TruPath™ Genome

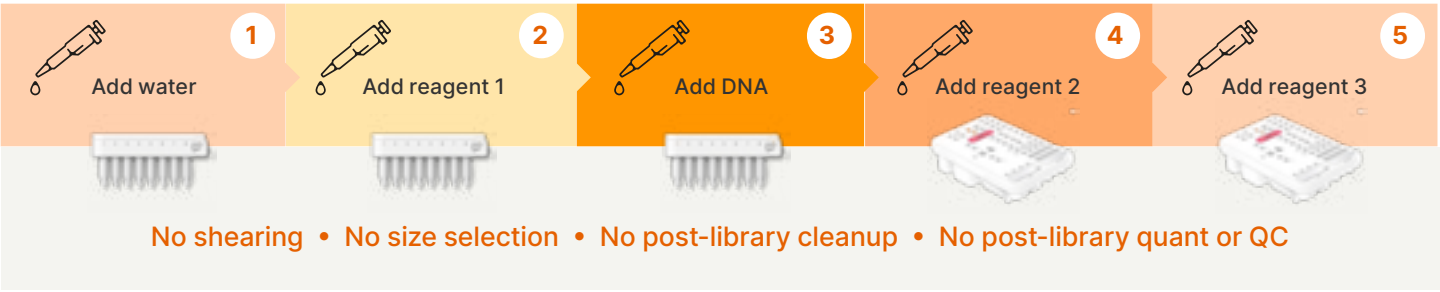
A faster, more scalable research solution for long-range genomic insights

TruPath Genome simplifies whole-genome sequencing (WGS) adoption and reduces hands-on time to ~10 minutes. Trusted Illumina transposase chemistry and on-flow cell library prep eliminates manual library prep steps.

Simplified sample preparation

TruPath reduces sample preparation to five steps, cutting down complexity and hands-on time to ~10 minutes for the 8-sample workflow.

The TruPath Genome workflow is 5 easy steps:



No shearing • No size selection • No post-library cleanup • No post-library quant or QC

Reduce labor & training costs

Reduce costly, complex automation

Avoid costly re-work

Turnaround time

Compared to current long read approaches, TruPath Genome delivers up to 4x more genomes per run and cuts turnaround time by more than half.

By nearly eliminating hands-on library preparation and leveraging the fast turnaround time of NovaSeq™ X sequencing, TruPath Genome dramatically reduces overall workflow time without compromising data quality—enabling up to 4,000 genomes per year (>30× coverage) on a single NovaSeq X Plus System.

- **~32 hours DNA-to-VCF** for up to 16 samples, including sequencing (~29 hours) and analysis (~3 hr)
- **Up to 4× more genomes per run** and ~2× faster turnaround

PacBio SMRTbell Prep kit 3.0 workflow:*

TruPath Genome workflow:

Reduced prep complexity and faster time to results.

TruPath Genome advantages

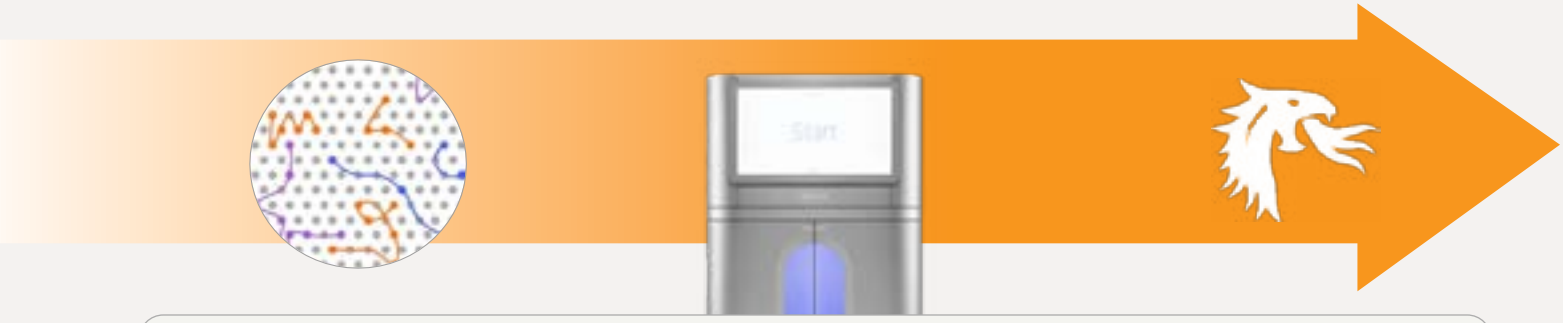
- **No manual library prep**, no DNA shearing, no size selection
- No post-library QC or rework required
- **~$395 per genome** (C8) with no added prep or instrument costs for automation, size selection, or shearing
- **>4,000 genomes/year** throughput capability

Long read WGS workflows add cost and complexity →

Workflow dimension	TruPath Genome	PacBio SMRTbell prep kit 3.0*
Pre-sequencing workflow	5 steps (integrated)	~10–12 steps (manual prep, QC, size selection, sequencing prep)
Prep time	~10 minutes	6 hours, multi-step
Library preparation	Step eliminated	Manual, multi-step; automation requires dedicated instrumentation
DNA shearing	Not required	Required
Size selection	Not required	Highly recommended
Analysis time	2.5–3.5 hours	9–16 hours
Throughput (30x)	Up to 16 genomes per run	Up to 4 genomes per run
Cost model	Single integrated workflow (prep + sequencing combined)	Multiple add-on components: prep + adapters + size selection + sequencing + analysis

TruPath Genome: Simplifying whole-genome analysis

While long read whole genome (WG) workflows are longer and more complex, requiring additional steps, additional instruments and reagents, longer sequencing and data analysis times, TruPath genome offers clear advantages.



Set up	Sequence	Analyze
TruPath™ Genome Streamlined, simple	**NovaSeq™ X Series** Proven accuracy	**DRAGEN™ Germline** Accurate, comprehensive, fast

Workflow components from single vendor enables researchers to scale operations confidently and eliminate workflow complexities.

Sources:
- https://www.pacb.com/wp-content/uploads/Revio-specification-sheet.pdf
- https://www.pacb.com/wp-content/uploads/Procedure-checklist-Preparing-whole-genome-and-metagenome-libraries-using-SMRTbell-prep-kit-3.0.pdf
- https://aws.amazon.com/blogs/publicsector/benchmarking-pacbio-whole-genome-sequencing-variant-pipeline-analysis-with-aws-healthomics-workflows/

Learn more about TruPath Genome

Bring long-range genomic insights into routine.