



Advancing microbial genomics with highly accurate short read and long read sequencing

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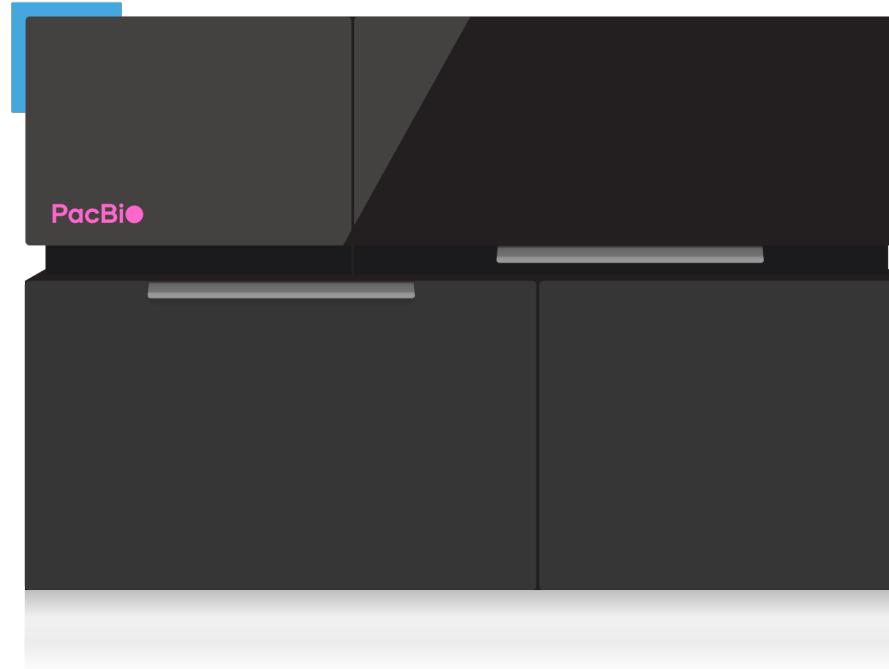
Onso system

Setting the bar for short-read accuracy



Sequencing by binding (SBB) enables extraordinary accuracy for short-read sequencing

Key platform specifications



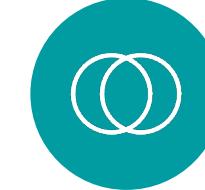
400 – 500 M reads (SE)
800 – 1,000M reads (PE)



Sequencing kits:
200-cycle kit: 1×200 and 2×100
300-cycle kit: 2×150



≥90% bases Q40+

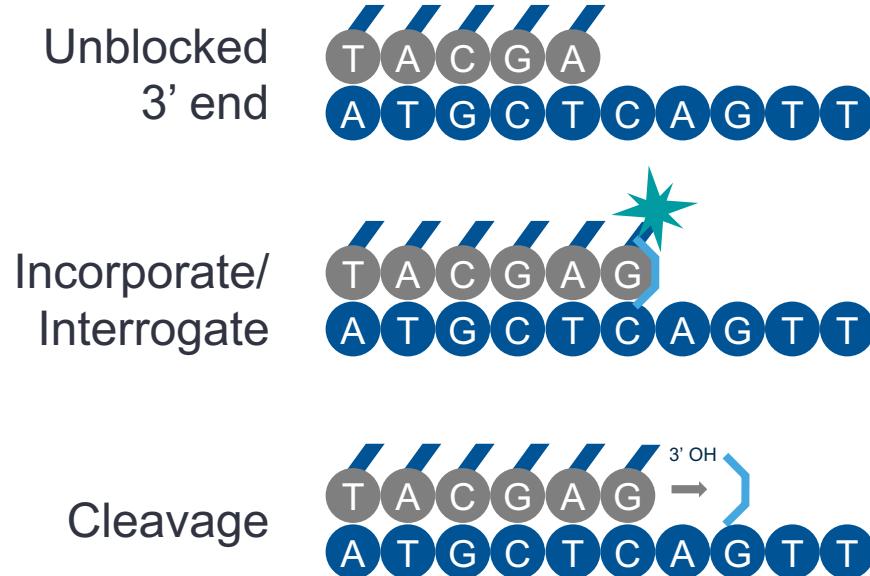


Seamless compatibility:
Conversion kit enabling existing P5/P7
libraries
Leverage existing short-read analysis
pipelines

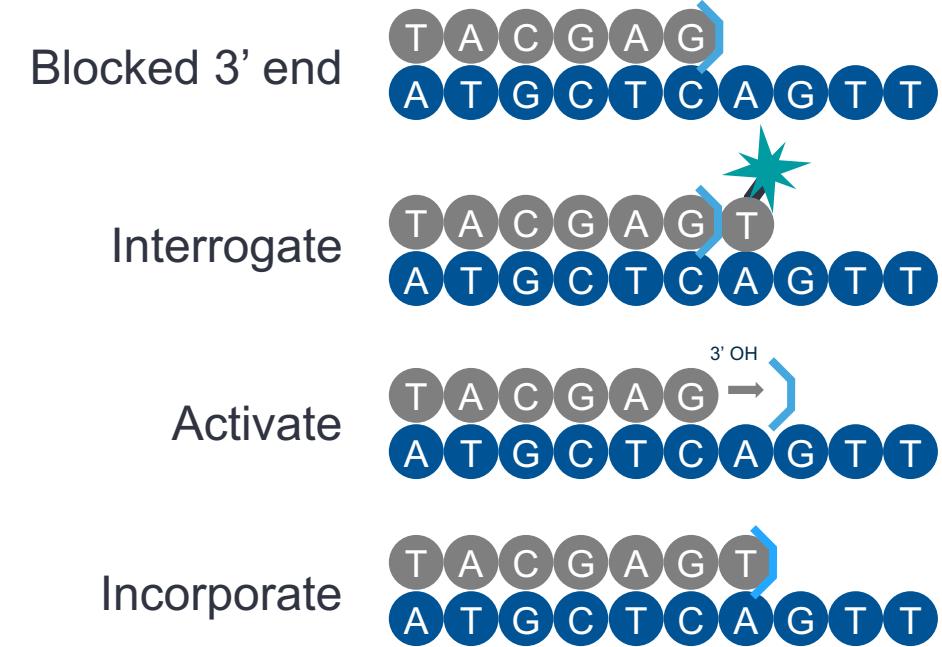
SBB chemistry enables highly accurate reads

Optimized steps, native nucleotide incorporation, scarless DNA strand formation

Sequencing by synthesis (SBS)



Sequencing by binding (SBB)



Benefits of SBB over SBS

>90%

Bases at Q40+

- Low sequencing noise = improved accuracy



Sequence through difficult / repetitive regions

- Better resolution of homopolymer regions



Negligible index hopping

- Reduced index mis-assignments



Low duplication rate

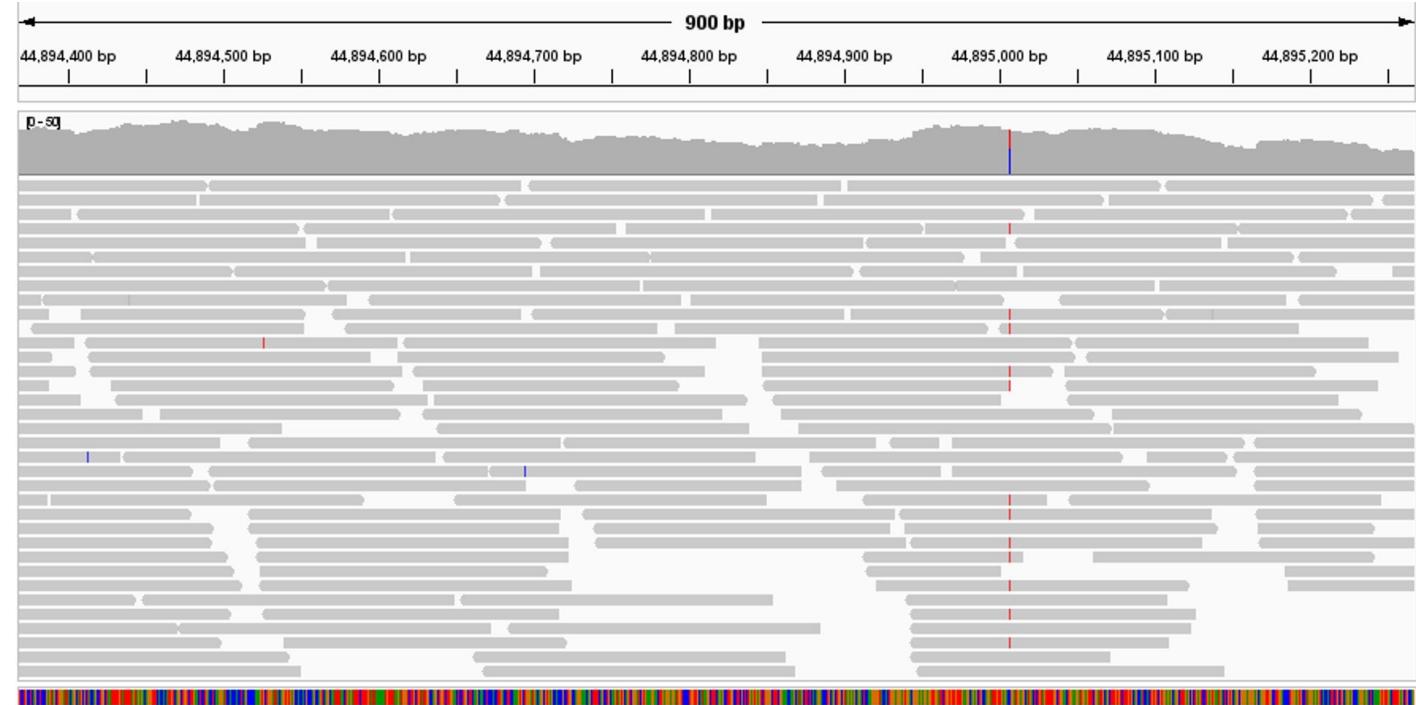
- Less sequencing redundancy



Lower input requirements

- Conserve your precious samples

SBB offers near perfect reads



HG002; chr19:44,894,368-44,895,266

Onso delivers a comprehensive solution for short-read customers leveraging our experience in sequencing



Onso sequencing system



Onso 200 + 300 cycle sequencing kits



Onso library prep + conversion kits

12+ years of commercial experience | Comprehensive service & support | Global organizational reach

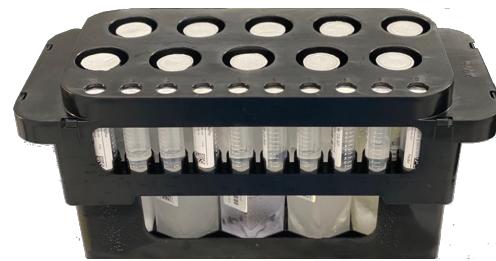
Onso sequencer setup and run

Designed for simplicity - less than 10 minutes from welcome screen to run start

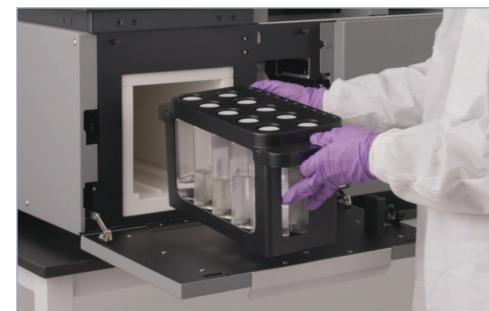
OPEN FLOW CELL LID &
REAGENT DRAWER



LOAD SEQUENCING
REAGENT PACK

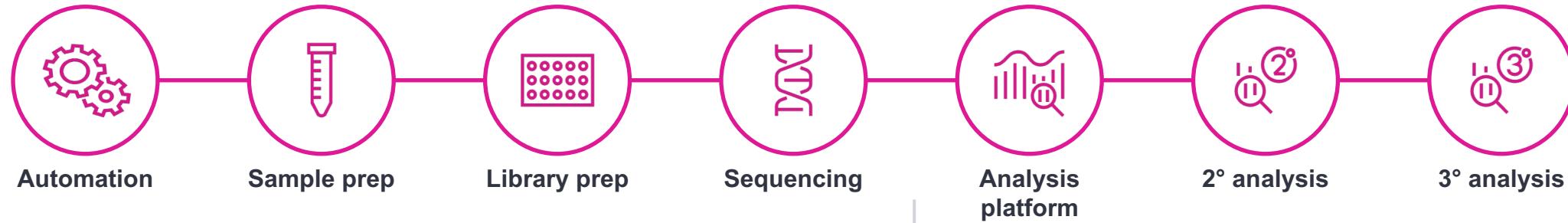


ENTER RUN PARAMETERS &
START SEQUENCING RUN



Onso sequencing ecosystem

Highly accurate short-read capability supported by trusted ecosystem partners



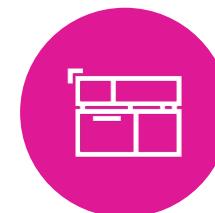
10X GENOMICS
Chromium Single Cell 3'

T W I S T
BIOSCIENCE

Exome 2.0
MRD Rapid 500

Agilent
SureSelect
Target Enrichment

QIAGEN
QIAseq Targeted Ultra



Google Health
DeepVariant

Sentieon
DNAscope
TNscope
TNseq

PacBio Compatible Full partner list:
pacb.com/compatible

Wastewater metagenomics comparison of SBB vs SBS

Sample ID	Sample site	Description
Sample 1	Influent from wastewater treatment plant 1	The raw wastewater without treatment
Sample 2	Influent from wastewater treatment plant 2	The raw wastewater without treatment
Sample 3	Primary Sludge	The sediment from primary treatment process

Sample preparation: DNA from each sample purified by ZymoPURE Water DNA/RNA kit from 10 mL raw wastewater or 1mL sludge sample

Main concerns in wastewater: 1. Dominant species/genus; 2. Functional groups that benefit or harmful to the treatment; 3. Pathogens; 4. AMR

Sequencing depth: 8M per sample for each - ILMN NextSeq & PacBio Onso

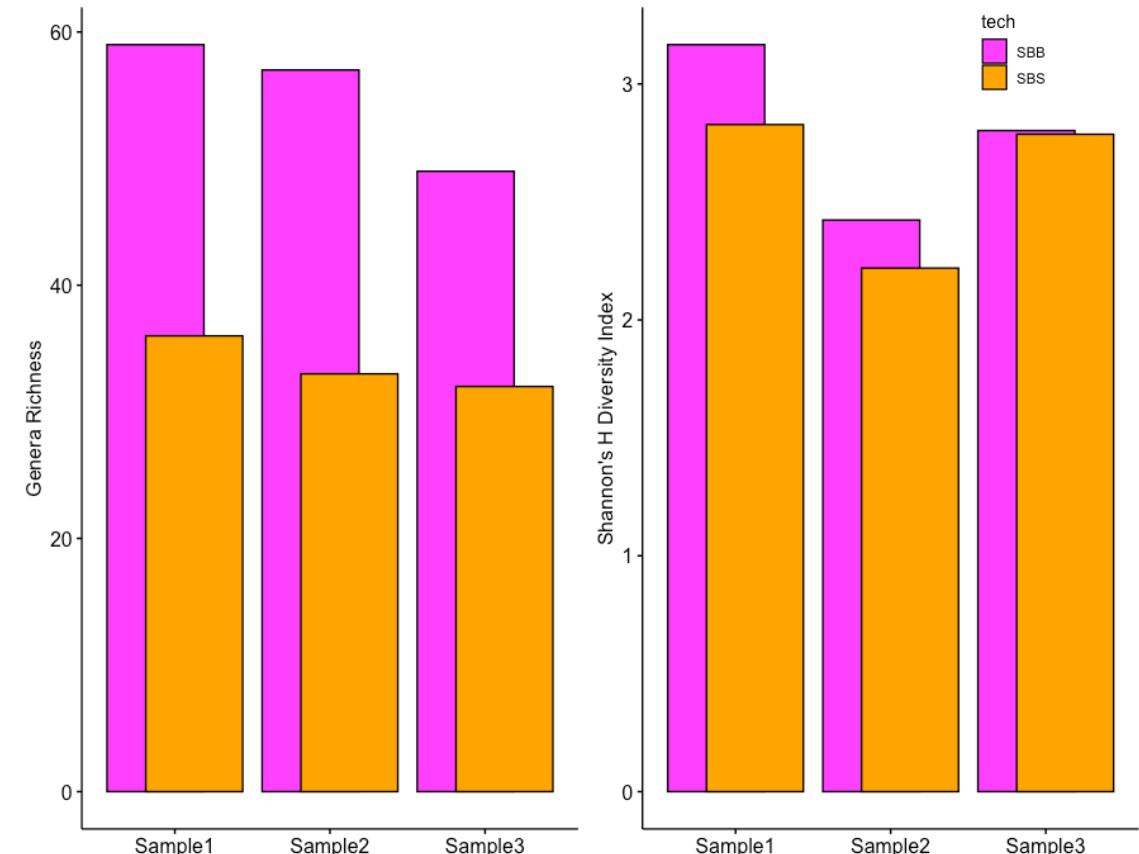
Analysis: Both technologies analyzed with the Zymo wastewater analysis workflow

More microbial diversity was able to be detected with SBB vs SBS

- More genera detected from SBB (121) than SBS (72), both using the Zymo analysis workflow

		Sample 1	Sample 2	Sample 3
Phylum	Onso	16	16	15
	NextSeq	10	8	12
Family	Onso	38	40	35
	NextSeq	24	22	25
Genus	Onso	61	59	50
	NextSeq	38	36	34
Species	Onso	75	106	81
	NextSeq	57	45	50

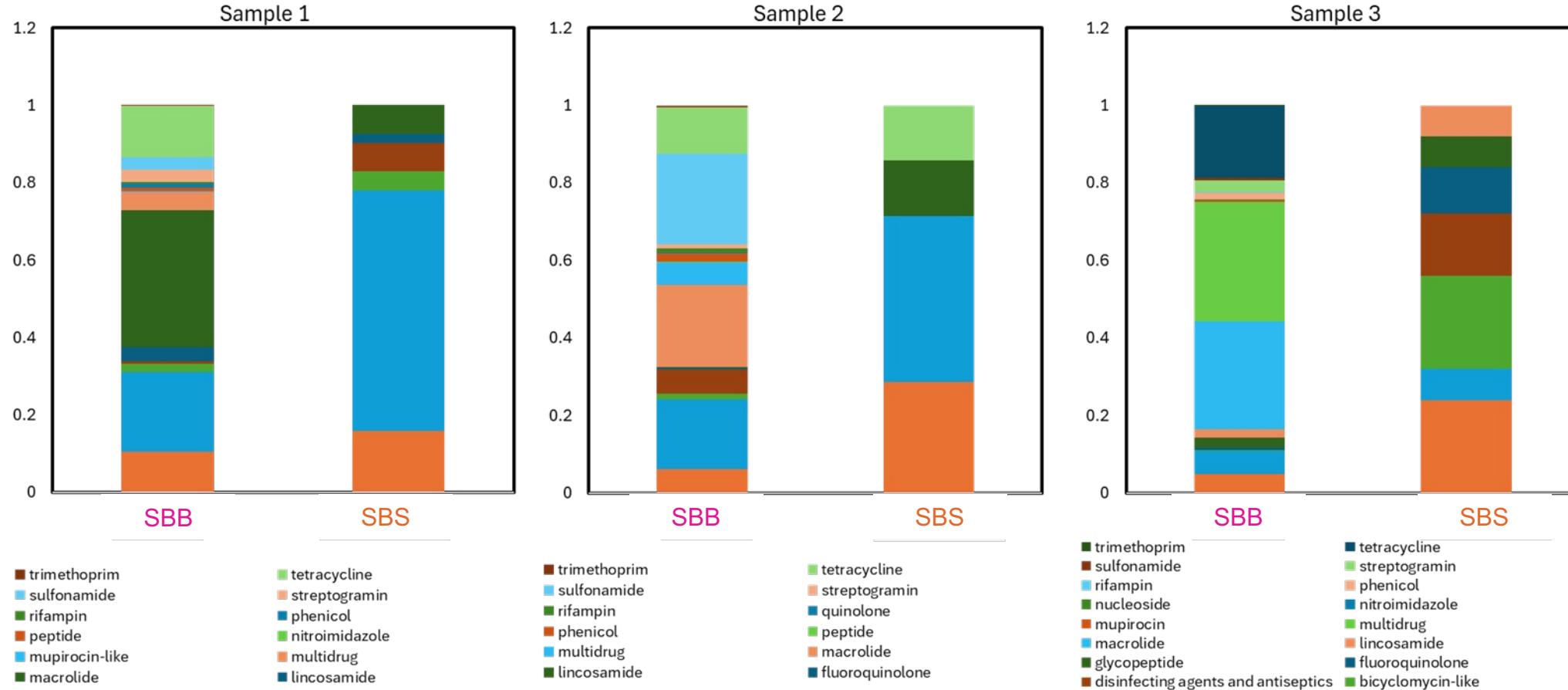
Number of taxa generated at each taxonomic level for Onso and NextSeq



Genera Richness and Shannon Diversity for Onso and NextSeq

More AMR classes were able to be detected with SBB vs SBS

- AMR classes vary across different technology
- More ARGs detected from SBB (21) than SBS (7), both using the Zymo analysis workflow



The Antimicrobial resistance classes in each sample presented in relative abundance from SSB and SBS

SBB outperforms SBS at detecting microbial genera, antimicrobial resistance classes, and functional bacteria in wastewater samples

Using shotgun metagenomics at the same number of reads: 8M reads per sample for 3 same samples

# detected	SBB	SBS
Microbial genera	121	72
AMR classes	21	7
Functional bacteria	16	13

Revio system

HiFi sequencing at scale



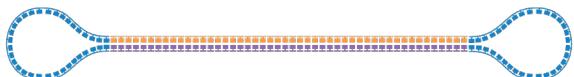
What is HiFi sequencing?

HiFi reads are both long (up to 25 kb) and highly accurate (99.9%)

Start with high-quality double-stranded DNA



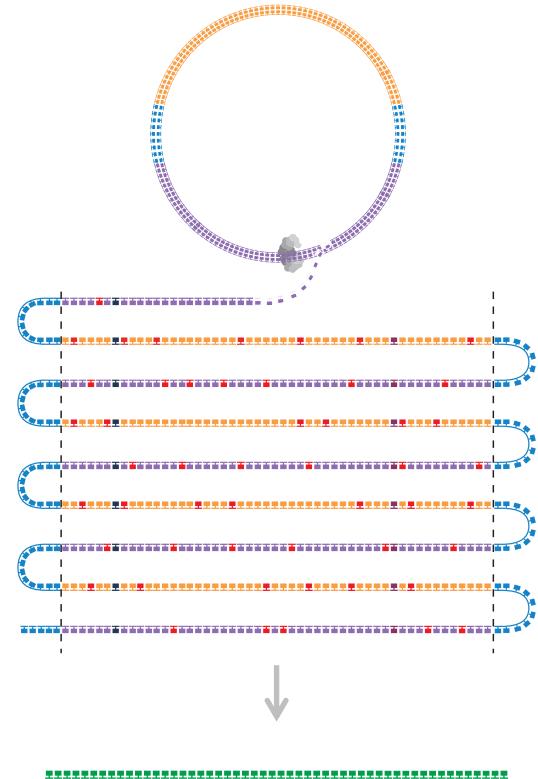
Ligate SMRTbell adaptors and size select



Anneal primers and bind DNA polymerase



Circularized DNA is sequenced in repeated passes



The polymerase reads are trimmed of adapters to yield subreads

Consensus is called from subreads

HiFi read
99.9% accuracy
Up to 25 kb

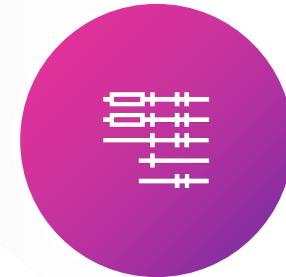
More complete + accurate long-read sequencing



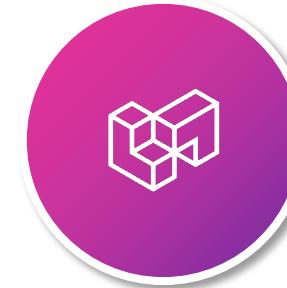
Metagenomics



16S sequencing



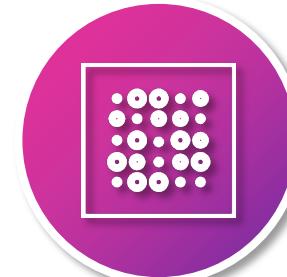
Microbial Assembly



Epigenetics



Viral sequencing

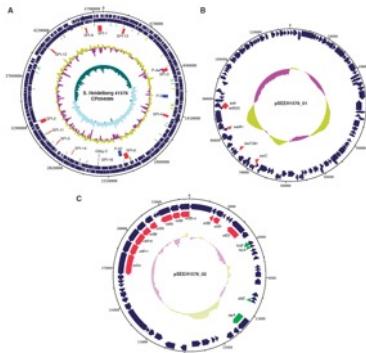


Targeted sequencing



HiFi sequencing delivers more comprehensive and higher quality data for microbial genomics from culture to culture-free

Microbial whole genome sequencing



Obtain single contig chromosomes for most bacteria + plasmids

Consensus accuracies >99.99%

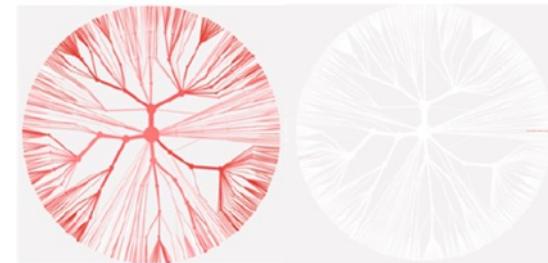
Detection of R-M system motifs

Identify strains, AMR genes, and mobile vectors mediating spread

Short-read polishing not needed

Competitive cost with short reads

Full-length 16S / ITS sequencing



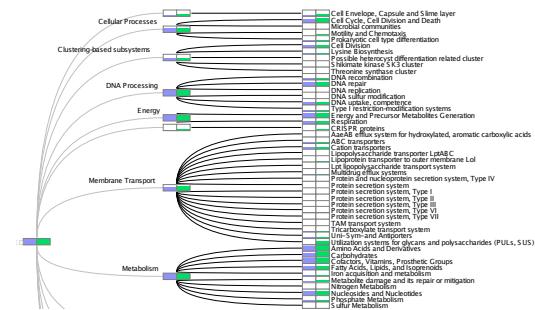
Species/strain-level resolution

More classified reads

Reveals true sample diversity

Competitive cost with partial 16S

Shotgun metagenome profiling



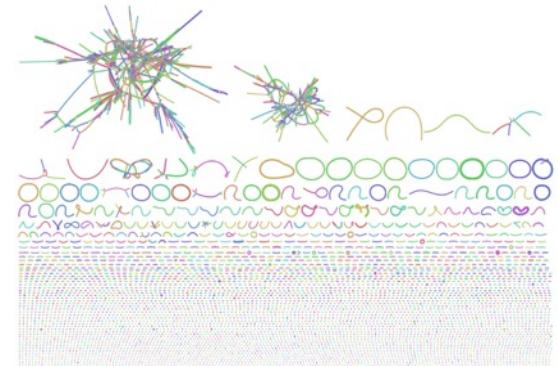
~8 genes per sequence read

~90% of reads with at least 1 gene

Profile taxonomy with high precision and recall

Competitive cost with short reads

Shotgun metagenome assembly



Obtain many high-quality MAGs

Complete, closed genomes

Resolves closely related strains

Short-read polishing (hybrid assembly) not needed

Four independent stages on Revio system enable flexible experimental designs



Metagenomes per year (estimate):

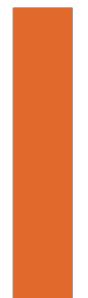
Revio system



MAGs*: ~4,000 metagenomes per year at 3-plex

Profiling: ~120,000 metagenomes per year at 96-plex

Sequel IIe system



MAGs*: ~250 metagenomes per year at 1-plex
Profiling: ~12,000 metagenomes per year at 48-plex



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