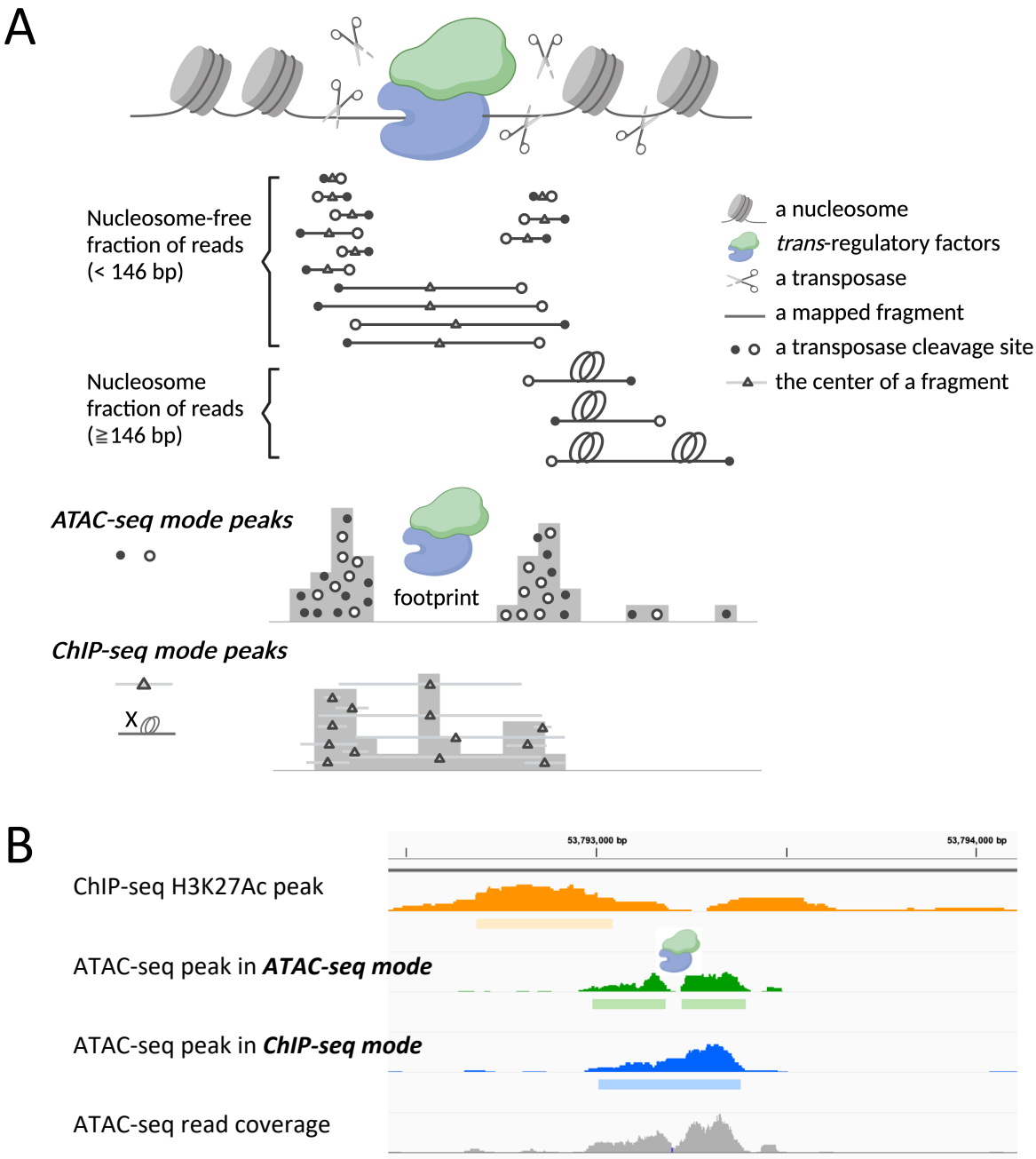

Supplemental Figure S3: (A) ATAC-seq peaks were called in two ways: (i) ATAC-seq mode focusing on open chromatin regions. Genomic loci cleaved by transposase (tags) (shown in small circles) were defined as 38-bp regions around the reads' 5'-ends (Adey *et al*., 2010, Buenrostro *et al*., 2013). Peaks (open chromatin regions) were identified by comparing the tag distribution of a sample to one from a purified genomic DNA control; and (ii) ChIP-seq mode to cover regions protected from transposase cleavage events due to binding(s) of *trans*-regulatory factor(s) like a transcription factor (so-called footprints in the ATAC-seq mode analysis). Peaks were called with a setting generally used for ChIP-seq analysis (MACS2 piles up entire sequencing fragments instead of focusing on transposase cleavage sites close to 5'-ends of reads). To avoid covering nucleosome positions, only nucleosome-free fraction of reads (mapped fragment size < 146 bp) was used. This figure was created with BioRender.com. **(B)** An example of liver ATAC-seq peaks called in either ATAC-seq (shown in green) or ChIP-seq (blue) mode in a putative enhancer region (chr3:53,792,472-53,793,916) overlapping with H3K27Ac ChIP-seq peaks in a cognate liver tissue (orange) (Villar *et al*., 2015). ChIP-seq mode of peaks facilitate to cover and identify *trans*-acting factor's footprints depleted in ATAC-seq mode peak calling.