

CRISPRclean™ Stranded Total RNA Prep with rRNA Depletion Portfolio Overview

NGS sensitivity is limited

Next-generation sequencing (NGS) has evolved into a powerful tool for genomic discovery and diagnosis by lowering cost and increasing throughput. Unfortunately, much of that sequencing power is spent decoding biologically uninformative sequences. Legacy targeted sequencing methods use amplification of specific sequences to eliminate background noise. However, these methods commonly introduce amplification bias and require a priori knowledge of which transcripts or variants will be relevant in each study.

CRISPRclean differs from these methods by removing specific abundant and uninformative sequences. By removing undesired sequences and leaving the remaining content unperturbed, sequencing power is refocused on biologically relevant content leading to greater insights and identification of novel transcripts or variants.

CRISPRclean technology

CRISPRclean technology harnesses the specificity of CRISPR-Cas9 to degrade abundant, uninformative sequences. This technology is integrated into a stranded total RNA sequencing library prep protocol after the adapter ligation step. CRISPR-Cas9 complexes are formed with a pool of designed guide RNAs, and the complexes are mixed with the adapter-ligated cDNA library. After the unwanted sequences are cut, they

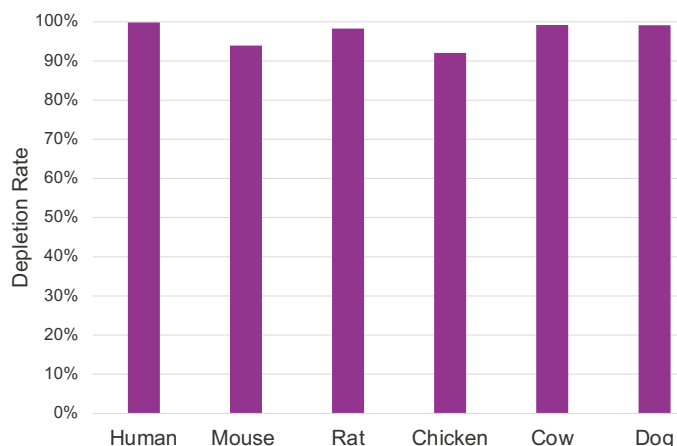


Figure 2. Using CRISPRclean™ Stranded Total RNA Prep with rRNA Depletion (Human, Mouse, Rat), greater than 90% depletion is seen across multiple species types.

cannot be substrates for PCR amplification and subsequent sequencing. The result is a refined NGS library with consistent full-length, uniform transcript coverage, high library complexity with minimum duplication and effective depletion of unwanted RNA sequences.

Application optimized depletion

Biological samples are complex, often containing contaminating nucleic acids from other species.

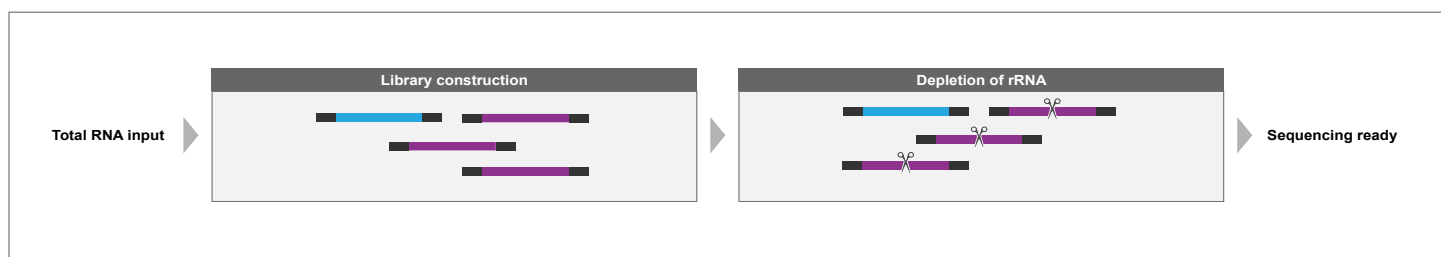


Figure 1: CRISPRclean workflow. CRISPRclean mediated depletion is integrated into a stranded RNA library prep after adapters are ligated on the cDNA libraries. The streamlined workflow takes 7.5-9 hours assay time and ~3 hours hands-on time.

Ribosomal, housekeeping or even common bacterial transcripts are significantly over expressed relative to transcripts of interest. Removal of contaminating or high expressing transcripts will enable better detection of biologically relevant signals. Currently Jumpcode Genomics offers products to enable the following applications:

Whole transcriptome profiling: Removing ribosomal RNA sequences shift sequencing reads to transcripts of biological interest including low expressing transcripts.

Microbiome: Removal of bacterial ribosomal RNA from 212 bacterial species, covering all phyla in a single depletion reaction. Increase the number of bacterial species detectable in a sample by 3-4X.

Infectious disease surveillance: Deplete both human and bacterial rRNA sequences from complex biological samples for greater sequencing coverage of viral and bacterial pathogens, and identifying low expressing human transcripts related to immune response in a single workflow.

CRISPRclean depletion is highly specific, unbiased and accurate

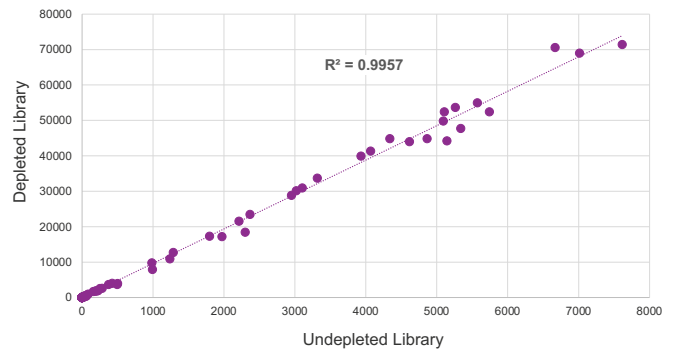


Figure 3. Highly specific CRISPRclean Stranded Total RNA Prep with rRNA Depletion (HMR) produces extremely low library bias. ERCC reads counts were highly correlated, between depleted (y-axis) and undepleted libraries (x-axis), indicating the CRISPRclean rRNA depletion method is highly specific, unbiased, and accurate. This allows for gene expression measurements to be more accurately represented than those that would be obtained from an undepleted sample.

Ordering information

Contact your sales representative to learn more

Catalog	Product name	Reactions
KIT1014	CRISPRclean™ Stranded Total RNA Prep with rRNA Depletion (Human, Mouse, Rat)	24
KIT1016	CRISPRclean™ Plus Stranded Total RNA Prep with rRNA Depletion (Human, Mouse, Rat, Pan Bacteria)	24
KIT1017	CRISPRclean™ Unique Dual Index Adapter Plate for RNA Prep (Set A)	96 UDI

To learn more, visit jumpcodegenomics.com