Bringing the "W" Back to Whole Genome Sequencing

Single molecule, real-time (SMRT®) Sequencing delivers long read lengths with unbiased coverage in the most comprehensive de novo genome assemblies generated today. True whole genome sequencing provides complete and accurate views of all types of genomic variation revealing structural variants, mobile elements, haplotypes, epigenetics, and low complexity regions.

- Go beyond draft genomes, generate megabase-sized contigs, and finish assemblies
- Access genomic variations beyond SNPs
- Reveal genomic regions inaccessible to amplification-based sequence methods
- Annotate complete gene models with promoter regions
- Phase haplotypes with diploid assembly
- Capture epigenetic information

Contig N50 Assembly Statistics of Genomes Assembled Using Only PacBio® Data

- Bacteria Finished Genomes
  - Yeast (12 Mb) N50: 7.1 Mb
  - Drosophila (170 Mb) N50: 4.5 Mb
  - Arabidopsis (120 Mb) N50: 2.4 Mb
- Panacoid grass (250 Mb) N50: 2.4 Mb
- Sea Bass (700 Mb) N50: 1 Mb
- Rice (370 Mb) N50: 4 Mb
- Spinach (1 Gb) N50: 920 kb
- Tetraploid Cotton (2.5 Gb) N50: 219 kb
- Goat (2.85 Gb) N50: 2.5 Mb
- Human (3.2 Gb) N50: 7.7 Mb

www.pacb.com/denovo
From DNA to Comprehensive Genome Assemblies

Long Insert Library Preparation
- Single library type required
- Size-selection options enrich for longest inserts
- Library input as low as 100 ng of gDNA
- Library automation supported

SMRT Sequencing on the PacBio® RS II
- Average read lengths 10-15 kb
- Scalable throughput:
  - Complete microbial genomes in 1 SMRT Cell
  - 5-10x coverage per genome recommended for gap filling
  - 25x coverage per genome for hybrid assembly
  - 50x coverage per genome recommended for de novo assembly
- Simultaneous capturing of epigenetic information using kinetics

De Novo Assembly & Structural Variation Detection
- Analysis tools available through SMRT Software Suite and community
- Megabase-sized contig N50s with demonstrated consensus accuracies >99.999%
- Diploid assemblies with haplotype information

References