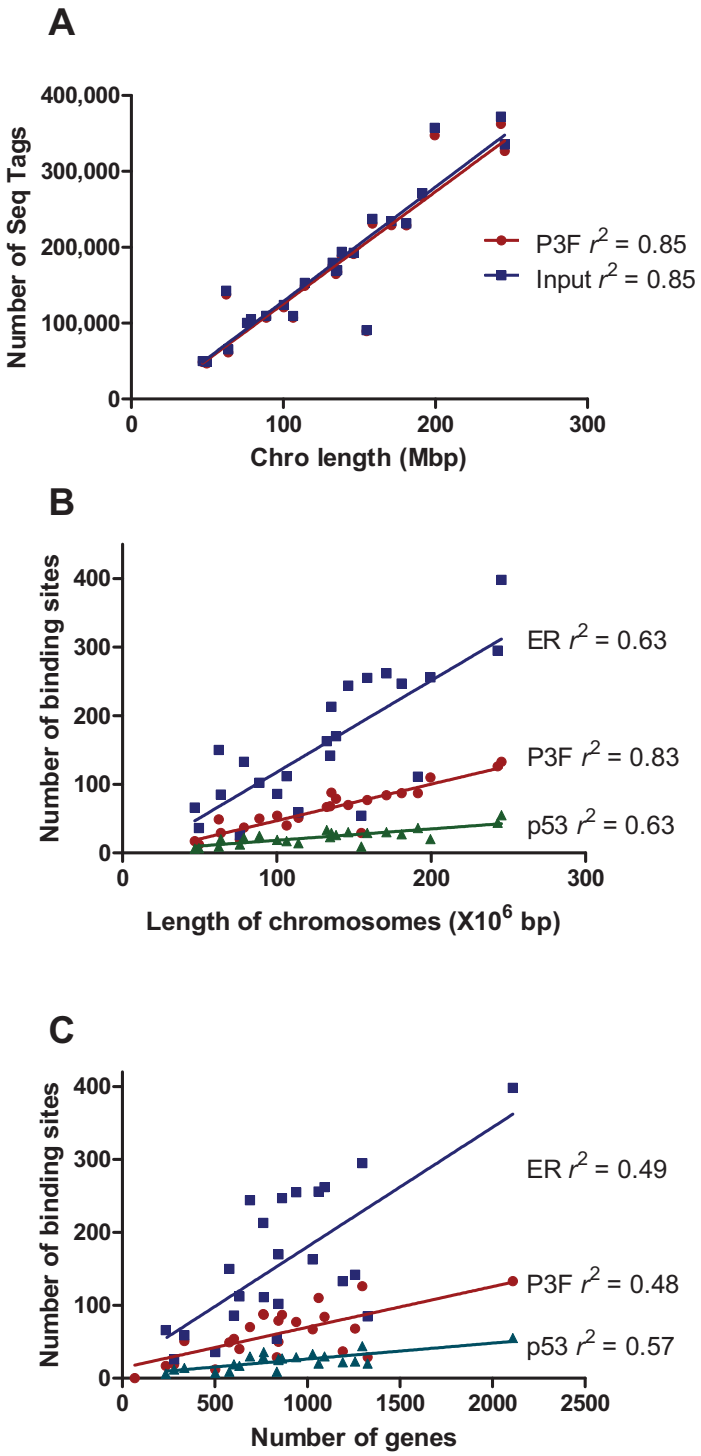

Figure S1. Chromosome distribution of PAX3-FKHR sites. (A) Chromosome distribution of all seqeunce tages. (B) Distribution of the binding sites based on the length of the chromosomes. (C) Distribution of the binding sites based on the number of the genes on each chromosome.

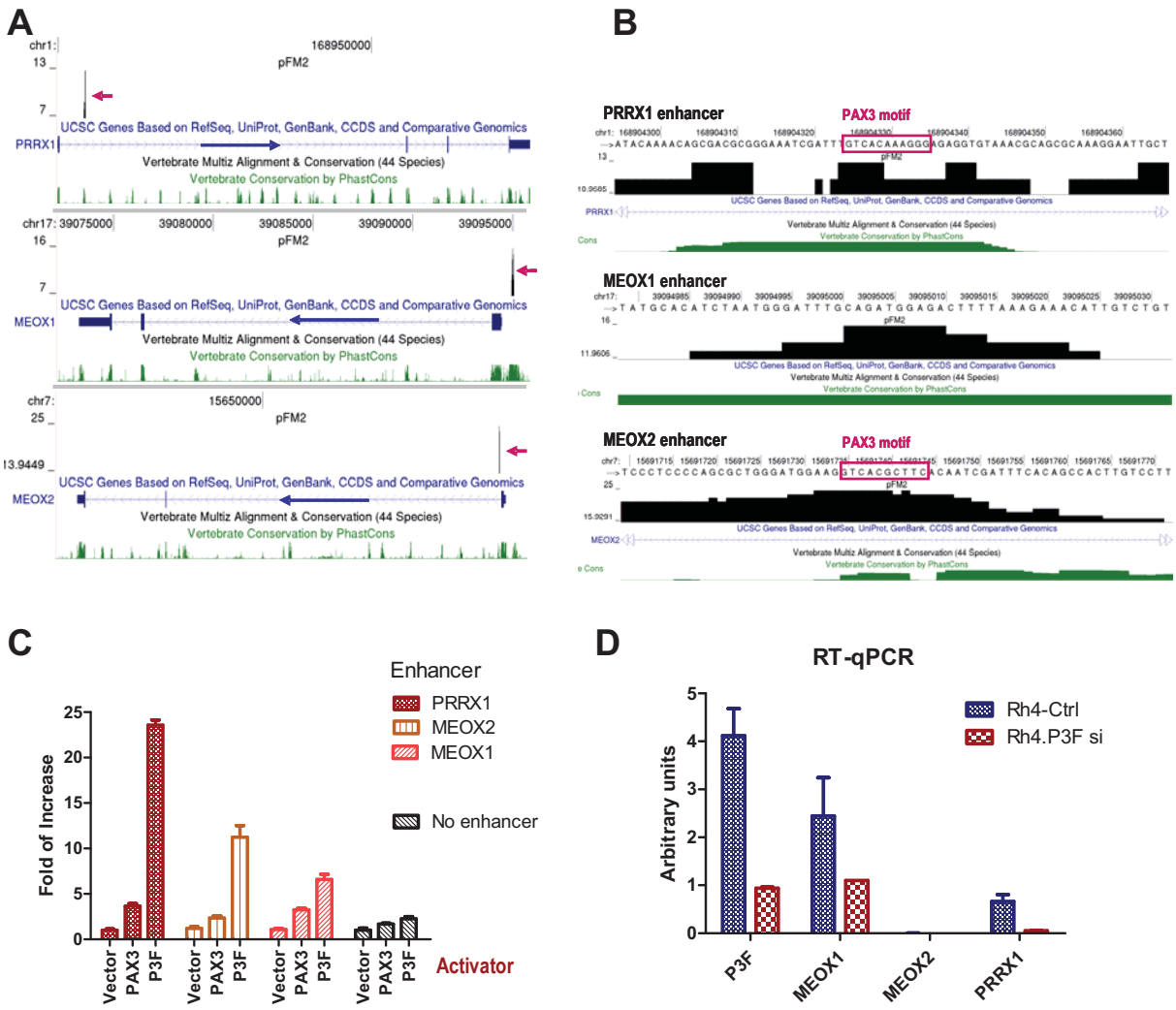

Figure S2. A group of muscular skeletal developmental homeobox genes as direct targets of PAX3-FKHR and PAX3. (A) Identification of homeobox genes with PAX3-FKHR binding sites. (B) Illustration of putative PAX3 recognition sequences associated with the peaks of the ChIP seq tags. (C) Enhancer activity for the binding sites in homeobox genes in response to PAX3 and PAX3-FKHR in co-transfected RD cells. (D) qPCR analysis of the expression levels of these homeobox genes in response to PAX3-FKHR knockdown in Rh4 cells.

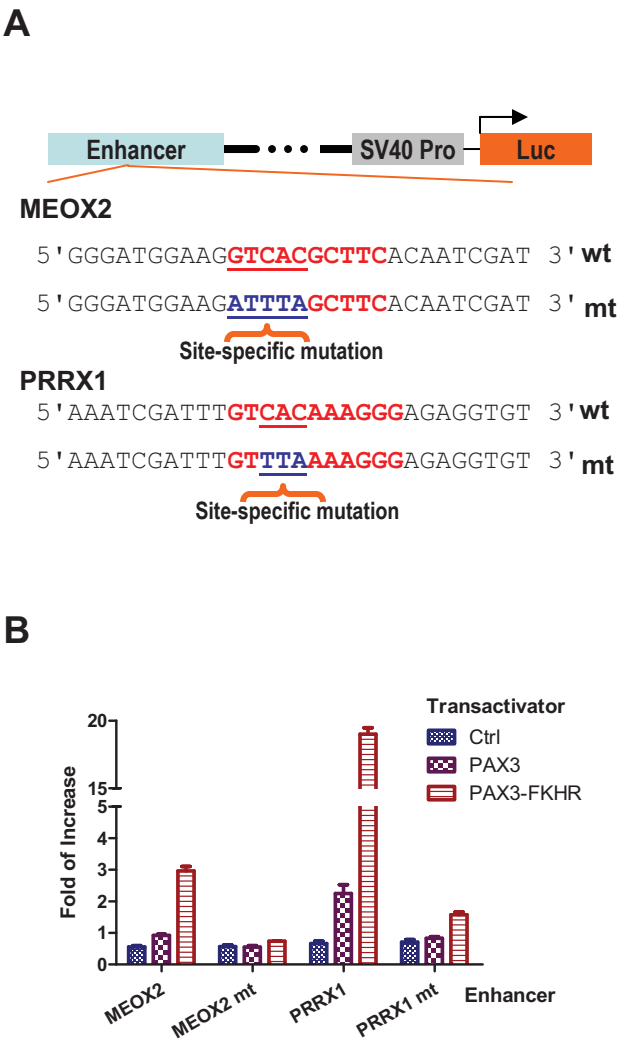

Figure S3. Identification of and verification of PAX3 recognition sequences in mediating PAX3 and PAX3-FKHR-mediated transactivation. (A) Site-direct mutagenesis of PAX3 recognition sequences at *MEOX2* and *PRRX1* enhancers. (B) Dependence of the PAX3 sequences for PAX and PAX3-FKHR dependent activation of *MEOX2* and *PRRX1* enhancers in co-transfected RD cells.

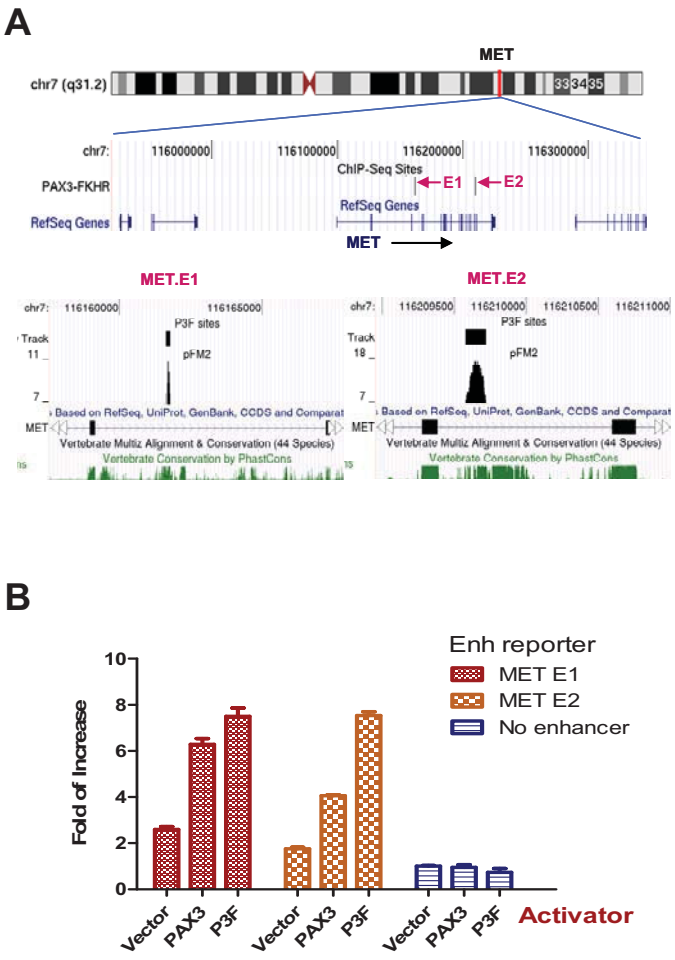

Figure S4. Characterization of PAX3 and PAX3-FKHR dependent enhancers at *MET*. (A) Identification of two PAX3-FKHR binding sites in the introns of *MET*. (B) Enhancer activities of two PAX3-FKHR binding sites at *MET* in enhancer assays. RD cells were co-transfected with 1:1 enhancer reporter and PAX3 or PAX3-FKHR plasmids for three days and analyzed with Promega dual luciferase assay kit.

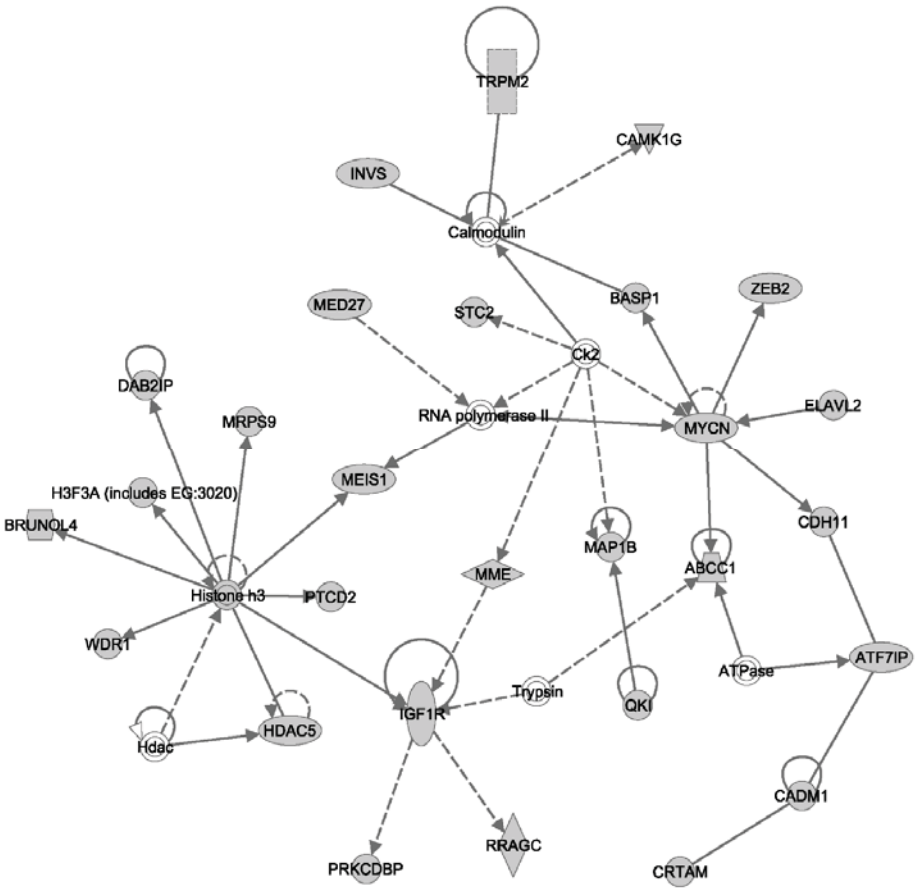

Figure S5. Genes with PAX3-FKHR bindings sites implicated in developmental skeletal, and muscular disorders network. Genes marked in grey are those with PAX3-FKHR sites. Figure obtained from IPA of Ingenuity.