

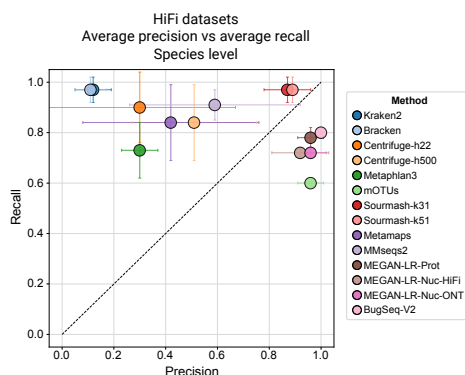
TAXONOMIC AND FUNCTIONAL PROFILING WITH HIFI METAGENOMICS

High-accuracy long-read sequencing to characterize complex microbial communities

HiFi metagenome profiling provides more (and richer) functional information and precise species classifications.

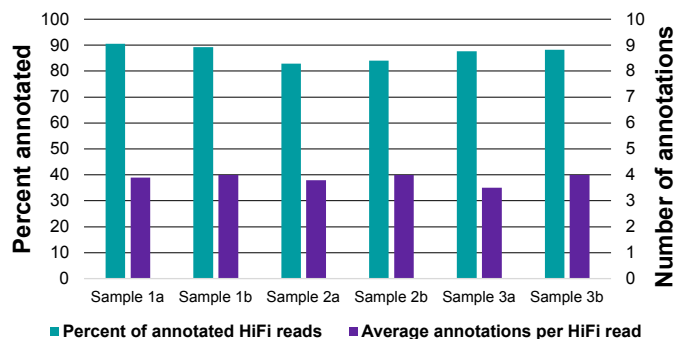
- Each HiFi read typically has an average of eight intact genes per read, providing richer information about genes that co-occur in a single microbe, and may be co-expressed
- 80-90% of HiFi reads have at least one functional annotation, and typically average four, whereas only ~1/3 of short reads can be annotated even once
- HiFi reads can assign taxonomy with high precision and recall

Shotgun metagenome taxonomic profiling



With highly accurate long-read metagenomic data, you can profile species with high precision and recall; tools/methods have been evaluated to provide recommendations to which work best for long-read metagenomic data.¹

Shotgun metagenome functional profiling



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

Typical workflow from DNA to metagenome taxonomic and functional resolution



Prepare SMRTbell® template

Create ~10–15 kb libraries for HiFi metagenome sequencing³



SMRT® sequencing and SMRT® analysis

Obtain HiFi reads with the Sequel® II/e or Revio™ system



Tertiary data analysis

Profile metagenome taxonomy and functions using our GitHub pipelines⁵ with Sourmash⁶ or Diamond⁷ + MEGAN-LR⁸, or with the BugSeq cloud-based platform⁹

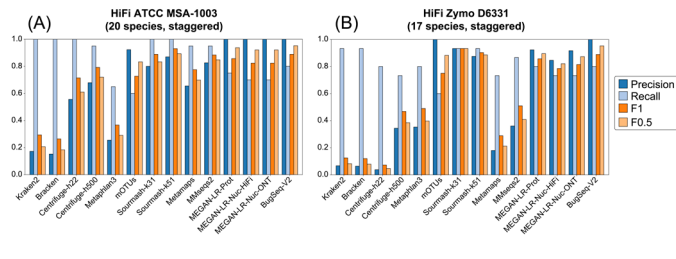
“Our comparisons between long-read sequencing technologies indicate that read quality remains critical for taxonomic profiling performance...The long-read datasets produced significantly better results than the short-read datasets.”

– Portik, Brown, and Pierce-Ward, 2022

The PacBio partnership with BugSeq empowers public health labs to solve complex microbial questions

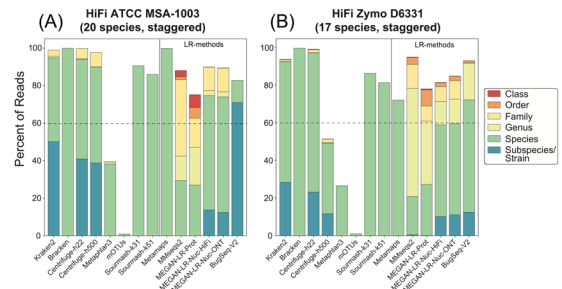


Yield top accuracy for taxonomic profiling



For the best precision/recall trade-off for taxonomic profiling, use BugSeq with HiFi reads.¹ BugSeq offers a curated reference database for analyses requiring the highest quality, and the NCBI nucleotide database for broader taxonomic representation.

Enable strain-level abundance



In a comparison of analytical tools, BugSeq produced the most accurate abundance estimates and classified the greatest number of reads to the strain rank using PacBio HiFi data.¹

Dive deep and analyze antimicrobial resistance

Klebsiella pneumoniae

| Antimicrobial | Class | Genotypic Predictor of Resistance | Confidence | Genotypic Determinant |
|-----------------------------|----------------|-----------------------------------|------------|---|
| Amikacin | Aminoglycoside | Present | Very High | aac(6)-Ib; aac(6)-Ib-cr; aph(3)-VI |
| Streptomycin | Aminoglycoside | Present | Very High | aadA1 |
| Tobramycin | Aminoglycoside | Present | Very High | aac(6)-Ib; aac(6)-Ib-cr |
| Gentamicin | Aminoglycoside | Not Detected | | |
| Amoxicillin clavulanic acid | Beta-Lactam | Present | Very High | blaNDM-5 |
| Ampicillin | Beta-Lactam | Present | Very High | blaCTX-M-15; blaNDM-5; blaSHV-11; blaTEM-1A |
| Aztreonam | Beta-Lactam | Present | Very High | blaCTX-M-15 |
| Cefepime | Beta-Lactam | Present | Very High | blaCTX-M-15; blaNDM-5 |
| Cefixime | Beta-Lactam | Present | Very High | blaCTX-M-15; blaNDM-5 |

Demo antimicrobial resistance report from BugSeq outputs. Beyond taxonomic profiling, BugSeq performs *de novo* assembly and identifies predictors of antimicrobial resistance (genes and mutations) as well as virulence factors using curated databases.¹⁰

Discover with simplicity

With HiFi data, it's as easy as uploading raw data. BugSeq is the only tool tested by Portik et al. (2022) that is cloud-based, has a graphical user interface, and performs quality control.¹

“Overall, we find that BugSeq, MEGAN-LR-prot, and MEGAN-LR-nuc provide the best tradeoffs for all long-read metagenomics data.”

– Portik, Brown, and Pierce-Ward, 2022



Learn more about PacBio microbial community applications and BugSeq:
pacb.com/metagenomics | bugseq.com/pacbio

KEY REFERENCES

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