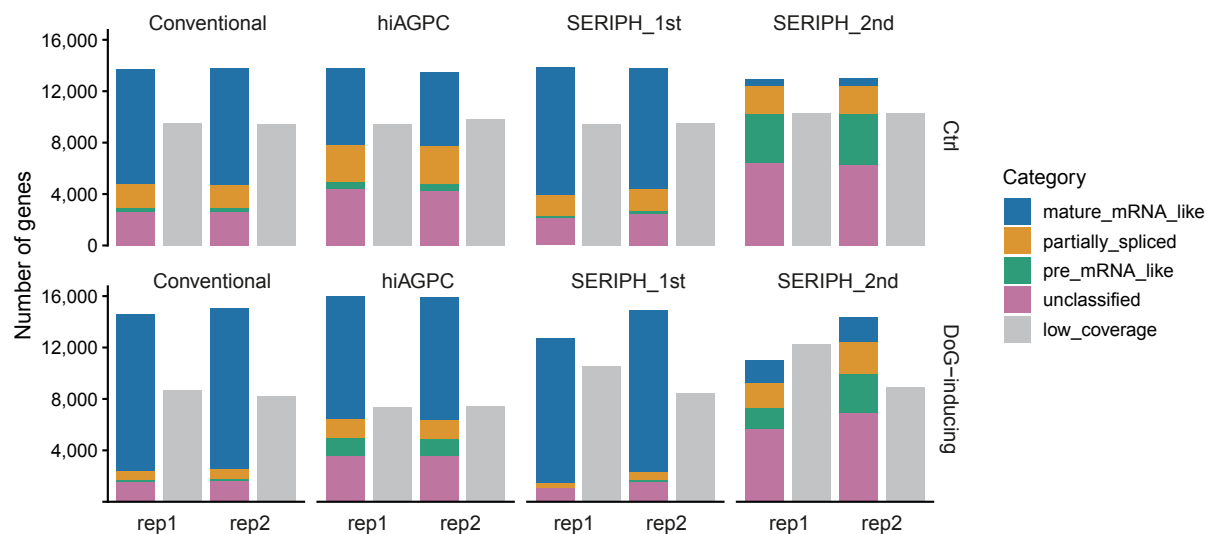
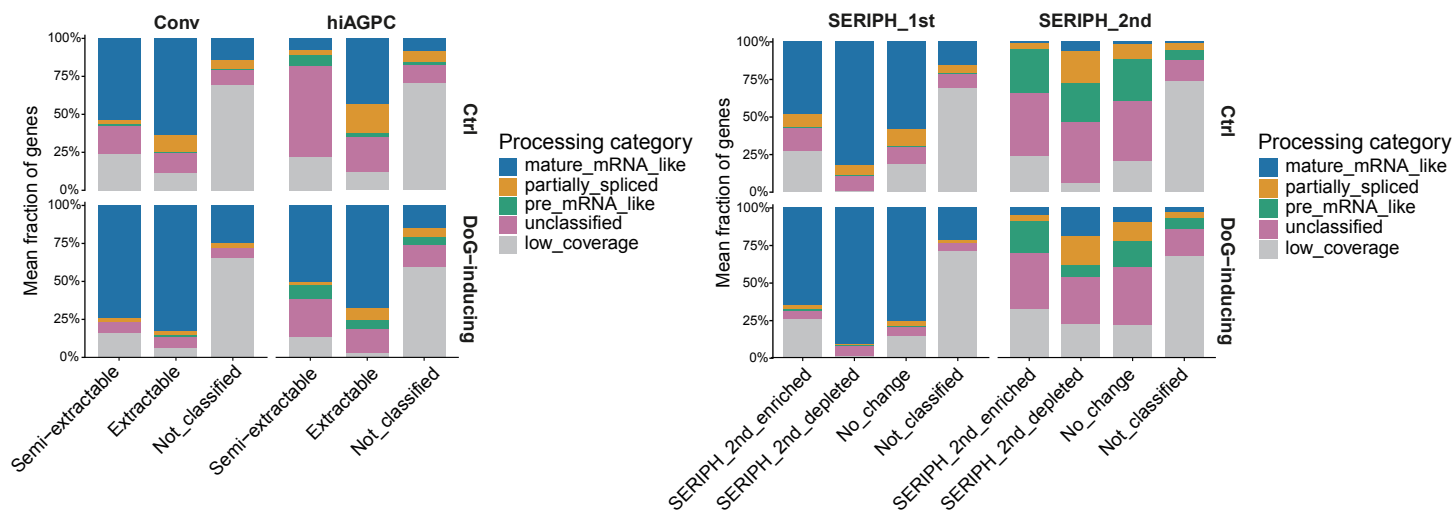


A



B



Supplemental Fig. 6

Supplemental Fig. S6: Gene-level classification of transcript processing patterns in relation to RNA preparation method, semi-extractability, and SERIPH enrichment.

(A) Fraction of genes assigned to each transcript processing category across RNA preparation methods under control and DoG-inducing conditions. Genes were classified into five categories based on exon and intron read patterns: *mature mRNA-like*, *partially spliced*, *pre-mRNA-like*, *unclassified*, and *low-coverage*. Biological replicates were collapsed by calculating the mean fraction across replicates.

(B) Fraction of genes in each transcript processing category according to semi-extractability and SERIPH enrichment classifications. For semi-extractability-based classification, category composition is shown in conventional and hiAGPC preparations. For SERIPH enrichment classification, category composition is shown in SERIPH 1st-step and 2nd-step preparations. Fractions are shown separately for control and DoG-inducing conditions, and biological replicates were collapsed by calculating the mean fraction across replicates.