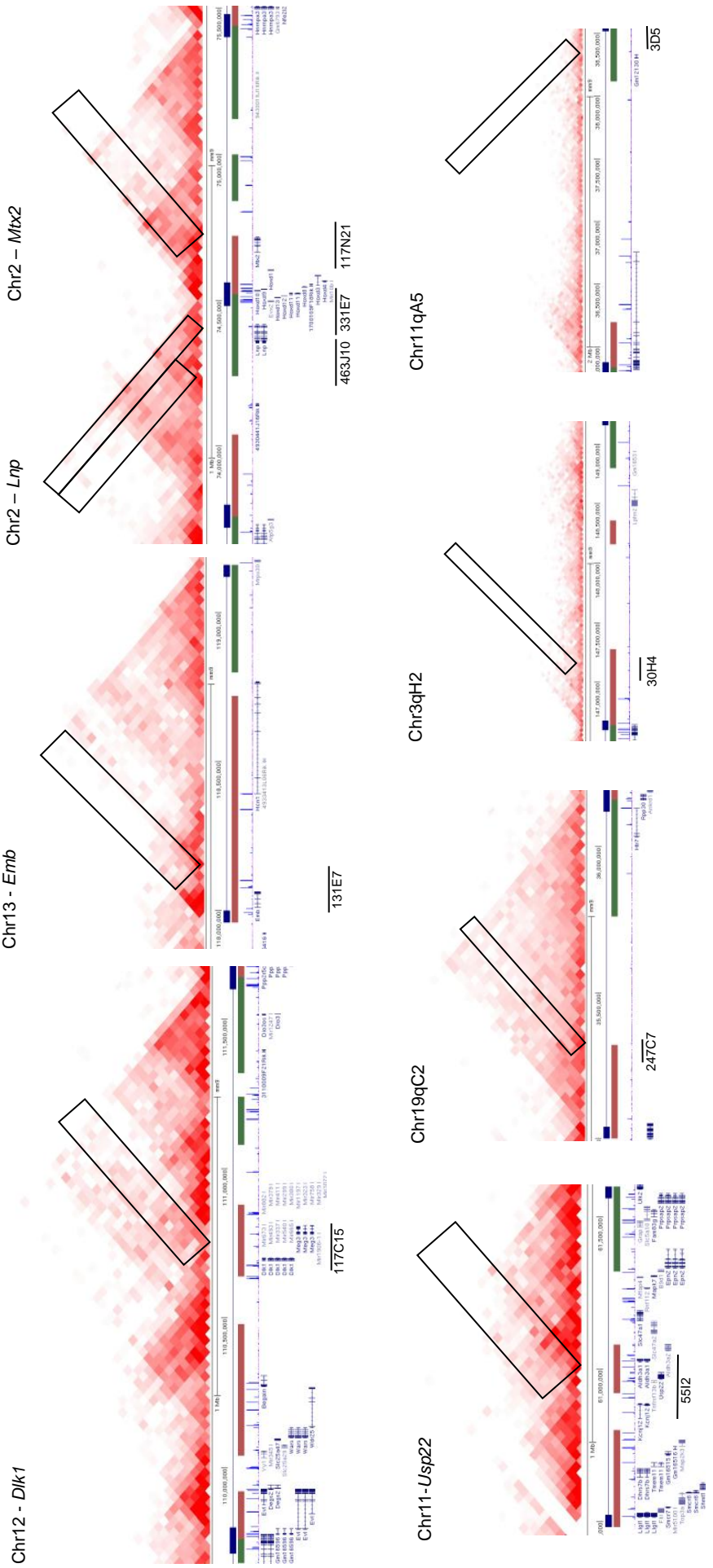
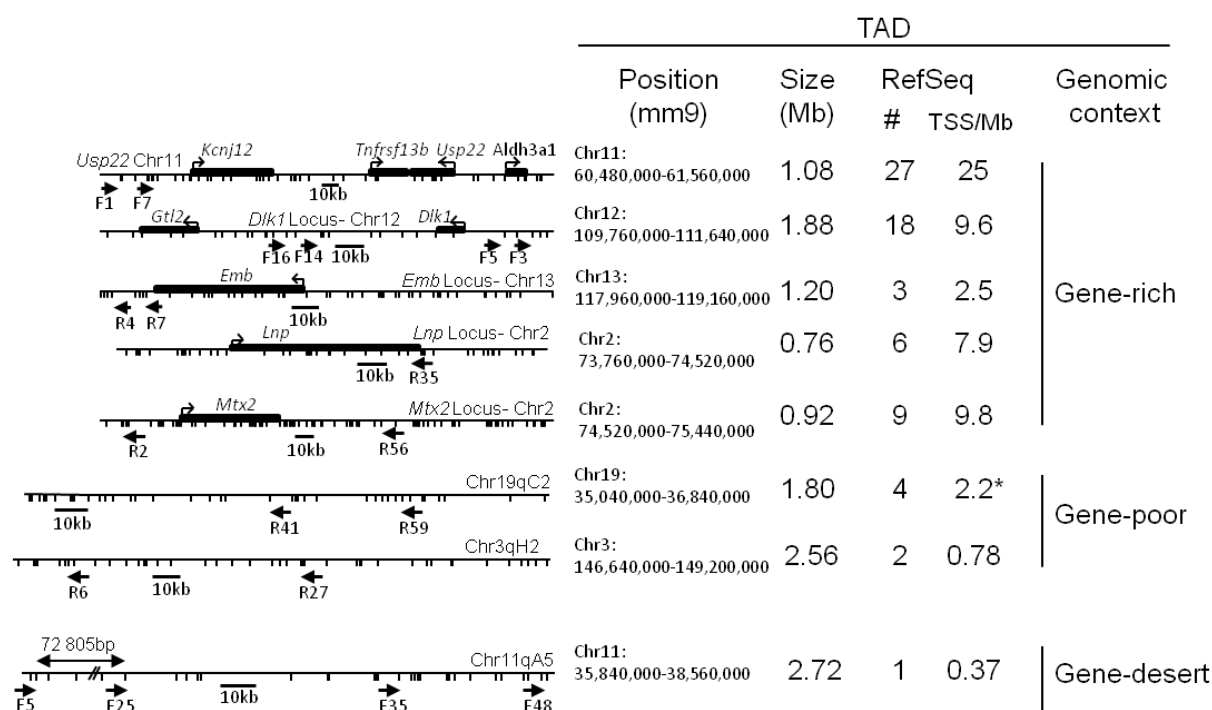


Additional file 1a



## Additional file 1b



\* This TAD possesses several genes near its borders. However, the gene-poor locus investigated is located far-away from them, in the center of the TAD (see Additional file 1a).

**Additional file 1 : Genomic maps of the TADs investigated in the present study. (a)** Map of the TADs containing the loci analyzed in mESC. The Hi-C data (<http://yuelab.org/hi-c/database.php>) ([1]) are displayed on the top of each map. Gene locations are presented as visualized in the UCSC browser. The black squares in the Hi-C data and the location of the BACs (black bars below the genes) help to demarcate the regions analyzed in our quantitative 3C experiments. Red and green rectangles indicate a negative or a positive directionality index respectively, as defined in ref. [1]. Blue rectangles are located at the borders of each TAD. **(b)** Detailed map of the loci investigated by quantitative 3C. Genes are indicated by full boxes and promoters by thick black arrows above these boxes. The scale-bar indicates the size of 10kb of sequence. The names of the loci and chromosomal location are indicated above each map. The HindIII (*Usp22*, *Emb*, *Lnp*, *Mtx2*, 19qC2, 3qH2 and 11qA5 loci) or EcoRI (*Dlk1* locus) sites investigated are indicated on the maps. Arrows labeled with a “F” (forward) or a “R” (reverse) indicate the positions of the primers used as anchors in quantitative 3C experiments. The location (mm9), size (in Mb) and gene density (TSS/Mb) of each TAD investigated are indicated on the right. Note that the very low contact frequencies observed for regions investigated on chromosomes 3 and 11qA5 impair the accurate location of TAD borders. TAD sizes provided here are those determined from data published in ref. [1].