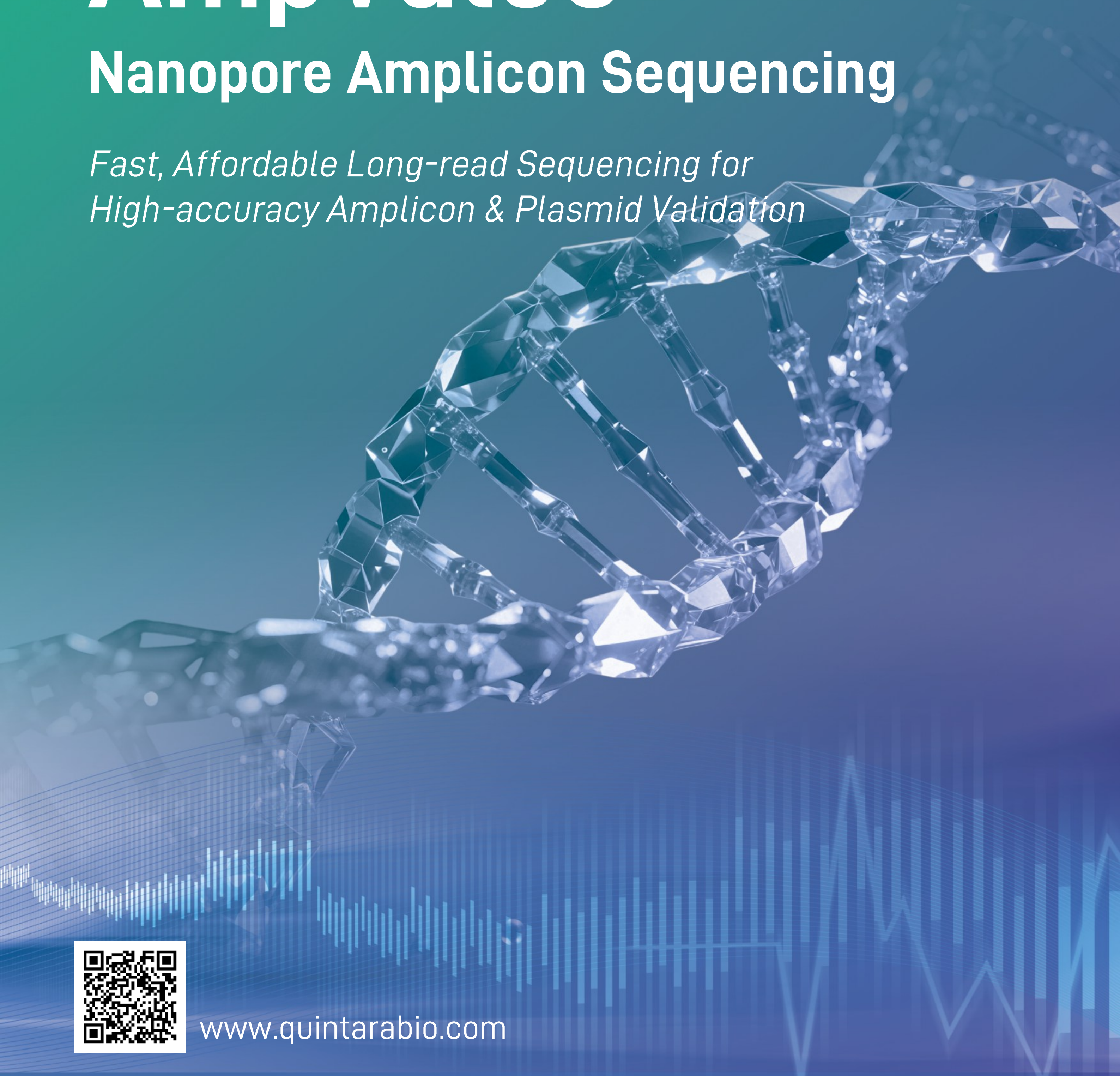
QUINTARA

Service Introduction | QTD26131 | 2026

AmpValue

Nanopore Amplicon Sequencing

Fast, Affordable Long-read Sequencing for High-accuracy Amplicon & Plasmid Validation



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Amplicon Value

Amplicon Value is a low-cost, nanopore-based amplicon sequencing service intended as an alternative to traditional Sanger sequencing. This service is well suited for sequencing clonal samples and resolving simple amplicon mixtures containing 2-3 variants, while providing full-length sequence information without common Sanger limitations such as primer design requirements and read-length constraints (e.g. <1,000 bp). Sequencing is performed using Oxford Nanopore R10.4.1 flow cells.

Library Preparation

Our library preparation workflow begins with end-repair of amplicon DNA to make the DNA ends compatible with downstream barcoding. Barcodes are then attached to the DNA ends using our proprietary in-house library preparation method, allowing samples to be 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 assembled into high-confidence consensus sequences representing the species present in each 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.

- 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.