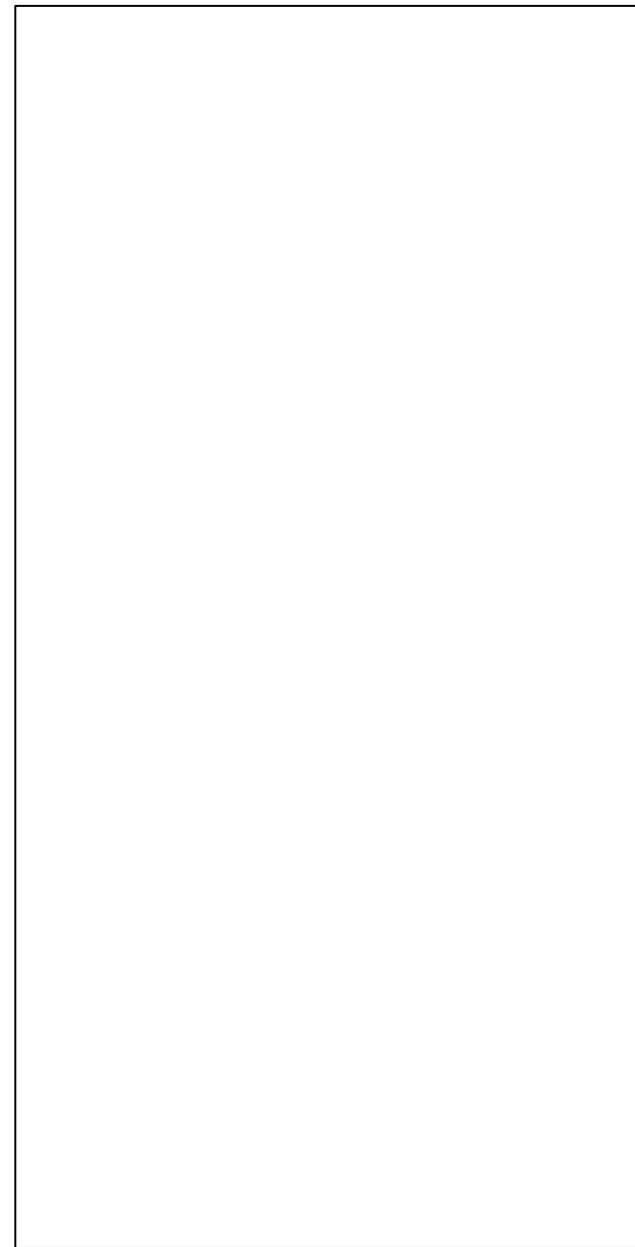
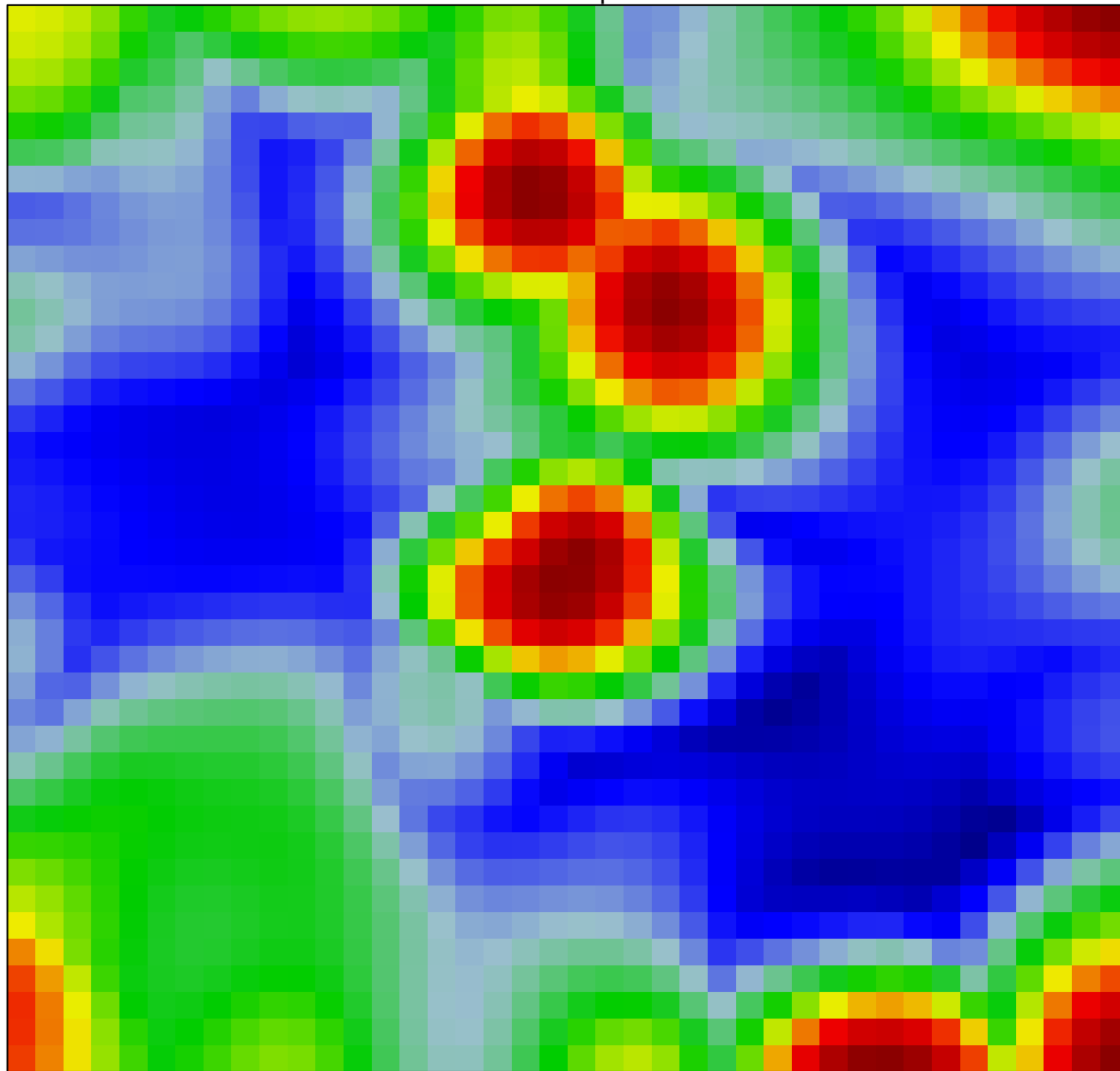


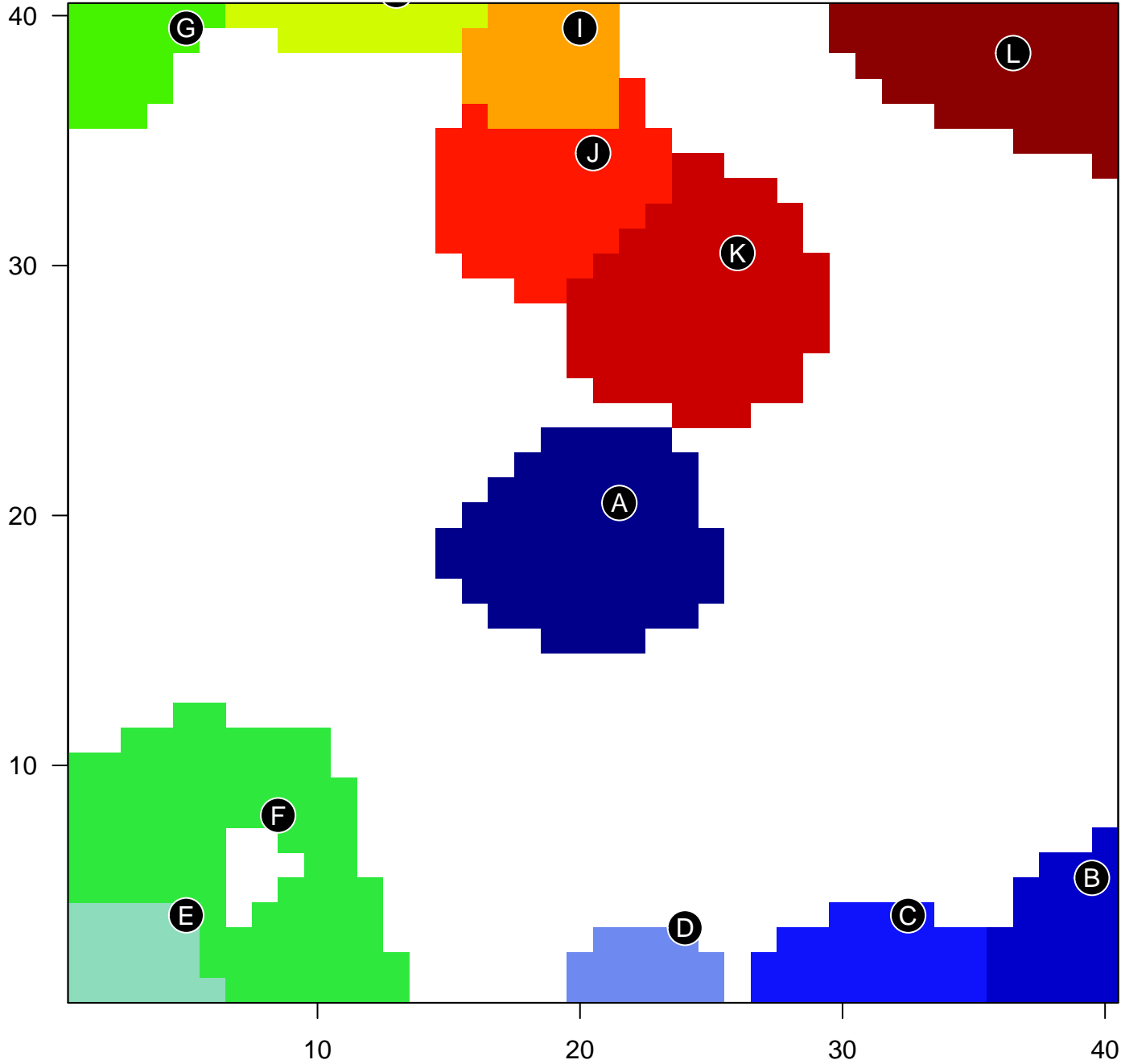
Group Overexpression Spots

landscape

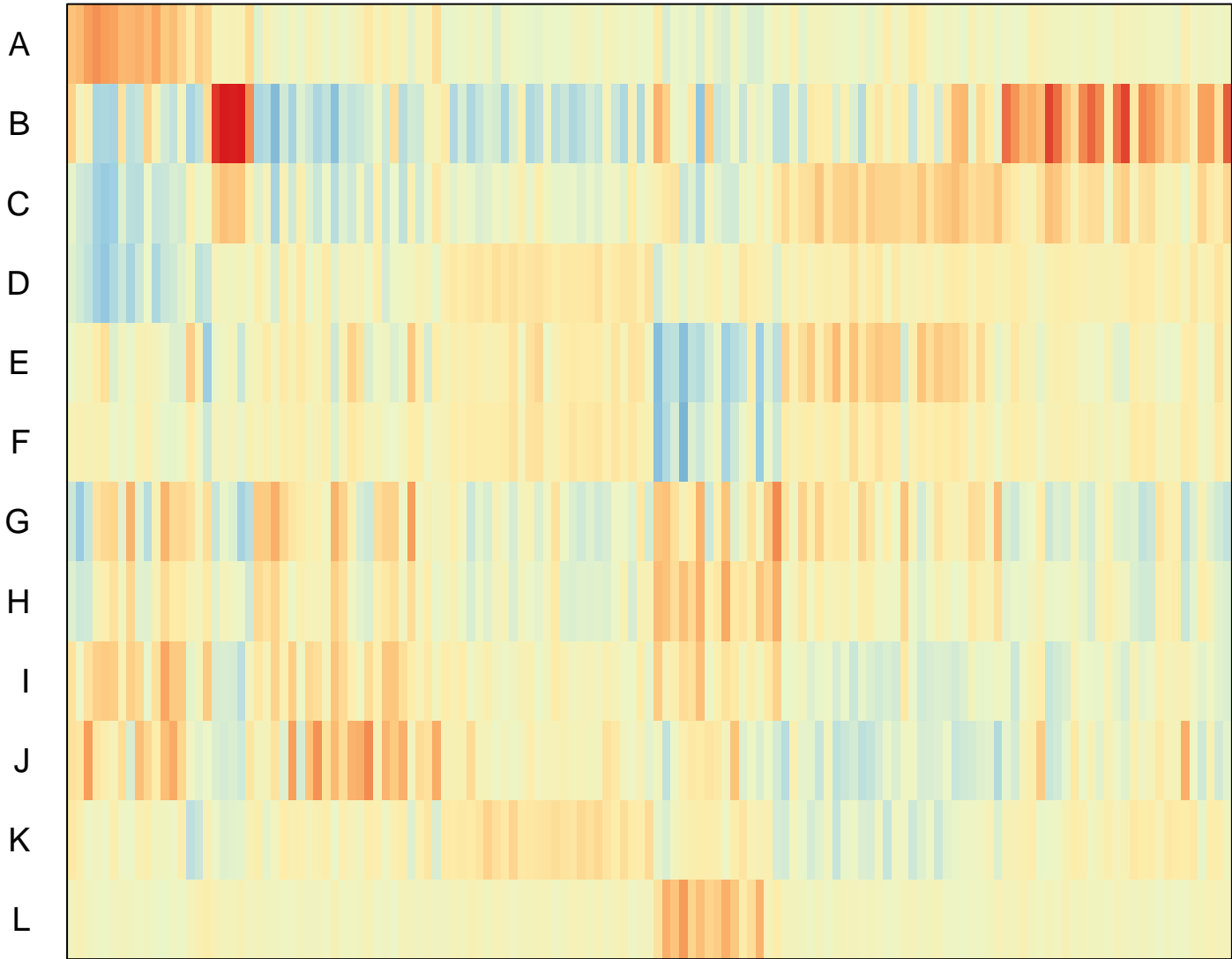


Group Overexpression Spots

annotation



- A ■ cell cycle
cell division
- B ■ synapse
chemical synaptic transmission
plasma membrane
- C ■ plasma membrane
synapse
membrane
- D ■ SRP-dependent cotranslational protein targeting to membrane
translational initiation
viral transcription
- E ■ regulation of transcription, DNA-templated
regulation of transcription by RNA polymerase II
- F ■ DNA-binding transcription factor activity, RNA polymerase II
cytosol
regulation of transcription by RNA polymerase II
cytoplasm
- G ■ regulation of alternative mRNA splicing, via spliceosome
erythrocyte development
chromatin organization
- H ■ negative regulation of transcription, DNA-templated
positive regulation of transcription by RNA polymerase II
chromatin binding
- I ■ cytoplasm
immune system process
defense response to virus
- J ■ immune system process
immune response
plasma membrane
- K ■ positive regulation of transcription by RNA polymerase II
cytosol
cytoplasm
- L ■ bicarbonate transport
cell communication
outer dynein arm assembly



- cell cycle
- cell division
- extracellular matrix organization

- synapse
- chemical synaptic transmission
- plasma membrane

- plasma membrane
- synapse
- membrane

- SRP-dependent cotranslational protein targeting to membrane
- translational initiation
- viral transcription

- regulation of transcription, DNA-templated
- regulation of transcription by RNA polymerase II
- DNA-binding transcription factor activity, RNA polymerase II-specific

- cytosol
- regulation of transcription by RNA polymerase II
- cytoplasm

- regulation of alternative mRNA splicing, via spliceosome
- erythrocyte development
- chromatin organization

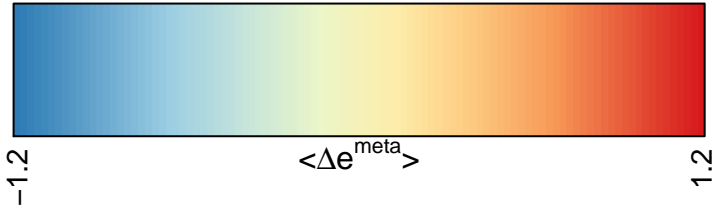
- negative regulation of transcription, DNA-templated
- positive regulation of transcription by RNA polymerase II
- chromatin binding

- cytoplasm
- immune system process
- defense response to virus

- immune system process
- immune response
- plasma membrane

- positive regulation of transcription by RNA polymerase II
- cytosol
- cytoplasm

- bicarbonate transport
- cell communication
- outer dynein arm assembly



Group Overexpression Spot

Spot Summary: A

metagenes = 73
genes = 1545

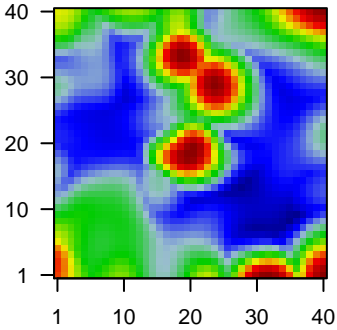
<r> metagenes = 0.71

beta: r2= 6.1 / log p= -Inf

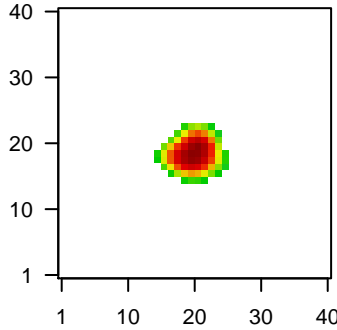
samples with spot = 17 (12.4 %)

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

Overview Map



Spot

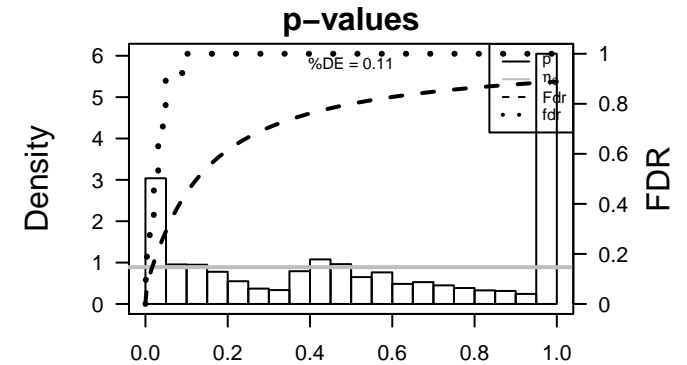
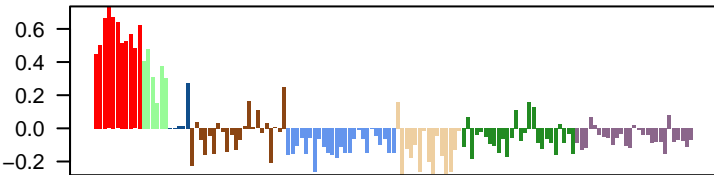


Spot Genelist

| Rank | ID | max e | r | Description | |
|------|-------------|-------|-------|-------------|--|
| | | min e | | Symbol | |
| 1 | 210809_s_at | 3.59 | -0.92 | 0.71 | POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953] |
| 2 | 243483_at | 3.39 | -0.59 | 0.6 | TRPM8 transient receptor potential cation channel subfamily M memt |
| 3 | 1555907_at | 3.31 | -0.45 | 0.49 | AGAP2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC: |
| 4 | 1555778_a_a | 3.29 | -0.53 | 0.68 | POSTN periostin [Source:HGNC Symbol;Acc:HGNC:16953] |
| 5 | 205858_at | 3.12 | -0.94 | 0.5 | NGFR nerve growth factor receptor [Source:HGNC Symbol;Acc:HGNC: |
| 6 | 242883_at | 3.11 | -0.37 | 0.39 | OTOS otospiralin [Source:HGNC Symbol;Acc:HGNC:22644] |
| 7 | 206858_s_at | 3.1 | -0.65 | 0.61 | HOXC6 homeobox C6 [Source:HGNC Symbol;Acc:HGNC:5128] |
| 8 | 228904_at | 3.05 | -0.62 | 0.72 | HOXB3 homeobox B3 [Source:HGNC Symbol;Acc:HGNC:5114] |
| 9 | 206154_at | 3.04 | -0.83 | 0.52 | RLBP1 retinaldehyde binding protein 1 [Source:HGNC Symbol;Acc:H |
| 10 | 222087_at | 3.01 | -0.48 | 0.39 | |
| 11 | 210135_s_at | 2.98 | -0.87 | 0.77 | SHOX2 short stature homeobox 2 [Source:HGNC Symbol;Acc:HGNC |
| 12 | 224588_at | 2.97 | -2.09 | 0.16 | X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC: |
| 13 | 203180_at | 2.88 | -0.89 | 0.47 | ALDH1A3 aldehyde dehydrogenase 1 family member A3 [Source:HGNC |
| 14 | 217057_s_at | 2.88 | -0.48 | 0.57 | GNAS GNAS complex locus [Source:HGNC Symbol;Acc:HGNC:439 |
| 15 | 220010_at | 2.87 | -0.81 | 0.35 | ACSL4 acyl-CoA synthetase long chain family member 4 [Source:HC |
| 16 | 242234_at | 2.84 | -0.62 | 0.74 | XAF1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:HGNC:: |
| 17 | 221577_x_at | 2.82 | -0.6 | 0.73 | GDF15 growth differentiation factor 15 [Source:HGNC Symbol;Acc:Hi |
| 18 | 218308_at | 2.79 | -0.78 | 0.59 | TACC3 transforming acidic coiled-coil containing protein 3 [Source:H |
| 19 | 227671_at | 2.79 | -1.83 | 0.16 | X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC: |
| 20 | 214218_s_at | 2.77 | -1.66 | 0.16 | X inactive specific transcript [Source:HGNC Symbol;Acc:HGNC: |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 2e-27 | 100 / 630 | BP cell cycle |
| 2 | 2e-26 | 76 / 394 | BP cell division |
| 3 | 4e-24 | 55 / 231 | BP extracellular matrix organization |
| 4 | 8e-17 | 48 / 254 | BP angiogenesis |
| 5 | 7e-16 | 27 / 85 | BP chromosome segregation |
| 6 | 6e-14 | 398 / 6202 | BP cytoplasm |
| 7 | 5e-11 | 30 / 158 | BP DNA replication |
| 8 | 3e-10 | 15 / 42 | BP mitotic spindle organization |
| 9 | 4e-10 | 64 / 594 | BP cell adhesion |
| 10 | 7e-09 | 14 / 44 | BP collagen fibril organization |
| 11 | 3e-08 | 40 / 327 | BP cell population proliferation |
| 12 | 4e-08 | 26 / 164 | BP mitotic cell cycle |
| 13 | 6e-08 | 90 / 1080 | BP multicellular organism development |
| 14 | 8e-08 | 11 / 31 | BP mitotic sister chromatid segregation |
| 15 | 9e-08 | 24 / 148 | BP skeletal system development |
| 16 | 1e-07 | 19 / 98 | BP G1/S transition of mitotic cell cycle |
| 17 | 2e-07 | 18 / 92 | BP wound healing |
| 18 | 3e-07 | 13 / 50 | BP mitotic cytokinesis |
| 19 | 4e-07 | 10 / 29 | BP blood vessel morphogenesis |
| 20 | 4e-07 | 10 / 29 | BP endodermal cell differentiation |
| 21 | 5e-07 | 30 / 233 | BP heart development |
| 22 | 6e-07 | 16 / 79 | BP microtubule-based movement |
| 23 | 1e-06 | 11 / 39 | BP CENP-A containing nucleosome assembly |
| 24 | 1e-06 | 11 / 39 | BP regulation of mitotic nuclear division |
| 25 | 1e-06 | 17 / 94 | BP cell-matrix adhesion |
| 26 | 3e-06 | 27 / 214 | BP cell migration |
| 27 | 4e-06 | 38 / 366 | BP DNA repair |
| 28 | 4e-06 | 33 / 299 | BP response to drug |
| 29 | 5e-06 | 57 / 657 | BP calcium ion binding |
| 30 | 6e-06 | 9 / 30 | BP sprouting angiogenesis |
| 31 | 6e-06 | 7 / 17 | BP DNA replication origin binding |
| 32 | 7e-06 | 279 / 4740 | BP cytosol |
| 33 | 8e-06 | 12 / 56 | BP DNA damage response, signal transduction by p53 class mediator resulting |
| 34 | 9e-06 | 45 / 484 | BP cellular response to DNA damage stimulus |
| 35 | 1e-05 | 14 / 76 | BP microtubule motor activity |
| 36 | 1e-05 | 6 / 13 | BP kinetochore assembly |
| 37 | 1e-05 | 9 / 33 | BP DNA replication initiation |
| 38 | 1e-05 | 9 / 33 | BP mitotic cell cycle checkpoint |
| 39 | 2e-05 | 17 / 112 | BP motor activity |
| 40 | 2e-05 | 46 / 513 | BP positive regulation of cell population proliferation |



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--------------------------------------|
| 1 | 2e-27 | 100 / 630 | cell cycle |
| 2 | 2e-26 | 76 / 394 | cell division |
| 3 | 4e-24 | 55 / 231 | extracellular matrix organization |
| 4 | 8e-17 | 48 / 254 | angiogenesis |
| 5 | 7e-16 | 27 / 85 | chromosome segregation |
| 6 | 6e-14 | 398 / 6202 | cytoplasm |
| 7 | 5e-11 | 30 / 158 | DNA replication |
| 8 | 3e-10 | 15 / 42 | mitotic spindle organization |
| 9 | 4e-10 | 64 / 594 | cell adhesion |
| 10 | 7e-09 | 14 / 44 | collagen fibril organization |
| 11 | 3e-08 | 40 / 327 | cell population proliferation |
| 12 | 4e-08 | 26 / 164 | mitotic cell cycle |
| 13 | 6e-08 | 90 / 1080 | multicellular organism development |
| 14 | 8e-08 | 11 / 31 | mitotic sister chromatid segregation |
| 15 | 9e-08 | 24 / 148 | skeletal system development |

Group Overexpression Spot

Spot Summary: B

metagenes = 27
genes = 987

<r> metagenes = 0.97
<r> genes = 0.61
beta: r2= 28.41 / log p= -Inf

samples with spot = 37 (27 %)

- group 1 : 2 (18.2 %)
- group 2 : 1 (16.7 %)
- group 3 : 5 (100 %)
- group 6 : 3 (20 %)
- group 7 : 3 (11.5 %)
- group 8 : 23 (85.2 %)

Spot Genelist

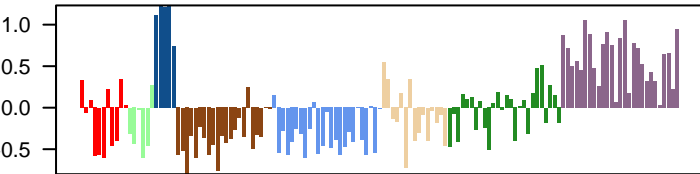
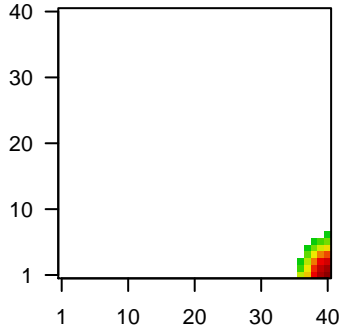
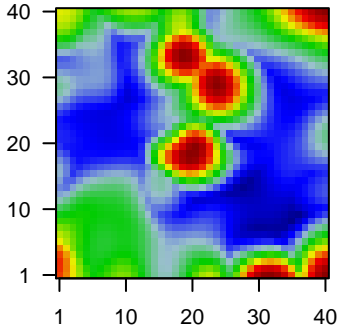
| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|---|
| | | | | | Symbol |
| 1 | 206803_at | 3.07 | -1.3 | 0.53 | PDYN prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820] |
| 2 | 206382_s_at | 2.85 | -0.87 | 0.6 | BDNF brain derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:1034] |
| 3 | 205901_at | 2.71 | -1.16 | 0.71 | PNOC prepronociceptin [Source:HGNC Symbol;Acc:HGNC:9163] |
| 4 | 229012_at | 2.64 | -0.83 | 0.71 | C9orf24 chromosome 9 open reading frame 24 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 5 | 1560652_at | 2.59 | -0.61 | 0.6 | novel transcript, overlapping to IRS4 |
| 6 | 207147_at | 2.55 | -0.86 | 0.6 | DLX2 distal-less homeobox 2 [Source:HGNC Symbol;Acc:HGNC:2082] |
| 7 | 206552_s_at | 2.4 | -1.6 | 0.75 | TAC1 tachykinin precursor 1 [Source:HGNC Symbol;Acc:HGNC:11111] |
| 8 | 228844_at | 2.39 | -0.8 | 0.8 | SLC13A5solute carrier family 13 member 5 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 9 | 207768_at | 2.35 | -0.93 | 0.85 | EGR4 early growth response 4 [Source:HGNC Symbol;Acc:HGNC:2082] |
| 10 | 214611_at | 2.29 | -0.89 | 0.57 | GRIK1 glutamate ionotropic receptor kainate type subunit 1 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 11 | 231391_at | 2.29 | -0.69 | 0.74 | CTXN3 cortixin 3 [Source:HGNC Symbol;Acc:HGNC:31110] |
| 12 | 222920_s_at | 2.29 | -1.17 | 0.88 | TESPA1 thymocyte expressed, positive selection associated 1 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 13 | 204380_s_at | 2.28 | -0.84 | 0.49 | FGFR3 fibroblast growth factor receptor 3 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 14 | 220025_at | 2.25 | -0.85 | 0.92 | TBR1 T-box, brain 1 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 15 | 242138_at | 2.23 | -1.27 | 0.74 | DLX1 distal-less homeobox 1 [Source:HGNC Symbol;Acc:HGNC:2082] |
| 16 | 219263_at | 2.22 | -1.06 | 0.74 | RNF128 ring finger protein 128, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:11590] |
| 17 | 232111_at | 2.18 | -0.91 | 0.81 | TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:11590] |
| 18 | 1555800_at | 2.18 | -1.12 | 0.88 | ZNF385Bzinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:2082] |
| 19 | 1559633_a_at | 2.16 | -1.09 | 0.85 | CHRM3 cholinergic receptor muscarinic 3 [Source:HGNC Symbol;Acc:HGNC:11590] |
| 20 | 211451_s_at | 2.15 | -0.89 | 0.8 | KCNJ4 potassium voltage-gated channel subfamily J member 4 [Source:HGNC Symbol;Acc:HGNC:11590] |

Geneset Overrepresentation

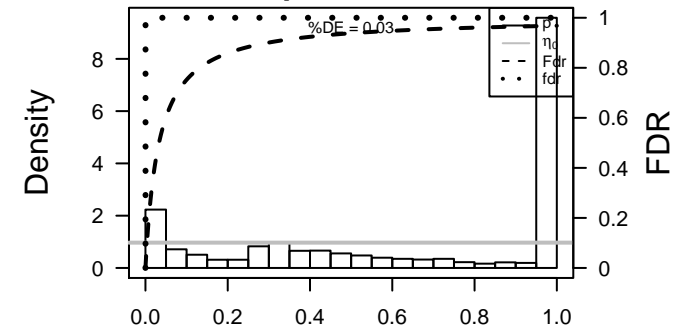
| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 1e-50 | 103 / 574 | BP synapse |
| 2 | 4e-44 | 65 / 236 | BP chemical synaptic transmission |
| 3 | 4e-36 | 266 / 4278 | BP plasma membrane |
| 4 | 3e-30 | 363 / 7387 | BP membrane |
| 5 | 3e-22 | 44 / 240 | BP postsynaptic membrane |
| 6 | 1e-19 | 67 / 627 | BP ion transport |
| 7 | 1e-18 | 58 / 505 | BP nervous system development |
| 8 | 9e-17 | 30 / 149 | BP regulation of ion transmembrane transport |
| 9 | 6e-12 | 94 / 1500 | BP signal transduction |
| 10 | 7e-12 | 22 / 119 | BP postsynapse |
| 11 | 1e-11 | 15 / 51 | BP neurotransmitter secretion |
| 12 | 1e-11 | 14 / 43 | BP neurotransmitter transport |
| 13 | 2e-11 | 60 / 777 | BP G protein-coupled receptor signaling pathway |
| 14 | 5e-11 | 22 / 131 | BP potassium ion transport |
| 15 | 5e-11 | 22 / 131 | BP presynapse |
| 16 | 9e-11 | 12 / 33 | BP regulation of exocytosis |
| 17 | 1e-10 | 17 / 79 | BP cellular response to calcium ion |
| 18 | 2e-10 | 14 / 51 | BP regulation of synaptic plasticity |
| 19 | 2e-10 | 11 / 28 | BP synaptic vesicle exocytosis |
| 20 | 2e-09 | 13 / 51 | BP regulation of synaptic vesicle exocytosis |
| 21 | 3e-09 | 10 / 27 | BP glutamate secretion |
| 22 | 4e-09 | 19 / 122 | BP potassium ion transmembrane transport |
| 23 | 4e-09 | 29 / 275 | BP ion transmembrane transport |
| 24 | 5e-09 | 49 / 657 | BP calcium ion binding |
| 25 | 6e-09 | 8 / 16 | BP positive regulation of calcium ion-dependent exocytosis |
| 26 | 8e-09 | 16 / 89 | BP locomotory behavior |
| 27 | 9e-09 | 10 / 30 | BP associative learning |
| 28 | 1e-08 | 15 / 79 | BP memory |
| 29 | 1e-08 | 12 / 48 | BP long-term synaptic potentiation |
| 30 | 1e-08 | 10 / 31 | BP regulation of NMDA receptor activity |
| 31 | 1e-08 | 18 / 118 | BP exocytosis |
| 32 | 2e-08 | 8 / 18 | BP regulation of neurotransmitter secretion |
| 33 | 2e-08 | 9 / 25 | BP calmodulin-dependent protein kinase activity |
| 34 | 3e-08 | 10 / 33 | BP long-term memory |
| 35 | 3e-08 | 7 / 13 | BP synaptic transmission, GABAergic |
| 36 | 3e-08 | 26 / 249 | BP brain development |
| 37 | 5e-08 | 12 / 54 | BP sensory perception of pain |
| 38 | 6e-08 | 15 / 89 | BP neuropeptide signaling pathway |
| 39 | 6e-08 | 19 / 144 | BP calcium ion transport |
| 40 | 9e-08 | 44 / 615 | BP transmembrane transport |

Overview Map

Spot



p-values



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 1e-50 | 103 / 574 | synapse |
| 2 | 4e-44 | 65 / 236 | chemical synaptic transmission |
| 3 | 4e-36 | 266 / 4278 | plasma membrane |
| 4 | 3e-30 | 363 / 7387 | membrane |
| 5 | 3e-22 | 44 / 240 | postsynaptic membrane |
| 6 | 1e-19 | 67 / 627 | ion transport |
| 7 | 1e-18 | 58 / 505 | nervous system development |
| 8 | 9e-17 | 30 / 149 | regulation of ion transmembrane transport |
| 9 | 6e-12 | 94 / 1500 | signal transduction |
| 10 | 7e-12 | 22 / 119 | postsynapse |
| 11 | 1e-11 | 15 / 51 | neurotransmitter secretion |
| 12 | 1e-11 | 14 / 43 | neurotransmitter transport |
| 13 | 2e-11 | 60 / 777 | G protein-coupled receptor signaling pathway |
| 14 | 5e-11 | 22 / 131 | potassium ion transport |
| 15 | 5e-11 | 22 / 131 | presynapse |

Group Overexpression Spot

Spot Summary: C

metagenes = 30
genes = 920

<r> metagenes = 0.94
<r> genes = 0.37
beta: r2= 9.57 / log p= -Inf

samples with spot = 30 (21.9 %)
group 3 : 4 (80 %)
group 7 : 19 (73.1 %)
group 8 : 7 (25.9 %)

Spot Genelist

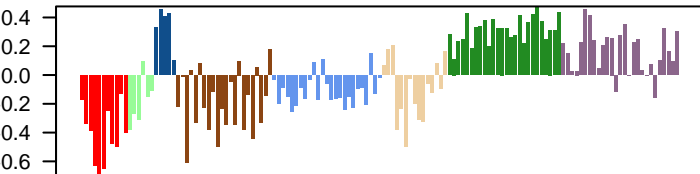
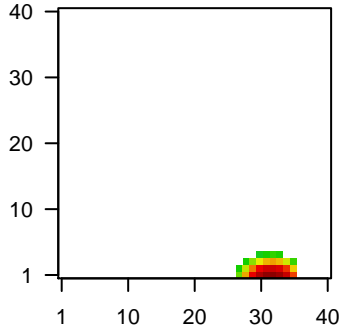
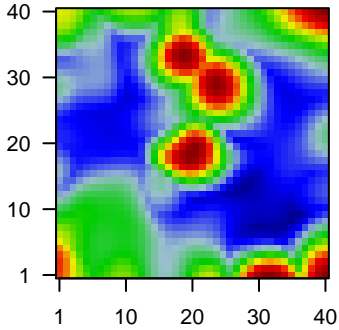
| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|---|
| 1 | 1556573_s_at | 2.93 | -1.3 | 0.35 | novel transcript |
| 2 | 243242_at | 2.38 | -0.75 | 0.48 | |
| 3 | 241883_x_at | 2.35 | -0.72 | 0.47 | |
| 4 | 1555230_a_at | 2.29 | -1.18 | 0.73 | KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC] |
| 5 | 1566772_at | 2.2 | -0.85 | 0.64 | |
| 6 | 236714_at | 2.14 | -1.26 | 0.72 | |
| 7 | 231029_at | 2.12 | -1.61 | 0.41 | |
| 8 | 1557215_at | 2.1 | -0.67 | 0.37 | long intergenic non-protein coding RNA 648 [Source:HGNC] |
| 9 | 1553415_at | 2.06 | -0.74 | 0.55 | SLC17A8 solute carrier family 17 member 8 [Source:HGNC Symbol;Acc:NM_014548] |
| 10 | 236111_at | 2.06 | -0.71 | 0.38 | long intergenic non-protein coding RNA 1238 [Source:HGNC] |
| 11 | 216672_s_at | 2.04 | -0.66 | 0.57 | MYT1L myelin transcription factor 1 like [Source:HGNC Symbol;Acc:NM_014548] |
| 12 | 229839_at | 2.04 | -0.64 | 0.45 | SCARA5 scavenger receptor class A member 5 [Source:HGNC Symbol;Acc:NM_014548] |
| 13 | 230112_at | 2.02 | -1.35 | 0.88 | MARCH4 membrane associated ring-CH-type finger 4 [Source:HGNC] |
| 14 | 244117_at | 1.97 | -0.81 | 0.47 | |
| 15 | 240450_at | 1.96 | -0.64 | 0.31 | |
| 16 | 221321_s_at | 1.96 | -1.19 | 0.75 | KCNIP2 potassium voltage-gated channel interacting protein 2 [Source:HGNC] |
| 17 | 1561324_at | 1.9 | -1.05 | 0.44 | |
| 18 | 227614_at | 1.89 | -0.91 | 0.48 | HKDC1 hexokinase domain containing 1 [Source:HGNC Symbol;Acc:NM_014548] |
| 19 | 224942_at | 1.89 | -0.71 | 0.36 | PAPPA pappalysin 1 [Source:HGNC Symbol;Acc:HGNC:8602] |
| 20 | 217085_at | 1.89 | -0.77 | 0.37 | novel transcript |

Geneset Overrepresentation

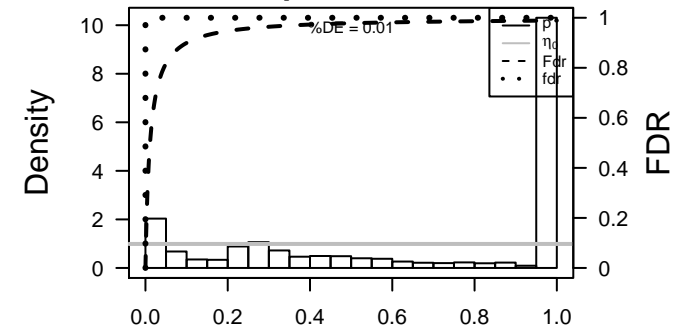
| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 5e-31 | 223 / 4278 | BP plasma membrane |
| 2 | 3e-26 | 67 / 574 | BP synapse |
| 3 | 2e-25 | 302 / 7387 | BP membrane |
| 4 | 1e-24 | 43 / 240 | BP postsynaptic membrane |
| 5 | 2e-12 | 49 / 627 | BP ion transport |
| 6 | 2e-12 | 43 / 505 | BP nervous system development |
| 7 | 3e-12 | 23 / 149 | BP regulation of ion transmembrane transport |
| 8 | 4e-12 | 16 / 65 | BP learning |
| 9 | 8e-12 | 28 / 236 | BP chemical synaptic transmission |
| 10 | 9e-11 | 16 / 79 | BP memory |
| 11 | 1e-10 | 13 / 48 | BP synapse organization |
| 12 | 5e-10 | 10 / 27 | BP positive regulation of excitatory postsynaptic potential |
| 13 | 6e-10 | 19 / 131 | BP potassium ion transport |
| 14 | 1e-09 | 9 / 22 | BP regulation of AMPA receptor activity |
| 15 | 2e-09 | 18 / 125 | BP calcium ion transmembrane transport |
| 16 | 3e-09 | 12 / 51 | BP neurotransmitter secretion |
| 17 | 6e-09 | 26 / 275 | BP ion transmembrane transport |
| 18 | 9e-09 | 17 / 122 | BP potassium ion transmembrane transport |
| 19 | 2e-08 | 11 / 48 | BP cardiac conduction |
| 20 | 3e-08 | 12 / 61 | BP positive regulation of synapse assembly |
| 21 | 1e-07 | 20 / 199 | BP axon guidance |
| 22 | 3e-07 | 6 / 13 | BP calcium ion transport into cytosol |
| 23 | 3e-07 | 6 / 13 | BP regulation of short-term neuronal synaptic plasticity |
| 24 | 5e-07 | 69 / 1500 | BP signal transduction |
| 25 | 6e-07 | 6 / 14 | BP vocalization behavior |
| 26 | 6e-07 | 16 / 144 | BP calcium ion transport |
| 27 | 9e-07 | 11 / 68 | BP regulation of insulin secretion |
| 28 | 9e-07 | 10 / 55 | BP social behavior |
| 29 | 2e-06 | 12 / 89 | BP locomotory behavior |
| 30 | 2e-06 | 6 / 17 | BP regulation of potassium ion transmembrane transport |
| 31 | 2e-06 | 9 / 48 | BP long-term synaptic potentiation |
| 32 | 3e-06 | 7 / 27 | BP glutamate secretion |
| 33 | 3e-06 | 9 / 50 | BP nervous system process |
| 34 | 4e-06 | 7 / 28 | BP regulation of presynapse assembly |
| 35 | 6e-06 | 5 / 12 | BP regulation of postsynaptic density assembly |
| 36 | 6e-06 | 34 / 594 | BP cell adhesion |
| 37 | 8e-06 | 13 / 118 | BP exocytosis |
| 38 | 8e-06 | 13 / 119 | BP postsynapse |
| 39 | 9e-06 | 6 / 21 | BP membrane depolarization |
| 40 | 1e-05 | 8 / 45 | BP neuromuscular process controlling balance |

Overview Map

Spot



p-values



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 5e-31 | 223 / 4278 | plasma membrane |
| 2 | 3e-26 | 67 / 574 | synapse |
| 3 | 2e-25 | 302 / 7387 | membrane |
| 4 | 1e-24 | 43 / 240 | postsynaptic membrane |
| 5 | 2e-12 | 49 / 627 | ion transport |
| 6 | 2e-12 | 43 / 505 | nervous system development |
| 7 | 3e-12 | 23 / 149 | regulation of ion transmembrane transport |
| 8 | 4e-12 | 16 / 65 | learning |
| 9 | 8e-12 | 28 / 236 | chemical synaptic transmission |
| 10 | 9e-11 | 16 / 79 | memory |
| 11 | 1e-10 | 13 / 48 | synapse organization |
| 12 | 5e-10 | 10 / 27 | positive regulation of excitatory postsynaptic potential |
| 13 | 6e-10 | 19 / 131 | potassium ion transport |
| 14 | 1e-09 | 9 / 22 | regulation of AMPA receptor activity |
| 15 | 2e-09 | 18 / 125 | calcium ion transmembrane transport |

Group Overexpression Spot

Spot Summary: D

metagenes = 16
genes = 532

<r> metagenes = 0.95
<r> genes = 0.32
beta: r2= 3.28 / log p= -Inf

samples with spot = 0 (0 %)

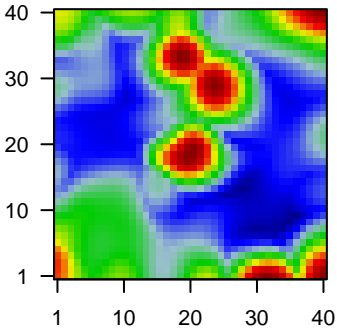
Spot Genelist

| Rank | ID | max e | r | min e | Description |
|------|-------------|-------|-------|-------|---|
| | | | | | Symbol |
| 1 | 206159_at | 2.05 | -1.3 | 0.42 | GDF10 growth differentiation factor 10 [Source:HGNC Symbol;Acc:HGNC:117] |
| 2 | 237622_at | 1.86 | -0.77 | 0.21 | ACO1 aconitase 1 [Source:HGNC Symbol;Acc:HGNC:117] |
| 3 | 208334_at | 1.84 | -1.17 | 0.56 | NDST4 N-deacetylase and N-sulfotransferase 4 [Source:HGNC Syrr] |
| 4 | 207276_at | 1.83 | -0.93 | 0.42 | CDR1 cerebellar degeneration related protein 1 [Source:HGNC Syrr] |
| 5 | 205262_at | 1.72 | -1.26 | 0.35 | KCNH2 potassium voltage-gated channel subfamily H member 2 [Source:HGNC Syrr] |
| 6 | 1560477_a_a | 1.68 | -1.08 | 0.4 | SAMD11 sterile alpha motif domain containing 11 [Source:HGNC Syml] |
| 7 | 215527_at | 1.68 | -0.78 | 0.41 | KHDRBS2 3'UTR overlapping transcript 1 [Source:HGNC Syrr] |
| 8 | 1553179_at | 1.64 | -1.07 | 0.44 | ADAMTS10 ADAM metalloproteinase with thrombospondin type 1 motif 19 |
| 9 | 239624_at | 1.63 | -1.79 | 0.27 | |
| 10 | 1556401_a_a | 1.62 | -0.78 | 0.45 | novel transcript |
| 11 | 244128_x_at | 1.54 | -1.34 | 0.29 | GLIS1 GLIS family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:117] |
| 12 | 244114_x_at | 1.52 | -1.63 | 0.33 | |
| 13 | 209652_s_at | 1.52 | -1.26 | 0.28 | PGF placental growth factor [Source:HGNC Symbol;Acc:HGNC:88] |
| 14 | 239230_at | 1.51 | -1.7 | 0.52 | HES5 hes family bHLH transcription factor 5 [Source:HGNC Symbol] |
| 15 | 1561479_at | 1.51 | -1.07 | 0.62 | TEC |
| 16 | 207505_at | 1.51 | -0.79 | 0.53 | PRKG2 protein kinase cGMP-dependent 2 [Source:HGNC Symbol;Acc:HGNC:117] |
| 17 | 214974_x_at | 1.5 | -1.14 | 0.47 | CXCL5 C-X-C motif chemokine ligand 5 [Source:HGNC Symbol;Acc:HGNC:117] |
| 18 | 242245_at | 1.49 | -1.48 | 0.58 | |
| 19 | 216594_x_at | 1.47 | -2.14 | 0.42 | AKR1C1 aldo-keto reductase family 1 member C1 [Source:HGNC Syn] |
| 20 | 228915_at | 1.46 | -1.66 | 0.43 | DACH1 dachshund family transcription factor 1 [Source:HGNC Syml] |

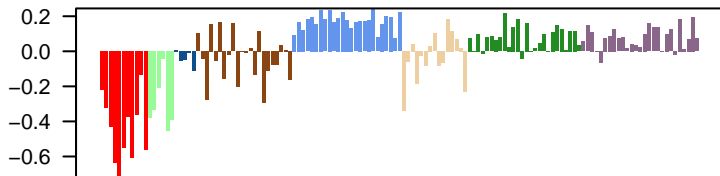
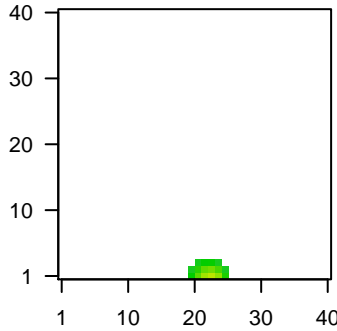
Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 2e-07 | 10 / 69 | BP SRP-dependent cotranslational protein targeting to membrane |
| 2 | 8e-07 | 12 / 120 | BP translational initiation |
| 3 | 3e-06 | 10 / 90 | BP viral transcription |
| 4 | 6e-06 | 10 / 98 | BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay |
| 5 | 1e-05 | 4 / 10 | BP cardiac left ventricle morphogenesis |
| 6 | 1e-04 | 21 / 505 | BP nervous system development |
| 7 | 2e-04 | 9 / 117 | BP negative regulation of cell migration |
| 8 | 2e-04 | 109 / 4740 | BP cytosol |
| 9 | 2e-04 | 9 / 119 | BP postsynapse |
| 10 | 2e-04 | 7 / 73 | BP modulation of chemical synaptic transmission |
| 11 | 3e-04 | 22 / 574 | BP synapse |
| 12 | 8e-04 | 13 / 276 | BP translation |
| 13 | 9e-04 | 3 / 12 | BP epithelial to mesenchymal transition involved in endocardial cushion formation |
| 14 | 1e-03 | 5 / 47 | BP response to ischemia |
| 15 | 1e-03 | 5 / 48 | BP inositol phosphate metabolic process |
| 16 | 1e-03 | 3 / 14 | BP cardiac muscle hypertrophy in response to stress |
| 17 | 2e-03 | 3 / 16 | BP glutamate receptor signaling pathway |
| 18 | 2e-03 | 3 / 16 | BP negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage |
| 19 | 2e-03 | 5 / 55 | BP somitogenesis |
| 20 | 2e-03 | 7 / 108 | BP neuron migration |
| 21 | 3e-03 | 18 / 513 | BP positive regulation of cell population proliferation |
| 22 | 3e-03 | 3 / 18 | BP action potential |
| 23 | 3e-03 | 3 / 18 | BP ionotropic glutamate receptor activity |
| 24 | 3e-03 | 11 / 249 | BP brain development |
| 25 | 3e-03 | 7 / 116 | BP steroid metabolic process |
| 26 | 4e-03 | 5 / 61 | BP positive regulation of synapse assembly |
| 27 | 4e-03 | 39 / 1500 | BP signal transduction |
| 28 | 4e-03 | 3 / 20 | BP axonal fasciculation |
| 29 | 4e-03 | 3 / 20 | BP neurotrophin TRK receptor signaling pathway |
| 30 | 6e-03 | 3 / 22 | BP ionotropic glutamate receptor signaling pathway |
| 31 | 6e-03 | 6 / 97 | BP transforming growth factor beta receptor signaling pathway |
| 32 | 6e-03 | 3 / 23 | BP synaptic membrane adhesion |
| 33 | 7e-03 | 7 / 131 | BP presynapse |
| 34 | 7e-03 | 5 / 71 | BP fat cell differentiation |
| 35 | 7e-03 | 8 / 165 | BP positive regulation of protein phosphorylation |
| 36 | 7e-03 | 5 / 72 | BP positive regulation of endothelial cell proliferation |
| 37 | 7e-03 | 7 / 133 | BP central nervous system development |
| 38 | 7e-03 | 4 / 46 | BP negative regulation of cold-induced thermogenesis |
| 39 | 7e-03 | 4 / 46 | BP neural tube development |
| 40 | 7e-03 | 3 / 24 | BP negative regulation of epithelial to mesenchymal transition |

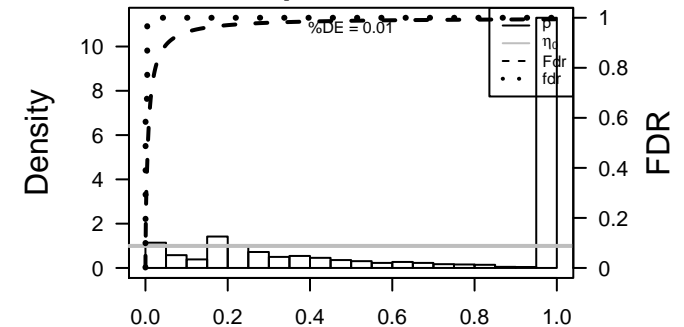
Overview Map



Spot



p-values



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 2e-07 | 10 / 69 | SRP-dependent cotranslational protein targeting to membrane |
| 2 | 8e-07 | 12 / 120 | translational initiation |
| 3 | 3e-06 | 10 / 90 | viral transcription |
| 4 | 6e-06 | 10 / 98 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay |
| 5 | 1e-05 | 4 / 10 | cardiac left ventricle morphogenesis |
| 6 | 1e-04 | 21 / 505 | nervous system development |
| 7 | 2e-04 | 9 / 117 | negative regulation of cell migration |
| 8 | 2e-04 | 109 / 4740 | cytosol |
| 9 | 2e-04 | 9 / 119 | postsynapse |
| 10 | 2e-04 | 7 / 73 | modulation of chemical synaptic transmission |
| 11 | 3e-04 | 22 / 574 | synapse |
| 12 | 8e-04 | 13 / 276 | translation |
| 13 | 9e-04 | 3 / 12 | epithelial to mesenchymal transition involved in endocardial cushion formation |
| 14 | 1e-03 | 5 / 47 | response to ischemia |
| 15 | 1e-03 | 5 / 48 | inositol phosphate metabolic process |

Group Overexpression Spot

Spot Summary: E

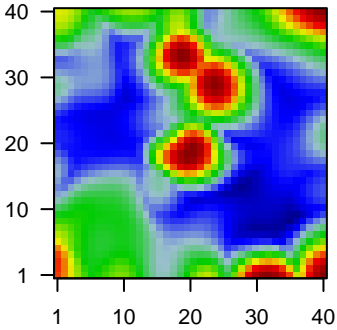
metagenes = 20
genes = 650

<r> metagenes = 0.94
<r> genes = 0.45
beta: r2= 8.62 / log p= -Inf

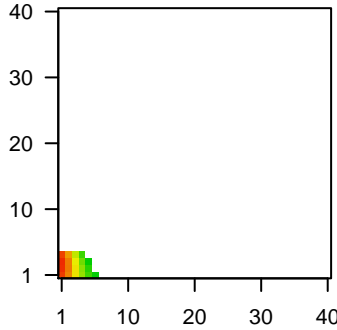
samples with spot = 18 (13.1 %)

group 2 : 1 (16.7 %)
group 4 : 2 (9.1 %)
group 5 : 1 (4 %)
group 7 : 14 (53.8 %)

Overview Map



Spot

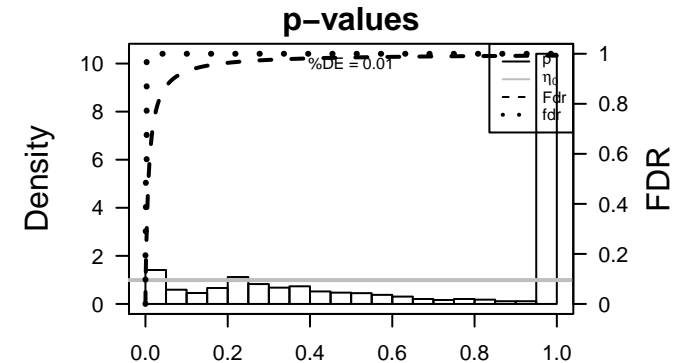
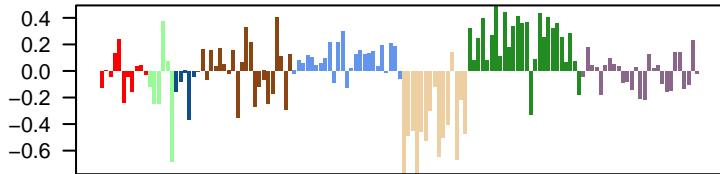


Spot Genelist

| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|---|
| 1 | 211879_x_at | 2.13 | -1.2 | 0.52 | PCDHGA9protocadherin gamma subfamily A, 3 [Source:HGNC Symbol; |
| 2 | 1569481_s_at | 2.03 | -0.89 | 0.4 | SNX22 sorting nexin 22 [Source:HGNC Symbol;Acc:HGNC:16315] |
| 3 | 1568795_at | 2 | -0.94 | 0.51 | |
| 4 | 1552662_a_at | 1.99 | -1.09 | 0.33 | PCDHGB7protocadherin gamma subfamily B, 7 [Source:HGNC Symbol; |
| 5 | 1558463_s_at | 1.98 | -0.77 | 0.5 | novel transcript |
| 6 | 231737_at | 1.95 | -0.93 | 0.66 | CACNG4calcium voltage-gated channel auxiliary subunit gamma 4 [S |
| 7 | 230809_at | 1.86 | -1.15 | 0.48 | |
| 8 | 221319_at | 1.85 | -0.86 | 0.36 | PCDHB8protocadherin beta 8 [Source:HGNC Symbol;Acc:HGNC:869; |
| 9 | 211020_at | 1.82 | -0.58 | 0.6 | GCNT2 glucosaminyl (N-acetyl) transferase 2 (I blood group) [Source |
| 10 | 1556147_at | 1.82 | -1.21 | 0.56 | novel transcript, antisense to PPM1L |
| 11 | 238784_at | 1.79 | -1.51 | 0.45 | DPY19L2dpy-19 like 2 [Source:HGNC Symbol;Acc:HGNC:19414] |
| 12 | 1569433_at | 1.78 | -0.84 | 0.56 | SAMD5 sterile alpha motif domain containing 5 [Source:HGNC Symb |
| 13 | 220619_at | 1.75 | -0.66 | 0.61 | CHD7 chromodomain helicase DNA binding protein 7 [Source:HGNC |
| 14 | 231789_at | 1.74 | -1.19 | 0.38 | PCDHB19protocadherin beta 15 [Source:HGNC Symbol;Acc:HGNC:86 |
| 15 | 243319_at | 1.73 | -0.64 | 0.63 | |
| 16 | 210359_at | 1.7 | -0.7 | 0.56 | MTSS1 MTSS1, I-BAR domain containing [Source:HGNC Symbol;Ac |
| 17 | 229779_at | 1.68 | -1.32 | 0.5 | COL4A4 collagen type IV alpha 4 chain [Source:HGNC Symbol;Acc:H |
| 18 | 233823_at | 1.68 | -1.15 | 0.4 | FAM184Bfamily with sequence similarity 184 member B [Source:HGNC |
| 19 | 241963_at | 1.66 | -0.57 | 0.52 | ZNF704 zinc finger protein 704 [Source:HGNC Symbol;Acc:HGNC:32 |
| 20 | 242450_at | 1.66 | -0.67 | 0.58 | RGMB repulsive guidance molecule BMP co-receptor b [Source:HG |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 4e-15 | 79 / 1387 | BP regulation of transcription, DNA-templated |
| 2 | 5e-15 | 70 / 1145 | BP regulation of transcription by RNA polymerase II |
| 3 | 3e-14 | 78 / 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 4 | 1e-06 | 29 / 484 | BP cellular response to DNA damage stimulus |
| 5 | 2e-06 | 24 / 366 | BP DNA repair |
| 6 | 2e-06 | 23 / 342 | BP chromatin organization |
| 7 | 4e-06 | 40 / 843 | BP DNA-binding transcription factor activity |
| 8 | 2e-05 | 7 / 40 | BP cytoplasmic microtubule organization |
| 9 | 3e-05 | 45 / 1086 | BP positive regulation of transcription by RNA polymerase II |
| 10 | 5e-05 | 140 / 4740 | BP cytosol |
| 11 | 1e-04 | 11 / 129 | BP rhythmic process |
| 12 | 3e-04 | 28 / 623 | BP protein phosphorylation |
| 13 | 5e-04 | 16 / 279 | BP RNA splicing |
| 14 | 5e-04 | 20 / 400 | BP chromatin binding |
| 15 | 6e-04 | 7 / 66 | BP double-strand break repair |
| 16 | 6e-04 | 14 / 233 | BP heart development |
| 17 | 8e-04 | 7 / 70 | BP transcription elongation from RNA polymerase II promoter |
| 18 | 9e-04 | 167 / 6202 | BP cytoplasm |
| 19 | 1e-03 | 18 / 358 | BP mRNA processing |
| 20 | 1e-03 | 9 / 119 | BP nucleic acid phosphodiester bond hydrolysis |
| 21 | 1e-03 | 19 / 400 | BP protein serine/threonine kinase activity |
| 22 | 2e-03 | 9 / 123 | BP transcription, DNA-templated |
| 23 | 2e-03 | 5 / 41 | BP nucleotide-excision repair |
| 24 | 2e-03 | 4 / 26 | BP response to gamma radiation |
| 25 | 2e-03 | 27 / 684 | BP phosphorylation |
| 26 | 3e-03 | 3 / 13 | BP regulation of mRNA splicing, via spliceosome |
| 27 | 3e-03 | 6 / 64 | BP cellular response to drug |
| 28 | 3e-03 | 20 / 459 | BP viral process |
| 29 | 3e-03 | 6 / 65 | BP roof of mouth development |
| 30 | 3e-03 | 4 / 28 | BP nucleotide-excision repair, preincision complex assembly |
| 31 | 3e-03 | 3 / 14 | BP positive regulation of interleukin-2 production |
| 32 | 3e-03 | 6 / 66 | BP regulation of circadian rhythm |
| 33 | 3e-03 | 5 / 46 | BP negative regulation of cold-induced thermogenesis |
| 34 | 3e-03 | 5 / 47 | BP response to UV |
| 35 | 4e-03 | 3 / 15 | BP gene silencing by miRNA |
| 36 | 4e-03 | 3 / 15 | BP regulation of cellular protein localization |
| 37 | 4e-03 | 4 / 30 | BP chromosome organization |
| 38 | 4e-03 | 4 / 30 | BP negative regulation of mitotic cell cycle |
| 39 | 4e-03 | 6 / 69 | BP transcription-coupled nucleotide-excision repair |
| 40 | 4e-03 | 7 / 93 | BP ciliary basal body-plasma membrane docking |



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 4e-15 | 79 / 1387 | regulation of transcription, DNA-templated |
| 2 | 5e-15 | 70 / 1145 | regulation of transcription by RNA polymerase II |
| 3 | 3e-14 | 78 / 1416 | DNA-binding transcription factor activity, RNA polymerase II-specific |
| 4 | 1e-06 | 29 / 484 | cellular response to DNA damage stimulus |
| 5 | 2e-06 | 24 / 366 | DNA repair |
| 6 | 2e-06 | 23 / 342 | chromatin organization |
| 7 | 4e-06 | 40 / 843 | DNA-binding transcription factor activity |
| 8 | 2e-05 | 7 / 40 | cytoplasmic microtubule organization |
| 9 | 3e-05 | 45 / 1086 | positive regulation of transcription by RNA polymerase II |
| 10 | 5e-05 | 140 / 4740 | cytosol |
| 11 | 1e-04 | 11 / 129 | rhythmic process |
| 12 | 3e-04 | 28 / 623 | protein phosphorylation |
| 13 | 5e-04 | 16 / 279 | RNA splicing |
| 14 | 5e-04 | 20 / 400 | chromatin binding |
| 15 | 6e-04 | 7 / 66 | double-strand break repair |

Group Overexpression Spot

Spot Summary: F

metagenes = 98
genes = 3111

<r> metagenes = 0.73

beta: r2= 6.01 / log p= -Inf

samples with spot = 0 (0 %)

Spot Genelist

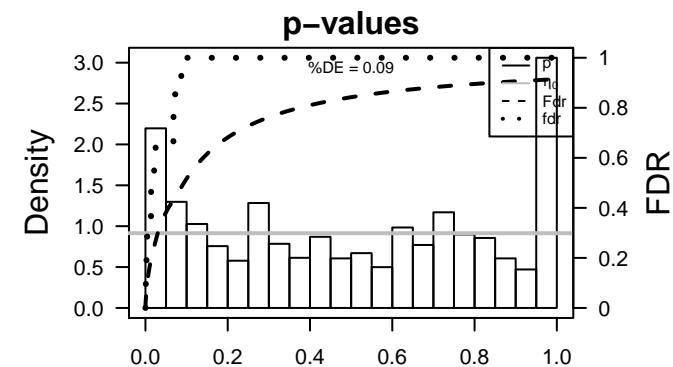
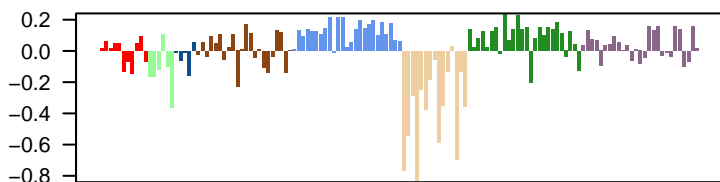
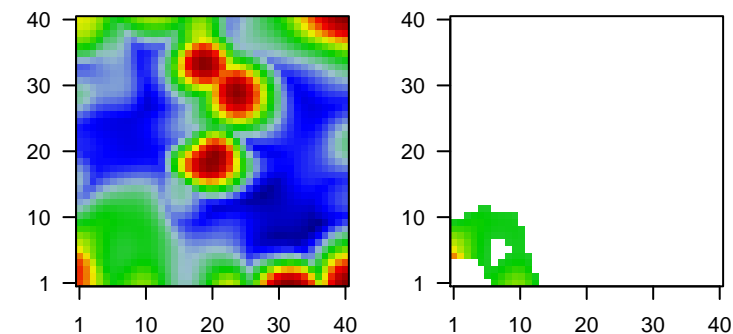
| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|--|
| | | | | | Symbol |
| 1 | 209772_s_at | 2.62 | -1.89 | 0.35 | CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 2 | 220241_at | 2.56 | -0.78 | 0.49 | TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 3 | 214079_at | 2.54 | -1.07 | 0.13 | DHRS2 dehydrogenase/reductase 2 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 4 | 242977_at | 2.4 | -0.78 | 0.27 | novel transcript |
| 5 | 1559712_at | 2.36 | -0.81 | 0.35 | long intergenic non-protein coding RNA 689 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 6 | 244308_at | 2.27 | -0.7 | 0.2 | novel transcript |
| 7 | 1559992_a_at | 2.23 | -1.21 | 0.28 | long intergenic non-protein coding RNA 645 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 8 | 215442_s_at | 2.13 | -0.8 | 0.35 | TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645] |
| 9 | 207978_s_at | 2.12 | -0.97 | 0.32 | NR4A3 nuclear receptor subfamily 4 group A member 3 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 10 | 229870_at | 2.1 | -0.96 | 0.48 | novel transcript, antisense to ZNF143 |
| 11 | 210055_at | 2.09 | -1.37 | 0.37 | TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:1645] |
| 12 | 208650_s_at | 2.09 | -2.09 | 0.24 | CD24 molecule pseudogene 4 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 13 | 220240_s_at | 2.09 | -1.17 | 0.47 | TMCO3 transmembrane and coiled-coil domains 3 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 14 | 1555191_a_at | 2.06 | -0.78 | 0.31 | FHL5 four and a half LIM domains 5 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 15 | 211607_x_at | 2.06 | -1.23 | 0.44 | EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:HGNC:1645] |
| 16 | 244517_x_at | 2.05 | -0.82 | 0.56 | novel transcript |
| 17 | 238717_at | 2 | -1.03 | 0.25 | novel transcript |
| 18 | 210984_x_at | 2 | -1.3 | 0.44 | EGFR epidermal growth factor receptor [Source:HGNC Symbol;Acc:HGNC:1645] |
| 19 | 201551_s_at | 1.99 | -1.97 | 0.22 | LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:1645] |
| 20 | 216379_x_at | 1.99 | -2.67 | 0.16 | CD24 CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645] |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 5e-23 | 656 / 4740 | BP cytosol |
| 2 | 5e-21 | 215 / 1145 | BP regulation of transcription by RNA polymerase II |
| 3 | 7e-21 | 806 / 6202 | BP cytoplasm |
| 4 | 2e-18 | 239 / 1387 | BP regulation of transcription, DNA-templated |
| 5 | 8e-18 | 241 / 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 6 | 1e-12 | 120 / 630 | BP protein transport |
| 7 | 3e-12 | 81 / 366 | BP DNA repair |
| 8 | 1e-11 | 97 / 484 | BP cellular response to DNA damage stimulus |
| 9 | 2e-08 | 70 / 358 | BP mRNA processing |
| 10 | 3e-08 | 45 / 192 | BP methylation |
| 11 | 1e-07 | 104 / 630 | BP cell cycle |
| 12 | 2e-07 | 10 / 15 | BP DNA double-strand break processing |
| 13 | 2e-07 | 73 / 400 | BP chromatin binding |
| 14 | 3e-07 | 40 / 173 | BP cilium assembly |
| 15 | 3e-07 | 129 / 843 | BP DNA-binding transcription factor activity |
| 16 | 2e-06 | 82 / 496 | BP negative regulation of apoptotic process |
| 17 | 4e-06 | 61 / 342 | BP chromatin organization |
| 18 | 7e-06 | 13 / 33 | BP tRNA methylation |
| 19 | 9e-06 | 24 / 93 | BP ciliary basal body-plasma membrane docking |
| 20 | 1e-05 | 34 / 158 | BP DNA replication |
| 21 | 1e-05 | 49 / 264 | BP vesicle-mediated transport |
| 22 | 1e-05 | 12 / 30 | BP chromosome organization |
| 23 | 1e-05 | 150 / 1086 | BP positive regulation of transcription by RNA polymerase II |
| 24 | 2e-05 | 168 / 1242 | BP Golgi apparatus |
| 25 | 2e-05 | 15 / 45 | BP non-motile cilium assembly |
| 26 | 2e-05 | 85 / 545 | BP protein ubiquitination |
| 27 | 3e-05 | 50 / 279 | BP RNA splicing |
| 28 | 3e-05 | 43 / 229 | BP mRNA splicing, via spliceosome |
| 29 | 4e-05 | 29 / 134 | BP cell cycle arrest |
| 30 | 5e-05 | 64 / 394 | BP cell division |
| 31 | 5e-05 | 28 / 129 | BP rhythmic process |
| 32 | 6e-05 | 91 / 613 | BP positive regulation of transcription, DNA-templated |
| 33 | 6e-05 | 72 / 459 | BP viral process |
| 34 | 6e-05 | 28 / 130 | BP regulation of signal transduction by p53 class mediator |
| 35 | 7e-05 | 47 / 267 | BP ubiquitin-protein transferase activity |
| 36 | 8e-05 | 20 / 80 | BP regulation of G2/M transition of mitotic cell cycle |
| 37 | 8e-05 | 11 / 30 | BP intrinsic apoptotic signaling pathway |
| 38 | 1e-04 | 8 / 17 | BP embryonic morphogenesis |
| 39 | 1e-04 | 23 / 101 | BP mRNA transport |
| 40 | 1e-04 | 21 / 89 | BP macroautophagy |

Overview Map

Spot



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 5e-23 | 656 / 4740 | cytosol |
| 2 | 5e-21 | 215 / 1145 | regulation of transcription by RNA polymerase II |
| 3 | 7e-21 | 806 / 6202 | cytoplasm |
| 4 | 2e-18 | 239 / 1387 | regulation of transcription, DNA-templated |
| 5 | 8e-18 | 241 / 1416 | DNA-binding transcription factor activity, RNA polymerase II-specific |
| 6 | 1e-12 | 120 / 630 | protein transport |
| 7 | 3e-12 | 81 / 366 | DNA repair |
| 8 | 1e-11 | 97 / 484 | cellular response to DNA damage stimulus |
| 9 | 2e-08 | 70 / 358 | mRNA processing |
| 10 | 3e-08 | 45 / 192 | methylation |
| 11 | 1e-07 | 104 / 630 | cell cycle |
| 12 | 2e-07 | 10 / 15 | DNA double-strand break processing |
| 13 | 2e-07 | 73 / 400 | chromatin binding |
| 14 | 3e-07 | 40 / 173 | cilium assembly |
| 15 | 3e-07 | 129 / 843 | DNA-binding transcription factor activity |

Group Overexpression Spot

Spot Summary: G

metagenes = 22
genes = 1448

<r> metagenes = 0.94

beta: r2= 10.11 / log p= -Inf

samples with spot = 27 (19.7 %)

group 1 : 3 (27.3 %)

group 2 : 3 (50 %)

group 4 : 9 (40.9 %)

group 6 : 6 (40 %)

group 7 : 6 (23.1 %)

Spot Genelist

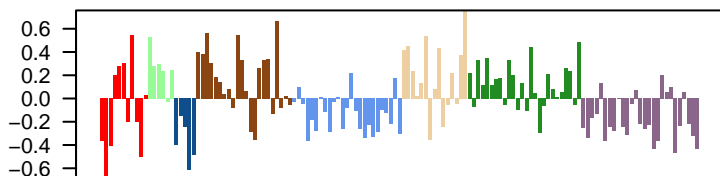
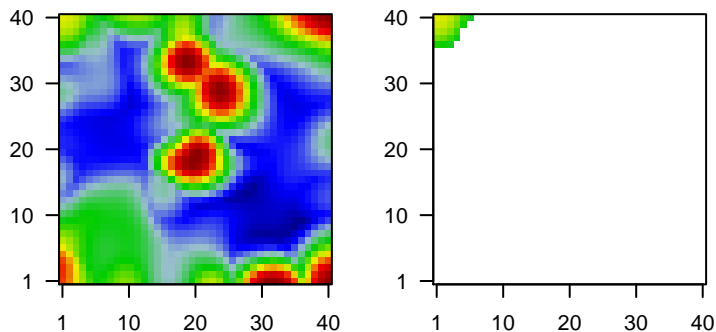
| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|--|
| | | | | | Symbol |
| 1 | 1562440_at | 2.29 | -0.64 | 0.64 | |
| 2 | 1566482_at | 2.19 | -0.81 | 0.55 | novel transcript |
| 3 | 215448_at | 2.16 | -1.33 | 0.48 | |
| 4 | 216007_at | 2.14 | -1.07 | 0.61 | |
| 5 | 1563331_at | 2.1 | -0.74 | 0.57 | |
| 6 | 232453_at | 2.1 | -1.18 | 0.45 | |
| 7 | 240728_at | 2.08 | -0.93 | 0.61 | |
| 8 | 244042_x_at | 2.08 | -1.91 | 0.49 | |
| 9 | 237943_at | 2.04 | -1.36 | 0.79 | TMCC1 transmembrane and coiled-coil domain family 1 [Source:HG] |
| 10 | 234597_at | 2.04 | -0.92 | 0.66 | |
| 11 | 216518_at | 2 | -0.75 | 0.47 | |
| 12 | 1563426_a_a | 1.96 | -0.74 | 0.66 | novel transcript |
| 13 | 233884_at | 1.96 | -0.95 | 0.5 | |
| 14 | 243428_at | 1.95 | -0.98 | 0.57 | KCNQ1 opposite strand/antisense transcript 1 [Source:HGNC] |
| 15 | 1552337_s_at | 1.95 | -0.8 | 0.42 | HOXD4 homeobox D4 [Source:NCBI gene;Acc:3233] |
| 16 | 1562898_at | 1.9 | -0.71 | 0.55 | |
| 17 | 232925_at | 1.9 | -1.69 | 0.66 | |
| 18 | 240158_at | 1.82 | -0.7 | 0.53 | |
| 19 | 234082_at | 1.82 | -1.64 | 0.27 | |
| 20 | 214235_at | 1.82 | -0.93 | 0.48 | CYP3A5 cytochrome P450 family 3 subfamily A member 5 [Source:HG] |

Geneset Overrepresentation

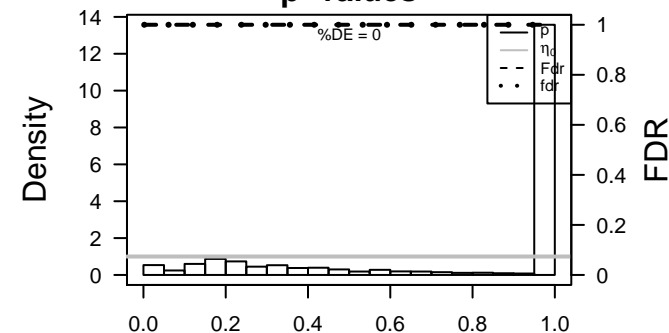
| Rank | p-value | #in/all | Geneset |
|------|---------|-----------|--|
| 1 | 0.002 | 5 / 61 | BP regulation of alternative mRNA splicing, via spliceosome |
| 2 | 0.002 | 3 / 19 | BP erythrocyte development |
| 3 | 0.004 | 12 / 342 | BP chromatin organization |
| 4 | 0.005 | 3 / 25 | BP mitochondrial calcium ion transmembrane transport |
| 5 | 0.005 | 3 / 25 | BP spliceosomal complex assembly |
| 6 | 0.006 | 3 / 26 | BP regulation of rhodopsin mediated signaling pathway |
| 7 | 0.007 | 5 / 83 | BP liver development |
| 8 | 0.007 | 3 / 28 | BP regulation of defense response to virus by virus |
| 9 | 0.007 | 4 / 54 | BP DNA duplex unwinding |
| 10 | 0.008 | 2 / 10 | BP IRES-dependent viral translational initiation |
| 11 | 0.010 | 85 / 4740 | BP cytosol |
| 12 | 0.010 | 4 / 59 | BP regulation of megakaryocyte differentiation |
| 13 | 0.010 | 2 / 11 | BP histone mRNA catabolic process |
| 14 | 0.010 | 2 / 11 | BP Leydig cell differentiation |
| 15 | 0.010 | 2 / 11 | BP positive regulation of extrinsic apoptotic signaling pathway in absence of ligand |
| 16 | 0.010 | 2 / 11 | BP protein quality control for misfolded or incompletely synthesized proteins |
| 17 | 0.010 | 3 / 32 | BP intra-Golgi vesicle-mediated transport |
| 18 | 0.011 | 4 / 61 | BP cell fate commitment |
| 19 | 0.011 | 3 / 33 | BP iron ion homeostasis |
| 20 | 0.012 | 2 / 12 | BP cytoplasmic translational initiation |
| 21 | 0.012 | 2 / 12 | BP formation of cytoplasmic translation initiation complex |
| 22 | 0.012 | 12 / 400 | BP chromatin binding |
| 23 | 0.013 | 7 / 175 | BP regulation of cell population proliferation |
| 24 | 0.014 | 2 / 13 | BP inflammatory response to antigenic stimulus |
| 25 | 0.014 | 2 / 13 | BP negative regulation of necroptotic process |
| 26 | 0.014 | 2 / 13 | BP positive regulation of keratinocyte differentiation |
| 27 | 0.016 | 2 / 14 | BP nuclear migration |
| 28 | 0.017 | 8 / 229 | BP mRNA splicing, via spliceosome |
| 29 | 0.018 | 16 / 630 | BP protein transport |
| 30 | 0.019 | 2 / 15 | BP embryonic hemopoiesis |
| 31 | 0.019 | 2 / 15 | BP gene silencing by miRNA |
| 32 | 0.019 | 2 / 15 | BP miRNA mediated inhibition of translation |
| 33 | 0.019 | 2 / 15 | BP muscle cell differentiation |
| 34 | 0.019 | 2 / 15 | BP negative regulation of androgen receptor signaling pathway |
| 35 | 0.019 | 2 / 15 | BP protein autoprocessing |
| 36 | 0.019 | 3 / 40 | BP regulation of cytokinesis |
| 37 | 0.021 | 2 / 16 | BP histone H4-K5 acetylation |
| 38 | 0.021 | 2 / 16 | BP histone H4-K8 acetylation |
| 39 | 0.021 | 2 / 16 | BP iron ion transport |
| 40 | 0.021 | 2 / 16 | BP sympathetic nervous system development |

Overview Map

Spot



p-values



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|-----------|---|
| 1 | 0.002 | 5 / 61 | regulation of alternative mRNA splicing, via spliceosome |
| 2 | 0.002 | 3 / 19 | erythrocyte development |
| 3 | 0.004 | 12 / 342 | chromatin organization |
| 4 | 0.005 | 3 / 25 | mitochondrial calcium ion transmembrane transport |
| 5 | 0.005 | 3 / 25 | spliceosomal complex assembly |
| 6 | 0.006 | 3 / 26 | regulation of rhodopsin mediated signaling pathway |
| 7 | 0.007 | 5 / 83 | liver development |
| 8 | 0.007 | 3 / 28 | regulation of defense response to virus by virus |
| 9 | 0.007 | 4 / 54 | DNA duplex unwinding |
| 10 | 0.008 | 2 / 10 | IRES-dependent viral translational initiation |
| 11 | 0.010 | 85 / 4740 | cytosol |
| 12 | 0.010 | 4 / 59 | regulation of megakaryocyte differentiation |
| 13 | 0.010 | 2 / 11 | histone mRNA catabolic process |
| 14 | 0.010 | 2 / 11 | Leydig cell differentiation |
| 15 | 0.010 | 2 / 11 | positive regulation of extrinsic apoptotic signaling pathway in absence of ligand |

Group Overexpression Spot

Spot Summary: H

metagenes = 17
genes = 1211

<r> metagenes = 0.85

beta: r2= 5.5 / log p= -Inf

samples with spot = 16 (11.7 %)

- group 1 : 1 (9.1 %)
- group 2 : 1 (16.7 %)
- group 4 : 4 (18.2 %)
- group 6 : 9 (60 %)
- group 7 : 1 (3.8 %)

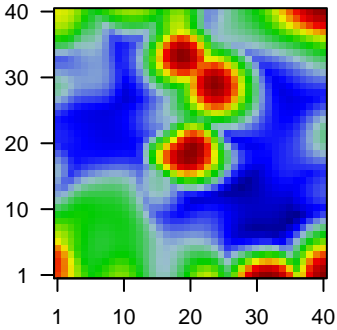
Spot Genelist

| Rank | ID | max e | r | min e | Description |
|------|-------------|-------|-------|-------|---|
| | | | | | Symbol |
| 1 | 204713_s_at | 2.44 | -1.56 | 0.31 | F5 coagulation factor V [Source:HGNC Symbol;Acc:HGNC:3542 |
| 2 | 214265_at | 2.22 | -0.74 | 0.32 | ITGA8 integrin subunit alpha 8 [Source:HGNC Symbol;Acc:HGNC:6 |
| 3 | 235059_at | 2.19 | -0.74 | 0.39 | RAB12 RAB12, member RAS oncogene family [Source:HGNC Symb |
| 4 | 215856_at | 2.13 | -0.6 | 0.59 | SIGLEC1 sialic acid binding Ig like lectin 15 [Source:HGNC Symbol;Acc |
| 5 | 226211_at | 2.09 | -1.04 | 0.42 | maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1 |
| 6 | 242319_at | 2.03 | -0.87 | 0.39 | DGKG diacylglycerol kinase gamma [Source:HGNC Symbol;Acc:HG |
| 7 | 243954_at | 2.03 | -0.77 | 0.49 | long intergenic non-protein coding RNA 877 [Source:HGNC : |
| 8 | 229775_s_at | 2.03 | -0.84 | 0.66 | |
| 9 | 207213_s_at | 1.95 | -1.36 | 0.48 | USP2 ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HG |
| 10 | 226210_s_at | 1.9 | -1.12 | 0.44 | maternally expressed 3 [Source:HGNC Symbol;Acc:HGNC:1 |
| 11 | 200952_s_at | 1.89 | -1.58 | 0.53 | CCND2 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 12 | 229985_at | 1.88 | -1.11 | 0.44 | |
| 13 | 240112_at | 1.88 | -1.05 | 0.67 | |
| 14 | 203479_s_at | 1.87 | -1.31 | 0.79 | OTUD4 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:33 |
| 15 | 238751_at | 1.84 | -1.21 | 0.49 | |
| 16 | 212821_at | 1.83 | -0.73 | 0.65 | PLEKHG3 pleckstrin homology and RhoGEF domain containing G3 [Sou |
| 17 | 200951_s_at | 1.81 | -1.28 | 0.51 | CCND2 cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583] |
| 18 | 1557044_at | 1.77 | -0.6 | 0.5 | long intergenic non-protein coding RNA 665 [Source:HGNC : |
| 19 | 1570035_at | 1.76 | -0.67 | 0.56 | |
| 20 | 1557170_at | 1.75 | -0.55 | 0.64 | NEK8 NIMA related kinase 8 [Source:NCBI gene;Acc:284086] |

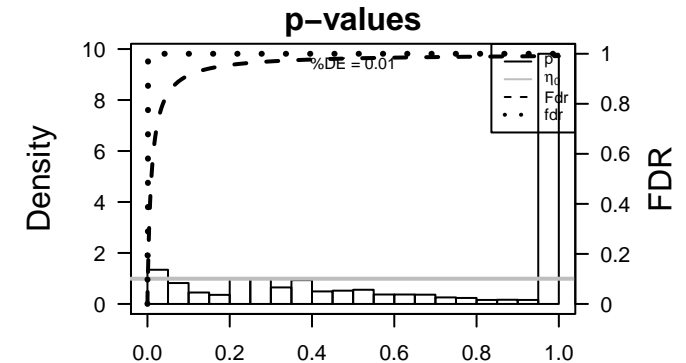
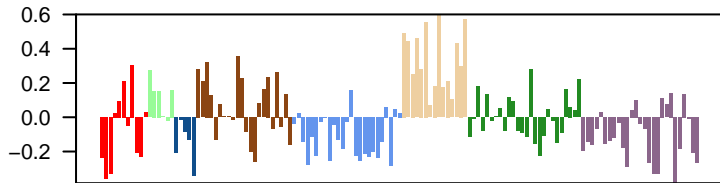
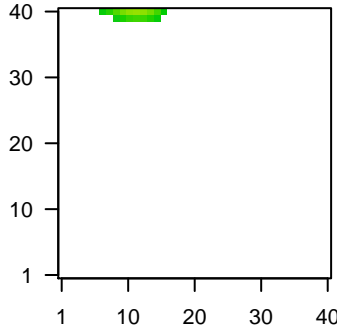
Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 4e-09 | 39 / 541 | BP negative regulation of transcription, DNA-templated |
| 2 | 1e-08 | 60 / 1086 | BP positive regulation of transcription by RNA polymerase II |
| 3 | 4e-07 | 29 / 400 | BP chromatin binding |
| 4 | 3e-06 | 55 / 1145 | BP regulation of transcription by RNA polymerase II |
| 5 | 4e-06 | 36 / 623 | BP protein phosphorylation |
| 6 | 6e-06 | 163 / 4740 | BP cytosol |
| 7 | 8e-06 | 62 / 1387 | BP regulation of transcription, DNA-templated |
| 8 | 9e-06 | 41 / 783 | BP negative regulation of transcription by RNA polymerase II |
| 9 | 1e-05 | 202 / 6202 | BP cytoplasm |
| 10 | 2e-05 | 18 / 227 | BP microtubule binding |
| 11 | 5e-05 | 60 / 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 12 | 6e-05 | 22 / 342 | BP chromatin organization |
| 13 | 6e-05 | 5 / 18 | BP myelination in peripheral nervous system |
| 14 | 9e-05 | 24 / 400 | BP protein serine/threonine kinase activity |
| 15 | 1e-04 | 11 / 112 | BP microtubule cytoskeleton organization |
| 16 | 2e-04 | 6 / 35 | BP metanephros development |
| 17 | 3e-04 | 33 / 684 | BP phosphorylation |
| 18 | 4e-04 | 9 / 90 | BP activation of protein kinase activity |
| 19 | 6e-04 | 4 / 16 | BP cytoskeleton-dependent intracellular transport |
| 20 | 6e-04 | 25 / 484 | BP cellular response to DNA damage stimulus |
| 21 | 7e-04 | 7 / 59 | BP regulation of megakaryocyte differentiation |
| 22 | 7e-04 | 30 / 630 | BP cell cycle |
| 23 | 7e-04 | 4 / 17 | BP alternative mRNA splicing, via spliceosome |
| 24 | 7e-04 | 17 / 279 | BP RNA splicing |
| 25 | 9e-04 | 29 / 613 | BP positive regulation of transcription, DNA-templated |
| 26 | 1e-03 | 25 / 505 | BP nervous system development |
| 27 | 1e-03 | 6 / 47 | BP signal transduction by protein phosphorylation |
| 28 | 1e-03 | 6 / 47 | BP stress-activated protein kinase signaling cascade |
| 29 | 1e-03 | 4 / 20 | BP actin filament-based movement |
| 30 | 1e-03 | 4 / 20 | BP camera-type eye morphogenesis |
| 31 | 2e-03 | 12 / 174 | BP protein autophosphorylation |
| 32 | 2e-03 | 3 / 10 | BP posttranscriptional gene silencing by RNA |
| 33 | 2e-03 | 4 / 21 | BP histone methylation |
| 34 | 2e-03 | 9 / 112 | BP animal organ morphogenesis |
| 35 | 2e-03 | 20 / 394 | BP cell division |
| 36 | 3e-03 | 35 / 843 | BP DNA-binding transcription factor activity |
| 37 | 3e-03 | 3 / 12 | BP generation of neurons |
| 38 | 3e-03 | 3 / 12 | BP histone deubiquitination |
| 39 | 3e-03 | 8 / 97 | BP transforming growth factor beta receptor signaling pathway |
| 40 | 3e-03 | 4 / 25 | BP activation of innate immune response |

Overview Map



Spot



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 4e-09 | 39 / 541 | negative regulation of transcription, DNA-templated |
| 2 | 1e-08 | 60 / 1086 | positive regulation of transcription by RNA polymerase II |
| 3 | 4e-07 | 29 / 400 | chromatin binding |
| 4 | 3e-06 | 55 / 1145 | regulation of transcription by RNA polymerase II |
| 5 | 4e-06 | 36 / 623 | protein phosphorylation |
| 6 | 6e-06 | 163 / 4740 | cytosol |
| 7 | 8e-06 | 62 / 1387 | regulation of transcription, DNA-templated |
| 8 | 9e-06 | 41 / 783 | negative regulation of transcription by RNA polymerase II |
| 9 | 1e-05 | 202 / 6202 | cytoplasm |
| 10 | 2e-05 | 18 / 227 | microtubule binding |
| 11 | 5e-05 | 60 / 1416 | DNA-binding transcription factor activity, RNA polymerase II-specific |
| 12 | 6e-05 | 22 / 342 | chromatin organization |
| 13 | 6e-05 | 5 / 18 | myelination in peripheral nervous system |
| 14 | 9e-05 | 24 / 400 | protein serine/threonine kinase activity |
| 15 | 1e-04 | 11 / 112 | microtubule cytoskeleton organization |

Group Overexpression Spot

Spot Summary: I

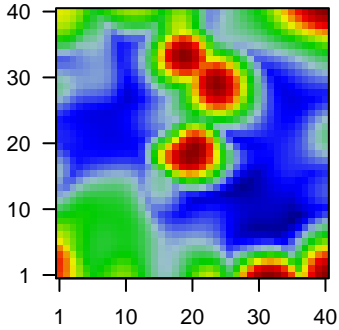
metagenes = 28
genes = 645

<r> metagenes = 0.89
<r> genes = 0.36
beta: r2= 5.52 / log p= -Inf

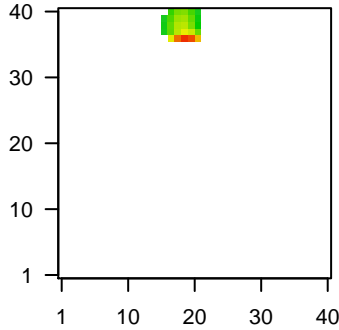
samples with spot = 21 (15.3 %)

group 1 : 5 (45.5 %)
group 2 : 4 (66.7 %)
group 4 : 8 (36.4 %)
group 6 : 4 (26.7 %)

Overview Map



Spot

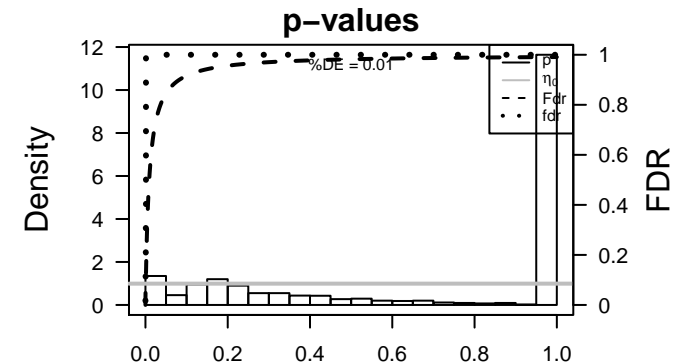
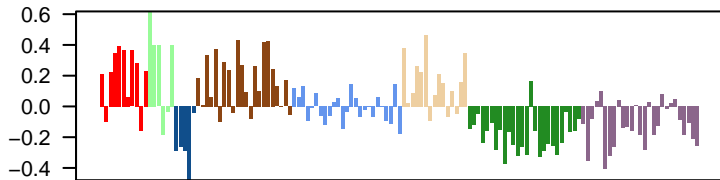


Spot Genelist

| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|---|
| | | | | | Symbol |
| 1 | 218959_at | 2.76 | -0.75 | 0.4 | HOXC10 homeobox C10 [Source:HGNC Symbol;Acc:HGNC:5122] |
| 2 | 243489_at | 2.73 | -0.86 | 0.41 | |
| 3 | 223836_at | 2.68 | -0.59 | 0.33 | FGFBP2 fibroblast growth factor binding protein 2 [Source:HGNC Sym] |
| 4 | 213728_at | 2.45 | -0.95 | 0.39 | LAMP1 lysosomal associated membrane protein 1 [Source:HGNC Sy |
| 5 | 210239_at | 2.44 | -0.59 | 0.46 | IRX5 iroquois homeobox 5 [Source:HGNC Symbol;Acc:HGNC:143] |
| 6 | 238327_at | 2.3 | -0.88 | 0.49 | ODF3B outer dense fiber of sperm tails 3B [Source:HGNC Symbol;Ac |
| 7 | 1569940_at | 2.23 | -0.67 | 0.5 | |
| 8 | 238999_at | 2.19 | -1.16 | 0.76 | |
| 9 | 228642_at | 2.13 | -1.09 | 0.56 | HOXA transcript antisense RNA, myeloid-specific 1 [Source:l |
| 10 | 236846_at | 2.13 | -0.5 | 0.66 | |
| 11 | 1568706_s_at | 2.13 | -0.69 | 0.68 | |
| 12 | 210507_s_at | 2.09 | -0.53 | 0.63 | AVIL advillin [Source:HGNC Symbol;Acc:HGNC:14188] |
| 13 | 207907_at | 2.04 | -0.49 | 0.46 | TNFSF14TNF superfamily member 14 [Source:HGNC Symbol;Acc:HGI |
| 14 | 205539_at | 2.03 | -0.85 | 0.58 | AVIL advillin [Source:HGNC Symbol;Acc:HGNC:14188] |
| 15 | 230601_s_at | 2.02 | -0.63 | 0.52 | LRRC46 leucine rich repeat containing 46 [Source:HGNC Symbol;Acc: |
| 16 | 222325_at | 1.99 | -1.11 | 0.57 | |
| 17 | 202238_s_at | 1.97 | -0.67 | 0.54 | NNMT nicotinamide N-methyltransferase [Source:HGNC Symbol;Ac |
| 18 | 241824_at | 1.89 | -0.86 | 0.35 | novel transcript, sense intronic to FOSL2 |
| 19 | 205569_at | 1.88 | -0.62 | 0.47 | LAMP3 lysosomal associated membrane protein 3 [Source:HGNC Sy |
| 20 | 240052_at | 1.84 | -0.81 | 0.48 | ITPR1 inositol 1,4,5-trisphosphate receptor type 1 [Source:HGNC S |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 3e-08 | 133 / 6202 | BP cytoplasm |
| 2 | 6e-06 | 23 / 564 | BP immune system process |
| 3 | 1e-05 | 12 / 184 | BP defense response to virus |
| 4 | 2e-05 | 40 / 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 5 | 4e-05 | 11 / 172 | BP positive regulation of I-kappaB kinase/NF-kappaB signaling |
| 6 | 7e-05 | 27 / 843 | BP DNA-binding transcription factor activity |
| 7 | 1e-04 | 17 / 417 | BP innate immune response |
| 8 | 1e-04 | 95 / 4740 | BP cytosol |
| 9 | 2e-04 | 31 / 1080 | BP multicellular organism development |
| 10 | 2e-04 | 31 / 1086 | BP positive regulation of transcription by RNA polymerase II |
| 11 | 2e-04 | 11 / 214 | BP cell migration |
| 12 | 3e-04 | 4 / 23 | BP proximal/distal pattern formation |
| 13 | 3e-04 | 3 / 10 | BP membranous septum morphogenesis |
| 14 | 3e-04 | 17 / 459 | BP viral process |
| 15 | 3e-04 | 10 / 185 | BP endocytosis |
| 16 | 3e-04 | 24 / 783 | BP negative regulation of transcription by RNA polymerase II |
| 17 | 4e-04 | 11 / 224 | BP negative regulation of gene expression |
| 18 | 5e-04 | 11 / 231 | BP extracellular matrix organization |
| 19 | 5e-04 | 20 / 613 | BP positive regulation of transcription, DNA-templated |
| 20 | 6e-04 | 4 / 28 | BP positive regulation of erythrocyte differentiation |
| 21 | 7e-04 | 7 / 103 | BP response to bacterium |
| 22 | 7e-04 | 9 / 168 | BP response to hypoxia |
| 23 | 7e-04 | 6 / 75 | BP response to wounding |
| 24 | 8e-04 | 16 / 455 | BP intracellular signal transduction |
| 25 | 8e-04 | 9 / 173 | BP cilium assembly |
| 26 | 9e-04 | 4 / 31 | BP mammary gland development |
| 27 | 1e-03 | 3 / 15 | BP NAD biosynthesis via nicotinamide riboside salvage pathway |
| 28 | 1e-03 | 8 / 148 | BP skeletal system development |
| 29 | 1e-03 | 4 / 34 | BP positive regulation of epithelial cell migration |
| 30 | 1e-03 | 3 / 16 | BP negative regulation of intrinsic apoptotic signaling pathway in response to D |
| 31 | 1e-03 | 3 / 16 | BP positive regulation of vascular associated smooth muscle cell migration |
| 32 | 1e-03 | 4 / 35 | BP positive regulation of substrate adhesion-dependent cell spreading |
| 33 | 1e-03 | 5 / 59 | BP glucose metabolic process |
| 34 | 2e-03 | 3 / 17 | BP regulation of extrinsic apoptotic signaling pathway via death domain recept |
| 35 | 2e-03 | 5 / 62 | BP circadian regulation of gene expression |
| 36 | 2e-03 | 10 / 233 | BP heart development |
| 37 | 2e-03 | 10 / 237 | BP regulation of apoptotic process |
| 38 | 2e-03 | 6 / 95 | BP anterior/posterior pattern specification |
| 39 | 2e-03 | 6 / 95 | BP lung development |
| 40 | 2e-03 | 4 / 40 | BP chondrocyte differentiation |



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 3e-08 | 133 / 6202 | cytoplasm |
| 2 | 6e-06 | 23 / 564 | immune system process |
| 3 | 1e-05 | 12 / 184 | defense response to virus |
| 4 | 2e-05 | 40 / 1416 | DNA-binding transcription factor activity, RNA polymerase II-specific |
| 5 | 4e-05 | 11 / 172 | positive regulation of I-kappaB kinase/NF-kappaB signaling |
| 6 | 7e-05 | 27 / 843 | DNA-binding transcription factor activity |
| 7 | 1e-04 | 17 / 417 | innate immune response |
| 8 | 1e-04 | 95 / 4740 | cytosol |
| 9 | 2e-04 | 31 / 1080 | multicellular organism development |
| 10 | 2e-04 | 31 / 1086 | positive regulation of transcription by RNA polymerase II |
| 11 | 2e-04 | 11 / 214 | cell migration |
| 12 | 3e-04 | 4 / 23 | proximal/distal pattern formation |
| 13 | 3e-04 | 3 / 10 | membranous septum morphogenesis |
| 14 | 3e-04 | 17 / 459 | viral process |
| 15 | 3e-04 | 10 / 185 | endocytosis |

Group Overexpression Spot

Spot Summary: J

metagenes = 52
genes = 1316

<r> metagenes = 0.88

beta: r2= 9.2 / log p= -Inf

samples with spot = 23 (16.8 %)

group 1 : 3 (27.3 %)

group 2 : 3 (50 %)

group 4 : 13 (59.1 %)

group 5 : 1 (4 %)

group 6 : 1 (6.7 %)

group 8 : 2 (7.4 %)

Spot Genelist

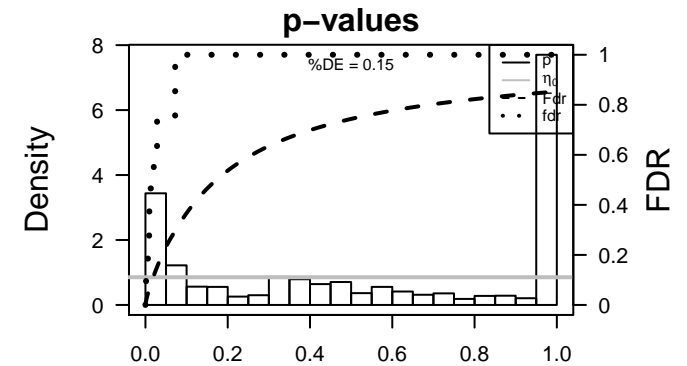
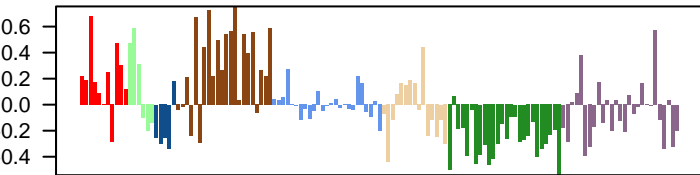
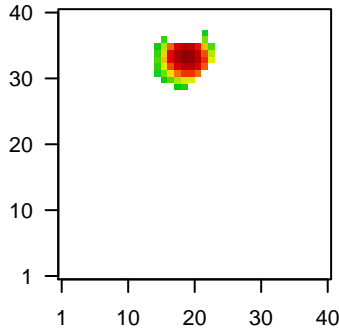
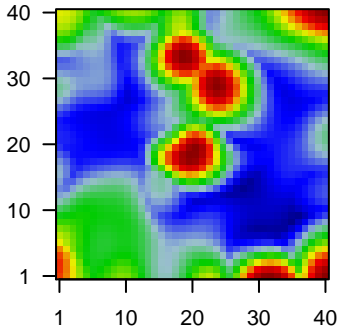
| Rank | ID | max e | r | min e | Description |
|------|-------------|-------|-------|-------|--|
| | | | | | Symbol |
| 1 | 211430_s_at | 3.66 | -1 | 0.56 | immunoglobulin heavy constant gamma 2 (G2m marker) [Sou |
| 2 | 209138_x_at | 3.42 | -0.97 | 0.61 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 3 | 215121_x_at | 3.38 | -1.11 | 0.59 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 4 | 217022_s_at | 3.37 | -0.9 | 0.56 | immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc |
| 5 | 214677_x_at | 3.36 | -1.19 | 0.62 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 6 | 215176_x_at | 3.32 | -0.8 | 0.57 | immunoglobulin kappa variable 1-39 (gene/pseudogene) [So |
| 7 | 204602_at | 3.11 | -0.63 | 0.28 | DKK1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S |
| 8 | 215379_x_at | 3.1 | -1.03 | 0.58 | immunoglobulin lambda constant 2 [Source:HGNC Symbol;A |
| 9 | 202018_s_at | 3.01 | -0.95 | 0.49 | LTF lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720] |
| 10 | 211634_x_at | 2.96 | -0.55 | 0.3 | immunoglobulin heavy variable 1-69 [Source:HGNC Symbol; |
| 11 | 216401_x_at | 2.95 | -0.59 | 0.42 | immunoglobulin kappa variable 1-37 (non-functional) [Sourc |
| 12 | 217148_x_at | 2.94 | -1 | 0.47 | immunoglobulin lambda variable 2-14 [Source:HGNC Symbc |
| 13 | 209560_s_at | 2.92 | -0.57 | 0.31 | DLK1 delta like non-canonical Notch ligand 1 [Source:HGNC Symb |
| 14 | 205207_at | 2.91 | -0.66 | 0.29 | IL6 interleukin 6 [Source:HGNC Symbol;Acc:HGNC:6018] |
| 15 | 216576_x_at | 2.88 | -0.61 | 0.41 | |
| 16 | 217378_x_at | 2.84 | -0.95 | 0.44 | immunoglobulin kappa variable 1/OR2-108 (non-functional) |
| 17 | 216557_x_at | 2.83 | -0.54 | 0.43 | immunoglobulin heavy variable 3-21 [Source:HGNC Symbol; |
| 18 | 214669_x_at | 2.74 | -0.74 | 0.52 | |
| 19 | 224061_at | 2.73 | -0.57 | 0.48 | INMT indolethylamine N-methyltransferase [Source:HGNC Symbol; |
| 20 | 211339_s_at | 2.73 | -0.49 | 0.59 | ITK IL2 inducible T cell kinase [Source:HGNC Symbol;Acc:HGNC |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 1e-99 | 168 / 564 | BP immune system process |
| 2 | 1e-78 | 122 / 388 | BP immune response |
| 3 | 4e-56 | 356 / 4278 | BP plasma membrane |
| 4 | 6e-56 | 104 / 417 | BP innate immune response |
| 5 | 4e-46 | 88 / 364 | BP inflammatory response |
| 6 | 6e-45 | 473 / 7387 | BP membrane |
| 7 | 7e-45 | 60 / 155 | BP regulation of immune response |
| 8 | 1e-42 | 94 / 460 | BP neutrophil degranulation |
| 9 | 1e-32 | 58 / 222 | BP adaptive immune response |
| 10 | 3e-30 | 33 / 64 | BP complement activation, classical pathway |
| 11 | 4e-29 | 46 / 152 | BP leukocyte migration |
| 12 | 8e-29 | 32 / 64 | BP regulation of complement activation |
| 13 | 3e-28 | 27 / 43 | BP antigen processing and presentation |
| 14 | 6e-27 | 59 / 289 | BP cytokine-mediated signaling pathway |
| 15 | 1e-26 | 27 / 47 | BP complement activation |
| 16 | 6e-24 | 27 / 56 | BP B cell receptor signaling pathway |
| 17 | 2e-22 | 16 / 17 | BP antigen processing and presentation of peptide or polysaccharide antigen v |
| 18 | 6e-21 | 30 / 89 | BP Fc-gamma receptor signaling pathway involved in phagocytosis |
| 19 | 2e-20 | 132 / 1500 | BP signal transduction |
| 20 | 1e-19 | 40 / 184 | BP defense response to virus |
| 21 | 1e-17 | 34 / 148 | BP chemotaxis |
| 22 | 4e-17 | 34 / 154 | BP receptor-mediated endocytosis |
| 23 | 9e-17 | 20 / 47 | BP phagocytosis, engulfment |
| 24 | 1e-15 | 21 / 59 | BP positive regulation of T cell proliferation |
| 25 | 6e-15 | 32 / 160 | BP T cell receptor signaling pathway |
| 26 | 8e-15 | 31 / 151 | BP defense response to bacterium |
| 27 | 6e-14 | 25 / 103 | BP response to bacterium |
| 28 | 4e-12 | 37 / 261 | BP cell surface receptor signaling pathway |
| 29 | 1e-11 | 13 / 29 | BP positive regulation of B cell activation |
| 30 | 1e-11 | 27 / 151 | BP cellular response to lipopolysaccharide |
| 31 | 2e-11 | 13 / 30 | BP immunoglobulin production |
| 32 | 2e-11 | 13 / 30 | BP phagocytosis, recognition |
| 33 | 5e-11 | 27 / 159 | BP response to lipopolysaccharide |
| 34 | 9e-11 | 57 / 594 | BP cell adhesion |
| 35 | 2e-10 | 11 / 23 | BP response to interferon-gamma |
| 36 | 2e-10 | 18 / 74 | BP neutrophil chemotaxis |
| 37 | 2e-10 | 12 / 29 | BP cytokine production |
| 38 | 5e-10 | 47 / 459 | BP viral process |
| 39 | 1e-09 | 17 / 72 | BP positive regulation of inflammatory response |
| 40 | 1e-09 | 12 / 33 | BP lipopolysaccharide-mediated signaling pathway |

Overview Map

Spot



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 1e-99 | 168 / 564 | immune system process |
| 2 | 1e-78 | 122 / 388 | immune response |
| 3 | 4e-56 | 356 / 4278 | plasma membrane |
| 4 | 6e-56 | 104 / 417 | innate immune response |
| 5 | 4e-46 | 88 / 364 | inflammatory response |
| 6 | 6e-45 | 473 / 7387 | membrane |
| 7 | 7e-45 | 60 / 155 | regulation of immune response |
| 8 | 1e-42 | 94 / 460 | neutrophil degranulation |
| 9 | 1e-32 | 58 / 222 | adaptive immune response |
| 10 | 3e-30 | 33 / 64 | complement activation, classical pathway |
| 11 | 4e-29 | 46 / 152 | leukocyte migration |
| 12 | 8e-29 | 32 / 64 | regulation of complement activation |
| 13 | 3e-28 | 27 / 43 | antigen processing and presentation |
| 14 | 6e-27 | 59 / 289 | cytokine-mediated signaling pathway |
| 15 | 1e-26 | 27 / 47 | complement activation |

Group Overexpression Spot

Spot Summary: K

metagenes = 78
genes = 1999

<r> metagenes = 0.74

beta: r2= 4.11 / log p= -Inf

samples with spot = 5 (3.6 %)
group 5 : 5 (20 %)

Spot Genelist

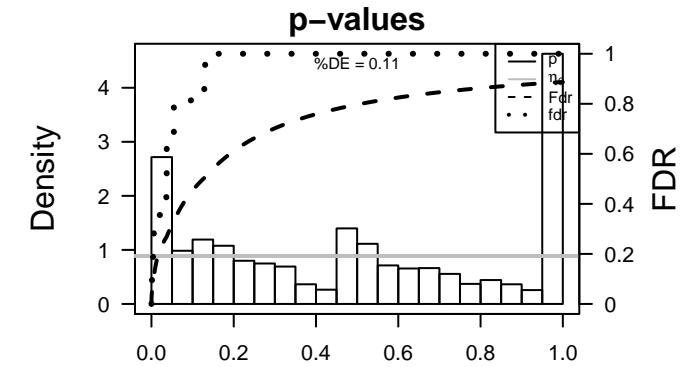
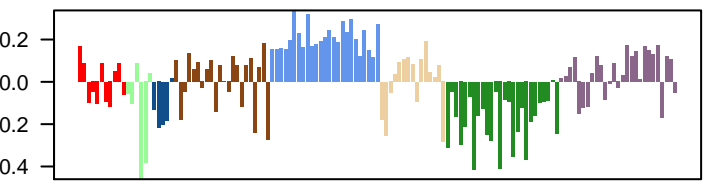
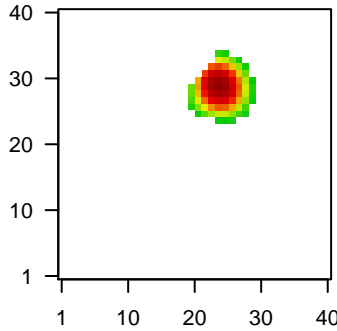
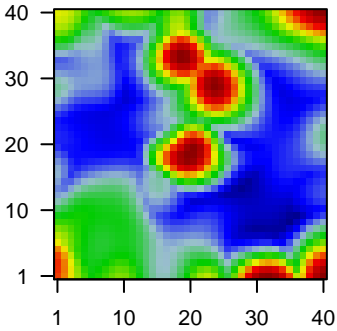
| Rank | ID | max e | r | min e | Description |
|------|-------------|-------|-------|-------|--|
| | | | | | Symbol |
| 1 | 231155_at | 2.98 | -0.75 | 0.37 | DEFB19 defensin beta 119 [Source:HGNC Symbol;Acc:HGNC:18099] |
| 2 | 237898_at | 2.62 | -1.03 | 0.39 | |
| 3 | 234830_at | 2.34 | -0.35 | 0.17 | FSHD region gene 2 family member E, pseudogene [Source:HGNC Symbol;Acc:HGNC:11830] |
| 4 | 213265_at | 2.32 | -0.88 | 0.4 | PGA4 pepsinogen 4, group 1 (pepsinogen A) [Source:HGNC Symbol;Acc:HGNC:10800] |
| 5 | 1557369_a_a | 2.31 | -0.92 | 0.31 | long intergenic non-protein coding RNA 698 [Source:HGNC Symbol;Acc:HGNC:19800] |
| 6 | 207148_x_at | 2.29 | -0.72 | 0.43 | MYOZ2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330] |
| 7 | 213782_s_at | 2.22 | -0.69 | 0.4 | MYOZ2 myozenin 2 [Source:HGNC Symbol;Acc:HGNC:1330] |
| 8 | 228504_at | 2.18 | -1.12 | 0.44 | SCN7A sodium voltage-gated channel alpha subunit 7 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 9 | 215443_at | 2.15 | -0.64 | 0.29 | TSHR thyroid stimulating hormone receptor [Source:HGNC Symbol;Acc:HGNC:10800] |
| 10 | 230661_at | 2.14 | -0.76 | 0.26 | |
| 11 | 220037_s_at | 2.13 | -1.17 | 0.49 | LYVE1 lymphatic vessel endothelial hyaluronan receptor 1 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 12 | 243952_at | 2.08 | -1.62 | 0.63 | TPTE pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:43600] |
| 13 | 228233_at | 2.06 | -1.09 | 0.43 | FREM1 FRAS1 related extracellular matrix 1 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 14 | 231626_at | 2.04 | -0.67 | 0.26 | TPH1 tryptophan hydroxylase 1 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 15 | 235892_at | 2.03 | -0.94 | 0.67 | COLCA1 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 16 | 210683_at | 2.03 | -0.52 | 0.28 | NRTN neuritin [Source:HGNC Symbol;Acc:HGNC:8007] |
| 17 | 214038_at | 2.02 | -0.83 | 0.27 | CCL8 C-C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 18 | 239984_at | 2.02 | -0.7 | 0.33 | SCN7A sodium voltage-gated channel alpha subunit 7 [Source:HGNC Symbol;Acc:HGNC:10800] |
| 19 | 216370_s_at | 2 | -0.84 | 0.51 | TKTL1 transketolase like 1 [Source:HGNC Symbol;Acc:HGNC:11830] |
| 20 | 206406_at | 1.98 | -0.7 | 0.24 | SMCP sperm mitochondria associated cysteine rich protein [Source:HGNC Symbol;Acc:HGNC:10800] |

Geneset Overrepresentation

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|--|
| 1 | 2e-09 | 112 / 1086 | BP positive regulation of transcription by RNA polymerase II |
| 2 | 6e-09 | 361 / 4740 | BP cytosol |
| 3 | 7e-09 | 453 / 6202 | BP cytoplasm |
| 4 | 5e-07 | 67 / 613 | BP positive regulation of transcription, DNA-templated |
| 5 | 7e-07 | 80 / 783 | BP negative regulation of transcription by RNA polymerase II |
| 6 | 5e-06 | 123 / 1416 | BP DNA-binding transcription factor activity, RNA polymerase II-specific |
| 7 | 1e-05 | 11 / 40 | BP regulation of neurogenesis |
| 8 | 1e-05 | 9 / 27 | BP hippo signaling |
| 9 | 2e-05 | 57 / 553 | BP oxidoreductase activity |
| 10 | 3e-05 | 44 / 398 | BP positive regulation of gene expression |
| 11 | 4e-05 | 29 / 222 | BP Wnt signaling pathway |
| 12 | 4e-05 | 13 / 61 | BP cell fate commitment |
| 13 | 5e-05 | 10 / 38 | BP protein kinase B signaling |
| 14 | 6e-05 | 19 / 120 | BP activation of MAPK activity |
| 15 | 8e-05 | 16 / 92 | BP wound healing |
| 16 | 8e-05 | 303 / 4278 | BP plasma membrane |
| 17 | 8e-05 | 8 / 26 | BP chondroitin sulfate biosynthetic process |
| 18 | 1e-04 | 63 / 671 | BP oxidation-reduction process |
| 19 | 1e-04 | 21 / 148 | BP positive regulation of NF-kappaB transcription factor activity |
| 20 | 2e-04 | 92 / 1080 | BP multicellular organism development |
| 21 | 2e-04 | 75 / 843 | BP DNA-binding transcription factor activity |
| 22 | 2e-04 | 15 / 89 | BP regulation of cell migration |
| 23 | 2e-04 | 8 / 29 | BP pituitary gland development |
| 24 | 2e-04 | 28 / 231 | BP extracellular matrix organization |
| 25 | 2e-04 | 12 / 62 | BP negative regulation of epithelial cell proliferation |
| 26 | 2e-04 | 10 / 45 | BP positive regulation of cell division |
| 27 | 2e-04 | 22 / 165 | BP positive regulation of protein phosphorylation |
| 28 | 3e-04 | 56 / 594 | BP cell adhesion |
| 29 | 3e-04 | 72 / 815 | BP protein homodimerization activity |
| 30 | 3e-04 | 28 / 237 | BP regulation of apoptotic process |
| 31 | 3e-04 | 10 / 47 | BP response to ischemia |
| 32 | 4e-04 | 21 / 159 | BP actin cytoskeleton organization |
| 33 | 5e-04 | 11 / 59 | BP retinoid metabolic process |
| 34 | 6e-04 | 7 / 26 | BP focal adhesion assembly |
| 35 | 6e-04 | 110 / 1387 | BP regulation of transcription, DNA-templated |
| 36 | 6e-04 | 41 / 412 | BP negative regulation of cell population proliferation |
| 37 | 6e-04 | 100 / 1242 | BP Golgi apparatus |
| 38 | 6e-04 | 8 / 34 | BP lamellipodium assembly |
| 39 | 6e-04 | 11 / 60 | BP vasculogenesis |
| 40 | 6e-04 | 21 / 165 | BP negative regulation of canonical Wnt signaling pathway |

Overview Map

Spot



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|------------|---|
| 1 | 2e-09 | 112 / 1086 | positive regulation of transcription by RNA polymerase II |
| 2 | 6e-09 | 361 / 4740 | cytosol |
| 3 | 7e-09 | 453 / 6202 | cytoplasm |
| 4 | 5e-07 | 67 / 613 | positive regulation of transcription, DNA-templated |
| 5 | 7e-07 | 80 / 783 | negative regulation of transcription by RNA polymerase II |
| 6 | 5e-06 | 123 / 1416 | DNA-binding transcription factor activity, RNA polymerase II-specific |
| 7 | 1e-05 | 11 / 40 | regulation of neurogenesis |
| 8 | 1e-05 | 9 / 27 | hippo signaling |
| 9 | 2e-05 | 57 / 553 | oxidoreductase activity |
| 10 | 3e-05 | 44 / 398 | positive regulation of gene expression |
| 11 | 4e-05 | 29 / 222 | Wnt signaling pathway |
| 12 | 4e-05 | 13 / 61 | cell fate commitment |
| 13 | 5e-05 | 10 / 38 | protein kinase B signaling |
| 14 | 6e-05 | 19 / 120 | activation of MAPK activity |
| 15 | 8e-05 | 16 / 92 | wound healing |

Group Overexpression Spot

Spot Summary: L

metagenes = 53
genes = 3454

<r> metagenes = 0.92

beta: r2= 2.89 / log p= -Inf

samples with spot = 10 (7.3 %)
group 6 : 10 (66.7 %)

Spot Genelist

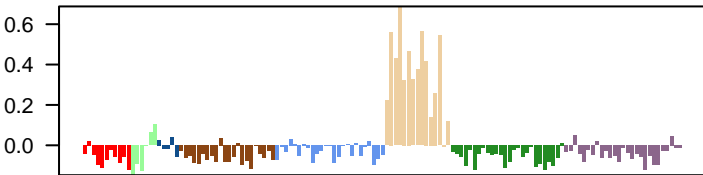
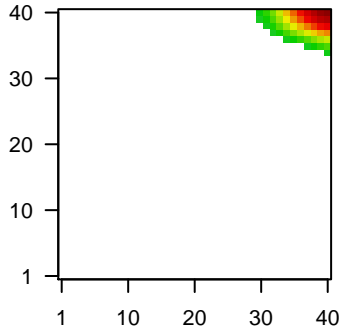
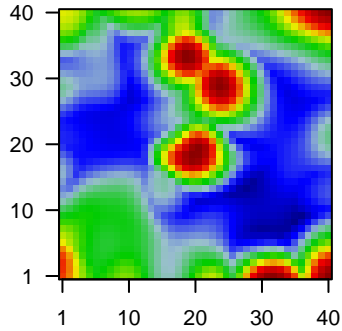
| Rank | ID | max e | r | min e | Description |
|------|--------------|-------|-------|-------|---|
| | | | | | Symbol |
| 1 | 1554648_a_at | 2.54 | -0.69 | 0.42 | DUOXA1 dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:HGNC:155464] |
| 2 | 214146_s_at | 2.49 | -0.81 | 0.26 | PPBP pro-platelet basic protein [Source:HGNC Symbol;Acc:HGNC:214146] |
| 3 | 1556711_at | 2.41 | -0.31 | 0.39 | FAM216B family with sequence similarity 216 member B [Source:HGNC Symbol;Acc:HGNC:155671] |
| 4 | 204419_x_at | 2.36 | -0.98 | 0.41 | HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:204419] |
| 5 | 231597_x_at | 2.31 | -0.71 | 0.43 | |
| 6 | 204848_x_at | 2.27 | -1.14 | 0.4 | HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:204848] |
| 7 | 207337_at | 2.19 | -0.54 | 0.38 | CTAG2 cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:207337] |
| 8 | 1559702_at | 2.16 | -0.61 | 0.47 | ZKSCAN2 divergent transcript [Source:HGNC Symbol;Acc:HGNC:155970] |
| 9 | 207739_s_at | 2.11 | -0.46 | 0.64 | GAGE2EG antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778] |
| 10 | 216648_s_at | 2.1 | -0.61 | 0.86 | |
| 11 | 221298_s_at | 2.08 | -0.57 | 0.46 | SLC22A8 absolute carrier family 22 member 8 [Source:HGNC Symbol;Acc:HGNC:221298] |
| 12 | 242135_at | 2.01 | -0.42 | 0.2 | |
| 13 | 219597_s_at | 2.01 | -0.65 | 0.26 | DUOX1 dual oxidase 1 [Source:HGNC Symbol;Acc:HGNC:3062] |
| 14 | 206359_at | 1.99 | -0.65 | 0.3 | SOCS3 suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:HGNC:206359] |
| 15 | 219914_at | 1.98 | -0.7 | 0.14 | ECEL1 endothelin converting enzyme like 1 [Source:HGNC Symbol;Acc:HGNC:219914] |
| 16 | 224997_x_at | 1.98 | -0.6 | 0.49 | H19, imprinted maternally expressed transcript [Source:HGNC Symbol;Acc:HGNC:224997] |
| 17 | 202222_s_at | 1.89 | -0.39 | 0.53 | DES desmin [Source:HGNC Symbol;Acc:HGNC:2770] |
| 18 | 1554420_at | 1.87 | -0.68 | 0.58 | ATF3 activating transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:155442] |
| 19 | 213515_x_at | 1.86 | -0.93 | 0.5 | HBG2 hemoglobin subunit gamma 2 [Source:HGNC Symbol;Acc:HGNC:213515] |
| 20 | 231078_at | 1.82 | -0.69 | 0.7 | SLC25A37 absolute carrier family 25 member 37 [Source:HGNC Symbol;Acc:HGNC:231078] |

Geneset Overrepresentation

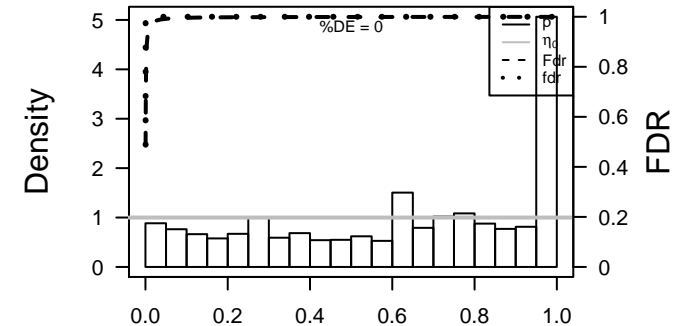
| Rank | p-value | #in/all | Geneset |
|------|---------|----------|--|
| 1 | 4e-04 | 11 / 38 | BP bicarbonate transport |
| 2 | 4e-04 | 12 / 44 | BP cell communication |
| 3 | 4e-04 | 7 / 17 | BP outer dynein arm assembly |
| 4 | 5e-04 | 25 / 138 | BP serine-type endopeptidase activity |
| 5 | 9e-04 | 27 / 159 | BP positive regulation of protein kinase B signaling |
| 6 | 1e-03 | 23 / 130 | BP serine-type peptidase activity |
| 7 | 1e-03 | 10 / 37 | BP peptide cross-linking |
| 8 | 1e-03 | 9 / 31 | BP mammary gland development |
| 9 | 1e-03 | 21 / 115 | BP keratinization |
| 10 | 1e-03 | 13 / 57 | BP odontogenesis of dentin-containing tooth |
| 11 | 2e-03 | 20 / 109 | BP glucose homeostasis |
| 12 | 2e-03 | 5 / 11 | BP epithelial cell development |
| 13 | 2e-03 | 6 / 16 | BP regulation of regulatory T cell differentiation |
| 14 | 2e-03 | 8 / 28 | BP pancreas development |
| 15 | 3e-03 | 5 / 12 | BP myotube differentiation |
| 16 | 3e-03 | 24 / 147 | BP positive regulation of cytosolic calcium ion concentration |
| 17 | 3e-03 | 7 / 23 | BP glucose transmembrane transport |
| 18 | 3e-03 | 14 / 70 | BP response to glucose |
| 19 | 4e-03 | 9 / 36 | BP photoreceptor cell maintenance |
| 20 | 4e-03 | 6 / 18 | BP positive regulation of actin cytoskeleton reorganization |
| 21 | 6e-03 | 10 / 45 | BP positive regulation of insulin secretion |
| 22 | 6e-03 | 5 / 14 | BP negative regulation of cell-cell adhesion |
| 23 | 6e-03 | 97 / 843 | BP DNA-binding transcription factor activity |
| 24 | 7e-03 | 8 / 33 | BP biomineral tissue development |
| 25 | 8e-03 | 5 / 15 | BP androgen metabolic process |
| 26 | 8e-03 | 5 / 15 | BP prostate gland development |
| 27 | 8e-03 | 7 / 27 | BP peripheral nervous system development |
| 28 | 9e-03 | 4 / 10 | BP carnitine shuttle |
| 29 | 1e-02 | 16 / 95 | BP anterior/posterior pattern specification |
| 30 | 1e-02 | 7 / 28 | BP neuronal action potential |
| 31 | 1e-02 | 5 / 16 | BP positive regulation of calcineurin-NFAT signaling cascade |
| 32 | 1e-02 | 5 / 16 | BP sympathetic nervous system development |
| 33 | 1e-02 | 12 / 65 | BP chemokine-mediated signaling pathway |
| 34 | 1e-02 | 7 / 29 | BP beta-catenin-TCF complex assembly |
| 35 | 1e-02 | 4 / 11 | BP enamel mineralization |
| 36 | 1e-02 | 4 / 11 | BP hormone biosynthetic process |
| 37 | 1e-02 | 4 / 11 | BP response to denervation involved in regulation of muscle adaptation |
| 38 | 1e-02 | 13 / 74 | BP neutrophil chemotaxis |
| 39 | 1e-02 | 6 / 23 | BP proximal/distal pattern formation |
| 40 | 1e-02 | 61 / 513 | BP positive regulation of cell population proliferation |

Overview Map

Spot



p-values



BP

| Rank | p-value | #in/all | Geneset |
|------|---------|----------|---|
| 1 | 4e-04 | 11 / 38 | bicarbonate transport |
| 2 | 4e-04 | 12 / 44 | cell communication |
| 3 | 4e-04 | 7 / 17 | outer dynein arm assembly |
| 4 | 5e-04 | 25 / 138 | serine-type endopeptidase activity |
| 5 | 9e-04 | 27 / 159 | positive regulation of protein kinase B signaling |
| 6 | 1e-03 | 23 / 130 | serine-type peptidase activity |
| 7 | 1e-03 | 10 / 37 | peptide cross-linking |
| 8 | 1e-03 | 9 / 31 | mammary gland development |
| 9 | 1e-03 | 21 / 115 | keratinization |
| 10 | 1e-03 | 13 / 57 | odontogenesis of dentin-containing tooth |
| 11 | 2e-03 | 20 / 109 | glucose homeostasis |
| 12 | 2e-03 | 5 / 11 | epithelial cell development |
| 13 | 2e-03 | 6 / 16 | regulation of regulatory T cell differentiation |
| 14 | 2e-03 | 8 / 28 | pancreas development |
| 15 | 3e-03 | 5 / 12 | myotube differentiation |