



Application		Whole genome sequencing				Viral sequencing	Full-length RNA sequencing			Metagenomics		Targeted sequencing	
Application		De novo genome assembly	Variant detection	Microbial de novo genome assembly	De novo genome assembly w/ ultralow input	Adeno-associated virus (AAV)	Whole transcriptome	Genome annotation	Single-cell	Full-length 16S rRNA	Shotgun profiling or assembly	Amplicons	Target enrichment
Experimental design													
Experimental design	Value proposition	Produce reference-quality, haplotype-phased genome assemblies including 5mC methylation profiles	Detect and phase 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 full-length AAV genomes in single reads	Discover and quantify full transcripts	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 / haplotype	10X for SVs; 30X for all variant classes	15X / microbe	15X / haplotype	40,000 full-length reads / sample	10M reads / sample	5M reads / sample	3,000 - 10,000 unique reads / single cell	8,000 reads / sample	See Best Practices Guide	50X / locus	50X / locus
	Library insert size	15 - 20 kb	15 - 20 kb	7 - 10 kb	10 - 12 kb	2 - 5 kb	500 bp to 3+ kb cDNA, 10 - 15 kb Kinnex array	500 bp to 3+ kb cDNA, 10 - 15 kb Kinnex array	500 bp to 1 kb cDNA, 10 - 15 kb Kinnex array	1.5 kb amplicon, 15 - 20 kb Kinnex array	10 kb	500 bp - 15 kb	3 - 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	2 samples	3 samples	1 sample	Up to 1,536 samples	Profile: 48 communities Assemble: 4 communities	Up to 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	24 AAV samples	4 samples	8 samples	1 sample	Up to 1,536 samples	Profile: 96 communities Assemble: 12 communities	Up to 1,000+ samples	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 [101-987-800]	Preparing multiplexed AAV SMRTbell libraries using SMRTbell prep kit 3.0 [102-126-400]	Preparing Kinnex libraries using the Kinnex full-length RNA kit [103-238-700]	Preparing MAS-Seq libraries using MAS-Seq for 10x Single Cell 3' kit [102-678-600]	Preparing Kinnex libraries from 16S rRNA amplicons [103-238-800]	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 [102-359-000]	HiFi sequencing with Twist Bioscience target enrichments [102-326-515]	
	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 / microbe	5 - 20 ng	1 µg total	300 ng total RNA / sample	15-75 ng of 10x Chromium single-cell cDNA	1 - 2 ng / sample (input into PCR)	300 ng / 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 / microbe	5 - 20 ng	1 µg total	300 ng total RNA / sample	15-75 ng of 10x Chromium single-cell cDNA	1 - 2 ng / sample (input into PCR)	300 ng / sample	300 ng for ≤3 kb 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	Read Segmentation and Iso-Seq Analysis	Read Segmentation and Single-cell Iso-Seq Analysis	Read Segmentation	n/a	n/a	n/a	HiFi Target Enrichment
	Community tools	hifiasm	DeepVariant	hifiasm	hifiasm	Form Bio	SQANTI3	Seurat	HiFi-16S-workflow	pb-metagenomics-tools	PacBio Amplicon Analysis (pbaa)	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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