

Universal Sequencing Technology Corp. Launches TELL-Meta Linked Read Software Pipeline for Metagenomics Applications

TELL-Meta software pipeline will revolutionize metagenomics research with Linked read for new species discovery, high quality metagenomic assembly and analysis.

CARLSBAD, CA, UNITED STATES,
October 1, 2024 /EINPresswire.com/ --
[Universal Sequencing Technology](#)
(UST), a global leader in Next
Generation DNA Sequencing (NGS)
innovations, announced today the
launch of [TELL-Meta software pipeline](#)
for metagenomics applications using
TELL-Seq linked read technology. This
groundbreaking technology is set to
revolutionize metagenomics research
with an accurate and cost-effective tool
for new species discovery and high
quality metagenomic assembly and
analysis.

UST's TELL-Seq linked read library
technology enables mainstream short
read NGS platforms, such as Illumina
sequencers, to produce super long
read results without using a long read
sequencer. The process is simple, fast
and cost effective. An Illumina
sequencing ready library can be

prepared in a PCR tube in 3 hours. It requires ultra low DNA input, 3-5ng for human genome, 0.1-0.5ng for microbial isolate and <0.1ng for targeted panels. The TELL-Meta software pipeline together with TELL-Seq linked read library prep kits is the ideal tool for metagenomic analysis

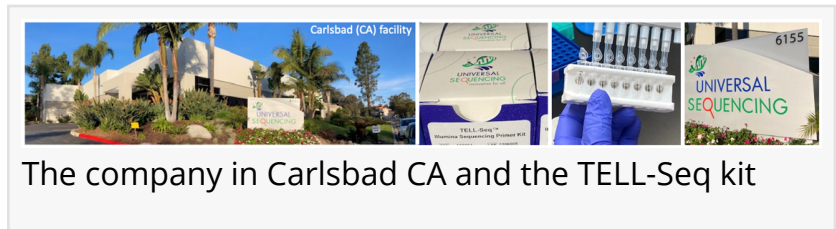


UST Logo

UNIVERSAL
SEQUENCING
innovation for all

Slogan

with accurate species identification, taxonomic classification and abundance estimation, performing exceptionally well for microbiome discovery. Recent publications (ref. 1-3) show that linked read method



outperforms both short read and long read methods in terms of producing more high-quality MAGs (metagenome-assembled genomes). UST's TELL-Seq is currently the best and only linked read technology commercially available in most regions of the world.

UST's TELL-Seq linked read library preparation kits include 8, 24, 96 and 384 sample indices, allowing users to pool different number of samples per lane (up to 3072 samples for 8 lanes) to sequence on low-cost high-throughput NGS platforms, such as Illumina NextSeq 2000, NovaSeq 6000 and NovaSeq X Plus, Element Bio Aviti and MGI DNBSEQ-G400, T7 and T20. This makes TELL-Seq a powerful tool for large scale metagenomics/microbiome research projects and applications.

UST's TELL-Meta software pipeline is available for download on UST's website <https://universalsequencing.com> along with a user guide and an application note to help researchers navigate and utilize the full potential of this innovative technology. UST's TELL-Seq linked read library preparation kits are available for order on the UST website as well as on the websites of [TELL-Seq distributors around the world](#) (see <https://universalsequencing.com/pages/distributors>).

ABOUT UNIVERSAL SEQUENCING TECHNOLOGY CORPORATION

Universal Sequencing Technology Corporation (<https://universalsequencing.com>), a Carlsbad (CA) based NGS biotechnology company, was established by a group of NGS veterans. UST is dedicated to the development and commercialization of the most advanced DNA sequencing technologies and has filed more than 25 PCT patent applications covering linked read library preparation, single-cell sequencing, and groundbreaking 5th generation nanosequencer technologies. UST is poised to lead the next wave of DNA sequencing innovations.

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Ru Zheng

Universal Sequencing Technology

+1 6173048425

[email us here](#)

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