Supplementary Table S1. ***prdm1a* target genes identified in both microarray analysis and as direct targets through ChIP** **Name**	**Gene function**
Downregulated Genes	
aldehyde dehydrogenase 3 family, member D1	cellular aldehyde metabolic process
annexin A2a	calcium ion binding
Cryptochrome DASH	FAD binding
epb41l5 - erythrocyte membrane protein band 4.1 like 5	cytoskeletal protein binding
glutamate -cysteine ligase, modifier subunit	ligase activity
integrin alpha 5	receptor, protein (ECM) binding
zN-Myc protein	DNA binding
microtubule associated protein, RP/EB family, member 1	microtubule binding
nuclear VCP-like	ATP binding
platelet activating factor acetylhydrolase, isoform 1b	hydrolase activity
Rho GTPase activating protein 12	protein binding/signal transduction
sec23 homolog b	protein binding/cartilage development
signal recognition particle 68	ER protein export pathway
solute carrier family 43, member 1	amino acid transport
TAF12 RNA polymerase II, TATA box	DNA Binding, transcription initiation

binding(TBP)-a	
TBC1 domain family, member 23	Rab GTPase activator activity
tumor necrosis factor, alpha-induced protein 8-like 3	unknown
visual system homeobox 1	DNA binding
SVOP-like	transport
zgc:55661	cysteine-type peptidase activity
zgc:55843	unknown
zgc: 64098	unknown
zgc: 66298	unknown
zgc: 77817	unknown
Upregulated Genes	
actin, alpha 1, skeletal muscle	ATP binding/protein binding
cyclin G2	cell cycle control
myosin, heavy polypeptide 2, fast muscle cell specific	ATP binding/ motor protein
myosin, light polypeptide 2, skeletal muscle	calcium ion binding
metaxin 1b	mitochondrial protein import
troponin T3a, skeletal, fast	interacts with tropomyosin/muscle contraction
tryptophan hydroxylase 1	aromatic amino acid family metabolic process
zgc: 92129	unknown

*Chip-on-chip analysis determined direct Prdm1a binding previously identified 381 putative Prdm1a targets involved in muscle development (von Hofsten *et al.*, 2008). We have identified 8 genes that are significantly upregulated and 24 significantly downregulated genes in our microarray analysis of whole embryos at 25 hpf that were also identified in the Chip-on-Chip analysis performed by von Hofstren and colleagues.