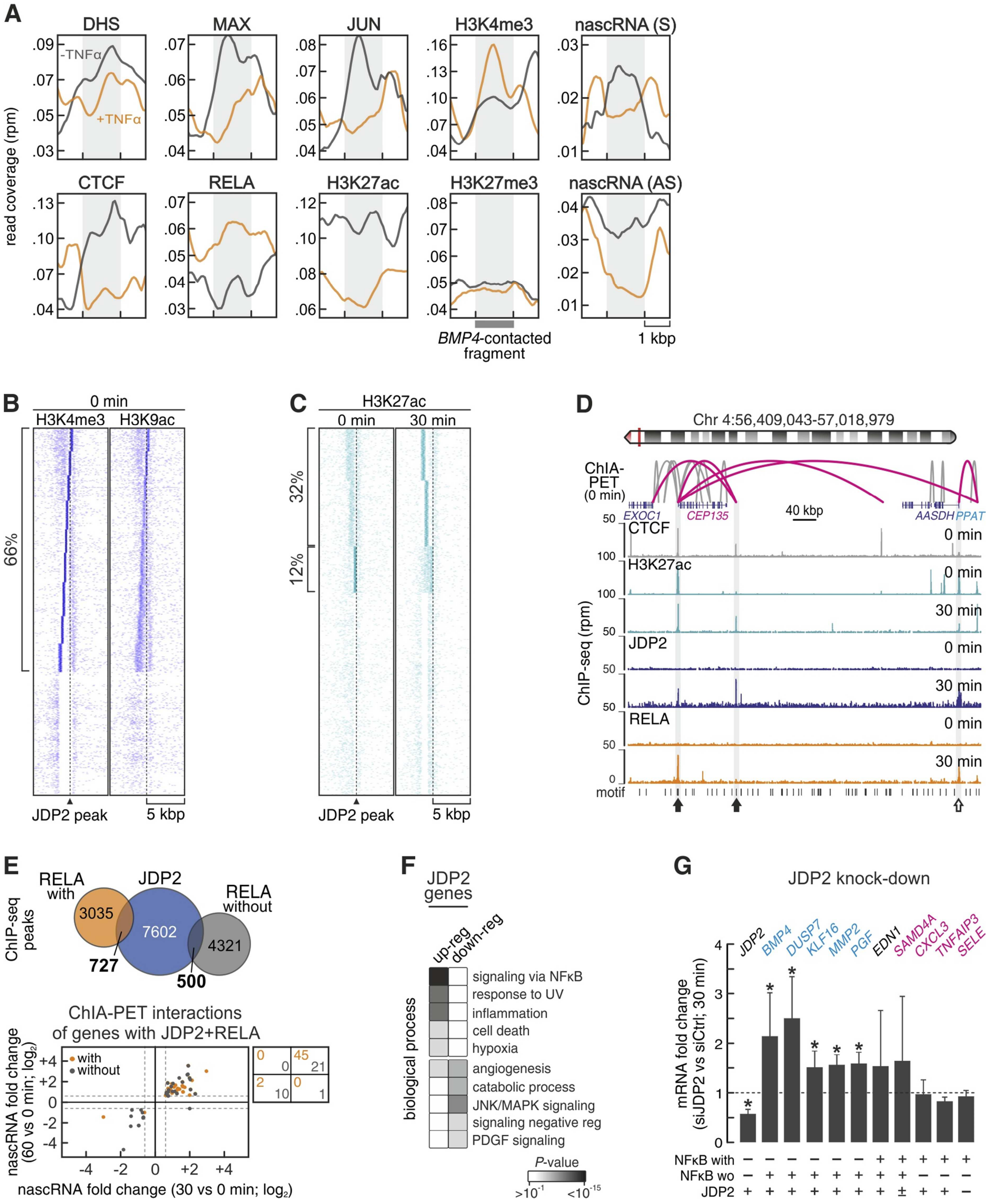

Supplemental Fig. S5. Regulatory properties of the JDP2 transcription factor. HUVECs were stimulated with TNF for 0 or 30 min and the function of JDP2 analyzed. (***A***) Raw read coverage (from ChIP- and nascent RNA-seq) along *Apo*I fragments (±1 kbp) contacted by *BMP4* at 0 (*grey*) or 30 min (*orange*) post-stimulation. Only contacted fragments with >100 rpm were used. Note that, with the exception of RELA, H3K27ac, and nascent RNA (sense strand – S, antisense strand – AS), all other datasets correspond to the 0-min time point. (***B***) Heat maps showing that 66% of JDP2 30-min peaks lie within <2 kbp of active gene promoters (as shown by the H3K4me3 and H3K9ac histone marks they carry; HUVEC ENCODE ChIP-seq data). (***C***) Heat maps showing that 32% and 12% of JDP2 30-min peaks lie within <2 kbp of H3K27ac-marked *cis*-elements that are further activated or suppressed at 30 min post-stimulation, respectively. (***D***) Typical profiles of JDP2 binding (*blue*) are shown alongside RELA, CTCF, and H3K27ac data in a locus harboring the TNF-induced *CEP135* (*red*) and TNF-repressed *PPAT* (*blue*) genes. ChIA-PET contacts (0 min; *on top*) bound by RELA are shown in magenta. (***E***) *Top*: Venn diagram showing the number of 30-min JDP2 ChIP-seq peaks (*blue*) that overlap RELA ones that either carry by the canonical motif ("with"; *orange*) or not ("without"; *grey*). *Bottom*: Log_2-fold changes in intronic RNA levels (30- or 60- versus 0-min; only changes of at least ±0.6 are shown) of genes bound by JDP2 and connected to RELA-bound enhancers in 30-min ChIA-PET data. Genes associated with "with" and "without" RELA peaks are shown as orange and black points, respectively, and their number in each quartile are shown (*right*). (***F***) The five most enriched GO terms for up- or down-regulated genes associated with a JDP2 peak at 30 min post-stimulation. (***G***) A ~50% knock-down of *JDP2* levels leads to increased mRNA levels of TNF-suppressed genes (*blue*), but does not significantly affect the levels of other TNF-responsive genes (*magenta*), as shown by RT-qPCR (±SD; n=3). *: significantly different; $P<0.05$, two-tailed Student's unpaired *t*-test.