

MSC2 vs MSC3

Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1589 (878 + / 711 -)
 # genes with fdr < 0.1 = 1144 (644 + / 500 -)
 # genes with fdr < 0.05 = 872 (508 + / 364 -)
 # genes with fdr < 0.01 = 541 (328 + / 213 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.14
 <fdr> = 0.86

Global Genelist

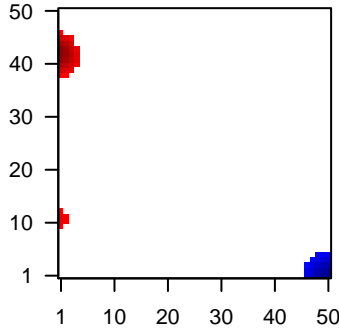
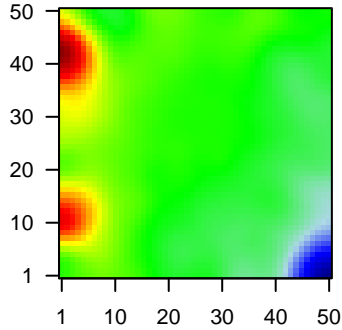
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ANXA1	-1.32	2e-16 1e-13	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	ARHGAP8	1.29	2e-16 1e-13	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:1480]
3	CAPN3	0.78	2e-16 1e-13	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
4	CDK2	0.87	2e-16 1e-13	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC:1480]
5	CHCHD6	1.04	2e-16 1e-13	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Source:HGNC Symbol;Acc:HGNC:1480]
6	DCTPP1	0.88	2e-16 1e-13	1 x 44 dCTP pyrophosphatase 1 [Source:HGNC Symbol;Acc:HGNC:1480]
7	EDIL3	-0.86	2e-16 1e-13	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol;Acc:HGNC:1480]
8	F2R	-0.88	2e-16 1e-13	50 x 1 coagulation factor II (thrombin) receptor [Source:HGNC Symbol;Acc:HGNC:1480]
9	FRMD6	-1	2e-16 1e-13	50 x 1 FERM domain containing 6 [Source:HGNC Symbol;Acc:HGNC:1480]
10	GAPDHS	1.01	2e-16 1e-13	1 x 43 glyceraldehyde-3-phosphate dehydrogenase, spermatogenic 1 [Source:HGNC Symbol;Acc:HGNC:1480]
11	MITF	0.79	2e-16 1e-13	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:1480]
12	MLANA	0.9	2e-16 1e-13	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
13	MYH10	0.75	2e-16 1e-13	1 x 44 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:HGNC:1480]
14	MYOF	-1.11	2e-16 1e-13	50 x 1 myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]
15	NMRK2	1.16	2e-16 1e-13	1 x 44 nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:HGNC:1480]
16	PTPRM	-0.96	2e-16 1e-13	50 x 1 protein tyrosine phosphatase, receptor type, M [Source:HGNC Symbol;Acc:HGNC:1480]
17	RAB27A	0.86	2e-16 1e-13	1 x 11 RAB27A, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:1480]
18	SLC24A5	0.86	2e-16 1e-13	1 x 43 solute carrier family 24 (sodium/potassium/calcium exchange) member 5 [Source:HGNC Symbol;Acc:HGNC:1480]
19	SNAI2	0.97	2e-16 1e-13	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1480]
20	ST6GALNAC1	1.09	2e-16 1e-13	1 x 44 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-transferase 1 [Source:HGNC Symbol;Acc:HGNC:1480]

Global Geneset Analysis

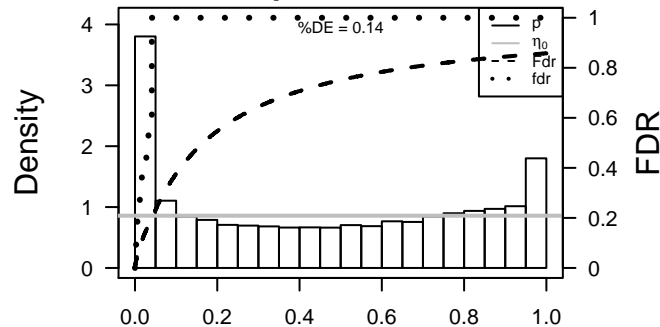
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.86	0e+00	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	13.57	0e+00	401	CC mitochondrial inner membrane
3	12.93	0e+00	405	GSEA C2MOOCHA_HUMAN_MITODB_6_2002
4	12.16	0e+00	1468	CC mitochondrion
5	11.74	0e+00	135	BP cellular metabolic process
6	11.7	0e+00	421	GSEA C2MOOCHA_MITOCHONDRIA
7	11.34	0e+00	368	GSEA C2STEIN_ESRRA_TARGETS_UP
8	11.3	0e+00	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
9	10.95	0e+00	94	BP respiratory electron transport chain
10	10.78	1e-05	213	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
11	10.53	1e-05	85	GSEA C2MOOCHA_VOXPPOS
12	10.49	1e-05	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
13	10.26	1e-05	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHASE
14	10.15	1e-05	102	GSEA C2KEGG_PARKINSONS_DISEASE
15	9.34	3e-05	500	GSEA C2STEIN_ESRRA_TARGETS
16	9.29	3e-05	18	BP melanocyte differentiation
17	9.25	3e-05	398	GSEA C2MOOCHA_PGC
18	8.99	3e-05	62	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
19	8.63	4e-05	1460	GSEA C2PUJANA_BRCA1_PCC_NETWORK
20	8.5	6e-05	142	GSEA C2KEGG_ALZHEIMERS_DISEASE
<i>Underexpressed</i>				
1	-9.28	3e-05	385	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
2	-9.15	3e-05	472	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
3	-8.99	3e-05	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
4	-8.64	4e-05	286	GSEA C2PASINI_SUZ12_TARGETS_DN
5	-8.37	7e-05	212	LymphomaENZ_Stromal signature 1
6	-8.14	8e-05	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
7	-8.06	9e-05	168	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
8	-7.6	2e-04	749	GSEA C2CUI_TCF21_TARGETS_2_DN
9	-7.54	2e-04	616	GSEA C2NABA_MATRISOME
10	-7.37	2e-04	425	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
11	-7.21	2e-04	683	GSEA C2RIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
12	-7.16	2e-04	281	Colon CancerTrack_CRC_TCGA_group.over_B_msi-h_UP
13	-7.15	2e-04	37	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_UP
14	-7.12	2e-04	28	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC
15	-7.04	3e-04	833	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
16	-7	3e-04	2188	LymphomaOPP_Poised_promoter
17	-6.86	3e-04	245	GSEA C2WANG_SMARCE1_TARGETS_UP
18	-6.84	4e-04	117	Colon CancerTrack_CRC-cluster-b
19	-6.82	4e-04	166	GSEA C2RODWELL_AGING_KIDNEY_NO_BLOOD_UP
20	-6.8	4e-04	3396	LymphomaOPP_Repressed

Profile

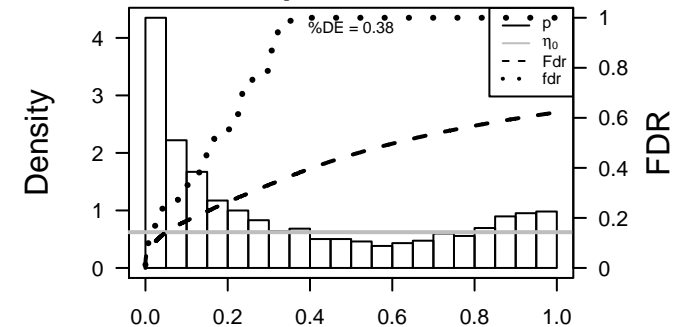
Regulated Spots



p-values



p-values



MSC2 vs MSC3

Local Summary

%DE = 0.92
 # metagenes = 6
 # genes = 142
 # genes in genesets = 141

 # genes with $fdr < 0.1$ = 117 (117 + / 0 -)
 # genes with $fdr < 0.05$ = 108 (108 + / 0 -)
 # genes with $fdr < 0.01$ = 90 (90 + / 0 -)

<r> metagenes = 1

<r> genes = 0.87

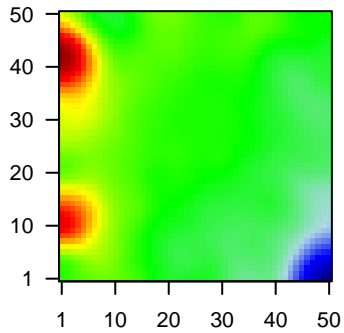
<FC> = 0.35

<shrinkage-t> = 1.6

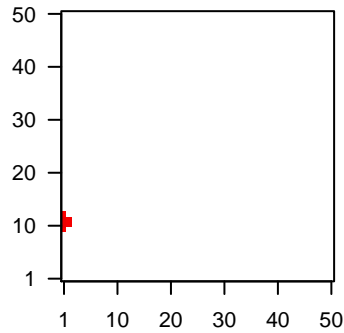
<p-value> = 0

<fdr> = 0.3

Profile



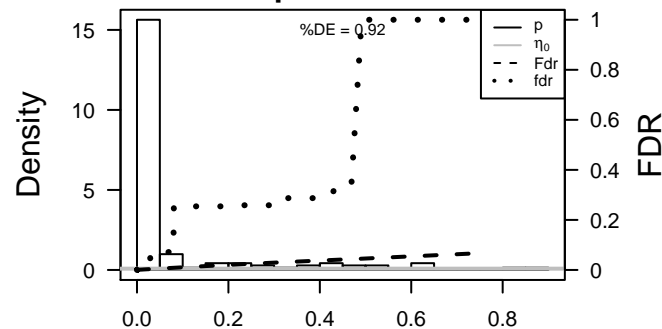
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	RAB27A	0.86	2e-16	1e-15	1 x 11 RAB27A, member RAS oncogene family [Source:HGNC Sym
2	SNAI2	0.97	2e-16	1e-15	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
3	GALNT3	0.82	8e-14	1e-11	1 x 12 polypeptide N-acetylgalactosaminyltransferase 3 [Source:HG
4	FAM69A	0.77	2e-12	1e-11	1 x 12 family with sequence similarity 69, member A [Source:HGNC
5	GDPD5	0.76	2e-12	1e-11	1 x 12 glycerophosphodiester phosphodiesterase domain containing
6	CCDC171	0.64	3e-12	2e-11	1 x 11 coiled-coil domain containing 171 [Source:HGNC Symbol;Ac
7	GALNTL6	0.73	5e-12	2e-11	1 x 11 polypeptide N-acetylgalactosaminyltransferase-like 6 [Sourc
8	HSPB8	0.69	6e-12	9e-10	1 x 11 heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGNC
9	PPARGC1A	0.68	9e-11	2e-09	1 x 10 peroxisome proliferator-activated receptor gamma, coactivat
10	BHLHE41	0.65	3e-10	2e-09	1 x 12 basic helix-loop-helix family, member e41 [Source:HGNC Sy
11	KCNAB2	0.63	4e-10	2e-09	1 x 10 potassium channel, voltage gated subfamily A regulatory beta
12	VEPH1	0.68	5e-10	1e-08	1 x 11 ventricular zone expressed PH domain-containing 1 [Source:
13	ROPN1B	0.64	3e-09	1e-08	1 x 10 rhophilin associated tail protein 1B [Source:HGNC Symbol;Ac
14	SGK1	0.48	4e-09	1e-08	1 x 13 serum/glucocorticoid regulated kinase 1 [Source:HGNC Syml
15	ID2	0.49	4e-09	1e-08	1 x 13 inhibitor of DNA binding 2, dominant negative helix-loop-heli
16	CDH3	0.61	6e-09	1e-08	1 x 11 cadherin 3, type 1, P-cadherin (placental) [Source:HGNC Sy
17	EDNRB	0.55	6e-09	1e-07	1 x 11 endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC
18	ATP6V0A1	0.55	2e-08	1e-07	1 x 10 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:Hi
19	DCT	0.58	3e-08	3e-07	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
20	DSTYK	0.49	6e-08	7e-07	1 x 12 dual serine/threonine and tyrosine protein kinase [Source:HG

p-values



MSC2 vs MSC3

Local Summary

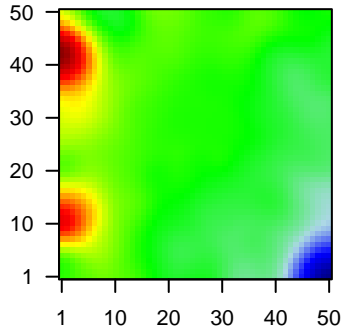
%DE = 0.94
 # metagenes = 28
 # genes = 401
 # genes in genesets = 399

 # genes with $fdr < 0.1$ = 355 (354 + / 1 -)
 # genes with $fdr < 0.05$ = 338 (338 + / 0 -)
 # genes with $fdr < 0.01$ = 285 (285 + / 0 -)

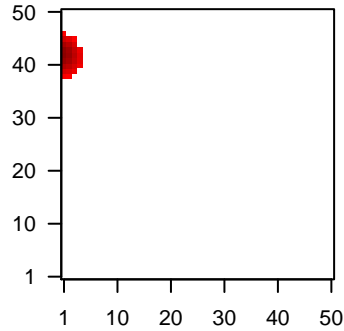
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.74

 $\langle FC \rangle$ = 0.37
 $\langle \text{shrinkage-t} \rangle$ = 1.76
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.25

Profile



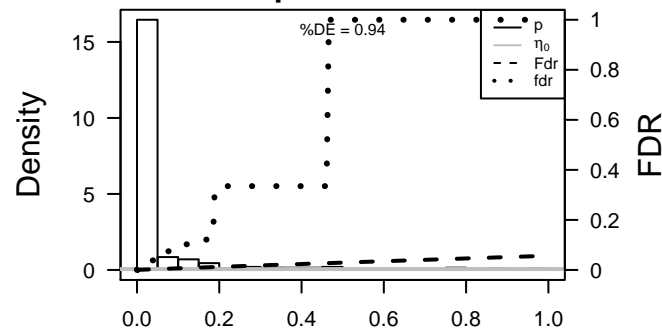
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ARHGAP8	1.29	2e-16	4e-16	1 x 43 Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:HGNC:1480]
2	CAPN3	0.78	2e-16	4e-16	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
3	CDK2	0.87	2e-16	4e-16	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC:1480]
4	CHCHD6	1.04	2e-16	4e-16	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Source:HGNC Symbol;Acc:HGNC:1480]
5	DCTPP1	0.88	2e-16	4e-16	1 x 44 dCTP pyrophosphatase 1 [Source:HGNC Symbol;Acc:HGNC:1480]
6	GAPDHS	1.01	2e-16	4e-16	1 x 43 glyceraldehyde-3-phosphate dehydrogenase, spermatogenic 1 [Source:HGNC Symbol;Acc:HGNC:1480]
7	MITF	0.79	2e-16	4e-16	1 x 41 microphthalmia-associated transcription factor [Source:HGNC Symbol;Acc:HGNC:1480]
8	MLANA	0.9	2e-16	4e-16	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
9	MYH10	0.75	2e-16	4e-16	1 x 44 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:HGNC:1480]
10	NMRK2	1.16	2e-16	4e-16	1 x 44 nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:HGNC:1480]
11	SLC24A5	0.86	2e-16	4e-16	1 x 43 solute carrier family 24 (sodium/potassium/calcium exchange) member 5 [Source:HGNC Symbol;Acc:HGNC:1480]
12	ST6GALNAC1	1.09	2e-16	4e-16	1 x 44 ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-transferase [Source:HGNC Symbol;Acc:HGNC:1480]
13	TRPM1	1	2e-16	4e-16	1 x 42 transient receptor potential cation channel, subfamily M, member 1 [Source:HGNC Symbol;Acc:HGNC:1480]
14	WDYHV1	0.93	2e-16	4e-16	4 x 43 WDYHV motif containing 1 [Source:HGNC Symbol;Acc:HGNC:1480]
15	EXOC3	0.66	4e-16	5e-14	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:HGNC:1480]
16	ATP1A1	0.71	3e-15	2e-12	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:HGNC:1480]
17	SLC18B1	0.72	7e-14	2e-12	1 x 42 solute carrier family 18, subfamily B, member 1 [Source:HGNC Symbol;Acc:HGNC:1480]
18	BIRC7	0.76	1e-13	2e-12	1 x 42 baculoviral IAP repeat containing 7 [Source:HGNC Symbol;Acc:HGNC:1480]
19	CITED1	0.72	2e-13	2e-12	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain 1 [Source:HGNC Symbol;Acc:HGNC:1480]
20	MBP	0.61	3e-13	4e-12	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925]

p-values



MSC2 vs MSC3

Local Summary

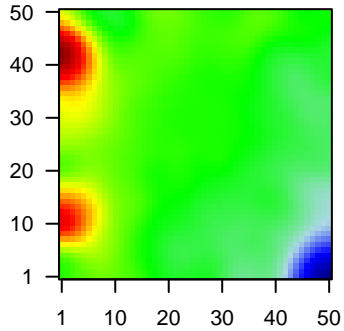
%DE = 0.97
 # metagenes = 22
 # genes = 332
 # genes in genesets = 332

 # genes with fdr < 0.1 = 317 (2 + / 315 -)
 # genes with fdr < 0.05 = 309 (1 + / 308 -)
 # genes with fdr < 0.01 = 275 (0 + / 275 -)

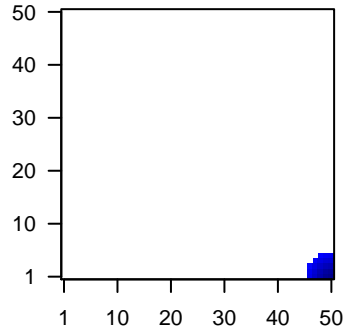
<r> metagenes = 1
 <r> genes = 0.76

 <FC> = -0.39
 <shrinkage-t> = -1.76
 <p-value> = 0
 <fdr> = 0.22

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ANXA1	-1.32	2e-16	2e-16	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	EDIL3	-0.86	2e-16	2e-16	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGI
3	F2R	-0.88	2e-16	2e-16	50 x 1 coagulation factor II (thrombin) receptor [Source:HGNC Synt
4	FRMD6	-1	2e-16	2e-16	50 x 1 FERM domain containing 6 [Source:HGNC Symbol;Acc:HGN
5	MYOF	-1.11	2e-16	2e-16	50 x 1 myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]
6	PTPRM	-0.96	2e-16	2e-16	50 x 1 protein tyrosine phosphatase, receptor type, M [Source:HGN
7	TMEM45A	-0.93	2e-16	2e-16	50 x 1 transmembrane protein 45A [Source:HGNC Symbol;Acc:HGN
8	TNFRSF12A	-1.21	2e-16	2e-16	50 x 1 tumor necrosis factor receptor superfamily, member 12A [Sou
9	TXNIP	-0.94	2e-16	2e-16	50 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:HC
10	SPOCK1	-0.82	1e-15	1e-14	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycar
11	CRYAB	-0.82	2e-15	6e-14	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
12	TPM4	-0.8	1e-14	6e-14	50 x 1 tropomyosin 4 [Source:HGNC Symbol;Acc:HGNC:12013]
13	LMO7	-0.86	1e-14	2e-13	50 x 2 LIM domain 7 [Source:HGNC Symbol;Acc:HGNC:6646]
14	THBS1	-0.8	4e-14	2e-12	50 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
15	SLIT2	-0.82	2e-13	5e-12	50 x 1 slit homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGN
16	TFPI	-0.79	1e-12	5e-12	50 x 1 tissue factor pathway inhibitor (lipoprotein-associated coagul:
17	C10orf10	-0.75	1e-12	1e-11	49 x 1 chromosome 10 open reading frame 10 [Source:HGNC Synt
18	SPARC	-0.62	2e-12	1e-11	50 x 2 secreted protein, acidic, cysteine-rich (osteonectin) [Source:t
19	AHNAK	-0.67	3e-12	1e-11	50 x 1 AHNAK nucleoprotein [Source:HGNC Symbol;Acc:HGNC:34:
20	LIMCH1	-0.77	4e-12	2e-10	50 x 1 LIM and calponin homology domains 1 [Source:HGNC Symb

p-values

