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Supplemental information

Interferons reshape the 3D conformation and accessibility of macrophage chromatin

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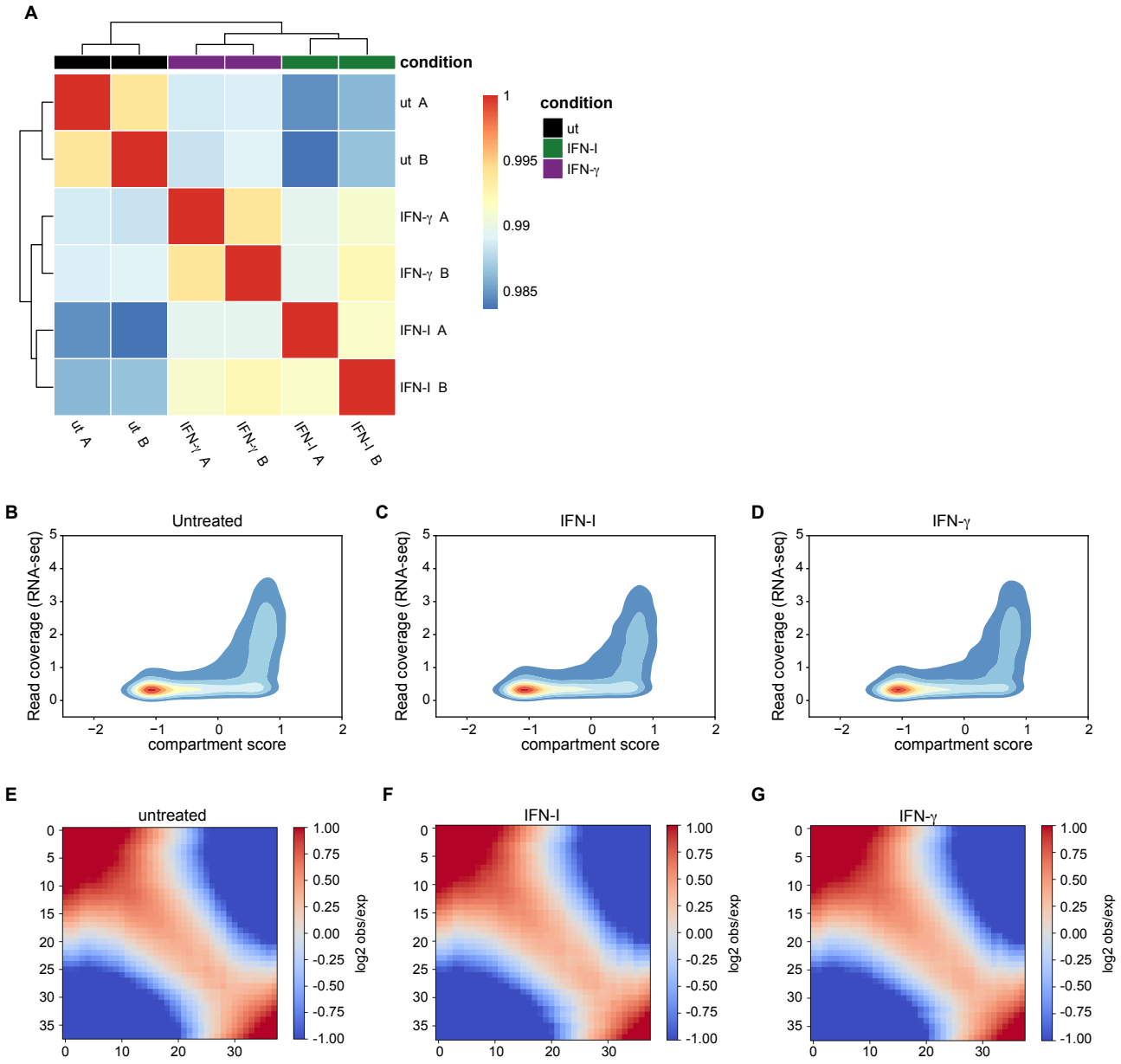

Figure S1. Quality control of HiC data. Related to figure 1. A Heatmap of sample similarity, as calculated with HiCRep (max. scanning distance 10Mbp, 10kbp bins). B-D Density plots of RNA-seq read coverage versus compartment score for each genomic bin (40kbp) of B untreated, C IFN-I treated (2h), D IFN-γ treated (2h) primary murine bone marrow-derived macrophages (BMDM). E-G Compartmentalization saddle plots showing the enrichment of interactions as a function of the compartment vector in E untreated, F IFN-I (2h) and G IFN-γ (2h) treated primary murine bone marrow-derived macrophages (kbp bins).

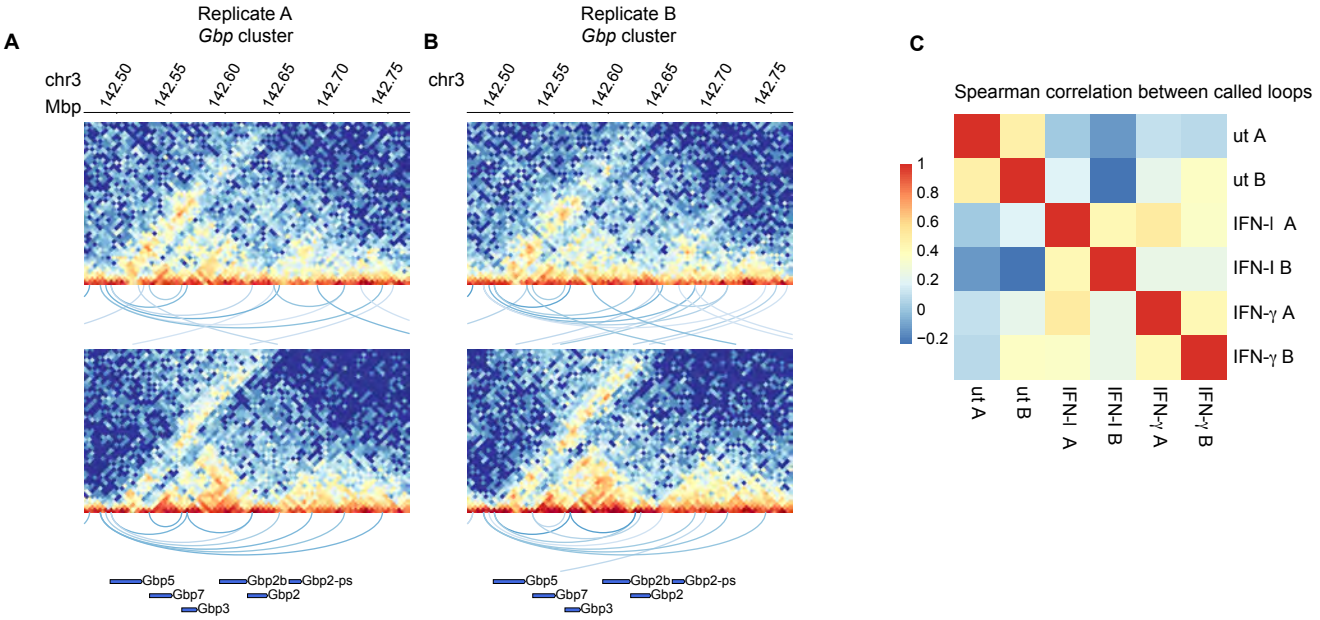

Figure S2. Correlation between HiC data replicates and correlation between loops called in individual samples. Related to figure 2. A, B Hi-C contact maps of untreated and IFN-I treated BMDM. Visualization of pattern detection with chromosight (loops between two loci are indicated as arcs). Color coding of arcs corresponds to Pearson correlation scores. Loops with a score > 0.35 are shown (maximum size/ylim = 500 kbp). Only ISG of the corresponding gene clusters are visualized. Single replicates are plotted next to each other. Only ISG of the corresponding gene clusters are visualized. C Spearman correlation of loop scores at ISG loci shown in Figures 2, 3, S3 (Gbp, Cxcl, Ifit, Irf1, Irf8, Oas, Mx, Rnf213) between individual samples.

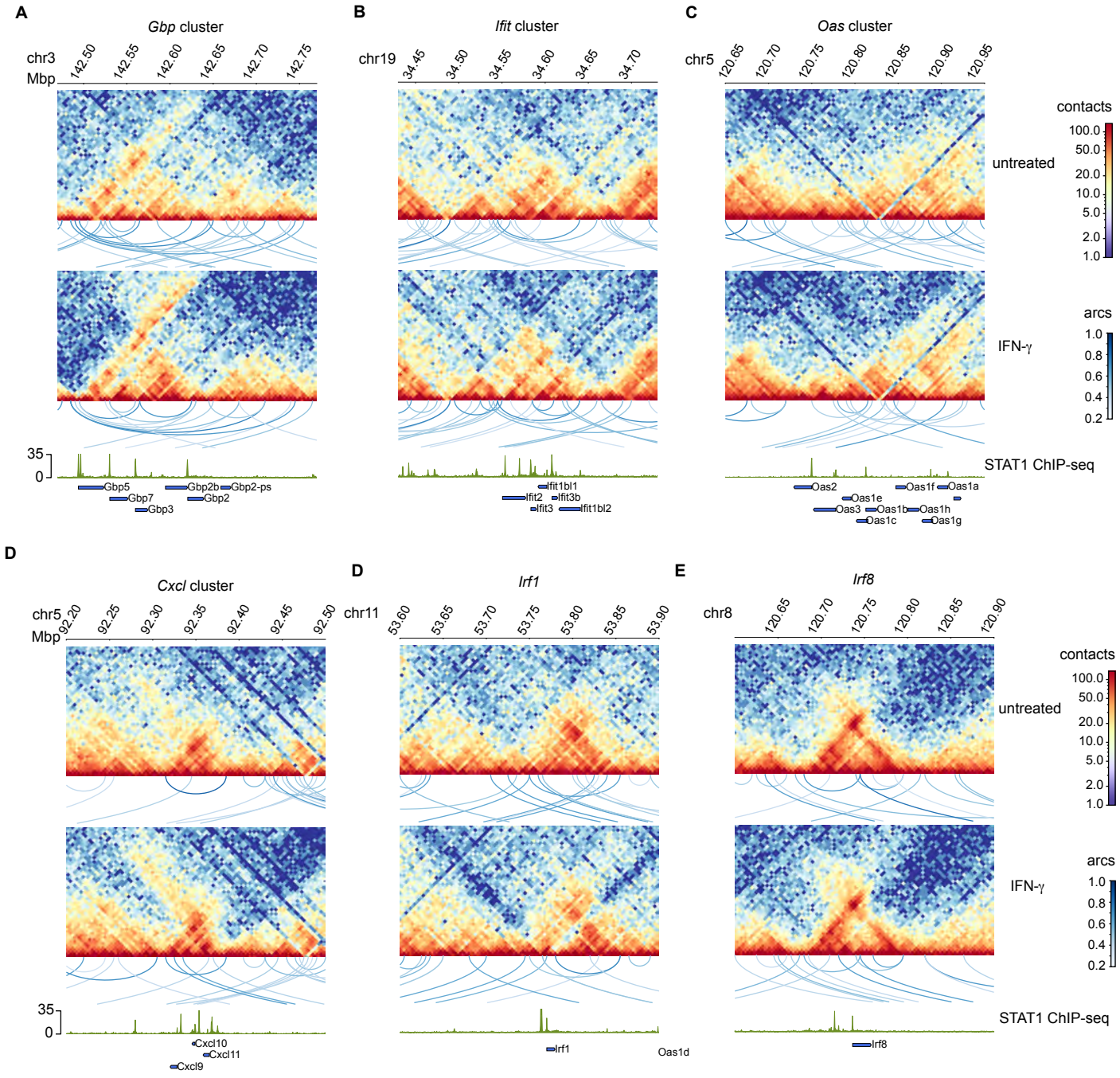

Figure S3. Effect of IFN-γ on the loop structure of ISG loci. Related to figure 2. A-F Hi-C contact maps (merge of 2 replicates per condition, log1p scale) of untreated and IFN-γ (2h) treated BMDM. Visualization of pattern detection with chromosight (loops between two loci are indicated as arcs). Color coding of arcs corresponds to Pearson correlation scores. Loops with a score > 0.35 are shown (maximum size/ylim = 500 kbp). Lower panel, STAT1 ChIP-seq tracks (1.5h IFN-γ treatment) and gene annotations are shown to visualize binding sites for both ISGF3 and STAT1 homodimers. Only ISG of the corresponding gene clusters are visualized.

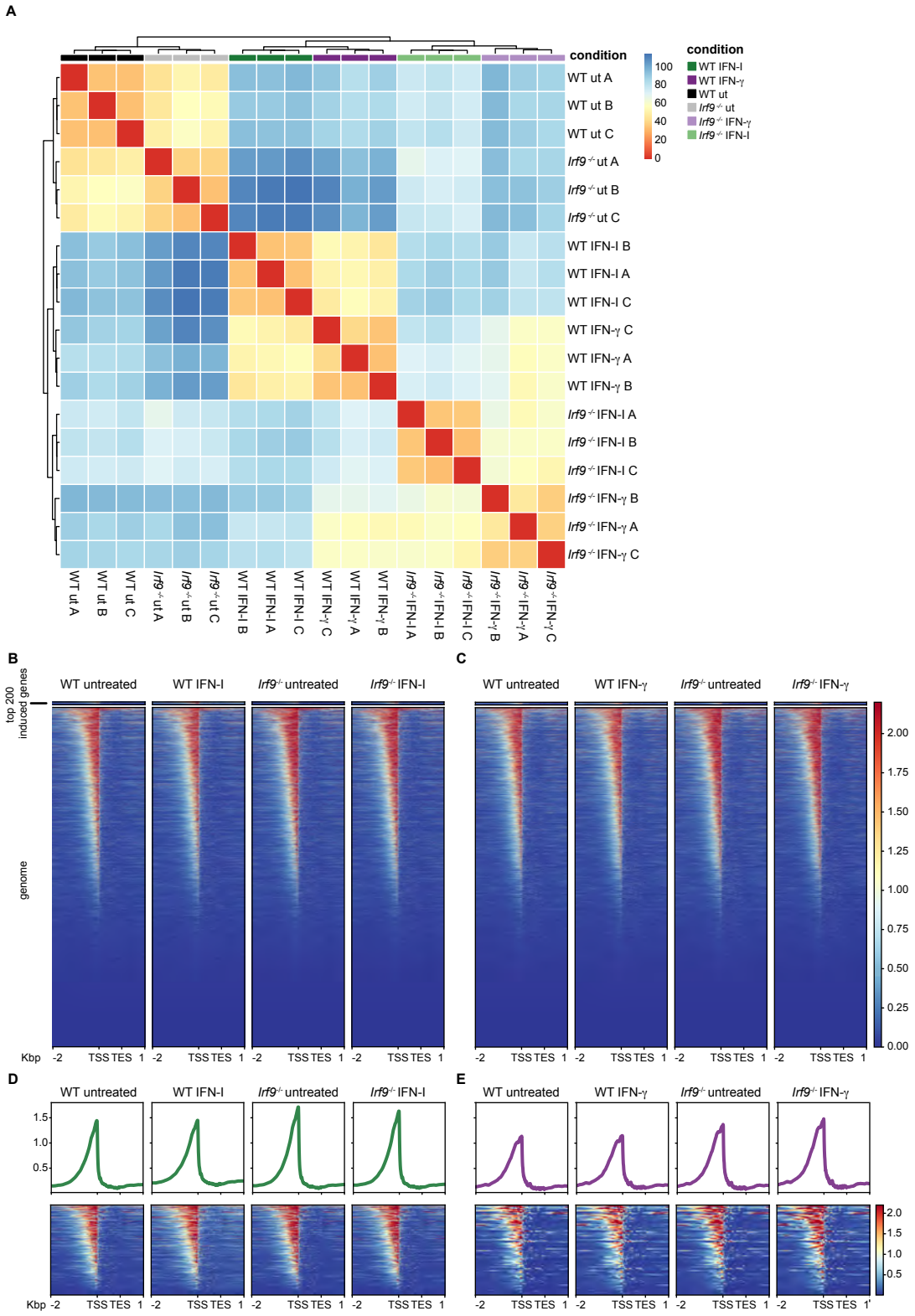

Figure S4. Similarity of ATAC-seq samples and effect of IFN and IRF9 deficiency on chromatin opening. Related to figures 4, 5 and 6. A Heatmap of sample similarity, generated from clustering by Euclidean distances between DESeq2 rlog values for each sample. B, C Heatmaps of chromatin accessibility in regions of the top 200 genes (log2FC) upregulated after IFN-I (2h) and IFN-γ (2h) treatment respectively according to RNA-seq and the remaining genome. Heatmaps are shown for the regions of the genes, including 2 kbp upstream of the TSS and 1kbp downstream of the TES as indicated below the plots. Data are derived from three biological replicates. D, E ATAC-seq intensities at TSS of genes specifically induced by IFN-I (D) or IFN-γ (E) according to RNA-seq. Top panels: Summary profile indicating the average ATAC-seq signal over all regions. Lower panels: Heatmaps of chromatin accessibility.

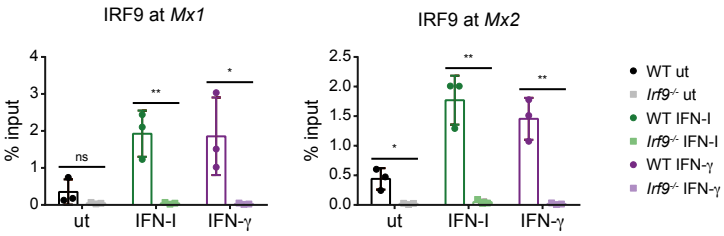

Figure S5. Control ChIP-qPCR showing association of IRF9 with the Mx1 and Mx2 promoters. Related to Figure 7. Site directed ChIP at the Mx1, Mx2 gene promoters was performed with anti-IRF9 mAb using bone marrow-derived macrophages isolated from wild-type and Irf9-/- BMDM, treated for 2h either with IFN-I or IFN-γ.

ChIP PCR Primers		
Gene name	Forward sequence 5'-3'	Reverse sequence 5'-3'
Oas1a	ATACAGAGCCCCACTCACAACT	TCTGGGTCTGTCGCATCG
Oas2	ATCCACGGCCTGGTCTATCT	TGTCTGAAGCAGATTGCGGT
Irf1	TCCCGCTAAGTGTTTAGATTTC	TTCGGTTCGGCTTAGACTG
Mx1	GCTCAGGCTTTTTCACGGTTTCA	GGCTTGAAGAGAGAGTGTGCAG
Mx2	CTTCTGCCCAGAATCAGGC	AGTTTCACTTTCATTTCTCTGGTT
untr6	TCAGGCATGAACCACCATAC	AACATCCACACGTCCAGTGA

Table S8: Primers used for ChIP-Q-PCR. Related to STAR methods.