Targeted Sequencing Solutions for PacBio RS Long Reads Using Partek® Flow™ and Partek® Genomics Suite™

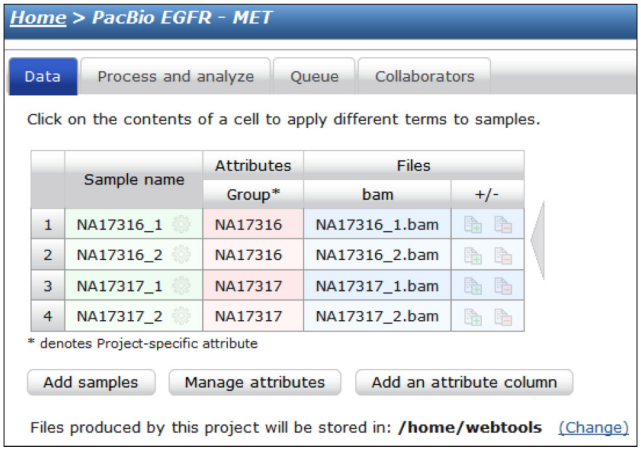
Overview

Partek provides a comprehensive solution for analysis, visualization, and integration with known variant databases for long read data from the PacBio RS Single Molecule Real Time (SMRT™) sequencing machine. The use of SMRT technology permits read lengths on average of 1,000 bp, instances over 10,000 bp, and observation of structural and cell type variation not accessible with other technologies.

Easily Import PacBio Data

With Partek Flow, easily import your PacBio RS data for maintaining attribute information throughout the analysis of your project.

Assign sample attributes using controlled vocabulary and perform in place editing of individual and group attributes to ensure the integrity of your sample attribute information.



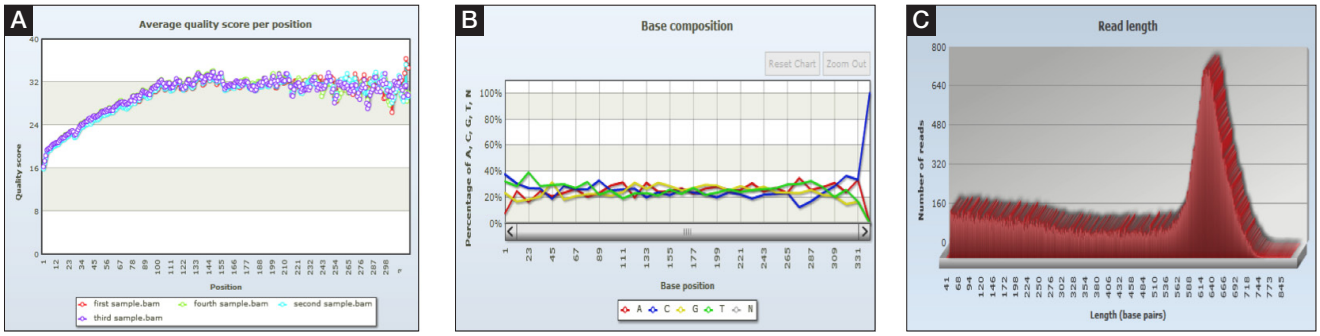
Multiple Levels of Genomic View

Visualization of PacBio long reads and detected variant can be accomplished using the Multi-Level Genome Browser in Partek Flow. Understanding the location of detected single nucleotide variations (SNV) is critical, but the overlay of this information with a database of known variant, respective chromosome position, and neighboring or overlapping genes in one view provides a greater insight into the genomic context.

Multi-Level View Chromosome Browser (chromosome, gene, SNPs)
Overlay with track of known SNVs (DGV, dbSNP)

QA/QC

Assessing read quality, both pre-aligned and post-aligned, will improve the accuracy of detecting SNVs. PacBio reads maintain high quality even at long reads.



QC metrics showing **A)** average quality score per position, **B)** base composition per position, and **C)** a quantitative number of reads.

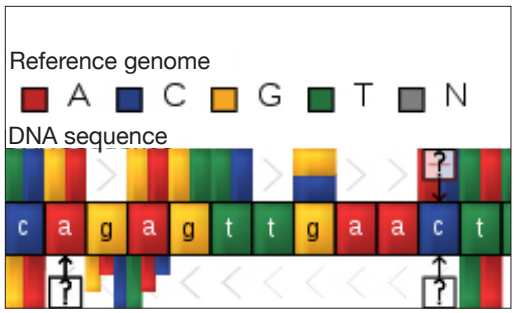
Partek Flow enables the inspection of important quality control metrics including:

- Individual and group QA/QC
- Coverage
- Average read quality per position
- Read length vs. number of reads
- Read filtering and trimming
- More

Detect SNVs Across Samples or Against a Reference

Partek has multiple methods to detect SNVs across samples or against a reference sample for the most complete SNV detection tool currently available. SNP detection, insertion and deletion detection, rare variant detection with confidence intervals, a genotype likelihood method, and a powerful covariate modeling method are available for identifying variants.

Homozygous SNP detected in NA17317 but not in NA17316



Detected SNPs with annotation tracks

Partek®
turning data into discovery®

North America +1-314-878-2329
Europe +44 (0) 7780 438753
Asia/Australasia +65-6478 9730
sales@partek.com | www.partek.com