

EXPLORE METAGENOMES IN HIGH RESOLUTION



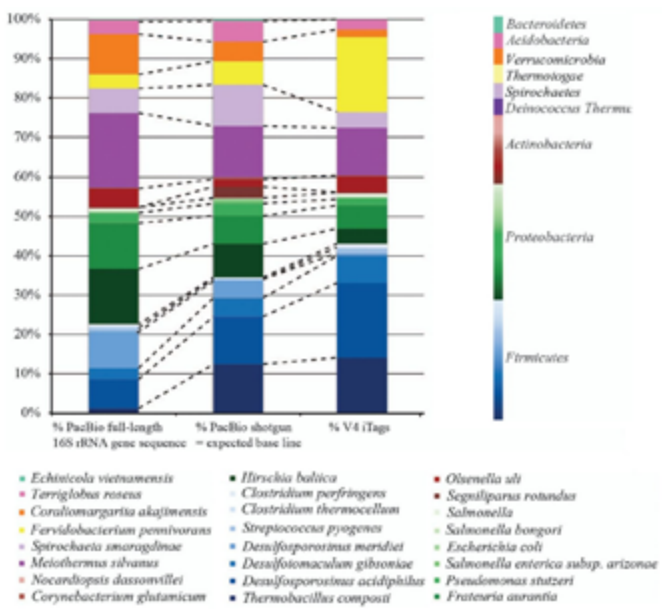
SEQUENCE WITH CONFIDENCE



The ability to identify and understand the functions of the complex microbial populations living in, on, and around us requires comprehensive characterization of each community member. Highly accurate long reads—HiFi reads—with single-molecule resolution make Single Molecule, Real-Time (SMRT®) Sequencing ideal for full-length 16S rRNA sequencing, long-read metagenomic profiling, and shotgun metagenomic assembly.

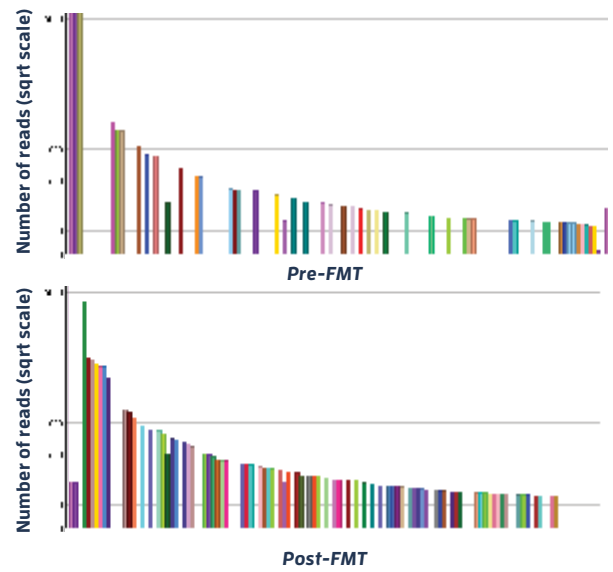
- Identify full-length genes within a microbial community using long-read metagenomic profiling with no assembly required
- Achieve deeper strain-level resolution of community composition and phylogeny
- Reconstruct longer contigs in whole-genome shotgun metagenomic assemblies and discover novel genes and gene clusters
- Leverage epigenomic data to associate contigs and plasmids from closely related strains

FULL-LENGTH 16S rRNA SEQUENCING: SPECIES-LEVEL PHYLOGENETIC RESOLUTION



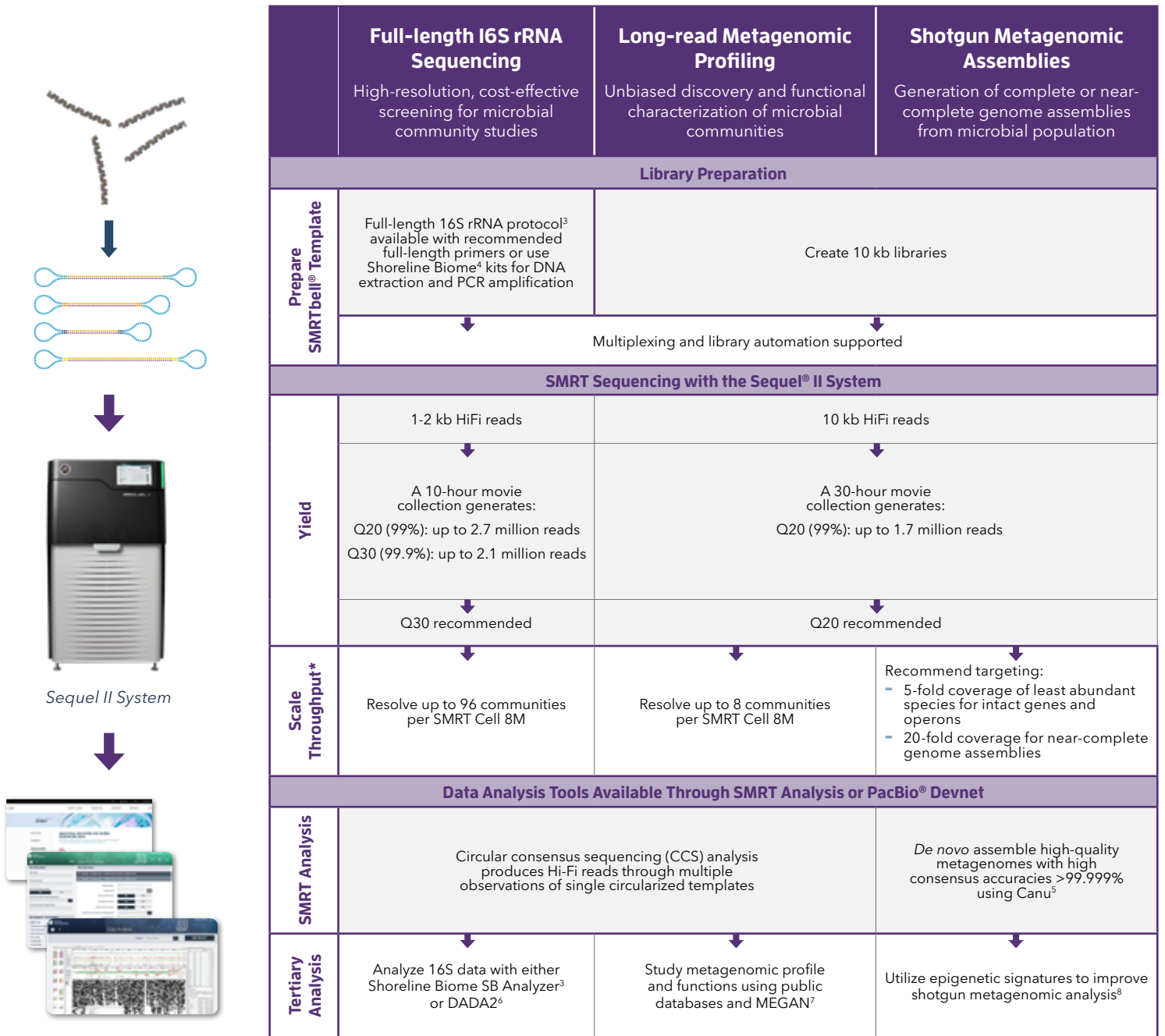
Full-length 16S rRNA sequences from a mock microbial community provided a more accurate community profile compared with short-read 16S rRNA and shotgun assembly results¹.

LONG-READ METAGENOMIC PROFILING: FECAL MICROBIOME DIVERSITY



Long, single-molecule reads generated high-resolution metagenomic profiles down to the species and strain level for pre- and post-fecal-microbiota-transplant (FMT) samples from an individual suffering from chronic *C. difficile* infection².

FROM DNA TO RESOLVED MICROBIAL COMMUNITIES



*Read lengths, reads/data per SMRT Cell 8M and other sequencing performance results vary based on sample quality/type and insert size.

KEY REFERENCES

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