

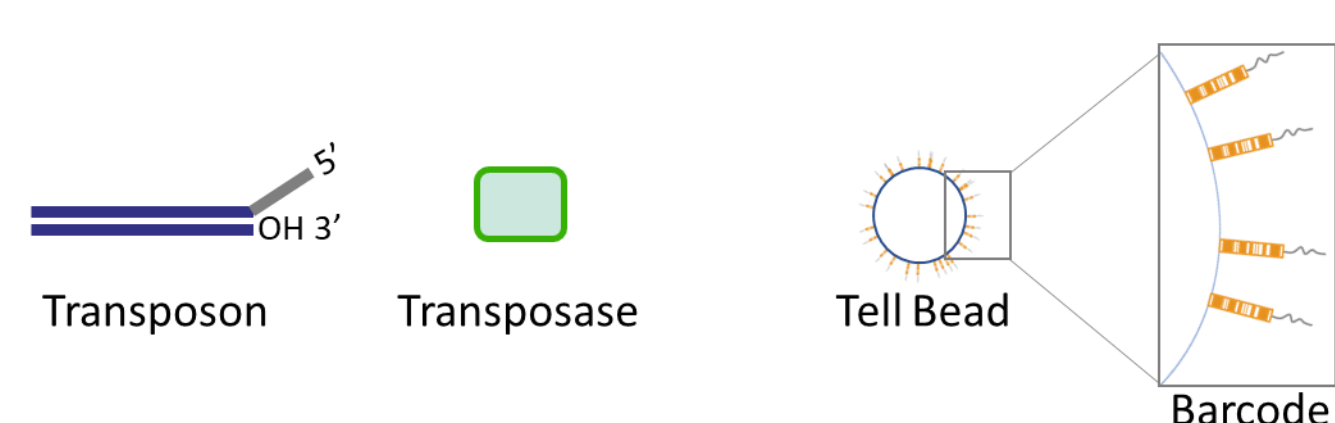
TELL-Seq™: Low input, single tube & highly scalable linked read library technology

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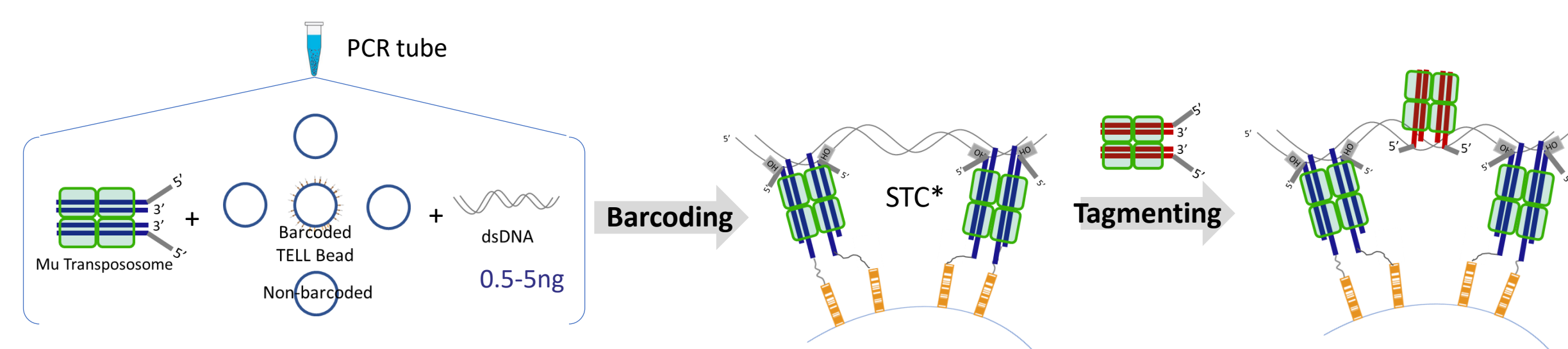


Transposase Enzyme Linked Long-read Sequencing (TELL-Seq) is a simple and scalable NGS library technology to generate barcode linked-reads for genome scale haplotype phasing and *de novo* sequencing. In a PCR tube, under a standard NGS laboratory setting and without the need for any expensive protocol-specific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

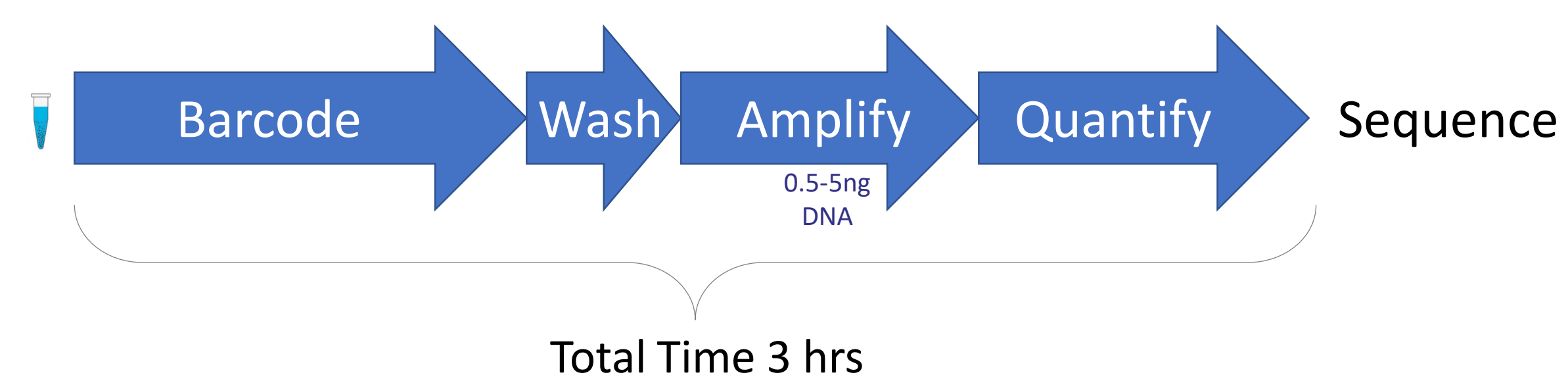
How TELL-Seq Works?



Transposase Enzyme Linked Long-Read Sequencing



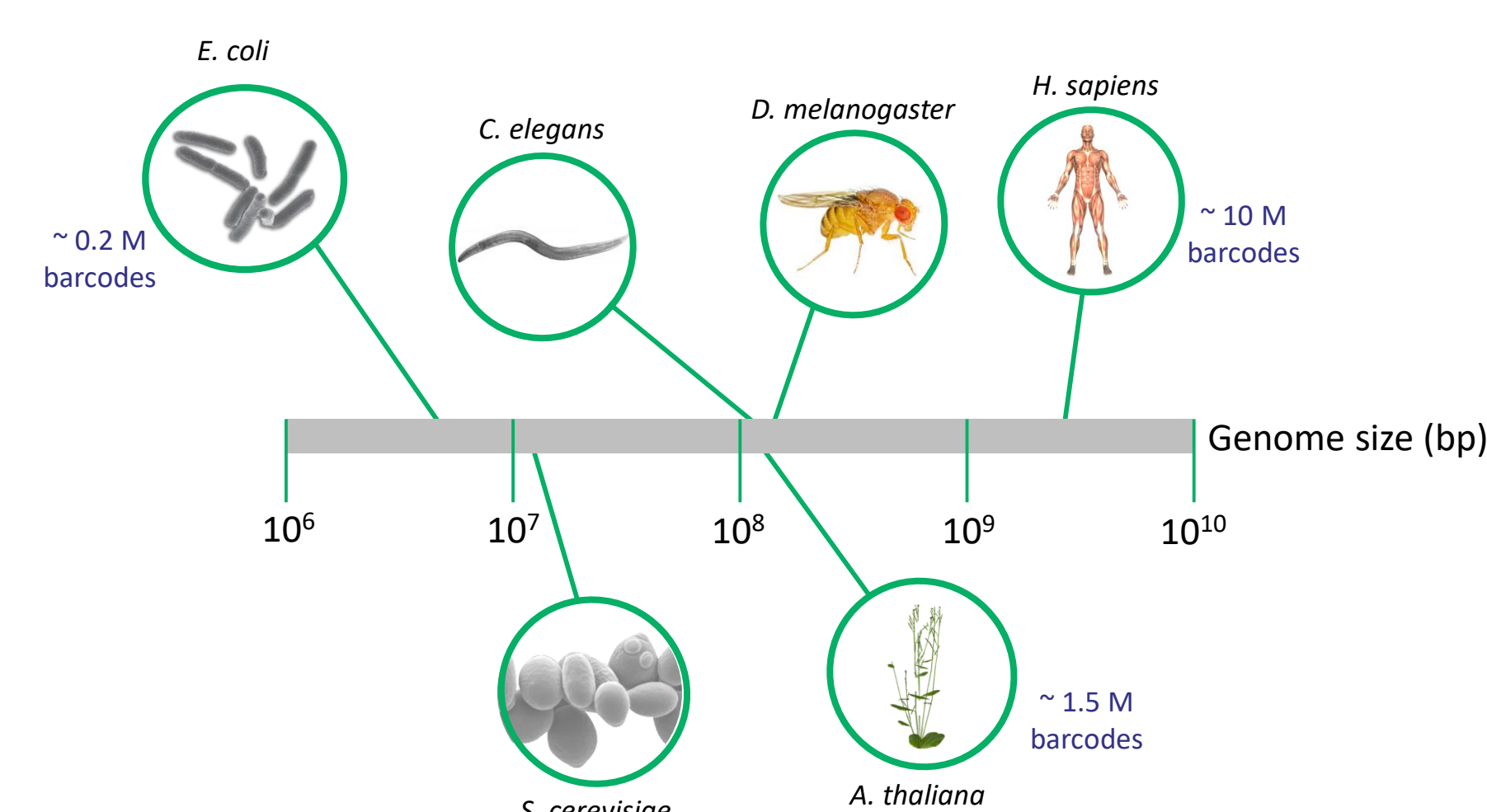
The TELL-Seq WGS Library Workflow is Simple



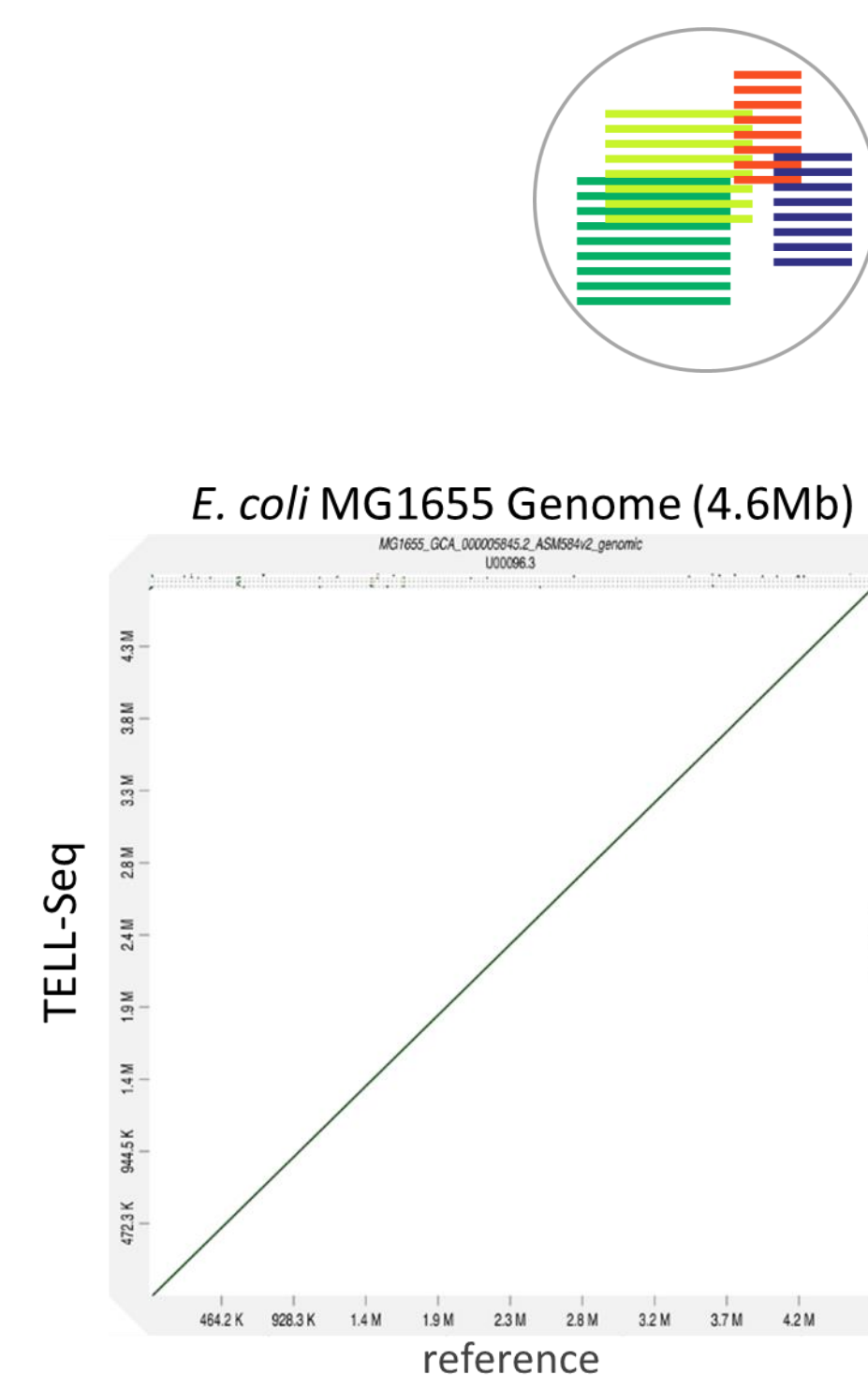
TELL-Seq Library Structure



Scalable for Small & Large Genomes



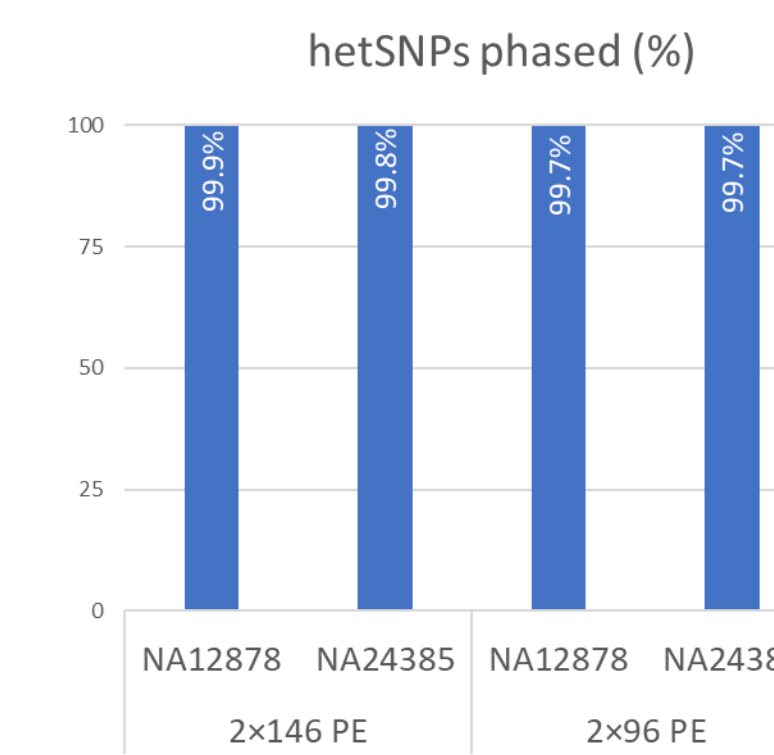
Genome Assembly



QUAST results	<i>E. coli</i> MG1655	<i>C. jejuni</i>	<i>R. sphaeroides</i>
# contigs (>= 1000 bp)	25	11	229
# contigs (>= 5000 bp)	3	1	7
Total length (>= 1000 bp)	4,725,322	1,674,730	5,173,415
Reference length	4,641,652	1,641,464	4,602,977
Largest contig	4,640,256	1,652,047	3,962,838
NG50	4,640,256	1,652,047	3,962,838
Genome fraction (%)	99.9	99.99	97.8
# misassemblies	0	0	52
# mismatches per 100 kbp	5.4	10.9	17.7
# indels per 100 kbp	0.4	4.0	2.1
Reference GC (%)	50.8	30.6	68.8

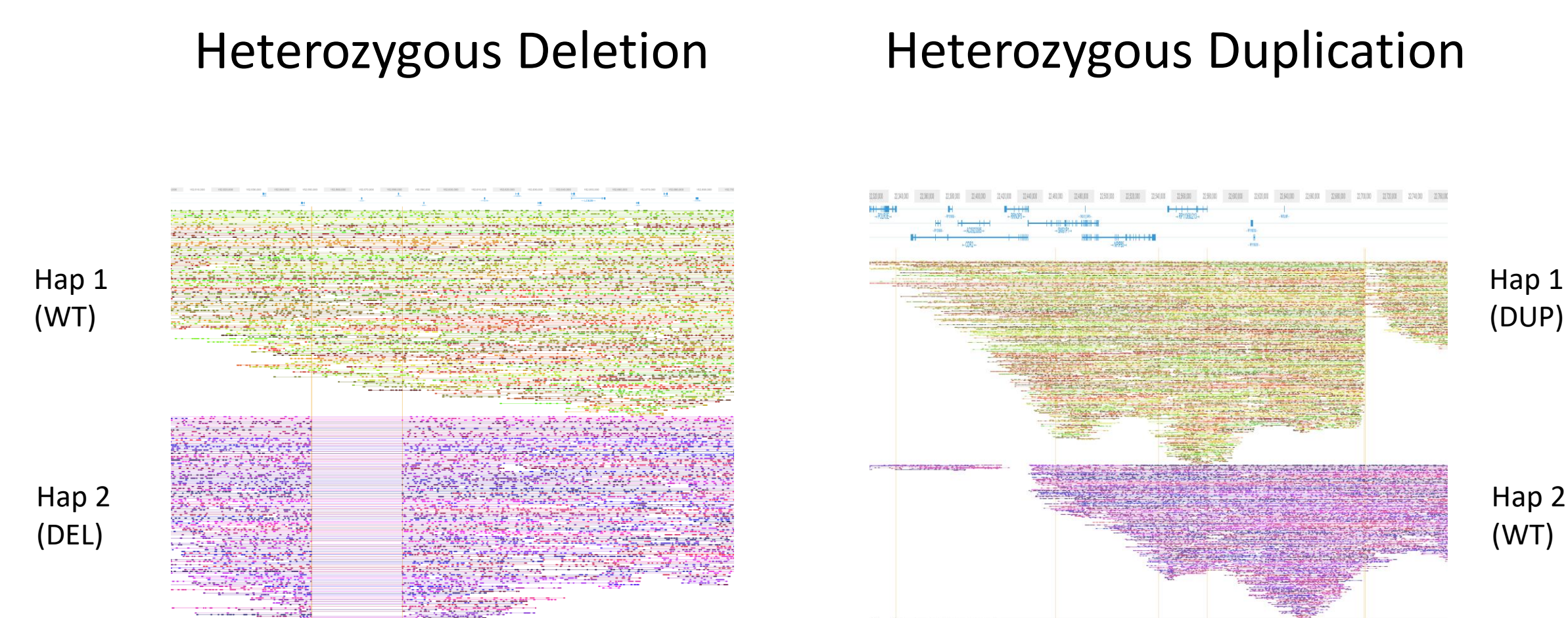
Whole Genome Phasing

	2x146 PE		2x96 PE	
	NA12878	NA24385	NA12878	NA24385
Coverage Depth (Unique)	38x	46x	25x	28x
Longest Phased Block	67.5 Mb	59.2 Mb	39.9 Mb	35.0 Mb
N50 Phased Block	14.4 Mb	13.4 Mb	8.0 Mb	9.4 Mb
Switch Error Rate	0.03%	0.07%	0.04%	0.08%



Structural Variation

Phased Reads Made SV Detection Simple



TELL-Seq Advantages

Technical Indices	TELL-Seq™
Instrument cost	Zero
Library prep cost	Low
Input DNA	<5 ng
Processing time	3 hours
Barcode capacity	>10 million
Genome size	≥ 1Mb

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

