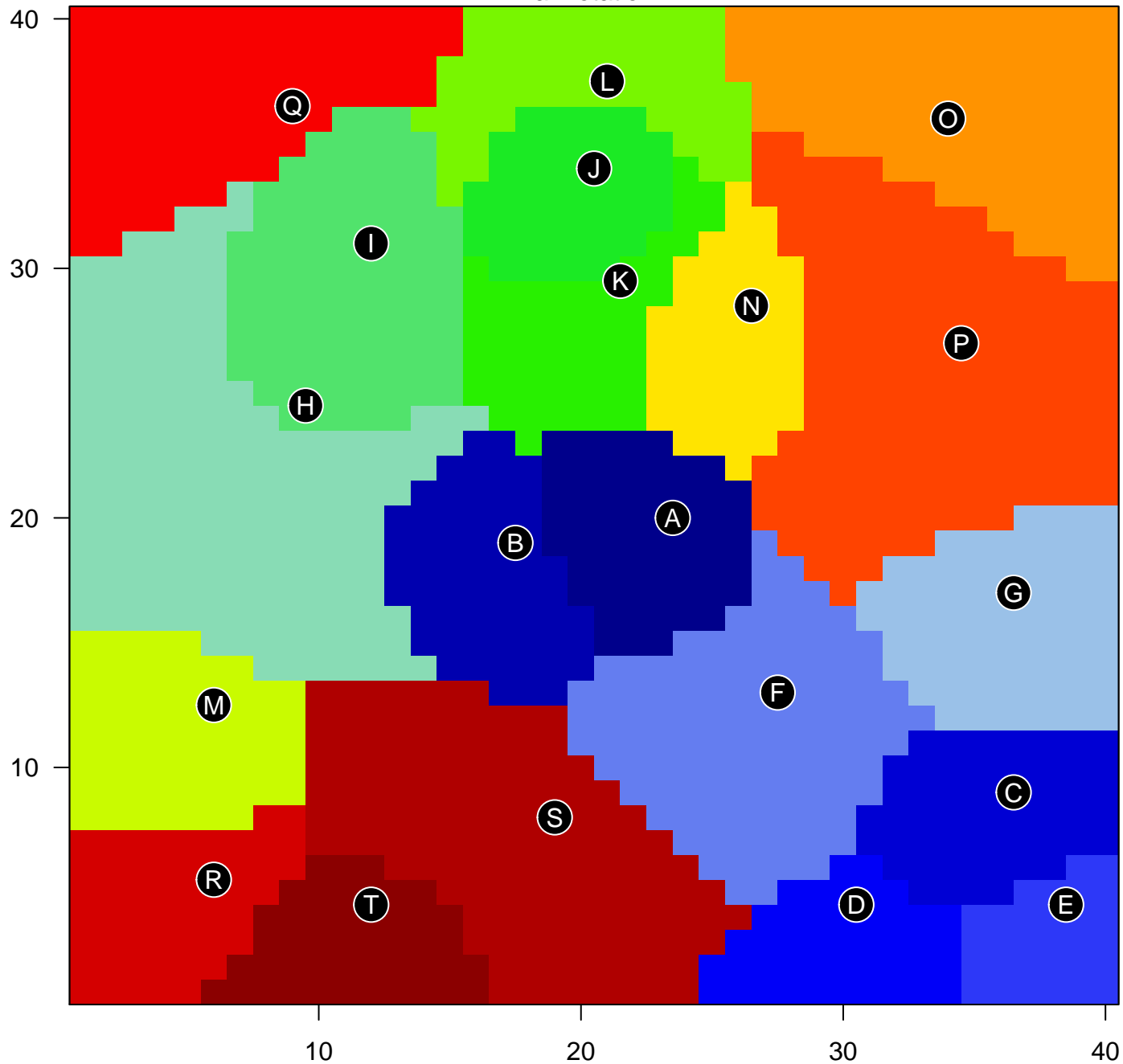


K-Means Cluster

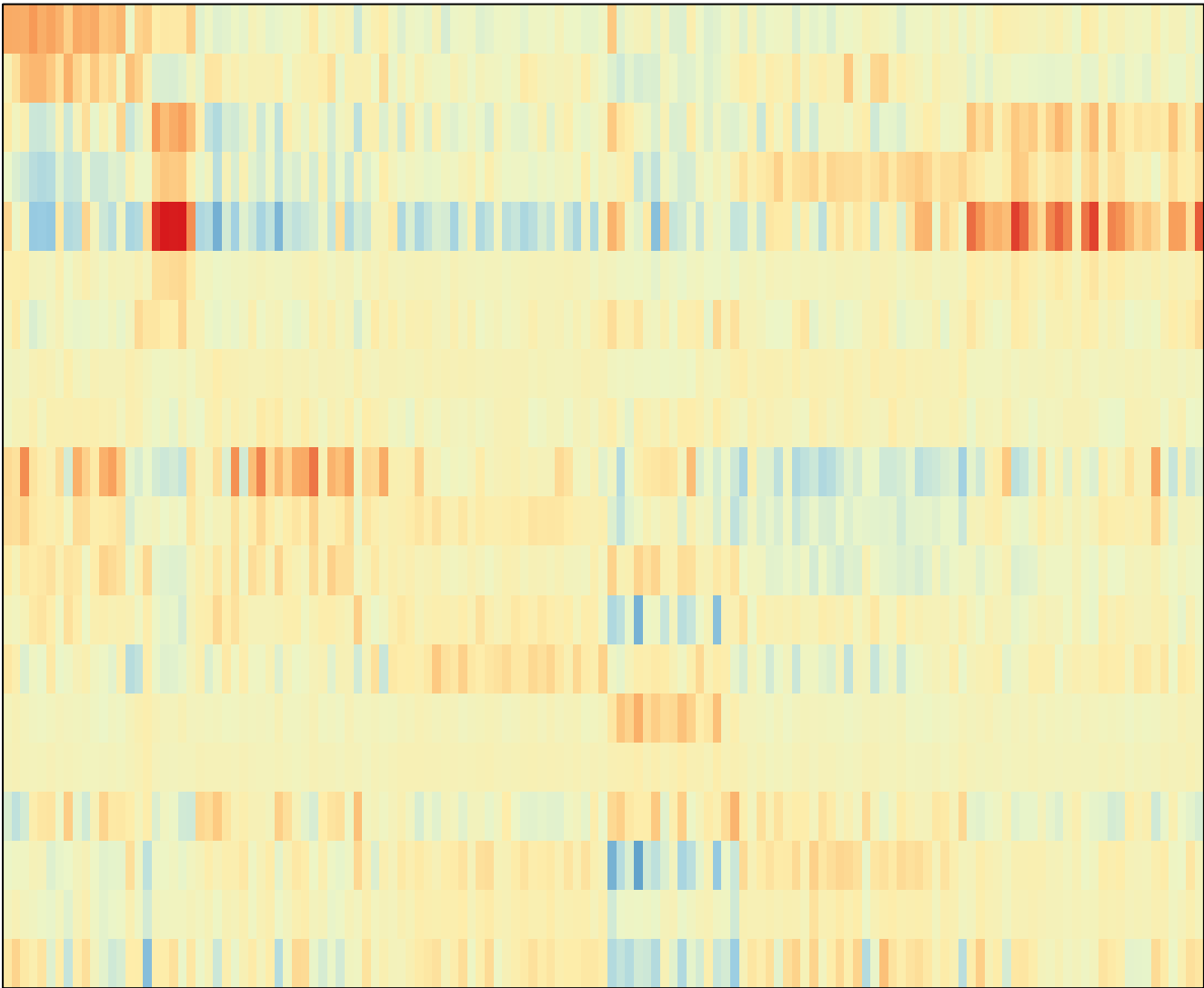
annotation



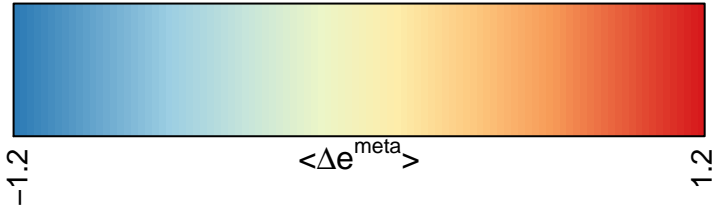
- A ■ cilium movement
extracellular matrix organization
- B ■ cell cycle
cell division
- C ■ membrane
plasma membrane
- D ■ synapse
plasma membrane
- E ■ synapse
chemical synaptic transmission
- F ■ membrane
plasma membrane
- G ■ cytoplasm
membrane
- H ■ mRNA processing
RNA splicing
- I ■ mitochondrion
translation
- J ■ immune system process
immune response
- K ■ Golgi apparatus
cytoplasm
- L ■ cytoplasm
membrane
- M ■ mRNA processing
cellular response to DNA damage stimulus
- N ■ cytoplasm
regulation of neurogenesis
- O ■ keratinization
intracellular receptor signaling pathway
- P ■ response to stimulus
sensory perception of smell
- Q ■ chromatin organization
chromatin binding
- R ■ DNA-binding transcription factor activity, RNA polymerase I
regulation of transcription by RNA polymerase II
- S ■ cytosol
cytoplasm
- T ■ cytosol
cytoplasm



A
B
C
D
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S
T



- cilium movement
- extracellular matrix organization
- cytoplasm
- cell cycle
- cell division
- DNA replication
- membrane
- plasma membrane
- ion transport
- synapse
- plasma membrane
- membrane
- synapse
- chemical synaptic transmission
- plasma membrane
- membrane
- plasma membrane
- cytoplasm
- cytoplasm
- membrane
- cytosol
- mRNA processing
- RNA splicing
- mRNA splicing, via spliceosome
- mitochondrion
- translation
- SRP-dependent cotranslational protein targeting to membrane
- immune system process
- immune response
- innate immune response
- Golgi apparatus
- cytoplasm
- cytosol
- cytoplasm
- membrane
- cytosol
- mRNA processing
- cellular response to DNA damage stimulus
- DNA repair
- cytoplasm
- regulation of neurogenesis
- protein homodimerization activity
- keratinization
- intracellular receptor signaling pathway
- regulation of regulatory T cell differentiation
- response to stimulus
- sensory perception of smell
- chromatin organization
- chromatin organization
- chromatin binding
- regulation of transcription, DNA-templated
- DNA-binding transcription factor activity, RNA polymerase II-specific
- regulation of transcription by RNA polymerase II
- regulation of transcription, DNA-templated
- cytosol
- cytoplasm
- mitochondrion
- cytosol
- cytoplasm
- membrane



K-Means Cluster

Spot Summary: A

metagenes = 58
genes = 1240

<r> metagenes = 0.8

beta: r2= 5.63 / log p= -Inf

samples with spot = 18 (13.1 %)

group 1 : 11 (100 %)

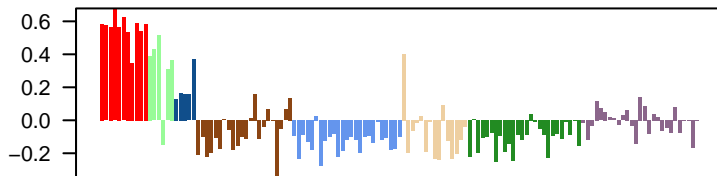
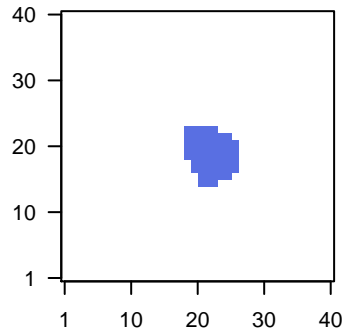
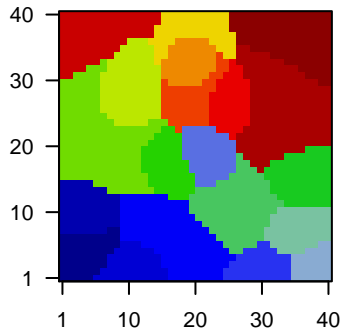
group 2 : 5 (83.3 %)

group 3 : 1 (20 %)

group 6 : 1 (6.7 %)

Overview Map

Spot

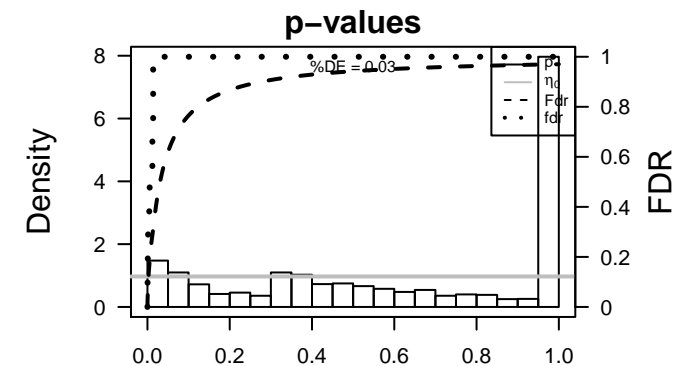


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	210809_s_at	3.59	-0.92	0.6	POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953]
2	243483_at	3.39	-0.59	0.53	TRPM8 transient receptor potential cation channel subfamily M memt
3	1555907_at	3.31	-0.45	0.46	AGAP2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
4	1555778_a_a	3.29	-0.53	0.56	POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953]
5	242883_at	3.11	-0.37	0.5	OTOS otospiralin [Source:HGNC Symbol;Acc:HGNC:22644]
6	206858_s_at	3.1	-0.65	0.55	HOXC6 homeobox C6 [Source:HGNC Symbol;Acc:HGNC:5128]
7	228904_at	3.05	-0.62	0.67	HOXB3 homeobox B3 [Source:HGNC Symbol;Acc:HGNC:5114]
8	206154_at	3.04	-0.83	0.54	RLBP1 retinaldehyde binding protein 1 [Source:HGNC Symbol;Acc:H
9	210135_s_at	2.98	-0.87	0.71	SHOX2 short stature homeobox 2 [Source:HGNC Symbol;Acc:HGNC
10	203180_at	2.88	-0.89	0.51	ALDH1A3aldehyde dehydrogenase 1 family member A3 [Source:HGNC
11	217057_s_at	2.88	-0.48	0.54	GNAS GNAS complex locus [Source:HGNC Symbol;Acc:HGNC:439
12	220010_at	2.87	-0.81	0.47	ACSL4 acyl-CoA synthetase long chain family member 4 [Source:HC
13	242234_at	2.84	-0.62	0.74	XAF1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:HGNC:1
14	221577_x_at	2.82	-0.6	0.66	GDF15 growth differentiation factor 15 [Source:HGNC Symbol;Acc:Hi
15	232539_at	2.76	-0.77	0.49	
16	206515_at	2.74	-0.84	0.4	CYP4F3 cytochrome P450 family 4 subfamily F member 3 [Source:HG
17	244731_at	2.72	-0.62	0.61	
18	206201_s_at	2.66	-0.92	0.76	MEOX2 mesenchyme homeobox 2 [Source:HGNC Symbol;Acc:HGNC
19	209396_s_at	2.66	-1.71	0.75	CHI3L1 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
20	220156_at	2.66	-0.54	0.25	EFCAB1 EF-hand calcium binding domain 1 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-13	15 / 32	BP cilium movement
2	6e-13	36 / 231	BP extracellular matrix organization
3	3e-07	302 / 6202	BP cytoplasm
4	8e-07	48 / 594	BP cell adhesion
5	1e-06	26 / 233	BP heart development
6	2e-06	27 / 254	BP angiogenesis
7	2e-06	7 / 17	BP cilium-dependent cell motility
8	2e-06	11 / 49	BP embryonic skeletal system morphogenesis
9	5e-06	10 / 44	BP collagen fibril organization
10	6e-06	49 / 657	BP calcium ion binding
11	7e-06	6 / 14	BP inner dynein arm assembly
12	8e-06	7 / 21	BP motile cilium assembly
13	1e-05	212 / 4278	BP plasma membrane
14	2e-05	69 / 1080	BP multicellular organism development
15	3e-05	5 / 11	BP axonemal dynein complex assembly
16	4e-05	10 / 55	BP embryonic limb morphogenesis
17	4e-05	13 / 92	BP wound healing
18	5e-05	17 / 148	BP skeletal system development
19	5e-05	6 / 19	BP axoneme assembly
20	6e-05	19 / 180	BP cell projection organization
21	8e-05	13 / 97	BP female pregnancy
22	2e-04	15 / 132	BP sensory perception of sound
23	2e-04	7 / 32	BP embryonic forelimb morphogenesis
24	2e-04	13 / 106	BP anatomical structure morphogenesis
25	3e-04	12 / 95	BP anterior/posterior pattern specification
26	3e-04	5 / 17	BP epithelial cilium movement
27	3e-04	5 / 17	BP outer dynein arm assembly
28	3e-04	13 / 112	BP motor activity
29	3e-04	17 / 173	BP cilium assembly
30	4e-04	10 / 73	BP epithelial cell differentiation
31	4e-04	6 / 27	BP keratan sulfate biosynthetic process
32	5e-04	7 / 38	BP bicarbonate transport
33	6e-04	13 / 118	BP platelet degranulation
34	6e-04	4 / 11	BP cilium movement involved in cell motility
35	6e-04	19 / 214	BP cell migration
36	7e-04	6 / 29	BP blood vessel morphogenesis
37	7e-04	9 / 65	BP pattern specification process
38	8e-04	4 / 12	BP sperm axoneme assembly
39	8e-04	7 / 41	BP negative regulation of viral genome replication
40	8e-04	34 / 500	BP catalytic activity



BP

Rank	p-value	#in/all	Geneset
1	1e-13	15 / 32	cilium movement
2	6e-13	36 / 231	extracellular matrix organization
3	3e-07	302 / 6202	cytoplasm
4	8e-07	48 / 594	cell adhesion
5	1e-06	26 / 233	heart development
6	2e-06	27 / 254	angiogenesis
7	2e-06	7 / 17	cilium-dependent cell motility
8	2e-06	11 / 49	embryonic skeletal system morphogenesis
9	5e-06	10 / 44	collagen fibril organization
10	6e-06	49 / 657	calcium ion binding
11	7e-06	6 / 14	inner dynein arm assembly
12	8e-06	7 / 21	motile cilium assembly
13	1e-05	212 / 4278	plasma membrane
14	2e-05	69 / 1080	multicellular organism development
15	3e-05	5 / 11	axonemal dynein complex assembly

K-Means Cluster

Spot Summary: B

metagenes = 60
genes = 1224

<r> metagenes = 0.78

beta: r2= 3.83 / log p= -Inf

samples with spot = 17 (12.4 %)

- group 1 : 9 (81.8 %)
- group 2 : 3 (50 %)
- group 4 : 2 (9.1 %)
- group 7 : 3 (11.5 %)

Spot Genelist

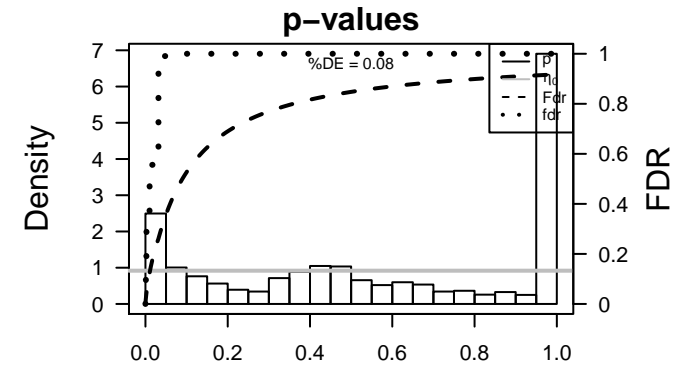
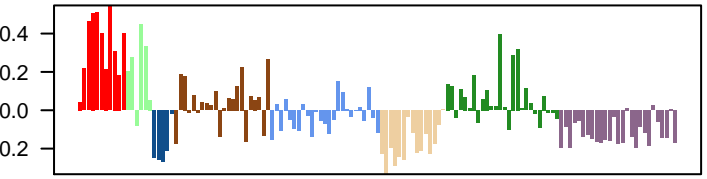
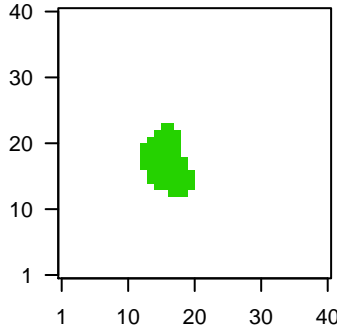
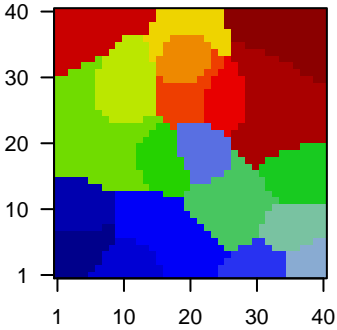
Rank	ID	max e	r	min e	Description
					Symbol
1	205858_at	3.12	-0.94	0.46	NGFR nerve growth factor receptor [Source:HGNC Symbol;Acc:HGNC:10000]
2	222087_at	3.01	-0.48	0.44	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
3	224588_at	2.97	-2.09	0.19	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
4	218308_at	2.79	-0.78	0.76	TACC3 transforming acidic coiled-coil containing protein 3 [Source:HGNC Symbol;Acc:HGNC:10000]
5	227671_at	2.79	-1.83	0.2	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
6	214218_s_at	2.77	-1.66	0.2	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
7	213492_at	2.77	-0.61	0.23	COL2A1 collagen type II alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:10000]
8	239153_at	2.75	-0.69	0.29	HOX transcript antisense RNA [Source:HGNC Symbol;Acc:HGNC:10000]
9	230746_s_at	2.67	-0.7	0.45	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
10	228481_at	2.66	-0.55	0.54	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
11	203936_s_at	2.62	-0.5	0.28	MMP9 matrix metalloproteinase 9 [Source:HGNC Symbol;Acc:HGNC:10000]
12	201852_x_at	2.61	-1.76	0.6	COL3A1 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:10000]
13	207199_at	2.61	-0.63	0.38	TERT telomerase reverse transcriptase [Source:HGNC Symbol;Acc:HGNC:10000]
14	221728_x_at	2.49	-1.68	0.19	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
15	224646_x_at	2.49	-0.89	0.34	H19, imprinted maternally expressed transcript [Source:HGNC Symbol;Acc:HGNC:10000]
16	1558834_s_at	2.45	-0.78	0.46	AKNAD1 AKNA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
17	204595_s_at	2.44	-0.67	0.5	STC1 stanniocalcin 1 [Source:HGNC Symbol;Acc:HGNC:11373]
18	224590_at	2.44	-1.42	0.21	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:10000]
19	217373_x_at	2.43	-0.86	0.52	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:10000]
20	201438_at	2.43	-0.93	0.33	COL6A3 collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:HGNC:10000]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-56	129 / 630	BP cell cycle
2	2e-44	91 / 394	BP cell division
3	6e-34	52 / 158	BP DNA replication
4	2e-23	32 / 85	BP chromosome segregation
5	1e-20	59 / 366	BP DNA repair
6	3e-18	37 / 164	BP mitotic cell cycle
7	3e-18	65 / 484	BP cellular response to DNA damage stimulus
8	5e-17	28 / 98	BP G1/S transition of mitotic cell cycle
9	2e-14	16 / 33	BP DNA replication initiation
10	1e-13	15 / 31	BP mitotic sister chromatid segregation
11	1e-13	28 / 130	BP G2/M transition of mitotic cell cycle
12	7e-12	15 / 39	BP CENP-A containing nucleosome assembly
13	1e-10	33 / 231	BP extracellular matrix organization
14	3e-10	14 / 42	BP mitotic spindle organization
15	4e-10	15 / 50	BP mitotic cytokinesis
16	8e-10	324 / 6202	BP cytoplasm
17	1e-09	18 / 80	BP regulation of G2/M transition of mitotic cell cycle
18	1e-09	13 / 39	BP regulation of mitotic nuclear division
19	2e-09	18 / 81	BP double-strand break repair via homologous recombination
20	2e-09	43 / 400	BP chromatin binding
21	2e-09	38 / 327	BP cell population proliferation
22	2e-09	15 / 56	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
23	3e-09	10 / 22	BP regulation of transcription involved in G1/S transition of mitotic cell cycle
24	4e-09	9 / 17	BP DNA replication origin binding
25	6e-09	32 / 254	BP angiogenesis
26	3e-08	11 / 33	BP mitotic cell cycle checkpoint
27	3e-08	21 / 130	BP regulation of signal transduction by p53 class mediator resulting in cell cycle arrest
28	5e-08	14 / 59	BP regulation of cyclin-dependent protein serine/threonine kinase activity
29	5e-08	22 / 145	BP regulation of cell cycle
30	6e-08	10 / 28	BP positive regulation of G2/M transition of mitotic cell cycle
31	6e-08	251 / 4740	BP cytosol
32	2e-07	7 / 13	BP kinetochore assembly
33	2e-07	17 / 97	BP DNA recombination
34	3e-07	12 / 49	BP interstrand cross-link repair
35	6e-07	16 / 93	BP ciliary basal body-plasma membrane docking
36	9e-07	12 / 54	BP DNA duplex unwinding
37	1e-06	9 / 29	BP endodermal cell differentiation
38	1e-06	8 / 22	BP mitotic spindle assembly checkpoint
39	1e-06	6 / 11	BP metaphase plate congression
40	1e-06	13 / 66	BP double-strand break repair

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	2e-56	129 / 630	cell cycle
2	2e-44	91 / 394	cell division
3	6e-34	52 / 158	DNA replication
4	2e-23	32 / 85	chromosome segregation
5	1e-20	59 / 366	DNA repair
6	3e-18	37 / 164	mitotic cell cycle
7	3e-18	65 / 484	cellular response to DNA damage stimulus
8	5e-17	28 / 98	G1/S transition of mitotic cell cycle
9	2e-14	16 / 33	DNA replication initiation
10	1e-13	15 / 31	mitotic sister chromatid segregation
11	1e-13	28 / 130	G2/M transition of mitotic cell cycle
12	7e-12	15 / 39	CENP-A containing nucleosome assembly
13	1e-10	33 / 231	extracellular matrix organization
14	3e-10	14 / 42	mitotic spindle organization
15	4e-10	15 / 50	mitotic cytokinesis

K-Means Cluster

Spot Summary: C

metagenes = 57
genes = 1396

<r> metagenes = 0.86

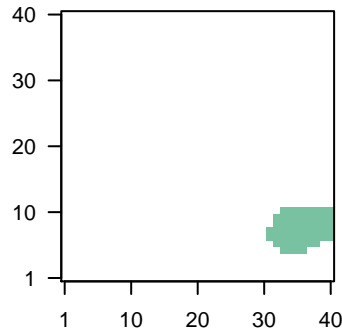
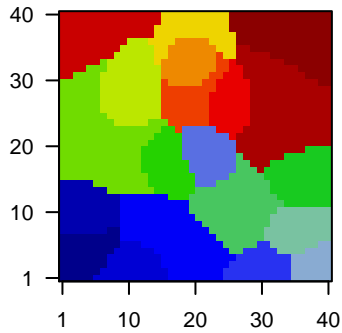
beta: r2= 8.44 / log p= -Inf

samples with spot = 24 (17.5 %)

- group 1 : 1 (9.1 %)
- group 2 : 1 (16.7 %)
- group 3 : 5 (100 %)
- group 6 : 1 (6.7 %)
- group 8 : 16 (59.3 %)

Overview Map

Spot

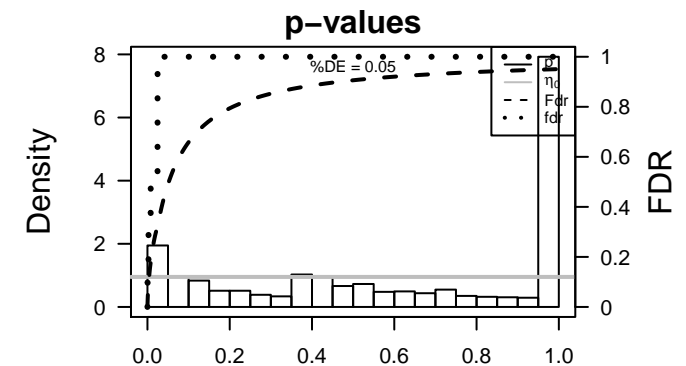
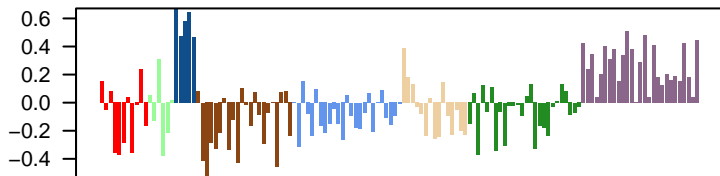


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	205350_at	3.07	-0.63	0.25	CRABP1 cellular retinoic acid binding protein 1 [Source:HGNC Symbol]
2	1554299_at	2.94	-0.48	0.3	NPAS4 neuronal PAS domain protein 4 [Source:HGNC Symbol;Acc:U1554299]
3	1560652_at	2.59	-0.61	0.54	novel transcript, overlapping to IRS4
4	201496_x_at	2.5	-0.77	0.5	MYH11 myosin heavy chain 11 [Source:HGNC Symbol;Acc:HGNC:7511]
5	206696_at	2.3	-0.64	0.61	GPR143 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:U206696]
6	204380_s_at	2.28	-0.84	0.46	FGFR3 fibroblast growth factor receptor 3 [Source:HGNC Symbol;Acc:U204380]
7	210729_at	2.23	-0.75	0.52	NPY2R neuropeptide Y receptor Y2 [Source:HGNC Symbol;Acc:HGNC:110729]
8	223704_s_at	2.21	-0.65	0.51	DMRT2 doublesex and mab-3 related transcription factor 2 [Source:HGNC Symbol;Acc:U223704]
9	205577_at	2.16	-1.35	0.6	PYGM glycogen phosphorylase, muscle associated [Source:HGNC Symbol;Acc:U205577]
10	239684_at	2.16	-0.57	0.4	TRPM3 transient receptor potential cation channel subfamily M member 3 [Source:HGNC Symbol;Acc:U239684]
11	235965_at	2.13	-0.53	0.46	
12	206898_at	2.09	-1.44	0.61	CDH19 cadherin 19 [Source:HGNC Symbol;Acc:HGNC:1758]
13	207317_s_at	2.08	-0.62	0.51	CASQ2 calsequestrin 2 [Source:HGNC Symbol;Acc:HGNC:1513]
14	206941_x_at	2.05	-0.9	0.39	SEMA3E semaphorin 3E [Source:HGNC Symbol;Acc:HGNC:10727]
15	239367_at	2.03	-0.73	0.35	BDNF brain derived neurotrophic factor [Source:HGNC Symbol;Acc:U239367]
16	207767_s_at	2.02	-0.61	0.6	EGR4 early growth response 4 [Source:HGNC Symbol;Acc:HGNC:107767]
17	212236_x_at	2.02	-0.65	0.7	KRT17 keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
18	231192_at	2.01	-0.53	0.54	LPAR3 lysophosphatidic acid receptor 3 [Source:HGNC Symbol;Acc:U231192]
19	226834_at	1.99	-0.74	0.52	CLMP CXADR like membrane protein [Source:HGNC Symbol;Acc:U226834]
20	207342_at	1.98	-0.64	0.58	CNGB1 cyclic nucleotide gated channel beta 1 [Source:HGNC Symbol;Acc:U207342]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-35	501 / 7387	BP membrane
2	7e-33	338 / 4278	BP plasma membrane
3	8e-13	69 / 627	BP ion transport
4	2e-10	35 / 236	BP chemical synaptic transmission
5	3e-10	354 / 6202	BP cytoplasm
6	6e-10	59 / 574	BP synapse
7	1e-09	26 / 149	BP regulation of ion transmembrane transport
8	4e-08	22 / 131	BP potassium ion transport
9	1e-07	56 / 615	BP transmembrane transport
10	2e-07	30 / 240	BP postsynaptic membrane
11	3e-07	48 / 505	BP nervous system development
12	4e-07	7 / 13	BP central nervous system myelination
13	1e-06	19 / 122	BP potassium ion transmembrane transport
14	4e-06	19 / 132	BP sensory perception of sound
15	1e-05	11 / 52	BP myelination
16	1e-05	18 / 131	BP presynapse
17	2e-05	98 / 1500	BP signal transduction
18	2e-05	28 / 275	BP ion transmembrane transport
19	3e-05	5 / 10	BP high voltage-gated calcium channel activity
20	5e-05	22 / 199	BP axon guidance
21	5e-05	10 / 51	BP regulation of synaptic plasticity
22	6e-05	17 / 133	BP protein localization to plasma membrane
23	6e-05	57 / 777	BP G protein-coupled receptor signaling pathway
24	7e-05	50 / 657	BP calcium ion binding
25	7e-05	21 / 190	BP actin filament binding
26	9e-05	5 / 12	BP auditory receptor cell stereocilium organization
27	9e-05	16 / 125	BP calcium ion transmembrane transport
28	9e-05	8 / 35	BP negative chemotaxis
29	1e-04	6 / 19	BP long-chain fatty-acyl-CoA biosynthetic process
30	1e-04	13 / 89	BP neuropeptide signaling pathway
31	1e-04	8 / 36	BP regulation of heart rate by cardiac conduction
32	1e-04	23 / 227	BP microtubule binding
33	2e-04	13 / 92	BP axonogenesis
34	2e-04	17 / 144	BP calcium ion transport
35	2e-04	37 / 455	BP intracellular signal transduction
36	2e-04	16 / 132	BP membrane organization
37	2e-04	9 / 48	BP cardiac conduction
38	2e-04	24 / 249	BP brain development
39	2e-04	28 / 315	BP positive regulation of GTPase activity
40	3e-04	10 / 61	BP adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway



BP

Rank	p-value	#in/all	Geneset
1	3e-35	501 / 7387	membrane
2	7e-33	338 / 4278	plasma membrane
3	8e-13	69 / 627	ion transport
4	2e-10	35 / 236	chemical synaptic transmission
5	3e-10	354 / 6202	cytoplasm
6	6e-10	59 / 574	synapse
7	1e-09	26 / 149	regulation of ion transmembrane transport
8	4e-08	22 / 131	potassium ion transport
9	1e-07	56 / 615	transmembrane transport
10	2e-07	30 / 240	postsynaptic membrane
11	3e-07	48 / 505	nervous system development
12	4e-07	7 / 13	central nervous system myelination
13	1e-06	19 / 122	potassium ion transmembrane transport
14	4e-06	19 / 132	sensory perception of sound
15	1e-05	11 / 52	myelination

K-Means Cluster

Spot Summary: D

metagenes = 44
genes = 1313

<r> metagenes = 0.89

beta: r2= 6.78 / log p= -Inf

samples with spot = 32 (23.4 %)

group 3 : 4 (80 %)
group 7 : 18 (69.2 %)
group 8 : 10 (37 %)

Spot Genelist

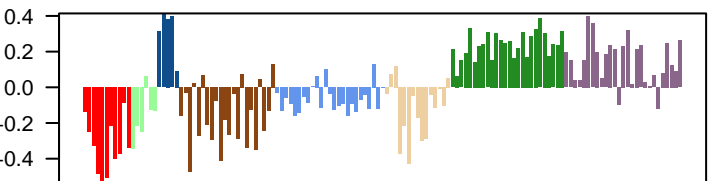
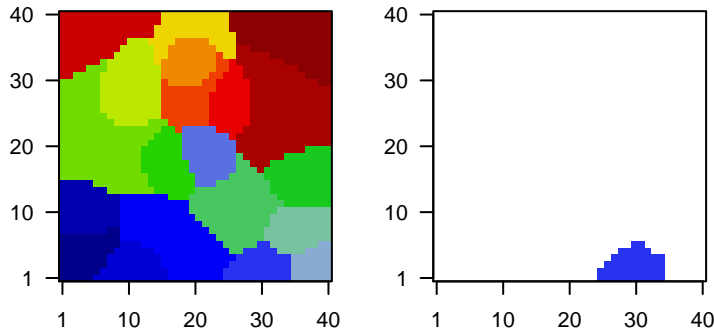
Rank	ID	max e	r	min e	Description
1	1556573_s_at	2.93	-1.3	0.33	novel transcript
2	243242_at	2.38	-0.75	0.44	
3	241883_x_at	2.35	-0.72	0.46	
4	1555230_a_at	2.29	-1.18	0.73	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC]
5	1566772_at	2.2	-0.85	0.64	
6	231029_at	2.12	-1.61	0.38	
7	1557215_at	2.1	-0.67	0.34	long intergenic non-protein coding RNA 648 [Source:HGNC]
8	213707_s_at	2.09	-0.79	0.23	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:HGNC:2
9	1553415_at	2.06	-0.74	0.53	SLC17A8 solute carrier family 17 member 8 [Source:HGNC Symbol;Acc:HGNC:1
10	236111_at	2.06	-0.71	0.39	long intergenic non-protein coding RNA 1238 [Source:HGNC]
11	216672_s_at	2.04	-0.66	0.54	MYT1L myelin transcription factor 1 like [Source:HGNC Symbol;Acc:HGNC:1
12	229839_at	2.04	-0.64	0.45	SCARA5 scavenger receptor class A member 5 [Source:HGNC Symbol;Acc:HGNC:1
13	230112_at	2.02	-1.35	0.86	MARCH4 membrane associated ring-CH-type finger 4 [Source:HGNC]
14	244117_at	1.97	-0.81	0.46	
15	240450_at	1.96	-0.64	0.28	
16	221321_s_at	1.96	-1.19	0.74	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC]
17	240911_at	1.96	-0.62	0.34	NOS1 nitric oxide synthase 1 [Source:HGNC Symbol;Acc:HGNC:78
18	1561324_at	1.9	-1.05	0.41	
19	227614_at	1.89	-0.91	0.46	HKDC1 hexokinase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1
20	224942_at	1.89	-0.71	0.34	PAPPA pappalysin 1 [Source:HGNC Symbol;Acc:HGNC:8602]

Geneset Overrepresentation

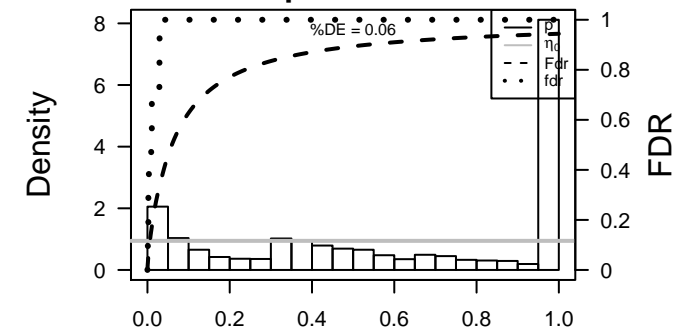
Rank	p-value	#in/all	Geneset
1	3e-27	85 / 574	BP synapse
2	4e-24	286 / 4278	BP plasma membrane
3	5e-24	423 / 7387	BP membrane
4	5e-23	50 / 240	BP postsynaptic membrane
5	9e-13	56 / 505	BP nervous system development
6	1e-10	33 / 236	BP chemical synaptic transmission
7	2e-10	17 / 65	BP learning
8	7e-10	16 / 61	BP positive regulation of synapse assembly
9	2e-09	11 / 27	BP glutamate secretion
10	2e-09	24 / 149	BP regulation of ion transmembrane transport
11	4e-09	54 / 594	BP cell adhesion
12	2e-08	13 / 48	BP synapse organization
13	2e-08	54 / 627	BP ion transport
14	3e-08	21 / 133	BP neuron projection development
15	2e-07	19 / 122	BP potassium ion transmembrane transport
16	2e-07	14 / 68	BP regulation of insulin secretion
17	3e-07	30 / 275	BP ion transmembrane transport
18	4e-07	12 / 51	BP neurotransmitter secretion
19	6e-07	19 / 131	BP presynapse
20	6e-07	9 / 28	BP regulation of presynapse assembly
21	7e-07	24 / 199	BP axon guidance
22	9e-07	8 / 22	BP regulation of AMPA receptor activity
23	1e-06	8 / 23	BP synaptic membrane adhesion
24	1e-06	18 / 125	BP calcium ion transmembrane transport
25	1e-06	11 / 48	BP cardiac conduction
26	2e-06	298 / 6202	BP cytoplasm
27	2e-06	6 / 12	BP regulation of postsynaptic density assembly
28	3e-06	18 / 131	BP potassium ion transport
29	3e-06	17 / 119	BP postsynapse
30	3e-06	13 / 73	BP modulation of chemical synaptic transmission
31	5e-06	8 / 27	BP positive regulation of excitatory postsynaptic potential
32	6e-06	11 / 55	BP social behavior
33	7e-06	8 / 28	BP regulation of synaptic transmission, glutamatergic
34	7e-06	8 / 28	BP synaptic transmission, glutamatergic
35	9e-06	13 / 79	BP memory
36	1e-05	78 / 1242	BP Golgi apparatus
37	2e-05	10 / 50	BP nervous system process
38	2e-05	5 / 10	BP high voltage-gated calcium channel activity
39	2e-05	6 / 16	BP glutamate receptor activity
40	2e-05	7 / 24	BP negative regulation of microtubule depolymerization

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	3e-27	85 / 574	synapse
2	4e-24	286 / 4278	plasma membrane
3	5e-24	423 / 7387	membrane
4	5e-23	50 / 240	postsynaptic membrane
5	9e-13	56 / 505	nervous system development
6	1e-10	33 / 236	chemical synaptic transmission
7	2e-10	17 / 65	learning
8	7e-10	16 / 61	positive regulation of synapse assembly
9	2e-09	11 / 27	glutamate secretion
10	2e-09	24 / 149	regulation of ion transmembrane transport
11	4e-09	54 / 594	cell adhesion
12	2e-08	13 / 48	synapse organization
13	2e-08	54 / 627	ion transport
14	3e-08	21 / 133	neuron projection development
15	2e-07	19 / 122	potassium ion transmembrane transport

K-Means Cluster

Spot Summary: E

metagenes = 30
genes = 1020

<r> metagenes = 0.95

beta: r2= 28.83 / log p= -Inf

samples with spot = 41 (29.9 %)

group 1 : 2 (18.2 %)

group 2 : 1 (16.7 %)

group 3 : 5 (100 %)

group 4 : 1 (4.5 %)

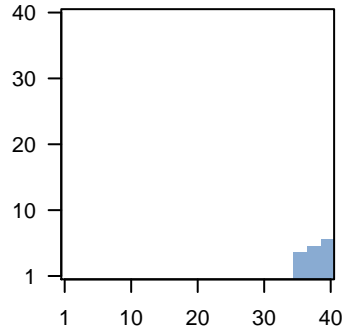
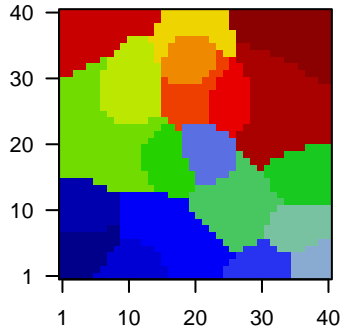
group 6 : 3 (20 %)

group 7 : 5 (19.2 %)

group 8 : 24 (88.9 %)

Overview Map

Spot

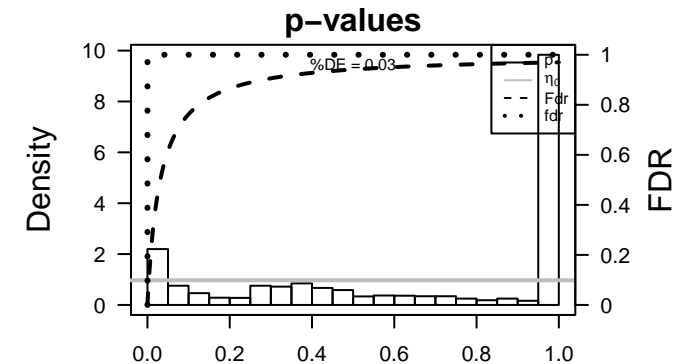
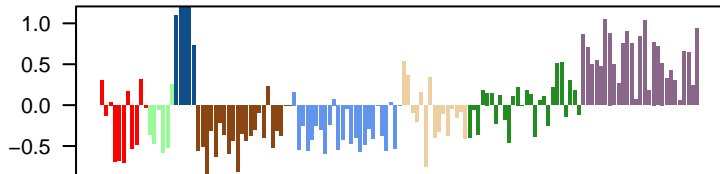


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	206803_at	3.07	-1.3	0.52	PDYN prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
2	206382_s_at	2.85	-0.87	0.57	BDNF brain derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:10343]
3	205901_at	2.71	-1.16	0.7	PNOC prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
4	229012_at	2.64	-0.83	0.69	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	0.74	TAC1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11111]
7	228844_at	2.39	-0.8	0.78	SLC13A5solute carrier family 13 member 5 [Source:HGNC Symbol;Acc:HGNC:19112]
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	0.54	GRIK1 glutamate ionotropic receptor kainate type subunit 1 [Source:HGNC Symbol;Acc:HGNC:20822]
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:19112]
12	220025_at	2.25	-0.85	0.91	TBR1 T-box, brain 1 [Source:HGNC Symbol;Acc:HGNC:11590]
13	242138_at	2.23	-1.27	0.72	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:20822]
14	219263_at	2.22	-1.06	0.72	RNF128 ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:19112]
15	232111_at	2.18	-0.91	0.81	TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:19112]
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	0.83	CHRM3 cholinergic receptor muscarinic 3 [Source:HGNC Symbol;Acc:HGNC:20822]
18	211451_s_at	2.15	-0.89	0.79	KCNJ4 potassium voltage-gated channel subfamily J member 4 [Source:HGNC Symbol;Acc:HGNC:20822]
19	236714_at	2.14	-1.26	0.63	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:HGNC:20822]
20	205914_s_at	2.14	-0.86	0.77	GRIN1 glutamate ionotropic receptor NMDA type subunit 1 [Source:HGNC Symbol;Acc:HGNC:20822]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-60	114 / 574	BP synapse
2	4e-48	69 / 236	BP chemical synaptic transmission
3	8e-46	290 / 4278	BP plasma membrane
4	4e-37	386 / 7387	BP membrane
5	2e-28	51 / 240	BP postsynaptic membrane
6	1e-23	74 / 627	BP ion transport
7	2e-20	34 / 149	BP regulation of ion transmembrane transport
8	2e-19	60 / 505	BP nervous system development
9	3e-13	14 / 33	BP regulation of exocytosis
10	1e-12	15 / 43	BP neurotransmitter transport
11	1e-12	16 / 51	BP neurotransmitter secretion
12	1e-12	16 / 51	BP regulation of synaptic plasticity
13	1e-12	24 / 131	BP potassium ion transport
14	4e-12	96 / 1500	BP signal transduction
15	1e-11	22 / 119	BP postsynapse
16	1e-11	23 / 131	BP presynapse
17	1e-11	12 / 28	BP synaptic vesicle exocytosis
18	2e-11	15 / 51	BP regulation of synaptic vesicle exocytosis
19	2e-11	18 / 79	BP memory
20	2e-11	33 / 275	BP ion transmembrane transport
21	5e-11	60 / 777	BP G protein-coupled receptor signaling pathway
22	5e-11	12 / 31	BP regulation of NMDA receptor activity
23	7e-11	21 / 118	BP exocytosis
24	9e-11	9 / 15	BP calcium ion-regulated exocytosis of neurotransmitter
25	2e-10	11 / 27	BP glutamate secretion
26	2e-10	17 / 79	BP cellular response to calcium ion
27	2e-10	21 / 125	BP calcium ion transmembrane transport
28	5e-10	22 / 144	BP calcium ion transport
29	9e-10	20 / 122	BP potassium ion transmembrane transport
30	2e-09	14 / 58	BP learning or memory
31	3e-09	48 / 615	BP transmembrane transport
32	3e-09	50 / 657	BP calcium ion binding
33	3e-09	10 / 27	BP gamma-aminobutyric acid signaling pathway
34	3e-09	10 / 27	BP positive regulation of excitatory postsynaptic potential
35	5e-09	9 / 21	BP positive regulation of dendrite extension
36	7e-09	8 / 16	BP positive regulation of calcium ion-dependent exocytosis
37	8e-09	10 / 29	BP calcium ion regulated exocytosis
38	1e-08	10 / 30	BP associative learning
39	2e-08	12 / 48	BP long-term synaptic potentiation
40	2e-08	8 / 18	BP regulation of neurotransmitter secretion



BP

Rank	p-value	#in/all	Geneset
1	6e-60	114 / 574	synapse
2	4e-48	69 / 236	chemical synaptic transmission
3	8e-46	290 / 4278	plasma membrane
4	4e-37	386 / 7387	membrane
5	2e-28	51 / 240	postsynaptic membrane
6	1e-23	74 / 627	ion transport
7	2e-20	34 / 149	regulation of ion transmembrane transport
8	2e-19	60 / 505	nervous system development
9	3e-13	14 / 33	regulation of exocytosis
10	1e-12	15 / 43	neurotransmitter transport
11	1e-12	16 / 51	neurotransmitter secretion
12	1e-12	16 / 51	regulation of synaptic plasticity
13	1e-12	24 / 131	potassium ion transport
14	4e-12	96 / 1500	signal transduction
15	1e-11	22 / 119	postsynapse

K-Means Cluster

Spot Summary: F

metagenes = 113
genes = 2645

<r> metagenes = 0.65

beta: r2= 1.33 / log p= -Inf

samples with spot = 4 (2.9 %)
group 3 : 4 (80 %)

Spot Genelist

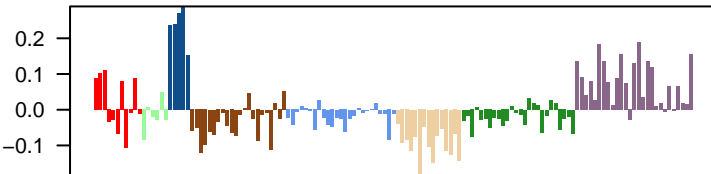
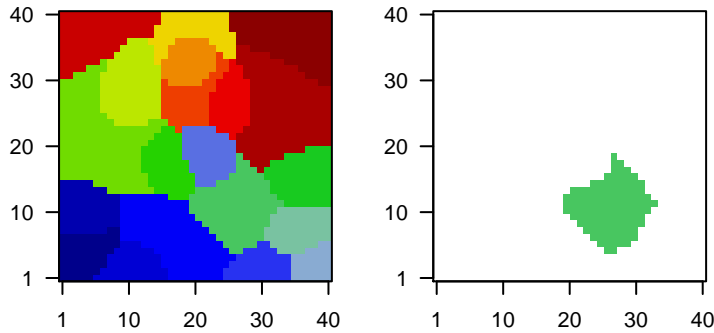
Rank	ID	max e	r	min e	Description
					Symbol
1	214612_x_at	2.85	-0.47	0.24	MAGEA3MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC]
2	213780_at	2.81	-0.6	0.22	TCHH trichohyalin [Source:HGNC Symbol;Acc:HGNC:11791]
3	207369_at	2.75	-0.35	0.15	BRS3 bombesin receptor subtype 3 [Source:HGNC Symbol;Acc:HGNC]
4	204938_s_at	2.58	-0.74	0.22	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
5	1554663_a_a	2.56	-0.58	0.04	NUMA1 nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC]
6	205828_at	2.38	-0.4	0.23	MMP3 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC]
7	209278_s_at	2.32	-0.44	0.27	TFPI2 tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:HGNC]
8	204940_at	2.3	-0.67	0.18	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
9	242680_at	2.26	-0.67	0.48	AVPR1A arginine vasopressin receptor 1A [Source:HGNC Symbol;Acc:HGNC]
10	238835_at	2.25	-0.6	0.47	AVPR1A arginine vasopressin receptor 1A [Source:HGNC Symbol;Acc:HGNC]
11	206528_at	2.23	-0.55	0.26	TRPC6 transient receptor potential cation channel subfamily C memb
12	236523_at	2.23	-0.47	0.3	C4orf54 chromosome 4 open reading frame 54 [Source:HGNC Symbol;Acc:HGNC]
13	230723_at	2.2	-0.48	0.24	SPATA18 spermatogenesis associated 18 [Source:HGNC Symbol;Acc:HGNC]
14	217287_s_at	2.16	-0.52	0.16	TRPC6 transient receptor potential cation channel subfamily C memb
15	211506_s_at	2.15	-0.46	0.22	CXCL8 C-X-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:HGNC]
16	231766_s_at	2.13	-0.51	0.51	COL12A1 collagen type XII alpha 1 chain [Source:HGNC Symbol;Acc:HGNC]
17	201108_s_at	2.08	-0.55	0.32	THBS1 thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
18	210730_s_at	2.08	-0.47	0.24	NPY2R neuropeptide Y receptor Y2 [Source:HGNC Symbol;Acc:HGNC]
19	1554997_a_a	2.07	-0.79	0.48	PTGS2 prostaglandin-endoperoxide synthase 2 [Source:HGNC Symbol;Acc:HGNC]
20	231879_at	2.06	-0.49	0.42	COL12A1 collagen type XII alpha 1 chain [Source:HGNC Symbol;Acc:HGNC]

Geneset Overrepresentation

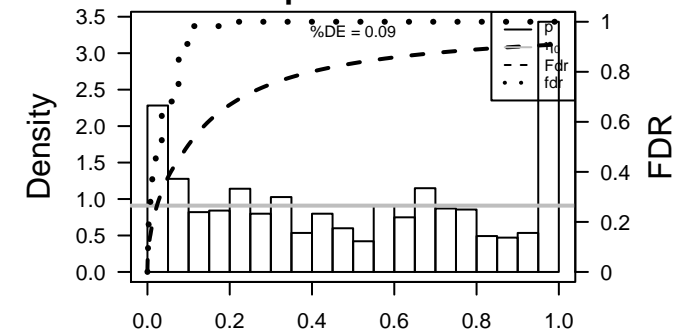
Rank	p-value	#in/all	Geneset
1	5e-19	809 / 7387	BP membrane
2	4e-13	488 / 4278	BP plasma membrane
3	1e-10	651 / 6202	BP cytoplasm
4	9e-09	504 / 4740	BP cytosol
5	8e-07	46 / 254	BP angiogenesis
6	2e-06	23 / 92	BP proton transmembrane transport
7	5e-06	93 / 684	BP phosphorylation
8	1e-05	149 / 1242	BP Golgi apparatus
9	1e-05	168 / 1435	BP mitochondrion
10	3e-05	9 / 21	BP proton-transporting ATPase activity, rotational mechanism
11	6e-05	15 / 57	BP blood vessel development
12	6e-05	10 / 28	BP ATP hydrolysis coupled proton transport
13	6e-05	42 / 264	BP vesicle-mediated transport
14	1e-04	10 / 30	BP sprouting angiogenesis
15	2e-04	12 / 43	BP gluconeogenesis
16	2e-04	7 / 16	BP G protein-coupled glutamate receptor signaling pathway
17	2e-04	80 / 630	BP protein transport
18	3e-04	28 / 163	BP autophagy
19	3e-04	7 / 17	BP face development
20	3e-04	55 / 400	BP protein serine/threonine kinase activity
21	3e-04	10 / 33	BP transferrin transport
22	4e-04	56 / 412	BP negative regulation of cell population proliferation
23	4e-04	70 / 545	BP protein ubiquitination
24	4e-04	23 / 126	BP response to oxidative stress
25	4e-04	77 / 615	BP transmembrane transport
26	6e-04	8 / 24	BP thyroid gland development
27	6e-04	15 / 69	BP positive regulation of protein catabolic process
28	6e-04	6 / 14	BP smooth muscle cell differentiation
29	6e-04	77 / 623	BP protein phosphorylation
30	6e-04	60 / 460	BP neutrophil degranulation
31	7e-04	163 / 1500	BP signal transduction
32	8e-04	8 / 25	BP positive regulation of focal adhesion assembly
33	8e-04	12 / 50	BP positive regulation of endothelial cell migration
34	8e-04	33 / 217	BP protein homooligomerization
35	9e-04	23 / 133	BP protein localization to plasma membrane
36	9e-04	21 / 117	BP negative regulation of cell growth
37	1e-03	12 / 51	BP positive regulation of protein localization to plasma membrane
38	1e-03	10 / 38	BP positive regulation of blood vessel endothelial cell migration
39	1e-03	27 / 168	BP response to hypoxia
40	1e-03	8 / 26	BP axon extension

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	5e-19	809 / 7387	membrane
2	4e-13	488 / 4278	plasma membrane
3	1e-10	651 / 6202	cytoplasm
4	9e-09	504 / 4740	cytosol
5	8e-07	46 / 254	angiogenesis
6	2e-06	23 / 92	proton transmembrane transport
7	5e-06	93 / 684	phosphorylation
8	1e-05	149 / 1242	Golgi apparatus
9	1e-05	168 / 1435	mitochondrion
10	3e-05	9 / 21	proton-transporting ATPase activity, rotational mechanism
11	6e-05	15 / 57	blood vessel development
12	6e-05	10 / 28	ATP hydrolysis coupled proton transport
13	6e-05	42 / 264	vesicle-mediated transport
14	1e-04	10 / 30	sprouting angiogenesis
15	2e-04	12 / 43	gluconeogenesis

K-Means Cluster

Spot Summary: G

metagenes = 73
genes = 2528

<r> metagenes = 0.72

beta: r2= 2.1 / log p= -Inf

samples with spot = 6 (4.4 %)

group 2 : 1 (16.7 %)

group 3 : 1 (20 %)

group 6 : 3 (20 %)

group 8 : 1 (3.7 %)

Spot Genelist

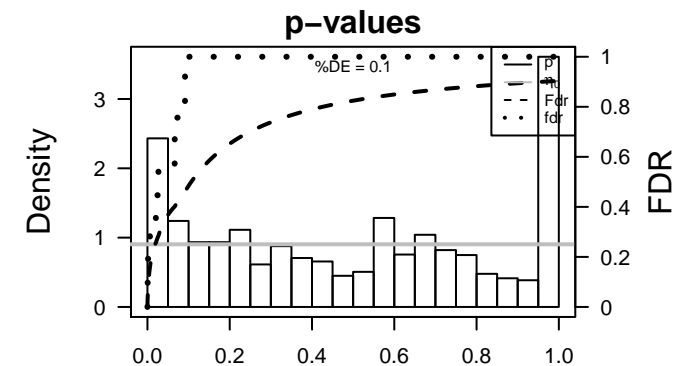
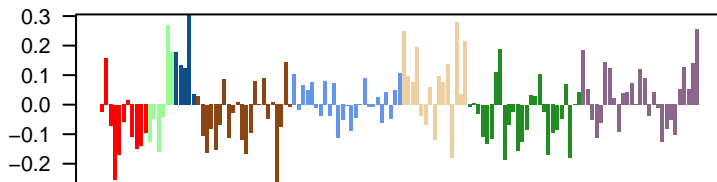
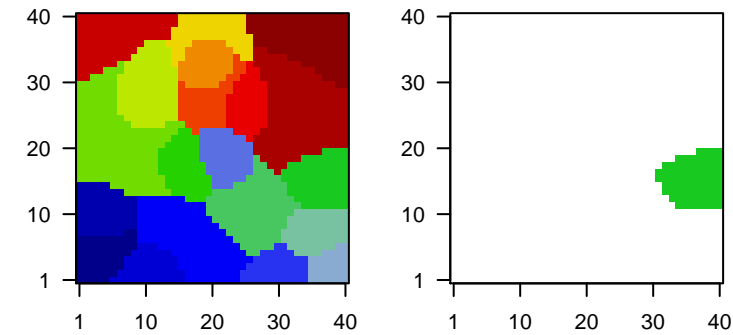
Rank	ID	max e	r	min e	Description
					Symbol
1	204086_at	3.41	-0.57	0.24	PRAME preferentially expressed antigen in melanoma [Source:HGNC
2	205576_at	2.92	-0.49	0.24	SERPIND1 serpin family D member 1 [Source:HGNC Symbol;Acc:HGNC
3	220226_at	2.43	-0.54	0.29	TRPM8 transient receptor potential cation channel subfamily M memt
4	243390_at	2.33	-0.72	0.31	
5	219614_s_at	2.3	-0.46	0.27	SLC6A20solute carrier family 6 member 20 [Source:HGNC Symbol;Acc
6	219824_at	2.23	-0.83	0.3	SLC13A4solute carrier family 13 member 4 [Source:HGNC Symbol;Acc
7	207184_at	2.04	-0.67	0.44	SLC6A13solute carrier family 6 member 13 [Source:HGNC Symbol;Acc
8	220231_at	1.96	-0.76	0.21	PPP1R1protein phosphatase 1 regulatory subunit 17 [Source:HGNC
9	210881_s_at	1.95	-0.6	0.46	INS-IGF2INS-IGF2 readthrough [Source:HGNC Symbol;Acc:HGNC:3
10	234291_s_at	1.91	-0.58	0.4	SLC6A20solute carrier family 6 member 20 [Source:HGNC Symbol;Acc
11	208255_s_at	1.87	-1.53	0.71	FKBP8 FKBP prolyl isomerase 8 [Source:HGNC Symbol;Acc:HGNC:
12	1560035_at	1.85	-0.64	0.36	RTP5 receptor transporter protein 5 (putative) [Source:HGNC Symb
13	236209_at	1.84	-0.81	0.14	
14	224505_s_at	1.82	-1.09	0.35	PLCD4 phospholipase C delta 4 [Source:HGNC Symbol;Acc:HGNC:5
15	227058_at	1.79	-0.72	0.27	MEDAG mesenteric estrogen dependent adipogenesis [Source:HGNC
16	216269_s_at	1.78	-0.69	0.19	ELN elastin [Source:HGNC Symbol;Acc:HGNC:3327]
17	230525_at	1.77	-0.58	0.22	novel protein
18	223149_s_at	1.73	-0.55	0.32	PTPN23 protein tyrosine phosphatase, non-receptor type 23 [Source:l
19	201495_x_at	1.72	-0.47	0.34	MYH11 myosin heavy chain 11 [Source:HGNC Symbol;Acc:HGNC:7E
20	1560100_at	1.71	-1.08	0.25	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-15	634 / 6202	BP cytoplasm
2	3e-14	725 / 7387	BP membrane
3	6e-10	475 / 4740	BP cytosol
4	4e-09	430 / 4278	BP plasma membrane
5	2e-08	84 / 574	BP synapse
6	3e-08	95 / 684	BP phosphorylation
7	7e-07	84 / 623	BP protein phosphorylation
8	1e-06	50 / 315	BP positive regulation of GTPase activity
9	4e-06	97 / 783	BP negative regulation of transcription by RNA polymerase II
10	8e-06	57 / 400	BP protein serine/threonine kinase activity
11	2e-05	162 / 1500	BP signal transduction
12	5e-05	60 / 455	BP intracellular signal transduction
13	6e-05	135 / 1242	BP Golgi apparatus
14	6e-05	11 / 36	BP semaphorin-plexin signaling pathway
15	7e-05	55 / 412	BP negative regulation of cell population proliferation
16	9e-05	64 / 505	BP nervous system development
17	1e-04	13 / 51	BP regulation of synaptic plasticity
18	1e-04	119 / 1086	BP positive regulation of transcription by RNA polymerase II
19	1e-04	12 / 45	BP negative regulation of cell cycle
20	1e-04	21 / 112	BP animal organ morphogenesis
21	2e-04	12 / 47	BP nuclear receptor activity
22	2e-04	23 / 131	BP presynapse
23	2e-04	52 / 400	BP chromatin binding
24	2e-04	8 / 23	BP negative regulation of axon extension involved in axon guidance
25	3e-04	10 / 36	BP negative regulation of Notch signaling pathway
26	3e-04	8 / 24	BP positive regulation of protein localization to nucleus
27	4e-04	72 / 613	BP positive regulation of transcription, DNA-templated
28	4e-04	65 / 541	BP negative regulation of transcription, DNA-templated
29	4e-04	15 / 72	BP negative regulation of protein binding
30	4e-04	16 / 80	BP protein localization
31	5e-04	8 / 25	BP response to lipid
32	5e-04	73 / 630	BP protein transport
33	5e-04	15 / 74	BP retrograde transport, endosome to Golgi
34	5e-04	13 / 59	BP glucose metabolic process
35	6e-04	7 / 20	BP cellular response to peptide hormone stimulus
36	6e-04	7 / 20	BP protein localization to Golgi apparatus
37	6e-04	34 / 240	BP postsynaptic membrane
38	6e-04	6 / 15	BP cellular response to estrogen stimulus
39	7e-04	12 / 53	BP IRE1-mediated unfolded protein response
40	9e-04	5 / 11	BP postsynapse organization

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	1e-15	634 / 6202	cytoplasm
2	3e-14	725 / 7387	membrane
3	6e-10	475 / 4740	cytosol
4	4e-09	430 / 4278	plasma membrane
5	2e-08	84 / 574	synapse
6	3e-08	95 / 684	phosphorylation
7	7e-07	84 / 623	protein phosphorylation
8	1e-06	50 / 315	positive regulation of GTPase activity
9	4e-06	97 / 783	negative regulation of transcription by RNA polymerase II
10	8e-06	57 / 400	protein serine/threonine kinase activity
11	2e-05	162 / 1500	signal transduction
12	5e-05	60 / 455	intracellular signal transduction
13	6e-05	135 / 1242	Golgi apparatus
14	6e-05	11 / 36	semaphorin-plexin signaling pathway
15	7e-05	55 / 412	negative regulation of cell population proliferation

K-Means Cluster

Spot Summary: H

metagenes = 174

genes = 6797

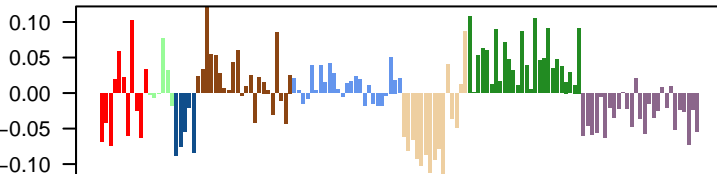
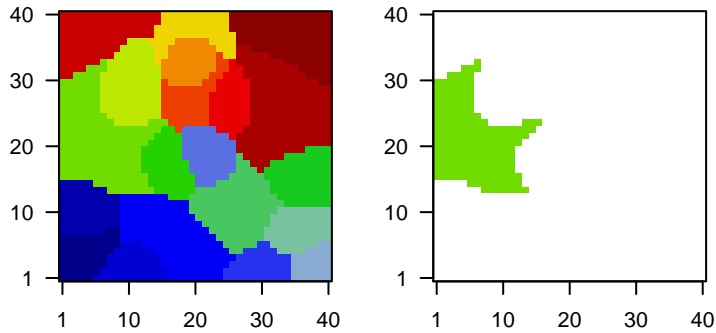
<r> metagenes = 0.49

beta: r2= 0.67 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map

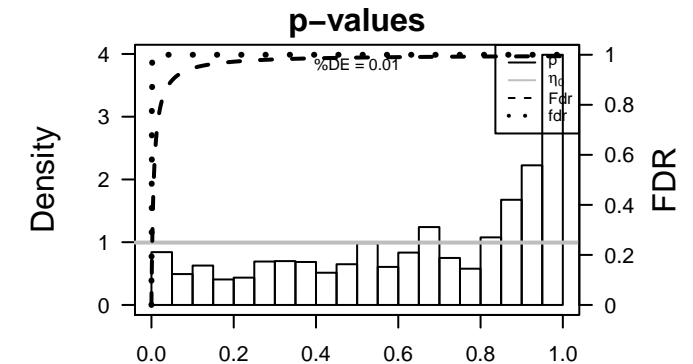
Spot



Geneset Overrepresentation

Rank p-value #in/all Geneset

Rank	p-value	#in/all	Geneset
1	2e-11	115 / 358	BP mRNA processing
2	2e-09	90 / 279	BP RNA splicing
3	1e-07	73 / 229	BP mRNA splicing, via spliceosome
4	6e-07	97 / 342	BP chromatin organization
5	3e-05	302 / 1387	BP regulation of transcription, DNA-templated
6	5e-05	34 / 99	BP mRNA export from nucleus
7	5e-05	24 / 61	BP regulation of alternative mRNA splicing, via spliceosome
8	7e-05	305 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
9	2e-04	31 / 94	BP RNA processing
10	2e-04	30 / 90	BP viral transcription
11	3e-04	12 / 24	BP mRNA cis splicing, via spliceosome
12	3e-04	15 / 34	BP tRNA export from nucleus
13	3e-04	17 / 41	BP regulation of glycolytic process
14	5e-04	8 / 13	BP positive regulation of RNA splicing
15	5e-04	14 / 32	BP histone H4 acetylation
16	6e-04	22 / 62	BP protein sumoylation
17	9e-04	7 / 11	BP epithelial cell development
18	1e-03	31 / 101	BP mRNA transport
19	1e-03	25 / 78	BP protein import into nucleus
20	2e-03	23 / 70	BP regulation of gene silencing by miRNA
21	2e-03	87 / 366	BP DNA repair
22	2e-03	7 / 12	BP homeostatic process
23	3e-03	11 / 26	BP maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S, 5.8S)
24	3e-03	8 / 16	BP sympathetic nervous system development
25	4e-03	226 / 1086	BP positive regulation of transcription by RNA polymerase II
26	4e-03	92 / 400	BP chromatin binding
27	4e-03	17 / 50	BP intracellular transport of virus
28	4e-03	31 / 110	BP meiotic cell cycle
29	5e-03	27 / 93	BP ribosome biogenesis
30	5e-03	178 / 843	BP DNA-binding transcription factor activity
31	5e-03	8 / 17	BP regulation of establishment of cell polarity
32	6e-03	235 / 1145	BP regulation of transcription by RNA polymerase II
33	6e-03	6 / 11	BP core promoter binding
34	6e-03	6 / 11	BP histone mRNA catabolic process
35	7e-03	15 / 44	BP negative regulation of gene expression, epigenetic
36	7e-03	10 / 25	BP DNA-dependent DNA replication
37	7e-03	10 / 25	BP endocrine pancreas development
38	8e-03	8 / 18	BP mitotic G2 DNA damage checkpoint
39	8e-03	12 / 33	BP ventricular septum development
40	1e-02	11 / 30	BP histone lysine methylation



BP

Rank	p-value	#in/all	Geneset
1	2e-11	115 / 358	mRNA processing
2	2e-09	90 / 279	RNA splicing
3	1e-07	73 / 229	mRNA splicing, via spliceosome
4	6e-07	97 / 342	chromatin organization
5	3e-05	302 / 1387	regulation of transcription, DNA-templated
6	5e-05	34 / 99	mRNA export from nucleus
7	5e-05	24 / 61	regulation of alternative mRNA splicing, via spliceosome
8	7e-05	305 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
9	2e-04	31 / 94	RNA processing
10	2e-04	30 / 90	viral transcription
11	3e-04	12 / 24	mRNA cis splicing, via spliceosome
12	3e-04	15 / 34	tRNA export from nucleus
13	3e-04	17 / 41	regulation of glycolytic process
14	5e-04	8 / 13	positive regulation of RNA splicing
15	5e-04	14 / 32	histone H4 acetylation

K-Means Cluster

Spot Summary: I

metagenes = 96
genes = 3108

<r> metagenes = 0.58

beta: r2= 1.16 / log p= -Inf

samples with spot = 0 (0 %)

Spot Genelist

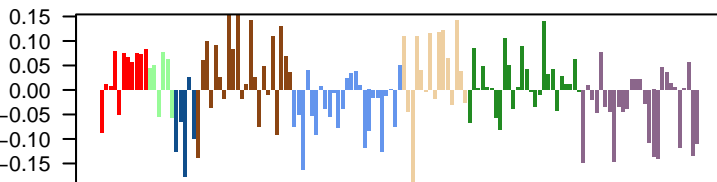
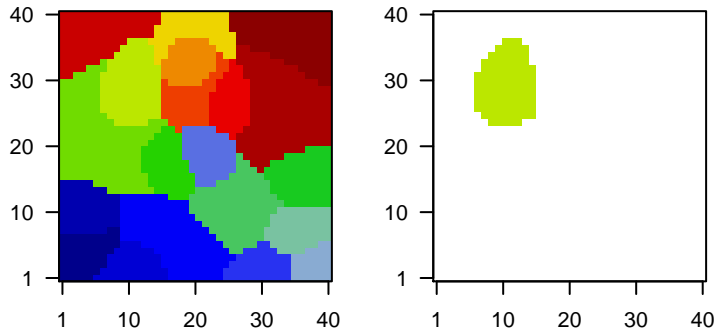
Rank	ID	max e	r	min e	Description
					Symbol
1	227952_at	3.07	-0.76	0.06	
2	210467_x_at	2.81	-0.3	0.17	MAGEA1 MAGE family member A12 [Source:HGNC Symbol;Acc:HGNC:10316]
3	208282_x_at	2.79	-0.42	0.12	DAZ1 deleted in azoospermia 1 [Source:HGNC Symbol;Acc:HGNC:10317]
4	1553296_at	2.77	-0.34	-0.06	ADGRG7 adhesion G protein-coupled receptor G7 [Source:HGNC Symbol;Acc:HGNC:10318]
5	206622_at	2.72	-0.72	0.17	TRH thyrotropin releasing hormone [Source:HGNC Symbol;Acc:HGNC:10319]
6	207909_x_at	2.71	-0.35	0.13	DAZ1 deleted in azoospermia 1 [Source:HGNC Symbol;Acc:HGNC:10317]
7	208168_s_at	2.53	-0.7	0.25	CHIT1 chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936]
8	211635_x_at	2.42	-0.91	0.19	immunoglobulin heavy variable 1-69 [Source:HGNC Symbol;Acc:HGNC:10320]
9	205242_at	2.41	-0.46	0.22	CXCL13 C-X-C motif chemokine ligand 13 [Source:HGNC Symbol;Acc:HGNC:10321]
10	209309_at	2.2	-1.3	0.18	AZGP1 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol;Acc:HGNC:10322]
11	206638_at	2.19	-0.62	0.17	HTR2B 5-hydroxytryptamine receptor 2B [Source:HGNC Symbol;Acc:HGNC:10323]
12	1555773_at	2.15	-0.4	0.18	BPIFC BPI fold containing family C [Source:HGNC Symbol;Acc:HGNC:10324]
13	220445_s_at	2.14	-0.3	0.29	CSAG3 CSAG family member 3 [Source:HGNC Symbol;Acc:HGNC:10325]
14	217179_x_at	2.08	-0.77	0.3	
15	1555480_a_at	2.06	-0.46	0.12	FBLIM1 filamin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGNC:10326]
16	219257_s_at	2.02	-0.71	0.24	SPHK1 sphingosine kinase 1 [Source:NCBI gene;Acc:8877]
17	209905_at	2	-0.38	0.15	HOXA9 homeobox A9 [Source:HGNC Symbol;Acc:HGNC:5109]
18	215894_at	1.97	-0.43	0.18	PTGDR prostaglandin D2 receptor [Source:HGNC Symbol;Acc:HGNC:10327]
19	211640_x_at	1.96	-0.29	0.06	
20	211649_x_at	1.94	-0.55	0.05	

Geneset Overrepresentation

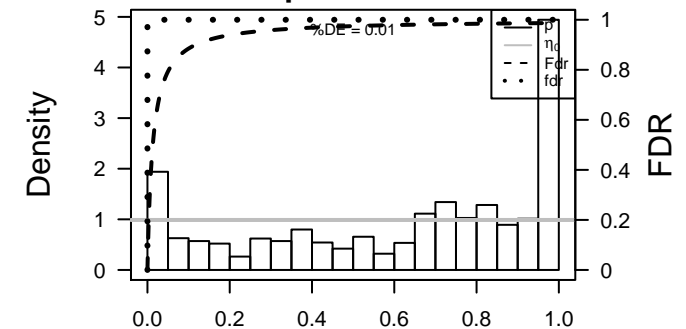
Rank	p-value	#in/all	Geneset
1	2e-63	364 / 1435	BP mitochondrion
2	9e-49	123 / 276	BP translation
3	1e-31	48 / 69	BP SRP-dependent cotranslational protein targeting to membrane
4	1e-30	52 / 83	BP mitochondrial translational elongation
5	7e-29	51 / 85	BP mitochondrial translational termination
6	9e-28	60 / 120	BP translational initiation
7	2e-26	698 / 4740	BP cytosol
8	1e-24	39 / 59	BP mitochondrial respiratory chain complex I assembly
9	5e-22	48 / 98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
10	1e-21	31 / 43	BP mitochondrial electron transport, NADH to ubiquinone
11	3e-21	45 / 90	BP viral transcription
12	2e-17	55 / 152	BP rRNA processing
13	4e-16	68 / 229	BP mRNA splicing, via spliceosome
14	9e-14	27 / 52	BP negative regulation of G2/M transition of mitotic cell cycle
15	5e-13	28 / 59	BP NIK/NF-kappaB signaling
16	7e-13	25 / 48	BP regulation of cellular amino acid metabolic process
17	2e-12	70 / 279	BP RNA splicing
18	2e-12	32 / 78	BP anaphase-promoting complex-dependent catabolic process
19	4e-12	29 / 67	BP antigen processing and presentation of exogenous peptide antigen via MHC class II, invariant chain containing
20	4e-12	29 / 67	BP regulation of transcription from RNA polymerase II promoter in response to hypoxia
21	3e-11	80 / 358	BP mRNA processing
22	6e-11	30 / 78	BP regulation of mitotic cell cycle phase transition
23	1e-10	36 / 108	BP regulation of mRNA stability
24	1e-10	31 / 84	BP SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
25	3e-10	17 / 29	BP cytoplasmic translation
26	3e-10	14 / 20	BP mitochondrial ATP synthase coupled proton transport
27	6e-10	17 / 30	BP cristae formation
28	9e-10	121 / 671	BP oxidation-reduction process
29	1e-09	25 / 63	BP regulation of hematopoietic stem cell differentiation
30	2e-09	767 / 6202	BP cytoplasm
31	3e-09	18 / 36	BP mitochondrial translation
32	4e-09	34 / 111	BP tumor necrosis factor-mediated signaling pathway
33	6e-09	16 / 30	BP ribosomal large subunit biogenesis
34	1e-08	25 / 69	BP transcription-coupled nucleotide-excision repair
35	1e-08	45 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
36	2e-08	14 / 25	BP cytochrome-c oxidase activity
37	3e-08	29 / 93	BP ribosome biogenesis
38	4e-08	11 / 16	BP ATP synthase coupled proton transport
39	5e-08	14 / 26	BP ATP biosynthetic process
40	9e-08	52 / 234	BP protein deubiquitination

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-63	364 / 1435	mitochondrion
2	9e-49	123 / 276	translation
3	1e-31	48 / 69	SRP-dependent cotranslational protein targeting to membrane
4	1e-30	52 / 83	mitochondrial translational elongation
5	7e-29	51 / 85	mitochondrial translational termination
6	9e-28	60 / 120	translational initiation
7	2e-26	698 / 4740	cytosol
8	1e-24	39 / 59	mitochondrial respiratory chain complex I assembly
9	5e-22	48 / 98	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
10	1e-21	31 / 43	mitochondrial electron transport, NADH to ubiquinone
11	3e-21	45 / 90	viral transcription
12	2e-17	55 / 152	rRNA processing
13	4e-16	68 / 229	mRNA splicing, via spliceosome
14	9e-14	27 / 52	negative regulation of G2/M transition of mitotic cell cycle
15	5e-13	28 / 59	NIK/NF-kappaB signaling

K-Means Cluster

Spot Summary: J

metagenes = 47
genes = 1161

<r> metagenes = 0.91

beta: r2= 10.77 / log p= -Inf

samples with spot = 33 (24.1 %)

group 1 : 6 (54.5 %)

group 2 : 3 (50 %)

group 3 : 1 (20 %)

group 4 : 16 (72.7 %)

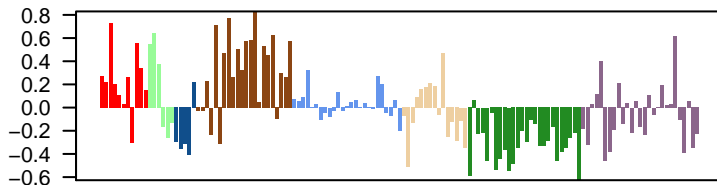
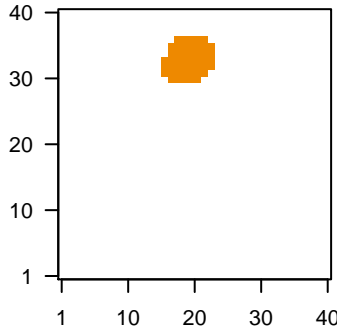
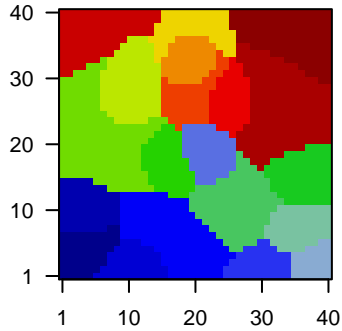
group 5 : 2 (8 %)

group 6 : 2 (13.3 %)

group 8 : 3 (11.1 %)

Overview Map

Spot

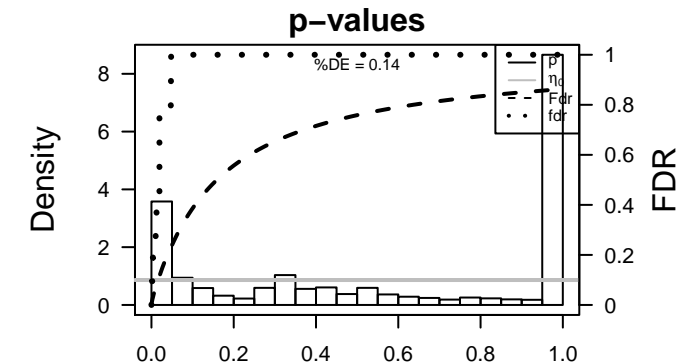


Spot Genelist

Rank	ID	max e	r	min e	Description
1	211430_s_at	3.66	-1	0.52	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
2	209138_x_at	3.42	-0.97	0.58	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
3	215121_x_at	3.38	-1.11	0.55	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
4	217022_s_at	3.37	-0.9	0.52	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	0.53	immunoglobulin kappa variable 1-39 (gene/pseudogene) [So
7	204602_at	3.11	-0.63	0.25	DKK1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
8	215379_x_at	3.1	-1.03	0.54	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
9	202018_s_at	3.01	-0.95	0.49	LTF lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
10	217148_x_at	2.94	-1	0.43	immunoglobulin lambda variable 2-14 [Source:HGNC Symbc
11	205207_at	2.91	-0.66	0.27	IL6 interleukin 6 [Source:HGNC Symbol;Acc:HGNC:6018]
12	216576_x_at	2.88	-0.61	0.38	
13	217378_x_at	2.84	-0.95	0.4	immunoglobulin kappa variable 1/OR2-108 (non-functional)
14	214669_x_at	2.74	-0.74	0.49	
15	224061_at	2.73	-0.57	0.47	INMT indolethylamine N-methyltransferase [Source:HGNC Symbol;
16	211339_s_at	2.73	-0.49	0.56	ITK IL2 inducible T cell kinase [Source:HGNC Symbol;Acc:HGNC
17	205374_at	2.72	-1.23	0.62	SLN sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]
18	214836_x_at	2.63	-0.83	0.5	
19	204614_at	2.61	-0.49	0.47	SERPINC2 serpin family B member 2 [Source:HGNC Symbol;Acc:HGNC
20	221651_x_at	2.59	-0.66	0.55	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-86	142 / 564	BP immune system process
2	7e-69	107 / 388	BP immune response
3	7e-53	95 / 417	BP innate immune response
4	9e-48	307 / 4278	BP plasma membrane
5	3e-47	84 / 364	BP inflammatory response
6	9e-40	85 / 460	BP neutrophil degranulation
7	8e-37	405 / 7387	BP membrane
8	2e-31	46 / 155	BP regulation of immune response
9	2e-27	56 / 289	BP cytokine-mediated signaling pathway
10	6e-25	24 / 43	BP antigen processing and presentation
11	3e-23	126 / 1500	BP signal transduction
12	4e-21	36 / 152	BP leukocyte migration
13	5e-21	15 / 17	BP antigen processing and presentation of peptide or polysaccharide antigen v
14	5e-20	38 / 184	BP defense response to virus
15	1e-19	24 / 64	BP regulation of complement activation
16	9e-19	40 / 222	BP adaptive immune response
17	6e-18	20 / 47	BP complement activation
18	3e-17	22 / 64	BP complement activation, classical pathway
19	9e-17	31 / 148	BP chemotaxis
20	1e-15	20 / 59	BP positive regulation of T cell proliferation
21	2e-15	25 / 103	BP response to bacterium
22	7e-14	28 / 151	BP cellular response to lipopolysaccharide
23	9e-14	18 / 56	BP B cell receptor signaling pathway
24	7e-13	21 / 89	BP Fc-gamma receptor signaling pathway involved in phagocytosis
25	1e-12	56 / 594	BP cell adhesion
26	3e-12	26 / 151	BP defense response to bacterium
27	6e-12	34 / 261	BP cell surface receptor signaling pathway
28	1e-11	26 / 160	BP T cell receptor signaling pathway
29	4e-11	12 / 29	BP cytokine production
30	7e-11	26 / 172	BP positive regulation of I-kappaB kinase/NF-kappaB signaling
31	2e-10	24 / 154	BP receptor-mediated endocytosis
32	3e-10	13 / 41	BP positive regulation of interferon-gamma production
33	4e-10	24 / 159	BP response to lipopolysaccharide
34	4e-10	18 / 88	BP cellular response to interferon-gamma
35	4e-10	18 / 88	BP positive regulation of peptidyl-tyrosine phosphorylation
36	8e-10	12 / 36	BP blood circulation
37	1e-09	10 / 23	BP response to interferon-gamma
38	1e-09	16 / 72	BP positive regulation of inflammatory response
39	2e-09	16 / 74	BP neutrophil chemotaxis
40	2e-09	42 / 459	BP viral process



BP

Rank	p-value	#in/all	Geneset
1	3e-86	142 / 564	immune system process
2	7e-69	107 / 388	immune response
3	7e-53	95 / 417	innate immune response
4	9e-48	307 / 4278	plasma membrane
5	3e-47	84 / 364	inflammatory response
6	9e-40	85 / 460	neutrophil degranulation
7	8e-37	405 / 7387	membrane
8	2e-31	46 / 155	regulation of immune response
9	2e-27	56 / 289	cytokine-mediated signaling pathway
10	6e-25	24 / 43	antigen processing and presentation
11	3e-23	126 / 1500	signal transduction
12	4e-21	36 / 152	leukocyte migration
13	5e-21	15 / 17	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
14	5e-20	38 / 184	defense response to virus
15	1e-19	24 / 64	regulation of complement activation

K-Means Cluster

Spot Summary: K

metagenes = 53
genes = 1181

<r> metagenes = 0.82

beta: r2= 4.09 / log p= -Inf

samples with spot = 11 (8 %)

group 1 : 5 (45.5 %)
group 4 : 4 (18.2 %)
group 5 : 1 (4 %)
group 8 : 1 (3.7 %)

Spot Genelist

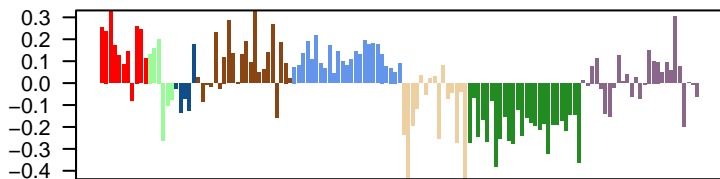
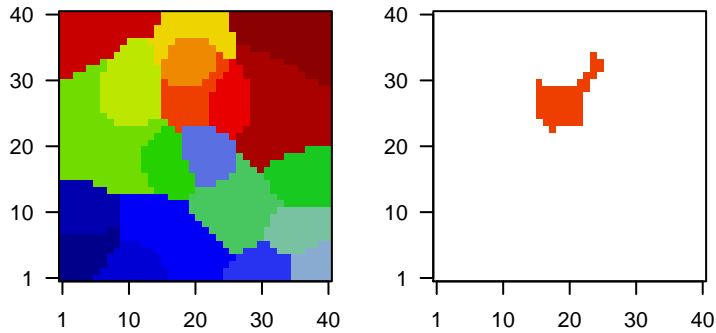
Rank	ID	max e	r	min e	Description
					Symbol
1	227678_at	2.67	-0.9	0.42	ATP23 ATP23 metallopeptidase and ATP synthase assembly factor h
2	205225_at	2.58	-0.59	0.28	ESR1 estrogen receptor 1 [Source:HGNC Symbol;Acc:HGNC:3467]
3	229377_at	2.37	-0.95	0.39	GRTF1 growth hormone regulated TBC protein 1 [Source:HGNC Syn
4	1557369_a_a	2.31	-0.92	0.35	long intergenic non-protein coding RNA 698 [Source:HGNC :
5	231380_at	2.14	-1.02	0.48	C8orf34 chromosome 8 open reading frame 34 [Source:HGNC Symbc
6	241535_at	2.14	-0.8	0.21	SNTG2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
7	214038_at	2.02	-0.83	0.35	CCL8 C-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:Hi
8	241470_x_at	2.02	-0.56	0.37	RASSF9 Ras association domain family member 9 [Source:HGNC Syr
9	216370_s_at	2	-0.84	0.55	TKTL1 transketolase like 1 [Source:HGNC Symbol;Acc:HGNC:1183f
10	241560_at	1.95	-0.58	0.3	
11	224463_s_at	1.94	-1.01	0.32	CFAP300cilia and flagella associated protein 300 [Source:HGNC Symt
12	1555416_a_a	1.94	-0.43	0.35	ALOX15B arachidonate 15-lipoxygenase, type B [Source:HGNC Symbc
13	207039_at	1.93	-1.04	0.16	CDKN2A cyclin dependent kinase inhibitor 2A [Source:HGNC Symbol;/
14	1553605_a_a	1.92	-0.61	0.37	ABCA13 ATP binding cassette subfamily A member 13 [Source:HGNC
15	204560_at	1.86	-1.38	0.49	FKBP5 FKBP prolyl isomerase 5 [Source:HGNC Symbol;Acc:HGNC:
16	207113_s_at	1.86	-1.01	0.35	TNF tumor necrosis factor [Source:HGNC Symbol;Acc:HGNC:118
17	230193_at	1.85	-0.69	0.28	WDR66 WD repeat domain 66 [Source:HGNC Symbol;Acc:HGNC:28f
18	234279_at	1.85	-1.4	0.33	
19	1562321_at	1.83	-1.71	0.33	PDK4 pyruvate dehydrogenase kinase 4 [Source:HGNC Symbol;Ac
20	210511_s_at	1.82	-1.25	0.28	INHBA inhibin subunit beta A [Source:HGNC Symbol;Acc:HGNC:60f

Geneset Overrepresentation

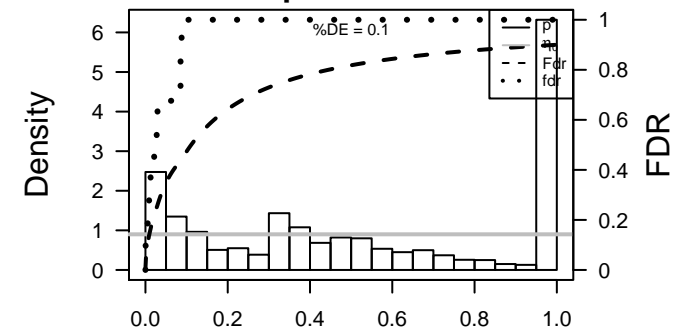
Rank	p-value	#in/all	Geneset
1	6e-14	103 / 1242	BP Golgi apparatus
2	2e-12	328 / 6202	BP cytoplasm
3	1e-09	254 / 4740	BP cytosol
4	1e-08	358 / 7387	BP membrane
5	6e-07	37 / 398	BP positive regulation of gene expression
6	6e-07	52 / 659	BP apoptotic process
7	9e-07	20 / 148	BP positive regulation of NF-kappaB transcription factor activity
8	1e-06	40 / 460	BP neutrophil degranulation
9	2e-06	88 / 1387	BP regulation of transcription, DNA-templated
10	5e-06	47 / 613	BP positive regulation of transcription, DNA-templated
11	5e-06	59 / 843	BP DNA-binding transcription factor activity
12	9e-06	8 / 29	BP positive regulation of interleukin-1 beta secretion
13	1e-05	14 / 92	BP wound healing
14	1e-05	9 / 38	BP protein kinase B signaling
15	1e-05	55 / 783	BP negative regulation of transcription by RNA polymerase II
16	1e-05	32 / 364	BP inflammatory response
17	1e-05	90 / 1500	BP signal transduction
18	1e-05	11 / 60	BP positive regulation of smooth muscle cell proliferation
19	3e-05	19 / 170	BP protein glycosylation
20	3e-05	22 / 216	BP carbohydrate metabolic process
21	3e-05	210 / 4278	BP plasma membrane
22	3e-05	7 / 25	BP antigen processing and presentation of peptide antigen via MHC class I
23	3e-05	8 / 34	BP lamellipodium assembly
24	4e-05	68 / 1086	BP positive regulation of transcription by RNA polymerase II
25	5e-05	5 / 12	BP negative regulation by host of viral transcription
26	6e-05	11 / 70	BP cellular response to organic cyclic compound
27	7e-05	10 / 59	BP response to cytokine
28	7e-05	11 / 71	BP hemopoiesis
29	8e-05	8 / 38	BP protein N-linked glycosylation
30	1e-04	11 / 74	BP negative regulation of NF-kappaB transcription factor activity
31	1e-04	23 / 254	BP angiogenesis
32	1e-04	17 / 159	BP response to lipopolysaccharide
33	1e-04	8 / 41	BP negative regulation of I-kappaB kinase/NF-kappaB signaling
34	2e-04	14 / 118	BP platelet degranulation
35	2e-04	5 / 15	BP regulation of I-kappaB kinase/NF-kappaB signaling
36	2e-04	14 / 119	BP cellular response to tumor necrosis factor
37	2e-04	5 / 16	BP negative regulation of cytokine production
38	2e-04	7 / 34	BP negative regulation of extrinsic apoptotic signaling pathway in absence of li
39	3e-04	13 / 109	BP response to virus
40	3e-04	31 / 412	BP negative regulation of cell population proliferation

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	6e-14	103 / 1242	Golgi apparatus
2	2e-12	328 / 6202	cytoplasm
3	1e-09	254 / 4740	cytosol
4	1e-08	358 / 7387	membrane
5	6e-07	37 / 398	positive regulation of gene expression
6	6e-07	52 / 659	apoptotic process
7	9e-07	20 / 148	positive regulation of NF-kappaB transcription factor activity
8	1e-06	40 / 460	neutrophil degranulation
9	2e-06	88 / 1387	regulation of transcription, DNA-templated
10	5e-06	47 / 613	positive regulation of transcription, DNA-templated
11	5e-06	59 / 843	DNA-binding transcription factor activity
12	9e-06	8 / 29	positive regulation of interleukin-1 beta secretion
13	1e-05	14 / 92	wound healing
14	1e-05	9 / 38	protein kinase B signaling
15	1e-05	55 / 783	negative regulation of transcription by RNA polymerase II

K-Means Cluster

Spot Summary: L

metagenes = 61
genes = 1694

<r> metagenes = 0.76

beta: r2= 3.94 / log p= -Inf

samples with spot = 18 (13.1 %)

- group 1 : 1 (9.1 %)
- group 2 : 4 (66.7 %)
- group 4 : 7 (31.8 %)
- group 6 : 6 (40 %)

Spot Genelist

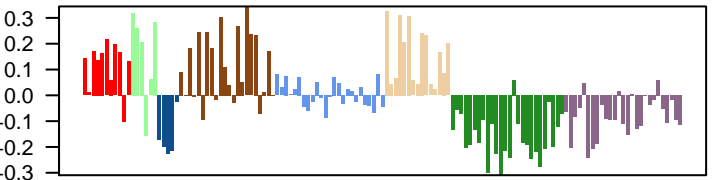
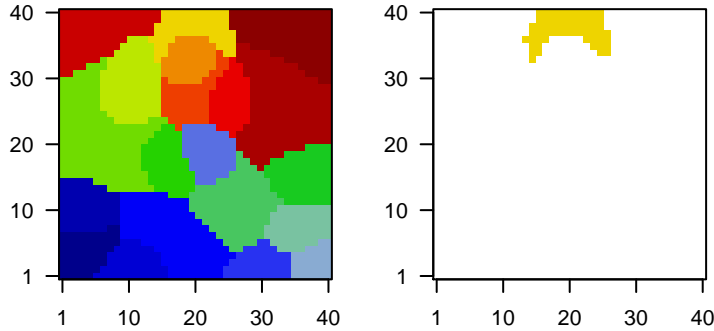
Rank	ID	max e	r	min e	Description
1	211634_x_at	2.96	-0.55	0.17	immunoglobulin heavy variable 1-69 [Source:HGNC Symbol;
2	216401_x_at	2.95	-0.59	0.35	immunoglobulin kappa variable 1-37 (non-functional) [Source
3	209560_s_at	2.92	-0.57	0.29	DLK1 delta like non-canonical Notch ligand 1 [Source:HGNC Symb
4	216351_x_at	2.87	-0.53	0.29	DAZ1 deleted in azoospermia 1 [Source:HGNC Symbol;Acc:HGNC:
5	216557_x_at	2.83	-0.54	0.33	immunoglobulin heavy variable 3-21 [Source:HGNC Symbol;
6	218959_at	2.76	-0.75	0.41	HOXC10 homeobox C10 [Source:HGNC Symbol;Acc:HGNC:5122]
7	243489_at	2.73	-0.86	0.35	
8	223836_at	2.68	-0.59	0.29	FGFBP2 fibroblast growth factor binding protein 2 [Source:HGNC Syml
9	213674_x_at	2.64	-0.43	0.19	immunoglobulin heavy constant delta [Source:HGNC Symbol
10	233887_at	2.55	-0.5	0.24	ADGRG6adhesion G protein-coupled receptor G6 [Source:HGNC Syrn
11	231044_at	2.55	-1.02	0.6	C1orf194chromosome 1 open reading frame 194 [Source:HGNC Symt
12	217258_x_at	2.5	-0.63	0.24	
13	216560_x_at	2.47	-0.39	0.24	immunoglobulin lambda variable 3-10 [Source:HGNC Symbc
14	214651_s_at	2.46	-0.44	0.27	HOXA9 homeobox A9 [Source:HGNC Symbol;Acc:HGNC:5109]
15	216491_x_at	2.46	-0.38	0.35	immunoglobulin heavy variable 4-61 [Source:HGNC Symbol;
16	217235_x_at	2.46	-0.46	0.36	
17	213728_at	2.45	-0.95	0.4	LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Sy
18	210239_at	2.44	-0.59	0.42	IRX5 iroquois homeobox 5 [Source:HGNC Symbol;Acc:HGNC:143
19	211881_x_at	2.42	-0.61	0.26	
20	219857_at	2.33	-0.78	0.36	PLEKHSpleckstrin homology domain containing S1 [Source:HGNC Sy

Geneset Overrepresentation

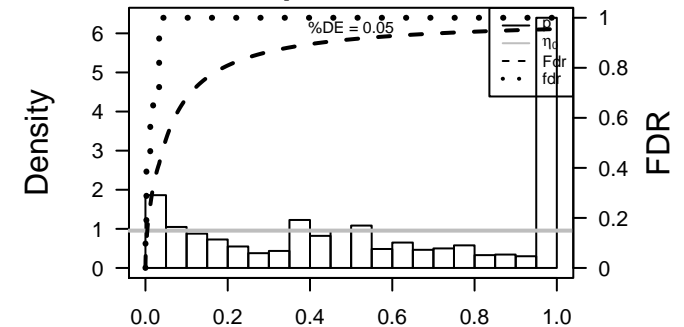
Rank	p-value	#in/all	Geneset
1	1e-14	391 / 6202	BP cytoplasm
2	2e-13	444 / 7387	BP membrane
3	3e-12	306 / 4740	BP cytosol
4	5e-09	58 / 564	BP immune system process
5	7e-07	255 / 4278	BP plasma membrane
6	2e-06	16 / 89	BP Fc-gamma receptor signaling pathway involved in phagocytosis
7	2e-06	54 / 613	BP positive regulation of transcription, DNA-templated
8	3e-06	7 / 16	BP negative regulation of growth
9	1e-05	66 / 843	BP DNA-binding transcription factor activity
10	1e-05	22 / 172	BP positive regulation of I-kappaB kinase/NF-kappaB signaling
11	1e-05	80 / 1086	BP positive regulation of transcription by RNA polymerase II
12	2e-05	9 / 35	BP positive regulation of substrate adhesion-dependent cell spreading
13	3e-05	22 / 185	BP endocytosis
14	3e-05	20 / 159	BP actin cytoskeleton organization
15	4e-05	38 / 417	BP innate immune response
16	8e-05	19 / 155	BP regulation of immune response
17	9e-05	85 / 1242	BP Golgi apparatus
18	1e-04	53 / 684	BP phosphorylation
19	1e-04	94 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
20	1e-04	51 / 659	BP apoptotic process
21	2e-04	23 / 222	BP adaptive immune response
22	3e-04	10 / 60	BP positive regulation of NIK/NF-kappaB signaling
23	3e-04	34 / 400	BP protein serine/threonine kinase activity
24	4e-04	8 / 40	BP carbohydrate transport
25	4e-04	6 / 23	BP cellular senescence
26	4e-04	6 / 23	BP proximal/distal pattern formation
27	5e-04	29 / 327	BP cell population proliferation
28	5e-04	5 / 16	BP 3'-UTR-mediated mRNA stabilization
29	5e-04	37 / 460	BP neutrophil degranulation
30	7e-04	4 / 10	BP cellular aldehyde metabolic process
31	7e-04	4 / 10	BP regulation of B cell differentiation
32	7e-04	19 / 184	BP defense response to virus
33	9e-04	9 / 56	BP B cell receptor signaling pathway
34	9e-04	18 / 173	BP cilium assembly
35	9e-04	6 / 26	BP glycosaminoglycan catabolic process
36	9e-04	6 / 26	BP regulation of actin filament polymerization
37	1e-03	17 / 160	BP T cell receptor signaling pathway
38	1e-03	5 / 18	BP cellular response to exogenous dsRNA
39	1e-03	21 / 219	BP positive regulation of cell migration
40	1e-03	7 / 36	BP positive regulation of intrinsic apoptotic signaling pathway

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	1e-14	391 / 6202	cytoplasm
2	2e-13	444 / 7387	membrane
3	3e-12	306 / 4740	cytosol
4	5e-09	58 / 564	immune system process
5	7e-07	255 / 4278	plasma membrane
6	2e-06	16 / 89	Fc-gamma receptor signaling pathway involved in phagocytosis
7	2e-06	54 / 613	positive regulation of transcription, DNA-templated
8	3e-06	7 / 16	negative regulation of growth
9	1e-05	66 / 843	DNA-binding transcription factor activity
10	1e-05	22 / 172	positive regulation of I-kappaB kinase/NF-kappaB signaling
11	1e-05	80 / 1086	positive regulation of transcription by RNA polymerase II
12	2e-05	9 / 35	positive regulation of substrate adhesion-dependent cell spreading
13	3e-05	22 / 185	endocytosis
14	3e-05	20 / 159	actin cytoskeleton organization
15	4e-05	38 / 417	innate immune response

K-Means Cluster

Spot Summary: M

metagenes = 64
genes = 2111

<r> metagenes = 0.87

beta: r2= 3.74 / log p= -Inf

samples with spot = 6 (4.4 %)

- group 1 : 1 (9.1 %)
- group 4 : 3 (13.6 %)
- group 5 : 1 (4 %)
- group 7 : 1 (3.8 %)

Spot Genelist

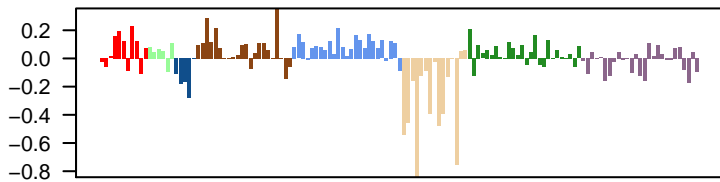
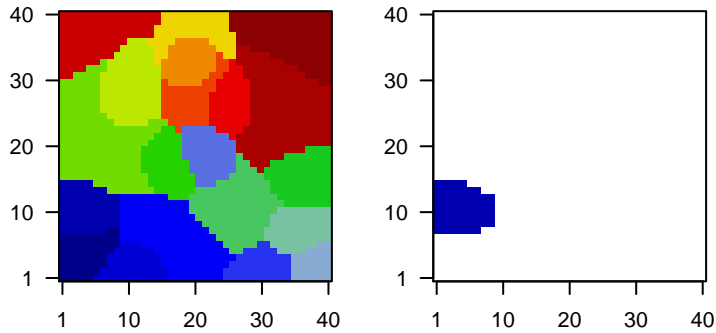
Rank	ID	max e	r	min e	Description
1	1559283_a_a	2.51	-0.6	0.41	novel transcript
2	235590_at	2.31	-0.78	0.52	SLF2 SMC5-SMC6 complex localization factor 2 [Source:HGNC S]
3	229870_at	2.1	-0.96	0.5	novel transcript, antisense to ZNF143
4	1558599_at	2.1	-0.72	0.41	
5	236017_at	2.09	-0.72	0.48	
6	244517_x_at	2.05	-0.82	0.54	
7	230598_at	1.99	-0.68	0.33	novel transcript
8	238107_at	1.97	-0.75	0.55	novel transcript
9	220399_at	1.95	-1.03	0.62	long intergenic non-protein coding RNA 115 [Source:HGNC :]
10	234787_at	1.95	-0.73	0.37	
11	1558600_a_a	1.95	-0.72	0.52	
12	224185_at	1.87	-0.9	0.6	TP53 tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]
13	205522_at	1.87	-1.37	0.35	
14	1563546_at	1.86	-0.73	0.33	
15	235319_at	1.86	-0.71	0.4	
16	239639_at	1.85	-0.68	0.5	long intergenic non-protein coding RNA 1977 [Source:HGNC]
17	236174_at	1.83	-0.92	0.5	novel transcript
18	1563229_at	1.83	-0.67	0.49	deleted in lymphocytic leukemia 2 [Source:HGNC Symbol;Ac]
19	240101_at	1.82	-0.76	0.51	STAM antisense RNA 1 (head to head) [Source:HGNC Symb]
20	239568_at	1.82	-0.93	0.35	PLEKHH2pleckstrin homology, MyTH4 and FERM domain containing H

Geneset Overrepresentation

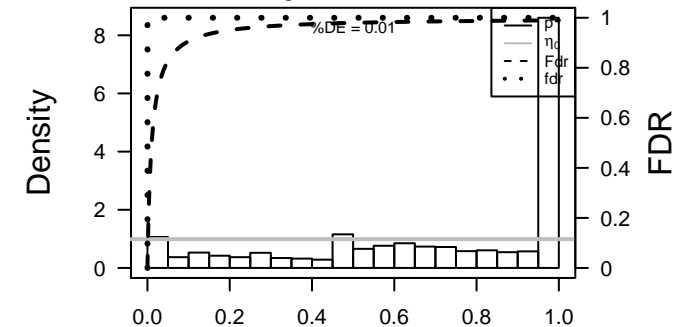
Rank	p-value	#in/all	Geneset
1	2e-18	70 / 358	BP mRNA processing
2	5e-18	83 / 484	BP cellular response to DNA damage stimulus
3	4e-15	65 / 366	BP DNA repair
4	4e-15	158 / 1387	BP regulation of transcription, DNA-templated
5	5e-15	55 / 279	BP RNA splicing
6	2e-14	136 / 1145	BP regulation of transcription by RNA polymerase II
7	2e-09	141 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
8	4e-09	39 / 229	BP mRNA splicing, via spliceosome
9	1e-08	32 / 173	BP cilium assembly
10	5e-08	33 / 192	BP methylation
11	1e-07	21 / 94	BP RNA processing
12	6e-07	20 / 93	BP ciliary basal body-plasma membrane docking
13	2e-06	44 / 342	BP chromatin organization
14	4e-06	28 / 180	BP cell projection organization
15	5e-06	48 / 400	BP chromatin binding
16	1e-05	66 / 630	BP cell cycle
17	1e-05	14 / 61	BP regulation of alternative mRNA splicing, via spliceosome
18	2e-05	11 / 40	BP intracellular transport involved in cilium assembly
19	2e-05	16 / 80	BP regulation of G2/M transition of mitotic cell cycle
20	3e-05	14 / 66	BP double-strand break repair
21	5e-05	9 / 30	BP ATP-dependent DNA helicase activity
22	5e-05	7 / 18	BP cilium organization
23	5e-05	8 / 24	BP replication fork processing
24	7e-05	344 / 4740	BP cytosol
25	7e-05	17 / 97	BP DNA recombination
26	7e-05	44 / 394	BP cell division
27	7e-05	12 / 54	BP DNA duplex unwinding
28	7e-05	437 / 6202	BP cytoplasm
29	8e-05	23 / 158	BP DNA replication
30	1e-04	17 / 101	BP mRNA transport
31	1e-04	15 / 83	BP thiol-dependent ubiquitin-specific protease activity
32	1e-04	10 / 41	BP RNA export from nucleus
33	2e-04	6 / 15	BP DNA double-strand break processing
34	2e-04	5 / 10	BP intracellular retrograde transport
35	2e-04	9 / 35	BP base-excision repair
36	2e-04	9 / 36	BP protein peptidyl-prolyl isomerization
37	3e-04	16 / 99	BP mRNA export from nucleus
38	3e-04	10 / 45	BP non-motile cilium assembly
39	3e-04	10 / 45	BP telomere maintenance
40	3e-04	19 / 130	BP G2/M transition of mitotic cell cycle

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-18	70 / 358	mRNA processing
2	5e-18	83 / 484	cellular response to DNA damage stimulus
3	4e-15	65 / 366	DNA repair
4	4e-15	158 / 1387	regulation of transcription, DNA-templated
5	5e-15	55 / 279	RNA splicing
6	2e-14	136 / 1145	regulation of transcription by RNA polymerase II
7	2e-09	141 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
8	4e-09	39 / 229	mRNA splicing, via spliceosome
9	1e-08	32 / 173	cilium assembly
10	5e-08	33 / 192	methylation
11	1e-07	21 / 94	RNA processing
12	6e-07	20 / 93	ciliary basal body-plasma membrane docking
13	2e-06	44 / 342	chromatin organization
14	4e-06	28 / 180	cell projection organization
15	5e-06	48 / 400	chromatin binding

K-Means Cluster

Spot Summary: N

metagenes = 51
genes = 1434

<r> metagenes = 0.78

beta: r2= 3.69 / log p= -Inf

samples with spot = 12 (8.8 %)

group 4 : 1 (4.5 %)
group 5 : 10 (40 %)
group 6 : 1 (6.7 %)

Spot Genelist

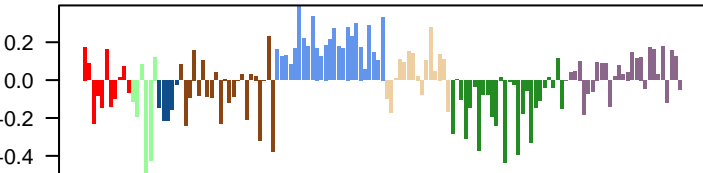
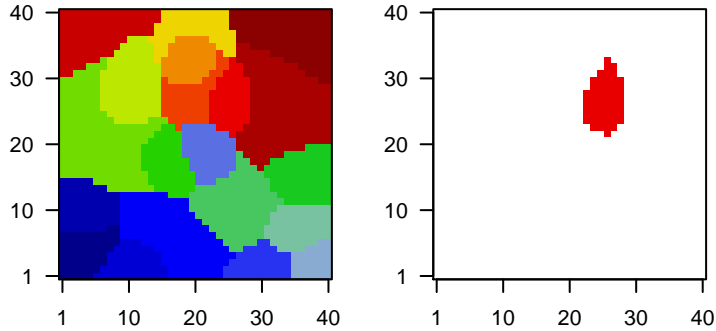
Rank	ID	max e	r	min e	Description
					Symbol
1	231155_at	2.98	-0.75	0.35	DEFB19 defensin beta 119 [Source:HGNC Symbol;Acc:HGNC:18099]
2	237898_at	2.62	-1.03	0.34	
3	240275_at	2.49	-0.68	0.3	ARMC3 armadillo repeat containing 3 [Source:HGNC Symbol;Acc:HGNC:1330]
4	1562371_s_at	2.33	-0.82	0.52	VWA3B von Willebrand factor A domain containing 3B [Source:HGNC Symbol;Acc:HGNC:1330]
5	213265_at	2.32	-0.88	0.35	PGA4 pepsinogen 4, group I (pepsinogen A) [Source:HGNC Symbol;Acc:HGNC:1330]
6	207148_x_at	2.29	-0.72	0.38	MYOZ2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
7	210452_x_at	2.25	-0.65	0.22	CYP4F2 cytochrome P450 family 4 subfamily F member 2 [Source:HGNC Symbol;Acc:HGNC:1330]
8	213782_s_at	2.22	-0.69	0.34	MYOZ2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
9	213764_s_at	2.19	-0.46	0.31	MFAP5 microfibril associated protein 5 [Source:HGNC Symbol;Acc:HGNC:1330]
10	206878_at	2.17	-0.71	0.32	DAO D-amino acid oxidase [Source:HGNC Symbol;Acc:HGNC:2666]
11	215443_at	2.15	-0.64	0.28	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1330]
12	230661_at	2.14	-0.76	0.27	
13	213765_at	2.14	-0.46	0.37	MFAP5 microfibril associated protein 5 [Source:HGNC Symbol;Acc:HGNC:1330]
14	220037_s_at	2.13	-1.17	0.45	LYVE1 lymphatic vessel endothelial hyaluronan receptor 1 [Source:HGNC Symbol;Acc:HGNC:1330]
15	209368_at	2.09	-1.05	0.55	EPHX2 epoxide hydrolase 2 [Source:HGNC Symbol;Acc:HGNC:3402]
16	243952_at	2.08	-1.62	0.54	TPTE pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:4366]
17	228233_at	2.06	-1.09	0.53	FREM1 FRAS1 related extracellular matrix 1 [Source:HGNC Symbol;Acc:HGNC:1330]
18	235892_at	2.03	-0.94	0.74	COLCA1 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:HGNC:1330]
19	210683_at	2.03	-0.52	0.28	NRTN neuritin [Source:HGNC Symbol;Acc:HGNC:8007]
20	237727_at	2.01	-0.84	0.38	

Geneset Overrepresentation

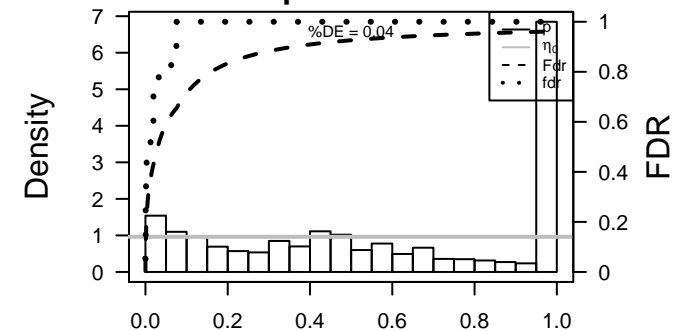
Rank	p-value	#in/all	Geneset
1	1e-06	326 / 6202	BP cytoplasm
2	3e-05	9 / 40	BP regulation of neurogenesis
3	7e-05	58 / 815	BP protein homodimerization activity
4	9e-05	43 / 553	BP oxidoreductase activity
5	1e-04	7 / 27	BP hippo signaling
6	1e-04	246 / 4740	BP cytosol
7	2e-04	11 / 70	BP smoothened signaling pathway
8	2e-04	71 / 1086	BP positive regulation of transcription by RNA polymerase II
9	2e-04	7 / 29	BP pituitary gland development
10	3e-04	10 / 64	BP camera-type eye development
11	3e-04	22 / 231	BP extracellular matrix organization
12	4e-04	10 / 65	BP pattern specification process
13	4e-04	7 / 33	BP regulation of canonical Wnt signaling pathway
14	4e-04	44 / 613	BP positive regulation of transcription, DNA-templated
15	5e-04	47 / 671	BP oxidation-reduction process
16	5e-04	6 / 25	BP positive regulation of cardiac muscle cell proliferation
17	5e-04	7 / 35	BP metanephros development
18	7e-04	5 / 18	BP nitric oxide mediated signal transduction
19	8e-04	4 / 11	BP response to pH
20	9e-04	13 / 113	BP muscle contraction
21	1e-03	4 / 12	BP developmental pigmentation
22	1e-03	4 / 12	BP negative regulation of amyloid-beta formation
23	1e-03	8 / 51	BP regulation of cardiac conduction
24	1e-03	11 / 89	BP regulation of cell migration
25	1e-03	41 / 594	BP cell adhesion
26	2e-03	6 / 32	BP cilium movement
27	2e-03	7 / 43	BP positive regulation of protein secretion
28	2e-03	4 / 14	BP ectoderm development
29	3e-03	8 / 57	BP RNA phosphodiester bond hydrolysis, endonucleolytic
30	3e-03	20 / 237	BP regulation of apoptotic process
31	3e-03	7 / 45	BP positive regulation of cell division
32	3e-03	214 / 4278	BP plasma membrane
33	3e-03	12 / 112	BP animal organ morphogenesis
34	3e-03	7 / 46	BP neural crest cell migration
35	3e-03	7 / 46	BP neural tube development
36	3e-03	4 / 15	BP definitive hemopoiesis
37	3e-03	4 / 15	BP production of miRNAs involved in gene silencing by miRNA
38	3e-03	5 / 25	BP response to cadmium ion
39	4e-03	8 / 61	BP cell fate commitment
40	4e-03	5 / 26	BP chondroitin sulfate biosynthetic process

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	1e-06	326 / 6202	cytoplasm
2	3e-05	9 / 40	regulation of neurogenesis
3	7e-05	58 / 815	protein homodimerization activity
4	9e-05	43 / 553	oxidoreductase activity
5	1e-04	7 / 27	hippo signaling
6	1e-04	246 / 4740	cytosol
7	2e-04	11 / 70	smoothened signaling pathway
8	2e-04	71 / 1086	positive regulation of transcription by RNA polymerase II
9	2e-04	7 / 29	pituitary gland development
10	3e-04	10 / 64	camera-type eye development
11	3e-04	22 / 231	extracellular matrix organization
12	4e-04	10 / 65	pattern specification process
13	4e-04	7 / 33	regulation of canonical Wnt signaling pathway
14	4e-04	44 / 613	positive regulation of transcription, DNA-templated
15	5e-04	47 / 671	oxidation-reduction process

K-Means Cluster

Spot Summary: O

metagenes = 112

genes = 6415

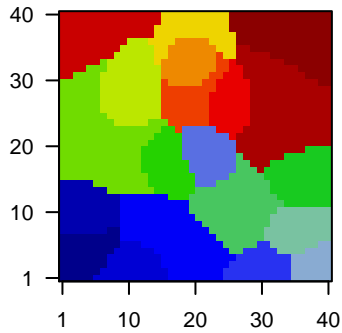
<r> metagenes = 0.83

beta: r2= 2.03 / log p= -Inf

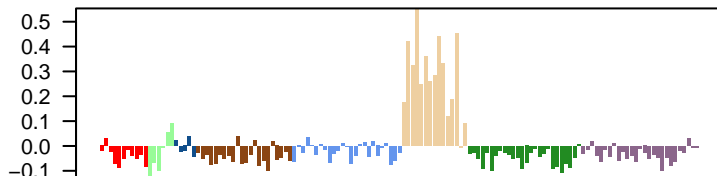
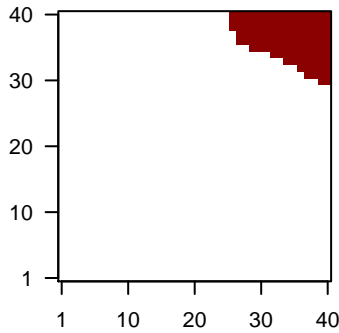
samples with spot = 10 (7.3 %)

group 6 : 10 (66.7 %)

Overview Map



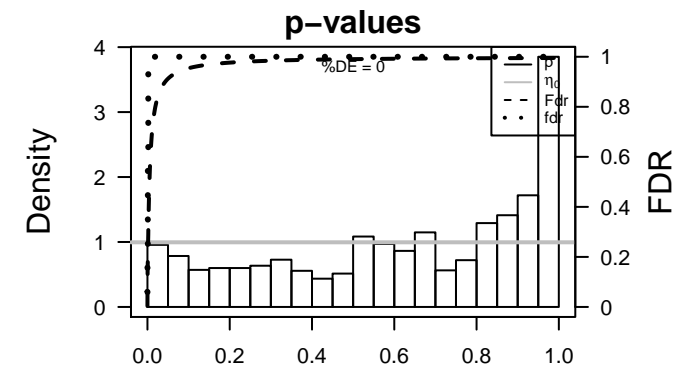
Spot



Geneset Overrepresentation

Rank p-value #in/all Geneset

Rank	p-value	#in/all	Geneset
1	1e-06	40 / 115	BP keratinization
2	4e-05	17 / 38	BP intracellular receptor signaling pathway
3	4e-05	10 / 16	BP regulation of regulatory T cell differentiation
4	1e-04	31 / 96	BP cornification
5	3e-04	14 / 32	BP positive regulation of vasoconstriction
6	3e-04	20 / 55	BP steroid hormone mediated signaling pathway
7	4e-04	15 / 37	BP peptide cross-linking
8	7e-04	38 / 138	BP serine-type endopeptidase activity
9	8e-04	27 / 89	BP epidermis development
10	8e-04	47 / 182	BP blood coagulation
11	9e-04	17 / 47	BP nuclear receptor activity
12	9e-04	161 / 777	BP G protein-coupled receptor signaling pathway
13	9e-04	12 / 28	BP pancreas development
14	9e-04	55 / 222	BP adaptive immune response
15	1e-03	10 / 22	BP cellular response to fatty acid
16	2e-03	31 / 111	BP sensory perception of smell
17	2e-03	92 / 418	BP regulation of signaling receptor activity
18	2e-03	14 / 38	BP bicarbonate transport
19	2e-03	8 / 16	BP positive regulation of calcineurin-NFAT signaling cascade
20	2e-03	19 / 59	BP regulation of megakaryocyte differentiation
21	2e-03	6 / 10	BP positive regulation of growth
22	3e-03	8 / 17	BP outer dynein arm assembly
23	3e-03	34 / 130	BP serine-type peptidase activity
24	4e-03	7 / 14	BP intestinal absorption
25	4e-03	10 / 25	BP cardiac muscle cell differentiation
26	4e-03	10 / 25	BP triglyceride homeostasis
27	4e-03	6 / 11	BP epithelial cell development
28	5e-03	116 / 564	BP immune system process
29	6e-03	9 / 22	BP sex differentiation
30	6e-03	10 / 26	BP chromatin silencing at rDNA
31	6e-03	55 / 241	BP response to stimulus
32	6e-03	16 / 51	BP antimicrobial humoral response
33	6e-03	18 / 60	BP response to nutrient levels
34	7e-03	6 / 12	BP positive regulation of insulin-like growth factor receptor signaling pathway
35	8e-03	36 / 147	BP positive regulation of cytosolic calcium ion concentration
36	8e-03	12 / 35	BP positive regulation of substrate adhesion-dependent cell spreading
37	8e-03	11 / 31	BP B cell activation
38	8e-03	11 / 31	BP mammary gland development
39	8e-03	17 / 57	BP odontogenesis of dentin-containing tooth
40	9e-03	7 / 16	BP sympathetic nervous system development



BP

Rank	p-value	#in/all	Geneset
1	1e-06	40 / 115	keratinization
2	4e-05	17 / 38	intracellular receptor signaling pathway
3	4e-05	10 / 16	regulation of regulatory T cell differentiation
4	1e-04	31 / 96	cornification
5	3e-04	14 / 32	positive regulation of vasoconstriction
6	3e-04	20 / 55	steroid hormone mediated signaling pathway
7	4e-04	15 / 37	peptide cross-linking
8	7e-04	38 / 138	serine-type endopeptidase activity
9	8e-04	27 / 89	epidermis development
10	8e-04	47 / 182	blood coagulation
11	9e-04	17 / 47	nuclear receptor activity
12	9e-04	161 / 777	G protein-coupled receptor signaling pathway
13	9e-04	12 / 28	pancreas development
14	9e-04	55 / 222	adaptive immune response
15	1e-03	10 / 22	cellular response to fatty acid

K-Means Cluster

Spot Summary: P

metagenes = 174

genes = 7023

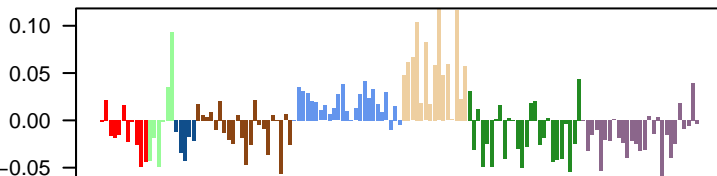
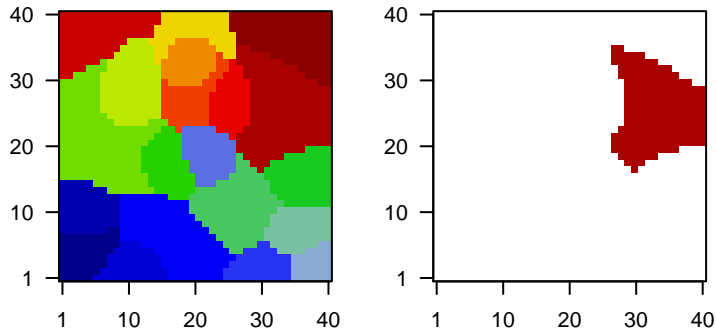
<r> metagenes = 0.37

beta: r2= 0.47 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map

Spot

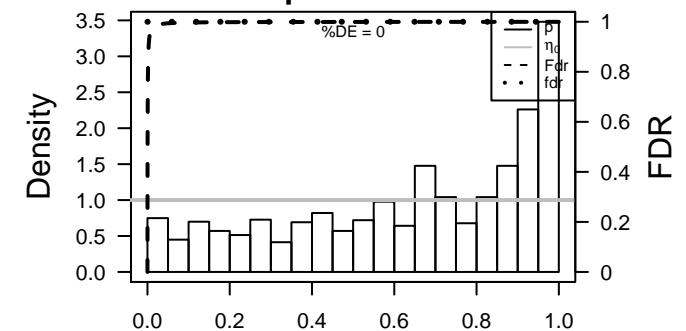


Geneset Overrepresentation

Rank p-value #in/all Geneset

Rank	p-value	#in/all	Geneset
1	6e-14	96 / 241	BP response to stimulus
2	5e-08	46 / 111	BP sensory perception of smell
3	2e-06	101 / 342	BP chromatin organization
4	3e-05	194 / 777	BP G protein-coupled receptor signaling pathway
5	2e-04	10 / 16	BP epithelial cell morphogenesis
6	2e-04	13 / 25	BP ventricular cardiac muscle tissue morphogenesis
7	4e-04	320 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
8	8e-04	14 / 31	BP ATP-dependent chromatin remodeling
9	9e-04	133 / 541	BP negative regulation of transcription, DNA-templated
10	1e-03	148 / 613	BP positive regulation of transcription, DNA-templated
11	2e-03	10 / 20	BP response to vitamin A
12	3e-03	7 / 12	BP estrogen biosynthetic process
13	3e-03	9 / 18	BP natural killer cell activation involved in immune response
14	3e-03	36 / 121	BP defense response
15	3e-03	242 / 1080	BP multicellular organism development
16	4e-03	31 / 102	BP chromatin remodeling
17	5e-03	34 / 115	BP keratinization
18	5e-03	6 / 10	BP posttranscriptional gene silencing by RNA
19	5e-03	26 / 83	BP xenobiotic metabolic process
20	5e-03	7 / 13	BP hematopoietic stem cell proliferation
21	6e-03	16 / 44	BP hormone-mediated signaling pathway
22	6e-03	190 / 843	BP DNA-binding transcription factor activity
23	8e-03	51 / 193	BP visual perception
24	8e-03	8 / 17	BP urogenital system development
25	9e-03	96 / 400	BP chromatin binding
26	9e-03	10 / 24	BP thyroid gland development
27	9e-03	6 / 11	BP immunological synapse formation
28	1e-02	32 / 112	BP animal organ morphogenesis
29	1e-02	250 / 1145	BP regulation of transcription by RNA polymerase II
30	1e-02	9 / 21	BP exogenous drug catabolic process
31	1e-02	9 / 21	BP T cell activation involved in immune response
32	1e-02	16 / 47	BP nuclear receptor activity
33	1e-02	28 / 96	BP cornification
34	1e-02	38 / 139	BP regulation of translation
35	1e-02	8 / 18	BP cell fate specification
36	1e-02	8 / 18	BP SUMO transferase activity
37	1e-02	13 / 36	BP binding of sperm to zona pellucida
38	1e-02	22 / 72	BP Rho protein signal transduction
39	1e-02	19 / 60	BP inner ear morphogenesis
40	1e-02	7 / 15	BP negative regulation of DNA recombination

p-values



BP

Rank	p-value	#in/all	Geneset
1	6e-14	96 / 241	response to stimulus
2	5e-08	46 / 111	sensory perception of smell
3	2e-06	101 / 342	chromatin organization
4	3e-05	194 / 777	G protein-coupled receptor signaling pathway
5	2e-04	10 / 16	epithelial cell morphogenesis
6	2e-04	13 / 25	ventricular cardiac muscle tissue morphogenesis
7	4e-04	320 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
8	8e-04	14 / 31	ATP-dependent chromatin remodeling
9	9e-04	133 / 541	negative regulation of transcription, DNA-templated
10	1e-03	148 / 613	positive regulation of transcription, DNA-templated
11	2e-03	10 / 20	response to vitamin A
12	3e-03	7 / 12	estrogen biosynthetic process
13	3e-03	9 / 18	natural killer cell activation involved in immune response
14	3e-03	36 / 121	defense response
15	3e-03	242 / 1080	multicellular organism development

K-Means Cluster

Spot Summary: Q

metagenes = 97

genes = 5140

<r> metagenes = 0.79

beta: r2= 5.87 / log p= -Inf

samples with spot = 20 (14.6 %)

group 1 : 1 (9.1 %)

group 2 : 1 (16.7 %)

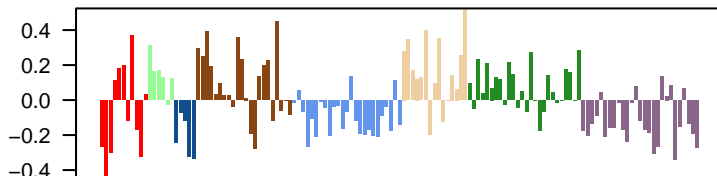
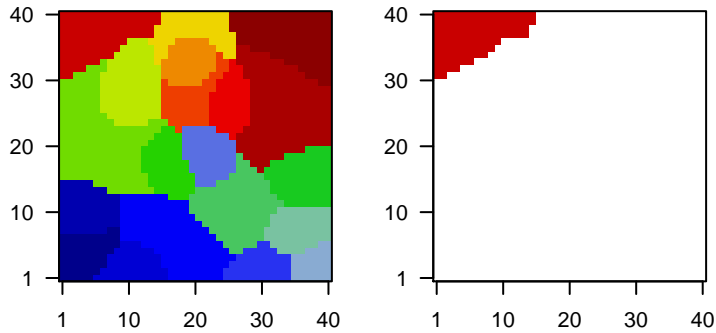
group 4 : 7 (31.8 %)

group 6 : 6 (40 %)

group 7 : 5 (19.2 %)

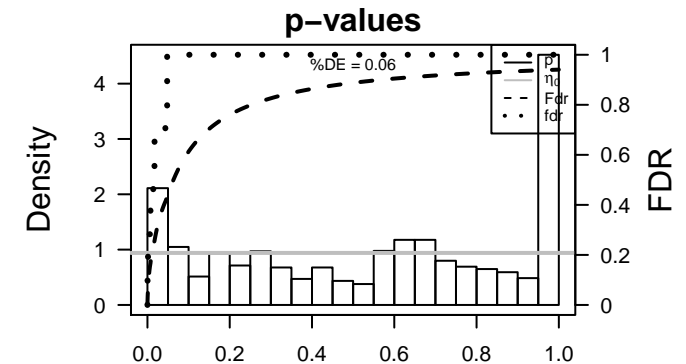
Overview Map

Spot



Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-13	70 / 342	BP chromatin organization
2	9e-13	77 / 400	BP chromatin binding
3	4e-12	186 / 1387	BP regulation of transcription, DNA-templated
4	2e-10	494 / 4740	BP cytosol
5	5e-10	153 / 1145	BP regulation of transcription by RNA polymerase II
6	5e-09	143 / 1086	BP positive regulation of transcription by RNA polymerase II
7	7e-09	612 / 6202	BP cytoplasm
8	2e-08	76 / 484	BP cellular response to DNA damage stimulus
9	9e-08	171 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
10	1e-07	71 / 459	BP viral process
11	1e-07	106 / 783	BP negative regulation of transcription by RNA polymerase II
12	9e-07	86 / 623	BP protein phosphorylation
13	1e-06	77 / 541	BP negative regulation of transcription, DNA-templated
14	3e-06	40 / 227	BP microtubule binding
15	4e-06	16 / 54	BP DNA duplex unwinding
16	8e-06	54 / 358	BP mRNA processing
17	9e-06	83 / 630	BP cell cycle
18	9e-06	83 / 630	BP protein transport
19	1e-05	7 / 12	BP centriole-centriole cohesion
20	2e-05	87 / 684	BP phosphorylation
21	2e-05	57 / 400	BP protein serine/threonine kinase activity
22	3e-05	10 / 27	BP regulation of cell morphogenesis
23	3e-05	19 / 83	BP thiol-dependent ubiquitin-specific protease activity
24	5e-05	43 / 281	BP ubiquitin-dependent protein catabolic process
25	8e-05	10 / 30	BP ATP-dependent DNA helicase activity
26	1e-04	10 / 31	BP ATP-dependent chromatin remodeling
27	2e-04	20 / 101	BP mRNA transport
28	2e-04	41 / 279	BP RNA splicing
29	2e-04	20 / 102	BP chromatin remodeling
30	2e-04	24 / 134	BP cell cycle arrest
31	2e-04	8 / 22	BP sister chromatid cohesion
32	2e-04	50 / 366	BP DNA repair
33	3e-04	6 / 13	BP negative regulation of protein localization to nucleus
34	3e-04	7 / 18	BP myelination in peripheral nervous system
35	4e-04	52 / 394	BP cell division
36	5e-04	21 / 117	BP negative regulation of cell migration
37	5e-04	7 / 19	BP nucleosome disassembly
38	5e-04	7 / 19	BP regulation of DNA replication
39	5e-04	7 / 19	BP TOR signaling
40	5e-04	18 / 94	BP RNA processing



BP

Rank	p-value	#in/all	Geneset
1	5e-13	70 / 342	chromatin organization
2	9e-13	77 / 400	chromatin binding
3	4e-12	186 / 1387	regulation of transcription, DNA-templated
4	2e-10	494 / 4740	cytosol
5	5e-10	153 / 1145	regulation of transcription by RNA polymerase II
6	5e-09	143 / 1086	positive regulation of transcription by RNA polymerase II
7	7e-09	612 / 6202	cytoplasm
8	2e-08	76 / 484	cellular response to DNA damage stimulus
9	9e-08	171 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
10	1e-07	71 / 459	viral process
11	1e-07	106 / 783	negative regulation of transcription by RNA polymerase II
12	9e-07	86 / 623	protein phosphorylation
13	1e-06	77 / 541	negative regulation of transcription, DNA-templated
14	3e-06	40 / 227	microtubule binding
15	4e-06	16 / 54	DNA duplex unwinding

K-Means Cluster

Spot Summary: R

metagenes = 53
genes = 1700

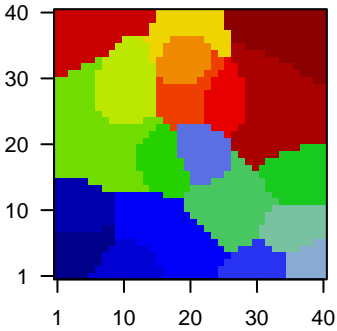
<r> metagenes = 0.86

beta: r2= 7.11 / log p= -Inf

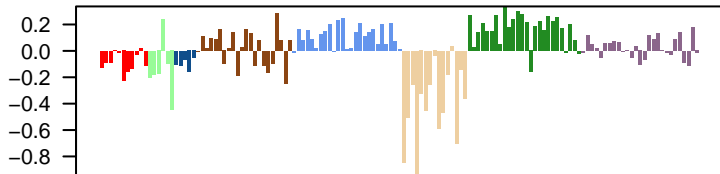
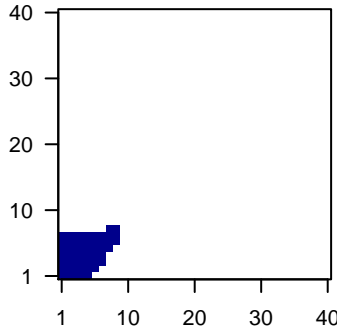
samples with spot = 20 (14.6 %)

- group 2 : 1 (16.7 %)
- group 4 : 1 (4.5 %)
- group 5 : 5 (20 %)
- group 7 : 13 (50 %)

Overview Map



Spot

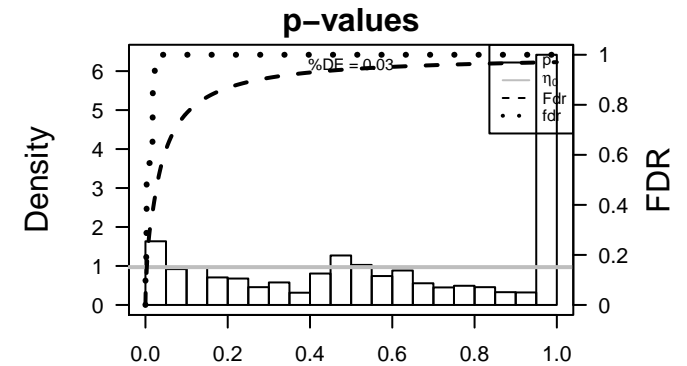


Spot Genelist

Rank	ID	max e	r	min e	Description
1	209772_s_at	2.62	-1.89	0.42	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645]
2	214079_at	2.54	-1.07	0.26	DHRS2 dehydrogenase/reductase 2 [Source:HGNC Symbol;Acc:HGNC:1645]
3	242977_at	2.4	-0.78	0.33	novel transcript
4	1559712_at	2.36	-0.81	0.38	long intergenic non-protein coding RNA 689 [Source:HGNC Symbol;Acc:HGNC:1645]
5	244308_at	2.27	-0.7	0.36	novel transcript
6	1559992_a_at	2.23	-1.21	0.3	long intergenic non-protein coding RNA 645 [Source:HGNC Symbol;Acc:HGNC:1645]
7	215442_s_at	2.13	-0.8	0.35	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645]
8	211879_x_at	2.13	-1.2	0.39	PCDHGA7 protocadherin gamma subfamily A, 3 [Source:HGNC Symbol;Acc:HGNC:1645]
9	210055_at	2.09	-1.37	0.37	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645]
10	208650_s_at	2.09	-2.09	0.32	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645]
11	1569481_s_at	2.03	-0.89	0.38	SNX22 sorting nexin 22 [Source:HGNC Symbol;Acc:HGNC:16315]
12	238717_at	2	-1.03	0.29	novel transcript
13	1568795_at	2	-0.94	0.45	novel transcript
14	1552662_a_at	1.99	-1.09	0.3	PCDHGB7 protocadherin gamma subfamily B, 7 [Source:HGNC Symbol;Acc:HGNC:1645]
15	216379_x_at	1.99	-2.67	0.26	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
16	205947_s_at	1.98	-1.02	0.45	VIPR2 vasoactive intestinal peptide receptor 2 [Source:HGNC Symbol;Acc:HGNC:1645]
17	1558463_s_at	1.98	-0.77	0.42	novel transcript
18	243261_at	1.98	-1.19	0.29	novel transcript
19	225149_at	1.96	-1.21	0.55	PCID2 PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:1645]
20	231737_at	1.95	-0.93	0.56	CACNG4 calcium voltage-gated channel auxiliary subunit gamma 4 [Source:HGNC Symbol;Acc:HGNC:1645]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-25	173 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	2e-25	150 / 1145	BP regulation of transcription by RNA polymerase II
3	4e-24	167 / 1387	BP regulation of transcription, DNA-templated
4	3e-11	53 / 366	BP DNA repair
5	4e-11	92 / 843	BP DNA-binding transcription factor activity
6	6e-09	58 / 484	BP cellular response to DNA damage stimulus
7	2e-08	45 / 342	BP chromatin organization
8	8e-07	35 / 267	BP ubiquitin-protein transferase activity
9	2e-06	56 / 545	BP protein ubiquitination
10	3e-06	316 / 4740	BP cytosol
11	4e-06	398 / 6202	BP cytoplasm
12	1e-05	91 / 1086	BP positive regulation of transcription by RNA polymerase II
13	2e-05	20 / 129	BP rhythmic process
14	3e-05	52 / 541	BP negative regulation of transcription, DNA-templated
15	3e-05	57 / 613	BP positive regulation of transcription, DNA-templated
16	3e-05	31 / 264	BP transcription by RNA polymerase II
17	4e-05	41 / 400	BP chromatin binding
18	8e-05	26 / 215	BP ubiquitin protein ligase activity
19	1e-04	31 / 281	BP ubiquitin-dependent protein catabolic process
20	1e-04	14 / 83	BP thiol-dependent ubiquitin-specific protease activity
21	2e-04	55 / 630	BP protein transport
22	3e-04	12 / 70	BP transcription elongation from RNA polymerase II promoter
23	4e-04	5 / 13	BP regulation of mRNA splicing, via spliceosome
24	4e-04	35 / 358	BP mRNA processing
25	6e-04	6 / 21	BP response to X-ray
26	6e-04	6 / 21	BP spinal cord motor neuron differentiation
27	7e-04	63 / 783	BP negative regulation of transcription by RNA polymerase II
28	7e-04	9 / 47	BP response to UV
29	7e-04	18 / 146	BP homophilic cell adhesion via plasma membrane adhesion molecules
30	1e-03	69 / 887	BP cell differentiation
31	1e-03	8 / 40	BP cytoplasmic microtubule organization
32	1e-03	5 / 16	BP positive regulation of ossification
33	1e-03	5 / 16	BP somite development
34	1e-03	5 / 16	BP sympathetic nervous system development
35	1e-03	7 / 32	BP embryonic cranial skeleton morphogenesis
36	1e-03	8 / 41	BP limb development
37	1e-03	13 / 93	BP Golgi organization
38	1e-03	10 / 61	BP double-strand break repair via nonhomologous end joining
39	1e-03	6 / 24	BP mRNA cis splicing, via spliceosome
40	1e-03	24 / 233	BP heart development



BP

Rank	p-value	#in/all	Geneset
1	1e-25	173 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
2	2e-25	150 / 1145	regulation of transcription by RNA polymerase II
3	4e-24	167 / 1387	regulation of transcription, DNA-templated
4	3e-11	53 / 366	DNA repair
5	4e-11	92 / 843	DNA-binding transcription factor activity
6	6e-09	58 / 484	cellular response to DNA damage stimulus
7	2e-08	45 / 342	chromatin organization
8	8e-07	35 / 267	ubiquitin-protein transferase activity
9	2e-06	56 / 545	protein ubiquitination
10	3e-06	316 / 4740	cytosol
11	4e-06	398 / 6202	cytoplasm
12	1e-05	91 / 1086	positive regulation of transcription by RNA polymerase II
13	2e-05	20 / 129	rhythmic process
14	3e-05	52 / 541	negative regulation of transcription, DNA-templated
15	3e-05	57 / 613	positive regulation of transcription, DNA-templated

K-Means Cluster

Spot Summary: S

metagenes = 137
genes = 3919

<r> metagenes = 0.67

beta: r2= 1.64 / log p= -Inf

samples with spot = 1 (0.7 %)
group 7 : 1 (3.8 %)

Spot Genelist

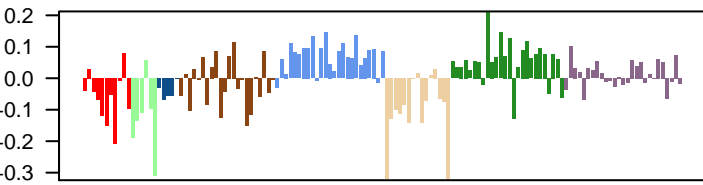
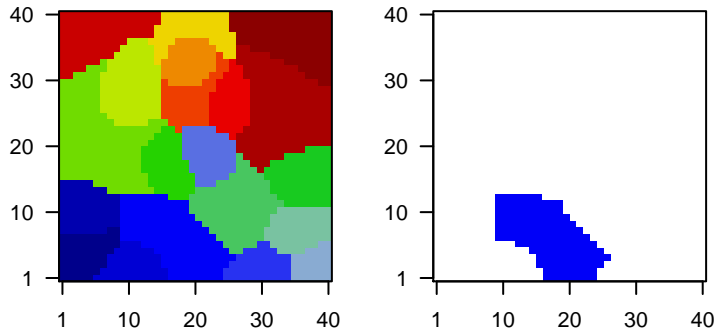
Rank	ID	max e	r	min e	Description
1	209942_x_at	3.15	-0.38	0.06	MAGEA3MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC
2	1555557_a_a	2.39	-0.52	0.25	microRNA 6829 [Source:HGNC Symbol;Acc:HGNC:50055]
3	229347_at	2.15	-1.11	0.11	MIR4458 host gene [Source:HGNC Symbol;Acc:HGNC:4900
4	228564_at	2.11	-0.92	0.2	long intergenic non-protein coding RNA 1116 [Source:HGNC
5	211877_s_at	2.07	-0.62	0.1	PCDHGA1rbt cadherin gamma subfamily A, 11 [Source:HGNC Symbc
6	206159_at	2.05	-1.3	0.29	GDF10 growth differentiation factor 10 [Source:HGNC Symbol;Acc:H
7	202859_x_at	1.99	-0.68	0.16	CXCL8 C-X-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
8	228202_at	1.94	-1.02	0.24	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
9	210155_at	1.93	-0.46	0.15	MYOC myocilin [Source:HGNC Symbol;Acc:HGNC:7610]
10	208387_s_at	1.88	-0.45	0.27	MMP24 matrix metalloproteinase 24 [Source:HGNC Symbol;Acc:HGN
11	240964_at	1.87	-0.56	0.38	PTEN phosphatase and tensin homolog [Source:HGNC Symbol;Acc
12	1556545_at	1.86	-0.79	0.26	TEC
13	237622_at	1.86	-0.77	0.21	ACO1 aconitase 1 [Source:HGNC Symbol;Acc:HGNC:117]
14	239078_at	1.86	-0.64	0.26	BROX BRO1 domain and CAAX motif containing [Source:HGNC Syr
15	208334_at	1.84	-1.17	0.38	NDST4 N-deacetylase and N-sulfotransferase 4 [Source:HGNC Syrr
16	207276_at	1.83	-0.93	0.11	CDR1 cerebellar degeneration related protein 1 [Source:HGNC Syrr
17	1562102_at	1.79	-0.66	0.32	
18	241933_at	1.78	-0.7	0.3	QRSL1 QRSL1, glutamyl-tRNA amidotransferase subunit A [Source
19	205262_at	1.72	-1.26	0.25	KCNH2 potassium voltage-gated channel subfamily H member 2 [So
20	234355_s_at	1.69	-0.68	0.22	DISP3 dispatched RND transporter family member 3 [Source:HGNC

Geneset Overrepresentation

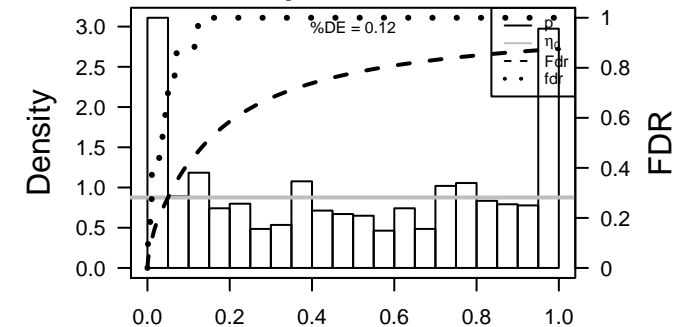
Rank	p-value	#in/all	Geneset
1	1e-51	898 / 4740	BP cytosol
2	2e-38	1053 / 6202	BP cytoplasm
3	5e-26	313 / 1435	BP mitochondrion
4	2e-23	168 / 630	BP protein transport
5	1e-18	141 / 545	BP protein ubiquitination
6	9e-18	104 / 358	BP mRNA processing
7	8e-17	76 / 229	BP mRNA splicing, via spliceosome
8	3e-14	79 / 267	BP ubiquitin-protein transferase activity
9	1e-12	78 / 279	BP RNA splicing
10	2e-12	86 / 324	BP intracellular protein transport
11	4e-12	68 / 234	BP protein deubiquitination
12	3e-11	75 / 281	BP ubiquitin-dependent protein catabolic process
13	4e-11	55 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
14	4e-10	47 / 149	BP protein folding
15	4e-10	60 / 215	BP ubiquitin protein ligase activity
16	6e-10	71 / 276	BP translation
17	5e-09	104 / 484	BP cellular response to DNA damage stimulus
18	8e-09	66 / 264	BP vesicle-mediated transport
19	2e-08	203 / 1145	BP regulation of transcription by RNA polymerase II
20	7e-08	29 / 83	BP thiol-dependent ubiquitin-specific protease activity
21	9e-08	57 / 228	BP protein polyubiquitination
22	1e-07	74 / 328	BP post-translational protein modification
23	1e-07	47 / 176	BP endoplasmic reticulum to Golgi vesicle-mediated transport
24	2e-07	24 / 63	BP ubiquitin-dependent ERAD pathway
25	2e-07	36 / 120	BP translational initiation
26	3e-07	22 / 56	BP mRNA 3'-end processing
27	4e-07	39 / 139	BP regulation of translation
28	4e-07	20 / 49	BP RNA metabolic process
29	1e-06	118 / 630	BP cell cycle
30	1e-06	24 / 70	BP transcription elongation from RNA polymerase II promoter
31	2e-06	207 / 1242	BP Golgi apparatus
32	2e-06	25 / 76	BP negative regulation of translation
33	2e-06	76 / 366	BP DNA repair
34	3e-06	19 / 50	BP protein K48-linked ubiquitination
35	4e-06	23 / 69	BP snRNA transcription by RNA polymerase II
36	5e-06	27 / 89	BP macroautophagy
37	5e-06	1008 / 7387	BP membrane
38	6e-06	21 / 61	BP regulation of alternative mRNA splicing, via spliceosome
39	1e-05	78 / 394	BP cell division
40	1e-05	88 / 459	BP viral process

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	1e-51	898 / 4740	cytosol
2	2e-38	1053 / 6202	cytoplasm
3	5e-26	313 / 1435	mitochondrion
4	2e-23	168 / 630	protein transport
5	1e-18	141 / 545	protein ubiquitination
6	9e-18	104 / 358	mRNA processing
7	8e-17	76 / 229	mRNA splicing, via spliceosome
8	3e-14	79 / 267	ubiquitin-protein transferase activity
9	1e-12	78 / 279	RNA splicing
10	2e-12	86 / 324	intracellular protein transport
11	4e-12	68 / 234	protein deubiquitination
12	3e-11	75 / 281	ubiquitin-dependent protein catabolic process
13	4e-11	55 / 179	proteasome-mediated ubiquitin-dependent protein catabolic process
14	4e-10	47 / 149	protein folding
15	4e-10	60 / 215	ubiquitin protein ligase activity

K-Means Cluster

Spot Summary: T

metagenes = 46
genes = 1626

<r> metagenes = 0.91

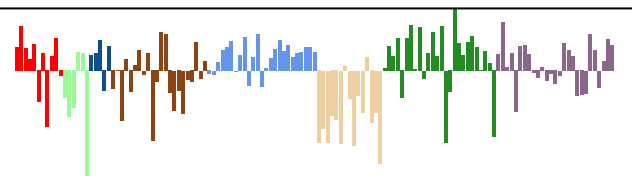
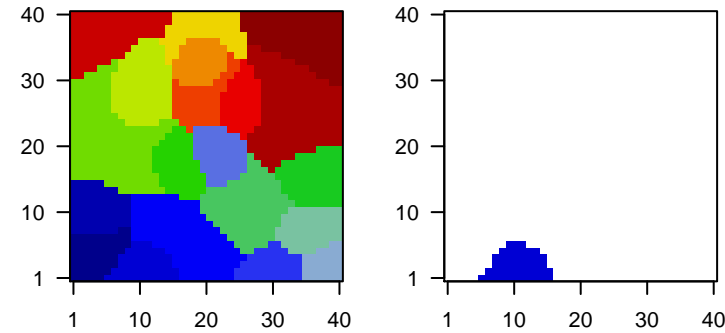
beta: r2= 6.8 / log p= -Inf

samples with spot = 22 (16.1 %)

- group 1 : 2 (18.2 %)
- group 3 : 1 (20 %)
- group 4 : 3 (13.6 %)
- group 5 : 4 (16 %)
- group 7 : 9 (34.6 %)
- group 8 : 3 (11.1 %)

Overview Map

Spot

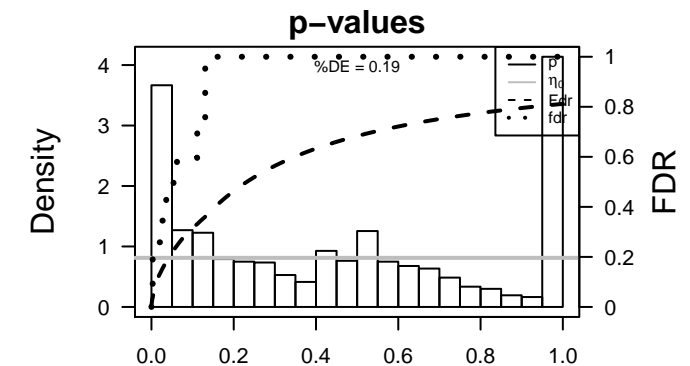


Spot Genelist

Rank	ID	max e	r	min e	Description
1	220241_at	2.56	-0.78	0.59	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Sy
2	203838_s_at	2.27	-0.97	0.44	TNK2 tyrosine kinase non receptor 2 [Source:HGNC Symbol;Acc:Hi
3	207978_s_at	2.12	-0.97	0.37	NR4A3 nuclear receptor subfamily 4 group A member 3 [Source:HGNC
4	220240_s_at	2.09	-1.17	0.69	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Sy
5	1555191_a_a	2.06	-0.78	0.52	FHL5 four and a half LIM domains 5 [Source:HGNC Symbol;Acc:HC
6	211607_x_at	2.06	-1.23	0.58	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
7	208889_s_at	2.05	-0.58	0.35	NCOR2 nuclear receptor corepressor 2 [Source:HGNC Symbol;Acc:H
8	210984_x_at	2	-1.3	0.56	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
9	201551_s_at	1.99	-1.97	0.48	LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Sy
10	200879_s_at	1.97	-1.12	0.64	EPAS1 endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc
11	216488_s_at	1.96	-1.14	0.53	ATP11A ATPase phospholipid transporting 11A [Source:HGNC Symbc
12	211899_s_at	1.87	-0.82	0.33	TRAF4 TNF receptor associated factor 4 [Source:HGNC Symbol;Acc
13	218948_at	1.84	-1.47	0.5	QRSL1 QRSL1, glutaminyl-tRNA amidotransferase subunit A [Source
14	207151_at	1.8	-0.85	0.58	ADCYAP1 ADCYAP receptor type I [Source:HGNC Symbol;Acc:HGNC:2
15	210790_s_at	1.8	-0.94	0.43	SAR1A secretion associated Ras related GTPase 1A [Source:HGNC
16	212940_at	1.79	-0.75	0.43	COL6A1 collagen type VI alpha 1 chain [Source:HGNC Symbol;Acc:Hi
17	204707_s_at	1.78	-0.7	0.47	MAPK4 mitogen-activated protein kinase 4 [Source:HGNC Symbol;A
18	230445_at	1.77	-1.09	0.42	BTBD17 BTB domain containing 17 [Source:HGNC Symbol;Acc:HGNC
19	222501_s_at	1.75	-1.44	0.75	REPIN1 replication initiator 1 [Source:HGNC Symbol;Acc:HGNC:1792
20	210973_s_at	1.72	-1.13	0.45	FGFR1 fibroblast growth factor receptor 1 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-45	490 / 4740	BP cytosol
2	1e-37	570 / 6202	BP cytoplasm
3	1e-34	637 / 7387	BP membrane
4	4e-20	155 / 1242	BP Golgi apparatus
5	3e-19	98 / 630	BP protein transport
6	5e-14	57 / 324	BP intracellular protein transport
7	4e-13	49 / 264	BP vesicle-mediated transport
8	1e-10	53 / 350	BP GTP binding
9	4e-10	29 / 132	BP membrane organization
10	4e-09	331 / 4278	BP plasma membrane
11	7e-09	136 / 1435	BP mitochondrion
12	2e-08	58 / 459	BP viral process
13	4e-08	76 / 684	BP phosphorylation
14	4e-08	31 / 179	BP protein dephosphorylation
15	5e-08	86 / 815	BP protein homodimerization activity
16	9e-08	17 / 64	BP response to unfolded protein
17	1e-07	59 / 496	BP negative regulation of apoptotic process
18	2e-07	28 / 162	BP dephosphorylation
19	8e-07	67 / 623	BP protein phosphorylation
20	1e-06	53 / 455	BP intracellular signal transduction
21	1e-06	28 / 176	BP endoplasmic reticulum to Golgi vesicle-mediated transport
22	1e-06	20 / 101	BP mRNA transport
23	1e-06	18 / 84	BP ephrin receptor signaling pathway
24	1e-06	23 / 129	BP rhythmic process
25	1e-06	60 / 545	BP protein ubiquitination
26	1e-06	24 / 139	BP regulation of translation
27	2e-06	11 / 34	BP membrane fusion
28	2e-06	31 / 214	BP cell migration
29	3e-06	17 / 80	BP response to endoplasmic reticulum stress
30	4e-06	16 / 74	BP retrograde transport, endosome to Golgi
31	5e-06	27 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
32	8e-06	46 / 400	BP protein serine/threonine kinase activity
33	9e-06	27 / 185	BP endocytosis
34	1e-05	10 / 33	BP regulation of cholesterol biosynthetic process
35	1e-05	14 / 63	BP ubiquitin-dependent ERAD pathway
36	1e-05	17 / 89	BP macroautophagy
37	2e-05	38 / 315	BP positive regulation of GTPase activity
38	2e-05	23 / 149	BP protein folding
39	2e-05	8 / 22	BP phosphatidylinositol dephosphorylation
40	2e-05	22 / 141	BP regulation of cell shape



BP

Rank	p-value	#in/all	Geneset
1	8e-45	490 / 4740	cytosol
2	1e-37	570 / 6202	cytoplasm
3	1e-34	637 / 7387	membrane
4	4e-20	155 / 1242	Golgi apparatus
5	3e-19	98 / 630	protein transport
6	5e-14	57 / 324	intracellular protein transport
7	4e-13	49 / 264	vesicle-mediated transport
8	1e-10	53 / 350	GTP binding
9	4e-10	29 / 132	membrane organization
10	4e-09	331 / 4278	plasma membrane
11	7e-09	136 / 1435	mitochondrion
12	2e-08	58 / 459	viral process
13	4e-08	76 / 684	phosphorylation
14	4e-08	31 / 179	protein dephosphorylation
15	5e-08	86 / 815	protein homodimerization activity