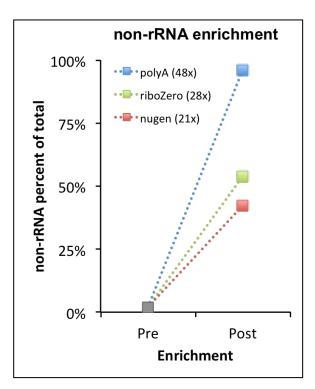
Supplemental Figure 2. Ribosomal RNA depletion leads to > 20-fold enrichment of non-rRNA sequencing coverage. The fraction (%) of non-rRNA compared to total RNA (y-axis) is plotted as a function of enrichment (x-axis). Enrichment of non-rRNA transcripts was calculated as the fold-increase from 2% pretreatment to Y% post-treatment,



assuming that rRNA constitutes 98% of the total cellular RNA. The different experimental treatments are indicated in the legend, with fold enrichment in parentheses.