

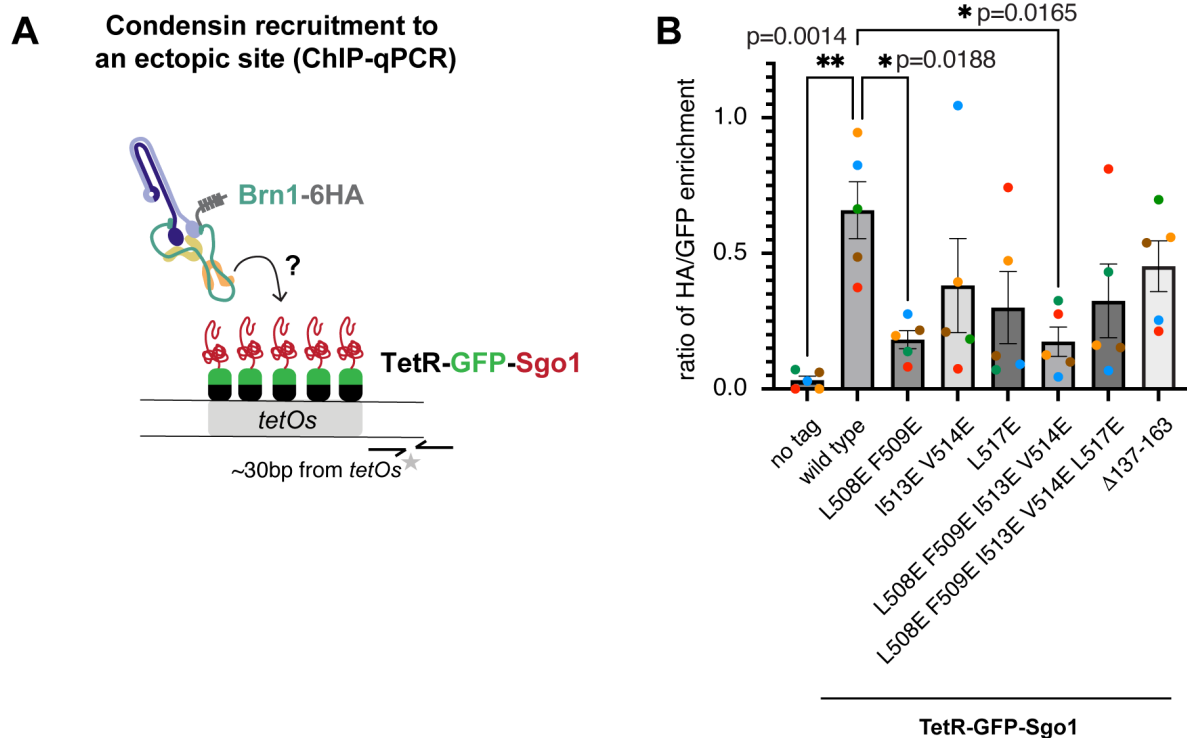
Molecular mechanism targeting condensin for chromosome condensation

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Appendix

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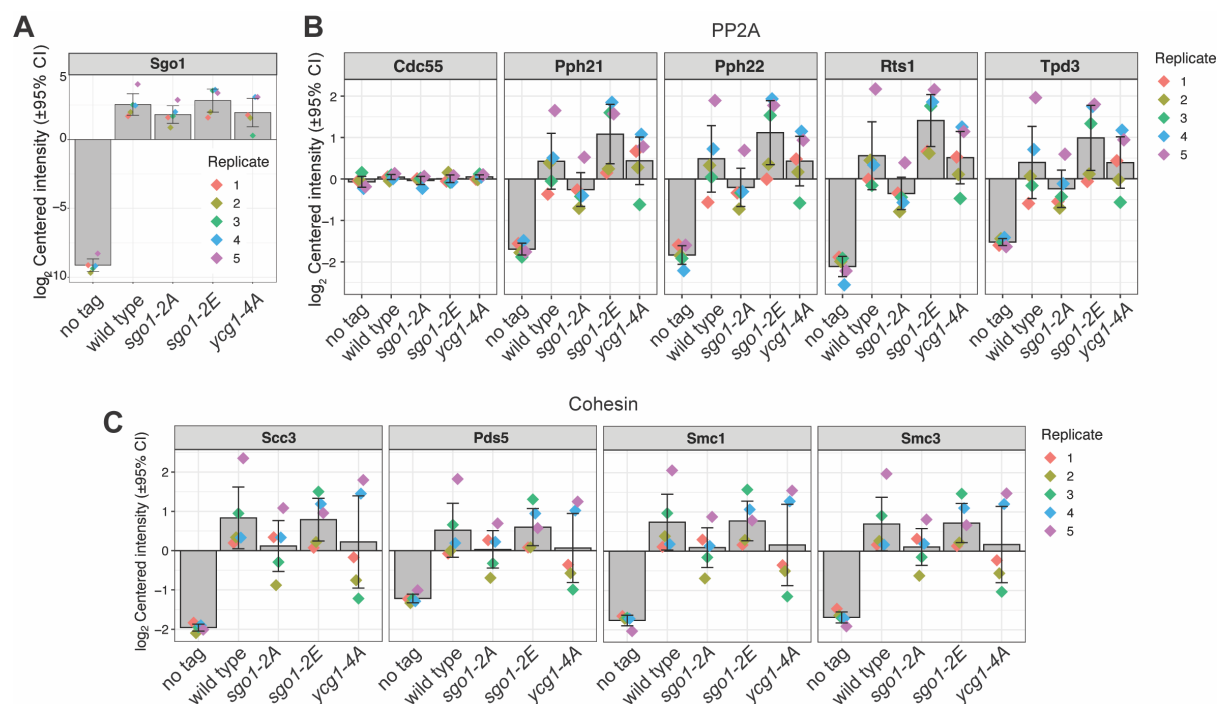
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Appendix Figure S1. Mutation of Sgo1 Conserved Region 1 (CR1) disrupts condensin recruitment to an ectopic site.

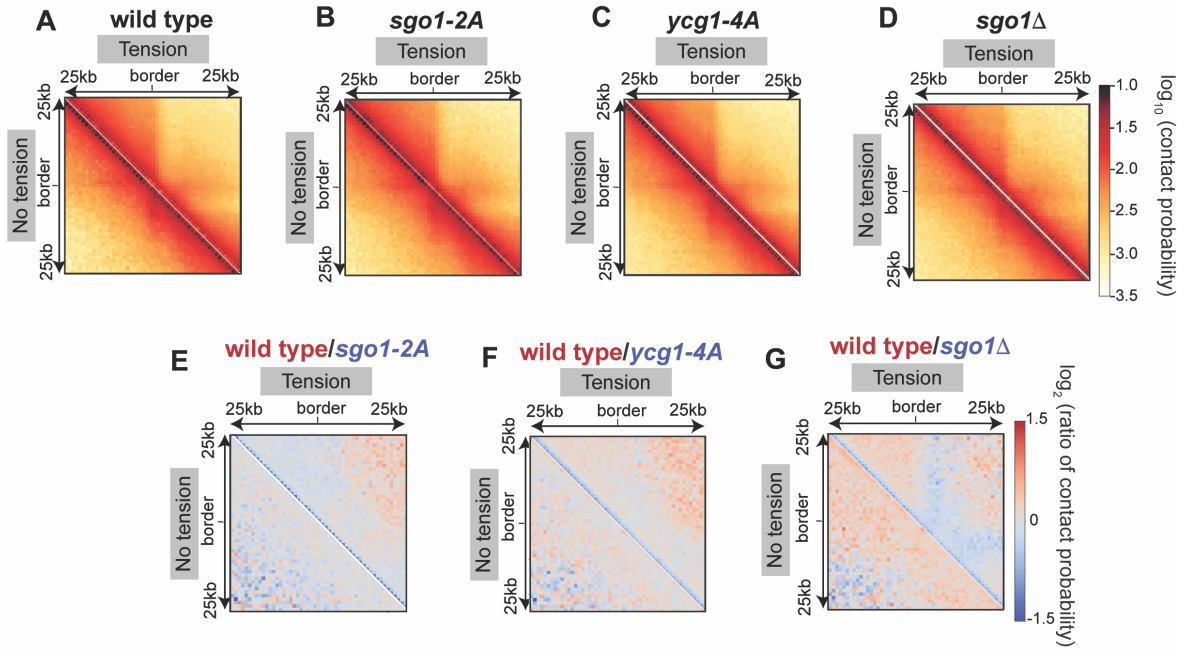
A, Schematic diagram showing tethered Sgo1 at an ectopic site recruits condensin, grey asterisk indicates the position of primers used for qPCR analysis, ~30 bp distant from the tethering site.

B, ChIP-qPCR measuring the levels of Brn1-6HA recruited to the tethered wild type and mutant Sgo1 variants. Strains were arrested in mitosis by treatment with nocodazole and benomyl for 2 hours. The ratios of Brn1 and Sgo1 enrichment (anti-HA/anti-GFP ChIP-qPCR values) were determined and the mean of four experimental repeats is shown with error bars representing standard error. * $p < 0.0332$; ** $p < 0.0021$, one-way ordinary ANOVA with Dunnetts correction, only comparisons significantly different from wild type are indicated. Strains used: no tag for anti-HA ChIP-qPCR (AM9655), no tag for anti-GFP ChIP-qPCR (AM20092), wild type (AM9847), L508E F509E (AM32194), I513E V514E (AM32195), L517E (AM32196), L508E F509E I513E V514E (AM32197), L508E F509E I513E V514E L517E (AM32198), Δ137-163 (AM32199).



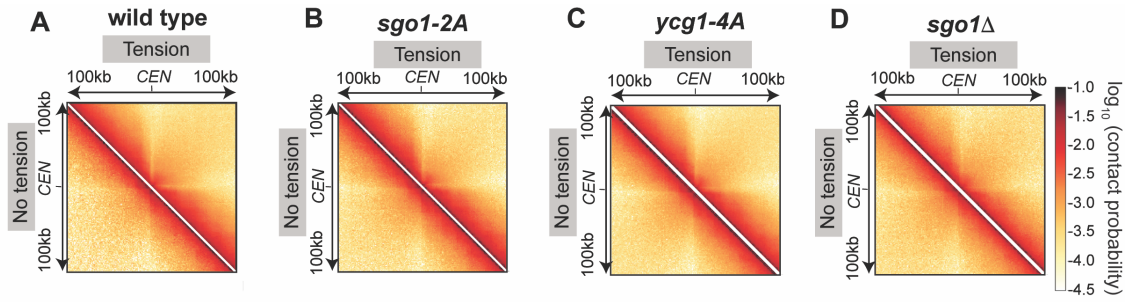
Appendix Figure S2. PP2A and cohesin association with Sgo1 is not affected by disruption of the CR1-Ycg1 interface.

Abundance of Sgo1 (**A**), PP2A (**B**), cohesin (**C**) in Sgo1-FLAG IP-MS. Plots show intensity values scaled to the mean of all conditions on a log₂ scale and therefore represent relative rather than absolute comparisons. Error bars represent the 95% confidence intervals. Data represents values from 5 biological replicates.



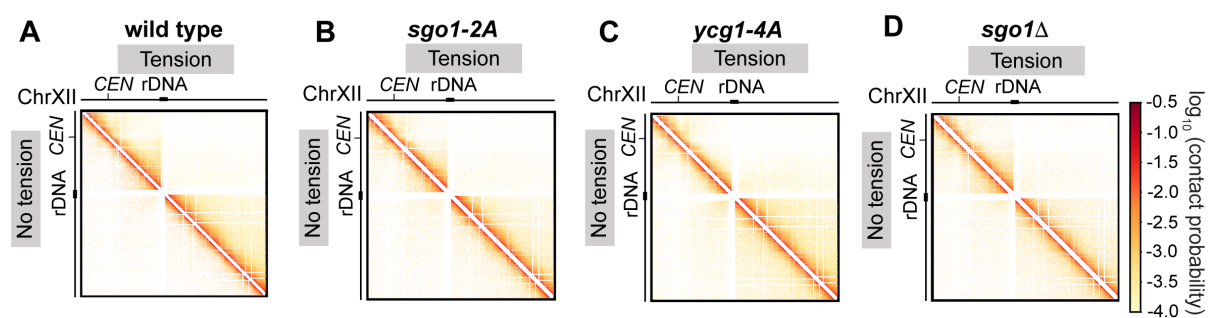
Appendix Figure S3. Hi-C heat map of borders.

A-G, Pile-ups (**A-D**, share the same scale bar on the right) and $\log_2$ ratio maps (**E-G**, share the same scale bar on the right) of *cis* contacts 25 kb surrounding all 32 borders for cells in the presence (upper right) or absence (lower left) of tension.



Appendix Figure S4. Hi-C heat map along chromosome arms.

A-D, Pile-ups (bin size 1kb) of *cis* contacts 100 kb surrounding all 16 centromeres for wild type, *sgo1-2A*, *ycg1-4A* and *sgo1Δ* in metaphase-arrested cells without spindle tension (lower left of the heatmap) or with tension (upper right). All Hi-C maps share the same scale bar on the right.



Appendix Figure S5. Hi-C heat map of ChrXII.

A-D, Hi-C maps of Chromosome XII in metaphase-arrested cells in the absence (lower left) and in the presence (upper right) of tension. All Hi-C maps share the same scale bar on the right.