PacBio sequencing machines and their applications

The Sequel is the second generation PacBio sequencer and generates up to 7x more reads per SMRT-cell compared to the first generation PacBio RSII sequencer. You will get very long reads (up to 50 kb) with a yield of up to 3-7 Gb of raw data per SMRT cell.

Sequel read lengths are currently shorter than what can be achieved on the RSII. However, pending chemistry improvements in the next quarter are expected to extend Sequel read lengths closer to that of the RSII.

The principles of the single molecule sequencing chemistry remain unchanged. The sequence coverage and the sequencing errors do not show any detectable sequence-specific biases. The sample requirements and the library prep protocols are essentially the same as for the RSII (requiring one additional column filtration).

	RS II	**Sequel**
data output per SMRT cell	0,75-1,5Gb	3-7Gb

What can be done on the PacBio Sequel:

- *De novo* sequencing of microbial/fungal/eukaryotic genomes (highly accurate finished genomes)
- Re-sequencing of complex genomes (to resolve structural variants)
- *De novo* sequencing of complex genomes
- Amplicon re-sequencing (e.g. for HLA typing that includes complete haplotype phasing information)
- Full-length transcript sequencing ("Iso-seq")
- Base modification analysis (epigenetic studies)

The PacBio sequencing technology currently has a higher cost per base than the illumina technology, but it offers some unique features, which enable e.g. more accurate genome assemblies.

For both sequencers we provide raw HDF5 base calls and FASTQs of filtered subreads (≥50 bp, ≥75 read quality) for all SMRT cells. We also have additional services for specific sequencing projects (e.g . HGAP 2 assembly, Reads of insert protocol).

Please also check pacbio websites for all background in long reads-sequencing technology:

http://www.pacb.com/products-and-services/pacbio-systems/
http://www.pacb.com/applications/