**Description Supplementary Material**

**Supplementary file 1**

An Excel file containing multiple tables in different tabs.

(a) Table S1. Proteins enriched in GFP::MEG-3 pulldowns. Proteins are sorted according to their p-value from the t SAM statistic as previously described (Chen et al., 2016). (b) Table S2. Similarity measures between predicted MIP LOTUS domain structures and LOTUS domains from other metazoans. Protein domains: M1, MIP-1; M2, MIP-2; L1, LOTUS1; L2, LOTUS2. SeqID, sequence identity; GDT, Global Distance Test parameters for best templates; PDB ID, protein databank identifier of the best template; RMSD, backbone root mean square distances in Å, with number of aligned residues in parentheses. Published structures used for comparison: D. melanogaster Oskar (PBD ID 5nt7), H. sapiens TDRD5 (PBD ID 3s93). (c) Table S3. Pairwise MIP LOTUS structural similarity analysis. Values shown are backbone rmsd values in Å and number of aligned residues (in parentheses). M1, MIP-1, M2, MIP-2; L1, LOTUS1; L2, LOTUS2. (d) Table S4. Description of MIP depletion phenotypes. (e) Table S5. Pairwise predicted binding affinities between MIP LOTUS domains and between MIP LOTUS domains and GLH-1. Affinities are in kcal/mol. M1, MIP-1; M2, MIP-2; L1, LOTUS1; L2, LOTUS2. Predictions for GLH-1 binding considered only the helicase CTD domain. Predictions for combinations with no values given were highly unfavorable (>0 kcal/mol). Predicted binding affinities for the native Drosophila complexes: Oskar LOTUS homodimer = −54.5 kcal/mol; Oskar LOTUS—Vasa helicase complex = −53.5 kcal/mol. (f) Table S6. Strains produced and used in this study. (g) Table S7. Guide RNA sequences, repair templates, and screening primers for CRISPR strains produced in this study. (h) Table S8. Plasmid DNA constructs for in vitro pulldown experiments.

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