

other_normHNPC vs

Global Summary

%DE = 0.09
 # genes with $fdr < 0.2 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.1 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.05 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.01 = 0$ (0 + / 0 -)

 # genes in genesets = 18990

 $\langle FC \rangle = 0$
 $\langle t\text{-score} \rangle = 0.17$
 $\langle p\text{-value} \rangle = 0.4$
 $\langle fdr \rangle = 0.91$

Global Genelist

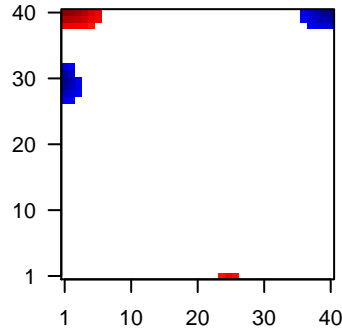
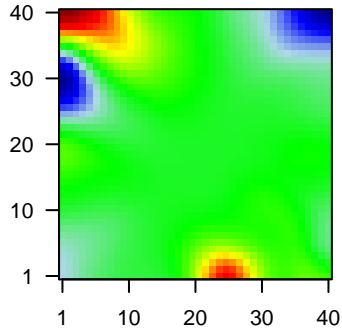
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG0000001	-0.03	7e-05	0.6 30 x 40 fibroblast growth factor receptor-like 1 [Source:HGNC Symbc
2	ENSG0000001	0	7e-05	0.9 23 x 18 von Willebrand factor C domain containing protein 2-like [Sou
3	ENSG0000002	0	2e-04	0.9 22 x 19 PRAME family member 19 [Source:HGNC Symbol;Acc:HGNC
4	ENSG0000000	0	2e-04	0.9 22 x 19 paired box 7 [Source:HGNC Symbol;Acc:HGNC:8621]
5	ENSG0000000	-0.03	3e-04	0.9 29 x 35 guanine nucleotide binding protein (G protein), alpha 15 (Gq)
6	ENSG0000001	0	9e-04	0.9 26 x 23 distal-less homeobox 4 [Source:HGNC Symbol;Acc:HGNC:2
7	ENSG0000001	0	9e-04	0.9 26 x 29 gasdermin A [Source:HGNC Symbol;Acc:HGNC:13311]
8	ENSG0000001	-0.02	9e-04	0.9 35 x 30 pleckstrin homology domain containing, family G (with RhoGe
9	ENSG0000001	-0.02	1e-03	0.9 31 x 31
10	ENSG0000001	-0.13	1e-03	0.9 1 x 5 store-operated calcium entry-associated regulatory factor [S
11	ENSG0000001	0	2e-03	0.9 23 x 18 S-antigen; retina and pineal gland (arrestin) [Source:HGNC S
12	ENSG0000001	0.01	2e-03	0.9 14 x 15 transcription elongation factor A (SII) N-terminal and central r
13	ENSG0000002	0	2e-03	0.9 21 x 20
14	ENSG0000001	0	2e-03	0.9 22 x 21 chromosome 1 open reading frame 87 [Source:HGNC Symbc
15	ENSG0000001	0	2e-03	0.9 21 x 19 transmembrane protein 247 [Source:HGNC Symbol;Acc:HGNC
16	ENSG0000001	0	2e-03	0.9 20 x 17 tripartite motif containing 43 [Source:HGNC Symbol;Acc:HGNC
17	ENSG0000000	0	2e-03	0.9 17 x 14 interleukin 12 receptor, beta 2 [Source:HGNC Symbol;Acc:HGNC
18	ENSG0000002	0	2e-03	0.9 26 x 25
19	ENSG0000002	0	2e-03	0.9 17 x 16
20	ENSG0000002	0	2e-03	0.9 25 x 20

Global Geneset Analysis

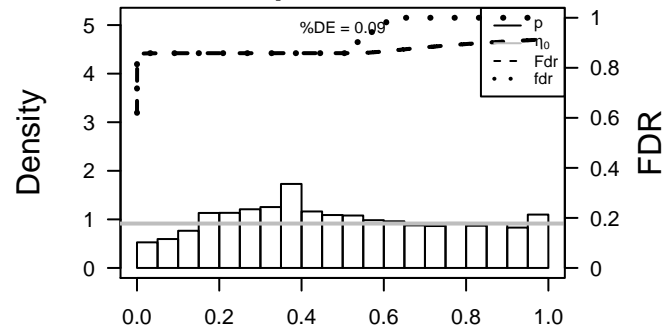
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.57	3e-05	3457	Lymphoma_Heterochrom
2	13.43	4e-05	1753	Colon_Cancer
3	13.09	4e-05	476	Tissue_WIRTH_Nervous System
4	12.35	6e-05	4879	Colon_Cancer1_Colon
5	11.66	7e-05	1281	Colon_Cancerpts_Colon
6	11.28	8e-05	1279	Brain_Overlap_fetal_midbrain_Enh
7	10.55	1e-04	1084	Brain_Overlap_fetal_midbrain_EnhG
8	10.37	1e-04	2658	Lymphoma_Heterochrom
9	10.04	2e-04	525	Colon_Cancer2_Colon
10	9.82	2e-04	712	Brain_Overlap_fetal_midbrain_EnhP
11	8.32	4e-04	2947	Colon_CancerPCWk_Colon
12	7.87	4e-04	1178	Colon_Cancer_Colon
13	7.73	5e-04	5039	Lymphoma_Heterochrom
14	7.59	5e-04	10278	Brain_Overlap_fetal_midbrain_ReprPCWk
15	7.56	5e-04	29	MF_retinoic acid receptor binding
16	7.55	5e-04	3406	Colon_CancerPC_Colon
17	7.24	6e-04	147	Glio_WILLSCHER_GBM_Verhaak-PN (mut&wt)_up_(MES&CL down)
18	7.15	7e-04	419	BP_synaptic transmission
19	7.11	7e-04	329	GSEA_C2REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
20	6.96	8e-04	106	Glio_WIRTH_Normal Brain
<i>Underexpressed</i>				
1	-19.27	3e-06	1298	GSEA_C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
2	-19.1	3e-06	713	Colon_Cancertrack_CRC_TCGA_group.over_C_normal_DN
3	-17.34	1e-05	550	Cancer_Lembcke_Normal vs Adenoma
4	-16.81	2e-05	859	GSEA_C2LEE_BMP2_TARGETS_DN
5	-16.18	2e-05	582	GSEA_C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	-16.11	2e-05	8123	Colon_CancerF_Colon
7	-15.56	2e-05	830	Colon_Cancertrack_CRC_TCGA_corr_R_normal_DN
8	-15.41	3e-05	944	GSEA_C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
9	-15.02	3e-05	10475	Colon_CancerA_Colon
10	-15.02	3e-05	5643	Lymphoma_Heterochrom
11	-14.92	3e-05	400	GSEA_C2VECCHI_GASTRIC_CANCER_EARLY_UP
12	-14.89	3e-05	1563	GSEA_C2PUJANA_BRCA1_PCC_NETWORK
13	-14.68	3e-05	813	GSEA_C2GRADE_COLON_CANCER_UP
14	-14.47	3e-05	775	GSEA_C2VEL_MYCN_TARGETS_WITH_E_BOX
15	-14.4	3e-05	9930	Colon_CancerB_Colon
16	-14.35	3e-05	850	GSEA_C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
17	-13.9	4e-05	747	GSEA_C2PUJANA_CHEK2_PCC_NETWORK
18	-13.83	4e-05	807	Lymphoma_Heterochrom
19	-13.82	4e-05	638	GSEA_C2MILL_PSEUDOPODIA_HAPTOTAXIS_DN
20	-13.77	4e-05	546	GSEA_C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP

Profile

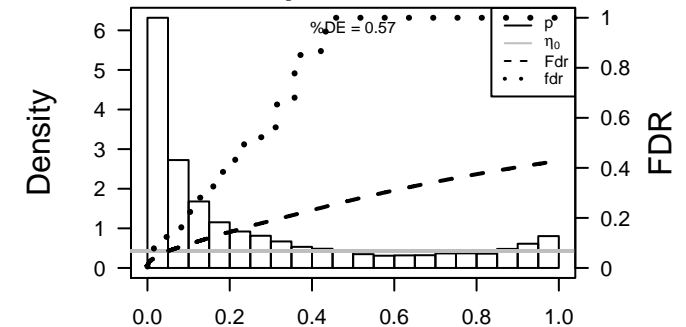
Regulated Spots



p-values



p-values



other_normHNPC vs

Local Summary

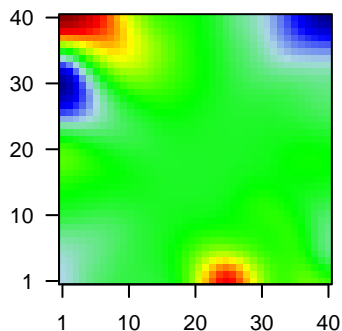
%DE = 0.95
 # metagenes = 3
 # genes = 119
 # genes in genesets = 118

 # genes with fdr < 0.1 = 116 (115 + / 1 -)
 # genes with fdr < 0.05 = 108 (107 + / 1 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)

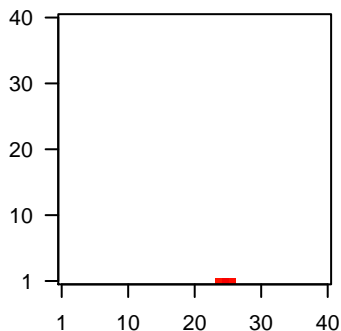
<r> metagenes = 1
 <r> genes = 0.7

 <FC> = 0.14
 <t-score> = 0.89
 <p-value> = 0.41
 <fdr> = 0.88

Profile



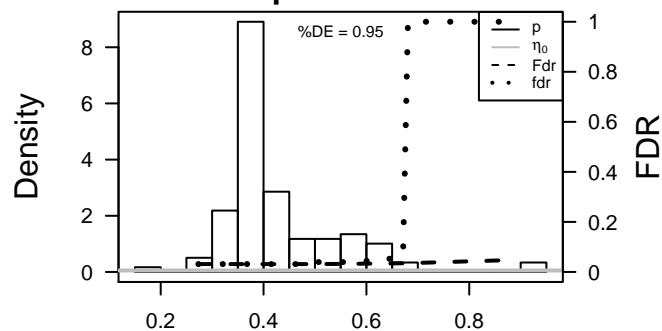
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000000	0.24	0.2	0.03	24 x 1 ornithine aminotransferase [Source:HGNC Symbol;Acc:HGNC:10000]
2	ENSG00000001	0.13	0.3	0.03	24 x 1 secreted frizzled-related protein 5 [Source:HGNC Symbol;Acc:HGNC:10001]
3	ENSG00000001	0.1	0.3	0.03	26 x 1 peptidase D [Source:HGNC Symbol;Acc:HGNC:8840]
4	ENSG00000001	0.13	0.3	0.03	25 x 1 acireductone dioxygenase 1 [Source:HGNC Symbol;Acc:HGNC:10002]
5	ENSG00000001	0.18	0.3	0.03	25 x 1 transmembrane 4 L six family member 4 [Source:HGNC Symbol;Acc:HGNC:10003]
6	ENSG00000001	0.44	0.3	0.03	25 x 1 retinol binding protein 2, cellular [Source:HGNC Symbol;Acc:HGNC:10004]
7	ENSG00000001	0.14	0.3	0.03	25 x 1 dipeptidyl-peptidase 4 [Source:HGNC Symbol;Acc:HGNC:30000]
8	ENSG00000001	0.12	0.3	0.03	24 x 1 NOP9 nucleolar protein [Source:HGNC Symbol;Acc:HGNC:10005]
9	ENSG00000001	0.17	0.3	0.03	25 x 1 ketohexokinase (fructokinase) [Source:HGNC Symbol;Acc:HGNC:10006]
10	ENSG00000001	0.1	0.3	0.03	26 x 1 phospholipase A2, group XIIB [Source:HGNC Symbol;Acc:HGNC:10007]
11	ENSG00000002	0.18	0.3	0.03	26 x 1 UDP glucuronosyltransferase 1 family, polypeptide A1 [Source:HGNC Symbol;Acc:HGNC:10008]
12	ENSG00000000	0.18	0.3	0.03	25 x 1 solute carrier family 15 (oligopeptide transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10009]
13	ENSG00000001	0.22	0.3	0.03	26 x 1 zinc finger protein 511 [Source:HGNC Symbol;Acc:HGNC:28000]
14	ENSG00000002	0.12	0.3	0.03	26 x 1 transmembrane 6 superfamily member 2 [Source:HGNC Symbol;Acc:HGNC:10010]
15	ENSG00000001	0.11	0.3	0.03	25 x 1 beta-carotene oxygenase 1 [Source:HGNC Symbol;Acc:HGNC:10011]
16	ENSG00000001	0.16	0.3	0.03	25 x 1 apolipoprotein B mRNA editing enzyme, catalytic polypeptide [Source:HGNC Symbol;Acc:HGNC:10012]
17	ENSG00000000	0.24	0.3	0.03	25 x 1 cAMP responsive element binding protein 3-like 3 [Source:HGNC Symbol;Acc:HGNC:10013]
18	ENSG00000001	0.11	0.4	0.03	24 x 1 nuclear receptor subfamily 0, group B, member 2 [Source:HGNC Symbol;Acc:HGNC:10014]
19	ENSG00000000	0.12	0.4	0.03	24 x 1 NPC1-like 1 [Source:HGNC Symbol;Acc:HGNC:7898]
20	ENSG00000001	0.22	0.4	0.03	25 x 1 carbonyl reductase 1 [Source:HGNC Symbol;Acc:HGNC:15400]

p-values



other_normHNPC vs

Local Summary

%DE = 0.4
 # metagenes = 17
 # genes = 354
 # genes in genesets = 349

 # genes with $fdr < 0.1 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.05 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.01 = 0$ (0 + / 0 -)

<r> metagenes = 0.99

<r> genes = 0.91

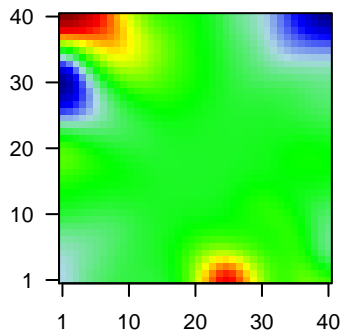
<FC> = 0.13

<t-score> = 0.81

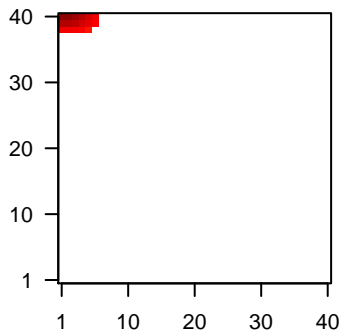
<p-value> = 0.42

<fdr> = 0.9

Profile



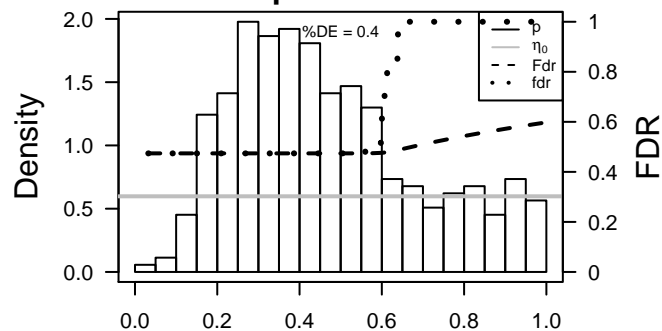
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.55	0.03	0.5	2 x 40 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
2	ENSG0000001	0.2	0.09	0.5	5 x 39 calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC S]
3	ENSG0000001	0.23	0.09	0.5	5 x 40 RASD family, member 2 [Source:HGNC Symbol;Acc:HGNC:1
4	ENSG0000001	0.15	0.12	0.5	6 x 39 CDC42 effector protein (Rho GTPase binding) 4 [Source:HG]
5	ENSG0000001	0.19	0.12	0.5	5 x 40 calcium/calmodulin-dependent protein kinase II gamma [Sou
6	ENSG0000001	0.27	0.12	0.5	4 x 40 EPH receptor A7 [Source:HGNC Symbol;Acc:HGNC:3390]
7	ENSG0000001	0.19	0.13	0.5	5 x 40 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:HGNC::
8	ENSG0000001	0.24	0.13	0.5	4 x 40 MAM domain containing 2 [Source:HGNC Symbol;Acc:HGNC
9	ENSG0000001	0.24	0.14	0.5	4 x 40 gremlin 2, DAN family BMP antagonist [Source:HGNC Symbc
10	ENSG0000001	0.16	0.15	0.5	6 x 40 Rho guanine nucleotide exchange factor (GEF) 26 [Source:H
11	ENSG0000001	0.31	0.15	0.5	2 x 40 forkhead box F2 [Source:HGNC Symbol;Acc:HGNC:3810]
12	ENSG0000001	0.23	0.15	0.5	3 x 40 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC::
13	ENSG0000000	0.17	0.16	0.5	6 x 40 glycoprotein M6B [Source:HGNC Symbol;Acc:HGNC:4461]
14	ENSG0000001	0.2	0.16	0.5	6 x 40 neuronal pentraxin I [Source:HGNC Symbol;Acc:HGNC:7952]
15	ENSG0000001	0.2	0.16	0.5	5 x 40 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086]
16	ENSG0000001	0.14	0.16	0.5	3 x 38 Shwachman-Bodian-Diamond syndrome [Source:HGNC Syr
17	ENSG0000001	0.26	0.16	0.5	1 x 39 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HG]
18	ENSG0000001	0.15	0.16	0.5	6 x 40 cadherin-like and PC-esterase domain containing 1 [Source:
19	ENSG0000001	0.19	0.17	0.5	5 x 40 sodium channel, voltage gated, type VII alpha subunit [Sourc
20	ENSG0000001	0.23	0.17	0.5	4 x 40 proline rich membrane anchor 1 [Source:HGNC Symbol;Acc:!

p-values



other_normHNPC vs

Local Summary

%DE = 0.92
 # metagenes = 15
 # genes = 238
 # genes in genesets = 237

 # genes with $fdr < 0.1$ = 207 (1 + / 206 -)
 # genes with $fdr < 0.05$ = 204 (1 + / 203 -)
 # genes with $fdr < 0.01$ = 0 (0 + / 0 -)

<r> metagenes = 0.99

<r> genes = 0.72

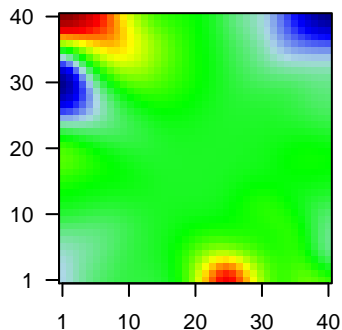
<FC> = -0.14

<t-score> = -1.09

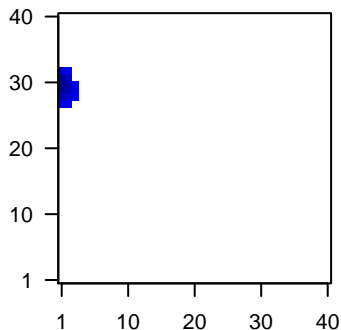
<p-value> = 0.34

<fdr> = 0.87

Profile



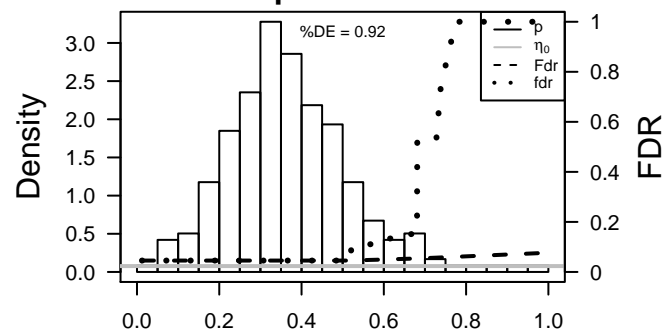
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.23	0.01	0.05	2 x 28 sulfatase 2 [Source:HGNC Symbol;Acc:HGNC:20392]
2	ENSG0000000	-0.31	0.06	0.05	1 x 29 vacuole membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:20392]
3	ENSG0000001	-0.26	0.06	0.05	1 x 31 jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6203]
4	ENSG0000001	-0.43	0.09	0.05	1 x 31 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:20392]
5	ENSG0000002	-0.26	0.09	0.05	1 x 30 nicotinamide phosphoribosyltransferase pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:20392]
6	ENSG0000001	-0.3	0.10	0.05	1 x 29 plasmalemma vesicle associated protein [Source:HGNC Symbol;Acc:HGNC:20392]
7	ENSG0000001	-0.28	0.11	0.05	1 x 31 superoxide dismutase 3, extracellular [Source:HGNC Symbol;Acc:HGNC:20392]
8	ENSG0000001	-0.21	0.13	0.05	1 x 30 nicotinamide phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:20392]
9	ENSG0000001	-0.5	0.13	0.05	1 x 30 biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
10	ENSG0000001	-0.12	0.14	0.05	3 x 29 protein S (alpha) [Source:HGNC Symbol;Acc:HGNC:9456]
11	ENSG0000001	-0.39	0.15	0.05	1 x 31 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:HGNC:20392]
12	ENSG0000001	-0.41	0.15	0.05	1 x 31 metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
13	ENSG0000001	-0.18	0.15	0.05	1 x 31 coagulation factor XIII, A1 polypeptide [Source:HGNC Symbol;Acc:HGNC:20392]
14	ENSG0000001	-0.23	0.15	0.05	1 x 31 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:HGNC:20392]
15	ENSG0000001	-0.14	0.16	0.05	2 x 32 lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
16	ENSG0000001	-0.37	0.17	0.05	1 x 31 nicotinamide N-methyltransferase [Source:HGNC Symbol;Acc:HGNC:20392]
17	ENSG0000000	-0.17	0.18	0.05	1 x 28 FK506 binding protein 1A, 12kDa [Source:HGNC Symbol;Acc:HGNC:20392]
18	ENSG0000001	-0.14	0.18	0.05	3 x 29 complement factor D (adipsin) [Source:HGNC Symbol;Acc:HGNC:20392]
19	ENSG0000001	-0.33	0.18	0.05	1 x 31 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:HGNC:20392]
20	ENSG0000000	-0.2	0.19	0.05	1 x 30 LIM and cysteine-rich domains 1 [Source:HGNC Symbol;Acc:HGNC:20392]

p-values



other_normHNPC vs

Local Summary

%DE = 0.77
 # metagenes = 14
 # genes = 294
 # genes in genesets = 289

 # genes with fdr < 0.1 = 0 (0 + / 0 -)
 # genes with fdr < 0.05 = 0 (0 + / 0 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)

<r> metagenes = 0.99

<r> genes = 0.85

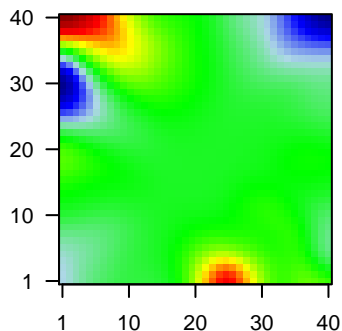
<FC> = -0.12

<t-score> = -1.35

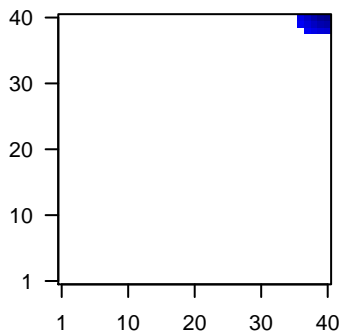
<p-value> = 0.22

<fdr> = 0.88

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.14	0.004	0.1	36 x 40 guanine nucleotide binding protein-like 3 (nucleolar) [Source:
2	ENSG0000000	-0.16	0.007	0.1	40 x 39 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc:
3	ENSG0000001	-0.2	0.016	0.1	39 x 40 transmembrane emp24 protein transport domain containing 9
4	ENSG0000001	-0.15	0.019	0.1	40 x 40 CDC42 effector protein (Rho GTPase binding) 1 [Source:HGNC
5	ENSG0000000	-0.13	0.019	0.1	36 x 39 methylenetetrahydrofolate dehydrogenase (NADP+ depende
6	ENSG0000000	-0.2	0.021	0.1	37 x 40 Sec61 alpha 1 subunit (S. cerevisiae) [Source:HGNC Symbol
7	ENSG0000001	-0.13	0.024	0.1	37 x 40 oligosaccharyltransferase complex subunit (non-catalytic) [S
8	ENSG0000001	-0.11	0.027	0.1	37 x 40 interleukin enhancer binding factor 2 [Source:HGNC Symbol;
9	ENSG0000000	-0.24	0.028	0.1	40 x 40 NME/NME2 nucleoside diphosphate kinase 2 [Source:HGNC
10	ENSG0000001	-0.16	0.028	0.1	40 x 40 eukaryotic translation initiation factor 4E binding protein 1 [So
11	ENSG0000001	-0.49	0.028	0.1	37 x 40 TIMP metalloproteinase inhibitor 1 [Source:HGNC Symbol;Acc:
12	ENSG0000001	-0.21	0.030	0.1	40 x 40 solute carrier family 1 (neutral amino acid transporter), memb
13	ENSG0000001	-0.18	0.030	0.1	40 x 38 solute carrier family 39 (zinc transporter), member 7 [Source:
14	ENSG0000002	-0.18	0.030	0.1	40 x 40 NME1-NME2 readthrough [Source:HGNC Symbol;Acc:HGNC
15	ENSG0000001	-0.82	0.035	0.1	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source
16	ENSG0000001	-0.29	0.036	0.1	40 x 40 tetraspanin 13 [Source:HGNC Symbol;Acc:HGNC:21643]
17	ENSG0000000	-0.15	0.039	0.1	40 x 38 reticulocalbin 1, EF-hand calcium binding domain [Source:HG
18	ENSG0000001	-0.19	0.044	0.1	40 x 40 transmembrane emp24 protein transport domain containing 3
19	ENSG0000001	-0.27	0.046	0.1	40 x 40 peptidylprolyl isomerase B (cyclophilin B) [Source:HGNC Syn
20	ENSG0000001	-0.27	0.048	0.1	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:

p-values

