

# MLH1\_normHNPC vs

## Global Summary

%DE = 0.52  
 # genes with fdr < 0.2 = 5532 ( 2525 + / 3007 - )  
 # genes with fdr < 0.1 = 2631 ( 985 + / 1646 - )  
 # genes with fdr < 0.05 = 1201 ( 352 + / 849 - )  
 # genes with fdr < 0.01 = 179 ( 34 + / 145 - )  
 # genes in genesets = 18990

<FC> = 0  
 <t-score> = -0.22  
 <p-value> = 0.12  
 <fdr> = 0.48

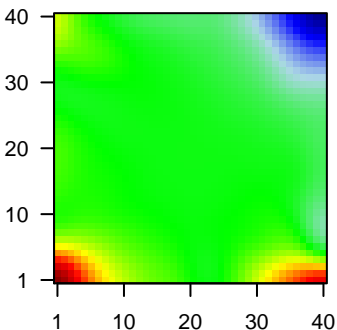
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000001	-0.13	3e-08	6e-04	38 x 34 proline/serine-rich coiled-coil 1 [Source:HGNC Symbol;Acc:HGNC:10381]
2	ENSG00000001	-0.04	1e-07	6e-04	36 x 26 p21 protein (Cdc42/Rac)-activated kinase 6 [Source:HGNC Symbol;Acc:HGNC:10381]
3	ENSG00000001	-0.33	2e-07	7e-04	37 x 40 sigma non-opioid intracellular receptor 1 [Source:HGNC Symbol;Acc:HGNC:10381]
4	ENSG00000001	-0.14	2e-07	1e-03	36 x 33 Obg-like ATPase 1 [Source:HGNC Symbol;Acc:HGNC:28833]
5	ENSG00000001	-0.03	6e-07	1e-03	21 x 35 zinc finger and BTB domain containing 8A [Source:HGNC Symbol;Acc:HGNC:10381]
6	ENSG00000001	0.14	9e-07	1e-03	1 x 24 WW domain binding protein 1-like [Source:HGNC Symbol;Acc:HGNC:10381]
7	ENSG00000001	-0.07	1e-06	1e-03	19 x 40 NAD kinase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:10381]
8	ENSG00000001	-0.08	1e-06	1e-03	33 x 33 coiled-coil domain containing 43 [Source:HGNC Symbol;Acc:HGNC:10381]
9	ENSG00000000	-0.13	1e-06	1e-03	35 x 36 thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:10381]
10	ENSG00000001	-0.54	1e-06	1e-03	40 x 40 ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:HGNC:10381]
11	ENSG00000001	0	1e-06	1e-03	18 x 24
12	ENSG00000001	-0.18	1e-06	1e-03	37 x 36 GrpE-like 1, mitochondrial (E. coli) [Source:HGNC Symbol;Acc:HGNC:10381]
13	ENSG00000001	0.13	2e-06	1e-03	9 x 1 cytochrome b561 family, member A3 [Source:HGNC Symbol;Acc:HGNC:10381]
14	ENSG00000000	-0.29	2e-06	1e-03	40 x 39 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc:HGNC:10381]
15	ENSG00000000	-0.16	2e-06	1e-03	38 x 36 aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393]
16	ENSG00000001	0.07	2e-06	1e-03	12 x 2 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:HGNC:10381]
17	ENSG00000001	0.33	2e-06	1e-03	6 x 36 methyltransferase like 7A [Source:HGNC Symbol;Acc:HGNC:10381]
18	ENSG00000002	-0.07	2e-06	1e-03	37 x 26 protein phosphatase methylesterase 1 [Source:HGNC Symbol;Acc:HGNC:10381]
19	ENSG00000001	-0.26	2e-06	1e-03	39 x 39 ribophorin I [Source:HGNC Symbol;Acc:HGNC:10381]
20	ENSG00000001	-0.09	2e-06	1e-03	39 x 31 MACRO domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10381]

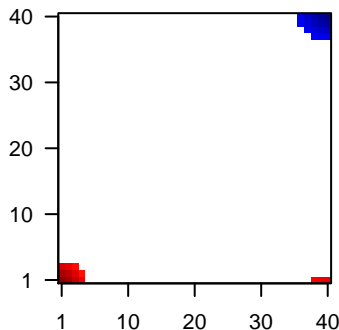
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.52	0e+00	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	22.05	0e+00	507	Colon Cancertrack_CRC_TCGA_corr_C_normal_UP
3	21.68	0e+00	844	Colon Cancertrack_CRC_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
4	19.5	3e-06	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
5	19.05	3e-06	427	Tissue WIRTH_Immune system
6	18.73	8e-06	347	LymphomaWIRTH_lymphoma937_spot H
7	18.56	1e-05	336	LymphomaWIRTH_lymphoma937_spot F
8	15.12	3e-05	3507	CC plasma membrane
9	14.29	3e-05	145	LymphomaWIRTH_lymphoma937_spot F
10	14.29	3e-05	145	LymphomaWIRTH_lymphoma937_spot F
11	13.75	4e-05	336	GSEA C2VEECHI_GASTRIC_CANCER_EARLY_DN
12	13.59	4e-05	175	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
13	13.31	4e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
14	13.17	4e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
15	13.01	4e-05	7592	LymphomaWIRTH_Strong_enhancer
16	12.69	5e-05	500	LymphomaWIRTH_lymphoma937_spot J
17	12.65	6e-05	484	LymphomaWIRTH_lymphoma937_spot K
18	12.32	6e-05	246	GSEA C2QI_PLASMACYTOMA_UP
19	12.3	6e-05	208	Tissue PALMER_B-Cell signature up
20	12.05	6e-05	368	GSEA C2INDGREN_BLADDER_CANCER_CLUSTER_2B
<i>Underexpressed</i>				
1	-33.92	0e+00	807	LymphomaWIRTH_lymphoma937_spot L
2	-33.81	0e+00	811	LymphomaWIRTH_lymphoma937_spot D
3	-32.1	0e+00	550	Cancer Lembecke_Normal vs Adenoma
4	-29.68	0e+00	713	Colon Cancertrack_CRC_TCGA_group.over_C_normal_DN
5	-29.65	0e+00	1298	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
6	-29.34	0e+00	830	Colon Cancertrack_CRC_TCGA_corr_R_normal_DN
7	-26.36	0e+00	582	GSEA C2AIRO_HEPATOBLASTOMA_CLASSES_UP
8	-25.22	0e+00	145	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
9	-23.97	0e+00	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
10	-23.47	0e+00	546	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	-22.97	0e+00	400	GSEA C2VEECHI_GASTRIC_CANCER_EARLY_UP
12	-22.58	0e+00	316	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
13	-22.55	0e+00	1228	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	-22.49	0e+00	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
15	-22.37	0e+00	859	GSEA C2LEE_BMP2_TARGETS_DN
16	-22.04	0e+00	282	GSEA C2MANALO_HYPOXIA_DN
17	-21.82	0e+00	446	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
18	-21.67	0e+00	327	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
19	-21.17	6e-04	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	-21.11	0e+00	775	GSEA C2WELMYCN_TARGETS_WITH_E_BOX

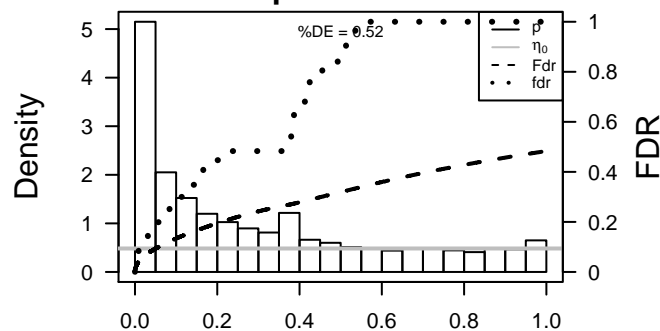
Profile



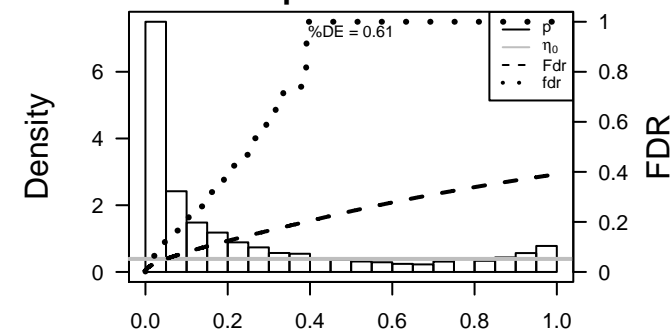
Regulated Spots



p-values



p-values



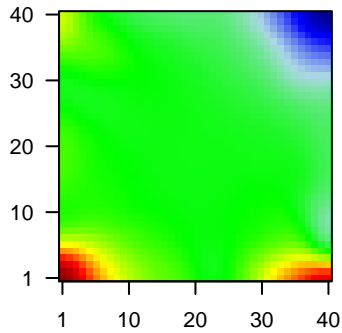
# MLH1\_normHNPC vs

## Local Summary

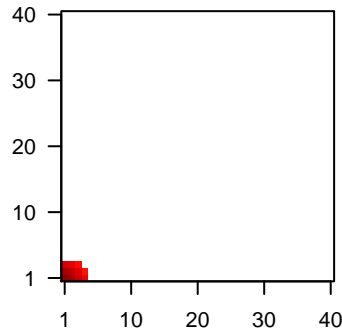
%DE = 0.98  
 # metagenes = 11  
 # genes = 238  
 # genes in genesets = 233  
  
 # genes with fdr < 0.1 = 226 ( 226 + / 0 -)  
 # genes with fdr < 0.05 = 226 ( 226 + / 0 -)  
 # genes with fdr < 0.01 = 214 ( 214 + / 0 -)

<r> metagenes = 1  
 <r> genes = 0.89  
  
 <FC> = 0.34  
 <t-score> = 3.53  
 <p-value> = 0.01  
 <fdr> = 0.13

Profile



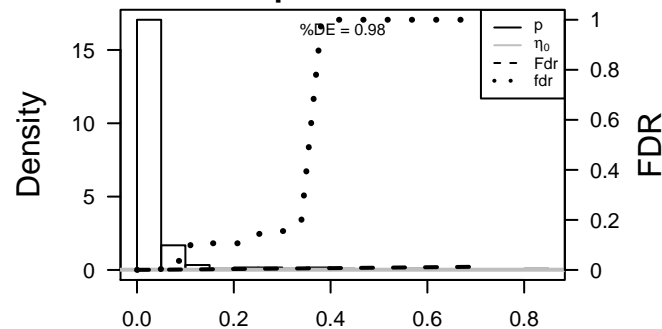
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG000002	0.41	2e-05	2e-04	3 x 1 Spi-B transcription factor (Spi-1/PU.1 related) [Source:HGNC]
2	ENSG000001	0.86	1e-04	2e-04	1 x 1 CD79a molecule, immunoglobulin-associated alpha [Source:
3	ENSG000001	0.28	2e-04	2e-04	4 x 1 pleckstrin homology domain containing, family F (with FYVE c
4	ENSG000002	0.37	2e-04	2e-04	3 x 3 apolipoprotein B mRNA editing enzyme, catalytic polypeptide
5	ENSG000001	0.71	2e-04	2e-04	1 x 1 pre-B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271
6	ENSG000001	1.3	4e-04	2e-04	1 x 1 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
7	ENSG000001	0.86	4e-04	2e-04	1 x 1 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
8	ENSG000002	0.52	5e-04	2e-04	1 x 1 protein tyrosine phosphatase, receptor type, C-associated pr
9	ENSG000001	0.98	6e-04	2e-04	1 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
10	ENSG000001	0.32	6e-04	2e-04	2 x 1 lymphocyte antigen 86 [Source:HGNC Symbol;Acc:HGNC:16
11	ENSG000001	0.34	6e-04	3e-04	3 x 1 family with sequence similarity 102, member A [Source:HGNC
12	ENSG000001	0.61	7e-04	3e-04	1 x 1 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
13	ENSG000000	0.34	8e-04	3e-04	4 x 1 ATPase, Ca++ transporting, ubiquitous [Source:HGNC Symb
14	ENSG000000	0.57	8e-04	5e-04	1 x 1 CD79b molecule, immunoglobulin-associated beta [Source:h
15	ENSG000001	0.59	1e-03	5e-04	1 x 1 clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
16	ENSG000001	0.28	1e-03	5e-04	4 x 2 tumor protein p53 inducible nuclear protein 1 [Source:HGNC
17	ENSG000001	1.06	1e-03	5e-04	1 x 1 follicular dendritic cell secreted protein [Source:HGNC Symb
18	ENSG000001	0.36	2e-03	5e-04	1 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:HGNC:18504]
19	ENSG000001	1.19	2e-03	5e-04	1 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
20	ENSG000001	0.26	2e-03	5e-04	4 x 1 CDC42 small effector 2 [Source:HGNC Symbol;Acc:HGNC:11

p-values



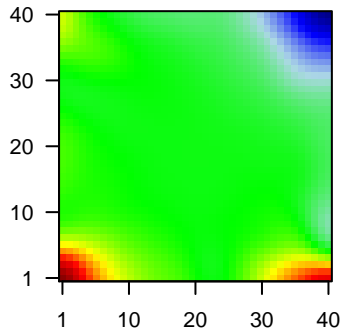
# MLH1\_normHNPC vs

## Local Summary

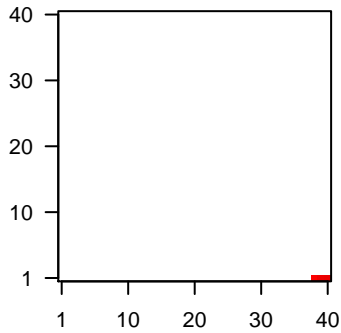
%DE = 0.71  
 # metagenes = 3  
 # genes = 124  
 # genes in genesets = 123  
  
 # genes with  $fdr < 0.1$  = 58 ( 58 + / 0 - )  
 # genes with  $fdr < 0.05$  = 57 ( 57 + / 0 - )  
 # genes with  $fdr < 0.01$  = 4 ( 4 + / 0 - )

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.44  
  
 $\langle FC \rangle$  = 0.39  
 $\langle t\text{-score} \rangle$  = 2.29  
 $\langle p\text{-value} \rangle$  = 0.06  
 $\langle fdr \rangle$  = 0.34

Profile



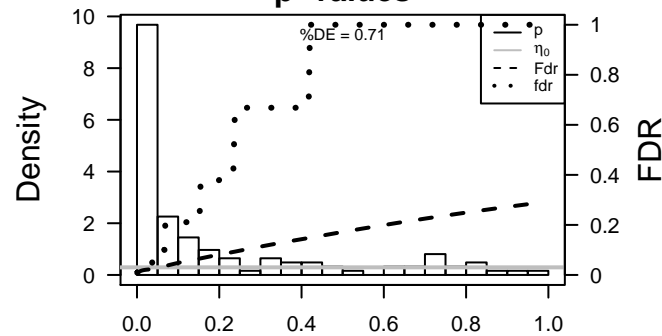
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.85	6e-04	0.009	39 x 1 coiled-coil domain containing 152 [Source:HGNC Symbol;Acc:HGNC:12691]
2	ENSG0000000	1.25	7e-04	0.009	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:12691]
3	ENSG0000001	0.92	1e-03	0.009	40 x 1 carbonic anhydrase II [Source:HGNC Symbol;Acc:HGNC:137]
4	ENSG0000002	0.77	1e-03	0.010	39 x 1 selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGNC:12691]
5	ENSG0000001	1.52	1e-03	0.014	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:12691]
6	ENSG0000001	0.82	2e-03	0.014	40 x 1 joining chain of multimeric IgA and IgM [Source:HGNC Symbol;Acc:HGNC:12691]
7	ENSG0000002	0.88	3e-03	0.014	40 x 1
8	ENSG0000001	0.64	3e-03	0.014	40 x 1 calcineurin-like EF-hand protein 2 [Source:HGNC Symbol;Acc:HGNC:12691]
9	ENSG0000001	0.39	3e-03	0.014	40 x 1 solute carrier family 9, subfamily A (NHE3, cation proton antiporter) [Source:HGNC Symbol;Acc:HGNC:12691]
10	ENSG0000001	1.21	3e-03	0.018	40 x 1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:12691]
11	ENSG0000001	0.48	4e-03	0.018	39 x 1 placenta-specific 8 [Source:HGNC Symbol;Acc:HGNC:19254]
12	ENSG0000001	0.81	5e-03	0.018	40 x 1 carbonic anhydrase I [Source:HGNC Symbol;Acc:HGNC:136]
13	ENSG0000001	0.7	6e-03	0.018	40 x 1 alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:HGNC:12691]
14	ENSG0000000	0.27	6e-03	0.018	39 x 1 ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
15	ENSG0000001	0.98	6e-03	0.018	40 x 1 keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
16	ENSG0000000	0.77	6e-03	0.018	40 x 1 membrane-spanning 4-domains, subfamily A, member 12 [Source:HGNC Symbol;Acc:HGNC:12691]
17	ENSG0000001	0.36	7e-03	0.018	39 x 1 polymerase (DNA-directed), delta 4, accessory subunit [Source:HGNC Symbol;Acc:HGNC:12691]
18	ENSG0000001	1.1	7e-03	0.026	40 x 1 aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
19	ENSG0000001	0.46	8e-03	0.026	38 x 1 protein kinase (cAMP-dependent, catalytic) inhibitor beta [Source:HGNC Symbol;Acc:HGNC:12691]
20	ENSG0000000	1	9e-03	0.026	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:12691]

p-values



# MLH1\_normHNPC vs

## Local Summary

%DE = 0.99  
 # metagenes = 17  
 # genes = 345  
 # genes in genesets = 340  
  
 # genes with  $fdr < 0.1$  = 343 ( 0 + / 343 -)  
 # genes with  $fdr < 0.05$  = 340 ( 0 + / 340 -)  
 # genes with  $fdr < 0.01$  = 319 ( 0 + / 319 -)

<r> metagenes = 0.99

<r> genes = 0.85

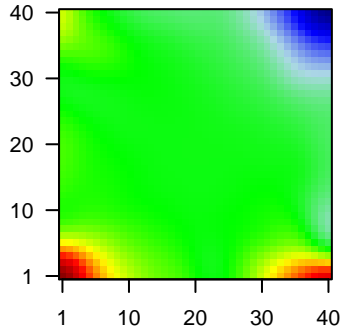
<FC> = -0.29

<t-score> = -4.91

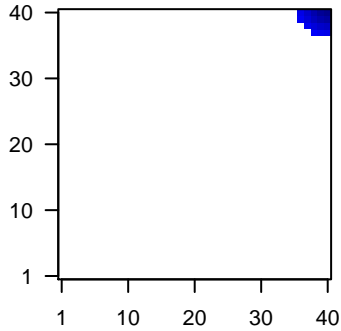
<p-value> = 0

<fdr> = 0.09

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.33	2e-07	1e-06	37 x 40 sigma non-opioid intracellular receptor 1 [Source:HGNC Syrr
2	ENSG0000001	-0.54	1e-06	1e-06	40 x 40 ribosomal protein L22-like 1 [Source:HGNC Symbol;Acc:HG
3	ENSG0000000	-0.29	2e-06	1e-06	40 x 39 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc
4	ENSG0000001	-0.26	2e-06	1e-06	39 x 39 ribophorin I [Source:HGNC Symbol;Acc:HGNC:10381]
5	ENSG0000001	-0.2	3e-06	1e-06	40 x 38 forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:3818]
6	ENSG0000001	-0.28	4e-06	1e-06	39 x 39 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;/
7	ENSG0000001	-0.27	5e-06	1e-06	38 x 40 regulator of chromosome condensation 1 [Source:HGNC Syn
8	ENSG0000002	-0.42	5e-06	1e-06	40 x 40 NME1-NME2 readthrough [Source:HGNC Symbol;Acc:HGNC
9	ENSG0000000	-0.23	5e-06	1e-06	40 x 39 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
10	ENSG0000000	-0.35	6e-06	1e-06	39 x 40 mitochondrial ribosomal protein S35 [Source:HGNC Symbol;/
11	ENSG0000001	-0.28	6e-06	1e-06	40 x 39 CD320 molecule [Source:HGNC Symbol;Acc:HGNC:16692]
12	ENSG0000001	-0.38	7e-06	1e-06	40 x 40 pleckstrin 2 [Source:HGNC Symbol;Acc:HGNC:19238]
13	ENSG0000002	-0.24	7e-06	2e-06	37 x 38 hematological and neurological expressed 1-like [Source:HG
14	ENSG0000001	-0.23	8e-06	5e-06	40 x 39 Tu translation elongation factor, mitochondrial [Source:HGNC
15	ENSG0000001	-0.38	1e-05	5e-06	40 x 40 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein ret
16	ENSG0000001	-0.17	1e-05	5e-06	39 x 37 Ran GTPase activating protein 1 [Source:HGNC Symbol;Acc:
17	ENSG0000000	-0.17	1e-05	5e-06	38 x 37 RAN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:98
18	ENSG0000001	-0.23	2e-05	5e-06	38 x 37 basic leucine zipper and W2 domains 2 [Source:HGNC Synt
19	ENSG0000000	-0.49	3e-05	5e-06	40 x 40 NME/NM23 nucleoside diphosphate kinase 2 [Source:HGNC
20	ENSG0000001	-0.24	3e-05	5e-06	39 x 39 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]

p-values

