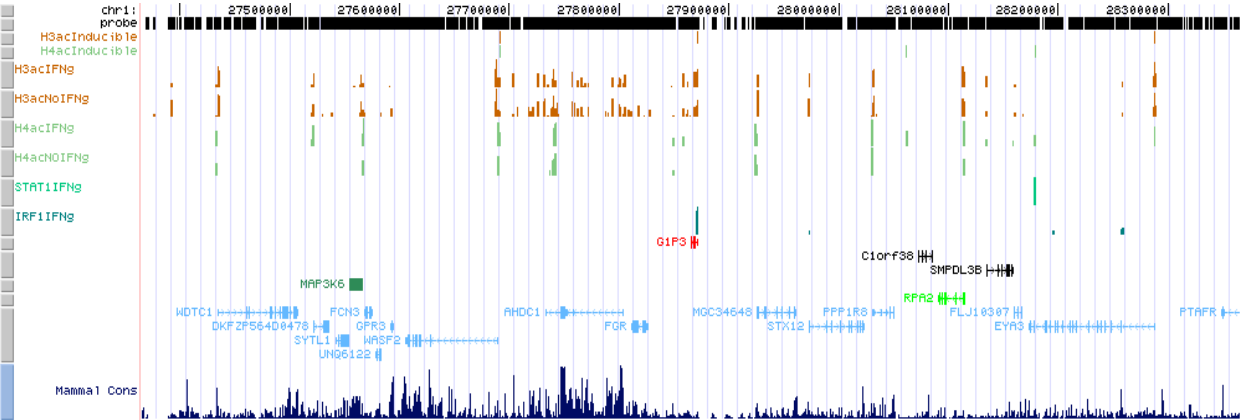
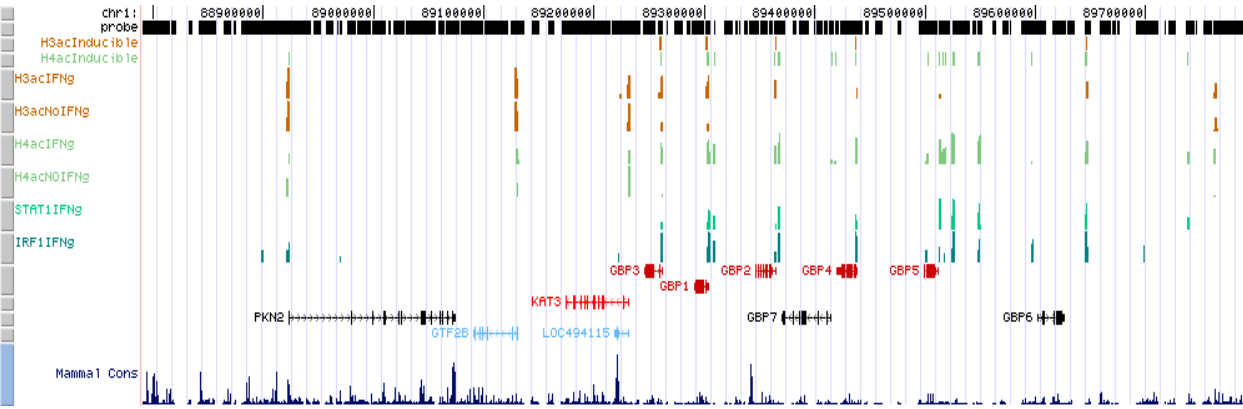


Supplementary Fig 1. H3ac and H4ac distribution at ISG-rich regions

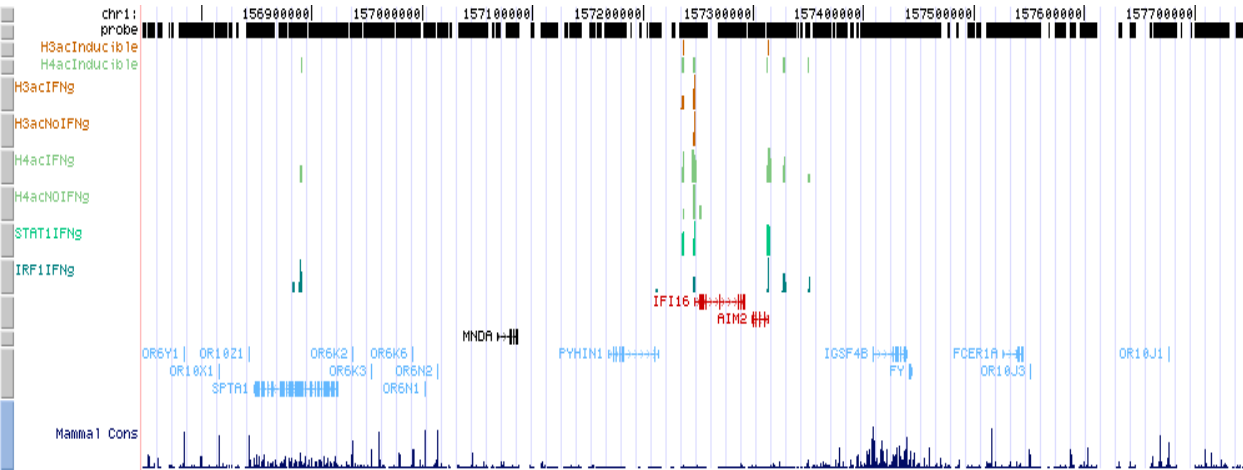
6-16(G1P3) locus chr1:27,365,167-28,365,167



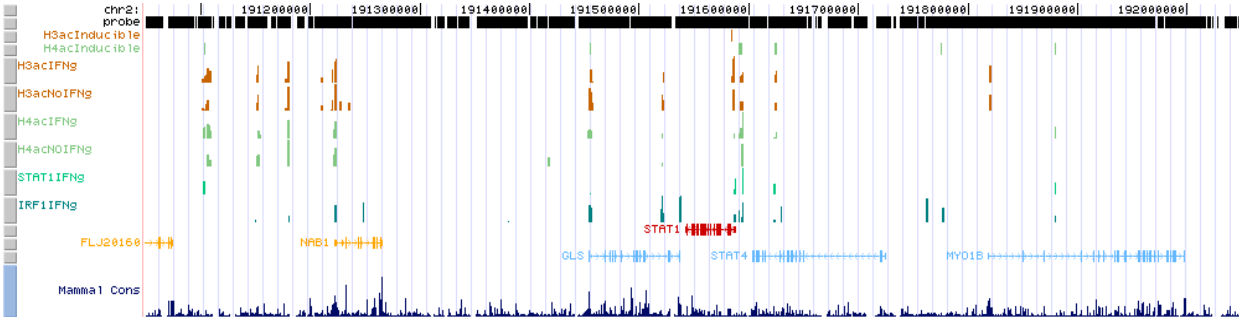
GBP1 cluster chr1:88,790,592-89,790,592



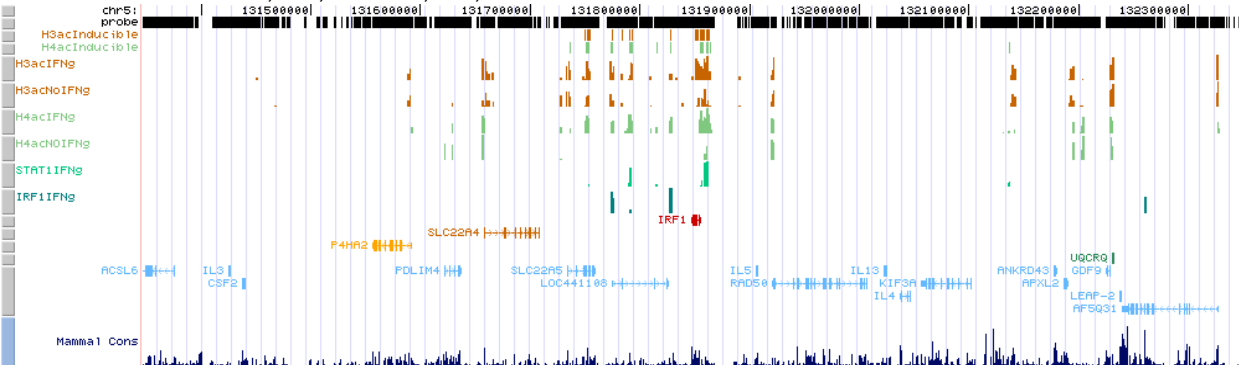
IFI16 cluster (IFI200 series) chr1:156,746,330 -157,746,330



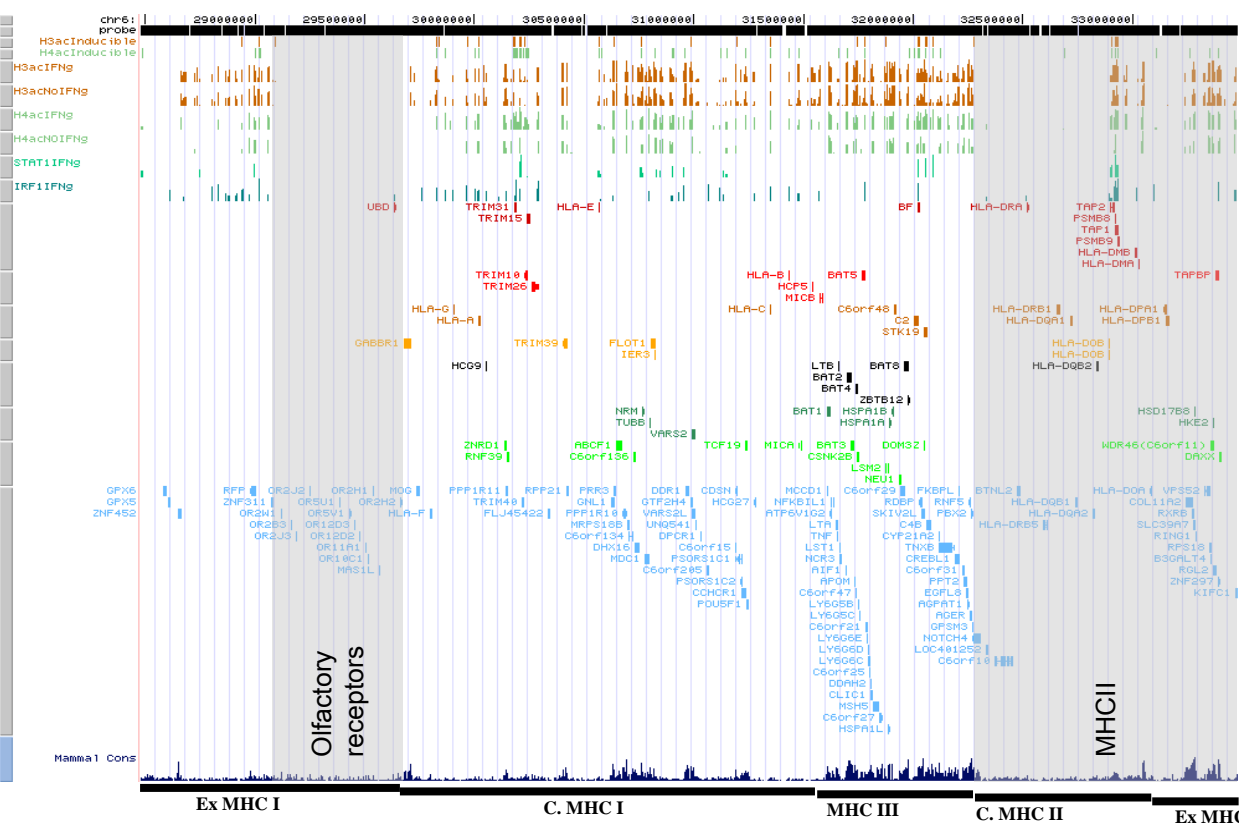
STAT1 locus chr2:191,048,779-192,048,779



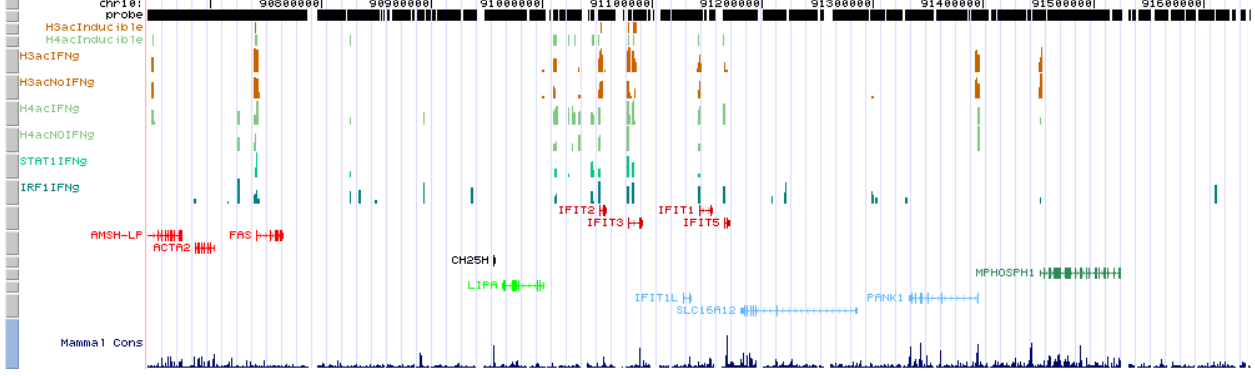
IRF1 locus chr5:131,346,678-132,346,678



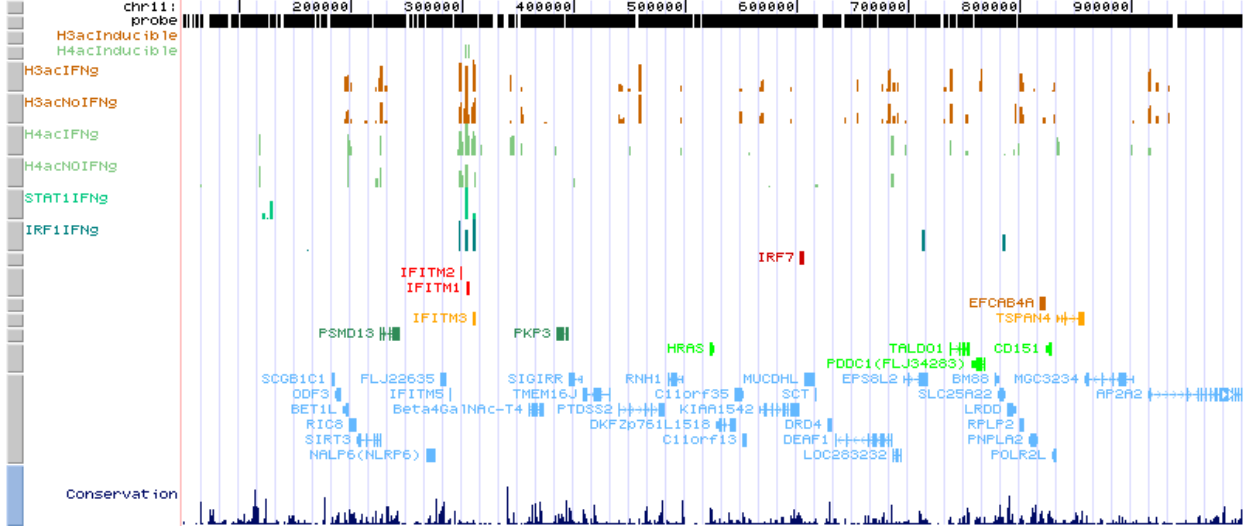
MHC locus chr6:28,478,769-33,478,769



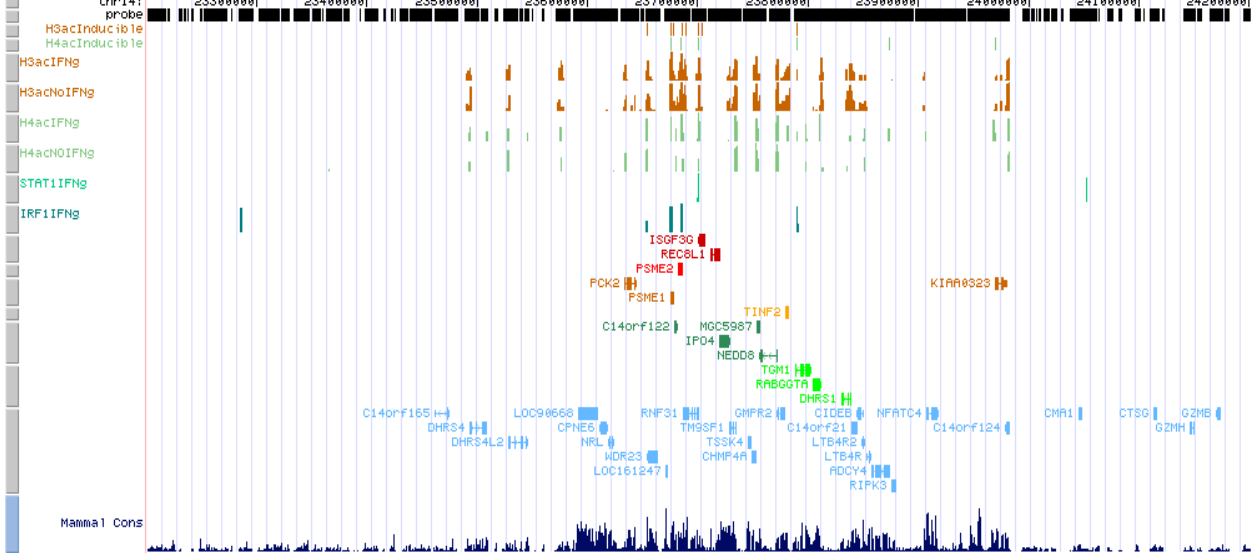
IFIT1 cluster chr10:90,642,357-91,642,357



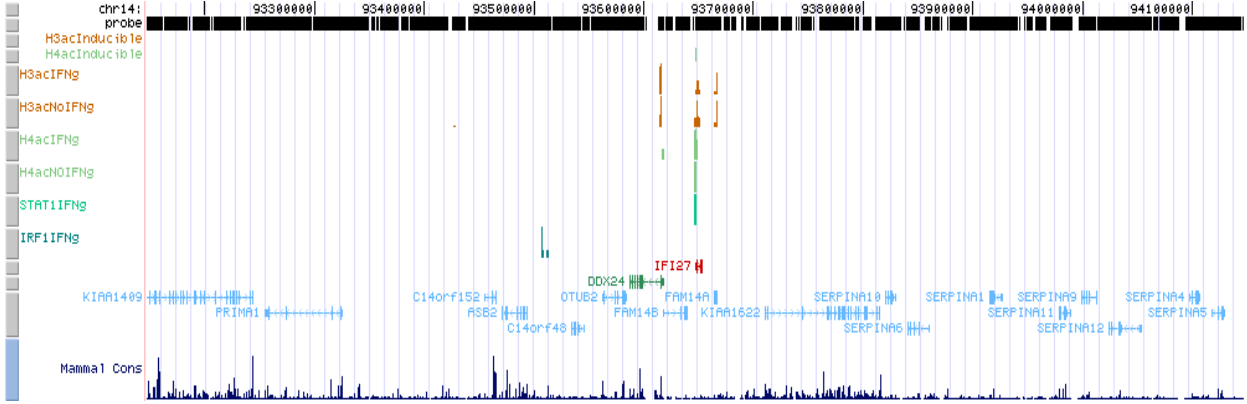
9-27(IFITM1) cluster, IFITM3 locus chr11:50001-1,000,000



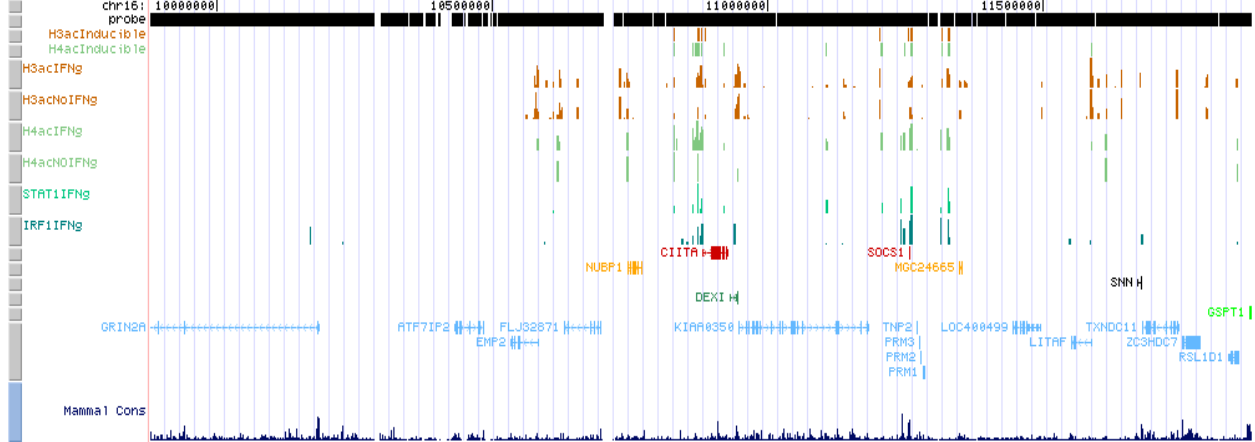
PSME cluster chr14:23,201,190-24,201,190



IFI27 locus chr14: 93,146,835-94,146,835

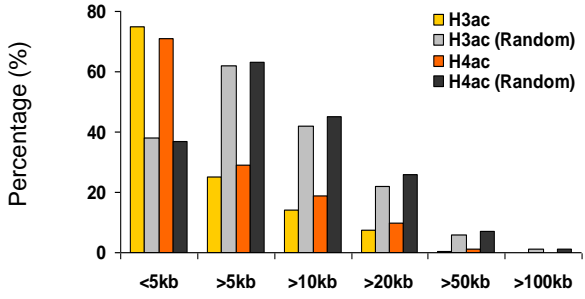


CIITA and SOCS1 loci chr16:9,878,539-11,878,539

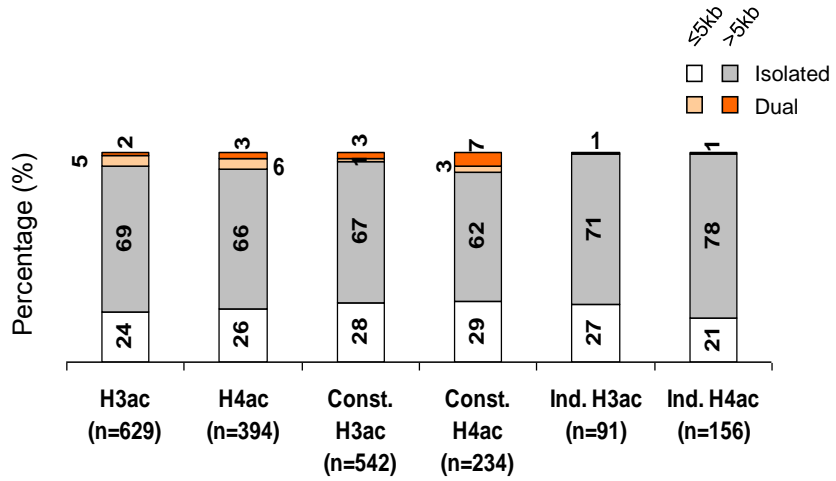


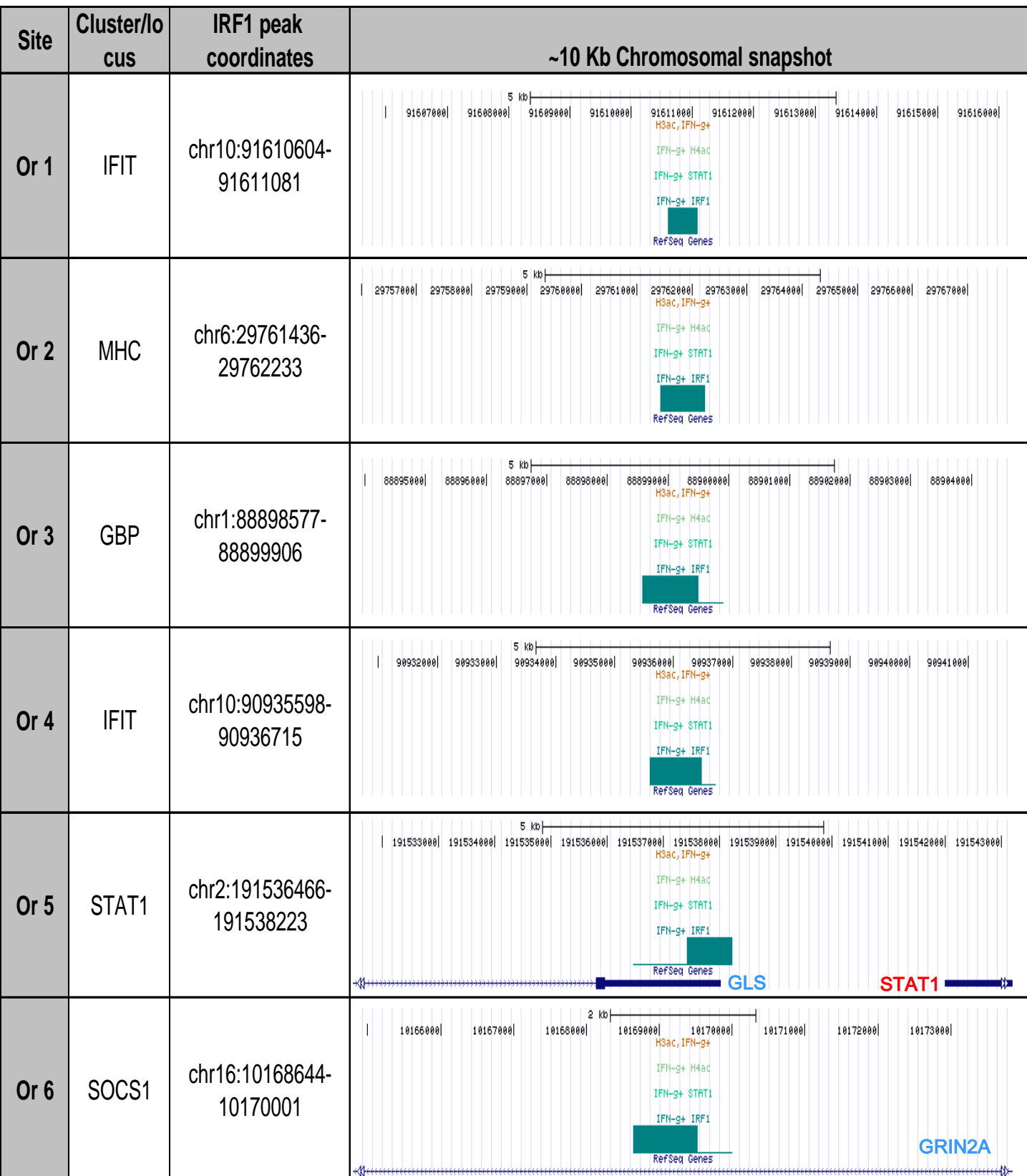
Supp Fig 2. Distribution of H3ac and H4ac relative to the TSS of all genes. (A) Bar graph summarizes the distribution of histone acetylation sites at increasing distance from the 5' ends of genes located within the studied 16 Mb (Known Genes, Refseq and Geneid Genes), and compared to equal numbers of randomly generated sites. **(B)** Percent of isolated or dual (i.e. overlapping) randomly generated sites corresponding to the number of total, constitutive and induced histone acetylation sites at proximal ($\leq 5\text{kb}$) or distal ($> 5\text{kb}$) distances from the TSS of Known genes.

A)



B)





Supp Fig 3. Chromosomal localization of a selected set of orphan IRF1 sites. Coordinates of randomly selected orphan IRF1 sites are provided. Snap shots show +/-5kb regions around the selected sites and show IRF1 binding in the absence of STAT1 binding or H3/4ac. Snap shots also show the inter- or intra-genic localization of the orphan sites. Overlapping or nearby genes were colored in red for early induced ISGS (eindISGs) and in blue for Other genes.

Supp Figures 3. Cont.

