



Supplementary Figure 22: Analysis of various sample quality metrics in our study's FFPE cohort vs. TCGA samples. A) Median per-sample TIN as density plots. B) Per-transcript coverage scatterplot shows that our study has better coverage for most transcripts. C) Per-transcript median TIN shows that, while most transcripts show concordance in quality, a subset of transcripts have higher quality in TCGA. These transcripts are significantly enriched in those coding for zinc finger genes.