TELL-Seq™: Ultra-low input, single tube & highly scalable linked read library technology

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Transposase Enzyme Linked Long-read Sequencing (TELL-Seq™) is a simple and scalable NGS library technology to generate barcode linked-reads for genome scale haplotype phasing and de novo sequencing. In a PCR tube, under a standard NGS laboratory setting and without the need for any expensive protocol-specific instrument, TELL-Seq Whole Genome Sequencing (WGS) Library Prep Kit will generate an Illumina sequencing library in 3 hours from as low as 0.1 ng DNA input. Multiple samples can be easily processed in parallel as needed. The library protocol can be adjusted and used for various sized genomes ranging from bacteria to human. The TELL-Seq library will replace both fragment library and mate-pair library altogether and become a new standard library method for WGS.

How TELL-Seq Works?

**Transposase Enzyme Linked Long-Read Sequencing**

The TELL-Seq WGS Library Workflow is Simple

- **Barcode**
- **Wash**
- **Amplify**
- **Quantify**
- **Sequencing**

Total Time 3 hrs

**The TELL-Seq Library Structure**

Scalable for Small & Large Genomes

- **E. coli**: ~0.2 M barcodes
- **C. elegans**: ~10 M barcodes
- **D. melanogaster**: ~1.5 M barcodes
- **H. sapiens**: ~10 M barcodes
- **S. cerevisiae**: ~10⁶ barcodes
- **A. thaliana**: ~10⁷ barcodes

**TELL-Seq Advantages**

- Low cost, no need of extra equipment
- Easy and fast process
- Broader applications
- Highly scalable for high throughput production / automation