Enhanced RiboZero™ Technology: Expanded Removal of Ribosomal RNA and Improved RNA-Seq Library Quality

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Introduction
Deep sequencing of cDNA prepared from total RNA (RNA-Seq) or mRNA (mRNA-Seq) has become the method of choice for transcript profiling, discovery of novel transcripts, and identification of alternative splicing events. However, standard deep sequencing of cDNA prepared from total RNA (RNA-Seq) or mRNA (mRNA-Seq) has become the method of choice.

Methods
Advances in Ribo-Zero technology enable removal of both mitochondrial ribosomal RNA (mtrRNA) and cytoplasmic rRNA from total RNA samples that provide excellent removal of rRNA, even from degraded and archived FFPE RNA samples. Recent noncoding RNAs.

Results
Removal of ribosomal RNAs from total RNA. Total RNA from MCF-7 cells was examined using a nanochip on a Bioanalyzer before and after treatment with the Ribo-Zero Gold Kit.

Conclusions
◆ Ribo-Zero kits remove >99% of rRNA from intact and partially degraded total RNA samples.
◆ Ribo-Zero treated RNA samples produce more uniquely mapped RNA-Seq reads compared to poly(A) enrichment.
◆ Ribo-Zero treatment recovers mRNA and ncRNA for whole transcriptome RNA-Seq.
◆ Ribo-Zero treatment maintains the nonribosomal RNA transcript profile of the original RNA sample.

Acknowledgements
We are grateful to Britten Haase (EMBL GeneCore, Heidelberg, Germany) for sequencing data using the Ribo-Zero Gold Kit.