UNIVERSAL SEQUENCING
innovation for all

UST TELL-Seq™ Library Prep Kit

Long-Read Sequencing Made Simple.

Generate a sequencing library

in just **3** hours

TELL-Seq™

Transposase **E**nzyme **L**inked **L**ong-read Sequencing

Transposase Enzyme Linked Long-read Sequencing is a simple and scalable NGS library technology that generates barcoded linked reads for genome scale sequencing applications. The whole barcoding procedure can be carried out in a PCR tube without the need for expensive instrumentation

TELL-Seq Library Prep kit

- One tube process, simple, fast and economic.
- Enable a short-read sequencer to produce super long-read results, average 20kb to 200kb, or longer
- Require ultra low DNA input, 3-5ng for human genome, 0.1-0.5ng for microbial genomes and target sequencing panels

TELL-Seq library **+** Illumina short-read

TELL-Seq applications:

- ✓ De novo Sequencing (small and large genomes）
- ✓ Microbiology and metagenomics
- ✓ Whole human genome phasing
- ✓ Whole exome and target phasing
- ✓ Structure variation detection

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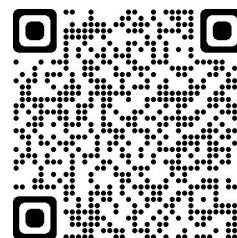
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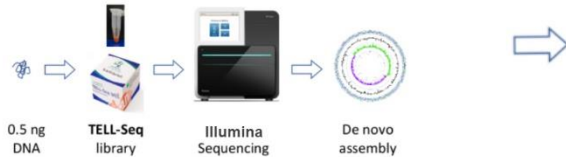we offer a full product guarantee

outstanding technical support

Microbial de novo Assembly

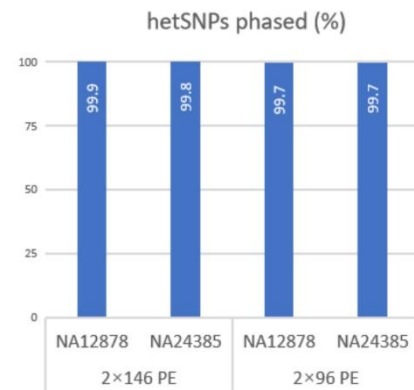## Turn 0.5 ng Microbial DNA Into an Accurate Genome

E. coli MG1655	TELL-seq
Genome fraction (%)	99.92
Largest alignment	4,630,233
Total aligned length	4,684,057
NA50	4,630,233
# misassemblies	0
# mismatches per 100 kbp	3.15
# indels per 100 kbp	0.34
# N's per 100 kbp	0

Human Genome Phasing Application

Method	TELL-Seq			
	NA12878		NA24385	
Coverage Depth (Unique)	38×	25×	46×	28×
Longest Phased Block	67.5 Mb	39.9 Mb	59.2 Mb	35.0Mb
N50 Phased Block	14.4 Mb	8.0 Mb	13.4 Mb	9.4 Mb
Switch Error Rate	0.04%	0.05%	0.08%	0.12%

hetSNPs phased (%)

	NA12878	NA24385	NA12878	NA24385
	99.9	99.8	99.7	99.7
	2×146 PE		2×96 PE	

Metagenomics

Metagenomic de novo Assembly and Taxonomic Analysis & Quantification

Taxonomy:
Species Name Abundance
Staphylococcus epidermis 17.9%
Streptococcus mutans 13.2%
Escherichia coli 7.1%
Rhodobacter sphaeroides 3.6%
Bacillus cereus 1.4%
... ...

① **TELL-Seq Library Prep kit** developed by UST to build linked-read libraries that CAPTURE long-range information in short-reads

② **Tell-Link for *de novo* genome assembly and Tell-TaxContigs software** for taxonomic classifications and abundance estimation, both developed by UST