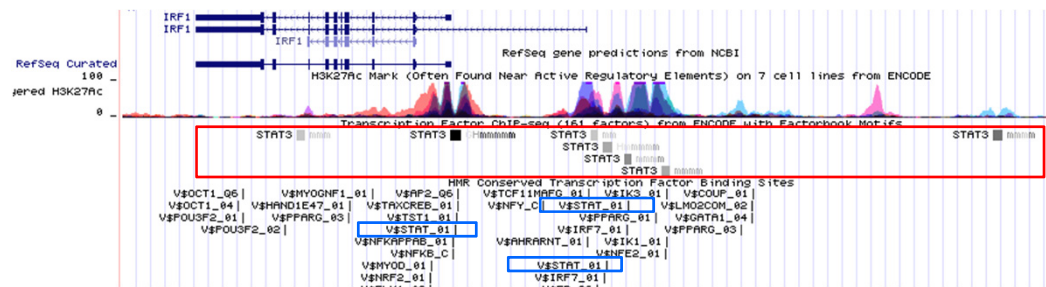
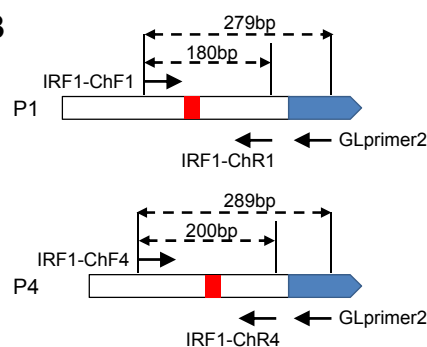


Figure 5-figure supplement 1

A



B



C



D



E

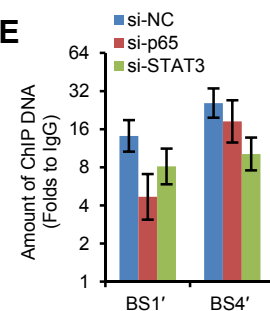


Figure 5-figure supplement 1. Predicted STAT3, NFkB and IRF1 binding sites on human IRF1 gene. **(A)** Screenshot (UCSC genome browser, GRCh37/hg19) shows STAT3 binding clusters from ENCODE ChIP-seq data. Three conserved STAT binding sites (in blue boxes) are predicted by “TFBS Conserved” tract. **(B)** Illustration of the locations of primers on the reporter constructs. **(C)** The sequences and the locations of STAT3 and NFkB binding motifs within P1 construct. The the sequence and the location of PCR primers used for ChIP (referred as BS1’) are shown in blue. **(D)** The sequences and the locations of STAT3, NFkB and IRF1 binding motifs within P4 construct. Non-canonical NFkB binding sites were predicted by AliBaba2.1. **(E)** ChIP-qPCR assays of BS1’ and BS4’ fragments bound by STAT3. HepG2 cells were transfected with indicated siRNAs (20nM) for 48 hours and then harvested for ChIP, with STAT3 antibody or normal rabbit IgG. The amount of ChIP DNAs was firstly normalized to that of input DNAs and then further normalized to that of IgG groups. Data are one experiment representative of three experiments (mean \pm SEM of technical triplicates).