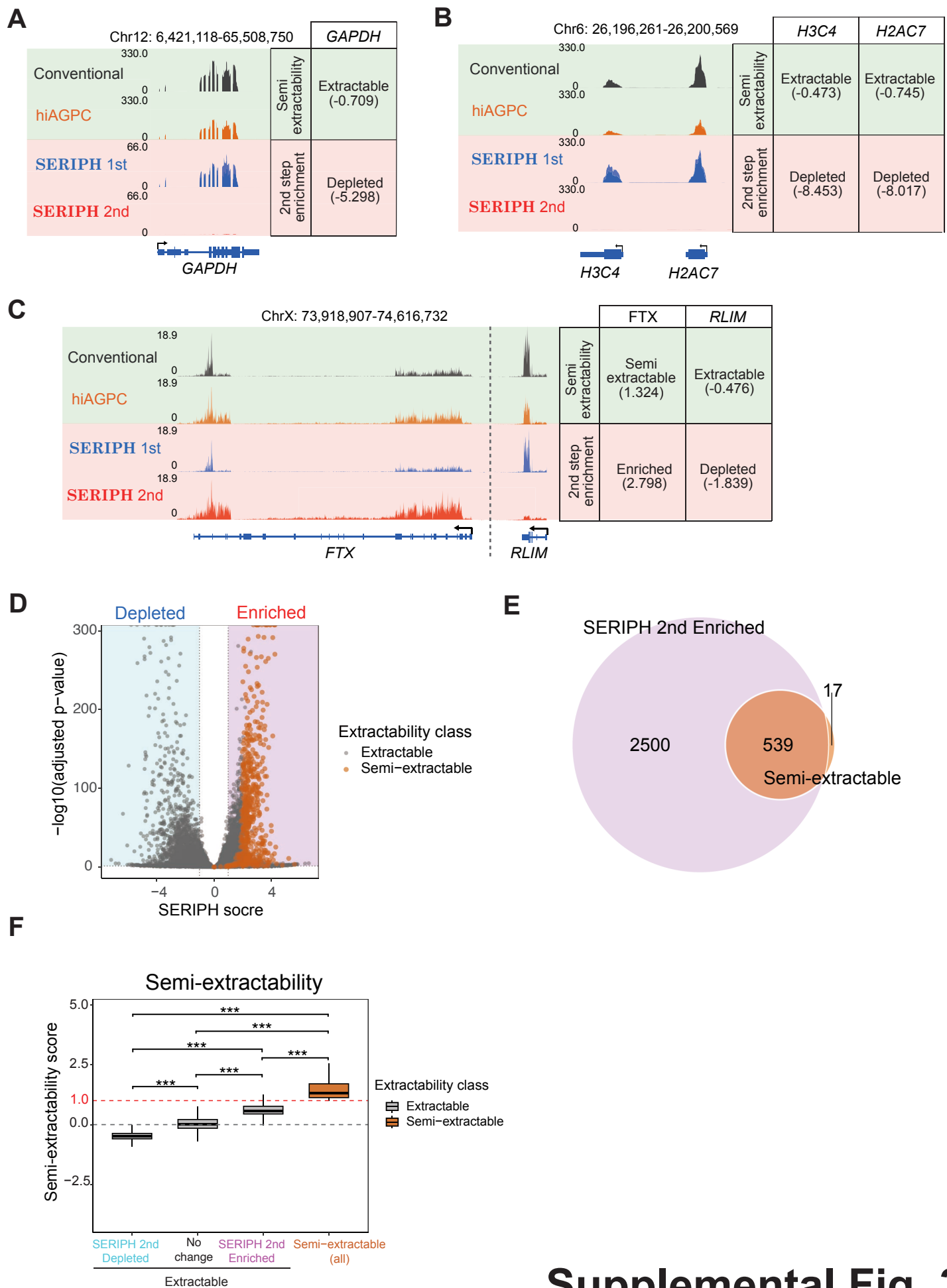




Supplemental Fig. 3

Supplemental Fig S3: SERIPH expands the semi-extractable repertoire at the gene-level.

(A, B) Genome browser views of the *GAPDH* locus (A) and the *H3C4–H2AC7* locus (B). Normalized coverage tracks are shown with biological replicates overlaid. Numbers in parentheses indicate scores derived from the indicated analyses. Black arrows indicate the direction of transcription.

(C) Genome browser view of the *FTX–RLIM* locus. Normalized coverage tracks are shown with replicates overlaid. Numbers in parentheses indicate scores derived from the indicated analyses. Black dotted lines denote omitted genomic regions for visualization. Black arrows indicate the direction of transcription.

(D–F) Analysis of semi-extractability in unspliced transcripts.

(D) Volcano plot showing the transcriptome-wide distribution of unspliced transcripts enriched or depleted in the SERIPH 2nd-step fraction relative to the 1st-step fraction, analogous to the analysis shown in Fig. 2C.

(E) Venn diagram illustrating the overlap between unspliced transcripts annotated as semi-extractable in the original improved vs. conventional dataset and unspliced transcripts enriched in the SERIPH 2nd-step fraction, analogous to Fig. 2D. Numbers denote the total transcripts in each group, as well as the shared and unique subsets.

(F) Distribution of semi-extractability scores for unspliced transcripts originally classified as extractable, grouped according to their enrichment status in the SERIPH 2nd-step fraction, analogous to Fig. 2E.