Supplemental Figures

Parallel analysis of replication timing, gene expression and copy number with PARTAGE

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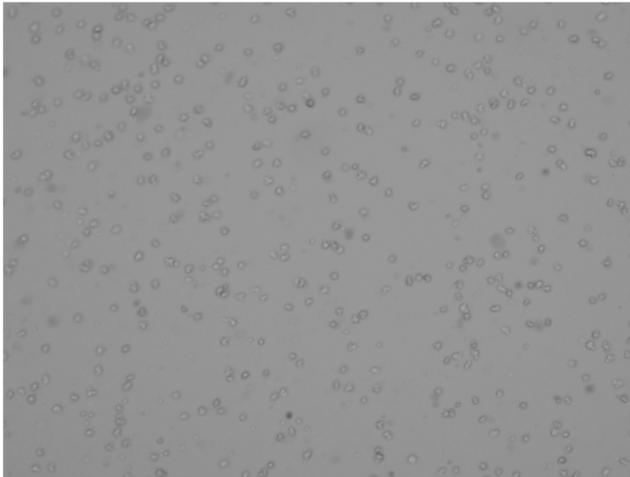[2]Masonic Cancer Center, University of Minnesota Medical School, Minneapolis, Minnesota
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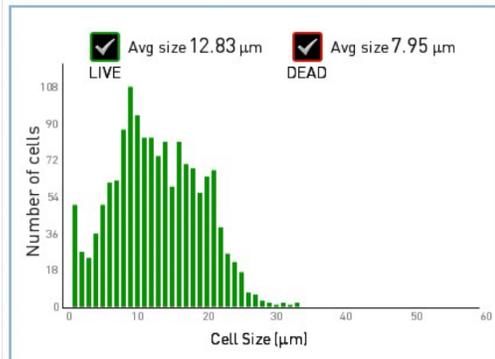
[†]These authors contributed equally to this work
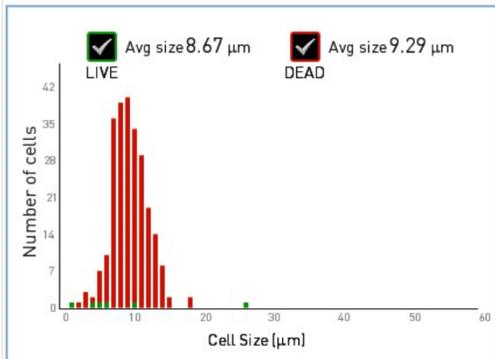
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A

Concentration		
Total		9.64 x 10⁶/mL
Live	92%	8.87 x 10⁶/mL
Dead	8%	7.68 x 10⁵/mL

Avg size 12.83 μm — LIVE   Avg size 7.95 μm — DEAD

B

| Concentration		
Total		1.48 x 10⁶/mL
Live	2%	3.52 x 10⁴/mL
Dead	98%	1.44 x 10⁶/mL

Avg size 8.67 μm — LIVE   Avg size 9.29 μm — DEAD

Supplemental Figure 1. A) Viability analysis after dissociation of HepG2 cells. B) Intact nuclei and lysis efficiency estimation. Cell viability assays were performed based on trypan blue staining on an automated cell counter (Invitrogen CountessII-FL).
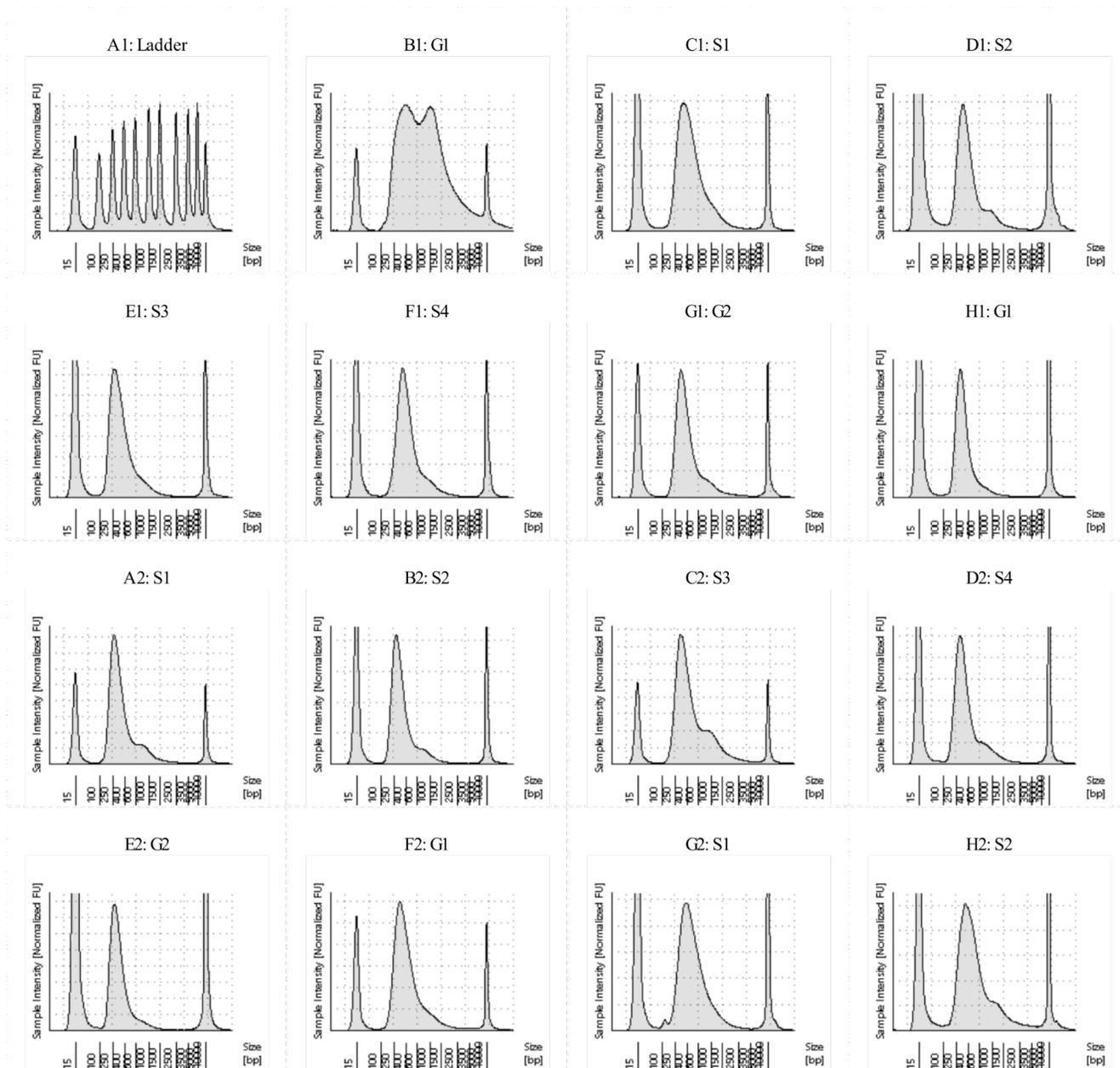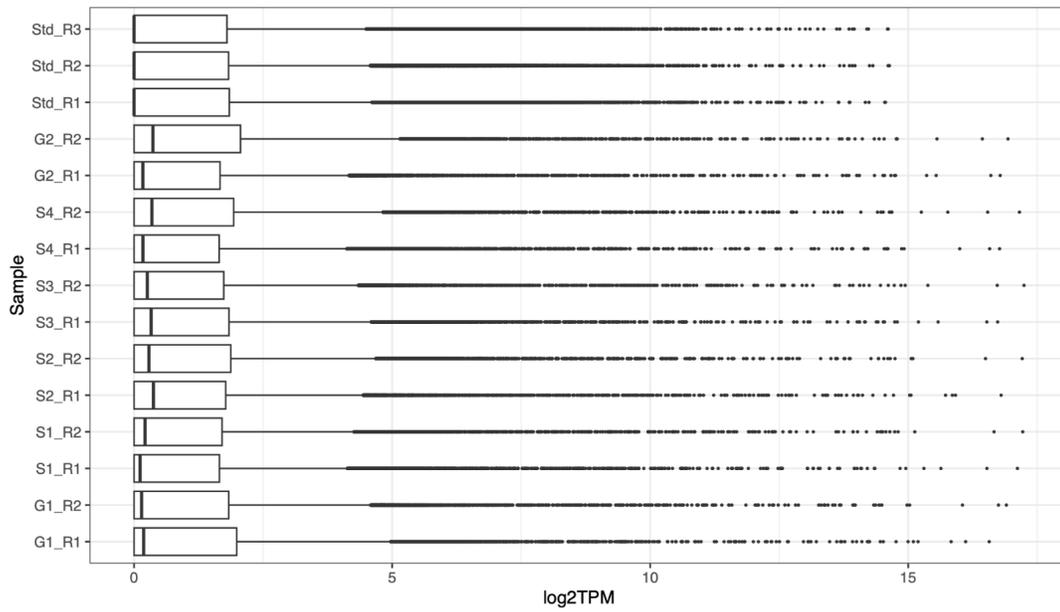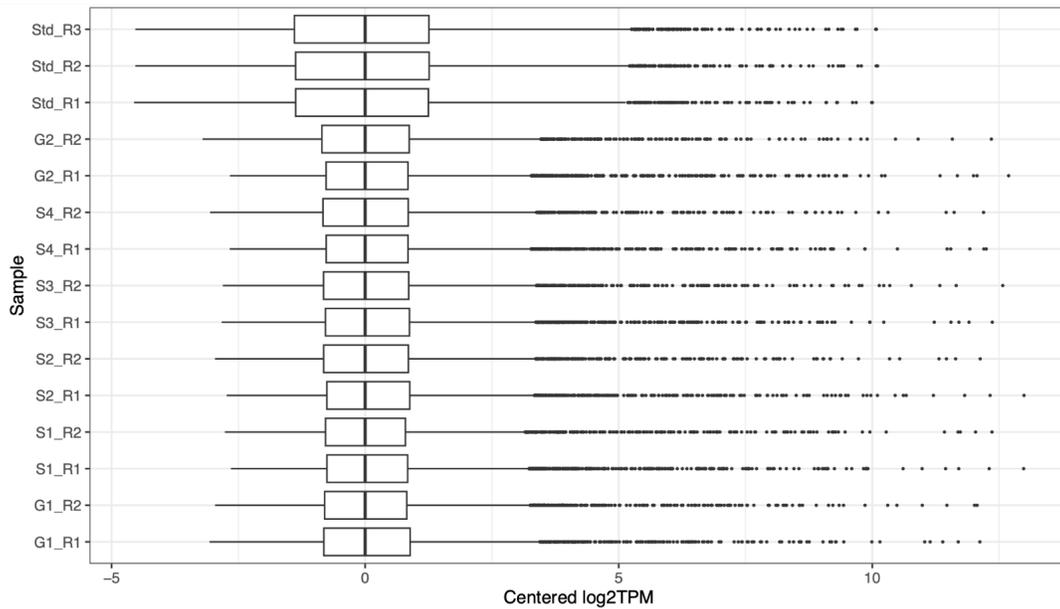
Supplemental Figure 2. Size distribution analysis of PARTAGE Repli-seq libraries performed on TapeStation with a High Sensitivity DNA ScreenTape.
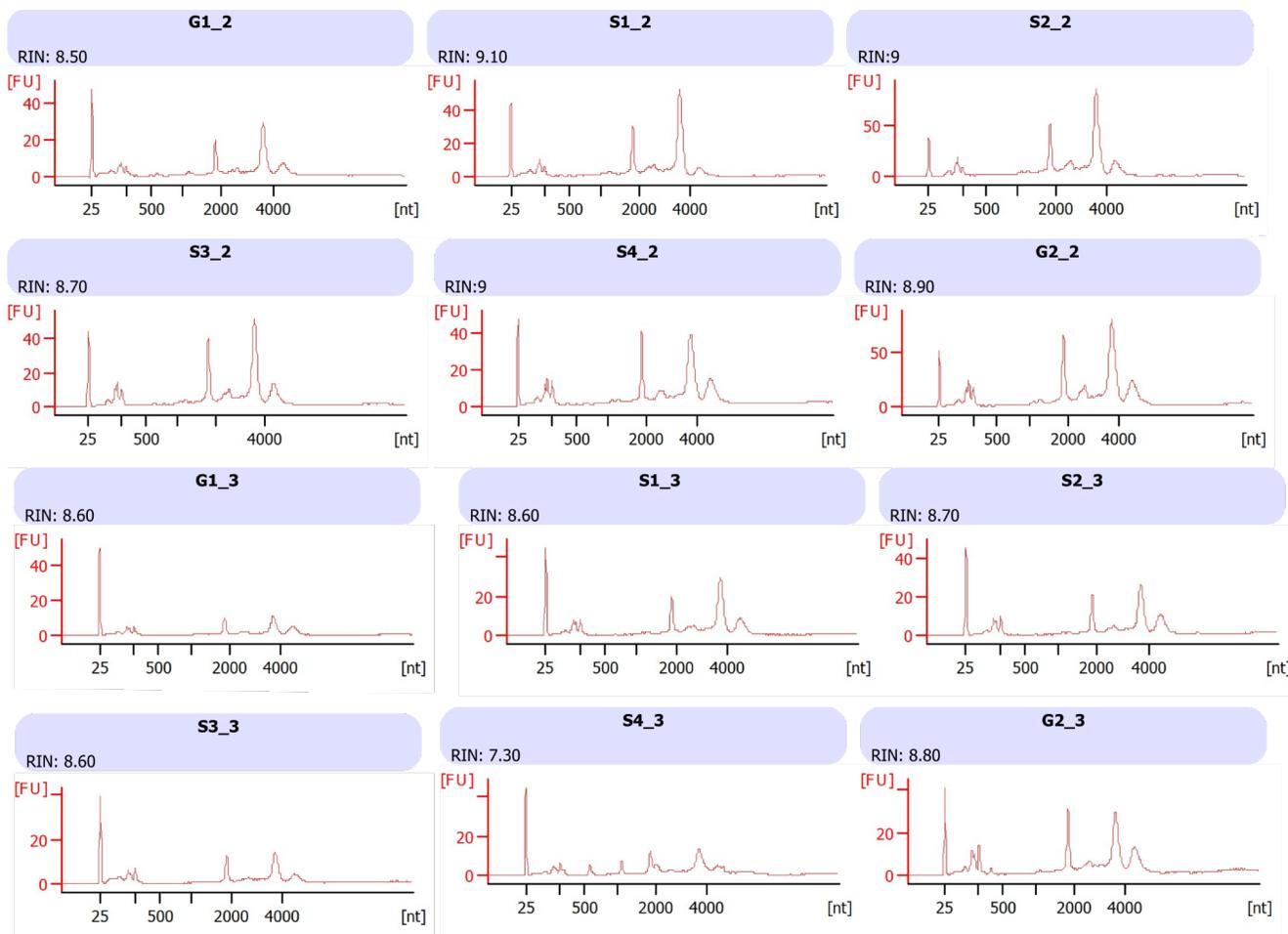
Supplemental Figure 3. Size distribution analysis of PARTAGE RNA-seq libraries performed on Bionalyzer with RNA 6000 Nano Kit.
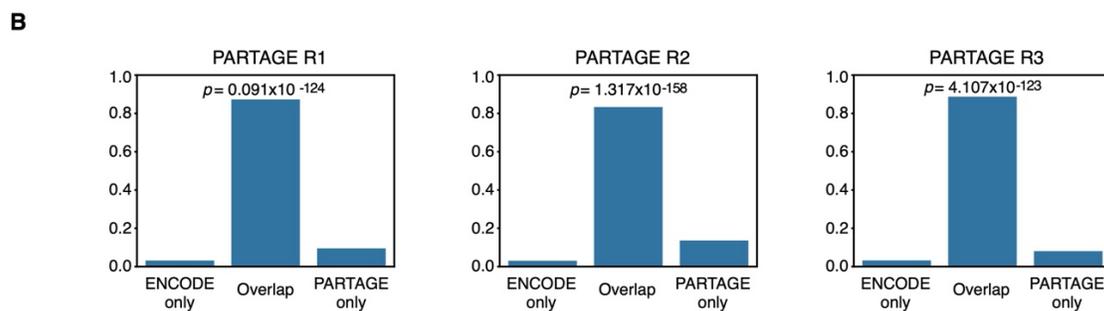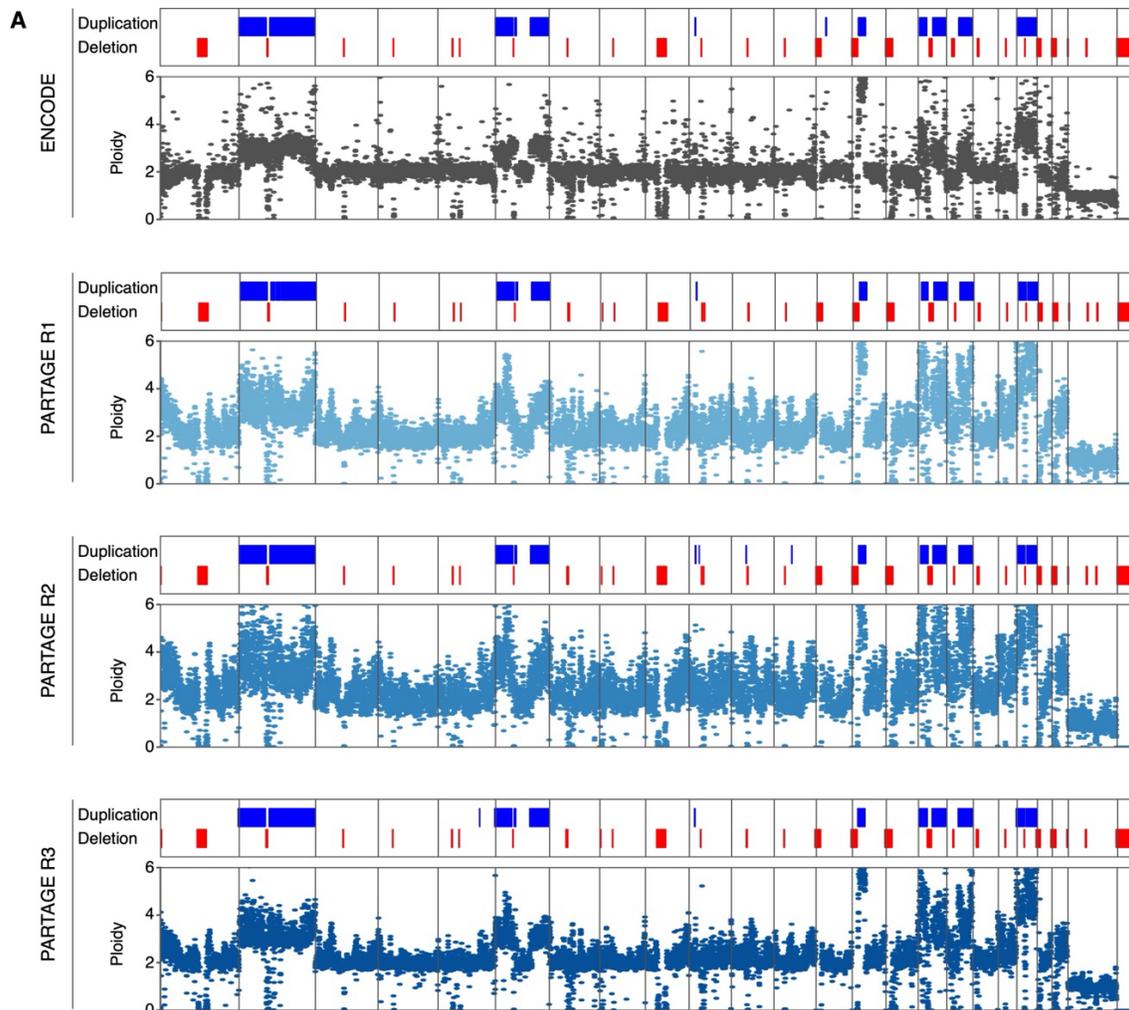
Supplemental Figure 4. A) Comparative CNV analysis at 200Kb resolution. CNV profiles derived from ENCODE high-coverage WGS (60X coverage; top track) and from PARTAGE (~0.5X coverage; three independent replicates) using CNVpytor (see methods). CNV events are shown as duplications (blue) and deletions (red). B) Overlap of CNV calls between ENCODE and PARTAGE replicates. PARTAGE correctly detected >85% of the ENCODE CNV events (n=75) across replicates. The statistical significance of the overlap between ENCODE and PARTAGE CNVs was assessed using ProOvErlap (see methods).

A

B

Supplemental Figure 5. Per sample gene expression distributions. A) Log2TPM values. B) Log2TPM values after removing non expressed genes (threshold ≥1 Log2TPM), median-centering, and batch correction using ComBat algorithm.
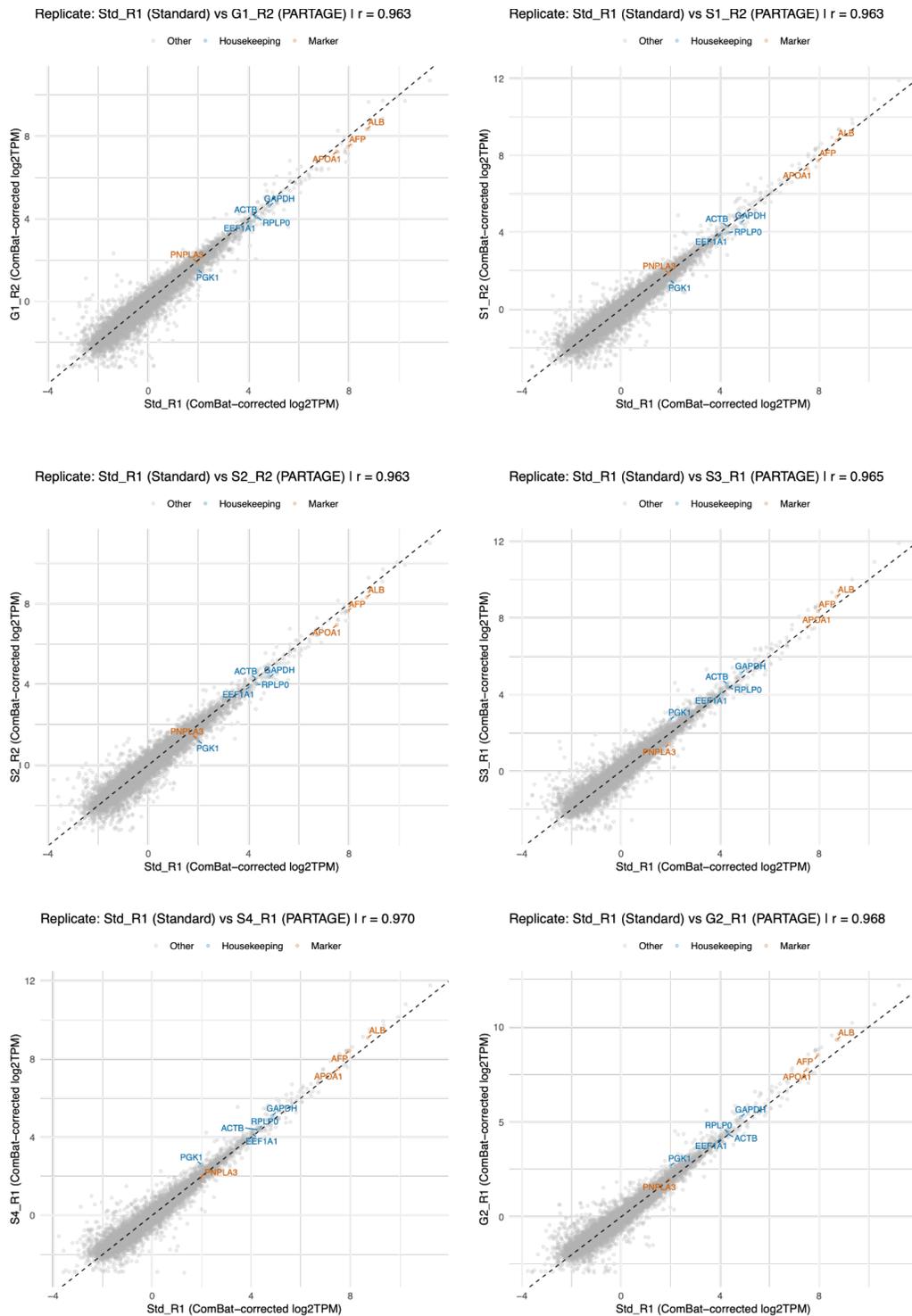
Supplemental Figure 6. Gene-by-gene, replicate-level scatterplots on batch-corrected gene expression values (log2TPM). Standard RNA-seq (x-axis) versus PARTAGE RNA-seq (y-axis) replicates are shown. Housekeeping genes (blue) and hepatic markers (red) are highlighted; all other genes are gray. Only genes expressed with TPM ≥ 1 in at least 2 samples were considered (11,630 protein-coding genes passed these filters).
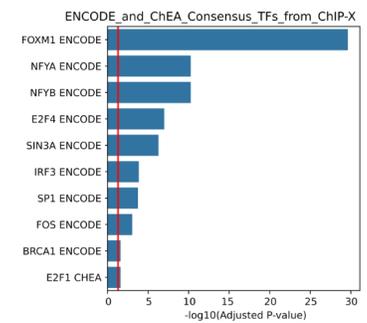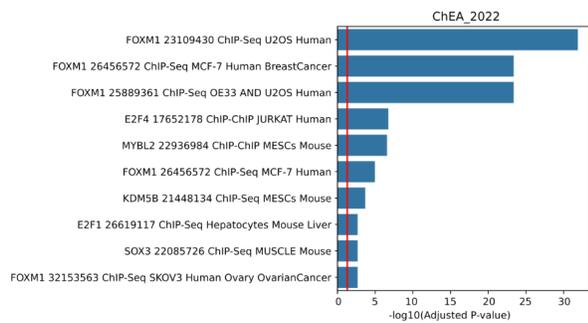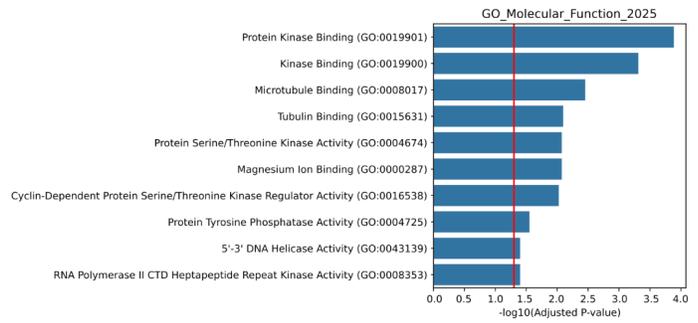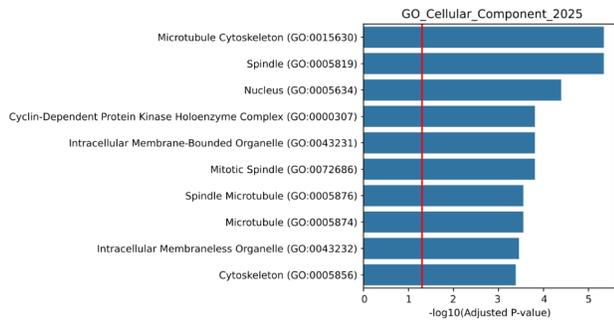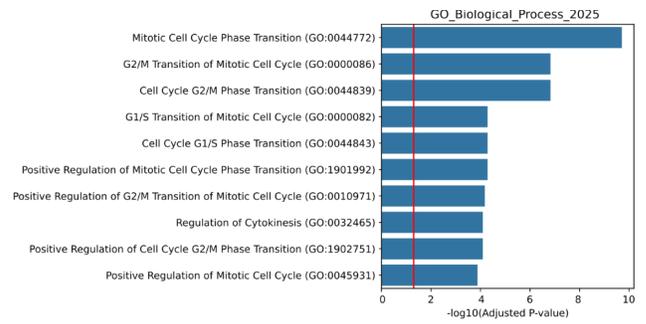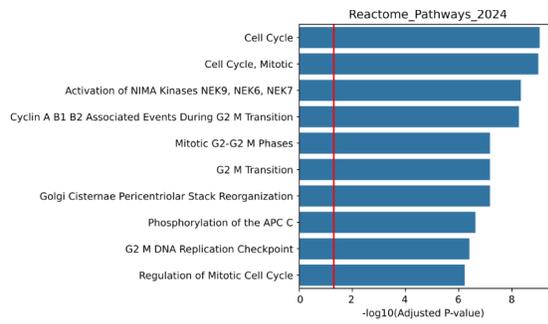
Supplemental Figure 7. Ontology analysis of cell cycle-regulated genes.