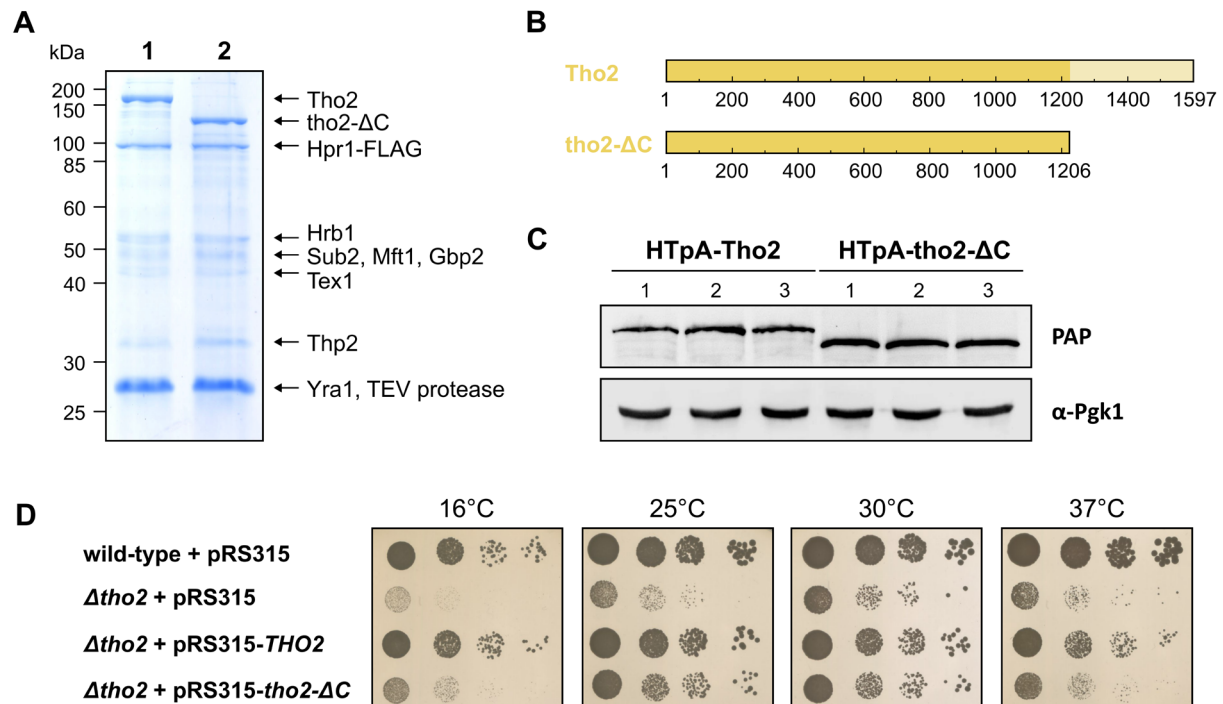


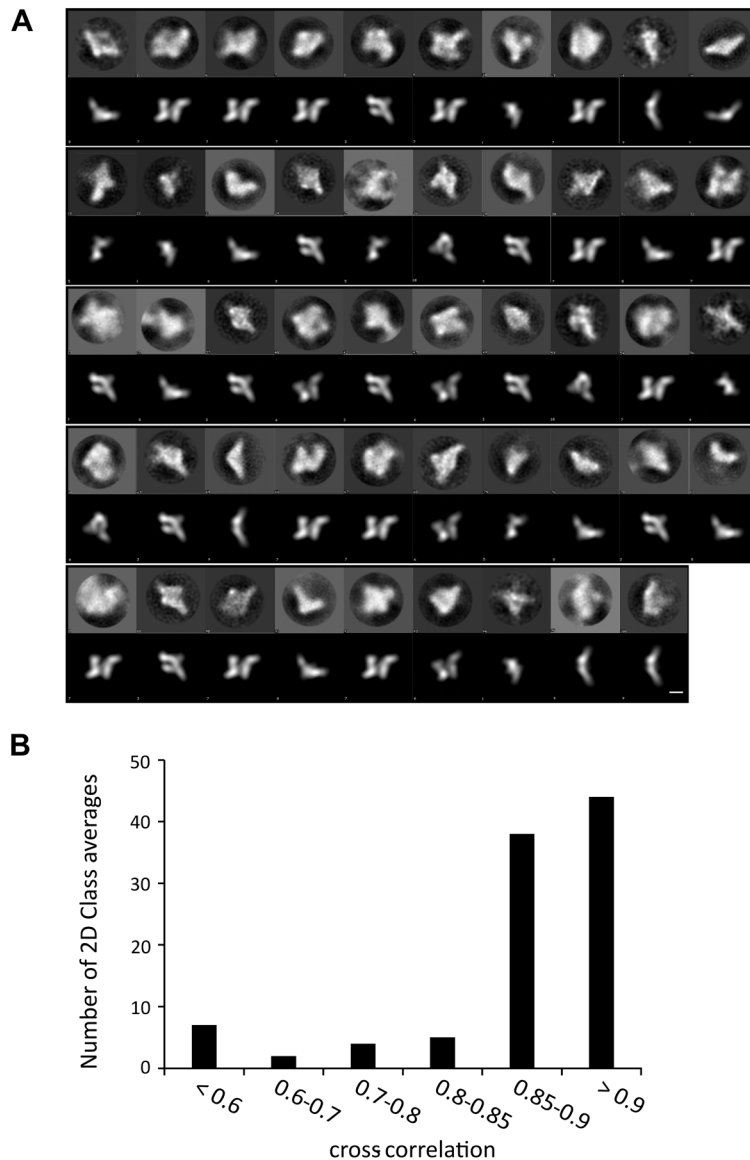
SUPPLEMENTAL MATERIAL

Cross-linking mass spectrometric analysis of the endogenous TREX complex from *S. cerevisiae*

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SUPPLEMENTAL FIGURE S1. The unstructured C-terminal domain of Tho2 is not necessary for TREX complex formation but for growth at low and high temperatures. (A) SDS-PAGE of the purified endogenous *S. cerevisiae* TREX complex containing full-length Tho2 (lane 1) or C-terminally truncated Tho2, named tho2-ΔC (lane 2). Molecular weight marker bands are indicated in kDa. (B) Schematic representation of full-length Tho2 and C-terminally truncated Tho2, tho2-ΔC. (C) Total protein levels of Tho2 and tho2-ΔC are similar. Protein levels of HTPA-Tho2 and HTPA-tho2-ΔC in whole cell extracts were determined by Western blot for three biological replicates. Pgk1 served as a loading control. (D) Dot spots of wild-type and the indicated *THO2* mutants (W303 background). Shown are 10-fold serial dilutions that were incubated for two days at 25°C, 30°C and 37°C or six days at 16°C.



SUPPLEMENTAL FIGURE S2. Negative stain analysis of the BS³ cross-linked *S.c.* TREX complex. (A) Selected 2D class averages of a 42,784 particle dataset (top row) and matching re-projections of pdb:7aqo (bottom row) lowpass-filtered to 25 Å. (B) Plot showing cross-correlation coefficient of 100 2D class averages from 42,784 particles obtained by projection matching.

SUPPLEMENTAL TABLE S1. Summary of the cross-linked peptide pairs identified in the different cross-linking experiments (as Microsoft Excel .x/sx file). The last tab of the spreadsheet contains detailed information on the table layout.