

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: ChIP-seq data used for correlation-based computational analysis and prioritization of TAD boundaries for deletion *in vivo*.

File name: Supplementary Data 2

Description: Correlation analyses and CTCF cluster scores used in the prioritization of TAD boundary loci for deletion *in vivo*.

File name: Supplementary Data 3

Description: Locus features of the TAD boundaries selected for individual deletions in this study.

File name: Supplementary Data 4

Description: Mendelian segregation data.

File name: Supplementary Data 5

Description: Statistically significant differentially expressed genes across select tissues in homozygous TAD boundary mutants versus wild-type embryos at E11.5.

File name: Supplementary Data 6

Description: qPCR source data.

File name: Supplementary Data 7

Description: Summary results from comprehensive phenotyping of adult mice in this study.

File name: Supplementary Data 8

Description: TAD boundaries and intra-TAD Boundary B2 sequences targeted for deletion *in vivo* and corresponding CRISPR sgRNA templates.

File name: Supplementary Data 9

Description: Primers used for screening and genotyping of TAD boundary and other loci generated using CRISPR-mediated deletions.

File name: Supplementary Data 10

Description: Availability of TAD boundary knockout mice.

File name: Supplementary Data 11

Description: qRT-PCR gene-specific primers.