

HIFI WGS AT SCALE ON THE SEQUEL IIe SYSTEM

Scale your whole genome sequencing (WGS) and epigenome workflows with PacBio® HiFi reads employing a single technician working one day a week. Sequence 25 human genomes at ≥ 30-fold coverage each month using four Sequel® II systems.*

1 technician + 1 day per week =
5 SMRT® Cells per Sequel IIe system for up to 4 Sequel IIe systems



LIBRARY PREP

SMRTbell® prep kit 3.0 +
AMPure® PB bead size selection

- 1 µg of DNA per SMRT Cell 8M
- Automation-friendly
- Up to 24 WGS samples prepared in 6.5 hours
- Single workflow for HiFi reads + 5mC base calling



SMRT® SEQUENCING

Sequel IIe system

- 6.5 days of walk-away automated runtime
- On-instrument base and 5mC calling allowing low compute costs
- Data transferred to server automatically after each SMRT Cell 8M is processed

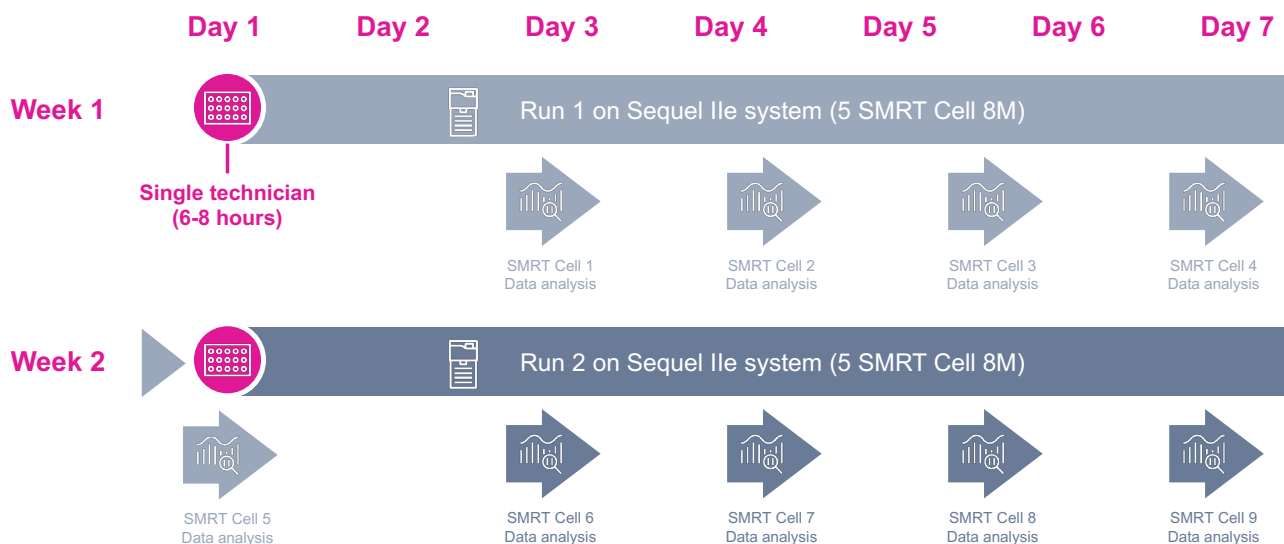


DATA ANALYSIS

SMRT® Link

- HiFi reads + 5mC calling allow complete view of the genome and epigenome from a single data type
- Low data storage costs with 35 GB file sizes per SMRT Cell (175 GB per week per instrument)

A convenient schedule that maximizes system utilization for 5 SMRT Cells a week is shown below.



*At 30 Gb of HiFi yield per SMRT Cell 8M. **Contact PacBio** for specific sequencing run parameters.

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