



Application		Whole genome sequencing				Viral sequencing	RNA sequencing			Metagenomics		Targeted sequencing	
Application		De novo genome assembly	Variant detection	Microbial de novo genome assembly	De novo genome assembly w/ ultraflow input	Adeno-associated virus (AAV)	Whole transcriptome (Iso-Seq method)	Genome annotation (Iso-Seq method)	Single-Cell Iso-Seq (MAS-Seq)	Full-length 16S rRNA sequencing	Shotgun metagenomic profiling or assembly	Amplicon sequencing	Target enrichment
Experimental design													
Experimental design	Value proposition	Produce reference-quality, haplotype-phased genome assemblies including 5mC methylation profiles.	Detect and phase all classes of variants: SNVs, indels, SVs, tandem repeats, DNA methylation.	Produce accurate, closed assemblies of chromosomes and plasmids. Detect DNA methylation profiles.	Produce high-quality, haplotype-phased genome assemblies.	Sequence 24 AAV samples	Characterize alternative splicing	Annotate a genome with full length transcripts	Characterize alternative splicing in single cells / cell types	Obtain strain level resolution from 16S rRNA	Generate near-complete assemblies of high-complexity samples (e.g. gut microbiome)	Generate sequences of complete long-range amplicons	Detect all classes of variant at scale for genes of interest
	Coverage	≥15X per haplotype	≥10X for SVs; ≥30X for all variant classes	≥15X per microbe	≥15X per haplotype	≥40,000 full-length reads per AAV sample	-	-	≥3,000 - 10,000 unique reads / single cell	≥8,000 HiFi reads / sample	See Best Practices Guide	≥50X per locus	≥50X per locus
	Library insert size	15 - 20 kb	15 - 20 kb	7 - 10 kb	10 - 12 kb	2 - 5 kb	500 bp to 3+ kb	500 bp to 3+ kb	11 - 14 kb	1 - 2 kb	10 kb	500 bp - 15 kb	5 - 8 kb
	Multiplexing: Sequel II/Ile SMRT Cell	1 Gb of genome	n/a	96 microbes up to 375 Mb of total genome	1 Gb of genome	24 AAV samples	1 sample	12 samples	n/a	192 samples	Profile: 48 communities Assemble: 4 communities	≥1,000 samples	Large 20 Mb panel: 4 samples Medium 2 Mb panel: 24 samples Small 100 kb panel: 96 samples
	Multiplexing: Revio SMRT Cell	3 Gb of genome	SV: 3 humans All variants: 1 human	96 microbes up to 1 Gb of total genome	3 Gb of genome	Not supported; coming soon	Not supported; coming soon	Not supported; coming soon	n/a	Not supported; coming soon	Profile: 96 communities Assemble: 12 communities	≥1,000 samples (only amplicons >3 kb)	Large 20 Mb panel: 12 samples Medium 2 Mb panel: 72 samples Small 100 kb panel: 288 samples
Sample + library preparation													
Sample + library preparation	Protocols	Preparing whole genome and metagenome libraries using SMRTbell prep kit 3.0 [102-166-600]		Procedure & Checklist – Preparing HiFi SMRTbell Libraries from Ultra-Low DNA Input input [101-987-800]	Preparing multiplexed AAV SMRTbell libraries using SMRTbell prep kit 3.0 [102-126-400]	Preparing Iso-seq libraries using SMRTbell prep kit 3.0 [102-396-000]	Preparing MAS-Seq libraries using MAS-Seq for 10x Single Cell 3' kit [102-678-600]	Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 [102-359-000]	Preparing whole genome and metagenome libraries using SMRTbell prep kit 3.0 [102-166-600]	Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 [101-921-300]	Preparing multiplexed amplicon libraries using SMRTbell prep kit 3.0 [102-359-000]	HiFi sequencing with Twist Bioscience target enrichments [192-326-515]	
	DNA input: Sequel II/Ile SMRT Cell	1 µg / Gb of genome (3 µg / human genome)	1 µg / Gb of genome (3 µg / human genome)	300 ng per microbe	5 - 20 ng	1000 ng total	300 ng total RNA for 1st Strand cDNA Synthesis	15-75 ng of 10x Chromium 3' single cell cDNA	1000 ng of pooled 16S samples	≥300 ng per sample	150 ng for <5 kb 200 ng for 5 - 7 kb 300 ng for ≥7 kb of total amplified DNA	200-300 ng of total enriched DNA	
	DNA input: Revio SMRT Cell	0.7 µg / Gb of genome (2 µg / human genome)	0.7 µg / Gb of genome (2 µg / human genome)	300 ng per microbe	5 - 20 ng	Not supported; coming soon	Not supported; coming soon	15-75 ng of 10x Chromium 3' single cell cDNA	Not supported; coming soon	≥300 ng per sample	500 ng for 3 - 12 kb 750 ng for ≥12 kb of total amplified DNA	500 ng of total enriched DNA	
Data analysis tools													
Data analysis tools	SMRT® Link workflows	Genome Assembly	Variant Calling	Microbial Genome Analysis	Genome Assembly	n/a	Iso-Seq	Read Segmentation and Single-cell Iso-Seq Analysis	n/a	n/a	n/a	n/a	
	Community tools	hifiasm	DeepVariant	hifiasm	hifiasm	Form Bio	SQANTI	SQANTI	pb-16S-nf	PB-metagenomics-tools	PacBio Amplicon Analysis (rbaa)	HiFiTargetEnrichment_snakemake	

Sequencing performance - including read lengths, yield, and read counts - vary based on sample quality, sample type, and fragment length.

[PacBio Glossary of Terms](#)

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