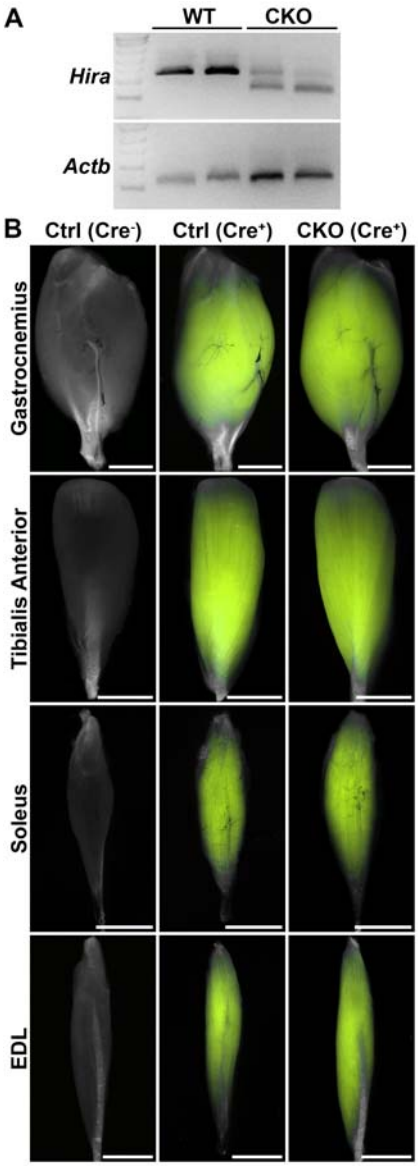

Fig. S1. Confirmation of *Hira* CKO in skeletal muscle. (A) *Hira* Δ exon 4 mRNA transcripts were detected in *Hira* CKO muscles but not wild type. Reverse-transcription PCR was performed using cDNA from tibialis anterior muscle. *Hira* primers flanked exon 4, which is deleted in the CKO. PCR for *Actb/β-actin* transcripts served as a loading control. (B) Stereoimages of hindlimb muscles from control and *Hira* CKO mice. YFP fluorescence images are overlaid with brightfield. YFP fluorescence was only detected in the muscles of mice harboring the $Myf6^{cre}$ allele. Scale bar, 2 mm. Ctrl, control; CKO, *Hira* conditional knockout; EDL, extensor digitorum longus; WT, wild type.

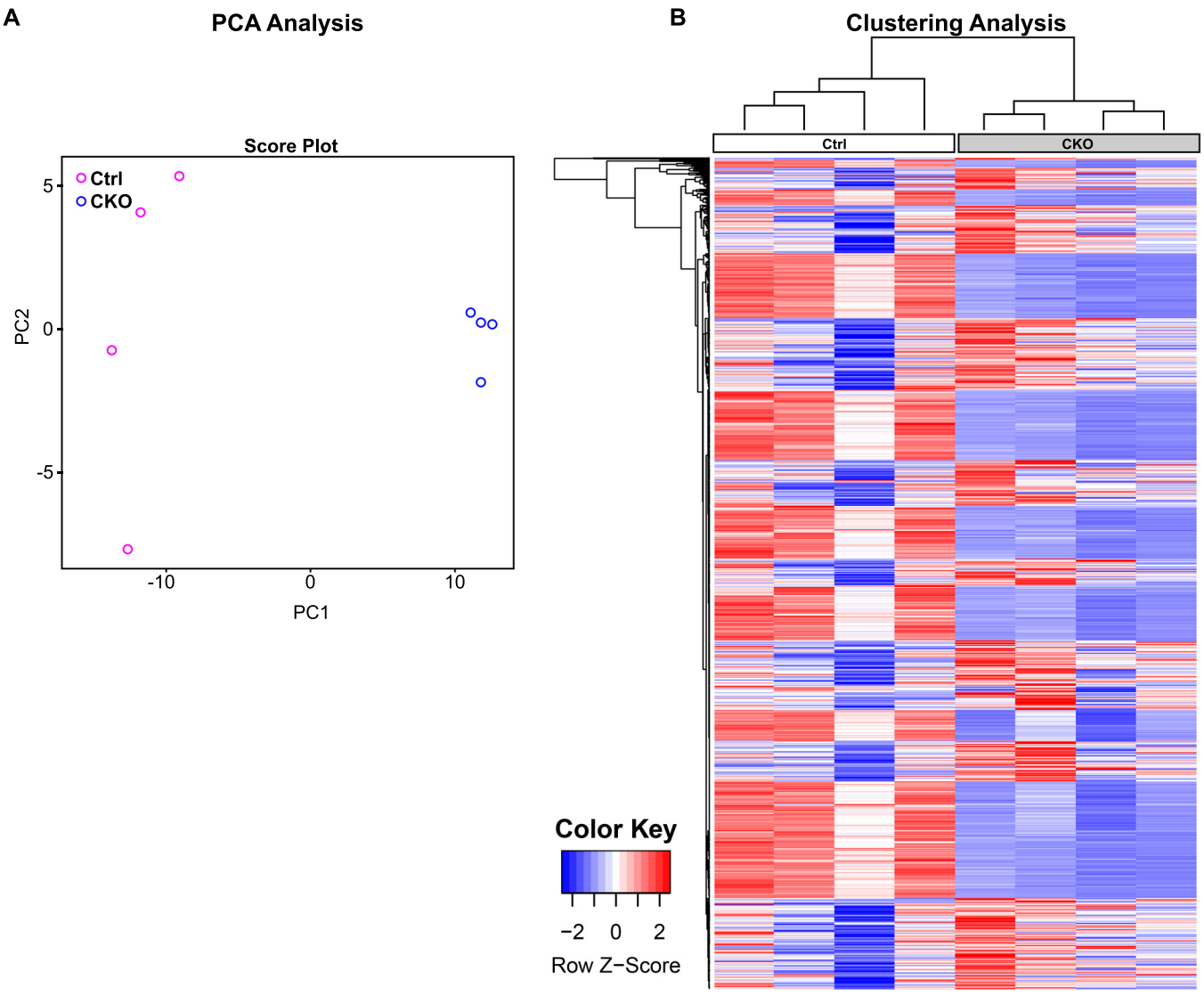

Fig. S2. Principal component analysis and clustering analysis of 6 week microarray data. Total RNA was extracted from tibialis anterior muscles at 6 weeks of age (n = 4 mice/group, hybridized in triplicate). (A) Principal Component Analysis (PCA) was performed to evaluate any differences among biological replicates and their treatment conditions. (B) Clustering analysis was performed to visualize the correlations among the replicates and varying sample conditions. Based on log2 fold change, we selected 1000 differentially expressed genes (500 from upregulated and 500 from downregulated sets) for clustering analysis. An unsupervised hierarchical clustering analysis on these 1000 genes revealed that samples representing the treatment and control conditions grouped together. Up- and down-regulated genes are represented in red and blue colors, respectively. $P < 0.05$ for all differentially expressed genes. Ctrl, control; CKO, Hira conditional knockout.

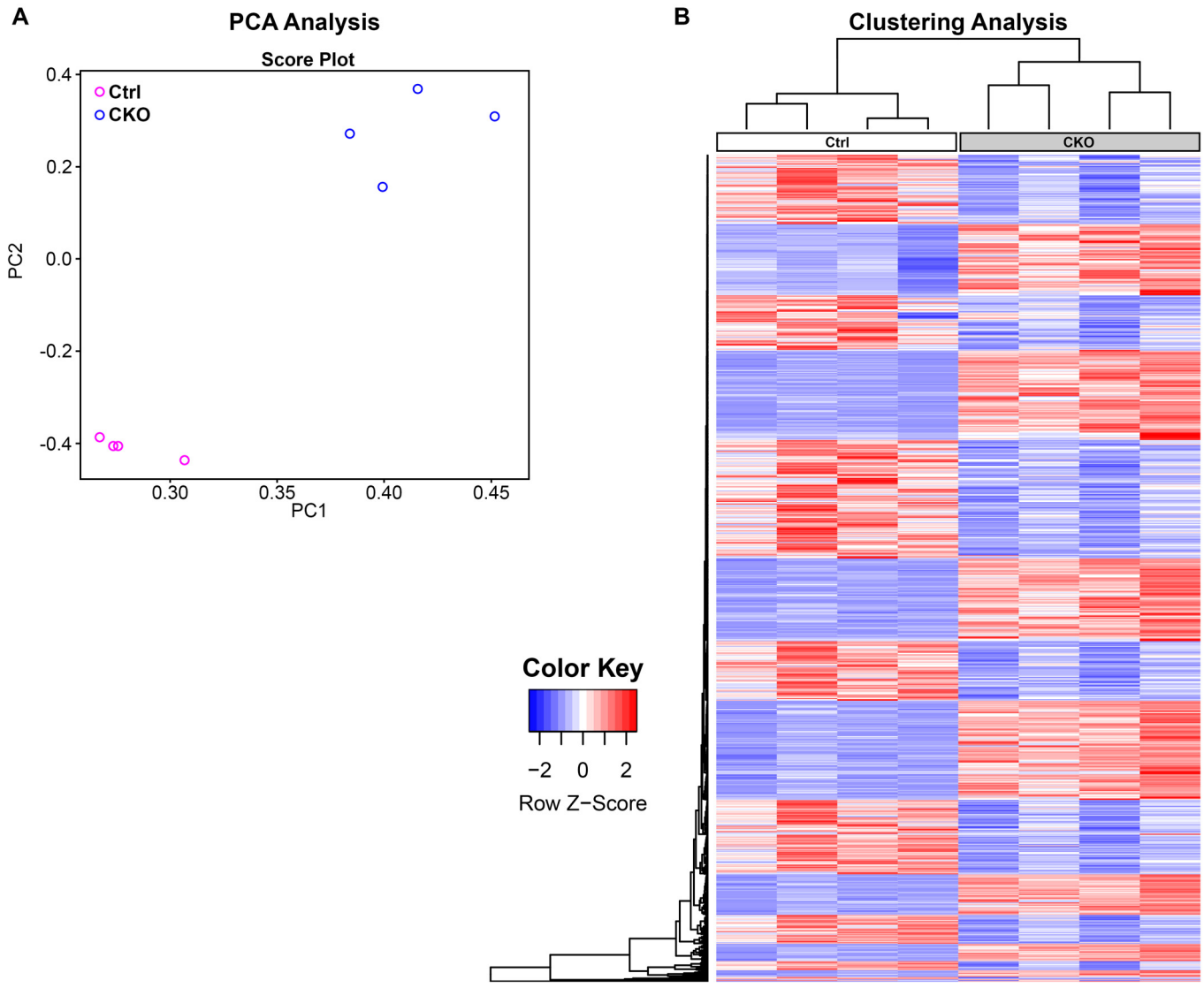

Fig. S3. Principal component analysis and clustering analysis of 6 month microarray data. Total RNA was extracted from tibialis anterior muscles at 6 months of age (n = 4 mice/group, hybridized in triplicate). (A) Principal Component Analysis (PCA) was performed to evaluate any differences among biological replicates and their treatment conditions. (B) Clustering analysis was performed to visualize the correlations among the replicates and varying sample conditions. Based on log2 fold change, we selected 1000 differentially expressed genes (500 from upregulated and 500 from downregulated sets) for clustering analysis. An unsupervised hierarchical clustering analysis on these 1000 genes revealed that samples representing the treatment and control conditions grouped together. Up- and down-regulated genes are represented in red and blue colors, respectively. $P < 0.05$ for all differentially expressed genes. Ctrl, control; CKO, *Hira* conditional knockout.

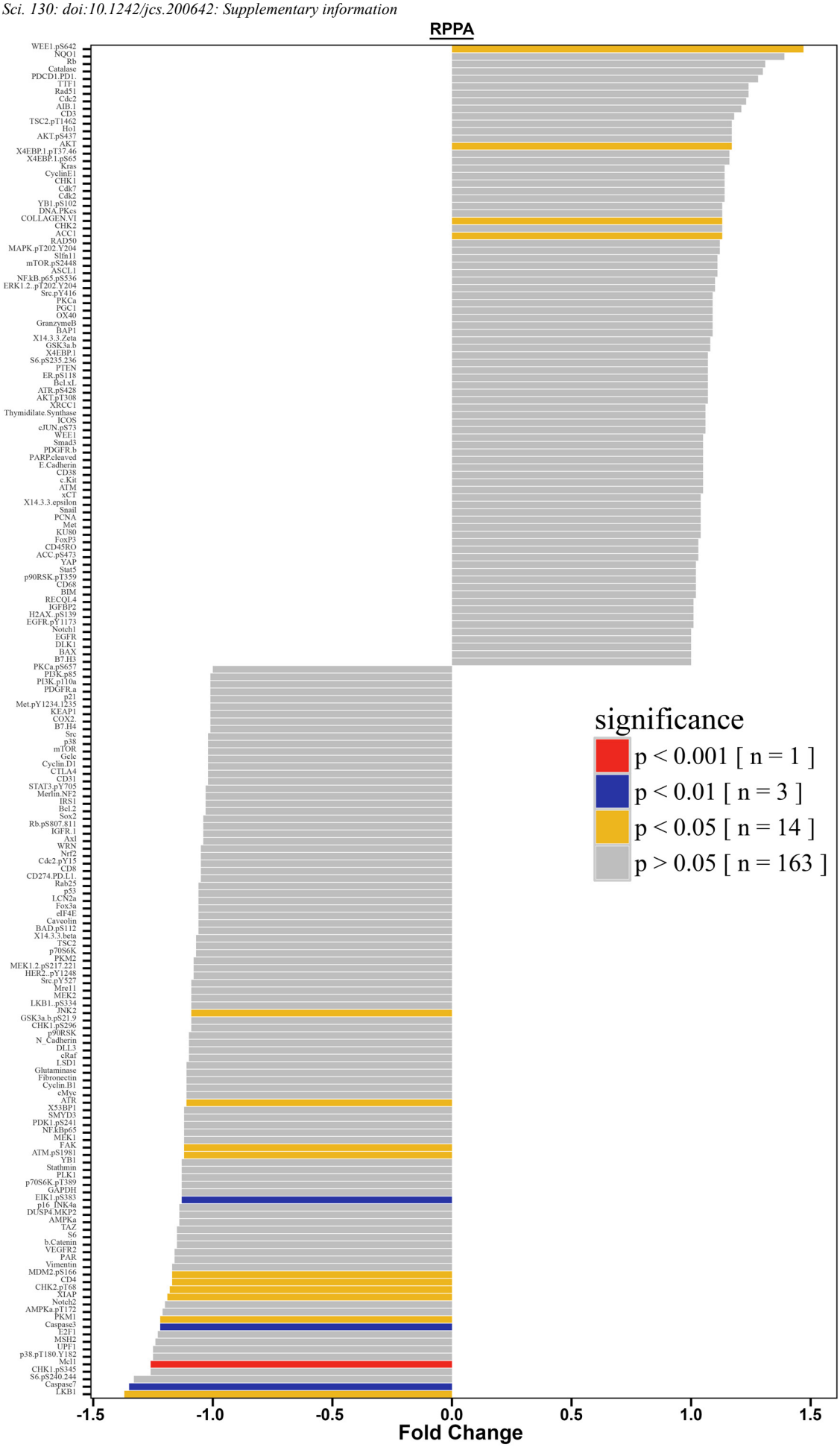

Fig. S4. Full results of the reverse phase protein array (RPPA). Whole cell extracts from the tibialis anterior of 6-month-old mice were assayed for differential protein expression by RPPA. Of the 181 antibodies on the array, 18 targets were identified to be differentially expressed ($P < 0.05$). Illustrated is the fold-change for each target in the *Hira* CKO relative to its level in extracts from control littermates ($n = 4$ animals/group).