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Cover: Image produced by Galaxy HiCExplorer (https://hicexplorer.usegalaxy.eu). Definition of a Topologically Associating Domains (TAD) and its boundaries. Starting from the top: Contact matrix heatmap (first track) visualizing low (blue), medium (yellow) or red (high) interaction frequencies between genomic regions. Topologically associated domains (TADs, second track) were annotated using the TAD-separation score (third track). TAD separation z-scores (third track) of different window sizes (10-40 kb, grey line) and the mean z-score score (blue line with error bars) are plotted. The chromatin state track (fourth track) shows annotated promoters (red), strong and weak enhancers, (orange, yellow) as well as transcribed (green), polycomb-repressed (black) heterochromatin (brown) and undefined (gray) regions. Principal component analysis reveals A (PC1 > 0) and B (PC1 < 0) compartments (track five). A compartments are associated with active and B compartments with inactive chromatin as indicated by H3K27ac enrichment (track six) and chromatin state annotation.

Raw data were taken from Nothjunge et al. 2017 (Nature Communications, 8:1667, doi: 10.1038/s41467-017-01724-9).