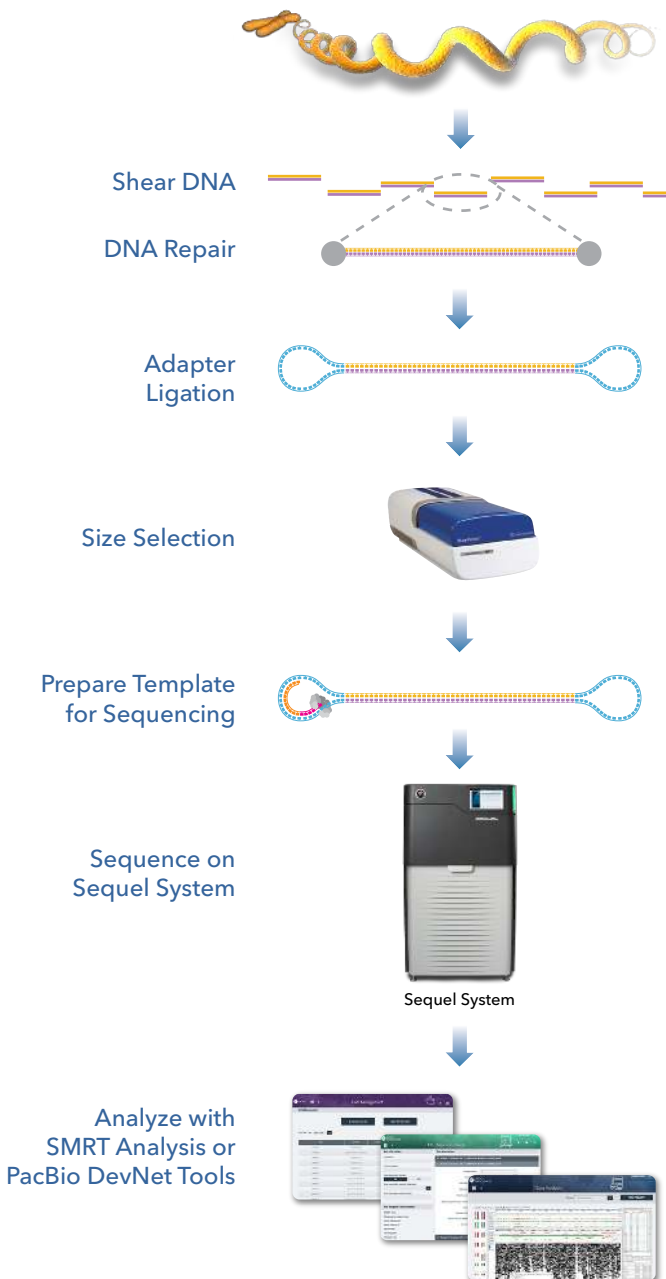




PLANT AND ANIMAL WHOLE GENOME SEQUENCING BEST PRACTICES

Single Molecule, Real-Time (SMRT®) Sequencing on the Sequel® System enables easy and affordable generation of high-quality *de novo* assemblies of even the most complex plant and animal genomes. With megabase-size contig N50s, consensus accuracies >99.99%, and tools for phasing haplotypes you can capture undetected SNVs, fully intact genes, and regulatory regions embedded in complex structures that fragmented draft genomes often miss.

FROM GENOMIC DNA TO A COMPLETE GENOME

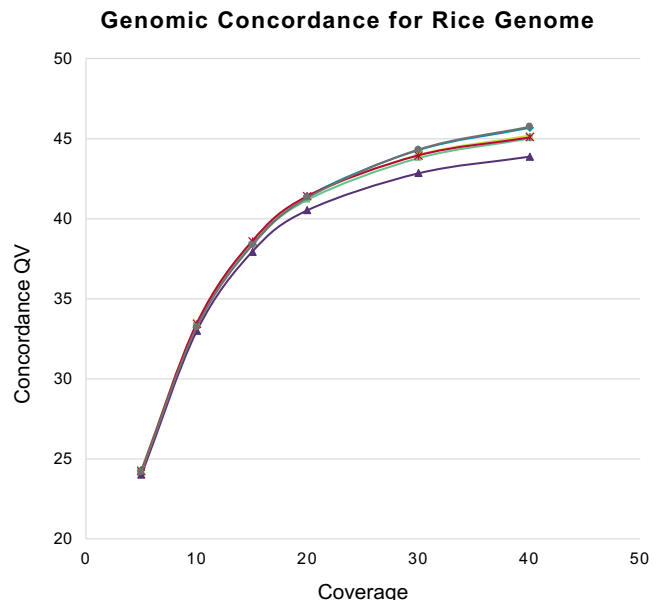


WORKFLOW RECOMMENDATIONS

- Start with high-quality, high molecular weight DNA¹
- Prepare long-insert SMRTbell® libraries² for sequencing
 - Sequence >20 SMRT Cells from 3 µg DNA*
 - Store library for several months without diminished sequencing performance
- Size select library for optimal yield and read lengths³
- Maximize output and turn-around-time with adjustable sequencing parameters⁴
 - 30 to 50-fold unique molecular coverage recommended for assembly and an additional 20 to 30-fold sequence coverage for polishing⁵
 - Yields up to 12 Gb per SMRT Cell 1M with 10-hour collection time
 - For a 1 Gb genome, ~5 SMRT Cells needed for a high-quality genome assembly
- Utilize the PacBio analytical portfolio for genome assembly⁶

*Number of SMRT Cells that can be run for a given library is a function of the size, cleanup yield, and loading of instrument

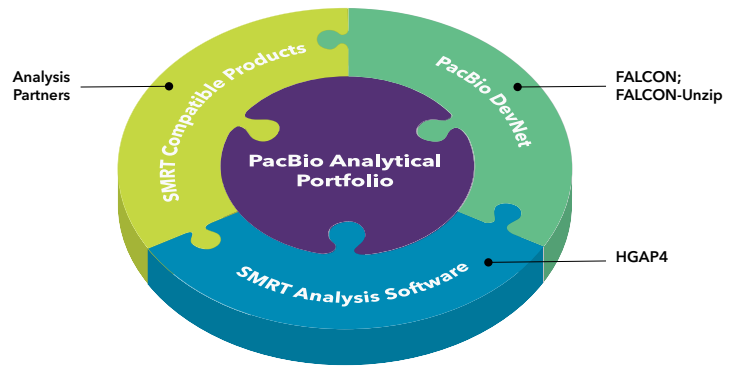
CONSENSUS ACCURACY >99.99% (QV40) WITH 40-FOLD COVERAGE, EVEN FOR COMPLEX GENOMES



Plot of QV scores across the genic regions of multiple data sets of the rice genome assembled to a high-contiguity. These data were generated on the Sequel System with chemistry 3.0 and Sequel System Software v6.0.

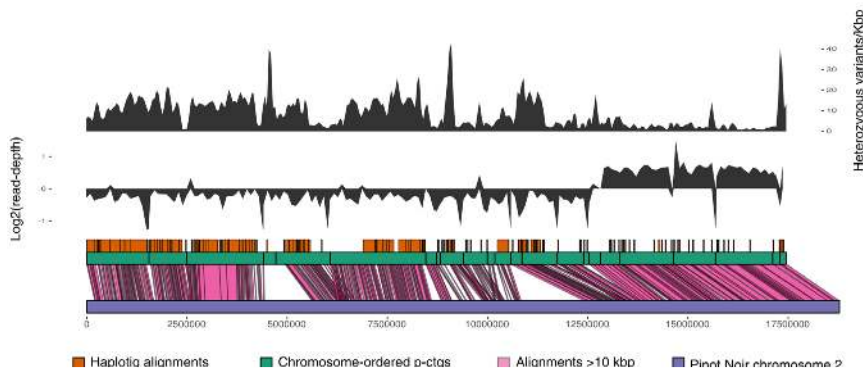
DATA ANALYSIS SOLUTIONS WITH THE PACBIO ANALYTICAL PORTFOLIO

- Generate highly accurate *de novo* assemblies with megabase-level contiguity⁷
 - Push-button assembly for small genomes with HGAP4 using SMRT Analysis
 - Phased assembly at the command line with FALCON, FALCON-Unzip, and FALCON-Phase from PacBio DevNet
 - Network of analysis partners for platform or full-service bioinformatics

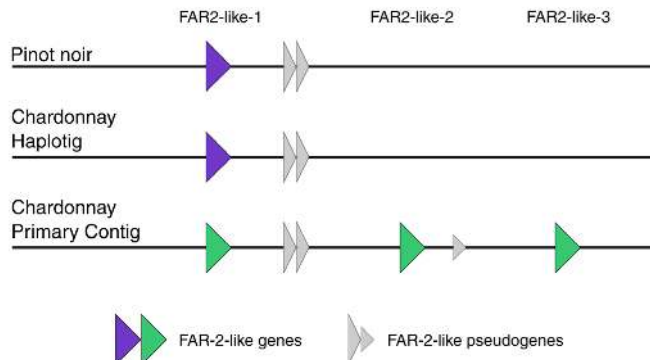


The PacBio analytical portfolio offers solutions for every user in the lab from easy-to-use interfaces to command line tools, and full-service genomics.

BUILDING BETTER GENOMES. ENABLING BREAKTHROUGH DISCOVERIES.



Expanded view of chromosome two showing the heterozygous variants (top track) and read-depth (second track) of the Chardonnay genome (orange and green tracks) and aligning to the Pinot noir genome (purple track).⁵



Genomic arrangement of the FAR2-like genes in Chardonnay with Pinot noir-derived (purple) and Gouais blanc-derived (green) genes shown.⁸

KEY REFERENCES

1. Preparing DNA for PacBio Whole Genome Sequencing for *De Novo* Assembly: Quality Control and Shearing
2. Procedure & Checklist - Preparing >30 kb Libraries Using SMRTbell® Express Template Preparation Kit
3. Preparing Libraries for PacBio Whole Genome Sequencing for *De Novo* Assembly: Quality Control and Size Selection
4. Quick Reference Card - Diffusion Loading and Pre-Extension Time Recommendations for the Sequel System
5. PacBio Assembly Tool Suite: FAQ - What Coverage do I Need for *De Novo* Assembly and Polishing?
6. PacBio Analytical Portfolio for Whole Genome Sequencing
7. *De Novo* Assembly Brochure: Assembly Options for Your SMRT Sequencing Data
8. Roach, M. J. et al. (2018) Population Sequencing Reveals Clonal Diversity and Ancestral Inbreeding in the Grapevine Cultivar Chardonnay. *bioRxiv*.