Additional File 6

A p65 mostly binds enhancers

B Examples of p65-induced intragenic nucleosome depletion
Additional File 6 | Characteristics of p65 binding genome-wide. (A) Sites binding p65 carry histone marks characteristic of enhancers. Strong peaks of p65 binding 10 or 30 min post-stimulation were selected (±20 reads/million; FDR <0.01; n=214 and 8,583, respectively). Left/middle: Venn diagrams showing that ~65% of 30-min peaks carry histone modifications typical of enhancers (i.e., H3K4me1, H3K27ac; determined using HUVEC ENCODE data [31]). Right: HUVEC chromatin, segmented using epigenetic marks and hidden Markov models (HMM [51]), was compared to 10- and 30-min p65 binding profiles; most 10-min peaks overlap repetitive elements, while >75% 30-min p65 sites are embedded in regions characterized as “strong” enhancers. (B) Examples of intra-genic p65 peaks. Browser tracks illustrate MNase-seq (0-min levels in grey underlie 10- and 30-min in green to facilitate comparison), p65 (black) or H3K4me1/3 ChiP-seq (orange and purple, respectively), and RNA-seq data (magenta) in the introns of TNFα-responsive genes EX71, SAMD4A, and SLC25A25.