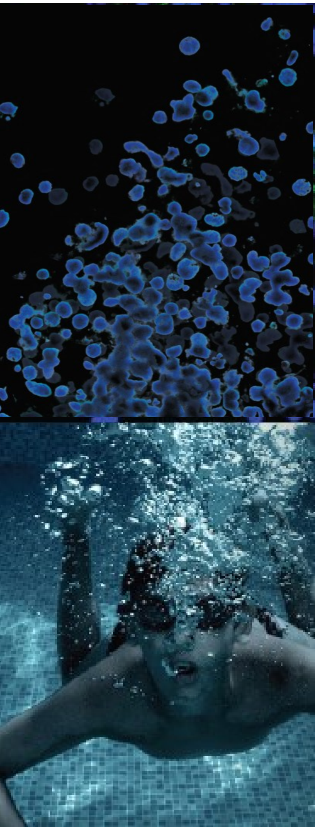


Making Sense Out of Microbiome Data – The Importance of Standards

Briana Benton, BS
Technical Manager, ATCC

Credible Leads to Incredible™

Agenda

- ✓ Background on American Type Culture Collection
- ✓ Challenges in microbiome research
  - ✓ Discuss why standards are essential
- ✓ Development of microbiome standards
- ✓ The ATCC® Microbiome Standards portfolio and upcoming new products
- ✓ Applications of standards in microbiome research
  - ✓ Extraction method, assay variability, NGS library preparation, and bioinformatics analysis
- ☒ Microbiome assay development
- ☒ Show the best data
- ☒ Recommend any specific assay, kit, protocol, or instrument

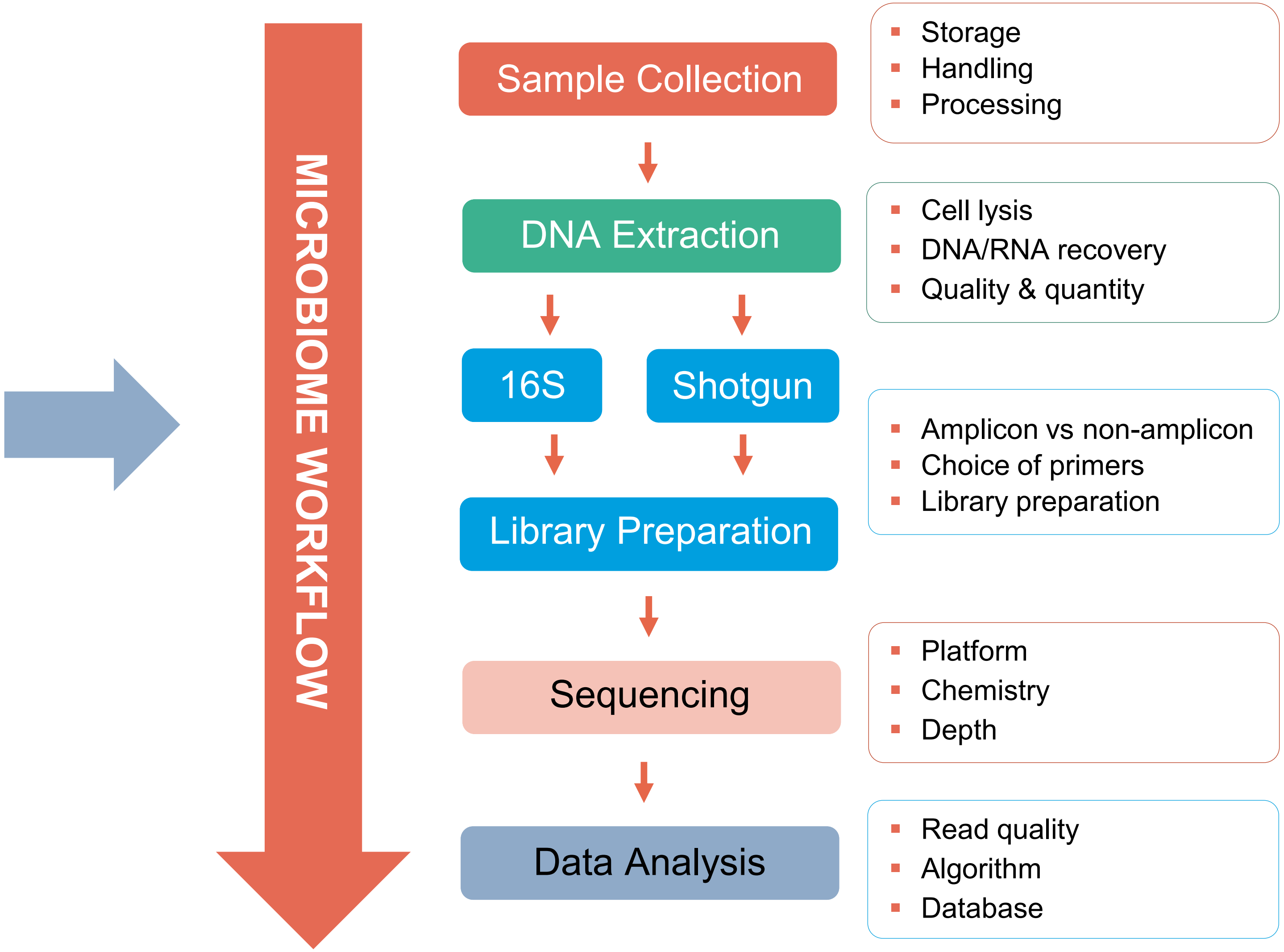
About ATCC

- Founded in 1925, ATCC is a non-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's largest, most diverse biological materials and information resource for microbes – the "*gold standard*"
- Innovative R&D company featuring gene editing, microbiome, NGS, advanced models
- cGMP biorepository
- Partner with government, industry, and academia
- Leading global supplier of authenticated cell lines, viral and microbial standards
- Sales and distribution in 150 countries, 18 international distributors
- Talented team of 450+ employees, over one-third with advanced degrees

Microbiome Research

The microbiome field is rapidly moving toward translational research pertinent to human health and disease, therapeutics, and personalized medicine

Challenges in Microbiome Research



Sample Collection
- Storage
- Handling
- Processing

DNA Extraction
- Cell lysis
- DNA/RNA recovery
- Quality & quantity

16S / **Shotgun**

Library Preparation
- Amplicon vs non-amplicon
- Choice of primers
- Library preparation

Sequencing
- Platform
- Chemistry
- Depth

Data Analysis
- Read quality
- Algorithm
- Database

Development of Mock Microbial Communities

Strain selection criteria

- Ability to lyse
- Gram stain
- GC content
- Genome size
- Spore formation
- Microbiome site
- 16S rRNA copy number
- Genome complexity
- ITS variability
- Assembled genomes
- Diagnostic relevance
- Aerobic/ anaerobic

Whole Cell Standards

- Authenticated ATCC cultures
- Growth and image cytometry cell counting
- Mixed in even proportions.
- Store at 4°C until ready to use

Genomic DNA Standards

- Authenticated ATCC nucleic acids
- Fluorescent dye-based quantification
- Mixed in even or staggered proportions based on genome copy number
- Store at -20°C

Assay development, optimization, verification, and quality control

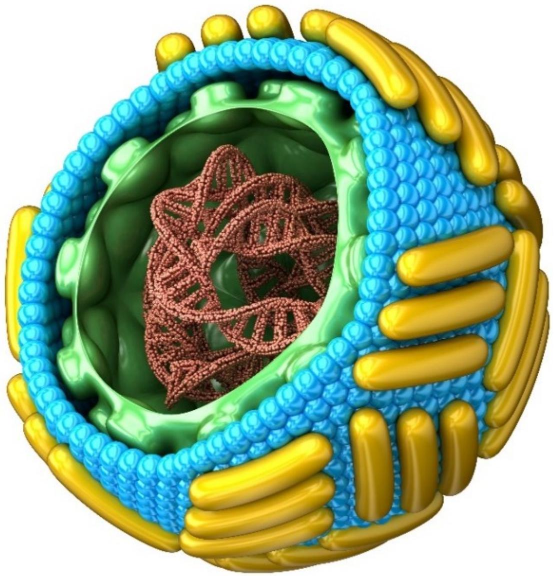
ATCC® Microbiome Standards Portfolio

Preparation	ATCC® Catalog No.	Number of Organisms	Composition	Complexity	Importance
Genomic DNA	MSA-1000™	10	Even	Medium	Standards for assay development and optimization
	MSA-1001™	10	Staggered	Medium	
	MSA-1002™	20	Even	High	
	MSA-1003™	20	Staggered	High	
Whole cell	MSA-2003™	10	Even	Medium	
	MSA-2002™	20	Even	High	
Genomic DNA	MSA-4000™	11	Staggered	Medium	NGS-based pathogen detection
Genomic DNA	MSA-3000™	6	Even	Low	Environmental studies
	MSA-3001™	10	Even	Medium	
	MSA-3002™	10	Staggered	Medium	

Site-specific Microbiome Standards

Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Importance
Oral	Whole cell	MSA-2004™	6	• Mock microbial communities representing the oral, skin, gut, and vaginal microbiomes • Comprises normal and atypical flora • Anaerobic and aerobic microbial strains • A combination of Gram-positive and -negative bacterial cultures • Even composition
	Genomic DNA	MSA-1004™		
Skin	Whole cell	MSA-2005™	6	
	Genomic DNA	MSA-1005™		
Gut	Whole cell	MSA-2006™	12	
	Genomic DNA	MSA-1006™		
Vaginal	Whole cell	MSA-2007™	6	
	Genomic DNA	MSA-1007™		

ATCC Virome Standards



Composition of Virome Standards
Human herpesvirus 5 strain AD169 (ATCC® VR-538™)
Human mastadenovirus strain F (ATCC® VR-931™)
Influenza B virus strain B/Florida/4/2006 (ATCC® VR-1804™)
Zika virus strain MR 766 (ATCC® VR-1838™)
Reovirus 3 strain Dearing (ATCC® VR-824™)
Human respiratory syncytial virus strain A2 (ATCC® VR-1540™)

Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Specification (ddPCR™)	Applications
Virome	Virus Mix	MSA-2008™	6	2 x 10^3 genome copies/µL per virus	Standards for virome assay development, optimization, verification, and validation; evaluating reproducibility; and use as a daily run quality control
	Nucleic Acid Mix	MSA-1008™	6	2 x 10^4 genome copies/µL per virus	

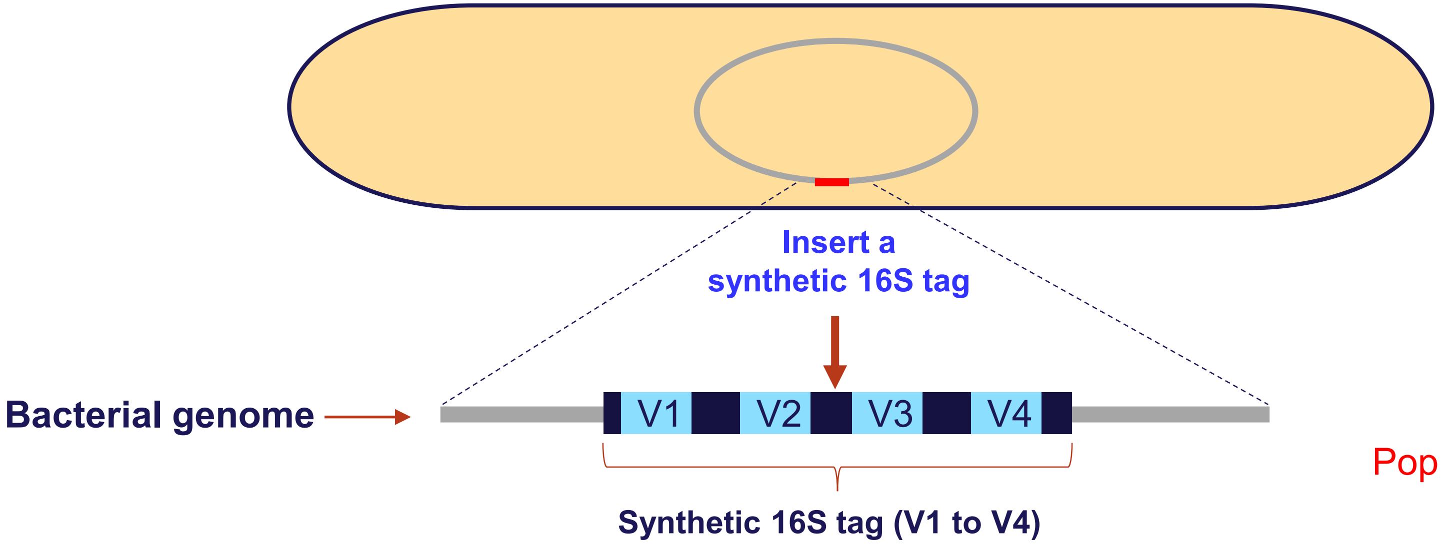
Spike-in Standards (3 Strain Tagged Mix)

Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Importance
3 Strain Tagged Mix	Whole cell	MSA-2014™	3	• Microbiome measurements and data normalization • 16S rRNA and shotgun assay verification, validation, and quality control
	Genomic	MSA-1014™		

Spike-in Composition

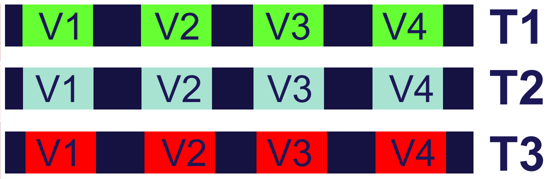
Species	Gram Stain	Genome size (Mb)	Tag size (bp)	G/C Content (%)	16S Copies	Tag copies	Cells per vial
Escherichia coli **Tag1**	Negative	4.59	829	50.8	7	1	2 x 10^7
Clostridium perfringens **Tag2**	Positive	3.25	799	29.0	10	1	2 x 10^7
Staphylococcus aureus **Tag3**	Positive	2.70	833	32.8	6	1	2 x 10^7

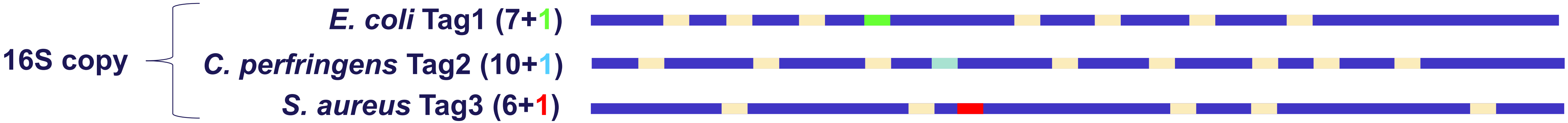
Engineering Synthetic 16S Tag Into Bacterial Genome



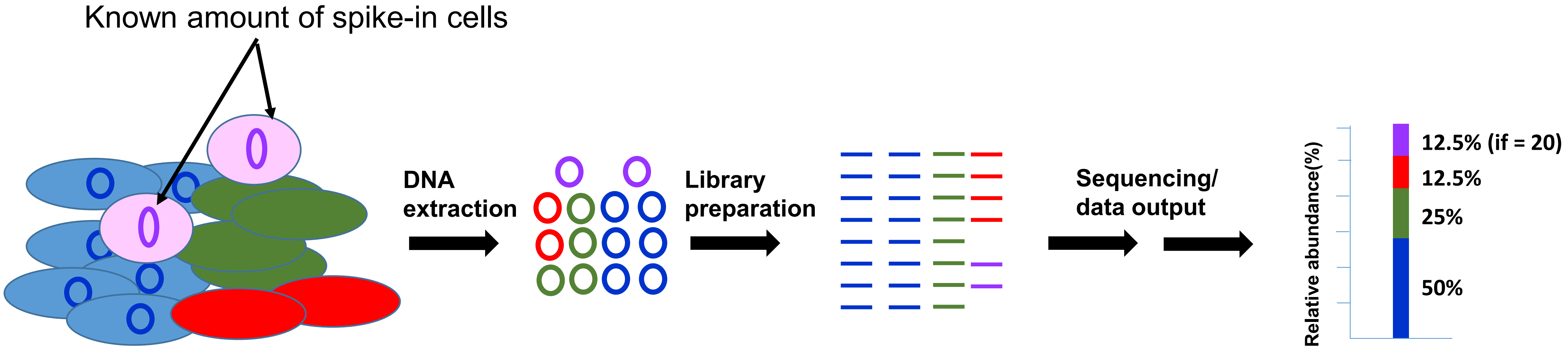
Popular regions: V1 to V4

Bacterial Strains	Gram Stain	Genome G/C (%)	Insertion loci	BSL
Escherichia coli Tag1	Negative	50.8	Beta galactosidase	1
Clostridium perfringens Tag2	Positive	29.0	Theta-toxin	2
Staphylococcus aureus Tag3	Positive	32.8	O-antigen polymerase	2





Spike-in Internal Control for Normalization

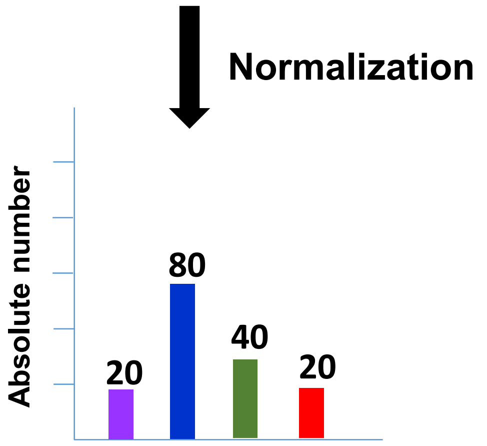


Known amount of spike-in cells

DNA extraction

Library preparation

Sequencing/ data output



Normalization

Spike-ins of known quantity can provide a baseline number for comparison with the number from unknown quantity, such that the data can be normalized within a sequencing assay and between different assays

Spike-in: Calculating Absolute Numbers in a Sample

Microorganisms	Cell# in Sample X	Relative abundance in X	Cell# in Sample Y	Relative abundance in X
A	6,000	60.00%	500	45.45%
B	2,000	20.00%	250	22.73%
C	2,000	20.00%	350	31.82%

↓ Mix with a known amount of spike-in cells (or DNA)

Microorganisms	Cell# in Sample X	Relative abundance in X	Cell# in Sample Y	Relative abundance in Y
A	6,000	59.41%	500	41.67%
B	2,000	19.80%	250	20.83%
C	2,000	19.80%	350	29.17%
Spike-in S	100	0.99%	100	8.33%

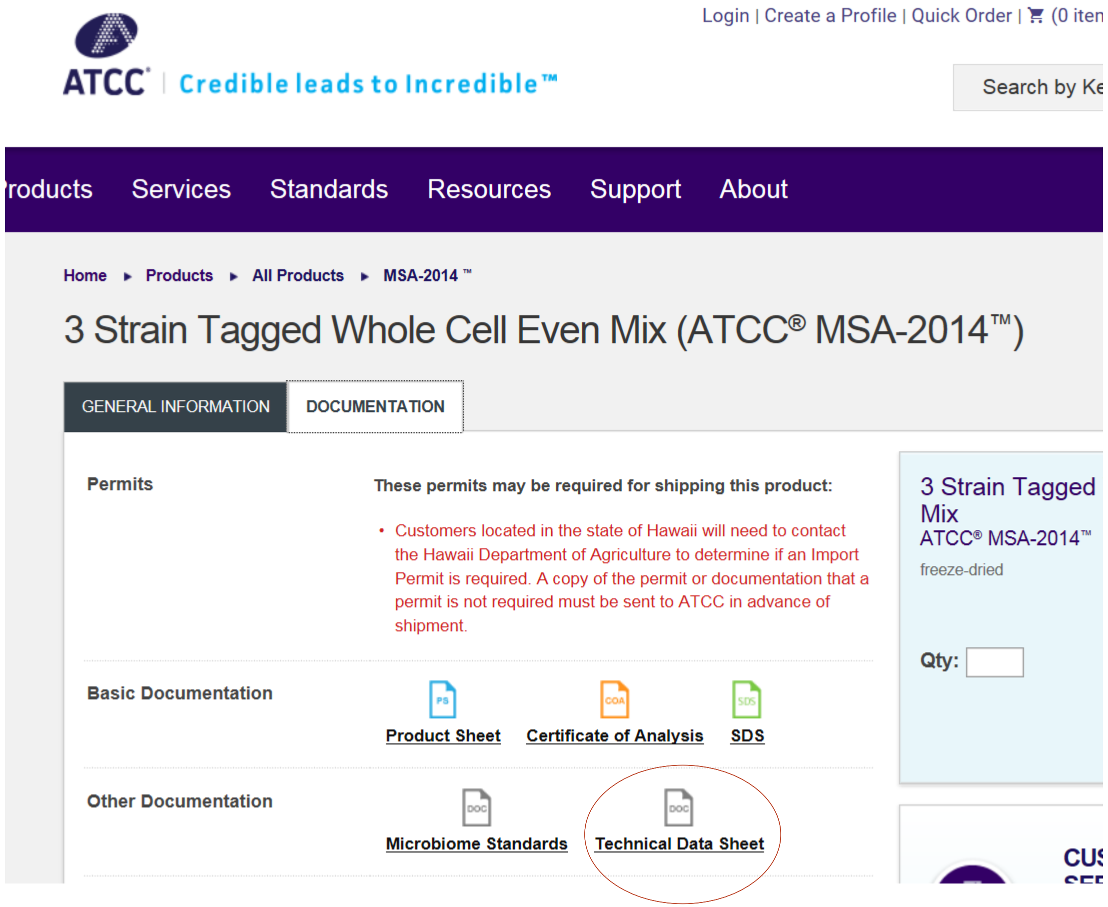
In sample X, if 0.99% Spike-in S = 100, then 19.80% B = 19.80% ÷ 0.99% x 100= 2,000
In sample Y, if 8.33% Spike-in S = 100, then 20.83% B = 20.8% ÷ 8.33% x 100= 250

Total cell#: In sample X, if 0.99% Spike-in S = 100, then total cell# of the sample X = 99% ÷ 0.99% x 100= 10,000

Criterium of a spike-in bacterial sequence: Uniqueness

Resources

Technical Data Sheet: 3 Strain Tagged Whole Cell Even Mix



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ATCC | Credible leads to Incredible™

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Home ▸ Products ▸ All Products ▸ MSA-2014 ™

3 Strain Tagged Whole Cell Even Mix (ATCC® MSA-2014™)

GENERAL INFORMATION | DOCUMENTATION

Permits

These permits may be required for shipping this product:

- Customers located in the state of Hawaii will need to contact the Hawaii Department of Agriculture to determine if an Import Permit is required. A copy of the permit or documentation that a permit is not required must be sent to ATCC in advance of shipment.

Basic Documentation

Product Sheet | Certificate of Analysis | SDS

Other Documentation

Microbiome Standards | Technical Data Sheet

3 Strain Tagged Mix
ATCC® MSA-2014™
freeze-dried

Qty:

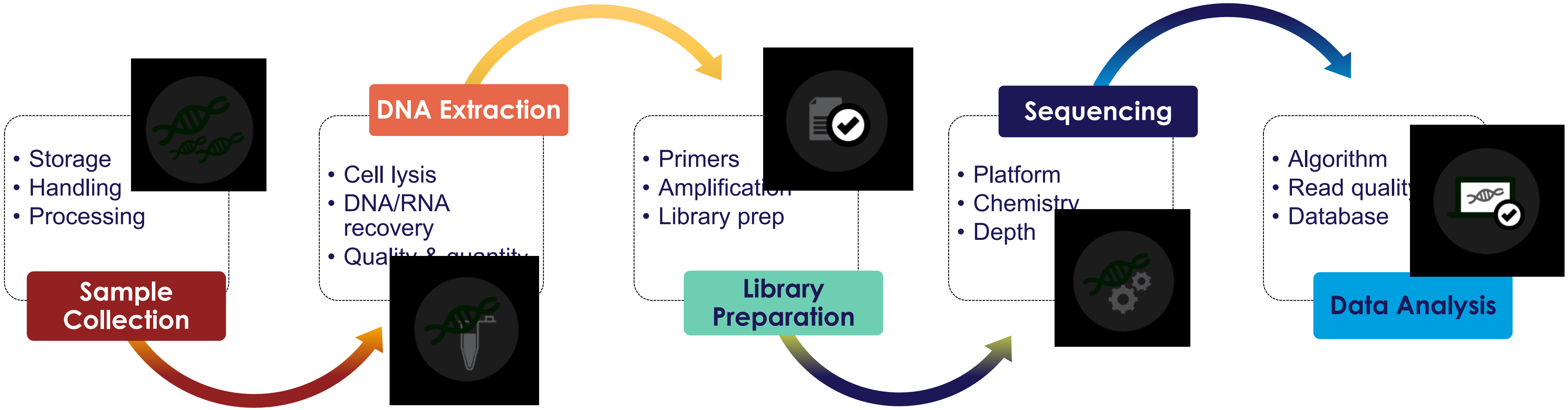
CUS

Coming Soon - Mycobiome (MSA-2010™ and MSA-1010™)

MSA-2010™	MSA-1010™
Whole cell	Genomic
In production now	Coming soon
Release date: 23Sep2019	Release: Q4

ATCC® No.	Species Name	Genome size (Mb)	Relevancy
MYA-4609™	*Aspergillus fumigatus Af293*	28.8	Opportunistic, airborne pathogen that is responsible for 90% of fungal infections in immunocompromised patients
10231™	*Candida albicans*	17.1	Commensal fungus of the oral cavity that can form biofilms on denture surfaces leading to mucosal infections
2001™	*Candida glabrata*	12.3	Commensal fungus of the oral cavity and human gut that can acquire resistance to azole antifungals leading to infection
208821™	*Cryptococcus neoformans var. grubii*	18.9	Responsible for cryptococcal meningitis in immunosuppressed patients
MYA-4612™	*Malassezia globosa CBS 7966*	9.0	Part of the normal skin flora but can be responsible for skin diseases such as dandruff, dermatitis, and folliculitis
201390™	*Saccharomyces cerevisiae*	12.2	Eukaryotic model organism used to study gene expression, signal transduction, the cell cycle, and metabolism
9533™	*Trichophyton interdigitale*	21.9	Can infect skin and nails to cause chronic infections such as athlete's foot and ringworm
204094™	*Cutaneotrichosporon dermatis(CBS2043)*	23.3	Emerging opportunistic agent of invasive fungal infections, particularly in severely immunocompromised patients
10106™	*Penicillium chrysogenum Thom*	32.5	Spore-former and source of beta-lactam antibiotics such as penicillin
36031™	*Fusarium keratoplasticum (F solani)*	48.6	Filamentous, opportunistic pathogen that causes fungal keratitis

Microbiome Workflow, Biases, and Standardization



Sample Collection
- Storage
- Handling
- Processing

DNA Extraction
- Cell lysis
- DNA/RNA recovery
- Quality & quantity

Library Preparation
- Primers
- Amplification
- Library prep

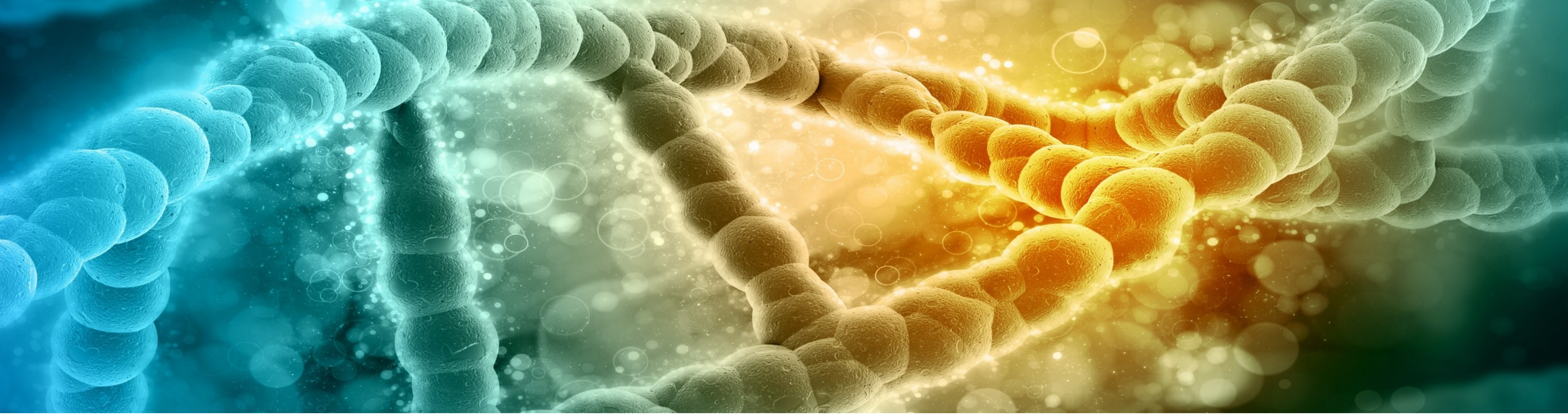
Sequencing
- Platform
- Chemistry
- Depth

Data Analysis
- Algorithm
- Read quality
- Database

❑ **Ideal use - Whole Cell Microbiomes (full process control)**

❑ **Ideal use – Genomic Microbiomes (assay control)**

❑ **One Codex Modules**



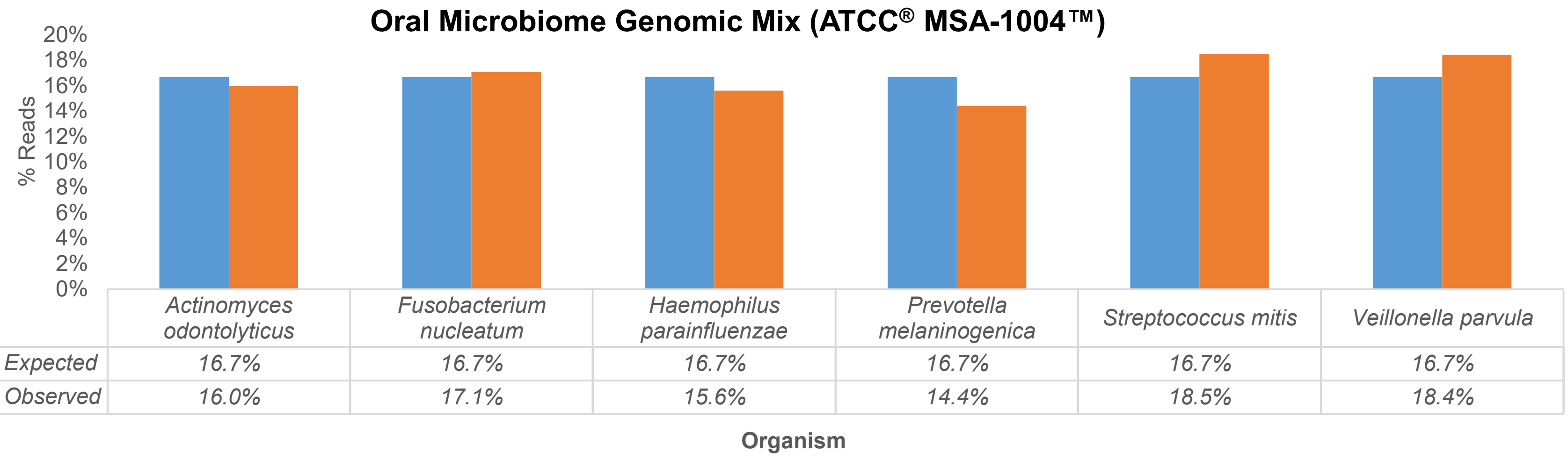
Applications of standards in microbiome research

- DNA extraction
- 16S rRNA amplification and library kits
- NGS platforms
- Bioinformatics and databases

Genomic Versus Whole Cell Standards

DNA extraction methods are not perfect

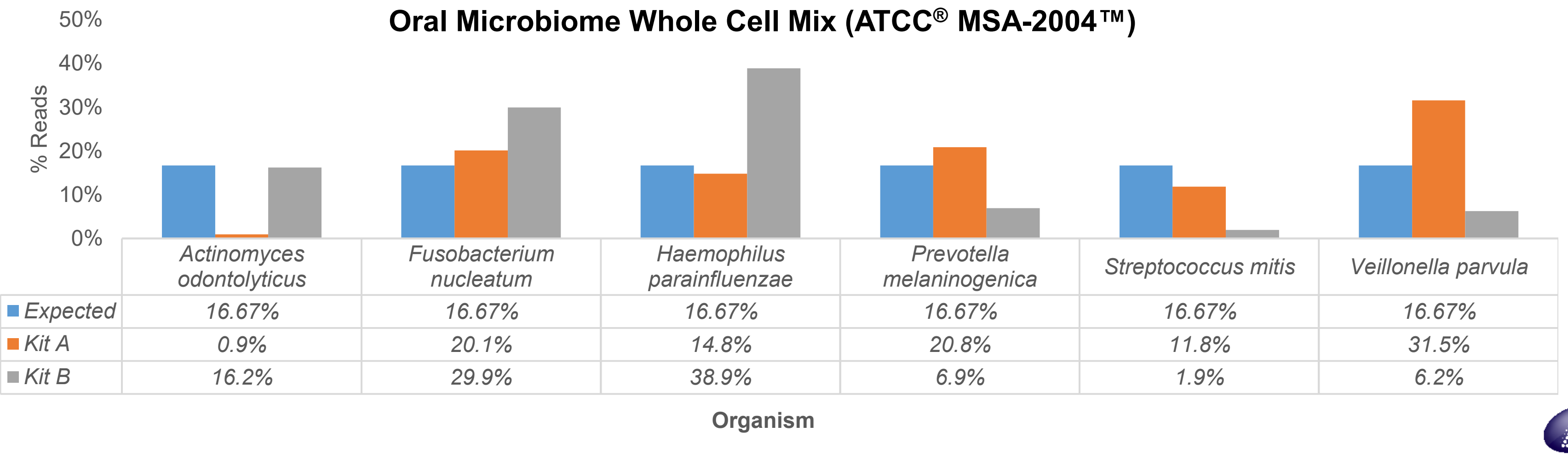
Shotgun metagenomic analysis of the Oral Microbiome Genomic Mix



Oral Microbiome Genomic Mix (ATCC® MSA-1004™)

	Actinomyces odontolyticus	*Fusobacterium nucleatum*	*Haemophilus parainfluenzae*	*Prevotella melaninogenica*	*Streptococcus mitis*	*Veillonella parvula*
🟦 *Expected*	*16.7%*	*16.7%*	*16.7%*	*16.7%*	*16.7%*	*16.7%*
🟧 *Observed*	*16.0%*	*17.1%*	*15.6%*	*14.4%*	*18.5%*	*18.4%*

DNA extraction from the Oral Microbiome Whole Cell Mix with two different kits followed by shotgun metagenomic analysis

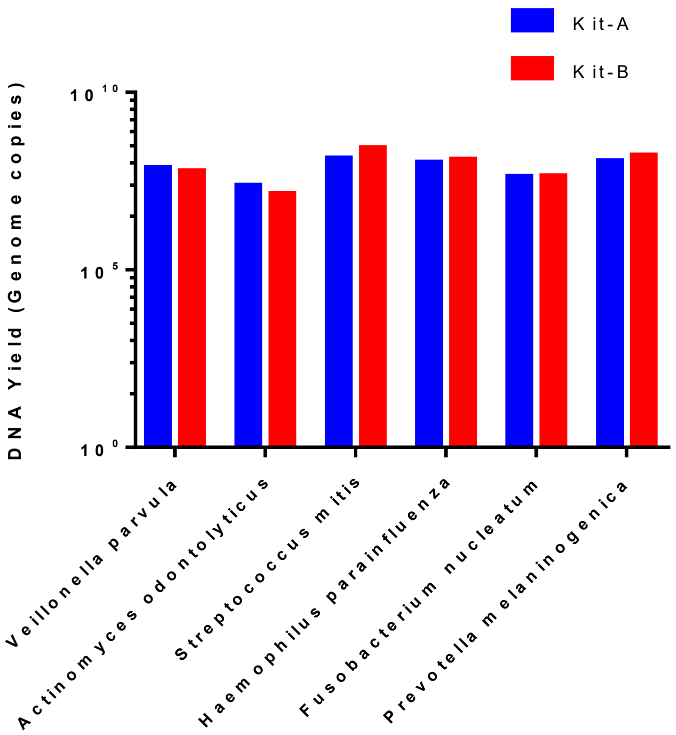


Oral Microbiome Whole Cell Mix (ATCC® MSA-2004™)

	Actinomyces odontolyticus	*Fusobacterium nucleatum*	*Haemophilus parainfluenzae*	*Prevotella melaninogenica*	*Streptococcus mitis*	*Veillonella parvula*
🟦 *Expected*	*16.67%*	*16.67%*	*16.67%*	*16.67%*	*16.67%*	*16.67%*
🟧 *Kit A*	*0.9%*	*20.1%*	*14.8%*	*20.8%*	*11.8%*	*31.5%*
⬜ *Kit B*	*16.2%*	*29.9%*	*38.9%*	*6.9%*	*1.9%*	*6.2%*

Assess Biases in DNA Extraction

Compare different pre-treatments and extraction methods, optimize protocols, and validate different kits



DNA extraction from individual components of the Oral Whole Cell Mix

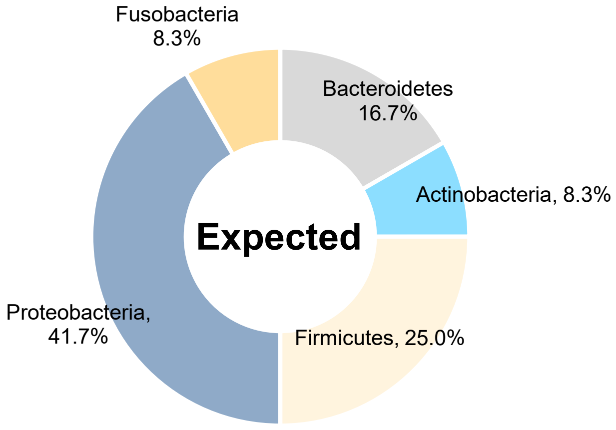
Organism	Number of Cells per Component	Gram Stain	Genome size Mb	%GC
Actinomyces odontolyticus	~2x10^7	+	2.39	65.5
Fusobacterium nucleatum		-	2.17	27.2
Haemophilus parainfluenzae		-	2.12	39.3
Prevotella melaninogenica		-	3.17	35.1
Streptococcus mitis		+	1.83	40.5
Veillonella parvula		-	2.16	38.6

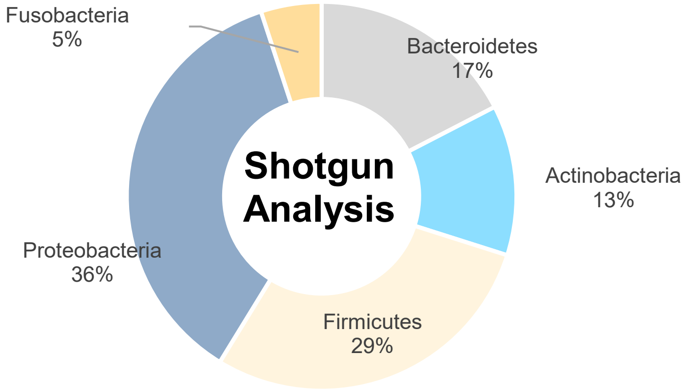
Gut Whole Cell Standard

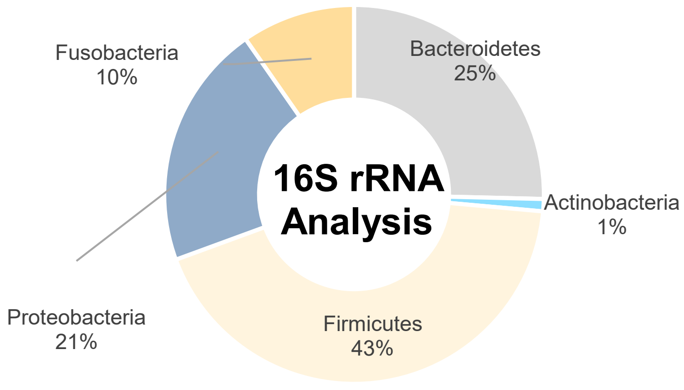
Profiling of gut microbiome standard at the phylum, genus, and species level

The Gut Whole Cell Microbiome Standard (ATCC® MSA-2006™) can be used as a full process control for shotgun and 16S rRNA assays

Phylum	Expected	Strain	Expected	Observed-Shotgun	Observed-16S (V1V2)
Bacteroidetes	16.6%	*Bacteroides fragilis*	8.3%	12.3%	17.0%
		Bacteroides vulgatus	8.3%	8.6%	8.4%
Actinobacteria	8.33%	*Bifidobacterium adolescentis*	8.3%	12.0%	1.0%
Firmicutes	25.0%	*Clostridium difficile*	8.3%	16.5%	29.0%
		Enterococcus faecalis	8.3%	3.1%	1.6%
		Lactobacilus plantarum	8.3%	8.1%	12.3%
Proteobacteria	41.7%	*Enterobacter cloacae*	8.3%	10.6%	4.0%
		Escherichia coli	8.3%	6.6%	3.3%
		Helicobacter pylori	8.3%	3.8%	7.7%
		Salmonella enterica	8.3%	4.9%	2.2%
		Yersinia enterocolitica	8.3%	8.8%	3.6%
Fusobacteria	8.3%	*Fusobacterium nucleatum*	8.3%	4.8%	9.7%



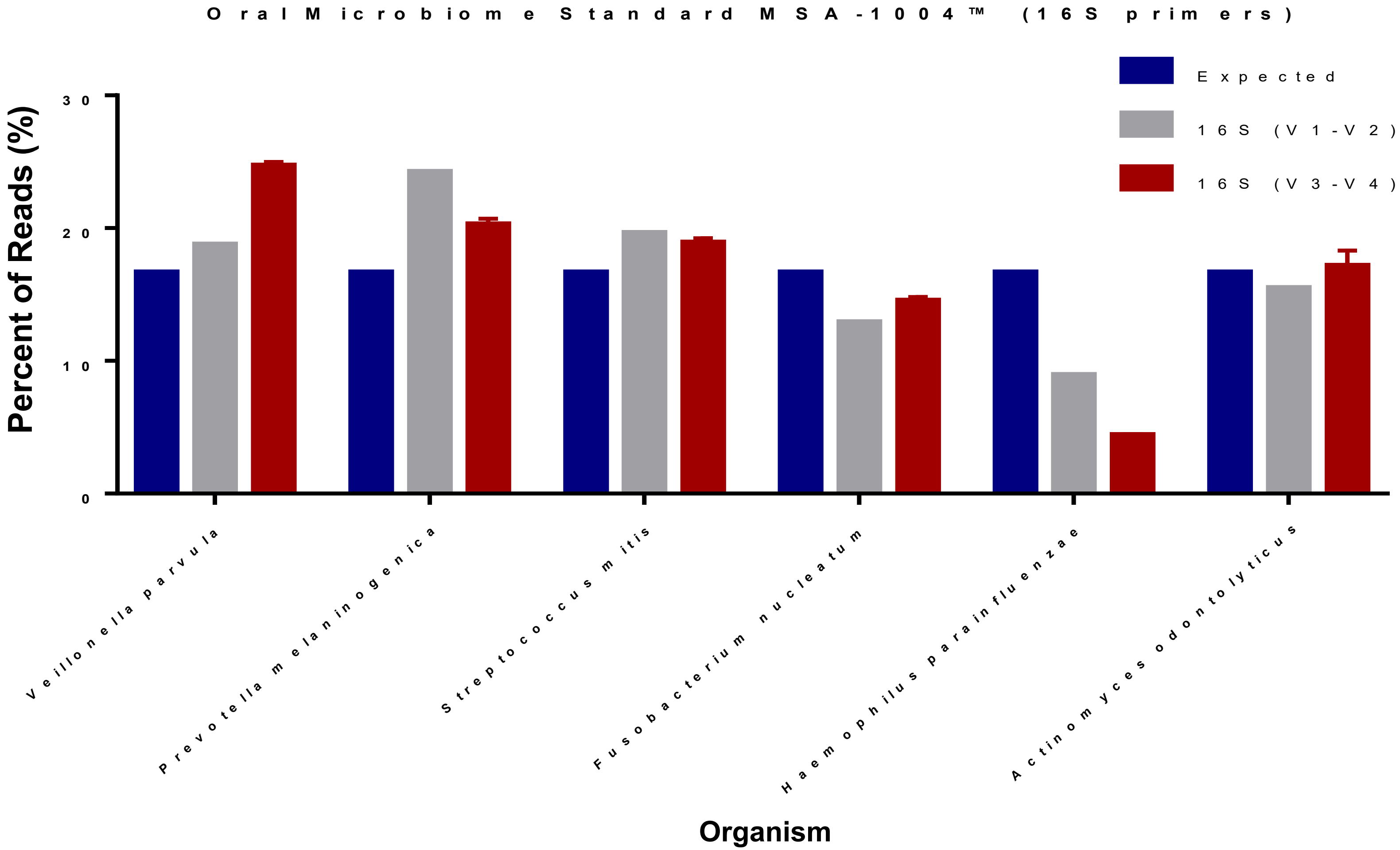




16S Amplicon-based Analysis: Primer Selection

Compare different primer sets, optimize amplification steps, and validate 16S analysis methods

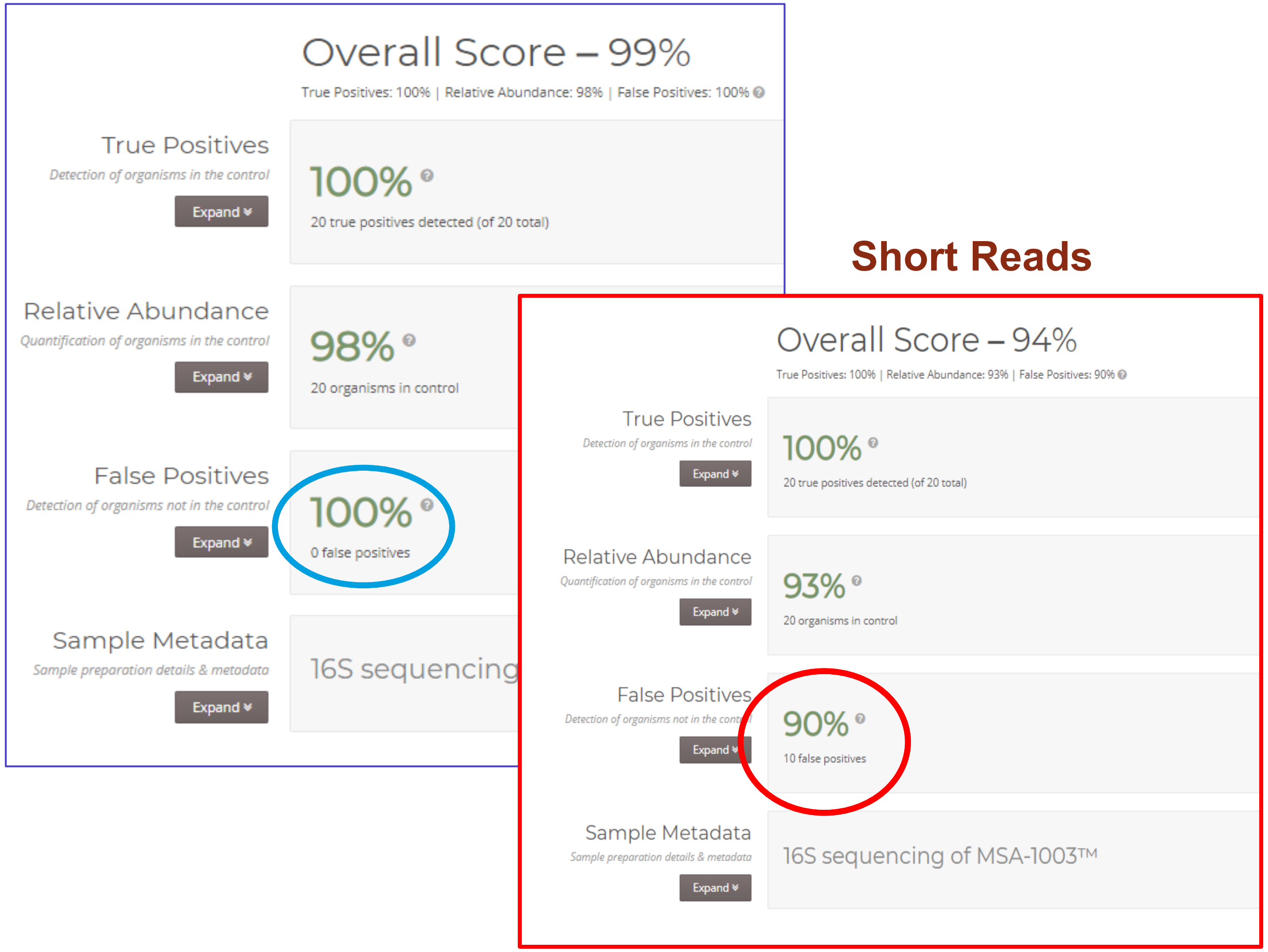
16S rRNA analysis of the Oral Genomic DNA Standard via two primer sets



Comparing Library Preparation Kits

The LoopSeq™ 16S rRNA long-read method allows highest sequence accuracy and species-level taxonomy

Loop Genomics



Overall Score – 99%

True Positives: 100% | Relative Abundance: 98% | False Positives: 100%

True Positives
Detection of organisms in the control
Expand

100%
20 true positives detected (of 20 total)

Relative Abundance
Quantification of organisms in the control
Expand

98%
20 organisms in control

False Positives
Detection of organisms not in the control
Expand

100%
0 false positives

Sample Metadata
Sample preparation details & metadata
Expand

16S sequencing

Short Reads

Overall Score – 94%

True Positives: 100% | Relative Abundance: 93% | False Positives: 90%

True Positives
Detection of organisms in the control
Expand

100%
20 true positives detected (of 20 total)

Relative Abundance
Quantification of organisms in the control
Expand

93%
20 organisms in control

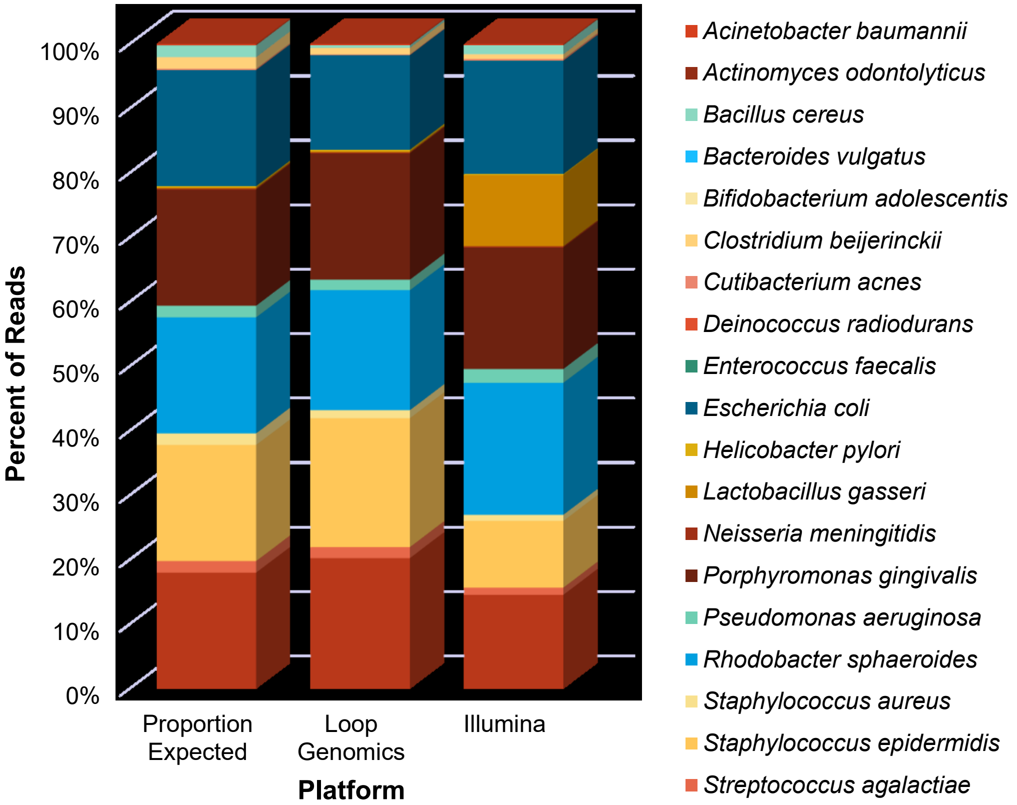
False Positives
Detection of organisms not in the cont
Expand

90%
10 false positives

Sample Metadata
Sample preparation details & metadata
Expand

16S sequencing of MSA-1003™

Genomic DNA (ATCC® MSA-1003™)



LoopSeq data courtesy of Tony Lialin, Loop Genomics

MSA-1004™/MSA-2004™ Oral Microbiome

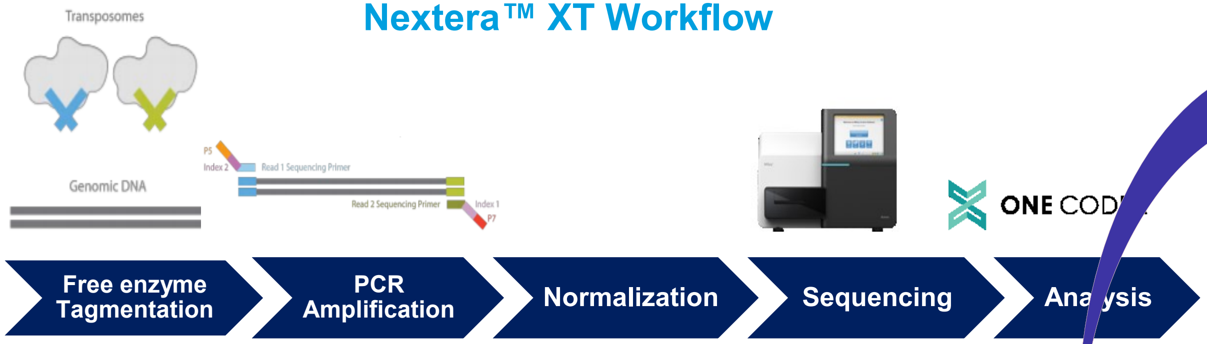
Name	Gram Stain	% GC	Genome Size (Mb)	16S rRNA Copies
Actinomyces odontolyticus	POS	65.5	2.39396	2
Fusobacterium nucleatum	NEG	27.2	2.1745	5
Haemophilus parainfluenzae	NEG	39.3	2.12476	9
Prevotella melaninogenica	NEG	35.1	3.16828	4
Streptococcus mitis	POS	40.5	1.83108	4
Veillonella parvula	NEG	38.6	2.16347	4

Comparing Library Preparation Kits

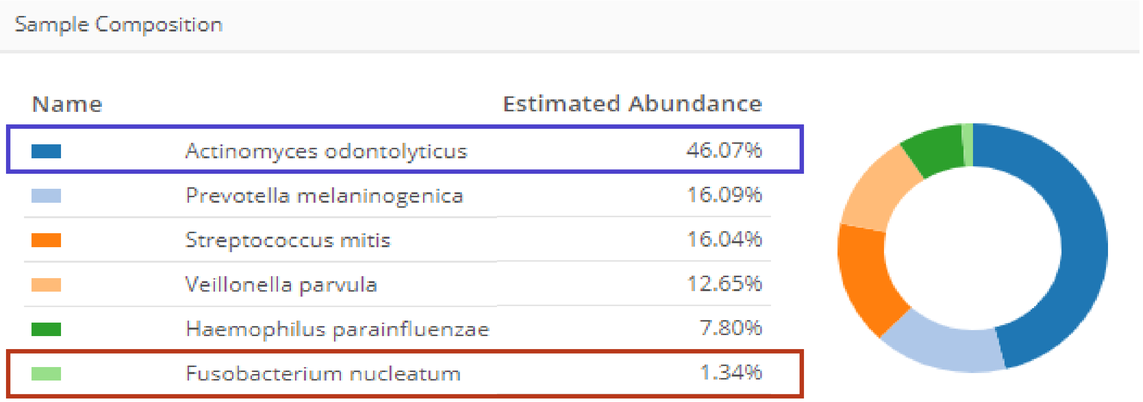
Nextera Flex enables uniform coverage of genomes of low GC content

Oral Microbiome Genomic DNA (ATCC® MSA-1004™)

Nextera™ XT Workflow



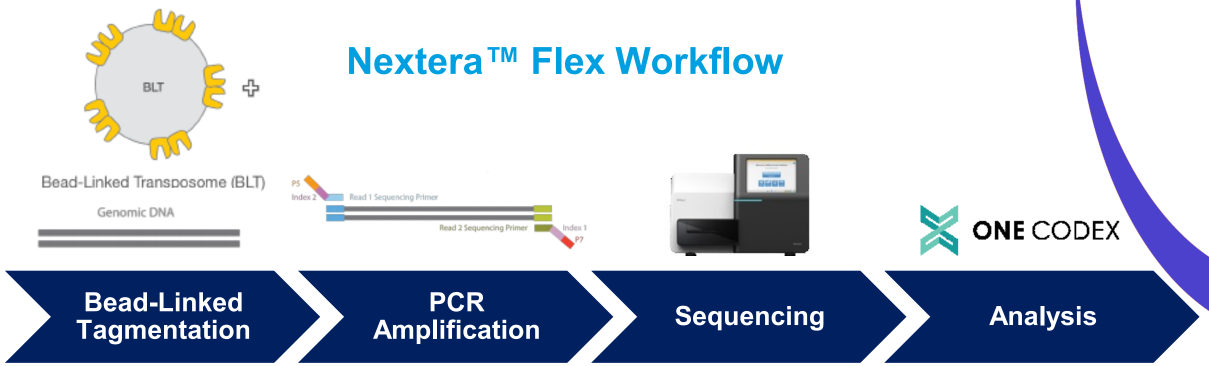
Free enzyme Tagmentation → PCR Amplification → Normalization → Sequencing → Analysis



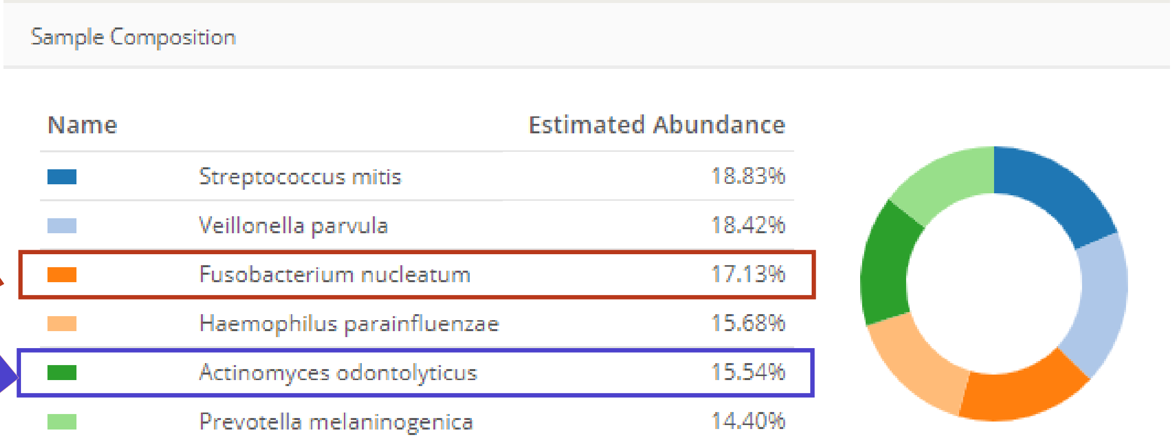
Sample Composition

	Name	Estimated Abundance
🟦	Actinomyces odontolyticus	46.07%
🟦	Prevotella melaninogenica	16.09%
🟧	Streptococcus mitis	16.04%
🟧	Veillonella parvula	12.65%
🟩	Haemophilus parainfluenzae	7.80%
🟩	Fusobacterium nucleatum	1.34%

Nextera™ Flex Workflow



Bead-Linked Tagmentation → PCR Amplification → Sequencing → Analysis



Sample Composition

	Name	Estimated Abundance
🟦	Streptococcus mitis	18.83%
🟦	Veillonella parvula	18.42%
🟧	Fusobacterium nucleatum	17.13%
🟧	Haemophilus parainfluenzae	15.68%
🟩	Actinomyces odontolyticus	15.54%
🟩	Prevotella melaninogenica	14.40%

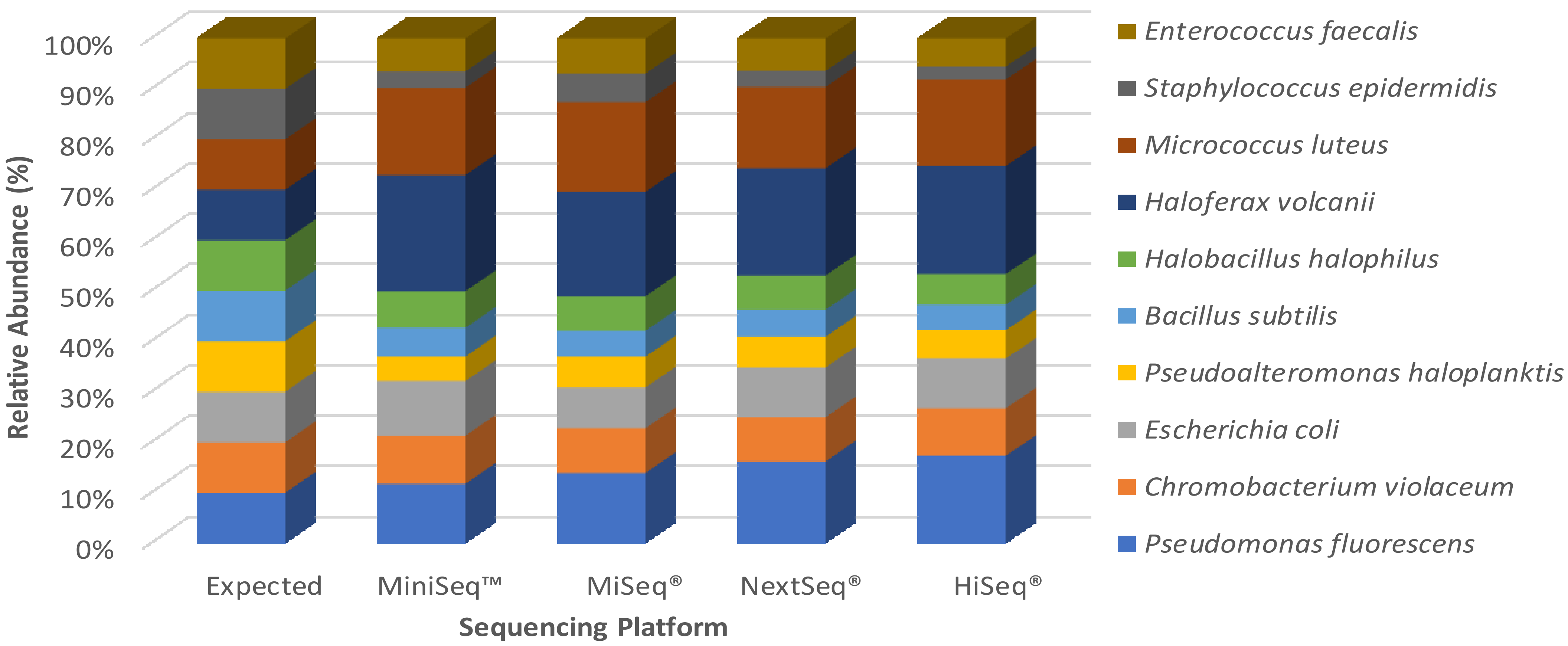
Data courtesy of Illumina

Evaluating NGS Platforms

Short-read Sequencing Platform: Illumina®

Assay reproducibility through different Illumina sequencing platforms

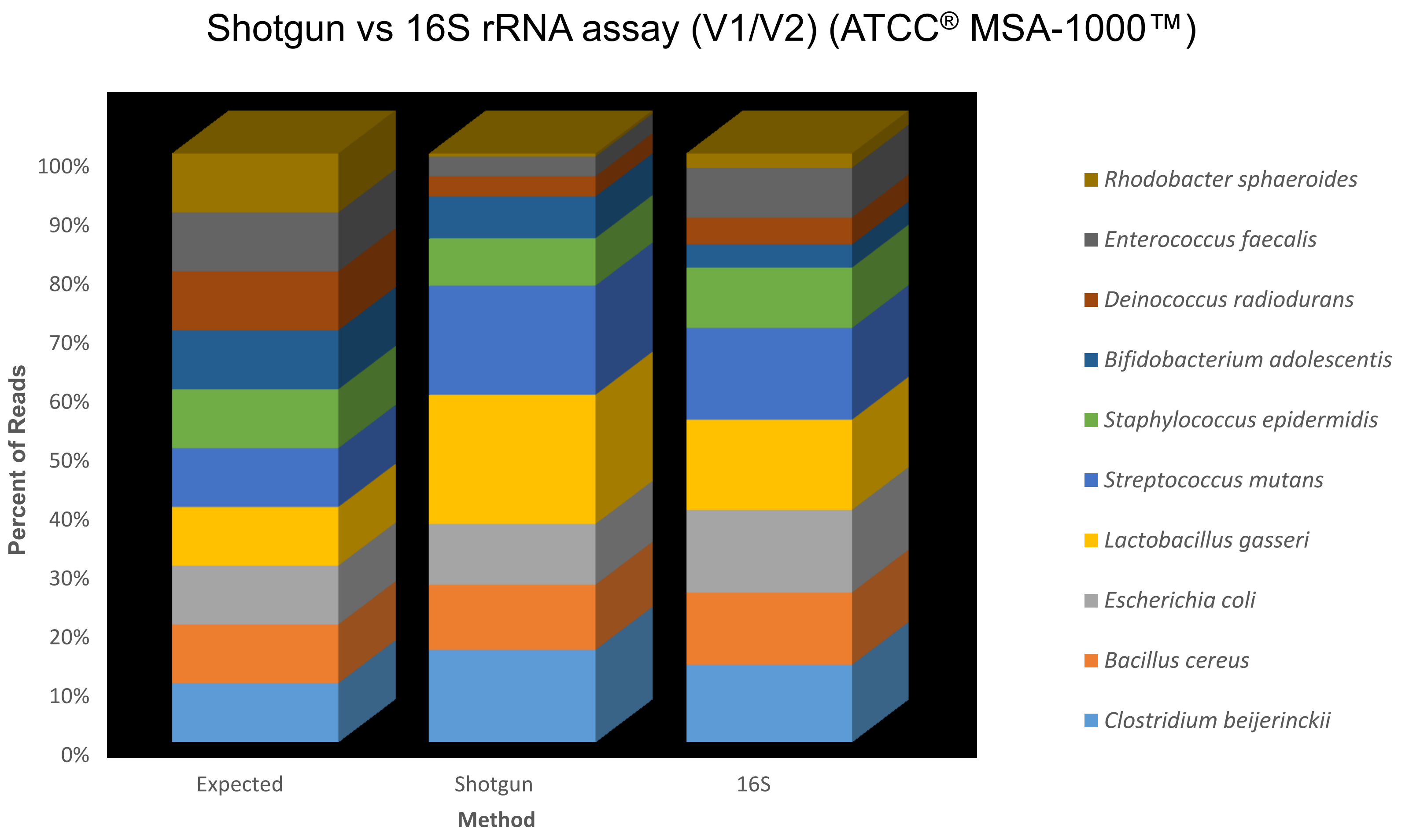
Shotgun Metagenomic Data (ATCC® MSA-3001™)



Data courtesy of Dr. Stefan Green, UIC (ABRF-MGRG)

Short-read Sequencing Platform: Ion Torrent™

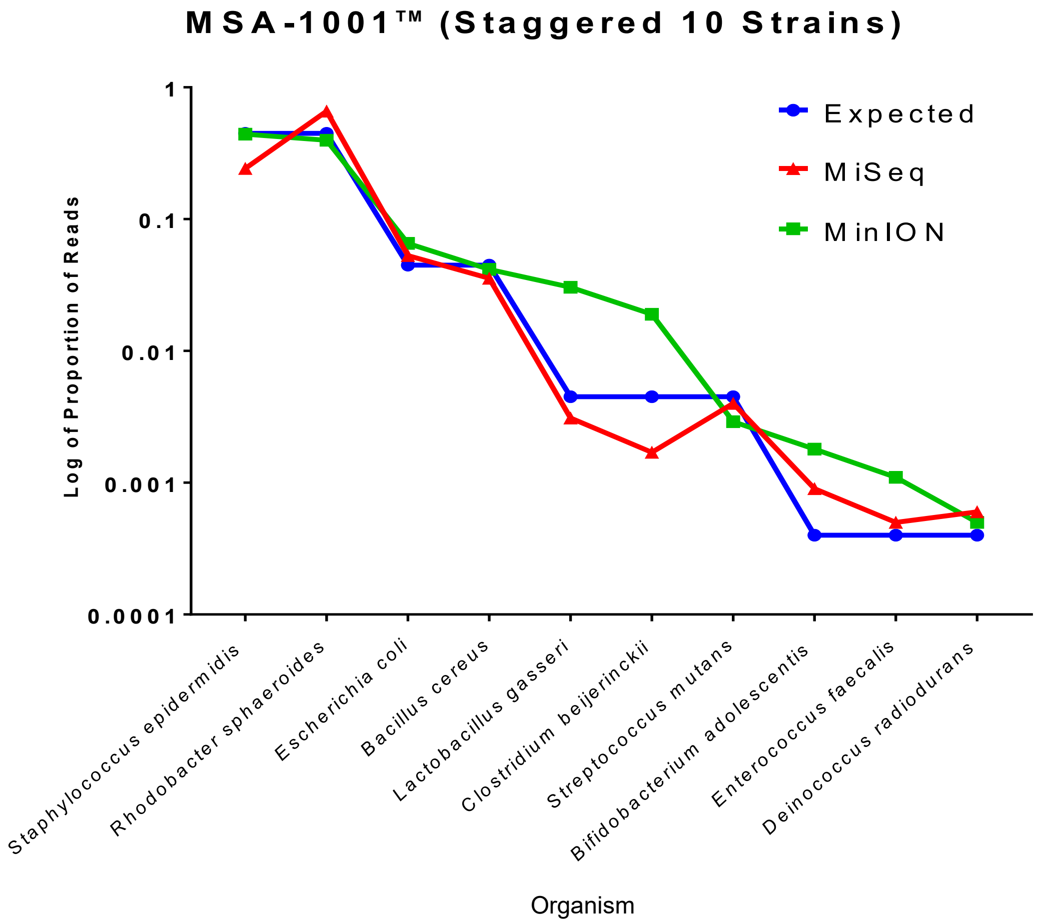
16S rRNA and shotgun data on the Ion GPM Platform (ATCC® MSA-1003™)

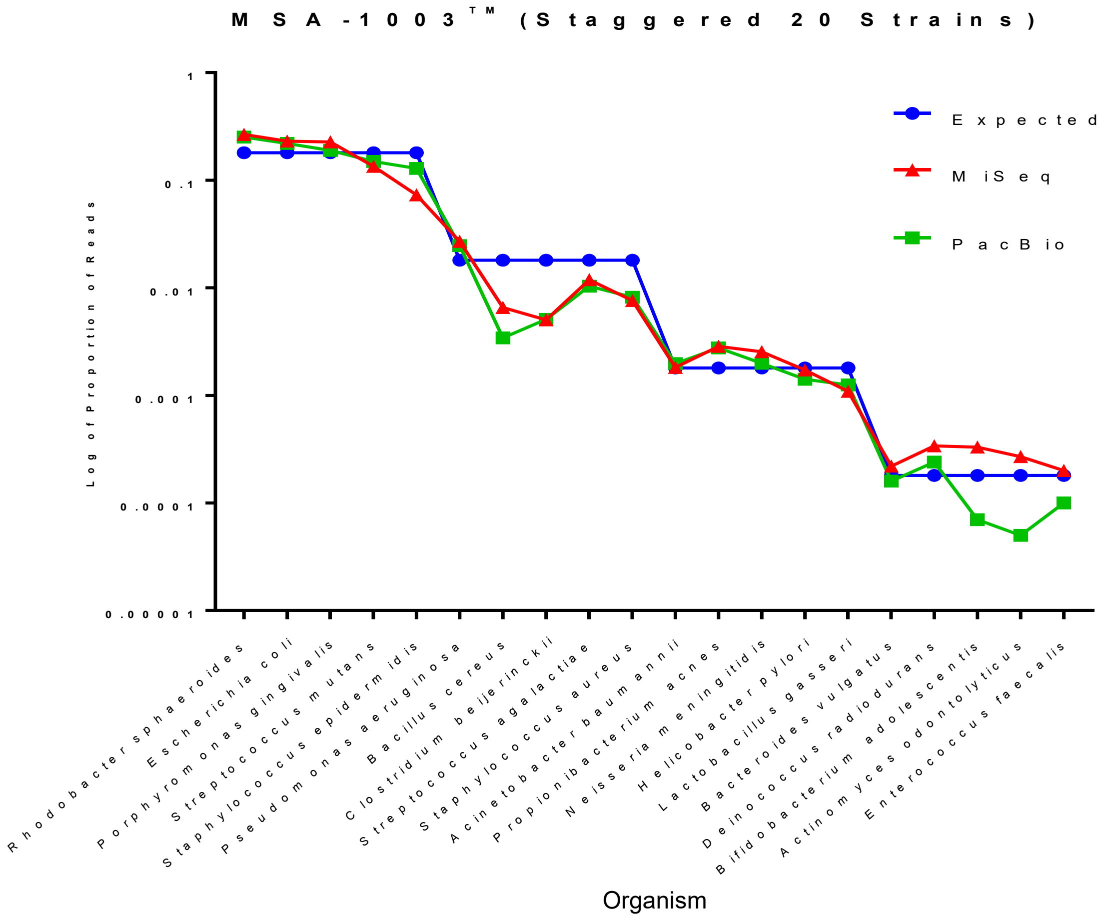


Data courtesy of Dr. Pat Gillevet and Rohan Patil (Microbiome Analysis Center, GMU)

Shotgun Metagenomic Analysis: Short vs Long Reads

ATCC Microbiome Standards are technology agnostic

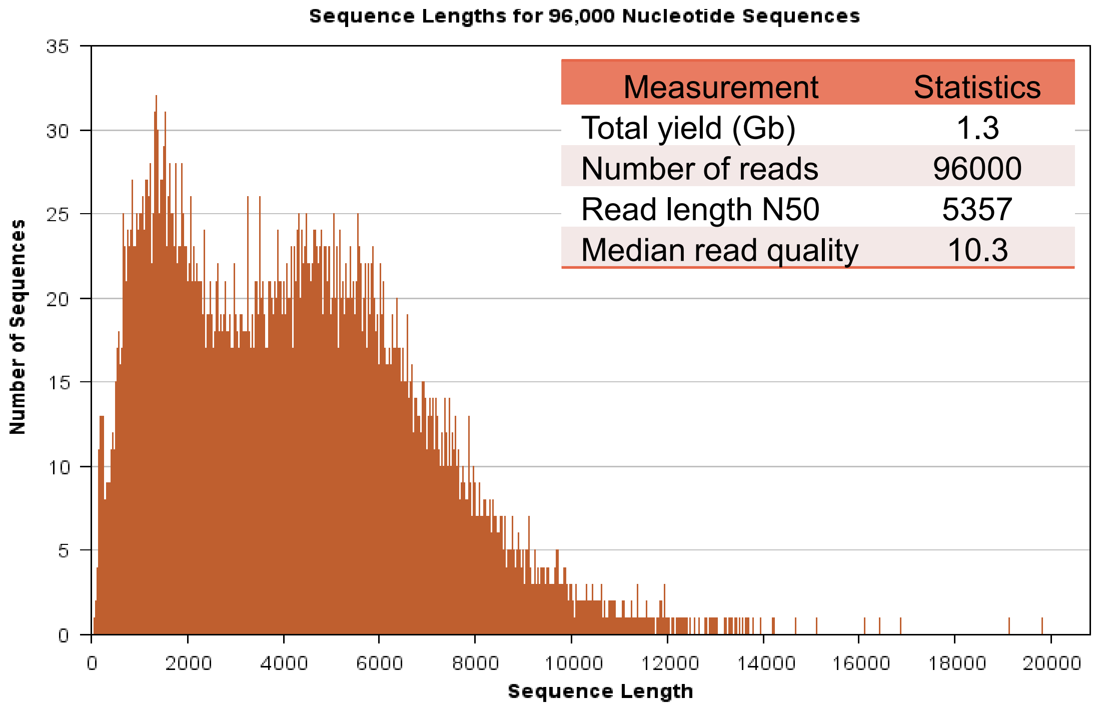

MSA-1001™ (Staggered 10 Strains)


MSA-1003™ (Staggered 20 Strains)

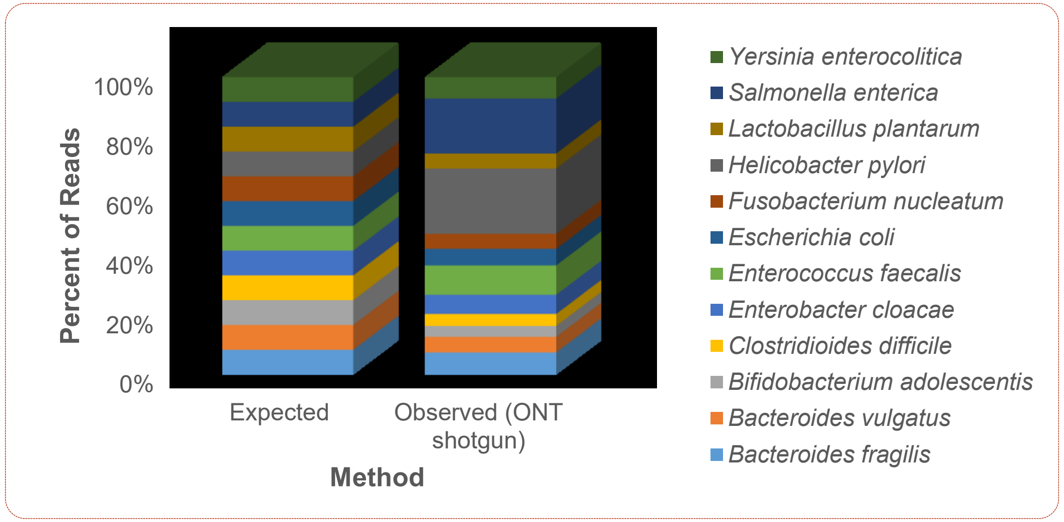
Long-read Sequencing Platform: Nanopore®

One hour sequencing coverage was enough to identify all organisms in the mix with sufficient genome coverage

The Gut Microbiome Whole Cell Standard (ATCC® MSA-1006™) was analyzed via shotgun sequencing on the MinION platform



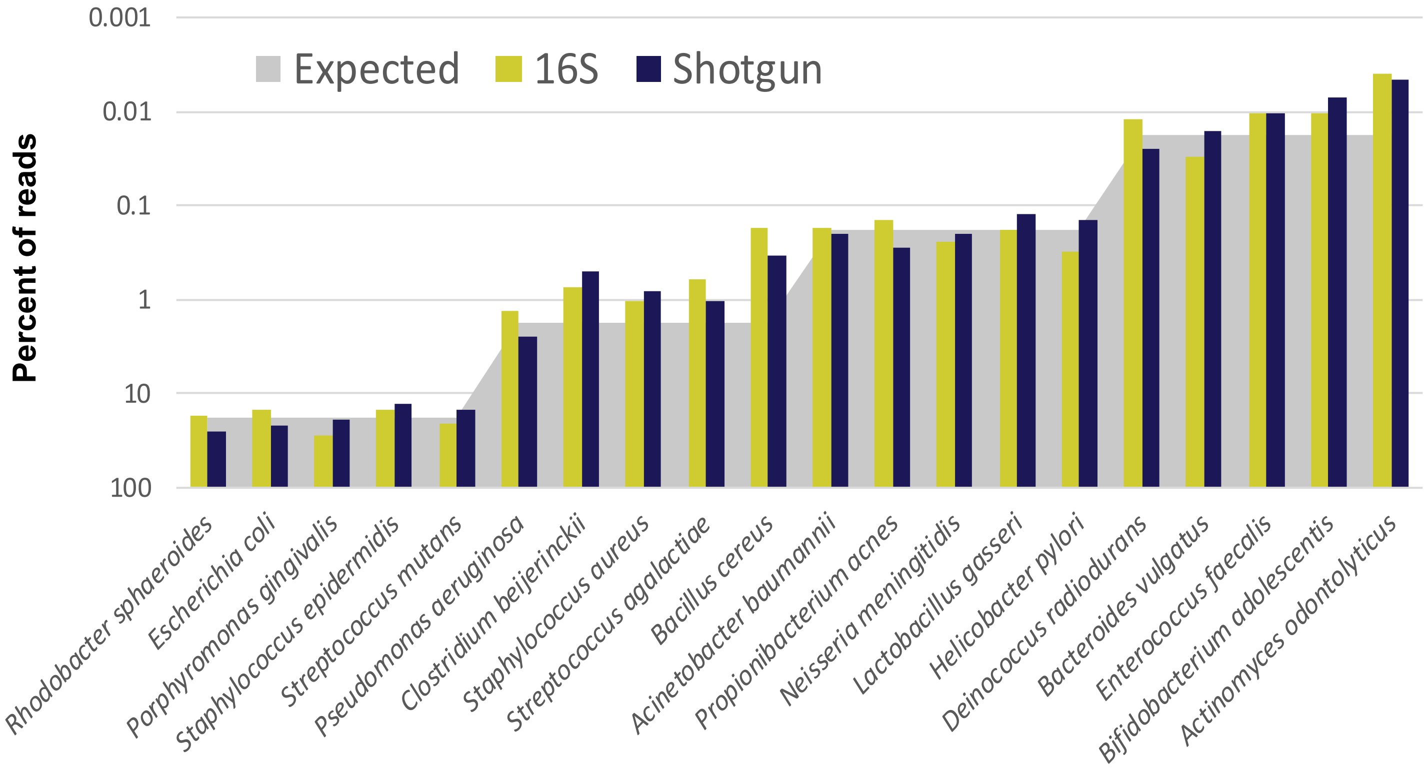
Measurement	Statistics
Total yield (Gb)	1.3
Number of reads	96000
Read length N50	5357
Median read quality	10.3



Organism	Genome Coverage (x)
Enterobacter cloacae	9.1
Enterococcus faecalis	14.1
Bacteroides fragilis	8.1
Bacteroides vulgatus	6.6
Bifidobacterium adolescentis	1.8
Clostridioides difficile	7.4
Escherichia coli	6.5
Fusobacterium nucleatum	4.6
Helicobacter pylori	16.6
Lactobacillus plantarum	6.0
Salmonella enterica	11.1
Yersinia enterocolitica	11.3

Long-read Sequencing Platform: PacBio®

16S rRNA (full-length) and shotgun data on the PacBio Sequel Platform (ATCC® MSA-1003™)



Organism

ATCC quality control score (One Codex)

One Codex Analysis	16S rRNA run 1	16S rRNA run 2	Shotgun run 1	Shotgun run 2
True positives	100%	100%	100%	100%
Relative abundance	95%	95%	97%	97%
False positives	100%	100%	88%	84%
Overall score	98%	98%	95%	95%

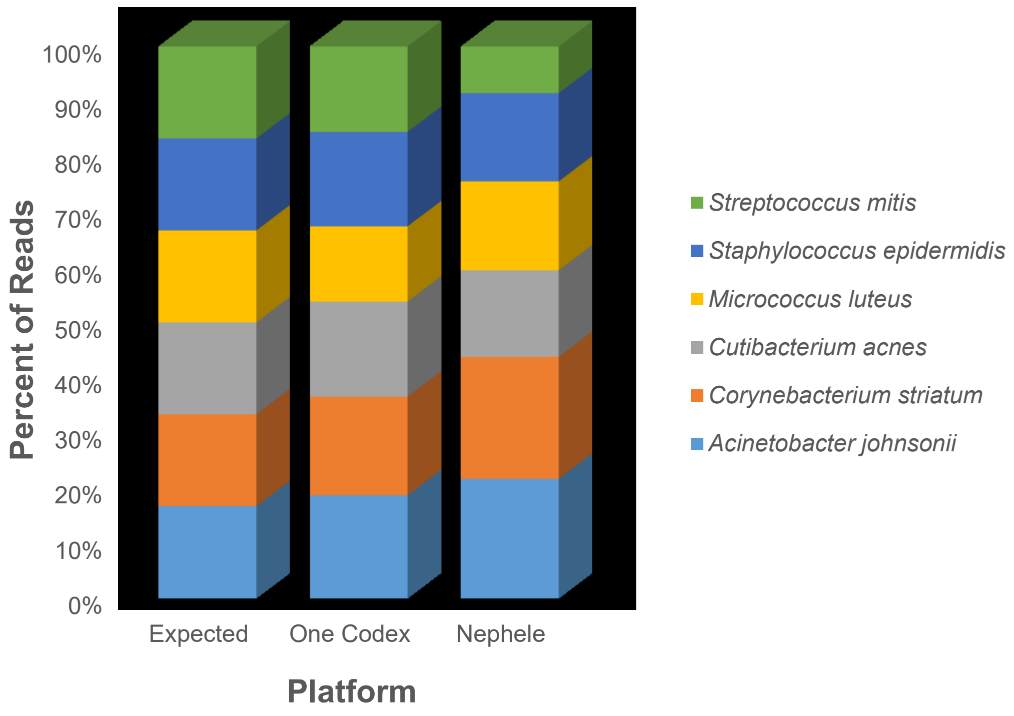
Data courtesy of Dr. Joan Wong, PACBIO®

Comparing Bioinformatics and Databases

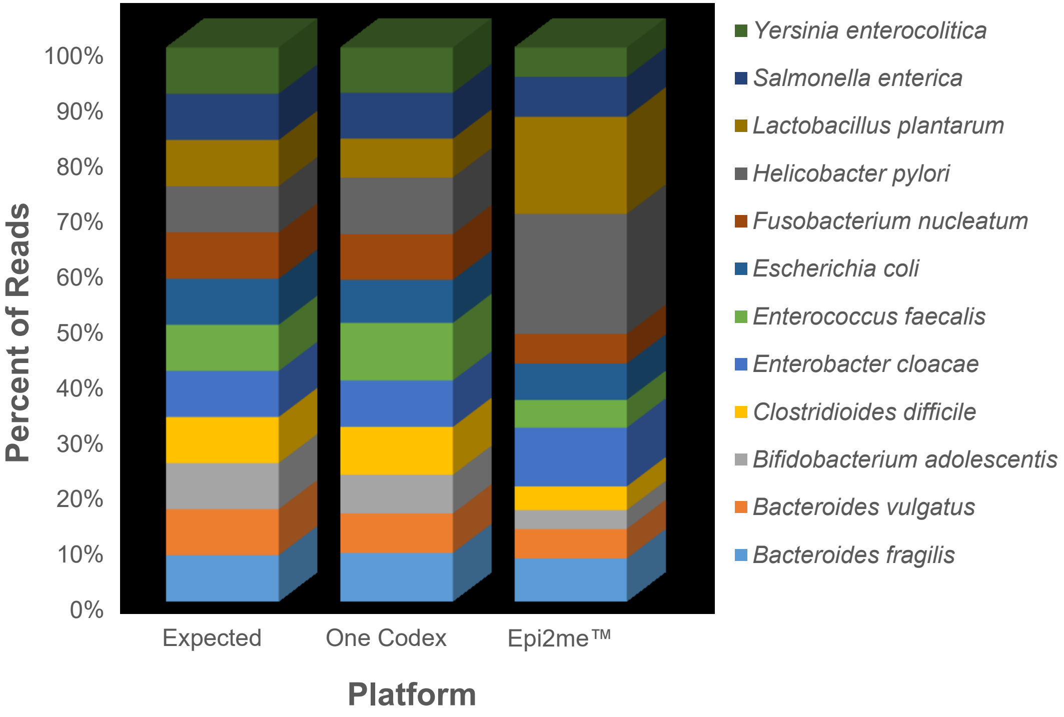
Data Analysis Using Different Databases

Evaluation of NGS data from microbiome standards in multiple analysis platforms and databases

Nephele vs One Codex
Short-read sequencing data from the Skin Genomic DNA Mix (ATCC® MSA-1005™)



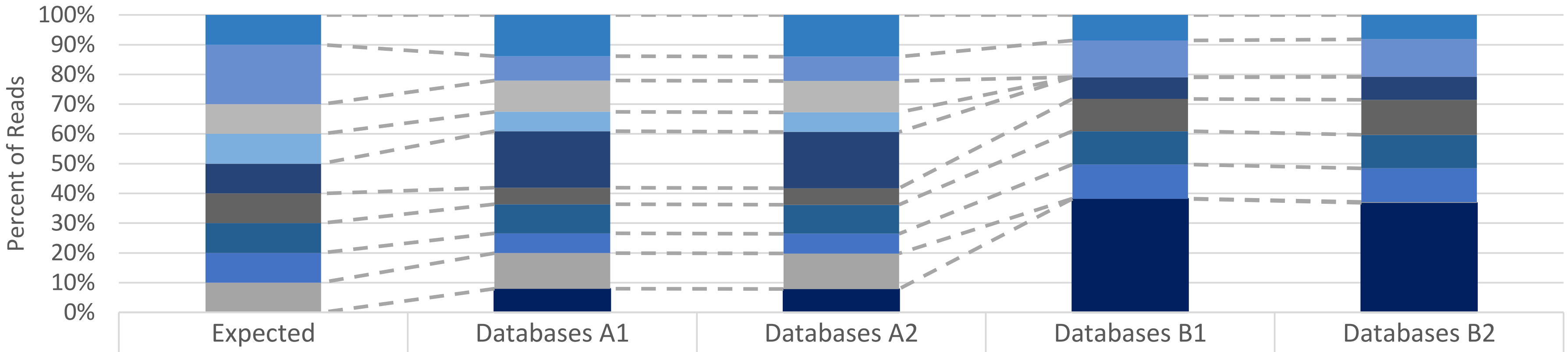
Epi2Me vs One Codex
Long-read sequencing data from the Gut Genomic DNA Mix (ATCC® MSA-1006™)



Mycobiome Standards

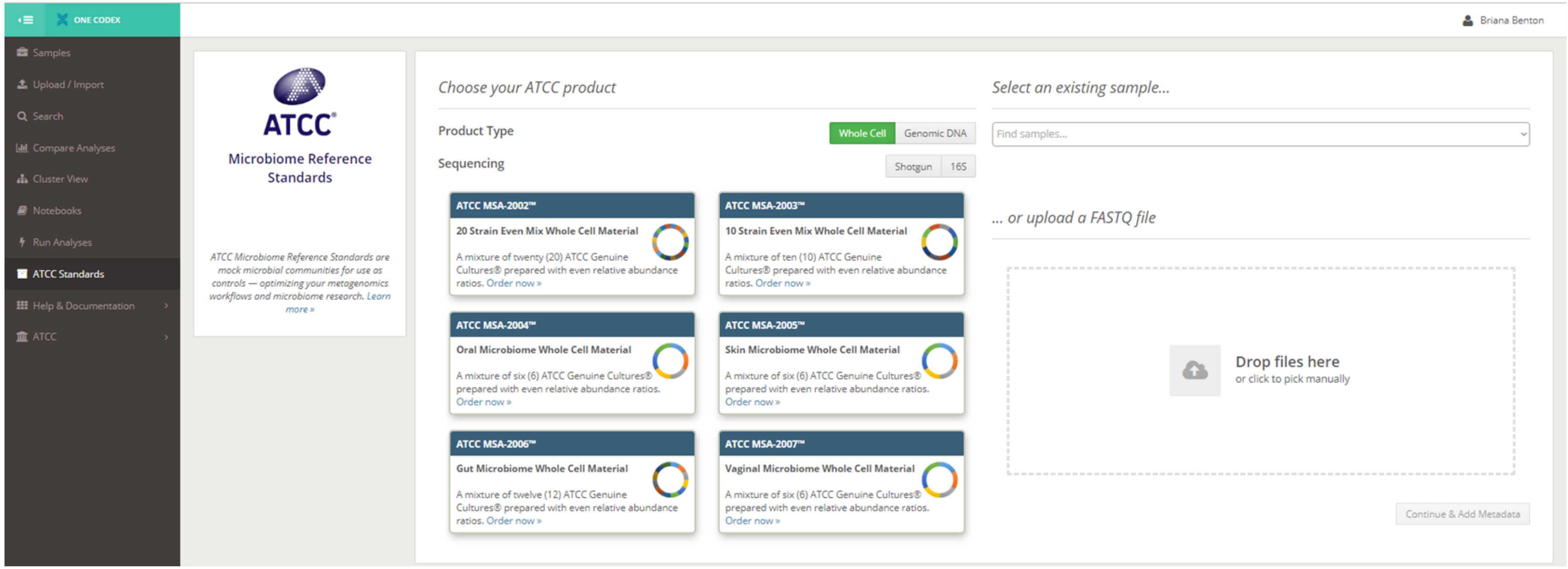
Data analysis platform impacts strain identification and taxonomic resolution

Shotgun Analysis of Genomic DNA standards (ATCC® MSA-1010™)



	Expected	Databases A1	Databases A2	Databases B1	Databases B2
■ Aspergillus	10%	13.88%	13.99%	8.60	8.16
■ Candida	20%	8.17%	8.22%	12.31	12.61
■ Cryptococcus	10%	10.52%	10.51%	0.00	0.00
■ Cutaneotrichosporon	10%	6.53%	6.61%	0.00	0.00
■ Fusarium	10%	19.00%	18.94%	7.32	7.78
■ Malassezia	10%	5.53%	5.55%	10.86	11.74
■ Penicillium	10%	9.81%	9.76%	11.17	11.25
■ Saccharomyces	10%	6.63%	6.62%	11.48	11.35
■ Trichophyton	10%	12.01%	11.98%	0.05	0.29
■ Unclasified	0%	7.93%	7.82%	38.21	36.82

ATCC Data Analysis Solution



ATCC Microbiome Reference Standards

ATCC Microbiome Reference Standards are mock microbial communities for use as controls — optimizing your metagenomics workflows and microbiome research. Learn more »

Choose your ATCC product

Product Type

Sequencing

ATCC MSA-2002™
20 Strain Even Mix Whole Cell Material
A mixture of twenty (20) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

ATCC MSA-2003™
10 Strain Even Mix Whole Cell Material
A mixture of ten (10) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

ATCC MSA-2004™
Oral Microbiome Whole Cell Material
A mixture of six (6) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

ATCC MSA-2005™
Skin Microbiome Whole Cell Material
A mixture of six (6) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

ATCC MSA-2006™
Gut Microbiome Whole Cell Material
A mixture of twelve (12) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

ATCC MSA-2007™
Vaginal Microbiome Whole Cell Material
A mixture of six (6) ATCC Genuine Cultures® prepared with even relative abundance ratios. Order now »

Select an existing sample...

... or upload a FASTQ file

WORKFLOW:

1. Drag and drop Fastq files or export via cloud
2. Choose your ATCC product and analysis (16s and shotgun)
3. Download your reports

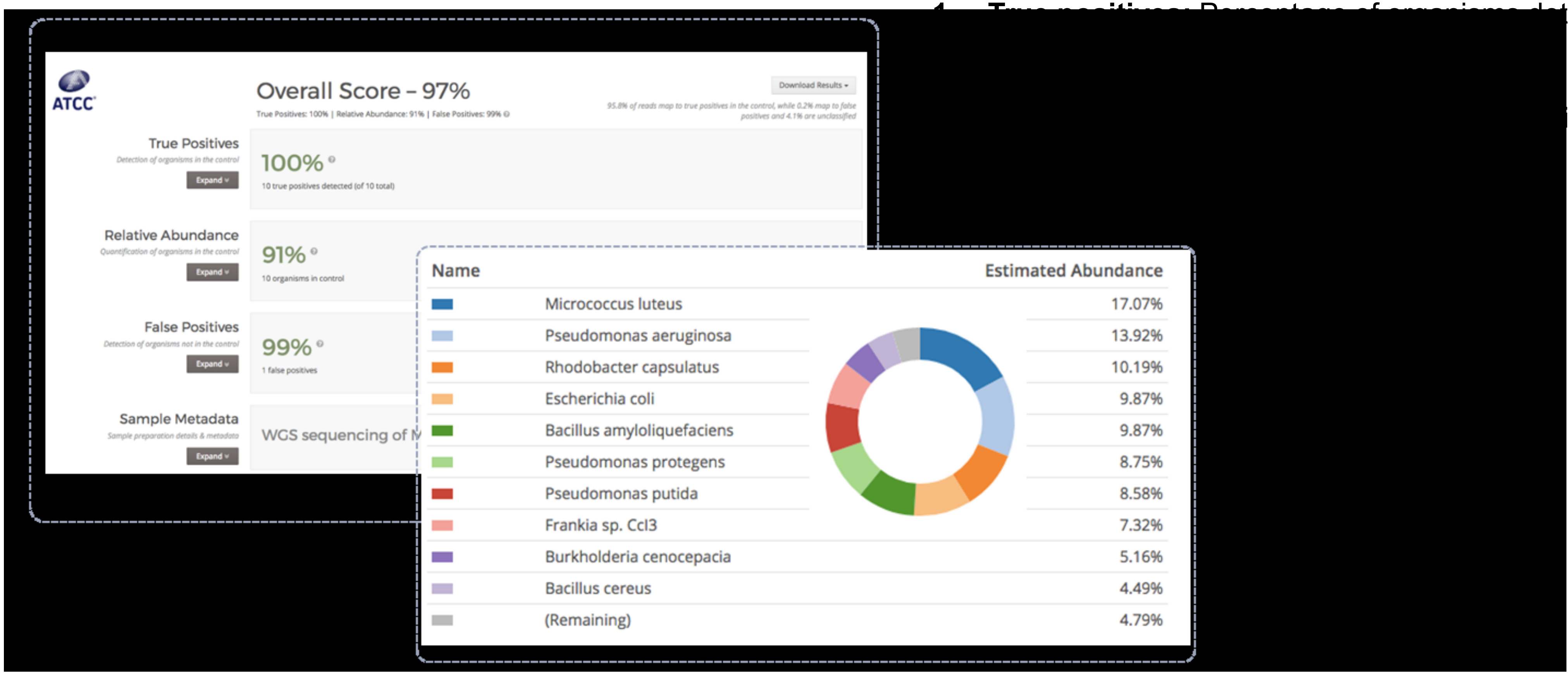
ATCC Data Analysis Solution

RESULTS ARE PROVIDED ON A SCORECARD REPORTS:

1. **True positives:** Percentage of organisms detected from the

in the control

isms in the control



Overall Score – 97%

True Positives: 100% | Relative Abundance: 91% | False Positives: 99%

95.8% of reads map to true positives in the control, while 0.2% map to false positives and 4.1% are unclassified

True Positives

Detection of organisms in the control

100%

10 true positives detected (of 10 total)

Relative Abundance

Quantification of organisms in the control

91%

10 organisms in control

False Positives

Detection of organisms not in the control

99%

1 false positives

Sample Metadata

Sample preparation details & metadata

WGS sequencing of M

	Name	Estimated Abundance
🟦	Micrococcus luteus	17.07%
🟦	Pseudomonas aeruginosa	13.92%
🟧	Rhodobacter capsulatus	10.19%
🟧	Escherichia coli	9.87%
🟩	Bacillus amyloliquefaciens	9.87%
🟩	Pseudomonas protegens	8.75%
🟥	Pseudomonas putida	8.58%
🟥	Frankia sp. Ccl3	7.32%
🟪	Burkholderia cenocepacia	5.16%
🟪	Bacillus cereus	4.49%
⬜	(Remaining)	4.79%

ATCC Data Analysis Solution

Mock Microbial Communities

- Genomic DNA and whole cell standards
- Even and staggered mixtures comprising 10 or 20 strains
- Environmental and pathogen mixtures

Site-specific Standards

- Genomic DNA and whole cell standards
- Even mixtures of 6-12 strains
- Bacterial strains prevalent in the oral, skin, gut, and vaginal microbiome

Spike-In Standards

- Recombinant strains with a unique DNA tag stably integrated into the chromosome
- Recombinant standards include the Gram-negative and Gram-positive bacteria

New Products

- Genomic DNA and whole cell mock communities representing:
  - Virome
  - Mycobiome

Bundled with data analysis on the One Codex platform

www.atcc.org/Microbiome

Conclusion

- ✓ The use of standards in all areas of research is absolutely essential.
- ✓ Microbiome research is challenging and flush with biases
- ✓ The ATCC® Microbiome Standards portfolio and upcoming new products
- ✓ Applications of standards in microbiome research
  - ✓ Extraction method, assay variability, NGS library preparation, and bioinformatics analysis

Acknowledgements

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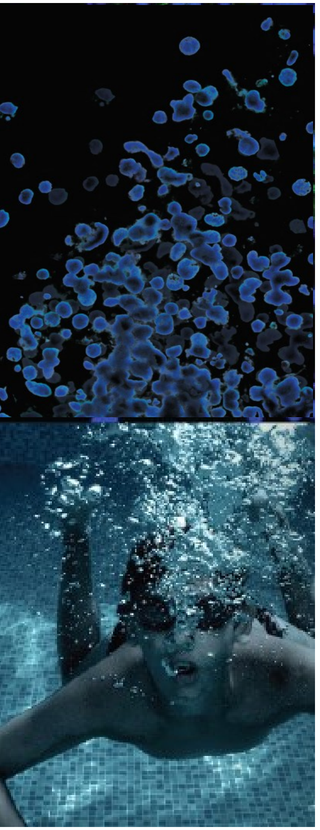
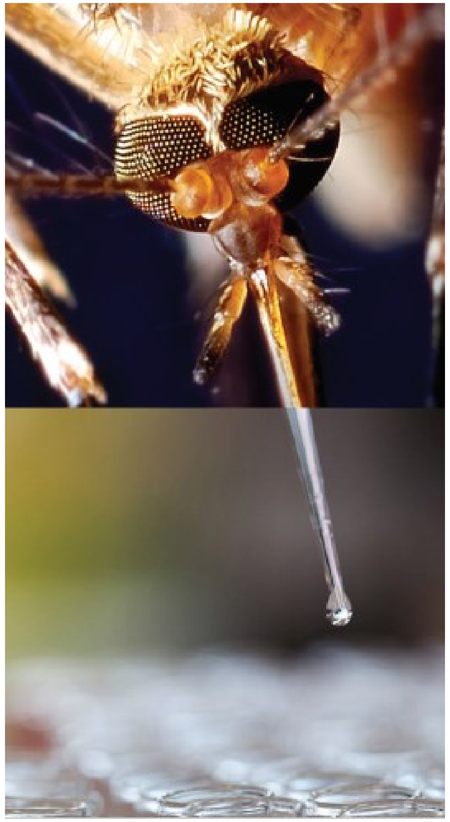
- Tony Lialin, Loop Genomics

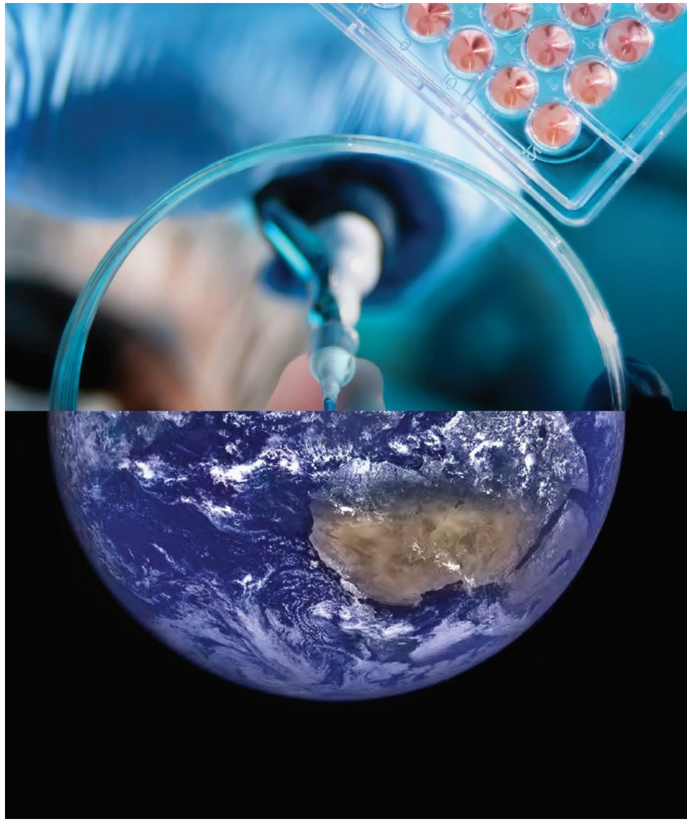


Thank you!

Questions?

Credible Leads to Incredible™





Cultivating collaboration to support global health

Upcoming webinars

- STR Profiling for Mouse Cell Lines: Another Tool to Combat Cell Line Misidentification | September 12, 12:00 ET

www.atcc.org/webinars