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<tr>
<td>De Novo Assembly - for whole genome up to 2.5 kb</td>
<td>Preparing whole genome and metagenome libraries using SMRTbell prep kit 3.0</td>
<td>1 µg of genome (3 µg for human genome)</td>
<td>SMRTbell prep kit 3.0</td>
<td>N/A</td>
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<tr>
<td>De Novo Assembly - for low-input DNA libraries</td>
<td>Preparing multiplexed SMRTbell libraries using SMRTbell prep kit 3.0</td>
<td>≥1 µg (≥600 Mb genome size)</td>
<td>SMRTbell prep kit 3.0</td>
<td>Two 600-Mb genomes</td>
<td>De Novo Assembly - for whole genome up to 2.5 kb</td>
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<tr>
<td>Variant Detection</td>
<td>Preparing single-cell libraries, splicing/annotating, and target capture library prep</td>
<td>≥50 ng per sample to 16 µg per sample</td>
<td>SMRTbell prep kit 3.0</td>
<td>Up to 24 AHD samples</td>
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<td>Targeted Sequencing Utilizing the CRISPR-Cas9 System [101-801-359]</td>
<td>Preparing single-cell libraries, splicing/annotating, and target capture library prep</td>
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<td>Low DNA Input (single-sample)</td>
<td>Preparing single-cell libraries, splicing/annotating, and target capture library prep</td>
<td>≥50 ng per sample to 16 µg per sample</td>
<td>SMRTbell prep kit 3.0</td>
<td>Up to 24 AHD samples</td>
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**Whole Genome Sequencing**

- De Novo Assembly - for whole genome up to 2.5 kb
- De Novo Assembly - for low-input DNA libraries
- Variant Detection

**Virus Sequencing**

- De Novo Assembly - for whole genome up to 2.5 kb
- De Novo Assembly - for low-input DNA libraries
- Variant Detection

**RNA Sequencing**

- De Novo Assembly - for whole genome up to 2.5 kb
- De Novo Assembly - for low-input DNA libraries
- Variant Detection

**Metagenomics**

- De Novo Assembly - for whole genome up to 2.5 kb
- De Novo Assembly - for low-input DNA libraries
- Variant Detection

**Targeted Sequencing**

- De Novo Assembly - for whole genome up to 2.5 kb
- De Novo Assembly - for low-input DNA libraries
- Variant Detection

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**Protocol**

- Preparing whole genome and metagenome libraries using SMRTbell prep kit 3.0
-Preparing multiplexed SMRTbell libraries using SMRTbell prep kit 3.0
- Preparing single-cell libraries, splicing/annotating, and target capture library prep

**Minimum Input Amount**

- 1 µg of genome (3 µg for human genome)
- ≥50 ng per sample to 16 µg per sample

**Recommended Pacific Biosciences Template Prep Kit**

- SMRTbell prep kit 3.0
- SMRTbell prep kit 3.0
- SMRTbell prep kit 3.0
- SMRTbell prep kit 3.0

**Multiplexing/SMRT Cell SM**

- N/A
- Two 600-Mb genomes
- Up to 96 micrograms

**Whole Genome Sequencing with the Sequel II and Sequel IIx Systems: Loading and Pre-Extension Recommendations**

- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0
- Desequencing kit loading kit 3.0

**Movie Collection Time**

- 30 h
- 15 h
- 15 h
- 24 h
- 24 h
- 15 h
- 15 h
- 15 h

**Gene Analysis Software Applications**

- De novo assembly powered by IPA
- HiFi Mapping
- Gene Analysis powered by IPA
- Microbial Gene Analysis
- NGS Sample Analysis powered by IPA
- SMRTbell Express TPK 2.0
- SMRTbell prep kit 3.0
- Iso-Seq
- HiFiViral
- HiFiViral
- HiFiViral
- HiFiViral
- HiFiViral
- HiFiViral
- HiFiViral

**Other Analysis Tools**

- Bovin, H. Cana
- HiSeq
- Bovin, H. Cana
- Bovin, H. Cana
- Bovin, H. Cana

**Read lengths, read counts per SMRT Cell and other performance results vary based on sample quality and insert size.**

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