF acetylcholine-activated cation-selective channel activity
16	2e-03	3 / 11	CC acetylcholine-gated channel complex
17	2e-03	3 / 11	BP male sex determination
18	2e-03	3 / 11	miRN Melanoma, cutaneous malignant, 2
19	2e-03	3 / 12	MF NAD-dependent histone deacetylase activity (H3-K14 specific)
20	3e-03	3 / 13	MF hormone binding
21	3e-03	4 / 27	miRN Colorectal cancer
22	3e-03	3 / 14	BP synaptic transmission, cholinergic
23	3e-03	6 / 66	BP biosynthetic process
24	4e-03	4 / 30	BP adenylylase-coupled G-protein coupled receptor signaling pathw
25	5e-03	2 / 5	H.Tis: WIRTH_Pituitary gland
26	5e-03	3 / 16	miRN Cervical cancer, somatic
27	5e-03	8 / 120	H.Tis: WIRTH_Testis
28	6e-03	4 / 34	miRN Pancreatic cancer
29	6e-03	4 / 34	miRN Squamous cell carcinoma, head and neck
30	6e-03	4 / 34	miRN Hematological
31	7e-03	3 / 18	MF aromatase activity
32	7e-03	4 / 35	MF transmembrane receptor protein tyrosine kinase activity
33	7e-03	4 / 35	miRN Prostate cancer
34	7e-03	38 / 1146	TF HEBENSTREIT_low expression TF
35	8e-03	91 / 3274	CC integral to membrane
36	8e-03	3 / 19	miRN Multiple myeloma
37	9e-03	4 / 38	miRN Breast cancer
38	1e-02	3 / 21	MF Rac GTPase binding
39	1e-02	6 / 85	miRN ATTA-380-3P
40	1e-02	2 / 8	GSE/ NAGY_STAGA_COMPONENTS_HUMAN

Overview Map

Spot



p-values





# Correlation Cluster

## Spot Summary: H

# metagenes = 49  
# genes = 480

<r> metagenes = 0.94  
<r> genes = 0.25  
beta: r2= 3.58 / log p= -Inf

# samples with spot = 29 ( 10.5 % )  
Atypical : 15 ( 20.3 % )  
Classical : 8 ( 25 % )  
Mesenchymal : 3 ( 3.5 % )  
Basal : 3 ( 3.6 % )

## Spot Genelist

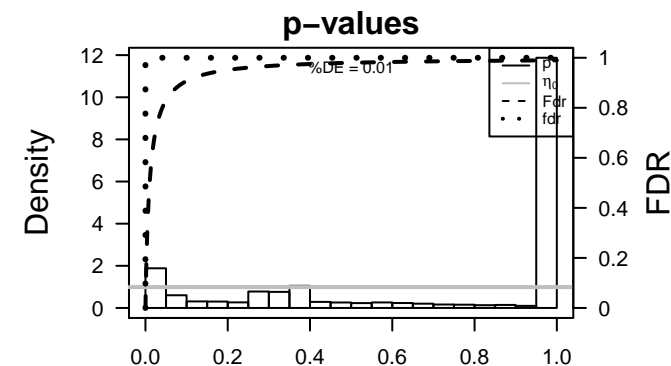
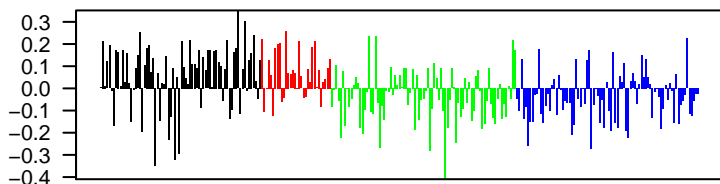
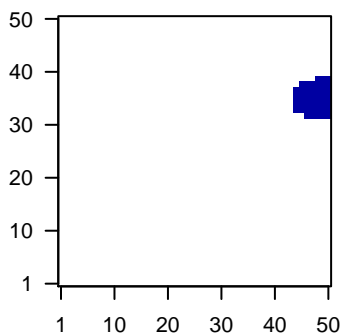
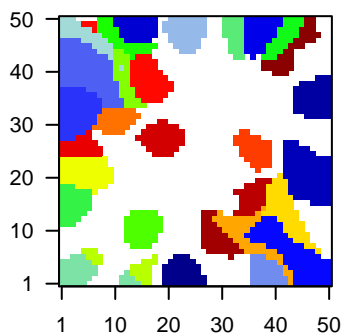
Rank	ID	max e	r	min e	Description
1	27075	1.78	-1.45	0.37	TSPAN13 tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
2	5274	1.74	-0.65	0.41	SERPIN1 serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
3	4254	1.49	-1.1	0.5	KITLG KIT ligand [Source:HGNC Symbol;Acc:6343]
4	10257	1.47	-0.85	0.54	ABCC4 ATP-binding cassette, sub-family C (CFTR/MRP), member 4
5	11212	1.46	-1.05	0.35	PROSC proline synthetase co-transcribed homolog (bacterial) [Sourc
6	57088	1.41	-1.2	0.24	PLSCR4 phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649]
7	60481	1.39	-1.17	0.5	ELOVL5 ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:213
8	4982	1.39	-0.58	0.28	TNFRSF10B tumor necrosis factor receptor superfamily, member 11b [Sou
9	54467	1.32	-0.78	0.42	ANKIB1 ankyrin repeat and IBR domain containing 1 [Source:HGNC S
10	7095	1.32	-0.69	0.46	SEC62 SEC62 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1
11	171586	1.32	-0.85	0.49	ABHD3 abhydrolase domain containing 3 [Source:HGNC Symbol;Acc
12	3730	1.32	-0.6	0.36	KAL1 Kallmann syndrome 1 sequence [Source:HGNC Symbol;Acc:
13	1429	1.26	-1.33	0.44	CRYZ crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
14	23215	1.25	-1.4	0.57	PRRC2C proline-rich coiled-coil 2C [Source:HGNC Symbol;Acc:2490
15	5934	1.22	-0.98	0.51	RBL2 retinoblastoma-like 2 (p130) [Source:HGNC Symbol;Acc:989
16	29919	1.22	-0.88	0.46	C18orf8 chromosome 18 open reading frame 8 [Source:HGNC Symb
17	26035	1.21	-0.95	0.43	GLCE glucuronic acid epimerase [Source:HGNC Symbol;Acc:1785
18	57045	1.18	-0.74	0.42	TWSG1 twisted gastrulation BMP signaling modulator 1 [Source:HGN
19	64747	1.18	-0.88	0.33	MFSD1 major facilitator superfamily domain containing 1 [Source:HGI
20	58527	1.18	-1.02	0.5	ABRACL1 ABRA C-terminal like [Source:HGNC Symbol;Acc:21230]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-13	53 / 595	MF RNA binding
2	7e-13	23 / 121	miRN hsa-miR-543
3	2e-12	206 / 4640	CC nucleus
4	3e-12	68 / 940	MF nucleic acid binding
5	3e-12	36 / 318	miRN hsa-miR-590-3p
6	1e-11	41 / 421	miRN hsa-let-7b
7	6e-11	45 / 517	miRN hsa-miR-106a
8	7e-11	35 / 335	miRN hsa-miR-142-5p
9	1e-10	23 / 153	miRN hsa-miR-450b-5p
10	2e-10	45 / 538	miRN hsa-miR-17
11	3e-10	41 / 463	miRN hsa-miR-301a
12	3e-10	48 / 603	miRN hsa-miR-20a
13	1e-09	37 / 412	miRN hsa-miR-372
14	2e-09	38 / 433	miRN hsa-miR-19b
15	2e-09	41 / 495	miRN hsa-miR-103
16	3e-09	31 / 311	miRN hsa-miR-98
17	3e-09	44 / 565	miRN hsa-miR-20b
18	4e-09	28 / 264	miRN hsa-miR-449a
19	4e-09	17 / 100	miRN hsa-miR-544
20	5e-09	50 / 699	Chr Chr 5
21	5e-09	41 / 511	miRN hsa-miR-106b
22	6e-09	35 / 396	miRN hsa-miR-301b
23	7e-09	23 / 188	miRN hsa-miR-548d-3p
24	7e-09	28 / 271	miRN hsa-miR-101
25	8e-09	34 / 381	miRN hsa-let-7c
26	8e-09	22 / 174	BP mRNA processing
27	8e-09	37 / 440	miRN hsa-miR-19a
28	1e-08	42 / 545	miRN hsa-miR-93
29	1e-08	16 / 93	miRN hsa-miR-10b
30	2e-08	20 / 150	miRN hsa-miR-633
31	2e-08	28 / 281	miRN hsa-miR-570
32	2e-08	23 / 197	miRN hsa-miR-568
33	2e-08	39 / 494	miRN hsa-miR-107
34	2e-08	29 / 303	miRN hsa-miR-302b
35	3e-08	21 / 171	miRN hsa-miR-452
36	3e-08	21 / 172	miRN hsa-miR-607
37	4e-08	22 / 189	miRN hsa-miR-1283
38	4e-08	35 / 426	miRN hsa-miR-519d
39	4e-08	32 / 368	miRN hsa-miR-144
40	5e-08	29 / 315	miRN hsa-miR-30e

## Overview Map

## Spot





# Correlation Cluster

## Spot Summary: I

# metagenes = 89  
# genes = 770

<r> metagenes = 0.95  
<r> genes = 0.46  
beta: r2= 18.54 / log p= -Inf

# samples with spot = 60 ( 21.8 % )  
Atypical : 45 ( 60.8 % )  
Mesenchymal : 10 ( 11.8 % )  
Basal : 5 ( 6 % )

## Spot Genelist

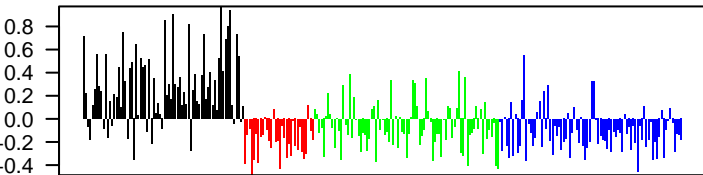
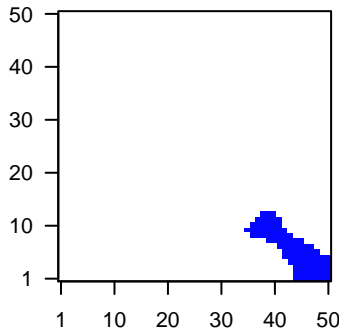
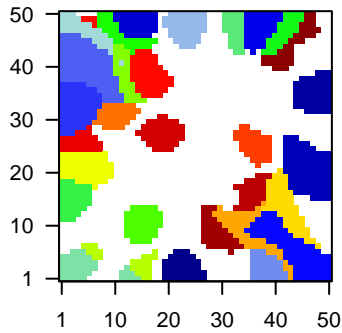
Rank	ID	max e	r	min e	Description
1	260436	4.41	-1.73	0.46	FDCSP follicular dendritic cell secreted protein [Source:HGNC Symbc
2	6363	3.84	-1.64	0.79	CCL19 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
3	3512	3.8	-2.52	0.56	IGJ immunoglobulin J polypeptide, linker protein for immunoglobu
4	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 sparco/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:H
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

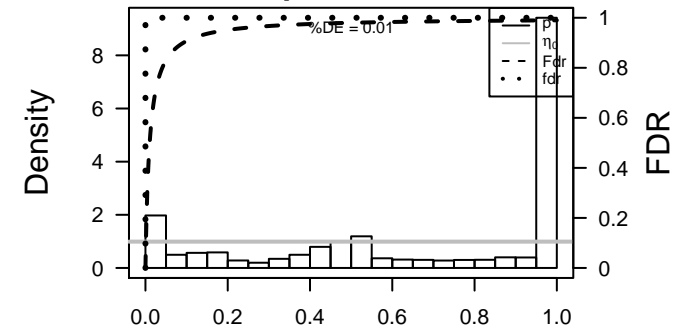
Rank	p-value	#in/all	Geneset
1	1e-99	178 / 417	H.Tis: WIRTH_Immune system
2	1e-99	189 / 553	Canci: Lembcke_Colonic Inflammation
3	8e-52	95 / 312	BP: immune response
4	2e-39	76 / 265	Glio: willscher_GBM_Verhaak-CL_expression_B_up
5	2e-39	76 / 265	Glio: willscher_GBM_Verhaak-MES_expression_B_up
6	2e-39	76 / 265	Glio: willscher_GBM_Verhaak-PNwt_expression_B_down
7	2e-39	76 / 265	Glio: willscher_GBM_Verhaak-PNmut_expression_B_down
8	2e-32	253 / 2659	CC: plasma membrane
9	7e-28	50 / 162	CC: external side of plasma membrane
10	8e-26	31 / 60	BP: T cell costimulation
11	1e-22	33 / 84	BP: T cell receptor signaling pathway
12	2e-22	63 / 327	Lymp: SPANG_CD40 6hrs UP
13	4e-21	30 / 74	BP: regulation of immune response
14	2e-19	46 / 204	BP: cell surface receptor signaling pathway
15	9e-19	76 / 530	BP: innate immune response
16	5e-18	51 / 269	BP: inflammatory response
17	7e-18	18 / 28	BP: B cell receptor signaling pathway
18	1e-17	55 / 316	Canci: SPANG_BCL6-index2
19	1e-16	119 / 1167	BP: signal transduction
20	4e-16	13 / 15	CC: MHC class II protein complex
21	2e-15	20 / 45	BP: T cell activation
22	2e-15	93 / 835	CC: integral to plasma membrane
23	8e-15	12 / 14	GSE/ FINETTI_BREAST_CANCER_KINOME_GREEN
24	1e-14	20 / 49	Glio: Donson-innate immunity-associated with LTS in HGA
25	4e-14	59 / 426	Lymp: SPANG_CD40 6hrs DN
26	2e-13	15 / 28	Lymp: DAVE_Immune response 1
27	7e-13	11 / 14	GSE/ BIOCARTE_NO2IL12_PATHWAY
28	1e-12	18 / 47	BP: antigen processing and presentation
29	2e-12	15 / 32	Glio: Donson-Misc immune function-associated with LTS in HGA
30	2e-12	17 / 43	BP: positive regulation of T cell proliferation
31	3e-12	10 / 12	CC: T cell receptor complex
32	4e-12	14 / 28	BP: B cell activation
33	7e-12	13 / 24	CC: immunological synapse
34	7e-12	11 / 16	GSE/ SU_THYMUS
35	1e-11	10 / 13	Canci: GENTLES_modul18
36	1e-11	16 / 41	MF: non-membrane spanning protein tyrosine kinase activity
37	1e-11	29 / 143	MF: transmembrane signaling receptor activity
38	2e-11	8 / 8	GSE/ BIOCARTE_TCRA_PATHWAY
39	3e-11	52 / 407	BP: blood coagulation
40	4e-11	46 / 336	BP: intracellular signal transduction

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: J

# metagenes = 56  
# genes = 227

<r> metagenes = 0.94  
<r> genes = 0.24  
beta: r2= 3.16 / log p= -Inf

# samples with spot = 20 ( 7.3 % )  
Atypical : 17 ( 23 % )  
Mesenchymal : 2 ( 2.4 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

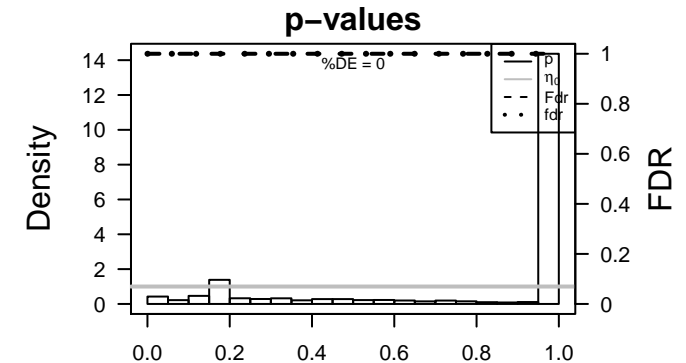
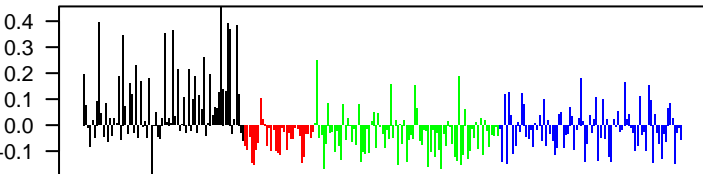
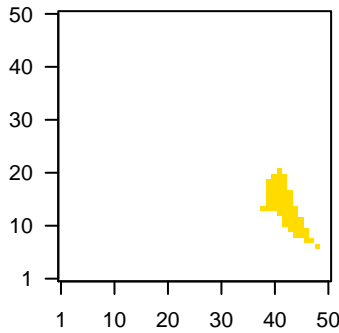
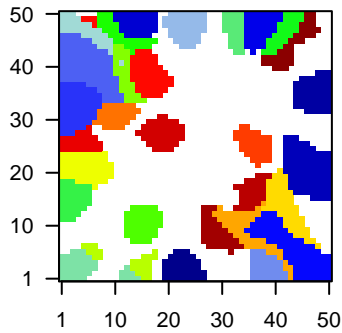
Rank	ID	max e	r	min e	Description
					Symbol
1	26824	1.91	-0.97	0.28	RNU11 RNA, U11 small nuclear [Source:HGNC Symbol;Acc:10108]
2	55769	1.53	-1.27	0.38	ZNF83 zinc finger protein 83 [Source:HGNC Symbol;Acc:13158]
3	23708	1.42	-1	0.44	GSPT2 G1 to S phase transition 2 [Source:HGNC Symbol;Acc:4622]
4	80237	1.39	-0.65	0.4	ELL3 elongation factor RNA polymerase II-like 3 [Source:HGNC S]
5	10370	1.37	-1.08	0.39	CITED2 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo
6	9045	1.34	-1.07	0.51	RPL14 ribosomal protein L14 [Source:HGNC Symbol;Acc:10305]
7	27248	1.27	-0.81	0.58	ERLEC1 endoplasmic reticulum lectin 1 [Source:HGNC Symbol;Acc:2f
8	827	1.26	-0.35	0.42	CAPN6 calpain 6 [Source:HGNC Symbol;Acc:1483]
9	4189	1.24	-0.8	0.54	DNAJB9 DnaJ (Hsp40) homolog, subfamily B, member 9 [Source:HGNC
10	3708	1.23	-0.79	0.57	ITPR1 inositol 1,4,5-trisphosphate receptor, type 1 [Source:HGNC S
11	9846	1.23	-0.71	0.55	GAB2 GRB2-associated binding protein 2 [Source:HGNC Symbol;A
12	387066	1.22	-1.28	0.43	
13	830	1.21	-0.77	0.27	CAPZA2 capping protein (actin filament) muscle Z-line, alpha 2 [Sourc
14	28972	1.16	-0.89	0.66	SPCS1 signal peptidase complex subunit 1 homolog (S. cerevisiae) [t
15	84870	1.15	-0.38	0.65	RSPO3 R-spondin 3 [Source:HGNC Symbol;Acc:20866]
16	88455	1.14	-0.8	0.56	ANKRD13A ankyrin repeat domain 13A [Source:HGNC Symbol;Acc:2126
17	1519	1.09	-0.97	0.59	CTSO cathepsin O [Source:HGNC Symbol;Acc:2542]
18	84314	1.08	-0.54	0.26	TMEM107 transmembrane protein 107 [Source:HGNC Symbol;Acc:2812
19	90594	1.07	-0.58	0.54	ZNF439 zinc finger protein 439 [Source:HGNC Symbol;Acc:20873]
20	51643	1.06	-0.92	0.53	TMBIM4 Protein lifeguard 4; Uncharacterized protein [Source:UniProt

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-08	35 / 914	Chr Chr 3
2	2e-05	8 / 87	BP translational termination
3	6e-05	9 / 128	BP translational initiation
4	7e-05	32 / 1142	CC intracellular
5	1e-04	7 / 81	BP viral transcription
6	1e-04	8 / 109	BP SRP-dependent cotranslational protein targeting to membrane
7	1e-04	5 / 37	CC cytosolic small ribosomal subunit
8	2e-04	8 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
9	3e-04	7 / 92	BP translational elongation
10	3e-04	7 / 92	BP viral life cycle
11	3e-04	4 / 25	CC small ribosomal subunit
12	4e-04	3 / 11	BP UV protection
13	5e-04	3 / 12	GSE/ YAMASHITA_LIVER_CANCER_STEM_CELL_DN
14	5e-04	3 / 12	GSE/ BIOCARTA_INTRINSIC_PATHWAY
15	8e-04	41 / 1820	MF metal ion binding
16	8e-04	3 / 14	GSE/ LIN_MELANOMA_COPY_NUMBER_DN
17	1e-03	25 / 940	MF nucleic acid binding
18	1e-03	5 / 57	BP phosphatidylinositol biosynthetic process
19	1e-03	5 / 58	BP regulation of insulin secretion
20	1e-03	8 / 153	MF structural constituent of ribosome
21	1e-03	3 / 16	GSE/ ROSS_AML_WITH_CBFB_MYH11_FUSION
22	1e-03	3 / 16	GSE/ WILLERT_WNT_SIGNALING
23	1e-03	36 / 1581	BP regulation of transcription, DNA-dependent
24	2e-03	11 / 280	Chr Chr 13
25	2e-03	8 / 167	miRN ATGC-103-107
26	2e-03	3 / 20	MF myosin binding
27	2e-03	10 / 253	BP translation
28	2e-03	4 / 42	miRN GTAC-486
29	4e-03	3 / 23	BP activation of protein kinase activity
30	4e-03	4 / 48	BP activation of phospholipase C activity
31	4e-03	3 / 24	BP T cell homeostasis
32	5e-03	2 / 8	GSE/ CASORELLI_APL_SECONDARY_VS_DE_NOVO_DN
33	6e-03	2 / 9	GSE/ ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
34	6e-03	2 / 9	GSE/ GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_UP
35	6e-03	2 / 9	GSE/ BIOCARTA_NUCLEARRS_PATHWAY
36	6e-03	2 / 9	GSE/ REACTOME_COMMON_PATHWAY
37	6e-03	14 / 482	BP cellular protein metabolic process
38	6e-03	3 / 28	BP spleen development
39	8e-03	2 / 10	MF protein kinase A regulatory subunit binding
40	8e-03	2 / 10	GSE/ LOPEZ_MESOTHELIOMA_SURVIVAL_UP

### Overview Map

### Spot







# Correlation Cluster

## Spot Summary: K

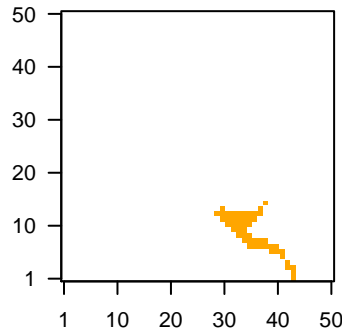
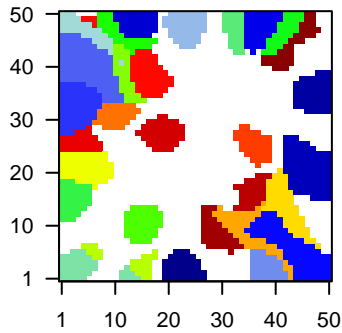
# metagenes = 50  
# genes = 128

<r> metagenes = 0.95  
<r> genes = 0.27  
beta: r2= 4.63 / log p= -Inf

# samples with spot = 33 ( 12 % )  
Atypical : 26 ( 35.1 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 3 ( 3.6 % )

Overview Map

Spot



## Spot Genelist

Rank	ID	max e	r	min e	Description
1	3127	4.47	-1.24	0.19	HLA-DRB3 major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:11356]
2	80162	1.79	-0.97	0.67	ATHL1 ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;Acc:11356]
3	84446	1.74	-1.13	0.68	BRSK1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:11356]
4	7127	1.66	-0.92	0.42	TNFAIP2 tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:11356]
5	10734	1.48	-0.48	0.52	STAG3 stromal antigen 3 [Source:HGNC Symbol;Acc:11356]
6	414918	1.39	-0.92	0.59	DENND6BENN/MADD domain containing 6B [Source:HGNC Symbol;Acc:11356]
7	4034	1.35	-0.87	0.68	LRCH4 leucine-rich repeats and calponin homology (CH) domain containing 4 [Source:HGNC Symbol;Acc:11356]
8	26580	1.31	-1.3	0.42	BSCL2 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:HGNC Symbol;Acc:11356]
9	23240	1.31	-0.96	0.49	KIAA0922 KIAA0922 [Source:HGNC Symbol;Acc:29146]
10	348094	1.26	-0.82	0.52	ANKDD1 Ankyrin repeat and death domain containing 1A [Source:HGNC Symbol;Acc:11356]
11	79090	1.25	-0.81	0.58	TRAPPC6 Trafficking protein particle complex 6A [Source:HGNC Symbol;Acc:11356]
12	56834	1.21	-0.78	0.64	GPR137 G protein-coupled receptor 137 [Source:HGNC Symbol;Acc:11356]
13	32	1.19	-0.78	0.71	ACACB acetyl-CoA carboxylase beta [Source:HGNC Symbol;Acc:85]
14	755	1.18	-0.7	0.78	C21orf2 chromosome 21 open reading frame 2 [Source:HGNC Symbol;Acc:11356]
15	11025	1.17	-0.82	0.6	LILRB3 leukocyte immunoglobulin-like receptor, subfamily B (with TV domain) 3 [Source:HGNC Symbol;Acc:11356]
16	10180	1.16	-0.89	0.73	RBM6 RNA binding motif protein 6 [Source:HGNC Symbol;Acc:9903]
17	140685	1.14	-0.61	0.58	ZBTB46 zinc finger and BTB domain containing 46 [Source:HGNC Symbol;Acc:11356]
18	84557	1.14	-0.98	0.42	MAP1LC3A Microtubule-associated protein 1 light chain 3 alpha [Source:HGNC Symbol;Acc:11356]
19	1445	1.13	-0.85	0.53	CSK c-src tyrosine kinase [Source:HGNC Symbol;Acc:2444]
20	126299	1.13	-0.97	0.68	ZNF428 zinc finger protein 428 [Source:HGNC Symbol;Acc:20804]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-04	5 / 64	BP activation of signaling protein activity involved in unfolded protein response
2	4e-04	5 / 82	BP endoplasmic reticulum unfolded protein response
3	4e-04	11 / 426	Lymp SPANG_CD40 6hrs DN
4	1e-03	4 / 64	MF mRNA binding
5	2e-03	3 / 31	BP adenylylate cyclase-inhibiting G-protein coupled receptor signaling pathway
6	2e-03	4 / 70	CC endomembrane system
7	2e-03	18 / 1135	Chr Chr 19
8	3e-03	2 / 11	BP negative regulation of lipid catabolic process
9	3e-03	2 / 11	GSE/ CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
10	3e-03	2 / 11	GSE/ GUTIERREZ_CHRONIC_LYMPHOBLASTIC_LEUKEMIA_UP
11	3e-03	3 / 39	BP erythrocyte differentiation
12	4e-03	2 / 12	GSE/ BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_DN
13	4e-03	2 / 12	GSE/ KIM_MYCN_AMPLIFICATION_TARGETS_UP
14	4e-03	2 / 12	GSE/ SYED ESTRADIOL_RESPONSE
15	4e-03	8 / 327	Lymp SPANG_CD40 6hrs UP
16	4e-03	2 / 13	MF spectrin binding
17	4e-03	2 / 13	BP temperature homeostasis
18	4e-03	2 / 13	GSE/ BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
19	5e-03	2 / 14	MF calcium-activated potassium channel activity
20	5e-03	2 / 14	GSE/ KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
21	5e-03	2 / 14	GSE/ DOANE_RESPONSE_TO_ANDROGEN_DN
22	5e-03	2 / 14	GSE/ ENGELMANN_CANCER_PROGENITORS_UP
23	6e-03	2 / 15	GSE/ MUELLER METHYLATED_IN_GLIOMASTOMA
24	6e-03	2 / 15	GSE/ LUI_THYROID_CANCER_CLUSTER_2
25	6e-03	2 / 15	GSE/ CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70
26	6e-03	2 / 15	GSE/ ABE_INNER_EAR
27	6e-03	2 / 16	BP positive regulation of viral genome replication
28	6e-03	2 / 16	GSE/ HUTTMANN_B CLL_POOR_SURVIVAL_DN
29	6e-03	2 / 16	GSE/ NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
30	6e-03	2 / 16	GSE/ POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP
31	6e-03	2 / 16	GSE/ DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN
32	6e-03	2 / 16	GSE/ PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
33	7e-03	2 / 17	CC autophagic vacuole membrane
34	8e-03	2 / 18	miRN CGCT-503
35	9e-03	2 / 19	BP spliceosomal complex assembly
36	9e-03	6 / 234	CC neuronal cell body
37	9e-03	16 / 1095	TF HEBENSTREIT_high expression TF
38	1e-02	4 / 116	CC cytoplasmic membrane-bounded vesicle
39	1e-02	2 / 22	MF Rab guanyl-nucleotide exchange factor activity
40	1e-02	2 / 23	BP positive regulation of protein secretion

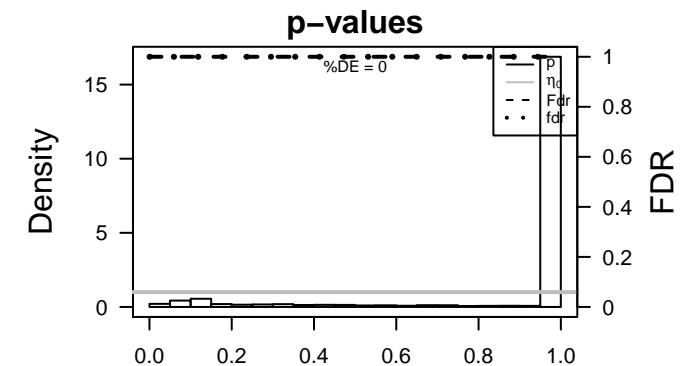
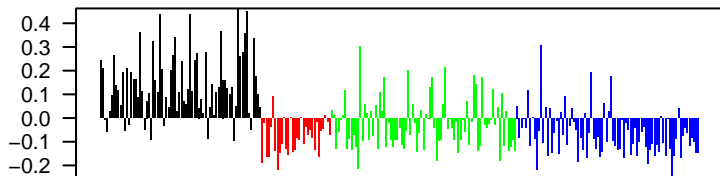


Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'activation of signaling protein activity involved in unfolded protein response'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists cancer types like 'LIU\_PROSTATE\_CANCER\_DN', 'Limbic\_Colonial Inflammation'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists cancer types like 'LIU\_PROSTATE\_CANCER\_DN', 'LIU\_COMMON\_CANCER\_GENES'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'mitochondrial system', 'autophagic vacuole membrane'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'mitochondrial system', 'autophagic vacuole membrane'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists chromosomes like 'Chr 19', 'Chr 16', 'Chr 11'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists diseases like 'GUJL Psoriasis down', 'GUJL Psoriasis up'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists diseases like 'GUJL Psoriasis down', 'GUJL Psoriasis up'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'willscher\_GBM\_Verhaak-PNwt\_expression\_N\_down'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'willscher\_GBM\_Verhaak-PNwt\_expression\_N\_down'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'CORCANNON APOPTOSIS BY EPOXOMICIN UP', 'GILTZANOFF CHRONIC LYMPHOCTIC LEUKEMIA UP'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'WIRTH Immune system', 'WIRTH Testis'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'WIRTH Immune system', 'WIRTH Testis'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'SPANG\_CD40\_6hrs DN', 'SPANG\_CD40\_6hrs UP'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'SPANG\_CD40\_6hrs DN', 'SPANG\_CD40\_6hrs UP'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'spectrin binding', 'calcium-activated potassium channel activity'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'ATGT-221--222', 'GTCT-7'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'ATGT-221--222', 'GTCT-7'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'MIRNA target', 'hsa-miR-125b'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'GUSTAFSSON PI3K UP', 'GUSTAFSSON PI3K\_DN'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'HEBESTREIT high expression TF', 'HEBESTREIT low expression TF'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'HEBESTREIT high expression TF', 'HEBESTREIT low expression TF'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'VAQUERIZAS Heart', 'VAQUERIZAS General'.

Table with 3 columns: Rank, p-value, #in/all, Geneset. Lists biological processes like 'VAQUERIZAS Heart', 'VAQUERIZAS General'.

# Correlation Cluster

## Spot Summary: L

# metagenes = 42  
# genes = 550

<r> metagenes = 0.93  
<r> genes = 0.3  
beta: r2= 15.28 / log p= -Inf

# samples with spot = 63 ( 22.9 % )  
Atypical : 8 ( 10.8 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 49 ( 57.6 % )  
Basal : 4 ( 4.8 % )

## Spot Genelist

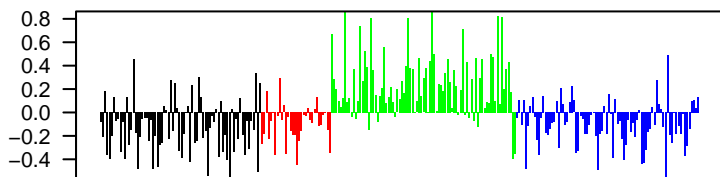
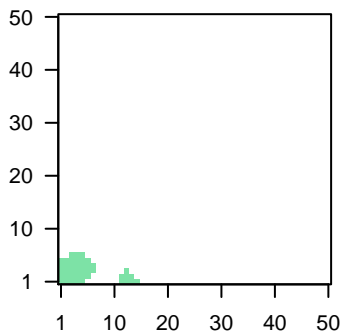
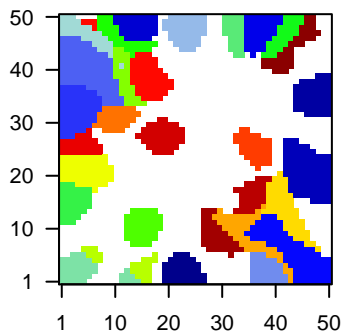
Rank	ID	max e	r	min e	Description
					Symbol
1	4319	4.09	-2.68	0.57	MMP10 matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
2	12	3.84	-2.36	0.4	RP11-986E7.7
3	3040	3.64	-2.76	0.32	HBA2 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	401138	3.58	-1.16	0.28	AMTN amelotin [Source:HGNC Symbol;Acc:33188]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

## Geneset Overrepresentation

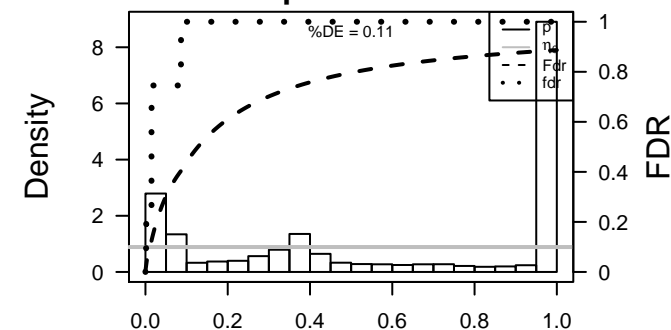
Rank	p-value	#in/all	Geneset
1	1e-65	87 / 250	Lymph LENZ_Stromal signature 1
2	3e-63	84 / 242	BP extracellular matrix organization
3	1e-58	73 / 190	CC extracellular matrix
4	1e-56	159 / 1182	CC extracellular region
5	2e-46	111 / 683	CC extracellular space
6	3e-45	99 / 553	Cancer Lembecke_Colonc Inflammation
7	3e-36	63 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
8	3e-36	63 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
9	3e-36	63 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
10	3e-36	63 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
11	3e-32	34 / 69	BP extracellular matrix disassembly
12	4e-32	33 / 64	BP collagen catabolic process
13	6e-31	70 / 403	BP cell adhesion
14	6e-31	49 / 183	CC proteinaceous extracellular matrix
15	5e-22	21 / 37	BP collagen fibril organization
16	8e-22	15 / 16	MMM MACIE_J_MMLL 1
17	5e-20	27 / 83	CC basement membrane
18	1e-19	23 / 57	MF extracellular matrix structural constituent
19	3e-17	13 / 16	GSE/FARMER_BREAST_CANCER_CLUSTER_5
20	9e-17	28 / 117	Glio GIEZELT_GBM_WT_up_VS_mut
21	3e-16	31 / 153	CC endoplasmic reticulum lumen
22	6e-16	12 / 15	GSE/FARMER_TUMORIGENESIS_UP
23	9e-16	35 / 204	BP angiogenesis
24	9e-16	50 / 407	BP blood coagulation
25	1e-15	13 / 19	MF extracellular matrix binding
26	3e-15	21 / 68	CC collagen
27	3e-13	24 / 114	BP positive regulation of cell migration
28	9e-13	24 / 119	Lymph ROSOLOWSKI_green total
29	2e-12	9 / 11	MF platelet-derived growth factor binding
30	2e-12	9 / 11	Glio Phillips MES up vs Prolif & PN
31	3e-12	20 / 85	MF integrin binding
32	4e-12	10 / 15	GSE/FARMER_ONDER_CDH1_TARGETS_2_UP
33	1e-11	18 / 72	CC extracellular vesicular exosome
34	2e-11	53 / 579	MF calcium ion binding
35	2e-11	34 / 269	BP inflammatory response
36	2e-11	38 / 330	CC cell surface
37	4e-11	18 / 76	BP wound healing
38	4e-11	13 / 35	Glio Colman_survival_associated
39	8e-11	14 / 44	MF collagen binding
40	2e-10	22 / 126	BP skeletal system development

## Overview Map

## Spot



## p-values





# Correlation Cluster

## Spot Summary: M

# metagenes = 25  
# genes = 123

<r> metagenes = 0.94  
<r> genes = 0.19  
beta: r2= 2.68 / log p= -Inf

# samples with spot = 22 ( 8 % )  
Atypical : 4 ( 5.4 % )  
Mesenchymal : 17 ( 20 % )  
Basal : 1 ( 1.2 % )

## Spot Genelist

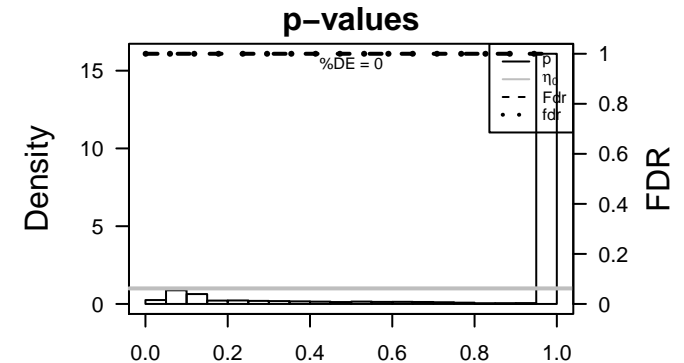
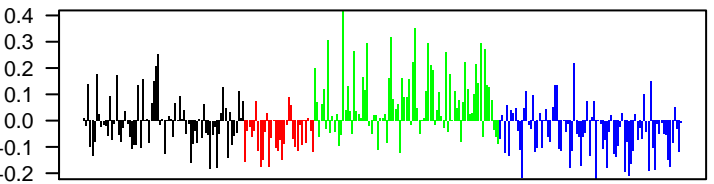
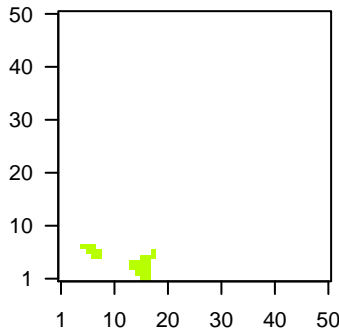
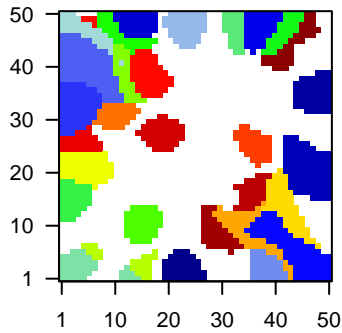
Rank	ID	max e	r	min e	Description
					Symbol
1	90637	1.72	-0.81	0.31	ZFAND2#zinc finger, AN1-type domain 2A [Source:HGNC Symbol;Acc:10120]
2	51312	1.67	-1.04	0.63	SLC25A3#olute carrier family 25 (mitochondrial iron transporter), memt
3	11213	1.59	-0.95	0.47	IRAK3 interleukin-1 receptor-associated kinase 3 [Source:HGNC S
4	26863	1.57	-1.39	0.28	RNU1-1 RNA, U1 small nuclear 1 [Source:HGNC Symbol;Acc:10120]
5	56675	1.56	-1.29	0.35	NRIP3 nuclear receptor interacting protein 3 [Source:HGNC Symbol;
6	26864	1.56	-1.2	0.28	RNVU1-RNA, variant U1 small nuclear 7 [Source:HGNC Symbol;Acc:
7	55321	1.56	-0.67	0.48	TMEM74#ansmembrane protein 74B [Source:HGNC Symbol;Acc:158
8	23551	1.52	-0.62	0.5	RASD2 RASD family, member 2 [Source:HGNC Symbol;Acc:18229]
9	1627	1.51	-1.29	0.62	DBN1 drebrin 1 [Source:HGNC Symbol;Acc:2695]
10	26869	1.5	-1.31	0.27	RNU1-1 RNA, U1 small nuclear 1 [Source:HGNC Symbol;Acc:10120]
11	7059	1.5	-1.04	0.59	THBS3 thrombospondin 3 [Source:HGNC Symbol;Acc:11787]
12	132625	1.46	-0.59	0.39	ZFP42 ZFP42 zinc finger protein [Source:HGNC Symbol;Acc:30949]
13	84969	1.36	-0.91	0.35	TOX2 TOX high mobility group box family member 2 [Source:HGNC
14	4499	1.32	-0.55	0.32	MT1M metallothionein 1M [Source:HGNC Symbol;Acc:14296]
15	1465	1.3	-0.94	0.57	CSRP1 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
16	79709	1.29	-1.19	0.7	COLGALT#ollagen beta(1-O)galactosyltransferase 1 [Source:HGNC Sy
17	1649	1.26	-0.76	0.31	DDIT3 DNA-damage-inducible transcript 3 [Source:HGNC Symbol;
18	1296	1.24	-0.79	0.49	COL8A2 collagen, type VIII, alpha 2 [Source:HGNC Symbol;Acc:2216]
19	10567	1.22	-0.9	0.7	RABAC1 Rab acceptor 1 (prenylated) [Source:HGNC Symbol;Acc:979
20	25825	1.21	-1.03	0.37	BACE2 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Ac

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-04	3 / 18	BP camera-type eye morphogenesis
2	6e-04	4 / 53	Glio Christensen_hypermethylated_in_primary_glioblastoma
3	8e-04	7 / 207	CC dendrite
4	2e-03	10 / 449	Chr Chr 20
5	2e-03	2 / 10	GSE# HELLER_HDAC_TARGETS_UP
6	3e-03	2 / 12	BP cAMP catabolic process
7	3e-03	2 / 12	GSE# NUTT_GBM_VS_AO_GLIOMA_UP
8	4e-03	2 / 13	BP synaptic vesicle endocytosis
9	4e-03	2 / 13	GSE# TOMLINS_METASTASIS_DN
10	4e-03	2 / 13	GSE# NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP
11	4e-03	2 / 13	GSE# KEGG_CIRCADIEN_RHYTHM_MAMMAL
12	5e-03	2 / 14	GSE# BENPORATH_ES_WITH_H3K27ME3
13	5e-03	2 / 14	GSE# BIOCARTA_GCR_PATHWAY
14	5e-03	2 / 15	BP regulation of neuronal synaptic plasticity
15	5e-03	2 / 15	GSE# MULLIGHAN_MLL_SIGNATURE_2_UP
16	5e-03	2 / 15	GSE# RAGHAVACHARI_PLATELET_SPECIFIC_GENES
17	5e-03	2 / 15	GSE# BLALOCK_ALZHEIMERS_DISEASE_DN
18	5e-03	5 / 153	CC endoplasmic reticulum lumen
19	6e-03	3 / 49	miRN hsa-miR-1201
20	6e-03	2 / 16	BP synaptic vesicle exocytosis
21	6e-03	2 / 16	GSE# HEIDENBLAD_AMPLICON_8Q24_DN
22	6e-03	2 / 16	GSE# BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_UP
23	6e-03	2 / 16	GSE# REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRF1_AND_NA
24	6e-03	2 / 16	GSE# ST_GRANULE_CELL_SURVIVAL_PATHWAY
25	7e-03	2 / 17	MF proline-rich region binding
26	7e-03	8 / 379	Glio Down_a
27	7e-03	3 / 53	CC endoplasmic reticulum-Golgi intermediate compartment
28	8e-03	2 / 19	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
29	9e-03	16 / 1135	Chr Chr 19
30	9e-03	4 / 110	Glio Christensen_hypermethylated_in_grade3_astrocytoma
31	9e-03	3 / 58	CC ruffle membrane
32	9e-03	2 / 20	BP phosphatidylinositol metabolic process
33	9e-03	2 / 20	BP positive regulation of synapse assembly
34	9e-03	8 / 400	H.Tis: WIRTH_Nervous System
35	1e-02	10 / 579	MF calcium ion binding
36	1e-02	2 / 21	MF aspartic-type endopeptidase activity
37	1e-02	2 / 21	BP female gonad development
38	1e-02	2 / 21	BP iron ion homeostasis
39	1e-02	2 / 21	Glio Martinezz_Glio_hypermeth
40	1e-02	5 / 182	miRN CTGA-24

## Overview Map

## Spot





# Correlation Cluster

## Spot Summary: N

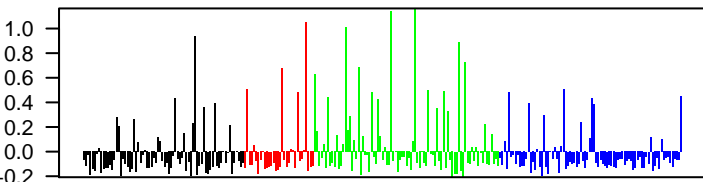
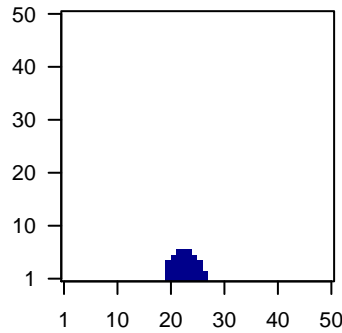
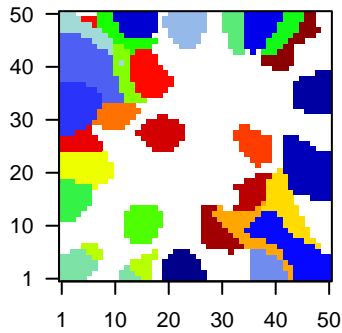
# metagenes = 38  
# genes = 224

<r> metagenes = 0.96  
<r> genes = 0.44  
beta: r2= 5.46 / log p= -Inf

# samples with spot = 38 ( 13.8 % )  
Atypical : 9 ( 12.2 % )  
Classical : 4 ( 12.5 % )  
Mesenchymal : 17 ( 20 % )  
Basal : 8 ( 9.5 % )

### Overview Map

### Spot



## Spot Genelist

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

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	88 / 127	H.Tis: WIRTH_Muscle
2	5e-37	24 / 36	BP muscle filament sliding
3	6e-34	24 / 44	MF structural constituent of muscle
4	3e-30	27 / 84	BP muscle contraction
5	4e-28	26 / 88	CC Z disc
6	2e-22	13 / 16	H.Tis: WIRTH_Hippocampus
7	9e-20	15 / 34	CC myofibril
8	3e-18	12 / 20	CC I band
9	9e-18	11 / 16	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_F
10	1e-17	10 / 12	CC myosin filament
11	2e-17	14 / 37	CC sarcomere
12	7e-17	29 / 297	MF actin binding
13	9e-15	9 / 13	CC muscle myosin complex
14	4e-14	12 / 37	BP cardiac muscle contraction
15	6e-14	9 / 15	BP striated muscle contraction
16	1e-13	9 / 16	CC M band
17	3e-12	8 / 14	CC contractile fiber
18	6e-12	8 / 15	GSE/ REACTOME_STRIATED_MUSCLE_CONTRACTION
19	1e-11	14 / 88	BP muscle organ development
20	6e-11	7 / 12	MF titin binding
21	1e-10	9 / 29	CC sarcoplasmic reticulum membrane
22	2e-10	8 / 21	BP sarcomere organization
23	6e-10	11 / 62	CC sarcolemma
24	9e-10	9 / 36	CC sarcoplasmic reticulum
25	1e-09	10 / 51	BP skeletal muscle tissue development
26	3e-09	6 / 11	CC A band
27	3e-09	6 / 11	BP cardiac muscle tissue morphogenesis
28	5e-09	6 / 12	BP skeletal muscle contraction
29	4e-08	9 / 53	MF cytoskeletal protein binding
30	7e-08	7 / 28	CC T-tubule
31	8e-08	8 / 42	CC myosin complex
32	9e-08	6 / 18	BP regulation of muscle contraction
33	9e-08	6 / 18	BP regulation of the force of heart contraction
34	1e-07	13 / 149	MF calmodulin binding
35	2e-07	20 / 375	Disea GUDJ_psoriasis down
36	2e-07	14 / 184	CC actin cytoskeleton
37	8e-07	5 / 14	MF tropomyosin binding
38	1e-06	5 / 15	GSE/ EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
39	2e-06	5 / 16	GSE/ KEGG_DILATED_CARDIOMYOPATHY
40	2e-06	6 / 29	BP regulation of heart contraction

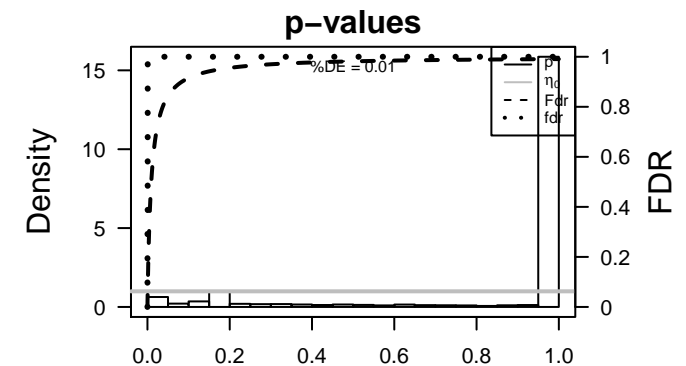


Table with 3 columns: p-value, #in/all, Geneset. Lists various biological processes such as muscle contraction, cardiac muscle contraction, and regulation of heart contraction.

Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes like muscle filament sliding, cardiac muscle contraction, and striated muscle contraction.

Table with 3 columns: p-value, #in/all, Geneset. Lists various cancer types and related processes, including prostate cancer, breast cancer, and lung cancer.

Table with 3 columns: p-value, #in/all, Geneset. Lists biological processes such as cell cycle, cell division, and cell growth.

Table with 3 columns: p-value, #in/all, Geneset. Lists various cellular structures and organelles, including mitochondria, cytoskeleton, and nucleus.

Table with 3 columns: p-value, #in/all, Geneset. Lists chromosomes and related genomic features.

Table with 3 columns: p-value, #in/all, Geneset. Lists various biological processes and pathways, including metabolic pathways and signaling.

Table with 3 columns: p-value, #in/all, Geneset. Lists various diseases and related conditions, including cancer, neurodegenerative diseases, and metabolic disorders.

Table with 3 columns: p-value, #in/all, Geneset. Lists various biological processes and pathways, including cell cycle and protein synthesis.

Table with 3 columns: p-value, #in/all, Geneset. Lists various biological processes and pathways, including cell cycle and cell growth.

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Table with 3 columns: p-value, #in/all, Geneset. Lists various biological processes and pathways, including cell cycle and cell growth.



# Correlation Cluster

## Spot Summary: O

# metagenes = 38  
# genes = 115

<r> metagenes = 0.94  
<r> genes = 0.18  
beta: r2= 0.79 / log p= -Inf

# samples with spot = 5 ( 1.8 % )  
Atypical : 3 ( 4.1 % )  
Mesenchymal : 2 ( 2.4 % )

## Spot Genelist

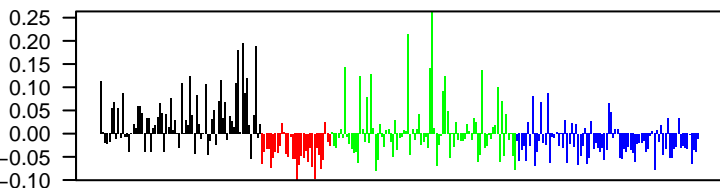
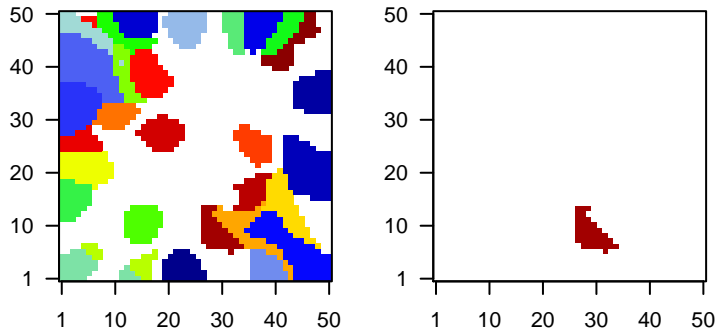
Rank	ID	max e	r	min e	Description
1	2710	1.79	-0.85	0.28	GK glycerol kinase [Source:HGNC Symbol;Acc:4289]
2	51561	1.25	-0.57	0.25	IL23A interleukin 23, alpha subunit p19 [Source:HGNC Symbol;Acc:
3	7850	1.16	-0.64	0.28	IL1R2 interleukin 1 receptor, type II [Source:HGNC Symbol;Acc:599
4	162989	1.05	-0.95	0.32	DEDD2 death effector domain containing 2 [Source:HGNC Symbol;Ac
5	1844	0.97	-0.49	0.48	DUSP2 dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:3C
6	221692	0.94	-0.29	0.5	PHACTR1 phosphatase and actin regulator 1 [Source:HGNC Symbol;Ac
7	6774	0.92	-0.92	0.21	STAT3 signal transducer and activator of transcription 3 (acute-phas
8	25953	0.89	-0.48	0.52	PNKD paroxysmal nonkinetogenic dyskinesia [Source:HGNC Symbc
9	80704	0.86	-0.36	0.37	SLC19A3 solute carrier family 19 (thiamine transporter), member 3 [So
10	83636	0.83	-0.54	0.4	C19orf12 chromosome 19 open reading frame 12 [Source:HGNC Symt
11	83938	0.8	-0.55	0.32	C10orf11 chromosome 10 open reading frame 11 [Source:HGNC Symt
12	943	0.77	-0.35	0.43	TNFRSF8 tumor necrosis factor receptor superfamily, member 8 [Source
13	9674	0.76	-0.35	0.29	KIAA0046 KIAA0040 [Source:HGNC Symbol;Acc:28950]
14	81553	0.73	-0.39	0.5	FAM49A family with sequence similarity 49, member A [Source:HGNC
15	64180	0.71	-0.23	0.37	DPEP3 dipeptidase 3 [Source:HGNC Symbol;Acc:23029]
16	56905	0.71	-0.67	0.37	C15orf39 chromosome 15 open reading frame 39 [Source:HGNC Symt
17	26823	0.7	-0.27	0.29	
18	5027	0.69	-0.34	0.26	P2RX7 purinergic receptor P2X, ligand-gated ion channel, 7 [Source
19	140	0.69	-0.29	0.39	ADORA3 adenosine A3 receptor [Source:HGNC Symbol;Acc:268]
20	9034	0.67	-0.33	0.62	CCRL2 chemokine (C-C motif) receptor-like 2 [Source:HGNC Symbc

## Geneset Overrepresentation

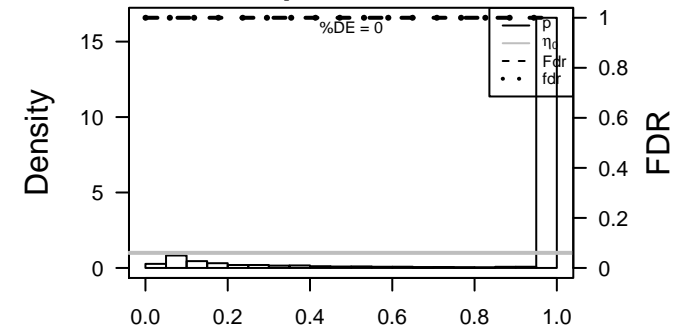
Rank	p-value	#in/all	Geneset
1	2e-08	43 / 2659	CC plasma membrane
2	3e-06	11 / 269	BP inflammatory response
3	1e-05	22 / 1167	BP signal transduction
4	3e-05	14 / 553	Cancer Lembecke_Colonc Inflammation
5	5e-05	3 / 11	BP negative regulation of interleukin-12 production
6	7e-05	13 / 530	BP innate immune response
7	2e-04	16 / 835	CC integral to plasma membrane
8	3e-04	4 / 45	BP cellular defense response
9	3e-04	9 / 312	BP immune response
10	5e-04	6 / 143	MF transmembrane signaling receptor activity
11	1e-03	3 / 29	BP receptor internalization
12	2e-03	2 / 9	GSE/ SA_MMP_CYTOKINE_CONNECTION
13	2e-03	4 / 74	BP regulation of immune response
14	2e-03	2 / 11	CC low-density lipoprotein particle
15	2e-03	2 / 11	GSE/ NAKAJIMA_EOSINOPHIL
16	3e-03	6 / 204	BP cell surface receptor signaling pathway
17	3e-03	2 / 12	GSE/ PEREZ_TP53_TARGETS
18	3e-03	2 / 12	GSE/ ROVERSI_GLIOMA_COPY_NUMBER_UP
19	3e-03	3 / 42	BP nucleotide-binding domain, leucine rich repeat containing receptor signalin
20	3e-03	9 / 435	BP G-protein coupled receptor signaling pathway
21	4e-03	2 / 13	MF mitogen-activated protein kinase binding
22	4e-03	2 / 13	GSE/ LIU_TARGETS_OF_VMYB_VS_CMYB_DN
23	4e-03	2 / 14	CC very-low-density lipoprotein particle
24	4e-03	2 / 14	GSE/ VALK_AML_CLUSTER_5
25	4e-03	2 / 14	GSE/ MAHAJAN_RESPONSE_TO_IL1A_UP
26	5e-03	2 / 15	GSE/ TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION GRANULOCYTE_D
27	5e-03	2 / 15	GSE/ KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY
28	5e-03	2 / 15	GSE/ BIOCARTA_NKCELLS_PATHWAY
29	5e-03	3 / 49	Glio Donson-innate immunity-associated with LTS in HGA
30	5e-03	6 / 227	MF receptor activity
31	5e-03	8 / 386	Chr Chr 22
32	5e-03	2 / 16	MF 14-3-3 protein binding
33	5e-03	2 / 16	MF chemokine receptor activity
34	5e-03	2 / 16	GSE/ GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP
35	5e-03	2 / 16	GSE/ SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP
36	5e-03	5 / 162	CC external side of plasma membrane
37	7e-03	2 / 18	BP positive regulation of T cell mediated cytotoxicity
38	7e-03	4 / 111	BP chemotaxis
39	7e-03	2 / 19	BP T cell proliferation
40	8e-03	3 / 59	MF protein phosphatase binding

Overview Map

Spot



p-values





# Correlation Cluster

## Spot Summary: P

# metagenes = 55  
# genes = 343

<r> metagenes = 0.94  
<r> genes = 0.23  
beta: r2= 3.3 / log p= -Inf

# samples with spot = 24 ( 8.7 % )  
Atypical : 10 ( 13.5 % )  
Classical : 1 ( 3.1 % )  
Mesenchymal : 6 ( 7.1 % )  
Basal : 7 ( 8.3 % )

## Spot Genelist

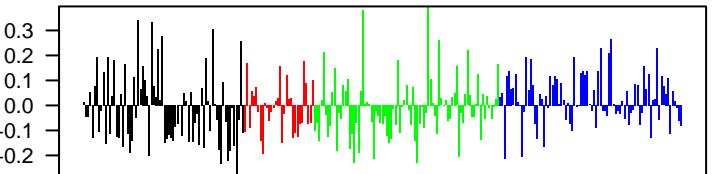
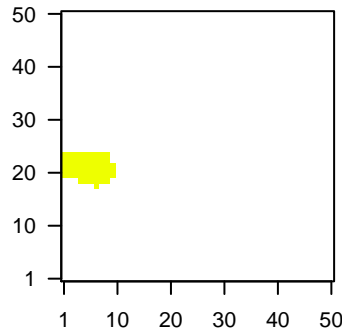
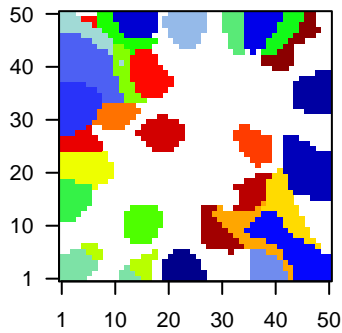
Rank	ID	max e	r	min e	Description
1	51702	2.13	-1.03	0.26	PADI3 peptidyl arginine deiminase, type III [Source:HGNC Symbol;Acc:10110]
2	3006	2.13	-1.48	0.19	HIST1H1D histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
3	430	1.64	-1.34	0.32	ASCL2 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:10110]
4	6884	1.58	-1	0.52	TAF13 TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor 13 [Source:HGNC Symbol;Acc:10110]
5	80154	1.54	-1.25	0.45	ARHGAP23 Rho guanine nucleotide exchange factor (GEF) 16 [Source:HGNC Symbol;Acc:10110]
6	27237	1.42	-1.48	0.44	ARHGAP23 Rho guanine nucleotide exchange factor (GEF) 16 [Source:HGNC Symbol;Acc:10110]
7	85019	1.37	-0.88	0.39	TMEM241 transmembrane protein 241 [Source:HGNC Symbol;Acc:3172]
8	90990	1.34	-1.06	0.46	KIFC2 kinesin family member C2 [Source:HGNC Symbol;Acc:29530]
9	8045	1.34	-1.07	0.55	RASSF7 Ras association (RalGDS/AF-6) domain family (N-terminal) member 7 [Source:HGNC Symbol;Acc:10110]
10	51337	1.33	-1.19	0.36	THEM6 thioesterase superfamily member 6 [Source:HGNC Symbol;Acc:10110]
11	79703	1.33	-1.36	0.37	C11orf80 chromosome 11 open reading frame 80 [Source:HGNC Symbol;Acc:10110]
12	2872	1.32	-1.1	0.39	MKNK2 MAP kinase interacting serine/threonine kinase 2 [Source:HGNC Symbol;Acc:10110]
13	85359	1.32	-0.72	0.5	DGCR6L DiGeorge syndrome critical region gene 6-like [Source:HGNC Symbol;Acc:10110]
14	100169760	1.3	-0.65	0.21	RNA5S9 RNA, 5S ribosomal 9 [Source:HGNC Symbol;Acc:34370]
15	5652	1.26	-1.57	0.49	PRSS8 protease, serine, 8 [Source:HGNC Symbol;Acc:9491]
16	6509	1.23	-0.94	0.21	SLC1A4 solute carrier family 1 (glutamate/neutral amino acid transport) member 4 [Source:HGNC Symbol;Acc:10110]
17	2717	1.23	-0.84	0.23	GLA galactosidase, alpha [Source:HGNC Symbol;Acc:4296]
18	3418	1.2	-1.07	0.33	IDH2 isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:HGNC Symbol;Acc:10110]
19	118881	1.2	-1.2	0.57	COMTDC1 catechol-O-methyltransferase domain containing 1 [Source:HGNC Symbol;Acc:10110]
20	83715	1.2	-0.73	0.5	ESPN espin [Source:HGNC Symbol;Acc:13281]

## Geneset Overrepresentation

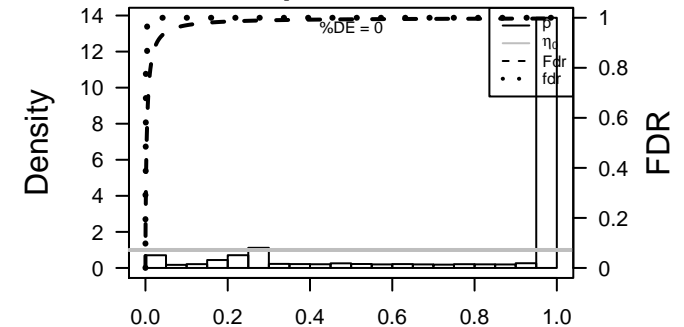
Rank	p-value	#in/all	Geneset
1	1e-10	58 / 1135	Chr Chr 19
2	1e-08	40 / 717	Chr Chr 16
3	8e-08	57 / 1318	CC mitochondrion
4	1e-06	37 / 755	Lymph SPANG_BCR_UP
5	6e-06	20 / 304	CC mitochondrial inner membrane
6	2e-05	13 / 152	BP cellular metabolic process
7	5e-05	9 / 83	BP respiratory electron transport chain
8	2e-04	45 / 1253	BP small molecule metabolic process
9	3e-04	4 / 16	GSE/ BERNARD_PPAPDC1B_TARGETS_UP
10	3e-04	4 / 16	GSE/ BIOCARTE_PTIDINS_PATHWAY
11	3e-04	7 / 62	BP negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
12	3e-04	4 / 17	CC proteasome accessory complex
13	4e-04	9 / 106	BP protein polyubiquitination
14	4e-04	7 / 66	BP positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
15	4e-04	6 / 48	BP regulation of cellular amino acid metabolic process
16	5e-04	27 / 649	BP gene expression
17	5e-04	8 / 89	CC microtubule organizing center
18	6e-04	21 / 455	CC perinuclear region of cytoplasm
19	6e-04	7 / 70	BP regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
20	8e-04	4 / 21	BP positive regulation of DNA repair
21	8e-04	7 / 74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-dependent proteolysis
22	1e-03	3 / 10	MF NADH dehydrogenase activity
23	1e-03	3 / 10	MF oxidoreductase activity, acting on NAD(P)H
24	1e-03	3 / 10	GSE/ REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE
25	1e-03	3 / 11	GSE/ AMIT_EGF_RESPONSE_20_MCF10A
26	2e-03	3 / 12	GSE/ REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE_NUCLEOTIDE_EXCHANGE_FACTOR_1
27	2e-03	6 / 63	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
28	2e-03	12 / 219	BP mRNA metabolic process
29	2e-03	3 / 13	GSE/ PENG_Glutamine_deprivation_DN
30	2e-03	3 / 13	GSE/ KEGG_RNA_DEGRADATION
31	2e-03	12 / 220	CC mitochondrial matrix
32	3e-03	4 / 28	BP exonucleolytic nuclear-transcribed mRNA catabolic process involved in development
33	3e-03	3 / 14	MF pseudouridine synthase activity
34	3e-03	3 / 14	GSE/ REACTOME_METABOLISM_OF_MRNA
35	3e-03	3 / 14	GSE/ ST_B_CELL_ANTIEN_RECEPTOR
36	3e-03	7 / 91	BP antigen processing and presentation of peptide antigen via MHC class I
37	3e-03	6 / 70	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
38	3e-03	3 / 15	GSE/ DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
39	3e-03	3 / 15	GSE/ OZEN_MIR125B1_TARGETS
40	3e-03	3 / 15	GSE/ SASSON_RESPONSE_TO_FORSKOLIN_UP

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: Q

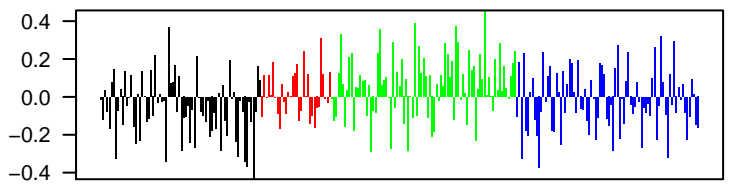
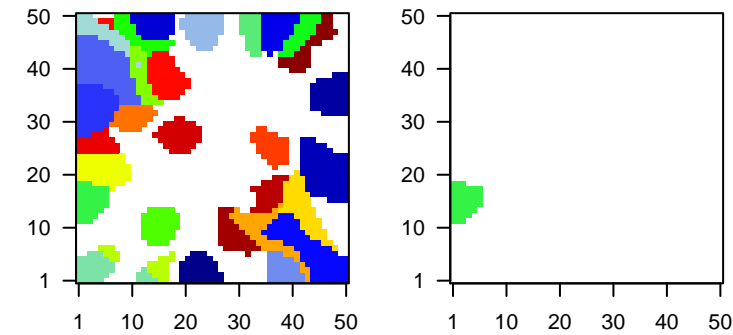
# metagenes = 39  
# genes = 357

<r> metagenes = 0.94  
<r> genes = 0.27  
beta: r2= 5.59 / log p= -Inf

# samples with spot = 42 ( 15.3 % )  
Atypical : 4 ( 5.4 % )  
Classical : 4 ( 12.5 % )  
Mesenchymal : 22 ( 25.9 % )  
Basal : 12 ( 14.3 % )

### Overview Map

### Spot

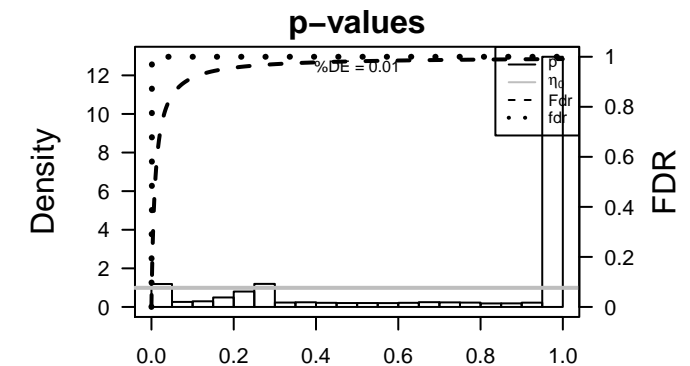


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	283869	2.84	-1.53	0.53	NPW neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	4495	2.82	-1.79	0.21	MT1G metallothionein 1G [Source:HGNC Symbol;Acc:7399]
3	220064	2.61	-1.08	0.48	ORAOV1 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175]
4	10202	2.48	-0.58	0.41	DHRS2 dehydrogenase/reductase (SDR family) member 2 [Source:HGNC Symbol;Acc:26874]
5	284085	2.29	-1.64	0.42	KRT18P5 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]
6	131076	2.28	-1.53	0.33	CCDC58 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:26874]
7	51083	2.28	-0.81	0.5	GAL galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:417]
8	8772	2.18	-1.29	0.52	FADD Fas (TNFRSF6)-associated via death domain [Source:HGNC Symbol;Acc:1991]
9	1152	2.07	-1.8	0.37	CKB creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
10	219931	2.01	-0.93	0.56	TPCN2 two pore segment channel 2 [Source:HGNC Symbol;Acc:208]
11	51373	1.97	-1.11	0.64	MRPS1728S ribosomal protein S17, mitochondrial; HCG1984214, isoform 2 [Source:HGNC Symbol;Acc:208]
12	2017	1.86	-1.24	0.42	CTTN cortactin [Source:HGNC Symbol;Acc:3338]
13	219927	1.84	-0.94	0.54	MRPL21 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;Acc:208]
14	2821	1.69	-0.94	0.44	GPI glucose-6-phosphate isomerase [Source:HGNC Symbol;Acc:15519]
15	23246	1.68	-1.14	0.75	BOP1 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
16	93273	1.67	-0.94	0.31	LEMD1 LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
17	230	1.64	-1.33	0.36	ALDOC aldolase C, fructose-bisphosphate [Source:HGNC Symbol;Acc:15519]
18	26873	1.55	-1.16	0.45	OPLAH 5-oxoprolinase (ATP-hydrolysing) [Source:HGNC Symbol;Acc:15519]
19	388581	1.55	-0.58	0.43	FAM132A family with sequence similarity 132, member A [Source:HGNC Symbol;Acc:15519]
20	142678	1.5	-1.09	0.53	MIB2 mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:15519]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-16	77 / 1318	CC mitochondrion
2	2e-12	41 / 530	Cancer_Lembcke_Normal vs Adenoma
3	9e-10	19 / 153	MF structural constituent of ribosome
4	1e-09	38 / 579	CC nucleolus
5	5e-09	50 / 949	CC nucleoplasm
6	7e-09	23 / 253	BP translation
7	2e-08	14 / 96	BP rRNA processing
8	2e-08	18 / 167	CC ribosome
9	2e-07	11 / 66	BP positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
10	2e-07	36 / 649	BP gene expression
11	3e-07	10 / 55	CC proteasome complex
12	3e-07	11 / 70	BP regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
13	5e-07	11 / 74	BP anaphase-promoting complex-dependent ubiquitin-dependent cell cycle regulation
14	8e-07	9 / 48	BP regulation of cellular amino acid metabolic process
15	8e-07	10 / 62	BP negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
16	9e-07	10 / 63	TF MYC_Targets_UP
17	1e-06	53 / 1233	TF KIM_MYC targets
18	3e-06	21 / 304	CC mitochondrial inner membrane
19	6e-06	18 / 242	BP RNA metabolic process
20	8e-06	9 / 63	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
21	1e-05	7 / 37	CC mitochondrial nucleoid
22	2e-05	5 / 16	GSE/ KORKOLA_EMBRYONAL_CARCINOMA_UP
23	2e-05	5 / 16	GSE/ WONG_EMBRYONIC_STEM_CELL_CORE
24	2e-05	30 / 595	MF RNA binding
25	2e-05	14 / 167	BP cellular nitrogen compound metabolic process
26	2e-05	19 / 287	BP viral process
27	2e-05	9 / 70	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
28	2e-05	22 / 370	BP mitotic cell cycle
29	2e-05	5 / 17	CC proteasome core complex
30	3e-05	9 / 74	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
31	3e-05	5 / 18	MF threonine-type endopeptidase activity
32	4e-05	4 / 10	GSE/ REACTOME_HIV_LIFE_CYCLE
33	4e-05	5 / 19	CC mitochondrial small ribosomal subunit
34	7e-05	134 / 4640	CC nucleus
35	9e-05	15 / 219	BP mRNA metabolic process
36	1e-04	10 / 106	BP protein polyubiquitination
37	1e-04	4 / 13	GSE/ XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
38	1e-04	4 / 13	GSE/ REACTOME_GLYCOLYSIS
39	1e-04	5 / 24	MF DNA helicase activity
40	2e-04	9 / 91	BP antigen processing and presentation of peptide antigen via MHC class I





# Correlation Cluster

## Spot Summary: R

# metagenes = 30  
# genes = 308

<r> metagenes = 0.97  
<r> genes = 0.37  
beta: r2= 6.83 / log p= -Inf

# samples with spot = 52 ( 18.9 % )  
Atypical : 12 ( 16.2 % )  
Classical : 11 ( 34.4 % )  
Mesenchymal : 26 ( 30.6 % )  
Basal : 3 ( 3.6 % )

## Spot Genelist

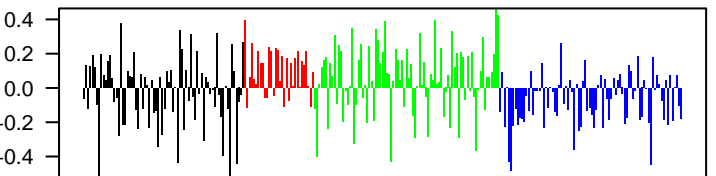
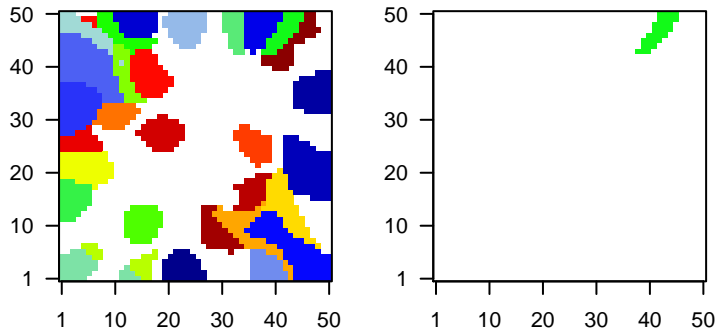
Rank	ID	max e	r	min e	Description
					Symbol
1	100008588	2.37	-0.91	0.23	RNA18S rRNA, 18S ribosomal 5 [Source:HGNC Symbol;Acc:37657]
2	8500	1.93	-1.22	0.43	PPF1A1 protein tyrosine phosphatase, receptor type, f polypeptide (P1)
3	9918	1.93	-1.18	0.52	NCAPD2 non-SMC condensin I complex, subunit D2 [Source:HGNC S
4	387103	1.83	-1.44	0.62	CENPW centromere protein W [Source:HGNC Symbol;Acc:21488]
5	81831	1.76	-1.65	0.52	NETO2 neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Sym
6	3992	1.73	-1.29	0.47	FADS1 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
7	7153	1.7	-1.84	0.83	TOP2A topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
8	1894	1.64	-1.47	0.85	ECT2 epithelial cell transforming sequence 2 oncogene [Source:HG
9	10635	1.63	-1.2	0.84	RAD51AP1 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
10	9319	1.58	-1.43	0.67	TRIP13 thyroid hormone receptor interactor 13 [Source:HGNC Symbc
11	8318	1.51	-1.6	0.76	CDC45 cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
12	54443	1.46	-1.74	0.71	ANLN anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
13	55353	1.45	-1.41	0.47	LAPTM4 lysosomal protein transmembrane 4 beta [Source:HGNC Sym
14	51659	1.45	-1.7	0.62	GINS2 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
15	55839	1.45	-1.29	0.62	CENPN centromere protein N [Source:HGNC Symbol;Acc:30873]
16	22974	1.44	-1.45	0.77	TPX2 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:1
17	113130	1.43	-1.66	0.69	CDCA5 cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
18	9133	1.42	-1.42	0.78	CCNB2 cyclin B2 [Source:HGNC Symbol;Acc:1580]
19	6611	1.4	-0.97	0.48	SMS spermine synthase [Source:HGNC Symbol;Acc:11123]
20	65062	1.4	-1.31	0.56	TMEM237 transmembrane protein 237 [Source:HGNC Symbol;Acc:144

## Geneset Overrepresentation

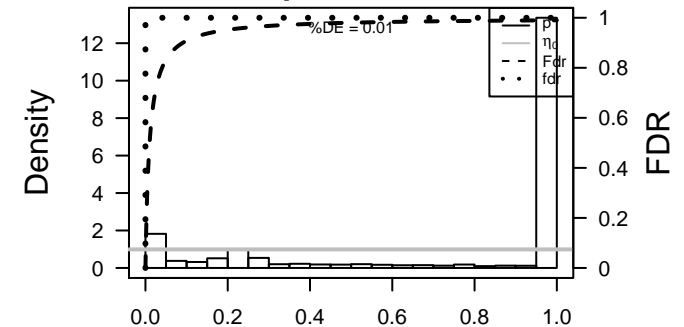
Rank	p-value	#in/all	Geneset
1	1e-99	79 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	1e-99	79 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	2e-68	84 / 370	BP mitotic cell cycle
4	3e-47	77 / 530	Cancer_Lembcke_Normal vs Adenoma
5	9e-38	49 / 232	BP mitosis
6	1e-35	85 / 949	CC nucleoplasm
7	3e-24	55 / 572	Disease_GUDJ_psooriasis up
8	2e-22	21 / 56	CC chromosome, centromeric region
9	3e-22	22 / 66	CC condensed chromosome kinetochore
10	1e-21	14 / 18	BP spindle organization
11	2e-19	19 / 57	Glio developing astrocytes
12	2e-18	12 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_2
13	2e-18	12 / 16	GSE/ FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
14	6e-18	157 / 4640	CC nucleus
15	3e-17	11 / 14	MMM MACIEJ_MMML 4
16	3e-17	18 / 61	CC kinetochore
17	1e-16	11 / 15	GSE/ FINETTI_BREAST_CANCER_KINOME_RED
18	1e-16	101 / 2378	CC cytosol
19	4e-16	24 / 148	BP G1/S transition of mitotic cell cycle
20	6e-16	19 / 83	CC spindle pole
21	1e-15	10 / 13	GSE/ CROONQUIST_IL6_DEPRIVATION_DN
22	4e-15	17 / 67	BP chromosome segregation
23	2e-13	9 / 13	GSE/ WINNEPENNINGCKX_MELANOMA_METASTASIS_UP
24	4e-13	9 / 14	GSE/ ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
25	4e-13	9 / 14	GSE/ AMUNDSON_GAMMA_RADIATION_RESPONSE
26	4e-13	9 / 14	GSE/ ZHAN_MULTIPLE_MYELOMA_PR_UP
27	6e-13	8 / 10	GSE/ MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
28	1e-12	9 / 15	GSE/ FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
29	2e-12	10 / 22	BP CENP-A containing nucleosome assembly at centromere
30	2e-12	9 / 16	GSE/ KANG_DOXORUBICIN_RESISTANCE_UP
31	4e-12	208 / 8023	MF protein binding
32	5e-12	20 / 149	BP DNA replication
33	2e-11	11 / 35	BP mitotic nuclear envelope disassembly
34	6e-11	26 / 298	BP DNA repair
35	7e-11	8 / 15	Cancer_SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
36	7e-11	8 / 15	GSE/ SMID_BREAST_CANCER_LUMINAL_A_DN
37	7e-11	8 / 15	GSE/ LEE_EARLY_T_LYMPHOCYTE_UP
38	7e-11	8 / 15	GSE/ WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
39	7e-11	8 / 15	GSE/ LY_AGING_MIDDLE_DN
40	1e-10	17 / 122	BP G2/M transition of mitotic cell cycle

Overview Map

Spot



p-values







# Correlation Cluster

## Spot Summary: S

# metagenes = 40  
# genes = 471

<r> metagenes = 0.94  
<r> genes = 0.27  
beta: r2= 4.23 / log p= -Inf

# samples with spot = 31 ( 11.3 % )  
Atypical : 2 ( 2.7 % )  
Classical : 7 ( 21.9 % )  
Mesenchymal : 15 ( 17.6 % )  
Basal : 7 ( 8.3 % )

## Spot Genelist

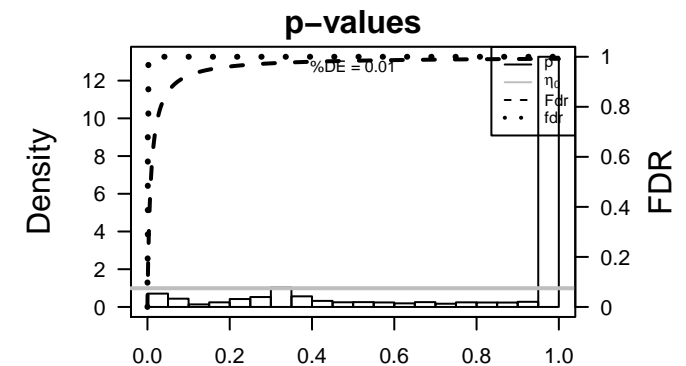
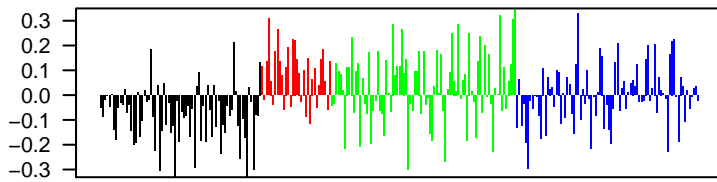
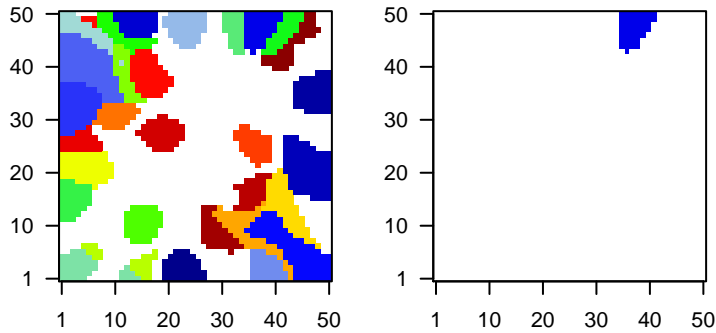
Rank	ID	max e	r	min e	Description
1	908	1.96	-0.89	0.63	CCT6A chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HGNC Symbol;Acc:1434]
2	793	1.83	-0.42	0.29	CALB1 calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
3	23480	1.83	-1.04	0.49	SEC61G Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
4	8836	1.83	-1.06	0.52	GGH gamma-glutamyl hydrolase (conjugase, folypolygamgluta
5	55915	1.8	-0.75	0.34	LANCL2 LanC lantibiotic synthetase component C-like 2 (bacterial) [S
6	2631	1.79	-0.97	0.4	GBAS glioblastoma amplified sequence [Source:HGNC Symbol;Acc
7	26872	1.76	-1.29	0.41	STEAP1 six transmembrane epithelial antigen of the prostate 1 [Sourc
8	3945	1.73	-1.73	0.38	LDHB lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
9	5321	1.65	-0.85	0.46	PLA2G4A phospholipase A2, group IVA (cytosolic, calcium-dependent)
10	643253	1.56	-0.75	0.7	
11	54802	1.51	-0.79	0.47	TRIT1 tRNA isopentenyltransferase 1 [Source:HGNC Symbol;Acc:21
12	134147	1.43	-1.05	0.27	CMBL carboxymethylenebutenolidase homolog (Pseudomonas) [So
13	10576	1.4	-0.82	0.54	CCT2 chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
14	5723	1.39	-0.48	0.53	PSPH phosphoserine phosphatase [Source:HGNC Symbol;Acc:957
15	51142	1.36	-0.79	0.45	CHCHD2 coiled-coil-helix-coiled-coil-helix domain containing 2 [Sour
16	154807	1.33	-0.77	0.62	VKORC1 vitamin K epoxide reductase complex, subunit 1-like 1 [Sourc
17	136	1.33	-1.43	0.63	ADORA2B adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
18	54517	1.32	-1.07	0.57	PUS7 pseudouridylyl synthase 7 homolog (S. cerevisiae) [Source:HG
19	388722	1.27	-0.85	0.53	C1orf53 chromosome 1 open reading frame 53 [Source:HGNC Symbol
20	51504	1.25	-0.91	0.45	TRMT112 RNA methyltransferase 11-2 homolog (S. cerevisiae) [Sourc

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-22	103 / 1318	CC mitochondrion
2	2e-12	79 / 1233	TF KIM_MYC targets
3	8e-11	50 / 649	BP gene expression
4	2e-09	42 / 534	Chr Chr 8
5	2e-09	44 / 579	CC nucleolus
6	4e-08	19 / 150	BP protein folding
7	6e-08	48 / 743	Chr Chr 7
8	9e-08	6 / 10	CC zona pellucida receptor complex
9	1e-07	8 / 23	CC mitochondrial ribosome
10	2e-07	24 / 253	BP translation
11	5e-07	54 / 949	CC nucleoplasm
12	1e-06	13 / 88	MF unfolded protein binding
13	1e-06	18 / 167	CC ribosome
14	1e-06	17 / 153	MF structural constituent of ribosome
15	1e-06	11 / 64	BP tRNA processing
16	2e-06	7 / 22	BP ncRNA metabolic process
17	2e-06	6 / 15	Canco GENTLES_modul6
18	2e-06	24 / 287	BP viral process
19	2e-06	21 / 229	BP RNA splicing
20	3e-06	55 / 1033	Chr Chr 2
21	5e-06	21 / 242	BP RNA metabolic process
22	5e-06	7 / 26	BP spliceosomal snRNP assembly
23	5e-06	8 / 36	BP 'de novo' posttranslational protein folding
24	1e-05	10 / 66	BP transcription elongation from RNA polymerase II promoter
25	3e-05	8 / 44	BP positive regulation of viral transcription
26	3e-05	6 / 23	BP binding of sperm to zona pellucida
27	4e-05	5 / 15	GSE/ REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_
28	4e-05	7 / 35	MF aminoacyl-tRNA ligase activity
29	6e-05	15 / 163	BP mRNA splicing, via spliceosome
30	6e-05	11 / 93	CC spliceosomal complex
31	9e-05	7 / 39	Canco ZHANG_MM up
32	1e-04	5 / 18	Lymp DAVE_c-myc BL UP
33	1e-04	15 / 174	BP mRNA processing
34	1e-04	21 / 304	CC mitochondrial inner membrane
35	2e-04	4 / 11	BP chaperone-mediated protein complex assembly
36	2e-04	6 / 31	BP 7-methylguanosine mRNA capping
37	2e-04	7 / 44	BP tRNA aminoacylation for protein translation
38	2e-04	5 / 21	BP termination of RNA polymerase I transcription
39	3e-04	4 / 12	BP mitochondrial fission
40	3e-04	11 / 112	MF methyltransferase activity

### Overview Map

### Spot





# Correlation Cluster

## Spot Summary: T

# metagenes = 55  
# genes = 301

<r> metagenes = 0.93  
<r> genes = 0.19  
beta: r2= 1.67 / log p= -Inf

# samples with spot = 18 ( 6.5 % )  
Atypical : 1 ( 1.4 % )  
Basal : 17 ( 20.2 % )

## Spot Genelist

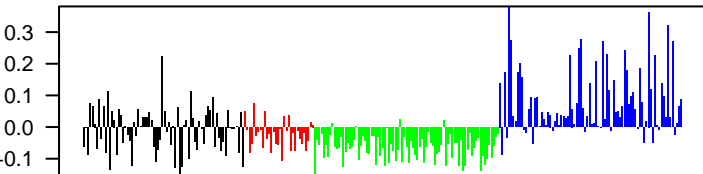
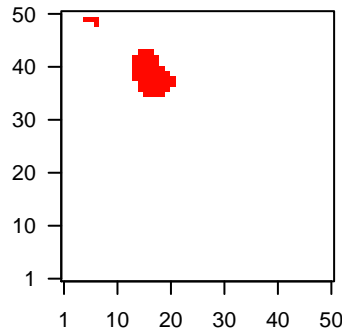
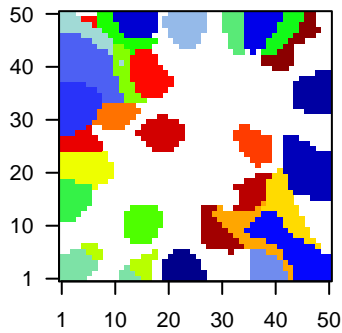
Rank	ID	max e	r	min e	Description
					Symbol
1	3933	2.9	-0.29	0.26	LCN1 lipocalin 1 [Source:HGNC Symbol;Acc:6525]
2	140683	1.96	-0.22	0.23	BPIFA2 BPI fold containing family A, member 2 [Source:HGNC Symb
3	3849	1.85	-0.46	0.31	KRT2 keratin 2 [Source:HGNC Symbol;Acc:6439]
4	239	1.65	-0.85	0.56	ALOX12 arachidonate 12-lipoxygenase [Source:HGNC Symbol;Acc:4:
5	10913	1.63	-0.56	0.38	EDAR ectodysplasin A receptor [Source:HGNC Symbol;Acc:2895]
6	79746	1.63	-1.28	0.23	ECHDC3enoyl CoA hydratase domain containing 3 [Source:HGNC Syr
7	3337	1.57	-1.37	0.48	DNAJB1 DnaJ (Hsp40) homolog, subfamily B, member 1 [Source:HGN
8	3656	1.46	-0.91	0.33	IRAK2 interleukin-1 receptor-associated kinase 2 [Source:HGNC S;
9	157638	1.46	-1.44	0.5	FAM84B family with sequence similarity 84, member B [Source:HGNC
10	8909	1.46	-0.48	0.75	ENDOU endonuclease, polyU-specific [Source:HGNC Symbol;Acc:14
11	10331	1.44	-0.51	0.42	B3GNT3 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransf
12	3359	1.44	-0.35	0.36	HTR3A 5-hydroxytryptamine (serotonin) receptor 3A, ionotropic [Sou
13	10451	1.43	-1.18	0.34	VAV3 vav 3 guanine nucleotide exchange factor [Source:HGNC Syr
14	55344	1.42	-0.83	0.29	PLCXD1 phosphatidylinositol-specific phospholipase C, X domain con
15	3850	1.41	-0.4	0.54	KRT3 keratin 3 [Source:HGNC Symbol;Acc:6440]
16	51350	1.4	-0.21	0.33	KRT76 keratin 76 [Source:HGNC Symbol;Acc:24430]
17	29949	1.4	-0.4	0.25	IL19 interleukin 19 [Source:HGNC Symbol;Acc:5990]
18	2952	1.38	-1.77	0.21	GSTT1 glutathione S-transferase theta 1 [Source:HGNC Symbol;Acc:
19	4217	1.33	-0.95	0.18	MAP3K5 mitogen-activated protein kinase kinase kinase 5 [Source:HC
20	2524	1.32	-1.05	0.7	FUT2 fucosyltransferase 2 (secretor status included) [Source:HGNC

## Geneset Overrepresentation

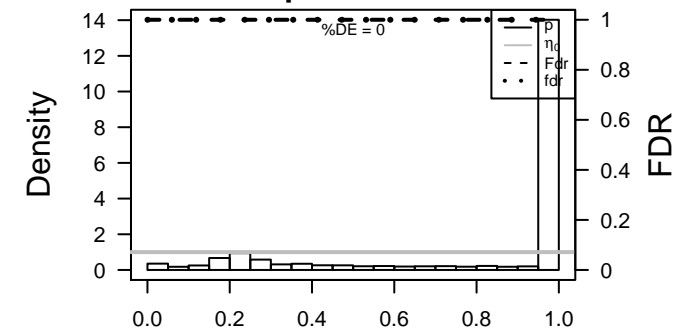
Rank	p-value	#in/all	Geneset
1	1e-05	7 / 44	CC keratin filament
2	3e-05	8 / 69	BP sphingolipid metabolic process
3	7e-04	22 / 572	Disea GUDJ_psooriasis up
4	9e-04	3 / 11	BP fatty acid beta-oxidation using acyl-Coa oxidase
5	9e-04	6 / 63	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
6	1e-03	3 / 12	GSE/ MANALO_HYPOXIA_UP
7	1e-03	68 / 2659	CC plasma membrane
8	1e-03	3 / 13	GSE/ KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLAC
9	2e-03	3 / 14	GSE/ MAINA_VHL_TARGETS_DN
10	2e-03	3 / 14	GSE/ CAIRO_HEPATOBLASTOMA_DN
11	2e-03	2 / 4	GSE/ GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
12	2e-03	3 / 15	GSE/ REACTOME_SPHINGOLIPID_METABOLISM
13	3e-03	22 / 633	Chr Chr 9
14	3e-03	3 / 16	GSE/ CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN
15	3e-03	3 / 16	GSE/ REACTOME_PEROXISOMAL_LIPID_METABOLISM
16	3e-03	4 / 33	BP sphingolipid biosynthetic process
17	3e-03	3 / 17	MF sulfuryl ester hydrolase activity
18	3e-03	4 / 35	BP glycosphingolipid metabolic process
19	3e-03	4 / 35	MF monooxygenase activity
20	4e-03	4 / 37	BP fatty acid beta-oxidation
21	5e-03	7 / 115	CC cell-cell junction
22	6e-03	2 / 7	GSE/ GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
23	7e-03	9 / 186	MF structural molecule activity
24	9e-03	4 / 46	BP chloride transport
25	1e-02	4 / 49	BP arachidonic acid metabolic process
26	1e-02	8 / 170	BP post-translational protein modification
27	1e-02	4 / 50	CC coated pit
28	1e-02	2 / 10	MF arylsulfatase activity
29	1e-02	2 / 10	BP centrosome localization
30	1e-02	2 / 10	BP epoxigenase P450 pathway
31	1e-02	2 / 10	MF fucosyltransferase activity
32	1e-02	2 / 10	CC Golgi-associated vesicle membrane
33	1e-02	2 / 10	BP negative regulation of translational initiation
34	1e-02	2 / 10	BP pantothenate metabolic process
35	1e-02	6 / 110	MF heme binding
36	2e-02	4 / 53	BP negative regulation of sequence-specific DNA binding transcription factor a
37	2e-02	17 / 529	MF protein homodimerization activity
38	2e-02	2 / 11	BP alpha-linolenic acid metabolic process
39	2e-02	2 / 11	CC HOPS complex
40	2e-02	2 / 11	BP sulfate transport

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: U

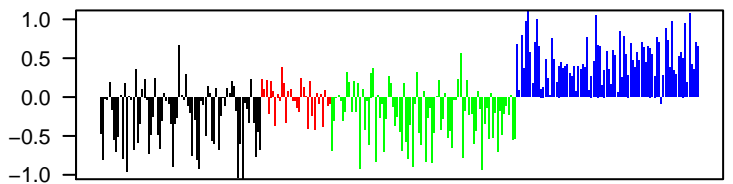
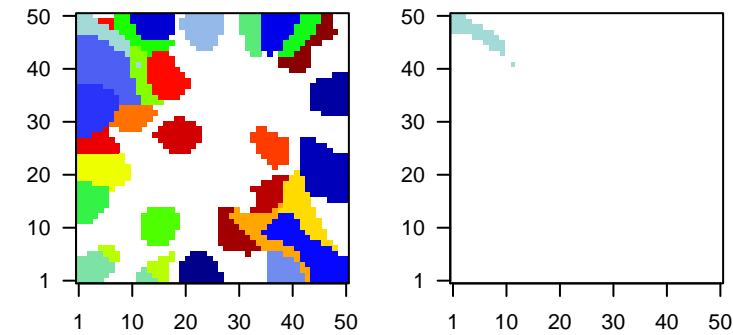
# metagenes = 35  
# genes = 354

<r> metagenes = 0.95  
<r> genes = 0.4  
beta: r2= 35.89 / log p= -Inf

# samples with spot = 100 ( 36.4 % )  
Atypical : 8 ( 10.8 % )  
Classical : 7 ( 21.9 % )  
Mesenchymal : 12 ( 14.1 % )  
Basal : 73 ( 86.9 % )

### Overview Map

### Spot

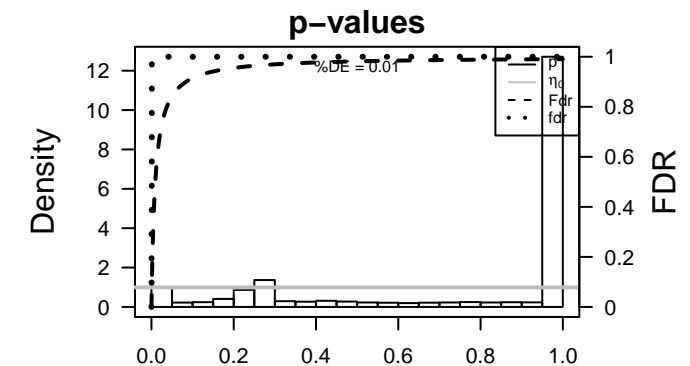


## Spot Genelist

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:6663]
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:11779]
12	2877	3.69	-3.11	0.44	GPX2 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Symbol;Acc:3048]
13	338324	3.66	-2.9	0.68	S100A7AS100 calcium binding protein A7A [Source:HGNC Symbol;Acc:11779]
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:16615]
18	84651	3.36	-1.82	0.74	SPINK7 serine peptidase inhibitor, Kazal type 7 (putative) [Source:HGNC Symbol;Acc:16615]
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:16615]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	82 / 135	H.Tis: WIRTH_Mucosa
2	5e-64	100 / 572	Disea: GUDJ_psooriasis up
3	1e-25	17 / 21	CC: cornified envelope
4	6e-25	23 / 53	BP: keratinocyte differentiation
5	3e-21	19 / 42	BP: keratinization
6	2e-19	22 / 76	BP: epidermis development
7	2e-14	11 / 19	BP: peptide cross-linking
8	4e-12	9 / 15	GSE/ WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
9	1e-11	23 / 186	MF: structural molecule activity
10	4e-10	8 / 16	GSE/ JAEGER_METASTASIS_DN
11	6e-10	59 / 1182	CC: extracellular region
12	3e-09	7 / 13	BP: negative regulation of peptidase activity
13	6e-09	7 / 14	GSE/ CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
14	7e-09	16 / 122	MF: serine-type endopeptidase activity
15	1e-08	7 / 15	GSE/ HINATA_NFKB_TARGETS KERATINOCYTE_DN
16	2e-08	7 / 16	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	2e-08	7 / 16	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
18	2e-08	7 / 16	GSE/ WANG_BARRETTES_ESOPHAGUS_DN
19	2e-08	7 / 16	GSE/ ONDER_CDH1_TARGETS_3_DN
20	2e-07	12 / 82	CC: intermediate filament
21	4e-07	51 / 1146	TF: HEBENSTREIT_low expression TF
22	6e-07	6 / 16	GSE/ CROMER_TUMORIGENESIS_DN
23	1e-06	5 / 10	MF: RAGE receptor binding
24	1e-06	9 / 52	BP: negative regulation of endopeptidase activity
25	4e-06	8 / 44	CC: keratin filament
26	5e-06	89 / 2659	CC: plasma membrane
27	7e-06	10 / 79	MF: serine-type endopeptidase inhibitor activity
28	1e-05	5 / 15	MF: retinol dehydrogenase activity
29	1e-05	5 / 15	GSE/ ONDER_CDH1_TARGETS_2_DN
30	2e-05	5 / 16	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
31	4e-05	4 / 10	GSE/ SMID_BREAST_CANCER_ERBB2_UP
32	4e-05	4 / 10	GSE/ REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_PROTEIN
33	6e-05	23 / 434	BP: oxidation-reduction process
34	6e-05	31 / 683	CC: extracellular space
35	7e-05	5 / 21	CC: desmosome
36	9e-05	4 / 12	BP: cellular aldehyde metabolic process
37	1e-04	7 / 51	MF: protein binding, bridging
38	1e-04	7 / 53	MF: serine-type peptidase activity
39	1e-04	4 / 13	H.Tis: WIRTH_Tonsil
40	1e-04	4 / 13	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP





# Correlation Cluster

## Spot Summary: V

# metagenes = 35  
# genes = 290

<r> metagenes = 0.96  
<r> genes = 0.22  
beta: r2= 5.44 / log p= -Inf

# samples with spot = 42 ( 15.3 % )  
Classical : 16 ( 50 % )  
Mesenchymal : 7 ( 8.2 % )  
Basal : 19 ( 22.6 % )

## Spot Genelist

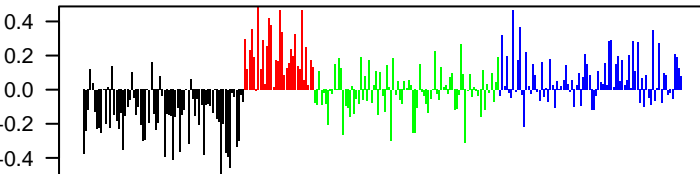
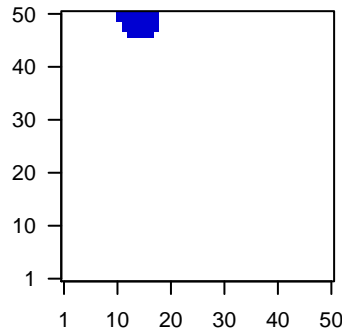
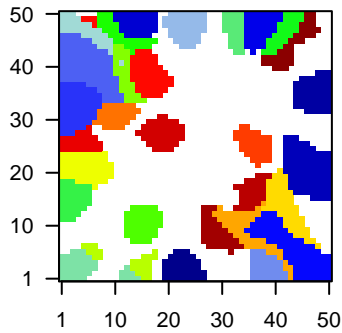
Rank	ID	max e	r	min e	Description
1	1109	3.73	-2.74	0.69	AKR1C4 aldo-keto reductase family 1, member C4 [Source:HGNC Sy]
2	57834	2.91	-1.53	0.7	CYP4F1 cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
3	1749	2.89	-1.7	0.51	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:2918]
4	1066	2.8	-0.72	0.47	CES1 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
5	1717	2.74	-1.44	0.42	DHCR7 7-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
6	140809	2.51	-1.38	0.73	SRXN1 sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
7	7102	2.39	-1.41	0.4	TSPAN7 tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
8	3485	2.34	-2.39	0.36	IGFBP2 insulin-like growth factor binding protein 2, 36kDa [Source:H
9	5217	2.22	-2.55	0.59	PFN2 profilin 2 [Source:HGNC Symbol;Acc:8882]
10	7062	2.14	-0.7	0.4	TCHH trichohyalin [Source:HGNC Symbol;Acc:11791]
11	7296	2.07	-0.96	0.54	TXNRD1 thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
12	493861	2.06	-0.82	0.49	EID3 EP300 interacting inhibitor of differentiation 3 [Source:HGNC
13	10457	2.06	-2.32	0.42	GPNUMB glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
14	57007	2.05	-2.01	0.49	ACKR3 atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
15	1646	2.04	-1.84	0.67	AKR1C2 aldo-keto reductase family 1, member C2 [Source:HGNC Sy]
16	24	1.91	-0.47	0.31	ABCA4 ATP-binding cassette, sub-family A (ABC1), member 4 [Sou
17	5445	1.91	-1.63	0.32	PON2 paraoxonase 2 [Source:HGNC Symbol;Acc:9205]
18	56666	1.9	-1.37	0.58	PANX2 pannexin 2 [Source:HGNC Symbol;Acc:8600]
19	406988	1.9	-1.65	0.3	MIR205H MIR205 host gene (non-protein coding) [Source:HGNC Sym]
20	4741	1.88	-0.55	0.38	NEFM neurofilament, medium polypeptide [Source:HGNC Symbol;A

## Geneset Overrepresentation

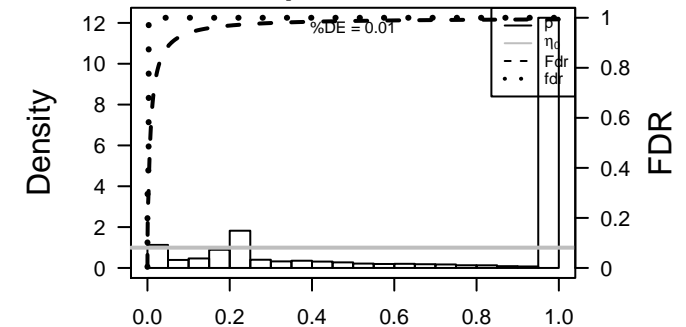
Rank	p-value	#in/all	Geneset
1	9e-07	33 / 743	Chr Chr 7
2	1e-06	19 / 296	MF oxidoreductase activity
3	2e-06	5 / 13	GSE/ SINGH_NFE2L2_TARGETS
4	3e-06	90 / 3274	CC integral to membrane
5	8e-06	22 / 434	BP oxidation-reduction process
6	2e-05	13 / 179	miRN hsa-miR-34b
7	2e-05	4 / 10	BP response to food
8	2e-05	17 / 299	BP axon guidance
9	3e-05	6 / 35	miRN hsa-miR-127-3p
10	4e-05	4 / 12	GSE/ DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
11	1e-04	4 / 15	GSE/ FARMER_BREAST_CANCER_CLUSTER_7
12	1e-04	7 / 65	BP response to glucocorticoid
13	2e-04	40 / 1253	BP small molecule metabolic process
14	2e-04	70 / 2659	CC plasma membrane
15	2e-04	5 / 32	MF ATPase activity, coupled to transmembrane movement of substances
16	2e-04	5 / 32	MF NADP binding
17	3e-04	8 / 96	BP lung development
18	3e-04	8 / 98	miRN ATGT-221-222
19	4e-04	6 / 56	miRN hsa-miR-151-3p
20	5e-04	8 / 104	miRN hsa-miR-605
21	5e-04	17 / 390	BP metabolic process
22	5e-04	51 / 1837	CC membrane
23	6e-04	5 / 39	BP retinoid metabolic process
24	6e-04	23 / 621	CC endoplasmic reticulum
25	7e-04	30 / 914	Chr Chr 3
26	7e-04	7 / 85	miRN hsa-miR-188-3p
27	7e-04	28 / 835	CC integral to plasma membrane
28	8e-04	6 / 63	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
29	9e-04	4 / 25	miRN hsa-miR-1273
30	1e-03	3 / 12	GSE/ REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN
31	1e-03	9 / 149	BP cellular lipid metabolic process
32	1e-03	6 / 69	BP response to toxic substance
33	1e-03	11 / 212	miRN hsa-miR-182
34	1e-03	16 / 387	miRN hsa-miR-519a
35	1e-03	6 / 71	BP pattern specification process
36	1e-03	6 / 71	BP response to nutrient
37	2e-03	13 / 284	miRN hsa-miR-503
38	2e-03	4 / 29	miRN hsa-miR-591
39	2e-03	8 / 125	MF iron ion binding
40	2e-03	17 / 433	miRN hsa-miR-19b

## Overview Map

## Spot



## p-values







# Correlation Cluster

## Spot Summary: W

# metagenes = 64  
# genes = 277

<r> metagenes = 0.94  
<r> genes = 0.21  
beta: r2= 3.09 / log p= -Inf

# samples with spot = 20 ( 7.3 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 16 ( 19 % )

## Spot Genelist

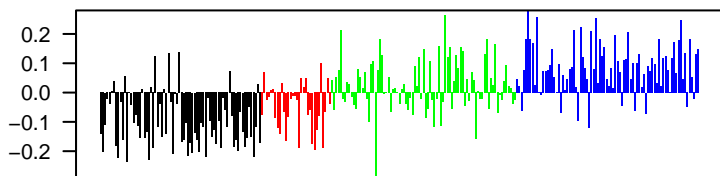
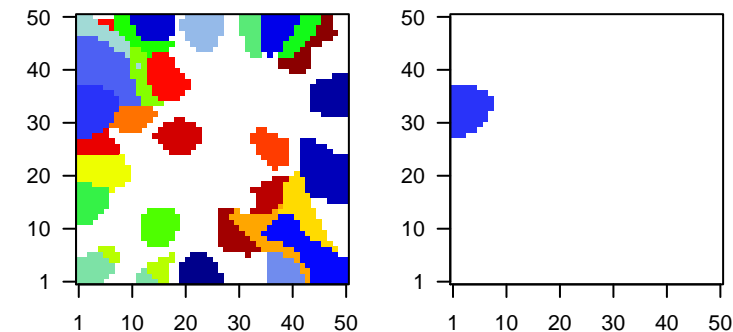
Rank	ID	max e	r	min e	Description
1	1984	1.86	-1.04	0.35	EIF5A eukaryotic translation initiation factor 5A [Source:HGNC Syml
2	170680	1.71	-0.44	0.43	PSORS1P1 psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;
3	8338	1.61	-1.41	0.32	HIST2H2A histone cluster 2, H2ac [Source:HGNC Symbol;Acc:4738]
4	6441	1.55	-0.67	0.36	SFTPD surfactant protein D [Source:HGNC Symbol;Acc:10803]
5	51278	1.45	-1.28	0.36	IER5 immediate early response 5 [Source:HGNC Symbol;Acc:5393]
6	8843	1.44	-0.83	0.43	HCAR3 hydroxycarboxylic acid receptor 3 [Source:HGNC Symbol;Acc:
7	54361	1.4	-0.63	0.47	WNT4 wingless-type MMTV integration site family, member 4 [Sour
8	338442	1.38	-0.84	0.49	HCAR2 hydroxycarboxylic acid receptor 2 [Source:HGNC Symbol;Acc:
9	10809	1.35	-0.99	0.37	STARD1 STAR-related lipid transfer (START) domain containing 10 [Sc
10	79670	1.31	-1	0.44	ZCCHC6 zinc finger, CCHC domain containing 6 [Source:HGNC Symb
11	83442	1.3	-1.19	0.55	SH3BGR3 SH3 domain binding glutamic acid-rich protein like 3 [Source
12	641649	1.3	-1.25	0.44	TMEM91 transmembrane protein 91 [Source:HGNC Symbol;Acc:32393]
13	55004	1.29	-0.83	0.32	LAMTOR1 late endosomal/lysosomal adaptor, MAPK and MTOR activat
14	83786	1.28	-0.95	0.4	FRMD8 FERM domain containing 8 [Source:HGNC Symbol;Acc:2546]
15	5672	1.28	-0.36	0.52	PSG4 pregnancy specific beta-1-glycoprotein 4 [Source:HGNC Syr
16	388555	1.27	-0.5	0.3	IGFL3 IGF-like family member 3 [Source:HGNC Symbol;Acc:32930]
17	134285	1.25	-0.91	0.35	TMEM17 transmembrane protein 171 [Source:HGNC Symbol;Acc:2703]
18	8689	1.24	-0.35	0.55	KRT36 keratin 36 [Source:HGNC Symbol;Acc:6454]
19	80765	1.24	-0.77	0.47	STARD5 STAR-related lipid transfer (START) domain containing 5 [Sou
20	118663	1.24	-0.39	0.34	BTBD16 BTB (POZ) domain containing 16 [Source:HGNC Symbol;Acc

## Geneset Overrepresentation

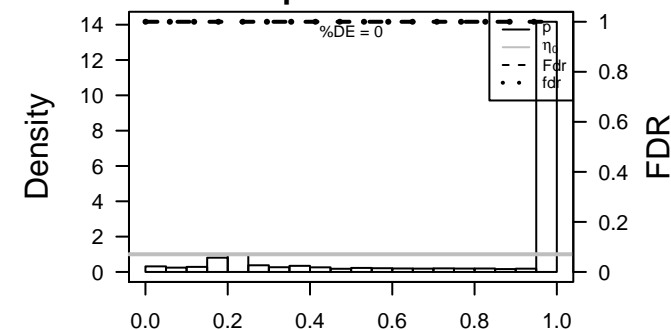
Rank	p-value	#in/all	Geneset
1	2e-07	33 / 717	Chr Chr 16
2	3e-05	5 / 23	BP endosome organization
3	1e-04	6 / 47	CC nucleosome
4	7e-04	8 / 115	MF lipid binding
5	7e-04	4 / 25	BP membrane fusion
6	1e-03	3 / 13	MF phosphatidylinositol-3,4-bisphosphate binding
7	2e-03	3 / 16	GSE/ AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
8	3e-03	2 / 5	miRN AGTG-521
9	3e-03	44 / 1720	Chr Chr 1
10	3e-03	13 / 320	BP small GTPase mediated signal transduction
11	3e-03	6 / 86	MF guanyl-nucleotide exchange factor activity
12	3e-03	6 / 86	BP nucleosome assembly
13	3e-03	7 / 115	BP endocytosis
14	4e-03	4 / 38	BP positive regulation of interleukin-6 production
15	4e-03	3 / 19	MF SNARE binding
16	6e-03	4 / 44	BP regulation of Rab GTPase activity
17	6e-03	3 / 23	BP positive regulation of release of cytochrome c from mitochondria
18	7e-03	5 / 71	miRN hsa-miR-1254
19	7e-03	4 / 46	MF Rab GTPase activator activity
20	8e-03	3 / 25	MF phosphatidylinositol-3,4,5-trisphosphate binding
21	9e-03	2 / 9	miRN TCCG-184
22	1e-02	9 / 215	CC lysosomal membrane
23	1e-02	3 / 28	CC Golgi stack
24	1e-02	2 / 10	MF 3-beta-hydroxy-delta5-steroid dehydrogenase activity
25	1e-02	2 / 10	CC DNA-directed RNA polymerase I complex
26	1e-02	2 / 10	GSE/ LUI_THYROID_CANCER_CLUSTER_5
27	1e-02	5 / 82	BP endoplasmic reticulum unfolded protein response
28	1e-02	3 / 29	BP positive regulation of interferon-gamma production
29	1e-02	12 / 342	MF protein heterodimerization activity
30	1e-02	3 / 30	CC SNARE complex
31	1e-02	2 / 11	BP regulation of fat cell differentiation
32	1e-02	2 / 11	GSE/ GALE_APL_WITH_FLT3_MUTATED_DN
33	1e-02	2 / 11	miRN GCGC-525--524
34	1e-02	4 / 56	CC recycling endosome
35	2e-02	6 / 120	miRN GAGC-149
36	2e-02	2 / 12	BP extracellular polysaccharide biosynthetic process
37	2e-02	2 / 12	BP rRNA transcription
38	2e-02	2 / 12	GSE/ LI_LUNG_CANCER
39	2e-02	2 / 12	GSE/ KEGG_GLYCEROPHOSPHOLIPID_METABOLISM
40	2e-02	2 / 12	miRN hsa-miR-639

## Overview Map

## Spot



## p-values





# Correlation Cluster

## Spot Summary: X

# metagenes = 95  
# genes = 685

<r> metagenes = 0.93  
<r> genes = 0.28  
beta: r2= 12.37 / log p= -Inf

# samples with spot = 64 ( 23.3 % )  
Mesenchymal : 31 ( 36.5 % )  
Basal : 33 ( 39.3 % )

## Spot Genelist

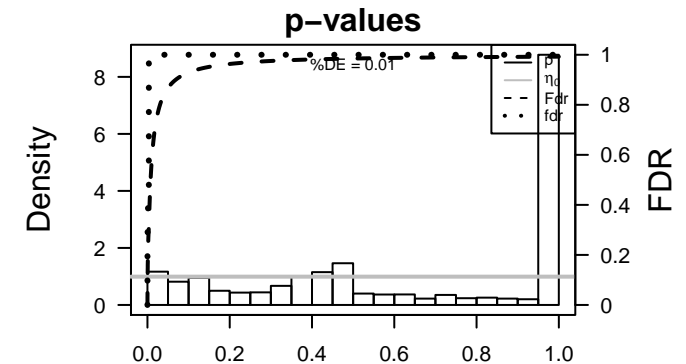
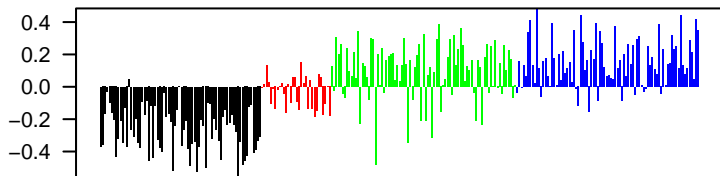
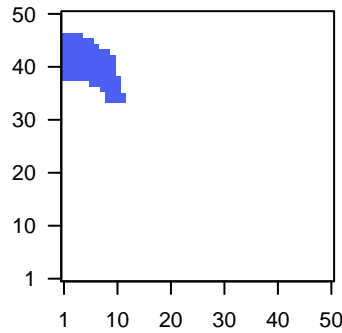
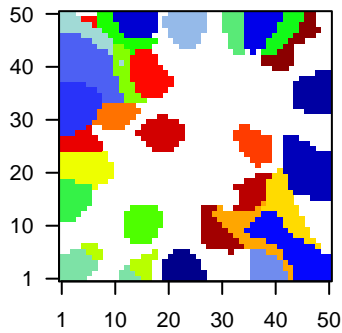
Rank	ID	max e	r	min e	Description
					Symbol
1	2167	5.04	-2.11	0.33	FABP4 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
2	374918	3.79	-1.25	0.43	IGFL1 IGF-like family member 1 [Source:HGNC Symbol;Acc:24093]
3	780854	3.58	-1.9	0.24	SNORD33small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc:15740]
4	404203	3.3	-0.91	0.51	SPINK6 serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symbol;Acc:15740]
5	780851	3.23	-1.91	0.23	SNORD33small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc:15740]
6	118430	3.17	-0.81	0.37	MUCL1 mucin-like 1 [Source:HGNC Symbol;Acc:30588]
7	780853	3.15	-1.74	0.25	SNORD33small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc:15740]
8	1041	3.12	-1.1	0.66	CDSN corneodesmosin [Source:HGNC Symbol;Acc:1802]
9	151516	2.97	-1.01	0.52	ASPRV1 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;Acc:15740]
10	3489	2.81	-2.42	0.59	IGFBP6 insulin-like growth factor binding protein 6 [Source:HGNC Symbol;Acc:15740]
11	760	2.81	-2.26	0.69	CA2 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	51200	2.78	-1.85	0.64	CPA4 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
13	2731	2.65	-0.96	0.22	GLDC glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:15740]
14	9119	2.63	-0.92	0.55	KRT75 keratin 75 [Source:HGNC Symbol;Acc:24431]
15	4015	2.63	-1.39	0.41	LOX lysyl oxidase [Source:HGNC Symbol;Acc:6664]
16	8710	2.62	-1.39	0.5	SERPINC1serpin peptidase inhibitor, clade B (ovalbumin), member 7 [Source:HGNC Symbol;Acc:15740]
17	5947	2.61	-2.47	0.45	RBP1 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:15740]
18	5744	2.59	-2.33	0.7	PTH1H parathyroid hormone-like hormone [Source:HGNC Symbol;Acc:15740]
19	1823	2.59	-0.82	0.61	DSC1 desmocollin 1 [Source:HGNC Symbol;Acc:3035]
20	4753	2.56	-1.8	0.39	NELL2 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-39	104 / 572	Disea GUDJ_psooriasis up
2	1e-12	28 / 135	H.Tiss WIRTH_Mucosa
3	6e-08	16 / 76	BP epidermis development
4	2e-07	16 / 82	CC intermediate filament
5	7e-07	11 / 42	BP keratinization
6	9e-07	7 / 15	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
7	1e-06	8 / 21	CC desmosome
8	1e-06	11 / 44	BP skin development
9	1e-06	231 / 4310	CC cytoplasm
10	2e-06	7 / 16	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	2e-06	45 / 519	Chr Chr 14
12	3e-06	154 / 2659	CC plasma membrane
13	2e-05	6 / 15	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
14	3e-05	21 / 186	MF structural molecule activity
15	7e-05	5 / 12	BP hemidesmosome assembly
16	7e-05	5 / 12	BP keratinocyte proliferation
17	9e-05	4 / 7	MMM MACIEJ_MMML 9
18	2e-04	6 / 22	MF cadherin binding
19	2e-04	5 / 15	GSE/ FARMER_BREAST_CANCER_CLUSTER_3
20	2e-04	36 / 470	miRN GCAC-17-5P--20A--106A--106B--20B--519D
21	3e-04	14 / 116	miRN GACA-219
22	3e-04	43 / 603	miRN hsa-miR-20a
23	3e-04	5 / 16	GSE/ FARMER_BREAST_CANCER_CLUSTER_4
24	3e-04	5 / 16	GSE/ XU_HGF_SIGNALING_NOT_VIA_AKT1_6HR
25	4e-04	33 / 426	miRN hsa-miR-519d
26	5e-04	12 / 95	miRN hsa-miR-133b
27	5e-04	11 / 82	MF structural constituent of cytoskeleton
28	5e-04	12 / 96	miRN hsa-miR-133a
29	6e-04	40 / 565	miRN hsa-miR-20b
30	7e-04	6 / 27	CC basal plasma membrane
31	7e-04	28 / 354	miRN CTTT-524
32	8e-04	13 / 114	miRN hsa-miR-875-3p
33	1e-03	13 / 117	Glio GIEZELT_GBM_WT_up_VS_mut
34	1e-03	15 / 147	miRN hsa-miR-143
35	1e-03	53 / 835	CC integral to plasma membrane
36	1e-03	5 / 20	MF scaffold protein binding
37	1e-03	4 / 12	GSE/ DOANE_RESPONSE_TO_ANDROGEN_UP
38	1e-03	4 / 12	GSE/ SESTO_RESPONSE_TO_UV_C3
39	1e-03	30 / 401	miRN ACCA-9
40	1e-03	3 / 6	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP

Overview Map

Spot





# Correlation Cluster

## Spot Summary: Y

# metagenes = 30  
# genes = 162

<r> metagenes = 0.94  
<r> genes = 0.26  
beta: r2= 6.47 / log p= -Inf

# samples with spot = 38 ( 13.8 % )  
Atypical : 4 ( 5.4 % )  
Classical : 7 ( 21.9 % )  
Basal : 27 ( 32.1 % )

## Spot Genelist

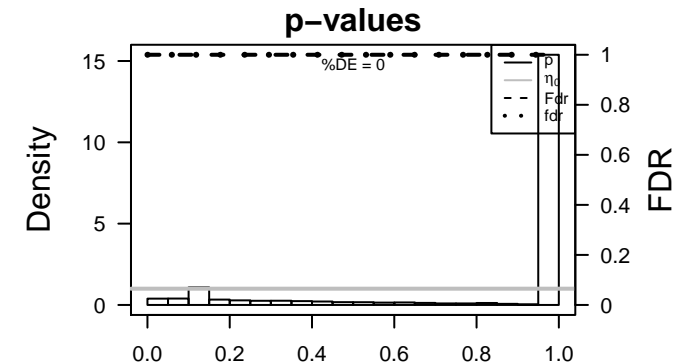
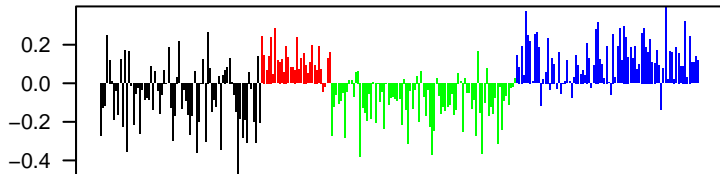
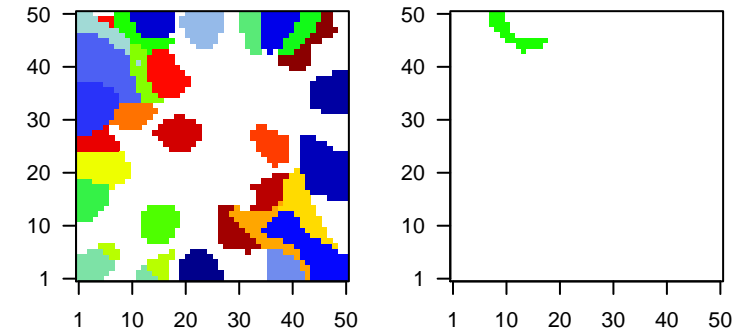
Rank	ID	max e	r	min e	Description
1	5327	2.56	-1.74	0.35	PLAT plasminogen activator, tissue [Source:HGNC Symbol;Acc:90f
2	9073	2.47	-0.88	0.44	CLDN8 claudin 8 [Source:HGNC Symbol;Acc:2050]
3	3881	1.91	-0.55	0.37	KRT31 keratin 31 [Source:HGNC Symbol;Acc:6448]
4	55191	1.84	-1.03	0.32	NADSYNNAD synthetase 1 [Source:HGNC Symbol;Acc:29832]
5	157506	1.8	-1.64	0.54	RDH10 retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;
6	100130691	1.72	-0.78	0.65	AC074286.1
7	2886	1.7	-0.89	0.49	GRB7 growth factor receptor-bound protein 7 [Source:HGNC Symb
8	1525	1.67	-2.17	0.52	CXADR coxsackie virus and adenovirus receptor [Source:HGNC Sym
9	8804	1.63	-1.52	0.38	CREG1 cellular repressor of E1A-stimulated genes 1 [Source:HGNC
10	81610	1.62	-1.63	0.55	FAM83D family with sequence similarity 83, member D [Source:HGNC
11	13	1.57	-0.5	0.47	AADAC arylacetamide deacetylase [Source:HGNC Symbol;Acc:17]
12	283422	1.5	-0.72	0.5	
13	2052	1.48	-0.85	0.41	EPHX1 epoxide hydrolase 1, microsomal (xenobiotic) [Source:HGNC
14	60437	1.46	-0.64	0.47	CDH26 cadherin 26 [Source:HGNC Symbol;Acc:15902]
15	26355	1.44	-1.04	0.58	FAM162A family with sequence similarity 162, member A [Source:HGNC
16	4257	1.42	-0.96	0.34	MGST1 microsomal glutathione S-transferase 1 [Source:HGNC Symt
17	55893	1.41	-1.13	0.37	ZNF395 zinc finger protein 395 [Source:HGNC Symbol;Acc:18737]
18	121273	1.4	-1.04	0.46	C12orf54 chromosome 12 open reading frame 54 [Source:HGNC Symt
19	2086	1.38	-0.79	0.51	ERV3-1 endogenous retrovirus group 3, member 1 [Source:HGNC Sy
20	1718	1.38	-1.74	0.61	DHCR24 24-dehydrocholesterol reductase [Source:HGNC Symbol;Acc

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-07	9 / 92	CC tight junction
2	2e-05	6 / 57	BP cell-cell junction organization
3	4e-04	14 / 504	Chr Chr 15
4	5e-04	4 / 37	CC adherens junction
5	5e-04	3 / 16	GSE/ LUCAS_HNF4A_TARGETS_UP
6	1e-03	4 / 49	CC peroxisomal membrane
7	2e-03	2 / 7	GSE/ REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT
8	2e-03	6 / 137	CC basolateral plasma membrane
9	3e-03	3 / 30	BP protein localization to plasma membrane
10	3e-03	2 / 9	GSE/ REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECUL
11	4e-03	3 / 33	CC intercalated disc
12	4e-03	3 / 33	BP tight junction assembly
13	4e-03	2 / 10	miRN CTAC-325
14	4e-03	10 / 379	Glio Down_a
15	5e-03	8 / 266	miRN AAGC-135A--135B
16	5e-03	2 / 11	BP cochlea development
17	5e-03	2 / 11	BP ear development
18	5e-03	2 / 11	BP fatty acid beta-oxidation using acyl-CoA oxidase
19	5e-03	2 / 11	GSE/ WHITESIDE_CISPLATIN_RESISTANCE_UP
20	5e-03	2 / 11	miRN GCGC-525--524
21	7e-03	4 / 76	BP wound healing
22	7e-03	4 / 77	CC late endosome membrane
23	7e-03	2 / 13	MF spectrin binding
24	7e-03	2 / 13	GSE/ BAELEDE_DIABETIC_NEPHROPATHY_DN
25	7e-03	2 / 13	GSE/ KEGG_CIRCADIAN_RHYTHM_MAMMAL
26	7e-03	2 / 13	miRN miR-1
27	8e-03	2 / 14	GSE/ FINETTI_BREAST_CANCERS_KINOME_BLUE
28	8e-03	2 / 14	GSE/ BIOCARTA_UCALPAIN_PATHWAY
29	8e-03	45 / 3274	CC integral to membrane
30	9e-03	3 / 43	CC neuromuscular junction
31	9e-03	8 / 296	MF oxidoreductase activity
32	9e-03	3 / 44	BP steroid metabolic process
33	9e-03	2 / 15	BP lens morphogenesis in camera-type eye
34	9e-03	2 / 15	GSE/ WATANABE_RECTAL_CANCER_RADIOOTHERAPY_RESPONSIVE_DN
35	9e-03	2 / 15	GSE/ WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN
36	9e-03	2 / 15	GSE/ AIGNER_ZEB1_TARGETS
37	9e-03	2 / 15	GSE/ BECKER_TAMOXIFEN_RESISTANCE_UP
38	9e-03	2 / 15	GSE/ YAGI_AML_RELAPSE_PROGNOSIS
39	9e-03	2 / 15	GSE/ BEIER_GLIOMA_STEM_CELL_UP
40	9e-03	2 / 15	GSE/ REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING

### Overview Map

### Spot





# Correlation Cluster

## Spot Summary: Z

# metagenes = 31  
# genes = 85

<r> metagenes = 0.95  
<r> genes = 0.23  
beta: r2= 1.05 / log p= -Inf

# samples with spot = 7 ( 2.5 % )  
Basal : 7 ( 8.3 % )

## Spot Genelist

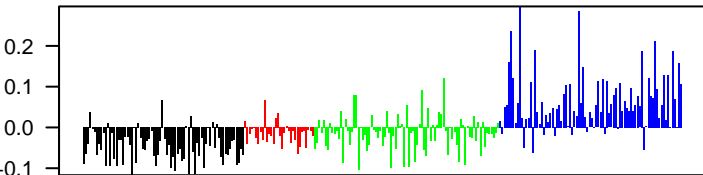
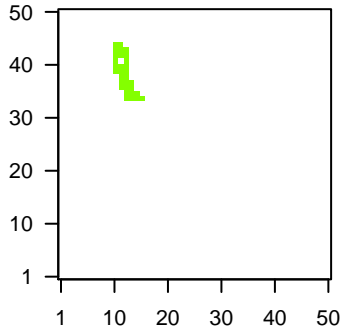
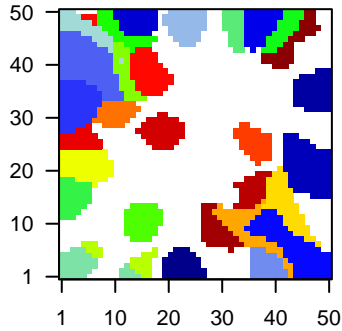
Rank	ID	max e	r	min e	Description
					Symbol
1	1373	1.32	-0.55	0.24	CPS1 carbamoyl-phosphate synthase 1, mitochondrial [Source:HGNC Symbol;Acc:1373]
2	337959	1.32	-0.23	0.15	KRTAP13 keratin associated protein 13-2 [Source:HGNC Symbol;Acc:337959]
3	388698	0.92	-0.16	0.5	FLG2 filaggrin family member 2 [Source:HGNC Symbol;Acc:33276]
4	83640	0.87	-0.46	0.5	FAM103A family with sequence similarity 103, member A1 [Source:HGNC Symbol;Acc:83640]
5	353133	0.85	-0.33	0.21	LCE1C late cornified envelope 1C [Source:HGNC Symbol;Acc:29464]
6	11254	0.82	-0.32	0.41	SLC6A14 solute carrier family 6 (amino acid transporter), member 14 [Source:HGNC Symbol;Acc:11254]
7	384	0.82	-0.45	0.38	ARG2 arginase 2 [Source:HGNC Symbol;Acc:664]
8	122553	0.81	-0.52	0.38	TRAPPC6B trafficking protein particle complex 6B [Source:HGNC Symbol;Acc:122553]
9	3622	0.77	-0.63	0.41	ING2 inhibitor of growth family, member 2 [Source:HGNC Symbol;Acc:3622]
10	353144	0.77	-0.26	0.2	LCE3C late cornified envelope 3C [Source:HGNC Symbol;Acc:16612]
11	3423	0.77	-0.64	0.27	IDS iduronate 2-sulfatase [Source:HGNC Symbol;Acc:5389]
12	2774	0.75	-0.39	0.25	GNAL guanine nucleotide binding protein (G protein), alpha activator
13	11219	0.69	-0.23	0.53	TREX2 three prime repair exonuclease 2 [Source:HGNC Symbol;Acc:11219]
14	10740	0.69	-0.23	0.41	RFPL1S RFPL1 antisense RNA 1 [Source:HGNC Symbol;Acc:9978]
15	4598	0.68	-0.42	0.63	MVK mevalonate kinase [Source:HGNC Symbol;Acc:7530]
16	100131551	0.67	-0.34	0.54	
17	55954	0.67	-0.36	0.41	ZMAT5 zinc finger, matrin-type 5 [Source:HGNC Symbol;Acc:28046]
18	9517	0.66	-0.53	0.52	SPTLC2 serine palmitoyltransferase, long chain base subunit 2 [Source:HGNC Symbol;Acc:9517]
19	83874	0.66	-0.42	0.5	TBC1D10B TBC1 domain family, member 10A [Source:HGNC Symbol;Acc:83874]
20	43847	0.66	-0.32	0.46	KLK14 kallikrein-related peptidase 14 [Source:HGNC Symbol;Acc:64384]

## Geneset Overrepresentation

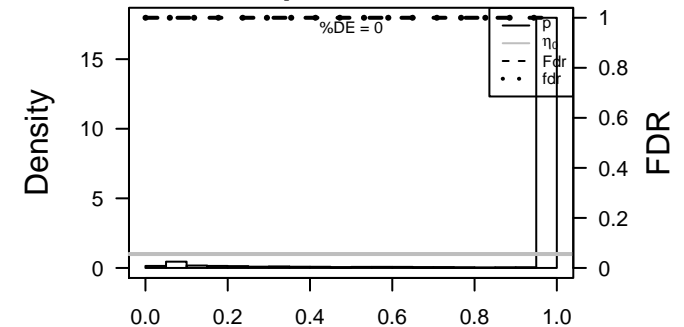
Rank	p-value	#in/all	Geneset
1	9e-07	6 / 66	BP lipid catabolic process
2	5e-04	10 / 572	Diseas GUDJ_psooriasis up
3	7e-04	3 / 35	MF hydrolase activity, acting on ester bonds
4	9e-04	2 / 9	GSE/ REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS
5	1e-03	2 / 10	BP urea cycle
6	1e-03	5 / 158	BP lipid metabolic process
7	1e-03	3 / 42	BP keratinization
8	2e-03	2 / 12	MF hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in line
9	2e-03	2 / 14	BP chondroitin sulfate catabolic process
10	3e-03	5 / 198	BP vesicle-mediated transport
11	6e-03	2 / 23	BP glycosaminoglycan catabolic process
12	7e-03	6 / 339	MF GTP binding
13	1e-02	2 / 33	BP sphingolipid biosynthetic process
14	1e-02	2 / 35	MF guanyl nucleotide binding
15	2e-02	2 / 38	MF G-protein beta/gamma-subunit complex binding
16	2e-02	2 / 44	BP regulation of Rab GTPase activity
17	2e-02	2 / 46	MF Rab GTPase activator activity
18	2e-02	4 / 220	CC mitochondrial matrix
19	2e-02	1 / 5	MMM MACIEJ_MMLL 28
20	3e-02	1 / 6	GSE/ MA_PITUITARY_FETAL_VS_ADULT_UP
21	3e-02	2 / 58	miRN hsa-miR-126*
22	3e-02	1 / 7	Glio oligodendrocytes_glio
23	3e-02	1 / 7	GSE/ SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_IN_CANCER
24	3e-02	1 / 7	GSE/ KEGG_SPHINGOLIPID_METABOLISM
25	3e-02	1 / 7	miRN miR-145
26	4e-02	4 / 256	MF GTPase activity
27	4e-02	1 / 8	GSE/ CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_UP
28	4e-02	1 / 8	GSE/ YAGI_AML_WITH_T_8_21_TRANSLOCATION
29	4e-02	2 / 65	BP response to glucocorticoid
30	4e-02	5 / 386	Chr Chr 22
31	4e-02	1 / 9	GSE/ GOZGIT_ESR1_TARGETS_DN
32	4e-02	1 / 9	GSE/ REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_CLASSES_II
33	4e-02	11 / 1253	BP small molecule metabolic process
34	5e-02	2 / 69	BP MAPK cascade
35	5e-02	2 / 69	BP response to toxic substance
36	5e-02	2 / 69	BP sphingolipid metabolic process
37	5e-02	2 / 70	MF phospholipid binding
38	5e-02	5 / 400	H.Tis: WIRTH_Nervous System
39	5e-02	1 / 10	BP anagen
40	5e-02	1 / 10	BP negative regulation of G-protein coupled receptor protein signaling pathway

### Overview Map

### Spot



### p-values







# Correlation Cluster

## Spot Summary: A1

# metagenes = 32  
# genes = 142

<r> metagenes = 0.95  
<r> genes = 0.14  
beta: r2= 0.47 / log p= -Inf

# samples with spot = 0 ( 0 % )

## Spot Genelist

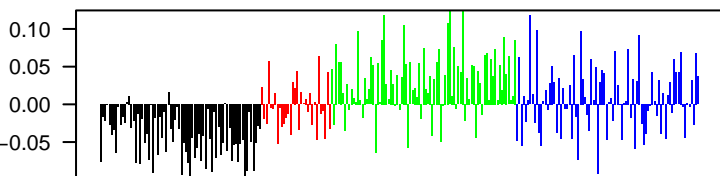
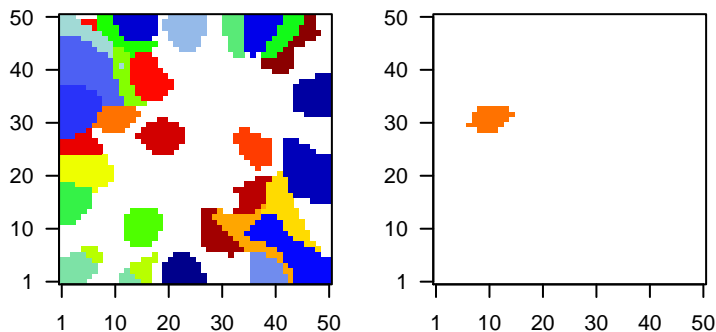
Rank	ID	max e	r	min e	Description
					Symbol
1	1907	1.81	-0.7	0.26	EDN2 endothelin 2 [Source:HGNC Symbol;Acc:3177]
2	89797	1.04	-0.83	0.21	NAV2 neuron navigator 2 [Source:HGNC Symbol;Acc:15997]
3	6330	0.96	-0.33	0.21	SCN4B sodium channel, voltage-gated, type IV, beta subunit [Source:HGNC Symbol;Acc:3177]
4	7088	0.88	-0.73	0.28	TLE1 transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) [Source:HGNC Symbol;Acc:3177]
5	145173	0.87	-0.62	0.24	B3GALT1 beta 1,3-galactosyltransferase-like [Source:HGNC Symbol;Acc:3177]
6	117195	0.87	-0.24	0.31	MRGPRX4 MAS-related GPR, member X3 [Source:HGNC Symbol;Acc:15997]
7	1312	0.87	-0.58	0.3	COMT catechol-O-methyltransferase [Source:HGNC Symbol;Acc:2:1312]
8	59274	0.78	-0.49	0.32	MESDC1 mesoderm development candidate 1 [Source:HGNC Symbol;Acc:3177]
9	8828	0.73	-0.26	0.35	NRP2 neuropilin 2 [Source:HGNC Symbol;Acc:8005]
10	89872	0.72	-0.26	0.28	AQP10 aquaporin 10 [Source:HGNC Symbol;Acc:16029]
11	2531	0.71	-0.62	0.27	KDSR 3-ketodihydroshingosine reductase [Source:HGNC Symbol;Acc:3177]
12	26031	0.69	-0.47	0.22	OSBPL3 oxysterol binding protein-like 3 [Source:HGNC Symbol;Acc:1:26031]
13	93145	0.69	-0.33	0.33	OLFM2 olfactomedin 2 [Source:HGNC Symbol;Acc:17189]
14	9231	0.68	-0.61	0.38	DLG5 discs, large homolog 5 (Drosophila) [Source:HGNC Symbol;Acc:3177]
15	54872	0.66	-0.35	0.32	PIGG phosphatidylinositol glycan anchor biosynthesis, class G [Source:HGNC Symbol;Acc:3177]
16	5047	0.65	-0.16	0.4	PAEP progesteragen-associated endometrial protein [Source:HGNC Symbol;Acc:3177]
17	2019	0.65	-0.25	0.35	EN1 engrailed homeobox 1 [Source:HGNC Symbol;Acc:3342]
18	377	0.65	-0.72	0.26	ARF3 ADP-ribosylation factor 3 [Source:HGNC Symbol;Acc:654]
19	23765	0.64	-0.37	0.28	IL17RA interleukin 17 receptor A [Source:HGNC Symbol;Acc:5985]
20	84248	0.64	-0.45	0.26	FYTTD1 forty-two-three domain containing 1 [Source:HGNC Symbol;Acc:3177]

## Geneset Overrepresentation

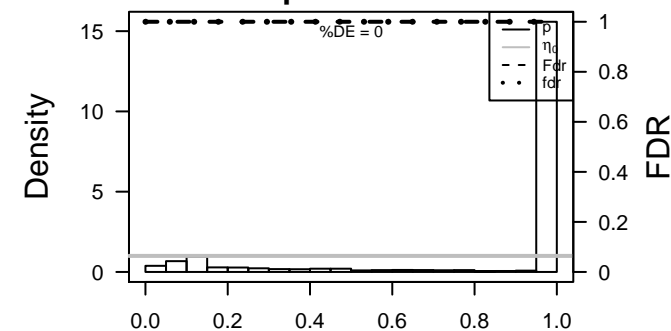
Rank	p-value	#in/all	Geneset
1	6e-06	4 / 15	BP anterior/posterior axis specification
2	4e-04	6 / 111	BP neuron differentiation
3	4e-04	7 / 157	BP Wnt signaling pathway
4	4e-04	3 / 18	MF transforming growth factor beta-activated receptor activity
5	5e-04	3 / 19	BP anatomical structure formation involved in morphogenesis
6	5e-04	3 / 19	BP regulation of protein binding
7	6e-04	29 / 1837	CC membrane
8	1e-03	3 / 26	MF growth factor binding
9	2e-03	6 / 153	CC endoplasmic reticulum lumen
10	2e-03	4 / 63	MF hormone activity
11	2e-03	8 / 274	BP nervous system development
12	3e-03	3 / 33	BP positive regulation of cell adhesion
13	3e-03	4 / 69	miRN AGCT-28
14	3e-03	3 / 34	BP thymus development
15	3e-03	3 / 35	MF protein self-association
16	3e-03	3 / 36	H.Tis: WIRTH_Placenta
17	3e-03	8 / 293	BP synaptic transmission
18	4e-03	8 / 294	miRN hsa-miR-202
19	4e-03	11 / 504	BP negative regulation of transcription from RNA polymerase II promoter
20	4e-03	2 / 11	BP chaperone mediated protein folding requiring cofactor
21	4e-03	2 / 11	BP embryonic viscerocranium morphogenesis
22	4e-03	3 / 37	MF symporter activity
23	4e-03	35 / 2659	CC plasma membrane
24	4e-03	3 / 38	MF transcription regulatory region sequence-specific DNA binding
25	4e-03	2 / 12	BP cerebellar Purkinje cell differentiation
26	4e-03	2 / 12	BP head development
27	5e-03	3 / 41	BP dorsal/ventral pattern formation
28	5e-03	3 / 41	MF SMAD binding
29	5e-03	2 / 13	BP hematopoietic progenitor cell differentiation
30	5e-03	2 / 13	MF transmembrane receptor protein serine/threonine kinase activity
31	5e-03	2 / 13	GSE/ WANG_METHYLATED_IN_BREAST_CANCER
32	6e-03	2 / 14	BP pharyngeal system development
33	6e-03	2 / 14	BP positive regulation of cell-cell adhesion
34	6e-03	2 / 14	GSE/ BIOCARTA_TOB1_PATHWAY
35	7e-03	2 / 15	BP female gamete generation
36	7e-03	2 / 15	BP mitochondrial transport
37	7e-03	2 / 15	BP positive regulation of extrinsic apoptotic signaling pathway via death domain
38	7e-03	2 / 15	BP regulation of ARF protein signal transduction
39	7e-03	2 / 15	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
40	7e-03	2 / 15	GSE/ BIOCARTA_TGFB_PATHWAY

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: B1

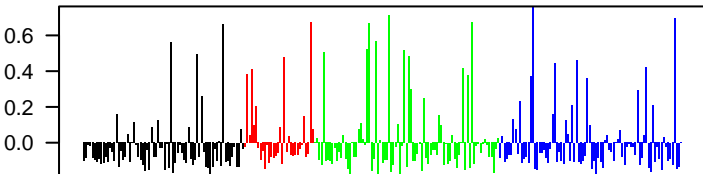
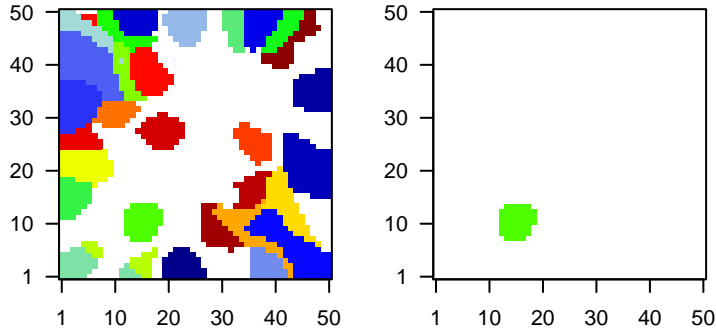
# metagenes = 42  
# genes = 172

<r> metagenes = 0.96  
<r> genes = 0.22  
beta: r2= 2.67 / log p= -Inf

# samples with spot = 32 ( 11.6 % )  
Atypical : 4 ( 5.4 % )  
Classical : 5 ( 15.6 % )  
Mesenchymal : 12 ( 14.1 % )  
Basal : 11 ( 13.1 % )

### Overview Map

### Spot

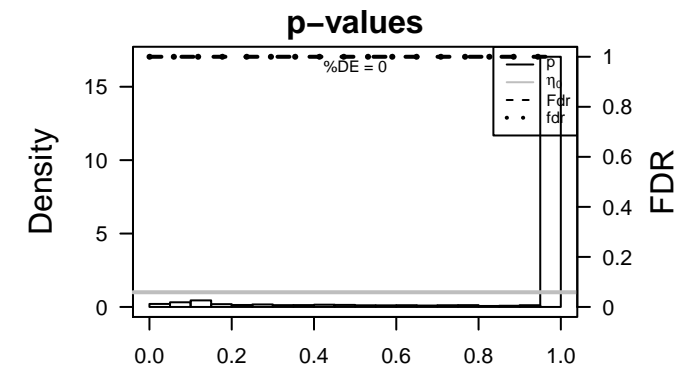


## Spot Genelist

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	4103	2.69	-0.85	0.47	MAGEA4melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
20	4100	2.59	-0.76	0.67	MAGEA1melanoma antigen family A, 1 (directs expression of antigen I

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-34	49 / 630	Chr Chr X
2	2e-12	14 / 120	H.Tis: WIRTH_Testis
3	4e-07	6 / 34	Chr Chr Y
4	1e-06	5 / 23	BP calcium-dependent cell-cell adhesion
5	7e-06	4 / 15	GSE/ MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
6	1e-05	3 / 6	miRN miR-181b
7	2e-05	11 / 259	BP spermatogenesis
8	2e-05	5 / 37	BP synapse assembly
9	3e-05	3 / 8	GSE/ ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
10	7e-05	7 / 118	Glio willscher_GBM_Verhaak-CL_expression_K_down
11	7e-05	7 / 118	Glio willscher_GBM_Verhaak-MES_expression_K_down
12	7e-05	7 / 118	Glio willscher_GBM_Verhaak-PNwt_expression_K_up
13	7e-05	7 / 118	Glio willscher_GBM_Verhaak-PNmut_expression_K_up
14	1e-04	6 / 89	Glio WIRTH_Normal Brain
15	2e-04	3 / 14	GSE/ MAHADEVAN_IMATINIB_RESISTANCE_UP
16	2e-04	6 / 99	BP homophilic cell adhesion
17	5e-04	3 / 19	BP oogenesis
18	7e-04	2 / 5	GSE/ MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
19	7e-04	2 / 5	miRN miR-181a
20	8e-04	10 / 346	BP cell differentiation
21	1e-03	9 / 293	BP synaptic transmission
22	1e-03	11 / 429	BP multicellular organismal development
23	2e-03	2 / 8	GSE/ WEBER_METHYLATED_ICP_IN_FIBROBLAST
24	3e-03	8 / 274	BP nervous system development
25	3e-03	2 / 10	MF L-glutamate transmembrane transporter activity
26	3e-03	2 / 10	BP piRNA metabolic process
27	3e-03	2 / 10	GSE/ CONRAD_STEM_CELL
28	3e-03	2 / 10	miRN hsa-miR-933
29	4e-03	2 / 11	Glio neurons_glio
30	5e-03	2 / 12	GSE/ RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
31	5e-03	2 / 12	GSE/ REACTOME_INORGANIC_CATION_ANION_SLC_TRANSPORTERS
32	5e-03	2 / 13	BP synapsis
33	5e-03	2 / 13	GSE/ PIEPOLI_LG11_TARGETS_DN
34	5e-03	2 / 13	GSE/ HATADA_METHYLATED_IN_LUNG_CANCER_DN
35	5e-03	2 / 13	GSE/ NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
36	5e-03	2 / 13	GSE/ REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTE
37	5e-03	2 / 13	GSE/ REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE
38	6e-03	2 / 14	BP DNA methylation involved in gamete generation
39	6e-03	2 / 14	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_B
40	6e-03	2 / 14	GSE/ REACTOME_Glutamate_NEUROTRANSMITTER_RELEASE_CYCLE





# Correlation Cluster

## Spot Summary: C1

# metagenes = 27  
# genes = 269

<r> metagenes = 0.96  
<r> genes = 0.25  
beta: r2= 3.56 / log p= -Inf

# samples with spot = 24 ( 8.7 % )  
Atypical : 5 ( 6.8 % )  
Classical : 3 ( 9.4 % )  
Mesenchymal : 4 ( 4.7 % )  
Basal : 12 ( 14.3 % )

## Spot Genelist

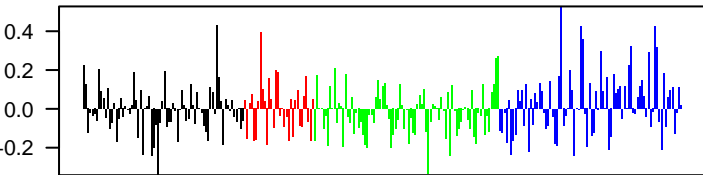
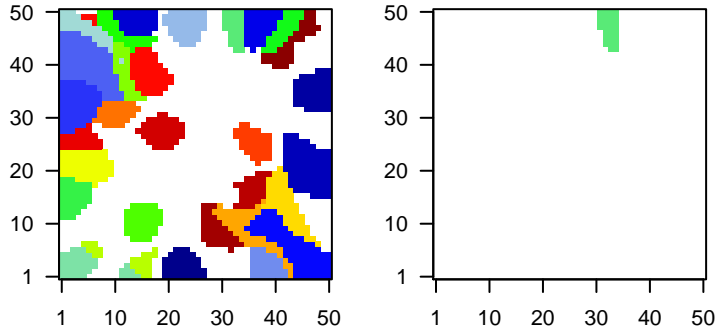
Rank	ID	max e	r	min e	Description
1	1207	1.52	-1.35	0.49	CLNS1A chloride channel, nucleotide-sensitive, 1A [Source:HGNC Sy
2	144363	1.49	-0.94	0.49	LYRM5 LYR motif containing 5 [Source:HGNC Symbol;Acc:27052]
3	100093630	1.47	-1.34	0.27	SNHG8 small nucleolar RNA host gene 8 (non-protein coding) [Sourc
4	84833	1.42	-0.97	0.4	USMG5 up-regulated during skeletal muscle growth 5 homolog (mous
5	5423	1.39	-1.04	0.26	POLB polymerase (DNA directed), beta [Source:HGNC Symbol;Acc
6	401505	1.36	-0.87	0.59	TOMM5 translocase of outer mitochondrial membrane 5 homolog (yea
7	139886	1.35	-1.31	0.32	SPIN4 spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
8	55848	1.34	-0.94	0.45	PLGRKT plasminogen receptor, C-terminal lysine transmembrane prot
9	6154	1.21	-0.73	0.6	RPL26 ribosomal protein L26 [Source:HGNC Symbol;Acc:10327]
10	27257	1.21	-0.84	0.36	LSM1 LSM1 homolog, U6 small nuclear RNA associated (S. cerevis
11	6160	1.2	-0.91	0.56	RPL31 ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]
12	6175	1.19	-1.11	0.67	RPLP0 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:1037
13	4712	1.17	-0.65	0.54	NDUFB6 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17
14	64776	1.12	-0.99	0.58	C11orf1 chromosome 11 open reading frame 1 [Source:HGNC Symbc
15	4724	1.12	-0.88	0.51	NDUFS4 NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (f
16	38	1.11	-0.8	0.45	ACAT1 acetyl-CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:9
17	83955	1.11	-0.73	0.53	NACAP1 nascent-polypeptide-associated complex alpha polypeptide i
18	1349	1.11	-1.08	0.69	COX7B cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;Ac
19	6165	1.1	-0.95	0.53	RPL35A ribosomal protein L35a [Source:HGNC Symbol;Acc:10345]
20	80227	1.1	-1.04	0.35	PAAF1 proteasomal ATPase-associated factor 1 [Source:HGNC Syrn

## Geneset Overrepresentation

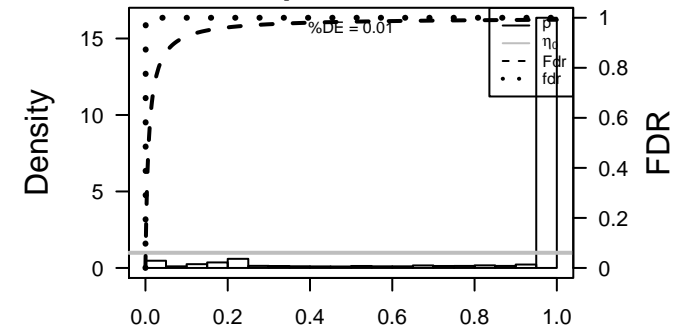
Rank	p-value	#in/all	Geneset
1	7e-27	26 / 83	BP respiratory electron transport chain
2	2e-24	77 / 1318	CC mitochondrion
3	3e-24	30 / 153	MF structural constituent of ribosome
4	4e-24	39 / 304	CC mitochondrial inner membrane
5	9e-22	34 / 253	BP translation
6	5e-20	22 / 92	BP translational elongation
7	6e-20	21 / 81	BP viral transcription
8	2e-19	26 / 152	BP cellular metabolic process
9	3e-19	21 / 87	BP translational termination
10	4e-19	24 / 128	BP translational initiation
11	1e-18	21 / 92	BP viral life cycle
12	3e-18	22 / 109	BP SRP-dependent cotranslational protein targeting to membrane
13	2e-17	25 / 167	CC ribosome
14	1e-16	21 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
15	3e-15	29 / 287	BP viral process
16	1e-14	42 / 649	BP gene expression
17	1e-14	25 / 219	BP mRNA metabolic process
18	2e-14	26 / 242	BP RNA metabolic process
19	4e-14	14 / 51	CC cytosolic large ribosomal subunit
20	6e-12	11 / 36	CC mitochondrial respiratory chain complex I
21	1e-11	32 / 482	BP cellular protein metabolic process
22	9e-11	10 / 34	MF NADH dehydrogenase (ubiquinone) activity
23	1e-10	10 / 35	BP mitochondrial electron transport, NADH to ubiquinone
24	8e-09	48 / 1233	TF KIM_MYC targets
25	1e-07	29 / 595	MF RNA binding
26	2e-07	5 / 10	CC large ribosomal subunit
27	4e-07	6 / 19	CC mitochondrial proton-transporting ATP synthase complex
28	4e-07	11 / 96	BP rRNA processing
29	7e-07	5 / 12	BP oxidative phosphorylation
30	1e-06	5 / 13	GSE/ REACTOME_ FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
31	2e-06	5 / 14	BP mitochondrial ATP synthesis coupled proton transport
32	3e-06	5 / 15	BP ATP synthesis coupled proton transport
33	2e-05	6 / 37	CC cytosolic small ribosomal subunit
34	4e-05	4 / 13	CC mitochondrial respiratory chain
35	5e-05	5 / 26	MF cytochrome-c oxidase activity
36	6e-05	7 / 62	Glio Stuehler_Proteins_up_in_STS
37	6e-05	5 / 27	MF rRNA binding
38	9e-05	11 / 169	Glio willscher_GBM_proteomics_wtOnly_Differencelist_
39	1e-04	4 / 16	BP mitochondrial respiratory chain complex I assembly
40	1e-04	4 / 16	Canc GENTLES_modul10

### Overview Map

### Spot



### p-values





# Correlation Cluster

## Spot Summary: D1

# metagenes = 44  
# genes = 435

<r> metagenes = 0.94  
<r> genes = 0.25  
beta: r2= 3.98 / log p= -Inf

# samples with spot = 25 ( 9.1 % )  
Atypical : 1 ( 1.4 % )  
Classical : 2 ( 6.2 % )  
Mesenchymal : 6 ( 7.1 % )  
Basal : 16 ( 19 % )

## 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:16262]
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:27110]
5	147463	1.9	-1.14	0.36	ANKRD29 ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
6	100006589	1.84	-1.52	0.29	RNA28S rRNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
7	1843	1.8	-2.27	0.6	DUSP1 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3012]
8	114908	1.77	-1.52	0.42	TMEM122 transmembrane protein 123 [Source:HGNC Symbol;Acc:3012]
9	1647	1.77	-1.07	0.3	GADD45 growth arrest and DNA-damage-inducible, alpha [Source:HGNC Symbol;Acc:11142]
10	25800	1.74	-1.25	0.54	SLC39A6 solute carrier family 39 (zinc transporter), member 6 [Source:HGNC Symbol;Acc:11142]
11	23645	1.71	-1.84	0.38	PPP1R15 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:11142]
12	1958	1.66	-2.12	0.48	EGR1 early growth response 1 [Source:HGNC Symbol;Acc:3238]
13	150094	1.57	-1.48	0.38	SIK1 salt-inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
14	10972	1.55	-1.23	0.61	TMED10 transmembrane emp24-like trafficking protein 10 (yeast) [Source:HGNC Symbol;Acc:11142]
15	7538	1.53	-2.16	0.59	ZFP36 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
16	5366	1.49	-1.15	0.43	PMAIP1 phorbol-12-myristate-13-acetate-induced protein 1 [Source:HGNC Symbol;Acc:12862]
17	57018	1.46	-1	0.51	CCNL1 cyclin L1 [Source:HGNC Symbol;Acc:20569]
18	3725	1.46	-1.81	0.53	JUN jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
19	6622	1.44	-0.92	0.28	SNCA synuclein, alpha (non A4 component of amyloid precursor) [Source:HGNC Symbol;Acc:6204]
20	2353	1.43	-3.04	0.61	FOS FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:16262]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-30	64 / 436	miRN hsa-miR-548n
2	2e-20	41 / 262	miRN hsa-miR-548l
3	2e-19	43 / 310	miRN hsa-miR-340
4	5e-18	35 / 217	miRN hsa-miR-548m
5	6e-17	52 / 517	miRN hsa-miR-106a
6	8e-17	40 / 313	Glio willscher_GBM_Verhaak-CL_expression_D_up
7	8e-17	40 / 313	Glio willscher_GBM_Verhaak-MES_expression_D_down
8	8e-17	40 / 313	Glio willscher_GBM_Verhaak-PNwt_expression_D_up
9	2e-16	41 / 336	miRN hsa-miR-548d-5p
10	5e-16	39 / 313	miRN hsa-miR-559
11	7e-16	36 / 269	miRN hsa-miR-1244
12	7e-16	50 / 511	miRN hsa-miR-106b
13	2e-15	38 / 307	miRN hsa-miR-548c-5p
14	2e-15	54 / 603	miRN hsa-miR-20a
15	4e-15	28 / 167	miRN hsa-miR-548g
16	4e-15	41 / 368	miRN hsa-miR-144
17	6e-15	35 / 271	miRN hsa-miR-548h
18	6e-15	50 / 538	miRN hsa-miR-17
19	1e-14	51 / 565	miRN hsa-miR-20b
20	5e-14	37 / 324	miRN hsa-miR-18a
21	6e-14	35 / 293	miRN hsa-miR-186
22	8e-14	31 / 232	miRN ACTT-142-5P
23	1e-13	37 / 336	miRN hsa-miR-548b-5p
24	2e-13	28 / 192	miRN hsa-miR-944
25	2e-13	48 / 545	miRN hsa-miR-93
26	2e-13	31 / 240	miRN hsa-miR-152
27	8e-13	34 / 302	miRN hsa-miR-548i
28	1e-12	24 / 150	miRN hsa-miR-200c
29	1e-12	44 / 494	miRN hsa-miR-107
30	1e-12	26 / 180	miRN hsa-miR-374a
31	1e-12	39 / 399	miRN hsa-miR-519c-3p
32	3e-12	33 / 300	miRN hsa-miR-561
33	4e-12	33 / 301	miRN hsa-miR-18b
34	4e-12	29 / 234	miRN hsa-miR-26a
35	4e-12	25 / 173	miRN hsa-miR-548k
36	5e-12	43 / 495	miRN hsa-miR-103
37	9e-12	41 / 463	miRN hsa-miR-301a
38	9e-12	23 / 151	miRN hsa-miR-429
39	1e-11	33 / 315	miRN hsa-miR-30e
40	1e-11	34 / 335	miRN hsa-miR-142-5p

### Overview Map

### Spot

