Expanded View Figures

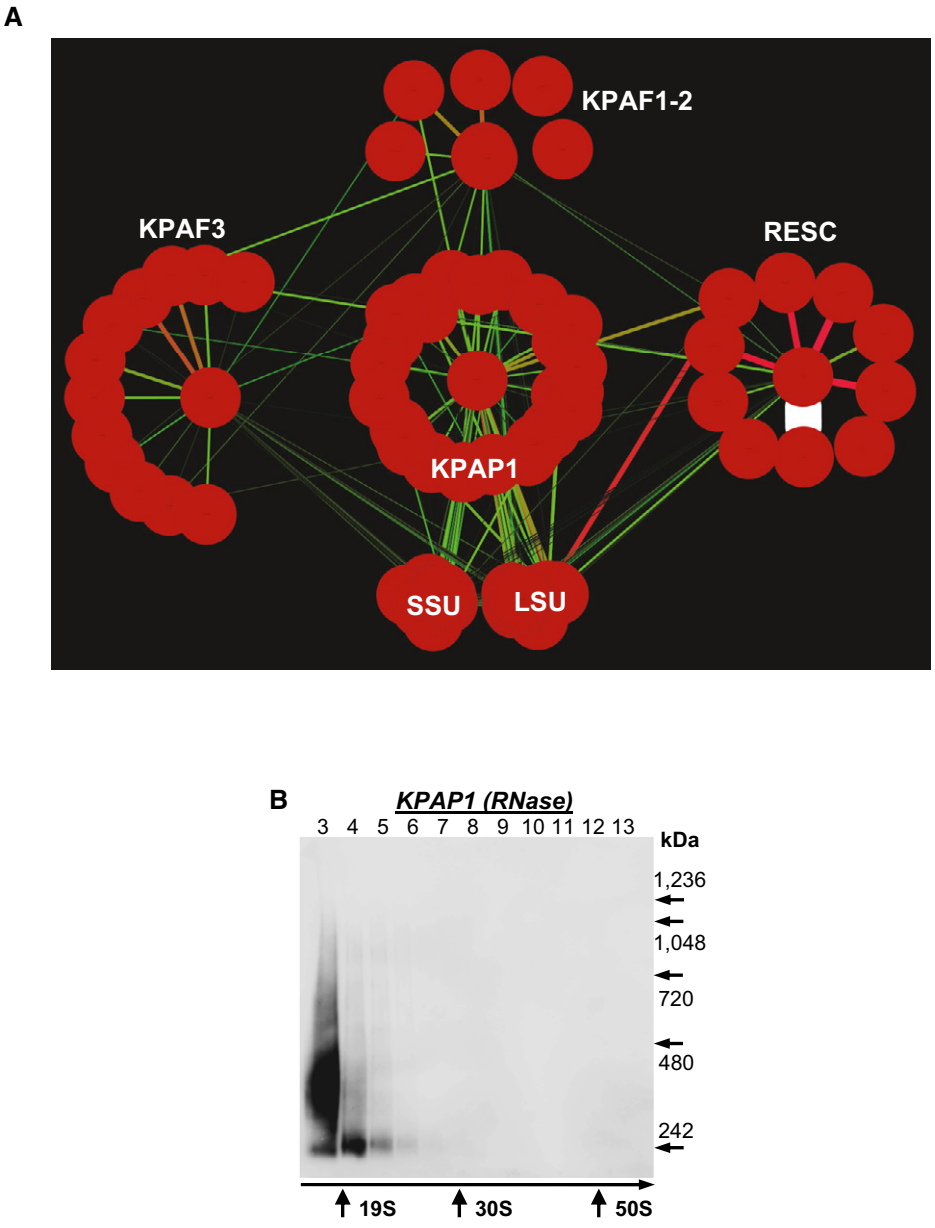

Figure EV1. Model of RNA-independent interactions between KPAP1 poly(A) polymerase, KPAF 1-2, KPAF3, RNA editing substrate binding complex (RESC), and the ribosome.

A KPAP1, KPAF2, KPAF3, GRBC1, L3, and S17 proteins were affinity purified from mitochondrial lysates in the presence of RNase A (0.1 mg/ml) and RNase T1 (500 U/ml). The network was generated in Cytoscape software from bait–prey pairs in which the prey protein was identified by five or more unique peptides (Table EV1). The edge thickness correlates with NSAF values.

B Mitochondrial fraction was extracted with detergent in the presence of RNase A (0.1 mg/ml) and RNase T1 (500 U/ml), and soluble contents were separated for 5 h at 178,000 *g* in 10–30% glycerol gradient. Each fraction was further resolved on 3–12% Bis-Tris native gel. Positions of native protein standards are denoted by arrows. KPAP1 was visualized by immunoblotting. Thyroglobulin (19S) and bacterial ribosomal subunits were used as apparent S-value standards.

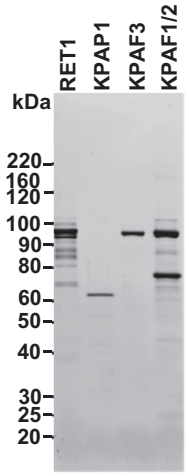

Figure EV2. Recombinant proteins used in reconstitution reactions.

Recombinant proteins were purified from *Escherichia coli* by sequential metal affinity, ion exchange, and size exclusion chromatographic steps. Final fractions were separated on 8–16% SDS–PAGE and stained with Sypro Ruby. Positions of molecular mass markers are indicated.

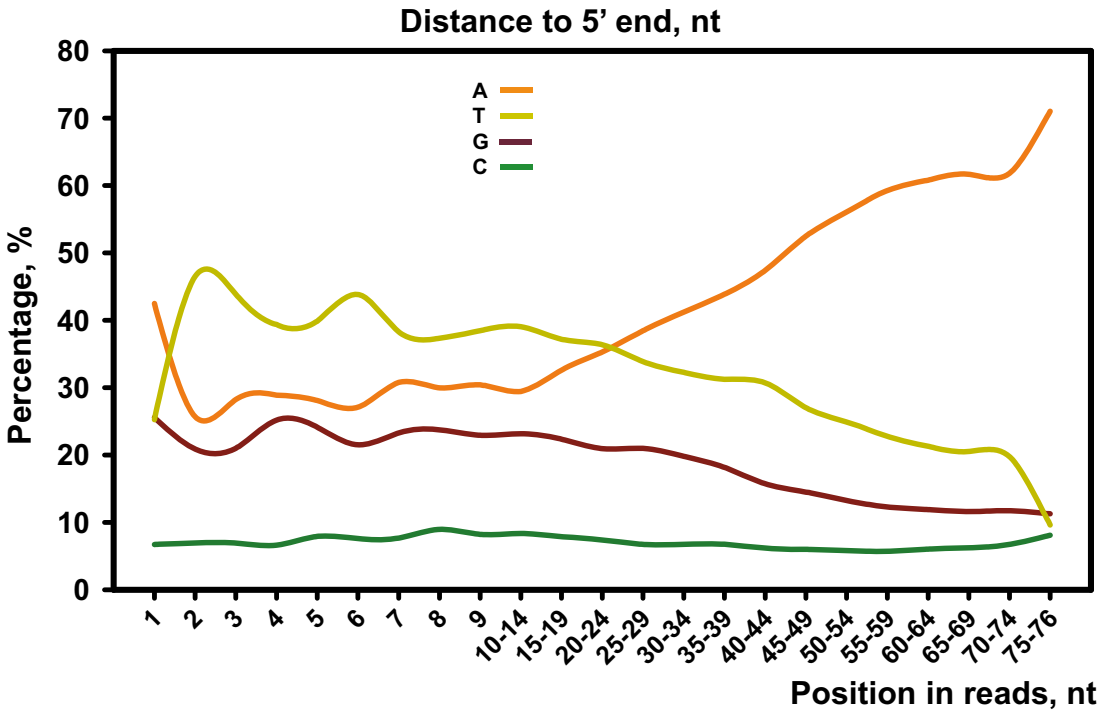

Figure EV3. Nucleotide frequency per each position in KPAF3-CLAP sequences.

Nucleotide frequency was calculated for each position of KPAF3-protected RNA sequence.