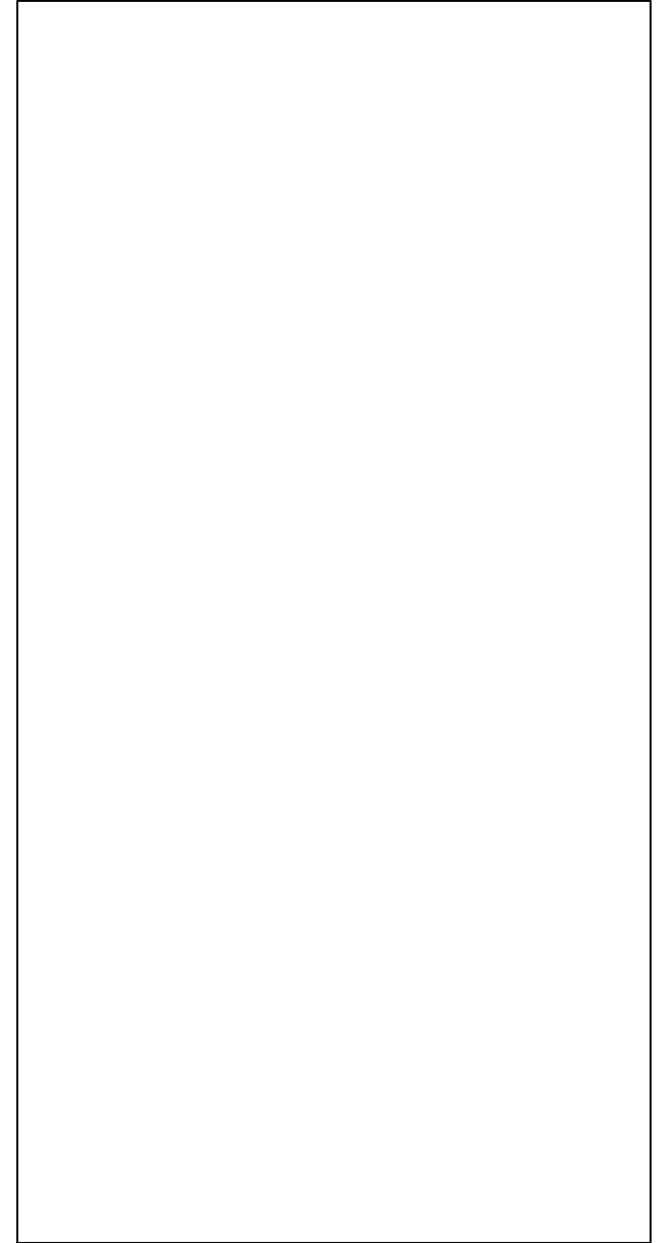
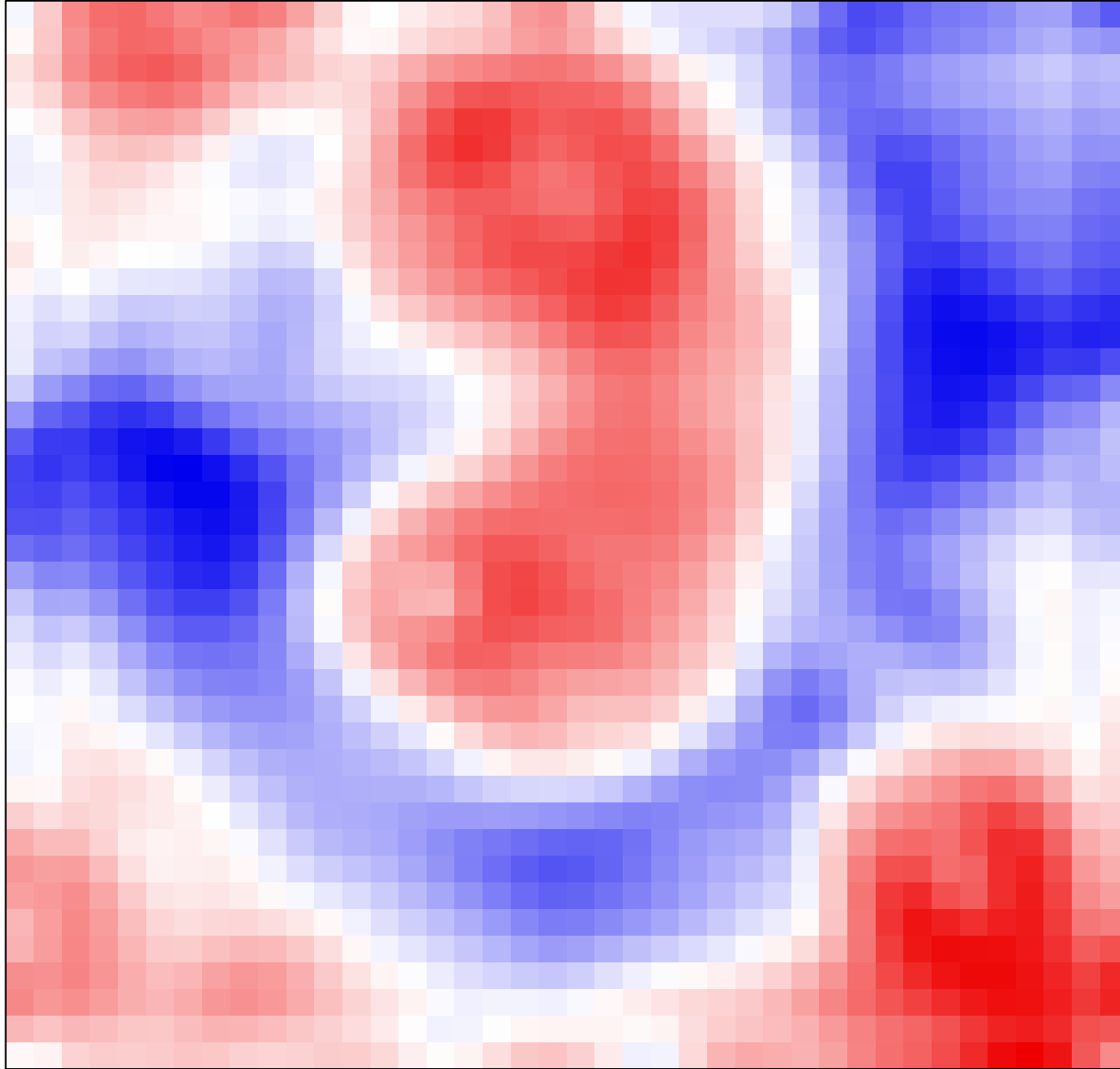


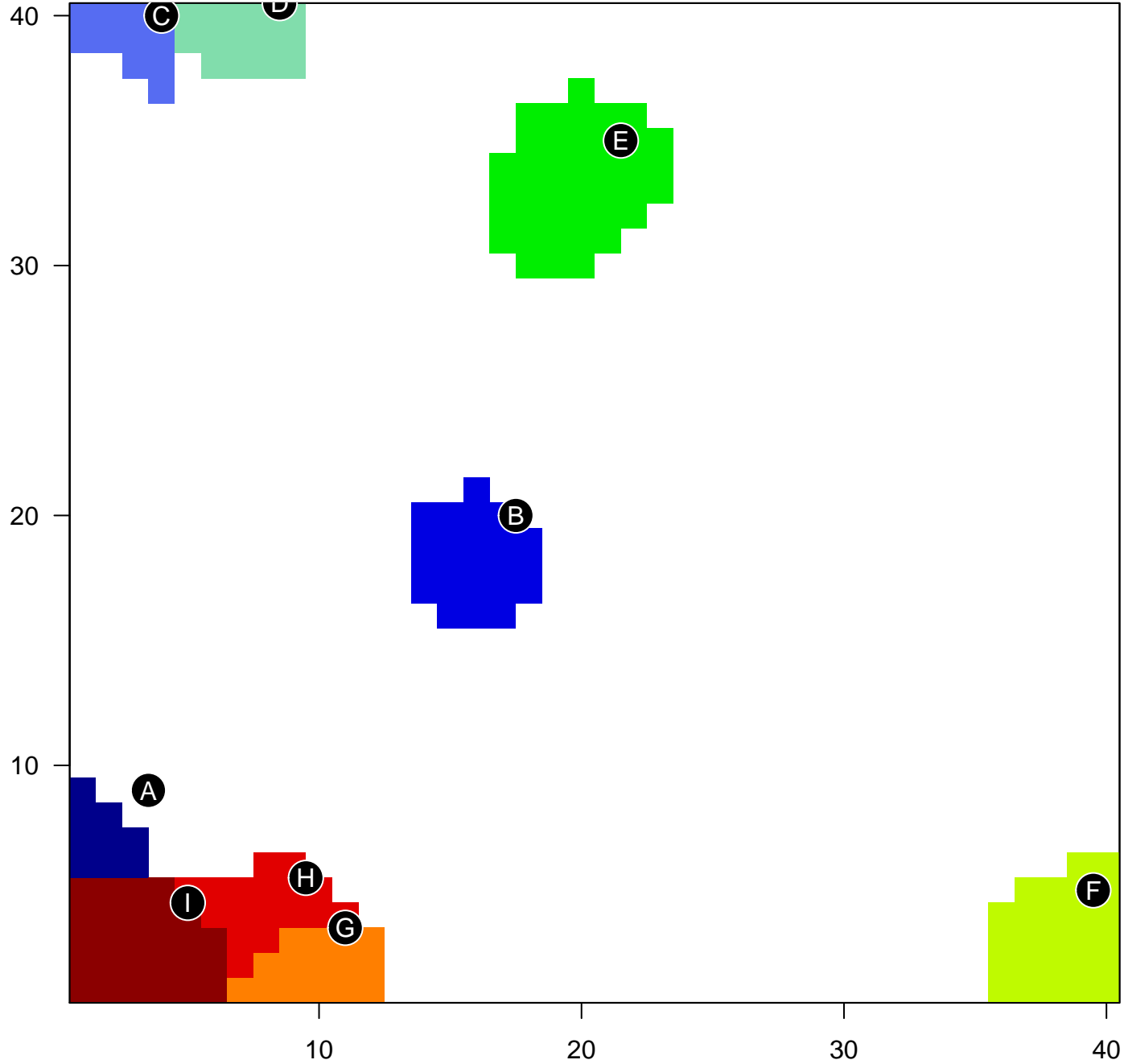
# D-Cluster

landscape

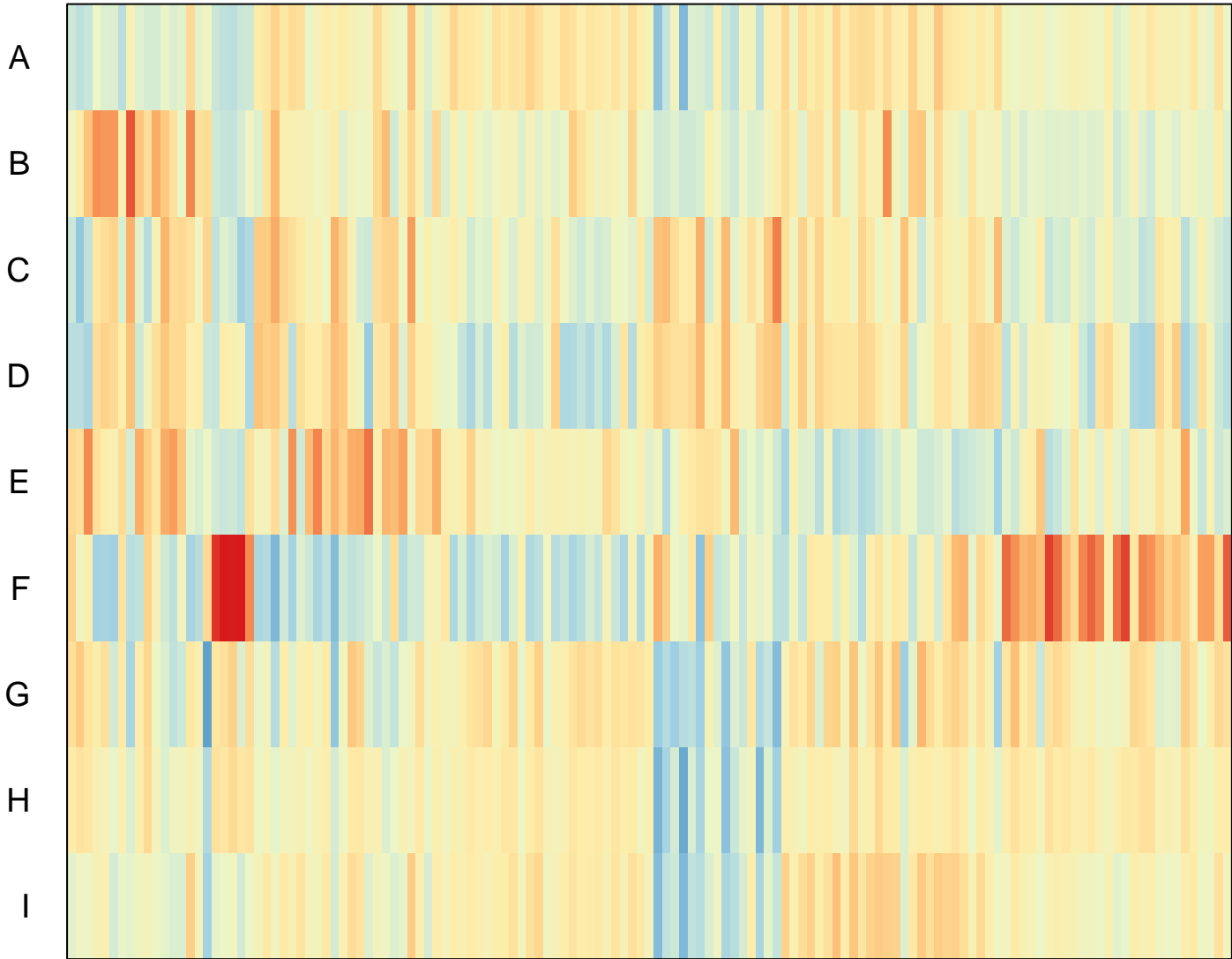


# D-Cluster

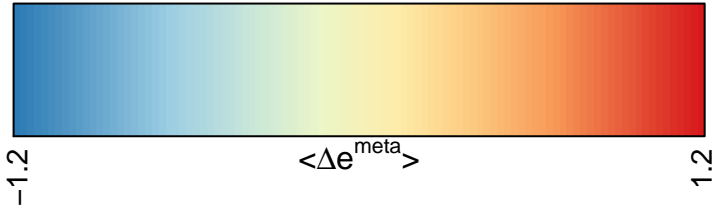
annotation



- A DNA-binding transcription factor activity, RNA polymerase I positive regulation of transcription, DNA-templated  
DNA-binding transcription factor activity
- B cell cycle  
cell division  
DNA replication
- C histone mRNA catabolic process  
regulation of transforming growth factor beta receptor signaling pathway  
DNA methylation
- D cytoplasm  
positive regulation of transcription by RNA polymerase II  
RNA splicing
- E immune system process  
immune response  
innate immune response
- F synapse  
chemical synaptic transmission  
plasma membrane
- G cytosol  
cytoplasm  
membrane
- H cytosol  
membrane  
Golgi apparatus
- I DNA-binding transcription factor activity, RNA polymerase I positive regulation of transcription, DNA-templated  
regulation of transcription, DNA-templated



- DNA-binding transcription factor activity, RNA polymerase II-specific  
positive regulation of transcription, DNA-templated  
DNA-binding transcription factor activity
- cell cycle  
cell division  
DNA replication
- histone mRNA catabolic process  
regulation of transforming growth factor beta receptor signaling pathway  
DNA methylation
- cytoplasm  
positive regulation of transcription by RNA polymerase II  
RNA splicing
- immune system process  
immune response  
innate immune response
- synapse  
chemical synaptic transmission  
plasma membrane
- cytosol  
cytoplasm  
membrane
- cytosol  
membrane  
Golgi apparatus
- DNA-binding transcription factor activity, RNA polymerase II-specific  
regulation of transcription by RNA polymerase II  
regulation of transcription, DNA-templated



# D-Cluster

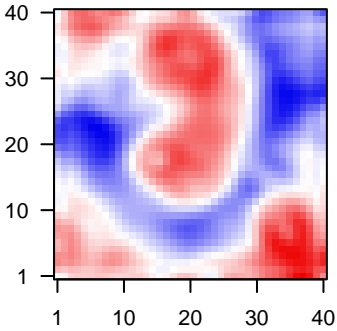
## Spot Summary: A

# metagenes = 9  
# genes = 354

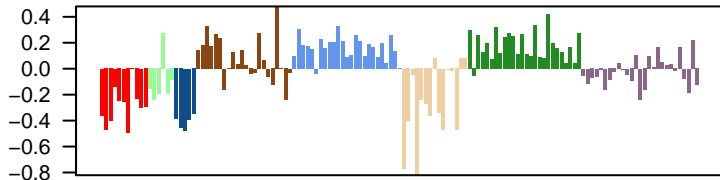
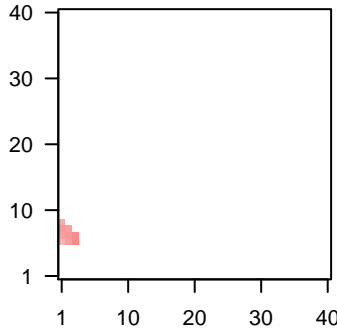
<r> metagenes = 0.97  
<r> genes = 0.38  
beta: r2= 6.85 / log p= -Inf

# samples with spot = 6 ( 4.4 %)  
group 4 : 2 ( 9.1 %)  
group 5 : 1 ( 4 %)  
group 7 : 3 ( 11.5 %)

Overview Map



Spot

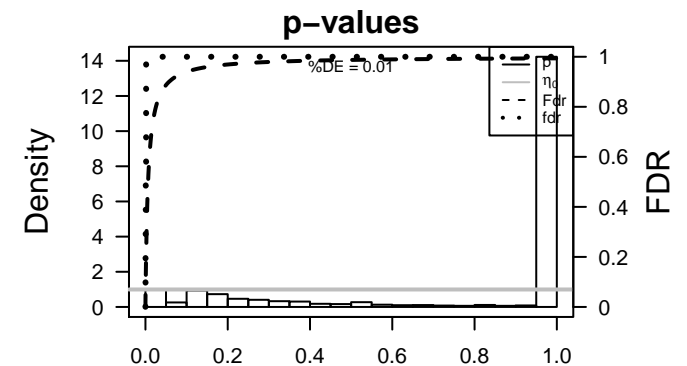


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	1559992_a_a	2.23	-1.21	0.39	long intergenic non-protein coding RNA 645 [Source:HGNC]
2	229870_at	2.1	-0.96	0.51	novel transcript, antisense to ZNF143
3	210055_at	2.09	-1.37	0.5	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;
4	244517_x_at	2.05	-0.82	0.6	
5	216379_x_at	1.99	-2.67	0.5	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
6	243261_at	1.98	-1.19	0.43	
7	1555520_at	1.94	-0.95	0.52	PTCH1 patched 1 [Source:HGNC Symbol;Acc:HGNC:9585]
8	230143_at	1.91	-1.62	0.55	RNF165 ring finger protein 165 [Source:HGNC Symbol;Acc:HGNC:311
9	232384_s_at	1.89	-1.36	0.71	novel transcript, antisense to SNX20
10	224185_at	1.87	-0.9	0.6	TP53 tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]
11	209771_x_at	1.85	-2.46	0.52	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
12	239639_at	1.85	-0.68	0.59	long intergenic non-protein coding RNA 1977 [Source:HGNC]
13	236174_at	1.83	-0.92	0.58	novel transcript
14	1559002_at	1.8	-0.69	0.57	MORF4L2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:1645]
15	238529_at	1.75	-0.7	0.53	novel transcript, antisense HIST2H4A
16	239347_at	1.75	-1.4	0.68	novel transcript
17	266_s_at	1.74	-2.48	0.5	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
18	1556294_at	1.73	-0.95	0.68	FXYP2 FXYP2 domain containing ion transport regulator 2 [Source:HGNC]
19	1559826_a_a	1.73	-0.98	0.46	long intergenic non-protein coding RNA 960 [Source:HGNC]
20	208651_x_at	1.71	-2.18	0.47	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-08	39 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	2e-07	23 / 613	BP positive regulation of transcription, DNA-templated
3	5e-07	27 / 843	BP DNA-binding transcription factor activity
4	1e-06	6 / 32	BP embryonic cranial skeleton morphogenesis
5	7e-06	34 / 1387	BP regulation of transcription, DNA-templated
6	2e-05	14 / 342	BP chromatin organization
7	5e-05	27 / 1086	BP positive regulation of transcription by RNA polymerase II
8	9e-05	17 / 541	BP negative regulation of transcription, DNA-templated
9	1e-04	27 / 1145	BP regulation of transcription by RNA polymerase II
10	1e-04	3 / 10	BP positive regulation of production of miRNAs involved in gene silencing by miRNAs
11	2e-04	5 / 49	BP embryonic skeletal system morphogenesis
12	2e-04	3 / 11	BP neural tube formation
13	3e-04	3 / 12	BP establishment of epithelial cell polarity
14	3e-04	3 / 13	BP eyelid development in camera-type eye
15	5e-04	5 / 60	BP inner ear morphogenesis
16	5e-04	4 / 35	BP embryonic organ development
17	7e-04	5 / 65	BP roof of mouth development
18	8e-04	3 / 17	BP pharyngeal system development
19	1e-03	3 / 19	BP positive regulation of branching involved in ureteric bud morphogenesis
20	1e-03	3 / 21	BP spinal cord motor neuron differentiation
21	2e-03	5 / 78	BP cartilage development
22	2e-03	3 / 22	BP innervation
23	2e-03	3 / 22	BP negative regulation of myoblast differentiation
24	2e-03	3 / 24	BP positive regulation of collagen biosynthetic process
25	2e-03	4 / 51	BP heart morphogenesis
26	2e-03	4 / 52	BP outflow tract morphogenesis
27	2e-03	3 / 25	BP endocrine pancreas development
28	4e-03	4 / 58	BP regulation of protein localization
29	4e-03	8 / 234	BP regulation of gene expression
30	4e-03	3 / 30	BP oligodendrocyte differentiation
31	4e-03	4 / 61	BP cell fate commitment
32	4e-03	11 / 400	BP chromatin binding
33	4e-03	3 / 31	BP negative regulation of DNA binding
34	4e-03	3 / 31	BP positive regulation of pri-miRNA transcription by RNA polymerase II
35	5e-03	3 / 32	BP positive regulation of BMP signaling pathway
36	5e-03	2 / 10	BP hindlimb morphogenesis
37	5e-03	2 / 10	BP keratinocyte proliferation
38	5e-03	5 / 102	BP chromatin remodeling
39	5e-03	3 / 33	BP liver regeneration
40	5e-03	3 / 33	BP spinal cord development



## BP

Rank	p-value	#in/all	Geneset
1	7e-08	39 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
2	2e-07	23 / 613	positive regulation of transcription, DNA-templated
3	5e-07	27 / 843	DNA-binding transcription factor activity
4	1e-06	6 / 32	embryonic cranial skeleton morphogenesis
5	7e-06	34 / 1387	regulation of transcription, DNA-templated
6	2e-05	14 / 342	chromatin organization
7	5e-05	27 / 1086	positive regulation of transcription by RNA polymerase II
8	9e-05	17 / 541	negative regulation of transcription, DNA-templated
9	1e-04	27 / 1145	regulation of transcription by RNA polymerase II
10	1e-04	3 / 10	positive regulation of production of miRNAs involved in gene silencing by miRNA
11	2e-04	5 / 49	embryonic skeletal system morphogenesis
12	2e-04	3 / 11	neural tube formation
13	3e-04	3 / 12	establishment of epithelial cell polarity
14	3e-04	3 / 13	eyelid development in camera-type eye
15	5e-04	5 / 60	inner ear morphogenesis

# D-Cluster

## Spot Summary: B

# metagenes = 23  
# genes = 419

<r> metagenes = 0.94  
<r> genes = 0.44  
beta: r2= 5.4 / log p= -Inf

# samples with spot = 16 ( 11.7 %)

group 1 : 7 ( 63.6 %)

group 2 : 2 ( 33.3 %)

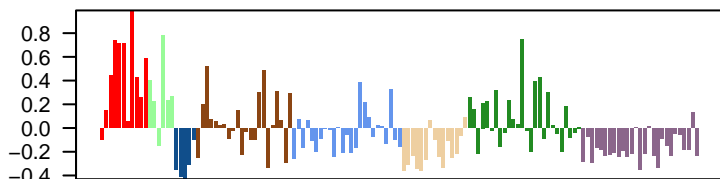
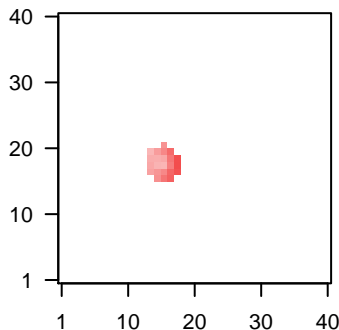
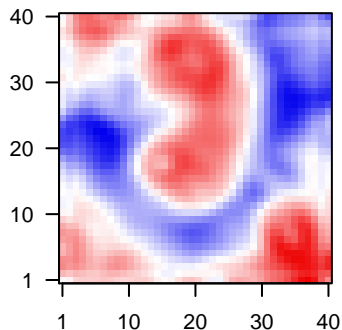
group 4 : 2 ( 9.1 %)

group 5 : 2 ( 8 %)

group 7 : 3 ( 11.5 %)

Overview Map

Spot

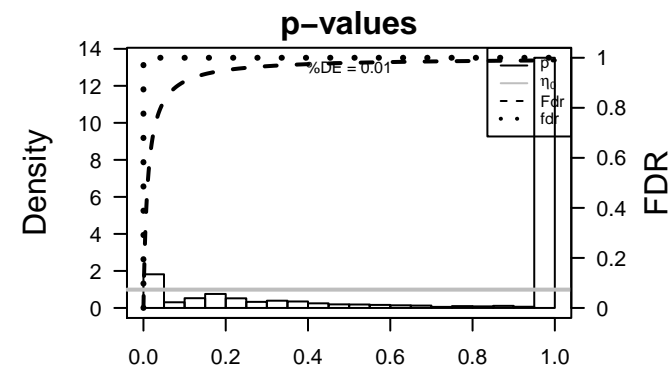


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	224588_at	2.97	-2.09	0.23	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588]
2	218308_at	2.79	-0.78	0.77	TACC3 transforming acidic coiled-coil containing protein 3 [Source:HGNC Symbol;Acc:HGNC:218308]
3	227671_at	2.79	-1.83	0.23	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:227671]
4	214218_s_at	2.77	-1.66	0.23	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:214218]
5	221728_x_at	2.49	-1.68	0.22	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:221728]
6	224646_x_at	2.49	-0.89	0.28	H19, imprinted maternally expressed transcript [Source:HGNC Symbol;Acc:HGNC:224646]
7	1558834_s_at	2.45	-0.78	0.5	AKNAD1 AKNA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1558834]
8	224590_at	2.44	-1.42	0.25	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224590]
9	217373_x_at	2.43	-0.86	0.51	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:217373]
10	205676_at	2.39	-0.65	0.5	CYP27B1 cytochrome P450 family 27 subfamily B member 1 [Source:HGNC Symbol;Acc:HGNC:205676]
11	224589_at	2.34	-1.31	0.24	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224589]
12	219773_at	2.34	-0.58	0.56	NOX4 NADPH oxidase 4 [Source:HGNC Symbol;Acc:HGNC:219773]
13	214451_at	2.18	-0.51	0.49	TFAP2B transcription factor AP-2 beta [Source:HGNC Symbol;Acc:HGNC:214451]
14	1559492_at	2.18	-0.71	0.4	AKNA AKNA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1559492]
15	226454_at	2.08	-0.5	0.38	MARCH9 membrane associated ring-CH-type finger 9 [Source:HGNC Symbol;Acc:HGNC:226454]
16	212670_at	2.07	-1.08	0.52	ELN elastin [Source:HGNC Symbol;Acc:HGNC:212670]
17	228033_at	2.04	-0.69	0.85	E2F7 E2F transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:228033]
18	244340_x_at	2	-0.95	0.4	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:244340]
19	237737_at	1.99	-0.88	0.49	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:237737]
20	238756_at	1.98	-0.92	0.72	GAS2L3 growth arrest specific 2 like 3 [Source:HGNC Symbol;Acc:HGNC:238756]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-85	103 / 630	BP cell cycle
2	1e-67	76 / 394	BP cell division
3	2e-40	40 / 158	BP DNA replication
4	1e-30	27 / 85	BP chromosome segregation
5	1e-28	43 / 366	BP DNA repair
6	3e-27	31 / 164	BP mitotic cell cycle
7	1e-24	44 / 484	BP cellular response to DNA damage stimulus
8	5e-20	21 / 98	BP G1/S transition of mitotic cell cycle
9	1e-18	22 / 130	BP G2/M transition of mitotic cell cycle
10	3e-17	13 / 31	BP mitotic sister chromatid segregation
11	4e-16	122 / 4740	BP cytosol
12	1e-15	13 / 39	BP CENP-A containing nucleosome assembly
13	4e-15	13 / 42	BP mitotic spindle organization
14	5e-15	12 / 33	BP DNA replication initiation
15	9e-15	14 / 56	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
16	9e-15	30 / 400	BP chromatin binding
17	2e-13	26 / 327	BP cell population proliferation
18	5e-13	18 / 145	BP regulation of cell cycle
19	1e-12	12 / 50	BP mitotic cytokinesis
20	2e-12	14 / 80	BP regulation of G2/M transition of mitotic cell cycle
21	4e-12	9 / 22	BP regulation of transcription involved in G1/S transition of mitotic cell cycle
22	1e-11	8 / 17	BP DNA replication origin binding
23	2e-11	20 / 227	BP microtubule binding
24	2e-11	13 / 79	BP microtubule-based movement
25	4e-11	12 / 66	BP double-strand break repair
26	8e-11	131 / 6202	BP cytoplasm
27	9e-11	7 / 13	BP kinetochore assembly
28	2e-10	8 / 22	BP mitotic spindle assembly checkpoint
29	2e-10	11 / 59	BP regulation of cyclin-dependent protein serine/threonine kinase activity
30	2e-10	12 / 76	BP microtubule motor activity
31	2e-10	9 / 33	BP mitotic cell cycle checkpoint
32	4e-10	9 / 35	BP mitotic metaphase plate congression
33	6e-10	10 / 49	BP interstrand cross-link repair
34	1e-09	8 / 27	BP mitotic spindle assembly
35	1e-09	9 / 39	BP regulation of mitotic nuclear division
36	2e-09	8 / 28	BP positive regulation of G2/M transition of mitotic cell cycle
37	2e-09	6 / 11	BP metaphase plate congression
38	4e-09	12 / 97	BP DNA recombination
39	5e-09	11 / 78	BP anaphase-promoting complex-dependent catabolic process
40	7e-09	11 / 81	BP double-strand break repair via homologous recombination



## BP

Rank	p-value	#in/all	Geneset
1	1e-85	103 / 630	cell cycle
2	1e-67	76 / 394	cell division
3	2e-40	40 / 158	DNA replication
4	1e-30	27 / 85	chromosome segregation
5	1e-28	43 / 366	DNA repair
6	3e-27	31 / 164	mitotic cell cycle
7	1e-24	44 / 484	cellular response to DNA damage stimulus
8	5e-20	21 / 98	G1/S transition of mitotic cell cycle
9	1e-18	22 / 130	G2/M transition of mitotic cell cycle
10	3e-17	13 / 31	mitotic sister chromatid segregation
11	4e-16	122 / 4740	cytosol
12	1e-15	13 / 39	CENP-A containing nucleosome assembly
13	4e-15	13 / 42	mitotic spindle organization
14	5e-15	12 / 33	DNA replication initiation
15	9e-15	14 / 56	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest

# D-Cluster

## Spot Summary: C

# metagenes = 10  
# genes = 597

<r> metagenes = 0.98

<r> genes = 0.55

beta: r2= 10.68 / log p= -Inf

# samples with spot = 23 ( 16.8 %)

group 1 : 2 ( 18.2 %)

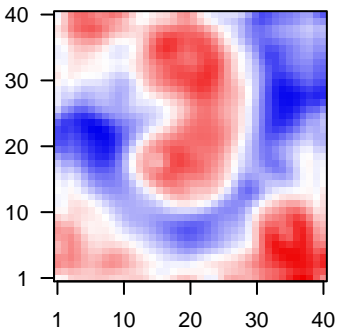
group 2 : 2 ( 33.3 %)

group 4 : 9 ( 40.9 %)

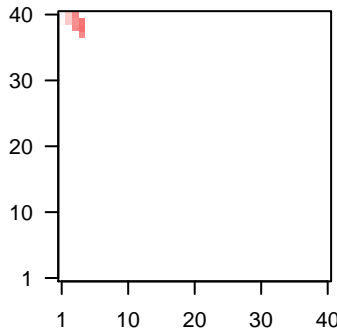
group 6 : 6 ( 40 %)

group 7 : 4 ( 15.4 %)

Overview Map



Spot

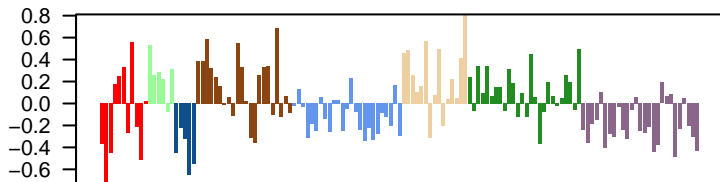


## Spot Genelist

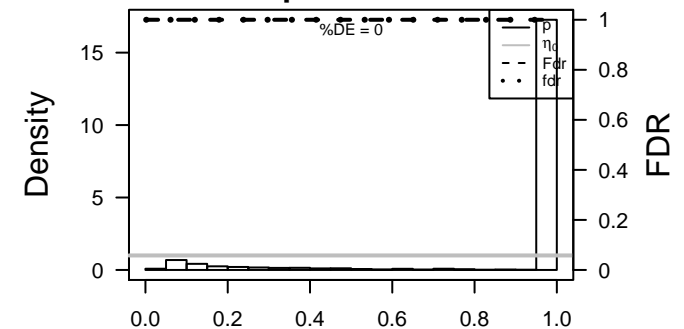
Rank	ID	max e	r	min e	Description
1	1562440_at	2.29	-0.64	0.63	
2	1566482_at	2.19	-0.81	0.53	novel transcript
3	1563426_a_a	1.96	-0.74	0.66	novel transcript
4	1552337_s_al	1.95	-0.8	0.43	HOXD4 homeobox D4 [Source:NCBI gene;Acc:3233]
5	232925_at	1.9	-1.69	0.67	
6	234082_at	1.82	-1.64	0.27	
7	214235_at	1.82	-0.93	0.47	CYP3A5 cytochrome P450 family 3 subfamily A member 5 [Source:HG]
8	215943_at	1.82	-1.1	0.74	
9	243077_at	1.74	-1.14	0.4	
10	240558_at	1.7	-0.93	0.53	
11	1563467_at	1.7	-0.84	0.65	
12	232120_at	1.68	-1.31	0.58	
13	233044_at	1.67	-1.22	0.61	
14	1558447_at	1.66	-1.19	0.72	
15	1568883_at	1.65	-0.53	0.55	
16	206558_at	1.64	-0.94	0.48	SIM2 SIM bHLH transcription factor 2 [Source:HGNC Symbol;Acc:HG]
17	241797_at	1.63	-1.44	0.74	
18	1554116_s_al	1.63	-0.94	0.74	PARP11 poly(ADP-ribose) polymerase family member 11 [Source:HG]
19	236976_at	1.61	-0.61	0.62	FANCA FA complementation group A [Source:HGNC Symbol;Acc:HG]
20	241726_at	1.6	-1.58	0.36	

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	0.002	2 / 11	BP histone mRNA catabolic process
2	0.006	2 / 20	BP regulation of transforming growth factor beta receptor signaling pathway
3	0.007	2 / 23	BP DNA methylation
4	0.009	2 / 26	BP positive regulation of muscle cell differentiation
5	0.009	2 / 26	BP regulation of rhodopsin mediated signaling pathway
6	0.016	2 / 35	BP spindle assembly
7	0.025	2 / 44	BP response to activity
8	0.031	2 / 49	BP embryonic skeletal system morphogenesis
9	0.043	5 / 342	BP chromatin organization
10	0.046	2 / 61	BP cell fate commitment
11	0.047	9 / 843	BP DNA-binding transcription factor activity
12	0.049	3 / 146	BP homophilic cell adhesion via plasma membrane adhesion molecules
13	0.053	2 / 66	BP protein autoubiquitination
14	0.055	1 / 10	BP cellular aldehyde metabolic process
15	0.055	1 / 10	BP deadenylation-dependent decapping of nuclear-transcribed mRNA
16	0.055	1 / 10	BP IRES-dependent viral translational initiation
17	0.055	1 / 10	BP low-density lipoprotein particle receptor catabolic process
18	0.055	1 / 10	BP positive regulation of blood vessel endothelial cell proliferation involved in sprouting
19	0.055	1 / 10	BP positive regulation of cell cycle G1/S phase transition
20	0.055	1 / 10	BP positive regulation of hormone secretion
21	0.055	1 / 10	BP positive regulation of methylation-dependent chromatin silencing
22	0.055	1 / 10	BP protein mono-ADP-ribosylation
23	0.056	2 / 68	BP retina development in camera-type eye
24	0.057	2 / 69	BP hippocampus development
25	0.060	1 / 11	BP erythrocyte homeostasis
26	0.060	1 / 11	BP Golgi ribbon formation
27	0.060	1 / 11	BP hematopoietic stem cell differentiation
28	0.060	1 / 11	BP limb bud formation
29	0.060	1 / 11	BP mesodermal cell differentiation
30	0.060	1 / 11	BP neural tube formation
31	0.060	1 / 11	BP ovulation
32	0.060	1 / 11	BP positive regulation of stem cell proliferation
33	0.060	1 / 11	BP protein auto-ADP-ribosylation
34	0.060	1 / 11	BP protein polyglutamylation
35	0.060	1 / 11	BP protein quality control for misfolded or incompletely synthesized proteins
36	0.060	1 / 11	BP regulation of microtubule polymerization
37	0.060	1 / 11	BP signal peptide processing
38	0.061	4 / 264	BP vesicle-mediated transport
39	0.065	2 / 74	BP retrograde transport, endosome to Golgi
40	0.065	1 / 12	BP commissural neuron axon guidance



p-values





## BP

Rank	p-value	#in/all	Geneset
1	0.002	2 / 11	histone mRNA catabolic process
2	0.006	2 / 20	regulation of transforming growth factor beta receptor signaling pathway
3	0.007	2 / 23	DNA methylation
4	0.009	2 / 26	positive regulation of muscle cell differentiation
5	0.009	2 / 26	regulation of rhodopsin mediated signaling pathway
6	0.016	2 / 35	spindle assembly
7	0.025	2 / 44	response to activity
8	0.031	2 / 49	embryonic skeletal system morphogenesis
9	0.043	5 / 342	chromatin organization
10	0.046	2 / 61	cell fate commitment
11	0.047	9 / 843	DNA-binding transcription factor activity
12	0.049	3 / 146	homophilic cell adhesion via plasma membrane adhesion molecules
13	0.053	2 / 66	protein autoubiquitination
14	0.055	1 / 10	cellular aldehyde metabolic process
15	0.055	1 / 10	deadenylation-dependent decapping of nuclear-transcribed mRNA

# D-Cluster

## Spot Summary: D

# metagenes = 14  
# genes = 693

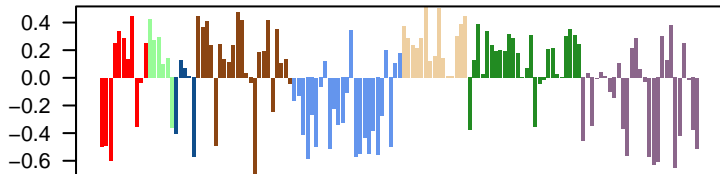
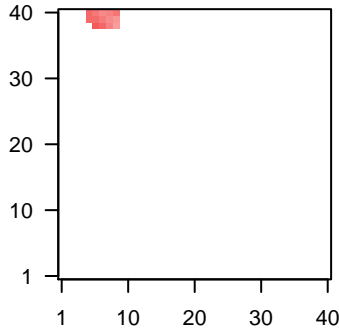
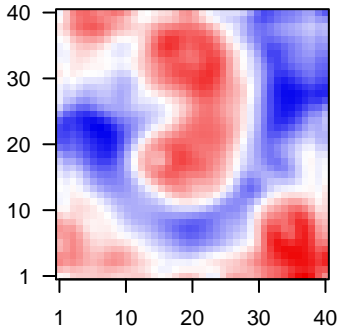
<r> metagenes = 0.97  
<r> genes = 0.55  
beta: r2= 10.26 / log p= -Inf

# samples with spot = 20 ( 14.6 %)

- group 1 : 2 ( 18.2 %)
- group 2 : 1 ( 16.7 %)
- group 4 : 7 ( 31.8 %)
- group 5 : 1 ( 4 %)
- group 6 : 5 ( 33.3 %)
- group 7 : 3 ( 11.5 %)
- group 8 : 1 ( 3.7 %)

Overview Map

Spot

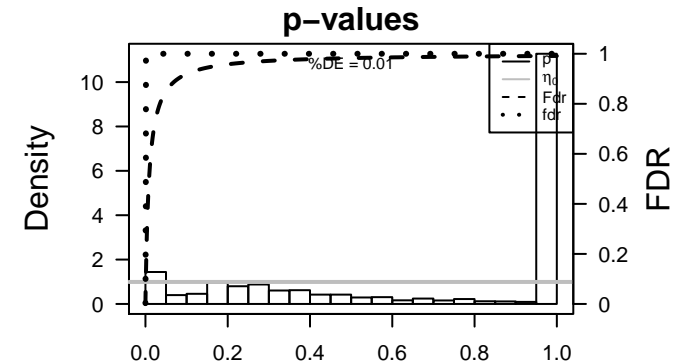


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	204713_s_at	2.44	-1.56	0.34	F5 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542]
2	214265_at	2.22	-0.74	0.42	ITGA8 integrin subunit alpha 8 [Source:HGNC Symbol;Acc:HGNC:6
3	215448_at	2.16	-1.33	0.55	
4	216007_at	2.14	-1.07	0.62	
5	1563331_at	2.1	-0.74	0.59	
6	226211_at	2.09	-1.04	0.46	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1
7	240728_at	2.08	-0.93	0.73	
8	237943_at	2.04	-1.36	0.81	TMCC1 transmembrane and coiled-coil domain family 1 [Source:HGNC
9	234597_at	2.04	-0.92	0.67	
10	242319_at	2.03	-0.87	0.58	DGKG diacylglycerol kinase gamma [Source:HGNC Symbol;Acc:HG
11	229775_s_at	2.03	-0.84	0.58	
12	216518_at	2	-0.75	0.45	
13	233884_at	1.96	-0.95	0.64	
14	207213_s_at	1.95	-1.36	0.69	USP2 ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG
15	244774_at	1.94	-1.09	0.36	PHACTR1 phosphatase and actin regulator 2 [Source:HGNC Symbol;Ac
16	226210_s_at	1.9	-1.12	0.48	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1
17	200952_s_at	1.89	-1.58	0.56	CCND2 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
18	240112_at	1.88	-1.05	0.66	
19	203479_s_at	1.87	-1.31	0.85	OTUD4 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:33
20	238751_at	1.84	-1.21	0.67	

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-08	163 / 6202	BP cytoplasm
2	1e-06	43 / 1086	BP positive regulation of transcription by RNA polymerase II
3	4e-06	18 / 279	BP RNA splicing
4	4e-06	16 / 227	BP microtubule binding
5	6e-06	123 / 4740	BP cytosol
6	2e-05	19 / 342	BP chromatin organization
7	2e-05	5 / 19	BP regulation of DNA replication
8	2e-05	27 / 613	BP positive regulation of transcription, DNA-templated
9	3e-05	19 / 358	BP mRNA processing
10	4e-05	20 / 400	BP chromatin binding
11	5e-05	40 / 1145	BP regulation of transcription by RNA polymerase II
12	8e-05	22 / 484	BP cellular response to DNA damage stimulus
13	1e-04	7 / 61	BP regulation of alternative mRNA splicing, via spliceosome
14	1e-04	23 / 541	BP negative regulation of transcription, DNA-templated
15	2e-04	4 / 16	BP cytoskeleton-dependent intracellular transport
16	2e-04	9 / 112	BP microtubule cytoskeleton organization
17	2e-04	25 / 630	BP cell cycle
18	2e-04	29 / 783	BP negative regulation of transcription by RNA polymerase II
19	4e-04	8 / 97	BP transforming growth factor beta receptor signaling pathway
20	4e-04	4 / 20	BP actin filament-based movement
21	4e-04	4 / 20	BP DNA replication-independent nucleosome assembly
22	4e-04	24 / 623	BP protein phosphorylation
23	6e-04	9 / 129	BP rhythmic process
24	9e-04	3 / 11	BP regulation of response to DNA damage stimulus
25	9e-04	6 / 62	BP circadian regulation of gene expression
26	9e-04	17 / 394	BP cell division
27	1e-03	42 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
28	1e-03	10 / 173	BP cilium assembly
29	2e-03	10 / 180	BP cell projection organization
30	2e-03	7 / 99	BP mRNA export from nucleus
31	2e-03	3 / 15	BP DNA damage response, signal transduction by p53 class mediator
32	2e-03	3 / 15	BP positive regulation of cilium assembly
33	2e-03	3 / 15	BP stress granule assembly
34	2e-03	40 / 1387	BP regulation of transcription, DNA-templated
35	2e-03	10 / 190	BP actin filament binding
36	3e-03	4 / 32	BP regulation of microtubule cytoskeleton organization
37	3e-03	8 / 132	BP membrane organization
38	3e-03	5 / 54	BP axon cytoplasm
39	3e-03	9 / 164	BP mitotic cell cycle
40	3e-03	5 / 55	BP bone development



## BP

Rank	p-value	#in/all	Geneset
1	2e-08	163 / 6202	cytoplasm
2	1e-06	43 / 1086	positive regulation of transcription by RNA polymerase II
3	4e-06	18 / 279	RNA splicing
4	4e-06	16 / 227	microtubule binding
5	6e-06	123 / 4740	cytosol
6	2e-05	19 / 342	chromatin organization
7	2e-05	5 / 19	regulation of DNA replication
8	2e-05	27 / 613	positive regulation of transcription, DNA-templated
9	3e-05	19 / 358	mRNA processing
10	4e-05	20 / 400	chromatin binding
11	5e-05	40 / 1145	regulation of transcription by RNA polymerase II
12	8e-05	22 / 484	cellular response to DNA damage stimulus
13	1e-04	7 / 61	regulation of alternative mRNA splicing, via spliceosome
14	1e-04	23 / 541	negative regulation of transcription, DNA-templated
15	2e-04	4 / 16	cytoskeleton-dependent intracellular transport

# D-Cluster

## Spot Summary: E

# metagenes = 40  
# genes = 999

<r> metagenes = 0.92

<r> genes = 0.47

beta: r2= 11.48 / log p= -Inf

# samples with spot = 22 ( 16.1 %)

group 1 : 3 ( 27.3 %)

group 2 : 3 ( 50 %)

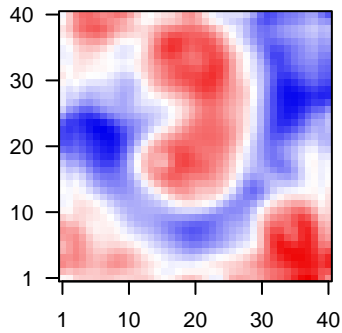
group 4 : 12 ( 54.5 %)

group 5 : 1 ( 4 %)

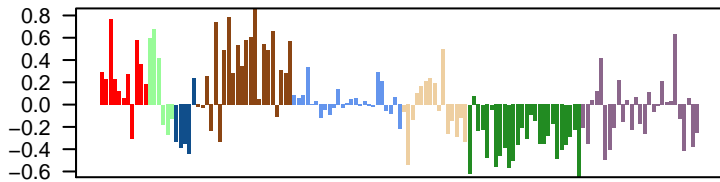
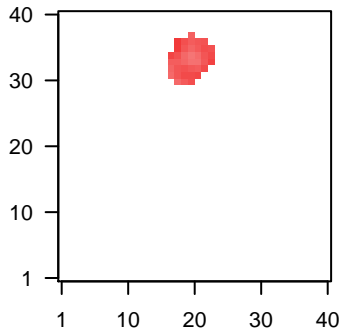
group 6 : 1 ( 6.7 %)

group 8 : 2 ( 7.4 %)

Overview Map



Spot

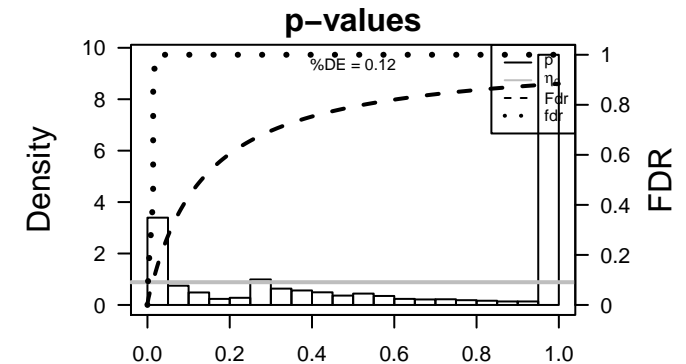


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	211430_s_at	3.66	-1	0.51	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
2	209138_x_at	3.42	-0.97	0.57	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
3	215121_x_at	3.38	-1.11	0.54	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
4	217022_s_at	3.37	-0.9	0.51	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
5	214677_x_at	3.36	-1.19	0.58	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215176_x_at	3.32	-0.8	0.52	immunoglobulin kappa variable 1-39 (gene/pseudogene) [So
7	215379_x_at	3.1	-1.03	0.53	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
8	202018_s_at	3.01	-0.95	0.49	LTF lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
9	214669_x_at	2.74	-0.74	0.48	
10	224061_at	2.73	-0.57	0.47	INMT indolethylamine N-methyltransferase [Source:HGNC Symbol
11	211339_s_at	2.73	-0.49	0.55	ITK IL2 inducible T cell kinase [Source:HGNC Symbol;Acc:HGNC
12	205374_at	2.72	-1.23	0.61	SLN sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]
13	214836_x_at	2.63	-0.83	0.49	
14	221651_x_at	2.59	-0.66	0.54	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
15	221671_x_at	2.58	-0.81	0.53	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
16	204575_s_at	2.56	-0.72	0.48	MMP19 matrix metalloproteinase 19 [Source:HGNC Symbol;Acc:HGN
17	209641_s_at	2.48	-0.8	0.62	ABCC3 ATP binding cassette subfamily C member 3 [Source:HGNC S
18	236028_at	2.46	-0.71	0.62	IBSP integrin binding sialoprotein [Source:HGNC Symbol;Acc:HGN
19	209374_s_at	2.46	-0.76	0.5	immunoglobulin heavy constant mu [Source:HGNC Symbol;A
20	37145_at	2.45	-0.6	0.61	GNLY granulysin [Source:HGNC Symbol;Acc:HGNC:4414]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-76	126 / 564	BP immune system process
2	2e-50	85 / 388	BP immune response
3	9e-49	86 / 417	BP innate immune response
4	2e-43	76 / 364	BP inflammatory response
5	2e-34	254 / 4278	BP plasma membrane
6	2e-33	73 / 460	BP neutrophil degranulation
7	1e-30	351 / 7387	BP membrane
8	5e-24	49 / 289	BP cytokine-mediated signaling pathway
9	1e-23	117 / 1500	BP signal transduction
10	7e-22	15 / 17	BP antigen processing and presentation of peptide or polysaccharide antigen v
11	5e-21	37 / 184	BP defense response to virus
12	5e-20	20 / 43	BP antigen processing and presentation
13	1e-19	33 / 155	BP regulation of immune response
14	1e-15	24 / 103	BP response to bacterium
15	1e-14	27 / 148	BP chemotaxis
16	3e-14	27 / 152	BP leukocyte migration
17	2e-13	17 / 56	BP B cell receptor signaling pathway
18	4e-13	17 / 59	BP positive regulation of T cell proliferation
19	2e-12	30 / 222	BP adaptive immune response
20	2e-12	17 / 64	BP regulation of complement activation
21	5e-12	25 / 160	BP T cell receptor signaling pathway
22	9e-12	24 / 151	BP cellular response to lipopolysaccharide
23	2e-11	16 / 64	BP complement activation, classical pathway
24	3e-11	49 / 594	BP cell adhesion
25	5e-11	18 / 88	BP cellular response to interferon-gamma
26	6e-11	23 / 151	BP defense response to bacterium
27	1e-10	24 / 172	BP positive regulation of I-kappaB kinase/NF-kappaB signaling
28	4e-10	13 / 47	BP complement activation
29	4e-10	16 / 77	BP cellular response to mechanical stimulus
30	5e-10	29 / 261	BP cell surface receptor signaling pathway
31	8e-10	13 / 49	BP positive regulation of tumor necrosis factor production
32	1e-09	12 / 41	BP positive regulation of interferon-gamma production
33	1e-09	22 / 159	BP response to lipopolysaccharide
34	2e-09	19 / 121	BP defense response
35	3e-09	16 / 88	BP positive regulation of peptidyl-tyrosine phosphorylation
36	4e-09	14 / 66	BP phagocytosis
37	6e-09	12 / 47	BP phagocytosis, engulfment
38	7e-09	9 / 23	BP response to interferon-gamma
39	9e-09	12 / 49	BP T cell activation
40	1e-08	52 / 777	BP G protein-coupled receptor signaling pathway



## BP

Rank	p-value	#in/all	Geneset
1	2e-76	126 / 564	immune system process
2	2e-50	85 / 388	immune response
3	9e-49	86 / 417	innate immune response
4	2e-43	76 / 364	inflammatory response
5	2e-34	254 / 4278	plasma membrane
6	2e-33	73 / 460	neutrophil degranulation
7	1e-30	351 / 7387	membrane
8	5e-24	49 / 289	cytokine-mediated signaling pathway
9	1e-23	117 / 1500	signal transduction
10	7e-22	15 / 17	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
11	5e-21	37 / 184	defense response to virus
12	5e-20	20 / 43	antigen processing and presentation
13	1e-19	33 / 155	regulation of immune response
14	1e-15	24 / 103	response to bacterium
15	1e-14	27 / 148	chemotaxis

# D-Cluster

## Spot Summary: F

# metagenes = 26  
# genes = 915

<r> metagenes = 0.97

<r> genes = 0.62

beta: r2= 29.95 / log p= -Inf

# samples with spot = 34 ( 24.8 %)

group 1 : 2 ( 18.2 %)

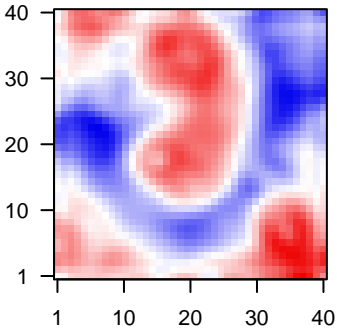
group 3 : 5 ( 100 %)

group 6 : 3 ( 20 %)

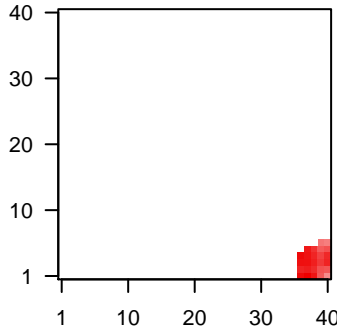
group 7 : 2 ( 7.7 %)

group 8 : 22 ( 81.5 %)

Overview Map



Spot

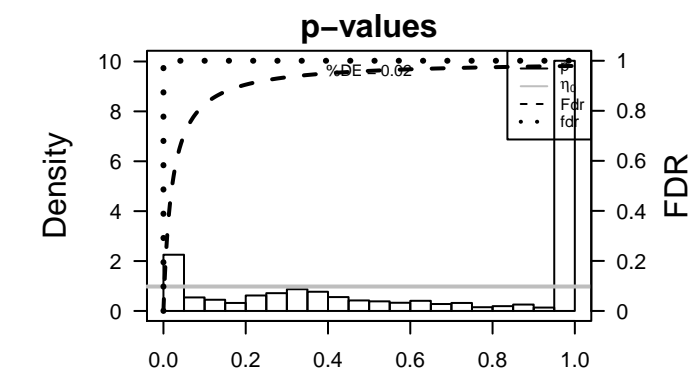
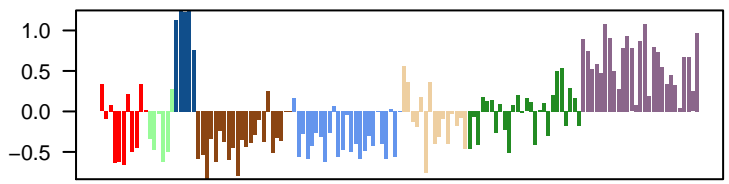


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	206803_at	3.07	-1.3	0.53	PDYN prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
2	206382_s_at	2.85	-0.87	0.59	BDNF brain derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:10342]
3	205901_at	2.71	-1.16	0.71	PNOC prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
4	229012_at	2.64	-0.83	0.7	C9orf24 chromosome 9 open reading frame 24 [Source:HGNC Symbol;Acc:HGNC:19112]
5	207147_at	2.55	-0.86	0.59	DLX2 distal-less homeobox 2 [Source:HGNC Symbol;Acc:HGNC:20822]
6	206552_s_at	2.4	-1.6	0.75	TAC1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11101]
7	228844_at	2.39	-0.8	0.79	SLC13A5solute carrier family 13 member 5 [Source:HGNC Symbol;Acc:HGNC:10342]
8	207768_at	2.35	-0.93	0.84	EGR4 early growth response 4 [Source:HGNC Symbol;Acc:HGNC:20822]
9	214611_at	2.29	-0.89	0.56	GRIK1 glutamate ionotropic receptor kainate type subunit 1 [Source:HGNC Symbol;Acc:HGNC:10342]
10	231391_at	2.29	-0.69	0.74	CTXN3 cortixin 3 [Source:HGNC Symbol;Acc:HGNC:31110]
11	222920_s_at	2.29	-1.17	0.88	TESPA1 thymocyte expressed, positive selection associated 1 [Source:HGNC Symbol;Acc:HGNC:10342]
12	220025_at	2.25	-0.85	0.92	TBR1 T-box, brain 1 [Source:HGNC Symbol;Acc:HGNC:11590]
13	242138_at	2.23	-1.27	0.73	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:20822]
14	219263_at	2.22	-1.06	0.74	RNF128 ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:10342]
15	232111_at	2.18	-0.91	0.81	TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:10342]
16	1555800_at	2.18	-1.12	0.87	ZNF385Bzinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:20822]
17	1559633_a_at	2.16	-1.09	0.84	CHRM3 cholinergic receptor muscarinic 3 [Source:HGNC Symbol;Acc:HGNC:10342]
18	211451_s_at	2.15	-0.89	0.8	KCNJ4 potassium voltage-gated channel subfamily J member 4 [Source:HGNC Symbol;Acc:HGNC:10342]
19	205914_s_at	2.14	-0.86	0.76	GRIN1 glutamate ionotropic receptor NMDA type subunit 1 [Source:HGNC Symbol;Acc:HGNC:10342]
20	231783_at	2.13	-1.47	0.92	CHRM1 cholinergic receptor muscarinic 1 [Source:HGNC Symbol;Acc:HGNC:10342]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-54	103 / 574	BP synapse
2	3e-46	65 / 236	BP chemical synaptic transmission
3	3e-37	254 / 4278	BP plasma membrane
4	9e-32	345 / 7387	BP membrane
5	1e-22	43 / 240	BP postsynaptic membrane
6	3e-20	65 / 627	BP ion transport
7	1e-17	30 / 149	BP regulation of ion transmembrane transport
8	2e-17	54 / 505	BP nervous system development
9	4e-12	15 / 51	BP neurotransmitter secretion
10	5e-12	14 / 43	BP neurotransmitter transport
11	1e-11	22 / 131	BP presynapse
12	1e-11	21 / 119	BP postsynapse
13	4e-11	87 / 1500	BP signal transduction
14	4e-11	12 / 33	BP regulation of exocytosis
15	7e-11	14 / 51	BP regulation of synaptic plasticity
16	8e-11	21 / 131	BP potassium ion transport
17	9e-11	11 / 28	BP synaptic vesicle exocytosis
18	3e-10	11 / 31	BP regulation of NMDA receptor activity
19	4e-10	16 / 79	BP cellular response to calcium ion
20	6e-10	54 / 777	BP G protein-coupled receptor signaling pathway
21	9e-10	13 / 51	BP regulation of synaptic vesicle exocytosis
22	1e-09	48 / 657	BP calcium ion binding
23	1e-09	10 / 27	BP glutamate secretion
24	3e-09	28 / 275	BP ion transmembrane transport
25	3e-09	8 / 16	BP positive regulation of calcium ion-dependent exocytosis
26	4e-09	15 / 79	BP memory
27	4e-09	18 / 118	BP exocytosis
28	4e-09	10 / 30	BP associative learning
29	7e-09	18 / 122	BP potassium ion transmembrane transport
30	1e-08	44 / 615	BP transmembrane transport
31	1e-08	8 / 18	BP regulation of neurotransmitter secretion
32	1e-08	9 / 25	BP calmodulin-dependent protein kinase activity
33	2e-08	7 / 13	BP synaptic transmission, GABAergic
34	2e-08	19 / 144	BP calcium ion transport
35	3e-08	25 / 249	BP brain development
36	5e-08	12 / 58	BP learning or memory
37	5e-08	9 / 29	BP calcium ion regulated exocytosis
38	6e-08	11 / 48	BP long-term synaptic potentiation
39	6e-08	7 / 15	BP calcium ion-regulated exocytosis of neurotransmitter
40	6e-08	17 / 125	BP calcium ion transmembrane transport



## BP

Rank	p-value	#in/all	Geneset
1	7e-54	103 / 574	synapse
2	3e-46	65 / 236	chemical synaptic transmission
3	3e-37	254 / 4278	plasma membrane
4	9e-32	345 / 7387	membrane
5	1e-22	43 / 240	postsynaptic membrane
6	3e-20	65 / 627	ion transport
7	1e-17	30 / 149	regulation of ion transmembrane transport
8	2e-17	54 / 505	nervous system development
9	4e-12	15 / 51	neurotransmitter secretion
10	5e-12	14 / 43	neurotransmitter transport
11	1e-11	22 / 131	presynapse
12	1e-11	21 / 119	postsynapse
13	4e-11	87 / 1500	signal transduction
14	4e-11	12 / 33	regulation of exocytosis
15	7e-11	14 / 51	regulation of synaptic plasticity

# D-Cluster

## Spot Summary: G

# metagenes = 15  
# genes = 599

<r> metagenes = 0.98

<r> genes = 0.55

beta: r2= 10.12 / log p= -Inf

# samples with spot = 15 ( 10.9 %)

group 1 : 1 ( 9.1 %)

group 3 : 1 ( 20 %)

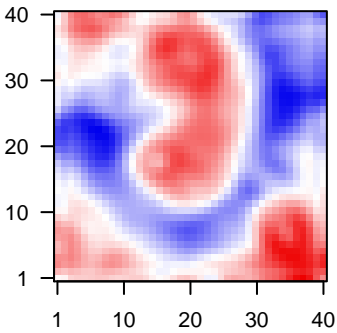
group 4 : 2 ( 9.1 %)

group 5 : 2 ( 8 %)

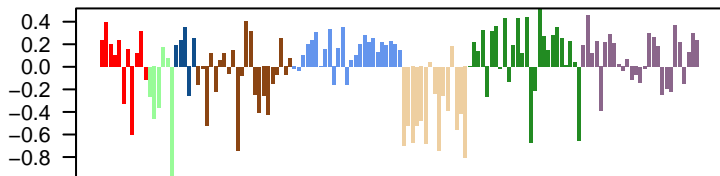
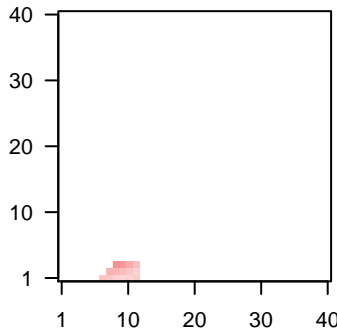
group 7 : 7 ( 26.9 %)

group 8 : 2 ( 7.4 %)

Overview Map



Spot

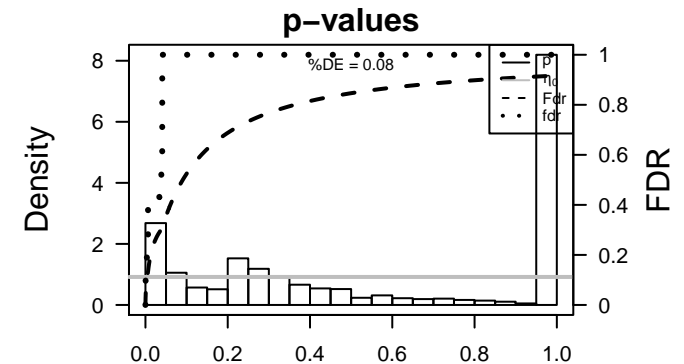


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	220241_at	2.56	-0.78	0.59	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Sy
2	220240_s_at	2.09	-1.17	0.69	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Sy
3	1555191_a_a	2.06	-0.78	0.53	FHL5 four and a half LIM domains 5 [Source:HGNC Symbol;Acc:HC
4	211607_x_at	2.06	-1.23	0.56	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
5	210984_x_at	2	-1.3	0.54	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
6	200879_s_at	1.97	-1.12	0.63	EPAS1 endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc:
7	210790_s_at	1.8	-0.94	0.43	SAR1A secretion associated Ras related GTPase 1A [Source:HGNC
8	222501_s_at	1.75	-1.44	0.71	REPIN1 replication initiator 1 [Source:HGNC Symbol;Acc:HGNC:1792
9	1554697_at	1.69	-1.41	0.51	ADAMTS10 metalloproteinase with thrombospondin type 1 motif 9 [
10	220029_at	1.67	-1.39	0.56	ELOVL2 ELOVL fatty acid elongase 2 [Source:HGNC Symbol;Acc:HGI
11	216352_x_at	1.65	-1.79	0.73	PCDHGA3 protocadherin gamma subfamily A, 3 [Source:HGNC Symbol;
12	233573_s_at	1.6	-1.05	0.74	WDR6 WD repeat domain 6 [Source:HGNC Symbol;Acc:HGNC:127
13	233638_s_at	1.57	-1.44	0.73	POMGN1 protein O-linked mannose N-acetylglucosaminyltransferase
14	228701_at	1.56	-1.43	0.72	VXN vexin [Source:HGNC Symbol;Acc:HGNC:28498]
15	214701_s_at	1.56	-1.04	0.6	FN1 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
16	215672_s_at	1.55	-1.13	0.73	AHCYL2 adenosylhomocysteinase like 2 [Source:HGNC Symbol;Acc:
17	1555716_a_a	1.55	-1.23	0.67	CXADR CXADR, Ig-like cell adhesion molecule [Source:HGNC Symb
18	211876_x_at	1.55	-1.95	0.74	PCDHGA3 protocadherin gamma subfamily A, 3 [Source:HGNC Symbol;
19	1555122_at	1.54	-0.91	0.71	ADGRA3 adhesion G protein-coupled receptor A3 [Source:HGNC Syrr
20	211124_s_at	1.53	-0.62	0.65	KITLG KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-18	193 / 4740	BP cytosol
2	8e-18	230 / 6202	BP cytoplasm
3	3e-15	252 / 7387	BP membrane
4	3e-12	46 / 630	BP protein transport
5	8e-09	17 / 132	BP membrane organization
6	3e-08	147 / 4278	BP plasma membrane
7	8e-08	10 / 47	BP activation of MAPKK activity
8	1e-07	58 / 1242	BP Golgi apparatus
9	5e-07	8 / 33	BP regulation of cholesterol biosynthetic process
10	7e-07	29 / 459	BP viral process
11	3e-06	16 / 179	BP protein dephosphorylation
12	4e-06	29 / 496	BP negative regulation of apoptotic process
13	6e-06	23 / 350	BP GTP binding
14	1e-05	58 / 1435	BP mitochondrion
15	2e-05	21 / 324	BP intracellular protein transport
16	2e-05	14 / 162	BP dephosphorylation
17	4e-05	18 / 264	BP vesicle-mediated transport
18	4e-05	12 / 129	BP rhythmic process
19	5e-05	8 / 58	BP learning or memory
20	7e-05	17 / 254	BP angiogenesis
21	2e-04	10 / 107	BP male gonad development
22	2e-04	4 / 14	BP vesicle organization
23	2e-04	8 / 72	BP protein heterooligomerization
24	2e-04	11 / 133	BP protein localization to plasma membrane
25	2e-04	35 / 815	BP protein homodimerization activity
26	3e-04	8 / 74	BP retrograde transport, endosome to Golgi
27	3e-04	43 / 1086	BP positive regulation of transcription by RNA polymerase II
28	3e-04	18 / 315	BP positive regulation of GTPase activity
29	4e-04	8 / 78	BP insulin receptor signaling pathway
30	4e-04	4 / 16	BP filopodium assembly
31	4e-04	10 / 120	BP activation of MAPK activity
32	5e-04	9 / 101	BP mRNA transport
33	5e-04	5 / 30	BP negative regulation of mitotic cell cycle
34	5e-04	8 / 82	BP chloride transmembrane transport
35	6e-04	9 / 105	BP actin filament organization
36	6e-04	6 / 47	BP thymus development
37	8e-04	4 / 19	BP branched-chain amino acid catabolic process
38	8e-04	4 / 19	BP regulation of nitric-oxide synthase activity
39	9e-04	6 / 50	BP sphingolipid biosynthetic process
40	9e-04	8 / 89	BP macroautophagy





## BP

Rank	p-value	#in/all	Geneset
1	1e-18	193 / 4740	cytosol
2	8e-18	230 / 6202	cytoplasm
3	3e-15	252 / 7387	membrane
4	3e-12	46 / 630	protein transport
5	8e-09	17 / 132	membrane organization
6	3e-08	147 / 4278	plasma membrane
7	8e-08	10 / 47	activation of MAPKK activity
8	1e-07	58 / 1242	Golgi apparatus
9	5e-07	8 / 33	regulation of cholesterol biosynthetic process
10	7e-07	29 / 459	viral process
11	3e-06	16 / 179	protein dephosphorylation
12	4e-06	29 / 496	negative regulation of apoptotic process
13	6e-06	23 / 350	GTP binding
14	1e-05	58 / 1435	mitochondrion
15	2e-05	21 / 324	intracellular protein transport

# D-Cluster

## Spot Summary: H

# metagenes = 17  
# genes = 437

<r> metagenes = 0.95  
<r> genes = 0.47  
beta: r2= 6.45 / log p= -Inf

# samples with spot = 0 ( 0 %)

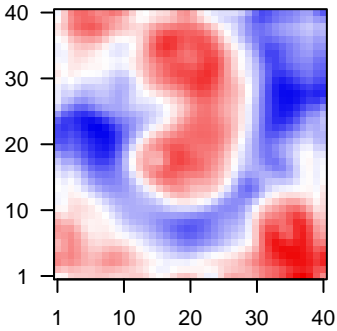
## Spot Genelist

Rank	ID	max e	r	min e	Description
1	207978_s_at	2.12	-0.97	0.4	NR4A3 nuclear receptor subfamily 4 group A member 3 [Source:HGNC]
2	225149_at	1.96	-1.21	0.6	PCID2 PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:12212]
3	218948_at	1.84	-1.47	0.53	QRSL1 QRSL1, glutamyl-tRNA amidotransferase subunit A [Source:HGNC Symbol;Acc:HGNC:12212]
4	217242_at	1.54	-0.81	0.51	ZNF154 zinc finger protein 154 [Source:HGNC Symbol;Acc:HGNC:12212]
5	239443_at	1.43	-1.59	0.36	PCDHB6 protocadherin beta 6 [Source:HGNC Symbol;Acc:HGNC:86912]
6	227059_at	1.43	-1.78	0.37	GPC6 glypican 6 [Source:HGNC Symbol;Acc:HGNC:4454]
7	40665_at	1.42	-0.74	0.48	FMO3 flavin containing monooxygenase 3 [Source:HGNC Symbol;Acc:HGNC:12212]
8	206070_s_at	1.38	-1.13	0.6	EPHA3 EPH receptor A3 [Source:HGNC Symbol;Acc:HGNC:3387]
9	202437_s_at	1.36	-1.49	0.49	CYP1B1 cytochrome P450 family 1 subfamily B member 1 [Source:HGNC Symbol;Acc:HGNC:12212]
10	231686_at	1.33	-1.02	0.43	
11	204304_s_at	1.32	-1.61	0.47	PROM1 prominin 1 [Source:HGNC Symbol;Acc:HGNC:9454]
12	227606_s_at	1.29	-1.58	0.68	STAMBP STAM binding protein like 1 [Source:HGNC Symbol;Acc:HGNC:12212]
13	229584_at	1.28	-1.69	0.54	LRRK2 leucine rich repeat kinase 2 [Source:HGNC Symbol;Acc:HGNC:12212]
14	223257_at	1.26	-1.35	0.74	G2E3 G2/M-phase specific E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:12212]
15	205501_at	1.24	-1.5	0.65	PDE10A phosphodiesterase 10A [Source:HGNC Symbol;Acc:HGNC:8664]
16	223235_s_at	1.23	-1.13	0.53	SMOC2 SPARC related modular calcium binding 2 [Source:HGNC Symbol;Acc:HGNC:12212]
17	203946_s_at	1.22	-1.03	0.46	ARG2 arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]
18	205728_at	1.22	-1.64	0.44	TENM1 teneurin transmembrane protein 1 [Source:HGNC Symbol;Acc:HGNC:12212]
19	236917_at	1.2	-1.12	0.39	LRRC34 leucine rich repeat containing 34 [Source:HGNC Symbol;Acc:HGNC:12212]
20	238819_at	1.19	-0.83	0.55	ZNF347 zinc finger protein 347 [Source:HGNC Symbol;Acc:HGNC:16212]

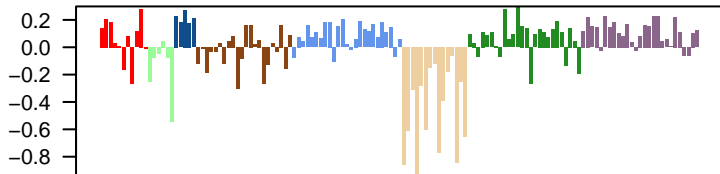
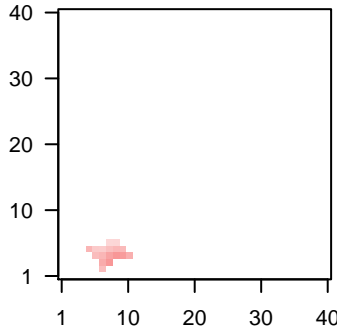
## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-07	116 / 4740	BP cytosol
2	7e-06	158 / 7387	BP membrane
3	2e-05	40 / 1242	BP Golgi apparatus
4	2e-05	135 / 6202	BP cytoplasm
5	1e-04	4 / 16	BP protein folding in endoplasmic reticulum
6	1e-04	7 / 70	BP positive regulation of proteasomal ubiquitin-dependent protein catabolic process
7	2e-04	5 / 35	BP cellular response to ionizing radiation
8	3e-04	10 / 163	BP autophagy
9	4e-04	3 / 10	BP cellular protein-containing complex localization
10	7e-04	4 / 26	BP intracellular transport
11	9e-04	14 / 328	BP post-translational protein modification
12	1e-03	4 / 31	BP positive regulation of TOR signaling
13	2e-03	3 / 15	BP endothelial cell proliferation
14	2e-03	4 / 32	BP regulation of microtubule cytoskeleton organization
15	2e-03	4 / 33	BP dendrite cytoplasm
16	2e-03	6 / 83	BP thiol-dependent ubiquitin-specific protease activity
17	2e-03	4 / 35	BP androgen receptor signaling pathway
18	2e-03	3 / 17	BP regulation of proteasomal protein catabolic process
19	3e-03	11 / 254	BP angiogenesis
20	3e-03	4 / 37	BP lung alveolus development
21	5e-03	5 / 68	BP positive regulation of protein ubiquitination
22	5e-03	5 / 68	BP regulation of autophagy
23	5e-03	11 / 273	BP MAPK cascade
24	5e-03	4 / 43	BP negative regulation of cell adhesion
25	5e-03	36 / 1435	BP mitochondrion
26	5e-03	6 / 99	BP mRNA export from nucleus
27	6e-03	3 / 23	BP cellular zinc ion homeostasis
28	6e-03	3 / 23	BP positive regulation of cardiac muscle hypertrophy
29	6e-03	3 / 23	BP zinc ion transport
30	6e-03	4 / 45	BP non-motile cilium assembly
31	6e-03	7 / 135	BP negative regulation of neuron apoptotic process
32	6e-03	4 / 46	BP phosphatidylinositol phosphorylation
33	7e-03	15 / 455	BP intracellular signal transduction
34	8e-03	8 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
35	8e-03	8 / 179	BP protein dephosphorylation
36	9e-03	5 / 80	BP response to endoplasmic reticulum stress
37	1e-02	3 / 28	BP mRNA polyadenylation
38	1e-02	2 / 10	BP deadenylation-dependent decapping of nuclear-transcribed mRNA
39	1e-02	2 / 10	BP mitotic DNA replication checkpoint
40	1e-02	2 / 10	BP protein deneddylation

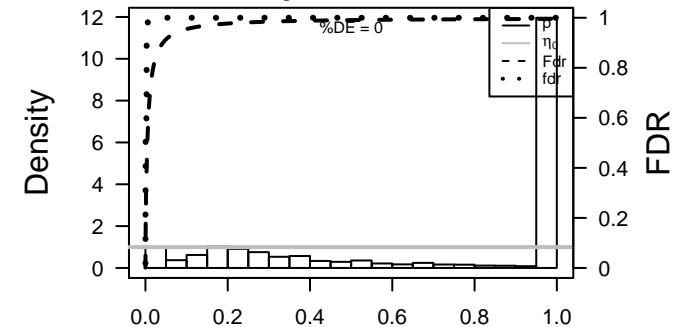
### Overview Map



### Spot



### p-values



## BP

Rank	p-value	#in/all	Geneset
1	5e-07	116 / 4740	cytosol
2	7e-06	158 / 7387	membrane
3	2e-05	40 / 1242	Golgi apparatus
4	2e-05	135 / 6202	cytoplasm
5	1e-04	4 / 16	protein folding in endoplasmic reticulum
6	1e-04	7 / 70	positive regulation of proteasomal ubiquitin-dependent protein catabolic process
7	2e-04	5 / 35	cellular response to ionizing radiation
8	3e-04	10 / 163	autophagy
9	4e-04	3 / 10	cellular protein-containing complex localization
10	7e-04	4 / 26	intracellular transport
11	9e-04	14 / 328	post-translational protein modification
12	1e-03	4 / 31	positive regulation of TOR signaling
13	2e-03	3 / 15	endothelial cell proliferation
14	2e-03	4 / 32	regulation of microtubule cytoskeleton organization
15	2e-03	4 / 33	dendrite cytoplasm

# D-Cluster

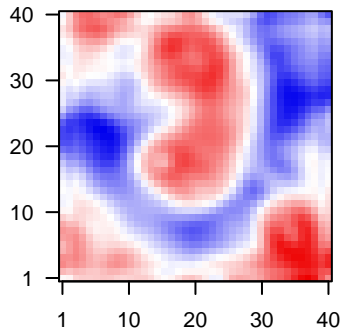
## Spot Summary: I

# metagenes = 27  
# genes = 879

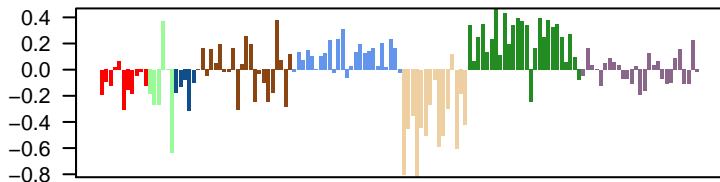
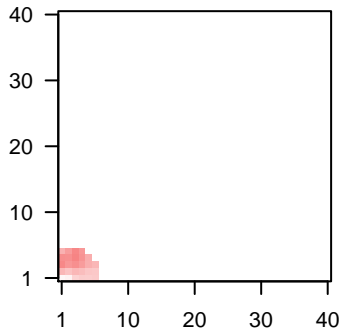
<r> metagenes = 0.92  
<r> genes = 0.41  
beta: r2= 8.3 / log p= -Inf

# samples with spot = 14 ( 10.2 %)  
group 2 : 1 ( 16.7 %)  
group 4 : 1 ( 4.5 %)  
group 7 : 12 ( 46.2 %)

Overview Map



Spot

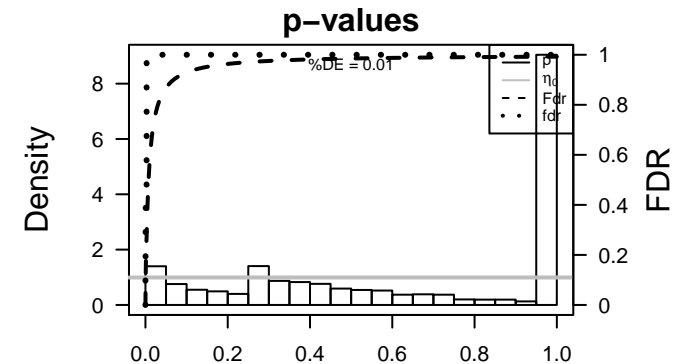


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	209772_s_at	2.62	-1.89	0.46	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:10040]
2	214079_at	2.54	-1.07	0.29	DHRS2 dehydrogenase/reductase 2 [Source:HGNC Symbol;Acc:HGNC:10040]
3	242977_at	2.4	-0.78	0.33	novel transcript
4	1559712_at	2.36	-0.81	0.4	long intergenic non-protein coding RNA 689 [Source:HGNC Symbol;Acc:HGNC:10040]
5	244308_at	2.27	-0.7	0.44	novel transcript
6	215442_s_at	2.13	-0.8	0.34	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:10040]
7	211879_x_at	2.13	-1.2	0.49	PCDHGA9 protocadherin gamma subfamily A, 3 [Source:HGNC Symbol;Acc:HGNC:10040]
8	208650_s_at	2.09	-2.09	0.36	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:10040]
9	1569481_s_at	2.03	-0.89	0.44	SNX22 sorting nexin 22 [Source:HGNC Symbol;Acc:HGNC:16315]
10	238717_at	2	-1.03	0.24	novel transcript
11	1568795_at	2	-0.94	0.51	novel transcript
12	1552662_a_at	1.99	-1.09	0.32	PCDHGB7 protocadherin gamma subfamily B, 7 [Source:HGNC Symbol;Acc:HGNC:10040]
13	205947_s_at	1.98	-1.02	0.46	VIPR2 vasoactive intestinal peptide receptor 2 [Source:HGNC Symbol;Acc:HGNC:10040]
14	1558463_s_at	1.98	-0.77	0.53	novel transcript
15	231737_at	1.95	-0.93	0.67	CACNG4 calcium voltage-gated channel auxiliary subunit gamma 4 [Source:HGNC Symbol;Acc:HGNC:10040]
16	230809_at	1.86	-1.15	0.48	novel transcript
17	221319_at	1.85	-0.86	0.32	PCDHB8 protocadherin beta 8 [Source:HGNC Symbol;Acc:HGNC:8690]
18	224940_s_at	1.84	-1.17	0.4	PAPPA pappalysin 1 [Source:HGNC Symbol;Acc:HGNC:8602]
19	211020_at	1.82	-0.58	0.59	GCNT2 glucosaminyl (N-acetyl) transferase 2 (I blood group) [Source:HGNC Symbol;Acc:HGNC:10040]
20	1556147_at	1.82	-1.21	0.6	novel transcript, antisense to PPM1L

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-17	101 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	6e-17	87 / 1145	BP regulation of transcription by RNA polymerase II
3	2e-15	95 / 1387	BP regulation of transcription, DNA-templated
4	2e-07	52 / 843	BP DNA-binding transcription factor activity
5	9e-07	29 / 366	BP DNA repair
6	2e-06	34 / 484	BP cellular response to DNA damage stimulus
7	2e-06	27 / 342	BP chromatin organization
8	3e-05	55 / 1086	BP positive regulation of transcription by RNA polymerase II
9	1e-04	7 / 40	BP cytoplasmic microtubule organization
10	1e-04	30 / 505	BP nervous system development
11	2e-04	4 / 11	BP positive regulation of double-strand break repair via nonhomologous end joining
12	3e-04	12 / 129	BP rhythmic process
13	5e-04	30 / 541	BP negative regulation of transcription, DNA-templated
14	6e-04	170 / 4740	BP cytosol
15	1e-03	23 / 400	BP chromatin binding
16	1e-03	4 / 18	BP ionotropic glutamate receptor activity
17	2e-03	11 / 133	BP neuron projection development
18	2e-03	17 / 264	BP transcription by RNA polymerase II
19	2e-03	15 / 224	BP negative regulation of gene expression
20	2e-03	31 / 623	BP protein phosphorylation
21	2e-03	10 / 119	BP nucleic acid phosphodiester bond hydrolysis
22	2e-03	5 / 33	BP phosphatidylinositol 3-kinase signaling
23	2e-03	210 / 6202	BP cytoplasm
24	3e-03	6 / 49	BP cellular response to UV
25	3e-03	4 / 21	BP positive regulation of neural precursor cell proliferation
26	3e-03	4 / 21	BP regulation of long-term neuronal synaptic plasticity
27	3e-03	4 / 21	BP spinal cord motor neuron differentiation
28	3e-03	7 / 66	BP double-strand break repair
29	3e-03	10 / 123	BP transcription, DNA-templated
30	3e-03	17 / 279	BP RNA splicing
31	3e-03	15 / 233	BP heart development
32	3e-03	4 / 22	BP ionotropic glutamate receptor signaling pathway
33	3e-03	11 / 146	BP homophilic cell adhesion via plasma membrane adhesion molecules
34	3e-03	3 / 11	BP establishment of protein localization to membrane
35	4e-03	20 / 358	BP mRNA processing
36	4e-03	4 / 23	BP histone H3-K4 methylation
37	4e-03	7 / 70	BP transcription elongation from RNA polymerase II promoter
38	4e-03	3 / 12	BP positive regulation of response to DNA damage stimulus
39	4e-03	3 / 12	BP receptor localization to synapse
40	4e-03	4 / 24	BP mRNA cis splicing, via spliceosome



## BP

Rank	p-value	#in/all	Geneset
1	1e-17	101 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
2	6e-17	87 / 1145	regulation of transcription by RNA polymerase II
3	2e-15	95 / 1387	regulation of transcription, DNA-templated
4	2e-07	52 / 843	DNA-binding transcription factor activity
5	9e-07	29 / 366	DNA repair
6	2e-06	34 / 484	cellular response to DNA damage stimulus
7	2e-06	27 / 342	chromatin organization
8	3e-05	55 / 1086	positive regulation of transcription by RNA polymerase II
9	1e-04	7 / 40	cytoplasmic microtubule organization
10	1e-04	30 / 505	nervous system development
11	2e-04	4 / 11	positive regulation of double-strand break repair via nonhomologous end joining
12	3e-04	12 / 129	rhythmic process
13	5e-04	30 / 541	negative regulation of transcription, DNA-templated
14	6e-04	170 / 4740	cytosol
15	1e-03	23 / 400	chromatin binding