



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 (SIEVERS *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.