Universal Prokaryotic RNA-Seq.

Complete metatranscriptomic library preparation solution for bacterial populations

RODUCT SHEET

The Universal Prokaryotic RNA-Seq with AnyDeplete[™] library preparation kit is an easy to use 'add and incubate' system ideal for microbial RNA sequencing studies. This strand-specific RNA-Seq kit provides a complete solution for library construction from pure cultures or mixed populations of bacteria. Integrated AnyDeplete technology enables rRNA depletion from a broad range of prokaryotes, enhancing informative reads and reducing sequencing cost.

Key benefits of the kit

- 1. Broad sample input range from 100 to 500 ng
- 2. Purified RNA from a wide variety of sample types cell lines, environmental samples and microbiome studies
- Customizable transcript depletion using AnyDeplete technology maximizes usable sequencing data
- 4. Compatible with samples with a wide range of GC content



Figure 1: Streamlined workflow for preparation of Illumina compatible libraries for microbiological RNA sequencing studies.

Applications

- Microbiome studies
- Environmental samples
- Whole transcriptome profiling
- Differential gene expression
- RNA sequencing

Without AnyDeplete With custom AnyDeplete



Figure 2: Custom depletion of *P. gingivalis* rRNA. Species-specific probes targeting rRNA were able to decrease the number of rRNA reads from 90% to 10%, significantly increasing the proportion of informative reads.

The Universal Prokaryotic RNA-Seq library preparation kit has been successfully used for preparation of high quality whole transcriptome libraries by researchers globally, with multiple publications in peer-reviewed journals:

 Sequencing libraries prepared using the Universal Prokaryotic RNA-Seq maximized informative reads to identify bacterial transcriptome signatures affected by plant immune activation.

Nobori, T et al. Transcriptome landscape of a bacterial pathogen under plant immunity. *PNAS*, 2018, **115**(13), E3055-E3064. doi: 10.1073/pnas.1800529115

2. A novel RNA-Seq data normalization method was developed using high quality sequencing data obtained from the Universal Prokaryotic RNA-Seq library preparation kit.

Berghoff, BA et al. RNA-sequence data normalization through in silico prediction of reference genes: the bacterial response to DNA damage as case study. *BioData Mining*, 2017, **10**, 30. doi:10.1186/s13040-017-0150-8 3. Tecan's Universal Prokaryotic RNA-Seq and Ovation Ultralow DNA-Seq library preparation kits successfully aided in a comprehensive analysis of the microbial population in diverse unexplored ecosystems.

Fortunato, C et al. Spatially distinct, temporally stable microbial populations mediate biogeochemical cycling at and below the seafloor in hydrothermal vent fluids. *Environmental Microbiology*, 2017, **20**(2), 769-784. doi: 10.1111/1462-2920.14011

4. Customized AnyDeplete probes allowed efficient rRNA depletion for termite-bacterial gut symbiosis study.

Peterson, BF & Scharf, ME. Metatranscriptome analysis reveals bacterial symbiont contributions to lower termite physiology and potential immune functions. *BMC Genomics*, 2016, **17**(1), 772. doi:10.1186/s12864-016-3126-z

Ordering information

Product Name	Part no.	No. of reactions
Universal Prokaryotic RNA-Seq, Prokaryotic AnyDeplete	0363	32

For Research Use Only. Not for use in diagnostic procedures.

www.tecan.com

Australia +61 3 9647 4100 Austria +43 62 46 89 330 Belgium +32 15 42 13 19 China +86 21 220 63 206 France +33 4 72 76 04 80 Germany +49 79 51 94 170 Italy +39 02 92 44 790 Japan +81 44 556 73 11 Netherlands +31 18 34 48 17 4 Nordic +46 8 750 39 40 Singapore +65 644 41 886 Spain +34 93 595 25 31 Switzerland +41 44 922 89 22 UK +44 118 9300 300 USA +1 919 361 5200 Other countries +41 44 922 81 11

Tecan is a registered trademark and AnyDeplete is a trademark of Tecan Group Ltd., Männedorf, Switzerland or of Tecan Genomics, Inc., Redwood City, USA.

© 2019 Tecan Genomics, Inc., all rights reserved. For disclaimer and trademarks please visit www.tecan.com

