Figure S1

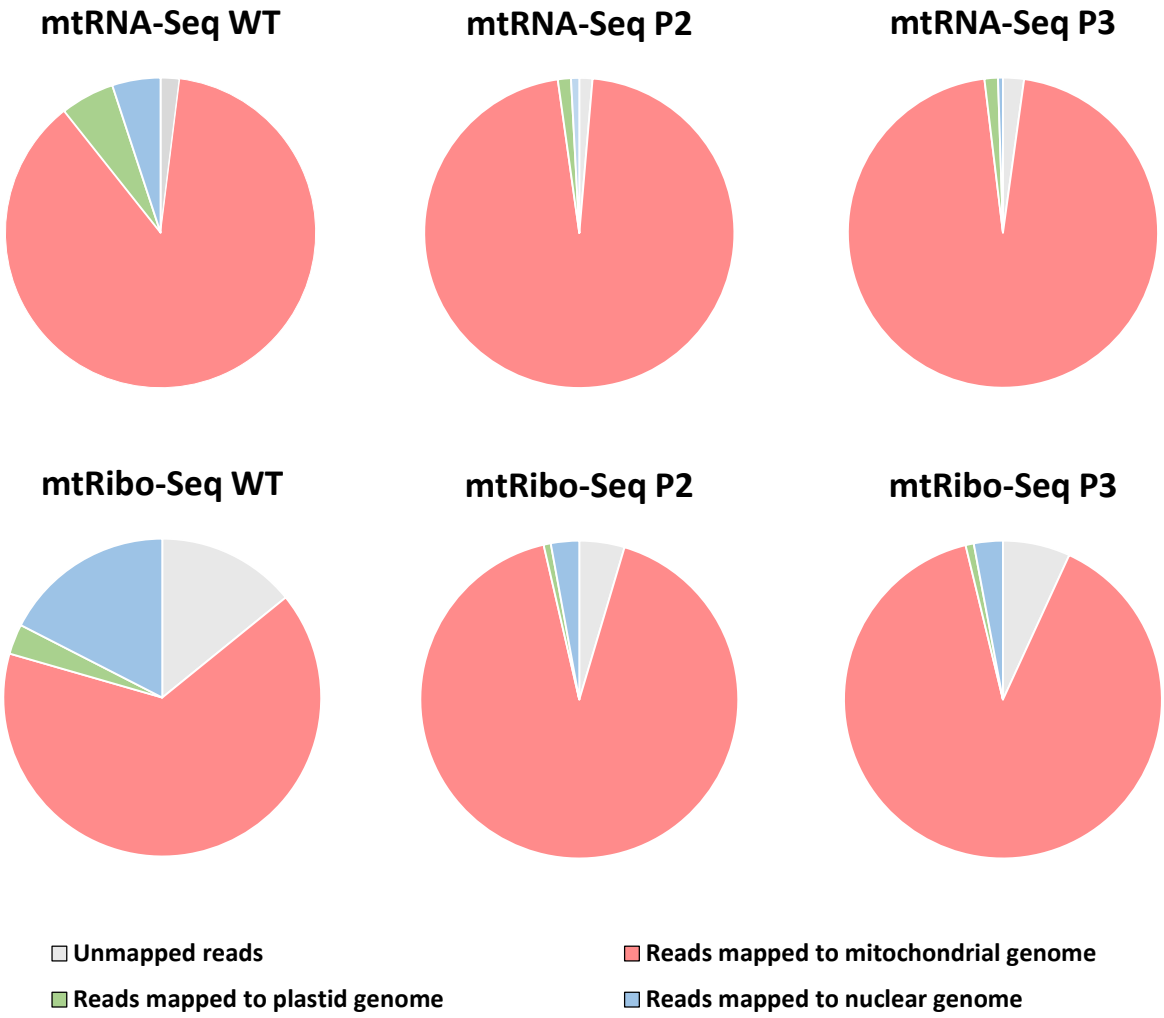

Figure S1. Percentage of mtRNA-Seq and mtRibo-Seq reads mapping to the mitochondrial, nuclear and plastid genomes, and unmapped ones, in P2 and P3 phenotypes of *rps10* and wild-type.

Figure S2

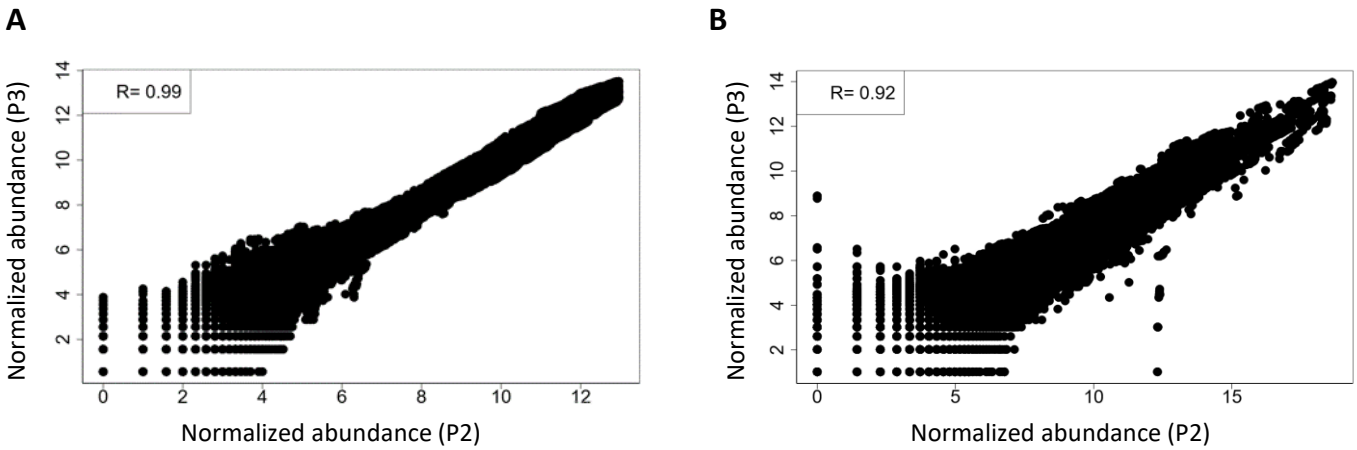

Figure S2. Reproducibility of mtRNA-Seq and mtRibo-Seq data for two phenotypes (P2 and P3) of the *rps10* mutant. **(A)** Correlation between mtRNA-Seq data sets. **(B)** Correlation between mtRibo-Seq data sets. Pearson correlation coefficients (R) are shown for total read counts between the P2 and P3 sets. Each dot corresponds to the number of reads mapped to a particular position on mitochondrial genome.

Figure S3

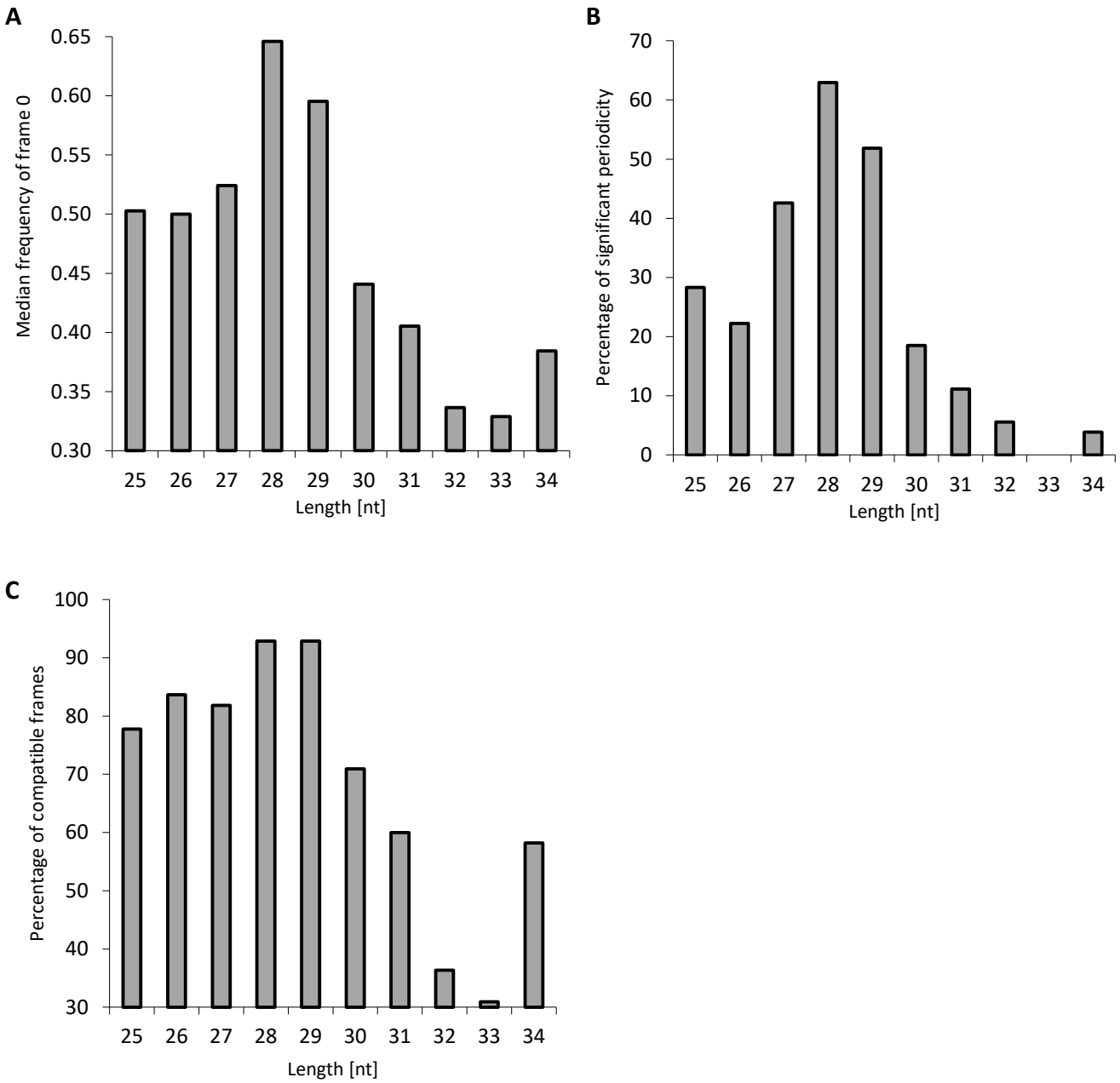

Figure S3. Correctness of translation frame for ribosome footprints of different lengths mapping to protein-coding genes in wild-type mitochondria. **(A)** Percentage of cases in which 3-nucleotide periodicity was statistically significant according to RiboTaper. **(B)** Percentage of correct frames. **(C)** Median frequency of correct frames.

Figure S4

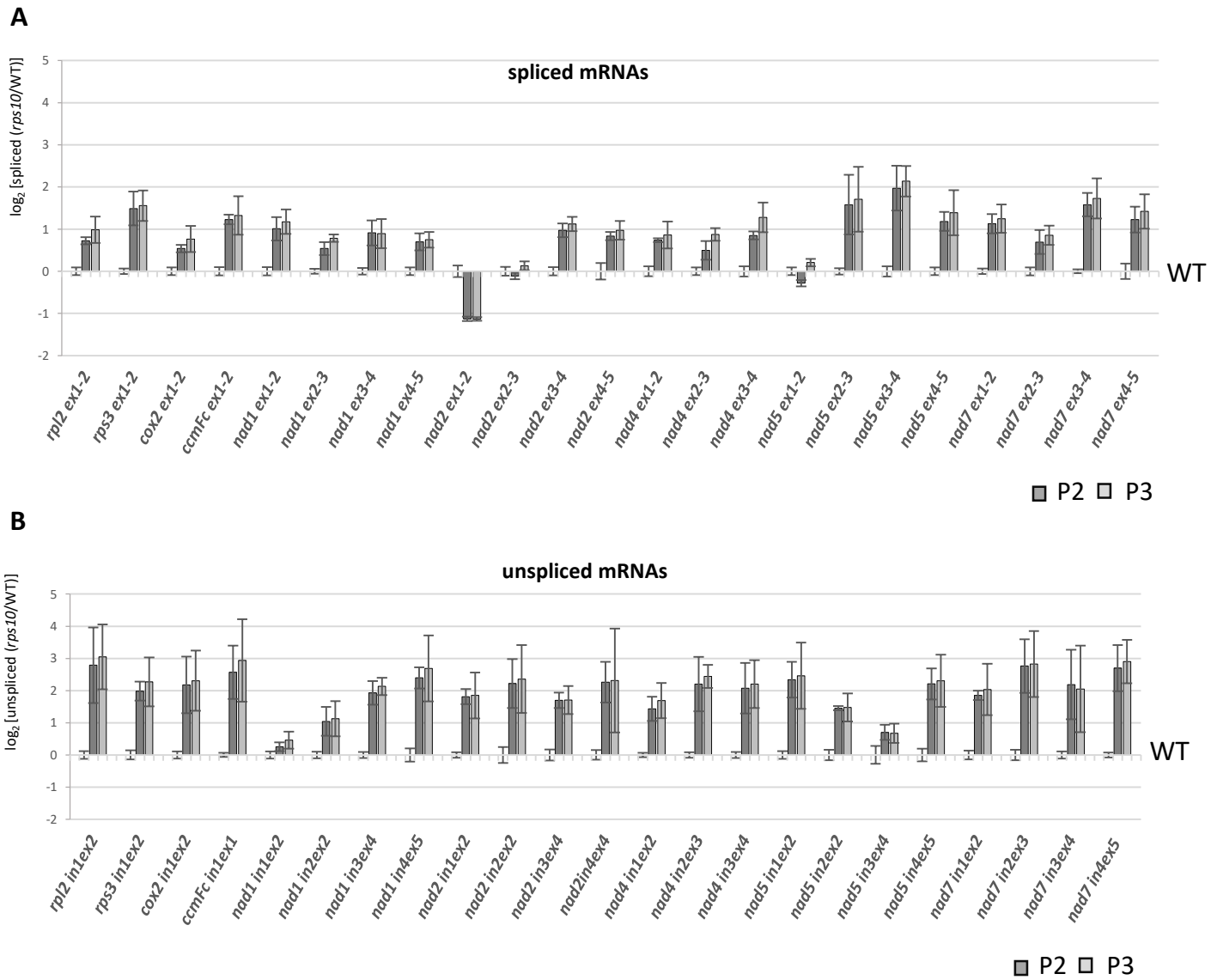

Figure S4. Relative steady-state transcript levels of mitochondrial genes containing introns in P2 and P3 phenotypes of *rps10* and wild-type. **(A)** Mature (spliced) transcripts. **(B)** Immature (unspliced) transcripts. Individual mRNA species were quantified by RT-qPCR with *ACT2* as reference. Log_2 of the ratios are shown. The values are means of five biological replicates, with standard errors.

Figure S5

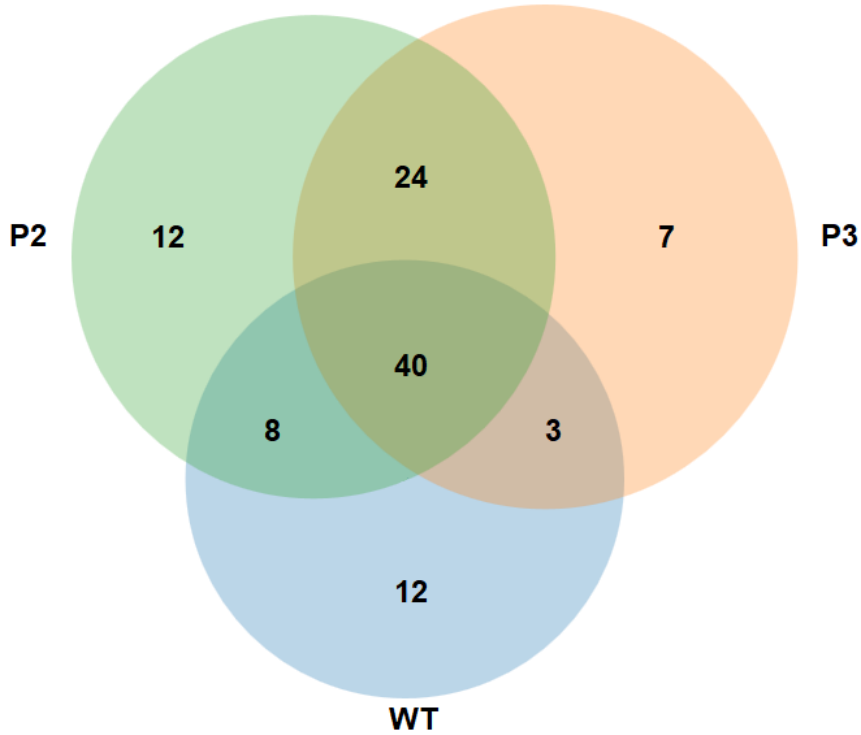

Figure S5. Distribution of common and specific mtRibo-Seq-sRNAs identified in P2 and P3 phenotypes of *rps10* and wild-type.

Figure S6

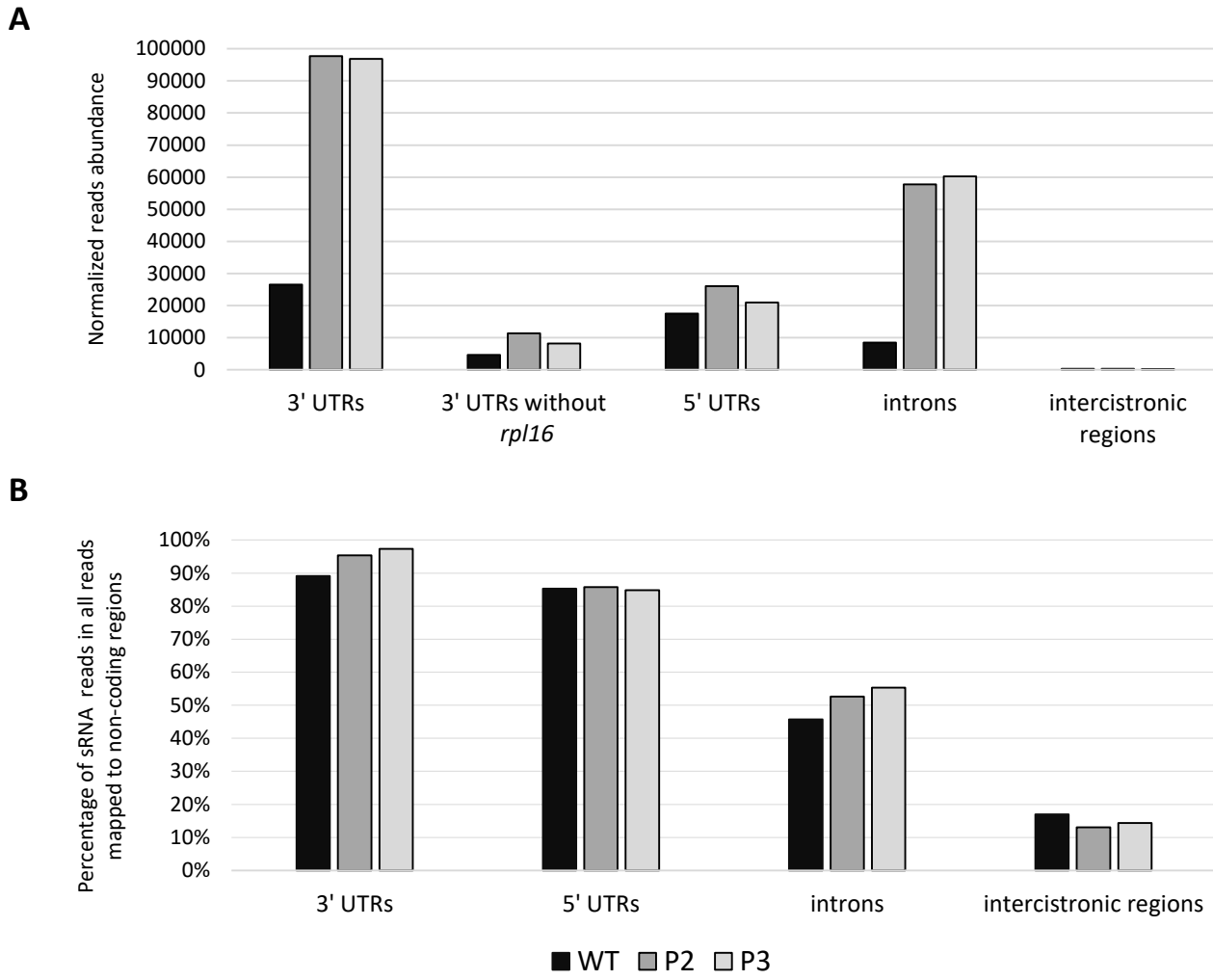

Figure S6. Putative mtRibo-Seq-sRNAs mapping to various non-coding regions of mitochondrial transcripts in P2 and P3 phenotypes of *rps10* and wild-type. mtRibo-Seq-sRNAs were identified using sRNA miner software (18). **(A)** Total number of mtRibo-Seq-sRNAs reads normalized to the number of all reads for respective libraries. For reads mapping to 3'UTRs two values are shown: for all such reads and after the extremely abundant *rpl16* mtRibo-Seq-sRNA reads have been removed. **(B)** Fraction of mtRibo-Seq-sRNAs reads among all mtRibo-Seq reads mapping to the respective non-coding regions.