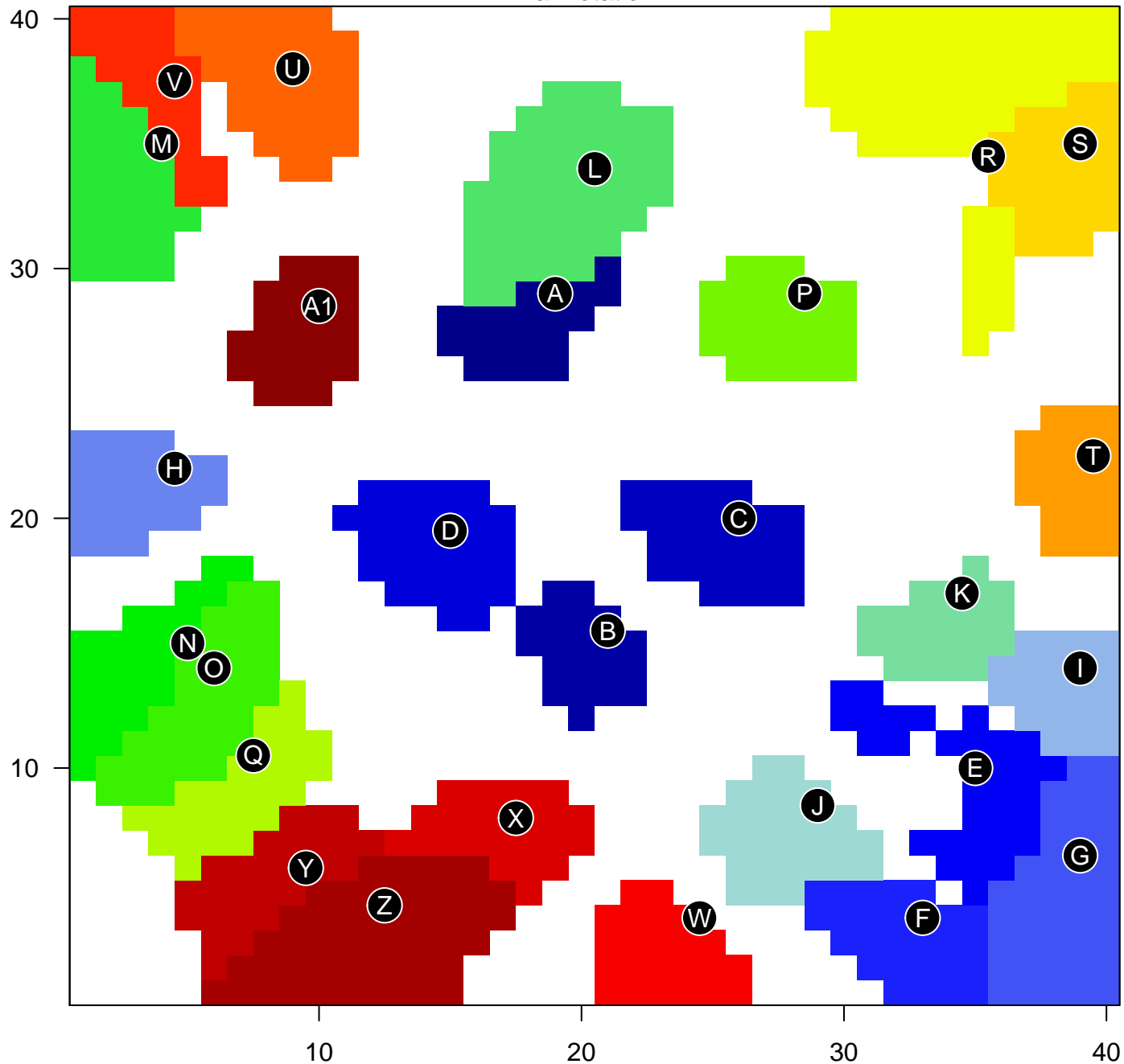


Correlation Cluster

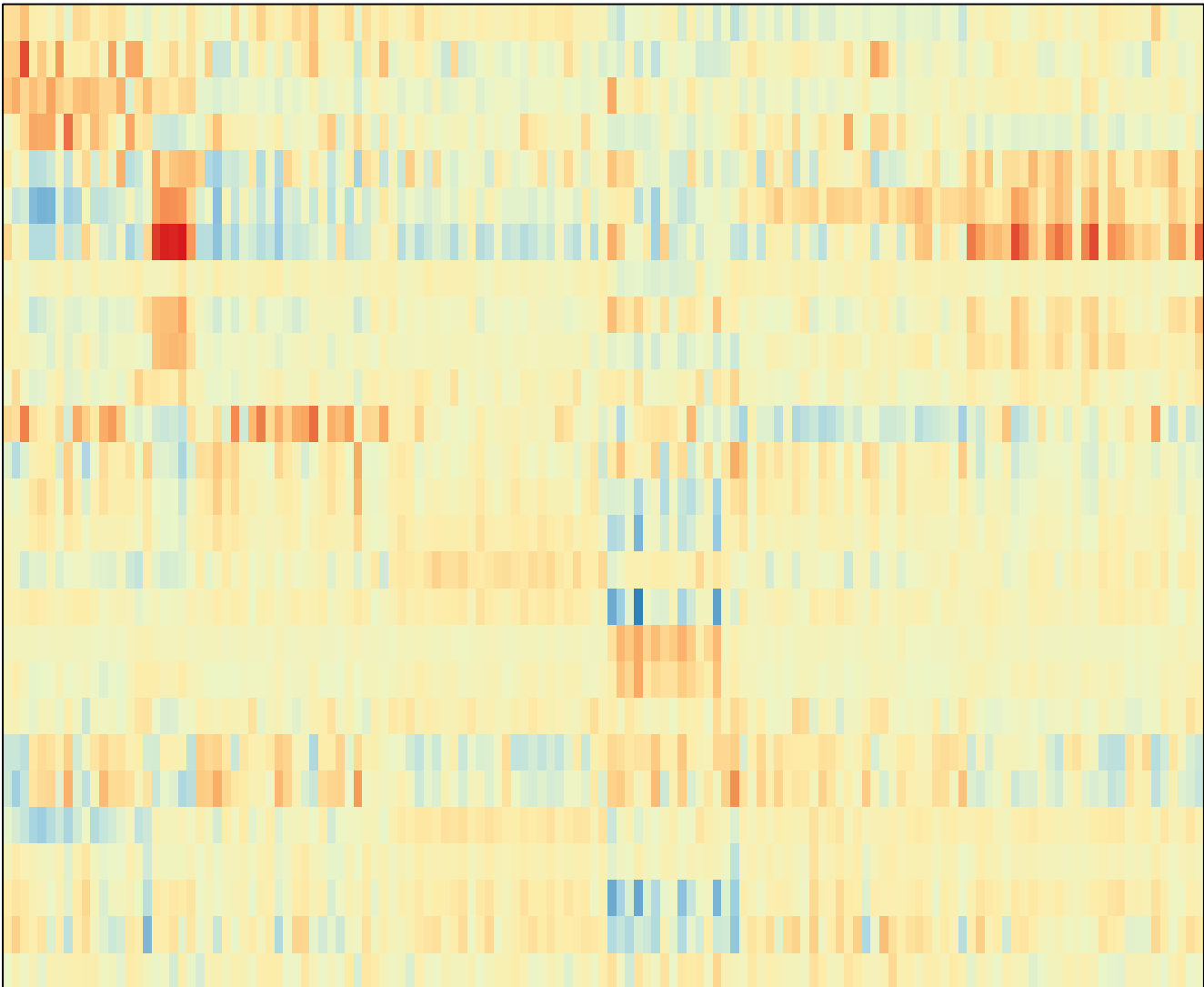
annotation



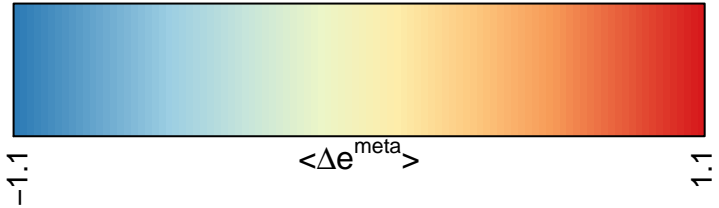
- A Golgi apparatus
- membrane
- B angiogenesis
- extracellular matrix organization
- C cilium movement
- cilium-dependent cell motility
- D cell cycle
- cell division
- E membrane
- plasma membrane
- F plasma membrane
- synapse
- G synapse
- chemical synaptic transmission
- H ATP-dependent microtubule motor activity, minus-end-dire
- positive regulation of response to DNA damage stimulus
- I membrane
- plasma membrane
- J cytosol
- cytoplasm
- K cell differentiation
- exogenous drug catabolic process
- L immune system process
- immune response
- M chromatin organization
- regulation of transcription, DNA-templated
- N mRNA processing
- cellular response to DNA damage stimulus
- O mRNA processing
- regulation of transcription by RNA polymerase II
- P cytosol
- cytoplasm
- Q regulation of transcription by RNA polymerase II
- regulation of transcription, DNA-templated
- R keratinization
- positive regulation of protein kinase B signaling
- S serine-type endopeptidase activity
- regulation of regulatory T cell differentiation
- T chromatin organization
- chromatin binding
- U cytoplasm
- cytosol
- V vesicle-mediated transport
- histone mRNA catabolic process
- W cytosol
- nervous system development



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- Golgi apparatus
- hemopoietic degranulation
- angiogenesis
- extracellular matrix organization
- plasma membrane
- cilium movement
- cilium movement involved in cell motility
- cell cycle
- DNA replication
- membrane
- plasma membrane
- cytoplasm
- plasma membrane
- membrane
- synapse
- chemical synaptic transmission
- plasma membrane
- ATP-dependent microtubule motor activity minus-end-directed
- protein localization to cell surface
- membrane
- synapse
- cytoplasm
- membrane
- cell differentiation
- exocytosis or catabolic process
- neural crest cell migration
- immune system process
- Innate immune response
- chromatin organization
- regulation of transcription, DNA-templated
- regulation of transcription by RNA polymerase II
- mRNA processing
- regulation of transcription, DNA-templated
- mRNA processing
- regulation of transcription by RNA polymerase II
- RNA splicing
- cytoplasm
- Wnt signaling pathway
- regulation of transcription by RNA polymerase II
- mRNA processing
- keratinization
- regulation of regulatory T cell differentiation
- serine-type endopeptidase activity
- regulation of synaptic vesicle exocytosis
- chromatin organization
- cytosol
- cytoplasm
- positive regulation of transcription by RNA polymerase II
- vesicle-mediated transport
- telomere maintenance
- cytosol
- nervous system development
- translational initiation
- protein transport
- cytosol
- mitochondrion
- cytosol
- protein transport
- cytosol
- membrane
- mitochondrion
- mitochondrial translational elongation
- mitochondrial translational termination



Correlation Cluster

Spot Summary: A

metagenes = 20
genes = 513

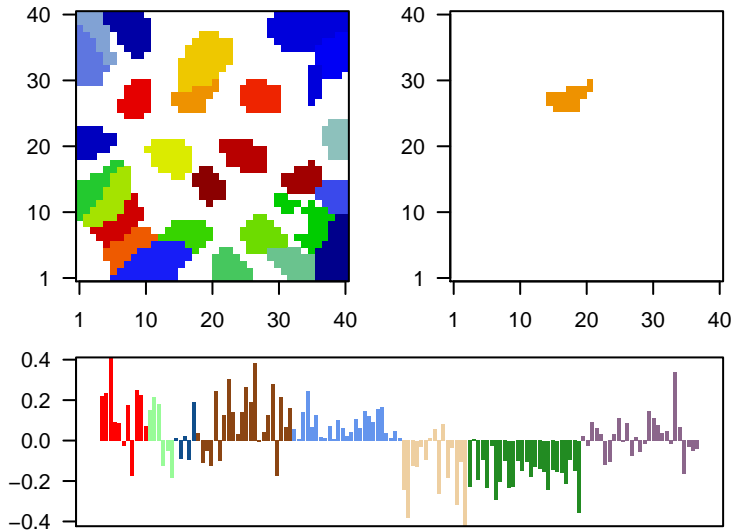
<r> metagenes = 0.95
<r> genes = 0.32
beta: r2= 3.3 / log p= -Inf

samples with spot = 14 (10.2 %)

- group 1 : 5 (45.5 %)
- group 2 : 1 (16.7 %)
- group 4 : 6 (27.3 %)
- group 5 : 1 (4 %)
- group 8 : 1 (3.7 %)

Overview Map

Spot

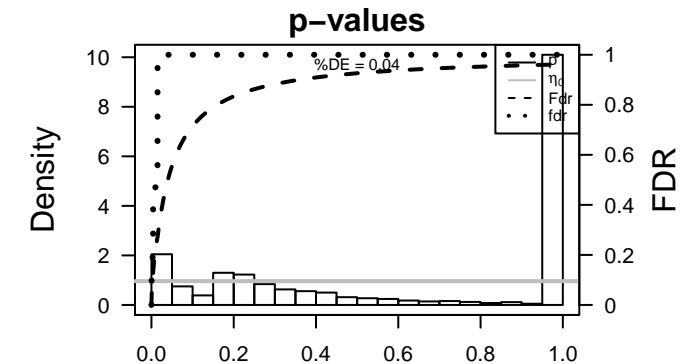


Spot Genelist

Rank	ID	max e	r	min e	Description
1	205225_at	2.58	-0.59	0.33	ESR1 estrogen receptor 1 [Source:HGNC Symbol;Acc:HGNC:3467]
2	1555416_a_a	1.94	-0.43	0.37	ALOX15Barachidonate 15-lipoxygenase, type B [Source:HGNC Symbc
3	204560_at	1.86	-1.38	0.52	FKBP5 FKBP prolyl isomerase 5 [Source:HGNC Symbol;Acc:HGNC:
4	1553775_at	1.83	-0.54	0.28	novel transcript, antisense to GOLGA4
5	225801_at	1.81	-0.89	0.6	FBXO32 F-box protein 32 [Source:HGNC Symbol;Acc:HGNC:16731]
6	208597_at	1.72	-0.55	0.34	CNTF ciliary neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:
7	229947_at	1.71	-0.85	0.34	PI15 peptidase inhibitor 15 [Source:HGNC Symbol;Acc:HGNC:894
8	213094_at	1.7	-1.08	0.52	ADGRG6adhesion G protein-coupled receptor G6 [Source:HGNC Syrr
9	211562_s_at	1.66	-0.6	0.33	LMOD1 leiomodin 1 [Source:HGNC Symbol;Acc:HGNC:6647]
10	1553027_a_a	1.62	-1.26	0.57	KLHL4 kelch like family member 4 [Source:HGNC Symbol;Acc:HGNC
11	209959_at	1.61	-1.14	0.46	NR4A3 nuclear receptor subfamily 4 group A member 3 [Source:HGN
12	1562597_at	1.59	-0.32	0.34	long intergenic non-protein coding RNA 2150 [Source:HGNC
13	216899_s_at	1.56	-1.38	0.72	SKAP2 src kinase associated phosphoprotein 2 [Source:HGNC Symt
14	202134_s_at	1.49	-0.81	0.58	WWTR1 WW domain containing transcription regulator 1 [Source:HGN
15	238583_at	1.47	-0.66	0.41	MSRB3 methionine sulfoxide reductase B3 [Source:HGNC Symbol;Ac
16	227314_at	1.45	-1.37	0.57	ITGA2 integrin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:6
17	235631_at	1.44	-1.29	0.64	DDR2 discoidin domain receptor tyrosine kinase 2 [Source:HGNC S
18	1554127_s_at	1.42	-0.97	0.5	MSRB3 methionine sulfoxide reductase B3 [Source:HGNC Symbol;Ac
19	1553787_at	1.42	-0.6	0.72	C11orf45chromosome 11 open reading frame 45 [Source:HGNC Symt
20	201552_at	1.41	-0.57	0.51	LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Sy

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-11	56 / 1242	BP Golgi apparatus
2	9e-11	189 / 7387	BP membrane
3	6e-10	30 / 460	BP neutrophil degranulation
4	5e-08	56 / 1500	BP signal transduction
5	6e-08	33 / 659	BP apoptotic process
6	1e-07	126 / 4740	BP cytosol
7	7e-07	9 / 59	BP response to cytokine
8	1e-06	34 / 783	BP negative regulation of transcription by RNA polymerase II
9	1e-06	113 / 4278	BP plasma membrane
10	3e-06	149 / 6202	BP cytoplasm
11	1e-05	5 / 18	BP negative regulation of protein localization to plasma membrane
12	1e-05	17 / 289	BP cytokine-mediated signaling pathway
13	1e-05	39 / 1086	BP positive regulation of transcription by RNA polymerase II
14	2e-05	11 / 132	BP membrane organization
15	2e-05	19 / 364	BP inflammatory response
16	2e-05	7 / 50	BP positive regulation of fat cell differentiation
17	3e-05	26 / 613	BP positive regulation of transcription, DNA-templated
18	4e-05	4 / 12	BP negative regulation of interleukin-12 production
19	4e-05	10 / 118	BP platelet degranulation
20	4e-05	12 / 170	BP protein glycosylation
21	4e-05	7 / 55	BP O-glycan processing
22	7e-05	19 / 398	BP positive regulation of gene expression
23	1e-04	11 / 159	BP actin cytoskeleton organization
24	1e-04	5 / 29	BP cytokine production
25	1e-04	4 / 16	BP negative regulation of cytokine production
26	2e-04	10 / 141	BP regulation of cell shape
27	2e-04	14 / 261	BP cell surface receptor signaling pathway
28	2e-04	5 / 32	BP positive regulation of vascular smooth muscle cell proliferation
29	2e-04	7 / 71	BP hemopoiesis
30	3e-04	10 / 148	BP positive regulation of NF-kappaB transcription factor activity
31	3e-04	7 / 74	BP negative regulation of NF-kappaB transcription factor activity
32	3e-04	42 / 1387	BP regulation of transcription, DNA-templated
33	3e-04	18 / 412	BP negative regulation of cell population proliferation
34	4e-04	5 / 37	BP positive regulation of glucose import
35	4e-04	4 / 21	BP regulation of bone mineralization
36	6e-04	3 / 10	BP cellular response to leptin stimulus
37	6e-04	3 / 10	BP oligosaccharide catabolic process
38	6e-04	6 / 60	BP positive regulation of smooth muscle cell proliferation
39	7e-04	5 / 41	BP receptor internalization
40	8e-04	5 / 42	BP toll-like receptor signaling pathway



BP

Rank	p-value	#in/all	Geneset
1	5e-11	56 / 1242	Golgi apparatus
2	9e-11	189 / 7387	membrane
3	6e-10	30 / 460	neutrophil degranulation
4	5e-08	56 / 1500	signal transduction
5	6e-08	33 / 659	apoptotic process
6	1e-07	126 / 4740	cytosol
7	7e-07	9 / 59	response to cytokine
8	1e-06	34 / 783	negative regulation of transcription by RNA polymerase II
9	1e-06	113 / 4278	plasma membrane
10	3e-06	149 / 6202	cytoplasm
11	1e-05	5 / 18	negative regulation of protein localization to plasma membrane
12	1e-05	17 / 289	cytokine-mediated signaling pathway
13	1e-05	39 / 1086	positive regulation of transcription by RNA polymerase II
14	2e-05	11 / 132	membrane organization
15	2e-05	19 / 364	inflammatory response

Correlation Cluster

Spot Summary: B

metagenes = 20
genes = 464

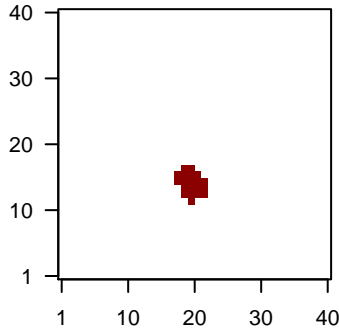
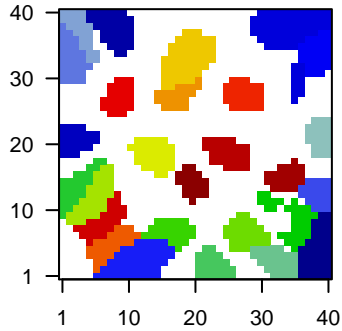
<r> metagenes = 0.92
<r> genes = 0.31
beta: r2= 4.02 / log p= -Inf

samples with spot = 17 (12.4 %)

- group 1 : 6 (54.5 %)
- group 2 : 3 (50 %)
- group 3 : 1 (20 %)
- group 4 : 3 (13.6 %)
- group 5 : 2 (8 %)
- group 7 : 2 (7.7 %)

Overview Map

Spot

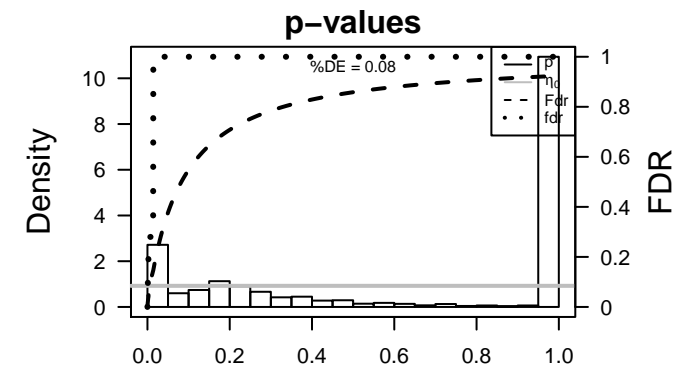
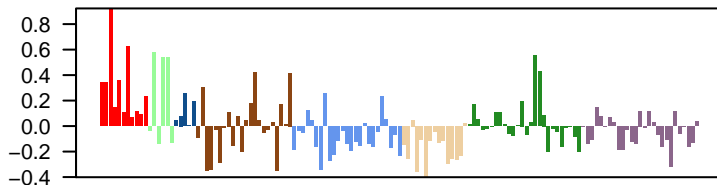


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	230746_s_at	2.67	-0.7	0.68	
2	203936_s_at	2.62	-0.5	0.45	MMP9 matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC:11373]
3	201852_x_at	2.61	-1.76	0.78	COL3A1 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:11373]
4	225681_at	2.53	-1.34	0.74	CTHRC1 collagen triple helix repeat containing 1 [Source:HGNC Symbol;Acc:HGNC:11373]
5	1552575_a_at	2.46	-0.51	0.41	C6orf141 chromosome 6 open reading frame 141 [Source:HGNC Symbol;Acc:HGNC:11373]
6	204595_s_at	2.44	-0.67	0.64	STC1 stanniocalcin 1 [Source:HGNC Symbol;Acc:HGNC:11373]
7	201438_at	2.43	-0.93	0.71	COL6A3 collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:HGNC:11373]
8	205828_at	2.38	-0.4	0.26	MMP3 matrix metallopeptidase 3 [Source:HGNC Symbol;Acc:HGNC:11373]
9	215076_s_at	2.34	-1.7	0.75	COL3A1 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:11373]
10	218730_s_at	2.32	-0.77	0.43	OGN osteoglycin [Source:HGNC Symbol;Acc:HGNC:8126]
11	211161_s_at	2.32	-1.4	0.81	COL3A1 collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:11373]
12	209278_s_at	2.32	-0.44	0.4	TFPI2 tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:11373]
13	206766_at	2.28	-0.8	0.65	ITGA10 integrin subunit alpha 10 [Source:HGNC Symbol;Acc:HGNC:11373]
14	202310_s_at	2.27	-1.2	0.67	COL1A1 collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:11373]
15	242680_at	2.26	-0.67	0.52	AVPR1A arginine vasopressin receptor 1A [Source:HGNC Symbol;Acc:HGNC:11373]
16	238835_at	2.25	-0.6	0.52	AVPR1A arginine vasopressin receptor 1A [Source:HGNC Symbol;Acc:HGNC:11373]
17	206528_at	2.23	-0.55	0.32	TRPC6 transient receptor potential cation channel subfamily C member 6 [Source:HGNC Symbol;Acc:HGNC:11373]
18	241942_at	2.22	-0.54	0.63	PXDNL peroxidasin like [Source:HGNC Symbol;Acc:HGNC:26359]
19	1559462_at	2.21	-0.56	0.52	
20	202404_s_at	2.2	-1.26	0.84	COL1A2 collagen type I alpha 2 chain [Source:HGNC Symbol;Acc:HGNC:11373]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-38	47 / 254	BP angiogenesis
2	1e-31	40 / 231	BP extracellular matrix organization
3	2e-25	142 / 4278	BP plasma membrane
4	1e-17	42 / 594	BP cell adhesion
5	7e-17	16 / 57	BP blood vessel development
6	2e-15	174 / 7387	BP membrane
7	2e-13	11 / 30	BP sprouting angiogenesis
8	4e-13	11 / 32	BP blood vessel remodeling
9	1e-11	14 / 84	BP negative regulation of angiogenesis
10	6e-11	16 / 131	BP positive regulation of angiogenesis
11	3e-10	19 / 214	BP cell migration
12	5e-10	10 / 44	BP collagen fibril organization
13	3e-09	18 / 219	BP positive regulation of cell migration
14	4e-09	8 / 28	BP branching involved in blood vessel morphogenesis
15	5e-09	15 / 152	BP leukocyte migration
16	5e-09	8 / 29	BP blood vessel morphogenesis
17	7e-09	6 / 12	BP lymph vessel development
18	2e-08	14 / 143	BP cell-cell adhesion
19	2e-08	6 / 14	BP vascular endothelial growth factor signaling pathway
20	3e-08	14 / 148	BP skeletal system development
21	4e-08	7 / 25	BP artery morphogenesis
22	8e-08	8 / 40	BP substrate adhesion-dependent cell spreading
23	1e-07	12 / 115	BP kidney development
24	1e-07	7 / 29	BP endodermal cell differentiation
25	2e-07	9 / 60	BP vasculogenesis
26	2e-07	6 / 19	BP embryonic heart tube development
27	3e-07	16 / 233	BP heart development
28	3e-07	38 / 1080	BP multicellular organism development
29	5e-07	8 / 50	BP positive regulation of endothelial cell migration
30	2e-06	32 / 887	BP cell differentiation
31	2e-06	30 / 815	BP protein homodimerization activity
32	2e-06	7 / 43	BP collagen catabolic process
33	4e-06	5 / 18	BP endocardial cushion morphogenesis
34	4e-06	10 / 111	BP positive regulation of MAPK cascade
35	6e-06	5 / 19	BP positive regulation of endothelial cell apoptotic process
36	7e-06	5 / 20	BP negative regulation of endothelial cell migration
37	8e-06	4 / 10	BP positive regulation of systemic arterial blood pressure
38	8e-06	19 / 412	BP negative regulation of cell population proliferation
39	8e-06	8 / 72	BP positive regulation of endothelial cell proliferation
40	9e-06	7 / 52	BP outflow tract morphogenesis



BP

Rank	p-value	#in/all	Geneset
1	2e-38	47 / 254	angiogenesis
2	1e-31	40 / 231	extracellular matrix organization
3	2e-25	142 / 4278	plasma membrane
4	1e-17	42 / 594	cell adhesion
5	7e-17	16 / 57	blood vessel development
6	2e-15	174 / 7387	membrane
7	2e-13	11 / 30	sprouting angiogenesis
8	4e-13	11 / 32	blood vessel remodeling
9	1e-11	14 / 84	negative regulation of angiogenesis
10	6e-11	16 / 131	positive regulation of angiogenesis
11	3e-10	19 / 214	cell migration
12	5e-10	10 / 44	collagen fibril organization
13	3e-09	18 / 219	positive regulation of cell migration
14	4e-09	8 / 28	branching involved in blood vessel morphogenesis
15	5e-09	15 / 152	leukocyte migration

Correlation Cluster

Spot Summary: C

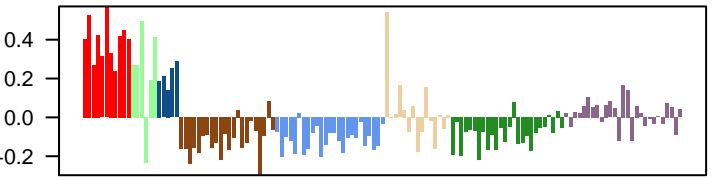
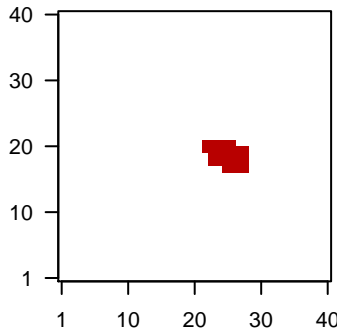
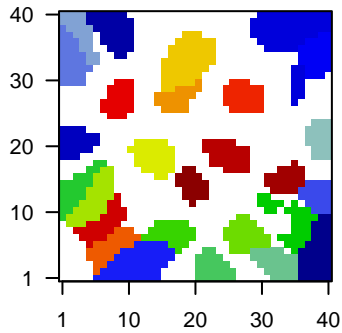
metagenes = 28
genes = 612

<r> metagenes = 0.92
<r> genes = 0.26
beta: r2= 3.45 / log p= -Inf

samples with spot = 19 (13.9 %)
group 1 : 11 (100 %)
group 2 : 4 (66.7 %)
group 3 : 3 (60 %)
group 6 : 1 (6.7 %)

Overview Map

Spot

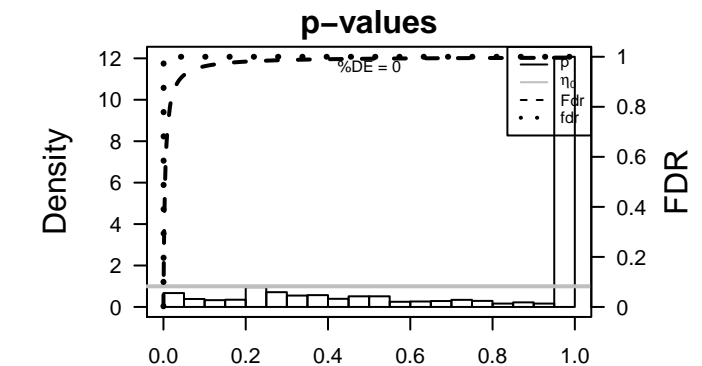


Spot Genelist

Rank	ID	max e	r	min e	Description
1	242883_at	3.11	-0.37	0.58	OTOS otospiralin [Source:HGNC Symbol;Acc:HGNC:22644]
2	206154_at	3.04	-0.83	0.56	RLBP1 retinaldehyde binding protein 1 [Source:HGNC Symbol;Acc:HGNC:206154]
3	220010_at	2.87	-0.81	0.61	ACSL4 acyl-CoA synthetase long chain family member 4 [Source:HGNC Symbol;Acc:HGNC:220010]
4	244731_at	2.72	-0.62	0.61	
5	231133_at	2.62	-0.56	0.67	DRC1 dynein regulatory complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:231133]
6	243087_at	2.6	-0.44	0.59	WDR63 WD repeat domain 63 [Source:HGNC Symbol;Acc:HGNC:243087]
7	209708_at	2.59	-0.95	0.83	MOXD1 monooxygenase DBH like 1 [Source:HGNC Symbol;Acc:HGNC:209708]
8	233516_s_at	2.55	-0.56	0.58	SPAG17 sperm associated antigen 17 [Source:HGNC Symbol;Acc:HGNC:233516]
9	214490_at	2.46	-0.63	0.52	ARSF arylsulfatase F [Source:HGNC Symbol;Acc:HGNC:214490]
10	211564_s_at	2.45	-0.73	0.82	PDLIM4 PDZ and LIM domain 4 [Source:HGNC Symbol;Acc:HGNC:211564]
11	228057_at	2.44	-1.04	0.76	DDIT4L DNA damage inducible transcript 4 like [Source:HGNC Symbol;Acc:HGNC:228057]
12	228307_at	2.37	-1.11	0.73	EMILIN3 elastin microfibril interfacer 3 [Source:HGNC Symbol;Acc:HGNC:228307]
13	231936_at	2.34	-0.45	0.43	HOXC9 homeobox C9 [Source:NCBI gene;Acc:3225]
14	205464_at	2.33	-0.43	0.34	SCNN1B sodium channel epithelial 1 beta subunit [Source:HGNC Symbol;Acc:HGNC:205464]
15	238755_at	2.32	-0.47	0.56	RASSF1 Ras association domain family member 10 [Source:HGNC Symbol;Acc:HGNC:238755]
16	227819_at	2.31	-0.88	0.75	LGR6 leucine rich repeat containing G protein-coupled receptor 6 [Source:HGNC Symbol;Acc:HGNC:227819]
17	1563830_at	2.3	-0.36	0.44	FHAD1 forkhead associated phosphopeptide binding domain 1 [Source:HGNC Symbol;Acc:HGNC:1563830]
18	1556190_s_at	2.29	-0.34	0.5	novel transcript
19	223609_at	2.27	-0.59	0.49	ROPN1L rhophilin associated tail protein 1 like [Source:HGNC Symbol;Acc:HGNC:223609]
20	209496_at	2.26	-0.77	0.84	RARRS2 retinoic acid receptor responder 2 [Source:HGNC Symbol;Acc:HGNC:209496]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-10	10 / 32	BP cilium movement
2	9e-07	6 / 17	BP cilium-dependent cell motility
3	2e-06	5 / 11	BP cilium movement involved in cell motility
4	2e-05	14 / 173	BP cilium assembly
5	6e-05	4 / 11	BP axonemal dynein complex assembly
6	7e-05	5 / 21	BP motile cilium assembly
7	1e-04	169 / 6202	BP cytoplasm
8	2e-04	4 / 14	BP inner dynein arm assembly
9	3e-04	8 / 79	BP microtubule-based movement
10	3e-04	7 / 61	BP flagellated sperm motility
11	4e-04	4 / 17	BP ATP-dependent microtubule motor activity, minus-end-directed
12	4e-04	4 / 17	BP epithelial cilium movement
13	4e-04	4 / 17	BP outer dynein arm assembly
14	6e-04	4 / 19	BP axoneme assembly
15	7e-04	9 / 112	BP motor activity
16	1e-03	27 / 657	BP calcium ion binding
17	1e-03	3 / 10	BP L-phenylalanine catabolic process
18	1e-03	7 / 76	BP microtubule motor activity
19	1e-03	22 / 500	BP catalytic activity
20	2e-03	3 / 12	BP positive regulation of triglyceride biosynthetic process
21	2e-03	9 / 132	BP sensory perception of sound
22	2e-03	3 / 13	BP negative regulation of keratinocyte proliferation
23	4e-03	4 / 30	BP behavioral fear response
24	4e-03	3 / 15	BP definitive hemopoiesis
25	4e-03	6 / 71	BP determination of left/right symmetry
26	4e-03	5 / 50	BP negative regulation of phosphoprotein phosphatase activity
27	5e-03	3 / 17	BP negative regulation of lipid catabolic process
28	5e-03	10 / 180	BP cell projection organization
29	6e-03	9 / 156	BP fatty acid metabolic process
30	7e-03	3 / 19	BP positive regulation of natural killer cell mediated cytotoxicity
31	1e-02	35 / 1080	BP multicellular organism development
32	1e-02	3 / 21	BP positive regulation of neural precursor cell proliferation
33	1e-02	5 / 61	BP negative regulation of signal transduction
34	2e-02	20 / 553	BP oxidoreductase activity
35	2e-02	16 / 416	BP spermatogenesis
36	2e-02	2 / 10	BP carnitine shuttle
37	2e-02	2 / 10	BP cellular aldehyde metabolic process
38	2e-02	2 / 10	BP epithelial cilium movement involved in determination of left/right asymmetry
39	2e-02	2 / 10	BP glial cell migration
40	2e-02	2 / 10	BP glycolipid biosynthetic process



BP

Rank	p-value	#in/all	Geneset
1	8e-10	10 / 32	cilium movement
2	9e-07	6 / 17	cilium-dependent cell motility
3	2e-06	5 / 11	cilium movement involved in cell motility
4	2e-05	14 / 173	cilium assembly
5	6e-05	4 / 11	axonemal dynein complex assembly
6	7e-05	5 / 21	motile cilium assembly
7	1e-04	169 / 6202	cytoplasm
8	2e-04	4 / 14	inner dynein arm assembly
9	3e-04	8 / 79	microtubule-based movement
10	3e-04	7 / 61	flagellated sperm motility
11	4e-04	4 / 17	ATP-dependent microtubule motor activity, minus-end-directed
12	4e-04	4 / 17	epithelial cilium movement
13	4e-04	4 / 17	outer dynein arm assembly
14	6e-04	4 / 19	axoneme assembly
15	7e-04	9 / 112	motor activity

Correlation Cluster

Spot Summary: D

metagenes = 31
genes = 654

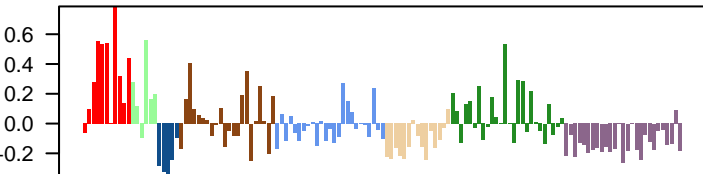
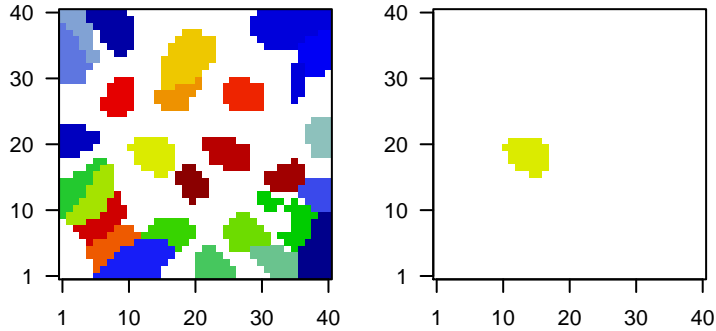
<r> metagenes = 0.93
<r> genes = 0.33
beta: r2= 3.35 / log p= -Inf

samples with spot = 21 (15.3 %)

- group 1 : 7 (63.6 %)
- group 2 : 3 (50 %)
- group 4 : 3 (13.6 %)
- group 5 : 2 (8 %)
- group 7 : 6 (23.1 %)

Overview Map

Spot

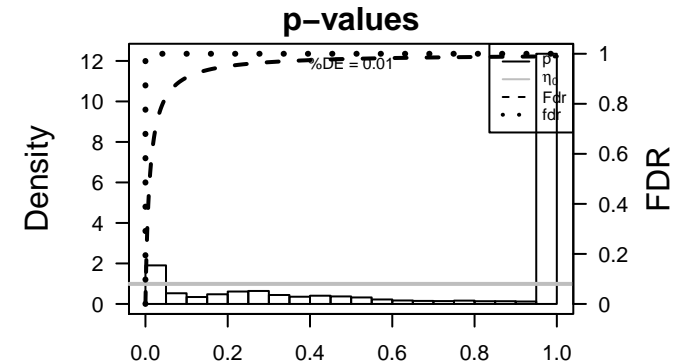


Spot Genelist

Rank	ID	max e	r	min e	Description
1	224588_at	2.97	-2.09	0.22	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588]
2	218308_at	2.79	-0.78	0.77	TACC3 transforming acidic coiled-coil containing protein 3 [Source:HGNC Symbol;Acc:HGNC:218308]
3	227671_at	2.79	-1.83	0.22	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:227671]
4	214218_s_at	2.77	-1.66	0.23	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:214218]
5	207199_at	2.61	-0.63	0.37	TERT telomerase reverse transcriptase [Source:HGNC Symbol;Acc:HGNC:207199]
6	204580_at	2.59	-0.3	0.29	MMP12 matrix metalloproteinase 12 [Source:HGNC Symbol;Acc:HGNC:204580]
7	221728_x_at	2.49	-1.68	0.22	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:221728]
8	1558834_s_at	2.45	-0.78	0.5	AKNAD1 AKNA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1558834]
9	224590_at	2.44	-1.42	0.24	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224590]
10	217373_x_at	2.43	-0.86	0.51	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:217373]
11	205676_at	2.39	-0.65	0.51	CYP27B1 cytochrome P450 family 27 subfamily B member 1 [Source:HGNC Symbol;Acc:HGNC:205676]
12	224589_at	2.34	-1.31	0.23	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224589]
13	211832_s_at	2.27	-0.48	0.36	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:211832]
14	214451_at	2.18	-0.51	0.49	TFAP2B transcription factor AP-2 beta [Source:HGNC Symbol;Acc:HGNC:214451]
15	1559492_at	2.18	-0.71	0.43	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:1559492]
16	226454_at	2.08	-0.5	0.39	MARCH9 membrane associated ring-CH-type finger 9 [Source:HGNC Symbol;Acc:HGNC:226454]
17	230861_at	2.07	-0.7	0.34	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:230861]
18	228033_at	2.04	-0.69	0.84	E2F7 E2F transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:228033]
19	237737_at	1.99	-0.88	0.48	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:237737]
20	237891_at	1.97	-0.78	0.49	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:237891]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-81	117 / 630	BP cell cycle
2	2e-61	83 / 394	BP cell division
3	2e-46	50 / 158	BP DNA replication
4	7e-30	30 / 85	BP chromosome segregation
5	2e-29	52 / 366	BP DNA repair
6	1e-28	37 / 164	BP mitotic cell cycle
7	1e-23	52 / 484	BP cellular response to DNA damage stimulus
8	4e-21	25 / 98	BP G1/S transition of mitotic cell cycle
9	3e-20	27 / 130	BP G2/M transition of mitotic cell cycle
10	1e-17	15 / 33	BP DNA replication initiation
11	2e-16	14 / 31	BP mitotic sister chromatid segregation
12	3e-16	15 / 39	BP CENP-A containing nucleosome assembly
13	2e-13	35 / 400	BP DNA replication binding
14	2e-13	159 / 4740	BP cytosol
15	8e-13	13 / 42	BP mitotic spindle organization
16	9e-13	21 / 145	BP regulation of cell cycle
17	3e-12	189 / 6202	BP cytoplasm
18	3e-12	14 / 56	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
19	3e-12	30 / 327	BP cell population proliferation
20	3e-12	16 / 80	BP regulation of G2/M transition of mitotic cell cycle
21	4e-12	10 / 22	BP regulation of transcription involved in G1/S transition of mitotic cell cycle
22	6e-12	14 / 59	BP regulation of cyclin-dependent protein serine/threonine kinase activity
23	1e-11	13 / 50	BP mitotic cytokinesis
24	7e-11	16 / 97	BP DNA recombination
25	7e-11	10 / 28	BP positive regulation of G2/M transition of mitotic cell cycle
26	1e-10	11 / 39	BP regulation of mitotic nuclear division
27	4e-10	8 / 17	BP DNA replication origin binding
28	4e-10	12 / 54	BP DNA duplex unwinding
29	2e-09	7 / 13	BP kinetochore assembly
30	2e-09	11 / 49	BP interstrand cross-link repair
31	4e-09	13 / 79	BP microtubule-based movement
32	5e-09	8 / 22	BP mitotic spindle assembly checkpoint
33	5e-09	12 / 66	BP double-strand break repair
34	6e-09	16 / 130	BP regulation of signal transduction by p53 class mediator resulting in cell cycle arrest
35	6e-09	13 / 81	BP double-strand break repair via homologous recombination
36	1e-08	9 / 33	BP mitotic cell cycle checkpoint
37	2e-08	9 / 35	BP DNA biosynthetic process
38	2e-08	9 / 35	BP mitotic metaphase plate congression
39	2e-08	6 / 11	BP metaphase plate congression
40	2e-08	20 / 227	BP microtubule binding



BP

Rank	p-value	#in/all	Geneset
1	5e-81	117 / 630	cell cycle
2	2e-61	83 / 394	cell division
3	2e-46	50 / 158	DNA replication
4	7e-30	30 / 85	chromosome segregation
5	2e-29	52 / 366	DNA repair
6	1e-28	37 / 164	mitotic cell cycle
7	1e-23	52 / 484	cellular response to DNA damage stimulus
8	4e-21	25 / 98	G1/S transition of mitotic cell cycle
9	3e-20	27 / 130	G2/M transition of mitotic cell cycle
10	1e-17	15 / 33	DNA replication initiation
11	2e-16	14 / 31	mitotic sister chromatid segregation
12	3e-16	15 / 39	CENP-A containing nucleosome assembly
13	2e-13	35 / 400	chromatin binding
14	2e-13	159 / 4740	cytosol
15	8e-13	13 / 42	mitotic spindle organization

Correlation Cluster

Spot Summary: E

metagenes = 32
genes = 592

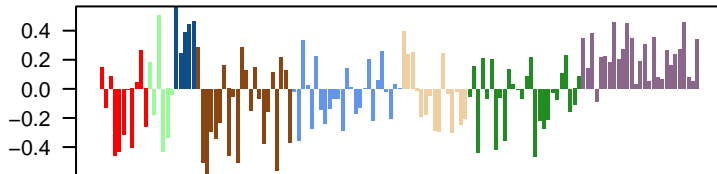
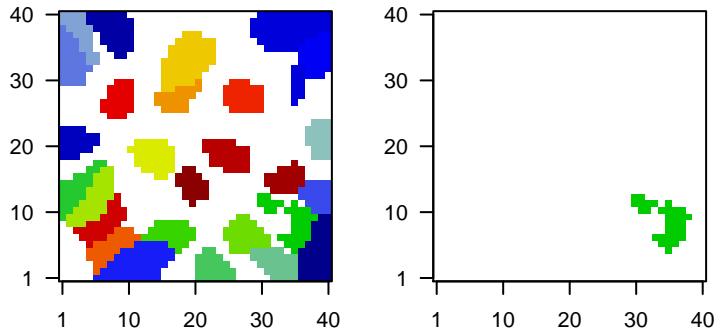
<r> metagenes = 0.92
<r> genes = 0.35
beta: r2= 6.16 / log p= -Inf

samples with spot = 38 (27.7 %)

- group 1 : 1 (9.1 %)
- group 2 : 1 (16.7 %)
- group 3 : 5 (100 %)
- group 4 : 3 (13.6 %)
- group 5 : 4 (16 %)
- group 6 : 4 (26.7 %)
- group 7 : 4 (15.4 %)
- group 8 : 16 (59.3 %)

Overview Map

Spot

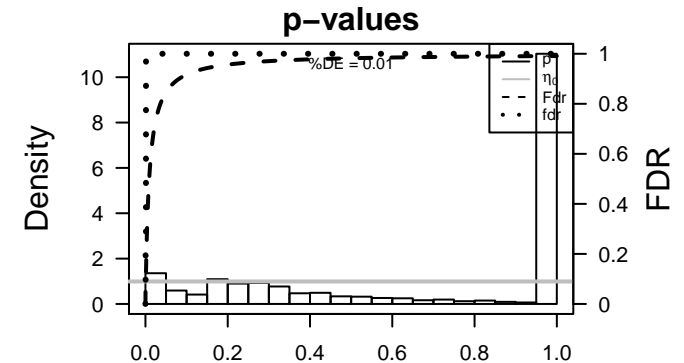


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	1554663_a_a	2.56	-0.58	0.15	NUMA1 nuclear mitotic apparatus protein 1 [Source:HGNC Symbol;Acc:HGNC:17513]
2	210729_at	2.23	-0.75	0.46	NPY2R neuropeptide Y receptor Y2 [Source:HGNC Symbol;Acc:HGNC:17513]
3	206898_at	2.09	-1.44	0.67	CDH19 cadherin 19 [Source:HGNC Symbol;Acc:HGNC:17513]
4	207317_s_at	2.08	-0.62	0.46	CASQ2 calsequestrin 2 [Source:HGNC Symbol;Acc:HGNC:1513]
5	239575_at	1.93	-1.67	0.88	OPALIN oligodendrocytic myelin paranodal and inner loop protein [Source:HGNC Symbol;Acc:HGNC:17513]
6	234130_at	1.93	-0.81	0.74	
7	235476_at	1.86	-1.05	0.65	novel tripartite motif-containing 59 (TRIM59) and intraflagella
8	219044_at	1.83	-0.88	0.47	THNSL2 threonine synthase like 2 [Source:HGNC Symbol;Acc:HGNC:17513]
9	237466_s_at	1.82	-0.75	0.76	HHIP hedgehog interacting protein [Source:HGNC Symbol;Acc:HGNC:17513]
10	219750_at	1.8	-1.55	0.77	TMEM144 transmembrane protein 144 [Source:HGNC Symbol;Acc:HGNC:17513]
11	239832_at	1.79	-0.65	0.27	
12	235614_at	1.78	-1.21	0.87	TMEM151 transmembrane protein 151A [Source:HGNC Symbol;Acc:HGNC:17513]
13	244297_at	1.78	-1.18	0.74	cytochrome P450, family 4, subfamily F family pseudogene
14	223757_at	1.77	-1.05	0.41	DIO3 opposite strand upstream RNA [Source:HGNC Symbol;Acc:HGNC:17513]
15	239500_at	1.76	-0.53	0.29	EFCAB1 EF-hand calcium binding domain 1 [Source:HGNC Symbol;Acc:HGNC:17513]
16	1563933_a_a	1.74	-1.3	0.54	PLD5 phospholipase D family member 5 [Source:HGNC Symbol;Acc:HGNC:17513]
17	217487_x_at	1.71	-1.42	0.79	FOLH1B folate hydrolase 1B [Source:HGNC Symbol;Acc:HGNC:13636]
18	221347_at	1.71	-0.52	0.37	CHRM5 cholinergic receptor muscarinic 5 [Source:HGNC Symbol;Acc:HGNC:17513]
19	218469_at	1.7	-1.27	0.81	GREM1 gremlin 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:17513]
20	213706_at	1.68	-1.55	0.61	GPD1 glycerol-3-phosphate dehydrogenase 1 [Source:HGNC Symbol;Acc:HGNC:17513]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-13	206 / 7387	BP membrane
2	4e-12	136 / 4278	BP plasma membrane
3	3e-09	167 / 6202	BP cytoplasm
4	2e-06	5 / 13	BP central nervous system myelination
5	2e-05	15 / 227	BP microtubule binding
6	5e-05	13 / 190	BP actin filament binding
7	1e-04	25 / 594	BP cell adhesion
8	2e-04	8 / 85	BP positive regulation of peptidyl-serine phosphorylation
9	2e-04	5 / 30	BP sterol biosynthetic process
10	2e-04	26 / 659	BP apoptotic process
11	2e-04	16 / 315	BP positive regulation of GTPase activity
12	3e-04	5 / 32	BP regulation of microtubule cytoskeleton organization
13	3e-04	4 / 19	BP lipid biosynthetic process
14	3e-04	6 / 52	BP myelination
15	3e-04	46 / 1500	BP signal transduction
16	5e-04	5 / 37	BP positive regulation of protein tyrosine kinase activity
17	6e-04	4 / 22	BP response to lead ion
18	7e-04	9 / 133	BP central nervous system development
19	7e-04	9 / 133	BP protein localization to plasma membrane
20	9e-04	3 / 11	BP establishment of protein localization to membrane
21	9e-04	10 / 165	BP positive regulation of protein phosphorylation
22	1e-03	9 / 138	BP regulation of small GTPase mediated signal transduction
23	1e-03	20 / 505	BP nervous system development
24	1e-03	5 / 43	BP substantia nigra development
25	1e-03	6 / 64	BP cellular response to drug
26	1e-03	3 / 12	BP detection of calcium ion
27	1e-03	23 / 627	BP ion transport
28	1e-03	4 / 27	BP microtubule bundle formation
29	1e-03	4 / 27	BP negative regulation of interleukin-6 production
30	1e-03	7 / 92	BP cholesterol metabolic process
31	1e-03	6 / 68	BP forebrain development
32	2e-03	3 / 14	BP nuclear migration
33	2e-03	3 / 14	BP positive regulation of myelination
34	2e-03	21 / 574	BP synapse
35	2e-03	4 / 30	BP oligodendrocyte differentiation
36	2e-03	10 / 185	BP endocytosis
37	2e-03	3 / 15	BP sodium-independent organic anion transport
38	3e-03	8 / 132	BP lipid transport
39	3e-03	8 / 132	BP membrane organization
40	3e-03	9 / 162	BP dephosphorylation



BP

Rank	p-value	#in/all	Geneset
1	1e-13	206 / 7387	membrane
2	4e-12	136 / 4278	plasma membrane
3	3e-09	167 / 6202	cytoplasm
4	2e-06	5 / 13	central nervous system myelination
5	2e-05	15 / 227	microtubule binding
6	5e-05	13 / 190	actin filament binding
7	1e-04	25 / 594	cell adhesion
8	2e-04	8 / 85	positive regulation of peptidyl-serine phosphorylation
9	2e-04	5 / 30	sterol biosynthetic process
10	2e-04	26 / 659	apoptotic process
11	2e-04	16 / 315	positive regulation of GTPase activity
12	3e-04	5 / 32	regulation of microtubule cytoskeleton organization
13	3e-04	4 / 19	lipid biosynthetic process
14	3e-04	6 / 52	myelination
15	3e-04	46 / 1500	signal transduction

Correlation Cluster

Spot Summary: F

metagenes = 27
genes = 677

<r> metagenes = 0.95
<r> genes = 0.43
beta: r2= 11.06 / log p= -Inf

samples with spot = 39 (28.5 %)
group 3 : 5 (100 %)
group 7 : 18 (69.2 %)
group 8 : 16 (59.3 %)

Spot Genelist

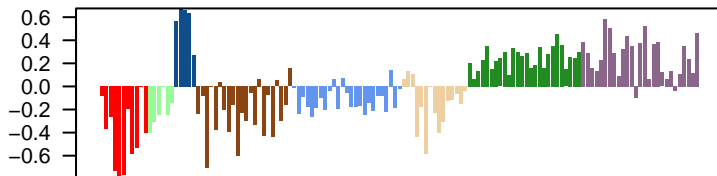
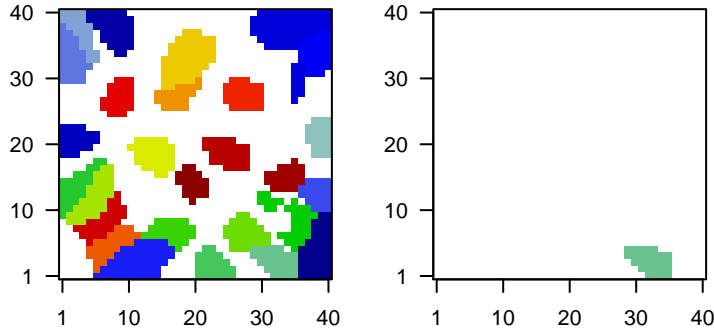
Rank	ID	max e	r	min e	Description
1	241883_x_at	2.35	-0.72	0.51	
2	1555230_a_a	2.29	-1.18	0.68	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC Symbol]
3	1566772_at	2.2	-0.85	0.65	
4	236714_at	2.14	-1.26	0.77	
5	229839_at	2.04	-0.64	0.43	SCARA5 scavenger receptor class A member 5 [Source:HGNC Symbol]
6	230112_at	2.02	-1.35	0.81	MARCH4 membrane associated ring-CH-type finger 4 [Source:HGNC Symbol]
7	221321_s_at	1.96	-1.19	0.7	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC Symbol]
8	202037_s_at	1.86	-1.75	0.46	SFRP1 secreted frizzled related protein 1 [Source:HGNC Symbol;Acc:HGNC:6720]
9	235666_at	1.85	-0.89	0.47	ITGA8 integrin subunit alpha 8 [Source:HGNC Symbol;Acc:HGNC:6720]
10	237933_at	1.82	-0.8	0.55	
11	228761_at	1.81	-1.4	0.72	SCRT1 scratch family transcriptional repressor 1 [Source:HGNC Symbol]
12	1552301_a_a	1.75	-1.03	0.67	CORO6 coronin 6 [Source:HGNC Symbol;Acc:HGNC:21356]
13	227827_at	1.74	-1.28	0.54	
14	1555935_s_at	1.72	-1.35	0.58	HUNK hormonally up-regulated Neu-associated kinase [Source:HGNC Symbol]
15	204585_s_at	1.71	-1.04	0.66	L1CAM L1 cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:6720]
16	244170_at	1.71	-1.59	0.85	RAB3C RAB3C, member RAS oncogene family [Source:HGNC Symbol]
17	1560525_at	1.69	-1.36	0.65	
18	227826_s_at	1.69	-1.58	0.55	
19	230896_at	1.68	-1.12	0.76	BEND4 BEN domain containing 4 [Source:HGNC Symbol;Acc:HGNC:6720]
20	226829_at	1.67	-1.42	0.46	AFAP1L2 actin filament associated protein 1 like 2 [Source:HGNC Symbol]

Geneset Overrepresentation

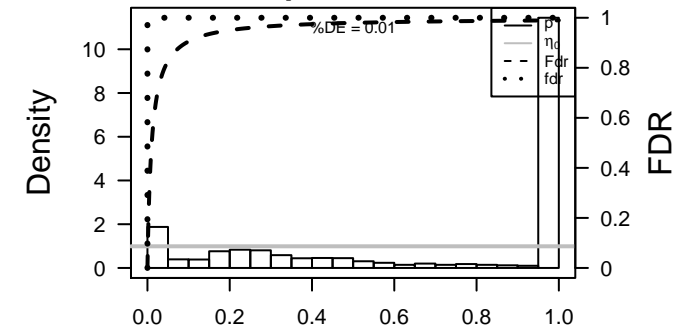
Rank	p-value	#in/all	Geneset
1	2e-26	177 / 4278	BP plasma membrane
2	3e-22	54 / 574	BP synapse
3	4e-20	234 / 7387	BP membrane
4	7e-19	33 / 240	BP postsynaptic membrane
5	2e-13	39 / 505	BP nervous system development
6	1e-12	15 / 65	BP learning
7	1e-11	20 / 149	BP regulation of ion transmembrane transport
8	3e-11	24 / 236	BP chemical synaptic transmission
9	4e-11	40 / 627	BP ion transport
10	3e-10	14 / 79	BP memory
11	8e-10	24 / 275	BP ion transmembrane transport
12	4e-09	8 / 22	BP regulation of AMPA receptor activity
13	2e-08	15 / 125	BP calcium ion transmembrane transport
14	3e-08	8 / 27	BP positive regulation of excitatory postsynaptic potential
15	6e-08	14 / 118	BP exocytosis
16	7e-08	11 / 68	BP regulation of insulin secretion
17	2e-07	6 / 15	BP exploration behavior
18	2e-07	10 / 61	BP positive regulation of synapse assembly
19	3e-07	17 / 199	BP axon guidance
20	5e-07	9 / 51	BP neurotransmitter secretion
21	6e-07	7 / 27	BP glutamate secretion
22	9e-07	9 / 55	BP social behavior
23	1e-06	11 / 89	BP locomotory behavior
24	1e-06	13 / 131	BP potassium ion transport
25	3e-06	25 / 455	BP intracellular signal transduction
26	3e-06	5 / 13	BP calcium ion transport into cytosol
27	3e-06	5 / 13	BP regulation of short-term neuronal synaptic plasticity
28	3e-06	8 / 48	BP cardiac conduction
29	4e-06	12 / 122	BP potassium ion transmembrane transport
30	4e-06	13 / 144	BP calcium ion transport
31	4e-06	5 / 14	BP vocalization behavior
32	5e-06	8 / 50	BP nervous system process
33	1e-05	6 / 27	BP gamma-aminobutyric acid signaling pathway
34	1e-05	53 / 1500	BP signal transduction
35	2e-05	7 / 45	BP neuromuscular process controlling balance
36	3e-05	4 / 10	BP high voltage-gated calcium channel activity
37	3e-05	7 / 48	BP negative regulation of phosphatase activity
38	3e-05	7 / 48	BP synapse organization
39	3e-05	6 / 33	BP regulation of exocytosis
40	4e-05	27 / 594	BP cell adhesion

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-26	177 / 4278	plasma membrane
2	3e-22	54 / 574	synapse
3	4e-20	234 / 7387	membrane
4	7e-19	33 / 240	postsynaptic membrane
5	2e-13	39 / 505	nervous system development
6	1e-12	15 / 65	learning
7	1e-11	20 / 149	regulation of ion transmembrane transport
8	3e-11	24 / 236	chemical synaptic transmission
9	4e-11	40 / 627	ion transport
10	3e-10	14 / 79	memory
11	8e-10	24 / 275	ion transmembrane transport
12	4e-09	8 / 22	regulation of AMPA receptor activity
13	2e-08	15 / 125	calcium ion transmembrane transport
14	3e-08	8 / 27	positive regulation of excitatory postsynaptic potential
15	6e-08	14 / 118	exocytosis

Correlation Cluster

Spot Summary: G

metagenes = 40
genes = 1442

<r> metagenes = 0.95

beta: r2= 21.34 / log p= -Inf

samples with spot = 35 (25.5 %)

group 1 : 2 (18.2 %)

group 2 : 1 (16.7 %)

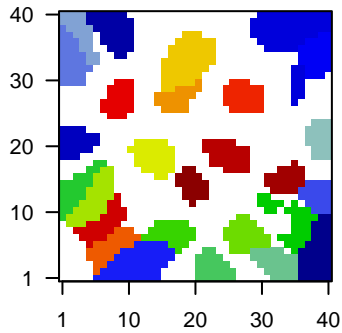
group 3 : 5 (100 %)

group 6 : 3 (20 %)

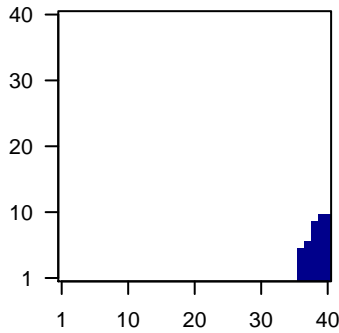
group 7 : 2 (7.7 %)

group 8 : 22 (81.5 %)

Overview Map



Spot

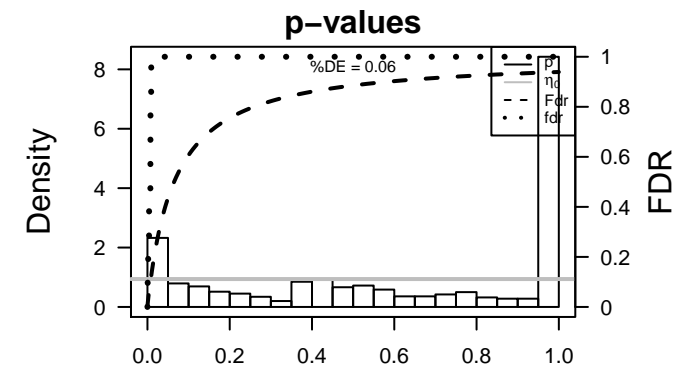
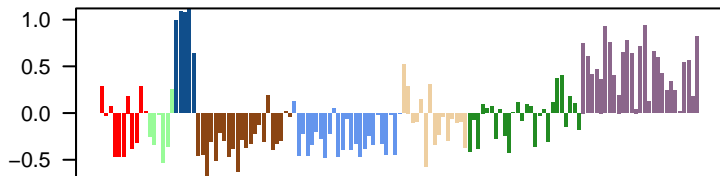


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	206803_at	3.07	-1.3	0.52	PDYN prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
2	1554299_at	2.94	-0.48	0.38	NPAS4 neuronal PAS domain protein 4 [Source:HGNC Symbol;Acc:HGNC:24211]
3	206382_s_at	2.85	-0.87	0.6	BDNF brain derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:10344]
4	205901_at	2.71	-1.16	0.71	PNOC prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
5	229012_at	2.64	-0.83	0.72	C9orf24 chromosome 9 open reading frame 24 [Source:HGNC Symbol;Acc:HGNC:24211]
6	1560652_at	2.59	-0.61	0.6	novel transcript, overlapping to IRS4
7	207147_at	2.55	-0.86	0.6	DLX2 distal-less homeobox 2 [Source:HGNC Symbol;Acc:HGNC:24211]
8	201496_x_at	2.5	-0.77	0.51	MYH11 myosin heavy chain 11 [Source:HGNC Symbol;Acc:HGNC:7520]
9	206552_s_at	2.4	-1.6	0.73	TAC1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11111]
10	228844_at	2.39	-0.8	0.81	SLC13A5solute carrier family 13 member 5 [Source:HGNC Symbol;Acc:HGNC:24211]
11	207768_at	2.35	-0.93	0.85	EGR4 early growth response 4 [Source:HGNC Symbol;Acc:HGNC:34211]
12	206696_at	2.3	-0.64	0.62	GPR143 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:HGNC:24211]
13	214611_at	2.29	-0.89	0.59	GRIK1 glutamate ionotropic receptor kainate type subunit 1 [Source:HGNC Symbol;Acc:HGNC:24211]
14	231391_at	2.29	-0.69	0.74	CTXN3 cortixin 3 [Source:HGNC Symbol;Acc:HGNC:31110]
15	222920_s_at	2.29	-1.17	0.88	TESPA1 thymocyte expressed, positive selection associated 1 [Source:HGNC Symbol;Acc:HGNC:24211]
16	204380_s_at	2.28	-0.84	0.51	FGFR3 fibroblast growth factor receptor 3 [Source:HGNC Symbol;Acc:HGNC:24211]
17	220025_at	2.25	-0.85	0.92	TBR1 T-box, brain 1 [Source:HGNC Symbol;Acc:HGNC:11590]
18	242138_at	2.23	-1.27	0.73	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:24211]
19	219263_at	2.22	-1.06	0.74	RNF128 ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:24211]
20	232111_at	2.18	-0.91	0.8	TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:24211]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-52	123 / 574	BP synapse
2	7e-48	78 / 236	BP chemical synaptic transmission
3	4e-43	361 / 4278	BP plasma membrane
4	1e-38	507 / 7387	BP membrane
5	3e-24	54 / 240	BP postsynaptic membrane
6	4e-23	88 / 627	BP ion transport
7	3e-21	40 / 149	BP regulation of ion transmembrane transport
8	3e-18	70 / 505	BP nervous system development
9	5e-16	32 / 131	BP potassium ion transport
10	7e-15	20 / 51	BP regulation of synaptic plasticity
11	1e-13	126 / 1500	BP signal transduction
12	7e-13	27 / 119	BP postsynapse
13	7e-13	79 / 777	BP G protein-coupled receptor signaling pathway
14	1e-12	28 / 131	BP presynapse
15	1e-12	14 / 28	BP synaptic vesicle exocytosis
16	6e-12	66 / 615	BP transmembrane transport
17	8e-12	14 / 31	BP regulation of NMDA receptor activity
18	9e-12	26 / 122	BP potassium ion transmembrane transport
19	2e-11	17 / 51	BP neurotransmitter secretion
20	2e-11	11 / 18	BP regulation of neurotransmitter secretion
21	4e-10	13 / 33	BP regulation of exocytosis
22	8e-10	20 / 89	BP locomotory behavior
23	1e-09	14 / 43	BP neurotransmitter transport
24	2e-09	63 / 657	BP calcium ion binding
25	2e-09	25 / 144	BP calcium ion transport
26	4e-09	9 / 16	BP positive regulation of calcium ion-dependent exocytosis
27	4e-09	18 / 79	BP cellular response to calcium ion
28	5e-09	15 / 54	BP sensory perception of pain
29	5e-09	22 / 118	BP exocytosis
30	5e-09	12 / 33	BP long-term memory
31	6e-09	11 / 27	BP glutamate secretion
32	7e-09	14 / 48	BP long-term synaptic potentiation
33	1e-08	8 / 13	BP synaptic transmission, GABAergic
34	1e-08	22 / 125	BP calcium ion transmembrane transport
35	2e-08	14 / 51	BP regulation of synaptic vesicle exocytosis
36	2e-08	11 / 30	BP associative learning
37	3e-08	17 / 79	BP memory
38	3e-08	18 / 89	BP neuropeptide signaling pathway
39	3e-08	10 / 25	BP calmodulin-dependent protein kinase activity
40	3e-08	10 / 25	BP regulation of dopamine secretion



BP

Rank	p-value	#in/all	Geneset
1	6e-52	123 / 574	synapse
2	7e-48	78 / 236	chemical synaptic transmission
3	4e-43	361 / 4278	plasma membrane
4	1e-38	507 / 7387	membrane
5	3e-24	54 / 240	postsynaptic membrane
6	4e-23	88 / 627	ion transport
7	3e-21	40 / 149	regulation of ion transmembrane transport
8	3e-18	70 / 505	nervous system development
9	5e-16	32 / 131	potassium ion transport
10	7e-15	20 / 51	regulation of synaptic plasticity
11	1e-13	126 / 1500	signal transduction
12	7e-13	27 / 119	postsynapse
13	7e-13	79 / 777	G protein-coupled receptor signaling pathway
14	1e-12	28 / 131	presynapse
15	1e-12	14 / 28	synaptic vesicle exocytosis

Correlation Cluster

Spot Summary: H

metagenes = 24
genes = 1376

<r> metagenes = 0.94

beta: r2= 0.66 / log p= -Inf

samples with spot = 0 (0 %)

Spot Genelist

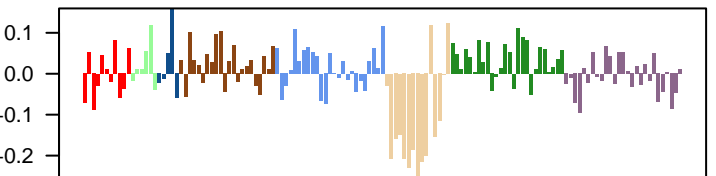
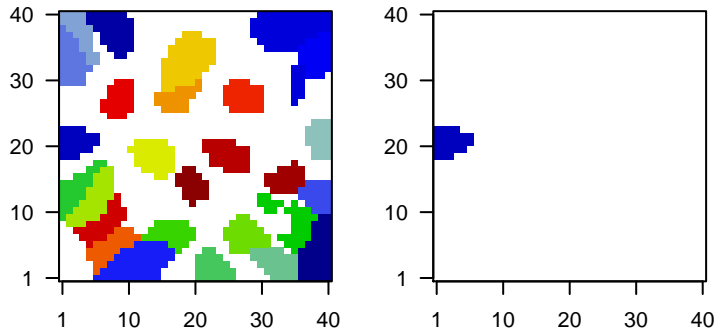
Rank	ID	max e	r	min e	Description Symbol
1	233092_s_at	2.87	-0.4	0.3	
2	237435_at	2.45	-0.37	0.34	
3	1558760_at	2	-0.66	0.34	
4	1553830_s_at	1.94	-0.51	0.23	MAGEA2 MAGE family member A2B [Source:HGNC Symbol;Acc:HGNC:10342]
5	216050_at	1.85	-0.55	0.43	
6	1562049_at	1.83	-0.56	0.38	novel transcript, antisense to SCTR
7	243110_x_at	1.73	-0.44	0.44	NPW neuropeptide W [Source:HGNC Symbol;Acc:HGNC:30509]
8	1562337_at	1.65	-0.63	0.17	OR7D2 olfactory receptor family 7 subfamily D member 2 [Source:NCBI RefSeq;Acc:NC_006265.3]
9	223994_s_at	1.5	-0.74	0.54	SLC12A9 solute carrier family 12 member 9 [Source:HGNC Symbol;Acc:HGNC:10342]
10	1562400_at	1.5	-0.39	0.43	
11	237101_at	1.49	-0.42	0.28	
12	217511_at	1.46	-0.93	0.26	KAZALD Kazal type serine peptidase inhibitor domain 1 [Source:HGNC Symbol;Acc:HGNC:10342]
13	237205_at	1.45	-0.34	0.32	CCDC199 coiled-coil domain containing 199 [Source:HGNC Symbol;Acc:HGNC:10342]
14	203809_s_at	1.44	-0.36	0.32	AKT2 AKT serine/threonine kinase 2 [Source:HGNC Symbol;Acc:HGNC:10342]
15	220786_s_at	1.34	-0.54	0.26	SLC38A4 solute carrier family 38 member 4 [Source:HGNC Symbol;Acc:HGNC:10342]
16	1564940_at	1.34	-0.67	0.24	novel transcript
17	243056_at	1.33	-0.71	0.25	C12orf60 chromosome 12 open reading frame 60 [Source:HGNC Symbol;Acc:HGNC:10342]
18	1557566_at	1.32	-0.52	0.18	
19	1556776_at	1.31	-0.99	0.33	ZNF426 divergent transcript [Source:HGNC Symbol;Acc:HGNC:10342]
20	235401_s_at	1.3	-0.47	0.36	FCRLA Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]

Geneset Overrepresentation

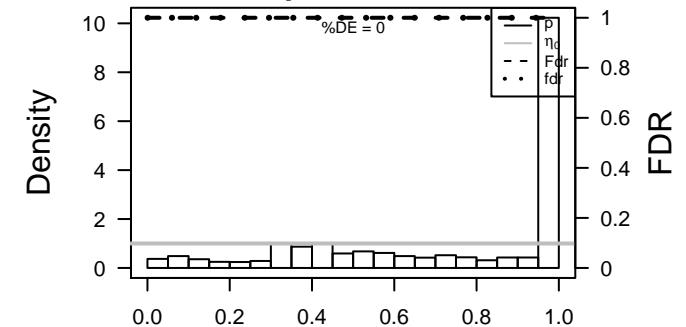
Rank	p-value	#in/all	Geneset
1	3e-04	5 / 17	BP ATP-dependent microtubule motor activity, minus-end-directed
2	6e-04	4 / 12	BP positive regulation of response to DNA damage stimulus
3	2e-03	5 / 25	BP protein localization to cell surface
4	2e-03	7 / 51	BP regulation of cardiac conduction
5	3e-03	10 / 101	BP ossification
6	4e-03	11 / 119	BP nucleic acid phosphodiester bond hydrolysis
7	5e-03	3 / 10	BP positive regulation of lymphocyte proliferation
8	5e-03	4 / 20	BP positive regulation of osteoclast differentiation
9	6e-03	3 / 11	BP positive regulation of fibroblast migration
10	8e-03	3 / 12	BP oocyte development
11	9e-03	6 / 50	BP positive regulation of cell adhesion
12	1e-02	4 / 24	BP female gonad development
13	1e-02	3 / 13	BP positive regulation of interleukin-2 biosynthetic process
14	1e-02	3 / 13	BP regulation of release of sequestered calcium ion into cytosol
15	1e-02	3 / 14	BP negative regulation of endocytosis
16	1e-02	3 / 14	BP negative regulation of interleukin-10 production
17	1e-02	4 / 26	BP focal adhesion assembly
18	1e-02	6 / 55	BP phospholipase C-activating G protein-coupled receptor signaling pathway
19	2e-02	3 / 15	BP positive regulation of glycogen biosynthetic process
20	2e-02	4 / 28	BP synapsis
21	2e-02	9 / 110	BP meiotic cell cycle
22	2e-02	7 / 76	BP B cell differentiation
23	2e-02	9 / 112	BP motor activity
24	2e-02	9 / 113	BP muscle contraction
25	2e-02	4 / 30	BP negative regulation of TOR signaling
26	2e-02	5 / 45	BP positive regulation of cell division
27	2e-02	13 / 193	BP visual perception
28	2e-02	8 / 98	BP cellular calcium ion homeostasis
29	3e-02	3 / 18	BP determination of adult lifespan
30	3e-02	3 / 18	BP mitotic G2 DNA damage checkpoint
31	3e-02	3 / 18	BP positive regulation of CREB transcription factor activity
32	3e-02	3 / 18	BP resolution of meiotic recombination intermediates
33	3e-02	3 / 18	BP response to vitamin D
34	3e-02	4 / 33	BP positive regulation of multicellular organism growth
35	3e-02	9 / 121	BP sodium ion transport
36	3e-02	5 / 49	BP epidermal growth factor receptor signaling pathway
37	3e-02	5 / 49	BP interstrand cross-link repair
38	3e-02	6 / 66	BP defense response to Gram-negative bacterium
39	3e-02	3 / 20	BP apoptotic cell clearance
40	3e-02	3 / 20	BP phosphate-containing compound metabolic process

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	3e-04	5 / 17	ATP-dependent microtubule motor activity, minus-end-directed
2	6e-04	4 / 12	positive regulation of response to DNA damage stimulus
3	2e-03	5 / 25	protein localization to cell surface
4	2e-03	7 / 51	regulation of cardiac conduction
5	3e-03	10 / 101	ossification
6	4e-03	11 / 119	nucleic acid phosphodiester bond hydrolysis
7	5e-03	3 / 10	positive regulation of lymphocyte proliferation
8	5e-03	4 / 20	positive regulation of osteoclast differentiation
9	6e-03	3 / 11	positive regulation of fibroblast migration
10	8e-03	3 / 12	oocyte development
11	9e-03	6 / 50	positive regulation of cell adhesion
12	1e-02	4 / 24	female gonad development
13	1e-02	3 / 13	positive regulation of interleukin-2 biosynthetic process
14	1e-02	3 / 13	regulation of release of sequestered calcium ion into cytosol
15	1e-02	3 / 14	negative regulation of endocytosis

Correlation Cluster

Spot Summary: I

metagenes = 21
genes = 770

<r> metagenes = 0.94
<r> genes = 0.37
beta: r2= 3.76 / log p= -Inf

samples with spot = 20 (14.6 %)
group 2 : 1 (16.7 %)
group 3 : 4 (80 %)
group 6 : 5 (33.3 %)
group 8 : 10 (37 %)

Spot Genelist

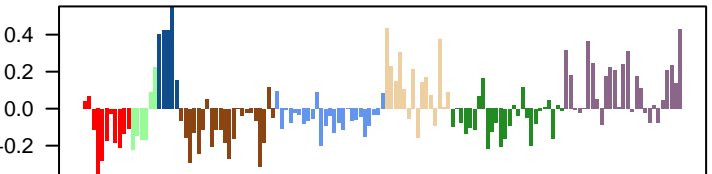
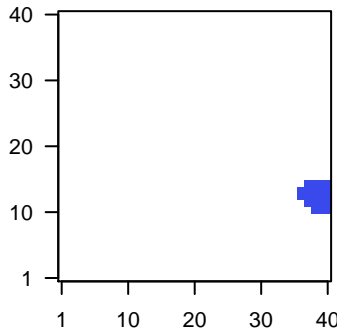
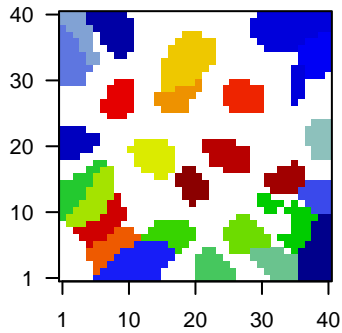
Rank	ID	max e	r	min e	Description
1	205350_at	3.07	-0.63	0.42	CRABP1 cellular retinoic acid binding protein 1 [Source:HGNC Symbol]
2	205576_at	2.92	-0.49	0.33	SERPINC1 serpin family D member 1 [Source:HGNC Symbol;Acc:HGNC:2155]
3	243390_at	2.33	-0.72	0.31	SLC6A13 solute carrier family 6 member 13 [Source:HGNC Symbol;Acc:HGNC:16067]
4	219824_at	2.23	-0.83	0.35	SLC13A4 solute carrier family 13 member 4 [Source:HGNC Symbol;Acc:HGNC:16067]
5	239684_at	2.16	-0.57	0.45	TRPM3 transient receptor potential cation channel subfamily M member 3 [Source:HGNC Symbol;Acc:HGNC:16067]
6	207184_at	2.04	-0.67	0.48	SLC6A13 solute carrier family 6 member 13 [Source:HGNC Symbol;Acc:HGNC:16067]
7	220231_at	1.96	-0.76	0.34	PPP1R17 protein phosphatase 1 regulatory subunit 17 [Source:HGNC Symbol;Acc:HGNC:16067]
8	208255_s_at	1.87	-1.53	0.67	FKBP8 FKBP prolyl isomerase 8 [Source:HGNC Symbol;Acc:HGNC:16067]
9	203951_at	1.85	-0.7	0.53	CNN1 calponin 1 [Source:HGNC Symbol;Acc:HGNC:2155]
10	227058_at	1.79	-0.72	0.44	MEDAG mesenteric estrogen dependent adipogenesis [Source:HGNC Symbol;Acc:HGNC:16067]
11	204687_at	1.75	-1.17	0.61	PARM1 prostate androgen-regulated mucin-like protein 1 [Source:HGNC Symbol;Acc:HGNC:16067]
12	237206_at	1.73	-0.55	0.49	MYOCD myocardin [Source:HGNC Symbol;Acc:HGNC:16067]
13	201495_x_at	1.72	-0.47	0.43	MYH11 myosin heavy chain 11 [Source:HGNC Symbol;Acc:HGNC:2155]
14	1560100_at	1.71	-1.08	0.43	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:2155]
15	221065_s_at	1.71	-0.71	0.49	CHST8 carbohydrate sulfotransferase 8 [Source:HGNC Symbol;Acc:HGNC:16067]
16	226129_at	1.64	-0.89	0.62	FAM83H family with sequence similarity 83 member H [Source:HGNC Symbol;Acc:HGNC:16067]
17	238654_at	1.63	-0.77	0.43	VSIG10LV-set and immunoglobulin domain containing 10 like [Source:HGNC Symbol;Acc:HGNC:16067]
18	37022_at	1.62	-0.79	0.58	PRELP proline and arginine rich end leucine rich repeat protein [Source:HGNC Symbol;Acc:HGNC:16067]
19	208335_s_at	1.61	-0.95	0.38	ACKR1 atypical chemokine receptor 1 (Duffy blood group) [Source:HGNC Symbol;Acc:HGNC:16067]
20	213955_at	1.6	-0.71	0.49	MYOZ3 myozenin 3 [Source:HGNC Symbol;Acc:HGNC:18565]

Geneset Overrepresentation

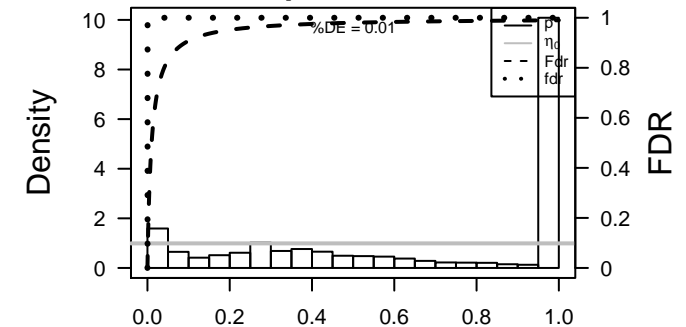
Rank	p-value	#in/all	Geneset
1	7e-19	300 / 7387	BP membrane
2	4e-16	196 / 4278	BP plasma membrane
3	3e-15	53 / 574	BP synapse
4	1e-11	240 / 6202	BP cytoplasm
5	6e-11	28 / 240	BP postsynaptic membrane
6	3e-08	45 / 684	BP phosphorylation
7	8e-08	11 / 51	BP neurotransmitter secretion
8	3e-07	178 / 4740	BP cytosol
9	4e-07	16 / 131	BP presynapse
10	5e-07	8 / 28	BP synaptic vesicle exocytosis
11	2e-06	7 / 23	BP positive regulation of protein dephosphorylation
12	7e-06	9 / 51	BP regulation of synaptic plasticity
13	1e-05	27 / 400	BP protein serine/threonine kinase activity
14	1e-05	7 / 30	BP associative learning
15	1e-05	7 / 30	BP synaptic membrane
16	2e-05	67 / 1500	BP signal transduction
17	4e-05	57 / 1242	BP Golgi apparatus
18	6e-05	8 / 51	BP regulation of synaptic vesicle exocytosis
19	6e-05	13 / 133	BP protein localization to plasma membrane
20	6e-05	6 / 27	BP positive regulation of excitatory postsynaptic potential
21	9e-05	35 / 657	BP calcium ion binding
22	9e-05	4 / 10	BP synaptic vesicle maturation
23	1e-04	5 / 20	BP response to corticosterone
24	2e-04	33 / 623	BP protein phosphorylation
25	2e-04	5 / 21	BP regulation of long-term neuronal synaptic plasticity
26	2e-04	4 / 12	BP regulation of synaptic vesicle endocytosis
27	2e-04	11 / 113	BP positive regulation of neuron projection development
28	2e-04	12 / 133	BP neuron projection development
29	3e-04	4 / 13	BP regulation of short-term neuronal synaptic plasticity
30	3e-04	6 / 36	BP negative regulation of Notch signaling pathway
31	4e-04	32 / 627	BP ion transport
32	4e-04	5 / 24	BP regulation of neuron apoptotic process
33	4e-04	9 / 84	BP ephrin receptor signaling pathway
34	4e-04	18 / 273	BP MAPK cascade
35	4e-04	5 / 25	BP calmodulin-dependent protein kinase activity
36	5e-04	27 / 505	BP nervous system development
37	5e-04	4 / 15	BP calcium ion-regulated exocytosis of neurotransmitter
38	5e-04	4 / 15	BP MAP kinase activity
39	6e-04	16 / 236	BP chemical synaptic transmission
40	6e-04	12 / 149	BP regulation of ion transmembrane transport

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	7e-19	300 / 7387	membrane
2	4e-16	196 / 4278	plasma membrane
3	3e-15	53 / 574	synapse
4	1e-11	240 / 6202	cytoplasm
5	6e-11	28 / 240	postsynaptic membrane
6	3e-08	45 / 684	phosphorylation
7	8e-08	11 / 51	neurotransmitter secretion
8	3e-07	178 / 4740	cytosol
9	4e-07	16 / 131	presynapse
10	5e-07	8 / 28	synaptic vesicle exocytosis
11	2e-06	7 / 23	positive regulation of protein dephosphorylation
12	7e-06	9 / 51	regulation of synaptic plasticity
13	1e-05	27 / 400	protein serine/threonine kinase activity
14	1e-05	7 / 30	associative learning
15	1e-05	7 / 30	synaptic membrane

Correlation Cluster

Spot Summary: J

metagenes = 28
genes = 744

<r> metagenes = 0.94
<r> genes = 0.34
beta: r2= 2.46 / log p= -Inf

samples with spot = 15 (10.9 %)
group 3 : 5 (100 %)
group 8 : 10 (37 %)

Spot Genelist

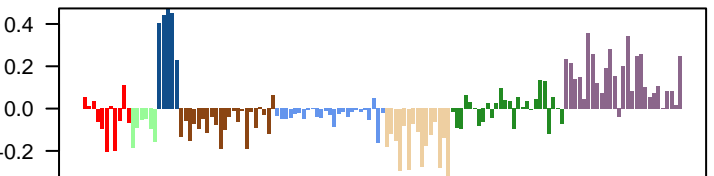
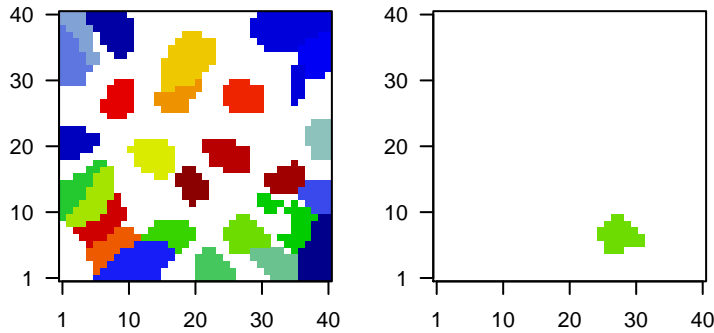
Rank	ID	max e	r	min e	Description
1	213780_at	2.81	-0.6	0.3	TCHH trichohyalin [Source:HGNC Symbol;Acc:HGNC:11791]
2	204938_s_at	2.58	-0.74	0.25	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
3	204940_at	2.3	-0.67	0.21	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
4	213707_s_at	2.09	-0.79	0.25	DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:HGNC:2
5	1554997_a_a	2.07	-0.79	0.52	PTGS2 prostaglandin-endoperoxide synthase 2 [Source:HGNC Sym
6	206805_at	1.97	-0.99	0.38	SEMA3Asemaphorin 3A [Source:HGNC Symbol;Acc:HGNC:10723]
7	240911_at	1.96	-0.62	0.36	NOS1 nitric oxide synthase 1 [Source:HGNC Symbol;Acc:HGNC:78
8	205978_at	1.95	-0.8	0.62	KL klotho [Source:HGNC Symbol;Acc:HGNC:6344]
9	224027_at	1.9	-0.45	0.57	CCL28 C-C motif chemokine ligand 28 [Source:HGNC Symbol;Acc:†
10	229199_at	1.84	-0.47	0.29	SCN9A sodium voltage-gated channel alpha subunit 9 [Source:HGNC
11	210367_s_at	1.83	-0.57	0.43	PTGES prostaglandin E synthase [Source:HGNC Symbol;Acc:HGNC
12	207717_s_at	1.8	-0.74	0.56	PKP2 plakophilin 2 [Source:HGNC Symbol;Acc:HGNC:9024]
13	206460_at	1.78	-0.88	0.47	AJAP1 adherens junctions associated protein 1 [Source:HGNC Sym
14	236591_at	1.77	-1.31	0.3	MIR4458 host gene [Source:HGNC Symbol;Acc:HGNC:4900
15	204501_at	1.75	-0.75	0.6	CCN3 cellular communication network factor 3 [Source:HGNC Sym
16	244163_at	1.74	-0.9	0.49	SEMA3Asemaphorin 3A [Source:HGNC Symbol;Acc:HGNC:10723]
17	241404_at	1.73	-0.72	0.39	
18	231750_at	1.62	-1.51	0.33	PCDHB4protocadherin beta 4 [Source:HGNC Symbol;Acc:HGNC:868
19	205908_s_at	1.59	-0.68	0.58	OMD osteomodulin [Source:HGNC Symbol;Acc:HGNC:8134]
20	205891_at	1.59	-1.04	0.58	ADORA2Badenosine A2b receptor [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

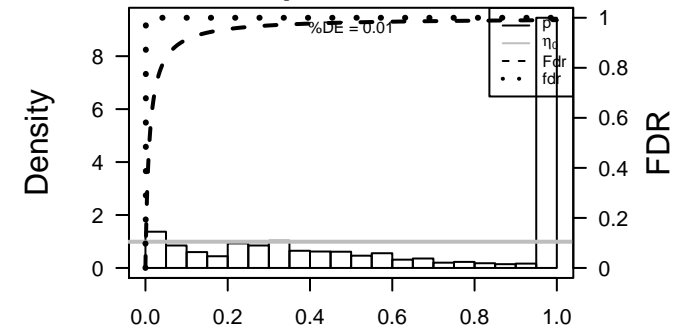
Rank	p-value	#in/all	Geneset
1	6e-13	195 / 4740	BP cytosol
2	3e-11	232 / 6202	BP cytoplasm
3	1e-08	254 / 7387	BP membrane
4	2e-06	22 / 267	BP ubiquitin-protein transferase activity
5	2e-06	60 / 1242	BP Golgi apparatus
6	4e-06	22 / 281	BP ubiquitin-dependent protein catabolic process
7	4e-06	12 / 92	BP proton transmembrane transport
8	1e-05	6 / 21	BP proton-transporting ATPase activity, rotational mechanism
9	1e-05	64 / 1435	BP mitochondrion
10	2e-05	33 / 574	BP synapse
11	2e-05	7 / 33	BP transferrin transport
12	4e-05	6 / 26	BP phagosome acidification
13	5e-05	27 / 455	BP intracellular signal transduction
14	6e-05	6 / 28	BP ATP hydrolysis coupled proton transport
15	7e-05	9 / 69	BP regulation of macroautophagy
16	1e-04	5 / 20	BP melanosome transport
17	2e-04	12 / 133	BP protein localization to plasma membrane
18	3e-04	6 / 36	BP synaptic vesicle endocytosis
19	4e-04	28 / 545	BP protein ubiquitination
20	4e-04	7 / 54	BP axon cytoplasm
21	5e-04	31 / 630	BP protein transport
22	5e-04	5 / 26	BP axon extension
23	6e-04	4 / 16	BP G protein-coupled glutamate receptor signaling pathway
24	6e-04	4 / 16	BP MAP kinase kinase activity
25	6e-04	11 / 133	BP positive regulation of canonical Wnt signaling pathway
26	8e-04	4 / 17	BP face development
27	9e-04	15 / 228	BP protein polyubiquitination
28	9e-04	8 / 78	BP insulin receptor signaling pathway
29	9e-04	7 / 61	BP peptidyl-threonine phosphorylation
30	1e-03	140 / 4278	BP plasma membrane
31	1e-03	6 / 45	BP protein targeting
32	1e-03	12 / 163	BP autophagy
33	1e-03	4 / 19	BP positive regulation of dendritic spine morphogenesis
34	1e-03	7 / 64	BP cellular response to drug
35	1e-03	8 / 84	BP SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
36	2e-03	8 / 86	BP regulation of GTPase activity
37	2e-03	11 / 149	BP protein folding
38	2e-03	31 / 684	BP phosphorylation
39	2e-03	5 / 35	BP negative chemotaxis
40	2e-03	16 / 273	BP MAPK cascade

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	6e-13	195 / 4740	cytosol
2	3e-11	232 / 6202	cytoplasm
3	1e-08	254 / 7387	membrane
4	2e-06	22 / 267	ubiquitin-protein transferase activity
5	2e-06	60 / 1242	Golgi apparatus
6	4e-06	22 / 281	ubiquitin-dependent protein catabolic process
7	4e-06	12 / 92	proton transmembrane transport
8	1e-05	6 / 21	proton-transporting ATPase activity, rotational mechanism
9	1e-05	64 / 1435	mitochondrion
10	2e-05	33 / 574	synapse
11	2e-05	7 / 33	transferrin transport
12	4e-05	6 / 26	phagosome acidification
13	5e-05	27 / 455	intracellular signal transduction
14	6e-05	6 / 28	ATP hydrolysis coupled proton transport
15	7e-05	9 / 69	regulation of macroautophagy

Correlation Cluster

Spot Summary: K

metagenes = 21
genes = 641

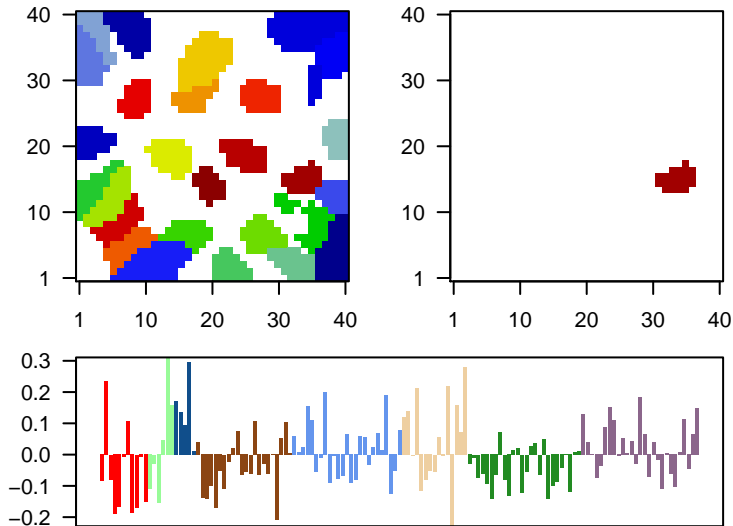
<r> metagenes = 0.92
<r> genes = 0.26
beta: r2= 1.28 / log p= -Inf

samples with spot = 6 (4.4 %)

group 1 : 1 (9.1 %)
group 2 : 1 (16.7 %)
group 3 : 1 (20 %)
group 6 : 3 (20 %)

Overview Map

Spot

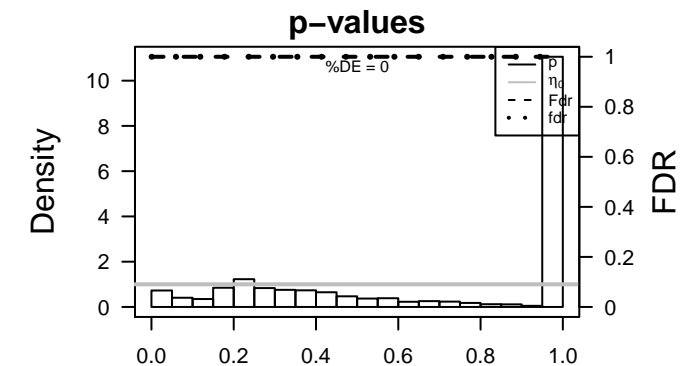


Spot Genelist

Rank	ID	max e	r	min e	Description
1	220226_at	2.43	-0.54	0.33	TRPM8 transient receptor potential cation channel subfamily M mem
2	219614_s_at	2.3	-0.46	0.25	SLC6A20solute carrier family 6 member 20 [Source:HGNC Symbol;Acc
3	234291_s_at	1.91	-0.58	0.4	SLC6A20solute carrier family 6 member 20 [Source:HGNC Symbol;Acc
4	203886_s_at	1.64	-0.61	0.38	FBLN2 fibulin 2 [Source:HGNC Symbol;Acc:HGNC:3601]
5	221991_at	1.41	-0.6	0.43	NXPH3 neurexophilin 3 [Source:HGNC Symbol;Acc:HGNC:8077]
6	231280_at	1.41	-0.52	0.48	HEBP2 heme binding protein 2 [Source:HGNC Symbol;Acc:HGNC:1f
7	233938_at	1.39	-0.64	0.59	C11orf86chromosome 11 open reading frame 86 [Source:HGNC Symt
8	228312_at	1.36	-0.93	0.4	PI16 peptidase inhibitor 16 [Source:HGNC Symbol;Acc:HGNC:212
9	207150_at	1.26	-0.66	0.42	SLC18A3solute carrier family 18 member A3 [Source:HGNC Symbol;A
10	236709_at	1.26	-0.87	0.48	CTXND1cortixin domain containing 1 [Source:HGNC Symbol;Acc:HG
11	217154_s_at	1.26	-0.56	0.54	EDN3 endothelin 3 [Source:HGNC Symbol;Acc:HGNC:3178]
12	230992_at	1.25	-0.94	0.43	
13	235383_at	1.24	-0.65	0.55	MYO7B myosin VIIB [Source:HGNC Symbol;Acc:HGNC:7607]
14	220653_at	1.23	-1.04	0.1	ZIM2 zinc finger imprinted 2 [Source:HGNC Symbol;Acc:HGNC:12
15	239993_at	1.17	-0.47	0.35	
16	239920_at	1.15	-0.77	0.53	
17	211111_at	1.13	-0.77	0.66	HGC6.3 uncharacterized LOC100128124 [Source:NCBI gene;Acc:10C
18	235870_at	1.13	-0.58	0.35	long intergenic non-protein coding RNA 1140 [Source:HGNC
19	229583_at	1.12	-0.93	0.6	
20	235958_at	1.11	-0.48	0.65	PLA2G4Bphospholipase A2 group IVF [Source:HGNC Symbol;Acc:HGI

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-04	32 / 887	BP cell differentiation
2	6e-04	4 / 21	BP exogenous drug catabolic process
3	2e-03	5 / 46	BP neural crest cell migration
4	2e-03	17 / 412	BP negative regulation of cell population proliferation
5	3e-03	3 / 15	BP adult heart development
6	3e-03	22 / 613	BP positive regulation of transcription, DNA-templated
7	4e-03	3 / 17	BP pharyngeal system development
8	4e-03	3 / 18	BP epoxygenase P450 pathway
9	4e-03	3 / 18	BP male genitalia development
10	4e-03	3 / 18	BP regulation of blood vessel size
11	5e-03	6 / 83	BP xenobiotic metabolic process
12	5e-03	3 / 19	BP embryonic heart tube development
13	5e-03	7 / 112	BP animal organ morphogenesis
14	6e-03	21 / 615	BP transmembrane transport
15	7e-03	3 / 21	BP positive regulation of heart rate
16	7e-03	3 / 21	BP regulation of cardiac muscle contraction
17	8e-03	4 / 42	BP skeletal muscle cell differentiation
18	8e-03	22 / 671	BP oxidation-reduction process
19	8e-03	4 / 43	BP neurotransmitter transport
20	9e-03	19 / 553	BP oxidoreductase activity
21	9e-03	3 / 23	BP negative regulation of axon extension involved in axon guidance
22	9e-03	3 / 23	BP regulation of vasoconstriction
23	9e-03	10 / 222	BP cell-cell signaling
24	1e-02	3 / 24	BP positive regulation of endocytosis
25	1e-02	11 / 261	BP cell surface receptor signaling pathway
26	1e-02	161 / 7387	BP membrane
27	1e-02	4 / 47	BP nuclear receptor activity
28	1e-02	4 / 48	BP positive regulation of cell differentiation
29	1e-02	31 / 1080	BP multicellular organism development
30	1e-02	3 / 27	BP positive regulation of mitotic nuclear division
31	1e-02	2 / 10	BP adrenergic receptor signaling pathway
32	1e-02	2 / 10	BP cardiac ventricle morphogenesis
33	1e-02	2 / 10	BP cellular response to potassium ion
34	1e-02	2 / 10	BP mitotic nuclear envelope reassembly
35	1e-02	2 / 10	BP negative regulation of reactive oxygen species biosynthetic process
36	1e-02	2 / 10	BP neuron projection maintenance
37	1e-02	2 / 10	BP positive regulation of systemic arterial blood pressure
38	2e-02	25 / 843	BP DNA-binding transcription factor activity
39	2e-02	2 / 11	BP potassium ion export across plasma membrane
40	2e-02	2 / 11	BP protein quality control for misfolded or incompletely synthesized proteins



BP

Rank	p-value	#in/all	Geneset
1	3e-04	32 / 887	cell differentiation
2	6e-04	4 / 21	exogenous drug catabolic process
3	2e-03	5 / 46	neural crest cell migration
4	2e-03	17 / 412	negative regulation of cell population proliferation
5	3e-03	3 / 15	adult heart development
6	3e-03	22 / 613	positive regulation of transcription, DNA-templated
7	4e-03	3 / 17	pharyngeal system development
8	4e-03	3 / 18	epoxygenase P450 pathway
9	4e-03	3 / 18	male genitalia development
10	4e-03	3 / 18	regulation of blood vessel size
11	5e-03	6 / 83	xenobiotic metabolic process
12	5e-03	3 / 19	embryonic heart tube development
13	5e-03	7 / 112	animal organ morphogenesis
14	6e-03	21 / 615	transmembrane transport
15	7e-03	3 / 21	positive regulation of heart rate

Correlation Cluster

Spot Summary: L

metagenes = 51
genes = 1246

<r> metagenes = 0.91

beta: r2= 10 / log p= -Inf

samples with spot = 33 (24.1 %)

group 1 : 7 (63.6 %)

group 2 : 3 (50 %)

group 3 : 1 (20 %)

group 4 : 16 (72.7 %)

group 5 : 2 (8 %)

group 6 : 2 (13.3 %)

group 8 : 2 (7.4 %)

Spot Genelist

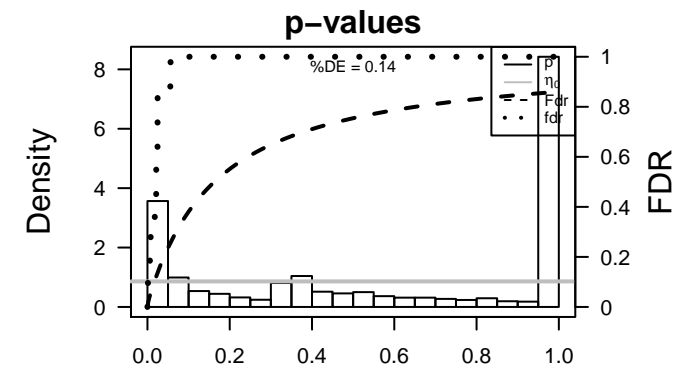
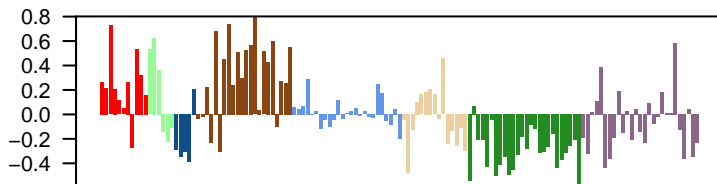
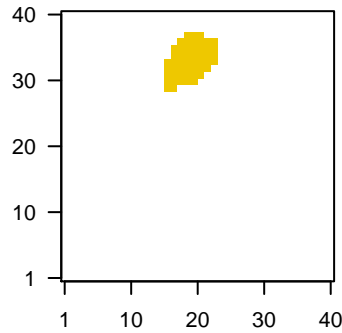
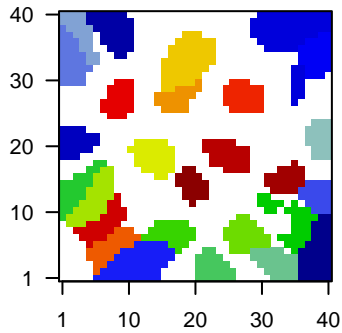
Rank	ID	max e	r	min e	Description
1	211430_s_at	3.66	-1	0.52	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
2	209138_x_at	3.42	-0.97	0.58	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
3	215121_x_at	3.38	-1.11	0.56	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
4	217022_s_at	3.37	-0.9	0.53	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
5	214677_x_at	3.36	-1.19	0.59	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215176_x_at	3.32	-0.8	0.54	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	0.55	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
9	202018_s_at	3.01	-0.95	0.5	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	0.48	INMT indolethylamine N-methyltransferase [Source:HGNC Symbol;
16	211339_s_at	2.73	-0.49	0.57	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	0.48	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	5e-89	150 / 564	BP immune system process
2	8e-67	109 / 388	BP immune response
3	4e-54	100 / 417	BP innate immune response
4	5e-46	86 / 364	BP inflammatory response
5	8e-45	321 / 4278	BP plasma membrane
6	8e-42	91 / 460	BP neutrophil degranulation
7	4e-37	436 / 7387	BP membrane
8	4e-34	50 / 155	BP regulation of immune response
9	1e-24	55 / 289	BP cytokine-mediated signaling pathway
10	2e-22	23 / 43	BP antigen processing and presentation
11	3e-22	42 / 184	BP defense response to virus
12	1e-21	130 / 1500	BP signal transduction
13	8e-21	37 / 152	BP leukocyte migration
14	2e-20	15 / 17	BP antigen processing and presentation of peptide or polysaccharide antigen v
15	8e-19	24 / 64	BP regulation of complement activation
16	2e-17	40 / 222	BP adaptive immune response
17	3e-17	20 / 47	BP complement activation
18	2e-16	22 / 64	BP complement activation, classical pathway
19	1e-15	31 / 148	BP chemotaxis
20	2e-15	26 / 103	BP response to bacterium
21	6e-15	20 / 59	BP positive regulation of T cell proliferation
22	2e-13	38 / 261	BP cell surface receptor signaling pathway
23	4e-13	18 / 56	BP B cell receptor signaling pathway
24	6e-13	28 / 151	BP defense response to bacterium
25	4e-12	21 / 89	BP Fc-gamma receptor signaling pathway involved in phagocytosis
26	4e-12	27 / 151	BP cellular response to lipopolysaccharide
27	7e-12	27 / 154	BP receptor-mediated endocytosis
28	1e-11	57 / 594	BP cell adhesion
29	2e-11	27 / 160	BP T cell receptor signaling pathway
30	2e-11	28 / 172	BP positive regulation of I-kappaB kinase/NF-kappaB signaling
31	3e-11	20 / 88	BP cellular response to interferon-gamma
32	1e-10	14 / 42	BP toll-like receptor signaling pathway
33	1e-10	11 / 23	BP response to interferon-gamma
34	1e-10	13 / 36	BP blood circulation
35	3e-10	22 / 121	BP defense response
36	3e-10	46 / 459	BP viral process
37	4e-10	17 / 72	BP positive regulation of inflammatory response
38	4e-10	25 / 159	BP response to lipopolysaccharide
39	9e-10	16 / 66	BP phagocytosis
40	9e-10	13 / 41	BP negative regulation of viral genome replication

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	5e-89	150 / 564	immune system process
2	8e-67	109 / 388	immune response
3	4e-54	100 / 417	innate immune response
4	5e-46	86 / 364	inflammatory response
5	8e-45	321 / 4278	plasma membrane
6	8e-42	91 / 460	neutrophil degranulation
7	4e-37	436 / 7387	membrane
8	4e-34	50 / 155	regulation of immune response
9	1e-24	55 / 289	cytokine-mediated signaling pathway
10	2e-22	23 / 43	antigen processing and presentation
11	3e-22	42 / 184	defense response to virus
12	1e-21	130 / 1500	signal transduction
13	8e-21	37 / 152	leukocyte migration
14	2e-20	15 / 17	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
15	8e-19	24 / 64	regulation of complement activation

Correlation Cluster

Spot Summary: M

metagenes = 30
genes = 1727

<r> metagenes = 0.94

beta: r2= 4.89 / log p= -Inf

samples with spot = 20 (14.6 %)

- group 1 : 1 (9.1 %)
- group 2 : 2 (33.3 %)
- group 4 : 7 (31.8 %)
- group 6 : 5 (33.3 %)
- group 7 : 5 (19.2 %)

Spot Genelist

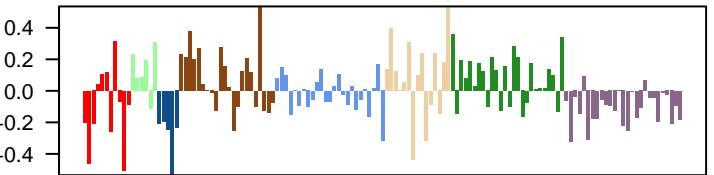
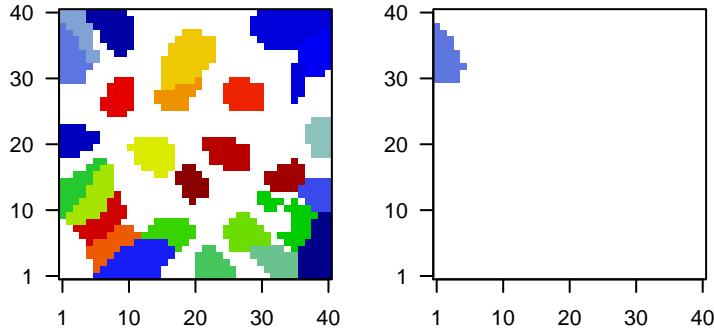
Rank	ID	max e	r	min e	Description
1	1561604_at	2.34	-0.84	0.47	
2	1556895_a_a	2.16	-0.46	0.28	
3	1555144_at	2.13	-0.64	0.48	
4	1553129_at	2.05	-0.56	0.32	SVEP1 sushi, von Willebrand factor type A, EGF and pentraxin doma
5	231630_at	1.98	-0.47	0.34	
6	243428_at	1.95	-0.98	0.58	KCNQ1 opposite strand/antisense transcript 1 [Source:HGNC
7	1562898_at	1.9	-0.71	0.55	
8	1554266_at	1.85	-0.48	0.31	
9	221969_at	1.82	-0.61	0.43	PAX5 paired box 5 [Source:HGNC Symbol;Acc:HGNC:8619]
10	242798_at	1.79	-0.48	0.39	long intergenic non-protein coding RNA 1424 [Source:HGNC
11	1562611_at	1.78	-1.01	0.44	
12	243112_at	1.76	-0.67	0.55	
13	1557835_at	1.75	-1.09	0.55	
14	217588_at	1.75	-0.72	0.51	CATSPER2 ion channel sperm associated 2 [Source:HGNC Symbol;A
15	232199_at	1.75	-0.66	0.43	novel transcript
16	1557825_at	1.74	-0.64	0.38	novel transcript, antisense to MSRA
17	239856_at	1.73	-1	0.25	
18	244239_at	1.72	-0.72	0.53	
19	238188_at	1.71	-0.5	0.48	IBA57 divergent transcript [Source:HGNC Symbol;Acc:HGNC
20	1567101_at	1.71	-0.72	0.47	

Geneset Overrepresentation

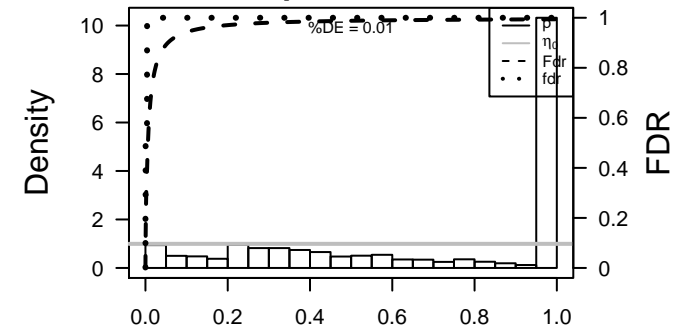
Rank	p-value	#in/all	Geneset
1	8e-08	28 / 342	BP chromatin organization
2	1e-06	66 / 1387	BP regulation of transcription, DNA-templated
3	1e-06	57 / 1145	BP regulation of transcription by RNA polymerase II
4	6e-06	27 / 400	BP chromatin binding
5	5e-05	61 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
6	5e-05	5 / 17	BP microtubule plus-end binding
7	3e-04	37 / 783	BP negative regulation of transcription by RNA polymerase II
8	3e-04	10 / 102	BP chromatin remodeling
9	3e-04	4 / 14	BP cardiac muscle cell proliferation
10	4e-04	5 / 25	BP positive regulation of microtubule polymerization
11	6e-04	5 / 27	BP microtubule bundle formation
12	1e-03	14 / 215	BP ubiquitin protein ligase activity
13	2e-03	26 / 545	BP protein ubiquitination
14	2e-03	14 / 227	BP microtubule binding
15	2e-03	3 / 11	BP actin filament depolymerization
16	2e-03	3 / 11	BP Leydig cell differentiation
17	2e-03	14 / 228	BP protein polyubiquitination
18	2e-03	21 / 412	BP negative regulation of cell population proliferation
19	3e-03	16 / 281	BP ubiquitin-dependent protein catabolic process
20	3e-03	14 / 234	BP protein deubiquitination
21	3e-03	4 / 24	BP negative regulation of neurogenesis
22	3e-03	3 / 12	BP negative regulation of oligodendrocyte differentiation
23	3e-03	3 / 12	BP positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
24	3e-03	11 / 162	BP transcription initiation from RNA polymerase II promoter
25	3e-03	12 / 188	BP in utero embryonic development
26	4e-03	6 / 58	BP protein processing
27	4e-03	5 / 41	BP limb development
28	4e-03	3 / 13	BP positive regulation of keratinocyte differentiation
29	5e-03	4 / 27	BP embryonic hindlimb morphogenesis
30	5e-03	4 / 27	BP regulation of cell morphogenesis
31	6e-03	3 / 15	BP positive regulation of cartilage development
32	6e-03	3 / 15	BP positive regulation of cilium assembly
33	6e-03	3 / 15	BP positive regulation of nuclear-transcribed mRNA catabolic process, deaden
34	7e-03	24 / 541	BP negative regulation of transcription, DNA-templated
35	7e-03	3 / 16	BP ventricular trabecula myocardium morphogenesis
36	7e-03	13 / 233	BP heart development
37	8e-03	146 / 4740	BP cytosol
38	8e-03	4 / 31	BP ATP-dependent chromatin remodeling
39	8e-03	21 / 459	BP viral process
40	8e-03	8 / 112	BP microtubule cytoskeleton organization

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	8e-08	28 / 342	chromatin organization
2	1e-06	66 / 1387	regulation of transcription, DNA-templated
3	1e-06	57 / 1145	regulation of transcription by RNA polymerase II
4	6e-06	27 / 400	chromatin binding
5	5e-05	61 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
6	5e-05	5 / 17	microtubule plus-end binding
7	3e-04	37 / 783	negative regulation of transcription by RNA polymerase II
8	3e-04	10 / 102	chromatin remodeling
9	3e-04	4 / 14	cardiac muscle cell proliferation
10	4e-04	5 / 25	positive regulation of microtubule polymerization
11	6e-04	5 / 27	microtubule bundle formation
12	1e-03	14 / 215	ubiquitin protein ligase activity
13	2e-03	26 / 545	protein ubiquitination
14	2e-03	14 / 227	microtubule binding
15	2e-03	3 / 11	actin filament depolymerization

Correlation Cluster

Spot Summary: N

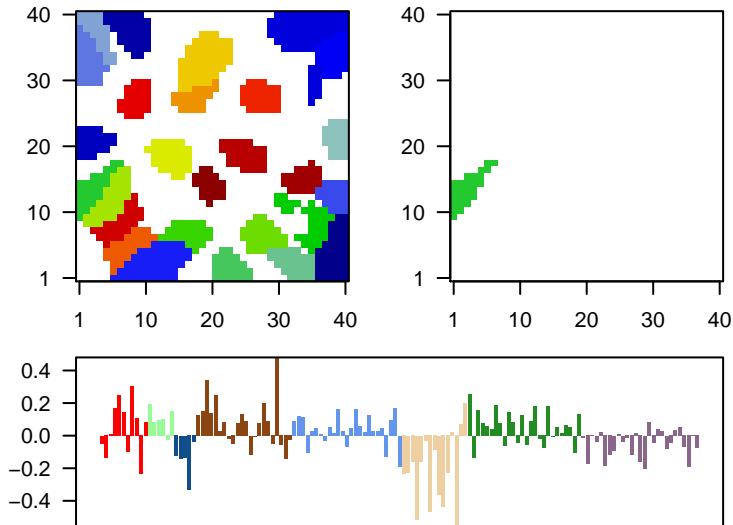
metagenes = 26
genes = 961

<r> metagenes = 0.96
<r> genes = 0.29
beta: r2= 2.81 / log p= -Inf

samples with spot = 7 (5.1 %)
group 1 : 2 (18.2 %)
group 4 : 3 (13.6 %)
group 6 : 1 (6.7 %)
group 7 : 1 (3.8 %)

Overview Map

Spot

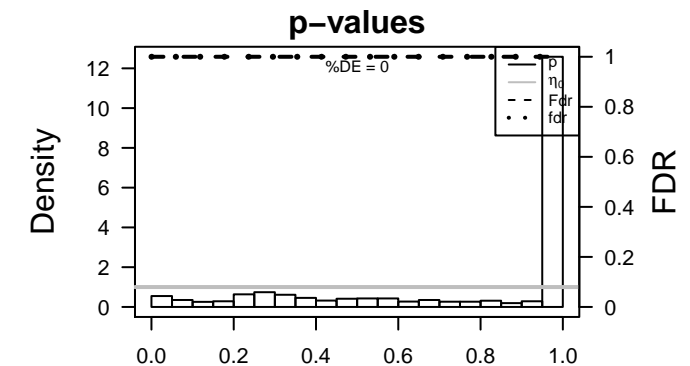


Spot Genelist

Rank	ID	max e	r	min e	Description
1	1559283_a_a	2.51	-0.6	0.44	novel transcript
2	235590_at	2.31	-0.78	0.59	SLF2 SMC5-SMC6 complex localization factor 2 [Source:HGNC S]
3	1558599_at	2.1	-0.72	0.49	
4	236017_at	2.09	-0.72	0.58	
5	230598_at	1.99	-0.68	0.43	novel transcript
6	238107_at	1.97	-0.75	0.58	novel transcript
7	220399_at	1.95	-1.03	0.57	long intergenic non-protein coding RNA 115 [Source:HGNC :
8	234787_at	1.95	-0.73	0.45	
9	1558600_a_a	1.95	-0.72	0.59	
10	219791_s_at	1.93	-0.35	0.18	HAND2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
11	205522_at	1.87	-1.37	0.43	
12	1563546_at	1.86	-0.73	0.33	
13	235319_at	1.86	-0.71	0.52	
14	1563229_at	1.83	-0.67	0.51	deleted in lymphocytic leukemia 2 [Source:HGNC Symbol;Ac
15	240101_at	1.82	-0.76	0.56	STAM antisense RNA 1 (head to head) [Source:HGNC Symb
16	239568_at	1.82	-0.93	0.37	PLEKHH2 pleckstrin homology, MyTH4 and FERM domain containi
17	233500_x_at	1.82	-0.97	0.64	CLEC2D C-type lectin domain family 2 member D [Source:HGNC Syrr
18	1561754_at	1.77	-0.86	0.35	
19	1570005_at	1.76	-0.43	0.28	
20	1567706_at	1.72	-1.01	0.5	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-05	23 / 358	BP mRNA processing
2	2e-04	26 / 484	BP cellular response to DNA damage stimulus
3	4e-04	55 / 1387	BP regulation of transcription, DNA-templated
4	7e-04	17 / 279	BP RNA splicing
5	7e-04	4 / 17	BP ATP-dependent microtubule motor activity, minus-end-directed
6	2e-03	19 / 366	BP DNA repair
7	2e-03	3 / 11	BP RNA cap binding
8	4e-03	3 / 13	BP glycerophospholipid catabolic process
9	4e-03	3 / 13	BP regulation of stem cell population maintenance
10	4e-03	4 / 27	BP positive regulation of viral genome replication
11	5e-03	3 / 14	BP intra-S DNA damage checkpoint
12	5e-03	7 / 83	BP activation of GTPase activity
13	5e-03	13 / 229	BP mRNA splicing, via spliceosome
14	6e-03	3 / 15	BP stress granule assembly
15	7e-03	3 / 16	BP preassembly of GPI anchor in ER membrane
16	7e-03	6 / 69	BP snRNA transcription by RNA polymerase II
17	8e-03	3 / 17	BP phosphatidylglycerol acyl-chain remodeling
18	9e-03	7 / 94	BP RNA processing
19	1e-02	5 / 56	BP mRNA 3'-end processing
20	1e-02	3 / 21	BP homeostasis of number of cells
21	1e-02	3 / 21	BP response to osmotic stress
22	2e-02	4 / 40	BP intracellular transport involved in cilium assembly
23	2e-02	9 / 158	BP DNA replication
24	2e-02	5 / 61	BP regulation of alternative mRNA splicing, via spliceosome
25	2e-02	4 / 41	BP RNA export from nucleus
26	2e-02	3 / 24	BP mRNA cis splicing, via spliceosome
27	2e-02	8 / 139	BP regulation of translation
28	2e-02	17 / 400	BP chromatin binding
29	2e-02	3 / 25	BP RNA splicing, via transesterification reactions
30	2e-02	3 / 25	BP spliceosomal complex assembly
31	2e-02	5 / 66	BP phospholipid metabolic process
32	2e-02	2 / 10	BP positive regulation of glucose metabolic process
33	2e-02	2 / 10	BP primary miRNA processing
34	3e-02	11 / 228	BP protein polyubiquitination
35	3e-02	3 / 27	BP mitotic spindle assembly
36	3e-02	4 / 47	BP response to UV
37	3e-02	2 / 11	BP histone mRNA catabolic process
38	3e-02	2 / 11	BP Leydig cell differentiation
39	3e-02	2 / 11	BP pyrimidine nucleotide-sugar transmembrane transport
40	3e-02	2 / 11	BP regulation of autophagosome assembly



BP

Rank	p-value	#in/all	Geneset
1	4e-05	23 / 358	mRNA processing
2	2e-04	26 / 484	cellular response to DNA damage stimulus
3	4e-04	55 / 1387	regulation of transcription, DNA-templated
4	7e-04	17 / 279	RNA splicing
5	7e-04	4 / 17	ATP-dependent microtubule motor activity, minus-end-directed
6	2e-03	19 / 366	DNA repair
7	2e-03	3 / 11	RNA cap binding
8	4e-03	3 / 13	glycerophospholipid catabolic process
9	4e-03	3 / 13	regulation of stem cell population maintenance
10	4e-03	4 / 27	positive regulation of viral genome replication
11	5e-03	3 / 14	intra-S DNA damage checkpoint
12	5e-03	7 / 83	activation of GTPase activity
13	5e-03	13 / 229	mRNA splicing, via spliceosome
14	6e-03	3 / 15	stress granule assembly
15	7e-03	3 / 16	preassembly of GPI anchor in ER membrane

Correlation Cluster

Spot Summary: O

metagenes = 33
genes = 964

<r> metagenes = 0.95
<r> genes = 0.34
beta: r2= 2.45 / log p= -Inf

samples with spot = 3 (2.2 %)
group 4 : 2 (9.1 %)
group 5 : 1 (4 %)

Spot Genelist

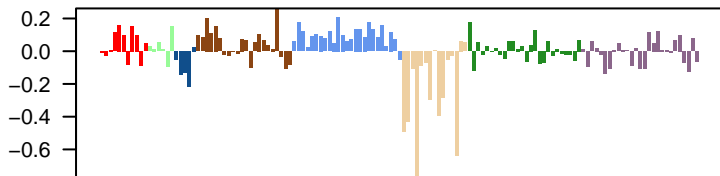
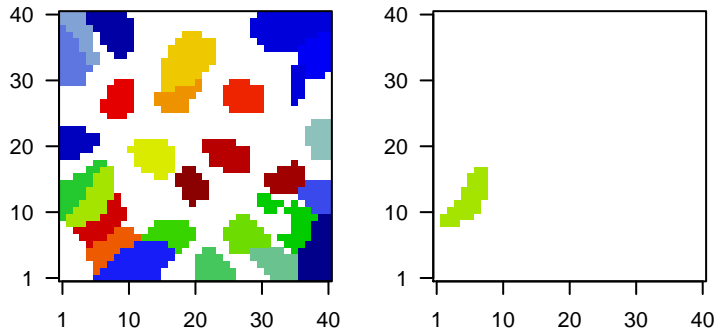
Rank	ID	max e	r	min e	Description
1	1562736_at	1.77	-0.86	0.24	LHX9 LIM homeobox 9 [Source:HGNC Symbol;Acc:HGNC:14222]
2	238207_at	1.72	-0.72	0.49	SMIM4 small integral membrane protein 4 [Source:HGNC Symbol;Acc:HGNC:14222]
3	235555_at	1.58	-1.4	0.74	
4	229407_at	1.56	-0.71	0.29	SDK1 sidekick cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:14222]
5	1570482_at	1.55	-0.67	0.3	
6	231331_at	1.5	-0.55	0.23	
7	241929_at	1.44	-0.44	0.26	
8	244319_at	1.44	-0.64	0.31	
9	230450_at	1.43	-0.97	0.56	
10	213582_at	1.42	-1.03	0.53	
11	227148_at	1.41	-1.86	0.66	PLEKHH2 pleckstrin homology, MyTH4 and FERM domain containing H
12	230314_at	1.41	-0.71	0.58	novel transcript
13	1560028_at	1.4	-0.72	0.45	NKAPD1 NKAP domain containing 1 [Source:HGNC Symbol;Acc:HGNC:14222]
14	238456_at	1.39	-1.67	0.63	
15	239041_at	1.37	-0.87	0.4	
16	231937_at	1.34	-0.81	0.52	novel transcript
17	235987_at	1.32	-1.15	0.45	novel transcript
18	1553299_at	1.31	-0.92	0.41	
19	236832_at	1.31	-1.51	0.64	adenylate cyclase 10, soluble pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:14222]
20	215563_s_at	1.31	-0.6	0.24	MST1L macrophage stimulating 1 like [Source:HGNC Symbol;Acc:HGNC:14222]

Geneset Overrepresentation

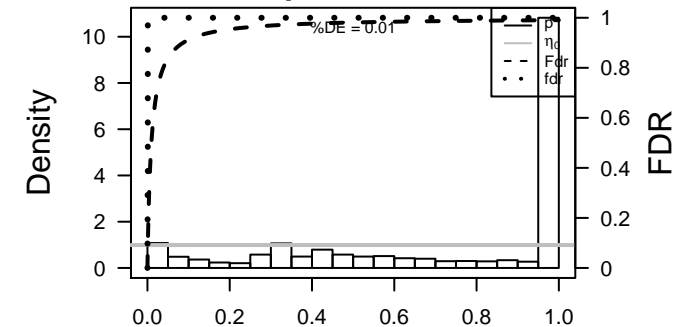
Rank	p-value	#in/all	Geneset
1	8e-12	40 / 358	BP mRNA processing
2	5e-11	80 / 1145	BP regulation of transcription by RNA polymerase II
3	5e-10	32 / 279	BP RNA splicing
4	2e-09	87 / 1387	BP regulation of transcription, DNA-templated
5	1e-08	35 / 366	BP DNA repair
6	3e-08	26 / 229	BP mRNA splicing, via spliceosome
7	4e-08	84 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
8	6e-08	40 / 484	BP cellular response to DNA damage stimulus
9	7e-07	30 / 342	BP chromatin organization
10	2e-06	14 / 94	BP RNA processing
11	3e-06	11 / 61	BP regulation of alternative mRNA splicing, via spliceosome
12	1e-05	200 / 4740	BP cytosol
13	1e-05	251 / 6202	BP cytoplasm
14	1e-05	6 / 18	BP cilium organization
15	2e-05	6 / 19	BP mRNA splice site selection
16	2e-05	13 / 101	BP mRNA transport
17	8e-05	14 / 130	BP regulation of signal transduction by p53 class mediator
18	8e-05	12 / 99	BP mRNA export from nucleus
19	2e-04	5 / 17	BP centriole replication
20	2e-04	5 / 17	BP miRNA metabolic process
21	2e-04	4 / 10	BP intracellular retrograde transport
22	2e-04	11 / 93	BP Golgi organization
23	3e-04	5 / 19	BP protein localization to centrosome
24	3e-04	6 / 30	BP histone lysine methylation
25	3e-04	37 / 630	BP cell cycle
26	4e-04	4 / 12	BP centriole-centriole cohesion
27	6e-04	14 / 158	BP DNA replication
28	8e-04	10 / 93	BP ciliary basal body-plasma membrane docking
29	8e-04	4 / 14	BP pre-miRNA processing
30	9e-04	7 / 49	BP cellular response to UV
31	9e-04	7 / 49	BP RNA metabolic process
32	1e-03	9 / 80	BP regulation of G2/M transition of mitotic cell cycle
33	1e-03	4 / 15	BP centrosome duplication
34	1e-03	25 / 400	BP chromatin binding
35	1e-03	25 / 400	BP protein serine/threonine kinase activity
36	1e-03	9 / 83	BP thiol-dependent ubiquitin-specific protease activity
37	1e-03	4 / 16	BP centrosome localization
38	1e-03	14 / 173	BP cilium assembly
39	2e-03	5 / 27	BP regulation of cell morphogenesis
40	2e-03	17 / 234	BP protein deubiquitination

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	8e-12	40 / 358	mRNA processing
2	5e-11	80 / 1145	regulation of transcription by RNA polymerase II
3	5e-10	32 / 279	RNA splicing
4	2e-09	87 / 1387	regulation of transcription, DNA-templated
5	1e-08	35 / 366	DNA repair
6	3e-08	26 / 229	mRNA splicing, via spliceosome
7	4e-08	84 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
8	6e-08	40 / 484	cellular response to DNA damage stimulus
9	7e-07	30 / 342	chromatin organization
10	2e-06	14 / 94	RNA processing
11	3e-06	11 / 61	regulation of alternative mRNA splicing, via spliceosome
12	1e-05	200 / 4740	cytosol
13	1e-05	251 / 6202	cytoplasm
14	1e-05	6 / 18	cilium organization
15	2e-05	6 / 19	mRNA splice site selection

Correlation Cluster

Spot Summary: P

metagenes = 26
genes = 809

<r> metagenes = 0.91
<r> genes = 0.26
beta: r2= 2.3 / log p= -Inf

samples with spot = 11 (8 %)
group 5 : 10 (40 %)
group 6 : 1 (6.7 %)

Spot Genelist

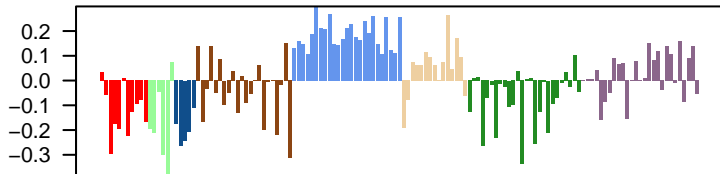
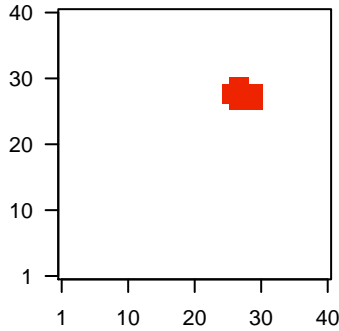
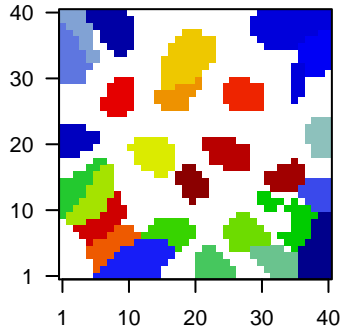
Rank	ID	max e	r	min e	Description
1	231155_at	2.98	-0.75	0.41	DEFB19 defensin beta 119 [Source:HGNC Symbol;Acc:HGNC:18099]
2	215443_at	2.15	-0.64	0.34	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;
3	231626_at	2.04	-0.67	0.22	TPH1 tryptophan hydroxylase 1 [Source:HGNC Symbol;Acc:HGNC:
4	235892_at	2.03	-0.94	0.69	COLCA1 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:H
5	210683_at	2.03	-0.52	0.28	NRTN neurturin [Source:HGNC Symbol;Acc:HGNC:8007]
6	206406_at	1.98	-0.7	0.41	SMCP sperm mitochondria associated cysteine rich protein [Source:
7	237471_at	1.92	-1.68	0.41	
8	1555854_at	1.9	-0.94	0.39	AKR1C1 aldo-keto reductase family 1 member C1 [Source:HGNC Syn
9	207302_at	1.9	-0.62	0.34	SGCG sarcoglycan gamma [Source:HGNC Symbol;Acc:HGNC:1080
10	236383_at	1.74	-0.92	0.58	
11	215059_at	1.72	-0.81	0.31	
12	232122_s_at	1.56	-1.54	0.6	VEPH1 ventricular zone expressed PH domain containing 1 [Source:!
13	229759_s_at	1.55	-0.86	0.41	VEPH1 ventricular zone expressed PH domain containing 1 [Source:!
14	238625_at	1.53	-1.1	0.46	FYB2 FYN binding protein 2 [Source:HGNC Symbol;Acc:HGNC:27
15	214601_at	1.52	-0.74	0.31	TPH1 tryptophan hydroxylase 1 [Source:HGNC Symbol;Acc:HGNC:
16	243060_at	1.52	-0.78	0.63	long intergenic non-protein coding RNA 1532 [Source:HGNC
17	1558858_at	1.51	-0.45	0.37	novel transcript, antisense to ID4
18	242601_at	1.49	-0.45	0.34	HEPACAM2 HEPACAM family member 2 [Source:HGNC Symbol;Acc:HG
19	208195_at	1.48	-0.87	0.52	TTN titin [Source:HGNC Symbol;Acc:HGNC:12403]
20	232481_s_at	1.48	-0.51	0.21	SLITRK6 SLIT and NTRK like family member 6 [Source:HGNC Symbol

Geneset Overrepresentation

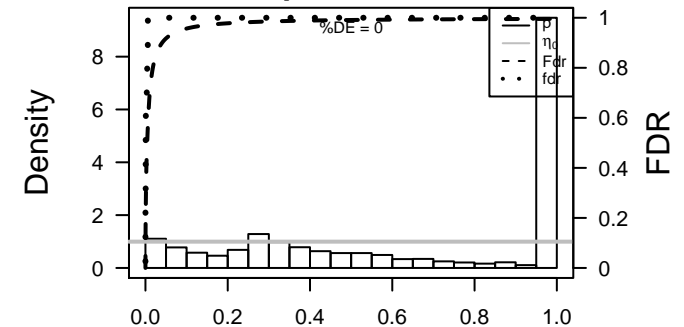
Rank	p-value	#in/all	Geneset
1	2e-10	188 / 4740	BP cytosol
2	9e-06	209 / 6202	BP cytoplasm
3	8e-05	17 / 222	BP Wnt signaling pathway
4	4e-04	23 / 400	BP protein serine/threonine kinase activity
5	4e-04	4 / 14	BP ectoderm development
6	5e-04	4 / 15	BP negative regulation of TORC1 signaling
7	5e-04	4 / 15	BP negative regulation of ubiquitin-dependent protein catabolic process
8	6e-04	33 / 684	BP phosphorylation
9	8e-04	12 / 156	BP fatty acid metabolic process
10	9e-04	24 / 455	BP intracellular signal transduction
11	2e-03	5 / 33	BP regulation of canonical Wnt signaling pathway
12	2e-03	11 / 148	BP neuron differentiation
13	2e-03	4 / 21	BP response to osmotic stress
14	2e-03	12 / 175	BP regulation of cell population proliferation
15	2e-03	3 / 11	BP positive regulation of extrinsic apoptotic signaling pathway in absence of lig
16	2e-03	3 / 11	BP regulation of protein kinase B signaling
17	3e-03	5 / 37	BP positive regulation of glucose import
18	3e-03	4 / 24	BP lipoprotein metabolic process
19	3e-03	3 / 12	BP developmental pigmentation
20	3e-03	3 / 12	BP negative regulation of oligodendrocyte differentiation
21	4e-03	5 / 40	BP chondrocyte differentiation
22	4e-03	3 / 13	BP alpha-linolenic acid metabolic process
23	4e-03	9 / 120	BP activation of MAPK activity
24	4e-03	4 / 26	BP chondroitin sulfate biosynthetic process
25	5e-03	4 / 27	BP hippo signaling
26	5e-03	6 / 62	BP response to calcium ion
27	6e-03	5 / 44	BP hormone-mediated signaling pathway
28	6e-03	4 / 28	BP pancreas development
29	6e-03	6 / 63	BP positive regulation of epithelial cell proliferation
30	6e-03	14 / 249	BP brain development
31	7e-03	5 / 46	BP fatty acid beta-oxidation
32	7e-03	23 / 505	BP nervous system development
33	7e-03	4 / 30	BP endoderm development
34	7e-03	11 / 179	BP protein dephosphorylation
35	8e-03	3 / 16	BP cytoskeleton-dependent intracellular transport
36	8e-03	3 / 16	BP heparan sulfate proteoglycan binding
37	8e-03	3 / 16	BP mitotic cell cycle arrest
38	9e-03	8 / 112	BP microtubule cytoskeleton organization
39	9e-03	24 / 545	BP protein ubiquitination
40	1e-02	13 / 237	BP regulation of apoptotic process

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-10	188 / 4740	cytosol
2	9e-06	209 / 6202	cytoplasm
3	8e-05	17 / 222	Wnt signaling pathway
4	4e-04	23 / 400	protein serine/threonine kinase activity
5	4e-04	4 / 14	ectoderm development
6	5e-04	4 / 15	negative regulation of TORC1 signaling
7	5e-04	4 / 15	negative regulation of ubiquitin-dependent protein catabolic process
8	6e-04	33 / 684	phosphorylation
9	8e-04	12 / 156	fatty acid metabolic process
10	9e-04	24 / 455	intracellular signal transduction
11	2e-03	5 / 33	regulation of canonical Wnt signaling pathway
12	2e-03	11 / 148	neuron differentiation
13	2e-03	4 / 21	response to osmotic stress
14	2e-03	12 / 175	regulation of cell population proliferation
15	2e-03	3 / 11	positive regulation of extrinsic apoptotic signaling pathway in absence of ligand

Correlation Cluster

Spot Summary: Q

metagenes = 26
genes = 807

<r> metagenes = 0.94
<r> genes = 0.46
beta: r2= 4.04 / log p= -Inf

samples with spot = 0 (0 %)

Spot Genelist

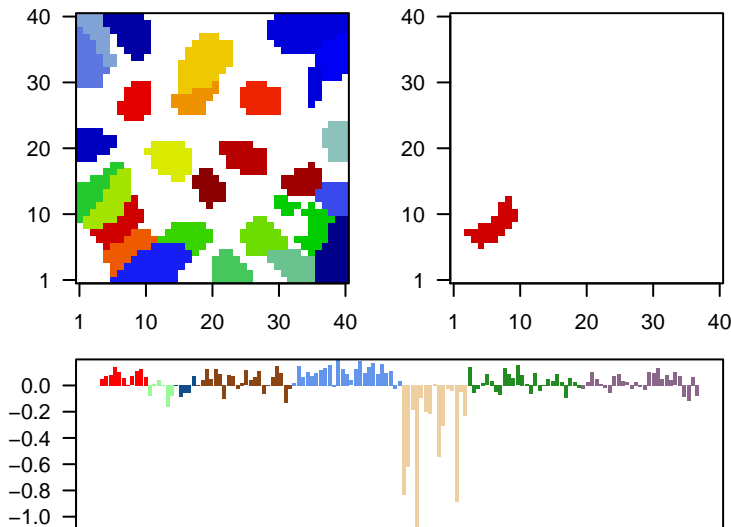
Rank	ID	max e	r	min e	Description
					Symbol
1	229352_at	1.47	-1	0.44	SPESP1 sperm equatorial segment protein 1 [Source:HGNC Symbol;A
2	235888_at	1.43	-1.21	0.4	glucuronidase, beta pseudogene 1 [Source:HGNC Symbol;Ar
3	235162_at	1.29	-0.92	0.59	MDM4 MDM4, p53 regulator [Source:HGNC Symbol;Acc:HGNC:697
4	238693_at	1.28	-1.02	0.6	PHC3 polyhomeotic homolog 3 [Source:HGNC Symbol;Acc:HGNC:1
5	243947_s_at	1.26	-0.81	0.49	
6	206546_at	1.17	-1.11	0.49	SYCP2 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
7	220397_at	1.15	-1.04	0.46	MDM1 Mdm1 nuclear protein [Source:HGNC Symbol;Acc:HGNC:295
8	1563483_at	1.15	-0.61	0.39	long intergenic non-protein coding RNA 869 [Source:HGNC :
9	230538_at	1.12	-1.64	0.71	SHC4 SHC adaptor protein 4 [Source:HGNC Symbol;Acc:HGNC:16
10	235947_at	1.12	-0.69	0.36	
11	238868_at	1.12	-0.81	0.47	UACA uveal autoantigen with coiled-coil domains and ankyrin repe
12	224441_s_at	1.11	-0.95	0.56	USP45 ubiquitin specific peptidase 45 [Source:HGNC Symbol;Acc:Hi
13	244033_at	1.11	-1.14	0.47	CEP128 centrosomal protein 128 [Source:HGNC Symbol;Acc:HGNC:2
14	214455_at	1.08	-1.03	0.31	HIST1H2B histone cluster 1 H2B family member c [Source:HGNC Symb
15	213652_at	1.07	-1.51	0.53	PCSK5 proprotein convertase subtilisin/kexin type 5 [Source:HGNC S
16	201664_at	1.06	-2.26	0.8	SMC4 structural maintenance of chromosomes 4 [Source:HGNC Sy
17	233058_at	1.05	-0.97	0.3	GPSM2 G protein signaling modulator 2 [Source:HGNC Symbol;Acc:G
18	220301_at	1.05	-1.49	0.52	CCDC102B coiled-coil domain containing 102B [Source:HGNC Symbol;A
19	209976_s_at	1.02	-1.08	0.4	CYP2E1 cytochrome P450 family 2 subfamily E member 1 [Source:HG
20	1553711_a_a	1.01	-0.9	0.37	FAM218A family with sequence similarity 218 member A [Source:HGNC

Geneset Overrepresentation

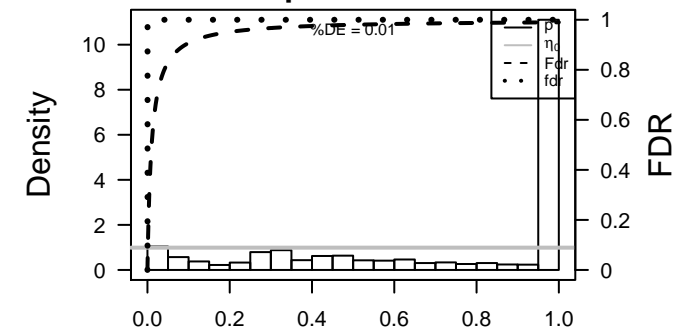
Rank	p-value	#in/all	Geneset
1	5e-15	85 / 1145	BP regulation of transcription by RNA polymerase II
2	1e-11	88 / 1387	BP regulation of transcription, DNA-templated
3	2e-10	36 / 358	BP mRNA processing
4	4e-10	85 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
5	2e-09	23 / 173	BP cilium assembly
6	2e-09	41 / 484	BP cellular response to DNA damage stimulus
7	3e-09	48 / 630	BP cell cycle
8	5e-09	34 / 366	BP DNA repair
9	5e-09	29 / 279	BP RNA splicing
10	1e-08	23 / 192	BP methylation
11	2e-08	10 / 33	BP tRNA methylation
12	3e-08	248 / 6202	BP cytoplasm
13	3e-07	32 / 394	BP cell division
14	2e-06	191 / 4740	BP cytosol
15	2e-06	19 / 180	BP cell projection organization
16	6e-06	12 / 83	BP thiol-dependent ubiquitin-specific protease activity
17	1e-05	23 / 281	BP ubiquitin-dependent protein catabolic process
18	2e-05	16 / 158	BP DNA replication
19	2e-05	5 / 13	BP regulation of mRNA splicing, via spliceosome
20	5e-05	8 / 45	BP non-motile cilium assembly
21	5e-05	5 / 15	BP DNA double-strand break processing
22	6e-05	19 / 229	BP mRNA splicing, via spliceosome
23	7e-05	5 / 16	BP establishment of planar polarity
24	1e-04	11 / 93	BP ciliary basal body-plasma membrane docking
25	1e-04	9 / 66	BP double-strand break repair
26	2e-04	20 / 267	BP ubiquitin-protein transferase activity
27	2e-04	10 / 84	BP tRNA processing
28	2e-04	6 / 30	BP ATP-dependent DNA helicase activity
29	2e-04	6 / 30	BP chromosome organization
30	2e-04	23 / 342	BP chromatin organization
31	3e-04	7 / 45	BP telomere maintenance
32	4e-04	25 / 400	BP chromatin binding
33	4e-04	8 / 61	BP double-strand break repair via nonhomologous end joining
34	4e-04	7 / 47	BP response to UV
35	5e-04	12 / 130	BP G2/M transition of mitotic cell cycle
36	5e-04	12 / 130	BP regulation of signal transduction by p53 class mediator
37	7e-04	9 / 81	BP double-strand break repair via homologous recombination
38	7e-04	12 / 134	BP cell cycle arrest
39	9e-04	30 / 545	BP protein ubiquitination
40	1e-03	7 / 54	BP DNA duplex unwinding

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	5e-15	85 / 1145	regulation of transcription by RNA polymerase II
2	1e-11	88 / 1387	regulation of transcription, DNA-templated
3	2e-10	36 / 358	mRNA processing
4	4e-10	85 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
5	2e-09	23 / 173	cilium assembly
6	2e-09	41 / 484	cellular response to DNA damage stimulus
7	3e-09	48 / 630	cell cycle
8	5e-09	34 / 366	DNA repair
9	5e-09	29 / 279	RNA splicing
10	1e-08	23 / 192	methylation
11	2e-08	10 / 33	tRNA methylation
12	3e-08	248 / 6202	cytoplasm
13	3e-07	32 / 394	cell division
14	2e-06	191 / 4740	cytosol
15	2e-06	19 / 180	cell projection organization

Correlation Cluster

Spot Summary: R

metagenes = 68
genes = 3940

<r> metagenes = 0.91

beta: r2= 2.11 / log p= -Inf

samples with spot = 12 (8.8 %)
group 6 : 12 (80 %)

Spot Genelist

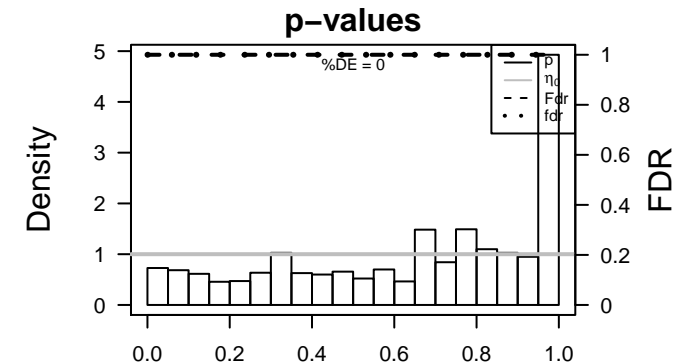
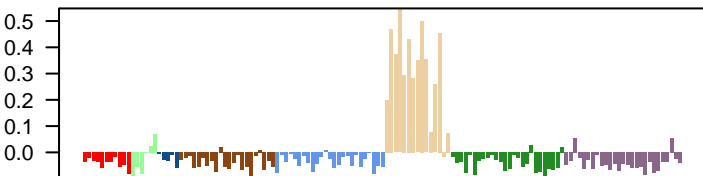
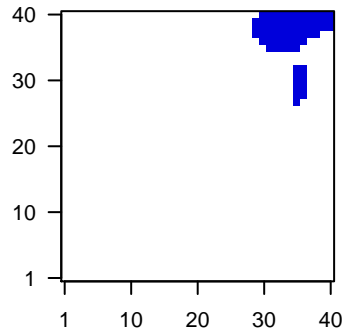
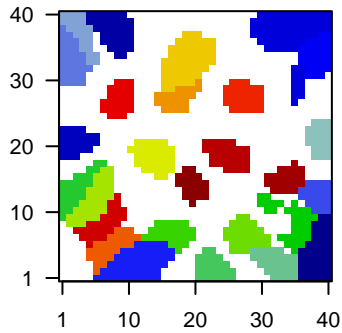
Rank	ID	max e	r	min e	Description
1	205033_s_at	2.95	-0.47	0.17	DEFA1 defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
2	1554648_a_at	2.54	-0.69	0.42	DUOXA1 dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC:24212]
3	214146_s_at	2.49	-0.81	0.25	PPBP pro-platelet basic protein [Source:HGNC Symbol;Acc:HGNC:25722]
4	1556711_at	2.41	-0.31	0.39	FAM216B family with sequence similarity 216 member B [Source:HGNC Symbol;Acc:HGNC:24212]
5	242009_at	2.4	-0.47	0.3	SLC6A4 solute carrier family 6 member 4 [Source:HGNC Symbol;Acc:HGNC:24212]
6	1555271_a_at	2.38	-0.63	0.15	TERT telomerase reverse transcriptase [Source:HGNC Symbol;Acc:HGNC:24212]
7	204419_x_at	2.36	-0.98	0.39	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:24212]
8	231597_x_at	2.31	-0.71	0.44	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:24212]
9	204848_x_at	2.27	-1.14	0.38	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:24212]
10	207337_at	2.19	-0.54	0.39	CTAG2 cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24212]
11	1559702_at	2.16	-0.61	0.49	ZKSCAN2 divergent transcript [Source:HGNC Symbol;Acc:HGNC:24212]
12	207739_s_at	2.11	-0.46	0.65	GAGE2EG antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
13	216648_s_at	2.1	-0.61	0.85	CPA3 carboxypeptidase A3 [Source:HGNC Symbol;Acc:HGNC:229]
14	205624_at	2.08	-0.45	0.36	CPA3 carboxypeptidase A3 [Source:HGNC Symbol;Acc:HGNC:229]
15	242135_at	2.01	-0.42	0.22	DUOX1 dual oxidase 1 [Source:HGNC Symbol;Acc:HGNC:3062]
16	219597_s_at	2.01	-0.65	0.26	DUOX1 dual oxidase 1 [Source:HGNC Symbol;Acc:HGNC:3062]
17	206359_at	1.99	-0.65	0.31	SOCS3 suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:HGNC:24212]
18	219914_at	1.98	-0.7	0.14	ECEL1 endothelin converting enzyme like 1 [Source:HGNC Symbol;Acc:HGNC:24212]
19	224997_x_at	1.98	-0.6	0.5	H19, imprinted maternally expressed transcript [Source:HGNC Symbol;Acc:HGNC:24212]
20	1565484_x_at	1.95	-0.68	0.3	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:HGNC:24212]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-04	25 / 115	BP keratinization
2	3e-04	31 / 159	BP positive regulation of protein kinase B signaling
3	6e-04	7 / 16	BP regulation of regulatory T cell differentiation
4	6e-04	6 / 12	BP positive regulation of insulin-like growth factor receptor signaling pathway
5	6e-04	15 / 59	BP regulation of megakaryocyte differentiation
6	9e-04	63 / 418	BP regulation of signaling receptor activity
7	2e-03	14 / 60	BP response to nutrient levels
8	2e-03	6 / 15	BP androgen metabolic process
9	3e-03	9 / 31	BP mammary gland development
10	4e-03	6 / 16	BP positive regulation of calcineurin-NFAT signaling cascade
11	4e-03	6 / 16	BP sympathetic nervous system development
12	4e-03	10 / 38	BP bicarbonate transport
13	4e-03	10 / 38	BP intracellular receptor signaling pathway
14	4e-03	102 / 777	BP G protein-coupled receptor signaling pathway
15	4e-03	8 / 27	BP peripheral nervous system development
16	4e-03	12 / 51	BP antimicrobial humoral response
17	5e-03	14 / 65	BP chemokine-mediated signaling pathway
18	5e-03	14 / 65	BP positive regulation of tyrosine phosphorylation of STAT protein
19	7e-03	18 / 95	BP anterior/posterior pattern specification
20	7e-03	8 / 29	BP adipose tissue development
21	7e-03	8 / 29	BP beta-catenin-TCF complex assembly
22	7e-03	5 / 13	BP male sex determination
23	8e-03	12 / 55	BP steroid hormone mediated signaling pathway
24	8e-03	8 / 30	BP response to testosterone
25	1e-02	5 / 14	BP ectoderm development
26	1e-02	5 / 14	BP negative regulation of cell-cell adhesion
27	1e-02	5 / 14	BP positive regulation of interleukin-17 production
28	1e-02	9 / 37	BP peptide cross-linking
29	1e-02	32 / 207	BP cytokine activity
30	1e-02	12 / 57	BP odontogenesis of dentin-containing tooth
31	1e-02	22 / 130	BP serine-type peptidase activity
32	1e-02	23 / 138	BP serine-type endopeptidase activity
33	1e-02	36 / 241	BP response to stimulus
34	1e-02	57 / 416	BP spermatogenesis
35	1e-02	6 / 20	BP telomere organization
36	1e-02	4 / 10	BP amelogenesis
37	1e-02	4 / 10	BP carnitine shuttle
38	1e-02	4 / 10	BP midgut development
39	1e-02	4 / 10	BP positive regulation of growth
40	1e-02	4 / 10	BP positive regulation of growth hormone secretion

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	2e-04	25 / 115	keratinization
2	3e-04	31 / 159	positive regulation of protein kinase B signaling
3	6e-04	7 / 16	regulation of regulatory T cell differentiation
4	6e-04	6 / 12	positive regulation of insulin-like growth factor receptor signaling pathway
5	6e-04	15 / 59	regulation of megakaryocyte differentiation
6	9e-04	63 / 418	regulation of signaling receptor activity
7	2e-03	14 / 60	response to nutrient levels
8	2e-03	6 / 15	androgen metabolic process
9	3e-03	9 / 31	mammary gland development
10	4e-03	6 / 16	positive regulation of calcineurin-NFAT signaling cascade
11	4e-03	6 / 16	sympathetic nervous system development
12	4e-03	10 / 38	bicarbonate transport
13	4e-03	10 / 38	intracellular receptor signaling pathway
14	4e-03	102 / 777	G protein-coupled receptor signaling pathway
15	4e-03	8 / 27	peripheral nervous system development

Correlation Cluster

Spot Summary: S

metagenes = 28
genes = 1844

<r> metagenes = 0.95

beta: r2= 1.69 / log p= -Inf

samples with spot = 9 (6.6 %)
group 6 : 9 (60 %)

Spot Genelist

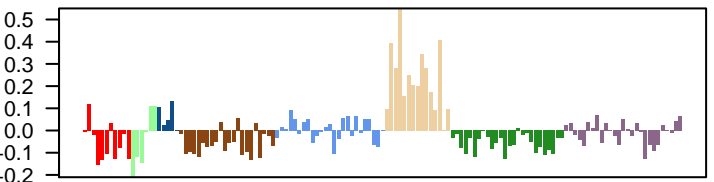
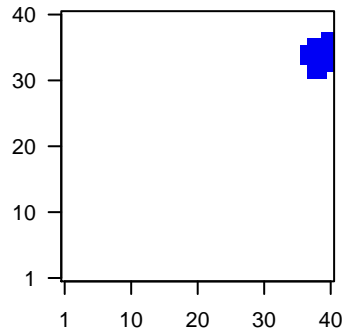
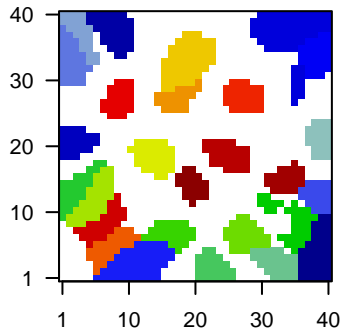
Rank	ID	max e	r	min e	Description
1	207519_at	2.46	-0.32	0.29	SLC6A4 solute carrier family 6 member 4 [Source:HGNC Symbol;Acc:HGNC:10000]
2	221298_s_at	2.08	-0.57	0.47	SLC22A8 solute carrier family 22 member 8 [Source:HGNC Symbol;Acc:HGNC:10000]
3	40284_at	1.95	-0.37	0.38	FOXA2 forkhead box A2 [Source:HGNC Symbol;Acc:HGNC:5022]
4	211560_s_at	1.93	-0.58	0.29	ALAS2 5'-aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
5	202222_s_at	1.89	-0.39	0.56	DES desmin [Source:HGNC Symbol;Acc:HGNC:2770]
6	231352_at	1.85	-0.63	0.3	SLC22A8 solute carrier family 22 member 8 [Source:HGNC Symbol;Acc:HGNC:10000]
7	207526_s_at	1.81	-0.67	0.45	IL1RL1 interleukin 1 receptor like 1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	239939_at	1.77	-0.67	0.42	novel transcript
9	1554097_a_a	1.75	-0.43	0.32	MIR31 host gene [Source:HGNC Symbol;Acc:HGNC:37187]
10	203673_at	1.71	-0.49	0.49	TG thyroglobulin [Source:HGNC Symbol;Acc:HGNC:11764]
11	243344_at	1.7	-0.51	0.32	novel transcript
12	206646_at	1.66	-0.56	0.35	GLI1 GLI family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:4200]
13	237775_x_at	1.65	-0.53	0.51	novel transcript
14	214642_x_at	1.62	-0.39	0.38	MAGEA10 MAGEA5 readthrough [Source:NCBI gene;Acc:NCBI:10000]
15	1555404_a_a	1.6	-0.44	0.4	DUOXA1 dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC:10000]
16	240033_at	1.59	-0.82	0.47	novel transcript
17	229096_at	1.57	-0.51	0.31	novel transcript
18	1562586_at	1.56	-0.44	0.56	novel transcript
19	209660_at	1.52	-0.4	0.37	TTR transthyretin [Source:HGNC Symbol;Acc:HGNC:12405]
20	1562903_at	1.5	-0.82	0.43	novel transcript

Geneset Overrepresentation

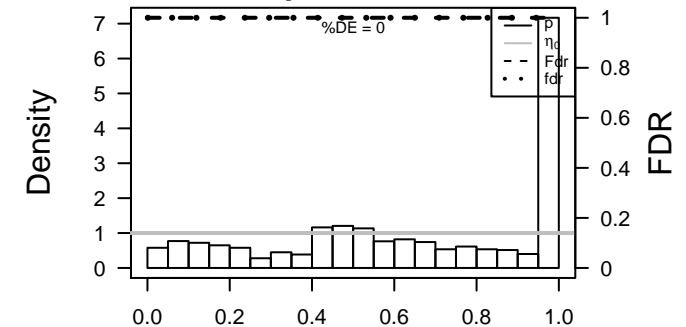
Rank	p-value	#in/all	Geneset
1	6e-04	17 / 138	BP serine-type endopeptidase activity
2	9e-04	5 / 16	BP regulation of regulatory T cell differentiation
3	9e-04	9 / 51	BP regulation of synaptic vesicle exocytosis
4	1e-03	13 / 96	BP cornification
5	2e-03	4 / 11	BP epithelial cell development
6	2e-03	9 / 55	BP steroid hormone mediated signaling pathway
7	2e-03	10 / 66	BP defense response to Gram-negative bacterium
8	2e-03	254 / 4278	BP plasma membrane
9	2e-03	4 / 12	BP low-density lipoprotein particle receptor activity
10	4e-03	10 / 74	BP defense response to Gram-positive bacterium
11	4e-03	8 / 52	BP T cell costimulation
12	5e-03	18 / 182	BP blood coagulation
13	5e-03	5 / 23	BP lipid storage
14	6e-03	14 / 130	BP serine-type peptidase activity
15	6e-03	5 / 24	BP G protein-coupled serotonin receptor signaling pathway
16	6e-03	5 / 24	BP thyroid gland development
17	7e-03	5 / 25	BP endocrine pancreas development
18	8e-03	8 / 57	BP odontogenesis of dentin-containing tooth
19	9e-03	5 / 26	BP protein kinase C-activating G protein-coupled receptor signaling pathway
20	1e-02	15 / 151	BP defense response to bacterium
21	1e-02	11 / 97	BP female pregnancy
22	1e-02	4 / 18	BP cell fate specification
23	1e-02	6 / 38	BP intracellular receptor signaling pathway
24	1e-02	15 / 154	BP receptor-mediated endocytosis
25	1e-02	3 / 10	BP cAMP biosynthetic process
26	1e-02	3 / 10	BP macrophage activation involved in immune response
27	1e-02	3 / 10	BP negative regulation of lipopolysaccharide-mediated signaling pathway
28	1e-02	12 / 115	BP keratinization
29	1e-02	4 / 19	BP response to iron ion
30	1e-02	7 / 51	BP antimicrobial humoral response
31	1e-02	10 / 89	BP epidermis development
32	1e-02	10 / 89	BP locomotory behavior
33	2e-02	3 / 11	BP negative regulation of growth of symbiont in host
34	2e-02	3 / 11	BP plasma membrane repair
35	2e-02	3 / 11	BP positive regulation of autophagosome assembly
36	2e-02	13 / 132	BP sensory perception of sound
37	2e-02	4 / 20	BP transmembrane receptor protein serine/threonine kinase signaling pathway
38	2e-02	53 / 777	BP G protein-coupled receptor signaling pathway
39	2e-02	20 / 236	BP chemical synaptic transmission
40	2e-02	5 / 31	BP homeostasis of number of cells within a tissue

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	6e-04	17 / 138	serine-type endopeptidase activity
2	9e-04	5 / 16	regulation of regulatory T cell differentiation
3	9e-04	9 / 51	regulation of synaptic vesicle exocytosis
4	1e-03	13 / 96	cornification
5	2e-03	4 / 11	epithelial cell development
6	2e-03	9 / 55	steroid hormone mediated signaling pathway
7	2e-03	10 / 66	defense response to Gram-negative bacterium
8	2e-03	254 / 4278	plasma membrane
9	2e-03	4 / 12	low-density lipoprotein particle receptor activity
10	4e-03	10 / 74	defense response to Gram-positive bacterium
11	4e-03	8 / 52	T cell costimulation
12	5e-03	18 / 182	blood coagulation
13	5e-03	5 / 23	lipid storage
14	6e-03	14 / 130	serine-type peptidase activity
15	6e-03	5 / 24	G protein-coupled serotonin receptor signaling pathway

Correlation Cluster

Spot Summary: T

metagenes = 21
genes = 1023

<r> metagenes = 0.94

beta: r2= 1.49 / log p= -Inf

samples with spot = 7 (5.1 %)

group 4 : 1 (4.5 %)

group 5 : 1 (4 %)

group 6 : 2 (13.3 %)

group 7 : 3 (11.5 %)

Spot Genelist

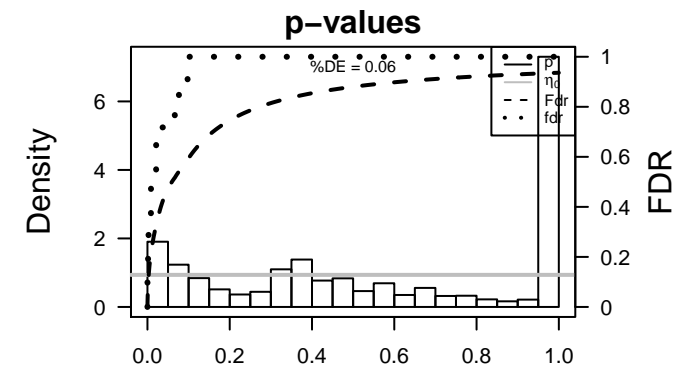
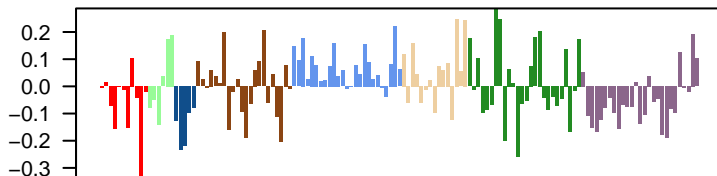
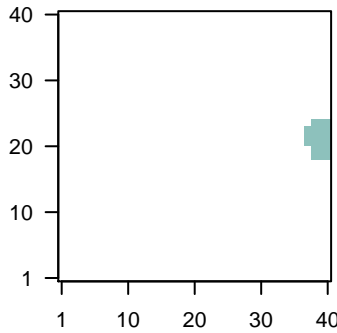
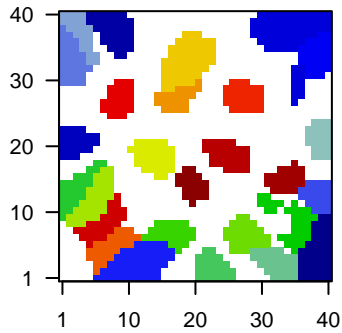
Rank	ID	max e	r	min e	Description
					Symbol
1	220205_at	2.17	-0.37	0.27	novel transcript
2	208468_at	2.15	-0.52	0.47	SOX21 SRY-box 21 [Source:HGNC Symbol;Acc:HGNC:11197]
3	230001_at	1.94	-0.59	0.25	MARCH9membrane associated ring-CH-type finger 9 [Source:HGNC
4	203365_s_at	1.87	-1.02	0.64	MMP15 matrix metallopeptidase 15 [Source:HGNC Symbol;Acc:HGN
5	1560035_at	1.85	-0.64	0.56	RTP5 receptor transporter protein 5 (putative) [Source:HGNC Symb
6	224505_s_at	1.82	-1.09	0.33	PLCD4 phospholipase C delta 4 [Source:HGNC Symbol;Acc:HGNC:5
7	1562169_at	1.81	-0.46	0.23	
8	216269_s_at	1.78	-0.69	0.36	ELN elastin [Source:HGNC Symbol;Acc:HGNC:3327]
9	223149_s_at	1.73	-0.55	0.48	PTPN23 protein tyrosine phosphatase, non-receptor type 23 [Source:l
10	213499_at	1.62	-0.99	0.37	CLCN2 chloride voltage-gated channel 2 [Source:HGNC Symbol;Acc
11	1556985_at	1.62	-0.73	0.32	
12	218892_at	1.62	-1.34	0.42	DCHS1 dachsous cadherin-related 1 [Source:HGNC Symbol;Acc:HG
13	206083_at	1.6	-1.24	0.33	ADGRB1adhesion G protein-coupled receptor B1 [Source:HGNC Syrr
14	213946_s_at	1.58	-0.99	0.41	OBSL1 obscurin like 1 [Source:HGNC Symbol;Acc:HGNC:29092]
15	1553139_s_at	1.57	-0.86	0.52	PLXNA3 plexin A3 [Source:HGNC Symbol;Acc:HGNC:9101]
16	229578_at	1.55	-0.68	0.26	JPH2 junctophilin 2 [Source:HGNC Symbol;Acc:HGNC:14202]
17	227496_at	1.47	-0.65	0.48	NR6A1 nuclear receptor subfamily 6 group A member 1 [Source:HGNC
18	207561_s_at	1.46	-1.41	0.6	ASIC3 acid sensing ion channel subunit 3 [Source:HGNC Symbol;Ac
19	204654_s_at	1.43	-0.83	0.45	TFAP2A transcription factor AP-2 alpha [Source:HGNC Symbol;Acc:H
20	203183_s_at	1.4	-0.87	0.67	SMARCD5W/SNF related, matrix associated, actin dependent regulatr

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-16	49 / 342	BP chromatin organization
2	7e-16	52 / 400	BP chromatin binding
3	2e-11	248 / 4740	BP cytosol
4	9e-10	299 / 6202	BP cytoplasm
5	3e-09	78 / 1086	BP positive regulation of transcription by RNA polymerase II
6	7e-09	80 / 1145	BP regulation of transcription by RNA polymerase II
7	1e-08	28 / 229	BP mRNA splicing, via spliceosome
8	2e-08	47 / 541	BP negative regulation of transcription, DNA-templated
9	7e-08	90 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
10	7e-08	10 / 31	BP ATP-dependent chromatin remodeling
11	8e-08	35 / 358	BP mRNA processing
12	3e-07	57 / 783	BP negative regulation of transcription by RNA polymerase II
13	8e-07	47 / 613	BP positive regulation of transcription, DNA-templated
14	1e-06	84 / 1387	BP regulation of transcription, DNA-templated
15	2e-06	39 / 484	BP cellular response to DNA damage stimulus
16	2e-06	15 / 99	BP mRNA export from nucleus
17	4e-06	11 / 56	BP mRNA 3'-end processing
18	6e-06	8 / 29	BP beta-catenin-TCF complex assembly
19	9e-06	26 / 279	BP RNA splicing
20	9e-06	9 / 40	BP histone deacetylation
21	9e-06	36 / 459	BP viral process
22	1e-05	14 / 101	BP mRNA transport
23	2e-05	14 / 102	BP chromatin remodeling
24	1e-04	13 / 106	BP positive regulation of DNA-binding transcription factor activity
25	1e-04	15 / 139	BP regulation of translation
26	2e-04	41 / 630	BP protein transport
27	2e-04	23 / 281	BP ubiquitin-dependent protein catabolic process
28	2e-04	7 / 36	BP endocytic recycling
29	3e-04	8 / 49	BP RNA metabolic process
30	3e-04	36 / 545	BP protein ubiquitination
31	4e-04	5 / 19	BP nucleosome disassembly
32	6e-04	6 / 30	BP histone lysine methylation
33	6e-04	6 / 30	BP negative regulation of proteasomal ubiquitin-dependent protein catabolic p
34	7e-04	9 / 69	BP snRNA transcription by RNA polymerase II
35	8e-04	9 / 70	BP transcription elongation from RNA polymerase II promoter
36	9e-04	4 / 13	BP protein deacetylation
37	9e-04	8 / 57	BP negative regulation of nucleic acid-templated transcription
38	9e-04	5 / 22	BP small GTPase binding
39	1e-03	30 / 455	BP intracellular signal transduction
40	1e-03	7 / 45	BP negative regulation of autophagy

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	1e-16	49 / 342	chromatin organization
2	7e-16	52 / 400	chromatin binding
3	2e-11	248 / 4740	cytosol
4	9e-10	299 / 6202	cytoplasm
5	3e-09	78 / 1086	positive regulation of transcription by RNA polymerase II
6	7e-09	80 / 1145	regulation of transcription by RNA polymerase II
7	1e-08	28 / 229	mRNA splicing, via spliceosome
8	2e-08	47 / 541	negative regulation of transcription, DNA-templated
9	7e-08	90 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
10	7e-08	10 / 31	ATP-dependent chromatin remodeling
11	8e-08	35 / 358	mRNA processing
12	3e-07	57 / 783	negative regulation of transcription by RNA polymerase II
13	8e-07	47 / 613	positive regulation of transcription, DNA-templated
14	1e-06	84 / 1387	regulation of transcription, DNA-templated
15	2e-06	39 / 484	cellular response to DNA damage stimulus

Correlation Cluster

Spot Summary: U

metagenes = 35
genes = 1469

<r> metagenes = 0.95

beta: r2= 5.79 / log p= -Inf

samples with spot = 26 (19 %)

group 1 : 2 (18.2 %)

group 2 : 1 (16.7 %)

group 4 : 7 (31.8 %)

group 5 : 1 (4 %)

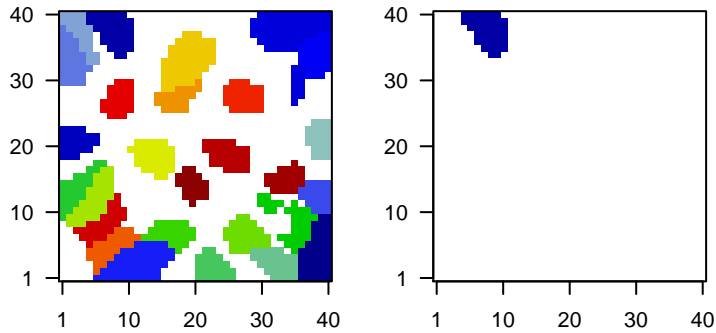
group 6 : 7 (46.7 %)

group 7 : 6 (23.1 %)

group 8 : 2 (7.4 %)

Overview Map

Spot

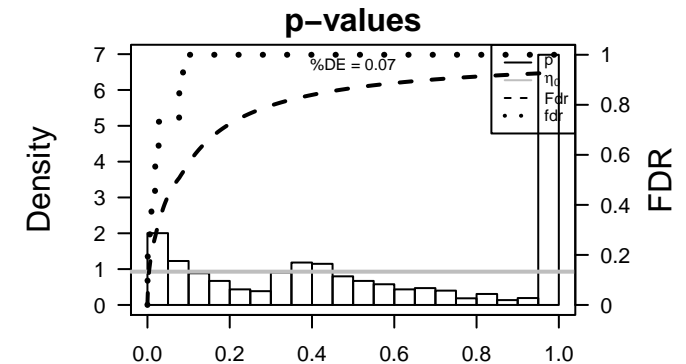
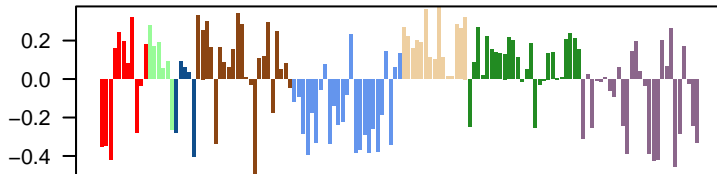


Spot Genelist

Rank	ID	max e	r	min e	Description
1	1553296_at	2.77	-0.34	0.21	ADGRG7adhesion G protein-coupled receptor G7 [Source:HGNC Syrn
2	205386_s_at	2.47	-0.83	0.4	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6
3	204713_s_at	2.44	-1.56	0.35	F5 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542
4	214265_at	2.22	-0.74	0.42	ITGA8 integrin subunit alpha 8 [Source:HGNC Symbol;Acc:HGNC:6
5	235059_at	2.19	-0.74	0.35	RAB12 RAB12, member RAS oncogene family [Source:HGNC Symb
6	215448_at	2.16	-1.33	0.54	
7	216007_at	2.14	-1.07	0.62	
8	1563331_at	2.1	-0.74	0.59	
9	226211_at	2.09	-1.04	0.45	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1-
10	240728_at	2.08	-0.93	0.72	
11	237943_at	2.04	-1.36	0.81	TMCC1 transmembrane and coiled-coil domain family 1 [Source:HGNC
12	234597_at	2.04	-0.92	0.65	
13	242319_at	2.03	-0.87	0.57	DGKG diacylglycerol kinase gamma [Source:HGNC Symbol;Acc:HG
14	229775_s_at	2.03	-0.84	0.59	
15	216518_at	2	-0.75	0.45	
16	233884_at	1.96	-0.95	0.63	
17	207213_s_at	1.95	-1.36	0.7	USP2 ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG
18	244774_at	1.94	-1.09	0.36	PHACTR2 phosphatase and actin regulator 2 [Source:HGNC Symbol;Ac
19	226210_s_at	1.9	-1.12	0.47	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1-
20	200952_s_at	1.89	-1.58	0.57	CCND2 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-15	344 / 6202	BP cytoplasm
2	6e-13	271 / 4740	BP cytosol
3	3e-11	88 / 1086	BP positive regulation of transcription by RNA polymerase II
4	2e-09	52 / 541	BP negative regulation of transcription, DNA-templated
5	1e-08	33 / 279	BP RNA splicing
6	2e-08	38 / 358	BP mRNA processing
7	2e-07	52 / 623	BP protein phosphorylation
8	2e-07	35 / 342	BP chromatin organization
9	4e-07	60 / 783	BP negative regulation of transcription by RNA polymerase II
10	6e-07	50 / 613	BP positive regulation of transcription, DNA-templated
11	9e-07	37 / 400	BP chromatin binding
12	9e-07	42 / 484	BP cellular response to DNA damage stimulus
13	2e-06	28 / 267	BP ubiquitin-protein transferase activity
14	3e-06	52 / 684	BP phosphorylation
15	4e-06	7 / 19	BP regulation of DNA replication
16	6e-06	35 / 400	BP protein serine/threonine kinase activity
17	1e-05	74 / 1145	BP regulation of transcription by RNA polymerase II
18	2e-05	85 / 1387	BP regulation of transcription, DNA-templated
19	2e-05	11 / 61	BP peptidyl-threonine phosphorylation
20	2e-05	11 / 61	BP regulation of alternative mRNA splicing, via spliceosome
21	2e-05	23 / 227	BP microtubule binding
22	5e-05	76 / 1242	BP Golgi apparatus
23	6e-05	45 / 630	BP protein transport
24	6e-05	22 / 224	BP negative regulation of gene expression
25	8e-05	40 / 545	BP protein ubiquitination
26	9e-05	13 / 97	BP transforming growth factor beta receptor signaling pathway
27	1e-04	15 / 129	BP rhythmic process
28	1e-04	7 / 31	BP anterograde axonal transport
29	1e-04	82 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
30	2e-04	7 / 32	BP regulation of microtubule cytoskeleton organization
31	2e-04	18 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
32	2e-04	9 / 54	BP axon cytoplasm
33	2e-04	10 / 66	BP protein autoubiquitination
34	2e-04	21 / 228	BP protein polyubiquitination
35	2e-04	43 / 630	BP cell cycle
36	2e-04	24 / 281	BP ubiquitin-dependent protein catabolic process
37	3e-04	5 / 16	BP positive regulation of neuron migration
38	3e-04	53 / 843	BP DNA-binding transcription factor activity
39	4e-04	13 / 112	BP microtubule cytoskeleton organization
40	5e-04	6 / 27	BP microtubule bundle formation



BP

Rank	p-value	#in/all	Geneset
1	3e-15	344 / 6202	cytoplasm
2	6e-13	271 / 4740	cytosol
3	3e-11	88 / 1086	positive regulation of transcription by RNA polymerase II
4	2e-09	52 / 541	negative regulation of transcription, DNA-templated
5	1e-08	33 / 279	RNA splicing
6	2e-08	38 / 358	mRNA processing
7	2e-07	52 / 623	protein phosphorylation
8	2e-07	35 / 342	chromatin organization
9	4e-07	60 / 783	negative regulation of transcription by RNA polymerase II
10	6e-07	50 / 613	positive regulation of transcription, DNA-templated
11	9e-07	37 / 400	chromatin binding
12	9e-07	42 / 484	cellular response to DNA damage stimulus
13	2e-06	28 / 267	ubiquitin-protein transferase activity
14	3e-06	52 / 684	phosphorylation
15	4e-06	7 / 19	regulation of DNA replication

Correlation Cluster

Spot Summary: V

metagenes = 23
genes = 1191

<r> metagenes = 0.96

beta: r2= 7.92 / log p= -Inf

samples with spot = 31 (22.6 %)

group 1 : 3 (27.3 %)

group 2 : 4 (66.7 %)

group 4 : 10 (45.5 %)

group 6 : 6 (40 %)

group 7 : 8 (30.8 %)

Spot Genelist

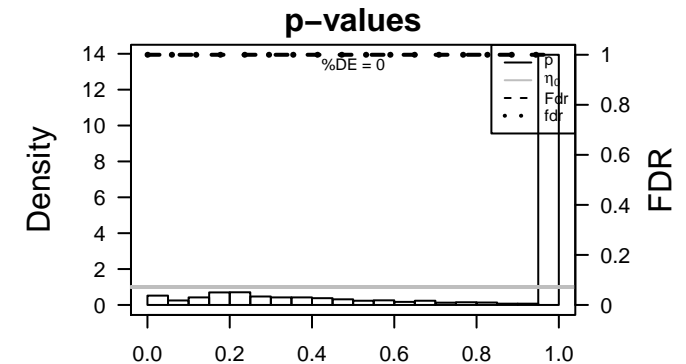
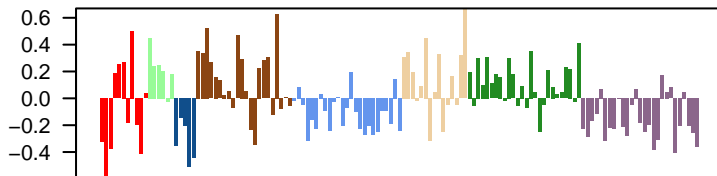
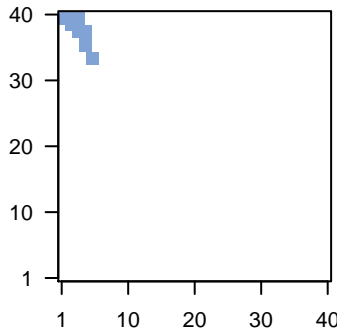
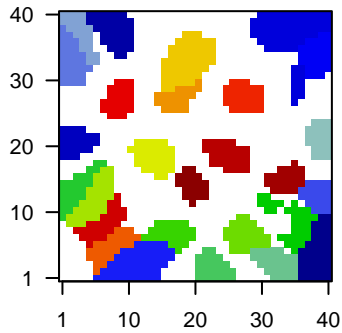
Rank	ID	max e	r	min e	Description
1	1562440_at	2.29	-0.64	0.64	
2	1566482_at	2.19	-0.81	0.53	novel transcript
3	232453_at	2.1	-1.18	0.44	
4	244042_x_at	2.08	-1.91	0.49	
5	1563426_a_a	1.96	-0.74	0.66	novel transcript
6	1552337_s_at	1.95	-0.8	0.42	HOXD4 homeobox D4 [Source:NCBI gene;Acc:3233]
7	232925_at	1.9	-1.69	0.66	
8	239591_at	1.89	-1.18	0.23	
9	240158_at	1.82	-0.7	0.54	
10	234082_at	1.82	-1.64	0.28	
11	214235_at	1.82	-0.93	0.48	CYP3A5 cytochrome P450 family 3 subfamily A member 5 [Source:HGNC]
12	211781_x_at	1.82	-0.75	0.63	
13	215943_at	1.82	-1.1	0.72	
14	233089_at	1.8	-0.76	0.71	QRSL1 QRSL1, glutaminyl-tRNA amidotransferase subunit A [Source:HGNC]
15	1558791_at	1.79	-0.6	0.43	firre intergenic repeating RNA element [Source:HGNC Symbol]
16	240663_at	1.78	-0.8	0.46	
17	216259_at	1.76	-1.04	0.49	
18	213247_at	1.76	-0.81	0.27	SVEP1 sushi, von Willebrand factor type A, EGF and pentraxin doma
19	243077_at	1.74	-1.14	0.39	
20	239602_at	1.71	-0.5	0.43	BRWD1 antisense RNA 2 [Source:HGNC Symbol;Acc:HGNC]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-04	13 / 264	BP vesicle-mediated transport
2	5e-04	3 / 11	BP histone mRNA catabolic process
3	5e-04	5 / 45	BP telomere maintenance
4	8e-04	7 / 101	BP mRNA transport
5	1e-03	4 / 30	BP ATP-dependent DNA helicase activity
6	1e-03	5 / 54	BP DNA duplex unwinding
7	1e-03	3 / 15	BP DNA double-strand break processing
8	2e-03	4 / 37	BP glycogen metabolic process
9	7e-03	3 / 26	BP protein export from nucleus
10	7e-03	18 / 630	BP protein transport
11	7e-03	5 / 81	BP double-strand break repair via homologous recombination
12	9e-03	5 / 85	BP positive regulation of neuron differentiation
13	9e-03	4 / 55	BP somitogenesis
14	9e-03	2 / 10	BP hepatocyte apoptotic process
15	9e-03	2 / 10	BP SRP-dependent cotranslational protein targeting to membrane, translocation
16	9e-03	12 / 366	BP DNA repair
17	1e-02	3 / 31	BP reciprocal meiotic recombination
18	1e-02	2 / 11	BP neural tube formation
19	1e-02	2 / 11	BP protein auto-ADP-ribosylation
20	1e-02	2 / 11	BP protein quality control for misfolded or incompletely synthesized proteins
21	1e-02	2 / 11	BP telomere maintenance via recombination
22	1e-02	3 / 32	BP positive regulation of BMP signaling pathway
23	1e-02	4 / 60	BP COPII vesicle coating
24	1e-02	4 / 61	BP double-strand break repair via nonhomologous end joining
25	1e-02	2 / 12	BP cell proliferation in forebrain
26	1e-02	2 / 12	BP positive regulation of double-strand break repair
27	1e-02	7 / 170	BP protein stabilization
28	1e-02	14 / 484	BP cellular response to DNA damage stimulus
29	2e-02	3 / 35	BP spindle assembly
30	2e-02	5 / 97	BP DNA recombination
31	2e-02	2 / 13	BP ear development
32	2e-02	2 / 13	BP inflammatory response to antigenic stimulus
33	2e-02	2 / 13	BP negative regulation of necroptotic process
34	2e-02	2 / 13	BP positive regulation of keratinocyte differentiation
35	2e-02	7 / 176	BP endoplasmic reticulum to Golgi vesicle-mediated transport
36	2e-02	2 / 15	BP muscle cell differentiation
37	2e-02	2 / 15	BP negative regulation of androgen receptor signaling pathway
38	2e-02	2 / 15	BP negative regulation of TORC1 signaling
39	2e-02	8 / 227	BP microtubule binding
40	2e-02	3 / 40	BP chondrocyte differentiation

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	2e-04	13 / 264	vesicle-mediated transport
2	5e-04	3 / 11	histone mRNA catabolic process
3	5e-04	5 / 45	telomere maintenance
4	8e-04	7 / 101	mRNA transport
5	1e-03	4 / 30	ATP-dependent DNA helicase activity
6	1e-03	5 / 54	DNA duplex unwinding
7	1e-03	3 / 15	DNA double-strand break processing
8	2e-03	4 / 37	glycogen metabolic process
9	7e-03	3 / 26	protein export from nucleus
10	7e-03	18 / 630	protein transport
11	7e-03	5 / 81	double-strand break repair via homologous recombination
12	9e-03	5 / 85	positive regulation of neuron differentiation
13	9e-03	4 / 55	somitogenesis
14	9e-03	2 / 10	hepatocyte apoptotic process
15	9e-03	2 / 10	SRP-dependent cotranslational protein targeting to membrane, translocation

Correlation Cluster

Spot Summary: W

metagenes = 23
genes = 749

<r> metagenes = 0.94
<r> genes = 0.32
beta: r2= 2.84 / log p= -Inf

samples with spot = 4 (2.9 %)
group 5 : 4 (16 %)

Spot Genelist

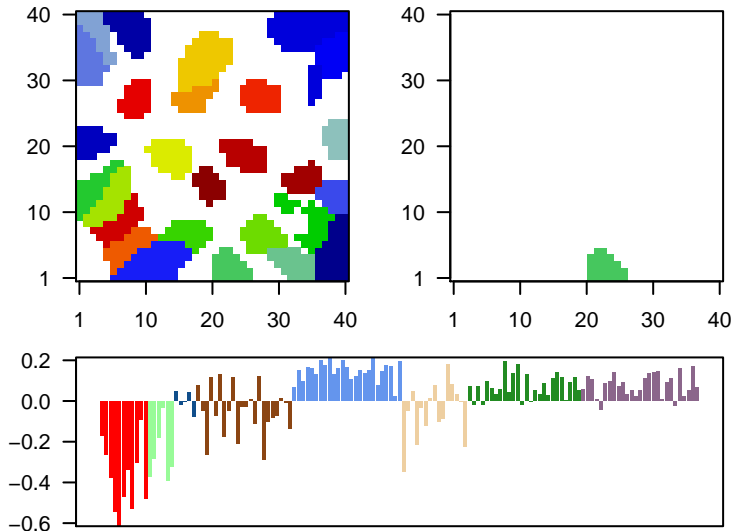
Rank	ID	max e	r	min e	Description
1	206159_at	2.05	-1.3	0.41	GDF10 growth differentiation factor 10 [Source:HGNC Symbol;Acc:HGNC:10000]
2	208334_at	1.84	-1.17	0.54	NDST4 N-deacetylase and N-sulfotransferase 4 [Source:HGNC Syrr]
3	207276_at	1.83	-0.93	0.39	CDR1 cerebellar degeneration related protein 1 [Source:HGNC Syrr]
4	1562102_at	1.79	-0.66	0.36	
5	1560477_a_a	1.68	-1.08	0.35	SAMD11 sterile alpha motif domain containing 11 [Source:HGNC Syml]
6	215527_at	1.68	-0.78	0.41	KHDRBS2 3'UTR overlapping transcript 1 [Source:HGNC Syr]
7	1553179_at	1.64	-1.07	0.45	ADAMTS4 ADAM metalloproteinase with thrombospondin type 1 motif 19
8	239624_at	1.63	-1.79	0.28	
9	1556401_a_a	1.62	-0.78	0.44	novel transcript
10	244128_x_at	1.54	-1.34	0.29	GLIS1 GLIS family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:10000]
11	244114_x_at	1.52	-1.63	0.34	
12	209652_s_at	1.52	-1.26	0.26	PGF placental growth factor [Source:HGNC Symbol;Acc:HGNC:88]
13	239230_at	1.51	-1.7	0.51	HES5 hes family bHLH transcription factor 5 [Source:HGNC Symbol]
14	1561479_at	1.51	-1.07	0.6	TEC
15	207505_at	1.51	-0.79	0.53	PRKG2 protein kinase cGMP-dependent 2 [Source:HGNC Symbol;Acc:HGNC:10000]
16	214974_x_at	1.5	-1.14	0.48	CXCL5 C-X-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:10000]
17	242245_at	1.49	-1.48	0.61	
18	216594_x_at	1.47	-2.14	0.4	AKR1C1 aldo-keto reductase family 1 member C1 [Source:HGNC Syn]
19	228915_at	1.46	-1.66	0.43	DACH1 dachshund family transcription factor 1 [Source:HGNC Symb]
20	232832_at	1.46	-0.72	0.38	novel transcript

Geneset Overrepresentation

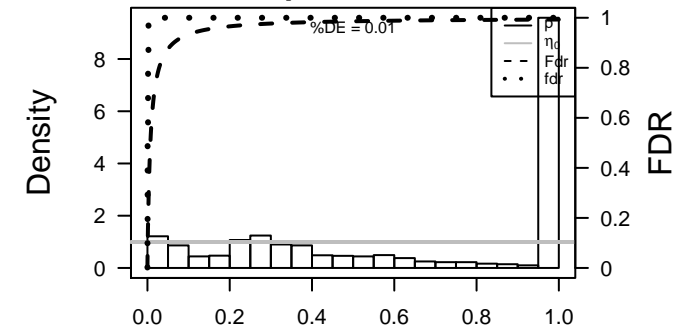
Rank	p-value	#in/all	Geneset
1	8e-11	177 / 4740	BP cytosol
2	6e-07	32 / 505	BP nervous system development
3	6e-06	13 / 120	BP translational initiation
4	1e-05	193 / 6202	BP cytoplasm
5	2e-05	31 / 574	BP synapse
6	3e-05	5 / 16	BP glutamate receptor signaling pathway
7	4e-05	9 / 69	BP SRP-dependent cotranslational protein targeting to membrane
8	6e-05	4 / 10	BP cardiac left ventricle morphogenesis
9	1e-04	11 / 117	BP negative regulation of cell migration
10	1e-04	10 / 98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
11	1e-04	7 / 48	BP inositol phosphate metabolic process
12	1e-04	11 / 119	BP postsynapse
13	3e-04	27 / 541	BP negative regulation of transcription, DNA-templated
14	3e-04	9 / 90	BP viral transcription
15	3e-04	7 / 55	BP somitogenesis
16	3e-04	8 / 73	BP modulation of chemical synaptic transmission
17	4e-04	11 / 133	BP central nervous system development
18	8e-04	4 / 18	BP action potential
19	1e-03	16 / 276	BP translation
20	1e-03	10 / 129	BP rhythmic process
21	1e-03	12 / 179	BP protein dephosphorylation
22	1e-03	7 / 70	BP positive regulation of translation
23	1e-03	3 / 10	BP locomotor rhythm
24	2e-03	4 / 23	BP synaptic membrane adhesion
25	2e-03	14 / 240	BP postsynaptic membrane
26	2e-03	4 / 24	BP negative regulation of epithelial to mesenchymal transition
27	3e-03	3 / 12	BP epithelial to mesenchymal transition involved in endocardial cushion formation
28	3e-03	23 / 513	BP positive regulation of cell population proliferation
29	3e-03	6 / 61	BP positive regulation of synapse assembly
30	4e-03	4 / 27	BP protein K63-linked deubiquitination
31	4e-03	13 / 233	BP heart development
32	4e-03	13 / 234	BP protein deubiquitination
33	6e-03	3 / 16	BP negative regulation of epithelial cell migration
34	6e-03	3 / 16	BP negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage
35	6e-03	4 / 31	BP anterograde axonal transport
36	6e-03	9 / 139	BP regulation of translation
37	6e-03	10 / 165	BP positive regulation of protein phosphorylation
38	7e-03	3 / 17	BP plasma membrane organization
39	7e-03	6 / 72	BP negative regulation of protein binding
40	8e-03	18 / 398	BP positive regulation of gene expression

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	8e-11	177 / 4740	cytosol
2	6e-07	32 / 505	nervous system development
3	6e-06	13 / 120	translational initiation
4	1e-05	193 / 6202	cytoplasm
5	2e-05	31 / 574	synapse
6	3e-05	5 / 16	glutamate receptor signaling pathway
7	4e-05	9 / 69	SRP-dependent cotranslational protein targeting to membrane
8	6e-05	4 / 10	cardiac left ventricle morphogenesis
9	1e-04	11 / 117	negative regulation of cell migration
10	1e-04	10 / 98	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
11	1e-04	7 / 48	inositol phosphate metabolic process
12	1e-04	11 / 119	postsynapse
13	3e-04	27 / 541	negative regulation of transcription, DNA-templated
14	3e-04	9 / 90	viral transcription
15	3e-04	7 / 55	somitogenesis

Correlation Cluster

Spot Summary: X

metagenes = 24
genes = 572

<r> metagenes = 0.94
<r> genes = 0.26
beta: r2= 1.09 / log p= -Inf

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

Spot Genelist

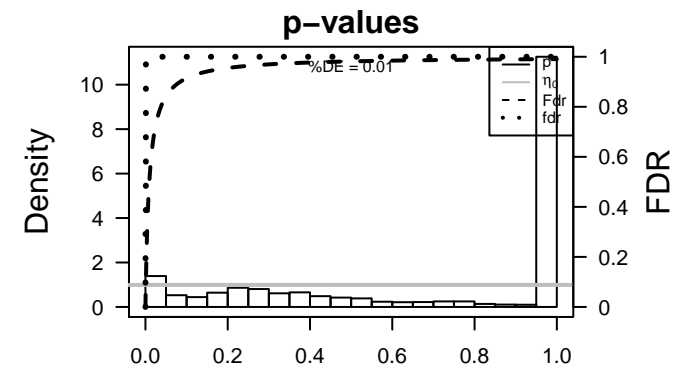
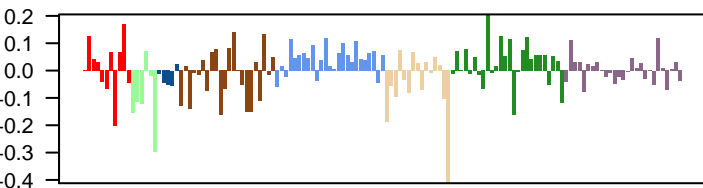
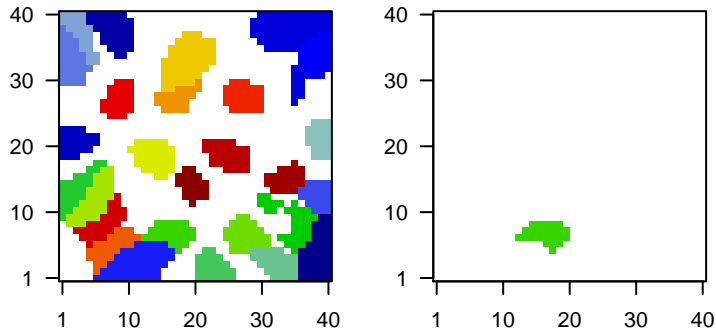
Rank	ID	max e	r	min e	Description
1	210155_at	1.93	-0.46	0.17	MYOC myocilin [Source:HGNC Symbol;Acc:HGNC:7610]
2	226564_at	1.42	-0.44	0.25	ZFAT zinc finger and AT-hook domain containing [Source:HGNC S
3	1552542_s_at	1.4	-0.58	0.43	TAGAP T cell activation RhoGTPase activating protein [Source:HGNC
4	201374_x_at	1.13	-0.57	0.34	PPP2CB protein phosphatase 2 catalytic subunit beta [Source:HGNC S
5	1552954_at	1.1	-0.31	0.25	chromosome 5 open reading frame 17 (putative) [Source:HGI
6	241951_at	1.09	-0.62	0.38	SLCO1C1olute carrier organic anion transporter family member 1C1 [S
7	235974_at	1.04	-0.59	0.31	EXOC4 exocyst complex component 4 [Source:HGNC Symbol;Acc:Hi
8	226467_at	1.02	-0.53	0.4	TANGO6 transport and golgi organization 6 homolog [Source:HGNC S]
9	1566147_a_a	0.98	-0.42	0.32	
10	236402_at	0.94	-0.68	0.43	BRAF B-Raf proto-oncogene, serine/threonine kinase [Source:HGI
11	220195_at	0.94	-0.79	0.3	MBD5 methyl-CpG binding domain protein 5 [Source:HGNC Symbc
12	1552299_at	0.93	-0.83	0.33	AK9 adenylate kinase 9 [Source:HGNC Symbol;Acc:HGNC:33814
13	1552980_at	0.92	-0.67	0.42	HAS3 hyaluronan synthase 3 [Source:HGNC Symbol;Acc:HGNC:48
14	230795_at	0.91	-0.84	0.44	
15	206389_s_at	0.9	-0.51	0.41	PDE3A phosphodiesterase 3A [Source:HGNC Symbol;Acc:HGNC:87
16	227741_at	0.89	-0.9	0.39	HACD2 3-hydroxyacyl-CoA dehydratase 2 [Source:HGNC Symbol;A
17	234902_s_at	0.87	-0.74	0.48	ZNF416 zinc finger protein 416 [Source:HGNC Symbol;Acc:HGNC:20
18	231258_at	0.86	-0.73	0.53	
19	1560560_at	0.84	-0.58	0.35	novel transcript
20	217430_x_at	0.82	-0.63	0.33	COL1A1 collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGI

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-14	48 / 630	BP protein transport
2	2e-13	171 / 4740	BP cytosol
3	3e-10	69 / 1435	BP mitochondrion
4	5e-10	28 / 324	BP intracellular protein transport
5	2e-08	23 / 264	BP vesicle-mediated transport
6	3e-07	184 / 6202	BP cytoplasm
7	3e-07	17 / 176	BP endoplasmic reticulum to Golgi vesicle-mediated transport
8	6e-07	19 / 229	BP mRNA splicing, via spliceosome
9	7e-07	54 / 1242	BP Golgi apparatus
10	1e-06	24 / 358	BP mRNA processing
11	2e-06	16 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
12	2e-06	10 / 68	BP positive regulation of protein ubiquitination
13	5e-06	11 / 93	BP Golgi organization
14	7e-06	9 / 62	BP protein targeting to peroxisome
15	1e-05	19 / 279	BP RNA splicing
16	4e-05	18 / 281	BP ubiquitin-dependent protein catabolic process
17	4e-05	8 / 60	BP COPII vesicle coating
18	6e-05	27 / 545	BP protein ubiquitination
19	7e-05	26 / 521	BP lipid metabolic process
20	7e-05	17 / 267	BP ubiquitin-protein transferase activity
21	9e-05	12 / 149	BP protein folding
22	2e-04	15 / 234	BP protein deubiquitination
23	4e-04	6 / 46	BP fatty acid beta-oxidation
24	6e-04	4 / 19	BP branched-chain amino acid catabolic process
25	8e-04	192 / 7387	BP membrane
26	9e-04	10 / 139	BP regulation of translation
27	9e-04	4 / 21	BP negative regulation of Rho protein signal transduction
28	9e-04	4 / 21	BP peroxisome organization
29	1e-03	3 / 10	BP production of siRNA involved in RNA interference
30	1e-03	5 / 38	BP positive regulation of ATPase activity
31	1e-03	8 / 99	BP mRNA export from nucleus
32	1e-03	4 / 23	BP nucleotide-excision repair, DNA damage recognition
33	1e-03	6 / 57	BP autophagosome assembly
34	1e-03	6 / 57	BP cellular iron ion homeostasis
35	1e-03	3 / 11	BP mitochondrial electron transport, ubiquinol to cytochrome c
36	1e-03	3 / 11	BP protein import into peroxisome matrix
37	1e-03	3 / 11	BP protein quality control for misfolded or incompletely synthesized proteins
38	2e-03	17 / 350	BP GTP binding
39	2e-03	7 / 80	BP response to endoplasmic reticulum stress
40	2e-03	4 / 25	BP cellular response to unfolded protein

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	3e-14	48 / 630	protein transport
2	2e-13	171 / 4740	cytosol
3	3e-10	69 / 1435	mitochondrion
4	5e-10	28 / 324	intracellular protein transport
5	2e-08	23 / 264	vesicle-mediated transport
6	3e-07	184 / 6202	cytoplasm
7	3e-07	17 / 176	endoplasmic reticulum to Golgi vesicle-mediated transport
8	6e-07	19 / 229	mRNA splicing, via spliceosome
9	7e-07	54 / 1242	Golgi apparatus
10	1e-06	24 / 358	mRNA processing
11	2e-06	16 / 179	proteasome-mediated ubiquitin-dependent protein catabolic process
12	2e-06	10 / 68	positive regulation of protein ubiquitination
13	5e-06	11 / 93	Golgi organization
14	7e-06	9 / 62	protein targeting to peroxisome
15	1e-05	19 / 279	RNA splicing

Correlation Cluster

Spot Summary: Y

metagenes = 26
genes = 718

<r> metagenes = 0.95
<r> genes = 0.45
beta: r2= 5.18 / log p= -Inf

samples with spot = 5 (3.6 %)
group 1 : 1 (9.1 %)
group 5 : 1 (4 %)
group 7 : 2 (7.7 %)
group 8 : 1 (3.7 %)

Spot Genelist

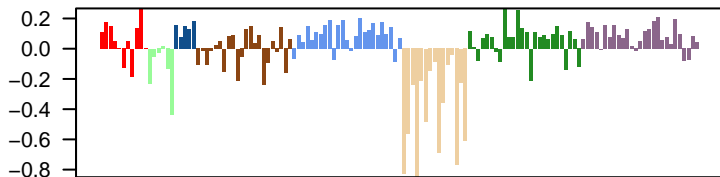
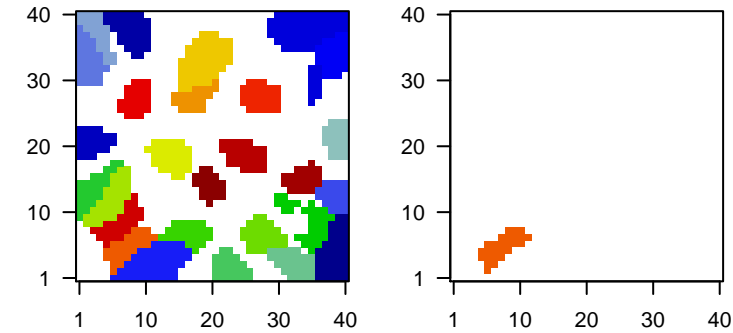
Rank	ID	max e	r	min e	Description
1	225149_at	1.96	-1.21	0.61	PCID2 PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10811]
2	243372_at	1.78	-0.86	0.59	PCID2 PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10811]
3	215779_s_at	1.55	-0.67	0.29	HIST1H2B histone cluster 1 H2B family member g [Source:HGNC Symbol;Acc:HGNC:10811]
4	239443_at	1.43	-1.59	0.34	PCDHB6 protocadherin beta 6 [Source:HGNC Symbol;Acc:HGNC:8699]
5	40665_at	1.42	-0.74	0.47	FMO3 flavin containing monooxygenase 3 [Source:HGNC Symbol;Acc:HGNC:10811]
6	204304_s_at	1.32	-1.61	0.48	PROM1 prominin 1 [Source:HGNC Symbol;Acc:HGNC:9454]
7	205214_at	1.32	-0.89	0.49	STK17B serine/threonine kinase 17b [Source:HGNC Symbol;Acc:HGNC:10811]
8	238537_at	1.3	-0.86	0.43	CA8 carbonic anhydrase 8 [Source:HGNC Symbol;Acc:HGNC:13811]
9	1559102_at	1.29	-1.15	0.69	novel transcript, antisense to AP1AR
10	229584_at	1.28	-1.69	0.53	LRRK2 leucine rich repeat kinase 2 [Source:HGNC Symbol;Acc:HGNC:10811]
11	223257_at	1.26	-1.35	0.77	G2E3 G2/M-phase specific E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:10811]
12	205501_at	1.24	-1.5	0.64	PDE10A phosphodiesterase 10A [Source:HGNC Symbol;Acc:HGNC:811]
13	223235_s_at	1.23	-1.13	0.51	SMOC2 SPARC related modular calcium binding 2 [Source:HGNC Symbol;Acc:HGNC:10811]
14	203946_s_at	1.22	-1.03	0.44	ARG2 arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]
15	205728_at	1.22	-1.64	0.42	TENM1 teneurin transmembrane protein 1 [Source:HGNC Symbol;Acc:HGNC:10811]
16	241925_x_at	1.22	-1.26	0.65	SLC16A7 solute carrier family 16 member 7 [Source:HGNC Symbol;Acc:HGNC:10811]
17	236917_at	1.2	-1.12	0.38	LRRC34 leucine rich repeat containing 34 [Source:HGNC Symbol;Acc:HGNC:10811]
18	238819_at	1.19	-0.83	0.56	ZNF347 zinc finger protein 347 [Source:HGNC Symbol;Acc:HGNC:1611]
19	223256_at	1.19	-1.39	0.82	G2E3 G2/M-phase specific E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:10811]
20	227874_at	1.17	-1.43	0.69	EMCN endomucin [Source:HGNC Symbol;Acc:HGNC:16041]

Geneset Overrepresentation

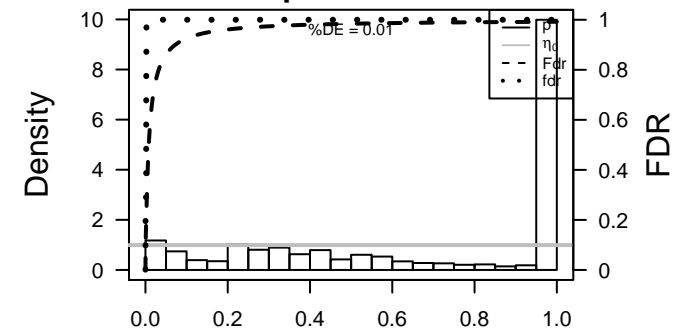
Rank	p-value	#in/all	Geneset
1	5e-09	180 / 4740	BP cytosol
2	5e-07	213 / 6202	BP cytoplasm
3	1e-06	38 / 630	BP protein transport
4	4e-06	59 / 1242	BP Golgi apparatus
5	1e-05	25 / 366	BP DNA repair
6	2e-05	237 / 7387	BP membrane
7	8e-05	30 / 545	BP protein ubiquitination
8	9e-05	33 / 630	BP cell cycle
9	1e-04	4 / 11	BP dosage compensation by inactivation of X chromosome
10	2e-04	6 / 33	BP bicellular tight junction assembly
11	2e-04	10 / 96	BP cellular response to leukemia inhibitory factor
12	6e-04	4 / 16	BP protein folding in endoplasmic reticulum
13	6e-04	9 / 93	BP Golgi organization
14	7e-04	5 / 28	BP mRNA polyadenylation
15	8e-04	25 / 484	BP cellular response to DNA damage stimulus
16	1e-03	4 / 18	BP negative regulation of DNA replication
17	1e-03	7 / 63	BP ubiquitin-dependent ERAD pathway
18	1e-03	7 / 64	BP response to unfolded protein
19	1e-03	16 / 264	BP transcription by RNA polymerase II
20	1e-03	16 / 264	BP vesicle-mediated transport
21	1e-03	13 / 192	BP methylation
22	1e-03	5 / 33	BP protein methylation
23	1e-03	5 / 33	BP spleen development
24	2e-03	5 / 34	BP endoplasmic reticulum organization
25	2e-03	7 / 68	BP regulation of autophagy
26	2e-03	3 / 10	BP positive regulation of endoplasmic reticulum stress-induced intrinsic apoptosis pathway
27	2e-03	5 / 35	BP androgen receptor signaling pathway
28	2e-03	3 / 11	BP interleukin-35-mediated signaling pathway
29	2e-03	3 / 11	BP postreplication repair
30	3e-03	6 / 55	BP phospholipid biosynthetic process
31	3e-03	3 / 12	BP negative regulation of autophagosome assembly
32	3e-03	11 / 163	BP autophagy
33	3e-03	17 / 315	BP positive regulation of GTPase activity
34	4e-03	20 / 400	BP chromatin binding
35	4e-03	33 / 783	BP negative regulation of transcription by RNA polymerase II
36	4e-03	3 / 13	BP protein localization to chromatin
37	4e-03	3 / 13	BP regulation of interferon-gamma-mediated signaling pathway
38	4e-03	4 / 26	BP intracellular transport
39	4e-03	17 / 324	BP intracellular protein transport
40	5e-03	6 / 61	BP double-strand break repair via nonhomologous end joining

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	5e-09	180 / 4740	cytosol
2	5e-07	213 / 6202	cytoplasm
3	1e-06	38 / 630	protein transport
4	4e-06	59 / 1242	Golgi apparatus
5	1e-05	25 / 366	DNA repair
6	2e-05	237 / 7387	membrane
7	8e-05	30 / 545	protein ubiquitination
8	9e-05	33 / 630	cell cycle
9	1e-04	4 / 11	dosage compensation by inactivation of X chromosome
10	2e-04	6 / 33	bicellular tight junction assembly
11	2e-04	10 / 96	cellular response to leukemia inhibitory factor
12	6e-04	4 / 16	protein folding in endoplasmic reticulum
13	6e-04	9 / 93	Golgi organization
14	7e-04	5 / 28	mRNA polyadenylation
15	8e-04	25 / 484	cellular response to DNA damage stimulus

Correlation Cluster

Spot Summary: Z

metagenes = 50
genes = 1667

<r> metagenes = 0.92

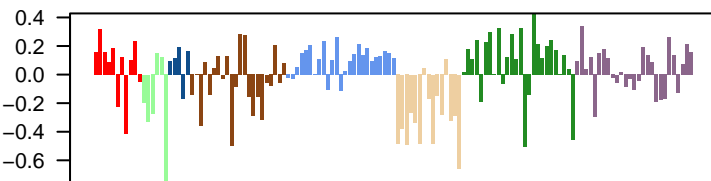
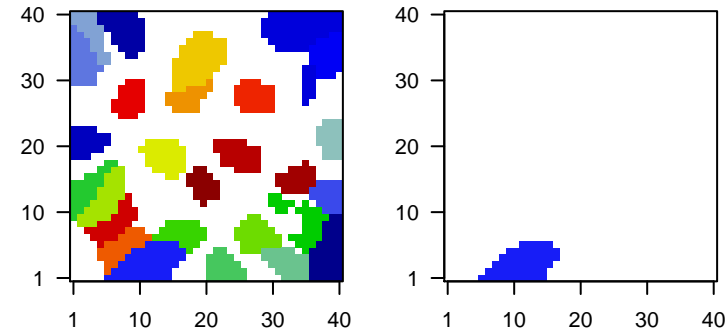
beta: r2= 6.22 / log p= -Inf

samples with spot = 21 (15.3 %)

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

Overview Map

Spot

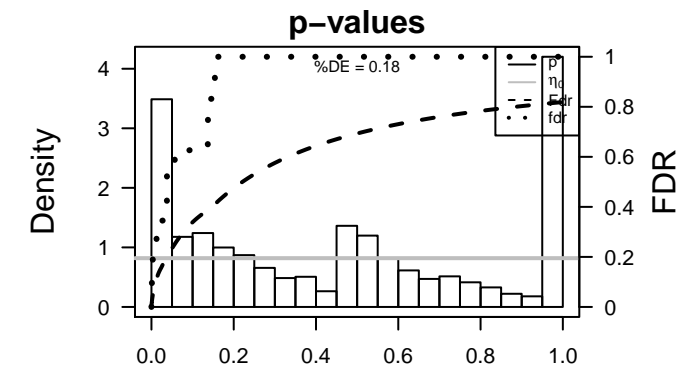


Spot Genelist

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	207978_s_at	2.12	-0.97	0.36	NR4A3 nuclear receptor subfamily 4 group A member 3 [Source:HGNC
3	220240_s_at	2.09	-1.17	0.7	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Sy
4	1555191_a_at	2.06	-0.78	0.52	FHL5 four and a half LIM domains 5 [Source:HGNC Symbol;Acc:HK
5	211607_x_at	2.06	-1.23	0.57	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
6	210984_x_at	2	-1.3	0.55	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:
7	201551_s_at	1.99	-1.97	0.48	LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Sy
8	200879_s_at	1.97	-1.12	0.63	EPAS1 endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc
9	216488_s_at	1.96	-1.14	0.52	ATP11A ATPase phospholipid transporting 11A [Source:HGNC Symbc
10	218948_at	1.84	-1.47	0.5	QRSL1 QRSL1, glutaminyl-tRNA amidotransferase subunit A [Source
11	207151_at	1.8	-0.85	0.58	ADCYAP1 ADCYAP receptor type I [Source:HGNC Symbol;Acc:HGNC:2
12	210790_s_at	1.8	-0.94	0.44	SAR1A secretion associated Ras related GTPase 1A [Source:HGNC
13	212940_at	1.79	-0.75	0.43	COL6A1 collagen type VI alpha 1 chain [Source:HGNC Symbol;Acc:Hi
14	204707_s_at	1.78	-0.7	0.46	MAPK4 mitogen-activated protein kinase 4 [Source:HGNC Symbol;A
15	230445_at	1.77	-1.09	0.43	BTBD17 BTB domain containing 17 [Source:HGNC Symbol;Acc:HGNC
16	222501_s_at	1.75	-1.44	0.74	REPIN1 replication initiator 1 [Source:HGNC Symbol;Acc:HGNC:1792
17	210973_s_at	1.72	-1.13	0.44	FGFR1 fibroblast growth factor receptor 1 [Source:HGNC Symbol;Acc
18	1554697_at	1.69	-1.41	0.51	ADAMTS10 ADAMTS metalloproteinase with thrombospondin type 1 motif 9 [
19	244561_at	1.69	-0.6	0.58	SLC9A7 solute carrier family 9 member A7 [Source:HGNC Symbol;Ac
20	205972_at	1.68	-1	0.35	SLC38A3 solute carrier family 38 member 3 [Source:HGNC Symbol;Acc

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-47	503 / 4740	BP cytosol
2	1e-38	580 / 6202	BP cytoplasm
3	9e-33	639 / 7387	BP membrane
4	1e-24	109 / 630	BP protein transport
5	3e-18	152 / 1242	BP Golgi apparatus
6	3e-17	63 / 324	BP intracellular protein transport
7	1e-16	55 / 264	BP vesicle-mediated transport
8	1e-10	30 / 132	BP membrane organization
9	1e-09	34 / 179	BP proteasome-mediated ubiquitin-dependent protein catabolic process
10	2e-09	51 / 350	BP GTP binding
11	3e-09	139 / 1435	BP mitochondrion
12	2e-08	23 / 101	BP mRNA transport
13	3e-08	20 / 80	BP response to endoplasmic reticulum stress
14	3e-08	49 / 358	BP mRNA processing
15	9e-08	17 / 63	BP ubiquitin-dependent ERAD pathway
16	1e-07	17 / 64	BP response to unfolded protein
17	1e-07	326 / 4278	BP plasma membrane
18	2e-07	56 / 459	BP viral process
19	2e-07	63 / 545	BP protein ubiquitination
20	3e-07	74 / 684	BP phosphorylation
21	1e-06	17 / 74	BP retrograde transport, endosome to Golgi
22	2e-06	28 / 179	BP protein dephosphorylation
23	3e-06	81 / 815	BP protein homodimerization activity
24	3e-06	26 / 162	BP dephosphorylation
25	4e-06	18 / 89	BP macroautophagy
26	4e-06	19 / 99	BP mRNA export from nucleus
27	5e-06	41 / 328	BP post-translational protein modification
28	5e-06	27 / 176	BP endoplasmic reticulum to Golgi vesicle-mediated transport
29	5e-06	9 / 24	BP mRNA cis splicing, via spliceosome
30	5e-06	55 / 496	BP negative regulation of apoptotic process
31	6e-06	22 / 129	BP rhythmic process
32	7e-06	24 / 149	BP protein folding
33	8e-06	36 / 279	BP RNA splicing
34	1e-05	9 / 26	BP Golgi to plasma membrane transport
35	1e-05	12 / 47	BP activation of MAPKK activity
36	1e-05	8 / 21	BP negative regulation of MAPK cascade
37	2e-05	63 / 623	BP protein phosphorylation
38	2e-05	29 / 214	BP cell migration
39	3e-05	16 / 84	BP ephrin receptor signaling pathway
40	3e-05	40 / 343	BP positive regulation of apoptotic process



BP

Rank	p-value	#in/all	Geneset
1	1e-47	503 / 4740	cytosol
2	1e-38	580 / 6202	cytoplasm
3	9e-33	639 / 7387	membrane
4	1e-24	109 / 630	protein transport
5	3e-18	152 / 1242	Golgi apparatus
6	3e-17	63 / 324	intracellular protein transport
7	1e-16	55 / 264	vesicle-mediated transport
8	1e-10	30 / 132	membrane organization
9	1e-09	34 / 179	proteasome-mediated ubiquitin-dependent protein catabolic process
10	2e-09	51 / 350	GTP binding
11	3e-09	139 / 1435	mitochondrion
12	2e-08	23 / 101	mRNA transport
13	3e-08	20 / 80	response to endoplasmic reticulum stress
14	3e-08	49 / 358	mRNA processing
15	9e-08	17 / 63	ubiquitin-dependent ERAD pathway

Correlation Cluster

Spot Summary: A1

metagenes = 24
genes = 901

<r> metagenes = 0.93
<r> genes = 0.29
beta: r2= 1.13 / log p= -Inf

samples with spot = 4 (2.9 %)
group 6 : 2 (13.3 %)
group 7 : 2 (7.7 %)

Spot Genelist

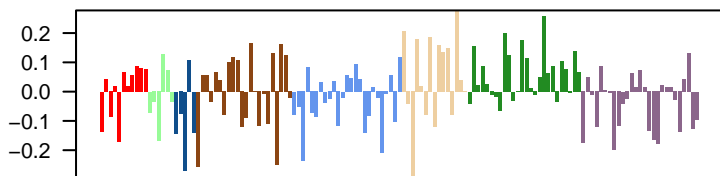
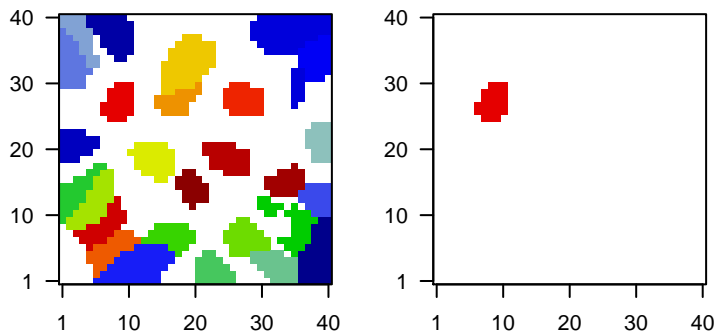
Rank	ID	max e	r	min e	Description
1	225767_at	1.94	-1.17	0.37	
2	204027_s_at	1.83	-0.74	0.45	METTL1 methyltransferase like 1 [Source:HGNC Symbol;Acc:HGNC:7
3	204179_at	1.69	-0.42	0.35	MB myoglobin [Source:HGNC Symbol;Acc:HGNC:6915]
4	214332_s_at	1.66	-0.63	0.33	novel protein
5	225616_at	1.64	-0.52	0.5	SPRYD4 SPRY domain containing 4 [Source:HGNC Symbol;Acc:HGNC:6915]
6	207813_s_at	1.61	-1.11	0.51	FDXR ferredoxin reductase [Source:HGNC Symbol;Acc:HGNC:3642]
7	230591_at	1.53	-0.77	0.51	novel transcript, antisense to MBTPS1
8	1565389_s_at	1.51	-0.51	0.27	GRM5 glutamate metabotropic receptor 5 [Source:HGNC Symbol;Acc:HGNC:3642]
9	206645_s_at	1.44	-0.74	0.28	NR0B1 nuclear receptor subfamily 0 group B member 1 [Source:HGNC Symbol;Acc:HGNC:3642]
10	211658_at	1.41	-1.36	0.45	
11	226546_at	1.41	-0.78	0.57	GIHCG, inhibitor of miR-200b/200a/429 expression [Source:HGNC Symbol;Acc:HGNC:3642]
12	1555865_at	1.4	-0.73	0.29	TOLLIP antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:3642]
13	1559532_at	1.36	-0.65	0.39	ARIH2OSRIadne RBR E3 ubiquitin protein ligase 2 opposite strand [Source:HGNC Symbol;Acc:HGNC:3642]
14	229338_at	1.34	-0.7	0.52	novel transcript
15	219254_at	1.33	-0.64	0.51	OGFOD32-oxoglutarate and iron dependent oxygenase domain containing 32 [Source:HGNC Symbol;Acc:HGNC:3642]
16	204175_at	1.33	-1.09	0.67	ZNF593 zinc finger protein 593 [Source:HGNC Symbol;Acc:HGNC:3642]
17	216177_at	1.32	-0.79	0.51	ribosomal protein L29 pseudogene 7 [Source:HGNC Symbol;Acc:HGNC:3642]
18	206956_at	1.31	-0.92	0.58	PMF1-BMP1-BGLAP readthrough [Source:HGNC Symbol;Acc:HGNC:3642]
19	227424_x_at	1.31	-0.69	0.47	URB1 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:3642]
20	219692_at	1.27	-0.46	0.27	KREMEN2 single containing transmembrane protein 2 [Source:HGNC Symbol;Acc:HGNC:3642]

Geneset Overrepresentation

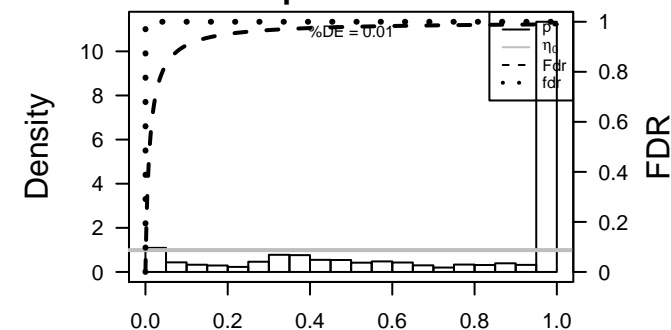
Rank	p-value	#in/all	Geneset
1	2e-67	194 / 1435	BP mitochondrion
2	5e-26	32 / 83	BP mitochondrial translational elongation
3	2e-24	31 / 85	BP mitochondrial translational termination
4	8e-22	25 / 59	BP mitochondrial respiratory chain complex I assembly
5	1e-19	46 / 276	BP translation
6	3e-17	19 / 43	BP mitochondrial electron transport, NADH to ubiquinone
7	6e-12	26 / 152	BP rRNA processing
8	2e-09	226 / 4740	BP cytosol
9	3e-09	28 / 229	BP mRNA splicing, via spliceosome
10	5e-09	31 / 279	BP RNA splicing
11	1e-08	11 / 36	BP mitochondrial translation
12	2e-08	52 / 671	BP oxidation-reduction process
13	5e-08	34 / 358	BP mRNA processing
14	1e-07	15 / 84	BP tRNA processing
15	2e-06	8 / 28	BP protein targeting to mitochondrion
16	8e-06	6 / 16	BP protein import into mitochondrial matrix
17	1e-05	8 / 33	BP exonucleolytic nuclear-transcribed mRNA catabolic process involved in development
18	1e-05	6 / 17	BP iron-sulfur cluster assembly
19	2e-05	6 / 18	BP mitochondrial respiratory chain complex IV assembly
20	2e-05	8 / 37	BP DNA-directed 5'-3' RNA polymerase activity
21	2e-05	9 / 48	BP regulation of cellular amino acid metabolic process
22	5e-05	7 / 30	BP cristae formation
23	5e-05	9 / 52	BP negative regulation of G2/M transition of mitotic cell cycle
24	5e-05	11 / 78	BP anaphase-promoting complex-dependent catabolic process
25	7e-05	10 / 67	BP regulation of transcription from RNA polymerase II promoter in response to stress
26	9e-05	5 / 15	BP ubiquinone biosynthetic process
27	1e-04	9 / 57	BP RNA phosphodiester bond hydrolysis, endonucleolytic
28	1e-04	6 / 24	BP positive regulation of viral transcription
29	1e-04	6 / 25	BP translational elongation
30	2e-04	5 / 17	BP positive regulation of mitochondrial translation
31	2e-04	8 / 49	BP RNA metabolic process
32	2e-04	4 / 10	BP protein maturation by iron-sulfur cluster transfer
33	3e-04	10 / 78	BP regulation of mitotic cell cycle phase transition
34	3e-04	11 / 93	BP ribosome biogenesis
35	4e-04	9 / 67	BP antigen processing and presentation of exogenous peptide antigen via MHC class II
36	4e-04	6 / 30	BP ribosomal large subunit biogenesis
37	4e-04	39 / 659	BP apoptotic process
38	5e-04	9 / 69	BP transcription-coupled nucleotide-excision repair
39	5e-04	4 / 12	BP tRNA 5'-leader removal
40	5e-04	7 / 43	BP tRNA aminoacylation for protein translation

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-67	194 / 1435	mitochondrion
2	5e-26	32 / 83	mitochondrial translational elongation
3	2e-24	31 / 85	mitochondrial translational termination
4	8e-22	25 / 59	mitochondrial respiratory chain complex I assembly
5	1e-19	46 / 276	translation
6	3e-17	19 / 43	mitochondrial electron transport, NADH to ubiquinone
7	6e-12	26 / 152	rRNA processing
8	2e-09	226 / 4740	cytosol
9	3e-09	28 / 229	mRNA splicing, via spliceosome
10	5e-09	31 / 279	RNA splicing
11	1e-08	11 / 36	mitochondrial translation
12	2e-08	52 / 671	oxidation-reduction process
13	5e-08	34 / 358	mRNA processing
14	1e-07	15 / 84	tRNA processing
15	2e-06	8 / 28	protein targeting to mitochondrion