Supplemental Materials

Supplementary Table 1

Gene lists of all upregulated genes in human CHC responder patients in their respective clusters 1 to 4 with the respective mean fold change at each time point.

Supplementary Table 2

Gene lists of all downregulated genes in human CHC responder patients with the respective mean fold change at each time point.

Supplementary Table 3

Gene list of all upregulated genes in human CHC responder patients at 144h treated with pegIFN-α2b (PegIntron®) or pegIFN-α2a (Pegasys®) with the respective mean fold change.

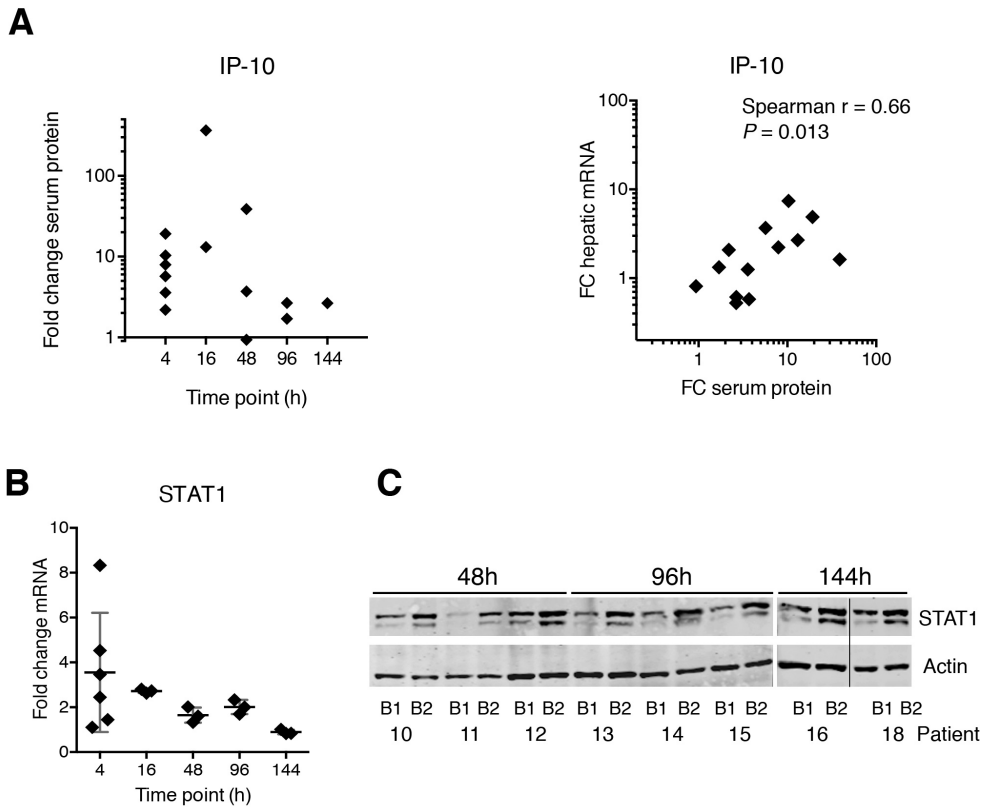
Supplementary Table 4

List of gene ontology terms and corresponding enrichment scores and significance of genes combined and differently upregulated in pegIFN-alpha (16h and 48h) and IFN-alpha (24h) treated patients.

Supplementary Table 5

Primer sequences used for quantitative real-time PCR.

Supplementary Figure 1



Supplementary Figure 1

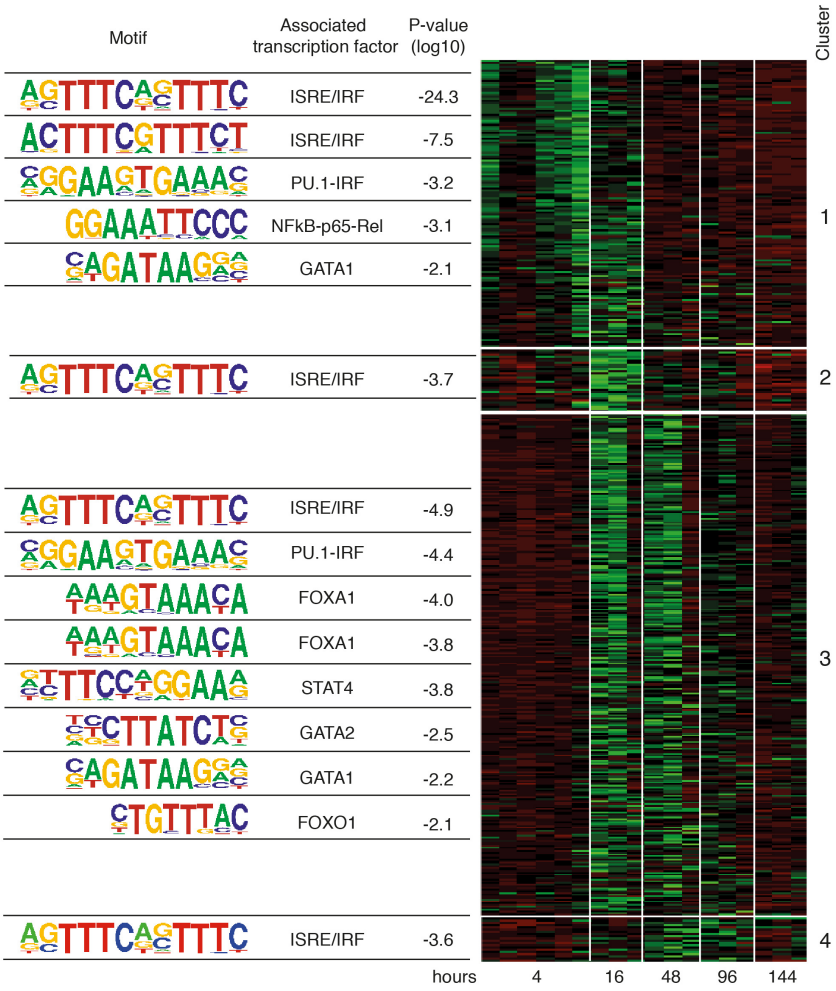
Gene expression induction is confirmed on protein level.

(A) IP-10 serum protein detected by ELISA significantly correlates with paired hepatic IP-10 mRNA. Shown are fold changes (FC) over time. Spearman correlation analysis was performed. Significance is indicated on the plot.

(B) Fold induction of STAT1 mRNA in paired liver samples at indicated time points. Indicated are additionally mean with SEM.

(B) STAT1 WB of paired liver samples shows increased protein levels in B2. Protein expression of the 4h time point was shown previously (Sarasin-Filipowicz et al., PNAS, 2008). The black line separates non-contiguous bands on the same gel.

Supplementary Figure 2



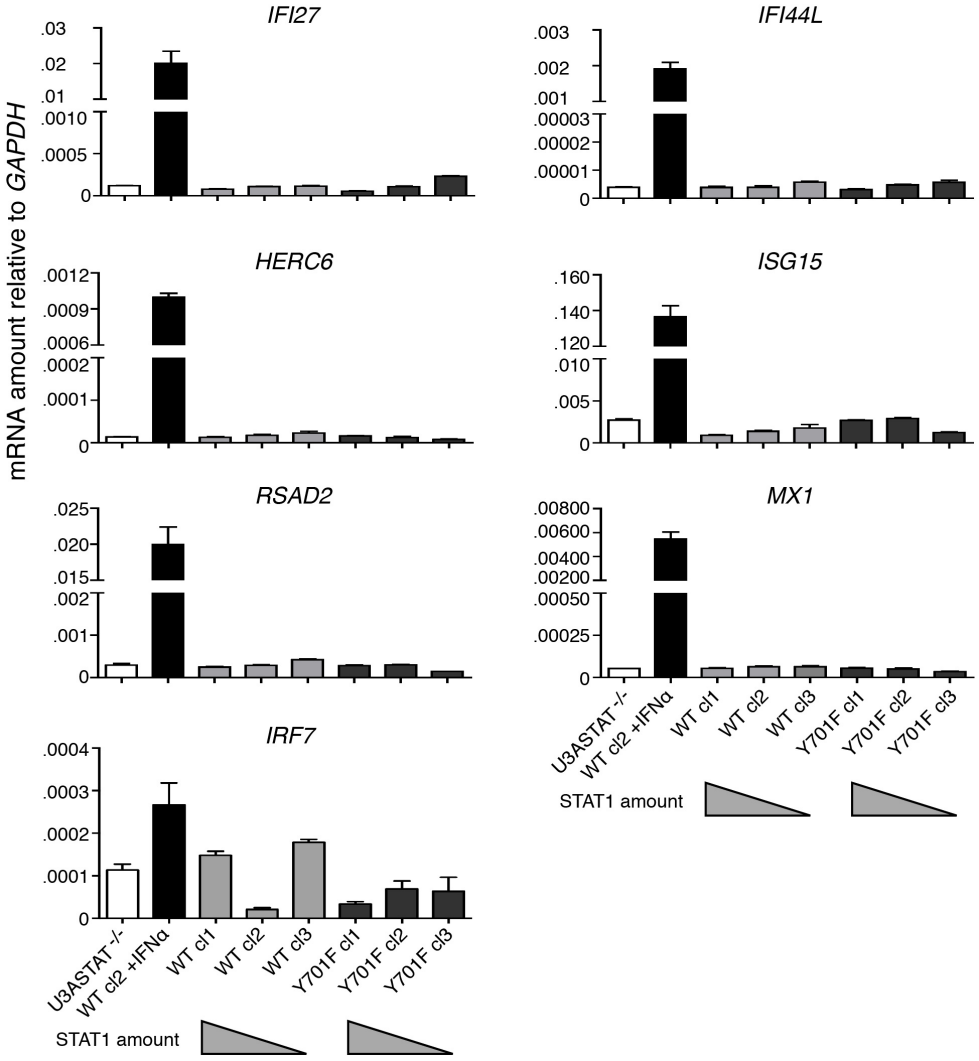
Supplementary Figure 2

In silico transcription factor binding analysis reveals ISRE as the main promoter binding site in every gene expression cluster.

Known TFBS in promoter regions (2 kbp upstream and 500 bp downstream of the transcription start site) of every gene in each cluster were analysed by HOMER software. Indicated are the motif, the name and the significance of enrichment of TFBS in each cluster. The heatmap represents all genes in the cluster normalized to the mean

expression of all samples for this gene, with green indicating higher than average and red below average expression.

Supplementary Figure 3



Supplementary Figure 3

mRNA expression assessed by quantitative RT-PCR of six representative ISGs (*IFI27, HERC6, RSAD2, IFI44L, ISG15, MX1*), and IRF7 without IFNα treatment not showing any upregulation in the different clones (WT cl1-3, Y701F cl1-3) compared to U3A STAT1$^{-/-}$ cells. As a positive control WT cl2 was treated with 1000 U/ml IFNα for 8 hours (lane 2). The relative amount of STAT1 protein per clone is illustrated graphically below. Shown are mean values of 3 replicates with SEM.