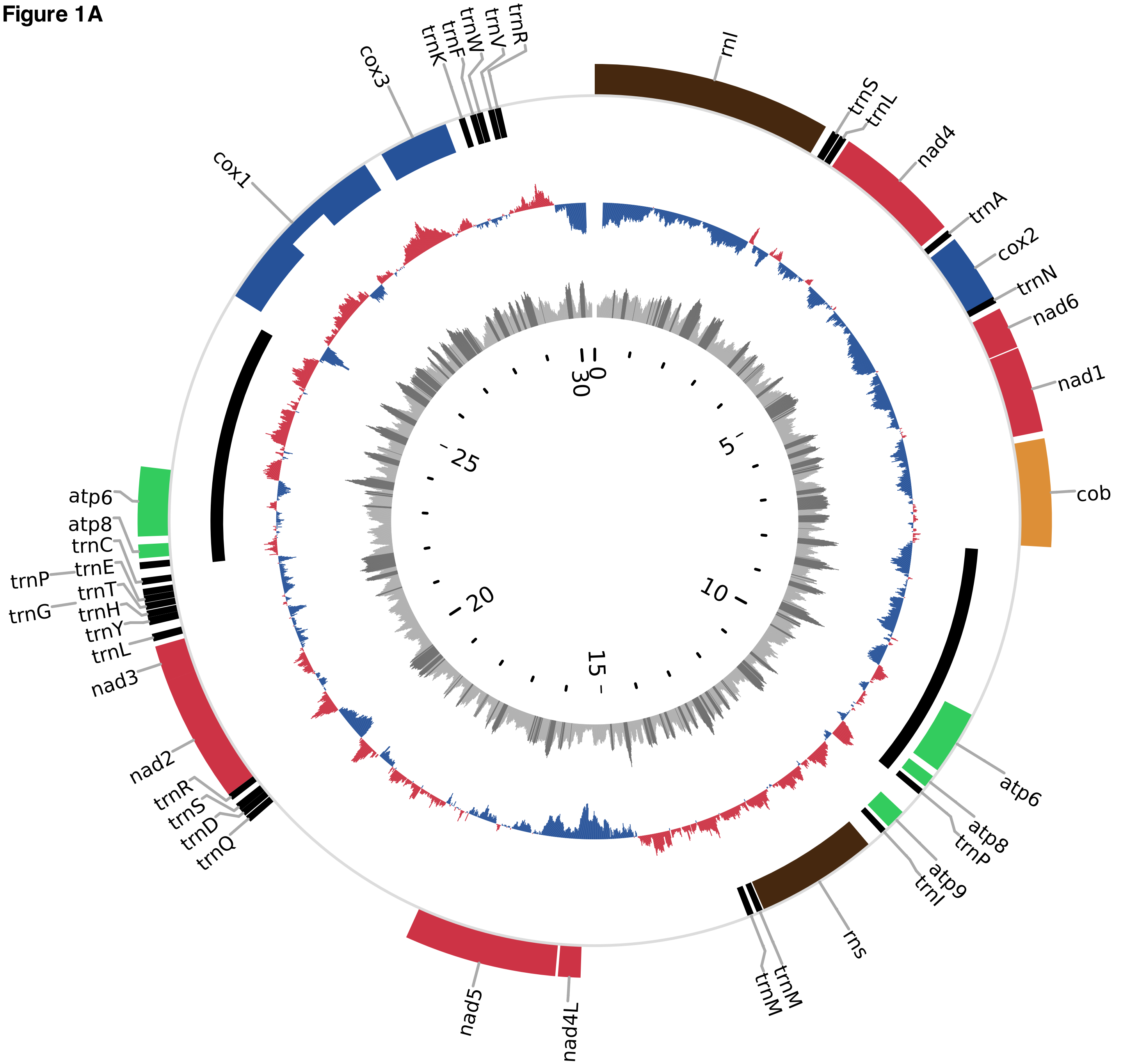
SUPPLEMENTARY MATERIAL

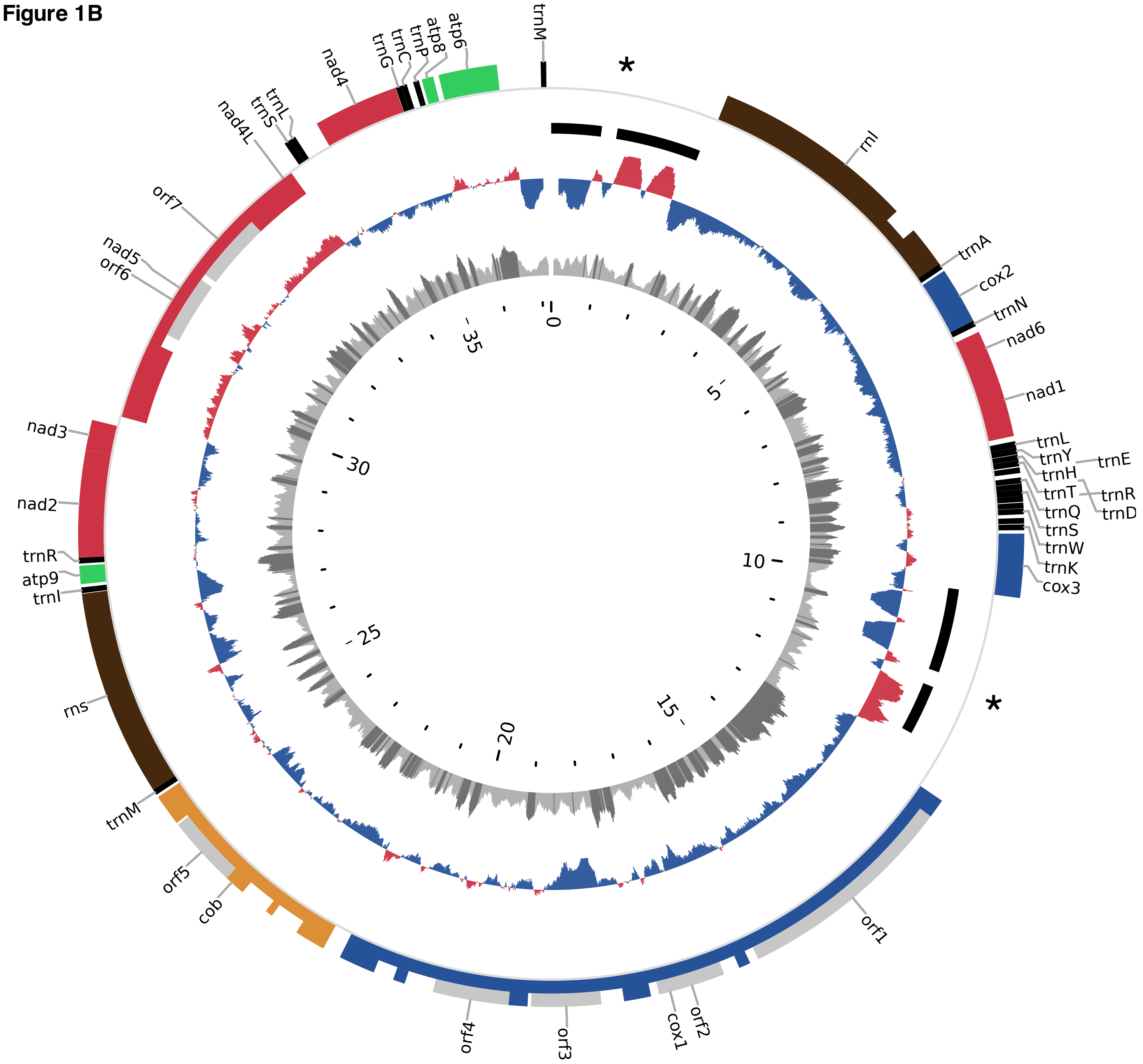
Supplementary Figure 1. Mitochondrial genome maps of *C. alai* **(A)**, *C. frijolesensis* **(B)**, *C. jiufengensis* **(C)**, *C. maltosa* **(D)**, *C. neerlandica* **(E)**, *C. salmanticensis* **(F)**, *C. sojae* **(G)**, and *C. viswanathii* **(H)**. The genetic maps were visualized using Circos (Krzywinski, M., Schein, J., Birol, I., Connors, J., Gascoyne, R., Horsman, D., Jones, S.J. and Marra, M.A. (2009) Circos: an information aesthetic for comparative genomics. *Genome Res*, 19, 1639-1645). All the genes are displayed on the outermost track with those coded on the direct and reverse strand shown on the outer and inner rim, respectively. The thin black arcs represent the regions of large inverted repeats (either terminal or internal). The middle track visualizes the GC-skew (window=250 and step=10 nucleotides) with positive values in red and negative in blue. The inner track represents the GC content plot (window=100 and step=10 nucleotides) with areas over 25% G+C in dark grey. The chromosome coordinates are shown in the innermost part of the map. Note that circular versions of *C. frijolesensis* and *C. viswanathii* mitochondrial genomes are shown (the asterisks indicate the positions of resolution elements involved in the genome linearization/fragmentation).

Supplementary Figure 2. Reconstruction of ancestral genome rearrangements. The figure shows possible ancestral gene orders (including tRNA genes) and the number of events on each branch found by local optimization for the double-cut-and-join (DCJ) model. The intervals show range of numbers of events in equally parsimonious histories. Red connectors in the gene orders for present-day and ancestral genomes represent inferred breakpoints on the branch to the nearest ancestor.

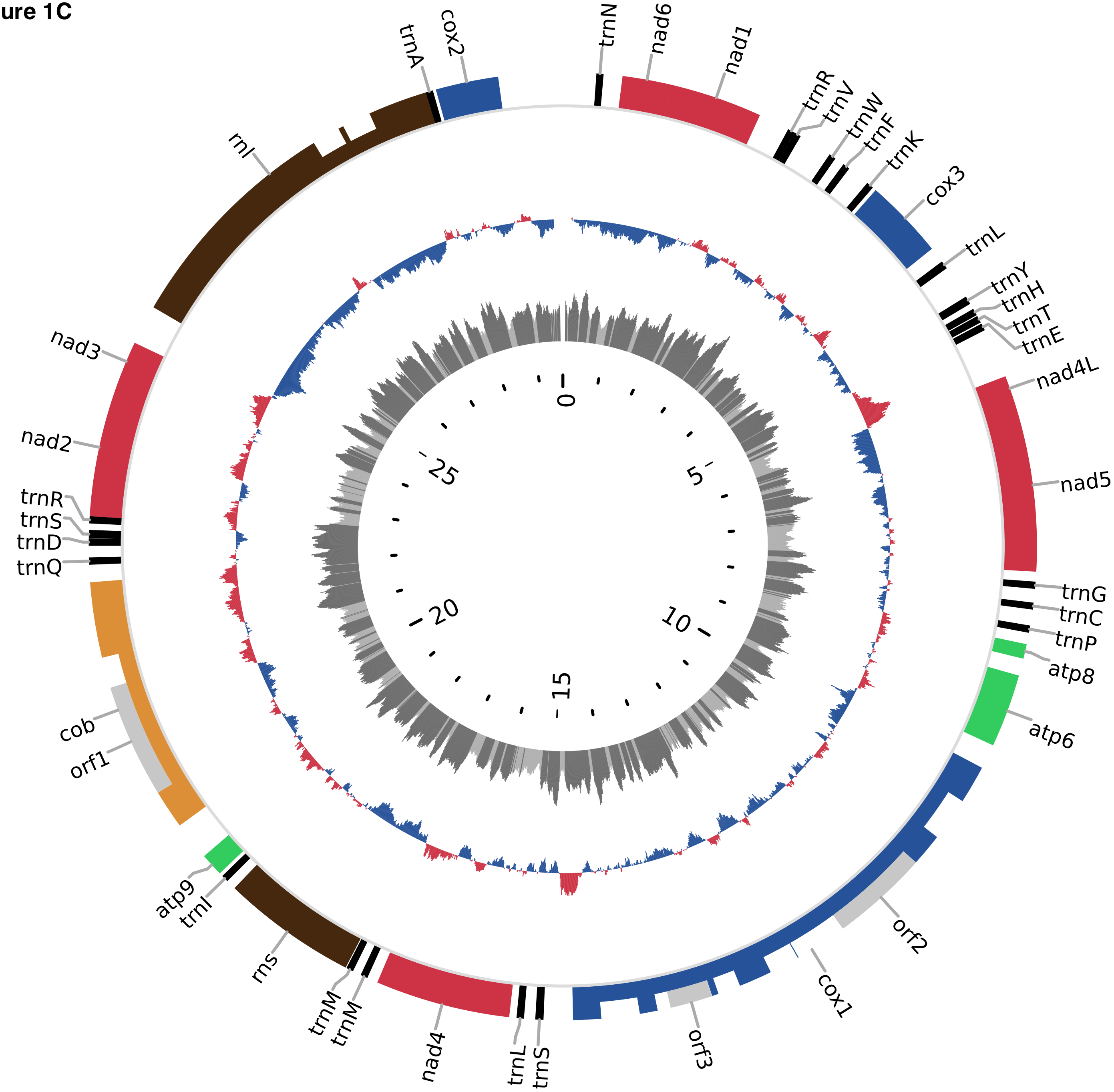
Supplementary Figure 1A



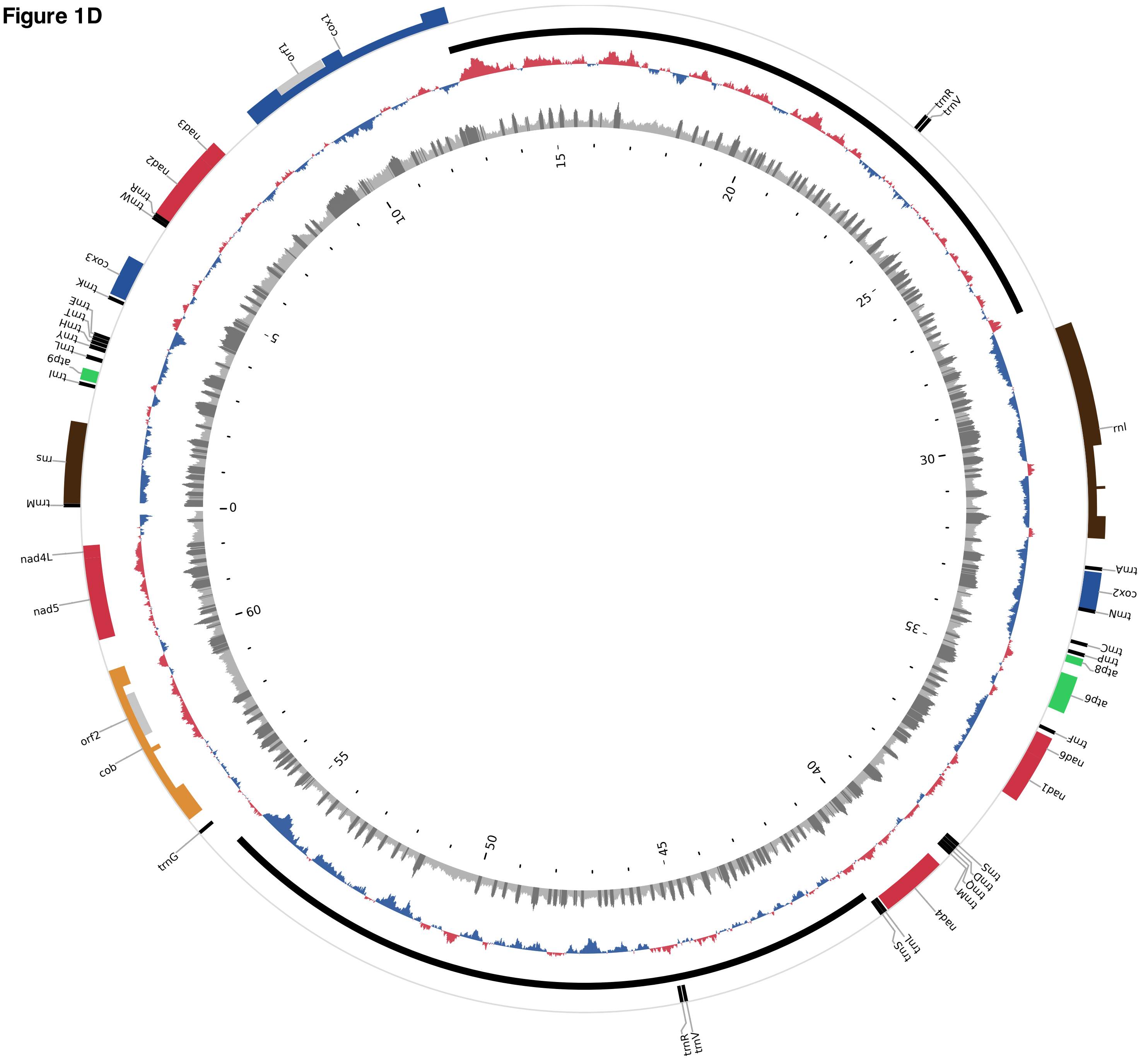
Supplementary Figure 1B



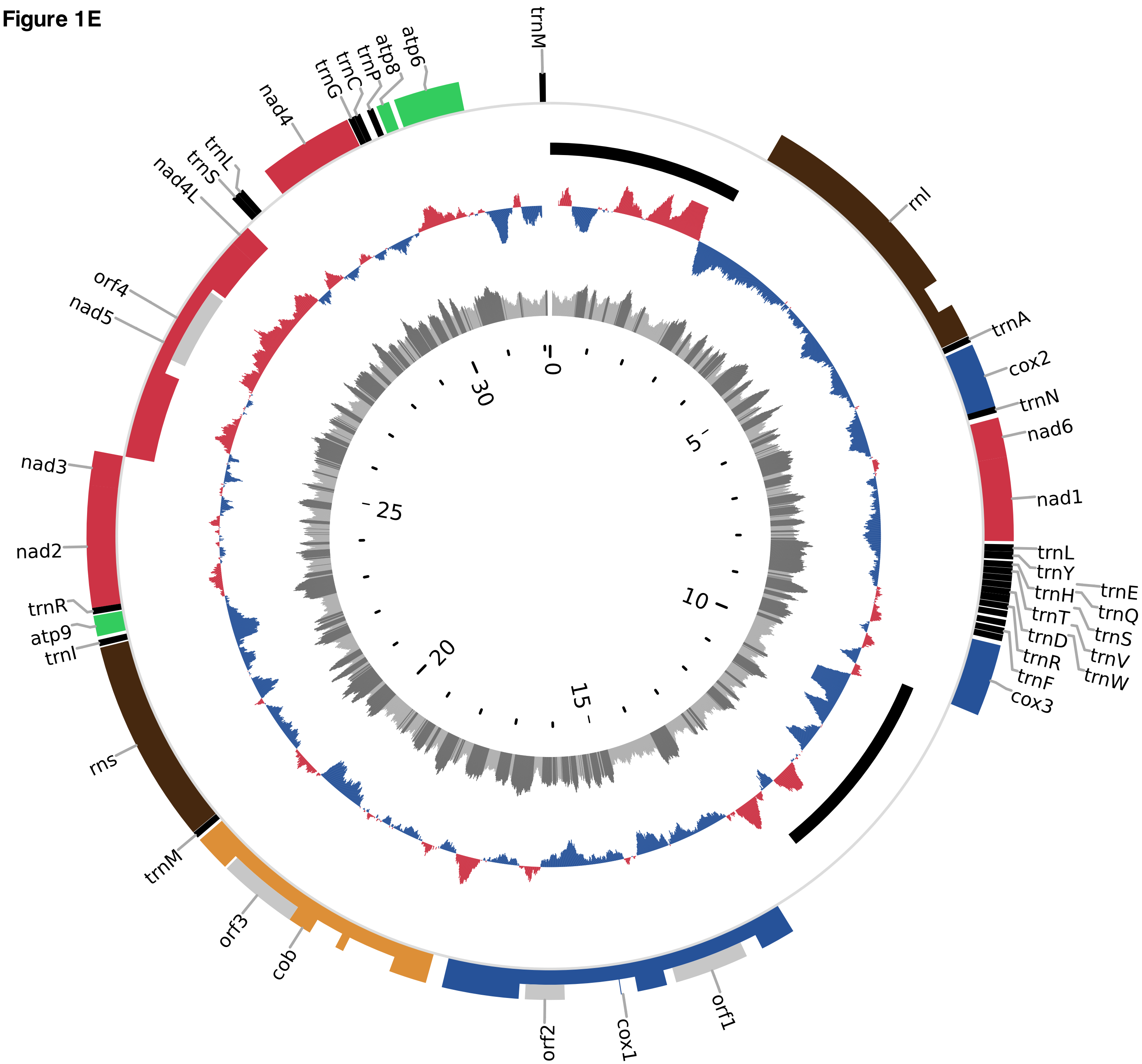
Supplementary Figure 1C



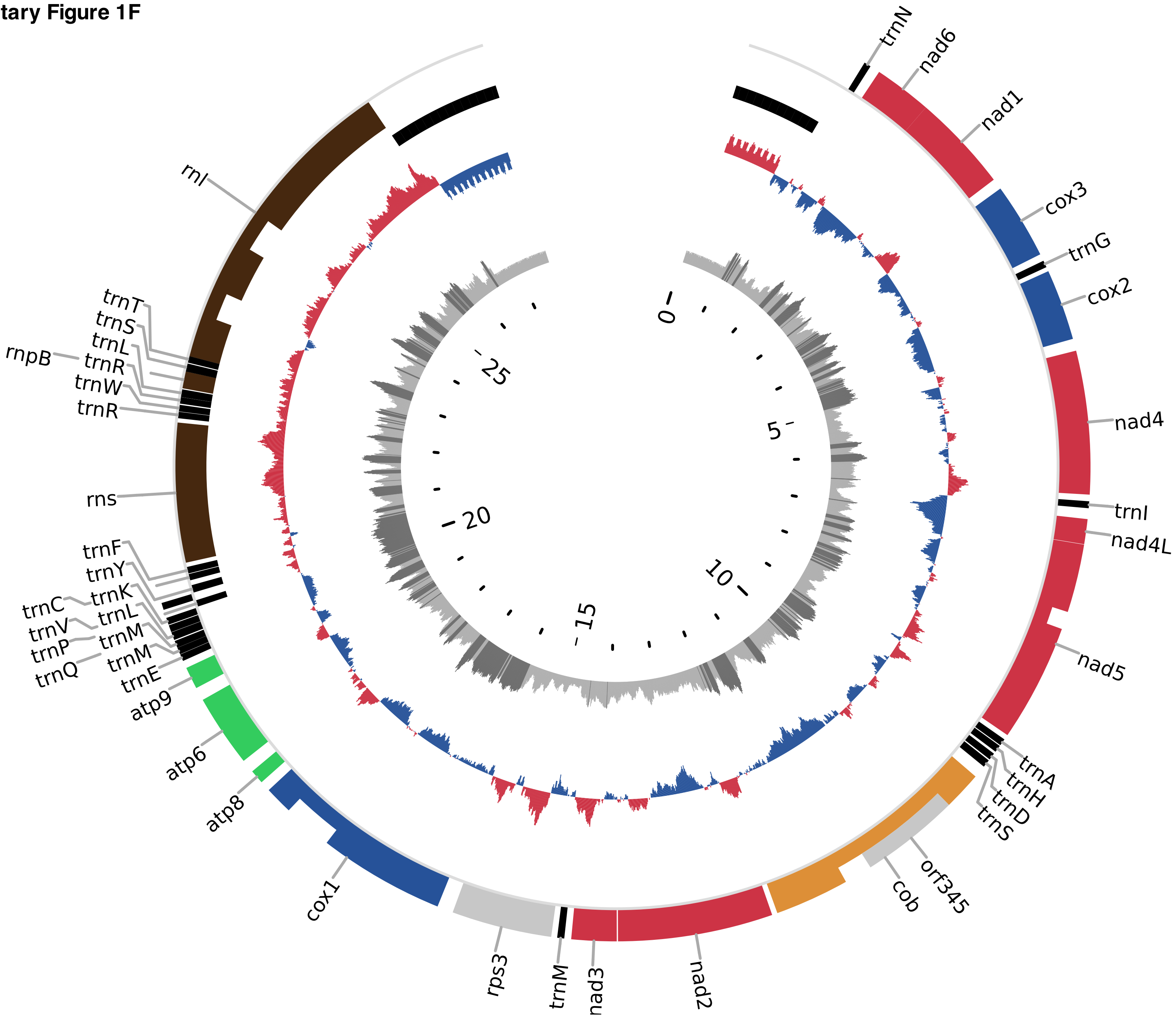
Supplementary Figure 1D



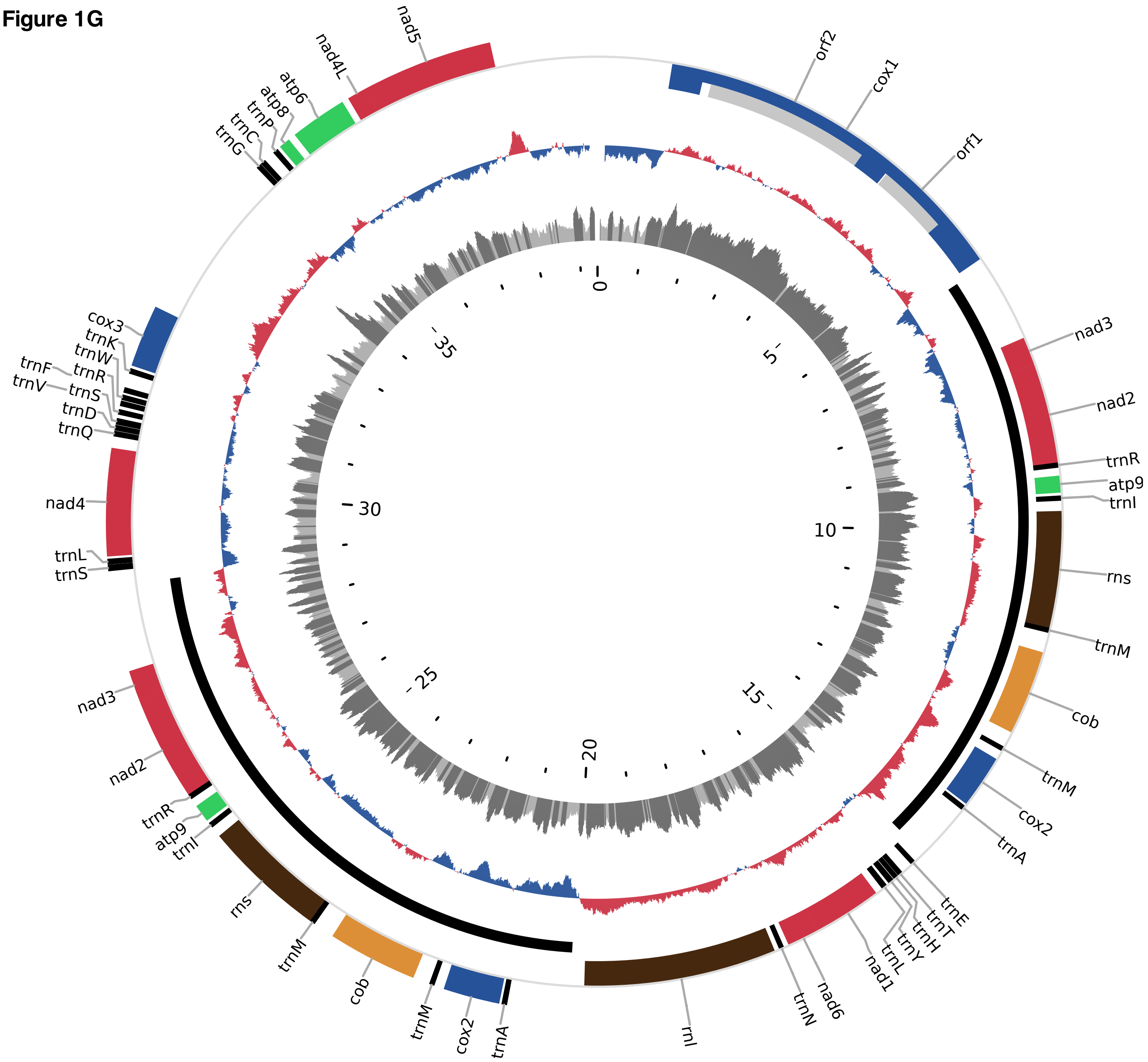
Supplementary Figure 1E



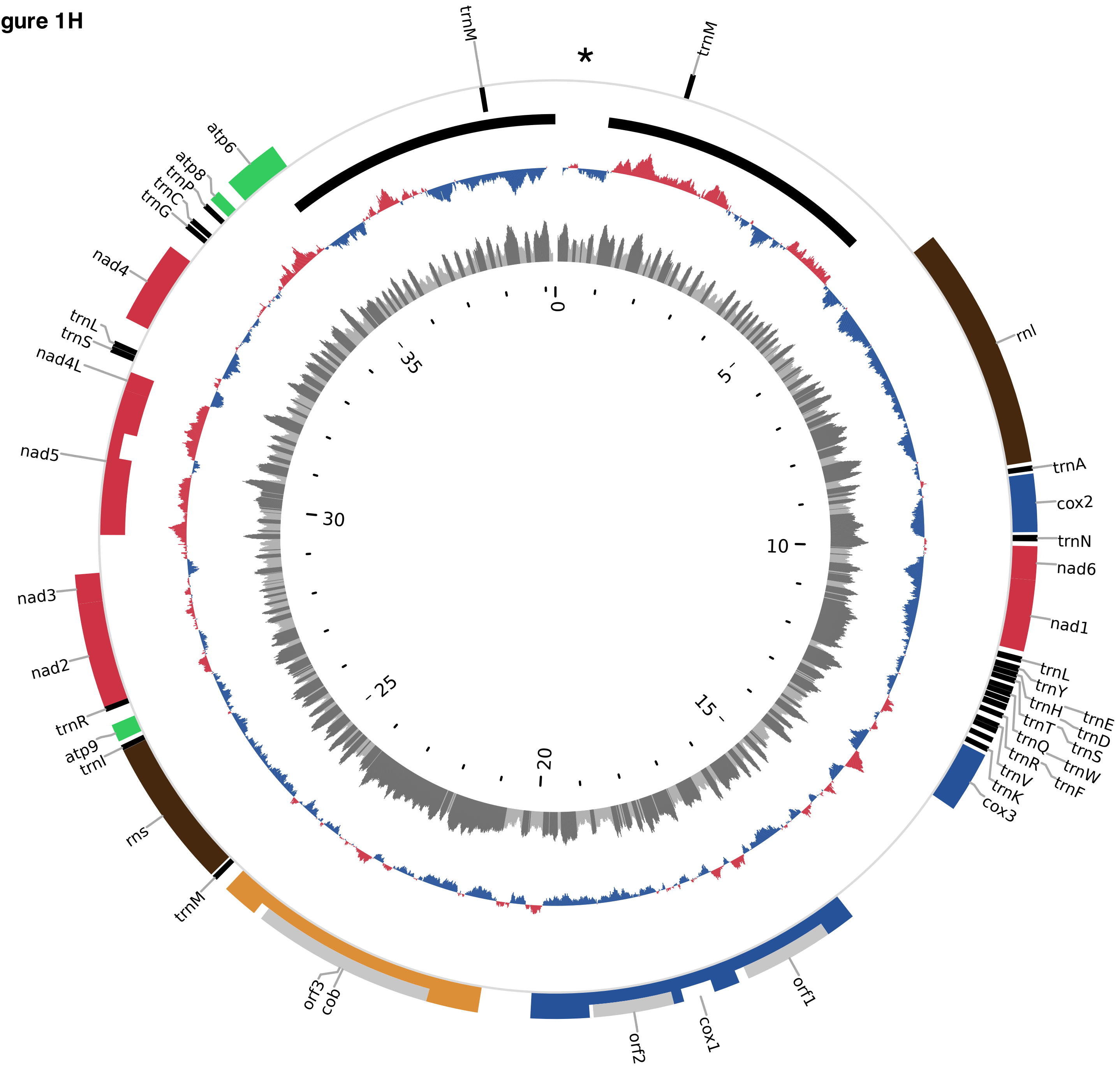
Supplementary Figure 1F



Supplementary Figure 1G



Supplementary Figure 1H



Supplementary Figure 2