

Expanded View Figures

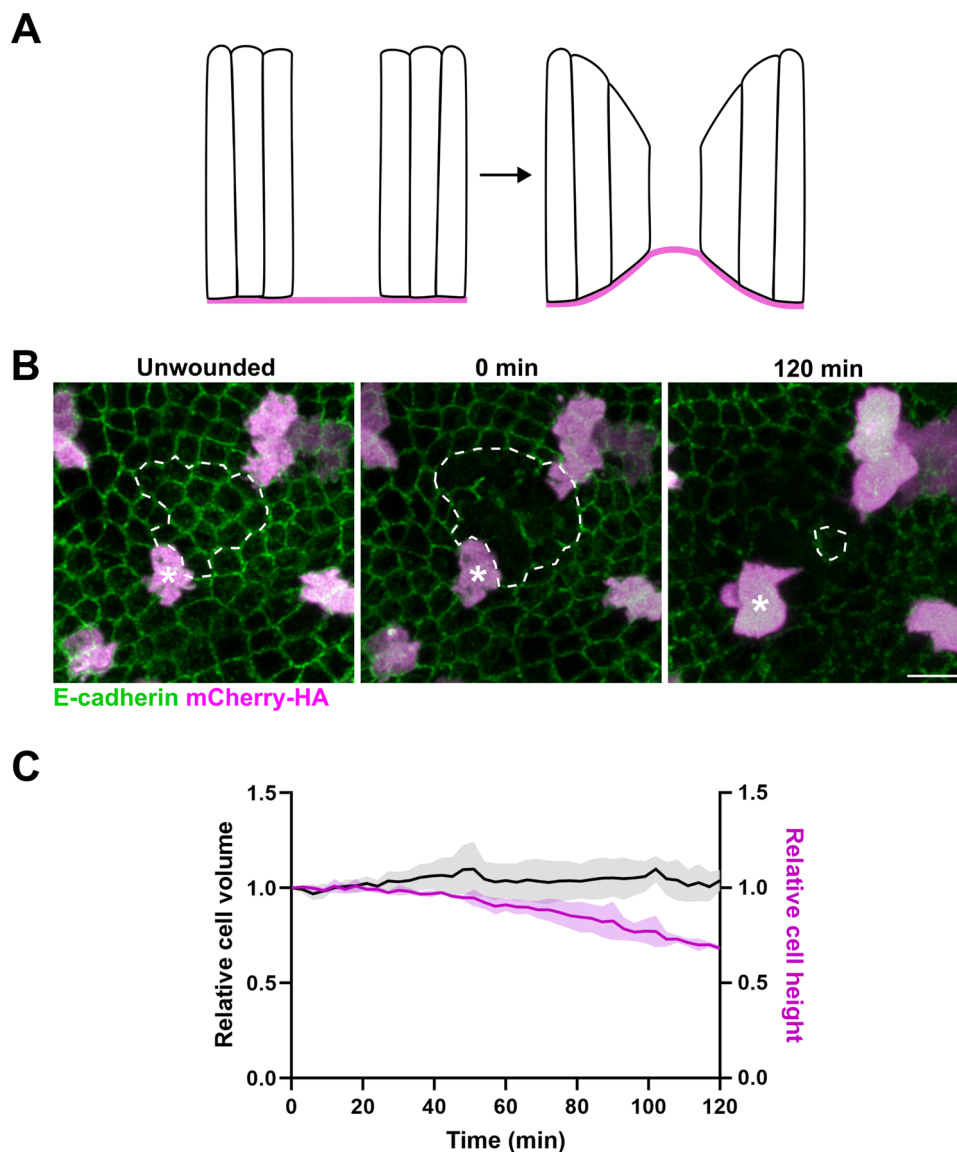


Figure EV1. Wound edge cell shortening hypothesis.

(A) Schematic of wound-edge cell shortening hypothesis. Cells are shown with a black outline and the basement membrane in magenta. (B) XY maximum projections of the apical surface of the unwounded area, immediately after wounding, and 120 min after wounding with E cadherin in green and mCherry-HA in magenta. The white dotted line indicates the wound area, and the white asterisk indicates the wound edge clone. By 120 min the wound edge clone has intercalated away from the wound edge. Scale bar, 5 μ m (C) Relative cell volume (black) and cell height (magenta) of the cytoplasmic mCherry clones ($n = 3$ wounds) over the first 120 min of healing. Solid lines are mean values and shaded regions represent SD.

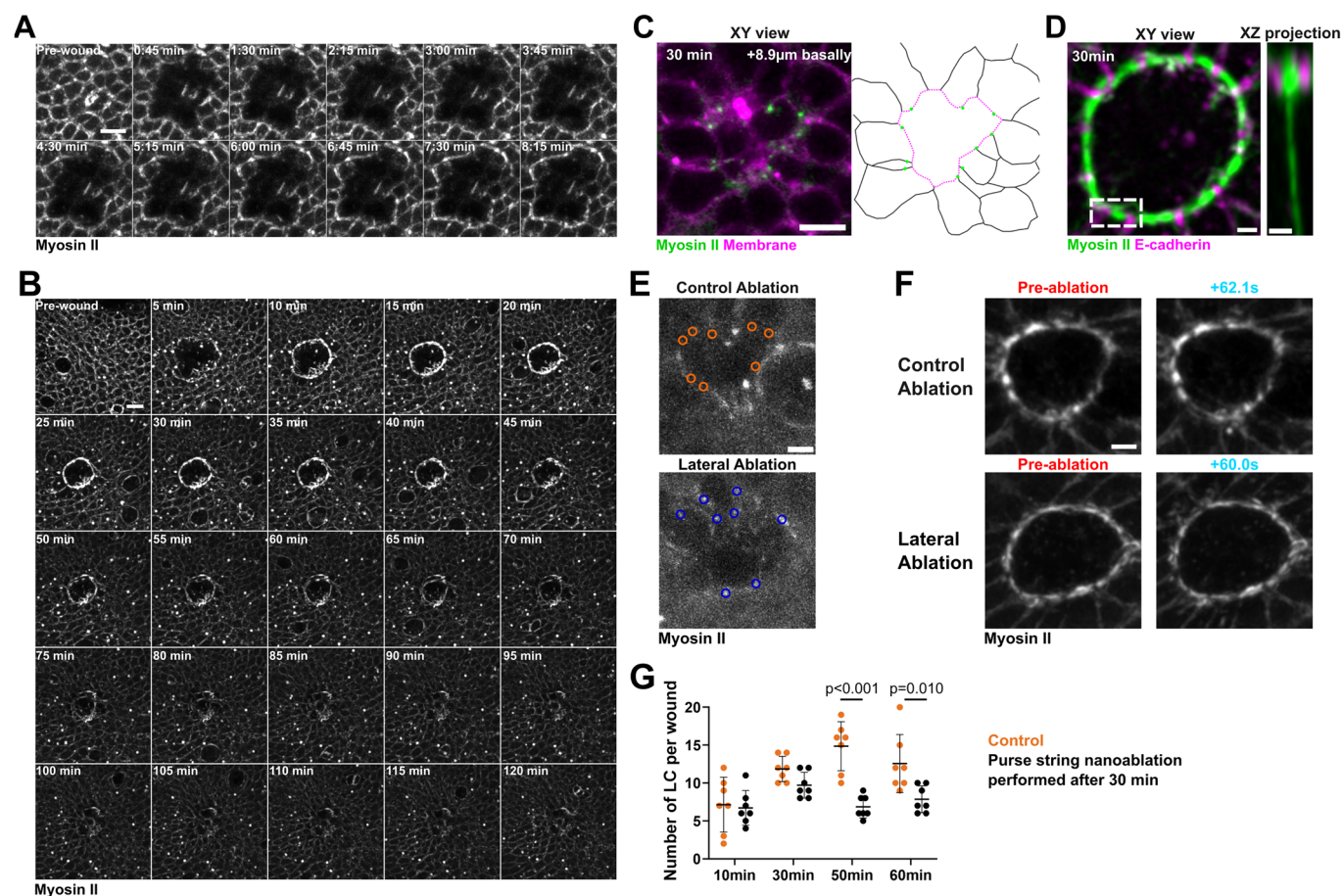
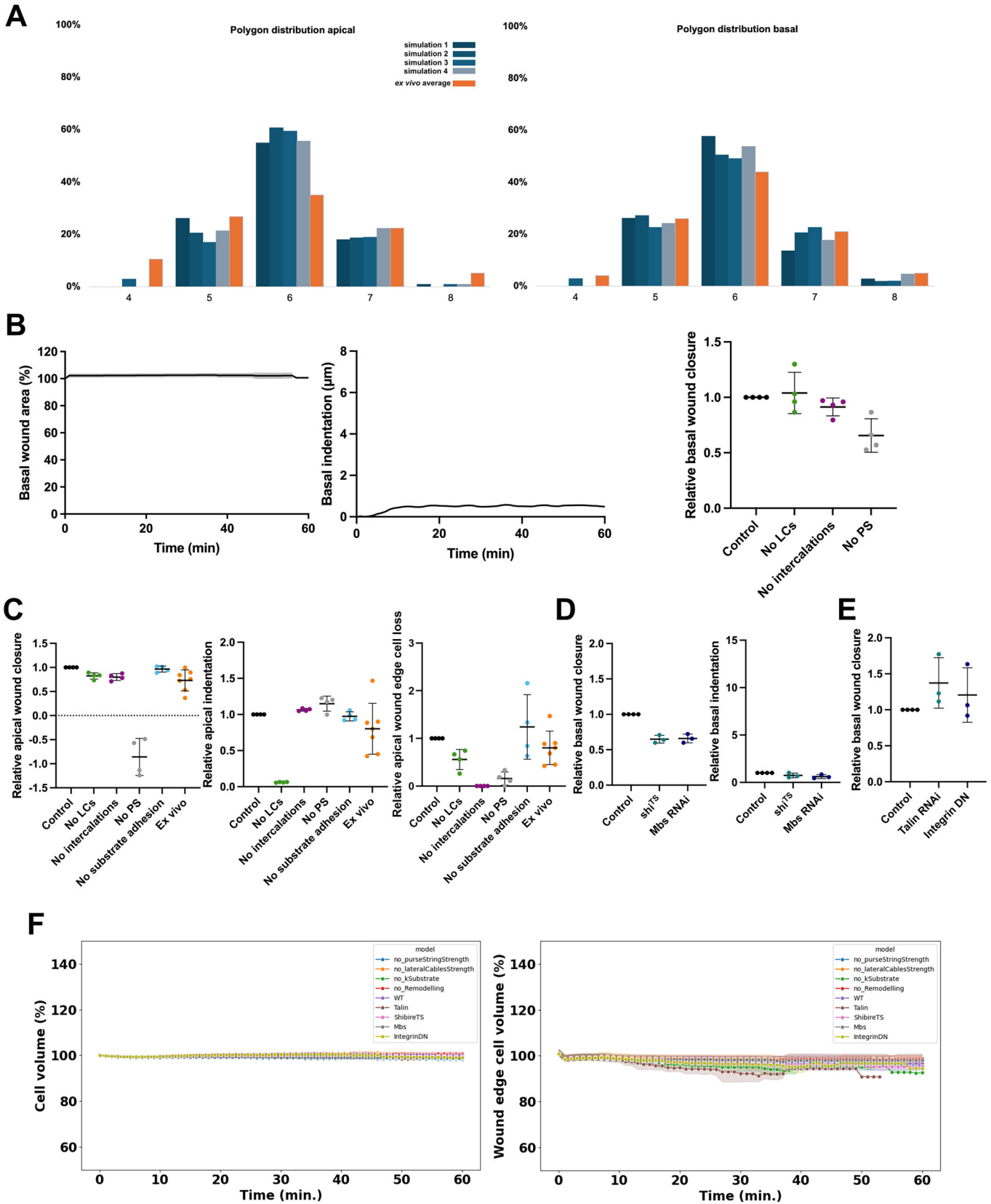


Figure EV2. Localisation of the lateral cables.

(A) Montage of XY max projections of the apical purse string from the wound in Fig. 2A with myosin II in grey. Scale bar, 5 μ m. (B) Montage of XY maximum projections of the apical purse string of the wound in Fig. 2B with myosin II in grey. Scale bar, 5 μ m. Pre-wound, 10 and 60 min images were reproduced in Figs. 2B and 4H. Pre-wound, 5, 60, and 120 min images were reproduced in Fig. 6A. (C) XY view of 8.9 μ m basally of the apical purse string 30 min after wounding with myosin II in green and membrane (CAAX-RFP) in magenta. Adjacent to a schematic showing the positions of the lateral cables. The magenta dotted line indicates the cell membranes at the wound edge, green dots indicate lateral cables, and black lines indicate the cell membrane away from the wound edge. Scale bar, 5 μ m. (D) XY maximum projection of the apical surface of the wound area 30 min after wounding with myosin II in green and e-cadherin in magenta. The white dotted box indicates the region of the adjacent XZ view showing that the cable is continuous with the purse string. Scale bar, 5 μ m. (E) XY maximum projection of wound area below the apical purse string before nano-ablation with myosin II in grey. Orange circles indicate examples of control ablation ROIs, and blue circles indicate lateral ablation ROIs. Scale bar, 2 μ m. (F) Grayscale images of timepoints of control and lateral ablation in Fig. 2J. Scale bar, 2 μ m. (G) Number of LC per wound upon nano-ablation of the apical purse string. Wing discs were wounded and normal wound healing was imaged until 30 min post-wounding, then the apical purse string was nano-ablated and wound healing was imaged for a further 20 min (50 min post-wounding) and 30 min (60 min post-wounding). Control wounds, which were not nano-ablated, are shown in orange and purse string nano-ablated wounds are shown in black. The plot shows individual data points with the mean (horizontal line), SD (bars) and p values from two-tailed Mann-Whitney tests.



◀ **Figure EV3. Computational model quantifications compared to ex vivo.**

(A) Polygon distribution of both apical (left) and basal sides (right). Blue-shaded colours relate to computational simulations. Orange refers to ex vivo. (B) Basal wound area of evolution (left), and indentation (middle) over time of control simulation; and compared to in silico perturbations (right). (C) Apical quantifications for all the computational perturbations related to ex vivo WT with relative apical wound closure (left), indentation (mid), and wound edge cell loss (right). (D) Basal quantifications of in silico *shi*^{TS}, and Mbs RNAi, relative to their control. (E) Basal wound closure of in silico Talin RNAi and Integrin DN relative to the in silico control. (F) Average volume of cells (left) and average volume of cells at the wound edge (right) regarding pre-wounding ($t = 0$) in percentage (%). Colours of (D–F) are related to Figs. 4 and 6, respectively.

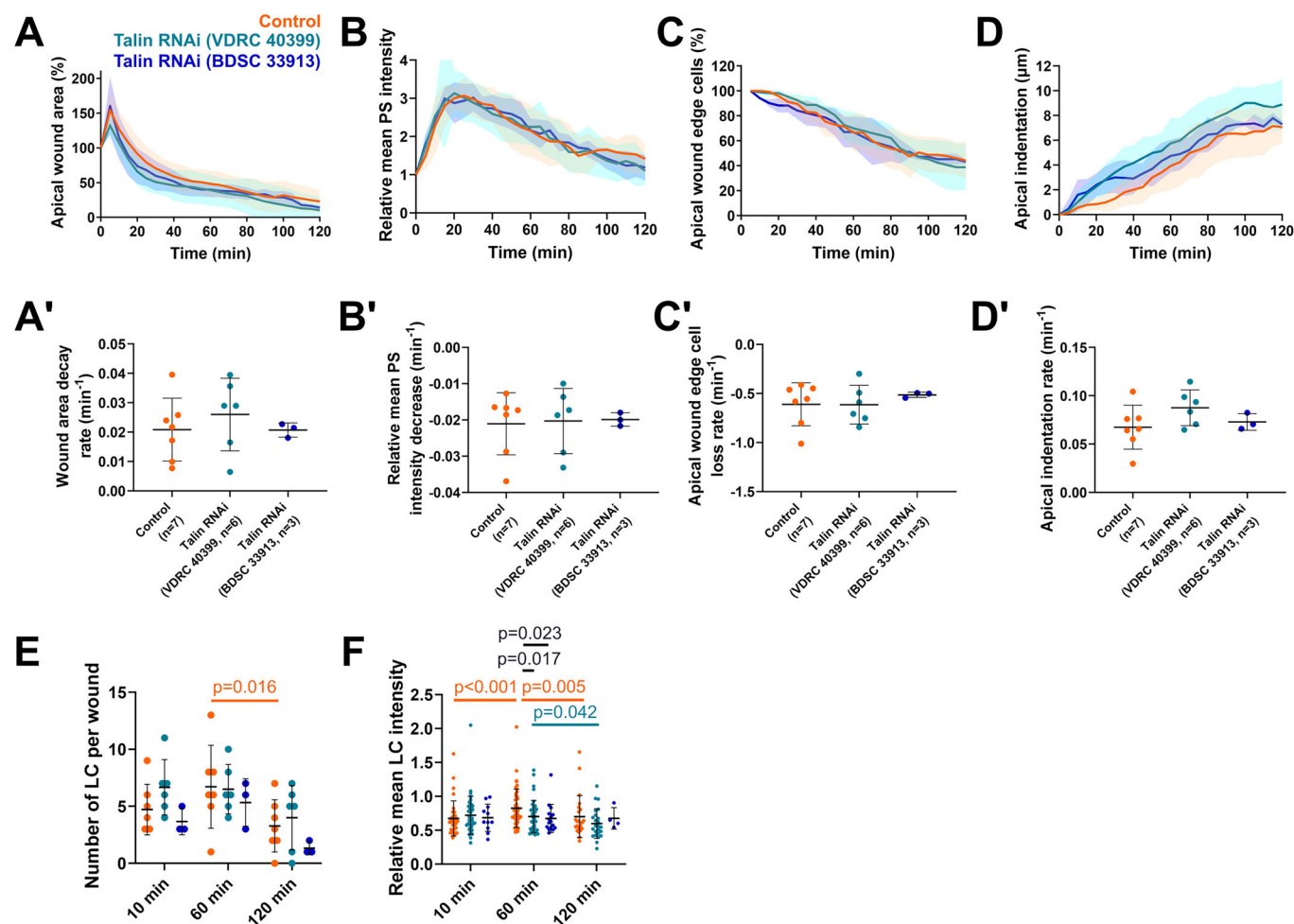


Figure EV4. Wound healing quantifications of a second Talin RNAi line (BDSC 33,913 in dark blue, $n = 3$) compared to the control (orange) and first Talin RNAi line (VDRG 40,399 in light blue, $n = 6$).

(A) Apical wound area. (A') Wound area decay rates from fitting one-phase decay curves of individual replicates from (A). (B) Relative mean PS myosin II intensity. (B') Relative PS myosin II intensity reduction rates from fitting straight lines of individual replicates from (B) from 20 min after wounding. (C) Percentage of apical wound edge cells remaining. (C') Apical wound edge cell loss rates from fitting straight lines of individual replicates from (C). (D) Apical indentation. (D') Apical indentation rates from fitting straight lines of individual replicates from (D). (E) Number of LC per wound 10, 60 and 120 min after wounding. (F) Relative mean LC myosin II intensity 10, 60 and 120 min after wounding. Plots show individual data points with the mean (horizontal line), SD (bars) and p values between genotypes from two-tailed Mann-Whitney tests.

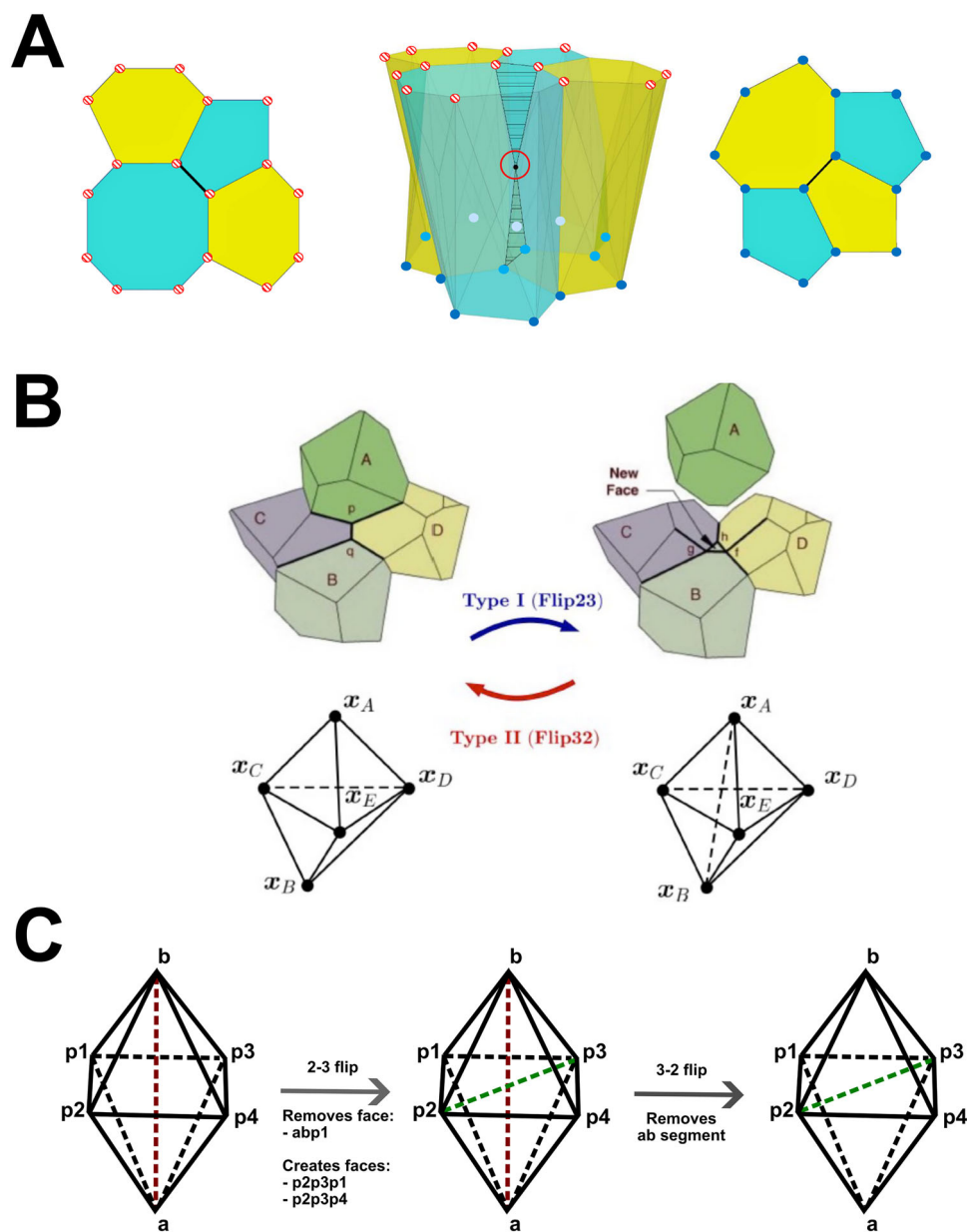


Figure EV5. 3D vertex model technical details.

(A) Four cells with a scutoid geometry were a point (vertex) where the four cells are connected at the same time (highlighted circle red). Top vertices are red spheres, and bottom vertices are blue spheres. Black highlights the intercalating face. (B) Flips 23 and 32 of the cell network (top) and nodal network (bottom) used for the model to remodel itself when intercalating. (C) Example of an intercalation where we performed the edge removal algorithm to remove the segment AB, executing 23 flips until the segment AB has three neighbours. Then, we performed a 32 flip, which means we can remove it without perturbing the network (see Methods).