



Service Introduction | QTD26135 | 2026

WPS Pro

Nanopore Whole Plasmid Sequencing

*Fast, Precise Long-read Sequencing for
Full-length Plasmid Mixture Resolution*



www.quintarabio.com

WPS Pro

WPS Pro is designed to preserve true full-length nanopore reads, where each read corresponds to a single plasmid molecule. In most library preparation workflows across providers, random linearization or fragmentation makes producing true full-length reads difficult, which limits analysis to consensus assemblies.

WPS Pro overcomes these limitations by optimizing for full-length molecules and minimizing random fragmentation during the library preparation process. Raw reads generated using this approach share identical start and end points in your vector backbone, allowing each read to be treated as a complete molecular sequence. This enables robust analysis of complex plasmid libraries and pooled plasmid samples.

This service excels at resolving plasmid mixtures and returning multiple distinct sequences per sample, providing insight into sample heterogeneity that cannot be captured by assembly-based approaches. Sequencing is performed using Oxford Nanopore R10.4.1 flow cells.

Library Preparation

Our library preparation workflow begins with sequence-dependent digestion of plasmid DNA to generate intact, full-length linear molecules. Barcodes are then attached to the DNA ends using a ligation-based library preparation method. Barcoded samples are multiplexed and sequenced on an Oxford Nanopore R10.4.1 flow cell.

Bioinformatics Analysis

After sequencing is complete, raw reads are basecalled using the latest Dorado Super Accuracy model. These high-accuracy reads are processed through our analysis pipeline, where they are grouped into multiple high-confidence consensus sequences, each representing a distinct plasmid population within the sample.

Once processing is complete, all results are uploaded to our secure customer portal, and you will receive an email notification when your data is ready. Details of all deliverables are outlined below.

Deliverables

Sequence Files

- FASTA file
A text-based file containing the final consensus DNA sequence.
- GenBank file
Includes the consensus sequence along with annotated genetic features.

- **AB1 file**
 A Sanger-style chromatogram view of the consensus sequence, allowing visualization of variants and low-confidence positions. Each peak color corresponds to a specific nucleotide.
- **Multi-FASTA file**
 A combined FASTA file containing all consensus sequences generated from the same sample.

Read-Level Data

- **Per-base data file**
 Provides a detailed breakdown of how individual raw reads support each base in the consensus sequence. This file is used to generate the AB1 chromatogram.
- **Alignment file**
 Displays the alignment of raw reads to the consensus sequence, enabling evaluation of sequencing data at a molecular level.
- **FASTQ file**
 Contains all raw sequencing reads generated for your sample.

Report(s)

- **Variant summary file**
 A table summarizing all detected variants, including the number of reads assigned to each variant and the corresponding sequence length.
- **QC report file**
 A comprehensive quality control report containing key metrics and visualizations, including:
 1. **Read-length histogram**
 Displays the distribution of raw read lengths. A single dominant peak typically indicates a pure sample, while multiple peaks may suggest concatemers or additional DNA species.
 2. **Virtual gel**
 A simulated gel image generated from raw read data, providing an intuitive view of sample composition.
 3. **Additional sample metrics**
 Including total reads, total bases, reads mapped to consensus, sample name, consensus length, and related statistics.

We Go Fast, You Go Forward



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