Supplemental Figures

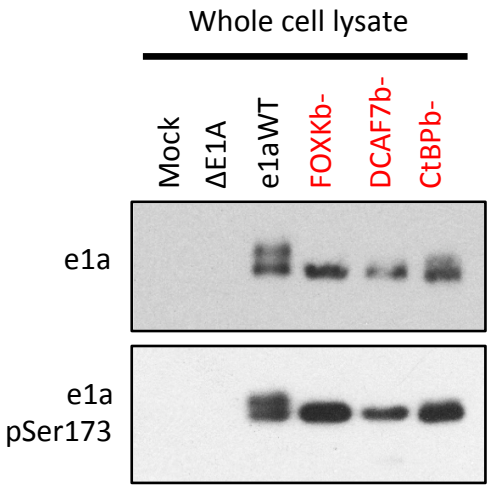

Fig S1. The e1a C-terminal mutations interfere with phosphorylation at Ser89 but not Ser173. Related to Fig 1
Western blot of protein extract from HBTEC 24h p.i. with the indicated vectors using monoclonal antibodies against e1a (M58, top) and e1a pSer173 (bottom).

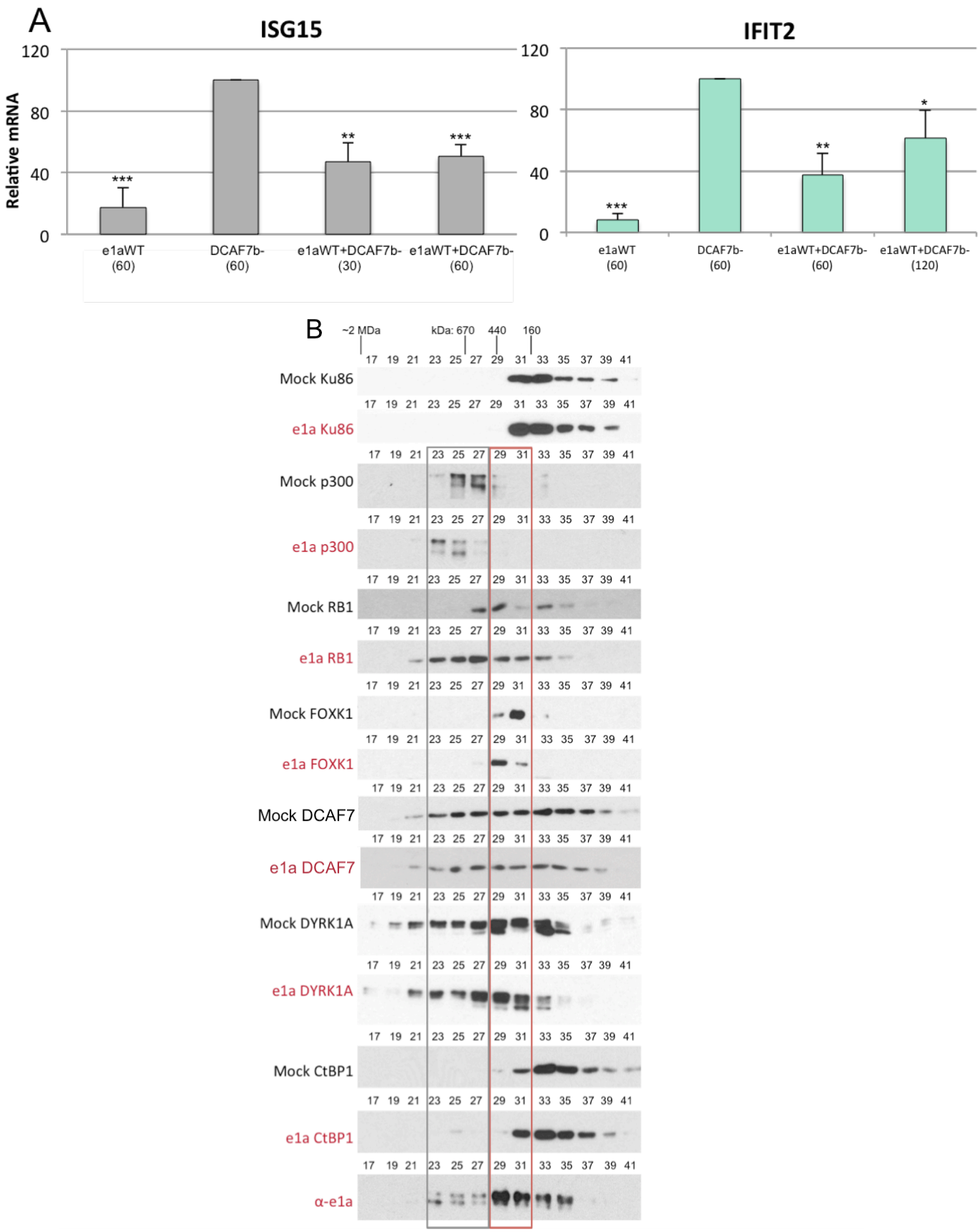

Figure S2. e1aWT and DCAF7b$^-$ coinfection and e1a nuclear protein complexes. Related to Fig 4
(**A**) Relative levels of ISG15 and IFIT2 mRNA as assayed by qRT-PCR from HBTECs infected or coinfected with indicated vectors. moi for individual vectors indicated in parentheses. Data are represented as averages of percent of DCAF7b- (moi 60) activation + S.D. (**B**) Western blots of Superose 6 column fractions from mock or e1aWT-vector infected HeLa nuclear extract (24 h p.i.). Non-e1a interacting nuclear factor Ku86 is shown as a control.

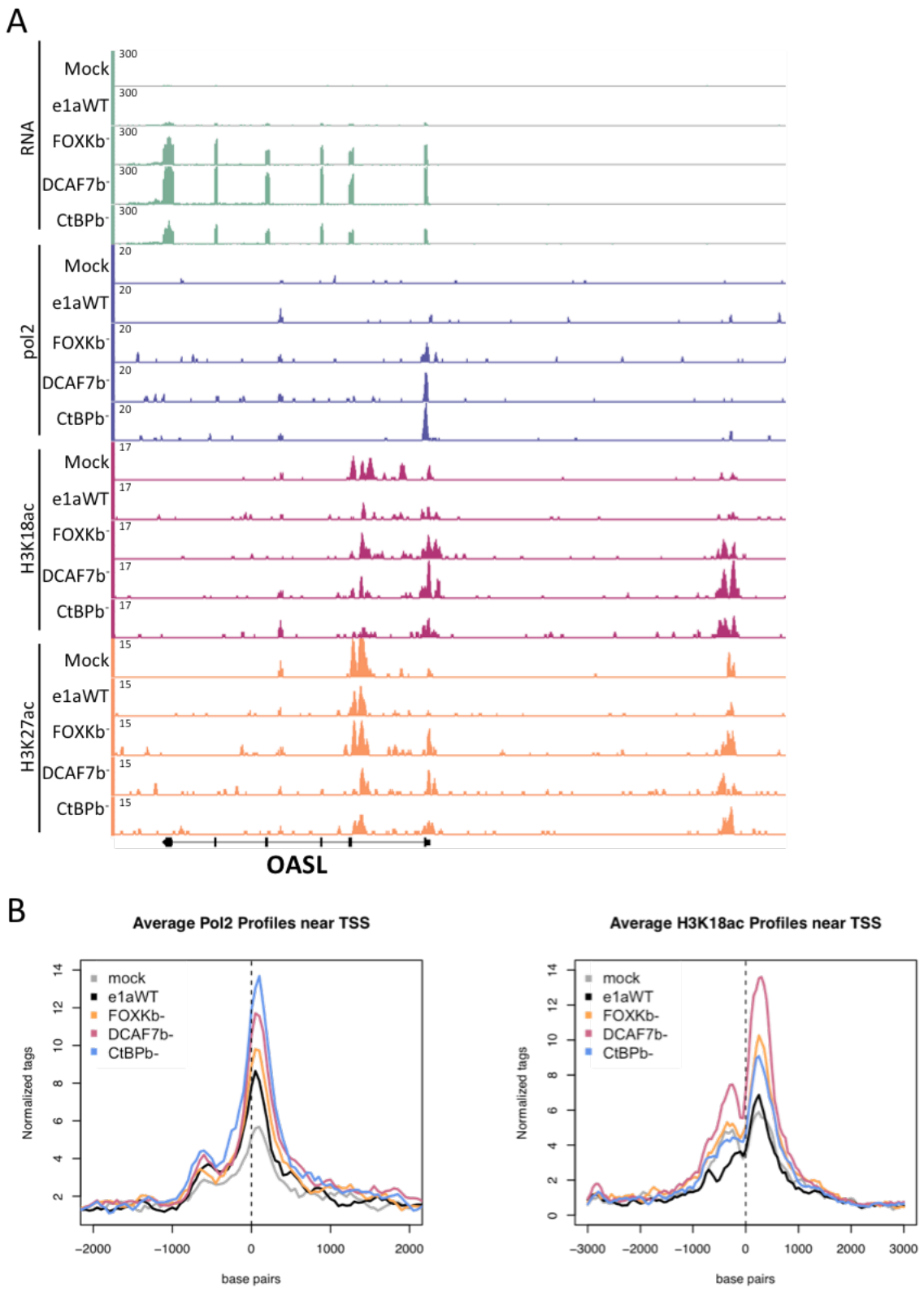

Figure S3. Chromatin marks related to transcriptional activation at e1a C-terminal induced ISGs. Related to Fig 5 (**A**) Genome browser track of RNA-seq and ChIP-seq enrichment upstream of and across the OASL gene from HBTEC infected for 24h. (**B**) Metagene plots showing average tag density of Pol2 or H3K18ac ChIP-seq enrichment around TSS of 52 genes expressed 2-fold higher by all three e1a C-terminal mutants using chromatin from cells mock-infected or infected with indicated e1a expressing Ad5 vector for 24 h. Data was normalized so there were equal numbers of mapped reads across samples.

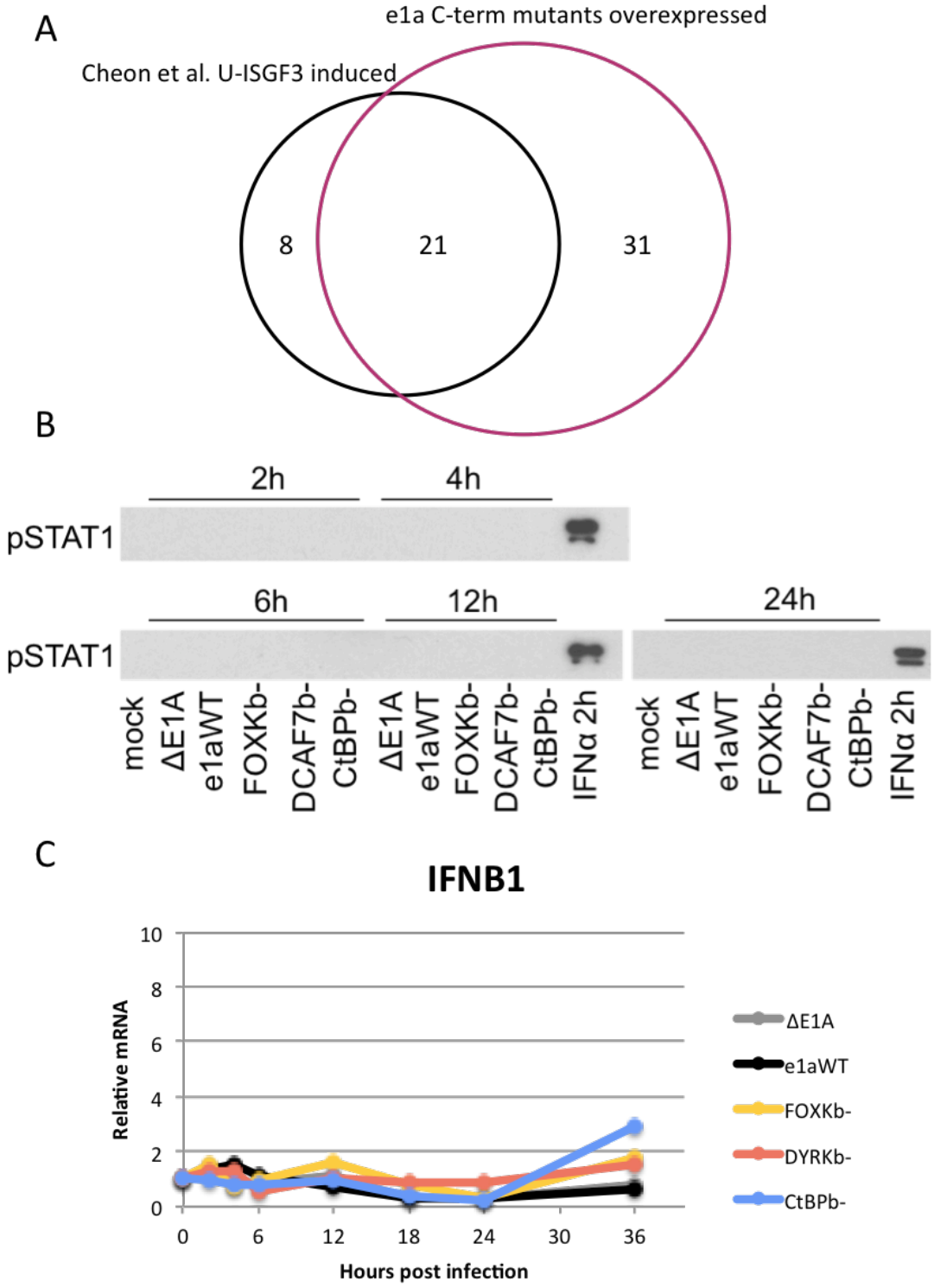

Figure S4. STAT1 is not phosphorylated at its activating site following infection. Related to Fig 6
(**A**) Venn diagram showing overlap of U-ISGF3 induced genes (Cheon et al., 2013) and e1a C-terminal mutant overexpressed genes. (**B**) Western blots for phosphorylated Y701 STAT1 from lysates of infected HBTEC at various times p.i. An extract from HTBEC treated with 10ng/mL IFNα for 2h was used as a positive control for STAT1 phosphorylated at Y701. (**C**) IFNB1 mRNA assayed by qRT-PCR during a time course of infection of HBTEC.

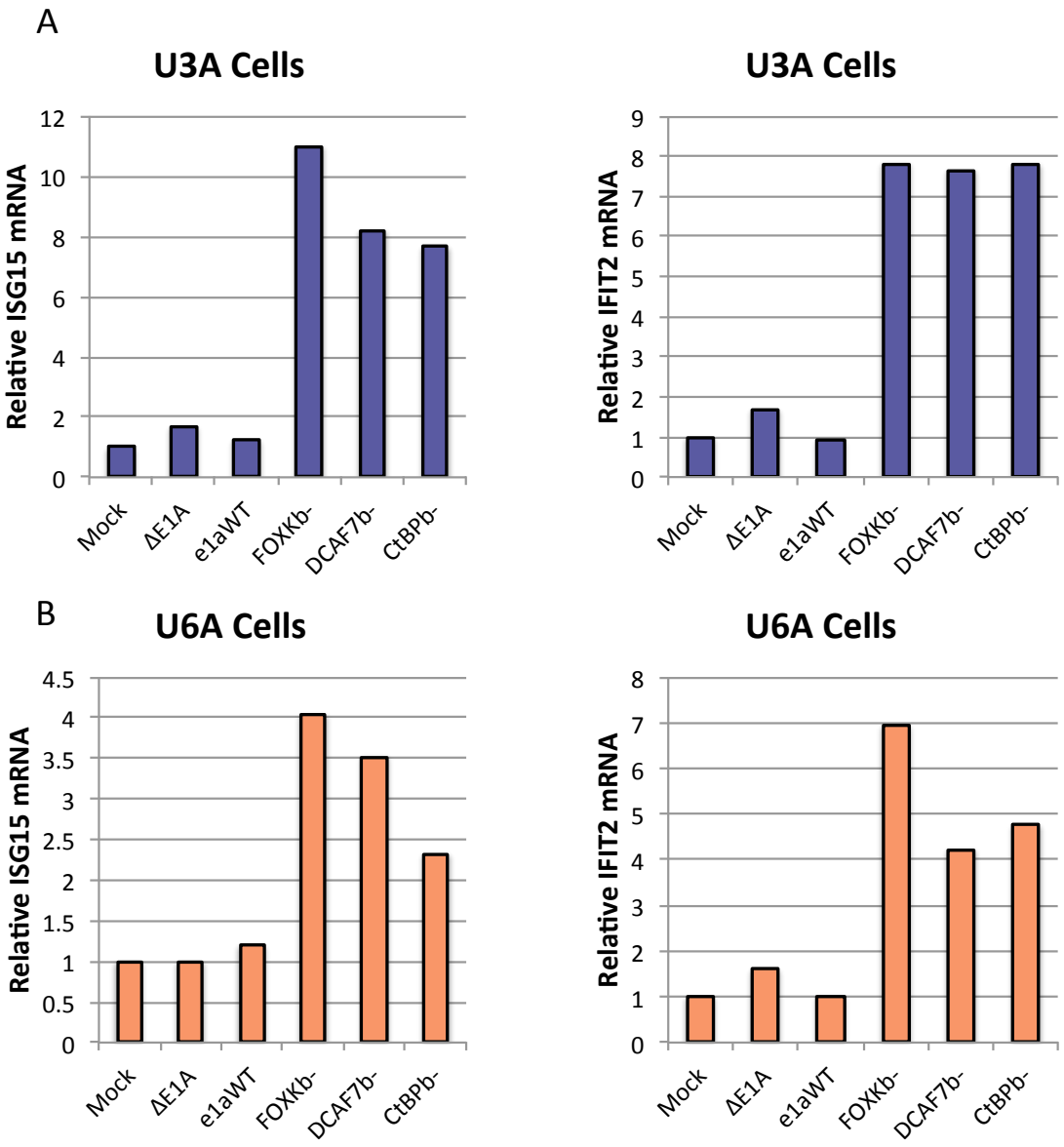

Figure S5. STAT1 and STAT2 are not necessary for e1a C-terminal activation of ISGs. Related to Fig 6
(**A**) STAT1 mutant U3A cells were infected for 24h with the indicated vectors prior to RNA isolation and qRT-PCR to determine relative ISG15 and IFIT2 mRNA levels. (**B**) Same as with **A** but in STAT2 mutant U6A cells.

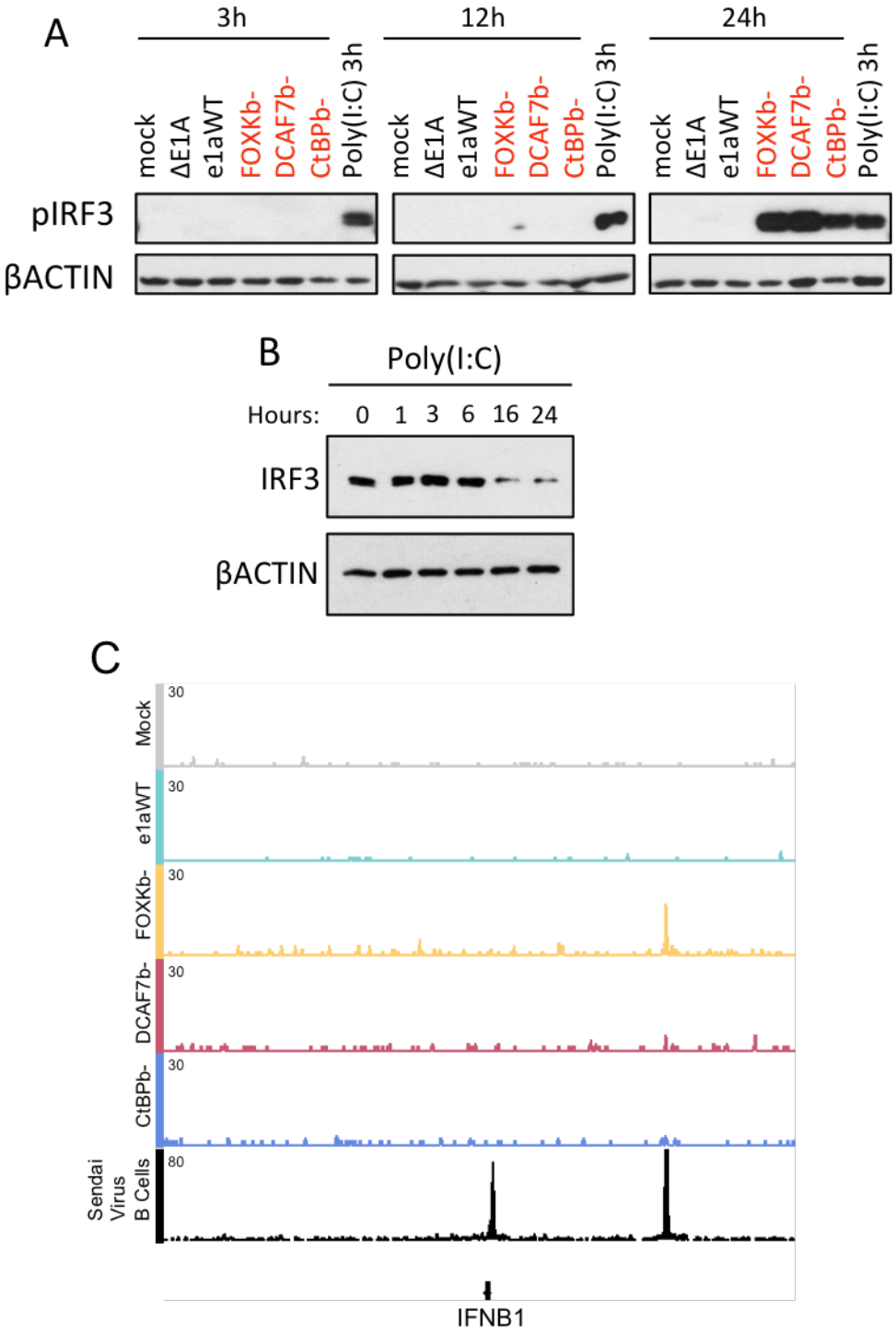

Figure S6. Phosphorylation of IRF3 protein by infections and Poly(I:C). Related to Fig 7
(**A**) HBTEC were infected for the indicated times or transfected with poly(I:C) 20ug/mL for 3h as a positive control for pIRF3. Level of pSer396 IRF3 was assayed by western blot. (**B**) HBTEC were transfected with Poly(I:C) 20ug/mL for the indicated times and total IRF3 protein was assayed by western blot. (**C**) Genome Browser image demonstrating the absence of IRF3 binding at its promoter following Ad5 vector infection/e1a expression, while Sendai virus infected B lymphocytes induces binding. GEO: GSE44939 (Freaney et al., 2013).

Table S1 Number of host cell genes expressed greater than two times higher and less than two times lower than in HBTECs infected with the e1aWT vector. Related to Fig 2

e1a mutant	Genes 2X > e1aWT	Genes 2X < e1aWT
P300b-	728	241
RBb-	454	790
FOXKb-	105	68
DCAF7b-	146	105
CtBPb-	119	138