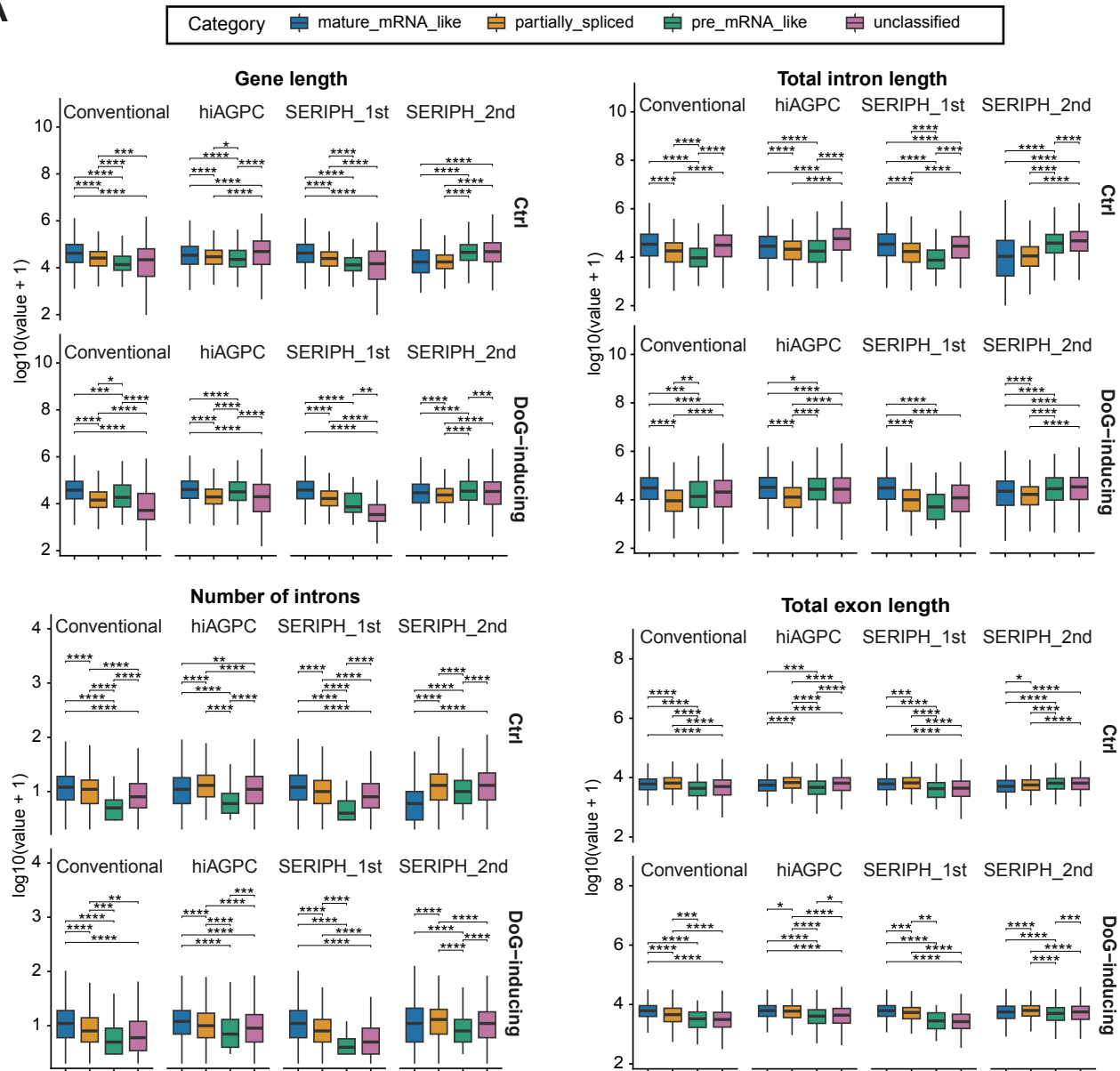
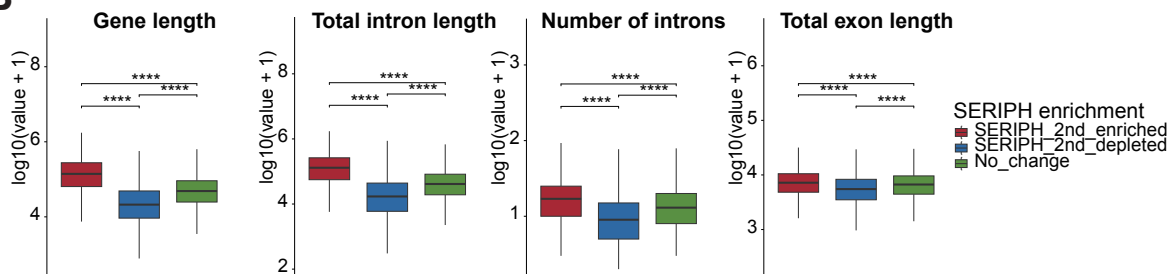


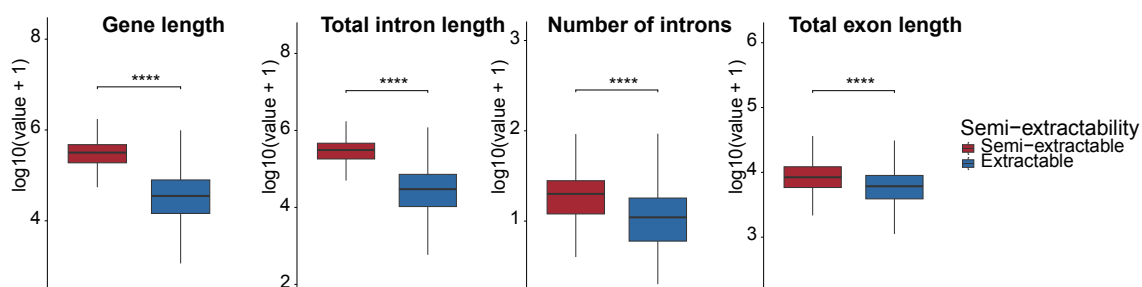
A



B



C



Supplemental Fig. 7

Supplemental Fig. S7: Relationship between transcript processing categories, semi-extractability, SERIPH enrichment, and gene features.

(A) Comparison of gene features among transcript processing categories. Gene length, total exon length, total intron length, and number of introns are shown after excluding low-coverage genes and genes with discordant classifications between replicates.

(B, C) Comparison of gene features among genes classified by SERIPH enrichment (B: *SERIPH 2nd-step enriched*, *SERIPH 2nd-step depleted*, or *No change*) or semi-extractability (C: *Semi-extractable* or *Extractable*). Gene features are shown as in (A). In all panels, boxplots show distributions of log₁₀-transformed values. Significant pairwise comparisons are indicated by brackets and were assessed using Wilcoxon rank-sum tests on log₁₀-transformed values, with Benjamini–Hochberg correction within each gene feature. *, **, ***, and **** indicate adjusted $P < 0.05$, < 0.01 , < 0.001 , and < 0.0001 , respectively.