Data File S1: Sequencing data for *rpl* and *rps* mutants, Related to Figures 1-3. Ribosome profiling data in RPKM (reads per kilobase million) are in columns B-Z, total RNA-seq data in RPKM are in columns AA-AY, TE (translation efficiency) values are in columns AZ-BX. Strains are sorted by growth rate, as presented in Figures 1-3. For TE, values were determined by calculating the ratio of ribosome footprint to mRNA-seq RPKM values. If total reads for mRNA and fps <48, a value of "ND" is shown.

Data File S2: mRNA synthesis for for *rpl* and *rps* mutants, Related to Figure 3. Data shown are for slope as determined by thioU incorporation measurements over time (0 hr to 15 min), as described in (Chan et al., 2018).

Data File S3: Mass spectrometry of 80S/monosome peak from *rpl* and *rps* mutants,
Related to Figure S2. TMT protein data quantification are shown, with mutants sorted by growth. Columns E to X represent data normalized to master mix to allow comparison of levels among all samples.

Data File S4: Mass spectrometry of extract from *rpl* and *rps* mutants, Related to Figure 4. Matched extract to that used for File S1 was subjected to TMT-based mass spectrometry. Mutants are sorted by growth. Columns F to X represent data normalized to master mix to allow comparison of levels among all samples.

Data File S5: Mass spectrometry of 60S peak from *rpl* and *rps* mutants, Related to Figure 5. TMT protein data are shown, with mutants sorted by growth. Values are normalized to total intensity.