

TELL-Seq™ Linked Read Library Prep Kit

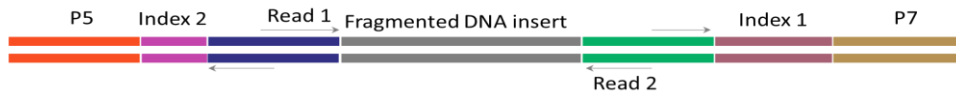
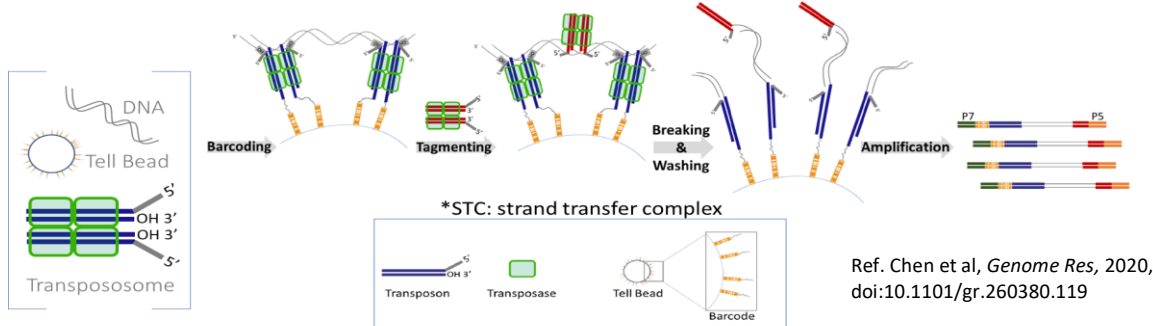
Transposase Enzyme Linked Long-Read Sequencing



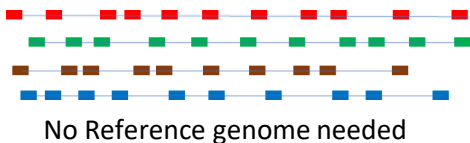
Applications:

- ✓ Microbial *de novo* assembly
- ✓ Microbiome discovery & analysis
- ✓ Animal/plant/insect *de novo* sequencing
- ✓ *De novo* sequencing scaffolding
- ✓ Whole human genome phasing
- ✓ Whole exome and target phasing
- ✓ Structure variation detection

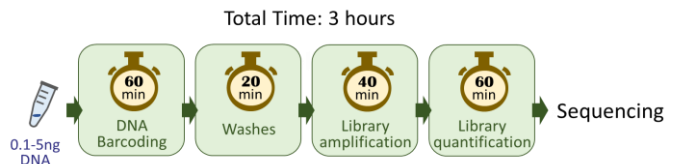
How Does TELL-Seq Linked Read Works?



Linked Read Assembly



Library Prep Workflow



Advantages of TELL-Seq:

- ✓ Enable short read NGS platforms to produce super long read results (20kb to 200kb or longer).
- ✓ A sequencing ready library can be prepared in a PCR tube in 3 hours, simple, fast and cost effective.
- ✓ Ultra low DNA input, 3-5ng for human genome and 0.1-0.5ng for microbial genome & target panels.
- ✓ 8, 24, 96, 384 sample indices available for pooling samples to be sequenced on high throughput sequencing platforms, such as Illumina NextSeq 2000, NovaSeq 6000, NovaSeq X and Element Aviti.

No bandwidth for library prep? No problem!
We provide services from HMW DNA extraction, library preparation, to sequencing and data analysis.



Microbial and Metagenomics Applications

Microbial de novo Assembly

Turn 0.5 ng Microbial DNA
Into an Accurate Genome



Microbial De Novo Assembly
Validated by Illumina

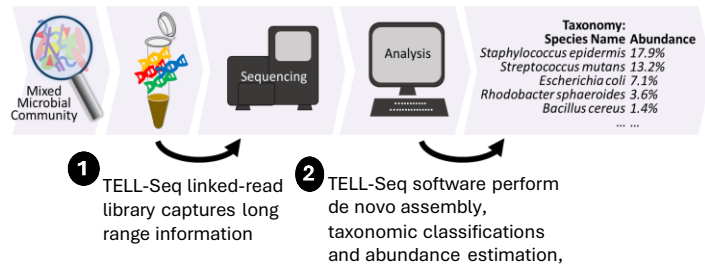
0.5ng DNA

	<i>C. perfringens</i>	<i>C. jejuni</i>	<i>B. cereus</i>	<i>B. subtilis</i>	<i>E. coli MG1655</i>	<i>R. palustris</i>
Genome size	~3.3 Mb	~1.6 Mb	~5.4 Mb	~4.3 Mb	~4.6 Mb	~5.3 Mb
GC content	28%	31%	35%	43%	51%	65%
Chromosome no./ plasmids no.	1/0	1/0	1/1	1/1	1/0	1/0
TELL-Read analysis metrics						
Read pairs	1,650,000	800,000	3,040,000	2,230,000	2,410,000	2,720,000
Mean coverage	100x	99x	100x	100x	100x	100x
Mean SLF size (bp)	25,416	24,903	15,219	23,533	21,226	20,761
Median SLF size (bp)	18,761	17,680	10,239	17,542	15,653	14,713
TELL-Link analysis metrics						
No. of contigs (≥ 10 kb)	1	1	2	2	1	1
Contig N50	3,237,188	1,615,713	5,315,730	4,184,919	4,618,375	5,242,132
Misassemblies	2	1	2	0	0	3
Genome fraction	99.11%	99.51%	99.03%	99.44%	97.71%	99.96%

Ref. Application Note on Microbial de novo assembly with linked-read technology on Illumina website

Microbiome Discovery & Analysis

Metagenomic de novo Assembly,
Taxonomic and Abundance Analysis



Validated with Mock 20

No.	ATCC Mock 20 Staggered Mix	Abundance		MIMAG quality	Completeness	Total length	N50
		Expected	Measured				
1	<i>Staphylococcus epidermidis</i> _ATCC_12228	18%	18.41%	NC	99.81%	2,463,688	2,178,314
2	<i>Streptococcus mutans</i> _ATCC_700610	18%	20.65%	NC	100%	1,963,101	1,522,430
3	<i>Escherichia coli</i> _ATCC_700926	18%	18.16%	HQ	99.97%	4,558,926	2,294,466
4	<i>Porphyromonas gingivalis</i> _ATCC_33277	18%	19.57%	HQ	99.92%	2,238,185	1,320,895
5	<i>Cereibacter sphaeroides</i> _ATCC_17029	18%	9.27%	NC	95.15%	3,122,569	3,110,016
6	<i>Staphylococcus aureus</i> _ATCC_BAA-1556	1.80%	1.62%	NC	98.74%	2,839,905	519,057
7	<i>Streptococcus agalactiae</i> _ATCC_BAA-611	1.80%	2.36%	NC	97.87%	2,053,975	554,467
8	<i>Bacillus pacificus</i> _ATCC_10987	1.80%	2.10%	NC	96.14%	4,992,077	1,039,542
9	<i>Clostridium beijerinckii</i> _ATCC_35702	1.80%	3.47%	NC	99.19%	5,932,616	151,545
10	<i>Pseudomonas aeruginosa</i> _ATCC_9027	1.80%	1.12%	NC	98.70%	6,150,350	4,060,264
11	<i>Lactobacillus gasseri</i> _ATCC_33323	0.18%	0.23%	MQ	55.71%	971,711	997
12	<i>Acinetobacter baumannii</i> _ATCC_17978	0.18%	0.23%	MQ	73.77%	1,870,326	954
13	<i>Helicobacter pylori</i> _ATCC_700392	0.18%	0.23%	LQ	39.86%	327,741	937
14	<i>Neisseria meningitidis</i> _ATCC_BAA-335	0.18%	0.23%	LQ	39.80%	551,692	877
15	<i>Cutibacterium acnes</i> _ATCC_11828	0.18%	0.19%	LQ	35.25%	563,852	736
16	<i>Enterococcus faecalis</i> _ATCC_47077	0.02%	N/A	UC	N/A	N/A	N/A
17	<i>Bifidobacterium adolescentis</i> _ATCC_15703	0.02%	N/A	UC	N/A	N/A	N/A
18	<i>Phocaeicola vulgatus</i> _ATCC_8482	0.02%	N/A	UC	N/A	N/A	N/A
19	<i>Deinococcus radiodurans</i> _ATCC_BAA-816	0.02%	N/A	UC	N/A	N/A	N/A
20	<i>Actinomyces odontolytica</i> _ATCC_17982	0.02%	N/A	UC	N/A	N/A	N/A

Note: Species with >0.18% abundance can be resolved by 98M reads; Higher sequencing depth needed for species with 0.02% abundance.



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