

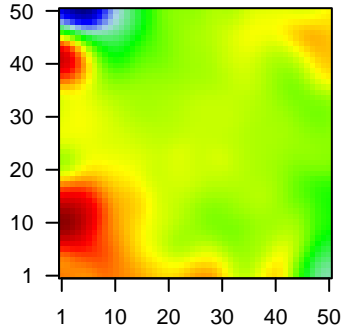
MSC2

Global Summary

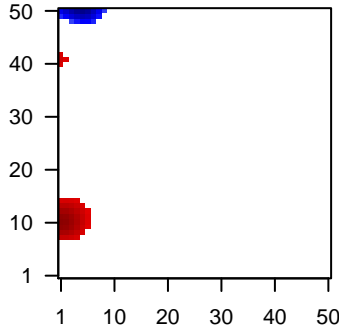
%DE = 0.15
 # genes with $fdr < 0.2$ = 1612 (809 + / 803 -)
 # genes with $fdr < 0.1$ = 1137 (554 + / 583 -)
 # genes with $fdr < 0.05$ = 917 (441 + / 476 -)
 # genes with $fdr < 0.01$ = 611 (290 + / 321 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.02
 <p-value> = 0.12
 <fdr> = 0.85

Profile



Regulated Spots

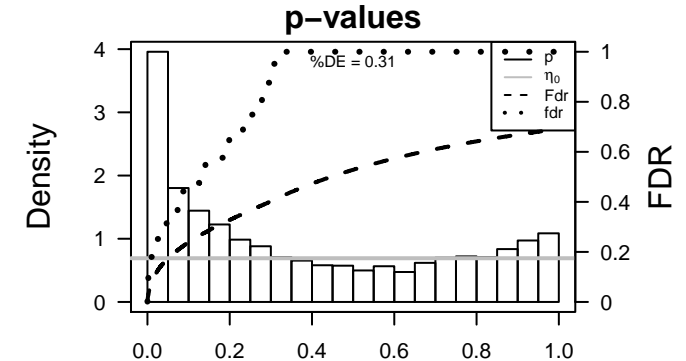
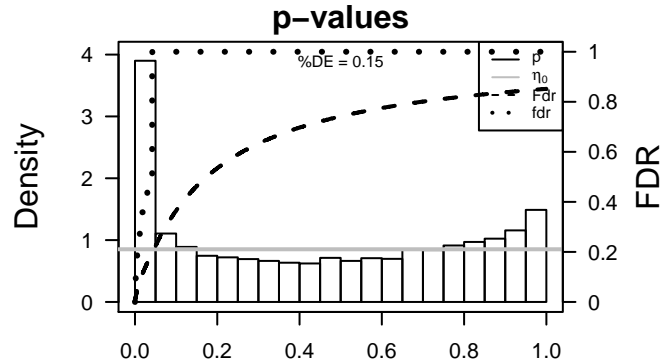


Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ANLN	-0.39	2e-16	5e-14	5 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:HGNC:10000]
2	ARHGAP8	0.49	2e-16	5e-14	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:10000]
3	ASF1B	-0.46	2e-16	5e-14	4 x 50 anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:HGNC:10000]
4	ASPM	-0.37	2e-16	5e-14	6 x 50 asp (abnormal spindle) homolog, microcephaly associated (D) [Source:HGNC Symbol;Acc:HGNC:10000]
5	ATP1A1	0.3	2e-16	5e-14	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:10000]
6	AURKB	-0.36	2e-16	5e-14	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
7	BLMH	-0.46	2e-16	5e-14	11 x 50 bleomycin hydrolase [Source:HGNC Symbol;Acc:HGNC:10565]
8	BUB1B	-0.49	2e-16	5e-14	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase B [Source:HGNC Symbol;Acc:HGNC:10000]
9	CALM2	-0.21	2e-16	5e-14	9 x 49 calmodulin 2 (phosphorylase kinase, delta) [Source:HGNC Symbol;Acc:HGNC:10000]
10	CCDC171	0.36	2e-16	5e-14	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Acc:HGNC:10000]
11	CDC20	-0.46	2e-16	5e-14	6 x 50 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:17225]
12	CDCA3	-0.34	2e-16	5e-14	6 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:10000]
13	CDCA5	-0.45	2e-16	5e-14	4 x 50 cell division cycle associated 5 [Source:HGNC Symbol;Acc:HGNC:10000]
14	CDK1	-0.49	2e-16	5e-14	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
15	CDK2	0.31	2e-16	5e-14	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
16	CENPQ	-0.32	2e-16	5e-14	2 x 50 centromere protein Q [Source:HGNC Symbol;Acc:HGNC:21325]
17	CENPU	-0.37	2e-16	5e-14	2 x 50 centromere protein U [Source:HGNC Symbol;Acc:HGNC:21325]
18	CHCHD6	0.39	2e-16	5e-14	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Source:HGNC Symbol;Acc:HGNC:10000]
19	CITED1	0.35	2e-16	5e-14	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1 [Source:HGNC Symbol;Acc:HGNC:10000]
20	CKAP2L	-0.42	2e-16	5e-14	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC:10000]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.11	2e-05	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	11.4	4e-05	401	CC mitochondrial inner membrane
3	10.98	6e-05	94	BP respiratory electron transport chain
4	10.69	7e-05	1468	CC mitochondrion
5	10.69	7e-05	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
6	10.43	8e-05	85	GSEA C2MOOTHA_VOXPHOS
7	10.22	8e-05	135	BP cellular metabolic process
8	10.2	8e-05	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
9	10.17	1e-04	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_Synthase
10	9.99	1e-04	102	GSEA C2KEGG_PARKINSONS_DISEASE
11	9.79	1e-04	405	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
12	9.37	2e-04	213	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
13	9.32	2e-04	18	BP melanocyte differentiation
14	9.17	2e-04	421	GSEA C2MOOTHA_MITOCHONDRIA
15	8.67	2e-04	13	BP melanin biosynthetic process
16	8.64	2e-04	368	GSEA C2STEIN_ESRRA_TARGETS_UP
17	8.5	3e-04	62	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
18	8.18	3e-04	142	GSEA C2KEGG_ALZHEIMERS_DISEASE
19	7.36	5e-04	19	CC mitochondrial proton-transporting ATP synthase complex
20	7.35	5e-04	63	Glio Stuehler_Proteins_up_in_STS
<i>Underexpressed</i>				
1	-35.82	0e+00	142	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
2	-33.59	0e+00	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	-31.26	0e+00	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	-30.9	0e+00	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	-30.59	0e+00	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	-28.5	0e+00	145	GSEA C2CHANG_CYCLING_GENES
7	-26.64	0e+00	93	GSEA C2KONG_E2F3_TARGETS
8	-25.96	0e+00	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
9	-25.71	1e-04	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	-24.97	0e+00	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
11	-24.67	0e+00	96	GSEA C2ROONQUIST_IL6_DEPRIVATION_DN
12	-24.51	0e+00	197	HM HALLMARK_E2F_TARGETS
13	-24.46	0e+00	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
14	-23.72	0e+00	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
15	-23.71	0e+00	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
16	-23.66	0e+00	99	GSEA C2BURTON_ADIPOGENESIS_3
17	-23.52	0e+00	99	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
18	-23.27	0e+00	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	-23.08	0e+00	81	GSEA C2GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	-23.07	0e+00	616	GSEA C2BENPORATH_CYCLING_GENES



MSC2

Local Summary

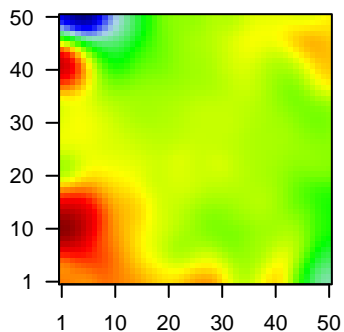
%DE = 0.9
 # metagenes = 42
 # genes = 429
 # genes in genesets = 426

 # genes with $fdr < 0.1$ = 328 (326 + / 2 -)
 # genes with $fdr < 0.05$ = 312 (311 + / 1 -)
 # genes with $fdr < 0.01$ = 193 (192 + / 1 -)

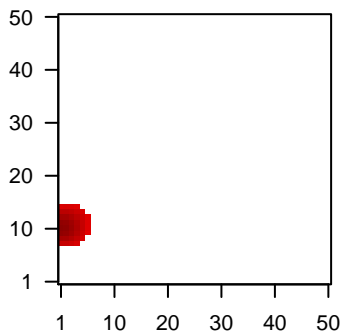
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.66

$\langle FC \rangle$ = 0.15
 $\langle \text{shrinkage-t} \rangle$ = 1.5
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.46

Profile



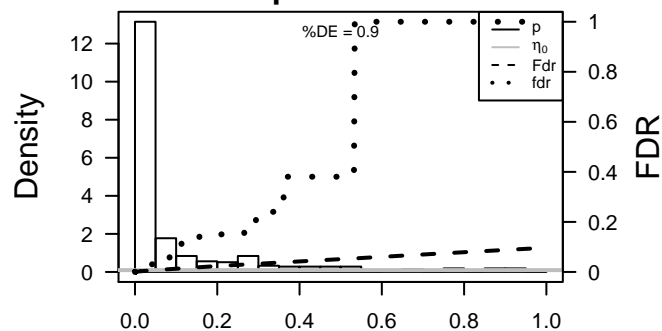
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CCDC171	0.36	2e-16	1e-15	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Ac
2	DSTYK	0.28	2e-16	1e-15	1 x 12 dual serine/threonine and tyrosine protein kinase [Source:HG
3	HSPB8	0.36	2e-16	1e-15	1 x 11 heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGNC
4	KLHL24	0.41	2e-16	1e-15	1 x 11 kelch-like family member 24 [Source:HGNC Symbol;Acc:HGNC
5	SEMA6A	0.19	2e-16	1e-15	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic
6	SGK1	0.24	2e-16	1e-15	1 x 13 serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
7	SNAI2	0.47	2e-16	1e-15	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
8	TMEM177	0.42	2e-14	5e-12	3 x 10 transmembrane protein 177 [Source:HGNC Symbol;Acc:HGNC
9	ATP6V0A1	0.31	1e-13	7e-12	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
10	RAB27A	0.38	4e-13	7e-12	1 x 11 RAB27A, member RAS oncogene family [Source:HGNC Sym
11	SOCS6	0.29	5e-13	1e-11	1 x 11 suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
12	BCCIP	0.22	8e-13	1e-11	2 x 15 BRCA2 and CDKN1A interacting protein [Source:HGNC Sym
13	PHACTR1	0.14	1e-12	6e-10	4 x 14 phosphatase and actin regulator 1 [Source:HGNC Symbol;Ac
14	SS18L1	0.31	4e-11	6e-10	1 x 10 synovial sarcoma translocation gene on chromosome 18-like
15	SDCBP	0.14	4e-11	6e-10	3 x 11 syndecan binding protein (syntenin) [Source:HGNC Symbol;A
16	GPR143	0.18	6e-11	6e-10	1 x 11 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:HGNC
17	EDNRB	0.25	6e-11	3e-09	1 x 11 endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC
18	ID2	0.19	1e-10	2e-08	1 x 13 inhibitor of DNA binding 2, dominant negative helix-loop-heli
19	MCF2	0.43	6e-10	2e-08	5 x 10 MCF2 cell line derived transforming sequence [Source:HGNC
20	ZNF330	0.22	1e-09	5e-08	2 x 13 zinc finger protein 330 [Source:HGNC Symbol;Acc:HGNC:15

p-values



MSC2

Local Summary

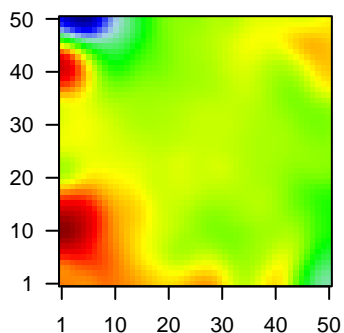
%DE = 0.92
 # metagenes = 4
 # genes = 100
 # genes in genesets = 99

 # genes with fdr < 0.1 = 86 (86 + / 0 -)
 # genes with fdr < 0.05 = 78 (78 + / 0 -)
 # genes with fdr < 0.01 = 64 (64 + / 0 -)

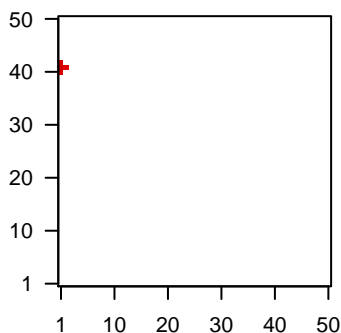
<r> metagenes = 1
 <r> genes = 0.91

<FC> = 0.19
 <shrinkage-t> = 2.25
 <p-value> = 0
 <fdr> = 0.3

Profile



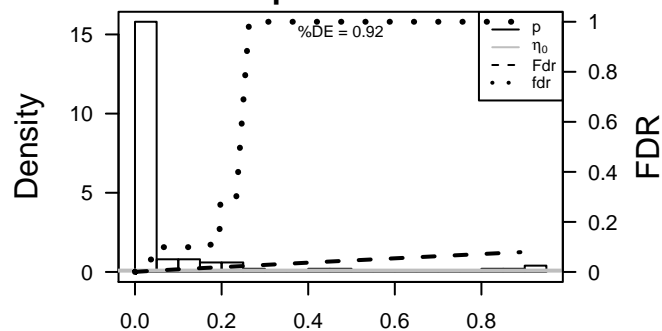
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ATP1A1	0.3	2e-16	2e-16	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:2528]
2	CITED1	0.35	2e-16	2e-16	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain [Source:HGNC Symbol;Acc:HGNC:2529]
3	CTSC	0.27	2e-16	2e-16	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
4	MBP	0.26	2e-16	2e-16	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]
5	MITF	0.34	2e-16	2e-16	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:2530]
6	NARS2	0.26	2e-16	2e-16	1 x 42 asparaginyl-tRNA synthetase 2, mitochondrial (putative) [Source:HGNC Symbol;Acc:HGNC:2531]
7	PLP1	0.28	2e-16	2e-16	1 x 42 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086]
8	SLC18B1	0.33	2e-16	2e-16	1 x 42 solute carrier family 18, subfamily B, member 1 [Source:HGNC Symbol;Acc:HGNC:2532]
9	TRPM1	0.39	2e-16	2e-16	1 x 42 transient receptor potential cation channel, subfamily M, member 1 [Source:HGNC Symbol;Acc:HGNC:2533]
10	TYR	0.25	2e-16	2e-16	1 x 42 tyrosinase [Source:HGNC Symbol;Acc:HGNC:12442]
11	STX7	0.28	9e-16	8e-14	1 x 42 syntaxin 7 [Source:HGNC Symbol;Acc:HGNC:11442]
12	SLC39A6	0.22	1e-14	1e-13	1 x 42 solute carrier family 39 (zinc transporter), member 6 [Source:HGNC Symbol;Acc:HGNC:2534]
13	BACE2	0.23	2e-14	4e-13	1 x 42 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Acc:HGNC:2535]
14	EXOC3	0.26	7e-14	3e-11	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:HGNC:2536]
15	MLST8	0.37	5e-12	3e-11	1 x 41 MTOR associated protein, LST8 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:2537]
16	SNCA	0.15	1e-11	3e-11	1 x 40 synuclein, alpha (non A4 component of amyloid precursor) [Source:HGNC Symbol;Acc:HGNC:2538]
17	MICAL1	0.33	1e-11	1e-10	1 x 41 microtubule associated monoxygenase, calponin and LIM domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2539]
18	ATP5G3	0.14	3e-11	2e-10	1 x 41 ATP synthase, H+ transporting, mitochondrial Fo complex, subunit 3 [Source:HGNC Symbol;Acc:HGNC:2540]
19	MTX2	0.19	5e-11	4e-10	1 x 42 metaxin 2 [Source:HGNC Symbol;Acc:HGNC:7506]
20	STARD10	0.38	1e-10	4e-10	1 x 40 STAR-related lipid transfer (START) domain containing 10 [Source:HGNC Symbol;Acc:HGNC:2541]

p-values



MSC2

Local Summary

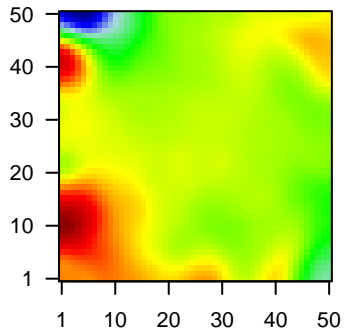
%DE = 0.95
 # metagenes = 22
 # genes = 335
 # genes in genesets = 335

 # genes with $fdr < 0.1$ = 310 (1 + / 309 -)
 # genes with $fdr < 0.05$ = 297 (1 + / 296 -)
 # genes with $fdr < 0.01$ = 280 (0 + / 280 -)

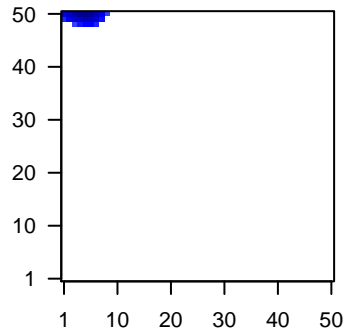
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.93

 $\langle FC \rangle$ = -0.21
 $\langle \text{shrinkage-t} \rangle$ = -2.58
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.15

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANLN	-0.39	2e-16	1e-16	5 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:HGNC:11390]
2	ASF1B	-0.46	2e-16	1e-16	4 x 50 anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:HGNC:11390]
3	ASPM	-0.37	2e-16	1e-16	6 x 50 asp (abnormal spindle) homolog, microcephaly associated (D
4	AURKB	-0.36	2e-16	1e-16	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
5	BUB1B	-0.49	2e-16	1e-16	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
6	CDC20	-0.46	2e-16	1e-16	6 x 50 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1722]
7	CDCA3	-0.34	2e-16	1e-16	6 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:1722]
8	CDCA5	-0.45	2e-16	1e-16	4 x 50 cell division cycle associated 5 [Source:HGNC Symbol;Acc:HGNC:1722]
9	CDK1	-0.49	2e-16	1e-16	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:1722]
10	CENPQ	-0.32	2e-16	1e-16	2 x 50 centromere protein Q [Source:HGNC Symbol;Acc:HGNC:213]
11	CENPU	-0.37	2e-16	1e-16	2 x 50 centromere protein U [Source:HGNC Symbol;Acc:HGNC:213]
12	CKAP2L	-0.42	2e-16	1e-16	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC:213]
13	ESCO2	-0.33	2e-16	1e-16	4 x 50 establishment of sister chromatid cohesion N-acetyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:213]
14	EXO1	-0.4	2e-16	1e-16	1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
15	HIST1H4C	-0.18	2e-16	1e-16	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:478]
16	HMGB2	-0.62	2e-16	1e-16	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:478]
17	KIF2C	-0.36	2e-16	1e-16	6 x 50 kinesin family member 2C [Source:HGNC Symbol;Acc:HGNC:478]
18	MELK	-0.35	2e-16	1e-16	5 x 50 maternal embryonic leucine zipper kinase [Source:HGNC Symbol;Acc:HGNC:478]
19	NCAPG	-0.46	2e-16	1e-16	6 x 50 non-SMC condensin I complex, subunit G [Source:HGNC Symbol;Acc:HGNC:478]
20	NDC80	-0.41	2e-16	1e-16	6 x 50 NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:HGNC:478]

p-values

