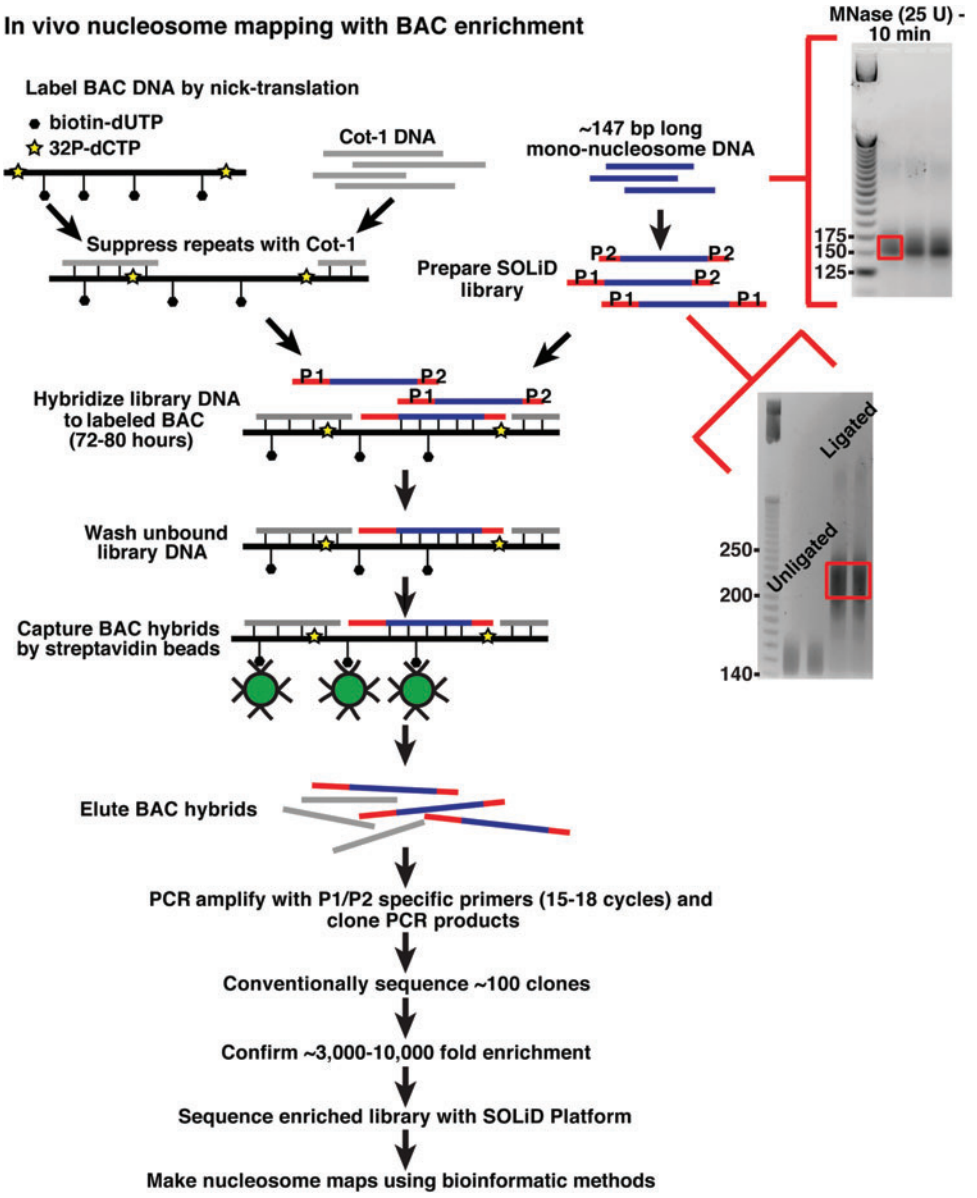
Supplementary Data



SUPPLEMENTARY FIG. S1. MNase-Seq coupled with direct genomic selection workflow (related to Fig. 2). Schematic depiction of direct genomic selection of nucleosome-protected DNA fragments coupled with next-generation sequencing. Cells were harvested at various times during the course of a Sendai virus infection. The nuclear fraction was isolated and subsequently digested by micrococcal nuclease treatment for 10 min. Sequencing libraries were prepared from mononucleosome-length DNA that was isolated and purified by agarose gel electrophoresis. In parallel, a binding affinity matrix was generated, which is composed of 3 biotin-labeled BACs that cover and span the entire type I IFN locus. The hybridized library DNA was washed, eluted, amplified, and sequenced to high depth using the SOLiD sequencing platform.