



SUPPLEMENTARY FIG. S2. Nucleosome sequence preferences and chromatin regulatory functions in the human type I IFN locus (related to Figs. 1 and 3). **(A)** Data are generated and represented as in Fig. 1B. Plotted is the *KLHL9* mRNA abundance before and after virus infection. Error bars denote standard deviation for triplicate PCRs. Results are representative of 3 independent infection experiments. **(B)** Data are generated and represented as in Fig. 3A. Density plots comparing the normalized nucleosome occupancy per base pair in the predicted nucleosome occupancy maps (based on data from the software tool NuPoP) (Xi and others 2010) and the *in vivo* nucleosome occupancy maps. **(C, D)** Data are generated and represented as in Fig. 3C and D. Magnified view of the *IFNA5* (C) and *IFNA8* (D) region. The gene is illustrated as a solid line, the TSS and directionality indicated by an arrow, and the gene body indicated with a box. Each row below depicts nucleosome occupancy per base pair. Positions of 5' and 3' NDRs and +1 and -1 nucleosomes flanking the TSS are indicated. The 2 genes are representative of the nucleosome organization found around the promoters of all the type I IFN genes (excluding *IFNE*). As the degree of Sendai virus-dependent induction is substantially lower in the *IFNA* and *IFNW1* genes relative to *IFNB1*, dramatic nucleosome rearrangements were not as clearly observed.