

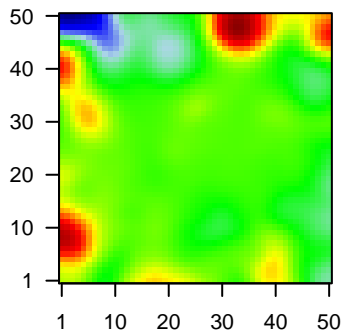
A5_mel

Global Summary

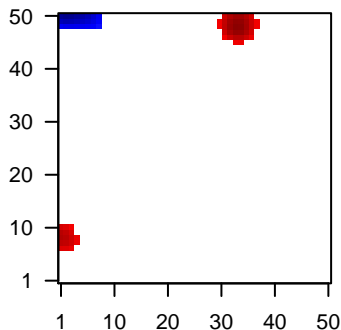
%DE = 0.2
 # genes with $fdr < 0.2$ = 2566 (1527 + / 1039 -)
 # genes with $fdr < 0.1$ = 2015 (1202 + / 813 -)
 # genes with $fdr < 0.05$ = 1714 (1037 + / 677 -)
 # genes with $fdr < 0.01$ = 1003 (595 + / 408 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.02
 <p-value> = 0.09
 <fdr> = 0.8

Profile



Regulated Spots



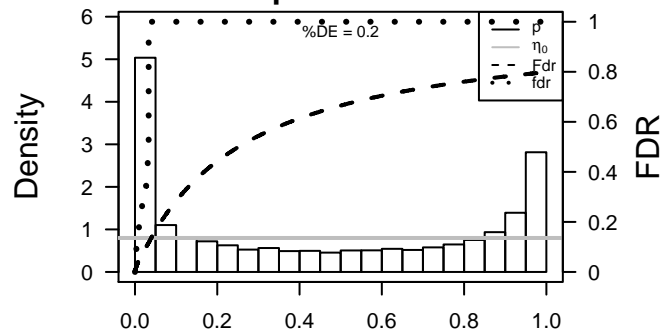
Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	-1.81	2e-16	1e-13	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ARL1	-1.57	2e-16	1e-13	25 x 49 ADP-ribosylation factor-like 1 [Source:HGNC Symbol;Acc:HGNC:24124]
3	BRD8	-1.73	2e-16	1e-13	50 x 39 bromodomain containing 8 [Source:HGNC Symbol;Acc:HGNC:24124]
4	BSCL2	-2.01	2e-16	1e-13	50 x 50 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:HGNC Symbol;Acc:HGNC:24124]
5	DAZAP2	-0.96	2e-16	1e-13	8 x 42 DAZ associated protein 2 [Source:HGNC Symbol;Acc:HGNC:24124]
6	DPY30	-1.67	2e-16	1e-13	22 x 46 dpy-30 homolog (C. elegans) [Source:HGNC Symbol;Acc:HGNC:24124]
7	EIF2A	-1.8	2e-16	1e-13	50 x 12 eukaryotic translation initiation factor 2A, 65kDa [Source:HGNC Symbol;Acc:HGNC:24124]
8	EIF3G	-1.69	2e-16	1e-13	47 x 39 eukaryotic translation initiation factor 3, subunit G [Source:HGNC Symbol;Acc:HGNC:24124]
9	EIF4A2	-1.19	2e-16	1e-13	50 x 11 eukaryotic translation initiation factor 4A2 [Source:HGNC Symbol;Acc:HGNC:24124]
10	ELOVL5	-1.51	2e-16	1e-13	18 x 48 ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:HGNC:24124]
11	EXOSC8	-1.71	2e-16	1e-13	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:24124]
12	FLII	-1.6	2e-16	1e-13	17 x 50 flightless I homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:24124]
13	HNRNPH3	-1.69	2e-16	1e-13	9 x 47 heterogeneous nuclear ribonucleoprotein H3 (2H9) [Source:HGNC Symbol;Acc:HGNC:24124]
14	SDF2	-1.67	2e-16	1e-13	48 x 50 stromal cell-derived factor 2 [Source:HGNC Symbol;Acc:HGNC:24124]
15	SHFM1	-0.88	2e-16	1e-13	25 x 44 split hand/foot malformation (ectrodactyly) type 1 [Source:HGNC Symbol;Acc:HGNC:24124]
16	TFRC	-0.98	2e-16	1e-13	6 x 15 transferrin receptor [Source:HGNC Symbol;Acc:HGNC:11763]
17	TMEM106C	-2.07	2e-16	1e-13	5 x 48 transmembrane protein 106C [Source:HGNC Symbol;Acc:HGNC:24124]
18	TXLNA	-1.26	2e-16	1e-13	12 x 43 taxilin alpha [Source:HGNC Symbol;Acc:HGNC:30685]
19	ANAPC5	-1.54	4e-16	9e-12	20 x 42 anaphase promoting complex subunit 5 [Source:HGNC Symbol;Acc:HGNC:24124]
20	SAE1	-1.44	4e-16	9e-12	4 x 47 SUMO1 activating enzyme subunit 1 [Source:HGNC Symbol;Acc:HGNC:24124]

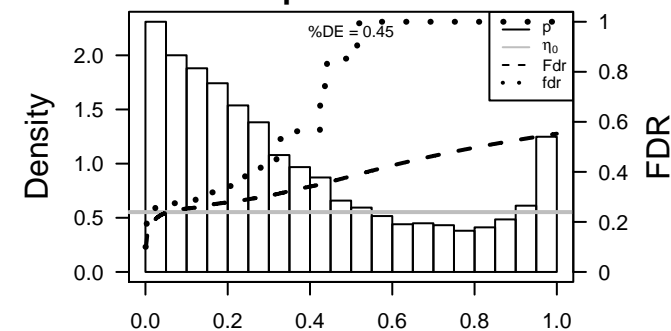
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.21	6e-04	401	CC mitochondrial inner membrane
2	7.03	1e-03	405	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
3	6.75	1e-03	421	GSEA C2MOOTHA_MITOCHONDRIA
4	6.69	1e-03	94	BP respiratory electron transport chain
5	6.61	1e-03	368	GSEA C2STEIN_ESRRA_TARGETS_UP
6	6.55	1e-03	213	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
7	6.49	1e-03	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	6.23	2e-03	1468	CC mitochondrion
9	6.14	2e-03	1730	BP small molecule metabolic process
10	5.73	2e-03	500	GSEA C2STEIN_ESRRA_TARGETS
11	5.54	2e-03	135	BP cellular metabolic process
12	5.53	2e-03	102	GSEA C2KEGG_PARKINSONS_DISEASE
13	5.38	3e-03	85	GSEA C2MOOTHA_VOXPPOS
14	5.34	3e-03	78	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
15	5.3	3e-03	107	GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION
16	5.27	3e-03	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
17	4.76	4e-03	83	BP mitochondrial translational elongation
18	4.68	4e-03	83	BP mitochondrial translational termination
19	4.61	5e-03	220	GSEA C2RICKMAN_METASTASIS_DN
20	4.6	5e-03	63	Glio Stuehler_Proteins_up_in_STS
<i>Underexpressed</i>				
1	-11.91	1e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
2	-11.52	2e-04	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
3	-11.23	2e-04	197	HM HALLMARK_E2F_TARGETS
4	-10.81	2e-04	1251	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
5	-10.61	2e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
6	-10.52	2e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	-10.37	2e-04	160	GSEA C2PUJANA_XPRSS_INT_NETWORK
8	-10.25	2e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
9	-9.67	3e-04	216	GSEA C2MARKEY_RB1_ACUTE_LOF_DN
10	-9.58	3e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
11	-9.23	4e-04	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
12	-9.15	4e-04	145	GSEA C2ZHANG_CYCLING_GENES
13	-9.01	4e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
14	-8.91	4e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
15	-8.9	4e-04	663	CC chromosome
16	-8.85	4e-04	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
17	-8.84	4e-04	113	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
18	-8.72	5e-04	616	GSEA C2BENPORATH_CYCLING_GENES
19	-8.7	5e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
20	-8.5	5e-04	99	GSEA C2BURTON_ADIPOGENESIS_3

p-values



p-values



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Local Summary

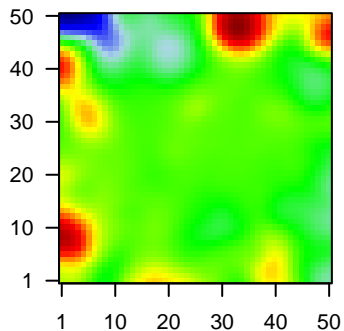
%DE = 0.72
 # metagenes = 17
 # genes = 233
 # genes in genesets = 231

 # genes with $fdr < 0.1$ = 115 (98 + / 17 -)
 # genes with $fdr < 0.05$ = 89 (78 + / 11 -)
 # genes with $fdr < 0.01$ = 65 (57 + / 8 -)

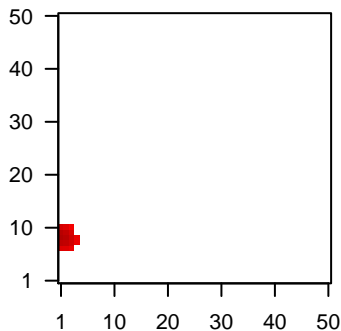
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = 0.34
 $\langle \text{shrinkage-t} \rangle$ = 5.43
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.58

Profile



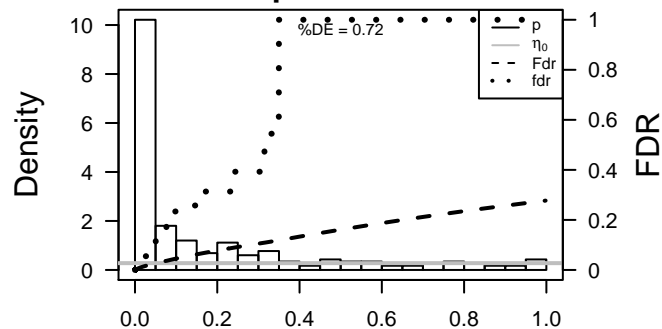
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	PLA2G4B	1.82	2e-13	2e-08	3 x 9 phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym]
2	OSBP	1.56	3e-10	1e-07	1 x 7 oxysterol binding protein [Source:HGNC Symbol;Acc:HGNC:1
3	ARHGAP35	1.49	2e-09	9e-07	4 x 8 Rho GTPase activating protein 35 [Source:HGNC Symbol;Acc
4	PIP5K1B	1.4	2e-08	9e-07	1 x 9 phosphatidylinositol-4-phosphate 5-kinase, type I, beta [Sou
5	CAMTA2	1.38	3e-08	6e-06	1 x 8 calmodulin binding transcription activator 2 [Source:HGNC S]
6	CTC-534A2.2	1.31	1e-07	7e-06	3 x 8
7	GAA	1.28	2e-07	2e-05	1 x 7 glucosidase, alpha, acid [Source:HGNC Symbol;Acc:HGNC:4
8	RAPGEF6	1.24	6e-07	2e-05	1 x 10 Rap guanine nucleotide exchange factor (GEF) 6 [Source:HG
9	LRRC8D	1.22	9e-07	2e-05	1 x 8 leucine rich repeat containing 8 family, member D [Source:HC
10	ROPN1B	1.21	1e-06	2e-05	1 x 10 rhophilin associated tail protein 1B [Source:HGNC Symbol;Ac
11	POPDC2	1.2	1e-06	1e-04	1 x 9 popeye domain containing 2 [Source:HGNC Symbol;Acc:HGNC
12	AGA	1.14	4e-06	1e-04	1 x 7 aspartylglucosaminidase [Source:HGNC Symbol;Acc:HGNC:1
13	PCSK2	1.13	6e-06	1e-04	1 x 10 proprotein convertase subtilisin/kexin type 2 [Source:HGNC S
14	TMEM101	1.1	7e-06	1e-04	1 x 11 transmembrane protein 101 [Source:HGNC Symbol;Acc:HGNC
15	SS18L1	1.1	9e-06	1e-04	1 x 10 synovial sarcoma translocation gene on chromosome 18-like
16	SEMA6D	1.1	9e-06	1e-04	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic
17	XG	1.09	1e-05	1e-04	2 x 9 Xg blood group [Source:HGNC Symbol;Acc:HGNC:12806]
18	ARMCX5	1.08	1e-05	1e-04	2 x 7 armadillo repeat containing, X-linked 5 [Source:HGNC Symb
19	KCNAB2	1.08	1e-05	4e-04	1 x 10 potassium channel, voltage gated subfamily A regulatory beta
20	VEPH1	1.03	3e-05	4e-04	1 x 11 ventricular zone expressed PH domain-containing 1 [Source:

p-values



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Local Summary

%DE = 0.79
 # metagenes = 36
 # genes = 250
 # genes in genesets = 249

 # genes with $fdr < 0.1$ = 156 (136 + / 20 -)
 # genes with $fdr < 0.05$ = 130 (119 + / 11 -)
 # genes with $fdr < 0.01$ = 101 (95 + / 6 -)

<r> metagenes = 0.87

<r> genes = 0.07

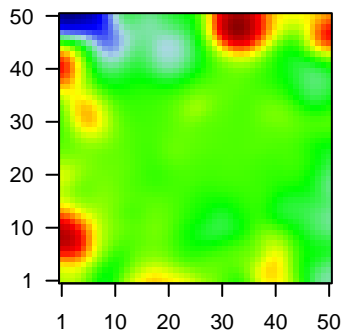
<FC> = 0.44

<shrinkage-t> = 7.17

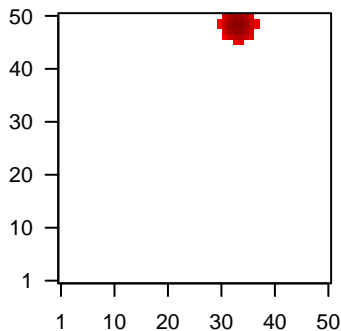
<p-value> = 0

<fdr> = 0.49

Profile



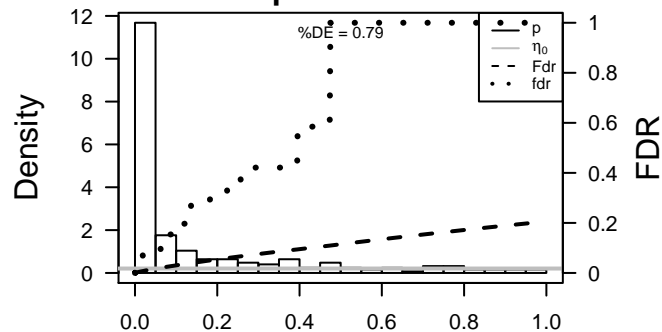
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SLC44A2	1.73	3e-12	3e-10	36 x 50 solute carrier family 44 (choline transporter), member 2 [Sour
2	ENPP5	1.7	8e-12	2e-09	34 x 47 ectonucleotide pyrophosphatase/phosphodiesterase 5 (putati
3	ZNF799	1.64	4e-11	2e-09	34 x 46 zinc finger protein 799 [Source:HGNC Symbol;Acc:HGNC:28
4	PLCD4	1.62	7e-11	1e-08	35 x 46 phospholipase C, delta 4 [Source:HGNC Symbol;Acc:HGNC:
5	ZRSR1	1.54	6e-10	1e-08	31 x 48 zinc finger (CCCH type), RNA-binding motif and serine/argini
6	HOGA1	1.52	8e-10	1e-08	35 x 46 4-hydroxy-2-oxoglutarate aldolase 1 [Source:HGNC Symbol
7	THAP10	1.52	9e-10	3e-08	32 x 46 THAP domain containing 10 [Source:HGNC Symbol;Acc:HG
8	METTL7A	1.5	1e-09	1e-07	33 x 46 methyltransferase like 7A [Source:HGNC Symbol;Acc:HGNC:
9	PLCG1	1.47	3e-09	1e-07	31 x 50 phospholipase C, gamma 1 [Source:HGNC Symbol;Acc:HGN
10	SLC44A3	1.43	8e-09	1e-07	34 x 46 solute carrier family 44, member 3 [Source:HGNC Symbol;Ac
11	YIPF7	1.43	9e-09	2e-07	33 x 46 Yip1 domain family, member 7 [Source:HGNC Symbol;Acc:Hi
12	SERPINA1	1.41	1e-08	2e-07	31 x 47 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ar
13	LOH12CR1	1.41	2e-08	3e-07	36 x 50 loss of heterozygosity, 12, chromosomal region 1 [Source:HG
14	GAGE12B	1.39	2e-08	5e-07	35 x 46 G antigen 12B [Source:HGNC Symbol;Acc:HGNC:26779]
15	ZNF708	1.37	3e-08	5e-07	33 x 47 zinc finger protein 708 [Source:HGNC Symbol;Acc:HGNC:12
16	SLC25A35	1.36	5e-08	5e-07	32 x 48 solute carrier family 25, member 35 [Source:HGNC Symbol;A
17	LRAT	1.36	5e-08	3e-06	34 x 47 lecithin retinol acyltransferase (phosphatidylcholine--retinol C
18	POLR3F	1.32	1e-07	6e-06	31 x 50 polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa [E
19	NFATC4	1.29	2e-07	6e-06	34 x 46 nuclear factor of activated T-cells, cytoplasmic, calcineurin-d
20	JMJD7-PLA2	1.27	3e-07	8e-06	34 x 47 JMJD7-PLA2G4B readthrough [Source:HGNC Symbol;Acc:J

p-values



A5_mel

Local Summary

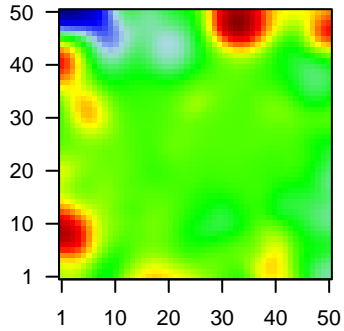
%DE = 0.84
 # metagenes = 24
 # genes = 359
 # genes in genesets = 358

 # genes with $fdr < 0.1$ = 227 (31 + / 196 -)
 # genes with $fdr < 0.05$ = 198 (26 + / 172 -)
 # genes with $fdr < 0.01$ = 115 (15 + / 100 -)

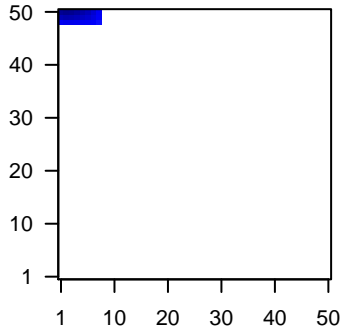
 $\langle r \rangle$ metagenes = 0.92
 $\langle r \rangle$ genes = 0.3

 $\langle FC \rangle = -0.42$
 $\langle \text{shrinkage-t} \rangle = -6.94$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.52$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	-1.81	2e-16	4e-15	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	EXOSC8	-1.71	2e-16	4e-15	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
3	TMEM106C	-2.07	2e-16	4e-15	5 x 48 transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
4	FANCL	-1.52	1e-13	2e-11	1 x 48 Fanconi anemia, complementation group L [Source:HGNC S
5	SMC4	-1.49	5e-13	7e-10	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Sy
6	HSPB11	-1.43	3e-11	7e-10	1 x 48 heat shock protein family B (small), member 11 [Source:HG
7	HLTF	-1.43	4e-11	7e-10	3 x 48 helicase-like transcription factor [Source:HGNC Symbol;Acc:
8	NUPL1	-1.43	4e-11	3e-09	1 x 48 nucleoporin like 1 [Source:HGNC Symbol;Acc:HGNC:20261]
9	HSD17B11	-1.4	1e-10	3e-09	8 x 50 hydroxysteroid (17-beta) dehydrogenase 11 [Source:HGNC :
10	LBR	-1.39	2e-10	3e-09	7 x 50 lamin B receptor [Source:HGNC Symbol;Acc:HGNC:6518]
11	RFC5	-1.39	2e-10	2e-08	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
12	ASRGL1	-1.35	7e-10	2e-08	1 x 50 asparaginase like 1 [Source:HGNC Symbol;Acc:HGNC:1644
13	DNMT1	-1.01	1e-09	2e-08	2 x 48 DNA (cytosine-5-)-methyltransferase 1 [Source:HGNC Symi
14	RRM1	-1.2	1e-09	1e-07	2 x 50 ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGI
15	CDKN3	-1.08	5e-09	1e-07	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
16	HIST1H4E	1.44	6e-09	1e-07	7 x 50 histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:47
17	CKLF	-1.3	9e-09	1e-07	3 x 49 chemokine-like factor [Source:HGNC Symbol;Acc:HGNC:13
18	MIS18A	-1.3	9e-09	3e-07	3 x 49 MIS18 kinetochore protein A [Source:HGNC Symbol;Acc:HGI
19	TUBB4B	-1.09	2e-08	3e-07	7 x 50 tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
20	PDS5B	-1.27	2e-08	3e-07	1 x 50 PDS5 cohesin associated factor B [Source:HGNC Symbol;Ac

p-values

