

## Supplemental Figure Legend

**Supplemental Figure 1. Extensive GH-induced histone H3 acetylation maps to the 5' ends of the *Igf1* and *Socs2* genes.** The graphs depict results of acetyl histone H3 ChIP-chip experiments using hepatic chromatin from pituitary deficient rats treated with systemic GH for 60 min. Illustrated is a 100 kb genomic segment containing *Igf1*, and 20 kb regions from the loci containing *Socs2* or *Spi 2.1*. Boxes represent exons and bent arrows transcription start sites. The vertical lines indicate regions of enhanced histone H3 acetylation consisting of four consecutive features from the tiled array with  $z$ -scores  $> +1.0$ . The dark boxes denote a  $z$ -score range of 0 to +1.0, and the larger light boxes from +1.0 to +5.0. For *Igf1*, thin vertical lines indicate Stat5b domains R34-35, R53-54, and R57-59. See Methods for details.

# Supplemental Fig. 1

