

# other\_normHNPC

## Global Summary

%DE = 0.09  
 # genes with fdr < 0.2 = 918 ( 5 + / 913 - )  
 # genes with fdr < 0.1 = 627 ( 1 + / 626 - )  
 # genes with fdr < 0.05 = 415 ( 0 + / 415 - )  
 # genes with fdr < 0.01 = 265 ( 0 + / 265 - )  
  
 # genes in genesets = 18990  
  
 <FC> = 0  
 <t-score> = -2  
 <p-value> = 0.21  
 <fdr> = 0.91

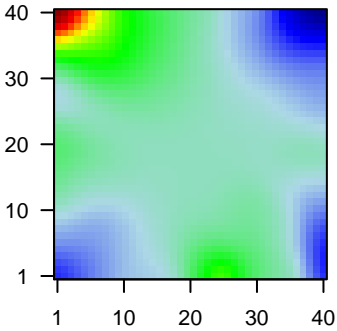
## Global Genelist

| Rank | ID         | log(FC) | fdr p-value | Description Metagene  |
|------|------------|---------|-------------|---|
| 1    | ENSG000002 | 0       | 3e-13 2e-08 | 22 x 13 chromosome 9 open reading frame 135 [Source:HGNC Synt           |
| 2    | ENSG000002 | 0       | 1e-12 9e-08 | 24 x 24   |
| 3    | ENSG000001 | 0       | 1e-11 9e-08 | 24 x 17 actin-like 7A [Source:HGNC Symbol;Acc:HGNC:161]                 |
| 4    | ENSG000001 | 0       | 2e-11 9e-08 | 26 x 26 fibrinogen-like 1 [Source:HGNC Symbol;Acc:HGNC:3695]            |
| 5    | ENSG000001 | 0       | 2e-11 9e-08 | 26 x 26 killer cell lectin-like receptor subfamily G, member 2 [Source: |
| 6    | ENSG000001 | 0       | 2e-11 9e-08 | 26 x 28 basic helix-loop-helix family, member a15 [Source:HGNC Sy       |
| 7    | ENSG000002 | -0.01   | 3e-11 9e-08 | 34 x 23   |
| 8    | ENSG000002 | -0.01   | 3e-11 2e-07 | 12 x 9  |
| 9    | ENSG000001 | -0.01   | 4e-11 3e-07 | 34 x 24   |
| 10   | ENSG000002 | 0       | 6e-11 3e-07 | 27 x 20   |
| 11   | ENSG000002 | -0.01   | 8e-11 3e-07 | 35 x 30   |
| 12   | ENSG000000 | -0.01   | 9e-11 3e-07 | 27 x 26 integrin-binding sialoprotein [Source:HGNC Symbol;Acc:HG        |
| 13   | ENSG000002 | 0       | 1e-10 8e-07 | 23 x 24 interferon, alpha 13 [Source:HGNC Symbol;Acc:HGNC:5419]         |
| 14   | ENSG000002 | 0       | 2e-10 1e-06 | 28 x 21 taste receptor, type 2, member 38 [Source:HGNC Symbol;Ac        |
| 15   | ENSG000001 | 0       | 2e-10 1e-06 | 23 x 23 interferon, alpha 1 [Source:HGNC Symbol;Acc:HGNC:5417]          |
| 16   | ENSG000001 | 0       | 3e-10 3e-06 | 24 x 24 dendrocyte expressed seven transmembrane protein [Source        |
| 17   | ENSG000001 | -0.04   | 7e-10 3e-06 | 30 x 40 transcobalamin I (vitamin B12 binding protein, R binder family  |
| 18   | ENSG000002 | 0       | 7e-10 3e-06 | 24 x 24   |
| 19   | ENSG000001 | -0.01   | 8e-10 3e-06 | 26 x 40 small proline-rich protein 2D [Source:HGNC Symbol;Acc:HG        |
| 20   | ENSG000001 | 0       | 1e-09 3e-06 | 27 x 24 interleukin 17A [Source:HGNC Symbol;Acc:HGNC:5981]              |

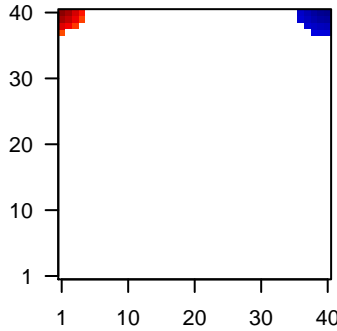
## Global Geneset Analysis

| Rank                  | GSZ    | p-value | #all  | Geneset  |
|-----------------------|--------|---------|-------|--|
| <i>Overexpressed</i>  |        |         |       |  |
| 1                     | 7.81   | 0.001   | 10239 | Brain Overlap_fetal_midbrain_ReprPC                                    |
| 2                     | 7.72   | 0.001   | 10475 | Colon CaRecteA_Colon   |
| 3                     | 7.57   | 0.001   | 9923  | Brain Overlap_fetal_midbrain_K9K27me3                                  |
| 4                     | 7.28   | 0.002   | 9470  | Colon CaRecte3_Colon   |
| 5                     | 7.21   | 0.002   | 9930  | Colon CaRecte_Colon  |
| 6                     | 6.95   | 0.002   | 9390  | Colon CaRecteWk_Colon  |
| 7                     | 6.8    | 0.002   | 11968 | Colon CaRecteWk_Colon  |
| 8                     | 6.55   | 0.002   | 10800 | Brain Overlap_fetal_midbrain_Quies                                     |
| 9                     | 6.26   | 0.002   | 10278 | Brain Overlap_fetal_midbrain_ReprPCWk                                  |
| 10                    | 6.11   | 0.002   | 11791 | Colon CaRecte_Colon  |
| 11                    | 6.04   | 0.002   | 6320  | Brain Overlap_fetal_midbrain_HetRpts                                   |
| 12                    | 5.98   | 0.002   | 8358  | LymphomaOPP_Active_promoter  |
| 13                    | 5.32   | 0.003   | 8123  | Colon CaRecteF_Colon   |
| 14                    | 5.19   | 0.003   | 8147  | LymphomaOPP_Weak_promoter  |
| 15                    | 4.91   | 0.003   | 7491  | LymphomaOPP_Txn_elongation   |
| 16                    | 4.79   | 0.003   | 7592  | LymphomaOPP_Strong_enhancer  |
| 17                    | 4.54   | 0.004   | 5889  | Colon CaRecteWk1_Colon   |
| 18                    | 4.52   | 0.004   | 6761  | Colon CaRecteD2_Colon  |
| 19                    | 4.4    | 0.004   | 10693 | MF protein binding   |
| 20                    | 4.19   | 0.004   | 7202  | TF ICGC_Runx3_targets  |
| <i>Underexpressed</i> |        |         |       |  |
| 1                     | -13.96 | 4e-04   | 13    | MF type I interferon receptor binding                                  |
| 2                     | -13.43 | 4e-04   | 14    | BP natural killer cell activation involved in immune response          |
| 3                     | -13.04 | 5e-04   | 15    | BP positive regulation of peptidyl-serine phosphorylation of STAT prot |
| 4                     | -12.38 | 5e-04   | 22    | MF cytokine receptor binding   |
| 5                     | -11.79 | 6e-04   | 18    | BP T cell activation involved in immune response                       |
| 6                     | -9.87  | 8e-04   | 26    | BP B cell proliferation  |
| 7                     | -9.81  | 8e-04   | 10    | BP mitochondrial calcium ion transport                                 |
| 8                     | -9.77  | 8e-04   | 24    | BP regulation of type I interferon-mediated signaling pathway          |
| 9                     | -9.61  | 9e-04   | 13    | BP negative regulation of myotube differentiation                      |
| 10                    | -8.94  | 1e-03   | 7     | GSEA C2RUNNE_GENDER_EFFECT_UP  |
| 11                    | -8.87  | 1e-03   | 31    | BP response to exogenous dsRNA   |
| 12                    | -8.53  | 1e-03   | 33    | GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE                                 |
| 13                    | -8.5   | 1e-03   | 29    | GSEA C2KEGG_REGULATION_OF_AUTOPHAGY                                    |
| 14                    | -8.44  | 1e-03   | 19    | CC male germ cell nucleus  |
| 15                    | -8.31  | 1e-03   | 111   | Glio Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN                      |
| 16                    | -7.49  | 1e-03   | 22    | CC cornified envelope  |
| 17                    | -7.4   | 1e-03   | 64    | GSEA C2KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY                      |
| 18                    | -7.2   | 2e-03   | 19    | GSEA C2BIOCARTA_CYTOKINE_PATHWAY                                       |
| 19                    | -7.07  | 2e-03   | 745   | Chr Chr 9  |
| 20                    | -6.94  | 2e-03   | 21    | GSEA C2WENG_POR_DOSAGE   |

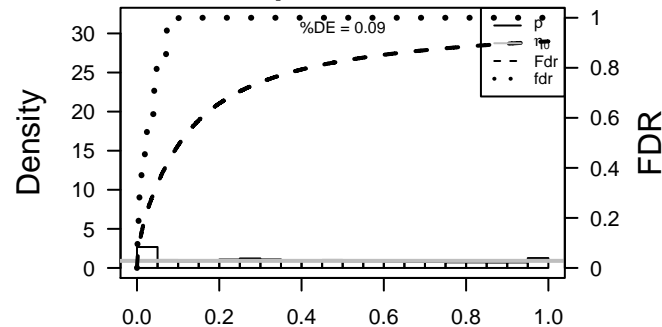
Profile



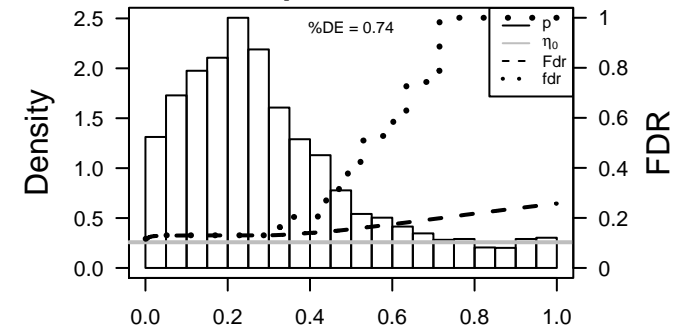
Regulated Spots



p-values



p-values



# other\_normHNPC

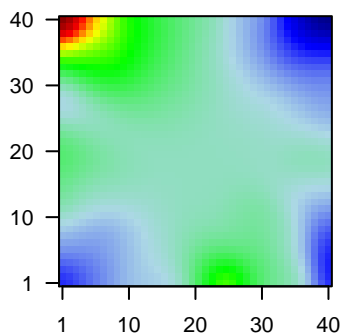
## Local Summary

%DE = 0.97  
 # metagenes = 12  
 # genes = 256  
 # genes in genesets = 254  
  
 # genes with fdr < 0.1 = 250 ( 250 + / 0 - )  
 # genes with fdr < 0.05 = 239 ( 239 + / 0 - )  
 # genes with fdr < 0.01 = 0 ( 0 + / 0 - )

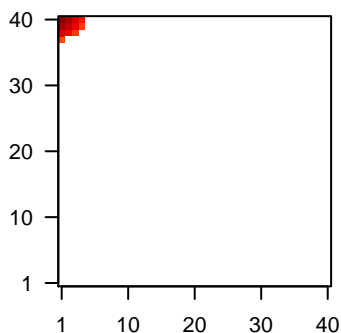
<r> metagenes = 1  
 <r> genes = 0.87

<FC> = 0.27  
 <t-score> = 1.33  
 <p-value> = 0.26  
 <fdr> = 1

Profile



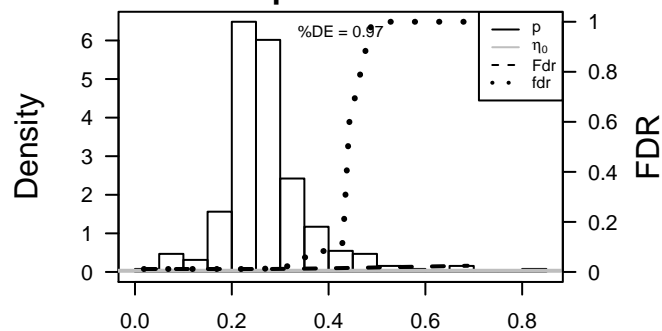
Spot



## Local Genelist

| Rank | ID          | log(FC) | p-value | fdr  | Description   |
|------|-------------|---------|---------|------|---|
| 1    | ENSG0000001 | 0.26    | 0.02    | 0.01 | 3 x 38 Shwachman-Bodian-Diamond syndrome [Source:HGNC Symb            |
| 2    | ENSG0000001 | 0.46    | 0.06    | 0.01 | 2 x 40 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC        |
| 3    | ENSG0000001 | 0.37    | 0.07    | 0.01 | 1 x 39 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC      |
| 4    | ENSG0000001 | 0.5     | 0.07    | 0.01 | 1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc     |
| 5    | ENSG0000000 | 0.18    | 0.07    | 0.01 | 1 x 37 phosphatidic acid phosphatase type 2A [Source:HGNC Symb        |
| 6    | ENSG0000000 | 0.3     | 0.08    | 0.01 | 3 x 40 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68            |
| 7    | ENSG0000001 | 0.24    | 0.10    | 0.01 | 3 x 40 related RAS viral (r-ras) oncogene homolog [Source:HGNC S      |
| 8    | ENSG0000001 | 0.29    | 0.11    | 0.01 | 1 x 40 receptor (G protein-coupled) activity modifying protein 1 [Sou |
| 9    | ENSG0000001 | 0.24    | 0.12    | 0.01 | 3 x 40 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:       |
| 10   | ENSG0000001 | 0.22    | 0.14    | 0.01 | 3 x 40 necdin, melanoma antigen (MAGE) family member [Source:H        |
| 11   | ENSG0000001 | 0.27    | 0.15    | 0.01 | 1 x 40 stomatin [Source:HGNC Symbol;Acc:HGNC:3383]                    |
| 12   | ENSG0000001 | 0.83    | 0.15    | 0.01 | 1 x 40 desmin [Source:HGNC Symbol;Acc:HGNC:2770]                      |
| 13   | ENSG0000001 | 0.25    | 0.16    | 0.01 | 3 x 40 chemokine (C-C motif) ligand 11 [Source:HGNC Symbol;Acc        |
| 14   | ENSG0000001 | 0.25    | 0.16    | 0.01 | 1 x 38 brain expressed, X-linked 4 [Source:HGNC Symbol;Acc:HGNC       |
| 15   | ENSG0000001 | 0.21    | 0.16    | 0.01 | 2 x 40 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [Sc   |
| 16   | ENSG0000001 | 0.28    | 0.16    | 0.01 | 3 x 40 inhibitor of DNA binding 2, dominant negative helix-loop-heli  |
| 17   | ENSG0000001 | 0.24    | 0.17    | 0.01 | 2 x 39 gelsolin [Source:HGNC Symbol;Acc:HGNC:4620]                    |
| 18   | ENSG0000001 | 0.35    | 0.17    | 0.01 | 1 x 40 microfibrillar-associated protein 4 [Source:HGNC Symbol;Ac     |
| 19   | ENSG0000001 | 0.33    | 0.17    | 0.01 | 1 x 40 A kinase (PRKA) anchor protein 12 [Source:HGNC Symbol;A        |
| 20   | ENSG0000001 | 0.41    | 0.18    | 0.01 | 1 x 40 F-box protein 32 [Source:HGNC Symbol;Acc:HGNC:16731]           |

p-values



# other\_normHNPPC

## Local Summary

%DE = 0.92  
 # metagenes = 17  
 # genes = 345  
 # genes in genesets = 340  
  
 # genes with  $fdr < 0.1$  = 296 ( 0 + / 296 -)  
 # genes with  $fdr < 0.05$  = 274 ( 0 + / 274 -)  
 # genes with  $fdr < 0.01$  = 161 ( 0 + / 161 -)

<r> metagenes = 0.99

<r> genes = 0.79

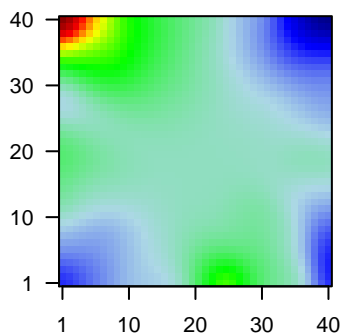
<FC> = -0.14

<t-score> = -4.53

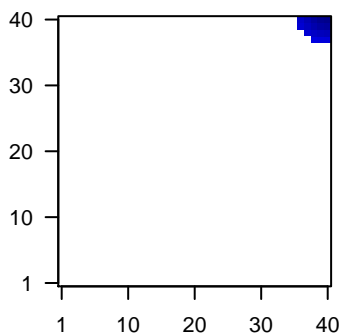
<p-value> = 0.02

<fdr> = 0.61

Profile



Spot



## Local Genelist

| Rank | ID         | log(FC) | p-value | fdr   | Description   |
|------|------------|---------|---------|-------|---|
| 1    | ENSG000000 | -0.05   | 5e-07   | 1e-05 | 37 x 40 claudin 18 [Source:HGNC Symbol;Acc:HGNC:2039]   |
| 2    | ENSG000001 | -0.15   | 9e-07   | 7e-05 | 40 x 37 ets variant 4 [Source:HGNC Symbol;Acc:HGNC:3493]  |
| 3    | ENSG000001 | -0.12   | 8e-06   | 7e-05 | 40 x 37 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:2032]     |
| 4    | ENSG000001 | -0.1    | 9e-06   | 7e-05 | 37 x 38 lamin B2 [Source:HGNC Symbol;Acc:HGNC:6638]   |
| 5    | ENSG000001 | -0.07   | 1e-05   | 7e-05 | 37 x 38 claudin 1 [Source:HGNC Symbol;Acc:HGNC:2032]  |
| 6    | ENSG000001 | -0.11   | 1e-05   | 7e-05 | 38 x 38 translocase of outer mitochondrial membrane 22 homolog (yeast)                          |
| 7    | ENSG000001 | -0.18   | 2e-05   | 7e-05 | 40 x 40 EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]                                      |
| 8    | ENSG000001 | -0.12   | 2e-05   | 2e-04 | 39 x 40 mitochondrial ribosomal protein S2 [Source:HGNC Symbol;Acc:HGNC:2032]                   |
| 9    | ENSG000001 | -0.08   | 2e-05   | 2e-04 | 37 x 38 proprotein convertase subtilisin/kexin type 9 [Source:HGNC Symbol;Acc:HGNC:2032]        |
| 10   | ENSG000001 | -0.18   | 3e-05   | 3e-04 | 39 x 40 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC:2032]                           |
| 11   | ENSG000001 | -0.15   | 4e-05   | 3e-04 | 40 x 40 EPH receptor B3 [Source:HGNC Symbol;Acc:HGNC:3394]                                      |
| 12   | ENSG000001 | -0.09   | 5e-05   | 1e-03 | 40 x 40 carbonic anhydrase IX [Source:HGNC Symbol;Acc:HGNC:13000]                               |
| 13   | ENSG000001 | -0.08   | 1e-04   | 1e-03 | 37 x 40 small nuclear ribonucleoprotein D1 polypeptide 16kDa [Source:HGNC Symbol;Acc:HGNC:2032] |
| 14   | ENSG000001 | -0.1    | 2e-04   | 1e-03 | 39 x 38 family with sequence similarity 57, member A [Source:HGNC Symbol;Acc:HGNC:2032]         |
| 15   | ENSG000001 | -0.1    | 2e-04   | 1e-03 | 36 x 40 dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Acc:HGNC:2032]                   |
| 16   | ENSG000001 | -0.11   | 3e-04   | 1e-03 | 38 x 40 tensin 4 [Source:HGNC Symbol;Acc:HGNC:24352]  |
| 17   | ENSG000001 | -0.13   | 3e-04   | 1e-03 | 37 x 40 phosphoribosylaminoimidazole carboxylase, phosphoribosyltransferase                     |
| 18   | ENSG000001 | -0.21   | 4e-04   | 1e-03 | 40 x 39 insulin-like growth factor binding protein 2, 36kDa [Source:HGNC Symbol;Acc:HGNC:2032]  |
| 19   | ENSG000001 | -0.14   | 4e-04   | 1e-03 | 36 x 40 EDAR-associated death domain [Source:HGNC Symbol;Acc:HGNC:2032]                         |
| 20   | ENSG000001 | -0.17   | 5e-04   | 1e-03 | 39 x 40 ectodermal-neural cortex 1 (with BTB domain) [Source:HGNC Symbol;Acc:HGNC:2032]         |

p-values

