A

Species Assembly

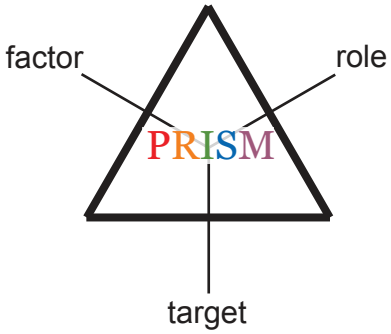
- Human NCBI build 36.1 (UCSC hg18, Mar 2006)
- Mouse NCBI build 37(UCSC mm9, Jul 2007)

browse

Perspective

Transcription factor regulator		search
Biological context		search
Target gene		search
Target genomic region		search

reset



B

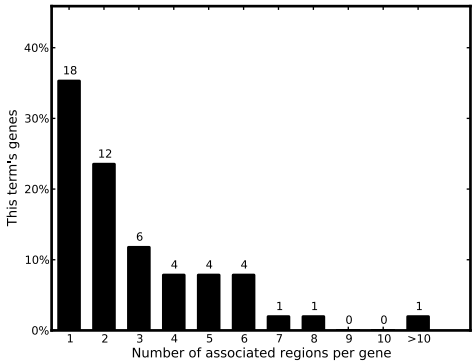
Transcription Factor	Ontology	Biological Function	E value	P-value	Fold Enrichment	Target Genes	Genes Hit	Binding Sites
/MYOG/					>=2.2			
MYOG	Mouse Phenotypes	abnormal muscle development	0.465	2.81e-25	2.69	*TBX1*, *PAX7*, *PAX1*, *DLL1*, *ACTA1* + 46 more	51	146 (to UCSC)
MYOG	GO Biological Process	skeletal muscle organ development	0.116	5.29e-13	2.22	*PAX7*, *ACTA1*, *SKI*, *CAV1*, *MET* + 43 more	48	102 (to UCSC)
MYOG	Mouse Phenotypes	abnormal diaphragm morphology	0.232	5.91e-13	2.22	*PAX7*, *CDKN1C*, *MET*, *MYOG*, *FGFRL1* + 37 more	42	102 (to UCSC)
MYOG	Mouse Phenotypes	dilated heart right ventricle	0.232	1.18e-11	2.31	*CXCR7*, *BAZ1B*, *PDGFB*, *CAV1*, *PDLIM3* + 26 more	31	83 (to UCSC)

C

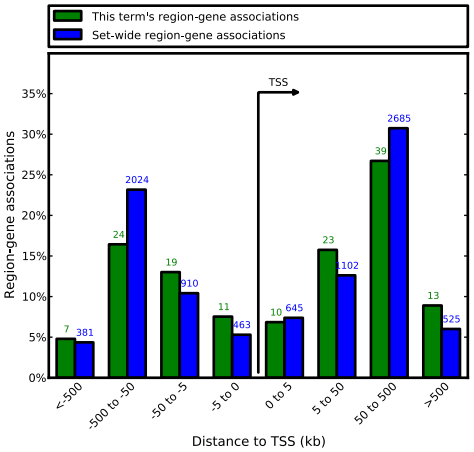
Term: *abnormal muscle development* (ID: MP:0000733) from MGIPhenotype .

This term's region-gene association graphs

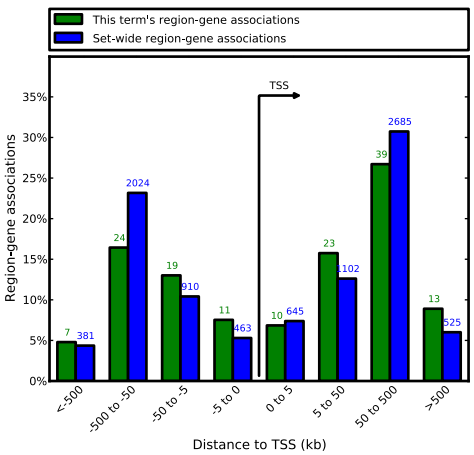
Number of associated regions per gene



Binned by orientation and distance to TSS



Binned by absolute distance to TSS



This term's genomic region-gene association tables

This term's genomic region -> gene association table

Region	Gene (distance to TSS)
G_MYOGENIN_01.22	PAX1 (+855,304)
G_MYOGENIN_01.35	PDGFC (-660)
G_MYOGENIN_01.53	MET (-2,463)
G_MYOGENIN_01.55	PRDM1 (-654,890)
G_MYOGENIN_01.86	CTBP2 (-56,990)
G_MYOGENIN_01.89	PAX7 (+14,545)
G_MYOGENIN_01.97	MET (-146,311)

This term's gene -> genomic region association table

Gene	Region (distance to TSS)
ACTA1	G_MYOGENIN_01.1751 (-1,623), G_MYOGENIN_01.880 (-707), G_MYOGENIN_01.2193 (-350), G_MYOGENIN_01.172 (+22,796), G_MYOGENIN_01.806 (+25,212)
AKT1	G_MYOGENIN_01.4596 (+10,617)
AKT2	G_MYOGENIN_01.3188 (+1,517), G_MYOGENIN_01.302 (+11,778)