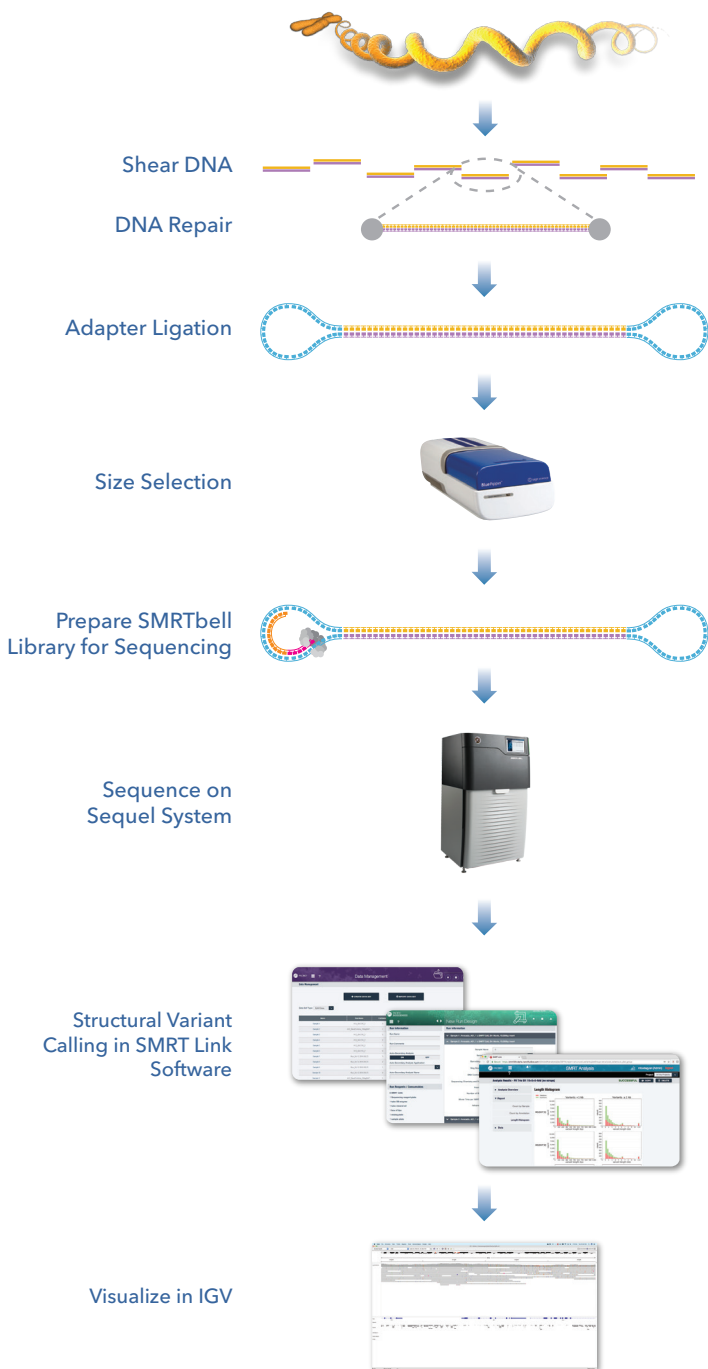


# LOW-COVERAGE, LONG-READ WHOLE GENOME SEQUENCING FOR STRUCTURAL VARIATION BEST PRACTICES

With the Sequel® System, you can affordably and sensitively characterize structural variation (SV) of all types ranging in size from tens to thousands of base pairs. Low-coverage, long-read whole genome sequencing (WGS) data provides rapid discovery of common SVs for population genetics studies and resolves rare SVs unique to an individual, with a very low false-discovery rate.

## FROM gDNA TO MOST COMPREHENSIVE SV CALL SET

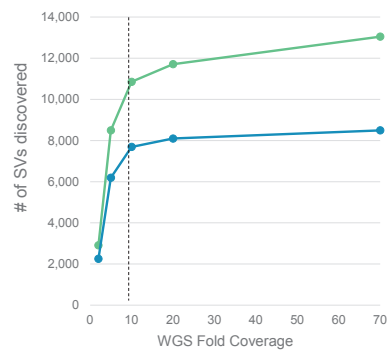


## SAMPLE PREPARATION RECOMMENDATIONS

- Use recommended high-quality *unamplified* genomic DNA input (>3 ug)
- Prepare >15 kb Library using SMRTbell® Express Template Preparation Kit<sup>1</sup>
- Enrich for longest inserts with size selection<sup>1</sup>
- Automated library-prep solutions available<sup>2</sup>
- Sequence to desired coverage based on study needs<sup>3</sup>:
  - 5 to 10-fold: population genetics studies - sensitivity limited per individual, but high for variants shared in the population using joint calling
  - 10-fold: rare undiagnosed disease studies - sensitivity high per individual allowing discovery of pathogenic SVs
  - 10 to >20-fold: genetic disease studies - identify a variant or gene that causes disease in a cohort of individuals with a shared phenotype. Higher coverage required for *de novo* SV detection in trios.
  - ~7.5 Gb per Sequel SMRT Cell 1M

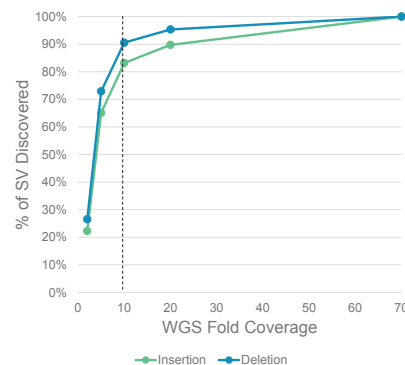
## SV DISCOVERY POWER AT VARIOUS COVERAGE LEVELS

Number of SVs Discovered vs. Coverage



A diploid human (HG00733) was sequenced to 70-fold coverage on the Sequel System. The reads were randomly sampled to various coverage levels, and the SV calls at each coverage were evaluated against the calls at full 70-fold coverage.

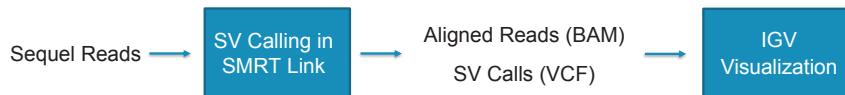
Sensitivity for SV Discovery vs. Coverage



Sensitivity increases sharply with coverage until about 10-fold, where it begins to level off. At 10-fold coverage, 10,854 insertions and 7,692 deletions are called (83% and 90.5% sensitivity respectively)<sup>4</sup>.

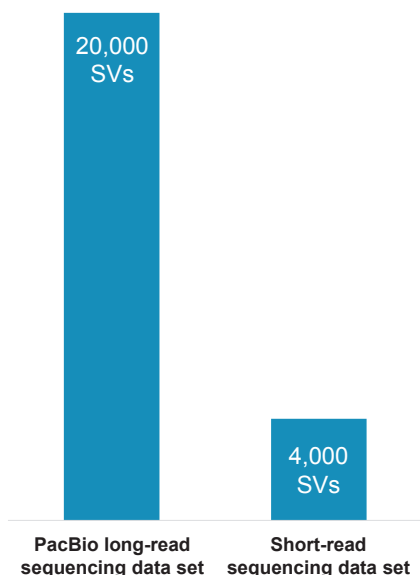
## DATA ANALYSIS SOLUTIONS WITH SMRT® ANALYSIS AND IGV

- Detect the broadest range of SV types including deletions, insertions, duplications, inversions, tandem repeats and translocations<sup>5</sup>
- Discover more SVs with the highest sensitivity - up to 20,000 SVs per genome<sup>4,6</sup>
- Identify common structural variants across multiple samples with joint calling
- Resolve breakpoints to sequence level<sup>7</sup>
- Limit costly validation efforts with a low false-discovery rate of 5-10%<sup>8</sup>
- Output data in standard file formats - BAM and VCF - for seamless integration with downstream analysis tools
- Confirm SV calls visually with IGV<sup>7,9</sup> and GenomeRibbon<sup>10</sup>



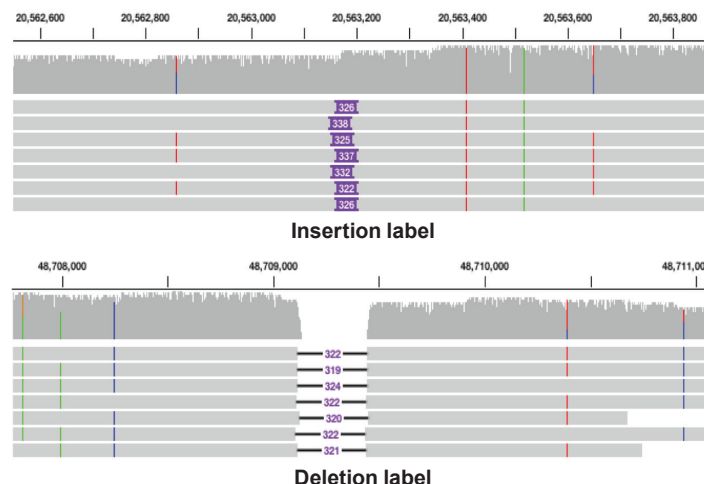
SMRT Link and IGV provide a complete workflow to call and visualize structural variants in PacBio reads.

## LONG-READ SMRT SEQUENCING PROVIDES HIGHER SENSITIVITY FOR SV DISCOVERY



A comparison of SV sensitivity across short-read sequencing and PacBio long-read sequencing for SV discovery in published human genomes<sup>8,11,12</sup>. PacBio long-read sequencing uncovers many structural variants missed by short-read methods, providing up to five-fold higher sensitivity for true SV discovery<sup>6,13</sup>.

## VISUALLY VALIDATE SV CALLS BY EXPLORING READ EVIDENCE IN IGV



Visualization of long-read sequencing evidence in support of an insertion and deletion structural variant in IGV. Insertions are indicated with a purple box with the width of the box proportional to the size of the insertion, and the basepair size is written on the box. Deletions are indicated by a black line. The basepair size of the deletion is written on a white box at the center of the line<sup>7</sup>.

## KEY REFERENCES

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