

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% pre-

treatment 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.

