Figure EV1. Structural alignments of the Dcc1 C-terminus with other WH domains.

A The Dcc1 C-terminus is shown in brown and indicated are the WH domains.
B Dcc1 C-terminus is shown in the same orientation as (A) and a structural alignment with three proteins containing WH domains, PKZ (PDB ID: 4KMF, blue), cullin-1 (PDB ID: 3TDU, orange) and DsrD (PDB ID: 1WQ2, green).
**Figure EV2.** Similar 'triple j-barrel' dimerisation folds.

RNase H2 complex (3PUF), A49/34.5 (3NFG) and Rap30/74 (1F3U) are presented for comparison with the heterotrimer Ctf18C-Dcc1-Ctf8. The dotted line indicates the area of structural similarity to the Ctf18C-Ctf8-Dcc1 structure.
Figure EV3. Additional DNA binding and functional analyses.

A. DNA EMSA showing residual binding to ssDNA (indicated by arrow) but not dsDNA by the WH3-deleted Dcc1 construct. Protein concentrations are given in μM.

B. DNA EMSA showing binding of Dcc1<sup>96–380</sup> to 18-bp substrates containing 7-bp 5’ or 3’ overhangs. Protein concentrations are given in μM.
Figure EV4. Expression of and complex formation by Dcc1 WH deletions.

A Western blot showing cellular expression levels of PK-tagged Dcc1 deletions employed for checkpoint activation and sister chromatid cohesion assays. Tubulin is shown as a loading control.

B SDS-PAGE gel of purified recombinant Dcc1-Ctf8-Ctf18C complexes containing indicated Dcc1 deletions. Protein complexes shown were purified in the same way as samples for crystallisation studies. Asterisks indicate impurities in the sample.

C Western blot showing cellular expression levels of Dcc1 deletion employed for ChIP analysis.