

Generate a sequencing library



in just **3** hours

# TELL-Seq™

Transposase Enzyme Linked Long-read Sequencing

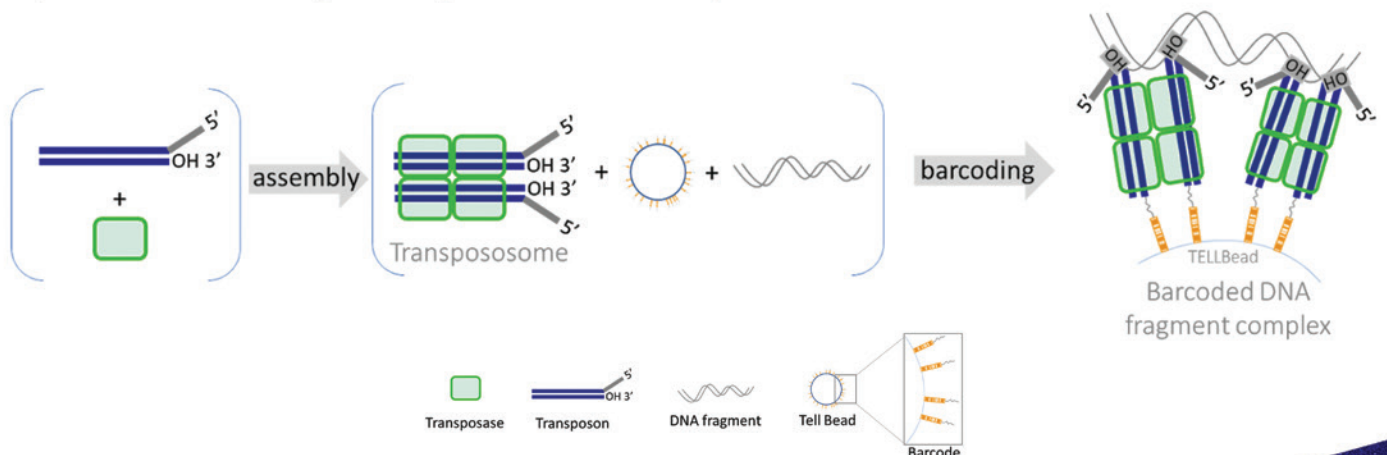
Transposase Enzyme Linked Long-read Sequencing is a simple and scalable NGS library technology that generates barcoded linked reads for genome scale sequencing applications. The whole barcoding procedure can be carried out in a PCR tube without the need for expensive instrumentation.

## The New Standard Library Method for WGS

The TELL-Seq™ Whole Genome Sequencing (WGS) Library Prep Kit generates a sequencing library in just 3 hours. The protocol can be easily adjusted based on the genome size to be analyzed. TELL-Seq™ WGS Library Prep Kit allows for *de novo* assembly of a wide range of genomes.

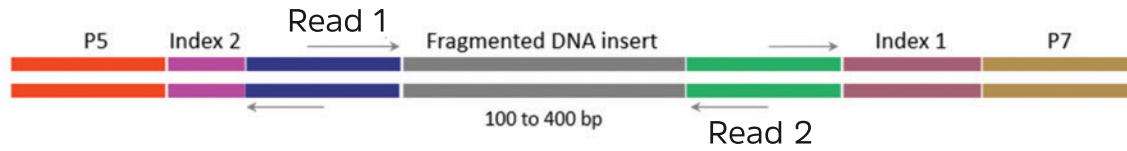
## How it works

TELL-Seq™ uses transposase tagging in combination with magnetic beads to capture and barcode long DNA fragments simultaneously.

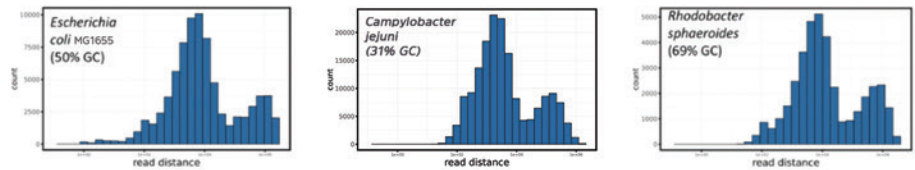


# TELL-Seq™ Library Structure

The TELL-Seq™ library is simple and compatible with all Illumina sequencers.



## TELL-Seq™ Results for Three Bacteria with Different GC Content



|                        | <i>E. Coli</i> MG1655 | <i>C. jejuni</i> | <i>R. sphaeroides</i> |
|------------------------|-----------------------|------------------|-----------------------|
| Total length (bp)      | 4,725,322             | 1,674,730        | 5,173,415             |
| Reference length (bp)  | 4,641,652             | 1,641,464        | 4,602,977             |
| Largest contig (bp)    | 4,640,256             | 1,652,047        | 3,962,838             |
| N50 Contig length (bp) | 4,640,256             | 1,652,047        | 3,962,838             |
| Misassemblies          | 0                     | 0                | 52                    |
| Mismatches per 100 kbp | 5.4                   | 10.9             | 17.7                  |
| Indels per 100 kbp     | 0.4                   | 4.0              | 3.5                   |
| Genome fraction (%)    | 99.9                  | 99.9             | 97.8                  |

TELL-Seq™ has successfully been used in the de novo sequencing of microbial samples, as well as large genome phasing and structural variant mapping (not shown here).



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