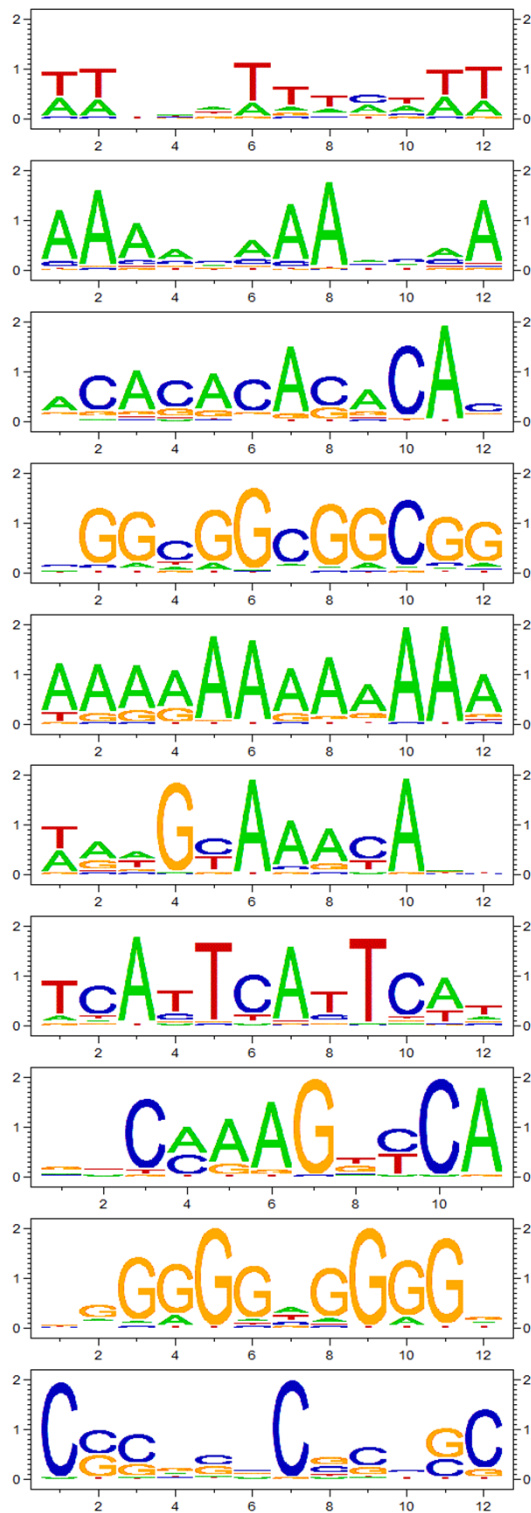


SUPPLEMENTAL FIGURE LEGENDS

SUPPLEMENTAL FIGURE S1. **Enriched motifs in HepG2 Smad2/3 binding regions.** *A.* Calculated motifs identified by CisGenome *de novo* motif prediction. Genomic sequences within 250 bp from the peak signal position of HepG2-specific Smad2/3 binding regions were used for the identification of enriched motifs. The eighth panel was the identified HNF4 α -like motif and shown in Figure 2*B*. *B.* Enriched motifs in Smad2/3 binding regions in HepG2 cells identified by using CEAS. Genomic sequences within 250 bp from the peak signal position of Smad2/3 binding data were analyzed to identify known transcription factor binding motifs. The results were sorted by fold enrichment compared to the background genome, and the top 3 motifs were shown.

SUPPLEMENTAL FIGURE S2. **Smad2/3 binding regions are weakly enriched in the genes up-regulated by TGF- β .** Expression microarray data for probe sets which have normalized signal values of at least 100 were sorted by their changes in expression after 1.5 h TGF- β stimulation and graphically represented using TM4 (58). Frequencies of Smad2/3 binding regions at moving average of 1001 probe sets are plotted in the right graph.

A



B

