Supplementary Figure S3

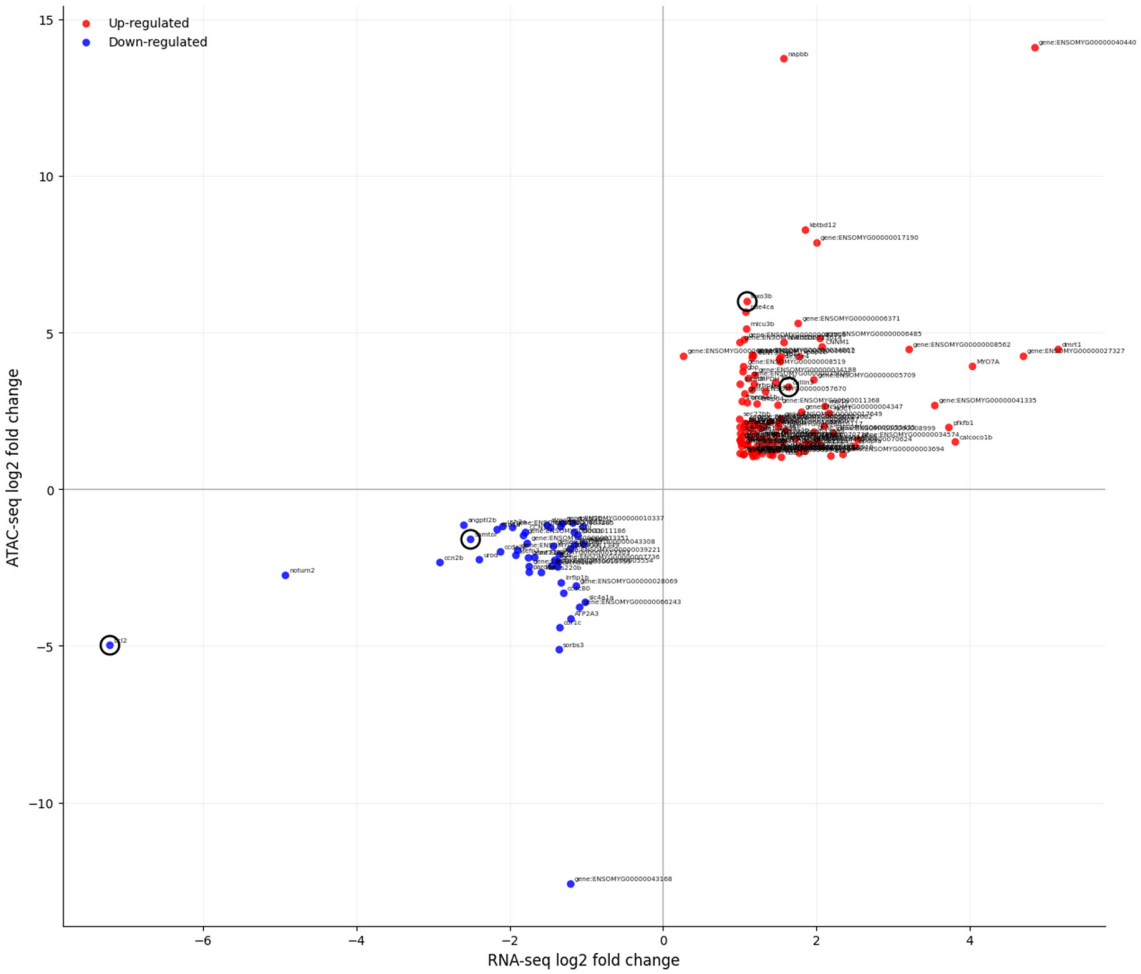


Figure S3. Integrated analysis of chromatin accessibility and gene expression in skeletal muscle following chronic cortisol exposure. Scatter plot showing the relationship between RNA-seq log2 fold change (x-axis) and ATAC-seq log2 fold change (y-axis). Each point represents a gene showing concordant changes in chromatin accessibility and transcript abundance. Upregulated genes are shown in red and downregulated genes in blue. The genes *foxo3b*, *cullin*-3, *bcl2*, and *samtor*, selected for RT-qPCR validation, are highlighted with black circles.