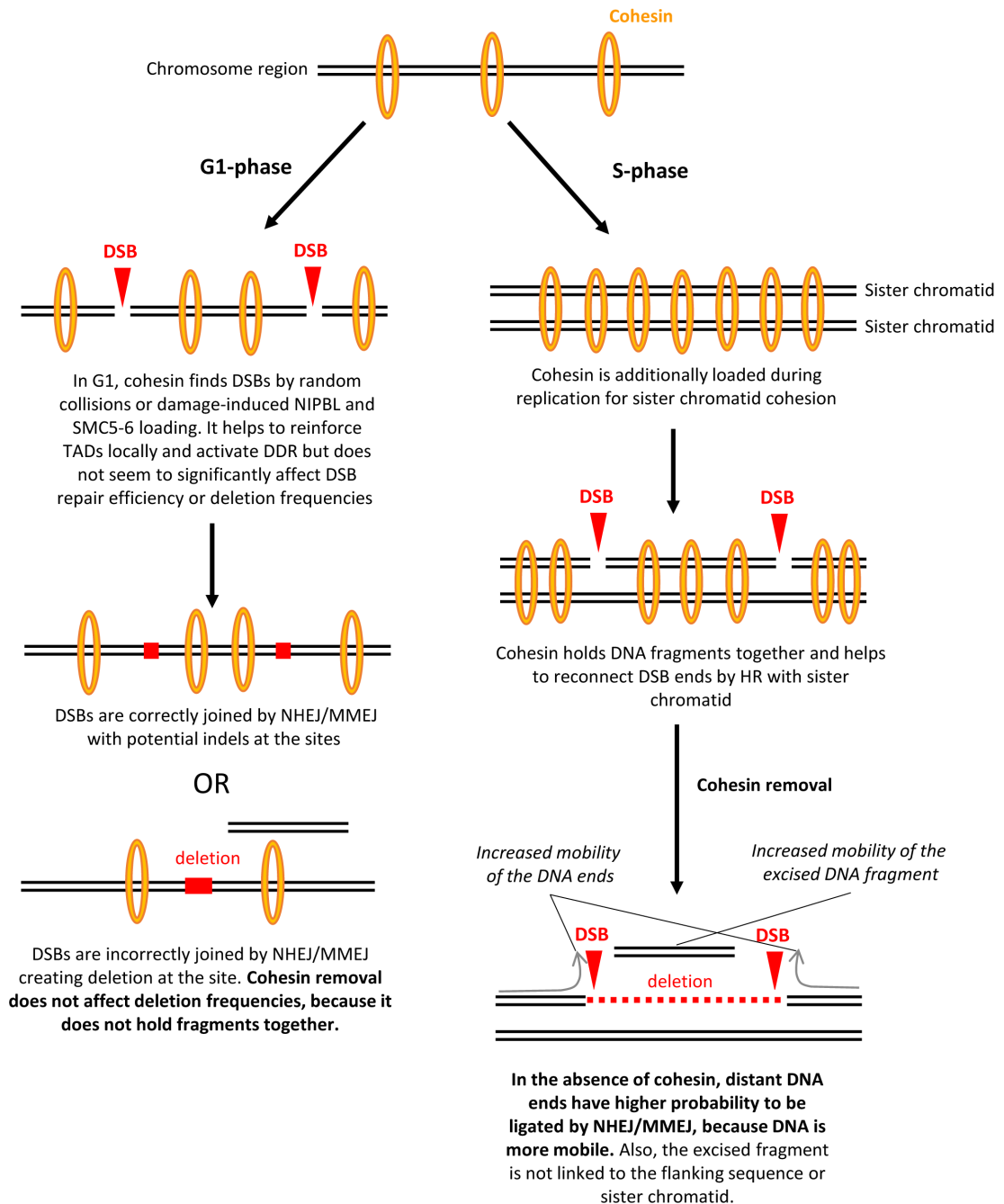


SUPPLEMENTARY MATERIALS

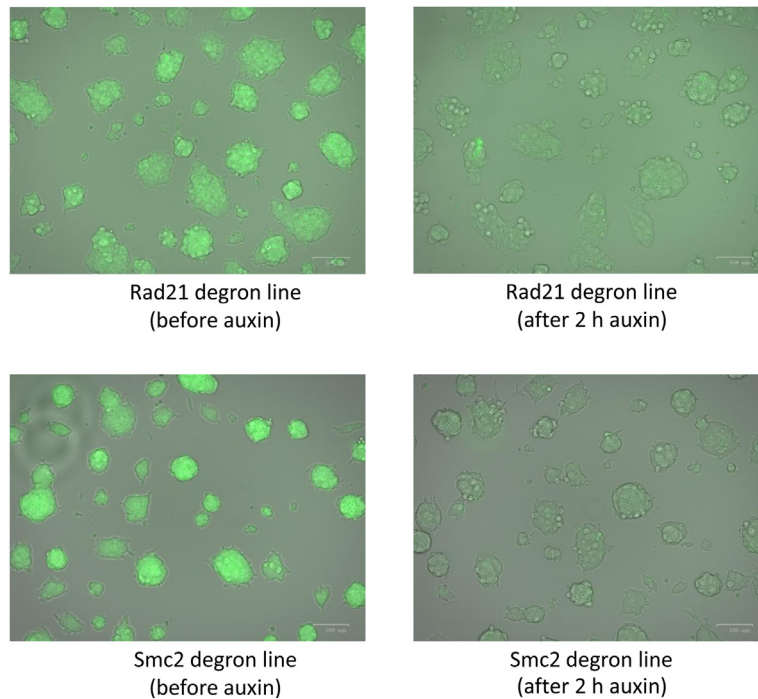
to the article A.V. Smirnov, A.S. Ryzhkova, A.M. Yunusova

“Effects of the auxin-dependent degradation of the cohesin and condensin complexes on the repair of distant DNA double-strand breaks in mouse embryonic stem cells”

Supplementary material 1. Cohesin protects genome from rearrangements by restraining DNA mobility after replication via sister chromatid cohesion

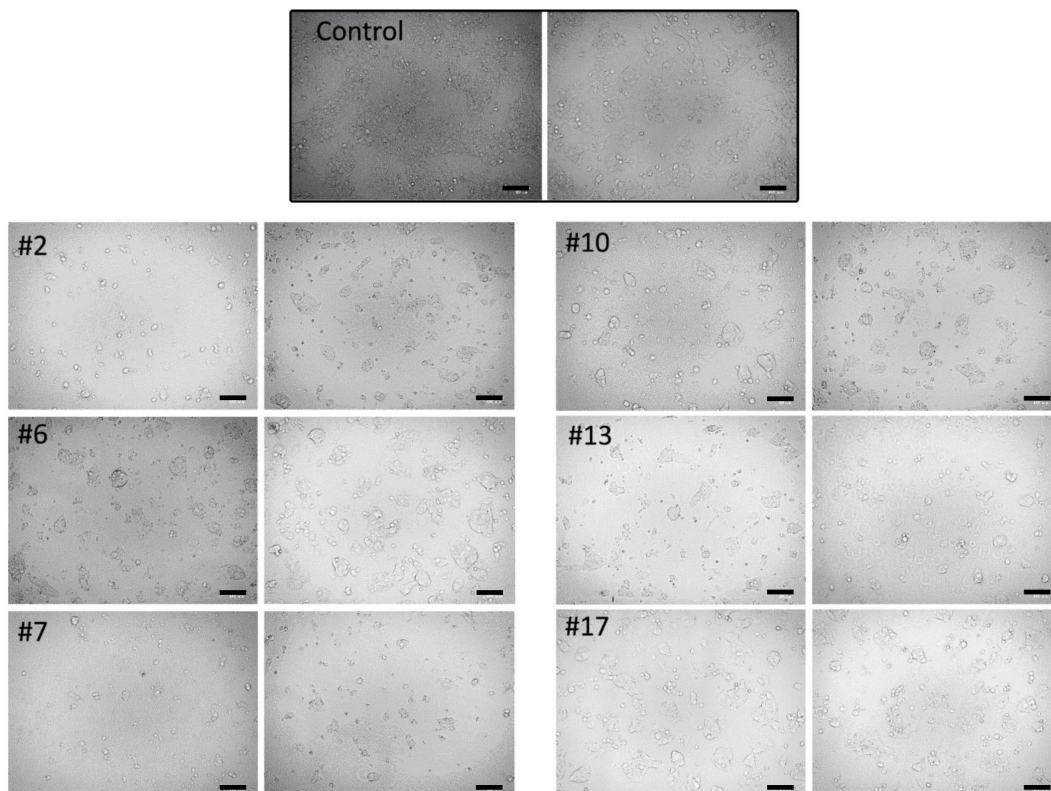


Supplementary material 2. Typical protein depletion picture after 2 hours with auxin. Most cells lose GFP signal



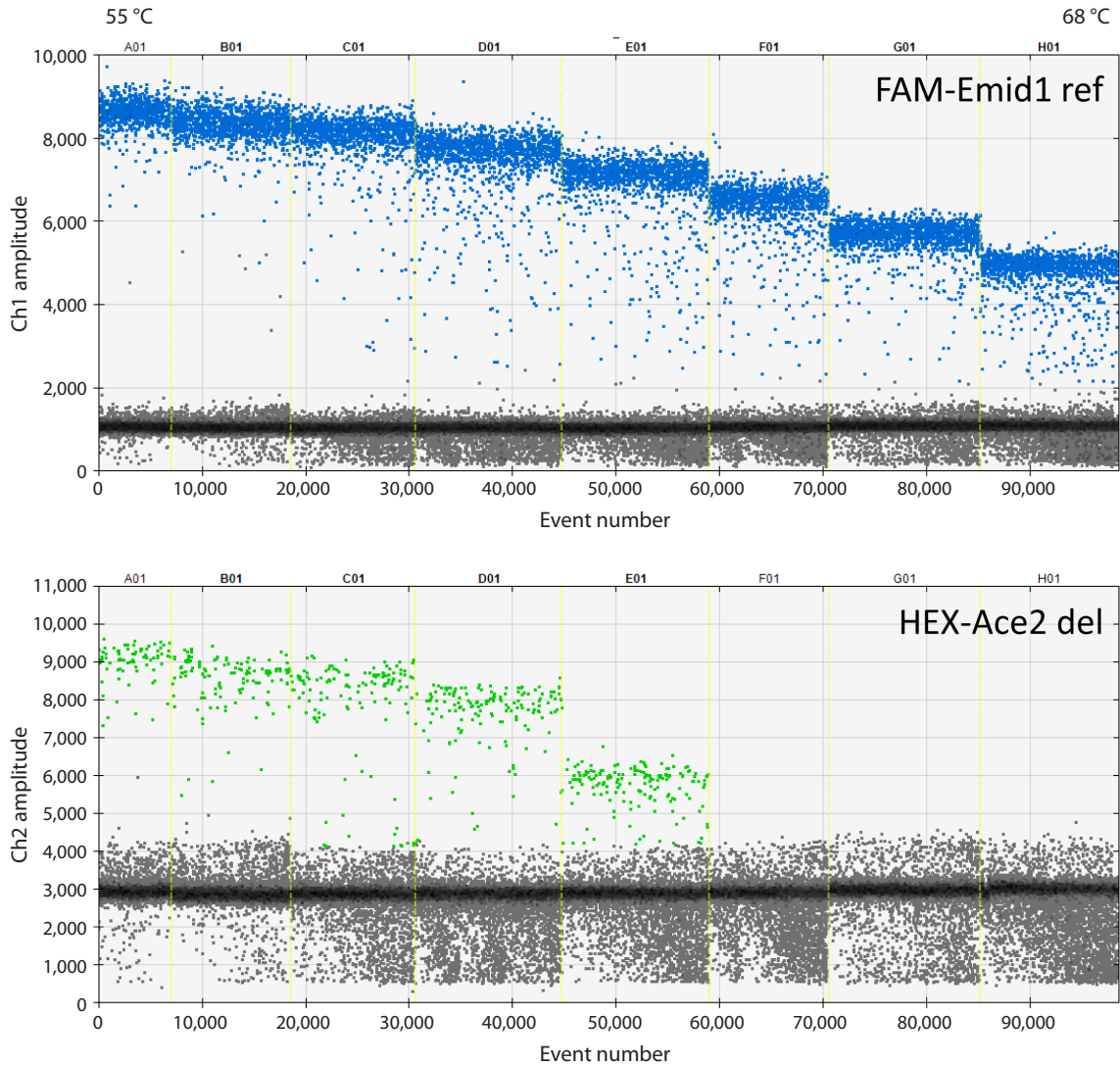
Scale bar – 100 μ m.

Supplementary material 3. mESCs survival after 24 hours post nucleofection, shown in duplicates



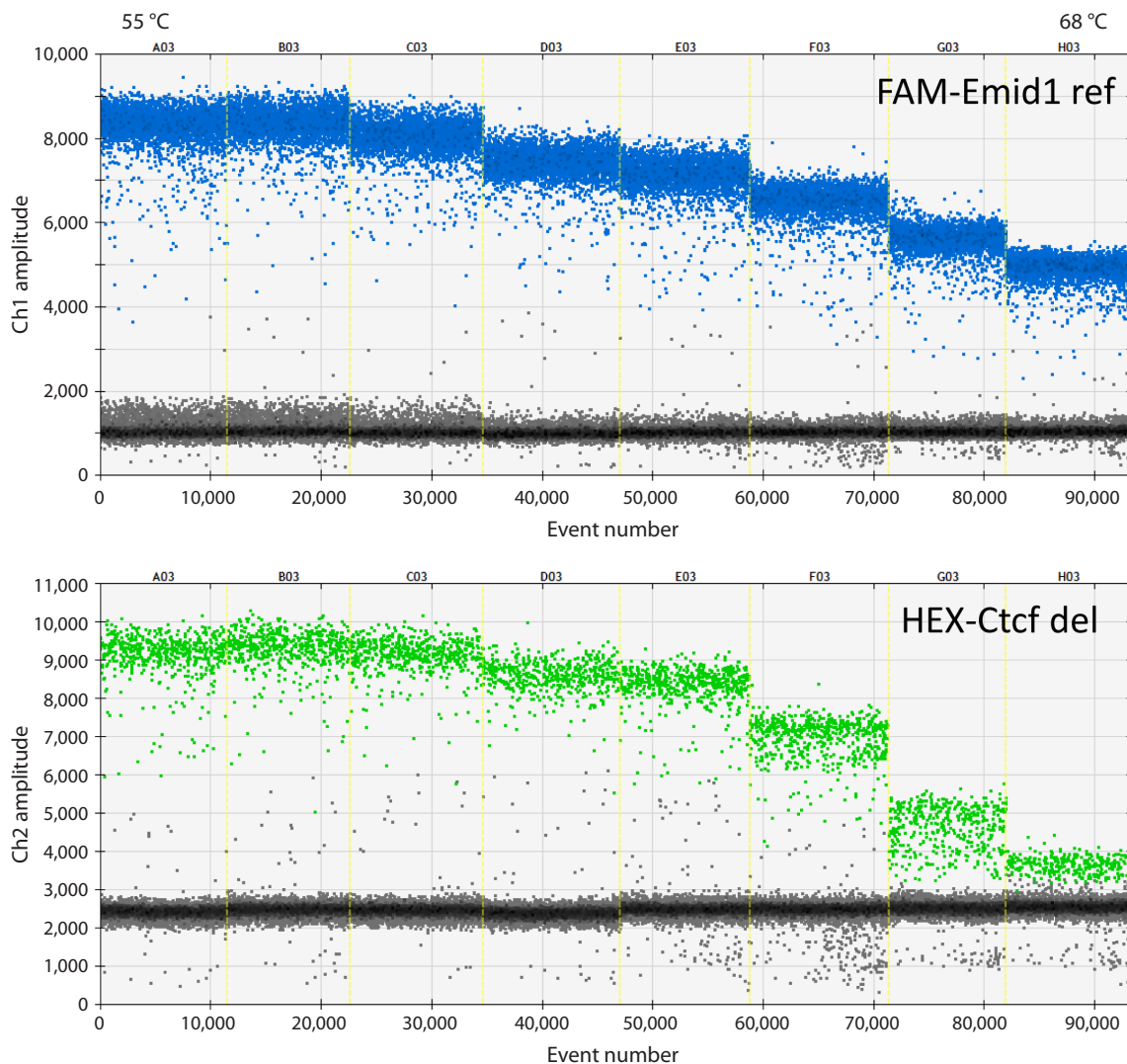
Neon settings are tagged in the corner. Control – untreated cells. Scale bar – 100 μ m.

Supplementary material 4. Gradient ddPCR for the Ace2 F-R2 region (primers for deletions)



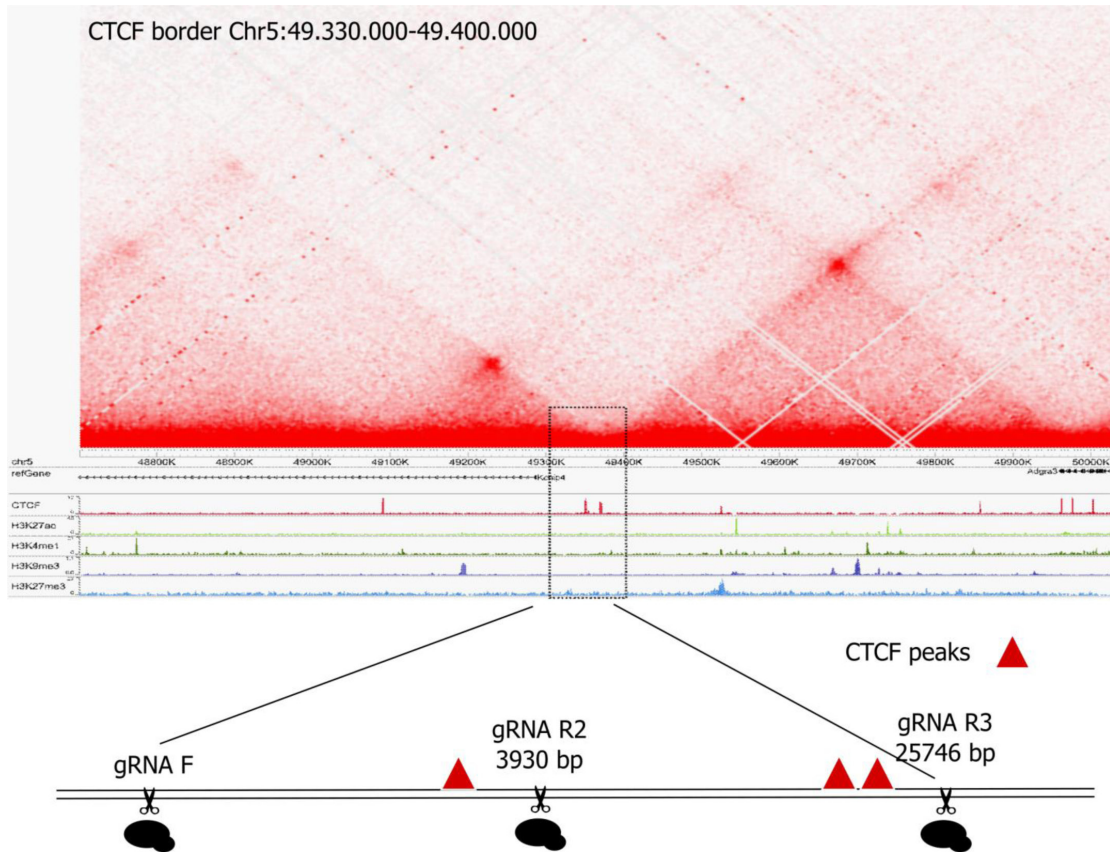
Optimal conditions were: 58 °C annealing and 45 cycles of amplification with standard oligos concentrations. X-axis – droplet counts and samples (yellow), gradient PCR from 55 °C to 68 °C, left to right. Y-axis – FAM/HEX signal levels.

Supplementary material 5. Gradient ddPCR for the Ctcf F-R2 region (primers for deletions)



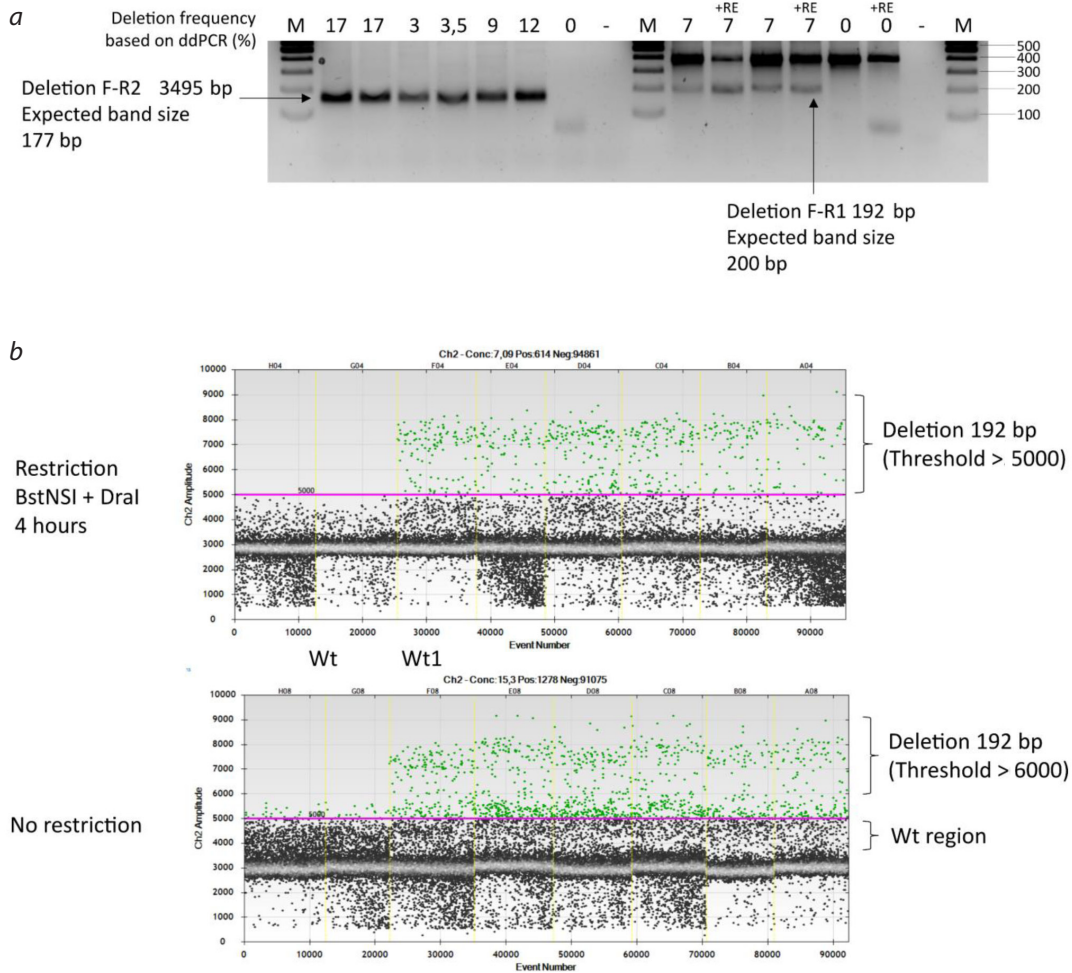
Optimal conditions were: 58 °C annealing and 45 cycles of amplification with standard oligos concentrations. X-axis – droplet counts and samples (yellow), gradient PCR from 55 °C to 68 °C, left to right. Y-axis – FAM/HEX signal levels.

Supplementary material 6. CTCF border which was studied in the paper (F-R2 deletion)



Topological organization of chromosomes is maintained by the cohesin complexes and Ctfc border elements which form topologically-associated domains (TADs). In the picture, Hi-C map from mESCs demonstrates two TADs, separated by Ctfc-bound sites (ChIP-seq data below, highlighted by a rectangle). It is not known whether end joining is affected by the proximity of TAD border and cohesin depletion is a good opportunity to study this process. Region F-R3 is currently under investigation.

Supplementary material 7. Restriction effect on a small deletion (F-R1,192 bp)



a – genomic DNA with various deletion percentages was amplified with ddPCR primers to test method sensitivity; *b* – restriction digestion effect on the deletion product amplification. Restriction does help to reduce background noise from wild-type amplification, but does not remove the signal completely.