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

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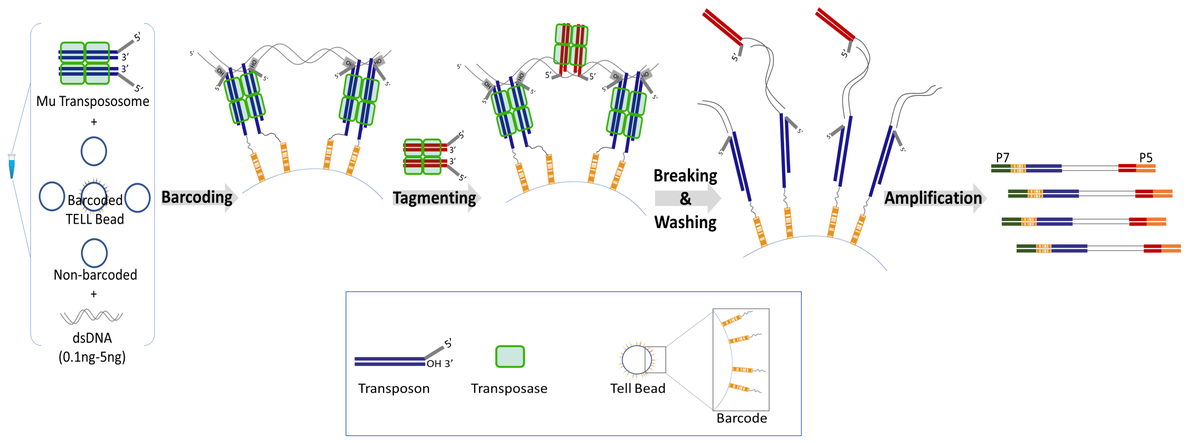
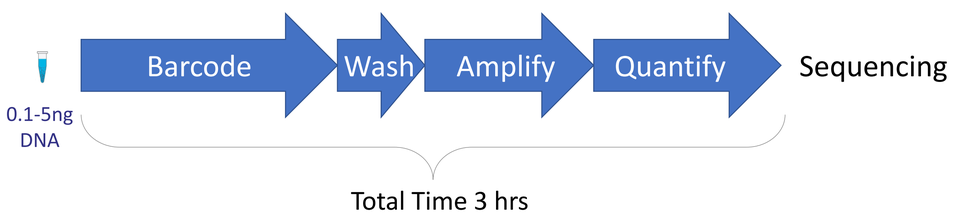
Transposase Enzyme Linked Long-read Sequencing (TELL-Seq™) is a simple and scalable NGS library technology to generate barcode linked-reads for genome scale haplotype phasing and *de novo* sequencing. In a PCR tube, under a standard NGS laboratory setting and without the need for any expensive protocol-specific instrument, TELL-Seq Whole Genome Sequencing (WGS) Library Prep Kit will generate an Illumina sequencing library in 3 hours from as low as 0.1ng 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?

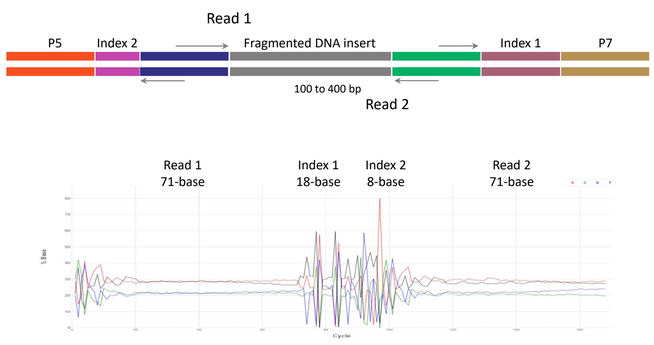
Transposase Enzyme Linked Long-Read Sequencing



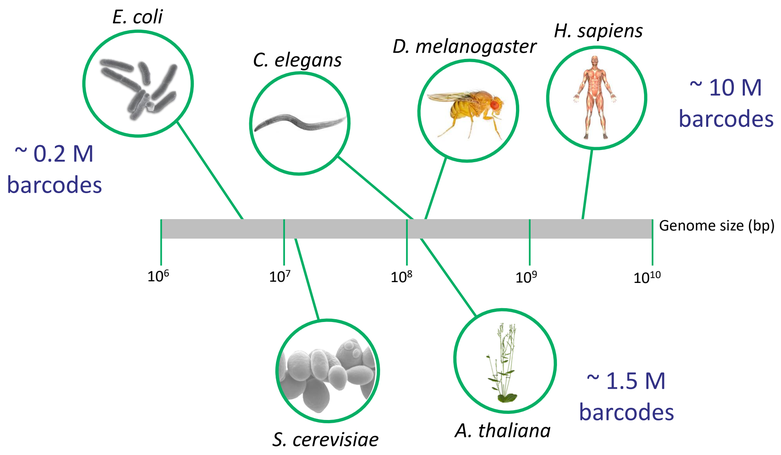
The TELL-Seq WGS Library Workflow is Simple



TELL-Seq Library Structure



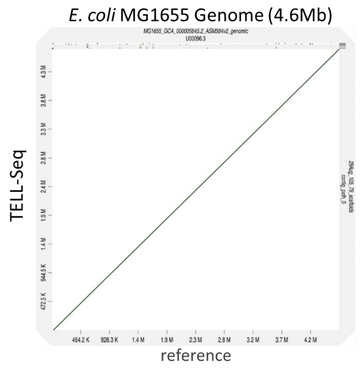
Scalable for Small & Large Genomes



Genome Assembly

TuringAssembler

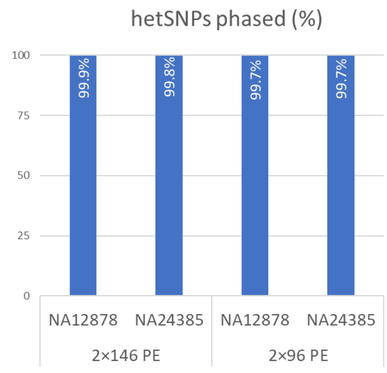
E. coli MG1655 Genome (4.6Mb)



QUAST results	*E. coli* MG1655	*C. jejuni*	*R. sphaeroides*
# contigs (>= 1000 bp)	25	11	213
# contigs (>= 5000 bp)	3	1	9
Total length (>= 1000 bp)	4,725,322	1,674,730	4,951,045
Reference length	4,641,652	1,641,464	4,602,977
Largest contig	4,640,256	1,652,047	3,839,617
NG50	4,640,256	1,652,047	3,839,617
Largest alignment	4,637,716	1,648,335	2,928,864
NGA50	4,637,716	1,648,335	2,928,864
Genome fraction (%)	99.9	99.99	99.4
# misassemblies	0	0	15
# mismatches per 100 kbp	5.4	10.9	10.3
# indels per 100 kbp	0.4	4.0	1.3
# N's per 100 kbp	0.0	0.0	458.8
Reference GC (%)	50.8	30.6	68.8

Whole Genome Phasing

	2×146 PE		2×96 PE	
	NA12878	NA24385	NA12878	NA24385
Coverage Depth (Unique)	38×	46×	25×	28×
Longest Phased Block	67.5 Mb	59.2 Mb	39.9 Mb	35.0Mb
N50 Phased Block	14.4 Mb	13.4 Mb	8.0 Mb	9.4 Mb
Switch Error Rate	0.04%	0.08%	0.05%	0.12%

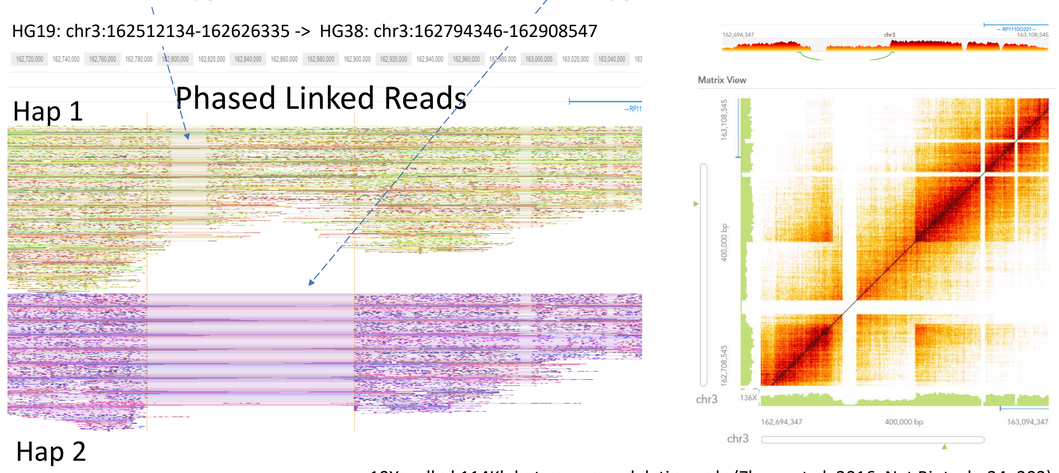


Structural Variation

Highly Sensitive Structural Variation Detection

A 19Kb homozygous deletion in a 114Kb heterozygous deletion

HG19: chr3:162512134-162626335 -> HG38: chr3:162794346-162908547



10X: called 114Kb heterozygous deletion only (Zheng et al. 2016. Nat Biotech. 34: 303)
stLFR: called 19Kb homozygous deletion only (Wang et al. 2019. Genome Res. 29: 798)

TELL-Seq Advantages

Technical Indices	TELL-Seq™
Instrument cost	Zero
Library prep cost	Low
Input DNA	0.1 ng – 5 ng
Processing time	3 hours
Barcode capacity	>2 billion
Genome size	≥ 1Mb

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

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