

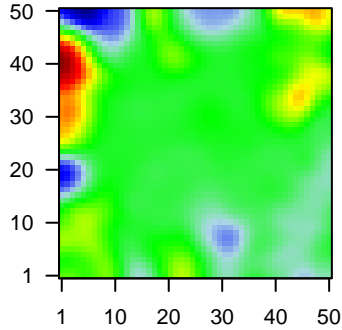
C10_mel

Global Summary

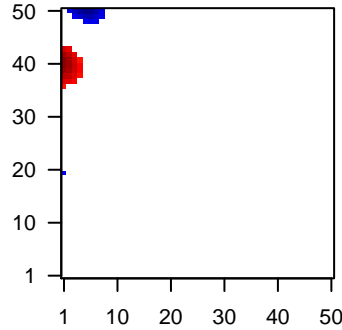
%DE = 0.23
 # genes with $fdr < 0.2$ = 2977 (1781 + / 1196 -)
 # genes with $fdr < 0.1$ = 2422 (1466 + / 956 -)
 # genes with $fdr < 0.05$ = 1906 (1199 + / 707 -)
 # genes with $fdr < 0.01$ = 1263 (805 + / 458 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.05
 <p-value> = 0.07
 <fdr> = 0.77

Profile



Regulated Spots



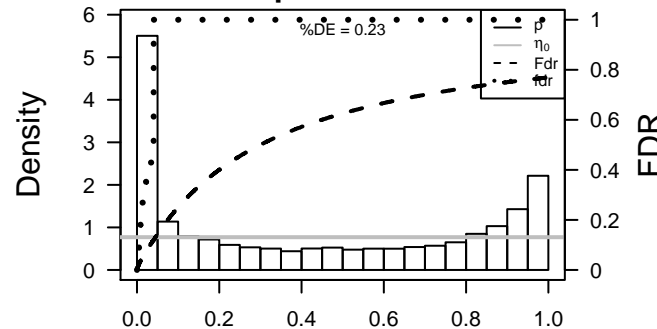
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ADSL	-1.58	2e-16	2e-13	28 x 50 adenylosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:21
2	BABAM1	-1.51	2e-16	2e-13	43 x 47 BRISC and BRCA1 A complex member 1 [Source:HGNC Syr
3	C1orf198	-1.39	2e-16	2e-13	49 x 1 chromosome 1 open reading frame 198 [Source:HGNC Synt
4	CCNDBP1	-1.68	2e-16	2e-13	1 x 21 cyclin D-type binding-protein 1 [Source:HGNC Symbol;Acc:t
5	CCNL1	-1.93	2e-16	2e-13	38 x 47 cyclin L1 [Source:HGNC Symbol;Acc:HGNC:20569]
6	DST	-1.51	2e-16	2e-13	46 x 1 dystonin [Source:HGNC Symbol;Acc:HGNC:1090]
7	E2F5	1.86	2e-16	2e-13	17 x 4 E2F transcription factor 5, p130-binding [Source:HGNC Symi
8	FBXO7	-1.53	2e-16	2e-13	1 x 20 F-box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586]
9	HDLBP	-0.98	2e-16	2e-13	44 x 42 high density lipoprotein binding protein [Source:HGNC Symb
10	MRPS35	-1.5	2e-16	2e-13	37 x 50 mitochondrial ribosomal protein S35 [Source:HGNC Symbol,t
11	NAE1	-1.53	2e-16	2e-13	10 x 45 NEDD8 activating enzyme E1 subunit 1 [Source:HGNC Synt
12	PSAT1	-1.72	2e-16	2e-13	14 x 50 phosphoserine aminotransferase 1 [Source:HGNC Symbol;Ar
13	SDF2	-1.67	2e-16	2e-13	48 x 50 stromal cell-derived factor 2 [Source:HGNC Symbol;Acc:HG
14	SH3BGRL3	-1.5	2e-16	2e-13	50 x 42 SH3 domain binding glutamate-rich protein like 3 [Source:HC
15	SMC4	-1.49	2e-16	2e-13	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Sy
16	SS18	-1.74	2e-16	2e-13	10 x 45 synovial sarcoma translocation, chromosome 18 [Source:HGI
17	YIPF3	-1.54	2e-16	2e-13	45 x 50 Yip1 domain family, member 3 [Source:HGNC Symbol;Acc:Hi
18	UCK2	-1.49	4e-16	3e-12	1 x 21 uridine-cytidine kinase 2 [Source:HGNC Symbol;Acc:HGNC:
19	CHN1	1.77	7e-16	3e-12	1 x 26 chimerin 1 [Source:HGNC Symbol;Acc:HGNC:1943]
20	ITPA	-1.05	9e-16	2e-11	5 x 40 inosine triphosphatase (nucleoside triphosphate pyrophosph

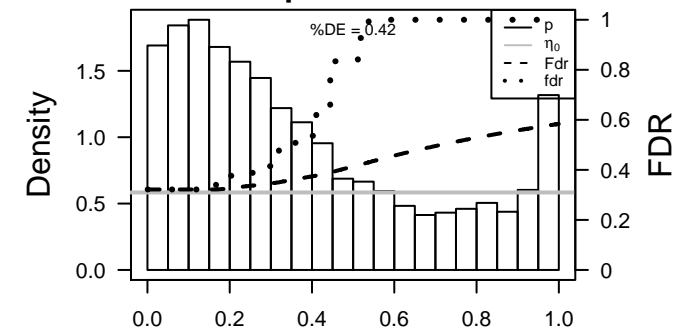
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.24	0.002	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5.75	0.002	1468	CC mitochondrion
3	5.46	0.003	401	CC mitochondrial inner membrane
4	5.17	0.003	159	Glio WILLSCHER_GBM_proteomics_wtOnly_Differencelst
5	5.13	0.003	42	LymphomaOARO_OxPhos_in_DLCL_UP
6	5.01	0.004	421	GSEA C2MOOHTA_MITOCHONDRIA
7	4.88	0.004	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
8	4.86	0.004	478	GSEA C2STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
9	4.84	0.004	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
10	4.81	0.004	135	BP cellular metabolic process
11	4.73	0.004	685	GSEA C2KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR
12	4.7	0.004	405	GSEA C2MOOHTA_HUMAN_MITODB_6_2002
13	4.67	0.005	102	GSEA C2KEGG_PARKINSONS_DISEASE
14	4.62	0.005	10	GSEA C2LIU_TOPBP1_TARGETS
15	4.61	0.005	85	GSEA C2MOOHTA_VOXPPOS
16	4.58	0.005	94	BP respiratory electron transport chain
17	4.55	0.005	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
18	4.49	0.005	398	GSEA C2MOOHTA_PGC
19	4.45	0.005	277	BP translation
20	4.43	0.005	41	CC mitochondrial nucleoid
<i>Underexpressed</i>				
1	-8.5	5e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
2	-8.16	6e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	-8.04	6e-04	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	-7.39	8e-04	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	-7.12	1e-03	944	GSEA C2NUYTEN_EZH2_TARGETS_DN
6	-7.04	1e-03	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BIL_LYMPHOCYTE_UP
7	-6.8	1e-03	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
8	-6.57	1e-03	93	GSEA C2KONG_E2F3_TARGETS
9	-6.34	5e-02	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	-6.31	2e-03	196	HM HALLMARK_G2M_CHECKPOINT
11	-6.31	2e-03	89	GSEA C2MORI_IMMATURE_B_LYMPHOCYTE_DN
12	-6.27	2e-03	165	GSEA C2XIANHANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
13	-6.25	2e-03	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
14	-6.24	2e-03	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
15	-6.19	2e-03	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
16	-6.06	2e-03	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	-6.05	2e-03	145	GSEA C2ZHANG_CYCLING_GENES
18	-6.03	2e-03	23	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
19	-6.01	2e-03	684	GSEA C2PATIL_LIVER_CANCER
20	-5.95	2e-03	87	GSEA C2ZHANG_TLX_TARGETS_UP

p-values



p-values



C10_mel

Local Summary

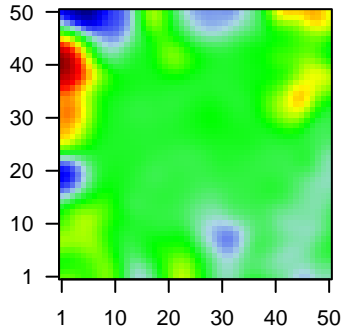
%DE = 0.77
 # metagenes = 25
 # genes = 335
 # genes in genesets = 334

 # genes with $fdr < 0.1$ = 215 (177 + / 38 -)
 # genes with $fdr < 0.05$ = 163 (136 + / 27 -)
 # genes with $fdr < 0.01$ = 141 (117 + / 24 -)

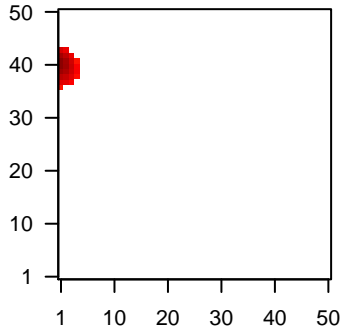
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.15

 $\langle FC \rangle$ = 0.28
 $\langle \text{shrinkage-t} \rangle$ = 5.22
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.48

Profile



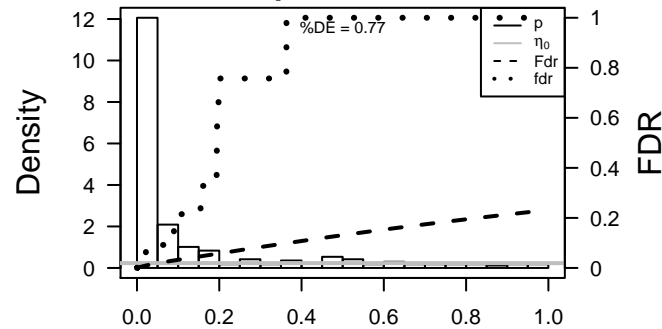
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CTSL	0.74	6e-15	9e-12	2 x 40 cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
2	SEPSECS	1.63	1e-13	5e-11	1 x 37 Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA syr
3	MRPS11	-1.39	8e-13	1e-09	1 x 37 mitochondrial ribosomal protein S11 [Source:HGNC Symbol;]
4	MTG1	-1.34	1e-11	7e-09	2 x 39 mitochondrial ribosome-associated GTPase 1 [Source:HGNC
5	TMEM199	-1.29	1e-10	1e-08	4 x 40 transmembrane protein 199 [Source:HGNC Symbol;Acc:HGNC:2537]
6	MAP3K6	1.39	3e-10	2e-08	1 x 37 mitogen-activated protein kinase kinase kinase 6 [Source:HGNC
7	MITF	0.61	6e-10	3e-08	1 x 41 microphthalmia-associated transcription factor [Source:HGNC
8	WIPF3	1.33	1e-09	3e-08	1 x 41 WAS/WASL interacting protein family, member 3 [Source:HGNC
9	LGALS3	1.17	1e-09	1e-07	1 x 43 lectin, galactoside-binding, soluble, 3 [Source:HGNC Symbol
10	UHRF2	1.3	3e-09	1e-07	1 x 36 ubiquitin-like with PHD and ring finger domains 2, E3 ubiquiti
11	HPS4	-1.2	8e-09	1e-07	1 x 42 Hermansky-Pudlak syndrome 4 [Source:HGNC Symbol;Acc:HGNC:2537]
12	ZNF577	1.26	8e-09	1e-07	2 x 39 zinc finger protein 577 [Source:HGNC Symbol;Acc:HGNC:2537]
13	BCS1L	1.26	8e-09	1e-07	1 x 38 BC1 (ubiquinol-cytochrome c reductase) synthesis-like [Sou
14	RBPMS2	1.26	9e-09	3e-07	1 x 42 RNA binding protein with multiple splicing 2 [Source:HGNC S
15	DAB2	0.5	2e-08	3e-07	3 x 41 Dab, mitogen-responsive phosphoprotein, homolog 2 (Droso
16	ANO2	1.24	2e-08	1e-06	1 x 42 anoctamin 2, calcium activated chloride channel [Source:HGNC
17	CAPG	1.2	4e-08	1e-06	1 x 43 capping protein (actin filament), gelsolin-like [Source:HGNC :
18	PLGRKT	1.19	7e-08	1e-06	1 x 41 plasminogen receptor, C-terminal lysine transmembrane prot
19	TMC6	-1.16	7e-08	2e-06	1 x 42 transmembrane channel-like 6 [Source:HGNC Symbol;Acc:HGNC:2537]
20	PFKM	1.01	1e-07	2e-06	1 x 41 phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HGNC:2537]

p-values



C10_mel

Local Summary

%DE = 0.67
 # metagenes = 1
 # genes = 64
 # genes in genesets = 64

 # genes with $fdr < 0.1$ = 33 (9 + / 24 -)
 # genes with $fdr < 0.05$ = 27 (7 + / 20 -)
 # genes with $fdr < 0.01$ = 21 (6 + / 15 -)

<r> metagenes = NA

<r> genes = 0.23

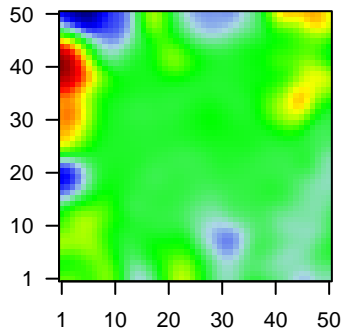
<FC> = -0.26

<shrinkage-t> = -4.57

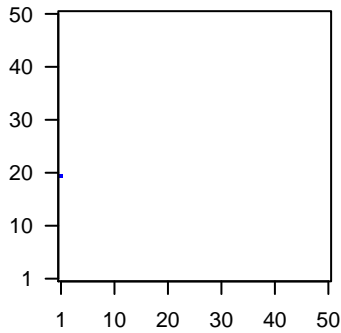
<p-value> = 0

<fdr> = 0.52

Profile



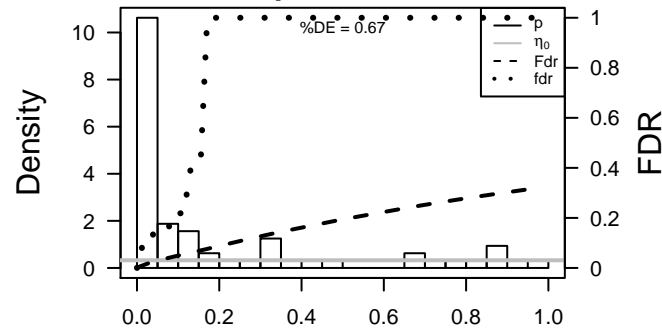
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	FBXO7	-1.53	2e-16	5e-15	1 x 20 F-box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586]
2	PRELID1	-1.24	1e-09	8e-08	1 x 20 PRELI domain containing 1 [Source:HGNC Symbol;Acc:HGNC:13587]
3	TMED3	-1.15	5e-09	2e-07	1 x 20 transmembrane emp24 protein transport domain containing 3
4	EIF2AK1	-1.17	1e-08	7e-06	1 x 20 eukaryotic translation initiation factor 2-alpha kinase 1 [Source:HGNC Symbol;Acc:HGNC:13588]
5	PTPN2	-0.98	3e-07	1e-05	1 x 20 protein tyrosine phosphatase, non-receptor type 2 [Source:HGNC Symbol;Acc:HGNC:13589]
6	ARF5	-1.06	1e-06	1e-05	1 x 20 ADP-ribosylation factor 5 [Source:HGNC Symbol;Acc:HGNC:13590]
7	STUB1	-1.06	1e-06	2e-05	1 x 20 STIP1 homology and U-box containing protein 1, E3 ubiquitin ligase
8	UOQRFS1	-1.01	2e-06	2e-05	1 x 20 ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
9	SLC11A2	-1.03	3e-06	6e-05	1 x 20 solute carrier family 11 (proton-coupled divalent metal ion transporter) member 2
10	EI24	0.99	6e-06	2e-04	1 x 20 etoposide induced 2.4 [Source:HGNC Symbol;Acc:HGNC:13591]
11	PGLS	-0.95	2e-05	2e-04	1 x 20 6-phosphogluconolactonase [Source:HGNC Symbol;Acc:HGNC:13592]
12	ZCCHC9	-0.92	3e-05	1e-03	1 x 20 zinc finger, CCHC domain containing 9 [Source:HGNC Symbol;Acc:HGNC:13593]
13	RIOK2	0.87	8e-05	1e-03	1 x 20 RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
14	UBE2J2	-0.84	1e-04	2e-03	1 x 20 ubiquitin-conjugating enzyme E2, J2 [Source:HGNC Symbol;Acc:HGNC:13594]
15	P4HB	-0.33	2e-04	4e-03	1 x 20 prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symbol;Acc:HGNC:13595]
16	NT5C3B	0.74	6e-04	4e-03	1 x 20 5'-nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:HGNC:13596]
17	SLC48A1	0.74	8e-04	4e-03	1 x 20 solute carrier family 48 (heme transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:13597]
18	GCSH	-0.73	8e-04	6e-03	1 x 20 glycine cleavage system protein H (aminomethyl carrier) [Source:HGNC Symbol;Acc:HGNC:13598]
19	POLDIP2	0.71	1e-03	1e-02	1 x 20 polymerase (DNA-directed), delta interacting protein 2 [Source:HGNC Symbol;Acc:HGNC:13599]
20	INSIG1	0.67	2e-03	1e-02	1 x 20 insulin induced gene 1 [Source:HGNC Symbol;Acc:HGNC:60]

p-values



C10_mel

Local Summary

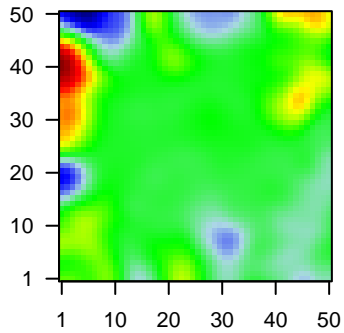
%DE = 0.82
 # metagenes = 16
 # genes = 223
 # genes in genesets = 223

 # genes with $fdr < 0.1$ = 148 (32 + / 116 -)
 # genes with $fdr < 0.05$ = 126 (26 + / 100 -)
 # genes with $fdr < 0.01$ = 75 (15 + / 60 -)

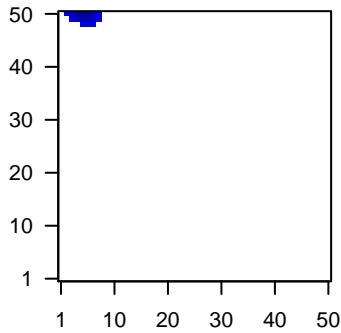
$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.39

 $\langle FC \rangle = -0.3$
 $\langle \text{shrinkage-t} \rangle = -4.73$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.48$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SMC4	-1.49	2e-16	9e-15	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Sy
2	HMGB2	-1.28	1e-10	6e-08	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
3	CENPN	-1.21	4e-09	6e-08	4 x 50 centromere protein N [Source:HGNC Symbol;Acc:HGNC:308
4	TMPO	-1.21	4e-09	6e-08	5 x 50 thymopoietin [Source:HGNC Symbol;Acc:HGNC:11875]
5	TRIP13	-1.2	6e-09	6e-08	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symb
6	ACTL6A	0.76	6e-09	3e-07	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
7	RACGAP1	1.24	1e-08	5e-07	7 x 50 Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:
8	MAD2L2	-1.18	3e-08	6e-07	2 x 50 MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S
9	NUSAP1	-1.17	4e-08	8e-07	6 x 50 nucleolar and spindle associated protein 1 [Source:HGNC Sy
10	SKP2	-1.16	7e-08	8e-07	3 x 50 S-phase kinase-associated protein 2, E3 ubiquitin protein lig
11	RFC5	-1.04	8e-08	1e-05	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
12	NUDT1	-1.08	6e-07	1e-05	5 x 48 nudix (nucleoside diphosphate linked moiety X)-type motif 1
13	BARD1	-1.08	6e-07	1e-05	2 x 50 BRCA1 associated RING domain 1 [Source:HGNC Symbol;A
14	UBE2T	-1.07	8e-07	1e-05	4 x 50 ubiquitin-conjugating enzyme E2T [Source:HGNC Symbol;Ac
15	CKAP2	-1	1e-06	1e-05	6 x 50 cytoskeleton associated protein 2 [Source:HGNC Symbol;Acc
16	UBE2C	-1.05	1e-06	2e-05	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;A
17	KIF23	-1.04	2e-06	2e-05	6 x 50 kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC
18	CDKN3	-0.76	3e-06	2e-05	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
19	FAM111A	-1.02	3e-06	2e-05	4 x 50 family with sequence similarity 111, member A [Source:HGNC
20	CENPF	-0.96	3e-06	3e-05	6 x 50 centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac

p-values

