

SUPPLEMENTARY INFORMATION

Cohesin is positioned in mammalian genomes by transcription, CTCF and Wapl

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Supplementary Table 1 | ChIP-seq experiments used in this study.

All ChIP-seq experiments used in this manuscript are listed in this table. The number of peaks identified by MACS peak calling is shown for each ChIP-seq experiment, and the common peaks between replica experiments are indicated. In the “merged replica ChIP” column, the ChIP data of the indicated rows were combined into one dataset and analyzed as described in Online Methods. n.a., not applicable.

Supplementary Table 2 | RNA-seq and GRO-seq experiments used in this study.

This table contains all RNA-seq and GRO-seq data analyzed in the manuscript.

Supplementary Table 3 | Oligonucleotide primers

This table contains all oligonucleotide primer pairs used for PCR genotyping, ChIP-qPCR and GRO-seq analyses.