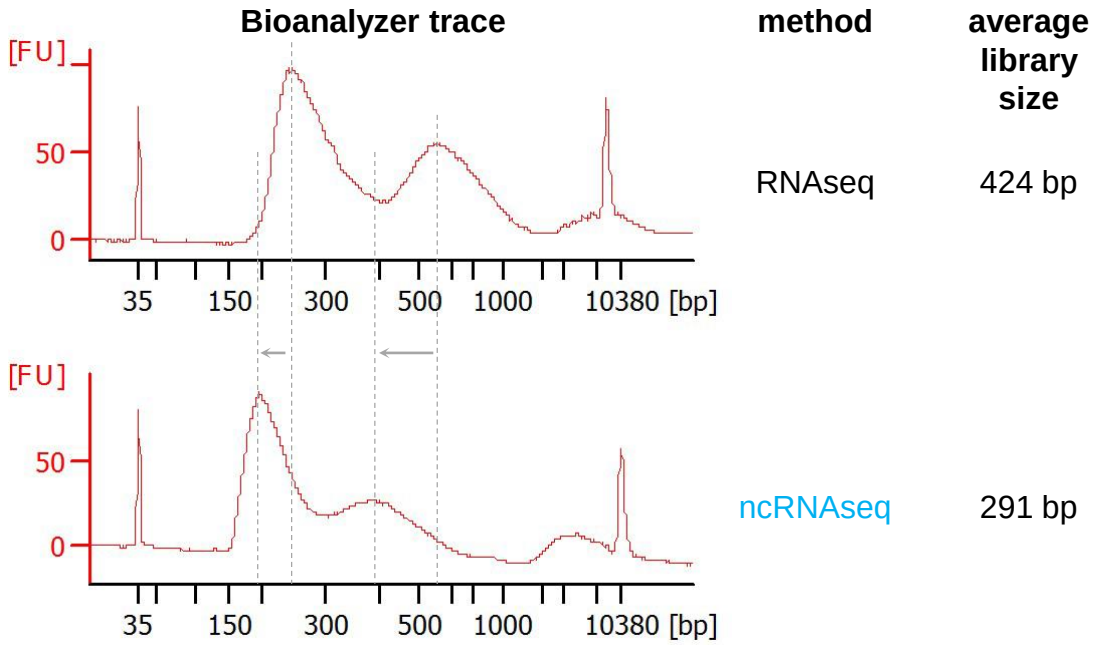

Figure S1: Bioanalyzer traces of sequencing libraries created side-by-side using standard (RNAseq) or modified (ncRNAseq) Illumina TruSeq protocols from the same RNA sample. The grey arrows illustrate the size shift of the two main peaks.

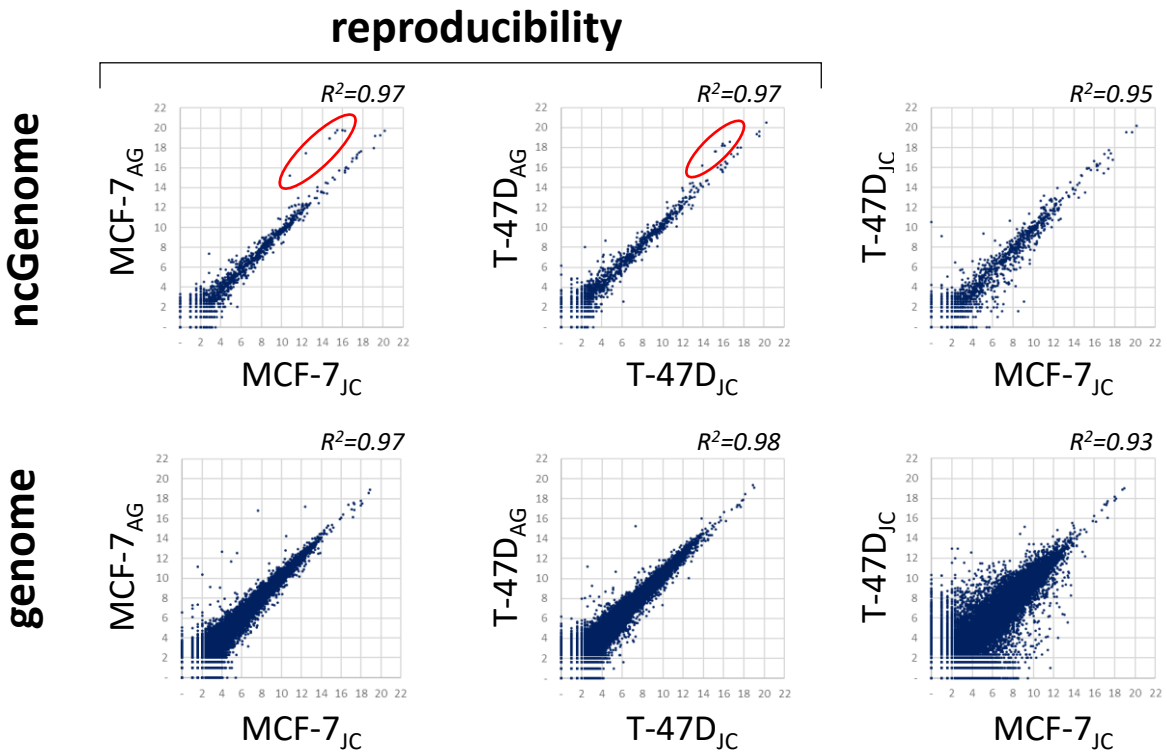

Figure S2: MCF-7 and T-47D breast cancer cell lines were obtained from two different laboratories (AG and JC). For each cell line, the two RNAs were independently extracted, the ncRNAseq libraries were prepared on different days, and the libraries were sequenced to different depths as part of independent sample pools on different flow cells. The correlations of linearly-scaled read counts ($\log_2$) for each cell line are presented on the left. For comparison, a similar correlation plotted for two different cell lines processed concomitantly is shown on the right. Data points for 28S, 18S and mitochondrial rRNA indicative of varying efficiency of rRNA depletion in independent library preparations are circled in red.