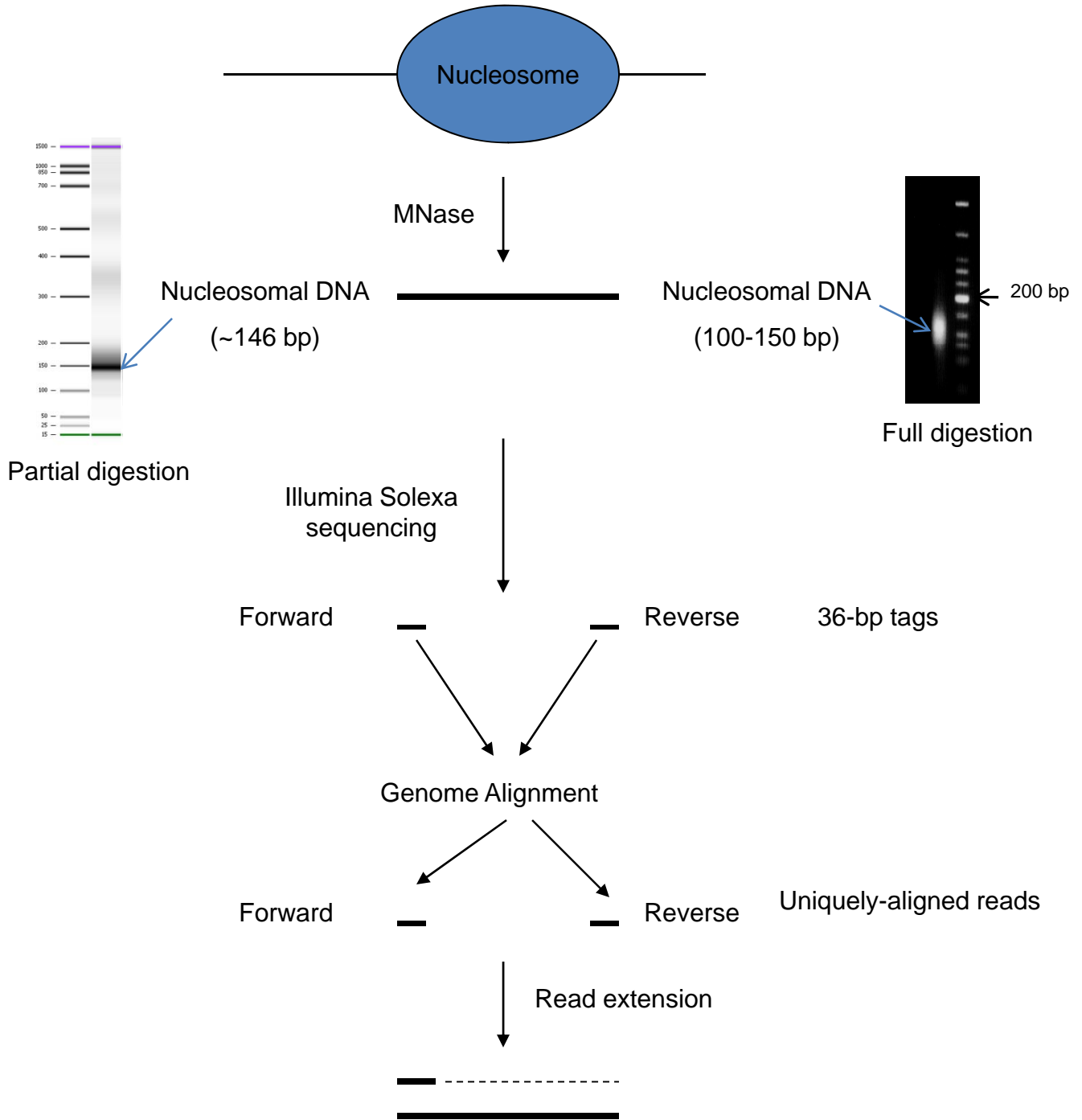


The Nucleosome Map of the Mammalian Liver

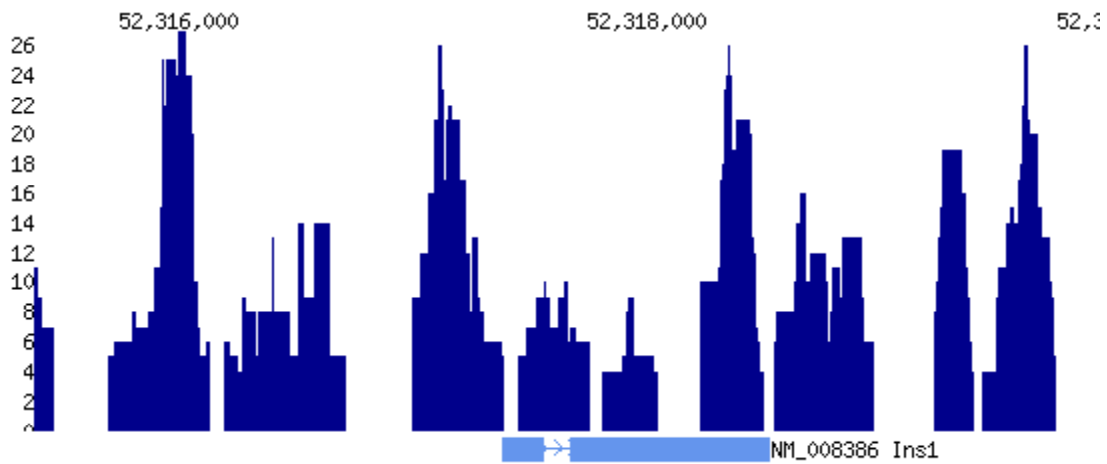
Zhaoyu Li, Jonathan Schug, Geetu Tuteja, Peter White
and Klaus H. Kaestner

This online supplementary information contains 9
supplementary figures.

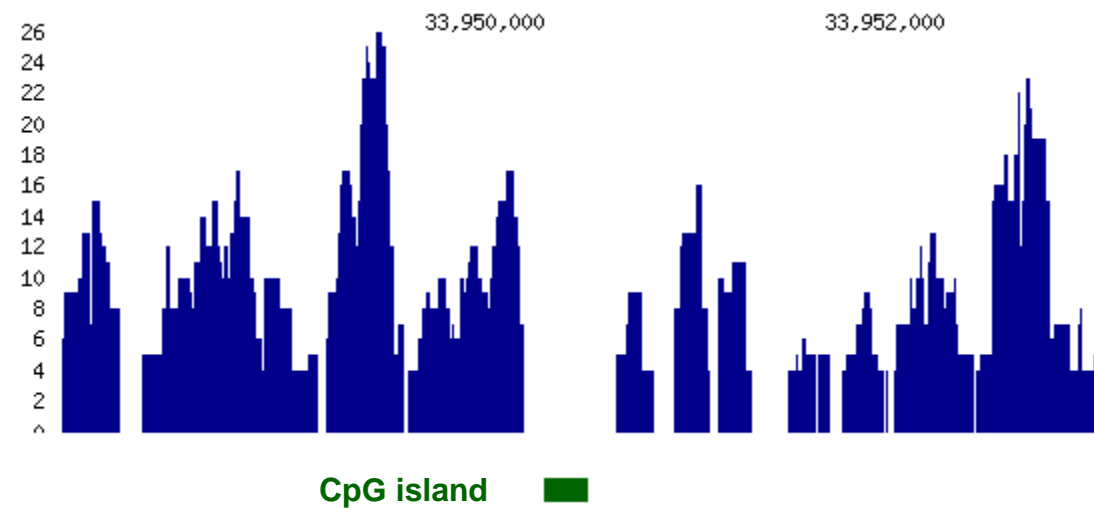
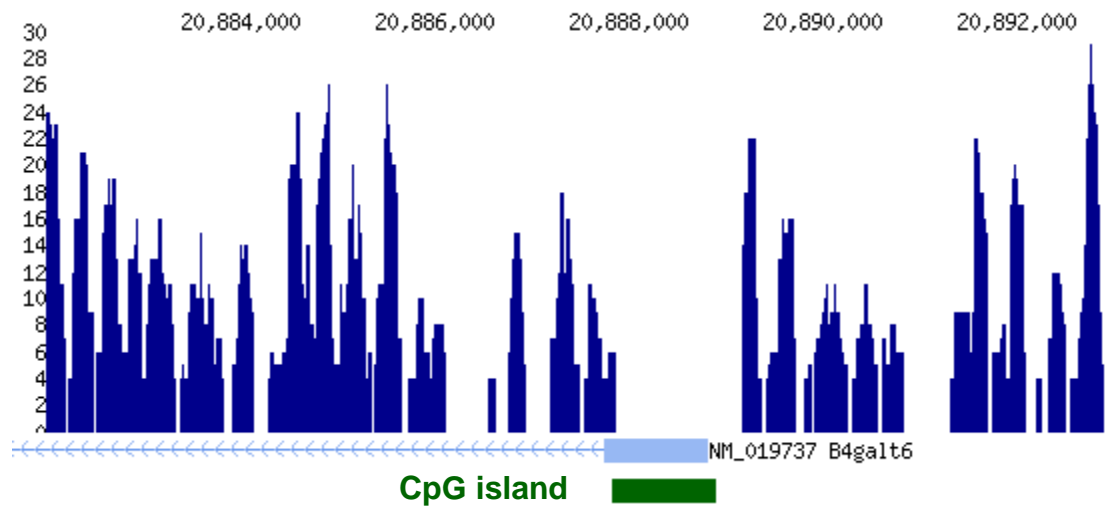
Nucleosome mapping I: high-throughput sequencing



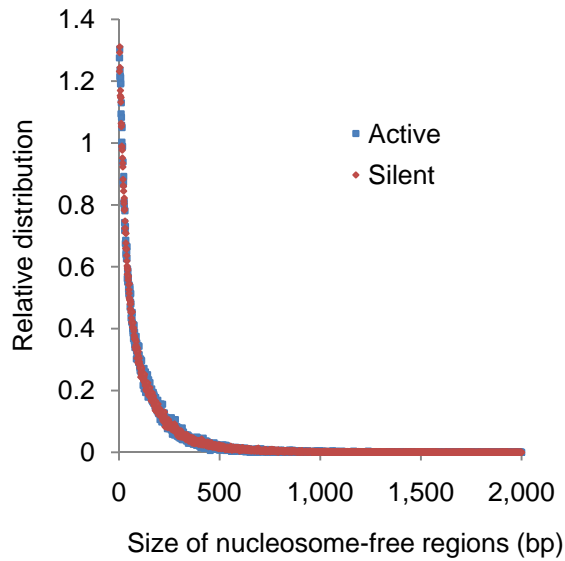
Supplementary Figure 1 Schematic view of Nucleosome mapping via high-throughput sequencing. MNase, micrococcal endonuclease.



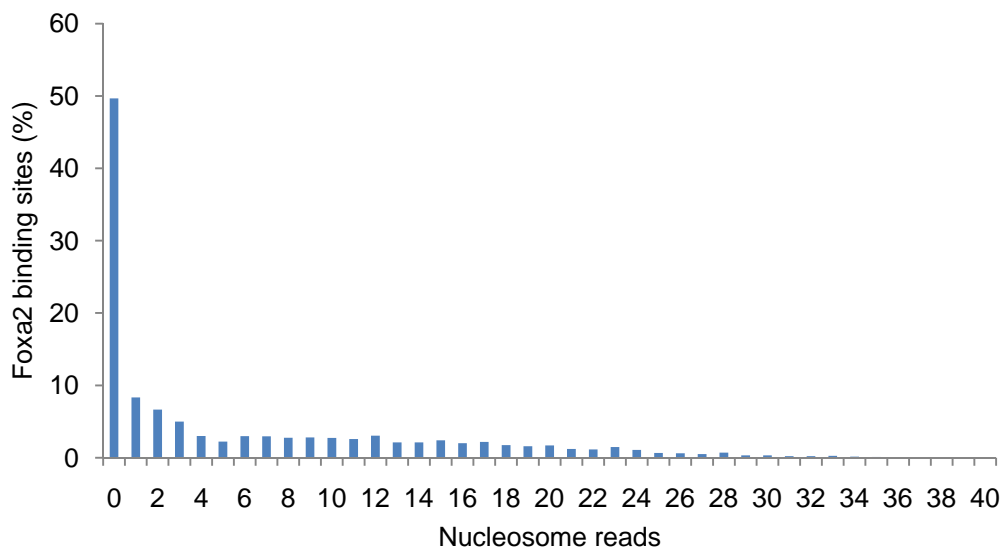
Supplementary Figure 2 Nucleosome positions at the *Insulin 1* gene, a gene that is not expressed in the liver. Note the occupancy of the transcriptional start site by nucleosomes.



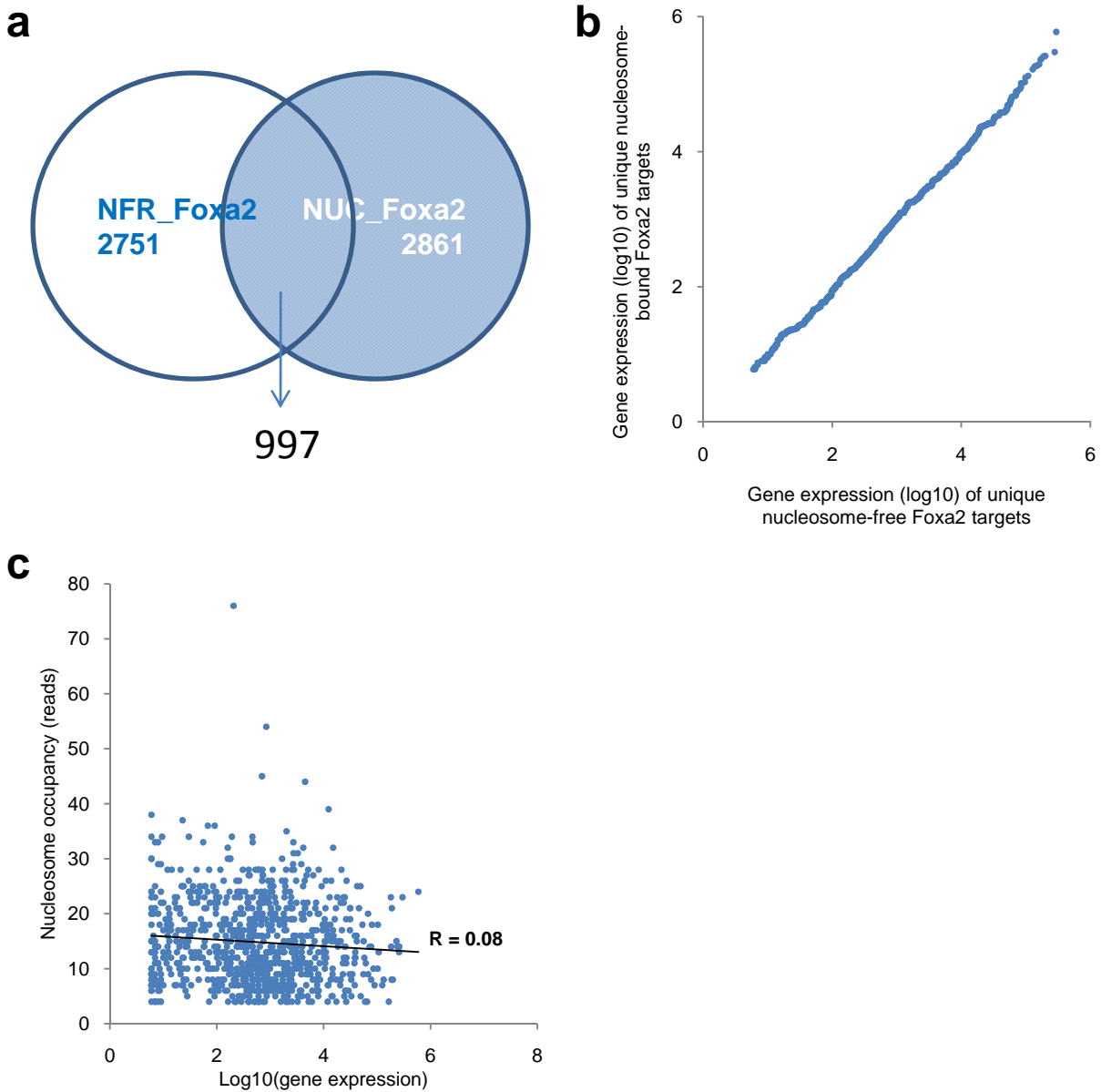
Supplementary Figure 3 Nucleosome positions and CpG islands (green) at promoter regions (upper panel) and intergenic regions (lower panel).



Supplementary Figure 4 Sizes of the nucleosome-free regions at gene body regions the 1000 genes with the highest expression in the liver compared to those of 1000 silent genes.



Supplementary Figure 5 The distribution of nucleosome reads at Foxa2 sites in the mouse liver.



Supplementary Figure 6 Gene expression level is not correlated with nucleosome occupancy at Foxa2 binding sites. (a) Foxa2 target genes are categorized by nucleosome-free (NFR) or nucleosome-bound (NUC) Foxa2. Among them, 997 genes have both nucleosome-free and nucleosome-bound Foxa2 sites. (b) The relationship of gene expression levels between nucleosome-free Foxa2 target genes and nucleosome-bound Foxa2 target genes. (c) Correlation between gene expression levels and nucleosome occupancy for unique nucleosome-bound Foxa2 targeting genes.

