Figure S1 Coiled-coil prediction of Corolla by the COILS program. Corolla is predicted to contain three coiled-coil regions based on the COILS program (LUPAS *et al.* 1991). These coiled-coil domains span the first two-thirds of the protein. Of note, the Eukaryotic Linear Motif (ELM) program (http://elm.eu.org/) identified only one coiled-coil domain in Corolla (aa 105–135) (DINKEL *et al.* 2014).
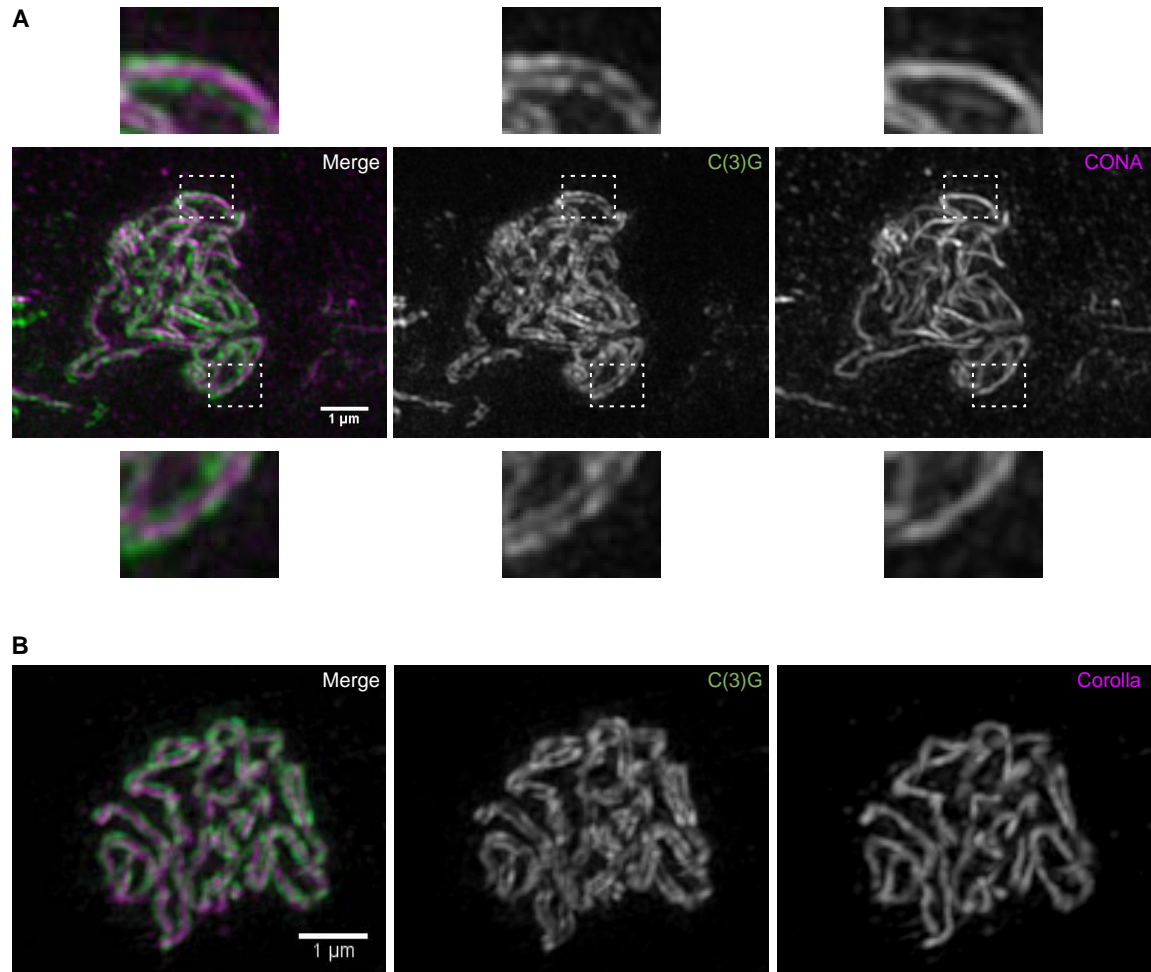
A

B

Figure S2   SIM imaging of a wild-type pachytene oocyte for Cona, C(3)G and Corolla. (A) DeltaVision OMX microscopy of C(3)G (C-terminal domain) (green, AF488) and Cona (magenta, AF555) in a wild-type pachytene oocyte. Maximum-intensity projection of Z-series though an entire pro-oocyte is shown. Two regions outlined with a dashed box are magnified above and below the image to show that Cona is clearly positioned between the two C(3)G tracks. **(B)** DeltaVision OMX microscopy of C(3)G (C-terminal domain) (green, AF488) and Corolla (magenta, AF555) in a wild-type pachytene oocyte. Maximum-intensity projection of Z-series though an entire pro-oocyte is shown.
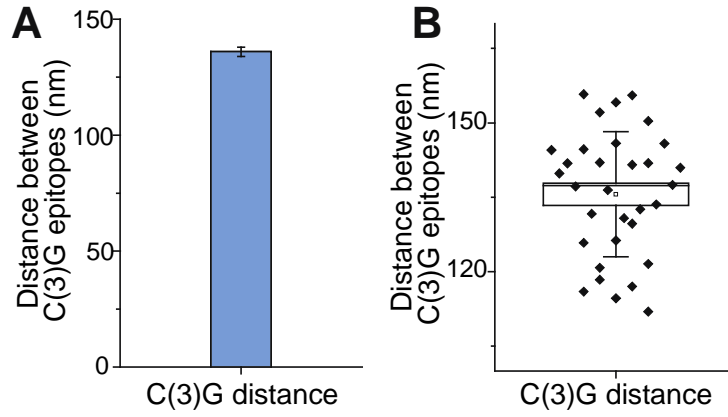
Figure S3 Measurements of the width of the SC by SIM. (A–B) Measurement of the width between C-terminal epitopes of C(3)G. In areas where the SC remained in the same *x-y* plane for an extended period, a line profile was generated and fit to two Gaussians. Error bar indicated the standard error in the mean. **(B)** A box and whisker plot showing the distance between C(3)G epitopes. The small box represents the standard error, the remaining line represents the median, and the whiskers represent standard deviation.
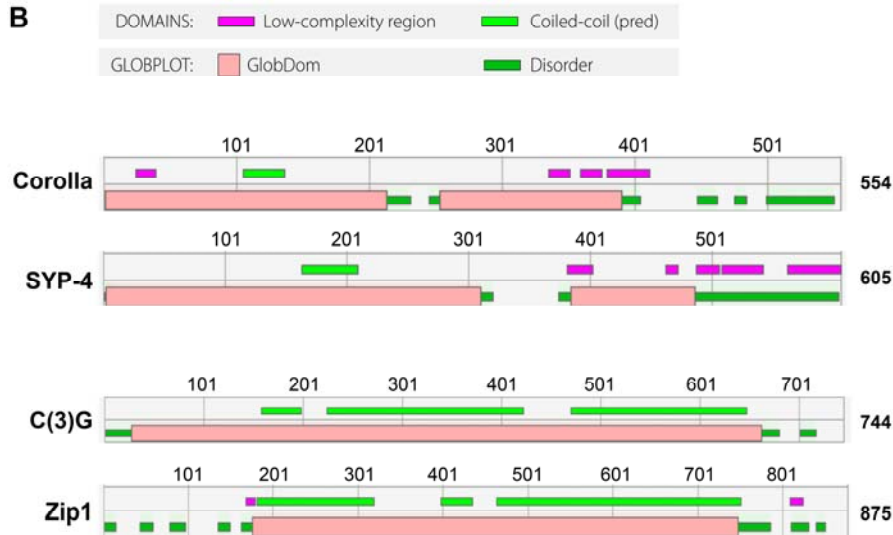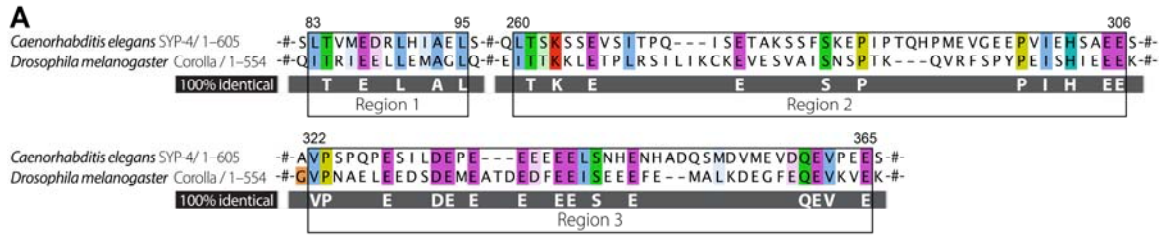
Figure S4 Alignment of protein sequence and predicted secondary structure of Corolla with SYP-4. (A) Clustal alignment of Corolla with SYP-4. *C. elegans* SYP-4 (http://www.ncbi.nlm.nih.gov/protein/CCD72468.1) was aligned to Corolla using Clustal Omega (Sɪᴇᴠᴇʀs *et al.* 2011). Three regions of potential homology were detected: region 1, from Corolla amino acids 83 to 95 (69% similarity, 38% identity); region 2, from amino acids 260 to 306 (28% similarity, 23% identity); and region 3, from amino acids 322 to 365 (43% similarity, 34% identity). Hash marks (#) denote removed sequence for ease of viewing the conserved regions and dashes (–) indicate gaps in alignment. Of these three similar regions, only region 3 falls within a predicted coiled-coil region of Corolla (Figure S1). **(B)** ELM analysis (http://elm.eu.org/) of Corolla (FBgn0030852), *C. elegans* SYP-4 (Accession CCD72468), Drosophila TF protein C(3)G (FBgn0000246) and *S. cerevisiae* TF protein Zip1 (Accession AAA35239) showing only the predicted coiled-coil domains, globular domains, low-complexity regions and disordered regions. Note that using the ELM resource, only one coiled-coil region was identified for Corolla and SYP-4, whereas COILS program identified three stretches of coiled-coil regions for both Corolla (Figure S1) and SYP-4 (Smolikov *et al*. 2009). The three coiled-coil stretches identified by COILS for Corolla are between amino acids 17 and 380. For comparison of the coiled-coil domains and flanking globular domains found in other TF proteins, Drosophila C(3)G and *S.cerevisiae* Zip1 are shown. Numbers above vertical lines correspond to amino acid number for each protein. Number at right-hand side corresponds to the total number of amino acids for each protein.

Files S1-S2

Available for download as .mov files at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.165290/-/DC1

File S1 Movie moves through Z slices of a representative nucleus with Corolla in magenta and C(3)G (C-terminal domain) in green as acquired on OMX Blaze microscope.

File S2 Corolla is continuous along the length of the SC. Movie shows rotation in X and Y of a representative nucleus with Corolla in magenta and C(3)G in green as acquired on OMX Blaze microscope.

K. A. Collins *et al.*

Table S1 Quantification of the centromere clustering defect in *corolla* mutants.

Genotype	Number of CID foci (%)						*n*	Average ± SD
	1	**2**	**3**	**4**	**5**	**6**		
wild type	16 (42.1)	13 (34.2)	9 (23.7)	0 (0)	0 (0)	0 (0)	38	1.80 ± 0.80
corolla	0 (0)	0 (0)	11 (34.4)	14 (43.8)	4 (12.5)	3 (9.4)	32	3.97 ± 0.93

The number of oocytes in region 3 of the germarium with a given number of CID foci are shown, followed in parentheses by the frequency that a given number of CID foci are seen in a genotype.

Table S2   Frequency of γ-H2AV foci in *corolla* as assayed in the DSB repair-deficient mutant *okra*

Genotype	Average number of foci per Region 3 oocyte	Standard deviation	% of control	Total oocytes analyzed
okra	22.3	1.9	100	10
corolla; *okra*	8.3	2.0	37	15