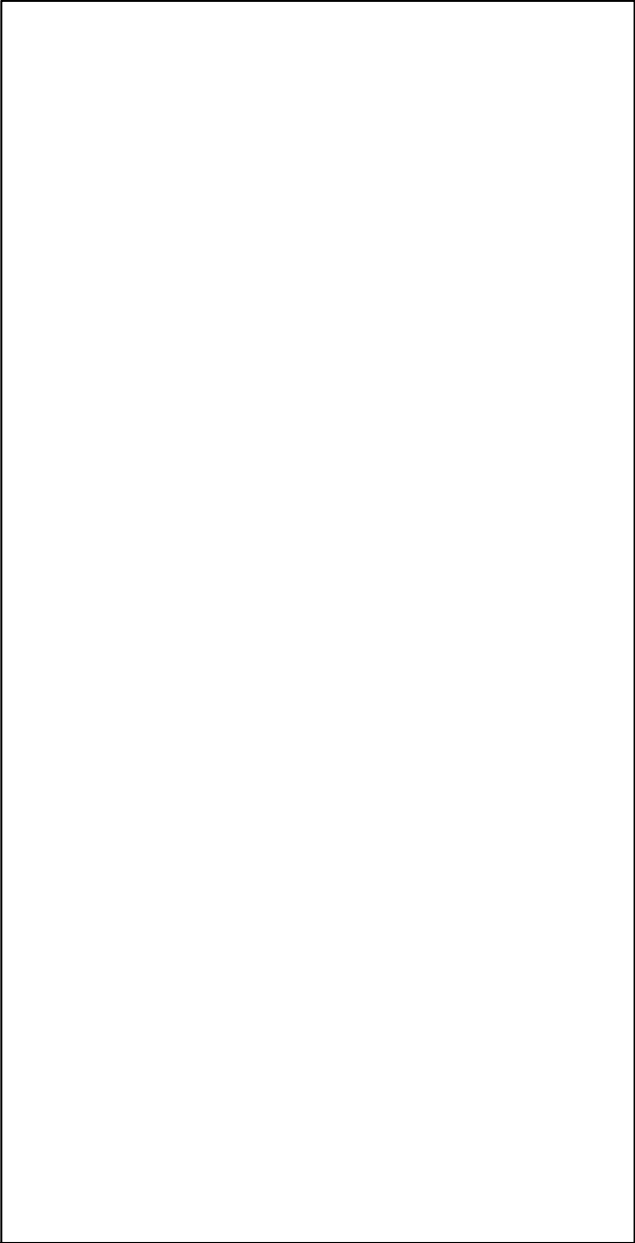
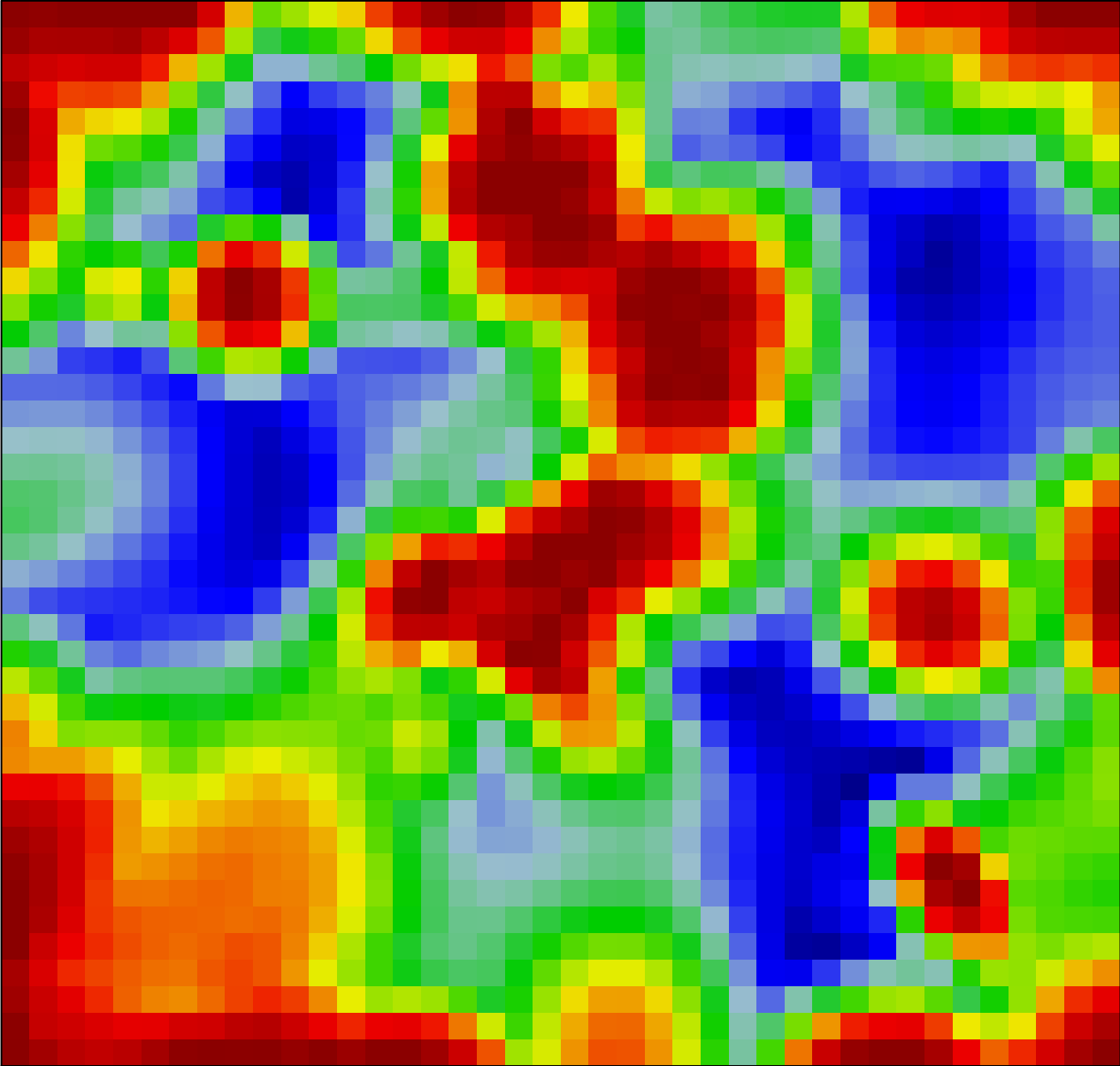
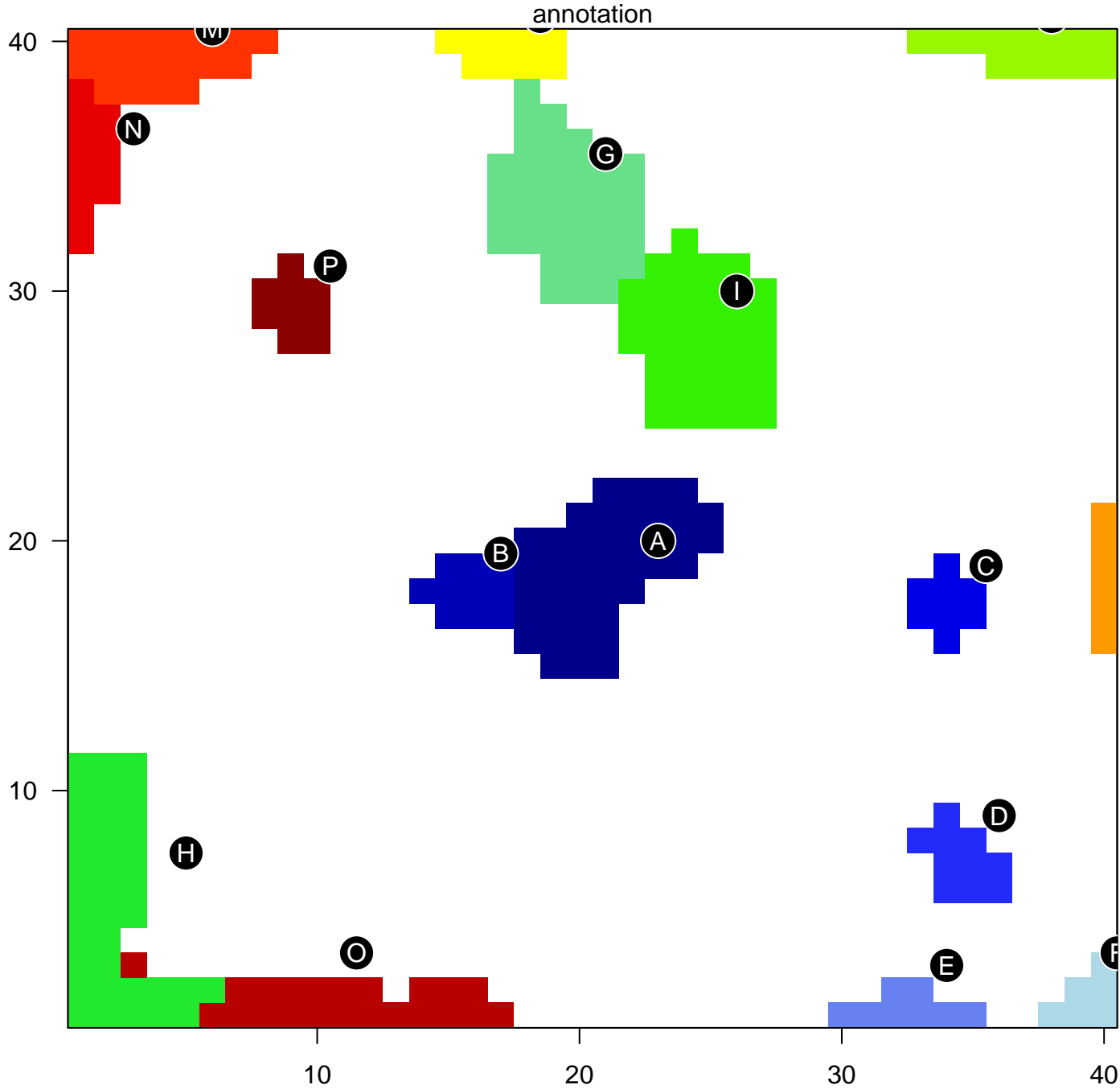


Overexpression Spots

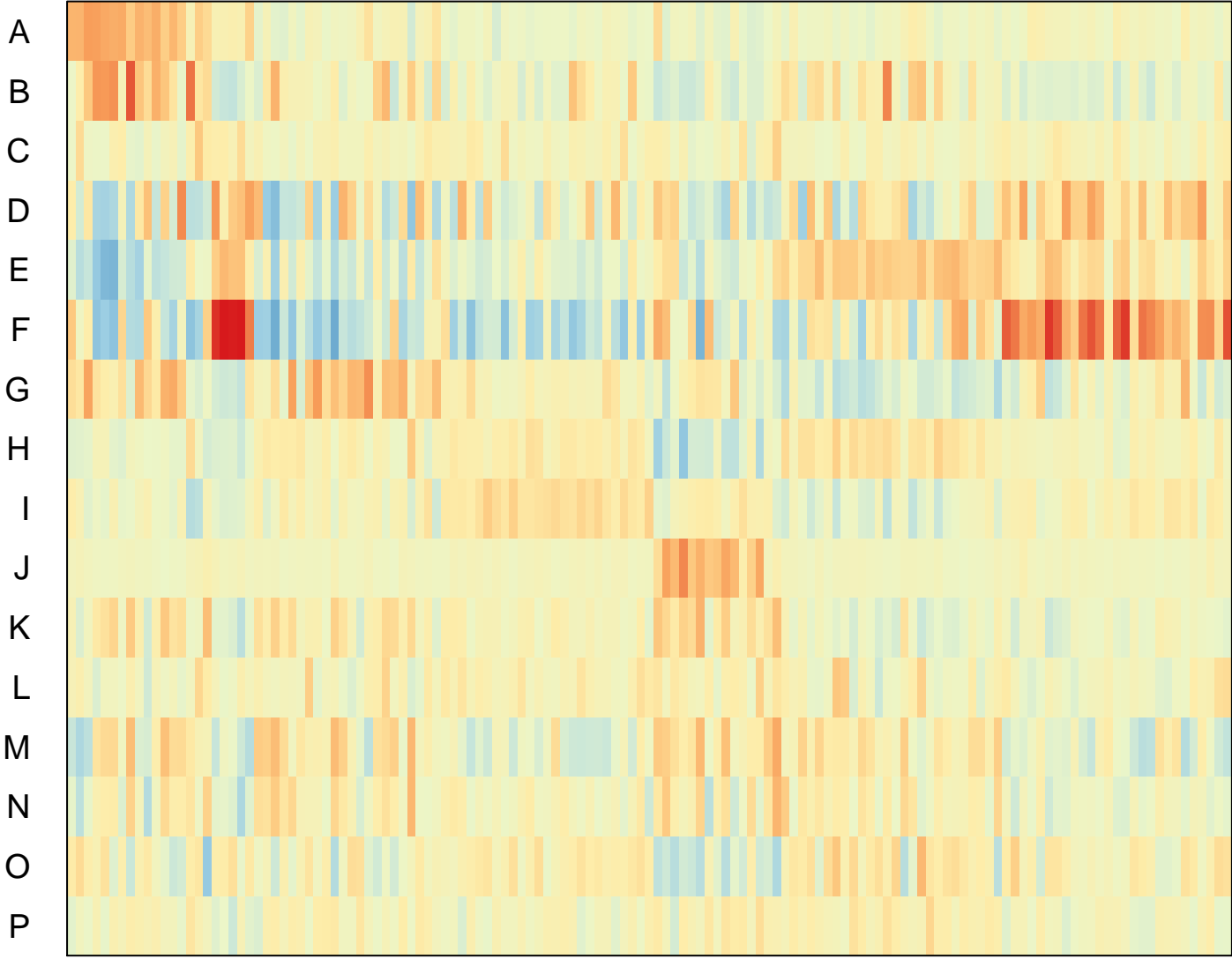
landscape



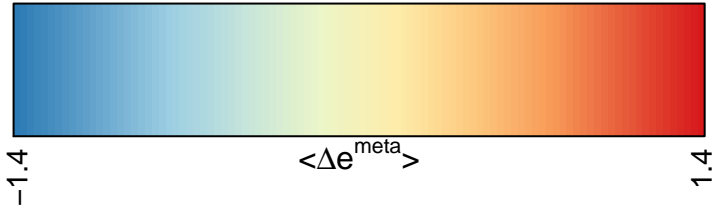
Overexpression Spots



- A ■ extracellular matrix organization
- angiogenesis
- B ■ cell cycle
- cell division
- C ■ positive regulation of protein localization to nucleus
- regulation of synaptic plasticity
- D ■ central nervous system myelination
- plasma membrane
- E ■ plasma membrane
- synapse
- F ■ synapse
- chemical synaptic transmission
- G ■ immune system process
- immune response
- H ■ DNA-binding transcription factor activity, RNA polymerase I
- regulation of transcription, DNA-templated
- I ■ positive regulation of gene expression
- positive regulation of transcription by RNA polymerase II
- J ■ positive regulation of insulin-like growth factor receptor sign
- blood circulation
- K ■ regulation of transcription, DNA-templated
- cytoplasm
- L ■ cytoplasm
- cytosol
- M ■ microtubule binding
- mRNA processing
- N ■ chromatin organization
- microtubule binding
- O ■ cytoplasm
- cytosol
- P ■ translation
- mitochondrion



- extracellular matrix organization
- angiogenesis
- collagen fibril organization
- cell cycle
- cell division
- chromosome segregation
- positive regulation of protein localization to nucleus
- regulation of synaptic plasticity
- rhodopsin mediated signaling pathway
- central nervous system myelination
- plasma membrane
- membrane
- plasma membrane
- synapse
- membrane
- synapse
- chemical synaptic transmission
- plasma membrane
- immune system process
- immune response
- innate immune response
- DNA-binding transcription factor activity, RNA polymerase II-specific
- regulation of transcription, DNA-templated
- regulation of transcription by RNA polymerase II
- positive regulation of gene expression
- positive regulation of transcription by RNA polymerase II
- regulation of neurogenesis
- positive regulation of insulin-like growth factor receptor signaling pathway
- blood circulation
- positive regulation of calcineurin-NFAT signaling cascade
- regulation of transcription, DNA-templated
- cytoplasm
- activation of GTPase activity
- cytoplasm
- cytosol
- viral process
- microtubule binding
- mRNA processing
- chromatin binding
- chromatin organization
- microtubule binding
- chromatin binding
- cytoplasm
- cytosol
- membrane
- translation
- mitochondrion
- SRP-dependent cotranslational protein targeting to membrane



Overexpression Spots

Spot Summary: A

metagenes = 41
genes = 874

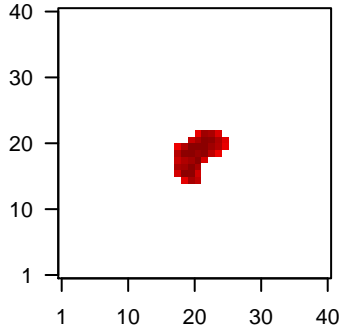
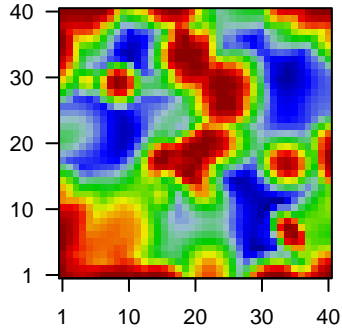
<r> metagenes = 0.77
<r> genes = 0.28
beta: r2= 6.61 / log p= -Inf

samples with spot = 18 (13.1 %)

- group 1 : 11 (100 %)
- group 2 : 5 (83.3 %)
- group 3 : 1 (20 %)
- group 6 : 1 (6.7 %)

Overview Map

Spot

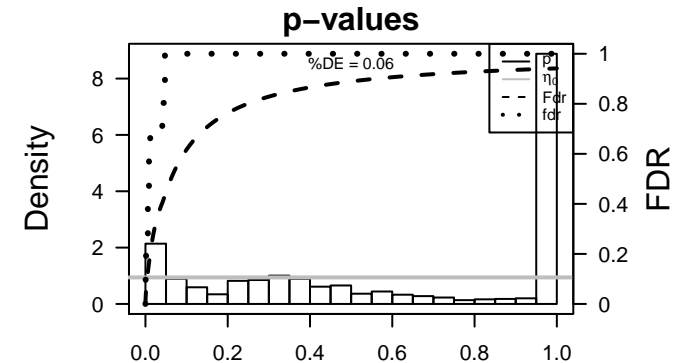
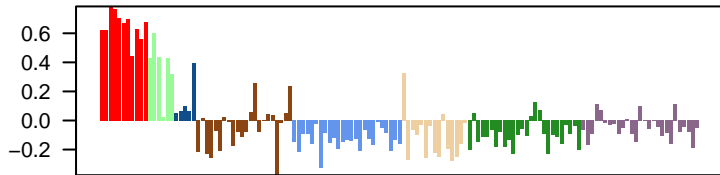


Spot Genelist

Rank	ID	max e	r	min e	Description
1	210809_s_at	3.59	-0.92	0.69	POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953]
2	243483_at	3.39	-0.59	0.6	TRPM8 transient receptor potential cation channel subfamily M memt
3	1555907_at	3.31	-0.45	0.48	AGAP2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
4	1555778_a_a	3.29	-0.53	0.65	POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953]
5	205858_at	3.12	-0.94	0.47	NGFR nerve growth factor receptor [Source:HGNC Symbol;Acc:HGNC:
6	242883_at	3.11	-0.37	0.44	OTOS otospiralin [Source:HGNC Symbol;Acc:HGNC:22644]
7	206858_s_at	3.1	-0.65	0.58	HOXC6 homeobox C6 [Source:HGNC Symbol;Acc:HGNC:5128]
8	228904_at	3.05	-0.62	0.71	HOXB3 homeobox B3 [Source:HGNC Symbol;Acc:HGNC:5114]
9	210135_s_at	2.98	-0.87	0.73	SHOX2 short stature homeobox 2 [Source:HGNC Symbol;Acc:HGNC
10	217057_s_at	2.88	-0.48	0.56	GNAS GNAS complex locus [Source:HGNC Symbol;Acc:HGNC:439
11	220010_at	2.87	-0.81	0.39	ACSL4 acyl-CoA synthetase long chain family member 4 [Source:HC
12	242234_at	2.84	-0.62	0.76	XAF1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:HGNC:
13	221577_x_at	2.82	-0.6	0.74	GDF15 growth differentiation factor 15 [Source:HGNC Symbol;Acc:Hi
14	232539_at	2.76	-0.77	0.5	
15	244731_at	2.72	-0.62	0.56	
16	230746_s_at	2.67	-0.7	0.34	
17	206201_s_at	2.66	-0.92	0.77	MEOX2 mesenchyme homeobox 2 [Source:HGNC Symbol;Acc:HGNC
18	209396_s_at	2.66	-1.71	0.74	CHI3L1 chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]
19	228481_at	2.66	-0.55	0.55	
20	231133_at	2.62	-0.56	0.63	DRC1 dynein regulatory complex subunit 1 [Source:HGNC Symbol;]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-29	49 / 231	BP extracellular matrix organization
2	3e-20	41 / 254	BP angiogenesis
3	3e-13	15 / 44	BP collagen fibril organization
4	5e-13	51 / 594	BP cell adhesion
5	3e-09	10 / 29	BP endodermal cell differentiation
6	3e-09	16 / 92	BP wound healing
7	6e-08	61 / 1080	BP multicellular organism development
8	1e-07	18 / 148	BP skeletal system development
9	2e-07	14 / 94	BP cell-matrix adhesion
10	4e-07	21 / 214	BP cell migration
11	5e-07	22 / 233	BP heart development
12	5e-07	166 / 4278	BP plasma membrane
13	2e-06	8 / 32	BP blood vessel remodeling
14	2e-06	40 / 657	BP calcium ion binding
15	3e-06	15 / 131	BP positive regulation of angiogenesis
16	4e-06	16 / 152	BP leukocyte migration
17	6e-06	11 / 75	BP response to wounding
18	1e-05	7 / 29	BP blood vessel morphogenesis
19	1e-05	5 / 12	BP lymphangiogenesis
20	1e-05	7 / 30	BP sprouting angiogenesis
21	2e-05	11 / 84	BP negative regulation of angiogenesis
22	2e-05	8 / 43	BP skin development
23	2e-05	13 / 118	BP platelet degranulation
24	2e-05	9 / 57	BP blood vessel development
25	3e-05	22 / 299	BP response to drug
26	3e-05	7 / 34	BP odontogenesis
27	3e-05	9 / 60	BP vasculogenesis
28	5e-05	11 / 93	BP integrin-mediated signaling pathway
29	5e-05	7 / 37	BP eye development
30	6e-05	12 / 112	BP animal organ morphogenesis
31	7e-05	11 / 97	BP female pregnancy
32	7e-05	9 / 66	BP response to mechanical stimulus
33	9e-05	7 / 40	BP substrate adhesion-dependent cell spreading
34	1e-04	11 / 105	BP platelet activation
35	2e-04	4 / 11	BP chondrocyte proliferation
36	2e-04	6 / 31	BP response to steroid hormone
37	2e-04	23 / 364	BP inflammatory response
38	2e-04	6 / 32	BP cilium movement
39	2e-04	11 / 111	BP positive regulation of MAPK cascade
40	3e-04	12 / 132	BP sensory perception of sound



BP

Rank	p-value	#in/all	Geneset
1	1e-29	49 / 231	extracellular matrix organization
2	3e-20	41 / 254	angiogenesis
3	3e-13	15 / 44	collagen fibril organization
4	5e-13	51 / 594	cell adhesion
5	3e-09	10 / 29	endodermal cell differentiation
6	3e-09	16 / 92	wound healing
7	6e-08	61 / 1080	multicellular organism development
8	1e-07	18 / 148	skeletal system development
9	2e-07	14 / 94	cell-matrix adhesion
10	4e-07	21 / 214	cell migration
11	5e-07	22 / 233	heart development
12	5e-07	166 / 4278	plasma membrane
13	2e-06	8 / 32	blood vessel remodeling
14	2e-06	40 / 657	calcium ion binding
15	3e-06	15 / 131	positive regulation of angiogenesis

Overexpression Spots

Spot Summary: B

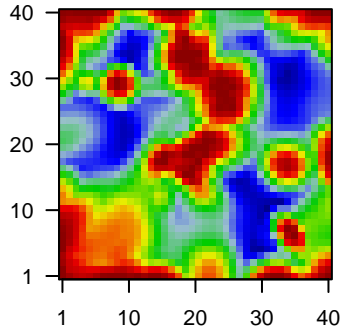
metagenes = 10
genes = 265

<r> metagenes = 0.98
<r> genes = 0.55
beta: r2= 6.28 / log p= -Inf

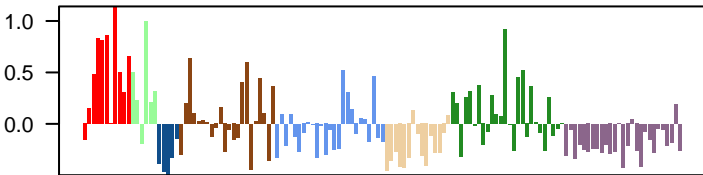
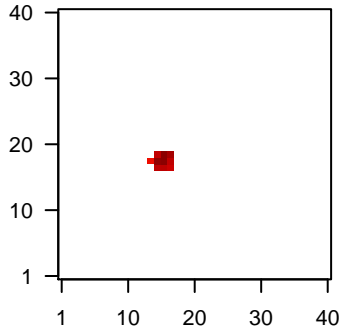
samples with spot = 23 (16.8 %)

- group 1 : 7 (63.6 %)
- group 2 : 3 (50 %)
- group 4 : 5 (22.7 %)
- group 5 : 2 (8 %)
- group 7 : 6 (23.1 %)

Overview Map



Spot

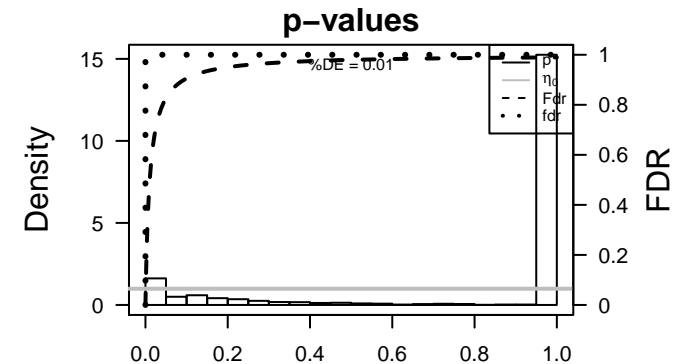


Spot Genelist

Rank	ID	max e	r	min e	Description
1	224588_at	2.97	-2.09	0.25	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224588]
2	218308_at	2.79	-0.78	0.76	TACC3 transforming acidic coiled-coil containing protein 3 [Source:HGNC Symbol;Acc:HGNC:218308]
3	227671_at	2.79	-1.83	0.25	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:227671]
4	214218_s_at	2.77	-1.66	0.25	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:214218]
5	221728_x_at	2.49	-1.68	0.24	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:221728]
6	1558834_s_at	2.45	-0.78	0.48	AKNAD1 AKNA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1558834]
7	224590_at	2.44	-1.42	0.27	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224590]
8	217373_x_at	2.43	-0.86	0.48	MDM2 MDM2 proto-oncogene [Source:HGNC Symbol;Acc:HGNC:217373]
9	224589_at	2.34	-1.31	0.26	X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC:224589]
10	214451_at	2.18	-0.51	0.48	TFAP2B transcription factor AP-2 beta [Source:HGNC Symbol;Acc:HGNC:214451]
11	228033_at	2.04	-0.69	0.84	E2F7 E2F transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:228033]
12	237737_at	1.99	-0.88	0.47	novel protein
13	219978_s_at	1.97	-1.17	0.82	novel protein
14	243327_at	1.95	-0.5	0.47	novel protein
15	218741_at	1.94	-0.94	0.86	CENPM centromere protein M [Source:HGNC Symbol;Acc:HGNC:218741]
16	230060_at	1.92	-0.67	0.7	CDCA7 cell division cycle associated 7 [Source:HGNC Symbol;Acc:HGNC:230060]
17	222680_s_at	1.91	-1.09	0.92	DTL denticleless E3 ubiquitin protein ligase homolog [Source:HGNC Symbol;Acc:HGNC:222680]
18	235287_at	1.91	-1.11	0.43	CDK6 cyclin dependent kinase 6 [Source:HGNC Symbol;Acc:HGNC:235287]
19	207746_at	1.88	-0.58	0.82	novel protein
20	202580_x_at	1.87	-1.14	0.89	FOXM1 forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:202580]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-88	89 / 630	BP cell cycle
2	3e-73	69 / 394	BP cell division
3	6e-36	27 / 85	BP chromosome segregation
4	6e-34	31 / 158	BP DNA replication
5	5e-26	26 / 164	BP mitotic cell cycle
6	1e-24	33 / 366	BP DNA repair
7	6e-23	35 / 484	BP cellular response to DNA damage stimulus
8	2e-19	18 / 98	BP G1/S transition of mitotic cell cycle
9	6e-19	94 / 4740	BP cytosol
10	9e-18	12 / 31	BP mitotic sister chromatid segregation
11	1e-17	13 / 42	BP mitotic spindle organization
12	7e-16	17 / 130	BP G2/M transition of mitotic cell cycle
13	1e-14	11 / 39	BP CENP-A containing nucleosome assembly
14	3e-14	12 / 56	BP DNA damage response, signal transduction by p53 class mediator resulting in
15	4e-14	24 / 400	BP chromatin binding
16	4e-14	22 / 327	BP cell population proliferation
17	5e-14	100 / 6202	BP cytoplasm
18	9e-14	10 / 33	BP DNA replication initiation
19	9e-12	10 / 50	BP mitotic cytokinesis
20	3e-11	11 / 76	BP microtubule motor activity
21	4e-11	8 / 27	BP mitotic spindle assembly
22	4e-11	7 / 17	BP DNA replication origin binding
23	5e-11	11 / 79	BP microtubule-based movement
24	6e-11	13 / 130	BP regulation of signal transduction by p53 class mediator
25	8e-11	16 / 227	BP microtubule binding
26	2e-10	10 / 66	BP double-strand break repair
27	2e-10	8 / 33	BP mitotic cell cycle checkpoint
28	2e-10	13 / 145	BP regulation of cell cycle
29	4e-10	7 / 22	BP mitotic spindle assembly checkpoint
30	4e-10	8 / 35	BP mitotic metaphase plate congression
31	5e-10	6 / 13	BP kinetochore assembly
32	9e-10	10 / 78	BP anaphase-promoting complex-dependent catabolic process
33	9e-10	8 / 39	BP regulation of mitotic nuclear division
34	1e-09	10 / 80	BP regulation of G2/M transition of mitotic cell cycle
35	1e-09	9 / 59	BP regulation of cyclin-dependent protein serine/threonine kinase activity
36	2e-09	7 / 28	BP positive regulation of G2/M transition of mitotic cell cycle
37	3e-09	6 / 17	BP spindle organization
38	4e-09	7 / 30	BP chromosome organization
39	6e-09	8 / 49	BP interstrand cross-link repair
40	8e-09	10 / 97	BP DNA recombination



BP

Rank	p-value	#in/all	Geneset
1	7e-88	89 / 630	cell cycle
2	3e-73	69 / 394	cell division
3	6e-36	27 / 85	chromosome segregation
4	6e-34	31 / 158	DNA replication
5	5e-26	26 / 164	mitotic cell cycle
6	1e-24	33 / 366	DNA repair
7	6e-23	35 / 484	cellular response to DNA damage stimulus
8	2e-19	18 / 98	G1/S transition of mitotic cell cycle
9	6e-19	94 / 4740	cytosol
10	9e-18	12 / 31	mitotic sister chromatid segregation
11	1e-17	13 / 42	mitotic spindle organization
12	7e-16	17 / 130	G2/M transition of mitotic cell cycle
13	1e-14	11 / 39	CENP-A containing nucleosome assembly
14	3e-14	12 / 56	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
15	4e-14	24 / 400	chromatin binding

Overexpression Spots

Spot Summary: C

metagenes = 8
genes = 367

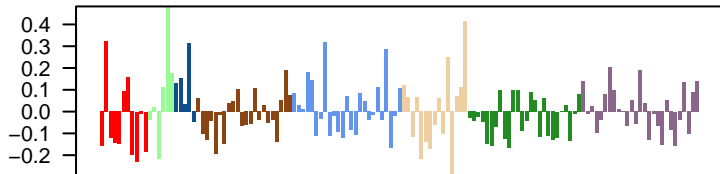
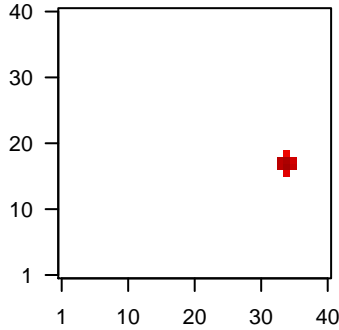
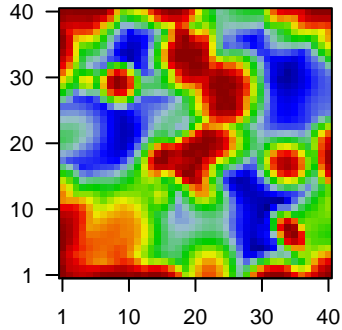
<r> metagenes = 0.97
<r> genes = 0.34
beta: r2= 1.36 / log p= -Inf

samples with spot = 5 (3.6 %)

- group 1 : 1 (9.1 %)
- group 2 : 1 (16.7 %)
- group 3 : 1 (20 %)
- group 5 : 1 (4 %)
- group 6 : 1 (6.7 %)

Overview Map

Spot

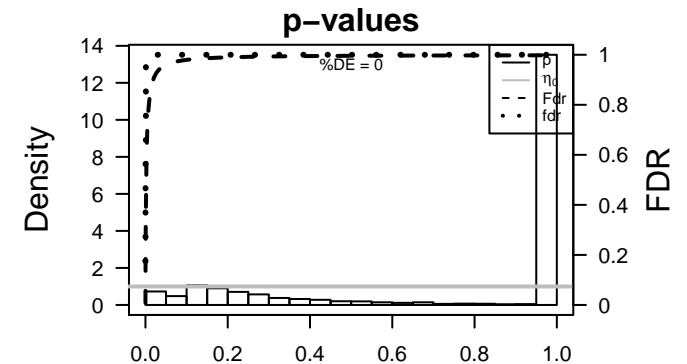


Spot Genelist

Rank	ID	max e	r	min e	Description
1	234291_s_at	1.91	-0.58	0.41	SLC6A20solute carrier family 6 member 20 [Source:HGNC Symbol;Acc:HGNC:8077]
2	236209_at	1.84	-0.81	0.28	
3	230525_at	1.77	-0.58	0.36	novel protein
4	211867_s_at	1.68	-0.54	0.38	PCDHA10protodherin alpha 10 [Source:HGNC Symbol;Acc:HGNC:8077]
5	221991_at	1.41	-0.6	0.45	NXP3H3 neurexophilin 3 [Source:HGNC Symbol;Acc:HGNC:8077]
6	233938_at	1.39	-0.64	0.66	C11orf86chromosome 11 open reading frame 86 [Source:HGNC Synt
7	237646_x_at	1.32	-1.21	0.69	PLEKHG9pleckstrin homology and RhoGEF domain containing G5 [Sou
8	238326_at	1.32	-0.6	0.75	
9	228580_at	1.3	-0.5	0.5	HTRA3 HtrA serine peptidase 3 [Source:HGNC Symbol;Acc:HGNC:3
10	207150_at	1.26	-0.66	0.45	SLC18A3solute carrier family 18 member A3 [Source:HGNC Symbol;A
11	236709_at	1.26	-0.87	0.51	CTXND1cortexin domain containing 1 [Source:HGNC Symbol;Acc:HG
12	235383_at	1.24	-0.65	0.52	MYO7B myosin VIIb [Source:HGNC Symbol;Acc:HGNC:7607]
13	230615_at	1.15	-0.6	0.75	DUOXA2dual oxidase maturation factor 2 [Source:HGNC Symbol;Acc:HGNC:8077]
14	239920_at	1.15	-0.77	0.67	
15	229583_at	1.12	-0.93	0.66	
16	233165_at	1.09	-0.41	0.58	
17	229726_at	1.07	-0.51	0.58	GRAP GRB2 related adaptor protein [Source:HGNC Symbol;Acc:HGNC:8077]
18	207106_s_at	1.07	-0.68	0.68	LTK leukocyte receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:8077]
19	231463_at	1.07	-0.51	0.46	CNTD1 cyclin N-terminal domain containing 1 [Source:HGNC Symbol;Acc:HGNC:8077]
20	211156_at	1.06	-0.48	0.77	CDKN2Acyclin dependent kinase inhibitor 2A [Source:HGNC Symbol;Acc:HGNC:8077]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-06	5 / 24	BP positive regulation of protein localization to nucleus
2	1e-04	5 / 51	BP regulation of synaptic plasticity
3	1e-04	3 / 11	BP rhodopsin mediated signaling pathway
4	2e-04	4 / 30	BP endothelial cell migration
5	7e-04	12 / 412	BP negative regulation of cell population proliferation
6	8e-04	5 / 75	BP response to wounding
7	1e-03	3 / 21	BP exogenous drug catabolic process
8	1e-03	4 / 47	BP nuclear receptor activity
9	2e-03	3 / 28	BP branching involved in blood vessel morphogenesis
10	4e-03	5 / 106	BP positive regulation of DNA-binding transcription factor activity
11	4e-03	16 / 777	BP G protein-coupled receptor signaling pathway
12	4e-03	7 / 204	BP cellular protein metabolic process
13	4e-03	2 / 10	BP negative regulation of reactive oxygen species biosynthetic process
14	4e-03	2 / 10	BP neuron projection maintenance
15	4e-03	3 / 34	BP acute-phase response
16	4e-03	3 / 34	BP excretion
17	5e-03	4 / 70	BP Ras protein signal transduction
18	5e-03	3 / 36	BP regulation of cytosolic calcium ion concentration
19	6e-03	2 / 12	BP commissural neuron axon guidance
20	6e-03	2 / 12	BP neuromuscular process controlling posture
21	7e-03	2 / 13	BP ear development
22	7e-03	2 / 13	BP negative regulation of DNA biosynthetic process
23	7e-03	2 / 13	BP negative regulation of vascular endothelial growth factor receptor signaling
24	7e-03	13 / 613	BP positive regulation of transcription, DNA-templated
25	7e-03	3 / 41	BP activation of adenylate cyclase activity
26	8e-03	2 / 14	BP nerve development
27	8e-03	4 / 81	BP activation of cysteine-type endopeptidase activity involved in apoptotic pro
28	8e-03	3 / 43	BP neurotransmitter transport
29	8e-03	3 / 43	BP skin development
30	9e-03	2 / 15	BP endothelial cell proliferation
31	9e-03	2 / 15	BP negative regulation of ubiquitin-dependent protein catabolic process
32	1e-02	2 / 16	BP neuron cellular homeostasis
33	1e-02	2 / 16	BP sympathetic nervous system development
34	1e-02	2 / 17	BP eye photoreceptor cell development
35	1e-02	2 / 17	BP pharyngeal system development
36	1e-02	2 / 17	BP positive regulation by host of viral transcription
37	1e-02	4 / 92	BP cholesterol metabolic process
38	1e-02	11 / 521	BP lipid metabolic process
39	1e-02	2 / 18	BP epoxygenase P450 pathway
40	1e-02	2 / 18	BP nitric oxide mediated signal transduction



BP

Rank	p-value	#in/all	Geneset
1	3e-06	5 / 24	positive regulation of protein localization to nucleus
2	1e-04	5 / 51	regulation of synaptic plasticity
3	1e-04	3 / 11	rhodopsin mediated signaling pathway
4	2e-04	4 / 30	endothelial cell migration
5	7e-04	12 / 412	negative regulation of cell population proliferation
6	8e-04	5 / 75	response to wounding
7	1e-03	3 / 21	exogenous drug catabolic process
8	1e-03	4 / 47	nuclear receptor activity
9	2e-03	3 / 28	branching involved in blood vessel morphogenesis
10	4e-03	5 / 106	positive regulation of DNA-binding transcription factor activity
11	4e-03	16 / 777	G protein-coupled receptor signaling pathway
12	4e-03	7 / 204	cellular protein metabolic process
13	4e-03	2 / 10	negative regulation of reactive oxygen species biosynthetic process
14	4e-03	2 / 10	neuron projection maintenance
15	4e-03	3 / 34	acute-phase response

Overexpression Spots

Spot Summary: D

metagenes = 10
genes = 283

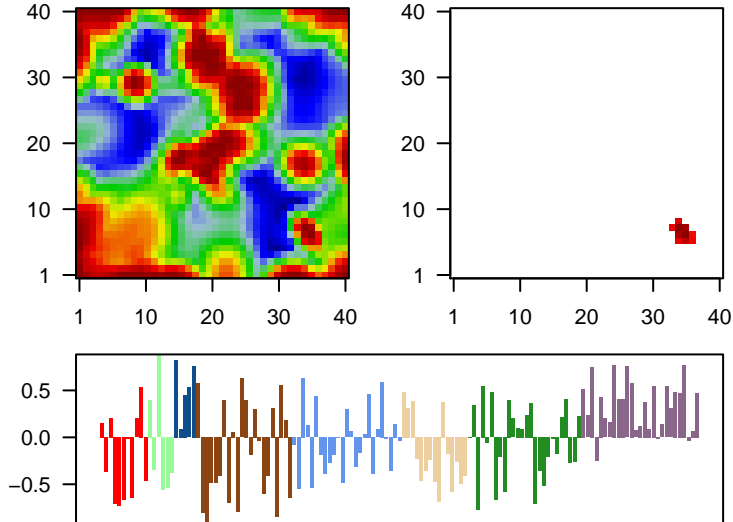
<r> metagenes = 0.98
<r> genes = 0.57
beta: r2= 12.37 / log p= -Inf

samples with spot = 42 (30.7 %)

- group 1 : 1 (9.1 %)
- group 2 : 2 (33.3 %)
- group 3 : 4 (80 %)
- group 4 : 6 (27.3 %)
- group 5 : 4 (16 %)
- group 6 : 4 (26.7 %)
- group 7 : 6 (23.1 %)
- group 8 : 15 (55.6 %)

Overview Map

Spot

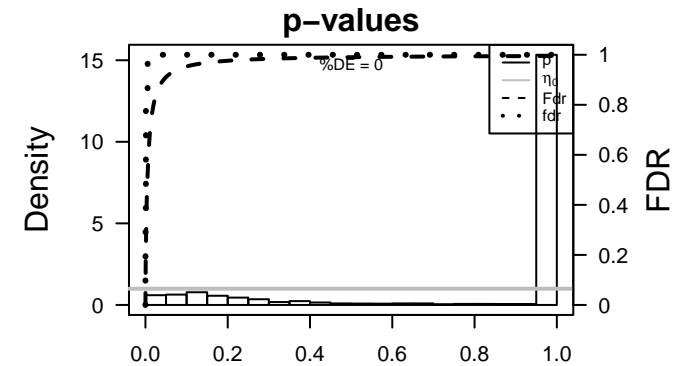


Spot Genelist

Rank	ID	max e	r	min e	Description
1	206898_at	2.09	-1.44	0.72	CDH19 cadherin 19 [Source:HGNC Symbol;Acc:HGNC:1758]
2	239575_at	1.93	-1.67	0.86	OPALIN oligodendrocytic myelin paranodal and inner loop protein [Source:HGNC Symbol;Acc:HGNC:1759]
3	234130_at	1.93	-0.81	0.75	
4	1554385_a_a	1.89	-1	0.52	PADI2 peptidyl arginine deiminase 2 [Source:HGNC Symbol;Acc:HGNC:1760]
5	235476_at	1.86	-1.05	0.69	novel tripartite motif-containing 59 (TRIM59) and intraflagella
6	237466_s_at	1.82	-0.75	0.74	HHIP hedgehog interacting protein [Source:HGNC Symbol;Acc:HGNC:1761]
7	219750_at	1.8	-1.55	0.83	TMEM144 transmembrane protein 144 [Source:HGNC Symbol;Acc:HGNC:1762]
8	235614_at	1.78	-1.21	0.82	TMEM151 transmembrane protein 151A [Source:HGNC Symbol;Acc:HGNC:1763]
9	244297_at	1.78	-1.18	0.78	cytochrome P450, family 4, subfamily F family pseudogene
10	209843_s_at	1.75	-1.05	0.64	SOX10 SRY-box 10 [Source:HGNC Symbol;Acc:HGNC:11190]
11	208285_at	1.74	-0.82	0.49	OR7A5 olfactory receptor family 7 subfamily A member 5 [Source:HGNC Symbol;Acc:HGNC:1764]
12	1563933_a_a	1.74	-1.3	0.52	PLD5 phospholipase D family member 5 [Source:HGNC Symbol;Acc:HGNC:1765]
13	217487_x_at	1.71	-1.42	0.88	FOLH1B folate hydrolase 1B [Source:HGNC Symbol;Acc:HGNC:13636]
14	232530_at	1.71	-0.71	0.61	PLD1 phospholipase D1 [Source:HGNC Symbol;Acc:HGNC:9067]
15	218469_at	1.7	-1.27	0.86	GREM1 gremlin 1, DAN family BMP antagonist [Source:HGNC Symbol;Acc:HGNC:1766]
16	223986_x_at	1.68	-1	0.71	DMRT2 doublesex and mab-3 related transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:1767]
17	213706_at	1.68	-1.55	0.58	GPD1 glycerol-3-phosphate dehydrogenase 1 [Source:HGNC Symbol;Acc:HGNC:1768]
18	220230_s_at	1.67	-1.04	0.81	CYB5R2 cytochrome b5 reductase 2 [Source:HGNC Symbol;Acc:HGNC:1769]
19	220026_at	1.66	-1.26	0.92	CLCA4 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:1770]
20	1569620_s_at	1.65	-0.76	0.72	novel transcript, antisense to a novel protein

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-10	6 / 13	BP central nervous system myelination
2	6e-10	70 / 4278	BP plasma membrane
3	3e-09	98 / 7387	BP membrane
4	2e-07	7 / 52	BP myelination
5	1e-04	7 / 133	BP central nervous system development
6	2e-04	3 / 14	BP magnesium ion transport
7	2e-04	3 / 14	BP positive regulation of myelination
8	5e-04	3 / 19	BP long-chain fatty-acyl-CoA biosynthetic process
9	6e-04	14 / 627	BP ion transport
10	7e-04	4 / 50	BP sphingolipid biosynthetic process
11	7e-04	6 / 132	BP membrane organization
12	8e-04	12 / 505	BP nervous system development
13	1e-03	12 / 521	BP lipid metabolic process
14	1e-03	3 / 26	BP oligodendrocyte development
15	2e-03	3 / 30	BP oligodendrocyte differentiation
16	2e-03	68 / 6202	BP cytoplasm
17	2e-03	4 / 70	BP Ras protein signal transduction
18	3e-03	12 / 594	BP cell adhesion
19	3e-03	3 / 37	BP positive regulation of protein tyrosine kinase activity
20	3e-03	2 / 11	BP amyloid precursor protein metabolic process
21	3e-03	2 / 11	BP negative regulation of pathway-restricted SMAD protein phosphorylation
22	4e-03	3 / 38	BP bicarbonate transport
23	4e-03	2 / 12	BP glycoprotein metabolic process
24	4e-03	2 / 12	BP regulation of exit from mitosis
25	5e-03	2 / 13	BP alpha-linolenic acid metabolic process
26	5e-03	2 / 13	BP very long-chain fatty acid biosynthetic process
27	5e-03	3 / 43	BP substantia nigra development
28	5e-03	2 / 14	BP negative regulation of cAMP-mediated signaling
29	5e-03	2 / 14	BP unsaturated fatty acid biosynthetic process
30	6e-03	6 / 199	BP axon guidance
31	6e-03	3 / 46	BP neural crest cell migration
32	6e-03	2 / 15	BP magnesium ion transmembrane transport
33	6e-03	2 / 15	BP sodium-independent organic anion transport
34	7e-03	7 / 275	BP ion transmembrane transport
35	7e-03	2 / 16	BP linoleic acid metabolic process
36	8e-03	2 / 17	BP regulation of protein localization to plasma membrane
37	1e-02	2 / 19	BP lipid biosynthetic process
38	1e-02	4 / 106	BP anatomical structure morphogenesis
39	1e-02	4 / 107	BP small GTPase mediated signal transduction
40	1e-02	11 / 615	BP transmembrane transport



BP

Rank	p-value	#in/all	Geneset
1	4e-10	6 / 13	central nervous system myelination
2	6e-10	70 / 4278	plasma membrane
3	3e-09	98 / 7387	membrane
4	2e-07	7 / 52	myelination
5	1e-04	7 / 133	central nervous system development
6	2e-04	3 / 14	magnesium ion transport
7	2e-04	3 / 14	positive regulation of myelination
8	5e-04	3 / 19	long-chain fatty-acyl-CoA biosynthetic process
9	6e-04	14 / 627	ion transport
10	7e-04	4 / 50	sphingolipid biosynthetic process
11	7e-04	6 / 132	membrane organization
12	8e-04	12 / 505	nervous system development
13	1e-03	12 / 521	lipid metabolic process
14	1e-03	3 / 26	oligodendrocyte development
15	2e-03	3 / 30	oligodendrocyte differentiation

Overexpression Spots

Spot Summary: E

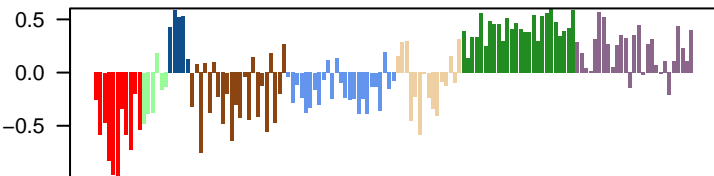
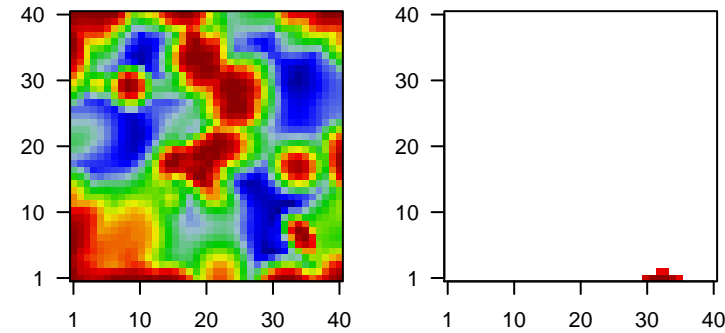
metagenes = 8
genes = 393

<r> metagenes = 0.97
<r> genes = 0.47
beta: r2= 13.77 / log p= -Inf

samples with spot = 37 (27 %)
group 3 : 4 (80 %)
group 6 : 1 (6.7 %)
group 7 : 22 (84.6 %)
group 8 : 10 (37 %)

Overview Map

Spot

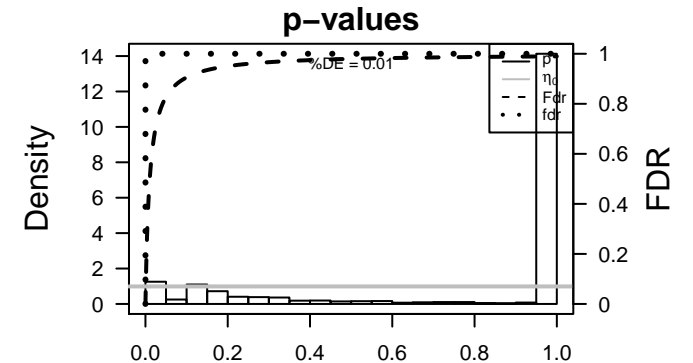


Spot Genelist

Rank	ID	max e	r	min e	Description
1	1556573_s_at	2.93	-1.3	0.35	novel transcript
2	243242_at	2.38	-0.75	0.5	
3	1555230_a_at	2.29	-1.18	0.71	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC Symbol]
4	1566772_at	2.2	-0.85	0.65	
5	236714_at	2.14	-1.26	0.72	
6	231029_at	2.12	-1.61	0.4	
7	1553415_at	2.06	-0.74	0.56	SLC17A8 solute carrier family 17 member 8 [Source:HGNC Symbol;Acc:U08547]
8	216672_s_at	2.04	-0.66	0.59	MYT1L myelin transcription factor 1 like [Source:HGNC Symbol;Acc:U08547]
9	230112_at	2.02	-1.35	0.89	MARCH4 membrane associated ring-CH-type finger 4 [Source:HGNC Symbol]
10	244117_at	1.97	-0.81	0.47	
11	221321_s_at	1.96	-1.19	0.73	KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC Symbol]
12	1561324_at	1.9	-1.05	0.44	
13	227614_at	1.89	-0.91	0.46	HKDC1 hexokinase domain containing 1 [Source:HGNC Symbol;Acc:U08547]
14	233433_at	1.88	-0.91	0.64	
15	215225_s_at	1.84	-2.02	0.55	GPR17 G protein-coupled receptor 17 [Source:HGNC Symbol;Acc:U08547]
16	1558945_s_at	1.83	-1.05	0.43	CACNA1A calcium voltage-gated channel subunit alpha1 A [Source:HGNC Symbol]
17	237933_at	1.82	-0.8	0.55	
18	228761_at	1.81	-1.4	0.78	SCRT1 scratch family transcriptional repressor 1 [Source:HGNC Symbol]
19	1563187_at	1.8	-0.91	0.57	
20	217130_at	1.76	-1.15	0.46	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-16	100 / 4278	BP plasma membrane
2	3e-16	34 / 574	BP synapse
3	1e-14	135 / 7387	BP membrane
4	1e-11	19 / 240	BP postsynaptic membrane
5	7e-11	18 / 236	BP chemical synaptic transmission
6	6e-10	27 / 627	BP ion transport
7	1e-09	10 / 65	BP learning
8	2e-09	7 / 22	BP regulation of AMPA receptor activity
9	6e-09	13 / 149	BP regulation of ion transmembrane transport
10	1e-08	10 / 79	BP memory
11	2e-08	22 / 505	BP nervous system development
12	6e-08	6 / 21	BP membrane depolarization
13	2e-07	15 / 275	BP ion transmembrane transport
14	3e-06	7 / 61	BP positive regulation of synapse assembly
15	6e-06	9 / 122	BP potassium ion transmembrane transport
16	7e-06	9 / 125	BP calcium ion transmembrane transport
17	8e-06	4 / 13	BP cerebellar Purkinje cell layer development
18	8e-06	4 / 13	BP regulation of short-term neuronal synaptic plasticity
19	8e-06	4 / 13	BP synapse maturation
20	8e-06	5 / 27	BP glutamate secretion
21	8e-06	5 / 27	BP positive regulation of excitatory postsynaptic potential
22	1e-05	5 / 28	BP regulation of presynapse assembly
23	1e-05	9 / 131	BP potassium ion transport
24	1e-05	6 / 48	BP cardiac conduction
25	1e-05	6 / 48	BP synapse organization
26	1e-05	4 / 14	BP vocalization behavior
27	1e-05	6 / 50	BP nervous system process
28	1e-05	4 / 15	BP exploration behavior
29	2e-05	6 / 51	BP neurotransmitter secretion
30	2e-05	9 / 144	BP calcium ion transport
31	2e-05	6 / 55	BP social behavior
32	2e-05	9 / 146	BP homophilic cell adhesion via plasma membrane adhesion molecules
33	3e-05	5 / 35	BP dendrite development
34	8e-05	6 / 68	BP regulation of insulin secretion
35	8e-05	8 / 133	BP neuron projection development
36	9e-05	4 / 23	BP synaptic membrane adhesion
37	1e-04	5 / 48	BP long-term synaptic potentiation
38	1e-04	5 / 48	BP negative regulation of phosphatase activity
39	2e-04	4 / 27	BP regulation of axonogenesis
40	2e-04	3 / 11	BP regulation of postsynaptic membrane neurotransmitter receptor levels



BP

Rank	p-value	#in/all	Geneset
1	1e-16	100 / 4278	plasma membrane
2	3e-16	34 / 574	synapse
3	1e-14	135 / 7387	membrane
4	1e-11	19 / 240	postsynaptic membrane
5	7e-11	18 / 236	chemical synaptic transmission
6	6e-10	27 / 627	ion transport
7	1e-09	10 / 65	learning
8	2e-09	7 / 22	regulation of AMPA receptor activity
9	6e-09	13 / 149	regulation of ion transmembrane transport
10	1e-08	10 / 79	memory
11	2e-08	22 / 505	nervous system development
12	6e-08	6 / 21	membrane depolarization
13	2e-07	15 / 275	ion transmembrane transport
14	3e-06	7 / 61	positive regulation of synapse assembly
15	6e-06	9 / 122	potassium ion transmembrane transport

Overexpression Spots

Spot Summary: F

metagenes = 6
genes = 366

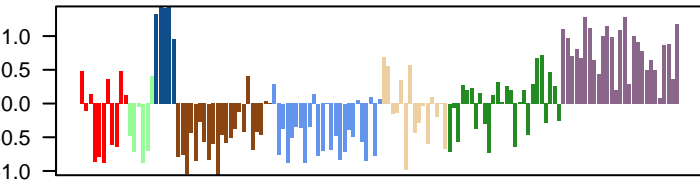
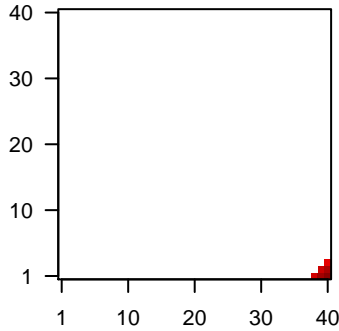
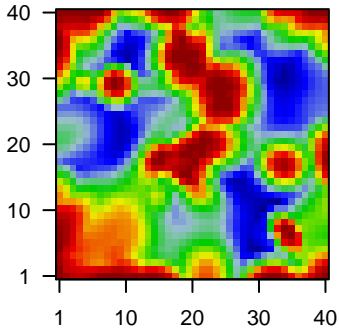
<r> metagenes = 1
<r> genes = 0.74
beta: r2= 43.24 / log p= -Inf

samples with spot = 42 (30.7 %)

- group 1 : 3 (27.3 %)
- group 2 : 1 (16.7 %)
- group 3 : 5 (100 %)
- group 4 : 1 (4.5 %)
- group 6 : 4 (26.7 %)
- group 7 : 4 (15.4 %)
- group 8 : 24 (88.9 %)

Overview Map

Spot

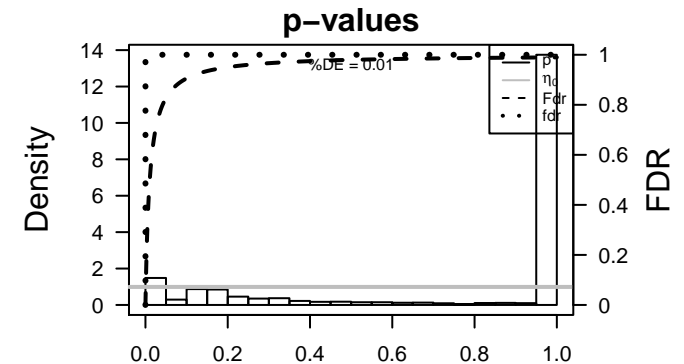


Spot Genelist

Rank	ID	max e	r	min e	Description
1	206803_at	3.07	-1.3	0.56	PDYN prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
2	205901_at	2.71	-1.16	0.73	PNOC prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163]
3	206552_s_at	2.4	-1.6	0.78	TAC1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11111]
4	207768_at	2.35	-0.93	0.83	EGR4 early growth response 4 [Source:HGNC Symbol;Acc:HGNC:22222]
5	222920_s_at	2.29	-1.17	0.88	TESPA1 thymocyte expressed, positive selection associated 1 [Source:HGNC Symbol;Acc:HGNC:11111]
6	220025_at	2.25	-0.85	0.9	TBR1 T-box, brain 1 [Source:HGNC Symbol;Acc:HGNC:11590]
7	242138_at	2.23	-1.27	0.73	DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:22222]
8	219263_at	2.22	-1.06	0.73	RNF128 ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:11111]
9	232111_at	2.18	-0.91	0.79	TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:11111]
10	1555800_at	2.18	-1.12	0.85	ZNF385B zinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:22222]
11	1559633_a_at	2.16	-1.09	0.82	CHRM3 cholinergic receptor muscarinic 3 [Source:HGNC Symbol;Acc:HGNC:11111]
12	231783_at	2.13	-1.47	0.92	CHRM1 cholinergic receptor muscarinic 1 [Source:HGNC Symbol;Acc:HGNC:11111]
13	219461_at	2.13	-1.27	0.87	PAK6 p21 (RAC1) activated kinase 6 [Source:HGNC Symbol;Acc:HGNC:11111]
14	207463_x_at	2.12	-0.73	0.85	PRSS3 serine protease 3 [Source:HGNC Symbol;Acc:HGNC:9486]
15	206084_at	2.12	-1.09	0.94	PTPRR protein tyrosine phosphatase, receptor type R [Source:HGNC Symbol;Acc:HGNC:11111]
16	213456_at	2.1	-0.73	0.83	SOSTDC4 sclerostin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:11111]
17	210408_s_at	2.08	-1.33	0.88	CPNE6 copine 6 [Source:HGNC Symbol;Acc:HGNC:2319]
18	210381_s_at	2.08	-1.05	0.92	CCKBR cholecystokinin B receptor [Source:HGNC Symbol;Acc:HGNC:11111]
19	208320_at	2.08	-2	0.83	CABP1 calcium binding protein 1 [Source:HGNC Symbol;Acc:HGNC:11111]
20	205625_s_at	2.06	-1.36	0.68	CALB1 calbindin 1 [Source:HGNC Symbol;Acc:HGNC:1434]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-34	55 / 574	BP synapse
2	3e-32	38 / 236	BP chemical synaptic transmission
3	2e-21	117 / 4278	BP plasma membrane
4	4e-17	152 / 7387	BP membrane
5	9e-17	25 / 240	BP postsynaptic membrane
6	1e-11	31 / 627	BP ion transport
7	2e-10	30 / 657	BP calcium ion binding
8	3e-10	10 / 51	BP neurotransmitter secretion
9	1e-09	9 / 43	BP neurotransmitter transport
10	1e-09	8 / 30	BP associative learning
11	4e-09	6 / 13	BP synaptic transmission, GABAergic
12	1e-08	12 / 119	BP postsynapse
13	2e-08	7 / 27	BP gamma-aminobutyric acid signaling pathway
14	3e-08	23 / 505	BP nervous system development
15	3e-08	9 / 60	BP neuron development
16	4e-08	43 / 1500	BP signal transduction
17	3e-07	9 / 79	BP cellular response to calcium ion
18	4e-07	11 / 131	BP presynapse
19	5e-07	9 / 82	BP chloride transmembrane transport
20	7e-07	6 / 28	BP synaptic vesicle exocytosis
21	1e-06	11 / 144	BP calcium ion transport
22	2e-06	7 / 50	BP nervous system process
23	2e-06	5 / 19	BP regulation of neuronal synaptic plasticity
24	5e-06	14 / 275	BP ion transmembrane transport
25	5e-06	25 / 777	BP G protein-coupled receptor signaling pathway
26	9e-06	5 / 25	BP calmodulin-dependent protein kinase activity
27	9e-06	5 / 25	BP regulation of dopamine secretion
28	1e-05	10 / 149	BP regulation of ion transmembrane transport
29	1e-05	5 / 27	BP glutamate secretion
30	2e-05	7 / 69	BP hippocampus development
31	2e-05	9 / 125	BP calcium ion transmembrane transport
32	2e-05	4 / 14	BP behavioral response to cocaine
33	2e-05	4 / 14	BP dopamine metabolic process
34	2e-05	6 / 48	BP long-term synaptic potentiation
35	2e-05	5 / 29	BP calcium ion regulated exocytosis
36	2e-05	9 / 131	BP potassium ion transport
37	3e-05	6 / 51	BP regulation of synaptic vesicle exocytosis
38	4e-05	7 / 79	BP memory
39	5e-05	4 / 18	BP regulation of neurotransmitter secretion
40	6e-05	5 / 36	BP synaptic vesicle endocytosis



BP

Rank	p-value	#in/all	Geneset
1	3e-34	55 / 574	synapse
2	3e-32	38 / 236	chemical synaptic transmission
3	2e-21	117 / 4278	plasma membrane
4	4e-17	152 / 7387	membrane
5	9e-17	25 / 240	postsynaptic membrane
6	1e-11	31 / 627	ion transport
7	2e-10	30 / 657	calcium ion binding
8	3e-10	10 / 51	neurotransmitter secretion
9	1e-09	9 / 43	neurotransmitter transport
10	1e-09	8 / 30	associative learning
11	4e-09	6 / 13	synaptic transmission, GABAergic
12	1e-08	12 / 119	postsynapse
13	2e-08	7 / 27	gamma-aminobutyric acid signaling pathway
14	3e-08	23 / 505	nervous system development
15	3e-08	9 / 60	neuron development

Overexpression Spots

Spot Summary: G

metagenes = 37
genes = 942

<r> metagenes = 0.9
<r> genes = 0.46
beta: r2= 11.79 / log p= -Inf

samples with spot = 22 (16.1 %)

- group 1 : 3 (27.3 %)
- group 2 : 3 (50 %)
- group 4 : 12 (54.5 %)
- group 5 : 1 (4 %)
- group 6 : 1 (6.7 %)
- group 8 : 2 (7.4 %)

Spot Genelist

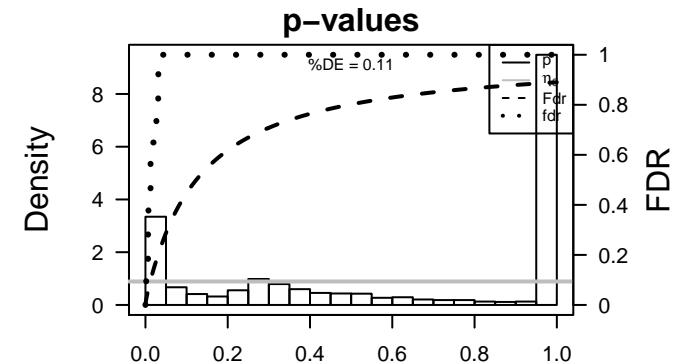
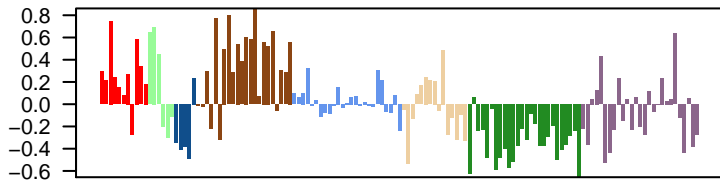
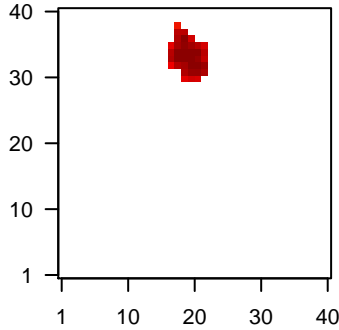
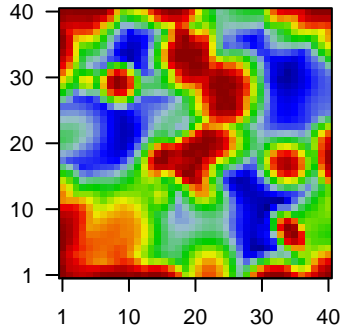
Rank	ID	max e	r	min e	Description
					Symbol
1	211430_s_at	3.66	-1	0.51	immunoglobulin heavy constant gamma 2 (G2m marker) [Sou
2	209138_x_at	3.42	-0.97	0.57	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
3	215121_x_at	3.38	-1.11	0.54	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
4	217022_s_at	3.37	-0.9	0.5	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
5	214677_x_at	3.36	-1.19	0.57	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
6	215176_x_at	3.32	-0.8	0.52	immunoglobulin kappa variable 1-39 (gene/pseudogene) [So
7	215379_x_at	3.1	-1.03	0.53	immunoglobulin lambda constant 2 [Source:HGNC Symbol;A
8	202018_s_at	3.01	-0.95	0.49	LTF lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
9	214669_x_at	2.74	-0.74	0.47	
10	224061_at	2.73	-0.57	0.46	INMT indolethylamine N-methyltransferase [Source:HGNC Symbol;
11	211339_s_at	2.73	-0.49	0.55	ITK IL2 inducible T cell kinase [Source:HGNC Symbol;Acc:HGNC
12	205374_at	2.72	-1.23	0.61	SLN sarcolipin [Source:HGNC Symbol;Acc:HGNC:11089]
13	223836_at	2.68	-0.59	0.33	FGFBP2 fibroblast growth factor binding protein 2 [Source:HGNC Syml
14	214836_x_at	2.63	-0.83	0.48	
15	221651_x_at	2.59	-0.66	0.53	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
16	221671_x_at	2.58	-0.81	0.53	immunoglobulin kappa constant [Source:HGNC Symbol;Acc:I
17	204575_s_at	2.56	-0.72	0.48	MMP19 matrix metalloproteinase 19 [Source:HGNC Symbol;Acc:HGN
18	209641_s_at	2.48	-0.8	0.61	ABCC3 ATP binding cassette subfamily C member 3 [Source:HGNC
19	236028_at	2.46	-0.71	0.61	IBSP integrin binding sialoprotein [Source:HGNC Symbol;Acc:HGN
20	209374_s_at	2.46	-0.76	0.49	immunoglobulin heavy constant mu [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-73	118 / 564	BP immune system process
2	8e-53	84 / 388	BP immune response
3	4e-47	81 / 417	BP innate immune response
4	2e-39	69 / 364	BP inflammatory response
5	2e-34	71 / 460	BP neutrophil degranulation
6	6e-33	234 / 4278	BP plasma membrane
7	1e-27	318 / 7387	BP membrane
8	6e-25	16 / 17	BP antigen processing and presentation of peptide or polysaccharide antigen v
9	2e-21	106 / 1500	BP signal transduction
10	2e-21	44 / 289	BP cytokine-mediated signaling pathway
11	8e-21	20 / 43	BP antigen processing and presentation
12	6e-18	30 / 155	BP regulation of immune response
13	1e-16	31 / 184	BP defense response to virus
14	2e-14	22 / 103	BP response to bacterium
15	2e-14	26 / 152	BP leukocyte migration
16	5e-13	16 / 56	BP B cell receptor signaling pathway
17	7e-13	24 / 148	BP chemotaxis
18	1e-12	16 / 59	BP positive regulation of T cell proliferation
19	5e-12	16 / 64	BP complement activation, classical pathway
20	5e-12	16 / 64	BP regulation of complement activation
21	8e-12	23 / 151	BP cellular response to lipopolysaccharide
22	1e-11	18 / 88	BP cellular response to interferon-gamma
23	1e-11	47 / 594	BP cell adhesion
24	2e-11	14 / 49	BP positive regulation of tumor necrosis factor production
25	3e-11	27 / 222	BP adaptive immune response
26	6e-11	22 / 151	BP defense response to bacterium
27	1e-10	13 / 47	BP complement activation
28	2e-10	22 / 160	BP T cell receptor signaling pathway
29	1e-09	14 / 66	BP phagocytosis
30	2e-09	12 / 47	BP phagocytosis, engulfment
31	2e-09	16 / 93	BP antigen processing and presentation of exogenous peptide antigen via MH
32	2e-09	18 / 121	BP defense response
33	4e-09	21 / 172	BP positive regulation of I-kappaB kinase/NF-kappaB signaling
34	5e-09	11 / 41	BP positive regulation of interferon-gamma production
35	5e-09	26 / 261	BP cell surface receptor signaling pathway
36	6e-09	14 / 74	BP neutrophil chemotaxis
37	7e-09	11 / 42	BP toll-like receptor signaling pathway
38	7e-09	10 / 33	BP lipopolysaccharide-mediated signaling pathway
39	7e-09	15 / 88	BP positive regulation of peptidyl-tyrosine phosphorylation
40	9e-09	15 / 89	BP Fc-gamma receptor signaling pathway involved in phagocytosis

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	5e-73	118 / 564	immune system process
2	8e-53	84 / 388	immune response
3	4e-47	81 / 417	innate immune response
4	2e-39	69 / 364	inflammatory response
5	2e-34	71 / 460	neutrophil degranulation
6	6e-33	234 / 4278	plasma membrane
7	1e-27	318 / 7387	membrane
8	6e-25	16 / 17	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
9	2e-21	106 / 1500	signal transduction
10	2e-21	44 / 289	cytokine-mediated signaling pathway
11	8e-21	20 / 43	antigen processing and presentation
12	6e-18	30 / 155	regulation of immune response
13	1e-16	31 / 184	defense response to virus
14	2e-14	22 / 103	response to bacterium
15	2e-14	26 / 152	leukocyte migration

Overexpression Spots

Spot Summary: H

metagenes = 36
genes = 1253

<r> metagenes = 0.83

beta: r2= 7.53 / log p= -Inf

samples with spot = 7 (5.1 %)

group 2 : 1 (16.7 %)

group 4 : 1 (4.5 %)

group 7 : 5 (19.2 %)

Spot Genelist

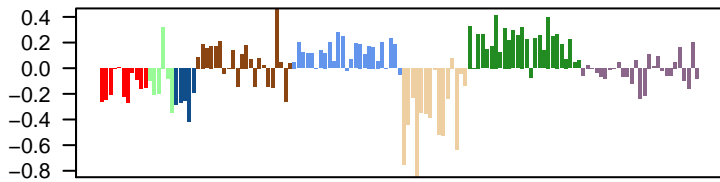
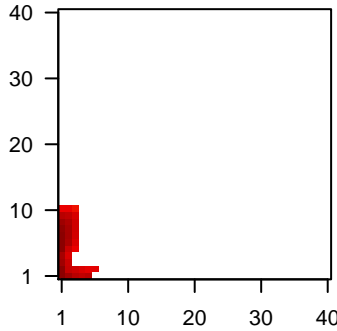
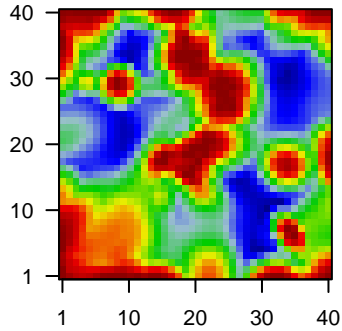
Rank	ID	max e	r	min e	Description
1	209772_s_at	2.62	-1.89	0.49	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645]
2	214079_at	2.54	-1.07	0.34	DHRS2 dehydrogenase/reductase 2 [Source:HGNC Symbol;Acc:HGNC:1645]
3	242977_at	2.4	-0.78	0.33	novel transcript
4	1559712_at	2.36	-0.81	0.46	long intergenic non-protein coding RNA 689 [Source:HGNC Symbol;Acc:HGNC:1645]
5	244308_at	2.27	-0.7	0.5	novel transcript
6	1559992_a_at	2.23	-1.21	0.3	long intergenic non-protein coding RNA 645 [Source:HGNC Symbol;Acc:HGNC:1645]
7	215442_s_at	2.13	-0.8	0.37	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645]
8	211879_x_at	2.13	-1.2	0.46	PCDHGB7 protocadherin gamma subfamily A, 3 [Source:HGNC Symbol;Acc:HGNC:1645]
9	229870_at	2.1	-0.96	0.6	novel transcript, antisense to ZNF143
10	210055_at	2.09	-1.37	0.4	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645]
11	208650_s_at	2.09	-2.09	0.42	CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645]
12	244517_x_at	2.05	-0.82	0.62	novel transcript
13	1569481_s_at	2.03	-0.89	0.45	SNX22 sorting nexin 22 [Source:HGNC Symbol;Acc:HGNC:16315]
14	238717_at	2	-1.03	0.25	novel transcript
15	1568795_at	2	-0.94	0.56	novel transcript
16	1552662_a_at	1.99	-1.09	0.29	PCDHGB7 protocadherin gamma subfamily B, 7 [Source:HGNC Symbol;Acc:HGNC:1645]
17	216379_x_at	1.99	-2.67	0.37	CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
18	205947_s_at	1.98	-1.02	0.52	VIPR2 vasoactive intestinal peptide receptor 2 [Source:HGNC Symbol;Acc:HGNC:1645]
19	1558463_s_at	1.98	-0.77	0.48	novel transcript
20	243261_at	1.98	-1.19	0.35	novel transcript

Geneset Overrepresentation

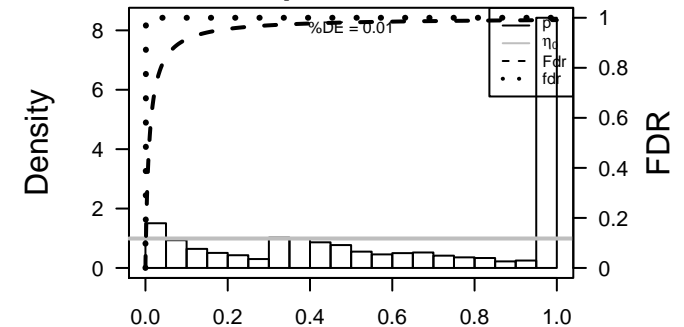
Rank	p-value	#in/all	Geneset
1	6e-20	124 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
2	1e-17	117 / 1387	BP regulation of transcription, DNA-templated
3	5e-17	102 / 1145	BP regulation of transcription by RNA polymerase II
4	5e-09	66 / 843	BP DNA-binding transcription factor activity
5	5e-08	35 / 342	BP chromatin organization
6	7e-07	36 / 400	BP chromatin binding
7	8e-07	72 / 1086	BP positive regulation of transcription by RNA polymerase II
8	1e-06	18 / 129	BP rhythmic process
9	2e-06	40 / 484	BP cellular response to DNA damage stimulus
10	5e-06	32 / 366	BP DNA repair
11	9e-06	8 / 30	BP chromosome organization
12	1e-05	41 / 541	BP negative regulation of transcription, DNA-templated
13	2e-05	44 / 613	BP positive regulation of transcription, DNA-templated
14	8e-05	6 / 21	BP spinal cord motor neuron differentiation
15	1e-04	14 / 119	BP nucleic acid phosphodiester bond hydrolysis
16	2e-04	5 / 16	BP sympathetic nervous system development
17	3e-04	5 / 17	BP embryonic morphogenesis
18	4e-04	12 / 102	BP chromatin remodeling
19	4e-04	8 / 49	BP embryonic skeletal system morphogenesis
20	5e-04	5 / 19	BP positive regulation of branching involved in ureteric bud morphogenesis
21	5e-04	34 / 505	BP nervous system development
22	6e-04	19 / 224	BP negative regulation of gene expression
23	6e-04	9 / 66	BP regulation of circadian rhythm
24	6e-04	47 / 783	BP negative regulation of transcription by RNA polymerase II
25	7e-04	8 / 54	BP DNA duplex unwinding
26	8e-04	33 / 496	BP negative regulation of apoptotic process
27	8e-04	7 / 42	BP branching involved in ureteric bud morphogenesis
28	9e-04	6 / 32	BP embryonic cranial skeleton morphogenesis
29	1e-03	11 / 100	BP osteoblast differentiation
30	1e-03	6 / 33	BP spinal cord development
31	2e-03	6 / 36	BP establishment of cell polarity
32	2e-03	5 / 25	BP endocrine pancreas development
33	2e-03	16 / 192	BP methylation
34	2e-03	4 / 16	BP positive regulation of ossification
35	3e-03	8 / 66	BP double-strand break repair
36	3e-03	13 / 146	BP homophilic cell adhesion via plasma membrane adhesion molecules
37	3e-03	4 / 17	BP alternative mRNA splicing, via spliceosome
38	4e-03	6 / 41	BP limb development
39	4e-03	4 / 18	BP ionotropic glutamate receptor activity
40	4e-03	5 / 29	BP pituitary gland development

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	6e-20	124 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
2	1e-17	117 / 1387	regulation of transcription, DNA-templated
3	5e-17	102 / 1145	regulation of transcription by RNA polymerase II
4	5e-09	66 / 843	DNA-binding transcription factor activity
5	5e-08	35 / 342	chromatin organization
6	7e-07	36 / 400	chromatin binding
7	8e-07	72 / 1086	positive regulation of transcription by RNA polymerase II
8	1e-06	18 / 129	rhythmic process
9	2e-06	40 / 484	cellular response to DNA damage stimulus
10	5e-06	32 / 366	DNA repair
11	9e-06	8 / 30	chromosome organization
12	1e-05	41 / 541	negative regulation of transcription, DNA-templated
13	2e-05	44 / 613	positive regulation of transcription, DNA-templated
14	8e-05	6 / 21	spinal cord motor neuron differentiation
15	1e-04	14 / 119	nucleic acid phosphodiester bond hydrolysis

Overexpression Spots

Spot Summary: I

metagenes = 38
genes = 998

<r> metagenes = 0.83
<r> genes = 0.29
beta: r2= 4.87 / log p= -Inf

samples with spot = 8 (5.8 %)
group 5 : 8 (32 %)

Spot Genelist

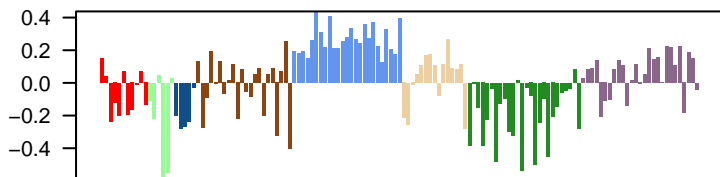
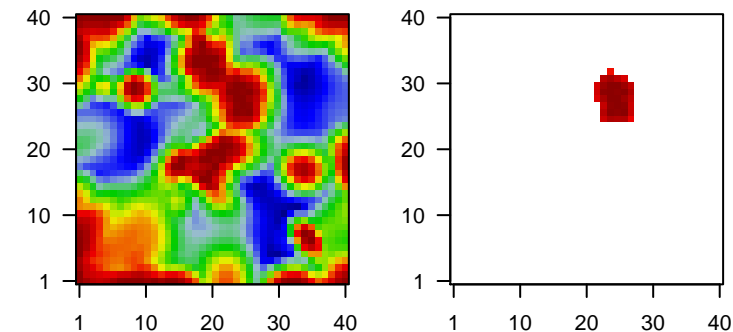
Rank	ID	max e	r	min e	Description
					Symbol
1	231155_at	2.98	-0.75	0.38	DEFB1 defensin beta 119 [Source:HGNC Symbol;Acc:HGNC:18099]
2	237898_at	2.62	-1.03	0.4	
3	213265_at	2.32	-0.88	0.39	PGA4 pepsinogen 4, group I (pepsinogen A) [Source:HGNC Symbo
4	1557369_a_at	2.31	-0.92	0.28	long intergenic non-protein coding RNA 698 [Source:HGNC :
5	207148_x_at	2.29	-0.72	0.43	MYO2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
6	213782_s_at	2.22	-0.69	0.4	MYO2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330]
7	215443_at	2.15	-0.64	0.31	TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;
8	220037_s_at	2.13	-1.17	0.51	LYVE1 lymphatic vessel endothelial hyaluronan receptor 1 [Source:H
9	243952_at	2.08	-1.62	0.63	TPTE pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:436
10	235892_at	2.03	-0.94	0.69	COLCA1 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:H
11	214038_at	2.02	-0.83	0.23	CCL8 C-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:Hi
12	216370_s_at	2	-0.84	0.47	TKTL1 transketolase like 1 [Source:HGNC Symbol;Acc:HGNC:1183
13	206406_at	1.98	-0.7	0.3	SMCP sperm mitochondria associated cysteine rich protein [Source:
14	211341_at	1.98	-0.77	0.42	POU4F1 POU class 4 homeobox 1 [Source:HGNC Symbol;Acc:HGNC
15	242345_at	1.95	-0.91	0.56	COL28A1 collagen type XXVIII alpha 1 chain [Source:HGNC Symbol;Ac
16	207695_s_at	1.94	-1.66	0.71	IGSF1 immunoglobulin superfamily member 1 [Source:HGNC Symb
17	237471_at	1.92	-1.68	0.31	
18	230319_at	1.91	-1.09	0.59	
19	1555854_at	1.9	-0.94	0.36	AKR1C1 aldo-keto reductase family 1 member C1 [Source:HGNC Syn
20	207302_at	1.9	-0.62	0.34	SGCG sarcoglycan gamma [Source:HGNC Symbol;Acc:HGNC:1080

Geneset Overrepresentation

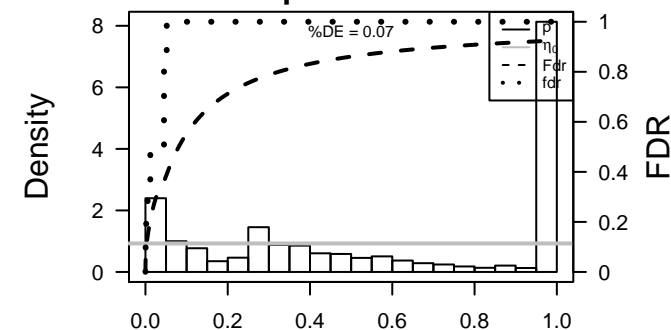
Rank	p-value	#in/all	Geneset
1	2e-07	32 / 398	BP positive regulation of gene expression
2	4e-07	61 / 1086	BP positive regulation of transcription by RNA polymerase II
3	2e-06	9 / 40	BP regulation of neurogenesis
4	2e-06	20 / 207	BP cytokine activity
5	9e-06	37 / 594	BP cell adhesion
6	1e-05	20 / 231	BP extracellular matrix organization
7	4e-05	32 / 513	BP positive regulation of cell population proliferation
8	5e-05	6 / 24	BP negative regulation of neurogenesis
9	6e-05	6 / 25	BP positive regulation of cardiac muscle cell proliferation
10	9e-05	35 / 613	BP positive regulation of transcription, DNA-templated
11	1e-04	6 / 28	BP glycosaminoglycan binding
12	1e-04	6 / 29	BP positive regulation of interleukin-1 beta secretion
13	2e-04	41 / 783	BP negative regulation of transcription by RNA polymerase II
14	2e-04	26 / 418	BP regulation of signaling receptor activity
15	2e-04	9 / 72	BP positive regulation of inflammatory response
16	3e-04	8 / 59	BP retinoid metabolic process
17	3e-04	7 / 45	BP positive regulation of cell division
18	3e-04	4 / 12	BP developmental pigmentation
19	3e-04	13 / 148	BP neuron differentiation
20	4e-04	15 / 188	BP positive regulation of ERK1 and ERK2 cascade
21	4e-04	8 / 62	BP negative regulation of epithelial cell proliferation
22	5e-04	8 / 64	BP camera-type eye development
23	5e-04	12 / 135	BP negative regulation of neuron apoptotic process
24	5e-04	8 / 65	BP chemokine-mediated signaling pathway
25	7e-04	6 / 38	BP positive regulation of bone mineralization
26	7e-04	6 / 38	BP protein kinase B signaling
27	7e-04	40 / 815	BP protein homodimerization activity
28	7e-04	8 / 68	BP retina development in camera-type eye
29	7e-04	4 / 15	BP regulation of I-kappaB kinase/NF-kappaB signaling
30	8e-04	5 / 26	BP focal adhesion assembly
31	9e-04	22 / 364	BP inflammatory response
32	9e-04	5 / 27	BP hippo signaling
33	9e-04	4 / 16	BP positive regulation of membrane protein ectodomain proteolysis
34	1e-03	5 / 28	BP regulation of synapse organization
35	1e-03	9 / 90	BP circadian rhythm
36	1e-03	13 / 168	BP response to hypoxia
37	1e-03	12 / 148	BP chemotaxis
38	1e-03	4 / 17	BP negative regulation of anoikis
39	1e-03	4 / 17	BP vasodilation
40	1e-03	8 / 74	BP neutrophil chemotaxis

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	2e-07	32 / 398	positive regulation of gene expression
2	4e-07	61 / 1086	positive regulation of transcription by RNA polymerase II
3	2e-06	9 / 40	regulation of neurogenesis
4	2e-06	20 / 207	cytokine activity
5	9e-06	37 / 594	cell adhesion
6	1e-05	20 / 231	extracellular matrix organization
7	4e-05	32 / 513	positive regulation of cell population proliferation
8	5e-05	6 / 24	negative regulation of neurogenesis
9	6e-05	6 / 25	positive regulation of cardiac muscle cell proliferation
10	9e-05	35 / 613	positive regulation of transcription, DNA-templated
11	1e-04	6 / 28	glycosaminoglycan binding
12	1e-04	6 / 29	positive regulation of interleukin-1 beta secretion
13	2e-04	41 / 783	negative regulation of transcription by RNA polymerase II
14	2e-04	26 / 418	regulation of signaling receptor activity
15	2e-04	9 / 72	positive regulation of inflammatory response

Overexpression Spots

Spot Summary: J

metagenes = 13
genes = 1099

<r> metagenes = 0.98

beta: r2= 4.28 / log p= -Inf

samples with spot = 11 (8 %)
group 6 : 11 (73.3 %)

Spot Genelist

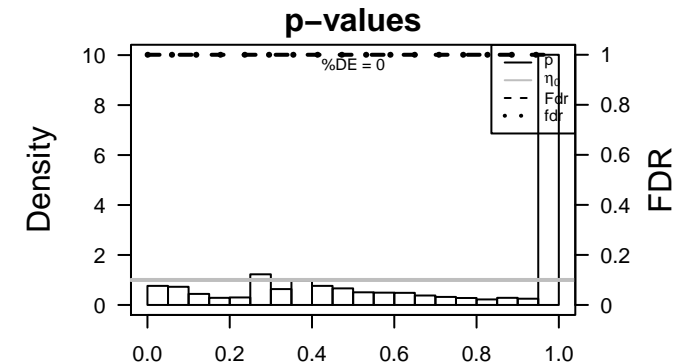
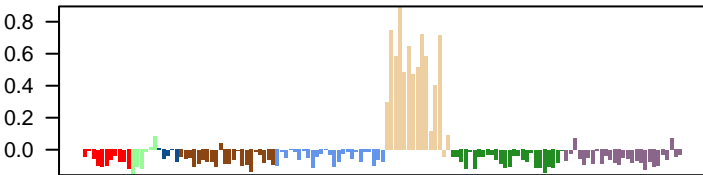
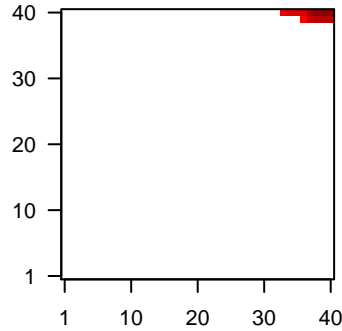
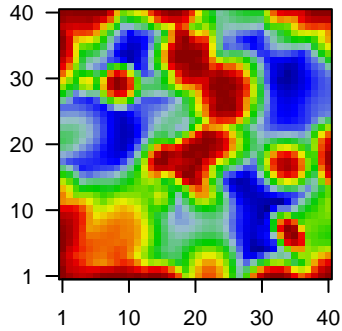
Rank	ID	max e	r	min e	Description
1	1554648_a_at	2.54	-0.69	0.43	DUOXA1 dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:NCBI]
2	214146_s_at	2.49	-0.81	0.26	PPBP pro-platelet basic protein [Source:HGNC Symbol;Acc:HGNC]
3	204419_x_at	2.36	-0.98	0.41	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC]
4	231597_x_at	2.31	-0.71	0.44	
5	204848_x_at	2.27	-1.14	0.41	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC]
6	1559702_at	2.16	-0.61	0.47	ZKSCAN2 divergent transcript [Source:HGNC Symbol;Acc:NCBI]
7	207739_s_at	2.11	-0.46	0.65	GAGE2EG antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
8	216648_s_at	2.1	-0.61	0.87	
9	224997_x_at	1.98	-0.6	0.49	H19, imprinted maternally expressed transcript [Source:HGNC Symbol;Acc:NCBI]
10	1554420_at	1.87	-0.68	0.62	ATF3 activating transcription factor 3 [Source:HGNC Symbol;Acc:NCBI]
11	213515_x_at	1.86	-0.93	0.5	HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC]
12	231078_at	1.82	-0.69	0.72	SLC25A37olute carrier family 25 member 37 [Source:HGNC Symbol;Acc:NCBI]
13	208145_at	1.81	-0.66	0.82	
14	242194_at	1.81	-0.62	0.55	CUL4A cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
15	204420_at	1.8	-0.84	0.54	FOSL1 FOS like 1, AP-1 transcription factor subunit [Source:HGNC Symbol;Acc:NCBI]
16	240897_at	1.77	-0.62	0.74	novel transcript
17	207546_at	1.75	-0.69	0.8	ATP4B ATPase H+/K+ transporting subunit beta [Source:HGNC Symbol;Acc:NCBI]
18	1553212_at	1.73	-0.73	0.84	KRT78 keratin 78 [Source:HGNC Symbol;Acc:HGNC:28926]
19	1566452_at	1.72	-0.57	0.5	
20	208558_at	1.71	-0.42	0.89	OR10H1 olfactory receptor family 10 subfamily H member 1 [Source:NCBI]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-04	4 / 12	BP positive regulation of insulin-like growth factor receptor signaling pathway
2	6e-04	6 / 36	BP blood circulation
3	1e-03	4 / 16	BP positive regulation of calcineurin-NFAT signaling cascade
4	1e-03	6 / 43	BP chemokine activity
5	2e-03	4 / 18	BP regulation of blood vessel size
6	2e-03	40 / 843	BP DNA-binding transcription factor activity
7	3e-03	5 / 35	BP lipid homeostasis
8	3e-03	3 / 11	BP rhodopsin mediated signaling pathway
9	3e-03	4 / 22	BP cellular response to fatty acid
10	4e-03	4 / 23	BP hydrogen peroxide catabolic process
11	4e-03	3 / 12	BP sperm axoneme assembly
12	5e-03	5 / 38	BP bicarbonate transport
13	5e-03	4 / 24	BP leukocyte chemotaxis
14	6e-03	7 / 74	BP neutrophil chemotaxis
15	7e-03	9 / 115	BP keratinization
16	7e-03	3 / 14	BP ectoderm development
17	7e-03	3 / 14	BP positive regulation of renal sodium excretion
18	7e-03	4 / 27	BP positive regulation of protein insertion into mitochondrial membrane involved in
19	1e-02	26 / 541	BP negative regulation of transcription, DNA-templated
20	1e-02	4 / 29	BP positive regulation of Ras protein signal transduction
21	1e-02	10 / 145	BP regulation of cell cycle
22	1e-02	3 / 16	BP regulation of blood vessel diameter
23	1e-02	4 / 30	BP activation of protein kinase B activity
24	1e-02	6 / 65	BP chemokine-mediated signaling pathway
25	1e-02	6 / 65	BP regulation of blood pressure
26	1e-02	10 / 148	BP chemotaxis
27	1e-02	4 / 31	BP stem cell differentiation
28	1e-02	3 / 17	BP positive regulation of T cell migration
29	1e-02	28 / 613	BP positive regulation of transcription, DNA-templated
30	2e-02	4 / 33	BP digestive tract development
31	2e-02	4 / 33	BP response to organonitrogen compound
32	2e-02	7 / 90	BP circadian rhythm
33	2e-02	24 / 513	BP positive regulation of cell population proliferation
34	2e-02	12 / 204	BP cellular protein metabolic process
35	2e-02	6 / 72	BP protein heterooligomerization
36	2e-02	3 / 20	BP response to vitamin A
37	2e-02	3 / 20	BP signal transduction involved in regulation of gene expression
38	2e-02	4 / 36	BP cell maturation
39	2e-02	4 / 36	BP photoreceptor cell maintenance
40	2e-02	20 / 418	BP regulation of signaling receptor activity

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	3e-04	4 / 12	positive regulation of insulin-like growth factor receptor signaling pathway
2	6e-04	6 / 36	blood circulation
3	1e-03	4 / 16	positive regulation of calcineurin-NFAT signaling cascade
4	1e-03	6 / 43	chemokine activity
5	2e-03	4 / 18	regulation of blood vessel size
6	2e-03	40 / 843	DNA-binding transcription factor activity
7	3e-03	5 / 35	lipid homeostasis
8	3e-03	3 / 11	rhodopsin mediated signaling pathway
9	3e-03	4 / 22	cellular response to fatty acid
10	4e-03	4 / 23	hydrogen peroxide catabolic process
11	4e-03	3 / 12	sperm axoneme assembly
12	5e-03	5 / 38	bicarbonate transport
13	5e-03	4 / 24	leukocyte chemotaxis
14	6e-03	7 / 74	neutrophil chemotaxis
15	7e-03	9 / 115	keratinization

Overexpression Spots

Spot Summary: K

metagenes = 9
genes = 434

<r> metagenes = 0.95
<r> genes = 0.44
beta: r2= 5.11 / log p= -Inf

samples with spot = 17 (12.4 %)

- group 1 : 2 (18.2 %)
- group 2 : 2 (33.3 %)
- group 4 : 6 (27.3 %)
- group 6 : 7 (46.7 %)

Spot Genelist

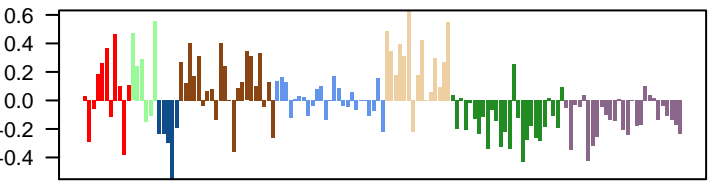
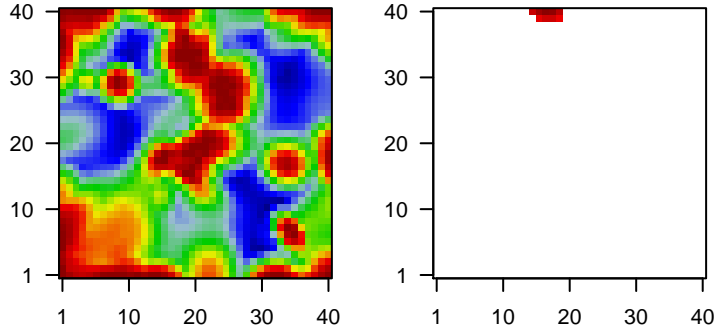
Rank	ID	max e	r	min e	Description
1	218959_at	2.76	-0.75	0.4	HOXC10 homeobox C10 [Source:HGNC Symbol;Acc:HGNC:5122]
2	1569940_at	2.23	-0.67	0.5	
3	1568706_s_at	2.13	-0.69	0.66	
4	222325_at	1.99	-1.11	0.51	
5	1559394_a_at	1.76	-0.67	0.45	
6	1557170_at	1.75	-0.55	0.68	NEK8 NIMA related kinase 8 [Source:NCBI gene;Acc:284086]
7	1562283_at	1.74	-0.77	0.59	
8	232002_at	1.73	-1.28	0.67	
9	242957_at	1.68	-0.8	0.39	VWCE von Willebrand factor C and EGF domains [Source:HGNC Sy
10	234247_at	1.65	-0.99	0.43	
11	218724_s_at	1.65	-0.96	0.52	TGIF2 TGFB induced factor homeobox 2 [Source:HGNC Symbol;Ac
12	236522_at	1.63	-0.51	0.7	
13	240156_at	1.59	-1.36	0.72	
14	1566232_at	1.58	-0.96	0.51	
15	215635_at	1.53	-1.03	0.7	
16	243454_at	1.53	-0.86	0.67	
17	1569578_at	1.53	-0.73	0.73	
18	218847_at	1.51	-1.44	0.64	IGF2BP2insulin like growth factor 2 mRNA binding protein 2 [Source:H
19	1559576_at	1.46	-0.98	0.64	
20	1557477_at	1.46	-0.89	0.61	

Geneset Overrepresentation

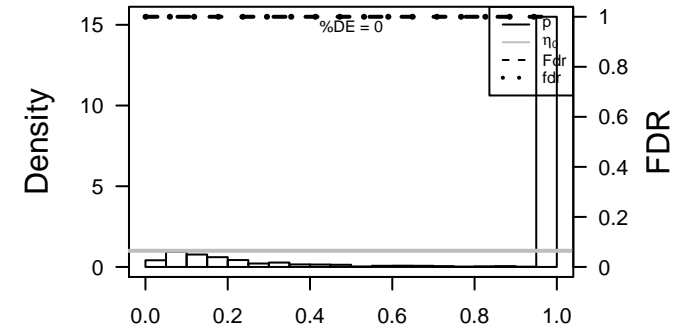
Rank	p-value	#in/all	Geneset
1	3e-05	22 / 1387	BP regulation of transcription, DNA-templated
2	5e-05	59 / 6202	BP cytoplasm
3	1e-04	5 / 83	BP activation of GTPase activity
4	2e-03	13 / 843	BP DNA-binding transcription factor activity
5	2e-03	18 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
6	2e-03	2 / 12	BP actin nucleation
7	2e-03	4 / 92	BP wound healing
8	2e-03	15 / 1086	BP positive regulation of transcription by RNA polymerase II
9	3e-03	43 / 4740	BP cytosol
10	3e-03	3 / 46	BP negative regulation of cold-induced thermogenesis
11	3e-03	6 / 229	BP mRNA splicing, via spliceosome
12	3e-03	12 / 783	BP negative regulation of transcription by RNA polymerase II
13	3e-03	3 / 47	BP regulation of cell adhesion
14	3e-03	5 / 164	BP cytoskeleton organization
15	3e-03	3 / 50	BP positive regulation of cell adhesion
16	4e-03	5 / 168	BP response to hypoxia
17	4e-03	2 / 16	BP positive regulation of tumor necrosis factor secretion
18	5e-03	2 / 18	BP actin filament capping
19	5e-03	2 / 18	BP myelination in peripheral nervous system
20	6e-03	9 / 541	BP negative regulation of transcription, DNA-templated
21	6e-03	2 / 19	BP axoneme assembly
22	6e-03	2 / 19	BP post-Golgi vesicle-mediated transport
23	6e-03	3 / 62	BP circadian regulation of gene expression
24	9e-03	3 / 71	BP hemopoiesis
25	9e-03	2 / 24	BP cellular response to interleukin-4
26	9e-03	3 / 72	BP negative regulation of protein binding
27	1e-02	2 / 27	BP mitotic spindle assembly
28	1e-02	5 / 227	BP microtubule binding
29	1e-02	2 / 28	BP mRNA polyadenylation
30	1e-02	3 / 81	BP regulation of Rho protein signal transduction
31	1e-02	5 / 233	BP heart development
32	1e-02	2 / 31	BP mammary gland development
33	1e-02	2 / 31	BP negative regulation of type I interferon production
34	2e-02	2 / 34	BP energy homeostasis
35	2e-02	2 / 34	BP positive regulation of epithelial cell migration
36	2e-02	3 / 93	BP ciliary basal body-plasma membrane docking
37	2e-02	2 / 36	BP positive regulation of intrinsic apoptotic signaling pathway
38	2e-02	4 / 173	BP cilium assembly
39	2e-02	2 / 37	BP negative regulation of protein catabolic process
40	2e-02	13 / 1145	BP regulation of transcription by RNA polymerase II

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	3e-05	22 / 1387	regulation of transcription, DNA-templated
2	5e-05	59 / 6202	cytoplasm
3	1e-04	5 / 83	activation of GTPase activity
4	2e-03	13 / 843	DNA-binding transcription factor activity
5	2e-03	18 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
6	2e-03	2 / 12	actin nucleation
7	2e-03	4 / 92	wound healing
8	2e-03	15 / 1086	positive regulation of transcription by RNA polymerase II
9	3e-03	43 / 4740	cytosol
10	3e-03	3 / 46	negative regulation of cold-induced thermogenesis
11	3e-03	6 / 229	mRNA splicing, via spliceosome
12	3e-03	12 / 783	negative regulation of transcription by RNA polymerase II
13	3e-03	3 / 47	regulation of cell adhesion
14	3e-03	5 / 164	cytoskeleton organization
15	3e-03	3 / 50	positive regulation of cell adhesion

Overexpression Spots

Spot Summary: L

metagenes = 6
genes = 543

<r> metagenes = 0.91
<r> genes = 0.36
beta: r2= 2.66 / log p= -Inf

samples with spot = 7 (5.1 %)

group 2 : 1 (16.7 %)

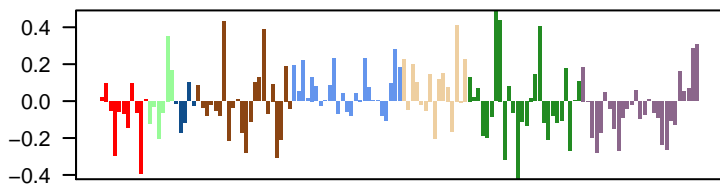
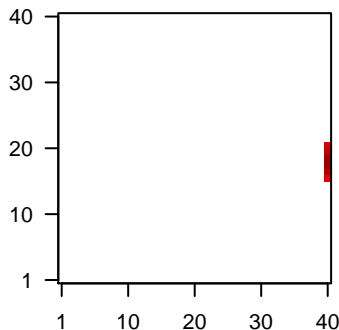
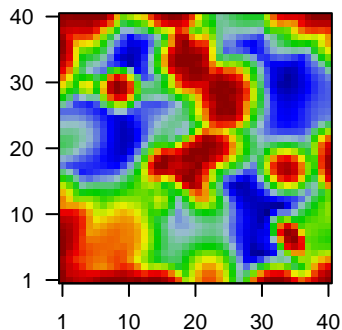
group 4 : 2 (9.1 %)

group 6 : 1 (6.7 %)

group 7 : 3 (11.5 %)

Overview Map

Spot

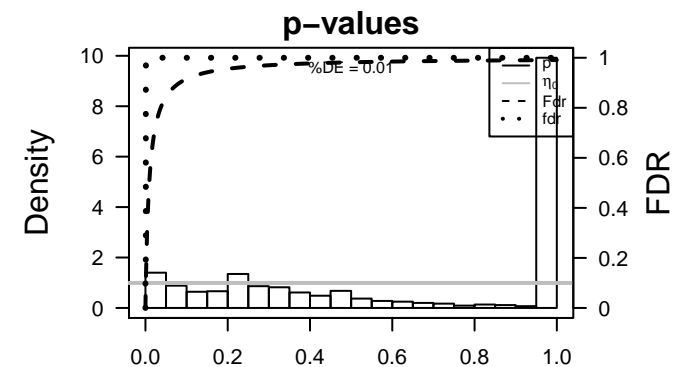


Spot Genelist

Rank	ID	max e	r	min e	Description
1	208468_at	2.15	-0.52	0.47	SOX21 SRY-box 21 [Source:HGNC Symbol;Acc:HGNC:11197]
2	210881_s_at	1.95	-0.6	0.51	INS-IGF2NS-IGF2 readthrough [Source:HGNC Symbol;Acc:HGNC:3327]
3	203365_s_at	1.87	-1.02	0.58	MMP15 matrix metalloproteinase 15 [Source:HGNC Symbol;Acc:HGNC:3327]
4	1560035_at	1.85	-0.64	0.57	RTP5 receptor transporter protein 5 (putative) [Source:HGNC Symbol;Acc:HGNC:3327]
5	216269_s_at	1.78	-0.69	0.4	ELN elastin [Source:HGNC Symbol;Acc:HGNC:3327]
6	223149_s_at	1.73	-0.55	0.61	PTPN23 protein tyrosine phosphatase, non-receptor type 23 [Source:HGNC Symbol;Acc:HGNC:3327]
7	215256_x_at	1.69	-0.71	0.62	ARHGAP33 GTPase activating protein 33 [Source:HGNC Symbol;Acc:HGNC:3327]
8	218892_at	1.62	-1.34	0.5	DCHS1 dachsous cadherin-related 1 [Source:HGNC Symbol;Acc:HGNC:3327]
9	206083_at	1.6	-1.24	0.29	ADGRB1 adhesion G protein-coupled receptor B1 [Source:HGNC Symbol;Acc:HGNC:3327]
10	222123_s_at	1.59	-1.24	0.33	HIF3A hypoxia inducible factor 3 subunit alpha [Source:HGNC Symbol;Acc:HGNC:3327]
11	213946_s_at	1.58	-0.99	0.35	OBSL1 obscurin like 1 [Source:HGNC Symbol;Acc:HGNC:29092]
12	1553139_s_at	1.57	-0.86	0.55	PLXNA3 plexin A3 [Source:HGNC Symbol;Acc:HGNC:9101]
13	205377_s_at	1.53	-0.96	0.44	ACHE acetylcholinesterase (Cartwright blood group) [Source:HGNC Symbol;Acc:HGNC:3327]
14	1555267_at	1.52	-0.85	0.6	
15	239361_at	1.51	-0.83	0.5	
16	227496_at	1.47	-0.85	0.41	NR6A1 nuclear receptor subfamily 6 group A member 1 [Source:HGNC Symbol;Acc:HGNC:3327]
17	207561_s_at	1.46	-1.41	0.57	ASIC3 acid sensing ion channel subunit 3 [Source:HGNC Symbol;Acc:HGNC:3327]
18	1553566_at	1.45	-0.77	0.53	PIANP PILR alpha associated neural protein [Source:HGNC Symbol;Acc:HGNC:3327]
19	218110_at	1.45	-1.16	0.77	XAB2 XPA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:14601]
20	228942_s_at	1.45	-0.52	0.5	DAB2IP DAB2 interacting protein [Source:HGNC Symbol;Acc:HGNC:3327]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-10	185 / 6202	BP cytoplasm
2	2e-08	146 / 4740	BP cytosol
3	7e-08	29 / 459	BP viral process
4	1e-07	8 / 31	BP ATP-dependent chromatin remodeling
5	1e-07	24 / 342	BP chromatin organization
6	2e-07	39 / 783	BP negative regulation of transcription by RNA polymerase II
7	7e-07	30 / 541	BP negative regulation of transcription, DNA-templated
8	1e-06	12 / 102	BP chromatin remodeling
9	2e-06	55 / 1416	BP DNA-binding transcription factor activity, RNA polymerase II-specific
10	7e-06	26 / 484	BP cellular response to DNA damage stimulus
11	7e-06	46 / 1145	BP regulation of transcription by RNA polymerase II
12	8e-06	23 / 400	BP chromatin binding
13	2e-05	43 / 1086	BP positive regulation of transcription by RNA polymerase II
14	3e-05	5 / 19	BP nucleosome disassembly
15	4e-05	189 / 7387	BP membrane
16	1e-04	12 / 163	BP autophagy
17	3e-04	8 / 83	BP activation of GTPase activity
18	5e-04	26 / 630	BP protein transport
19	5e-04	4 / 19	BP ubiquitin-dependent protein catabolic process via the multivesicular body pathway
20	6e-04	4 / 20	BP entrainment of circadian clock by photoperiod
21	6e-04	4 / 20	BP protein localization to Golgi apparatus
22	7e-04	24 / 574	BP synapse
23	7e-04	16 / 315	BP positive regulation of GTPase activity
24	7e-04	7 / 74	BP retrograde transport, endosome to Golgi
25	7e-04	5 / 36	BP establishment of cell polarity
26	7e-04	5 / 36	BP semaphorin-plexin signaling pathway
27	9e-04	4 / 22	BP chromatin silencing
28	9e-04	6 / 56	BP DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
29	1e-03	3 / 11	BP anoikis
30	1e-03	41 / 1242	BP Golgi apparatus
31	1e-03	12 / 214	BP cell migration
32	2e-03	3 / 12	BP branching involved in mammary gland duct morphogenesis
33	2e-03	3 / 12	BP response to acidic pH
34	2e-03	11 / 188	BP in utero embryonic development
35	2e-03	22 / 545	BP protein ubiquitination
36	2e-03	12 / 222	BP Wnt signaling pathway
37	2e-03	7 / 90	BP activation of protein kinase activity
38	2e-03	24 / 630	BP cell cycle
39	2e-03	6 / 68	BP cellular response to hydrogen peroxide
40	2e-03	5 / 47	BP positive regulation of protein serine/threonine kinase activity



BP

Rank	p-value	#in/all	Geneset
1	6e-10	185 / 6202	cytoplasm
2	2e-08	146 / 4740	cytosol
3	7e-08	29 / 459	viral process
4	1e-07	8 / 31	ATP-dependent chromatin remodeling
5	1e-07	24 / 342	chromatin organization
6	2e-07	39 / 783	negative regulation of transcription by RNA polymerase II
7	7e-07	30 / 541	negative regulation of transcription, DNA-templated
8	1e-06	12 / 102	chromatin remodeling
9	2e-06	55 / 1416	DNA-binding transcription factor activity, RNA polymerase II-specific
10	7e-06	26 / 484	cellular response to DNA damage stimulus
11	7e-06	46 / 1145	regulation of transcription by RNA polymerase II
12	8e-06	23 / 400	chromatin binding
13	2e-05	43 / 1086	positive regulation of transcription by RNA polymerase II
14	3e-05	5 / 19	nucleosome disassembly
15	4e-05	189 / 7387	membrane

Overexpression Spots

Spot Summary: M

metagenes = 19
genes = 1156

<r> metagenes = 0.92

beta: r2= 11.46 / log p= -Inf

samples with spot = 24 (17.5 %)

group 1 : 3 (27.3 %)

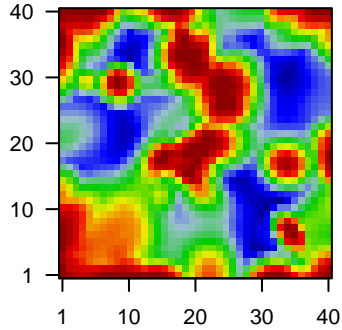
group 2 : 2 (33.3 %)

group 4 : 8 (36.4 %)

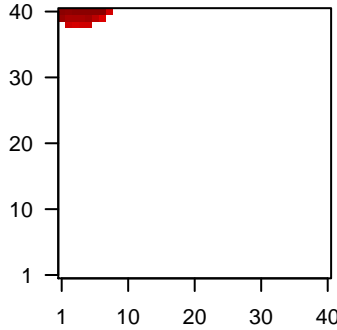
group 6 : 6 (40 %)

group 7 : 5 (19.2 %)

Overview Map



Spot

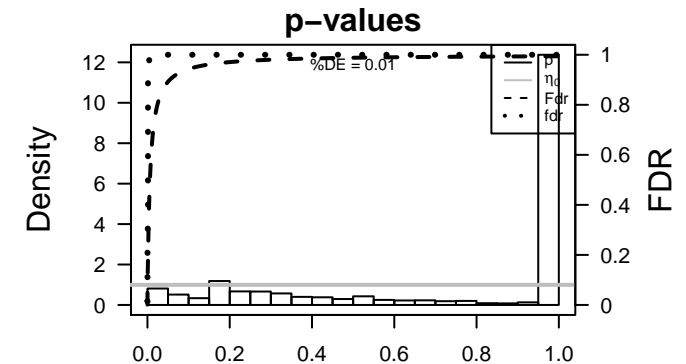
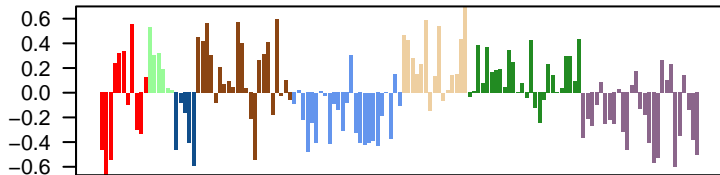


Spot Genelist

Rank	ID	max e	r	min e	Description
1	204713_s_at	2.44	-1.56	0.26	F5 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542]
2	1566482_at	2.19	-0.81	0.54	novel transcript
3	215448_at	2.16	-1.33	0.53	
4	216007_at	2.14	-1.07	0.67	
5	1563331_at	2.1	-0.74	0.62	
6	226211_at	2.09	-1.04	0.44	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1
7	240728_at	2.08	-0.93	0.7	
8	244042_x_at	2.08	-1.91	0.5	
9	237943_at	2.04	-1.36	0.87	TMCC1 transmembrane and coiled-coil domain family 1 [Source:HGNC
10	234597_at	2.04	-0.92	0.7	
11	242319_at	2.03	-0.87	0.51	DGKG diacylglycerol kinase gamma [Source:HGNC Symbol;Acc:HG
12	216518_at	2	-0.75	0.5	
13	1563426_a_at	1.96	-0.74	0.62	novel transcript
14	233884_at	1.96	-0.95	0.59	
15	207213_s_at	1.95	-1.36	0.46	USP2 ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG
16	1552337_s_at	1.95	-0.8	0.41	HOXD4 homeobox D4 [Source:NCBI gene;Acc:3233]
17	226210_s_at	1.9	-1.12	0.44	maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1
18	232925_at	1.9	-1.69	0.67	
19	200952_s_at	1.89	-1.58	0.56	CCND2 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
20	240112_at	1.88	-1.05	0.58	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-07	17 / 227	BP microtubule binding
2	1e-05	19 / 358	BP mRNA processing
3	2e-05	20 / 400	BP chromatin binding
4	2e-05	38 / 1086	BP positive regulation of transcription by RNA polymerase II
5	3e-05	18 / 342	BP chromatin organization
6	3e-05	16 / 279	BP RNA splicing
7	8e-05	7 / 61	BP regulation of alternative mRNA splicing, via spliceosome
8	9e-05	21 / 484	BP cellular response to DNA damage stimulus
9	1e-04	4 / 16	BP cytoskeleton-dependent intracellular transport
10	2e-04	8 / 93	BP regulation of lipid metabolic process
11	3e-04	109 / 4740	BP cytosol
12	6e-04	6 / 62	BP circadian regulation of gene expression
13	7e-04	4 / 24	BP positive regulation of receptor-mediated endocytosis
14	7e-04	4 / 24	BP regulation of glucose metabolic process
15	8e-04	4 / 25	BP spliceosomal complex assembly
16	8e-04	134 / 6202	BP cytoplasm
17	1e-03	3 / 13	BP positive regulation of keratinocyte differentiation
18	1e-03	3 / 13	BP protein targeting to vacuole
19	1e-03	22 / 630	BP cell cycle
20	1e-03	16 / 394	BP cell division
21	2e-03	8 / 129	BP rhythmic process
22	2e-03	11 / 229	BP mRNA splicing, via spliceosome
23	3e-03	3 / 17	BP alternative mRNA splicing, via spliceosome
24	4e-03	9 / 180	BP cell projection organization
25	4e-03	3 / 19	BP erythrocyte development
26	4e-03	3 / 19	BP regulation of DNA replication
27	4e-03	24 / 783	BP negative regulation of transcription by RNA polymerase II
28	4e-03	32 / 1145	BP regulation of transcription by RNA polymerase II
29	4e-03	6 / 90	BP circadian rhythm
30	4e-03	20 / 613	BP positive regulation of transcription, DNA-templated
31	4e-03	3 / 20	BP actin filament-based movement
32	4e-03	3 / 20	BP DNA replication-independent nucleosome assembly
33	4e-03	3 / 20	BP positive regulation of mRNA splicing, via spliceosome
34	4e-03	3 / 20	BP regulation of transforming growth factor beta receptor signaling pathway
35	5e-03	3 / 21	BP hindbrain development
36	6e-03	18 / 541	BP negative regulation of transcription, DNA-templated
37	6e-03	3 / 22	BP sister chromatid cohesion
38	7e-03	3 / 23	BP aorta development
39	7e-03	3 / 23	BP DNA methylation
40	8e-03	6 / 102	BP chromatin remodeling



BP

Rank	p-value	#in/all	Geneset
1	4e-07	17 / 227	microtubule binding
2	1e-05	19 / 358	mRNA processing
3	2e-05	20 / 400	chromatin binding
4	2e-05	38 / 1086	positive regulation of transcription by RNA polymerase II
5	3e-05	18 / 342	chromatin organization
6	3e-05	16 / 279	RNA splicing
7	8e-05	7 / 61	regulation of alternative mRNA splicing, via spliceosome
8	9e-05	21 / 484	cellular response to DNA damage stimulus
9	1e-04	4 / 16	cytoskeleton-dependent intracellular transport
10	2e-04	8 / 93	regulation of lipid metabolic process
11	3e-04	109 / 4740	cytosol
12	6e-04	6 / 62	circadian regulation of gene expression
13	7e-04	4 / 24	positive regulation of receptor-mediated endocytosis
14	7e-04	4 / 24	regulation of glucose metabolic process
15	8e-04	4 / 25	spliceosomal complex assembly

Overexpression Spots

Spot Summary: N

metagenes = 11
genes = 942

<r> metagenes = 0.97
<r> genes = 0.49
beta: r2= 6.53 / log p= -Inf

samples with spot = 14 (10.2 %)

- group 1 : 1 (9.1 %)
- group 2 : 2 (33.3 %)
- group 4 : 4 (18.2 %)
- group 6 : 4 (26.7 %)
- group 7 : 3 (11.5 %)

Spot Genelist

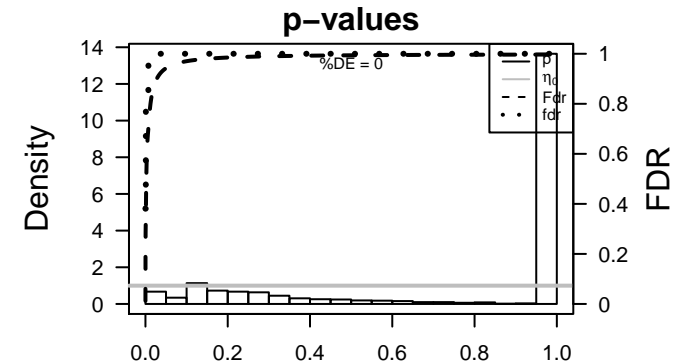
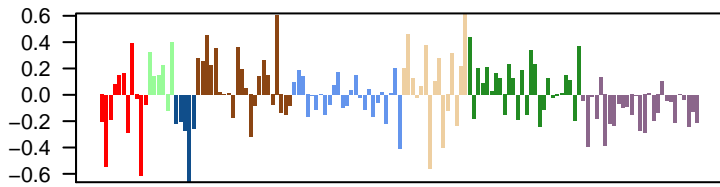
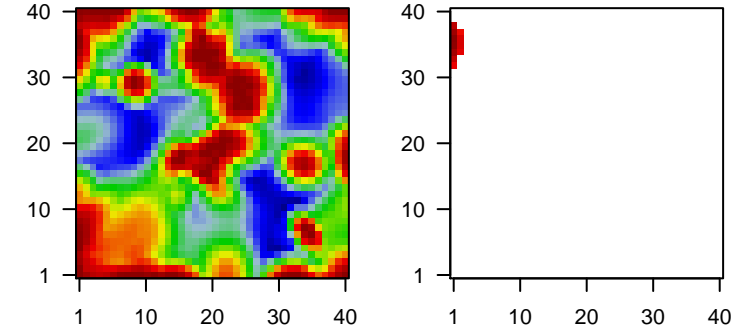
Rank	ID	max e	r	min e	Description
1	243428_at	1.95	-0.98	0.56	KCNQ1 opposite strand/antisense transcript 1 [Source:HGNC
2	1562898_at	1.9	-0.71	0.57	
3	243112_at	1.76	-0.67	0.52	
4	1557835_at	1.75	-1.09	0.57	
5	217588_at	1.75	-0.72	0.52	CATSPER2 catanin channel sperm associated 2 [Source:HGNC Symbol;A
6	244239_at	1.72	-0.72	0.53	
7	214967_at	1.67	-1.16	0.55	
8	235551_at	1.65	-0.73	0.51	
9	1563597_at	1.64	-0.7	0.52	
10	1558828_s_at	1.64	-1.16	0.48	cardiac mesoderm enhancer-associated non-coding RNA [S
11	1557104_at	1.64	-0.81	0.58	
12	232480_at	1.62	-1.17	0.65	MIRLET7B host gene [Source:HGNC Symbol;Acc:HGNC:371
13	1558987_at	1.62	-1	0.64	
14	1553524_at	1.56	-0.56	0.55	DGKB diacylglycerol kinase beta [Source:HGNC Symbol;Acc:HGNC
15	215761_at	1.54	-0.93	0.79	DMXL2 Dmx like 2 [Source:HGNC Symbol;Acc:HGNC:2938]
16	1562276_at	1.54	-1.03	0.55	
17	236717_at	1.54	-1.51	0.25	TOGARAM12G array regulator of axonemal microtubules 2 [Source:HGI
18	1557025_a_at	1.53	-0.5	0.54	novel transcript
19	243480_at	1.53	-0.93	0.78	
20	232701_at	1.52	-1.17	0.57	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-06	15 / 342	BP chromatin organization
2	2e-04	10 / 227	BP microtubule binding
3	4e-04	13 / 400	BP chromatin binding
4	5e-04	3 / 15	BP positive regulation of cilium assembly
5	6e-04	25 / 1145	BP regulation of transcription by RNA polymerase II
6	7e-04	72 / 4740	BP cytosol
7	9e-04	28 / 1387	BP regulation of transcription, DNA-templated
8	1e-03	3 / 19	BP nucleosome disassembly
9	1e-03	13 / 459	BP viral process
10	2e-03	12 / 412	BP negative regulation of cell population proliferation
11	2e-03	8 / 215	BP ubiquitin protein ligase activity
12	2e-03	3 / 25	BP positive regulation of microtubule polymerization
13	3e-03	3 / 27	BP microtubule bundle formation
14	3e-03	3 / 27	BP regulation of cell morphogenesis
15	4e-03	4 / 62	BP somatic stem cell population maintenance
16	5e-03	2 / 10	BP positive regulation of transcription of nucleolar large rRNA by RNA polymerase I
17	5e-03	2 / 10	BP primary miRNA processing
18	5e-03	2 / 10	BP regulation of DNA damage checkpoint
19	5e-03	3 / 33	BP midbrain development
20	6e-03	2 / 11	BP actin filament depolymerization
21	6e-03	2 / 11	BP regulation of microtubule polymerization
22	7e-03	2 / 12	BP homeostatic process
23	7e-03	2 / 12	BP microtubule polymerization
24	7e-03	2 / 12	BP negative regulation of oligodendrocyte differentiation
25	7e-03	2 / 12	BP oxidative phosphorylation
26	7e-03	2 / 12	BP positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
27	7e-03	2 / 12	BP regulation of microtubule polymerization or depolymerization
28	7e-03	4 / 71	BP hemopoiesis
29	7e-03	23 / 1242	BP Golgi apparatus
30	8e-03	14 / 630	BP protein transport
31	8e-03	5 / 117	BP negative regulation of cell migration
32	9e-03	3 / 40	BP cytoplasmic microtubule organization
33	9e-03	2 / 14	BP cardiac muscle cell proliferation
34	9e-03	2 / 14	BP regulation of osteoblast differentiation
35	1e-02	83 / 6202	BP cytoplasm
36	1e-02	2 / 15	BP positive regulation of cartilage development
37	1e-02	2 / 15	BP positive regulation of histone H3-K4 methylation
38	1e-02	2 / 15	BP positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent
39	1e-02	2 / 16	BP negative regulation of epithelial cell migration
40	1e-02	7 / 233	BP heart development

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	4e-06	15 / 342	chromatin organization
2	2e-04	10 / 227	microtubule binding
3	4e-04	13 / 400	chromatin binding
4	5e-04	3 / 15	positive regulation of cilium assembly
5	6e-04	25 / 1145	regulation of transcription by RNA polymerase II
6	7e-04	72 / 4740	cytosol
7	9e-04	28 / 1387	regulation of transcription, DNA-templated
8	1e-03	3 / 19	nucleosome disassembly
9	1e-03	13 / 459	viral process
10	2e-03	12 / 412	negative regulation of cell population proliferation
11	2e-03	8 / 215	ubiquitin protein ligase activity
12	2e-03	3 / 25	positive regulation of microtubule polymerization
13	3e-03	3 / 27	microtubule bundle formation
14	3e-03	3 / 27	regulation of cell morphogenesis
15	4e-03	4 / 62	somatic stem cell population maintenance

Overexpression Spots

Spot Summary: O

metagenes = 22
genes = 971

<r> metagenes = 0.9
<r> genes = 0.44
beta: r2= 8.09 / log p= -Inf

samples with spot = 6 (4.4 %)
group 1 : 1 (9.1 %)
group 7 : 4 (15.4 %)
group 8 : 1 (3.7 %)

Spot Genelist

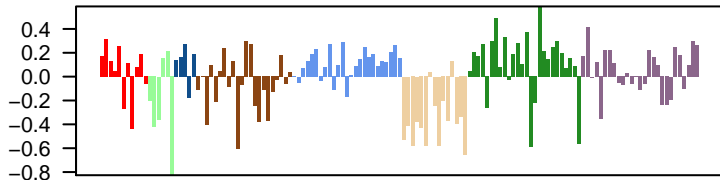
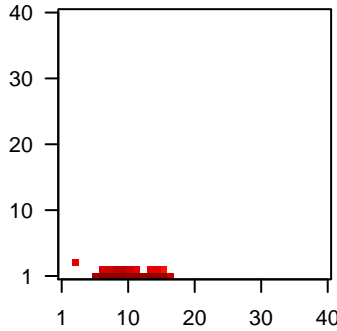
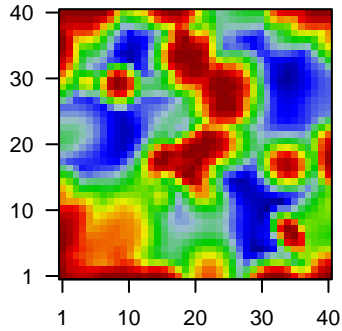
Rank	ID	max e	r	min e	Description
1	155557_a_at	2.39	-0.52	0.47	microRNA 6829 [Source:HGNC Symbol;Acc:HGNC:50055]
2	203838_s_at	2.27	-0.97	0.53	TNK2 tyrosine kinase non receptor 2 [Source:HGNC Symbol;Acc:HGNC:203838]
3	220240_s_at	2.09	-1.17	0.68	TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Symbol;Acc:HGNC:220240]
4	211877_s_at	2.07	-0.62	0.21	PCDHGA1 protocadherin gamma subfamily A, 11 [Source:HGNC Symbol;Acc:HGNC:211877]
5	1555191_a_at	2.06	-0.78	0.51	FHL5 four and a half LIM domains 5 [Source:HGNC Symbol;Acc:HGNC:1555191]
6	211607_x_at	2.06	-1.23	0.59	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:HGNC:211607]
7	208889_s_at	2.05	-0.58	0.42	NCOR2 nuclear receptor corepressor 2 [Source:HGNC Symbol;Acc:HGNC:208889]
8	210984_x_at	2	-1.3	0.57	EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:HGNC:210984]
9	201551_s_at	1.99	-1.97	0.48	LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:201551]
10	200879_s_at	1.97	-1.12	0.67	EPAS1 endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc:HGNC:200879]
11	211899_s_at	1.87	-0.82	0.37	TRAF4 TNF receptor associated factor 4 [Source:HGNC Symbol;Acc:HGNC:211899]
12	207151_at	1.8	-0.85	0.62	ADCYAP1 ADCYAP receptor type I [Source:HGNC Symbol;Acc:HGNC:207151]
13	210790_s_at	1.8	-0.94	0.43	SAR1A secretion associated Ras related GTPase 1A [Source:HGNC Symbol;Acc:HGNC:210790]
14	212940_at	1.79	-0.75	0.48	COL6A1 collagen type VI alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:212940]
15	204707_s_at	1.78	-0.7	0.48	MAPK4 mitogen-activated protein kinase 4 [Source:HGNC Symbol;Acc:HGNC:204707]
16	230445_at	1.77	-1.09	0.46	BTBD17 BTB domain containing 17 [Source:HGNC Symbol;Acc:HGNC:230445]
17	222501_s_at	1.75	-1.44	0.79	REPIN1 replication initiator 1 [Source:HGNC Symbol;Acc:HGNC:222501]
18	210973_s_at	1.72	-1.13	0.48	FGFR1 fibroblast growth factor receptor 1 [Source:HGNC Symbol;Acc:HGNC:210973]
19	1554697_at	1.69	-1.41	0.52	ADAMTS1 ADAM metalloproteinase with thrombospondin type 1 motif 9 [Source:HGNC Symbol;Acc:HGNC:1554697]
20	244561_at	1.69	-0.6	0.59	SLC9A7 solute carrier family 9 member A7 [Source:HGNC Symbol;Acc:HGNC:244561]

Geneset Overrepresentation

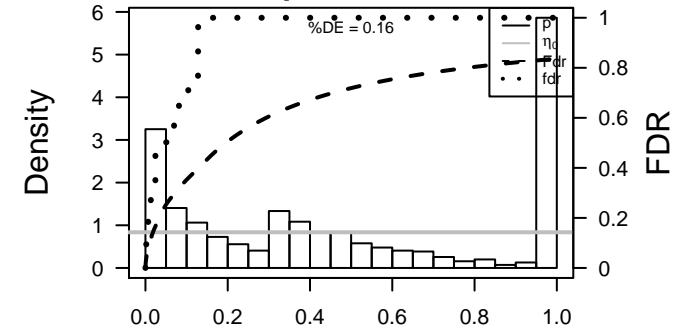
Rank	p-value	#in/all	Geneset
1	1e-25	366 / 6202	BP cytoplasm
2	2e-25	302 / 4740	BP cytosol
3	2e-23	408 / 7387	BP membrane
4	1e-13	100 / 1242	BP Golgi apparatus
5	6e-13	241 / 4278	BP plasma membrane
6	8e-09	54 / 630	BP protein transport
7	2e-08	43 / 459	BP viral process
8	4e-08	34 / 324	BP intracellular protein transport
9	9e-08	35 / 350	BP GTP binding
10	2e-07	50 / 623	BP protein phosphorylation
11	3e-07	19 / 129	BP rhythmic process
12	3e-07	60 / 815	BP protein homodimerization activity
13	7e-07	52 / 684	BP phosphorylation
14	7e-07	31 / 315	BP positive regulation of GTPase activity
15	8e-07	11 / 47	BP activation of MAPKK activity
16	2e-06	9 / 33	BP regulation of cholesterol biosynthetic process
17	4e-06	70 / 1086	BP positive regulation of transcription by RNA polymerase II
18	6e-06	37 / 455	BP intracellular signal transduction
19	1e-05	33 / 400	BP protein serine/threonine kinase activity
20	2e-05	23 / 234	BP protein deubiquitination
21	2e-05	12 / 76	BP negative regulation of translation
22	3e-05	12 / 78	BP insulin receptor signaling pathway
23	3e-05	83 / 1435	BP mitochondrion
24	3e-05	16 / 132	BP membrane organization
25	3e-05	25 / 273	BP MAPK cascade
26	3e-05	18 / 162	BP dephosphorylation
27	3e-05	7 / 26	BP regulation of cytoskeleton organization
28	4e-05	37 / 496	BP negative regulation of apoptotic process
29	4e-05	7 / 27	BP metal ion transport
30	4e-05	5 / 12	BP Lys63-specific deubiquitinase activity
31	4e-05	80 / 1387	BP regulation of transcription, DNA-templated
32	4e-05	43 / 613	BP positive regulation of transcription, DNA-templated
33	4e-05	42 / 594	BP cell adhesion
34	5e-05	24 / 264	BP vesicle-mediated transport
35	5e-05	16 / 138	BP regulation of small GTPase mediated signal transduction
36	5e-05	39 / 541	BP negative regulation of transcription, DNA-templated
37	6e-05	11 / 72	BP Rho protein signal transduction
38	7e-05	5 / 13	BP positive regulation of cell-cell adhesion
39	8e-05	6 / 21	BP negative regulation of intrinsic apoptotic signaling pathway
40	9e-05	7 / 30	BP negative regulation of mitotic cell cycle

Overview Map

Spot



p-values



BP

Rank	p-value	#in/all	Geneset
1	1e-25	366 / 6202	cytoplasm
2	2e-25	302 / 4740	cytosol
3	2e-23	408 / 7387	membrane
4	1e-13	100 / 1242	Golgi apparatus
5	6e-13	241 / 4278	plasma membrane
6	8e-09	54 / 630	protein transport
7	2e-08	43 / 459	viral process
8	4e-08	34 / 324	intracellular protein transport
9	9e-08	35 / 350	GTP binding
10	2e-07	50 / 623	protein phosphorylation
11	3e-07	19 / 129	rhythmic process
12	3e-07	60 / 815	protein homodimerization activity
13	7e-07	52 / 684	phosphorylation
14	7e-07	31 / 315	positive regulation of GTPase activity
15	8e-07	11 / 47	activation of MAPKK activity

Overexpression Spots

Spot Summary: P

metagenes = 9
genes = 389

<r> metagenes = 0.96
<r> genes = 0.39
beta: r2= 1.6 / log p= -Inf

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

Spot Genelist

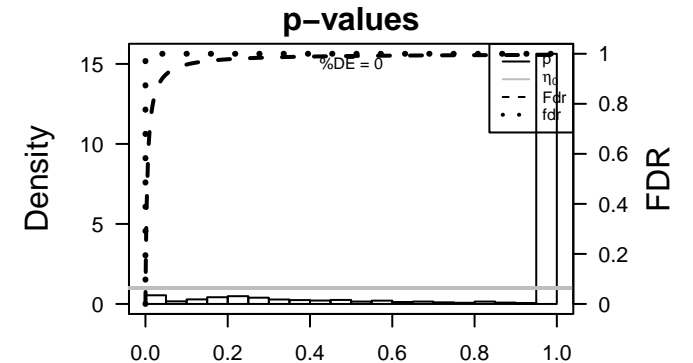
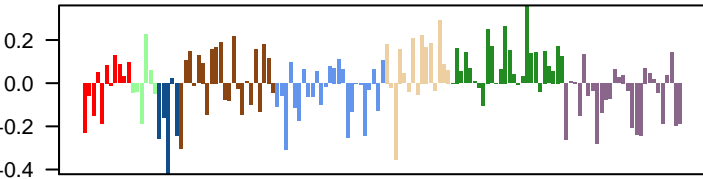
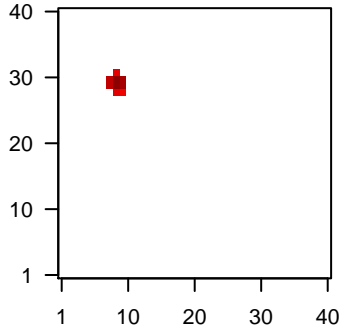
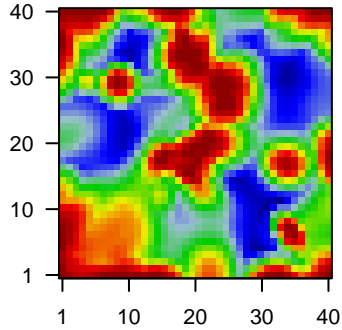
Rank	ID	max e	r	min e	Description
					Symbol
1	204179_at	1.69	-0.42	0.31	MB myoglobin [Source:HGNC Symbol;Acc:HGNC:6915]
2	225616_at	1.64	-0.52	0.44	SPRYD4 SPRY domain containing 4 [Source:HGNC Symbol;Acc:HGNC:10842]
3	207813_s_at	1.61	-1.11	0.46	FDXR ferredoxin reductase [Source:HGNC Symbol;Acc:HGNC:3642]
4	230591_at	1.53	-0.77	0.51	novel transcript, antisense to MBTPS1
5	1565389_s_at	1.51	-0.51	0.3	GRM5 glutamate metabotropic receptor 5 [Source:HGNC Symbol;Acc:HGNC:10842]
6	206645_s_at	1.44	-0.74	0.32	NR0B1 nuclear receptor subfamily 0 group B member 1 [Source:HGNC Symbol;Acc:HGNC:10842]
7	226546_at	1.41	-0.78	0.62	GIHCG, inhibitor of miR-200b/200a/429 expression [Source:HGNC Symbol;Acc:HGNC:10842]
8	1559532_at	1.36	-0.65	0.37	ARIH2OARIadne RBR E3 ubiquitin protein ligase 2 opposite strand [Source:HGNC Symbol;Acc:HGNC:10842]
9	229338_at	1.34	-0.7	0.56	novel transcript
10	216177_at	1.32	-0.79	0.61	ribosomal protein L29 pseudogene 7 [Source:HGNC Symbol;Acc:HGNC:10842]
11	235770_at	1.32	-0.83	0.38	MASP1 mannan binding lectin serine peptidase 1 [Source:HGNC Symbol;Acc:HGNC:10842]
12	206956_at	1.31	-0.92	0.56	PMF1-BMP1-BGLAP readthrough [Source:HGNC Symbol;Acc:HGNC:10842]
13	227424_x_at	1.31	-0.69	0.52	URB1 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:10842]
14	238389_s_at	1.21	-0.77	0.56	novel transcript
15	214463_x_at	1.19	-0.92	0.56	HIST1H4K histone cluster 1 H4 family member k [Source:HGNC Symbol;Acc:HGNC:10842]
16	216881_x_at	1.11	-0.6	0.34	PRB4 proline rich protein BstNI subfamily 4 [Source:HGNC Symbol;Acc:HGNC:10842]
17	223706_at	1.1	-0.58	0.39	C22orf23 chromosome 22 open reading frame 23 [Source:HGNC Symbol;Acc:HGNC:10842]
18	236400_at	1.06	-0.52	0.47	IDH1 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:40]
19	219138_at	1.02	-0.66	0.62	novel transcript
20	229423_at	1.02	-0.71	0.48	novel transcript

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-22	35 / 276	BP translation
2	6e-22	74 / 1435	BP mitochondrion
3	6e-14	15 / 69	BP SRP-dependent cotranslational protein targeting to membrane
4	9e-14	20 / 152	BP rRNA processing
5	1e-12	16 / 98	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
6	1e-12	15 / 83	BP mitochondrial translational elongation
7	2e-12	15 / 85	BP mitochondrial translational termination
8	2e-12	17 / 120	BP translational initiation
9	4e-12	15 / 90	BP viral transcription
10	1e-07	7 / 28	BP protein targeting to mitochondrion
11	4e-06	16 / 279	BP RNA splicing
12	6e-06	18 / 358	BP mRNA processing
13	8e-06	14 / 229	BP mRNA splicing, via spliceosome
14	2e-05	4 / 12	BP ribosomal small subunit assembly
15	6e-05	5 / 29	BP cytoplasmic translation
16	9e-05	4 / 17	BP positive regulation of mitochondrial translation
17	2e-04	5 / 36	BP mitochondrial translation
18	2e-04	4 / 21	BP ribosomal large subunit assembly
19	4e-04	7 / 93	BP ribosome biogenesis
20	4e-04	4 / 25	BP translational elongation
21	5e-04	4 / 26	BP spliceosomal snRNP assembly
22	9e-04	4 / 30	BP ribosomal large subunit biogenesis
23	1e-03	3 / 15	BP ubiquinone biosynthetic process
24	1e-03	5 / 57	BP RNA phosphodiester bond hydrolysis, endonucleolytic
25	2e-03	92 / 4740	BP cytosol
26	3e-03	3 / 19	BP import into nucleus
27	3e-03	13 / 366	BP DNA repair
28	3e-03	6 / 97	BP chaperone binding
29	6e-03	3 / 26	BP ATP biosynthetic process
30	6e-03	3 / 26	BP maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, and 5S rRNA)
31	8e-03	5 / 84	BP tRNA processing
32	8e-03	4 / 54	BP nucleobase-containing compound metabolic process
33	9e-03	3 / 29	BP response to tumor necrosis factor
34	9e-03	2 / 10	BP DNA dealkylation involved in DNA repair
35	9e-03	2 / 10	BP positive regulation of establishment of protein localization to telomere
36	9e-03	2 / 10	BP protein maturation by iron-sulfur cluster transfer
37	9e-03	3 / 30	BP cristae formation
38	1e-02	2 / 11	BP positive regulation of double-strand break repair via nonhomologous end joining
39	1e-02	2 / 12	BP cytoplasmic translational initiation
40	1e-02	2 / 12	BP endothelial cell differentiation

Overview Map

Spot



BP

Rank	p-value	#in/all	Geneset
1	1e-22	35 / 276	translation
2	6e-22	74 / 1435	mitochondrion
3	6e-14	15 / 69	SRP-dependent cotranslational protein targeting to membrane
4	9e-14	20 / 152	rRNA processing
5	1e-12	16 / 98	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
6	1e-12	15 / 83	mitochondrial translational elongation
7	2e-12	15 / 85	mitochondrial translational termination
8	2e-12	17 / 120	translational initiation
9	4e-12	15 / 90	viral transcription
10	1e-07	7 / 28	protein targeting to mitochondrion
11	4e-06	16 / 279	RNA splicing
12	6e-06	18 / 358	mRNA processing
13	8e-06	14 / 229	mRNA splicing, via spliceosome
14	2e-05	4 / 12	ribosomal small subunit assembly
15	6e-05	5 / 29	cytoplasmic translation