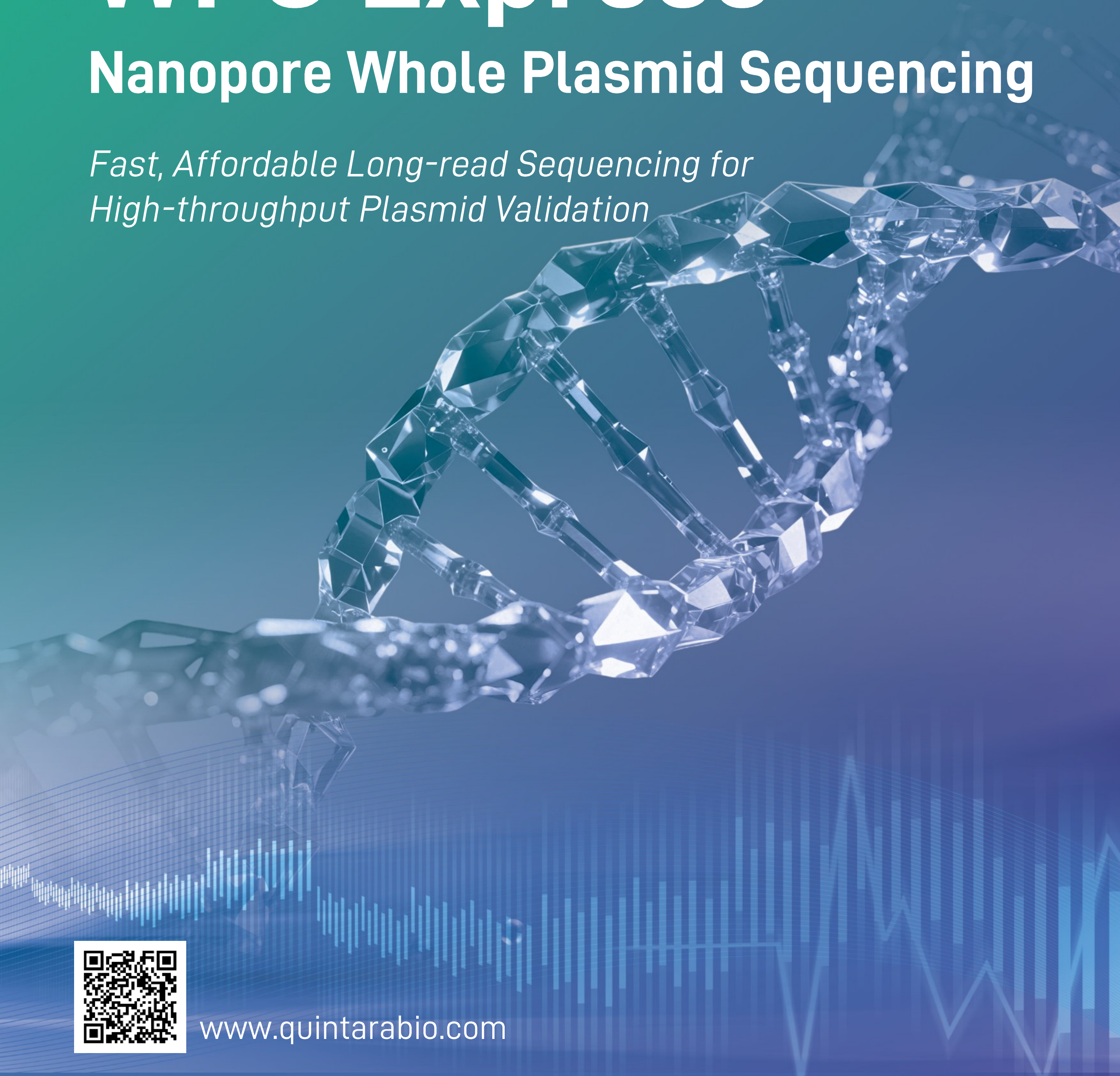
QUINTARA

Service Introduction | QTD26132 | 2026

WPS Express

Nanopore Whole Plasmid Sequencing

Fast, Affordable Long-read Sequencing for High-throughput Plasmid Validation



www.quintarabio.com

Overview

WPS Express is a cost-effective whole plasmid sequencing service designed for high-throughput colony screening and clonal plasmid verification. It provides the advantages of long-read nanopore sequencing while optimizing for both speed and affordability.

This service is intended for sequencing clonal plasmids without high-complexity sequences such as high-GC (e.g. CAG promoter) regions and strong secondary structures (e.g. hairpins, ITRs, LTRs). Sequencing is performed using Oxford Nanopore R10.4.1 flow cells.

Workflow

1. Sample Submission

   Primer-free sample submission supports plasmid, RCA, and bacterial samples, with access to over 1,000 convenient drop-off locations.

2. Library Preparation

   Libraries are constructed using optimized Oxford Nanopore Technologies (ONT) workflows alongside Quintara's proprietary in-house methods.

3. Sequencing

   Sequencing is performed via ONT long-read technology, delivering ultra-high coverage depth and real-time data acquisition capabilities.

4. Data Analysis

   Analysis encompasses de novo circular assembly, full-spectrum functional annotation, and provision of ready-to-use, publication-ready deliverables.

Library Preparation

Our library preparation workflow begins with sequence-dependent linearization of plasmid DNA, followed by barcoding using our proprietary in-house method. Barcoded samples are then multiplexed and sequenced on an Oxford Nanopore R10.4.1 flow cell, enabling efficient processing of large numbers of samples in a single run.

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 to generate a full-length consensus plasmid sequence. The analysis is optimized for rapid, reliable single-consensus generation for clonal samples.

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.

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.

Report(s)

- Summary file

  A concise report containing key sample-level metrics, including:

  1. reaction status (successful or failed)
  2. plasmid length
  3. final consensus plasmid sequence

We Go Fast,
You Go Forward

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