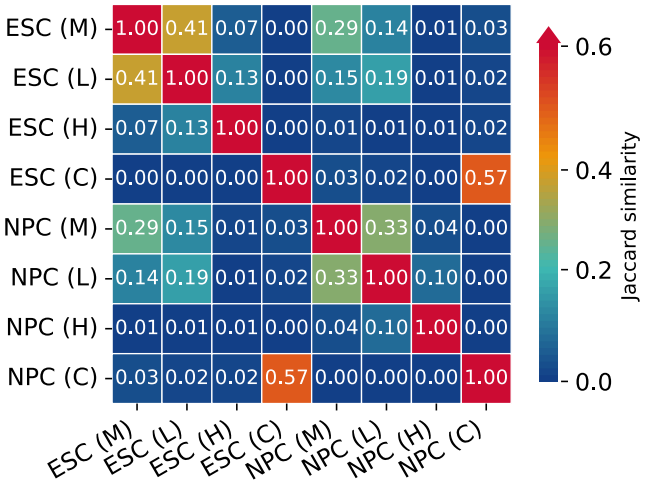
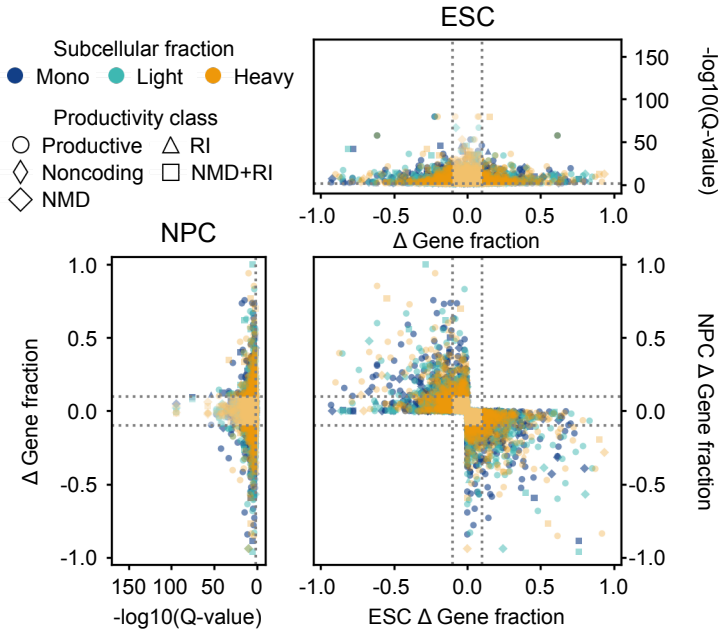
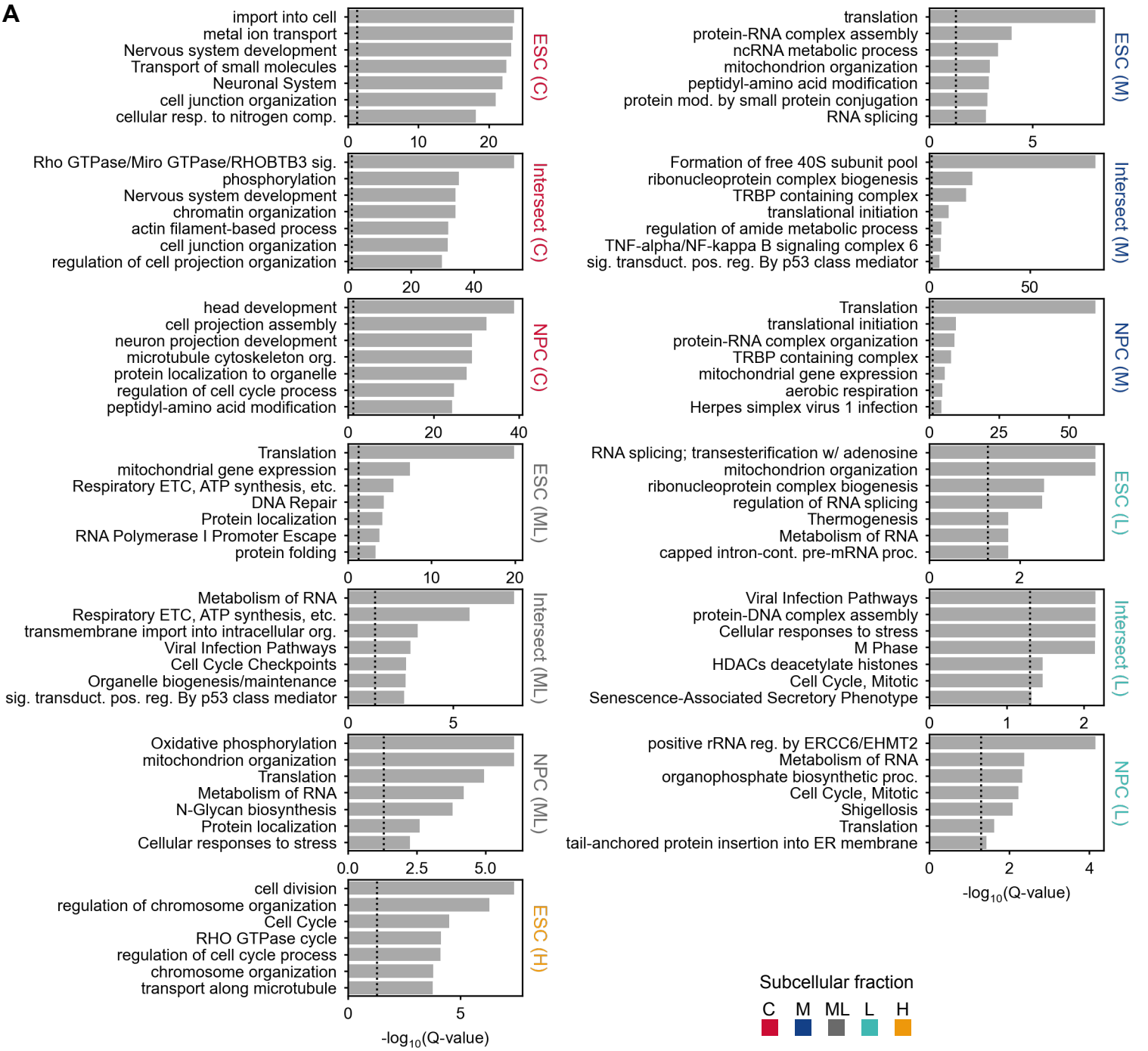


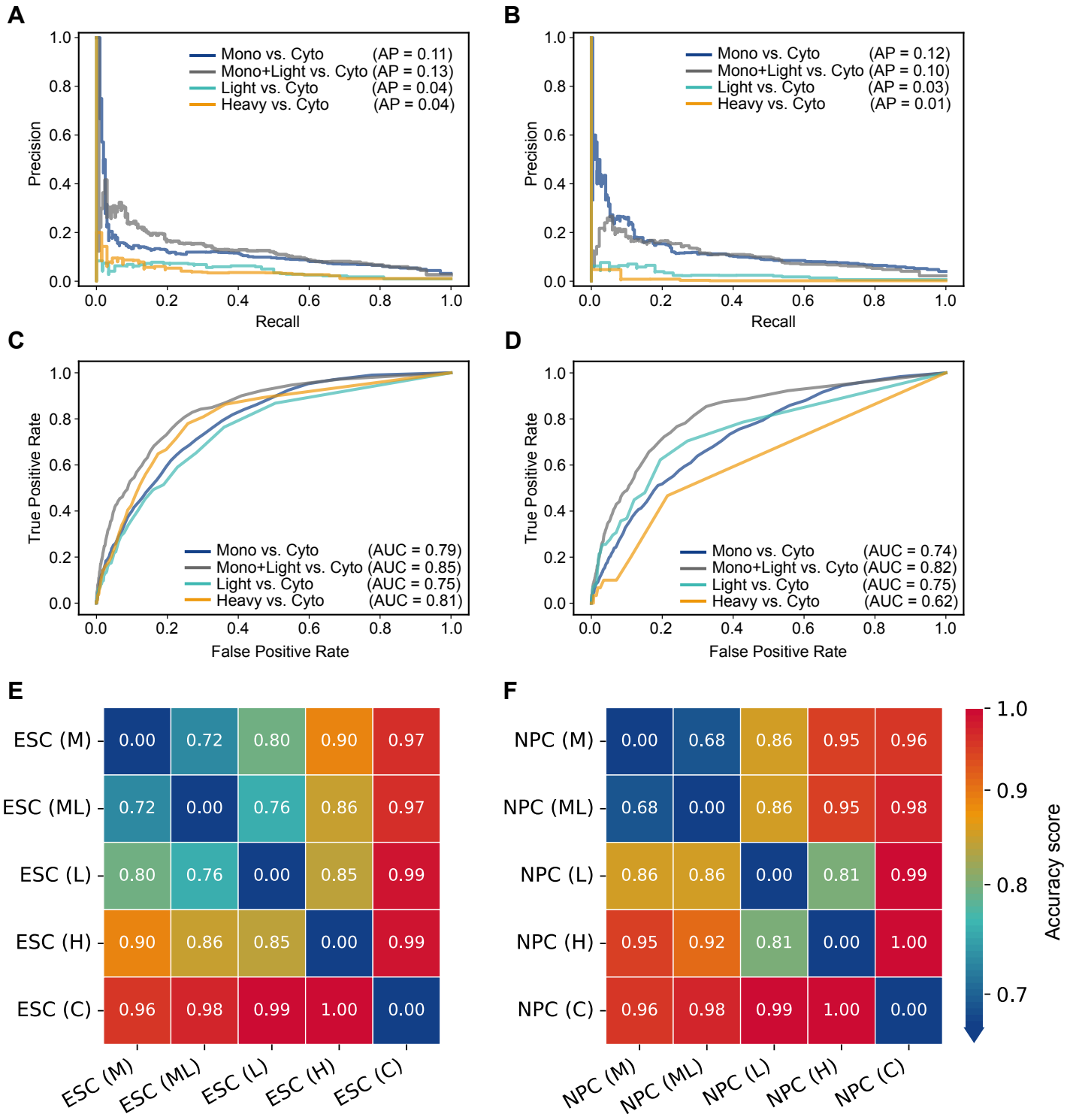
Supplemental Figure 1. Overlap of transcript subpopulations associated with particular subcellular fractions relative to their cognate cytosolic fraction ($log_2FC \geq 1.0$, p-value ≤ 0.05). The fractions include: monosome (M), light polyribosome (L), heavy polyribosome (H) and cytosol (C). Cytosol subpopulations represent those not enriched in any subcellular fractions.



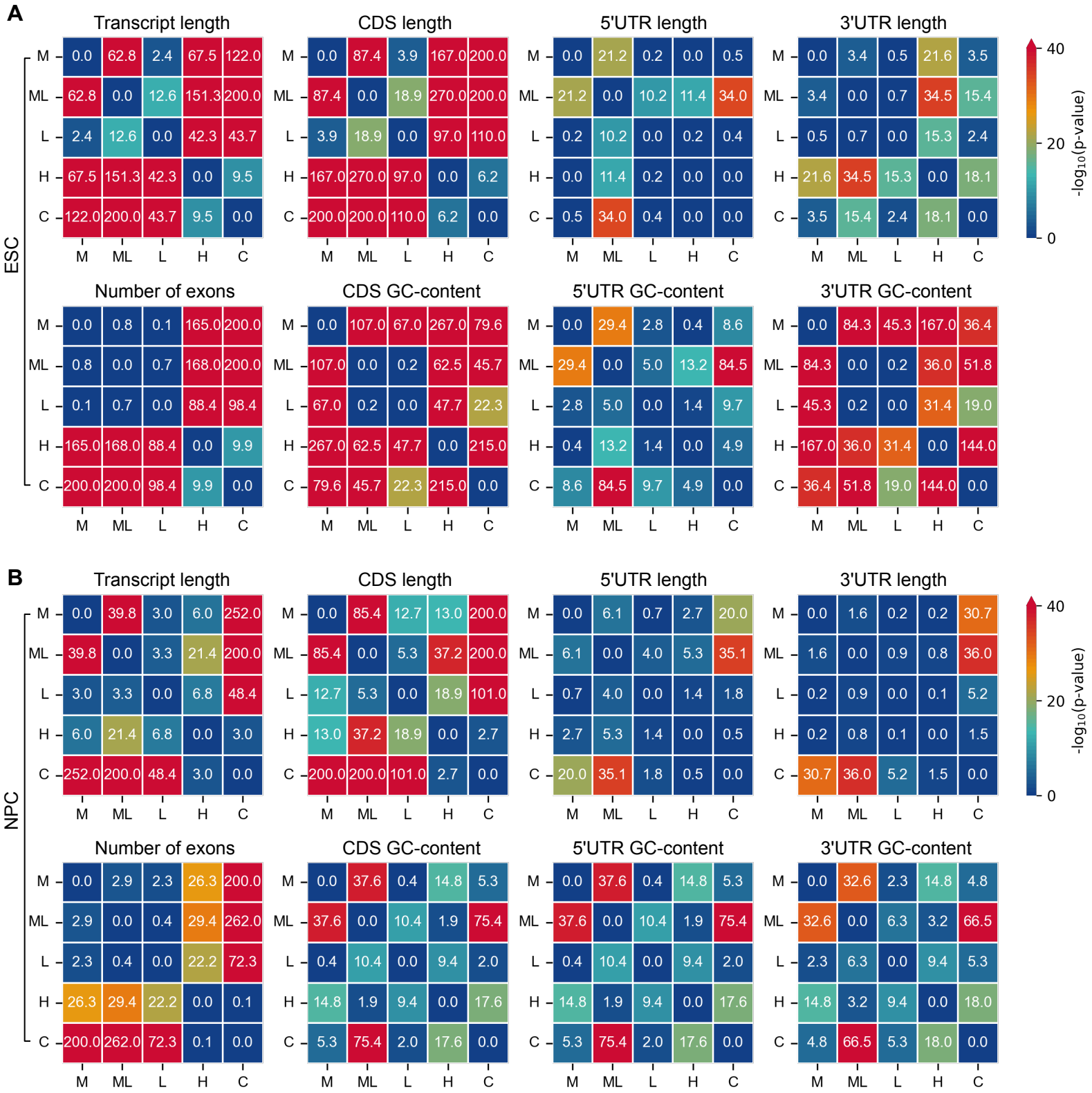
Supplemental Figure 2. Divergent isoform sedimentation observed in 3,085 transcripts in 1,506 genes between ESC and NPC. The volcano plots represent differential isoform sedimentation in terms of gene fraction relative to the cytosol ($|\Delta \text{ Gene fraction}| \geq 0.1$, Q-value ≤ 0.05). The central plot shows changes in gene fraction, with Q-value ≤ 0.05, of isoforms present in both ESC and NPC.



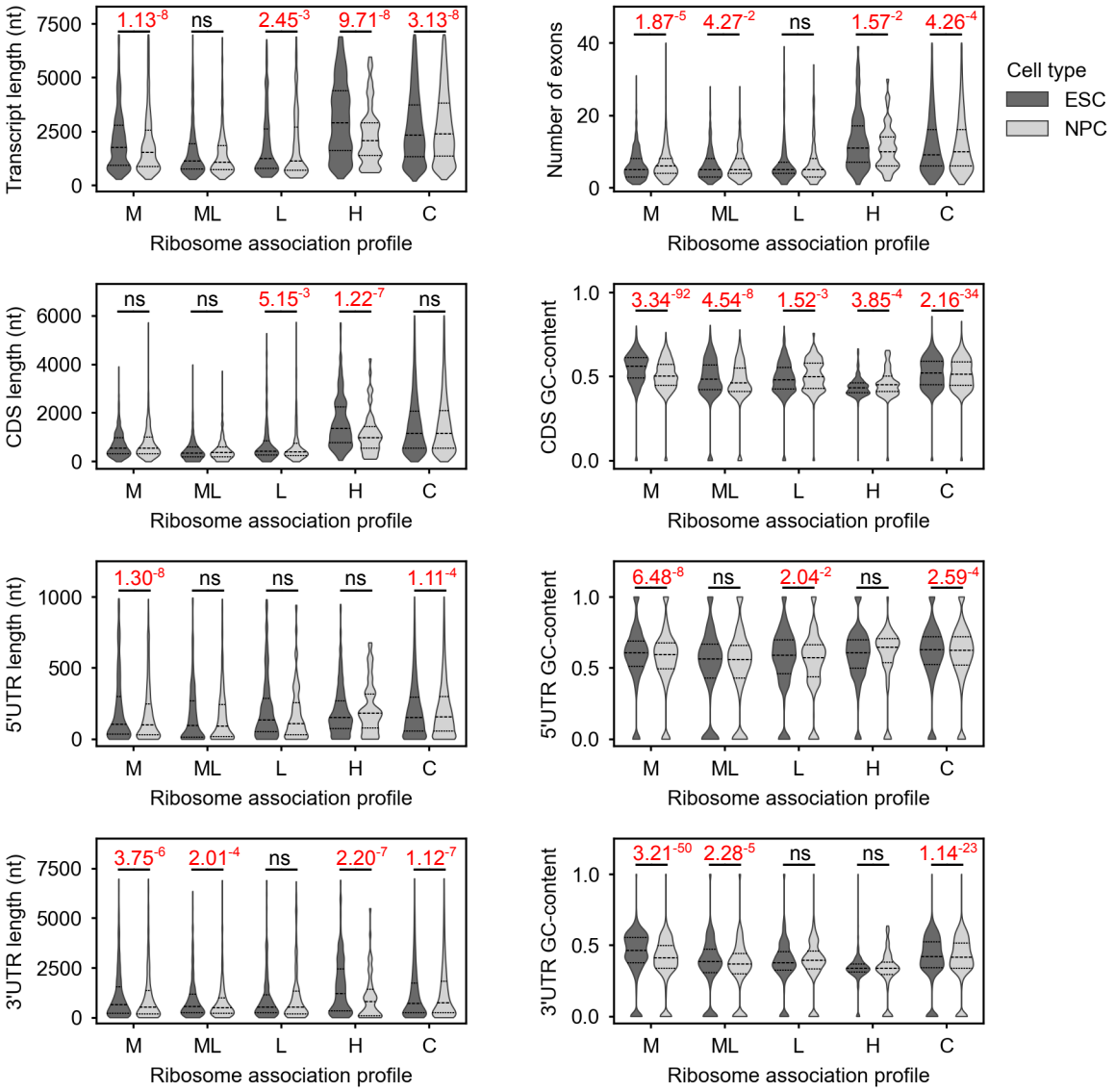
Supplemental Figure 3. Metascape analysis of transcripts enriched in subcellular fractions relative to cytosol. The top 7 terms are shown for each fraction: monosome (M), monosome *and* light polyribosome (ML), light polyribosome (L) and heavy polyribosome (H). Cytosol (C) represents transcripts that aren't enriched in a fraction. Each set of transcripts was analyzed in terms of those that are unique to each cell type (ESC and NPC) and those that are shared by them (Intersect).



Supplemental Figure 4. Assessing binary classification performance of Random Forest Classifiers in distinguishing between transcripts with expression profiles associated with monosome (M), monosome *and* light polyribosome (ML), light polyribosome (L), heavy polyribosome (H) and cytosol (C). (A-B) Precision-Recall of binary classification with average precision (AP) noted for each class versus cytosol in ESC and NPC respectively. (C-D) Receiver Operating Characteristic of binary classification with area under curve (AUC) noted for each class versus cytosol in ESC and NPC respectively. (E-F) Mean accuracy score for each pairwise class comparison in ESC and NPC respectively.



Supplemental Figure 5. Comparison of transcript feature measurements between transcript sets with particular ribosome association profiles. (A-B) Heatmaps of -$\log_{10}$(p-value) derived from Wilcoxon rank-sum tests to assess inter-fraction feature measurement differences. The transcript sets were associated with monosome exclusively (M), monosome *and* light polyribosome (ML), light polyribosome exclusively (L), heavy polyribosome (H) and cytosol (C).



Supplemental Figure 6. Comparison of transcript feature measurements between cognate subcellular fractions across cell types. P-values were derived from Wilcoxon rank-sum tests. Significant p-values (p-value ≤ 0.05) are highlighted in red, while non-significant p-values are presented as "ns".