SUPPLEMENTARY FIGURE LEGENDS

SUP. 1. **Human NF-YC mRNAs alignment**. The full alignment of 13 human NF-YC mRNAs present within the GenBank database is reporter. The exonic structure of the originally cloned NF-YC is indicated by black lines. Start (ATG) and Stop (TGA) codons are in bold.

SUP. 2. **Intermediate NF-YC mRNAs**. RT-PCRs performed with the Ex8-Ex10 primer pair, after 46 cycles. Intermediates amplicons, not corresponding to the previously reported 37 kDa, 48kDa and 50 kDa transcripts, are present, suggesting other possible arrangements of exons in-between 8 and 10.

SUP. 3 **NF-YC isoform Western Blot.** Full scan of the NF-YC Western Blot showed in FIG 1D. Intermediate isoforms are presents, supporting RT-PCR findings (Sup. 2)

SUP.4 **Human and mouse P1 and P2 alignments.** Sequence alignment of human and mouse P1 and P2 regions, +-500 bp from the annotated TSS (arrow). P1 CCAAT boxes downstream to TSS are also shown.