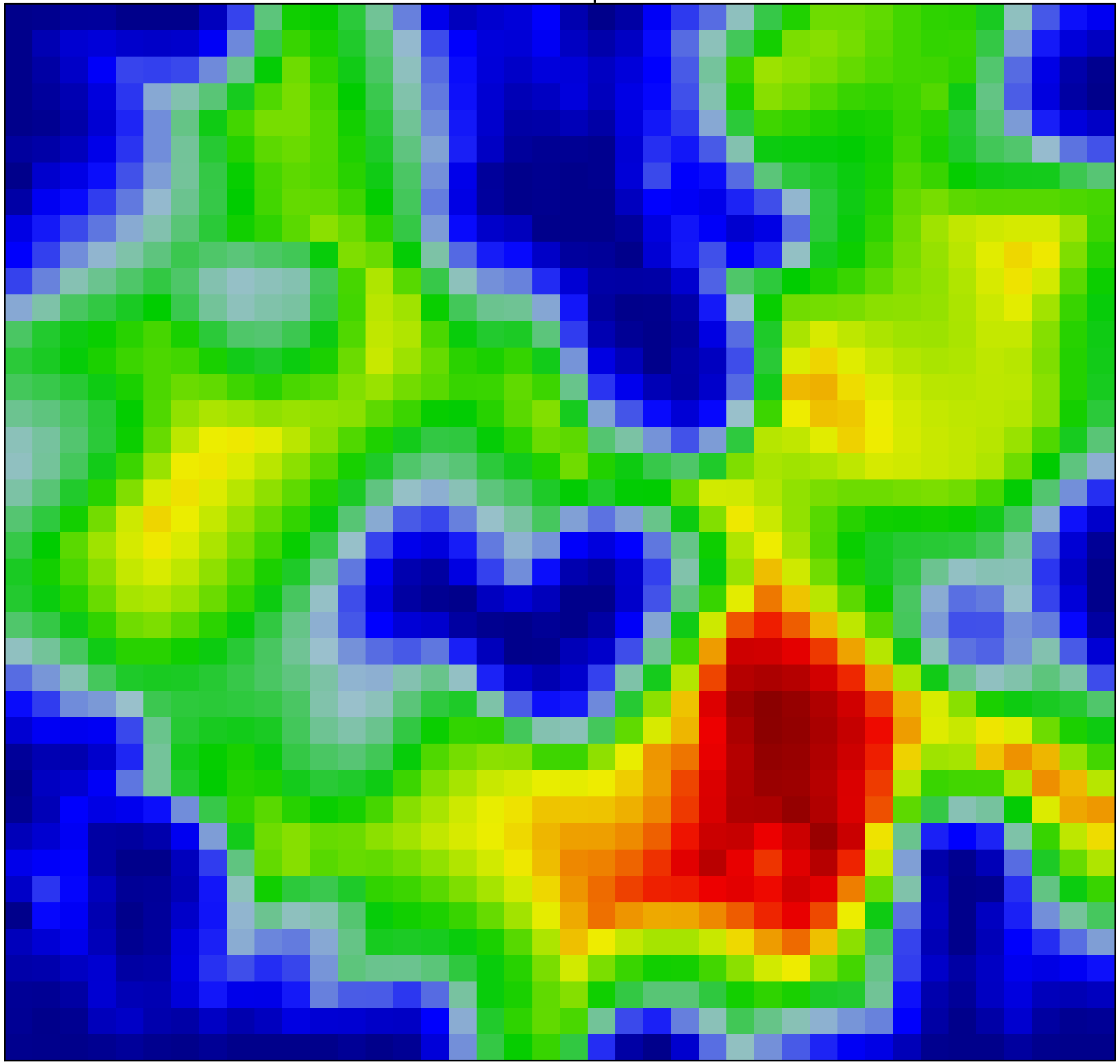
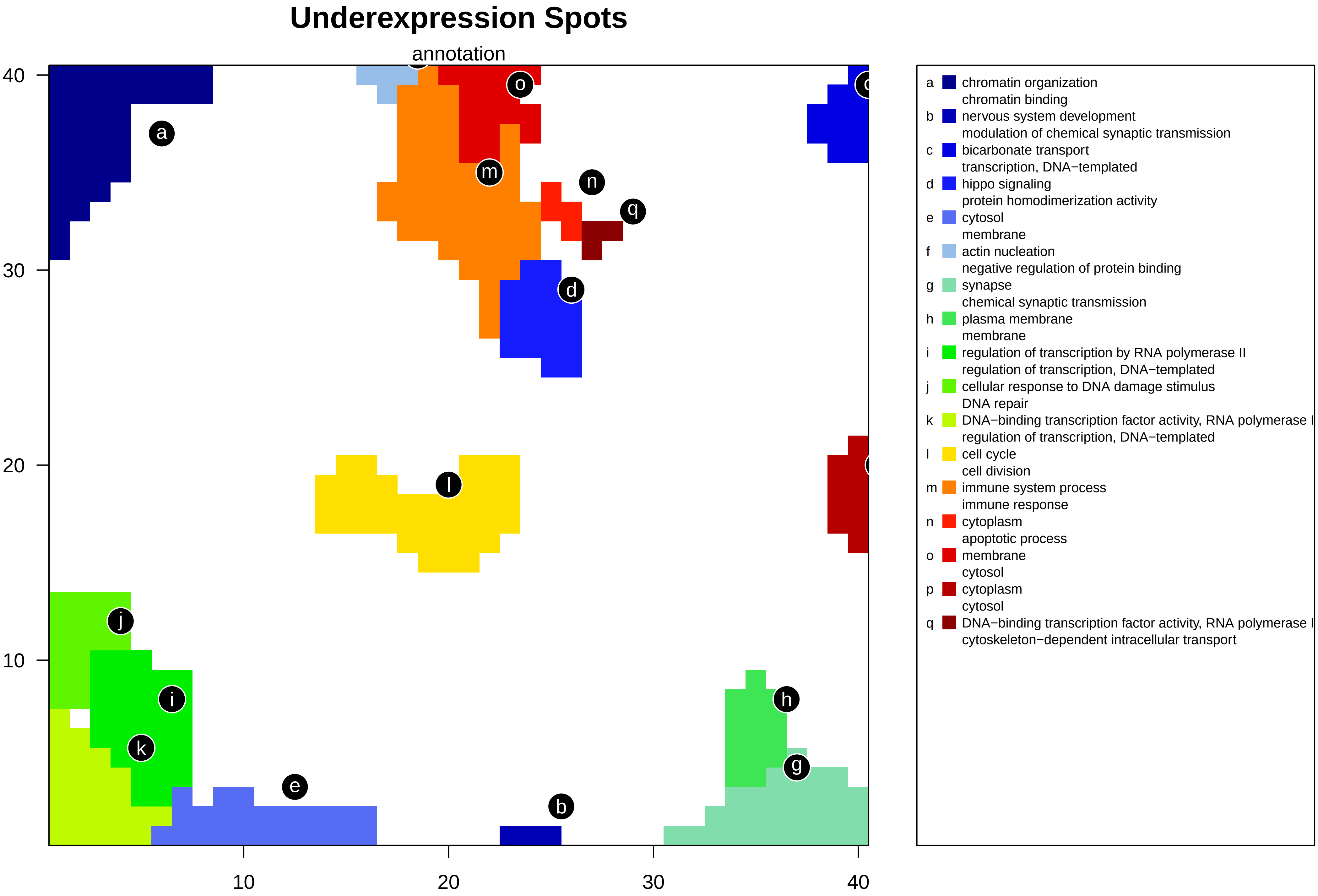
Underexpression Spots

landscape




Underexpression Spots
annotation
40
30
20
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a
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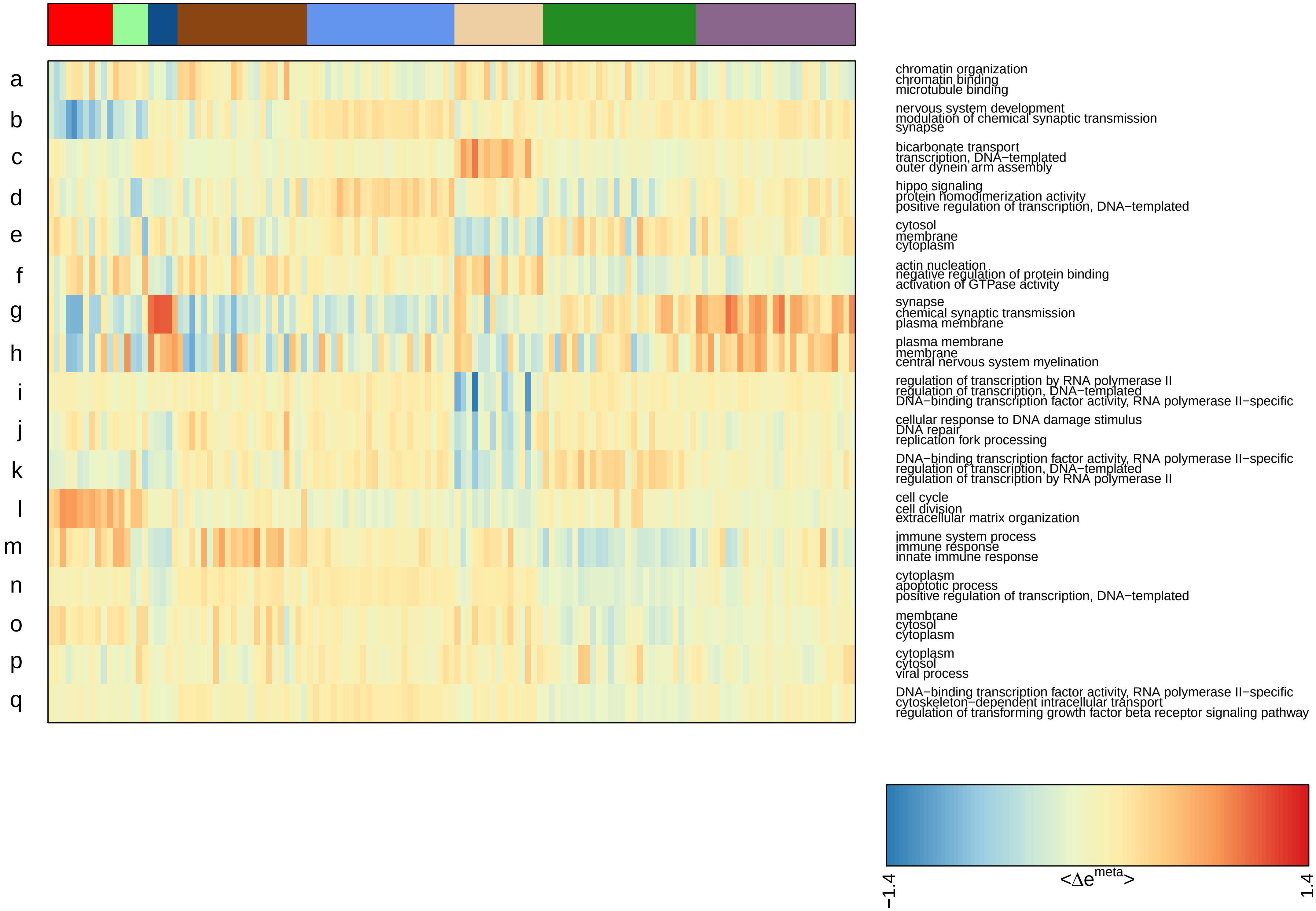
k
l
m
n
o
q
a chromatin organization
chromatin binding
b nervous system development
modulation of chemical synaptic transmission
c bicarbonate transport
transcription, DNA−templated
d hippo signaling
protein homodimerization activity
e cytosol
membrane
f actin nucleation
negative regulation of protein binding
g synapse
chemical synaptic transmission
h plasma membrane
membrane
i regulation of transcription by RNA polymerase II
regulation of transcription, DNA−templated
j cellular response to DNA damage stimulus
DNA repair
k DNA−binding transcription factor activity, RNA polymerase I
regulation of transcription, DNA−templated
l cell cycle
cell division
m immune system process
immune response
n cytoplasm
apoptotic process
o membrane
cytosol
p cytoplasm
cytosol
q DNA−binding transcription factor activity, RNA polymerase I
cytoskeleton−dependent intracellular transport


a
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p
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chromatin organization
chromatin binding
microtubule binding
nervous system development
modulation of chemical synaptic transmission
synapse
bicarbonate transport
transcription, DNA−templated
outer dynein arm assembly
hippo signaling
protein homodimerization activity
positive regulation of transcription, DNA−templated
cytosol
membrane
cytoplasm
actin nucleation
negative regulation of protein binding
activation of GTPase activity
synapse
chemical synaptic transmission
plasma membrane
plasma membrane
membrane
central nervous system myelination
regulation of transcription by RNA polymerase II
regulation of transcription, DNA−templated
DNA−binding transcription factor activity, RNA polymerase II−specific
cellular response to DNA damage stimulus
DNA repair
replication fork processing
DNA−binding transcription factor activity, RNA polymerase II−specific
regulation of transcription, DNA−templated
regulation of transcription by RNA polymerase II
cell cycle
cell division
extracellular matrix organization
immune system process
immune response
innate immune response
cytoplasm
apoptotic process
positive regulation of transcription, DNA−templated
membrane
cytosol
cytoplasm
cytoplasm
cytosol
viral process
DNA−binding transcription factor activity, RNA polymerase II−specific
cytoskeleton−dependent intracellular transport
regulation of transforming growth factor beta receptor signaling pathway
−1.4
$\langle \Delta e^{meta} \rangle$
1.4

Underexpression Spots

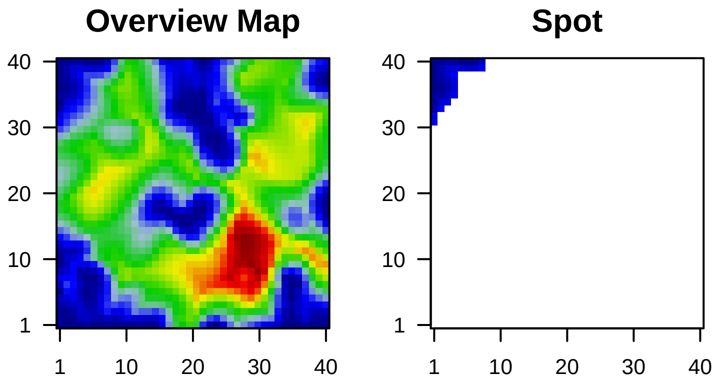
Spot Summary: a

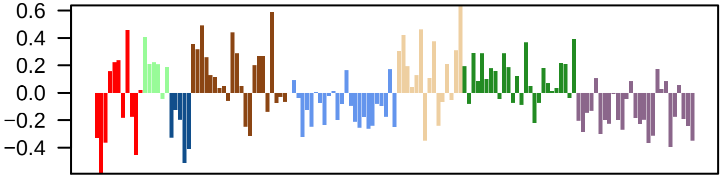
metagenes = 39
genes = 2563

<r> metagenes = 0.85

beta: r2= 8.25 / log p= −Inf

samples with spot = 17 (12.4 %)
group 1 : 4 (36.4 %)
group 3 : 3 (60 %)
group 4 : 1 (4.5 %)
group 5 : 1 (4 %)
group 6 : 1 (6.7 %)
group 8 : 7 (25.9 %)



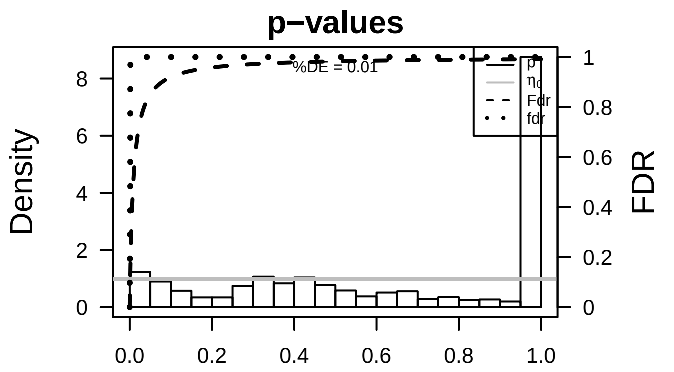


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	240502_at	0.83	−2.47	0.51		
2	204913_s_at	1	−2.35	0.6	SOX11	SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
3	1552455_at	1.17	−2.27	0.42	PRUNE2	prune homolog 2 with BCH domain [Source:HGNC Symbol;A
4	215571_at	0.94	−2.23	0.55		
5	242405_at	0.86	−2.22	0.7		
6	234084_x_at	1.08	−2.2	0.56		
7	203849_s_at	1.03	−2.19	0.36	KIF1A	kinesin family member 1A [Source:HGNC Symbol;Acc:HGNC
8	239884_at	1	−2.18	0.34	CADPS	calcium dependent secretion activator [Source:HGNC Symbo
9	216563_at	0.94	−2.09	0.37		
10	214422_at	0.76	−2.04	0.65		
11	243756_at	1.25	−2.02	0.47		
12	239096_at	0.69	−1.98	0.59		
13	1560741_at	0.56	−1.96	0.22		
14	212057_at	0.72	−1.96	0.47	GSE1	Gse1 coiled−coil protein [Source:HGNC Symbol;Acc:HGNC:
15	232541_at	1.34	−1.95	0.49		
16	244112_x_at	0.6	−1.95	0.62		
17	1569312_at	0.96	−1.91	0.64		
18	242024_at	1.13	−1.91	0.63		
19	244042_x_at	2.08	−1.91	0.49		
20	235388_at	0.75	−1.89	0.49	CHD9	chromodomain helicase DNA binding protein 9 [Source:HGN

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−09	36 / 342	BP	chromatin organization
2	1e−08	38 / 400	BP	chromatin binding
3	6e−08	26 / 227	BP	microtubule binding
4	2e−06	213 / 4740	BP	cytosol
5	2e−06	69 / 1145	BP	regulation of transcription by RNA polymerase II
6	3e−06	66 / 1086	BP	positive regulation of transcription by RNA polymerase II
7	2e−05	35 / 484	BP	cellular response to DNA damage stimulus
8	5e−05	41 / 630	BP	cell cycle
9	6e−05	74 / 1387	BP	regulation of transcription, DNA−templated
10	7e−05	6 / 22	BP	embryonic pattern specification
11	8e−05	29 / 394	BP	cell division
12	2e−04	12 / 102	BP	chromatin remodeling
13	2e−04	9 / 61	BP	regulation of alternative mRNA splicing, via spliceosome
14	2e−04	39 / 630	BP	protein transport
15	2e−04	6 / 27	BP	regulation of cell morphogenesis
16	4e−04	251 / 6202	BP	cytoplasm
17	4e−04	8 / 54	BP	DNA duplex unwinding
18	4e−04	6 / 30	BP	ATP−dependent DNA helicase activity
19	5e−04	4 / 12	BP	centriole−centriole cohesion
20	5e−04	25 / 358	BP	mRNA processing
21	6e−04	5 / 21	BP	hindbrain development
22	7e−04	5 / 22	BP	sister chromatid cohesion
23	7e−04	44 / 783	BP	negative regulation of transcription by RNA polymerase II
24	9e−04	70 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
25	1e−03	17 / 215	BP	ubiquitin protein ligase activity
26	1e−03	5 / 24	BP	negative regulation of neurogenesis
27	1e−03	4 / 15	BP	positive regulation of cilium assembly
28	1e−03	6 / 37	BP	glycogen metabolic process
29	2e−03	4 / 16	BP	cytoskeleton−dependent intracellular transport
30	2e−03	17 / 229	BP	mRNA splicing, via spliceosome
31	2e−03	4 / 17	BP	alternative mRNA splicing, via spliceosome
32	2e−03	4 / 17	BP	microtubule plus−end binding
33	3e−03	7 / 56	BP	SMAD protein signal transduction
34	3e−03	31 / 541	BP	negative regulation of transcription, DNA−templated
35	3e−03	19 / 279	BP	RNA splicing
36	3e−03	14 / 180	BP	cell projection organization
37	3e−03	4 / 19	BP	nucleosome disassembly
38	3e−03	23 / 366	BP	DNA repair
39	3e−03	13 / 162	BP	transcription initiation from RNA polymerase II promoter
40	3e−03	31 / 545	BP	protein ubiquitination



BP

Rank	p−value	#in/all	Geneset
1	2e−09	36 / 342	chromatin organization
2	1e−08	38 / 400	chromatin binding
3	6e−08	26 / 227	microtubule binding
4	2e−06	213 / 4740	cytosol
5	2e−06	69 / 1145	regulation of transcription by RNA polymerase II
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7	2e−05	35 / 484	cellular response to DNA damage stimulus
8	5e−05	41 / 630	cell cycle
9	6e−05	74 / 1387	regulation of transcription, DNA−templated
10	7e−05	6 / 22	embryonic pattern specification
11	8e−05	29 / 394	cell division
12	2e−04	12 / 102	chromatin remodeling
13	2e−04	9 / 61	regulation of alternative mRNA splicing, via spliceosome
14	2e−04	39 / 630	protein transport
15	2e−04	6 / 27	regulation of cell morphogenesis

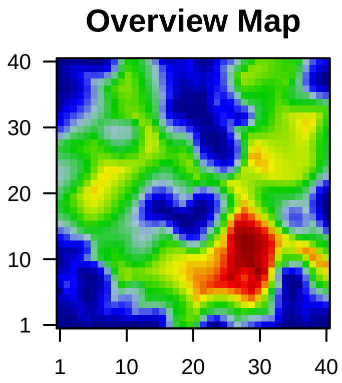
Underexpression Spots

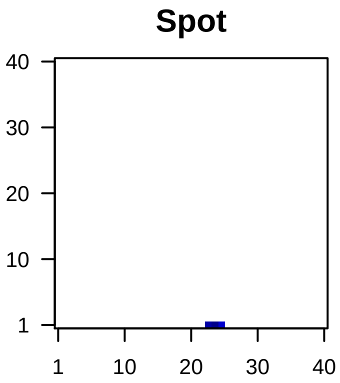
Spot Summary: b

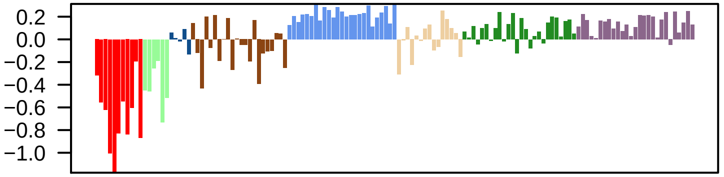
metagenes = 3
genes = 215

<r> metagenes = 0.99
<r> genes = 0.37
beta: r2= 4.42 / log p= −Inf

samples with spot = 18 (13.1 %)
group 1 : 10 (90.9 %)
group 2 : 4 (66.7 %)
group 4 : 3 (13.6 %)
group 6 : 1 (6.7 %)





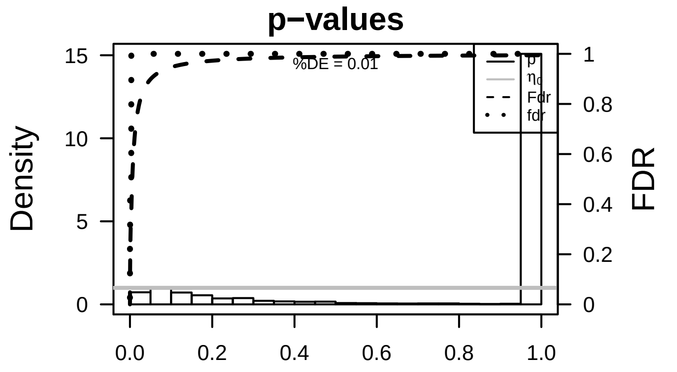


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	205751_at	0.73	−3	0.77	SH3GL2	SH3 domain containing GRB2 like 2, endophilin A1 [Source:H
2	203131_at	0.77	−2.96	0.63	PDGFRA	platelet derived growth factor receptor alpha [Source:HGNC S
3	222784_at	0.71	−2.9	0.68	SMOC1	SPARC related modular calcium binding 1 [Source:HGNC Sy
4	223557_s_at	0.66	−2.88	0.82	TMEFF2	transmembrane protein with EGF like and two follistatin like d
5	223122_s_at	1.44	−2.8	0.79	SFRP2	secreted frizzled related protein 2 [Source:HGNC Symbol;Acc
6	219732_at	0.78	−2.78	0.76	PLPPR1	phospholipid phosphatase related 1 [Source:HGNC Symbol;A
7	229831_at	0.85	−2.75	0.79	CNTN3	contactin 3 [Source:HGNC Symbol;Acc:HGNC:2173]
8	232377_at	0.71	−2.73	0.56	NXPH1	neurexophilin 1 [Source:HGNC Symbol;Acc:HGNC:20693]
9	228956_at	0.67	−2.69	0.77	UGT8	UDP glycosyltransferase 8 [Source:HGNC Symbol;Acc:HGN
10	227949_at	0.41	−2.68	0.64	PHACTR3	phosphatase and actin regulator 3 [Source:HGNC Symbol;Ac
11	208358_s_at	0.59	−2.63	0.75	UGT8	UDP glycosyltransferase 8 [Source:HGNC Symbol;Acc:HGN
12	207480_s_at	0.3	−2.54	0.51	MEIS2	Meis homeobox 2 [Source:HGNC Symbol;Acc:HGNC:7001]
13	234472_at	0.66	−2.53	0.8	GALNT13	polypeptide N−acetylgalactosaminyltransferase 13 [Source:H
14	239481_at	0.89	−2.53	0.78	FAM133A	family with sequence similarity 133 member A [Source:HGNC
15	236536_at	0.56	−2.5	0.82	GALNT13	polypeptide N−acetylgalactosaminyltransferase 13 [Source:H
16	228640_at	0.54	−2.5	0.69	PCDH7	protocadherin 7 [Source:HGNC Symbol;Acc:HGNC:8659]
17	209160_at	0.75	−2.5	0.63	AKR1C3	aldo−keto reductase family 1 member C3 [Source:HGNC Syn
18	1568603_at	0.75	−2.49	0.57	CADPS	calcium dependent secretion activator [Source:HGNC Symbo
19	206850_at	0.9	−2.48	0.71	RASL10A	RAS like family 10 member A [Source:HGNC Symbol;Acc:HG
20	1568604_a_a	0.55	−2.37	0.58	CADPS	calcium dependent secretion activator [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−09	18 / 505	BP	nervous system development
2	1e−05	6 / 73	BP	modulation of chemical synaptic transmission
3	3e−05	14 / 574	BP	synapse
4	5e−05	49 / 4278	BP	plasma membrane
5	2e−04	3 / 16	BP	glutamate receptor signaling pathway
6	2e−04	3 / 18	BP	action potential
7	4e−04	5 / 92	BP	axonogenesis
8	4e−04	7 / 199	BP	axon guidance
9	7e−04	11 / 513	BP	positive regulation of cell population proliferation
10	7e−04	4 / 61	BP	positive regulation of synapse assembly
11	1e−03	7 / 240	BP	postsynaptic membrane
12	2e−03	3 / 37	BP	eye development
13	2e−03	2 / 10	BP	cellular protein−containing complex localization
14	2e−03	2 / 10	BP	cellular response to brain−derived neurotrophic factor stimulus
15	2e−03	2 / 10	BP	negative regulation of transcription by competitive promoter binding
16	2e−03	2 / 10	BP	progesterone metabolic process
17	2e−03	5 / 133	BP	central nervous system development
18	2e−03	4 / 83	BP	cell chemotaxis
19	2e−03	16 / 1080	BP	multicellular organism development
20	3e−03	3 / 42	BP	branching involved in ureteric bud morphogenesis
21	3e−03	2 / 12	BP	pathway−restricted SMAD protein phosphorylation
22	3e−03	66 / 7387	BP	membrane
23	3e−03	2 / 13	BP	induction of positive chemotaxis
24	3e−03	2 / 13	BP	retinal metabolic process
25	3e−03	2 / 13	BP	sensory perception of light stimulus
26	4e−03	3 / 46	BP	neural tube development
27	4e−03	3 / 48	BP	inositol phosphate metabolic process
28	4e−03	3 / 49	BP	embryonic skeletal system morphogenesis
29	4e−03	2 / 15	BP	detection of temperature stimulus involved in sensory perception of pain
30	4e−03	2 / 15	BP	positive regulation of nuclear−transcribed mRNA catabolic process, deader
31	5e−03	2 / 16	BP	inositol trisphosphate biosynthetic process
32	5e−03	2 / 16	BP	negative regulation of intrinsic apoptotic signaling pathway in response to D
33	5e−03	2 / 16	BP	positive regulation of sodium ion transport
34	5e−03	3 / 53	BP	cellular response to amino acid stimulus
35	5e−03	3 / 53	BP	transmembrane receptor protein tyrosine kinase activity
36	6e−03	2 / 17	BP	negative regulation of anoikis
37	6e−03	4 / 107	BP	small GTPase mediated signal transduction
38	6e−03	2 / 18	BP	ionotropic glutamate receptor activity
39	6e−03	2 / 18	BP	male genitalia development
40	6e−03	2 / 18	BP	positive regulation of monocyte chemotaxis



BP

Rank	p−value	#in/all	Geneset
1	9e−09	18 / 505	nervous system development
2	1e−05	6 / 73	modulation of chemical synaptic transmission
3	3e−05	14 / 574	synapse
4	5e−05	49 / 4278	plasma membrane
5	2e−04	3 / 16	glutamate receptor signaling pathway
6	2e−04	3 / 18	action potential
7	4e−04	5 / 92	axonogenesis
8	4e−04	7 / 199	axon guidance
9	7e−04	11 / 513	positive regulation of cell population proliferation
10	7e−04	4 / 61	positive regulation of synapse assembly
11	1e−03	7 / 240	postsynaptic membrane
12	2e−03	3 / 37	eye development
13	2e−03	2 / 10	cellular protein−containing complex localization
14	2e−03	2 / 10	cellular response to brain−derived neurotrophic factor stimulus
15	2e−03	2 / 10	negative regulation of transcription by competitive promoter binding

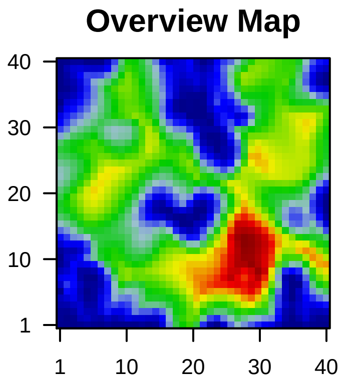
Underexpression Spots

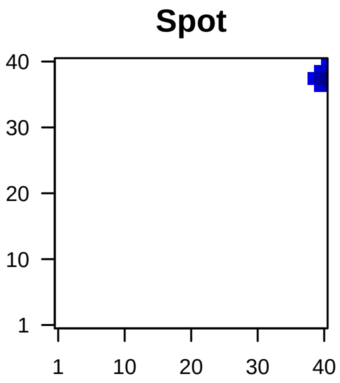
Spot Summary: c

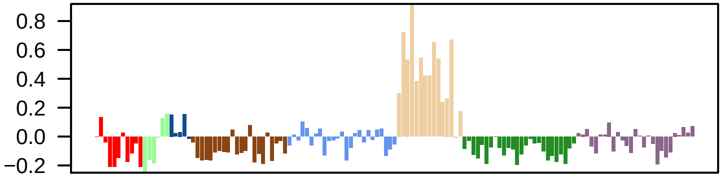
metagenes = 11
genes = 833

<r> metagenes = 0.99
<r> genes = 0.5
beta: r2= 4.37 / log p= −Inf

samples with spot = 0 (0 %)





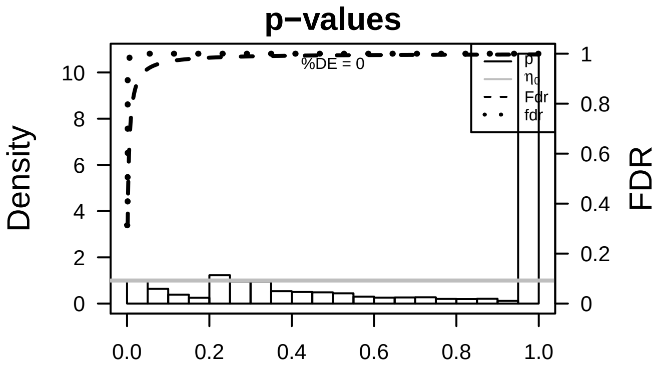


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209116_x_at	1.36	−2.42	0.32	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
2	217232_x_at	1.33	−1.89	0.35	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
3	211696_x_at	1.18	−1.3	0.36	HBB	hemoglobin subunit beta [Source:HGNC Symbol;Acc:HGNC:
4	217793_at	1.02	−1.25	0.69	RAB11B	RAB11B, member RAS oncogene family [Source:HGNC Sym
5	1553594_a_a	1.17	−1.18	0.62	INSL3	insulin like 3 [Source:HGNC Symbol;Acc:HGNC:6086]
6	216696_s_at	1.09	−1.16	0.55	PRODH2	proline dehydrogenase 2 [Source:HGNC Symbol;Acc:HGNC:
7	244516_at	1.18	−1.15	0.54		
8	204848_x_at	2.27	−1.14	0.44	HBG2	hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:H
9	205200_at	1.23	−1.14	0.38	CLEC3B	C−type lectin domain family 3 member B [Source:HGNC Sym
10	206128_at	1.2	−1.12	0.81	ADRA2C	adrenoceptor alpha 2C [Source:HGNC Symbol;Acc:HGNC:2
11	1558766_at	0.85	−1.12	0.45		
12	211076_x_at	1.13	−1.12	0.61	ATN1	atrophin 1 [Source:HGNC Symbol;Acc:HGNC:3033]
13	211699_x_at	1.13	−1.11	0.42	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HG
14	203750_s_at	1.02	−1.1	0.73	RARA	retinoic acid receptor alpha [Source:HGNC Symbol;Acc:HGN
15	209458_x_at	1.23	−1.08	0.43	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HG
16	243766_s_at	0.98	−1.08	0.71	TEAD2	TEA domain transcription factor 2 [Source:HGNC Symbol;Ac
17	204018_x_at	1.21	−1.07	0.43	HBA2	hemoglobin subunit alpha 2 [Source:HGNC Symbol;Acc:HG
18	236136_at	0.87	−1.04	0.66	CYTH3	cytohesin 3 [Source:HGNC Symbol;Acc:HGNC:9504]
19	240424_s_at	0.97	−1.03	0.35		novel transcript
20	221650_s_at	0.94	−1.03	0.59	MED18	mediator complex subunit 18 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−04	6 / 38	BP	bicarbonate transport
2	5e−04	10 / 123	BP	transcription, DNA−templated
3	5e−04	4 / 17	BP	outer dynein arm assembly
4	6e−04	6 / 47	BP	nuclear receptor activity
5	6e−04	6 / 47	BP	positive regulation of cell death
6	7e−04	5 / 32	BP	positive regulation of vasoconstriction
7	9e−04	6 / 51	BP	regulation of synaptic plasticity
8	1e−03	4 / 21	BP	positive regulation of glycolytic process
9	1e−03	10 / 138	BP	serine−type endopeptidase activity
10	1e−03	3 / 10	BP	carnitine shuttle
11	1e−03	6 / 55	BP	steroid hormone mediated signaling pathway
12	1e−03	123 / 4278	BP	plasma membrane
13	2e−03	5 / 38	BP	intracellular receptor signaling pathway
14	3e−03	4 / 26	BP	inorganic anion transport
15	3e−03	9 / 130	BP	serine−type peptidase activity
16	3e−03	5 / 44	BP	hormone−mediated signaling pathway
17	4e−03	3 / 15	BP	cellular response to estrogen stimulus
18	4e−03	3 / 15	BP	positive regulation of glycogen biosynthetic process
19	4e−03	5 / 48	BP	cardiac conduction
20	5e−03	10 / 168	BP	response to hypoxia
21	5e−03	4 / 31	BP	anion transmembrane transport
22	5e−03	3 / 16	BP	positive regulation of calcineurin−NFAT signaling cascade
23	5e−03	4 / 32	BP	cilium movement
24	6e−03	23 / 577	BP	proteolysis
25	6e−03	9 / 147	BP	positive regulation of cytosolic calcium ion concentration
26	6e−03	3 / 17	BP	phosphatidylglycerol acyl−chain remodeling
27	6e−03	4 / 33	BP	digestive tract development
28	7e−03	4 / 34	BP	acute−phase response
29	7e−03	3 / 18	BP	phosphatidylserine acyl−chain remodeling
30	9e−03	6 / 79	BP	positive regulation of catalytic activity
31	1e−02	3 / 20	BP	anion transport
32	1e−02	5 / 59	BP	antimicrobial humoral immune response mediated by antimicrobial peptide
33	1e−02	5 / 60	BP	response to estrogen
34	1e−02	5 / 60	BP	response to nutrient levels
35	1e−02	3 / 21	BP	arachidonic acid secretion
36	1e−02	23 / 613	BP	positive regulation of transcription, DNA−templated
37	1e−02	10 / 193	BP	visual perception
38	1e−02	3 / 22	BP	positive regulation of blood pressure
39	1e−02	4 / 41	BP	phosphatidic acid biosynthetic process
40	1e−02	5 / 63	BP	positive regulation of epithelial cell proliferation



BP

Rank	p−value	#in/all	Geneset
1	2e−04	6 / 38	bicarbonate transport
2	5e−04	10 / 123	transcription, DNA−templated
3	5e−04	4 / 17	outer dynein arm assembly
4	6e−04	6 / 47	nuclear receptor activity
5	6e−04	6 / 47	positive regulation of cell death
6	7e−04	5 / 32	positive regulation of vasoconstriction
7	9e−04	6 / 51	regulation of synaptic plasticity
8	1e−03	4 / 21	positive regulation of glycolytic process
9	1e−03	10 / 138	serine−type endopeptidase activity
10	1e−03	3 / 10	carnitine shuttle
11	1e−03	6 / 55	steroid hormone mediated signaling pathway
12	1e−03	123 / 4278	plasma membrane
13	2e−03	5 / 38	intracellular receptor signaling pathway
14	3e−03	4 / 26	inorganic anion transport
15	3e−03	9 / 130	serine−type peptidase activity

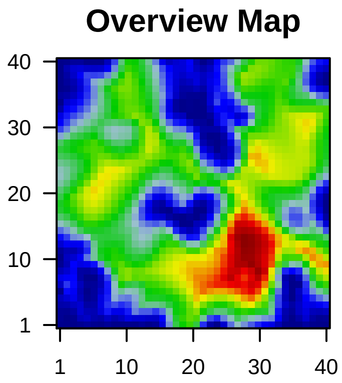
Underexpression Spots

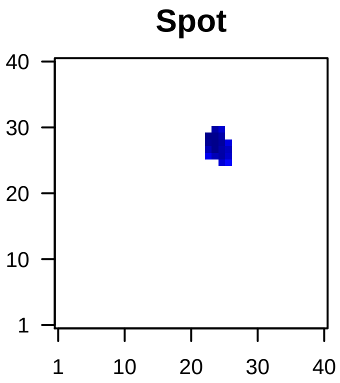
Spot Summary: d

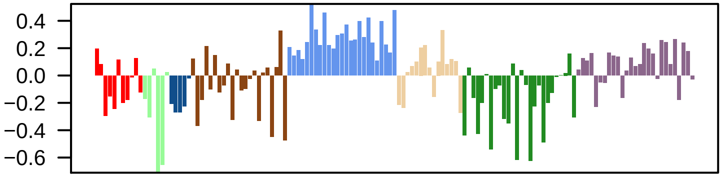
metagenes = 19
genes = 539

<r> metagenes = 0.9
<r> genes = 0.34
beta: r2= 5.18 / log p= −Inf

samples with spot = 21 (15.3 %)
group 1 : 1 (9.1 %)
group 2 : 3 (50 %)
group 3 : 2 (40 %)
group 4 : 5 (22.7 %)
group 6 : 1 (6.7 %)
group 7 : 9 (34.6 %)





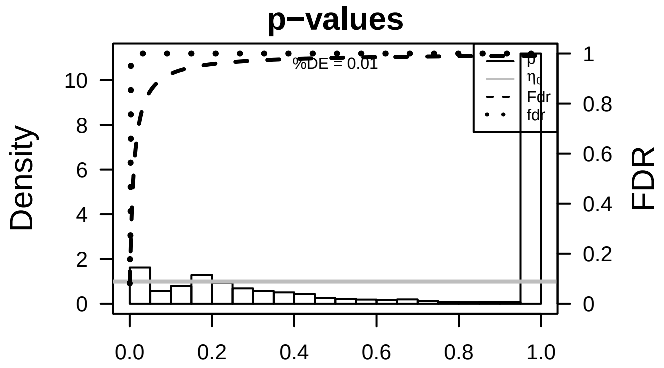


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	230865_at	0.72	−3.12	0.83	LIX1	limb and CNS expressed 1 [Source:HGNC Symbol;Acc:HGN
2	221008_s_at	0.82	−3.06	0.68	ETNPPL	ethanolamine−phosphate phospho−lyase [Source:HGNC Sy
3	230781_at	0.98	−2.93	0.7		long intergenic non−protein coding RNA 1088 [Source:HGNC
4	228018_at	0.83	−2.86	0.57	NKAIN4	sodium/potassium transporting ATPase interacting 4 [Source:
5	229800_at	0.58	−2.85	0.65	DCLK1	doublecortin like kinase 1 [Source:HGNC Symbol;Acc:HGNC
6	205903_s_at	0.65	−2.78	0.67	KCNN3	potassium calcium−activated channel subfamily N member 3
7	242579_at	0.78	−2.61	0.58	BMPR1B	bone morphogenetic protein receptor type 1B [Source:HGNC
8	229975_at	0.52	−2.56	0.79	BMPR1B	bone morphogenetic protein receptor type 1B [Source:HGNC
9	229151_at	1.16	−2.51	0.7	SLC14A1	solute carrier family 14 member 1 (Kidd blood group) [Source
10	215306_at	0.98	−2.5	0.61		
11	230720_at	0.59	−2.47	0.63	RNF182	ring finger protein 182 [Source:HGNC Symbol;Acc:HGNC:28
12	205856_at	1.26	−2.47	0.7	SLC14A1	solute carrier family 14 member 1 (Kidd blood group) [Source
13	204955_at	0.92	−2.45	0.36	SRPX	sushi repeat containing protein X−linked [Source:HGNC Sym
14	205902_at	0.8	−2.42	0.63	KCNN3	potassium calcium−activated channel subfamily N member 3
15	244040_at	0.78	−2.4	0.78	KCNN3	potassium calcium−activated channel subfamily N member 3
16	204563_at	1.28	−2.39	0.52	SELL	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
17	220460_at	0.94	−2.36	0.67	SLCO1C1	solute carrier organic anion transporter family member 1C1 [
18	213395_at	0.76	−2.35	0.65	MLC1	megalencephalic leukoencephalopathy with subcortical cysts
19	228017_s_at	0.79	−2.29	0.5	NKAIN4	sodium/potassium transporting ATPase interacting 4 [Source:
20	242828_at	0.58	−2.28	0.36	FIGN	fidgetin, microtubule severing factor [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	5e−05	5 / 27	BP	hippo signaling
2	8e−05	28 / 815	BP	protein homodimerization activity
3	1e−04	23 / 613	BP	positive regulation of transcription, DNA−templated
4	1e−04	4 / 17	BP	vasodilation
5	1e−04	4 / 18	BP	nitric oxide mediated signal transduction
6	4e−04	5 / 40	BP	regulation of neurogenesis
7	4e−04	6 / 62	BP	negative regulation of epithelial cell proliferation
8	5e−04	19 / 513	BP	positive regulation of cell population proliferation
9	5e−04	9 / 148	BP	neuron differentiation
10	6e−04	3 / 11	BP	positive regulation of extrinsic apoptotic signaling pathway in absence of lig
11	6e−04	4 / 25	BP	positive regulation of cardiac muscle cell proliferation
12	7e−04	6 / 68	BP	retina development in camera−type eye
13	7e−04	3 / 12	BP	developmental pigmentation
14	7e−04	3 / 12	BP	negative regulation of amyloid−beta formation
15	8e−04	6 / 70	BP	smoothened signaling pathway
16	9e−04	8 / 128	BP	peptidyl−tyrosine phosphorylation
17	1e−03	4 / 29	BP	pituitary gland development
18	1e−03	11 / 231	BP	extracellular matrix organization
19	1e−03	3 / 14	BP	toll−like receptor 4 signaling pathway
20	1e−03	5 / 53	BP	negative regulation of neuron death
21	1e−03	3 / 15	BP	definitive hemopoiesis
22	2e−03	15 / 398	BP	positive regulation of gene expression
23	2e−03	4 / 33	BP	regulation of canonical Wnt signaling pathway
24	2e−03	3 / 16	BP	heparan sulfate proteoglycan binding
25	2e−03	3 / 16	BP	positive regulation of macrophage derived foam cell differentiation
26	2e−03	89 / 4278	BP	plasma membrane
27	2e−03	141 / 7387	BP	membrane
28	2e−03	4 / 35	BP	response to interleukin−1
29	2e−03	3 / 17	BP	positive regulation of cellular protein metabolic process
30	3e−03	5 / 61	BP	adenylate cyclase−inhibiting G protein−coupled receptor signaling pathway
31	3e−03	9 / 188	BP	positive regulation of ERK1 and ERK2 cascade
32	3e−03	6 / 90	BP	circadian rhythm
33	3e−03	8 / 154	BP	receptor−mediated endocytosis
34	3e−03	3 / 19	BP	glutathione derivative biosynthetic process
35	3e−03	3 / 19	BP	response to food
36	3e−03	5 / 64	BP	camera−type eye development
37	4e−03	10 / 233	BP	heart development
38	4e−03	4 / 43	BP	positive regulation of protein secretion
39	5e−03	7 / 133	BP	neuron projection development
40	5e−03	3 / 23	BP	cGMP−mediated signaling



BP

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 27	hippo signaling
2	8e−05	28 / 815	protein homodimerization activity
3	1e−04	23 / 613	positive regulation of transcription, DNA−templated
4	1e−04	4 / 17	vasodilation
5	1e−04	4 / 18	nitric oxide mediated signal transduction
6	4e−04	5 / 40	regulation of neurogenesis
7	4e−04	6 / 62	negative regulation of epithelial cell proliferation
8	5e−04	19 / 513	positive regulation of cell population proliferation
9	5e−04	9 / 148	neuron differentiation
10	6e−04	3 / 11	positive regulation of extrinsic apoptotic signaling pathway in absence of ligand
11	6e−04	4 / 25	positive regulation of cardiac muscle cell proliferation
12	7e−04	6 / 68	retina development in camera−type eye
13	7e−04	3 / 12	developmental pigmentation
14	7e−04	3 / 12	negative regulation of amyloid−beta formation
15	8e−04	6 / 70	smoothened signaling pathway

Underexpression Spots

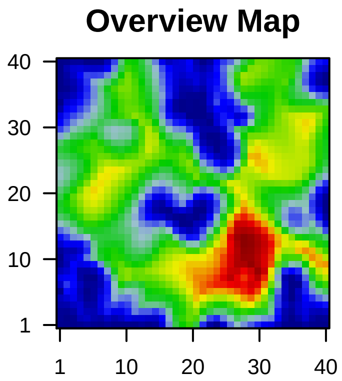
Spot Summary: e

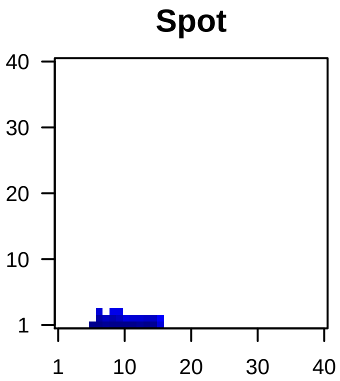
metagenes = 24
genes = 1002

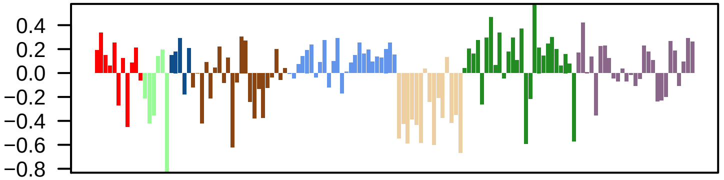
<r> metagenes = 0.92

beta: r2= 8.24 / log p= −Inf

samples with spot = 23 (16.8 %)
group 1 : 2 (18.2 %)
group 2 : 3 (50 %)
group 4 : 4 (18.2 %)
group 6 : 11 (73.3 %)
group 7 : 2 (7.7 %)
group 8 : 1 (3.7 %)


Overview Map


Spot

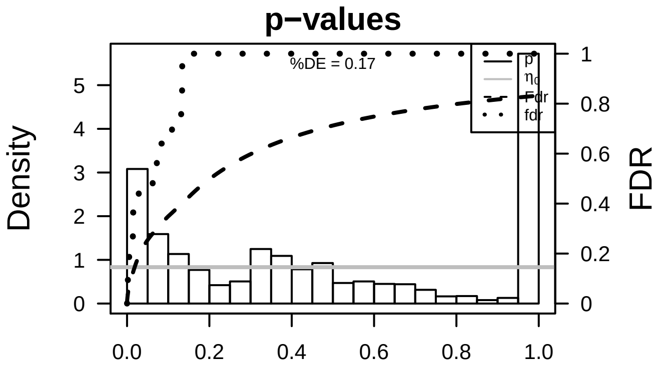


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	1558010_s_at	1.35	−2.72	0.74	SLC1A2	solute carrier family 1 member 2 [Source:HGNC Symbol;Acc:
2	210067_at	1.2	−2.48	0.55	AQP4	aquaporin 4 [Source:HGNC Symbol;Acc:HGNC:637]
3	231576_at	0.93	−2.42	0.81		
4	231166_at	0.92	−2.35	0.53	GPR155	G protein−coupled receptor 155 [Source:HGNC Symbol;Acc:
5	211090_s_at	0.45	−2.33	0.75	PRPF4B	pre−mRNA processing factor 4B [Source:HGNC Symbol;Acc:
6	206692_at	1.15	−2.29	0.79	KCNJ10	potassium voltage−gated channel subfamily J member 10 [Sc
7	211162_x_at	1.01	−2.29	0.75	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC
8	228695_at	0.92	−2.24	0.66	VXN	vexin [Source:HGNC Symbol;Acc:HGNC:28498]
9	1554679_a_at	0.67	−2.17	0.76	LAPTM4B	lysosomal protein transmembrane 4 beta [Source:HGNC Sym
10	232591_s_at	0.63	−2.13	0.9	TMEM30A	transmembrane protein 30A [Source:HGNC Symbol;Acc:HGN
11	1558014_s_at	0.65	−2.1	0.74	FAR1	fatty acyl−CoA reductase 1 [Source:HGNC Symbol;Acc:HGN
12	218748_s_at	0.5	−2.09	0.81		exocyst complex component 5 pseudogene 1 [Source:HGNC
13	211203_s_at	0.79	−2.07	0.63	CNTN1	contactin 1 [Source:HGNC Symbol;Acc:HGNC:2171]
14	1552978_a_at	0.68	−2.05	0.66	SCAMP1	secretory carrier membrane protein 1 [Source:HGNC Symbol
15	229676_at	0.76	−2.05	0.74		
16	201123_s_at	1.33	−2.04	0.3	EIF5A	eukaryotic translation initiation factor 5A [Source:HGNC Syml
17	203293_s_at	0.78	−2.03	0.88	LMAN1	lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC
18	229994_at	0.76	−2.02	0.52		
19	211379_x_at	0.71	−2.02	0.58	B3GALNT1	beta−1,3−N−acetylgalactosaminyltransferase 1 (globoside blc
20	211708_s_at	1	−2.01	0.77	SCD	stearoyl−CoA desaturase [Source:HGNC Symbol;Acc:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−27	313 / 4740	BP	cytosol
2	6e−26	423 / 7387	BP	membrane
3	7e−25	370 / 6202	BP	cytoplasm
4	1e−17	111 / 1242	BP	Golgi apparatus
5	1e−11	41 / 324	BP	intracellular protein transport
6	1e−11	240 / 4278	BP	plasma membrane
7	4e−11	60 / 630	BP	protein transport
8	2e−08	37 / 350	BP	GTP binding
9	1e−07	20 / 132	BP	membrane organization
10	1e−07	42 / 459	BP	viral process
11	3e−07	29 / 264	BP	vesicle−mediated transport
12	3e−07	61 / 815	BP	protein homodimerization activity
13	3e−07	75 / 1086	BP	positive regulation of transcription by RNA polymerase II
14	4e−07	19 / 129	BP	rhythmic process
15	4e−07	32 / 315	BP	positive regulation of GTPase activity
16	4e−07	50 / 623	BP	protein phosphorylation
17	6e−07	40 / 455	BP	intracellular signal transduction
18	1e−06	11 / 47	BP	activation of MAPKK activity
19	1e−06	52 / 684	BP	phosphorylation
20	2e−06	9 / 33	BP	regulation of cholesterol biosynthetic process
21	3e−06	20 / 162	BP	dephosphorylation
22	4e−06	21 / 179	BP	protein dephosphorylation
23	2e−05	6 / 16	BP	axon regeneration
24	2e−05	85 / 1435	BP	mitochondrion
25	2e−05	33 / 400	BP	protein serine/threonine kinase activity
26	2e−05	12 / 76	BP	negative regulation of translation
27	3e−05	38 / 496	BP	negative regulation of apoptotic process
28	3e−05	12 / 78	BP	insulin receptor signaling pathway
29	4e−05	7 / 26	BP	regulation of cytoskeleton organization
30	4e−05	25 / 273	BP	MAPK cascade
31	5e−05	5 / 12	BP	Lys63−specific deubiquitinase activity
32	5e−05	7 / 27	BP	metal ion transport
33	6e−05	16 / 138	BP	regulation of small GTPase mediated signal transduction
34	7e−05	12 / 84	BP	ephrin receptor signaling pathway
35	7e−05	43 / 613	BP	positive regulation of transcription, DNA−templated
36	7e−05	11 / 72	BP	Rho protein signal transduction
37	7e−05	5 / 13	BP	positive regulation of cell−cell adhesion
38	8e−05	16 / 141	BP	regulation of cell shape
39	8e−05	39 / 541	BP	negative regulation of transcription, DNA−templated
40	9e−05	6 / 21	BP	negative regulation of intrinsic apoptotic signaling pathway


p−values

BP

Rank	p−value	#in/all	Geneset
1	2e−27	313 / 4740	cytosol
2	6e−26	423 / 7387	membrane
3	7e−25	370 / 6202	cytoplasm
4	1e−17	111 / 1242	Golgi apparatus
5	1e−11	41 / 324	intracellular protein transport
6	1e−11	240 / 4278	plasma membrane
7	4e−11	60 / 630	protein transport
8	2e−08	37 / 350	GTP binding
9	1e−07	20 / 132	membrane organization
10	1e−07	42 / 459	viral process
11	3e−07	29 / 264	vesicle−mediated transport
12	3e−07	61 / 815	protein homodimerization activity
13	3e−07	75 / 1086	positive regulation of transcription by RNA polymerase II
14	4e−07	19 / 129	rhythmic process
15	4e−07	32 / 315	positive regulation of GTPase activity

Underexpression Spots

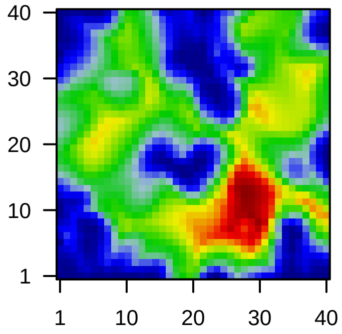
Spot Summary: f

metagenes = 4
genes = 246

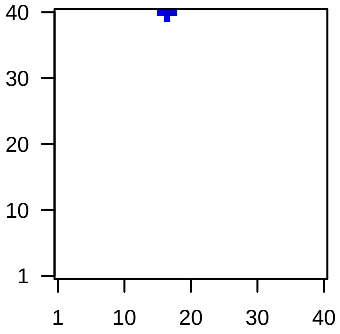
<r> metagenes = 0.99
<r> genes = 0.46
beta: r2= 5.3 / log p= −Inf

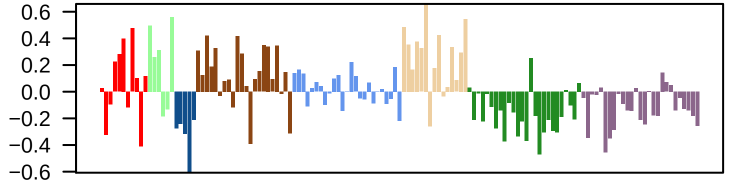
samples with spot = 19 (13.9 %)
group 1 : 2 (18.2 %)
group 3 : 3 (60 %)
group 4 : 2 (9.1 %)
group 7 : 8 (30.8 %)
group 8 : 4 (14.8 %)

Overview Map



Spot





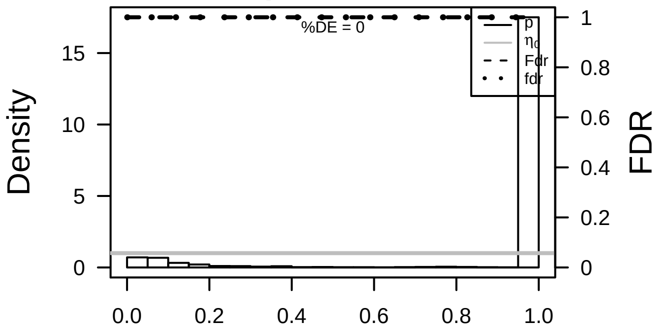
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	230707_at	0.95	−1.79	0.64	SORL1	sortilin related receptor 1 [Source:HGNC Symbol;Acc:HGNC:
2	1570511_at	0.95	−1.67	0.83		
3	234074_at	0.89	−1.59	0.45		
4	242507_at	1.38	−1.57	0.66		UBXN7 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:
5	216465_at	1.4	−1.51	0.52		
6	220467_at	0.81	−1.5	0.73		
7	243450_at	0.86	−1.48	0.84		
8	201693_s_at	1.05	−1.46	0.38	EGR1	early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3
9	242310_at	1.06	−1.42	0.67		
10	242611_at	1.04	−1.41	0.78	DOCK7	dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:HGNC
11	1555372_at	0.74	−1.4	0.7	BCL2L11	BCL2 like 11 [Source:HGNC Symbol;Acc:HGNC:994]
12	240156_at	1.59	−1.36	0.72		
13	243431_at	1.05	−1.3	0.65		
14	207672_at	1.05	−1.29	0.67	RFX4	regulatory factor X4 [Source:HGNC Symbol;Acc:HGNC:9985
15	232002_at	1.73	−1.28	0.66		
16	240254_at	1.14	−1.28	0.71		
17	232882_at	1.44	−1.26	0.67		
18	243745_at	0.98	−1.26	0.68		
19	214295_at	0.8	−1.25	0.87		
20	239448_at	1.15	−1.25	0.7		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−04	2 / 12	BP	actin nucleation
2	9e−04	3 / 72	BP	negative regulation of protein binding
3	1e−03	3 / 83	BP	activation of GTPase activity
4	3e−03	4 / 227	BP	microtubule binding
5	3e−03	2 / 31	BP	mammary gland development
6	3e−03	10 / 1387	BP	regulation of transcription, DNA−templated
7	3e−03	4 / 237	BP	regulation of apoptotic process
8	7e−03	2 / 47	BP	regulation of cell adhesion
9	7e−03	2 / 47	BP	response to ischemia
10	9e−03	3 / 164	BP	cytoskeleton organization
11	1e−02	2 / 56	BP	mRNA 3'−end processing
12	1e−02	25 / 6202	BP	cytoplasm
13	1e−02	9 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
14	1e−02	3 / 190	BP	actin filament binding
15	1e−02	2 / 69	BP	positive regulation of protein catabolic process
16	1e−02	4 / 358	BP	mRNA processing
17	2e−02	4 / 398	BP	positive regulation of gene expression
18	2e−02	4 / 400	BP	chromatin binding
19	2e−02	3 / 229	BP	mRNA splicing, via spliceosome
20	2e−02	6 / 843	BP	DNA−binding transcription factor activity
21	2e−02	7 / 1086	BP	positive regulation of transcription by RNA polymerase II
22	2e−02	2 / 92	BP	wound healing
23	3e−02	2 / 94	BP	cell−matrix adhesion
24	3e−02	1 / 10	BP	epithelial cilium movement involved in determination of left/right asymmetry
25	3e−02	1 / 10	BP	hepatocyte apoptotic process
26	3e−02	1 / 10	BP	locomotor rhythm
27	3e−02	1 / 10	BP	lymphocyte homeostasis
28	3e−02	1 / 10	BP	negative regulation of histone acetylation
29	3e−02	1 / 10	BP	notochord development
30	3e−02	1 / 10	BP	positive regulation of chemokine biosynthetic process
31	3e−02	1 / 10	BP	positive regulation of endoplasmic reticulum stress−induced intrinsic apopto
32	3e−02	1 / 10	BP	positive regulation of interferon−alpha secretion
33	3e−02	1 / 10	BP	positive regulation of protein homooligomerization
34	3e−02	1 / 10	BP	protein O−linked glycosylation via serine
35	3e−02	1 / 10	BP	sequestering of actin monomers
36	3e−02	2 / 99	BP	mRNA export from nucleus
37	3e−02	1 / 11	BP	axonemal dynein complex assembly
38	3e−02	1 / 11	BP	cerebral cortex cell migration
39	3e−02	1 / 11	BP	limb bud formation
40	3e−02	1 / 11	BP	negative regulation of epithelial cell differentiation

p−values



BP

Rank	p−value	#in/all	Geneset
1	4e−04	2 / 12	actin nucleation
2	9e−04	3 / 72	negative regulation of protein binding
3	1e−03	3 / 83	activation of GTPase activity
4	3e−03	4 / 227	microtubule binding
5	3e−03	2 / 31	mammary gland development
6	3e−03	10 / 1387	regulation of transcription, DNA−templated
7	3e−03	4 / 237	regulation of apoptotic process
8	7e−03	2 / 47	regulation of cell adhesion
9	7e−03	2 / 47	response to ischemia
10	9e−03	3 / 164	cytoskeleton organization
11	1e−02	2 / 56	mRNA 3'−end processing
12	1e−02	25 / 6202	cytoplasm
13	1e−02	9 / 1416	DNA−binding transcription factor activity, RNA polymerase II−specific
14	1e−02	3 / 190	actin filament binding
15	1e−02	2 / 69	positive regulation of protein catabolic process

Underexpression Spots

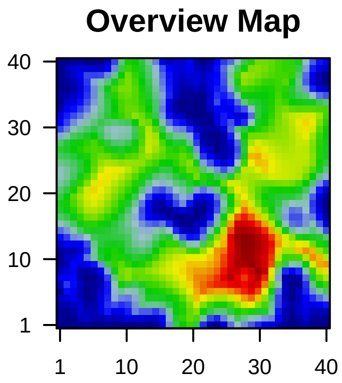
Spot Summary: g

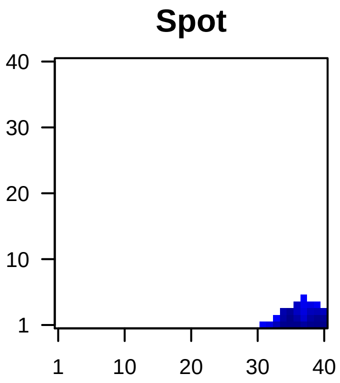
metagenes = 30
genes = 1011

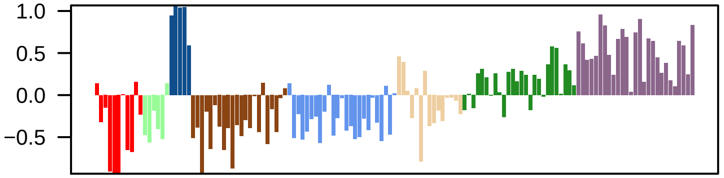
<r> metagenes = 0.91

beta: r2= 27.38 / log p= −Inf

samples with spot = 46 (33.6 %)
group 1 : 6 (54.5 %)
group 2 : 4 (66.7 %)
group 4 : 15 (68.2 %)
group 5 : 16 (64 %)
group 6 : 5 (33.3 %)


Overview Map


Spot

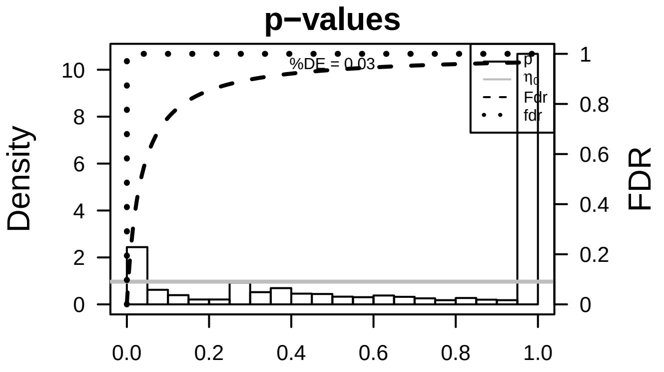


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204953_at	0.79	−3.03	0.71	SNAP91	synaptosome associated protein 91 [Source:HGNC Symbol;A
2	229294_at	0.86	−2.93	0.7	JPH3	junctophilin 3 [Source:HGNC Symbol;Acc:HGNC:14203]
3	204465_s_at	0.92	−2.85	0.72	INA	internexin neuronal intermediate filament protein alpha [Sourc
4	226612_at	0.96	−2.75	0.86	UBE2QL1	ubiquitin conjugating enzyme E2 Q family like 1 [Source:HGN
5	203000_at	1.2	−2.74	0.78	STMN2	stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
6	227769_at	0.72	−2.71	0.6	GPR27	G protein−coupled receptor 27 [Source:HGNC Symbol;Acc:H
7	205737_at	0.71	−2.69	0.67	KCNQ2	potassium voltage−gated channel subfamily Q member 2 [So
8	203001_s_at	1.27	−2.64	0.79	STMN2	stathmin 2 [Source:HGNC Symbol;Acc:HGNC:10577]
9	221805_at	1.83	−2.62	0.84	NEFL	neurofilament light [Source:HGNC Symbol;Acc:HGNC:7739]
10	205110_s_at	0.74	−2.61	0.63	FGF13	fibroblast growth factor 13 [Source:HGNC Symbol;Acc:HGNC
11	206385_s_at	0.86	−2.57	0.74	ANK3	ankyrin 3 [Source:HGNC Symbol;Acc:HGNC:494]
12	214111_at	0.72	−2.55	0.73	OPCML	opioid binding protein/cell adhesion molecule like [Source:HG
13	219671_at	1.36	−2.53	0.77	HPCAL4	hippocalcin like 4 [Source:HGNC Symbol;Acc:HGNC:18212]
14	221916_at	1.57	−2.51	0.83	NEFL	neurofilament light [Source:HGNC Symbol;Acc:HGNC:7739]
15	224458_at	0.6	−2.51	0.67	TMEM246	transmembrane protein 246 [Source:HGNC Symbol;Acc:HGN
16	226918_at	0.62	−2.5	0.6	JPH4	junctophilin 4 [Source:HGNC Symbol;Acc:HGNC:20156]
17	202508_s_at	0.94	−2.48	0.9	SNAP25	synaptosome associated protein 25 [Source:HGNC Symbol;A
18	1556904_at	0.85	−2.48	0.59		novel transcript, overlapping GABRB1
19	1568612_at	1.27	−2.48	0.87	GABRG2	gamma−aminobutyric acid type A receptor gamma2 subunit [
20	213307_at	0.91	−2.47	0.74	SHANK2	SH3 and multiple ankyrin repeat domains 2 [Source:HGNC S

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	4e−69	120 / 574	BP	synapse
2	2e−52	71 / 236	BP	chemical synaptic transmission
3	8e−50	285 / 4278	BP	plasma membrane
4	7e−45	384 / 7387	BP	membrane
5	7e−36	57 / 240	BP	postsynaptic membrane
6	1e−24	73 / 627	BP	ion transport
7	7e−21	60 / 505	BP	nervous system development
8	3e−17	30 / 149	BP	regulation of ion transmembrane transport
9	8e−17	19 / 51	BP	neurotransmitter secretion
10	5e−15	37 / 275	BP	ion transmembrane transport
11	1e−14	19 / 65	BP	learning
12	5e−14	25 / 131	BP	presynapse
13	6e−14	20 / 79	BP	memory
14	1e−12	93 / 1500	BP	signal transduction
15	3e−12	12 / 27	BP	gamma−aminobutyric acid signaling pathway
16	3e−12	12 / 27	BP	glutamate secretion
17	3e−12	24 / 144	BP	calcium ion transport
18	8e−12	14 / 43	BP	neurotransmitter transport
19	2e−11	21 / 118	BP	exocytosis
20	2e−11	12 / 31	BP	regulation of NMDA receptor activity
21	2e−11	21 / 119	BP	postsynapse
22	4e−11	14 / 48	BP	long−term synaptic potentiation
23	6e−11	12 / 33	BP	regulation of exocytosis
24	6e−11	18 / 89	BP	locomotory behavior
25	6e−11	21 / 125	BP	calcium ion transmembrane transport
26	8e−11	14 / 50	BP	nervous system process
27	8e−11	11 / 27	BP	positive regulation of excitatory postsynaptic potential
28	1e−10	11 / 28	BP	synaptic vesicle exocytosis
29	2e−10	21 / 131	BP	potassium ion transport
30	3e−10	11 / 30	BP	associative learning
31	4e−10	50 / 657	BP	calcium ion binding
32	5e−10	8 / 13	BP	synaptic transmission, GABAergic
33	2e−09	8 / 15	BP	calcium ion−regulated exocytosis of neurotransmitter
34	4e−09	9 / 22	BP	regulation of AMPA receptor activity
35	1e−08	18 / 122	BP	potassium ion transmembrane transport
36	2e−08	12 / 51	BP	regulation of synaptic plasticity
37	2e−08	7 / 13	BP	calcium ion transport into cytosol
38	5e−08	9 / 28	BP	synaptic transmission, glutamatergic
39	6e−08	8 / 21	BP	membrane depolarization
40	6e−08	8 / 21	BP	positive regulation of dendrite extension


p−values

BP

Rank	p−value	#in/all	Geneset
1	4e−69	120 / 574	synapse
2	2e−52	71 / 236	chemical synaptic transmission
3	8e−50	285 / 4278	plasma membrane
4	7e−45	384 / 7387	membrane
5	7e−36	57 / 240	postsynaptic membrane
6	1e−24	73 / 627	ion transport
7	7e−21	60 / 505	nervous system development
8	3e−17	30 / 149	regulation of ion transmembrane transport
9	8e−17	19 / 51	neurotransmitter secretion
10	5e−15	37 / 275	ion transmembrane transport
11	1e−14	19 / 65	learning
12	5e−14	25 / 131	presynapse
13	6e−14	20 / 79	memory
14	1e−12	93 / 1500	signal transduction
15	3e−12	12 / 27	gamma−aminobutyric acid signaling pathway

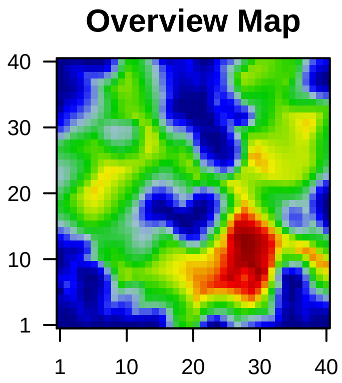
Underexpression Spots

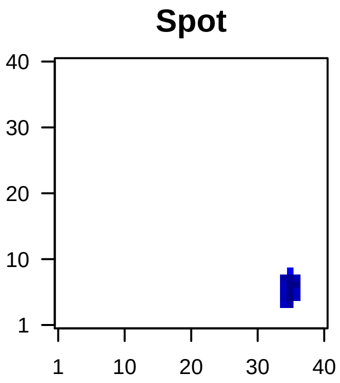
Spot Summary: h

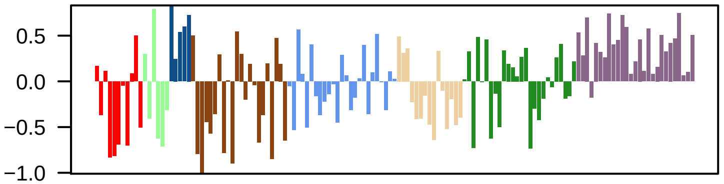
metagenes = 15
genes = 302

<r> metagenes = 0.94
<r> genes = 0.54
beta: r2= 13.34 / log p= −Inf

samples with spot = 41 (29.9 %)
group 1 : 6 (54.5 %)
group 2 : 4 (66.7 %)
group 4 : 11 (50 %)
group 5 : 7 (28 %)
group 6 : 7 (46.7 %)
group 7 : 6 (23.1 %)





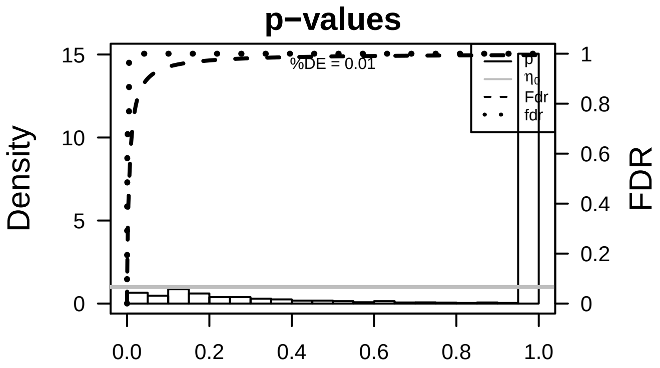


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	209072_at	0.94	−3.53	0.87	MBP	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
2	207010_at	0.71	−3.13	0.39	GABRB1	gamma−aminobutyric acid type A receptor beta1 subunit [Sou
3	227441_s_at	0.73	−2.71	0.67	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B [
4	231911_at	1.22	−2.69	0.92	ERMN	ermin [Source:HGNC Symbol;Acc:HGNC:29208]
5	207323_s_at	1.1	−2.68	0.9	MBP	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
6	1557256_a_a	0.71	−2.66	0.4		
7	235794_at	1.54	−2.65	0.89	MOBP	myelin−associated oligodendrocyte basic protein [Source:HG
8	207659_s_at	1.52	−2.64	0.89	MOBP	myelin−associated oligodendrocyte basic protein [Source:HG
9	229110_at	0.94	−2.56	0.77	SLC24A2	solute carrier family 24 member 2 [Source:HGNC Symbol;Ac
10	204777_s_at	1.35	−2.55	0.9	MAL	mal, T cell differentiation protein [Source:HGNC Symbol;Acc:
11	206899_at	1.46	−2.54	0.53	NTSR2	neurotensin receptor 2 [Source:HGNC Symbol;Acc:HGNC:80
12	226213_at	0.98	−2.51	0.57	ERBB3	erb−b2 receptor tyrosine kinase 3 [Source:HGNC Symbol;Ac
13	225275_at	0.82	−2.5	0.68	EDIL3	EGF like repeats and discoidin domains 3 [Source:HGNC Sy
14	223699_at	1.53	−2.49	0.91	CNDP1	carnosine dipeptidase 1 [Source:HGNC Symbol;Acc:HGNC:2
15	227440_at	0.82	−2.47	0.67	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B [
16	209631_s_at	1.08	−2.46	0.67	GPR37	G protein−coupled receptor 37 [Source:HGNC Symbol;Acc:H
17	210944_s_at	0.95	−2.46	0.73		novel transcript
18	210193_at	1.38	−2.41	0.89	MOBP	myelin−associated oligodendrocyte basic protein [Source:HG
19	214650_x_at	0.97	−2.4	0.91	MOG	myelin oligodendrocyte glycoprotein [Source:HGNC Symbol;
20	210839_s_at	1.2	−2.4	0.89	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−12	80 / 4278	BP	plasma membrane
2	4e−10	107 / 7387	BP	membrane
3	7e−10	6 / 13	BP	central nervous system myelination
4	3e−07	7 / 52	BP	myelination
5	7e−06	83 / 6202	BP	cytoplasm
6	2e−05	8 / 132	BP	membrane organization
7	1e−04	4 / 30	BP	oligodendrocyte differentiation
8	2e−04	14 / 505	BP	nervous system development
9	2e−04	7 / 133	BP	central nervous system development
10	2e−04	3 / 14	BP	positive regulation of myelination
11	5e−04	4 / 43	BP	substantia nigra development
12	6e−04	14 / 574	BP	synapse
13	8e−04	14 / 594	BP	cell adhesion
14	1e−03	14 / 627	BP	ion transport
15	1e−03	5 / 94	BP	response to toxic substance
16	1e−03	3 / 26	BP	oligodendrocyte development
17	2e−03	4 / 61	BP	negative regulation of signal transduction
18	2e−03	12 / 521	BP	lipid metabolic process
19	3e−03	5 / 107	BP	small GTPase mediated signal transduction
20	3e−03	5 / 112	BP	microtubule cytoskeleton organization
21	3e−03	24 / 1500	BP	signal transduction
22	3e−03	2 / 10	BP	cytoskeletal anchoring at plasma membrane
23	4e−03	2 / 11	BP	negative regulation of pathway−restricted SMAD protein phosphorylation
24	4e−03	3 / 37	BP	positive regulation of protein tyrosine kinase activity
25	5e−03	11 / 500	BP	catalytic activity
26	5e−03	2 / 12	BP	glycoprotein metabolic process
27	5e−03	2 / 12	BP	microtubule polymerization
28	5e−03	2 / 12	BP	regulation of exit from mitosis
29	5e−03	7 / 236	BP	chemical synaptic transmission
30	5e−03	7 / 240	BP	postsynaptic membrane
31	5e−03	3 / 41	BP	phosphatidic acid biosynthetic process
32	6e−03	5 / 133	BP	neuron projection development
33	6e−03	2 / 14	BP	central nervous system neuron development
34	6e−03	2 / 14	BP	negative regulation of cAMP−mediated signaling
35	7e−03	8 / 315	BP	positive regulation of GTPase activity
36	7e−03	3 / 44	BP	cell communication
37	7e−03	2 / 15	BP	positive regulation of dendrite development
38	7e−03	2 / 15	BP	sodium−independent organic anion transport
39	8e−03	12 / 615	BP	transmembrane transport
40	9e−03	2 / 17	BP	negative regulation of adenylate cyclase activity



BP

Rank	p−value	#in/all	Geneset
1	2e−12	80 / 4278	plasma membrane
2	4e−10	107 / 7387	membrane
3	7e−10	6 / 13	central nervous system myelination
4	3e−07	7 / 52	myelination
5	7e−06	83 / 6202	cytoplasm
6	2e−05	8 / 132	membrane organization
7	1e−04	4 / 30	oligodendrocyte differentiation
8	2e−04	14 / 505	nervous system development
9	2e−04	7 / 133	central nervous system development
10	2e−04	3 / 14	positive regulation of myelination
11	5e−04	4 / 43	substantia nigra development
12	6e−04	14 / 574	synapse
13	8e−04	14 / 594	cell adhesion
14	1e−03	14 / 627	ion transport
15	1e−03	5 / 94	response to toxic substance

Underexpression Spots

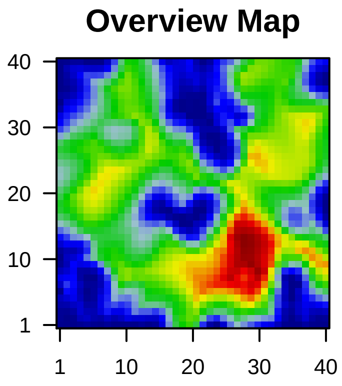
Spot Summary: i

metagenes = 32
genes = 982

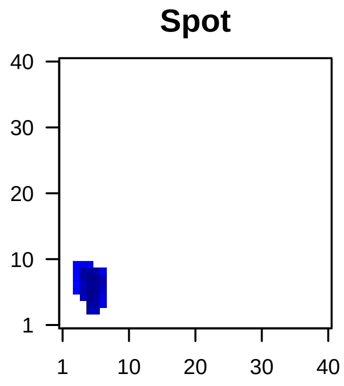
<r> metagenes = 0.91
<r> genes = 0.5
beta: r2= 6.02 / log p= −Inf

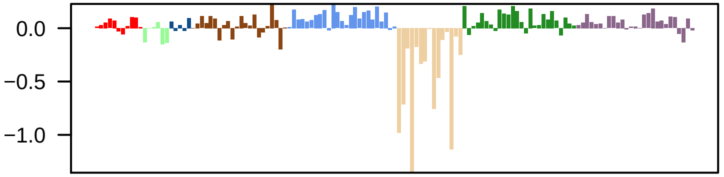
samples with spot = 8 (5.8 %)
group 6 : 8 (53.3 %)

Overview Map



Spot



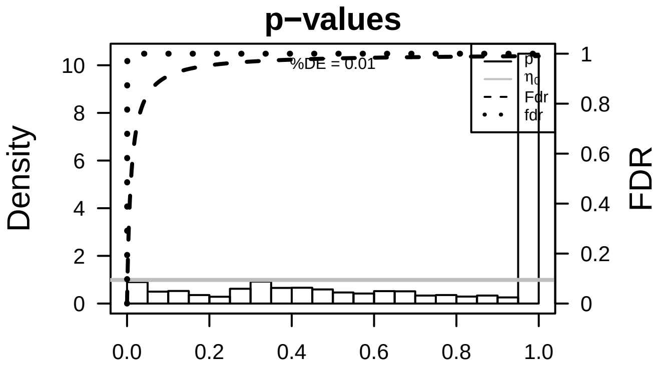


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	212179_at	0.53	−3.33	0.9	PNISR	PNN interacting serine and arginine rich protein [Source:HGN
2	228030_at	0.88	−2.91	0.73		
3	213359_at	0.61	−2.9	0.73	HNRNPD	heterogeneous nuclear ribonucleoprotein D [Source:HGNC S
4	232297_at	0.48	−2.84	0.72		
5	210425_x_at	0.61	−2.77	0.85	GOLGA8A	golgin A8 family member A [Source:HGNC Symbol;Acc:HGN
6	226591_at	0.53	−2.69	0.55		small nucleolar RNA host gene 14 [Source:HGNC Symbol;Ac
7	227260_at	0.97	−2.68	0.79		
8	225107_at	0.71	−2.63	0.86	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGN
9	213677_s_at	0.33	−2.59	0.86	PMS1	PMS1 homolog 1, mismatch repair system component [Sourc
10	221763_at	0.51	−2.58	0.88	JMJD1C	jumonji domain containing 1C [Source:HGNC Symbol;Acc:HG
11	230220_at	0.73	−2.57	0.68	UNC80	unc−80 homolog, NALCN channel complex subunit [Source:H
12	230624_at	0.48	−2.5	0.79	SLC25A27	solute carrier family 25 member 27 [Source:HGNC Symbol;Ac
13	240433_x_at	0.65	−2.49	0.7	CADM2	cell adhesion molecule 2 [Source:HGNC Symbol;Acc:HGNC:
14	203253_s_at	0.57	−2.48	0.88	PPIP5K2	diphosphoinositol pentakisphosphate kinase 2 [Source:HGNC
15	225885_at	0.57	−2.47	0.77	EEA1	early endosome antigen 1 [Source:HGNC Symbol;Acc:HGNC
16	221196_x_at	0.36	−2.45	0.69	BRCC3	BRCA1/BRCA2−containing complex subunit 3 [Source:HGNC
17	217317_s_at	0.55	−2.43	0.8		hect domain and RLD 2 pseudogene 2 [Source:HGNC Symb
18	200685_at	0.52	−2.41	0.83	SRSF11	serine and arginine rich splicing factor 11 [Source:HGNC Syn
19	213376_at	0.39	−2.4	0.69	ZBTB1	zinc finger and BTB domain containing 1 [Source:HGNC Sym
20	218757_s_at	0.3	−2.38	0.79	UPF3B	UPF3B, regulator of nonsense mediated mRNA decay [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−15	94 / 1145	BP	regulation of transcription by RNA polymerase II
2	1e−11	97 / 1387	BP	regulation of transcription, DNA−templated
3	7e−11	96 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
4	9e−11	40 / 366	BP	DNA repair
5	4e−10	46 / 484	BP	cellular response to DNA damage stimulus
6	5e−09	24 / 173	BP	cilium assembly
7	2e−08	225 / 4740	BP	cytosol
8	3e−08	34 / 342	BP	chromatin organization
9	2e−07	11 / 45	BP	non−motile cilium assembly
10	7e−07	22 / 192	BP	methylation
11	2e−06	269 / 6202	BP	cytoplasm
12	3e−06	14 / 93	BP	ciliary basal body−plasma membrane docking
13	4e−06	20 / 180	BP	cell projection organization
14	4e−06	13 / 83	BP	thiol−dependent ubiquitin−specific protease activity
15	6e−06	30 / 358	BP	mRNA processing
16	1e−05	8 / 33	BP	tRNA methylation
17	2e−05	13 / 93	BP	Golgi organization
18	5e−05	23 / 267	BP	ubiquitin−protein transferase activity
19	6e−05	41 / 630	BP	cell cycle
20	8e−05	12 / 94	BP	RNA processing
21	1e−04	20 / 227	BP	microtubule binding
22	1e−04	20 / 229	BP	mRNA splicing, via spliceosome
23	1e−04	29 / 400	BP	chromatin binding
24	1e−04	10 / 71	BP	determination of left/right symmetry
25	2e−04	16 / 164	BP	mitotic cell cycle
26	2e−04	22 / 279	BP	RNA splicing
27	3e−04	5 / 18	BP	cilium organization
28	4e−04	4 / 11	BP	dosage compensation by inactivation of X chromosome
29	7e−04	21 / 281	BP	ubiquitin−dependent protein catabolic process
30	7e−04	5 / 22	BP	mitotic spindle assembly checkpoint
31	7e−04	4 / 13	BP	regulation of mRNA splicing, via spliceosome
32	1e−03	8 / 61	BP	double−strand break repair via nonhomologous end joining
33	1e−03	14 / 158	BP	DNA replication
34	1e−03	26 / 394	BP	cell division
35	1e−03	4 / 15	BP	centrosome duplication
36	1e−03	4 / 15	BP	DNA double−strand break processing
37	2e−03	9 / 80	BP	regulation of G2/M transition of mitotic cell cycle
38	2e−03	4 / 16	BP	establishment of planar polarity
39	2e−03	19 / 264	BP	transcription by RNA polymerase II
40	2e−03	5 / 27	BP	mitotic spindle assembly



BP

Rank	p−value	#in/all	Geneset
1	2e−15	94 / 1145	regulation of transcription by RNA polymerase II
2	1e−11	97 / 1387	regulation of transcription, DNA−templated
3	7e−11	96 / 1416	DNA−binding transcription factor activity, RNA polymerase II−specific
4	9e−11	40 / 366	DNA repair
5	4e−10	46 / 484	cellular response to DNA damage stimulus
6	5e−09	24 / 173	cilium assembly
7	2e−08	225 / 4740	cytosol
8	3e−08	34 / 342	chromatin organization
9	2e−07	11 / 45	non−motile cilium assembly
10	7e−07	22 / 192	methylation
11	2e−06	269 / 6202	cytoplasm
12	3e−06	14 / 93	ciliary basal body−plasma membrane docking
13	4e−06	20 / 180	cell projection organization
14	4e−06	13 / 83	thiol−dependent ubiquitin−specific protease activity
15	6e−06	30 / 358	mRNA processing

Underexpression Spots

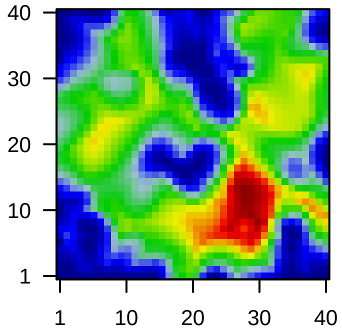
Spot Summary: j

metagenes = 18
genes = 622

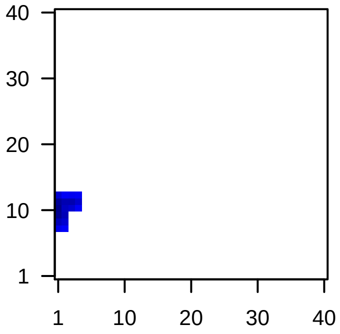
<r> metagenes = 0.95
<r> genes = 0.4
beta: r2= 5.17 / log p= −Inf

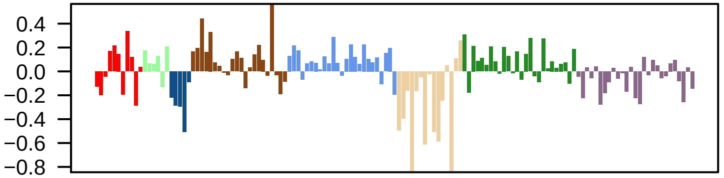
samples with spot = 13 (9.5 %)
group 1 : 1 (9.1 %)
group 3 : 3 (60 %)
group 6 : 7 (46.7 %)
group 8 : 2 (7.4 %)

Overview Map



Spot





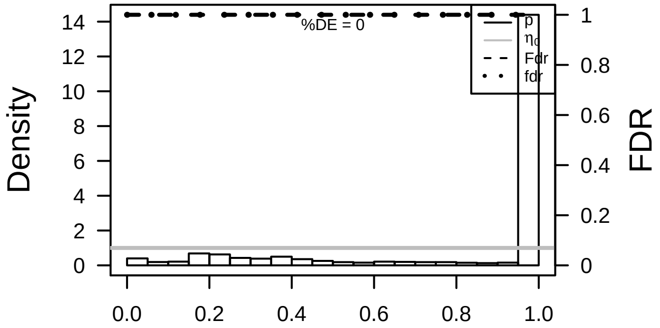
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	230142_s_at	0.54	−2.4	0.66	CIRBP	cold inducible RNA binding protein [Source:HGNC Symbol;Ac
2	207797_s_at	0.75	−2.21	0.59	LRP2BP	LRP2 binding protein [Source:HGNC Symbol;Acc:HGNC:254
3	1556088_at	0.65	−2.21	0.91		
4	229692_at	0.62	−2.21	0.73		
5	241774_at	0.65	−2.15	0.8		
6	221919_at	0.6	−2.1	0.82	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1 [Source:HGNC
7	212980_at	0.82	−2.06	0.79		activator of HSP90 ATPase homolog 2, pseudogene [Source:
8	228144_at	0.98	−2.05	0.78	ZNF300	zinc finger protein 300 [Source:HGNC Symbol;Acc:HGNC:13
9	217986_s_at	0.61	−2.02	0.74	BAZ1A	bromodomain adjacent to zinc finger domain 1A [Source:HG
10	219482_at	0.63	−2.02	0.7	SETD4	SET domain containing 4 [Source:HGNC Symbol;Acc:HGNC:
11	1563629_a_a	0.64	−1.99	0.83		endogenous retrovirus group K13 member 1 [Source:HGNC
12	219218_at	0.7	−1.98	0.46	BAHCC1	BAH domain and coiled−coil containing 1 [Source:HGNC Sy
13	242669_at	0.52	−1.97	0.77		
14	225062_at	0.72	−1.94	0.64	LOC102724219	uncharacterized LOC102724219 [Source:NCBI gene;Acc:102
15	243338_at	0.81	−1.92	0.69		novel transcript
16	230312_at	1.52	−1.91	0.74		
17	225017_at	0.63	−1.9	0.77	CCDC14	coiled−coil domain containing 14 [Source:HGNC Symbol;Acc
18	229795_at	0.73	−1.88	0.7		novel transcript
19	224558_s_at	0.92	−1.88	0.72		metastasis associated lung adenocarcinoma transcript 1 [Sou
20	209889_at	0.64	−1.86	0.66	SEC31B	SEC31 homolog B, COPII coat complex component [Source:

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−06	24 / 484	BP	cellular response to DNA damage stimulus
2	1e−04	17 / 366	BP	DNA repair
3	6e−04	4 / 24	BP	replication fork processing
4	1e−03	3 / 13	BP	replicative senescence
5	1e−03	9 / 158	BP	DNA replication
6	1e−03	4 / 30	BP	chromosome organization
7	4e−03	3 / 19	BP	negative regulation of mRNA splicing, via spliceosome
8	5e−03	6 / 94	BP	RNA processing
9	5e−03	36 / 1387	BP	regulation of transcription, DNA−templated
10	7e−03	4 / 45	BP	telomere maintenance
11	7e−03	6 / 102	BP	chromatin remodeling
12	7e−03	13 / 358	BP	mRNA processing
13	7e−03	11 / 279	BP	RNA splicing
14	7e−03	14 / 400	BP	chromatin binding
15	9e−03	4 / 49	BP	cellular response to UV
16	9e−03	4 / 49	BP	interstrand cross−link repair
17	1e−02	5 / 80	BP	protein localization
18	1e−02	2 / 10	BP	positive regulation of transcription from RNA polymerase II promoter in resp
19	1e−02	2 / 10	BP	positive regulation of transcription of nucleolar large rRNA by RNA polymer
20	1e−02	2 / 10	BP	primary miRNA processing
21	1e−02	3 / 29	BP	cytokine production
22	1e−02	3 / 30	BP	positive regulation of DNA replication
23	1e−02	3 / 30	BP	response to testosterone
24	1e−02	2 / 11	BP	regulation of mitochondrial membrane permeability
25	1e−02	3 / 31	BP	anion transmembrane transport
26	1e−02	6 / 119	BP	nucleic acid phosphodiester bond hydrolysis
27	2e−02	8 / 192	BP	methylation
28	2e−02	2 / 12	BP	centriole−centriole cohesion
29	2e−02	2 / 12	BP	positive regulation of double−strand break repair
30	2e−02	2 / 12	BP	positive regulation of histone deacetylation
31	2e−02	10 / 276	BP	translation
32	2e−02	2 / 13	BP	rRNA transcription
33	2e−02	5 / 93	BP	mitochondrion organization
34	2e−02	2 / 14	BP	cardiac septum morphogenesis
35	2e−02	5 / 97	BP	DNA recombination
36	2e−02	4 / 66	BP	double−strand break repair
37	2e−02	3 / 38	BP	cellular response to nerve growth factor stimulus
38	3e−02	2 / 15	BP	Golgi to endosome transport
39	3e−02	2 / 15	BP	regulation of I−kappaB kinase/NF−kappaB signaling
40	3e−02	28 / 1145	BP	regulation of transcription by RNA polymerase II

p−values



BP

Rank	p−value	#in/all	Geneset
1	2e−06	24 / 484	cellular response to DNA damage stimulus
2	1e−04	17 / 366	DNA repair
3	6e−04	4 / 24	replication fork processing
4	1e−03	3 / 13	replicative senescence
5	1e−03	9 / 158	DNA replication
6	1e−03	4 / 30	chromosome organization
7	4e−03	3 / 19	negative regulation of mRNA splicing, via spliceosome
8	5e−03	6 / 94	RNA processing
9	5e−03	36 / 1387	regulation of transcription, DNA−templated
10	7e−03	4 / 45	telomere maintenance
11	7e−03	6 / 102	chromatin remodeling
12	7e−03	13 / 358	mRNA processing
13	7e−03	11 / 279	RNA splicing
14	7e−03	14 / 400	chromatin binding
15	9e−03	4 / 49	cellular response to UV

Underexpression Spots

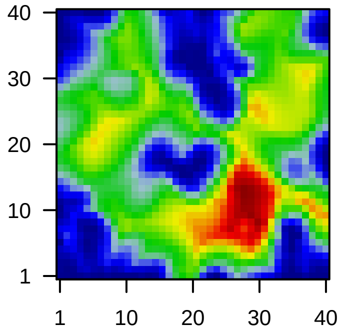
Spot Summary: k

metagenes = 25
genes = 912

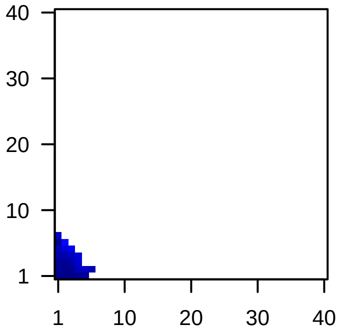
<r> metagenes = 0.91
<r> genes = 0.36
beta: r2= 8.15 / log p= −Inf

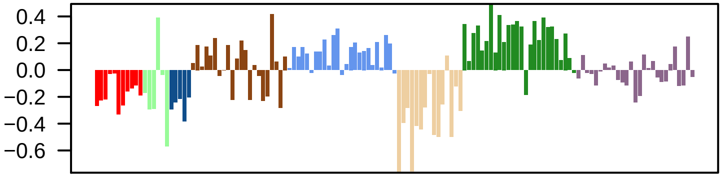
samples with spot = 19 (13.9 %)
group 1 : 2 (18.2 %)
group 2 : 3 (50 %)
group 3 : 2 (40 %)
group 4 : 1 (4.5 %)
group 6 : 11 (73.3 %)

Overview Map



Spot





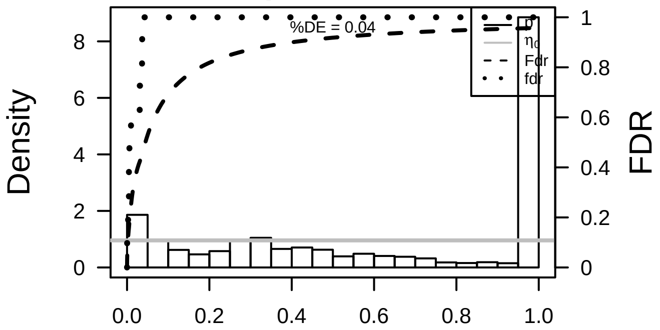
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	204851_s_at	0.79	−2.98	0.53	DCX	doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
2	222898_s_at	1.34	−2.77	0.62	DLL3	delta like canonical Notch ligand 3 [Source:NCBI gene;Acc:1
3	204850_s_at	0.73	−2.76	0.59	DCX	doublecortin [Source:HGNC Symbol;Acc:HGNC:2714]
4	216379_x_at	1.99	−2.67	0.36	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
5	236538_at	0.64	−2.59	0.59	GRIA2	glutamate ionotropic receptor AMPA type subunit 2 [Source:H
6	219537_x_at	0.97	−2.57	0.5	DLL3	delta like canonical Notch ligand 3 [Source:NCBI gene;Acc:1
7	236761_at	0.76	−2.54	0.62		
8	219196_at	0.84	−2.54	0.6	SCG3	secretogranin III [Source:HGNC Symbol;Acc:HGNC:13707]
9	213859_x_at	0.6	−2.54	0.61	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulat
10	210815_s_at	1	−2.54	0.67	CALCRL	calcitonin receptor like receptor [Source:HGNC Symbol;Acc:
11	201416_at	0.72	−2.52	0.45	SOX4	SRY−box 4 [Source:HGNC Symbol;Acc:HGNC:11200]
12	60474_at	0.8	−2.51	0.52	FERMT1	fermitin family member 1 [Source:HGNC Symbol;Acc:HGNC:
13	227921_at	0.74	−2.5	0.62		novel transcript
14	266_s_at	1.74	−2.48	0.35	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
15	209771_x_at	1.85	−2.46	0.38	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
16	238526_at	0.74	−2.38	0.65	RAB3IP	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
17	205290_s_at	0.83	−2.34	0.49	BMP2	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:H
18	220770_s_at	0.63	−2.34	0.77	ZBED8	zinc finger BED−type containing 8 [Source:HGNC Symbol;Ac
19	206331_at	0.68	−2.32	0.58	CALCRL	calcitonin receptor like receptor [Source:HGNC Symbol;Acc:
20	206785_s_at	1.39	−2.3	0.64	KLRC2	killer cell lectin like receptor C2 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−20	106 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
2	1e−17	99 / 1387	BP	regulation of transcription, DNA−templated
3	3e−17	87 / 1145	BP	regulation of transcription by RNA polymerase II
4	2e−10	59 / 843	BP	DNA−binding transcription factor activity
5	2e−08	64 / 1086	BP	positive regulation of transcription by RNA polymerase II
6	7e−07	29 / 366	BP	DNA repair
7	2e−06	27 / 342	BP	chromatin organization
8	3e−06	33 / 484	BP	cellular response to DNA damage stimulus
9	6e−06	38 / 613	BP	positive regulation of transcription, DNA−templated
10	2e−05	6 / 21	BP	spinal cord motor neuron differentiation
11	2e−05	32 / 505	BP	nervous system development
12	6e−05	5 / 16	BP	sympathetic nervous system development
13	8e−05	13 / 129	BP	rhythmic process
14	1e−04	5 / 19	BP	positive regulation of branching involved in ureteric bud morphogenesis
15	2e−04	7 / 42	BP	branching involved in ureteric bud morphogenesis
16	2e−04	31 / 541	BP	negative regulation of transcription, DNA−templated
17	2e−04	4 / 11	BP	neural tube formation
18	2e−04	29 / 496	BP	negative regulation of apoptotic process
19	2e−04	17 / 224	BP	negative regulation of gene expression
20	2e−04	6 / 32	BP	embryonic cranial skeleton morphogenesis
21	3e−04	13 / 146	BP	homophilic cell adhesion via plasma membrane adhesion molecules
22	4e−04	17 / 233	BP	heart development
23	4e−04	7 / 49	BP	embryonic skeletal system morphogenesis
24	5e−04	6 / 36	BP	establishment of cell polarity
25	5e−04	8 / 65	BP	pattern specification process
26	5e−04	8 / 65	BP	roof of mouth development
27	5e−04	10 / 100	BP	osteoblast differentiation
28	6e−04	5 / 25	BP	endocrine pancreas development
29	7e−04	4 / 15	BP	regulation of cellular protein localization
30	8e−04	6 / 40	BP	cytoplasmic microtubule organization
31	9e−04	31 / 594	BP	cell adhesion
32	9e−04	4 / 16	BP	positive regulation of ossification
33	9e−04	32 / 623	BP	protein phosphorylation
34	1e−03	4 / 17	BP	embryonic morphogenesis
35	1e−03	5 / 29	BP	pituitary gland development
36	1e−03	7 / 58	BP	regulation of protein localization
37	1e−03	5 / 30	BP	oligodendrocyte differentiation
38	1e−03	4 / 18	BP	ionotropic glutamate receptor activity
39	1e−03	41 / 887	BP	cell differentiation
40	2e−03	8 / 78	BP	cartilage development

p−values



BP

Rank	p−value	#in/all	Geneset
1	2e−20	106 / 1416	DNA−binding transcription factor activity, RNA polymerase II−specific
2	1e−17	99 / 1387	regulation of transcription, DNA−templated
3	3e−17	87 / 1145	regulation of transcription by RNA polymerase II
4	2e−10	59 / 843	DNA−binding transcription factor activity
5	2e−08	64 / 1086	positive regulation of transcription by RNA polymerase II
6	7e−07	29 / 366	DNA repair
7	2e−06	27 / 342	chromatin organization
8	3e−06	33 / 484	cellular response to DNA damage stimulus
9	6e−06	38 / 613	positive regulation of transcription, DNA−templated
10	2e−05	6 / 21	spinal cord motor neuron differentiation
11	2e−05	32 / 505	nervous system development
12	6e−05	5 / 16	sympathetic nervous system development
13	8e−05	13 / 129	rhythmic process
14	1e−04	5 / 19	positive regulation of branching involved in ureteric bud morphogenesis
15	2e−04	7 / 42	branching involved in ureteric bud morphogenesis

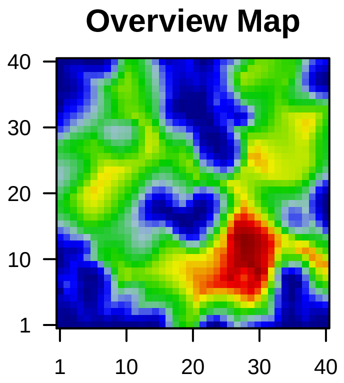
Underexpression Spots

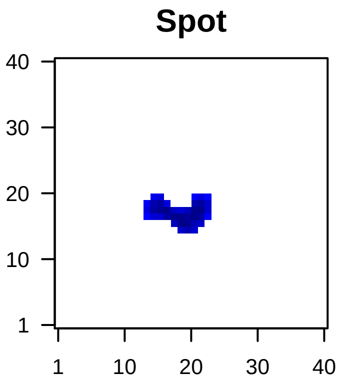
Spot Summary: I

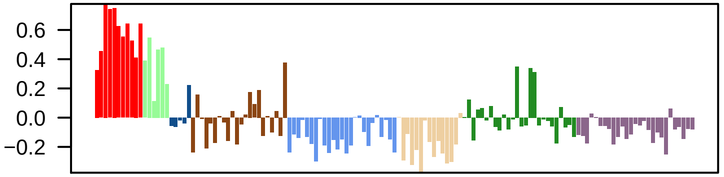
metagenes = 40
genes = 887

<r> metagenes = 0.72
<r> genes = 0.27
beta: r2= 6.4 / log p= −Inf

samples with spot = 7 (5.1 %)
group 5 : 1 (4 %)
group 6 : 6 (40 %)


Overview Map


Spot

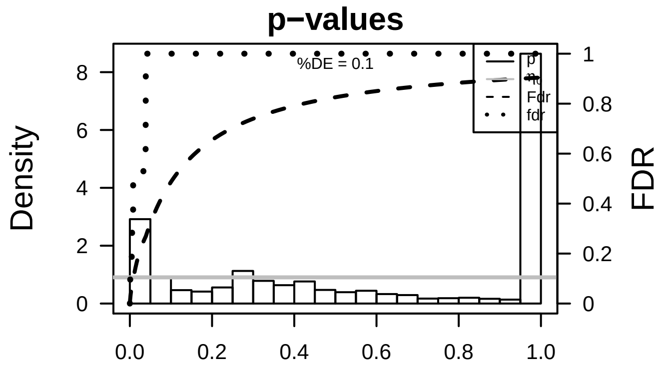


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	224999_at	1.42	−2.54	0.26	EGFR	epidermal growth factor receptor [Source:HGNC Symbol;Acc:
2	204041_at	1.48	−2.53	0.2	MAOB	monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
3	213142_x_at	1.01	−2.34	0.47	GSAP	gamma−secretase activating protein [Source:HGNC Symbol;
4	222150_s_at	1.07	−2.17	0.5	GSAP	gamma−secretase activating protein [Source:HGNC Symbol;
5	201291_s_at	1.64	−2.11	0.47	TOP2A	DNA topoisomerase II alpha [Source:HGNC Symbol;Acc:HG
6	224588_at	2.97	−2.09	0.19		X inactive specific transcript [Source:HGNC Symbol;Acc:HG
7	202589_at	1.3	−1.9	0.64	TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12
8	203358_s_at	1.08	−1.87	0.4	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit [
9	201792_at	1.67	−1.87	0.37	AEBP1	AE binding protein 1 [Source:HGNC Symbol;Acc:HGNC:303]
10	227671_at	2.79	−1.83	0.19		X inactive specific transcript [Source:HGNC Symbol;Acc:HG
11	228776_at	0.98	−1.79	0.65	GJC1	gap junction protein gamma 1 [Source:HGNC Symbol;Acc:H
12	218039_at	1.09	−1.77	0.53	NUSAP1	nucleolar and spindle associated protein 1 [Source:HGNC Sy
13	212298_at	1.28	−1.77	0.51	NRP1	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]
14	201852_x_at	2.61	−1.76	0.59	COL3A1	collagen type III alpha 1 chain [Source:HGNC Symbol;Acc:H
15	225911_at	1.73	−1.76	0.63	NPNT	nephronectin [Source:HGNC Symbol;Acc:HGNC:27405]
16	206306_at	2.14	−1.76	0.51	RYR3	ryanodine receptor 3 [Source:HGNC Symbol;Acc:HGNC:104
17	205029_s_at	1.38	−1.75	0.44	FABP7	fatty acid binding protein 7 [Source:HGNC Symbol;Acc:HGN
18	202450_s_at	1.05	−1.74	0.52	CTSK	cathepsin K [Source:HGNC Symbol;Acc:HGNC:2536]
19	210095_s_at	1.5	−1.72	0.38	IGFBP3	insulin like growth factor binding protein 3 [Source:HGNC Sy
20	201663_s_at	1.25	−1.72	0.72	SMC4	structural maintenance of chromosomes 4 [Source:HGNC Sy

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−51	103 / 630	BP	cell cycle
2	3e−45	78 / 394	BP	cell division
3	5e−26	45 / 231	BP	extracellular matrix organization
4	2e−22	35 / 158	BP	DNA replication
5	4e−22	27 / 85	BP	chromosome segregation
6	1e−15	35 / 254	BP	angiogenesis
7	2e−15	42 / 366	BP	DNA repair
8	4e−15	28 / 164	BP	mitotic cell cycle
9	4e−15	48 / 484	BP	cellular response to DNA damage stimulus
10	1e−14	22 / 98	BP	G1/S transition of mitotic cell cycle
11	3e−12	242 / 6202	BP	cytoplasm
12	4e−12	14 / 44	BP	collagen fibril organization
13	8e−12	48 / 594	BP	cell adhesion
14	1e−11	12 / 31	BP	mitotic sister chromatid segregation
15	4e−11	13 / 42	BP	mitotic spindle organization
16	6e−11	33 / 327	BP	cell population proliferation
17	2e−10	14 / 56	BP	DNA damage response, signal transduction by p53 class mediator resulting
18	2e−10	12 / 39	BP	CENP−A containing nucleosome assembly
19	5e−10	11 / 33	BP	DNA replication initiation
20	2e−09	19 / 130	BP	G2/M transition of mitotic cell cycle
21	2e−09	10 / 29	BP	endodermal cell differentiation
22	5e−09	12 / 50	BP	mitotic cytokinesis
23	1e−08	19 / 145	BP	regulation of cell cycle
24	1e−08	7 / 13	BP	kinetochore assembly
25	2e−08	10 / 35	BP	mitotic metaphase plate congression
26	5e−08	10 / 39	BP	regulation of mitotic nuclear division
27	1e−07	31 / 400	BP	chromatin binding
28	1e−07	9 / 33	BP	mitotic cell cycle checkpoint
29	1e−07	7 / 17	BP	DNA replication origin binding
30	1e−07	14 / 92	BP	wound healing
31	1e−07	6 / 11	BP	metaphase plate congression
32	2e−07	14 / 94	BP	cell−matrix adhesion
33	2e−07	178 / 4740	BP	cytosol
34	3e−07	8 / 27	BP	mitotic spindle assembly
35	4e−07	11 / 59	BP	regulation of cyclin−dependent protein serine/threonine kinase activity
36	5e−07	8 / 28	BP	positive regulation of G2/M transition of mitotic cell cycle
37	7e−07	12 / 76	BP	microtubule motor activity
38	8e−07	8 / 30	BP	sprouting angiogenesis
39	1e−06	7 / 22	BP	mitotic spindle assembly checkpoint
40	1e−06	7 / 22	BP	regulation of transcription involved in G1/S transition of mitotic cell cycle


p−values

BP

Rank	p−value	#in/all	Geneset
1	1e−51	103 / 630	cell cycle
2	3e−45	78 / 394	cell division
3	5e−26	45 / 231	extracellular matrix organization
4	2e−22	35 / 158	DNA replication
5	4e−22	27 / 85	chromosome segregation
6	1e−15	35 / 254	angiogenesis
7	2e−15	42 / 366	DNA repair
8	4e−15	28 / 164	mitotic cell cycle
9	4e−15	48 / 484	cellular response to DNA damage stimulus
10	1e−14	22 / 98	G1/S transition of mitotic cell cycle
11	3e−12	242 / 6202	cytoplasm
12	4e−12	14 / 44	collagen fibril organization
13	8e−12	48 / 594	cell adhesion
14	1e−11	12 / 31	mitotic sister chromatid segregation
15	4e−11	13 / 42	mitotic spindle organization

Underexpression Spots

Spot Summary: m

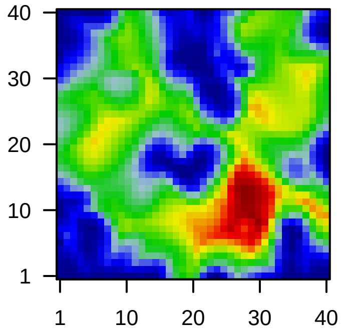
metagenes = 54
genes = 1204

<r> metagenes = 0.82

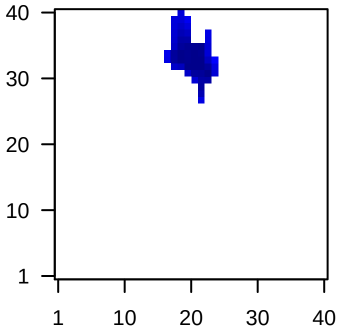
beta: r2= 10.61 / log p= −Inf

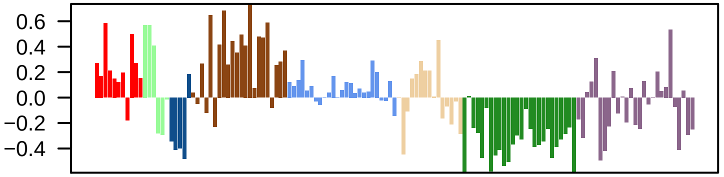
samples with spot = 32 (23.4 %)
group 2 : 2 (33.3 %)
group 3 : 4 (80 %)
group 6 : 2 (13.3 %)
group 7 : 19 (73.1 %)
group 8 : 5 (18.5 %)

Overview Map



Spot





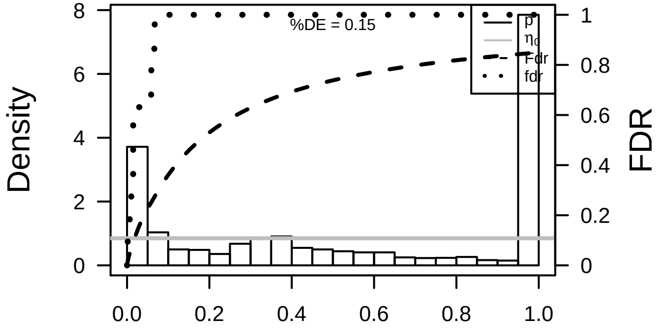
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202376_at	1.55	−2.59	0.61	SERPINA3	serpin family A member 3 [Source:HGNC Symbol;Acc:HGNC
2	223395_at	0.96	−2.55	0.41	ABI3BP	ABI family member 3 binding protein [Source:HGNC Symbol;
3	216834_at	1.24	−2.52	0.52	RGS1	regulator of G protein signaling 1 [Source:HGNC Symbol;Acc
4	214511_x_at	0.9	−2.28	0.78	FCGR1A	Fc fragment of IgG receptor Ia [Source:HGNC Symbol;Acc:H
5	205114_s_at	1.39	−2.26	0.22	CCL3	C−C motif chemokine ligand 3 [Source:HGNC Symbol;Acc:H
6	201645_at	0.91	−2.25	0.57	TNC	tenascin C [Source:HGNC Symbol;Acc:HGNC:5318]
7	224102_at	1.02	−2.23	0.38	P2RY12	purinergic receptor P2Y12 [Source:HGNC Symbol;Acc:HGNC
8	211991_s_at	1.21	−2.19	0.83	HLA−DPA1	major histocompatibility complex, class II, DP alpha 1 [Source
9	227266_s_at	1.05	−2.19	0.76	FYB1	FYN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:40
10	213566_at	1.01	−2.14	0.81	RNASE6	ribonuclease A family member k6 [Source:HGNC Symbol;Acc
11	201012_at	1.61	−2.14	0.66	ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
12	201141_at	1.77	−2.13	0.38	GPNMB	glycoprotein nmb [Source:HGNC Symbol;Acc:HGNC:4462]
13	216005_at	1.14	−2.1	0.51	TNC	tenascin C [Source:HGNC Symbol;Acc:HGNC:5318]
14	204174_at	1.14	−2.1	0.84	ALOX5AP	arachidonate 5−lipoxygenase activating protein [Source:HGN
15	204320_at	1.47	−2.1	0.28	COL11A1	collagen type XI alpha 1 chain [Source:HGNC Symbol;Acc:H
16	209846_s_at	0.85	−2.1	0.58	BTN3A2	butyrophilin subfamily 3 member A2 [Source:HGNC Symbol;
17	202988_s_at	1.52	−2.09	0.53	RGS1	regulator of G protein signaling 1 [Source:HGNC Symbol;Acc
18	230258_at	1.15	−2.09	0.57	GLIS3	GLIS family zinc finger 3 [Source:HGNC Symbol;Acc:HGNC:
19	204472_at	1.29	−2.08	0.69	GEM	GTP binding protein overexpressed in skeletal muscle [Sourc
20	230252_at	0.87	−2.07	0.76	LPAR5	lysophosphatidic acid receptor 5 [Source:HGNC Symbol;Acc:

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−64	122 / 564	BP	immune system process
2	5e−47	87 / 388	BP	immune response
3	3e−46	89 / 417	BP	innate immune response
4	1e−40	78 / 364	BP	inflammatory response
5	4e−32	278 / 4278	BP	plasma membrane
6	2e−31	76 / 460	BP	neutrophil degranulation
7	7e−28	389 / 7387	BP	membrane
8	3e−25	54 / 289	BP	cytokine−mediated signaling pathway
9	7e−22	125 / 1500	BP	signal transduction
10	8e−21	15 / 17	BP	antigen processing and presentation of peptide or polysaccharide antigen v
11	1e−19	38 / 184	BP	defense response to virus
12	3e−17	19 / 43	BP	antigen processing and presentation
13	6e−17	25 / 88	BP	cellular response to interferon−gamma
14	8e−17	32 / 155	BP	regulation of immune response
15	1e−15	30 / 148	BP	chemotaxis
16	2e−14	29 / 152	BP	leukocyte migration
17	4e−14	24 / 103	BP	response to bacterium
18	2e−13	20 / 74	BP	neutrophil chemotaxis
19	4e−13	18 / 59	BP	positive regulation of T cell proliferation
20	8e−13	27 / 151	BP	cellular response to lipopolysaccharide
21	8e−12	55 / 594	BP	cell adhesion
22	2e−11	13 / 33	BP	lipopolysaccharide−mediated signaling pathway
23	2e−11	16 / 56	BP	B cell receptor signaling pathway
24	7e−11	30 / 222	BP	adaptive immune response
25	1e−10	24 / 148	BP	positive regulation of NF−kappaB transcription factor activity
26	2e−10	32 / 261	BP	cell surface receptor signaling pathway
27	2e−10	29 / 219	BP	positive regulation of cell migration
28	4e−10	13 / 41	BP	positive regulation of interferon−gamma production
29	6e−10	13 / 42	BP	toll−like receptor signaling pathway
30	6e−10	25 / 172	BP	positive regulation of I−kappaB kinase/NF−kappaB signaling
31	8e−10	13 / 43	BP	positive regulation of phagocytosis
32	8e−10	26 / 188	BP	positive regulation of ERK1 and ERK2 cascade
33	9e−10	29 / 231	BP	extracellular matrix organization
34	1e−09	23 / 151	BP	defense response to bacterium
35	1e−09	16 / 72	BP	positive regulation of inflammatory response
36	2e−09	28 / 222	BP	cell−cell signaling
37	2e−09	19 / 105	BP	platelet activation
38	2e−09	15 / 64	BP	complement activation, classical pathway
39	2e−09	15 / 64	BP	regulation of complement activation
40	3e−09	20 / 121	BP	defense response

p−values



BP

Rank	p−value	#in/all	Geneset
1	3e−64	122 / 564	immune system process
2	5e−47	87 / 388	immune response
3	3e−46	89 / 417	innate immune response
4	1e−40	78 / 364	inflammatory response
5	4e−32	278 / 4278	plasma membrane
6	2e−31	76 / 460	neutrophil degranulation
7	7e−28	389 / 7387	membrane
8	3e−25	54 / 289	cytokine−mediated signaling pathway
9	7e−22	125 / 1500	signal transduction
10	8e−21	15 / 17	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
11	1e−19	38 / 184	defense response to virus
12	3e−17	19 / 43	antigen processing and presentation
13	6e−17	25 / 88	cellular response to interferon−gamma
14	8e−17	32 / 155	regulation of immune response
15	1e−15	30 / 148	chemotaxis

Underexpression Spots

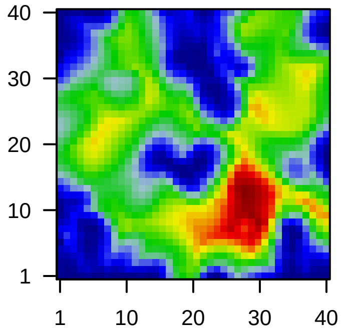
Spot Summary: n

metagenes = 4
genes = 95

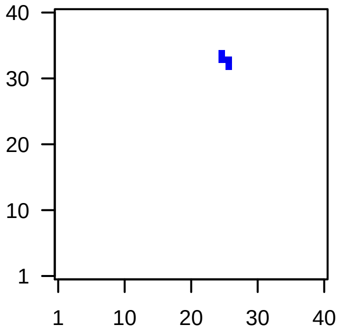
<r> metagenes = 0.97
<r> genes = 0.36
beta: r2= 3.35 / log p= −Inf

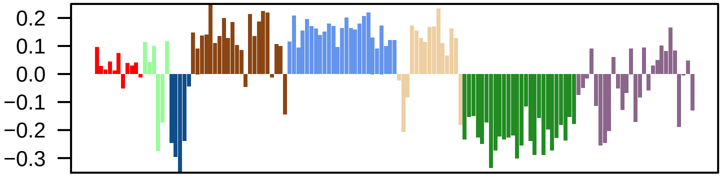
samples with spot = 9 (6.6 %)
group 2 : 1 (16.7 %)
group 3 : 2 (40 %)
group 7 : 6 (23.1 %)

Overview Map



Spot





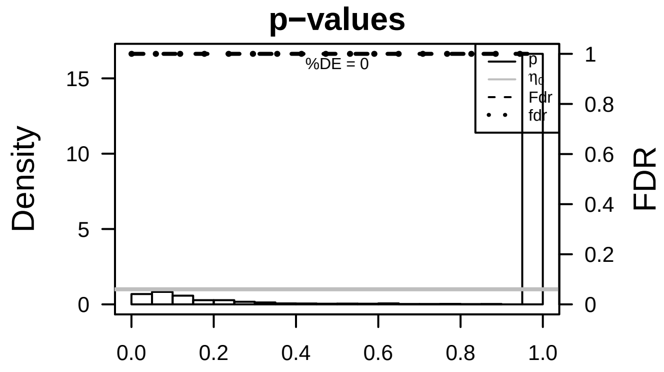
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	236361_at	0.99	−1.63	0.41	GALNT15	polypeptide N−acetylgalactosaminyltransferase 15 [Source:H
2	209230_s_at	0.59	−1.55	0.47	NUPR1	nuclear protein 1, transcriptional regulator [Source:HGNC Sy
3	209644_x_at	1.49	−1.39	0.35	CDKN2A	cyclin dependent kinase inhibitor 2A [Source:HGNC Symbol;
4	226020_s_at	0.38	−1.3	0.5	OMA1	OMA1 zinc metallopeptidase [Source:HGNC Symbol;Acc:HG
5	225912_at	0.42	−1.28	0.54	TP53INP1	tumor protein p53 inducible nuclear protein 1 [Source:HGNC
6	212188_at	0.6	−1.22	0.47	KCTD12	potassium channel tetramerization domain containing 12 [Sou
7	223421_at	0.6	−1.17	0.56	CYHR1	cysteine and histidine rich 1 [Source:HGNC Symbol;Acc:HG
8	48531_at	0.75	−1.12	0.61	TNIP2	TNFAIP3 interacting protein 2 [Source:HGNC Symbol;Acc:H
9	214346_at	1.35	−1.11	0.41		
10	237337_at	0.66	−1.11	0.72		
11	230269_at	1.25	−1.1	0.47	B3GALT5	beta−1,3−galactosyltransferase 5 [Source:HGNC Symbol;Acc
12	223234_at	0.49	−1.09	0.6	MAD2L2	mitotic arrest deficient 2 like 2 [Source:HGNC Symbol;Acc:H
13	203504_s_at	0.6	−1.09	0.53	ABCA1	ATP binding cassette subfamily A member 1 [Source:HGNC
14	1553890_s_a	0.88	−1.08	0.58	NTN5	netrin 5 [Source:HGNC Symbol;Acc:HGNC:25208]
15	1557433_at	0.63	−1.08	0.75		
16	218280_x_at	0.95	−1.07	0.43	HIST2H2AA3	histone cluster 2 H2A family member a3 [Source:HGNC Sym
17	243423_at	1	−1.06	0.61		
18	211126_s_at	0.81	−1.04	0.5	CSRP2	cysteine and glycine rich protein 2 [Source:HGNC Symbol;Ac
19	227749_at	1.08	−1.01	0.4	POU2F2	POU class 2 homeobox 2 [Source:HGNC Symbol;Acc:HGNC
20	207069_s_at	0.94	−1.01	0.45	SMAD6	SMAD family member 6 [Source:HGNC Symbol;Acc:HGNC:6

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−05	39 / 6202	BP	cytoplasm
2	9e−05	10 / 659	BP	apoptotic process
3	3e−04	9 / 613	BP	positive regulation of transcription, DNA−templated
4	5e−04	2 / 10	BP	negative regulation of erythrocyte differentiation
5	9e−04	2 / 13	BP	negative regulation of transcription regulatory region DNA binding
6	1e−03	11 / 1080	BP	multicellular organism development
7	1e−03	2 / 15	BP	negative regulation of androgen receptor signaling pathway
8	1e−03	2 / 15	BP	pulmonary valve morphogenesis
9	2e−03	7 / 496	BP	negative regulation of apoptotic process
10	2e−03	4 / 159	BP	actin cytoskeleton organization
11	3e−03	2 / 22	BP	positive regulation of oligodendrocyte differentiation
12	3e−03	12 / 1387	BP	regulation of transcription, DNA−templated
13	3e−03	4 / 170	BP	protein stabilization
14	4e−03	2 / 26	BP	negative regulation of fibroblast proliferation
15	5e−03	2 / 30	BP	T cell differentiation in thymus
16	6e−03	2 / 33	BP	midbrain development
17	6e−03	7 / 630	BP	cell cycle
18	9e−03	8 / 843	BP	DNA−binding transcription factor activity
19	9e−03	2 / 41	BP	negative regulation of I−kappaB kinase/NF−kappaB signaling
20	1e−02	3 / 134	BP	cell cycle arrest
21	1e−02	5 / 400	BP	chromatin binding
22	1e−02	2 / 51	BP	adenylate cyclase−modulating G protein−coupled receptor signaling pathw
23	1e−02	5 / 412	BP	negative regulation of cell population proliferation
24	2e−02	3 / 151	BP	cellular response to lipopolysaccharide
25	2e−02	2 / 57	BP	autophagosome assembly
26	2e−02	2 / 57	BP	odontogenesis of dentin−containing tooth
27	2e−02	2 / 58	BP	embryonic digit morphogenesis
28	2e−02	2 / 60	BP	response to estrogen
29	2e−02	3 / 165	BP	negative regulation of canonical Wnt signaling pathway
30	2e−02	7 / 815	BP	protein homodimerization activity
31	2e−02	2 / 67	BP	regulation of cell growth
32	2e−02	2 / 68	BP	regulation of autophagy
33	2e−02	10 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
34	2e−02	2 / 69	BP	negative regulation of DNA−binding transcription factor activity
35	2e−02	2 / 70	BP	Ras protein signal transduction
36	3e−02	2 / 73	BP	cellular response to interleukin−1
37	3e−02	4 / 327	BP	cell population proliferation
38	3e−02	2 / 74	BP	negative regulation of NF−kappaB transcription factor activity
39	3e−02	2 / 79	BP	positive regulation of catalytic activity
40	3e−02	2 / 81	BP	activation of cysteine−type endopeptidase activity involved in apoptotic pro

p−values



BP

Rank	p−value	#in/all	Geneset
1	2e−05	39 / 6202	cytoplasm
2	9e−05	10 / 659	apoptotic process
3	3e−04	9 / 613	positive regulation of transcription, DNA−templated
4	5e−04	2 / 10	negative regulation of erythrocyte differentiation
5	9e−04	2 / 13	negative regulation of transcription regulatory region DNA binding
6	1e−03	11 / 1080	multicellular organism development
7	1e−03	2 / 15	negative regulation of androgen receptor signaling pathway
8	1e−03	2 / 15	pulmonary valve morphogenesis
9	2e−03	7 / 496	negative regulation of apoptotic process
10	2e−03	4 / 159	actin cytoskeleton organization
11	3e−03	2 / 22	positive regulation of oligodendrocyte differentiation
12	3e−03	12 / 1387	regulation of transcription, DNA−templated
13	3e−03	4 / 170	protein stabilization
14	4e−03	2 / 26	negative regulation of fibroblast proliferation
15	5e−03	2 / 30	T cell differentiation in thymus

Underexpression Spots

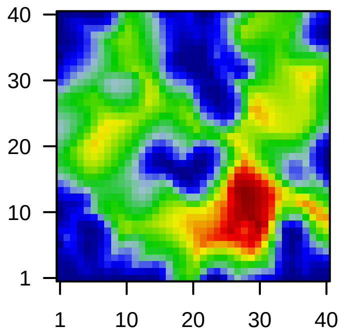
Spot Summary: o

metagenes = 17
genes = 489

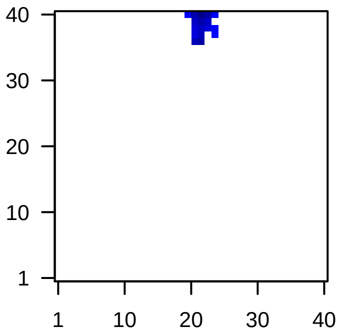
<r> metagenes = 0.92
<r> genes = 0.36
beta: r2= 4.18 / log p= −Inf

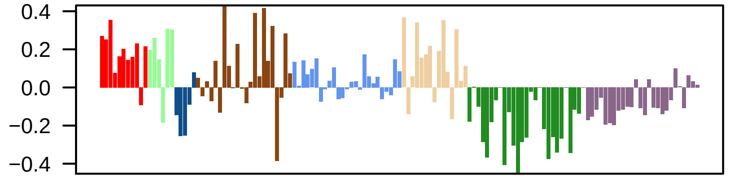
samples with spot = 11 (8 %)
group 4 : 1 (4.5 %)
group 7 : 10 (38.5 %)

Overview Map



Spot





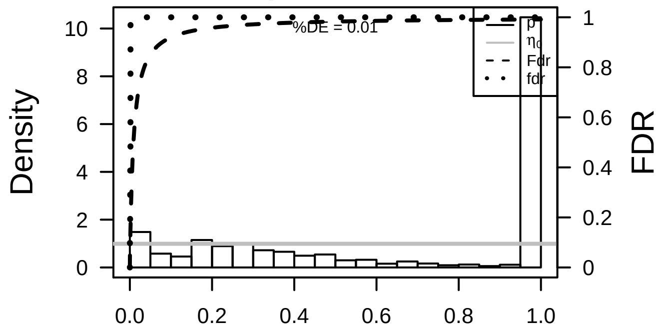
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	210090_at	1.93	−1.98	0.4	ARC	activity regulated cytoskeleton associated protein [Source:HG
2	205002_at	1	−1.61	0.7	AHDC1	AT−hook DNA binding motif containing 1 [Source:HGNC Sym
3	216862_s_at	0.54	−1.5	0.46	MTCP1	mature T cell proliferation 1 [Source:HGNC Symbol;Acc:HGN
4	224576_at	0.54	−1.5	0.54	ERGIC1	endoplasmic reticulum−golgi intermediate compartment 1 [Sc
5	204990_s_at	1.1	−1.49	0.78	ITGB4	integrin subunit beta 4 [Source:HGNC Symbol;Acc:HGNC:61
6	219505_at	0.89	−1.43	0.64	ADA2	adenosine deaminase 2 [Source:HGNC Symbol;Acc:HGNC:1
7	201367_s_at	1.07	−1.42	0.6	ZFP36L2	ZFP36 ring finger protein like 2 [Source:HGNC Symbol;Acc:H
8	215364_s_at	0.59	−1.41	0.68	SZT2	SZT2, KICSTOR complex subunit [Source:HGNC Symbol;Ac
9	40560_at	1.08	−1.4	0.52	TBX2	T−box 2 [Source:HGNC Symbol;Acc:HGNC:11597]
10	204070_at	1.16	−1.34	0.59	RARRES3	retinoic acid receptor responder 3 [Source:HGNC Symbol;Ac
11	217844_at	0.55	−1.34	0.64	CTDSP1	CTD small phosphatase 1 [Source:HGNC Symbol;Acc:HGNC
12	208033_s_at	0.94	−1.33	0.52	ZFHX3	zinc finger homeobox 3 [Source:HGNC Symbol;Acc:HGNC:7
13	212613_at	0.82	−1.33	0.46	BTN3A2	butyrophilin subfamily 3 member A2 [Source:HGNC Symbol;
14	204989_s_at	1.82	−1.32	0.64	ITGB4	integrin subunit beta 4 [Source:HGNC Symbol;Acc:HGNC:61
15	218918_at	0.92	−1.32	0.53	MAN1C1	mannosidase alpha class 1C member 1 [Source:HGNC Sym
16	213713_s_at	1.7	−1.31	0.37	GLB1L2	galactosidase beta 1 like 2 [Source:HGNC Symbol;Acc:HGN
17	228343_at	0.95	−1.31	0.48	POU2F2	POU class 2 homeobox 2 [Source:HGNC Symbol;Acc:HGNC
18	212300_at	0.61	−1.3	0.68	TXLNA	taxilin alpha [Source:HGNC Symbol;Acc:HGNC:30685]
19	201598_s_at	0.69	−1.28	0.68	INPPL1	inositol polyphosphate phosphatase like 1 [Source:HGNC Sy
20	212923_s_at	0.59	−1.27	0.55	PXDC1	PX domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−10	194 / 7387	BP	membrane
2	6e−10	138 / 4740	BP	cytosol
3	1e−09	167 / 6202	BP	cytoplasm
4	1e−06	13 / 138	BP	regulation of small GTPase mediated signal transduction
5	3e−06	46 / 1242	BP	Golgi apparatus
6	7e−06	5 / 16	BP	negative regulation of growth
7	2e−05	6 / 31	BP	cellular response to cadmium ion
8	3e−05	18 / 327	BP	cell population proliferation
9	5e−05	109 / 4278	BP	plasma membrane
10	8e−05	31 / 815	BP	protein homodimerization activity
11	1e−04	21 / 460	BP	neutrophil degranulation
12	1e−04	12 / 185	BP	endocytosis
13	2e−04	4 / 17	BP	cellular response to zinc ion
14	3e−04	11 / 172	BP	positive regulation of I−kappaB kinase/NF−kappaB signaling
15	4e−04	5 / 35	BP	positive regulation of substrate adhesion−dependent cell spreading
16	5e−04	4 / 21	BP	cellular response to copper ion
17	5e−04	4 / 21	BP	positive regulation of epidermal growth factor receptor signaling pathway
18	7e−04	6 / 59	BP	response to cytokine
19	7e−04	9 / 133	BP	protein localization to plasma membrane
20	7e−04	29 / 843	BP	DNA−binding transcription factor activity
21	7e−04	4 / 23	BP	cellular zinc ion homeostasis
22	7e−04	19 / 459	BP	viral process
23	8e−04	14 / 289	BP	cytokine−mediated signaling pathway
24	1e−03	3 / 12	BP	regulation of type I interferon production
25	1e−03	3 / 13	BP	interleukin−15−mediated signaling pathway
26	1e−03	7 / 93	BP	integrin−mediated signaling pathway
27	1e−03	10 / 178	BP	metabolic process
28	1e−03	4 / 28	BP	cellular response to vascular endothelial growth factor stimulus
29	2e−03	43 / 1500	BP	signal transduction
30	2e−03	14 / 315	BP	positive regulation of GTPase activity
31	2e−03	7 / 97	BP	transforming growth factor beta receptor signaling pathway
32	2e−03	6 / 72	BP	positive regulation of endothelial cell proliferation
33	2e−03	3 / 15	BP	dendritic spine development
34	2e−03	12 / 254	BP	angiogenesis
35	2e−03	4 / 32	BP	positive regulation of vascular smooth muscle cell proliferation
36	3e−03	3 / 16	BP	positive regulation of vascular associated smooth muscle cell migration
37	3e−03	4 / 34	BP	negative regulation of extrinsic apoptotic signaling pathway in absence of li
38	3e−03	4 / 34	BP	reactive oxygen species metabolic process
39	3e−03	23 / 684	BP	phosphorylation
40	4e−03	3 / 18	BP	myeloid dendritic cell differentiation

p−values



BP

Rank	p−value	#in/all	Geneset
1	2e−10	194 / 7387	membrane
2	6e−10	138 / 4740	cytosol
3	1e−09	167 / 6202	cytoplasm
4	1e−06	13 / 138	regulation of small GTPase mediated signal transduction
5	3e−06	46 / 1242	Golgi apparatus
6	7e−06	5 / 16	negative regulation of growth
7	2e−05	6 / 31	cellular response to cadmium ion
8	3e−05	18 / 327	cell population proliferation
9	5e−05	109 / 4278	plasma membrane
10	8e−05	31 / 815	protein homodimerization activity
11	1e−04	21 / 460	neutrophil degranulation
12	1e−04	12 / 185	endocytosis
13	2e−04	4 / 17	cellular response to zinc ion
14	3e−04	11 / 172	positive regulation of I−kappaB kinase/NF−kappaB signaling
15	4e−04	5 / 35	positive regulation of substrate adhesion−dependent cell spreading

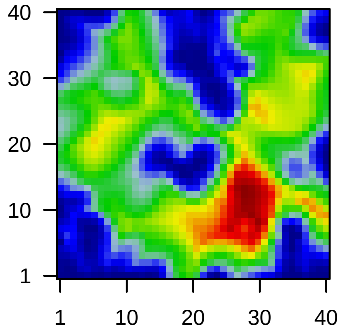
Underexpression Spots

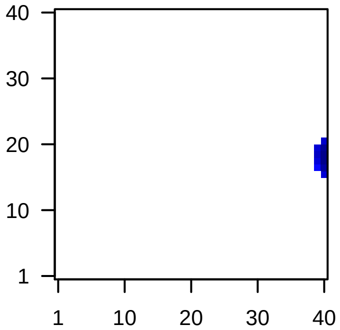
Spot Summary: p

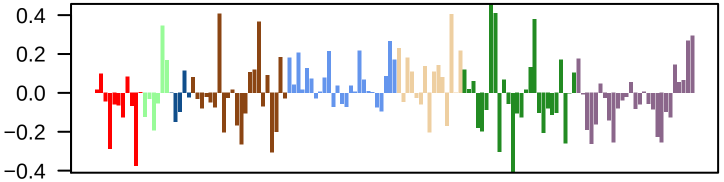
metagenes = 10
genes = 634

<r> metagenes = 0.93
<r> genes = 0.35
beta: r2= 2.61 / log p= −Inf

samples with spot = 5 (3.6 %)
group 1 : 2 (18.2 %)
group 4 : 1 (4.5 %)
group 7 : 2 (7.7 %)


Overview Map


Spot

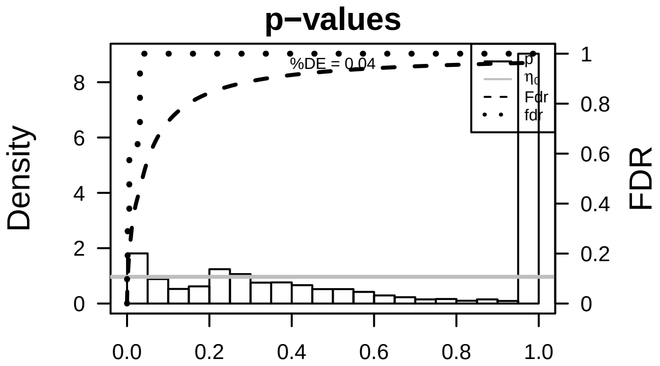


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	202861_at	0.76	−1.89	0.4	PER1	period circadian regulator 1 [Source:NCBI gene;Acc:5187]
2	225249_at	1.11	−1.82	0.6	SPPL2B	signal peptide peptidase like 2B [Source:HGNC Symbol;Acc:
3	221747_at	0.7	−1.73	0.38	TNS1	tensin 1 [Source:HGNC Symbol;Acc:HGNC:11973]
4	219264_s_at	1.15	−1.63	0.4	PPP2R3B	protein phosphatase 2 regulatory subunit B"beta [Source:HG
5	221838_at	0.62	−1.59	0.41	KLHL22	kelch like family member 22 [Source:HGNC Symbol;Acc:HGN
6	236688_at	1.19	−1.55	0.4	FRMPD3	FERM and PDZ domain containing 3 [Source:HGNC Symbol;
7	213038_at	0.81	−1.55	0.36	RNF19B	ring finger protein 19B [Source:HGNC Symbol;Acc:HGNC:26
8	227330_x_at	0.74	−1.53	0.28		MAFF interacting protein (pseudogene)
9	217948_at	0.6	−1.53	0.39	RTL8A	retrotransposon Gag like 8A [Source:HGNC Symbol;Acc:HGN
10	202045_s_at	0.62	−1.48	0.35	ARHGAP35	Rho GTPase activating protein 35 [Source:HGNC Symbol;Ac
11	202928_s_at	0.89	−1.47	0.55	PHF1	PHD finger protein 1 [Source:HGNC Symbol;Acc:HGNC:891
12	204805_s_at	0.53	−1.47	0.62	H1FX	H1 histone family member X [Source:HGNC Symbol;Acc:HG
13	200766_at	0.47	−1.45	0.41	CTSD	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
14	207561_s_at	1.46	−1.41	0.56	ASIC3	acid sensing ion channel subunit 3 [Source:HGNC Symbol;A
15	212563_at	0.8	−1.4	0.61	BOP1	BOP1 ribosomal biogenesis factor [Source:HGNC Symbol;Ac
16	209468_at	1.08	−1.39	0.59	LRP5	LDL receptor related protein 5 [Source:HGNC Symbol;Acc:H
17	204736_s_at	1.12	−1.39	0.32	CSPG4	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
18	1553479_at	0.98	−1.39	0.61	TMEM145	transmembrane protein 145 [Source:HGNC Symbol;Acc:HGN
19	226111_s_at	0.96	−1.38	0.65	ZNF385A	zinc finger protein 385A [Source:HGNC Symbol;Acc:HGNC:1
20	213121_at	1.08	−1.38	0.45	SNRNP70	small nuclear ribonucleoprotein U1 subunit 70 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	3e−10	209 / 6202	BP	cytoplasm
2	7e−09	165 / 4740	BP	cytosol
3	4e−08	32 / 459	BP	viral process
4	6e−08	44 / 783	BP	negative regulation of transcription by RNA polymerase II
5	1e−07	26 / 342	BP	chromatin organization
6	2e−07	34 / 541	BP	negative regulation of transcription, DNA−templated
7	2e−07	28 / 400	BP	chromatin binding
8	4e−07	8 / 31	BP	ATP−dependent chromatin remodeling
9	6e−07	54 / 1145	BP	regulation of transcription by RNA polymerase II
10	7e−07	13 / 102	BP	chromatin remodeling
11	1e−06	62 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
12	7e−06	49 / 1086	BP	positive regulation of transcription by RNA polymerase II
13	8e−06	218 / 7387	BP	membrane
14	1e−05	28 / 484	BP	cellular response to DNA damage stimulus
15	2e−05	7 / 36	BP	establishment of cell polarity
16	4e−05	10 / 90	BP	activation of protein kinase activity
17	6e−05	5 / 19	BP	nucleosome disassembly
18	8e−05	5 / 20	BP	protein localization to Golgi apparatus
19	8e−05	4 / 11	BP	anoikis
20	1e−04	5 / 22	BP	chromatin silencing
21	1e−04	9 / 83	BP	activation of GTPase activity
22	2e−04	10 / 105	BP	actin filament organization
23	2e−04	4 / 14	BP	stress fiber assembly
24	2e−04	29 / 613	BP	positive regulation of transcription, DNA−templated
25	3e−04	8 / 74	BP	retrograde transport, endosome to Golgi
26	4e−04	48 / 1242	BP	Golgi apparatus
27	4e−04	52 / 1387	BP	regulation of transcription, DNA−templated
28	4e−04	12 / 163	BP	autophagy
29	4e−04	26 / 545	BP	protein ubiquitination
30	5e−04	13 / 188	BP	in utero embryonic development
31	7e−04	14 / 222	BP	Wnt signaling pathway
32	7e−04	6 / 47	BP	positive regulation of protein serine/threonine kinase activity
33	8e−04	28 / 630	BP	cell cycle
34	8e−04	4 / 19	BP	TOR signaling
35	8e−04	4 / 19	BP	ubiquitin−dependent protein catabolic process via the multivesicular body s
36	1e−03	4 / 20	BP	entrainment of circadian clock by photoperiod
37	1e−03	20 / 400	BP	protein serine/threonine kinase activity
38	1e−03	17 / 315	BP	positive regulation of GTPase activity
39	1e−03	11 / 159	BP	actin cytoskeleton organization
40	1e−03	4 / 21	BP	histone methylation


p−values

BP

Rank	p−value	#in/all	Geneset
1	3e−10	209 / 6202	cytoplasm
2	7e−09	165 / 4740	cytosol
3	4e−08	32 / 459	viral process
4	6e−08	44 / 783	negative regulation of transcription by RNA polymerase II
5	1e−07	26 / 342	chromatin organization
6	2e−07	34 / 541	negative regulation of transcription, DNA−templated
7	2e−07	28 / 400	chromatin binding
8	4e−07	8 / 31	ATP−dependent chromatin remodeling
9	6e−07	54 / 1145	regulation of transcription by RNA polymerase II
10	7e−07	13 / 102	chromatin remodeling
11	1e−06	62 / 1416	DNA−binding transcription factor activity, RNA polymerase II−specific
12	7e−06	49 / 1086	positive regulation of transcription by RNA polymerase II
13	8e−06	218 / 7387	membrane
14	1e−05	28 / 484	cellular response to DNA damage stimulus
15	2e−05	7 / 36	establishment of cell polarity

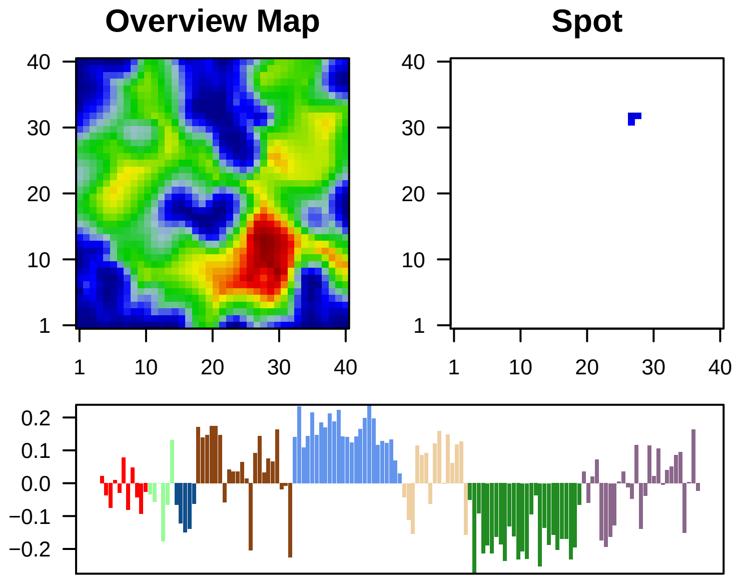
Underexpression Spots

Spot Summary: q

metagenes = 3
genes = 113

<r> metagenes = 0.99
<r> genes = 0.34
beta: r2= 1.96 / log p= −Inf

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

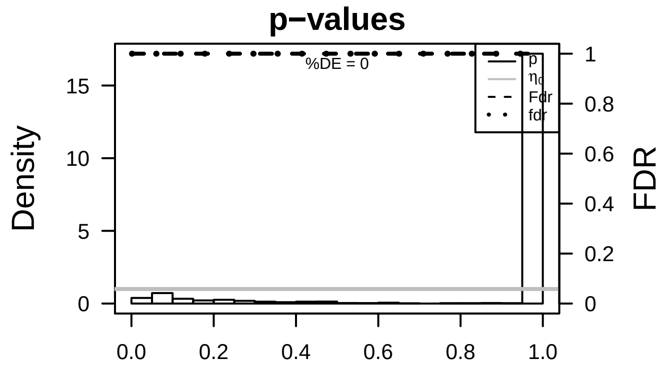


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	233498_at	1.07	−1.75	0.51		
2	227620_at	0.45	−1.33	0.52	SLC44A1	solute carrier family 44 member 1 [Source:HGNC Symbol;Ac
3	227228_s_at	1.38	−1.25	0.49	CCDC88C	coiled−coil domain containing 88C [Source:HGNC Symbol;Ac
4	1555967_at	0.79	−1.18	0.55		
5	218149_s_at	0.35	−1.13	0.5	ZNF395	zinc finger protein 395 [Source:HGNC Symbol;Acc:HGNC:18
6	230848_s_at	0.42	−1.11	0.5		
7	216398_at	0.94	−1.07	0.4		
8	1557224_at	0.94	−1.07	0.4		novel transcript, antisense to FAR2
9	209705_at	0.44	−1.07	0.66	MTF2	metal response element binding transcription factor 2 [Sourc
10	239303_at	1.48	−1.04	0.6	PIWIL2	piwi like RNA−mediated gene silencing 2 [Source:HGNC Sy
11	228593_at	0.65	−1.04	0.46		myotubularin related protein 9−like, pseudogene [Source:HG
12	204740_at	0.63	−1.02	0.6	CNKSR1	connector enhancer of kinase suppressor of Ras 1 [Source:H
13	238117_at	0.69	−1.01	0.51	PPOX	protoporphyrinogen oxidase [Source:HGNC Symbol;Acc:HG
14	231978_at	0.91	−0.99	0.46	TPCN2	two pore segment channel 2 [Source:HGNC Symbol;Acc:HG
15	226132_s_at	0.47	−0.99	0.59	MANEAL	mannosidase endo−alpha like [Source:HGNC Symbol;Acc:H
16	227729_at	0.63	−0.98	0.61	ZNF134	zinc finger protein 134 [Source:HGNC Symbol;Acc:HGNC:12
17	204937_s_at	0.38	−0.97	0.54	ZNF274	zinc finger protein 274 [Source:HGNC Symbol;Acc:HGNC:13
18	218284_at	0.45	−0.97	0.52	SMAD3	SMAD family member 3 [Source:HGNC Symbol;Acc:HGNC:6
19	220952_s_at	0.63	−0.94	0.47	PLEKHA5	pleckstrin homology domain containing A5 [Source:HGNC Sy
20	1554636_at	0.52	−0.93	0.61		

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	0.001	14 / 1416	BP	DNA−binding transcription factor activity, RNA polymerase II−specific
2	0.002	2 / 16	BP	cytoskeleton−dependent intracellular transport
3	0.003	2 / 20	BP	regulation of transforming growth factor beta receptor signaling pathway
4	0.003	8 / 613	BP	positive regulation of transcription, DNA−templated
5	0.003	2 / 22	BP	small GTPase binding
6	0.005	11 / 1145	BP	regulation of transcription by RNA polymerase II
7	0.006	9 / 843	BP	DNA−binding transcription factor activity
8	0.007	2 / 32	BP	oogenesis
9	0.008	2 / 35	BP	embryonic organ development
10	0.008	2 / 35	BP	gastrulation
11	0.009	2 / 37	BP	eye development
12	0.009	2 / 37	BP	lysosome organization
13	0.009	2 / 37	BP	negative regulation of protein catabolic process
14	0.010	2 / 38	BP	positive regulation of protein import into nucleus
15	0.011	5 / 342	BP	chromatin organization
16	0.012	4 / 227	BP	microtubule binding
17	0.020	11 / 1387	BP	regulation of transcription, DNA−templated
18	0.021	2 / 56	BP	gene silencing by RNA
19	0.021	2 / 57	BP	heart looping
20	0.022	3 / 152	BP	rRNA processing
21	0.027	9 / 1086	BP	positive regulation of transcription by RNA polymerase II
22	0.039	1 / 10	BP	cellular response to brain−derived neurotrophic factor stimulus
23	0.039	1 / 10	BP	epithelial cilium movement involved in determination of left/right asymmetry
24	0.039	1 / 10	BP	negative regulation of circadian rhythm
25	0.039	1 / 10	BP	positive regulation of growth hormone secretion
26	0.039	1 / 10	BP	positive regulation of interferon−alpha secretion
27	0.039	1 / 10	BP	positive regulation of interleukin−1 beta production
28	0.039	1 / 10	BP	primary miRNA processing
29	0.042	1 / 11	BP	core promoter binding
30	0.042	1 / 11	BP	intracellular cholesterol transport
31	0.042	1 / 11	BP	negative regulation of axon regeneration
32	0.042	1 / 11	BP	phospholipid efflux
33	0.042	1 / 11	BP	phospholipid homeostasis
34	0.042	1 / 11	BP	porphyrin−containing compound biosynthetic process
35	0.042	1 / 11	BP	positive regulation of positive chemotaxis
36	0.042	1 / 11	BP	positive regulation of type I interferon−mediated signaling pathway
37	0.042	1 / 11	BP	regulation of fibroblast migration
38	0.042	1 / 11	BP	regulation of mRNA processing
39	0.042	1 / 11	BP	t−circle formation
40	0.042	1 / 11	BP	UV−damage excision repair



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14	0.010	2 / 38	positive regulation of protein import into nucleus
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