Supplementary Information Guide

Supplementary Note 1: Outline of the SLICE model

This document provides the mathematical derivation of the SLICE model, and outlines how it is applied to the mESC-400 GAM dataset.

Supplementary Note 2: Detection of the most prominently interacting loci with the SLICE model

This documents shows how the SLICE model can be used as the basis for a statistical test, and how that test is applied to obtain the most prominently interacting pairs of loci.

Supplementary Note 3: Mathematical equations

Mathematical equations used to estimate sequencing saturation, estimate non-interacting distances between FISH probes and to calculate linkage disequilibrium.

Supplementary Table 1: Details of sequencing datasets

Details of sequencing datasets generated for this study (NPs, negative and positive control), including experimental batch, sequencing depth, and all metrics used to judge the quality of each NP.

Supplementary Table 2: Top 2% most interacting TAD triplets

List of TADs forming the top 2% most interacting TAD triplets, including their transcriptional/se class.

Supplementary Table 3: Details of published datasets

Details of published genome-wide datasets used in this study, including accession numbers.

Supplementary Table 4: Details of FISH probes

Details of FISH probes used for validating long-range interactions.

Supplementary Table 5: FISH edge-to-edge distances

Measurements of distances between the edges of two FISH probe signals.