Highly accurate long reads - HiFi reads - are the new benchmark for full length 16S, metagenome profiling, and metagenome assembly

- Determine community composition at the species or strain level with competitively priced full-length 16S sequencing
- Profile metagenomes efficiently and cost-effectively with an average of 8 full-length genes in every HiFi read
- Generate hundreds of high-quality (HQ) metagenome assembled genomes (MAGs), many of which are single-contig, circular MAGs.
- Leverage epigenomic data to associate contigs and plasmids from closely related strains

Full-length 16S rRNA sequencing
Species-level phylogenetic resolution

The proportion of 16S sequences from each bacterial genus that cannot be identified at the species level varies significantly depending on which variable region is used. Since the human gut can harbor a broad diversity of bacterial clades, only full-length sequences (V1-V9) can provide unbiased resolution of all the species that may be present.¹

HiFi metagenomics
Precise species profiling, more functional annotations, more high-quality MAGs, and more circular MAGs, even at lower coverage

With up to 9 complete genes per HiFi read, PacBio® data provides rich functional information; nearly every read contributes to your understanding of the biological functions present in your microbial community.²

Obtain more and richer metagenome functional information:

- ~80–90% of HiFi reads are functionally annotatable
- Each HiFi read typically has an average of four functional annotations

Achieve standout metagenome assemblies:

- ~90–125 HQ-MAGs per sample with ~17 Gb data; many are single contig with ~50 per sample
- 417 HQ-MAGs in total across four samples
From DNA to resolved microbial communities

<table>
<thead>
<tr>
<th>Library preparation</th>
<th>Full-length 16S rRNA sequencing</th>
<th>Metagenome profiling</th>
<th>Metagenome assembly</th>
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<tr>
<td>Prepare SMRTbell® template</td>
<td>High-resolution, cost-effective screening for microbial community studies</td>
<td>Unbiased compositional and functional characterization of microbial communities</td>
<td>Generation of complete or near-complete genome assemblies from microbial populations</td>
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<td>Follow full-length 16S rRNA protocol with recommended primers or use Intus Biosciences StrainID</td>
<td>Create ~10–15 kb libraries for HiFi metagenomics</td>
<td>Multiplexing and library automation supported</td>
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SMRT sequencing with the Sequel II® or Sequel IIe system

- Yield on the Sequel II or IIe system*: 1.6 kb HiFi reads ~10–15 kb HiFi reads
- A 10-hour movie collection generates up to 3.5 million >Q20 reads
- A 30-hour movie collection generates up to 3 million >Q20 reads
- Scale throughput on the Sequel II or IIe system*: Resolve up to 192 communities per SMRT® Cell 8M for $9/sample
- Multiplex up to 48 communities per SMRT Cell 8M for $85 / sample for taxonomic or functional profiling
- Recover up to 45 high-quality (HQ) MAGs for up to 4 multiplexed samples or up to 110 HQ MAGs for 1 sample for ~$10 / HQ MAG

Data analysis tools available through SMRT® Analysis or PacBio DevNet

- Tertiary analysis
  - Analyze 16S data with either DADA2®, QIIME2®, microbiomehelper®, One Codex®, EZBiome®, or with our GitHub-posted pipeline
  - Study metagenome compositions and functions using DIAMOND and MEGAN-LR®, or Sourmash® with our GitHub-posted pipeline or with BugSeq® (a PacBio Compatible Partner)
  - De novo assemble high-quality metagenomes to high consensus accuracies >99.999% (Q50) with hifiasm-meta®, metaFlye®, or HiCanu® and perform QC, binning, classification, and evaluation with our streamlined GitHub-posted pipeline

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* Prices, listed in USD, are approximate and may vary by region. Pricing includes library and sequencing reagents run on a Sequel II or IIe system and does not include instrument amortization or other reagents.

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KEY REFERENCES

2. Gehrig, J., et al. (2022) Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. Microbial Genomics, 8(3), 10.1099/mgen.0.000794
3. https://github.com/PacificBiosciences/pb-metagenomics-tools/blob/master/docs/PacBio-Data.md
7. Intus Biosciences
13. https://github.com/PacificBiosciences(pb-16S-nf

Learn about metagenome sequencing: pacb.com/microbial-pop