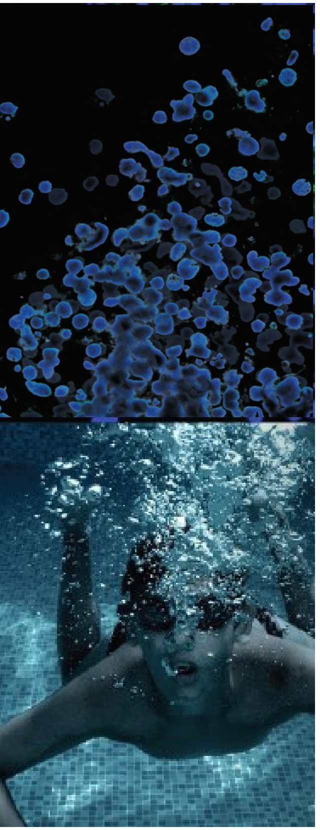


ATCC® NGS Standards and Their Applications

How Standards Help Establish Reliable Workflows for Microbiome Analysis

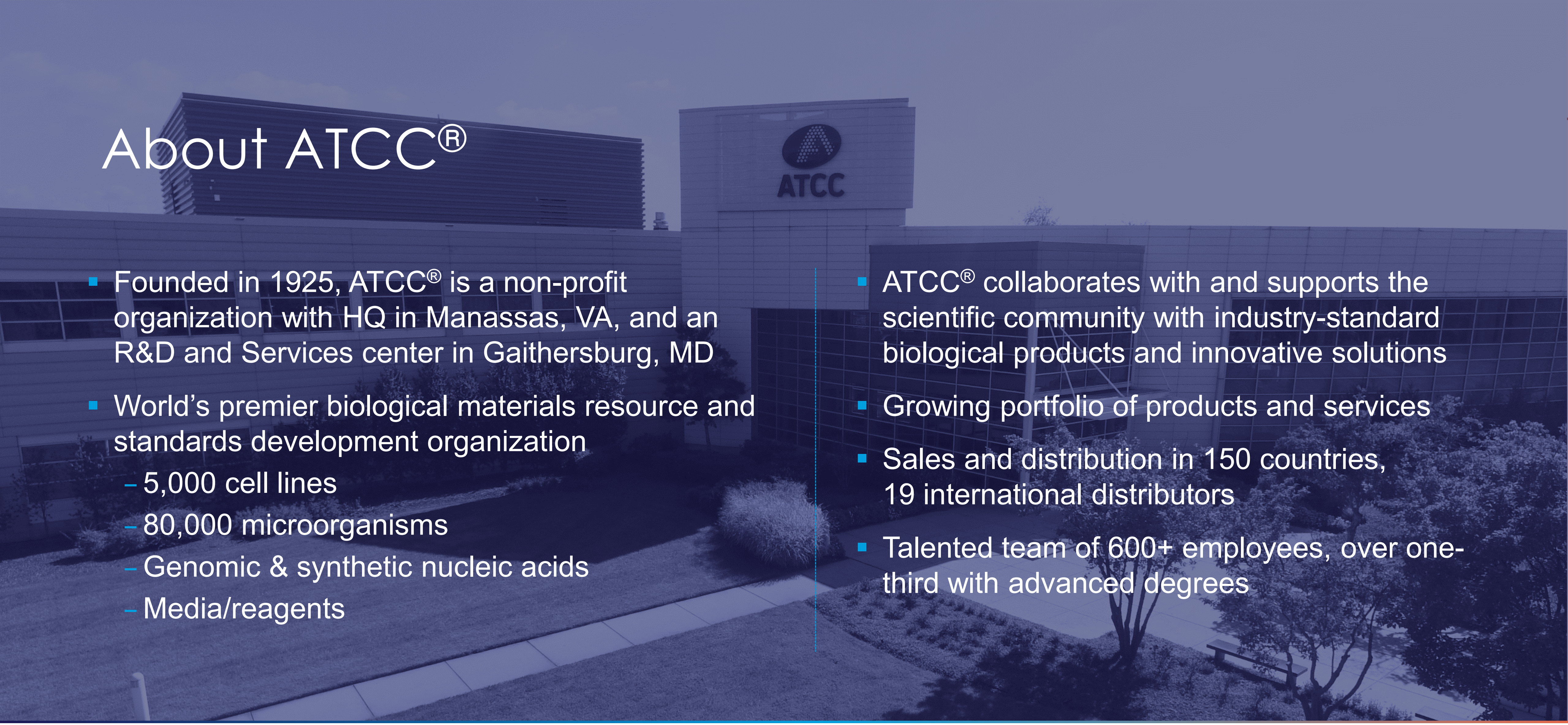
Kyle Young, BS, MBA
Product Manager, ATCC

Credible Leads to InCredible™

Introduction

Kyle Young *Product Manager, Bioprocessing (Microbiology)*

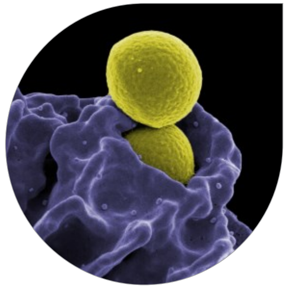
- Education
  - B.S. Biochemistry and Cellular & Molecular Biology,
    University of Tennessee (Knoxville, TN)
  - M.B.A.
    George Mason University (Fairfax, VA)
- American Type Culture Collection (ATCC)
  - 20 years at ATCC
    - Quality control testing (Cell Biology and Virology)
    - Virology Production
    - Virology R&D
    - High Containment Biomaterials (Virology and Bacteriology)
    - Product line management (Microbiology portfolio)



About ATCC®

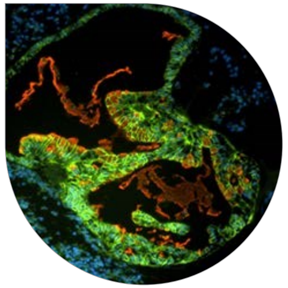
- Founded in 1925, ATCC® is a non-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's premier biological materials resource and standards development organization
  - 5,000 cell lines
  - 80,000 microorganisms
  - Genomic & synthetic nucleic acids
  - Media/reagents
- ATCC® collaborates with and supports the scientific community with industry-standard biological products and innovative solutions
- Growing portfolio of products and services
- Sales and distribution in 150 countries, 19 international distributors
- Talented team of 600+ employees, over one-third with advanced degrees

Our Offerings



Credible Collections

- The ATCC® collection of cell and microbial reference materials remain at the heart of incredible breakthroughs in scientific exploration.

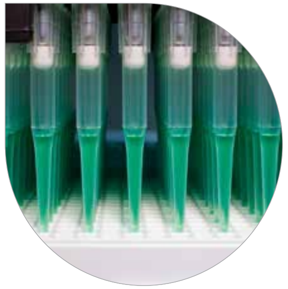


Advance Cell Models

- Advanced biological models enable greater specificity and functionality to the researcher's toolkit.

Authentication Resources

- ATCC® offers a range of high-quality cell authentication testing services backed by nearly 60 years of experience in biomaterial management and authentication standards.



Quality Standards

- ATCC® is a leader in the creation and maintenance of biological and published laboratory standards that protect public interests and provide quality reference material, education, accreditation, and certification services to the industry.

Offering Large Custom Solutions

- With an unmatched combination of extensive expertise, cutting edge technologies, best practices, and a world-renowned collection of cells and microbes, ATCC® is your ideal solutions partner.

cGMP Manufacturing & Biorepository Services

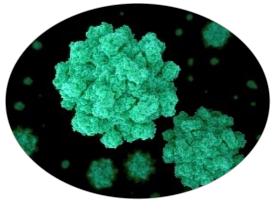
- Our longevity in the industry and reputation for quality ensures confidence for your Master and Working Mammalian Cell Banks and cGMP-compliant storage.

Innovations at ATCC®

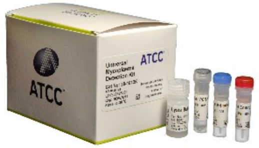
Much more than a culture collection!

ATCC® is more than culture management. New formats save time and money for our customers!

- Precisely quantitative, single-use, lyophilized pellets for the control of compendial assays: bioburden, antimicrobial effectiveness, sterility testing, environmental monitoring, and growth promotion.



- High-titer, high-purity viruses for viral clearance challenge studies and other adventitious agent testing.

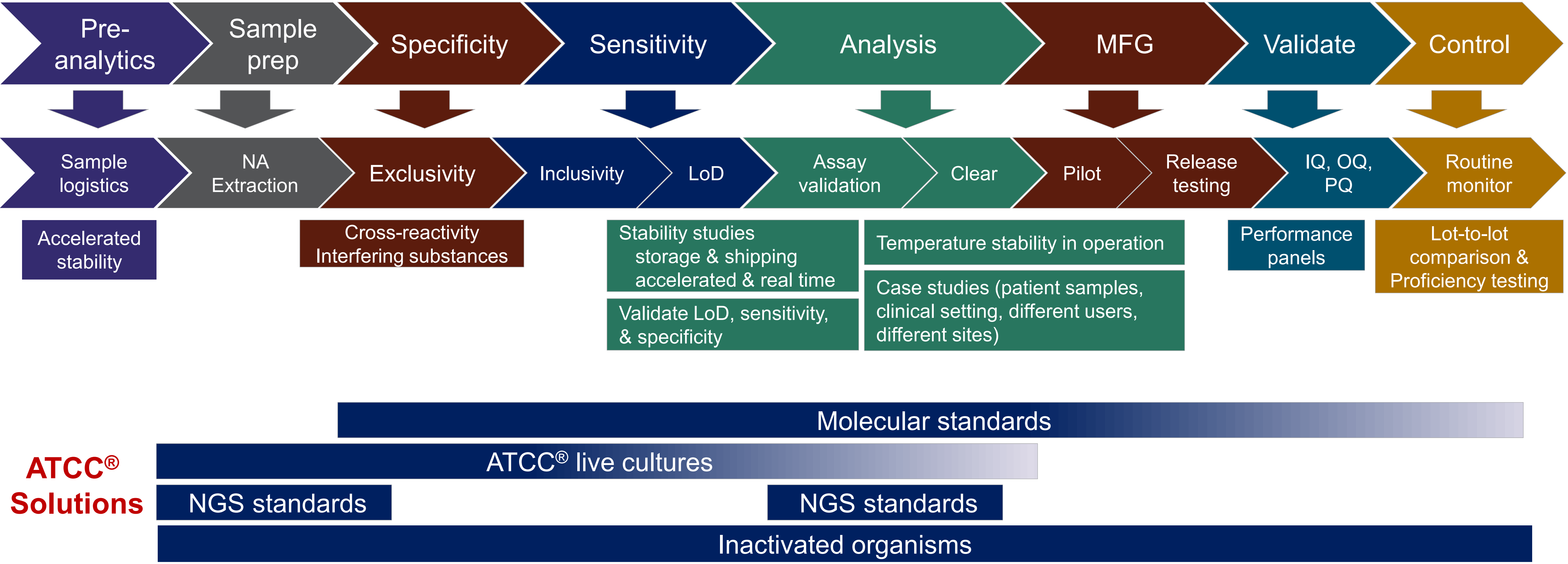


- Highly sensitive *Mycoplasma* testing kit with broad range of detection.
- Precisely quantitative DNA controls for *Mycoplasma* testing by compendial standards.

- Precisely quantitative DNA from bioproduction cell lines to control measurements of residual DNA. Developed in partnership with US Pharmacopoeia!

Numerous other products are in development that will serve needs for Oncology, Toxicology, Bioprocessing, Infectious Disease Diagnostics, and research.

Molecular Diagnostics (Dx) Workstream



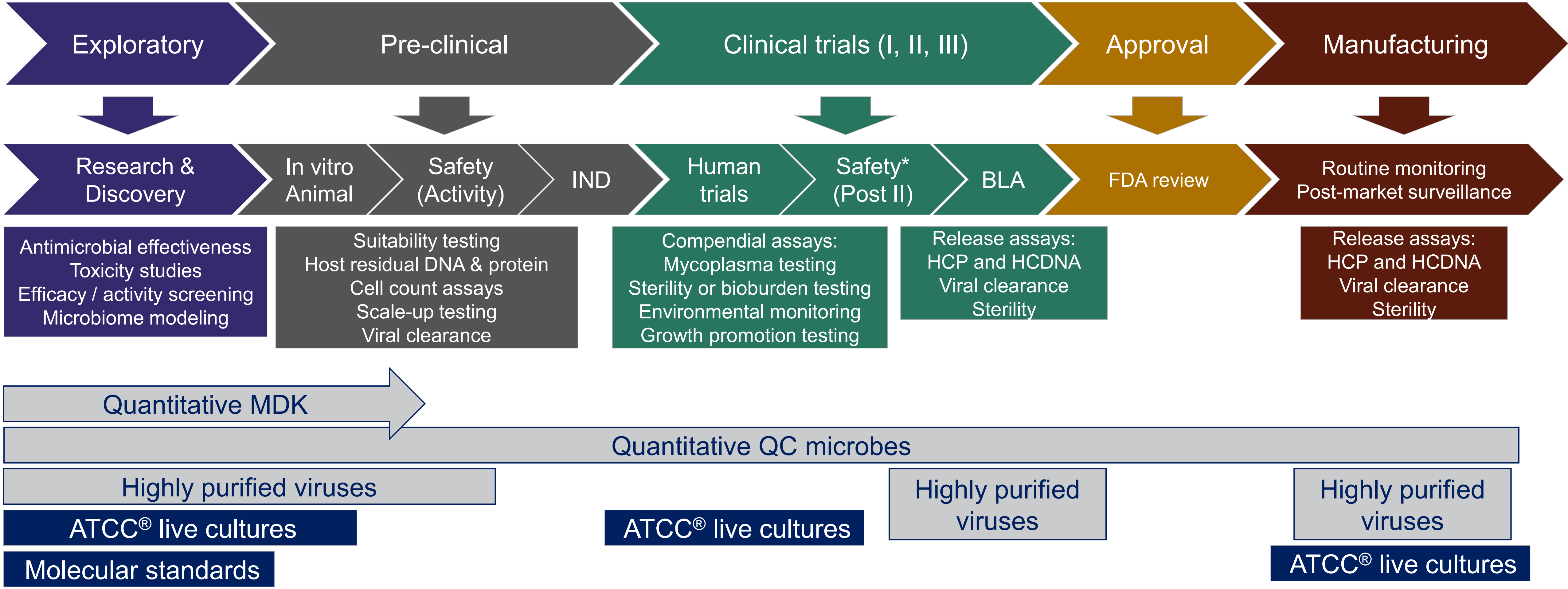
Pre-analytics → Sample prep → Specificity → Sensitivity → Analysis → MFG → Validate → Control

- Pre-analytics
  - Sample logistics
    - Accelerated stability
- Sample prep
  - NA Extraction
- Specificity
  - Exclusivity
    - Cross-reactivity
Interfering substances
- Sensitivity
  - Inclusivity
  - LoD
    - Stability studies
      - storage & shipping
      - accelerated & real time
    - Validate LoD, sensitivity, & specificity
- Analysis
  - Assay validation
  - Clear
    - Temperature stability in operation
    - Case studies (patient samples, clinical setting, different users, different sites)
- MFG
  - Pilot
  - Release testing
- Validate
  - IQ, OQ, PQ
    - Performance panels
- Control
  - Routine monitor
    - Lot-to-lot comparison & Proficiency testing

ATCC® Solutions

- Molecular standards
- ATCC® live cultures
- NGS standards
- NGS standards
- Inactivated organisms

Biologics Development Workstream



Exploratory

Pre-clinical

Clinical trials (I, II, III)

Approval

Manufacturing

Research & Discovery

In vitro Animal

Safety (Activity)

IND

Human trials

Safety* (Post II)

BLA

FDA review

Routine monitoring
Post-market surveillance

Antimicrobial effectiveness
Toxicity studies
Efficacy / activity screening
Microbiome modeling

Suitability testing
Host residual DNA & protein
Cell count assays
Scale-up testing
Viral clearance

Compendial assays:
Mycoplasma testing
Sterility or bioburden testing
Environmental monitoring
Growth promotion testing

Release assays:
HCP and HCDNA
Viral clearance
Sterility

Release assays:
HCP and HCDNA
Viral clearance
Sterility

Quantitative MDK

Quantitative QC microbes

Highly purified viruses

ATCC® live cultures

Molecular standards

ATCC® live cultures

Highly purified viruses

Highly purified viruses

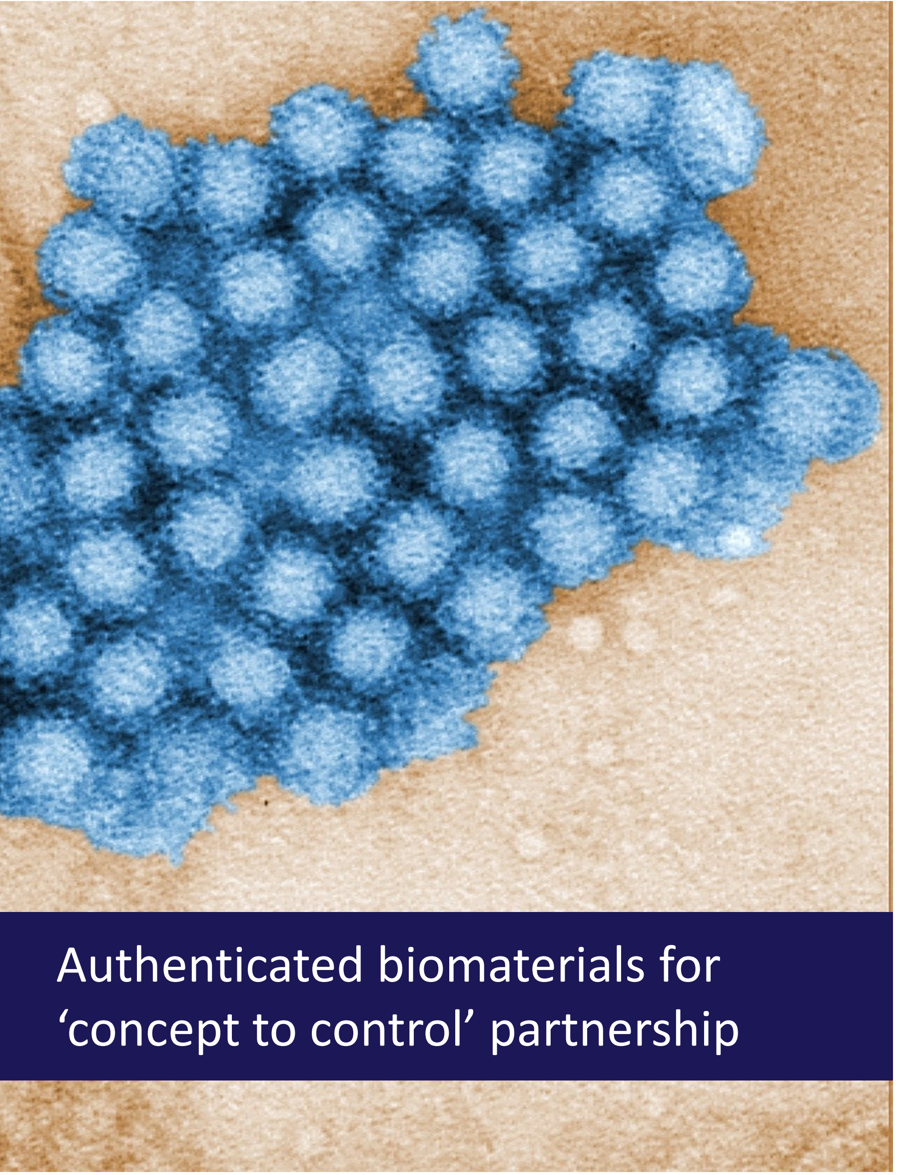
ATCC® live cultures

ATCC® Catalog

ATCC® Development

ATCC® Solutions

Molecular Diagnostics Portfolio

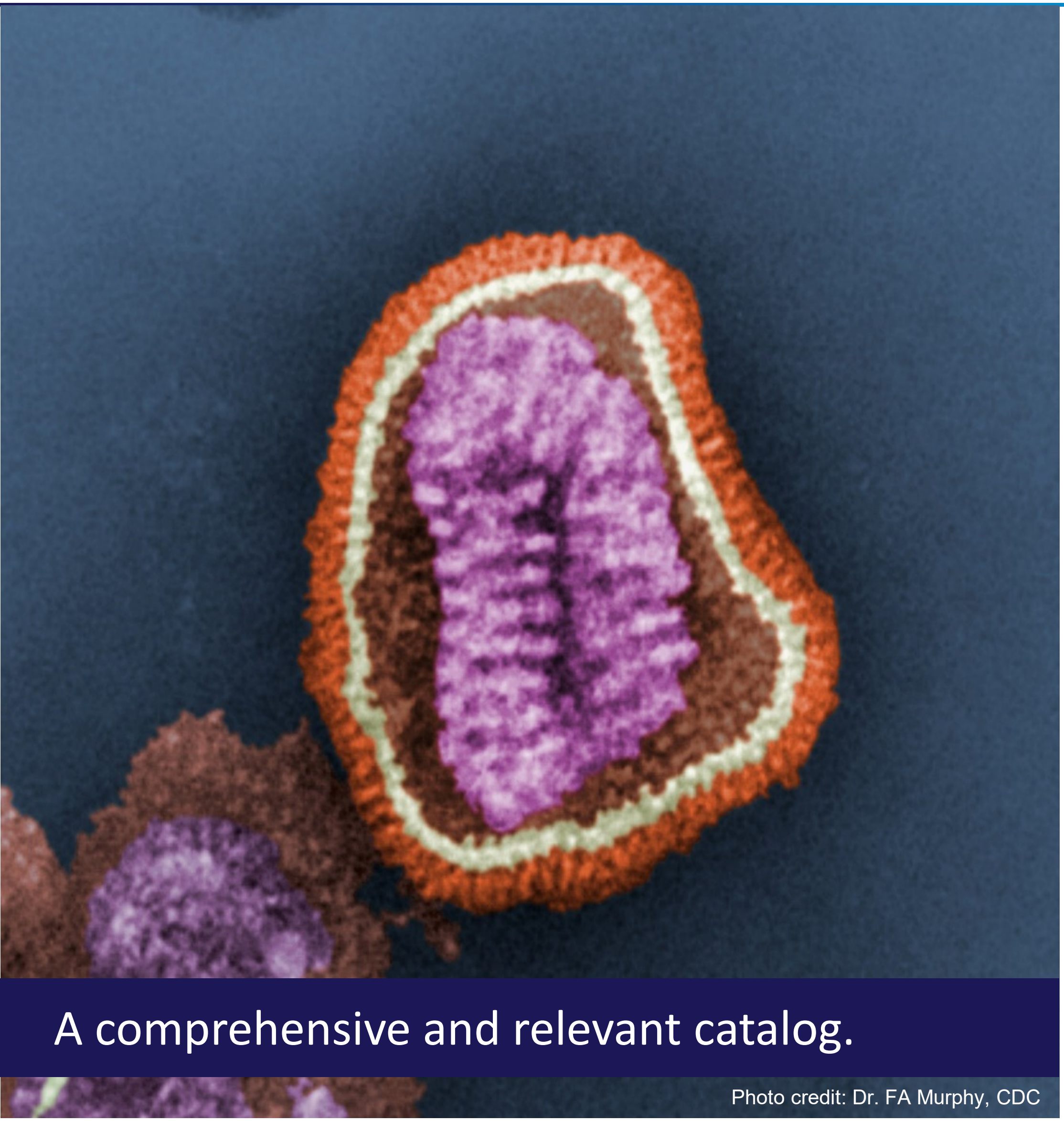


Authenticated biomaterials for ‘concept to control’ partnership

Molecular diagnostics:

- Molecular Standards (270+ quantitative nucleic acids)
- NGS standards (24+)
- Inactivated organisms
- Antimicrobial resistant bacteria and fungi (600+)
- Pathogens of relevance
  - Respiratory (540+)
  - Bloodborne (40+)
  - Enteric (570+)
  - Vector-borne (85+)
  - Sexually transmitted infections (130+)

Virology Portfolio



A comprehensive and relevant catalog.

Photo credit: Dr. FA Murphy, CDC

Virology:

- Viruses (3,000+)
  - With host cells and media
- High titer, semi-purified viruses (16+)
- Inactivated viruses (8+)
- Highly purified viruses
  - Adventitious agents in development for viral clearance testing and control.

Mycoplasma Detection

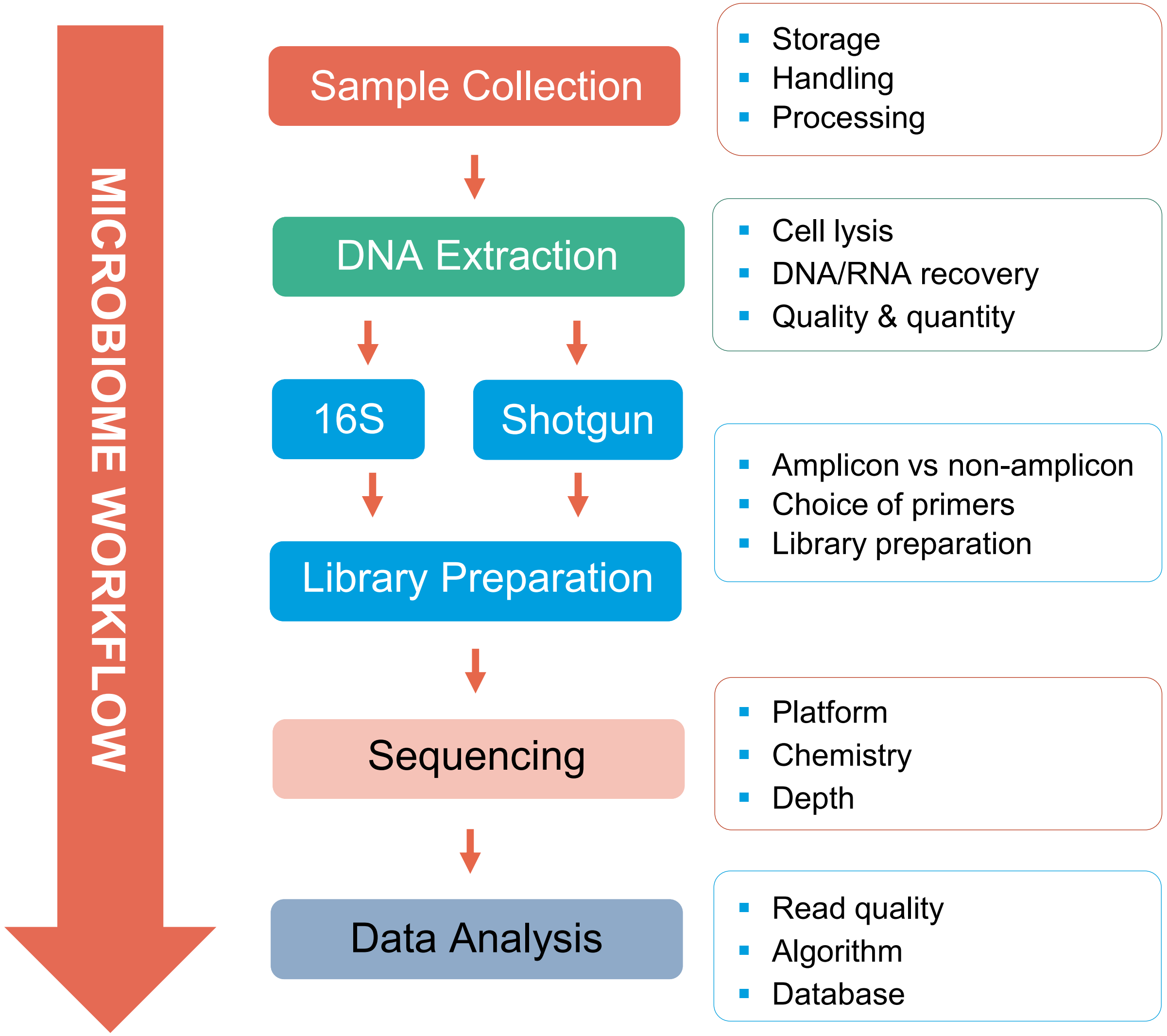
- Universal Mycoplasma Detection Kit (ATCC® 30-1012K™)
  - PCR and electrophoresis-based assay
  - Lysis buffer included – no DNA extraction kit necessary
  - Detects over 60 species, including compendial strains & common culture contaminants
  - Limit of detection is < 20 genomes (*M. arginine* and *A. laidlawii*)
- Quantitative Mycoplasma Detection Kit (dPCR assay in development)
- Certified Reference Material (CRM) DNA preparations
  - Ten strains cited by the harmonized compendia
  - Produced under ISO 17034 certification
  - Quantified by ddPCR™ (n = 9) at 1 x 10^6 to 1 x 10^7 genome copies/µL
- Titered live strains
  - Ten strains cited by the harmonized compendia
  - Quantified by CFU / mL (n = 3) at ≥ 2 x 10^4 CFU / mL

Species	Live, titered	DNA, quantified
Mycoplasma hominis	27545-TTR™	qCRM-27545D™
Mycoplasma pneumoniae	15531-TTR™	qCRM-15531D™
Acholeplasma laidlawii	23206-TTR™	qCRM-23206D™
Mycoplasma salivarium	23064-TTR™	qCRM-23064D™
Mycoplasma synoviae	25204-TTR™	qCRM-25204D™
Mycoplasma fermentans	19989-TTR™	qCRM-19989D™
Mycoplasma arginini	23838-TTR™	qCRM-23838D™
Mycoplasma gallisepticum	19610-TTR™	qCRM-19610D™
Mycoplasma hyorhinis	17981-TTR™	qCRM-17981D™
Mycoplasma orale	23714-TTR™	qCRM-23714D™

Microbiome Research and Applications

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

Challenges in Microbiome Research and Applications



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

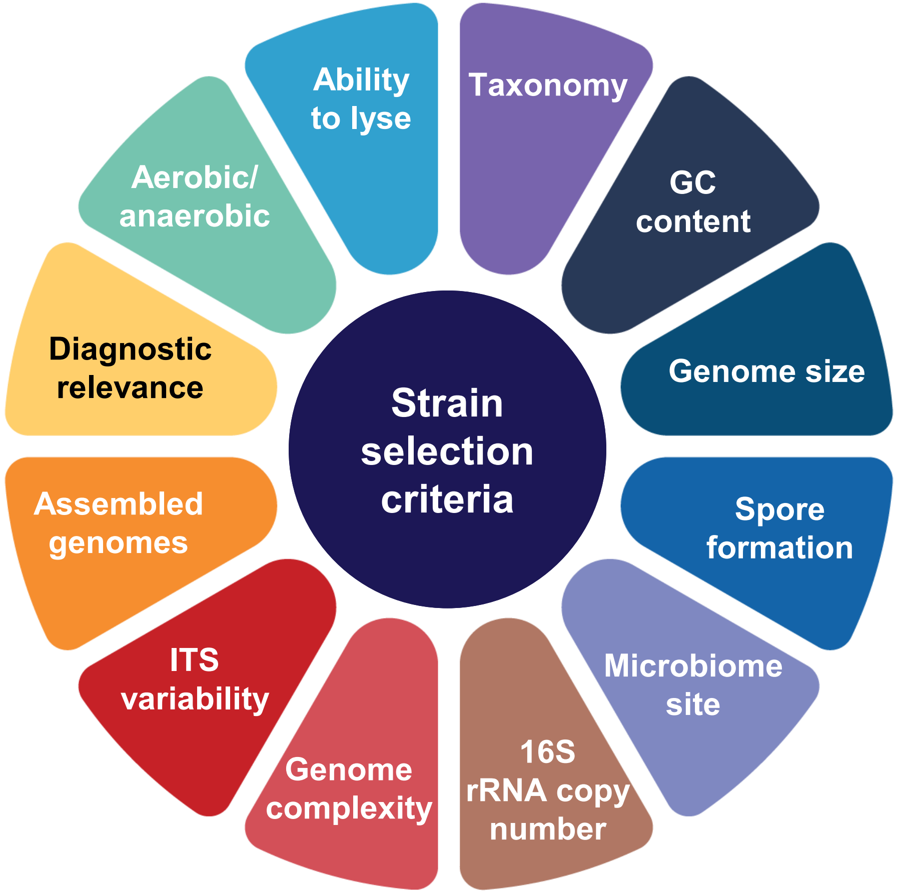
Sequencing

- Platform
- Chemistry
- Depth

Data Analysis

- Read quality
- Algorithm
- Database

Development of ATCC NGS Standards



Strain selection criteria

- Ability to lyse
- Taxonomy
- 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 proportion-based cell numbers cells
- Storage at 4°C

Genomic DNA Standards

- Authenticated ATCC® nucleic acids
- Fluorescent dye-based quantification
- Mixed in even proportions-based genome copy number
- Storage at -20°C

Assay development, optimization, verification, and quality control

ATCC® Genome Portal

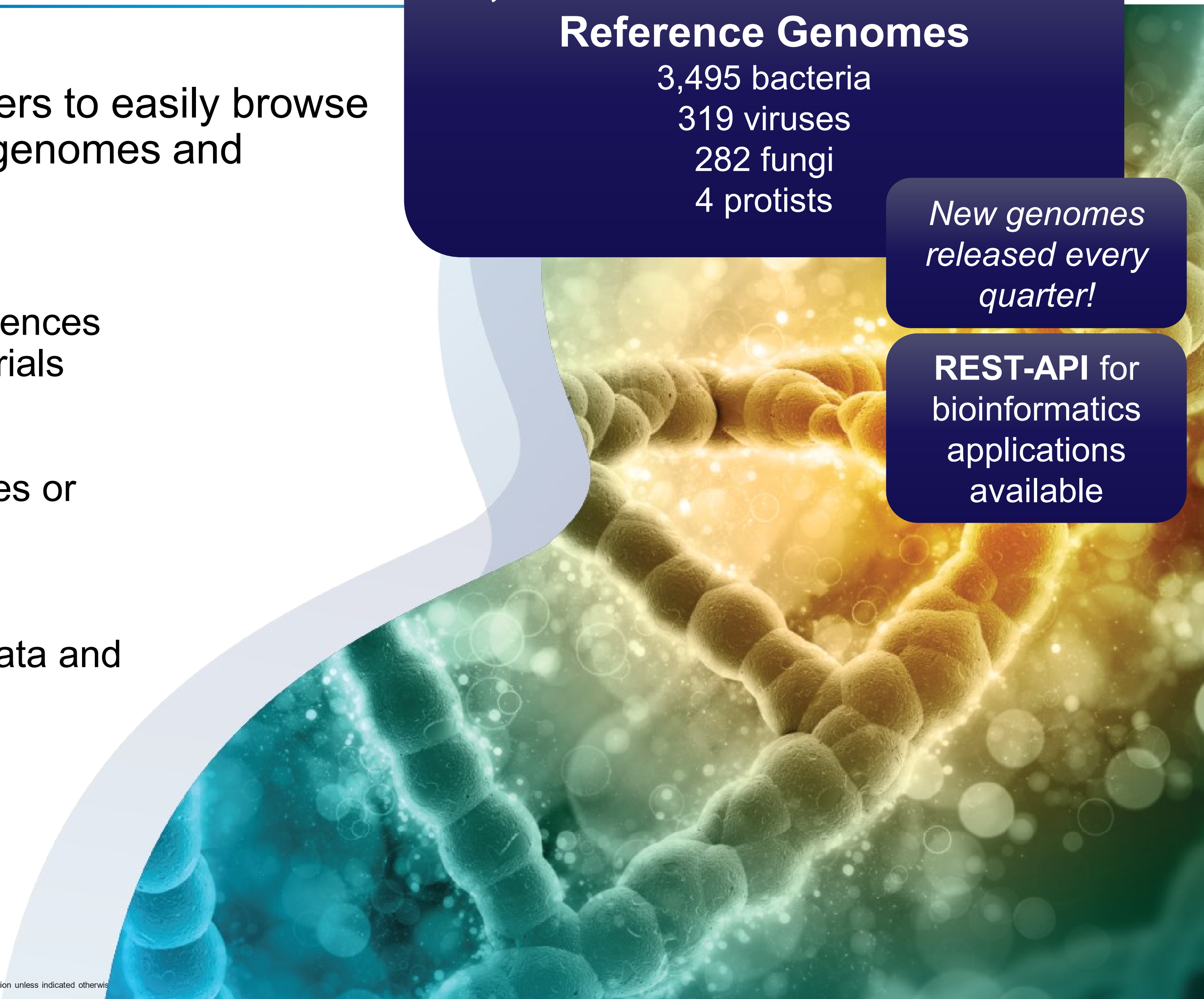
A cloud-based platform that enables users to easily browse authenticated and traceable reference genomes and metadata.

Download whole-genome sequences and annotations of ATCC materials

Search for nucleotide sequences or genes within genomes

View genome assembly metadata and quality metrics

genomes.atcc.org



4,100 Authenticated Microbial Reference Genomes
3,495 bacteria
319 viruses
282 fungi
4 protists

New genomes released every quarter!

REST-API for bioinformatics applications available

Yarmosh DA, et al. Comparative Analysis and Data Provenance for 1,113 Bacterial Genome Assemblies. Msphere 7(3): e00077-22, 2022

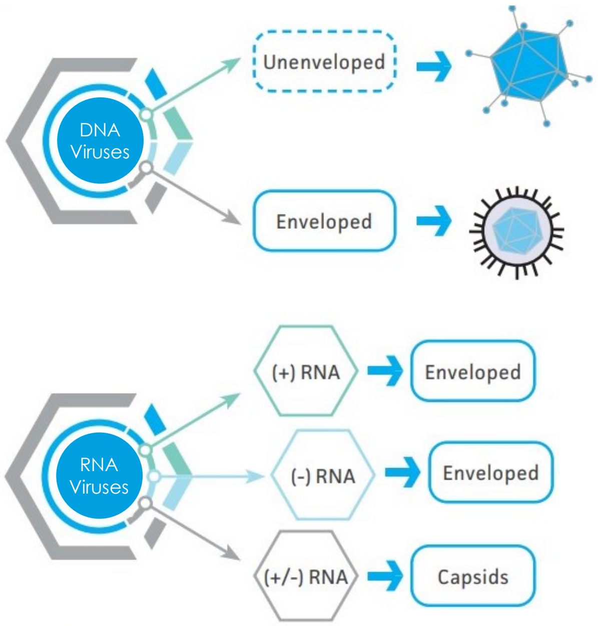
ATCC® NGS Standards Portfolio

Preparation	ATCC® Catalog No.	Number of Organisms	Composition	Complexity	Utility
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	

ATCC® Site-specific NGS 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 Gram-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	Structure
Human adenovirus 40 (ATCC® VR-931™)	dsDNA, unenveloped
Human herpesvirus 5 strain AD169 (ATCC® VR-538™)	dsDNA, enveloped
Zika virus strain MR 766 (ATCC® VR-1838™)	(+) ssRNA, enveloped
Influenza B virus strain B/Florida/4/2006 (ATCC® VR-1804™)	(-) ssRNA, enveloped
Human respiratory syncytial virus strain A2 (ATCC® VR-1540™)	(-) ssRNA, enveloped
Reovirus 3 strain Dearing (ATCC® VR-824™)	dsRNA, capsid

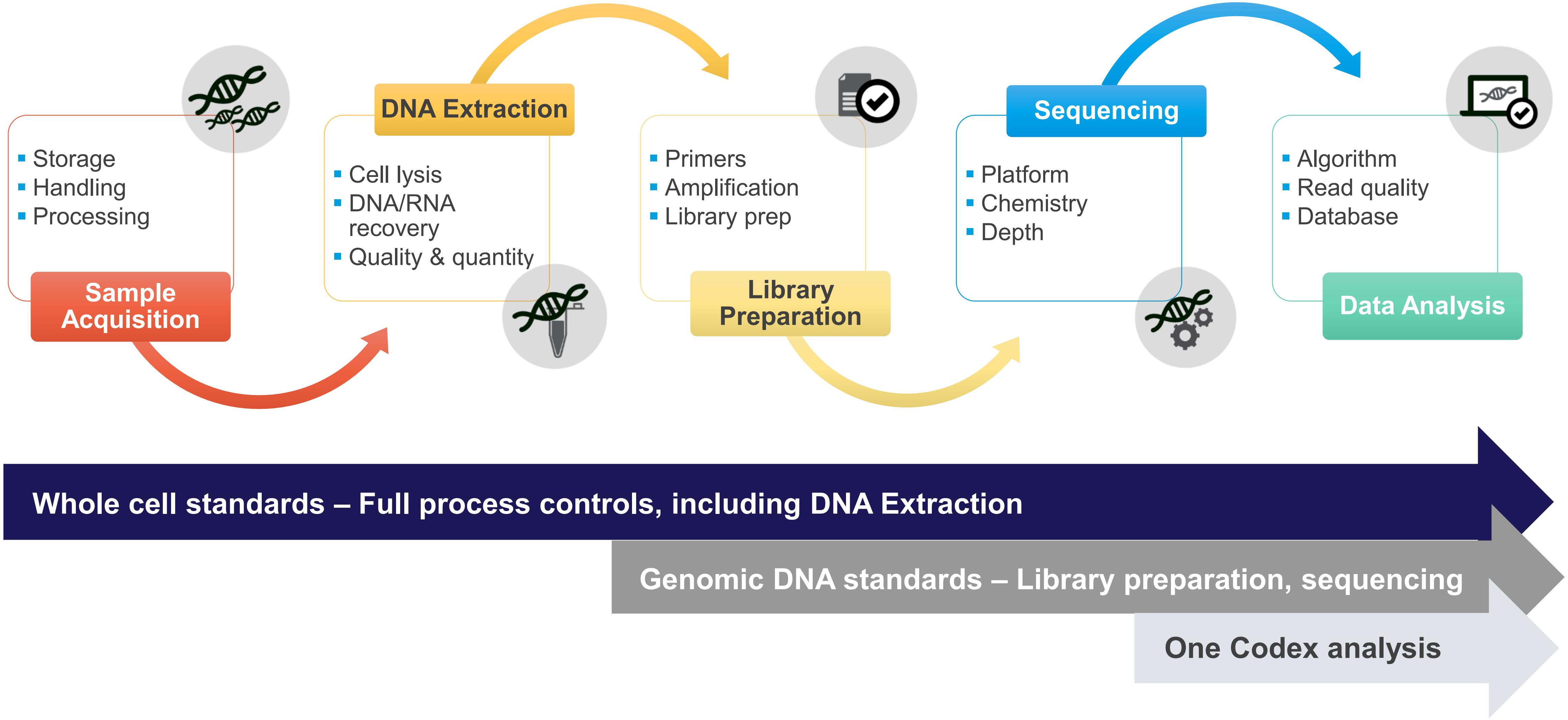
Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Specification (ddPCR™)	Applications
Virome	Virus Mix	MSA-2008™	6	2 × 10^3 genome copies/µL per virus	Standards for virome assay development, optimization, verification, and validation; evaluating reproducibility; and use as a daily run quality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

ATCC® Spike-in and Mycobiome Standards

Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Application
Spike-in	Whole cell	MSA-2014™	3	▪ Microbiome measurements and data normalization ▪ 16S rRNA and shotgun assay verification, validation, and quality control
	Genomic	MSA-1014™		

Standard	Preparation	ATCC® Catalog No.	Number of Organisms	Application
Mycobiome	Whole cell	MSA-2010™	10	▪ Fungal mock community standards for assay development, optimization, verification, and validation; evaluating reproducibility; and use as a daily run quality control
	Genomic	MSA-1010™		

Microbiome Workflow, Biases, and Standardization



Sample Acquisition

- 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

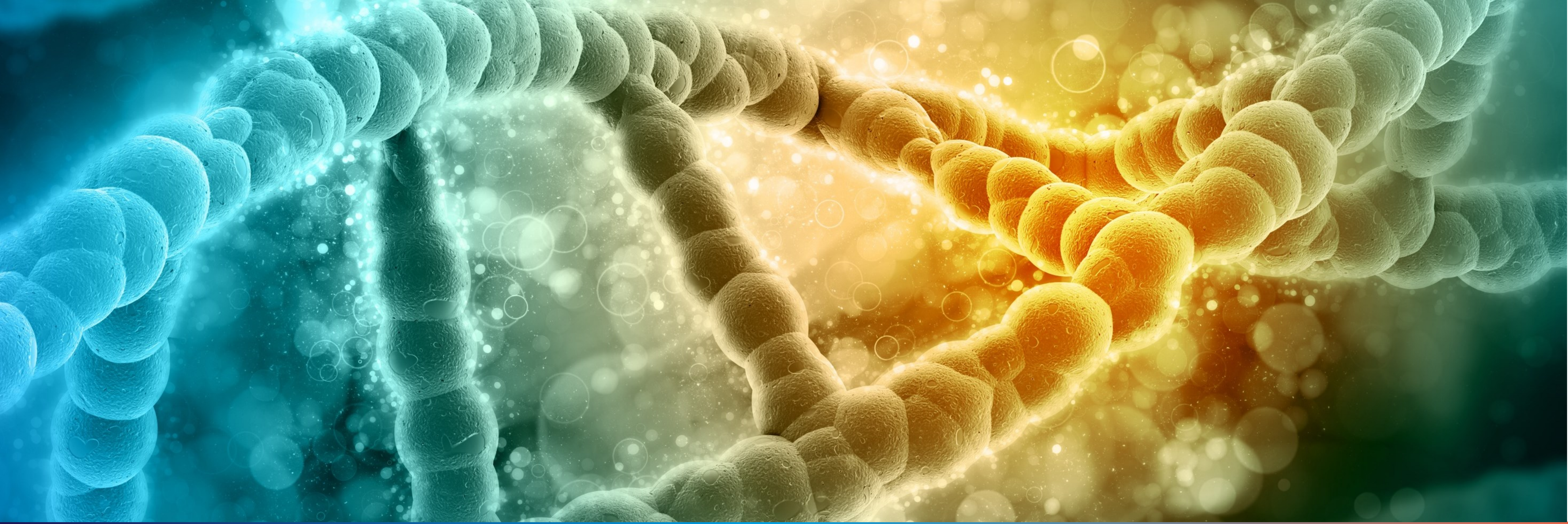
Whole cell standards – Full process controls, including DNA Extraction

Genomic DNA standards – Library preparation, sequencing

One Codex analysis

Utility and Application of NGS Standards

- Evaluating DNA extraction methods and kits
- Evaluating 16S rRNA and WGS library kits
- Evaluating NGS platforms

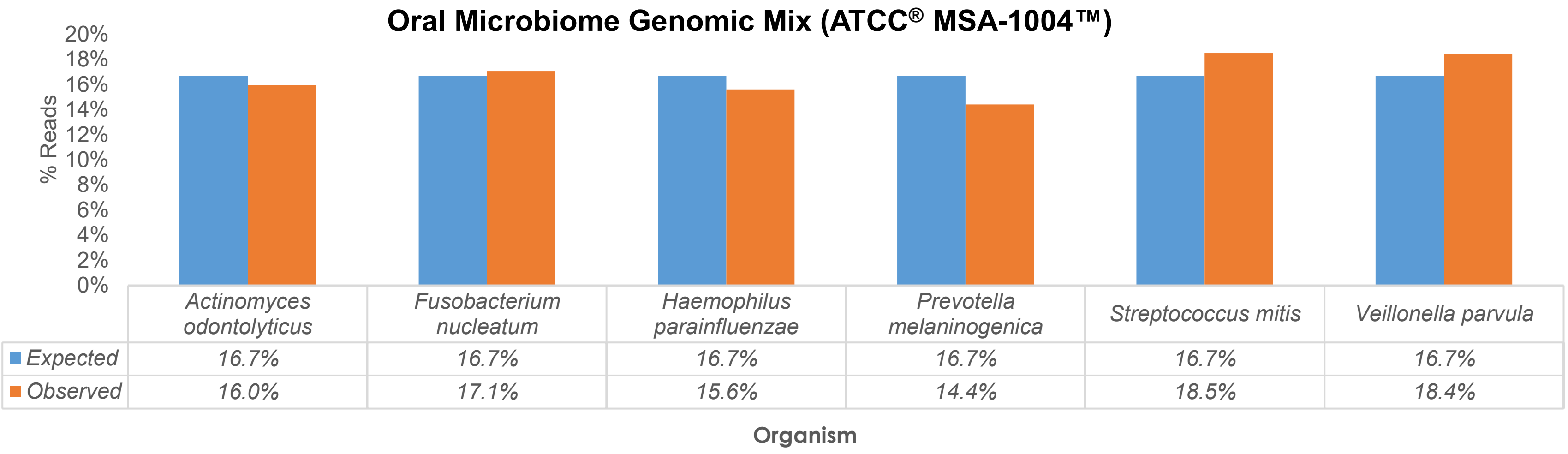


Evaluating DNA Extraction Methods and Kits

Genomic Versus Whole Cell Standards

DNA extraction methods are not perfect

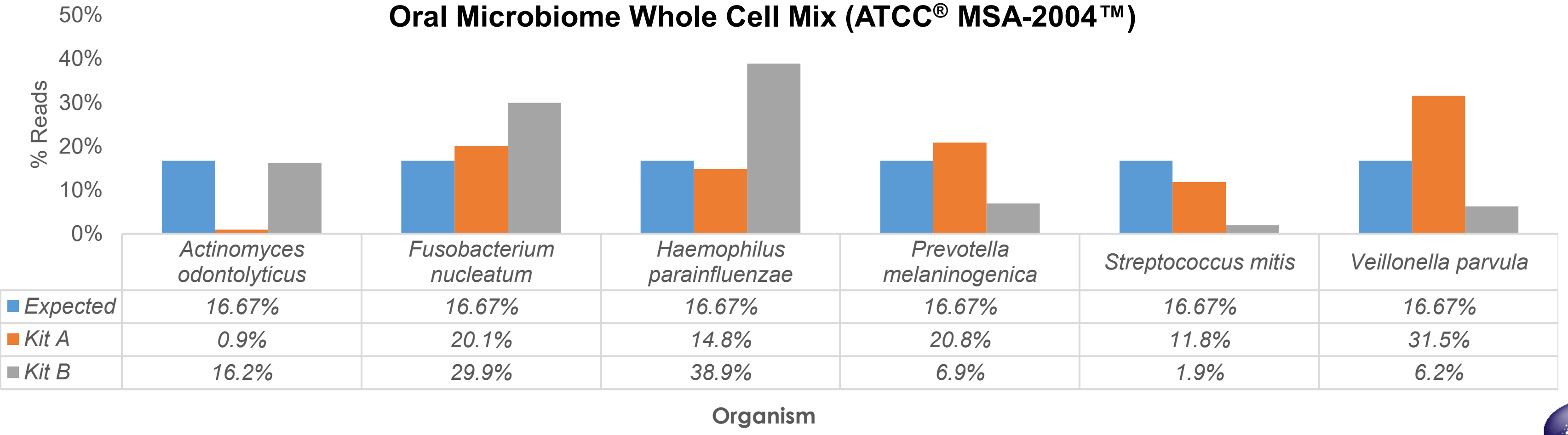
Shotgun metagenomic analysis of the Oral Microbiome Genomic Mix



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™)

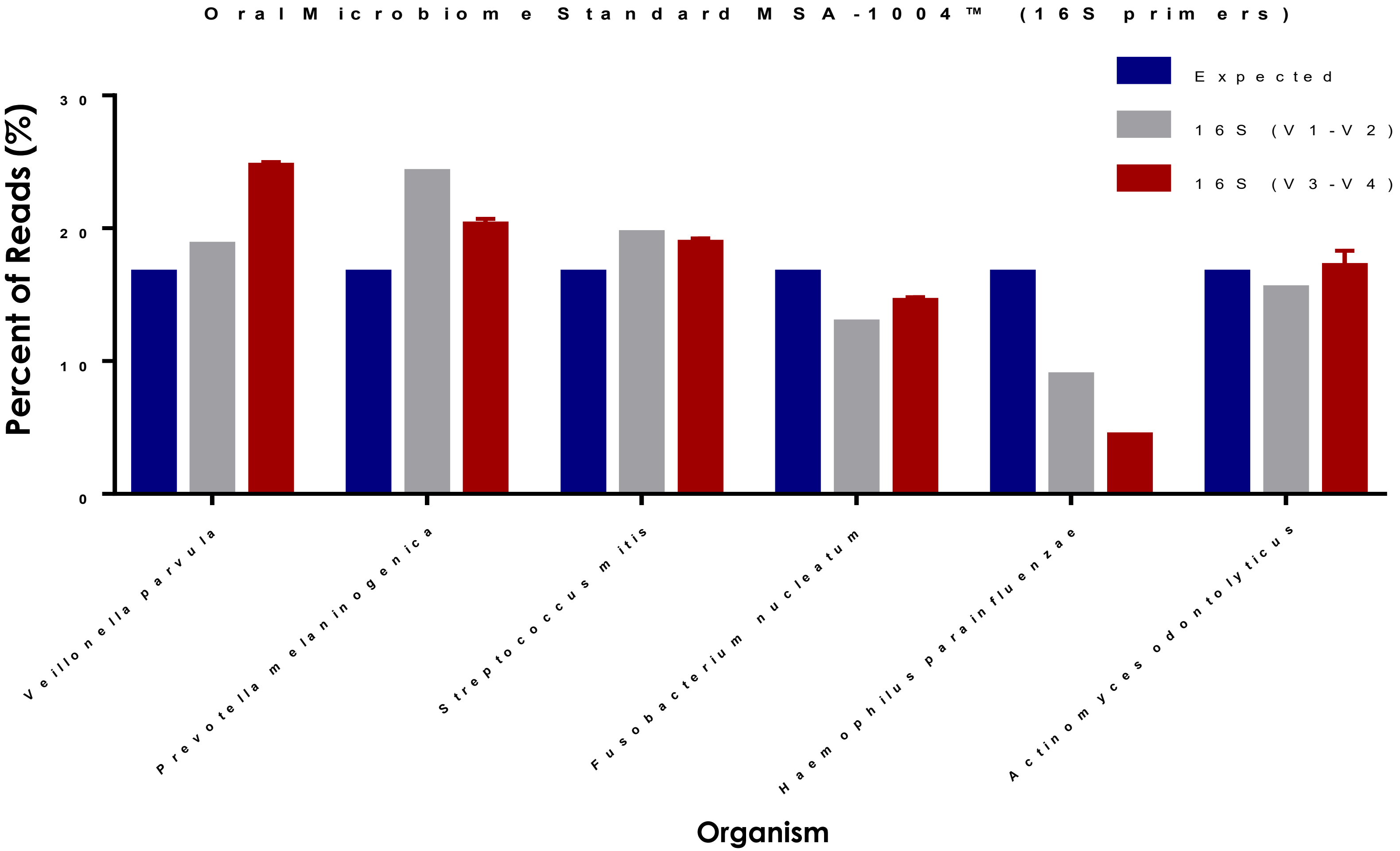
	Actinomyces odontolyticus	*Fusobacterium nucleatum*	*Haemophilus parainfluenzae*	*Prevotella melaninogenica*	*Streptococcus mitis*	*Veillonella parvula*
■ *Expected*	*16.67%*	*16.67%*	*16.67%*	*16.67%*	*16.67%*	*16.67%*
■ *Kit A*	*0.9%*	*20.1%*	*14.8%*	*20.8%*	*11.8%*	*31.5%*
■ *Kit B*	*16.2%*	*29.9%*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

Evaluating 16S rRNA and WGS Library Kits

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

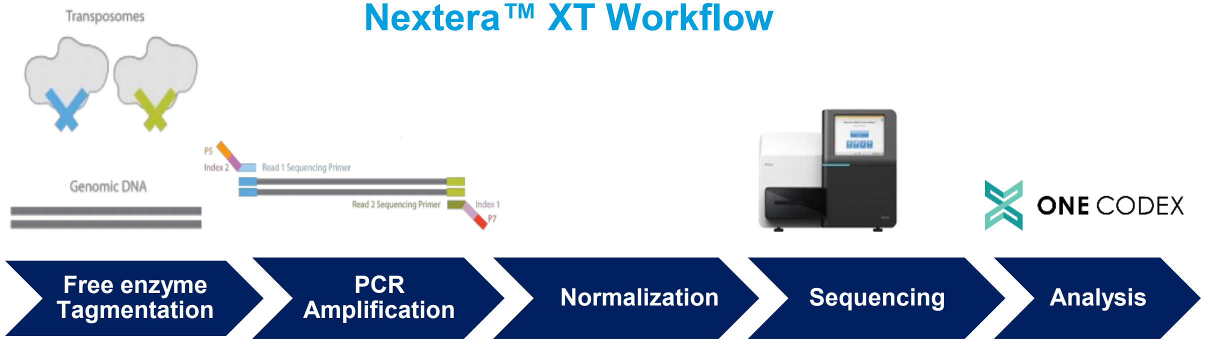


Comparing Library Preparation Kits

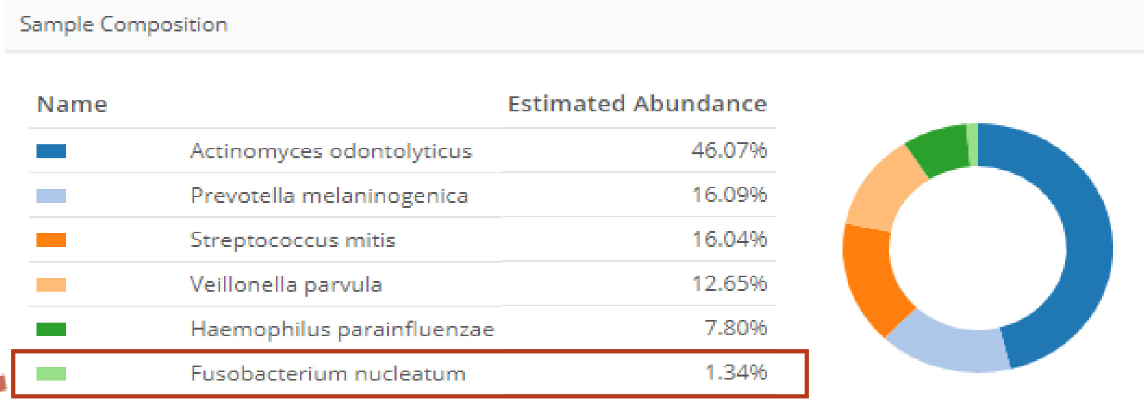
Nextera™ Flex enables uniform coverage of genomes of low GC content

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

Nextera™ XT Workflow



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

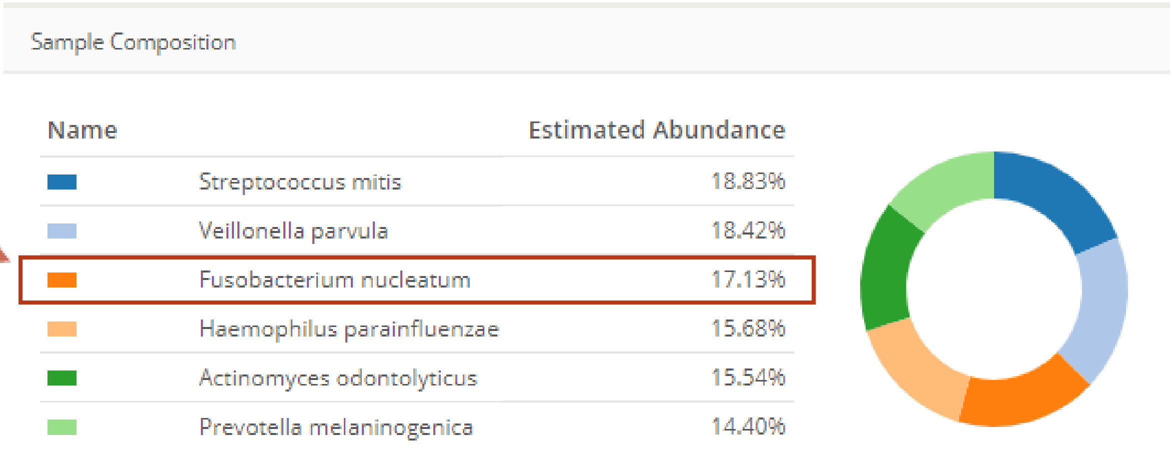


Sample Composition

	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

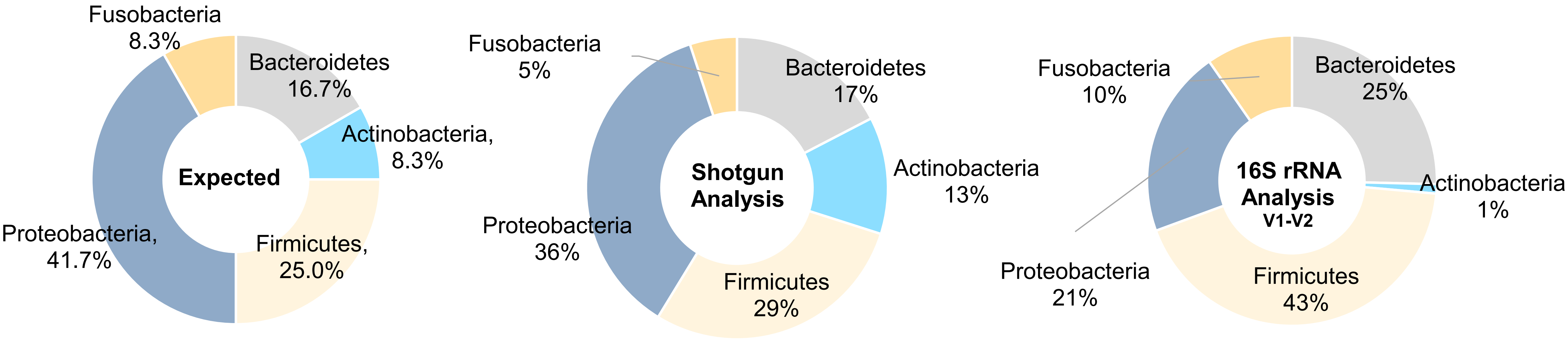
	Name	Estimated Abundance
🟦	Streptococcus mitis	18.83%
🟦	Veillonella parvula	18.42%
🟧	Fusobacterium nucleatum	17.13%
🟧	Haemophilus parainfluenzae	15.68%
🟩	Actinomyces odontolyticus	15.54%
🟩	Prevotella melaninogenica	14.40%

Data courtesy of Illumina®

Gut Whole Cell Standard

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

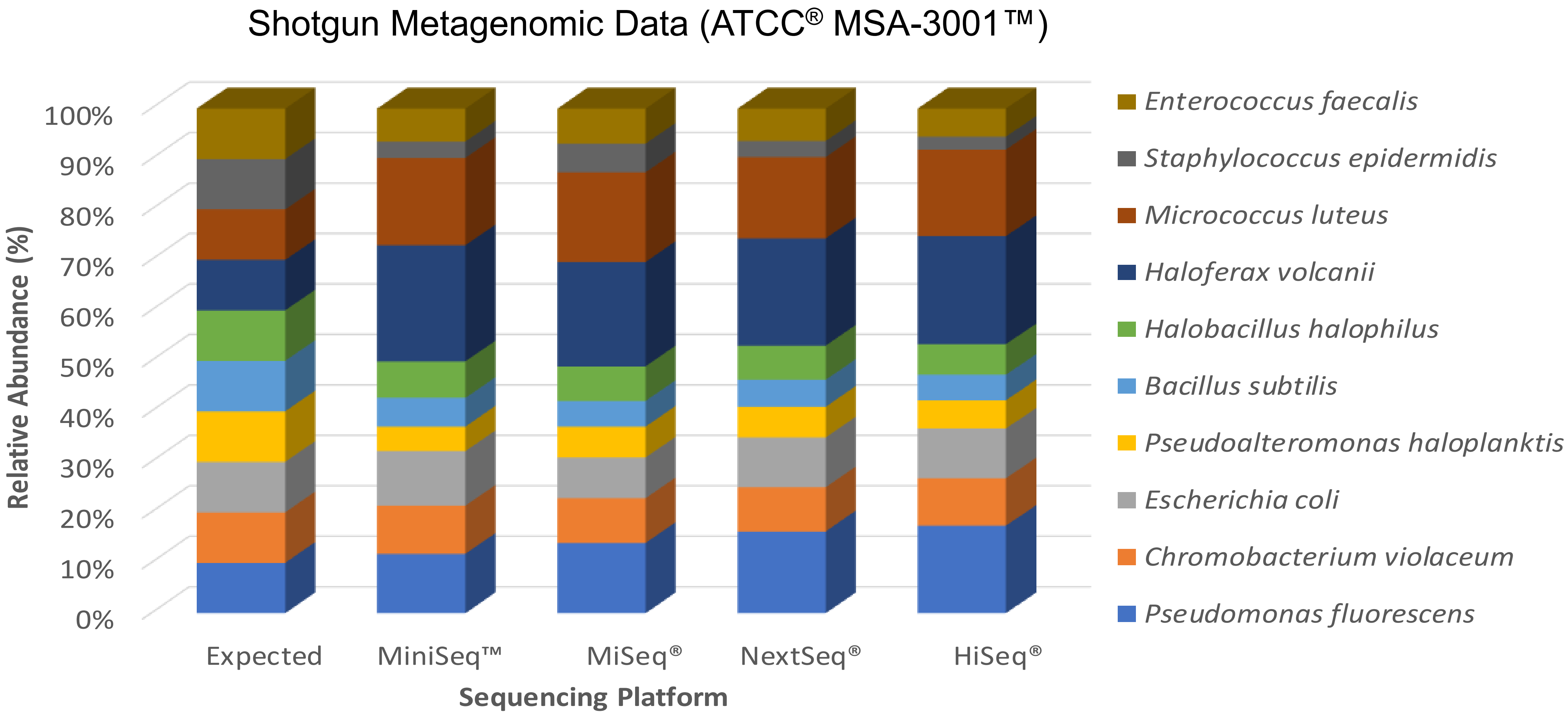
The Gut Whole Cell Microbiome Standard (ATCC® MSA-2006™) can be used as a full process control for shotgun and 16S rRNA assays



Evaluating NGS Platforms

Short-read Sequencing Platform: Illumina®

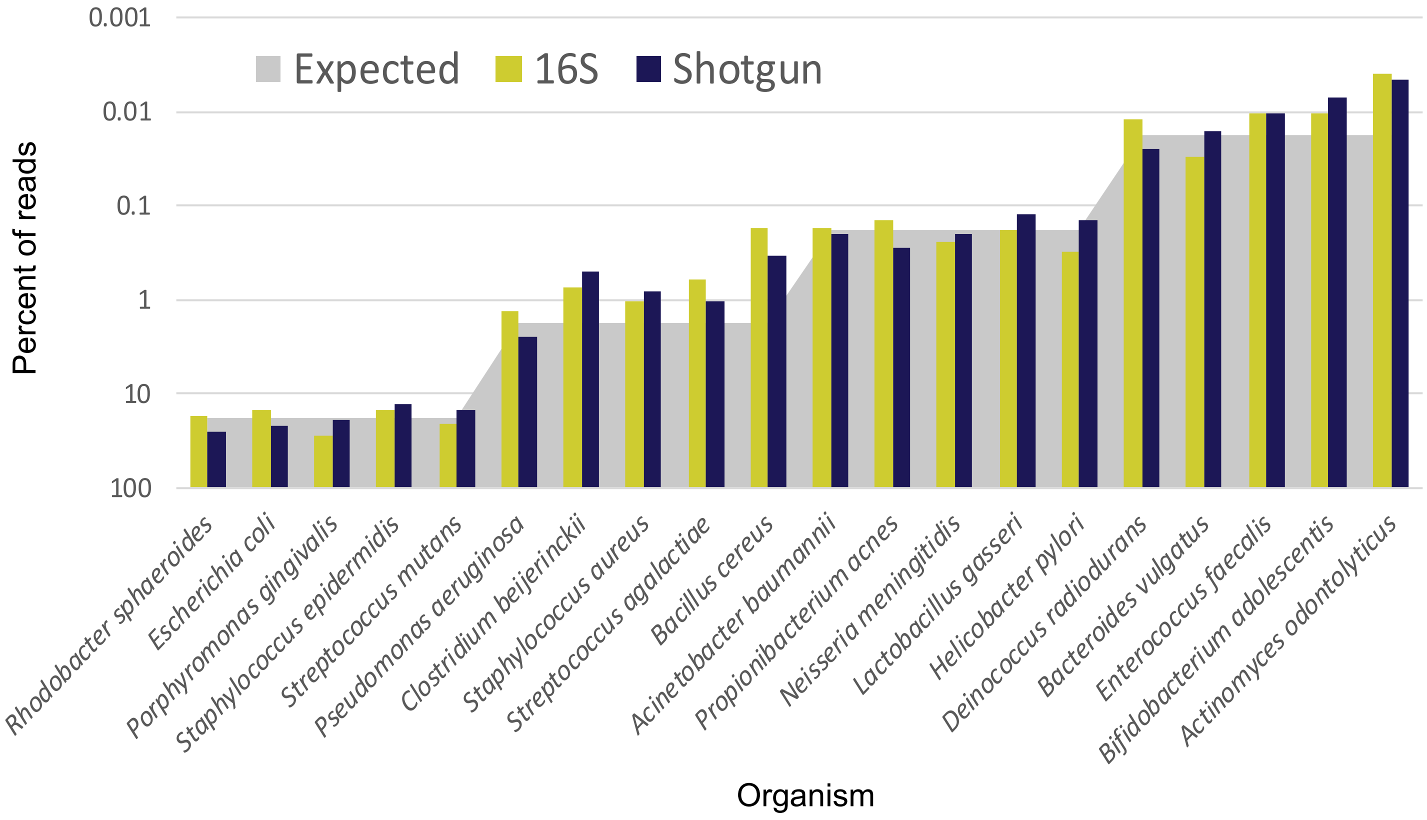
Assay reproducibility through different Illumina® sequencing platforms



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

Long-read Sequencing Platform: PACBIO®

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



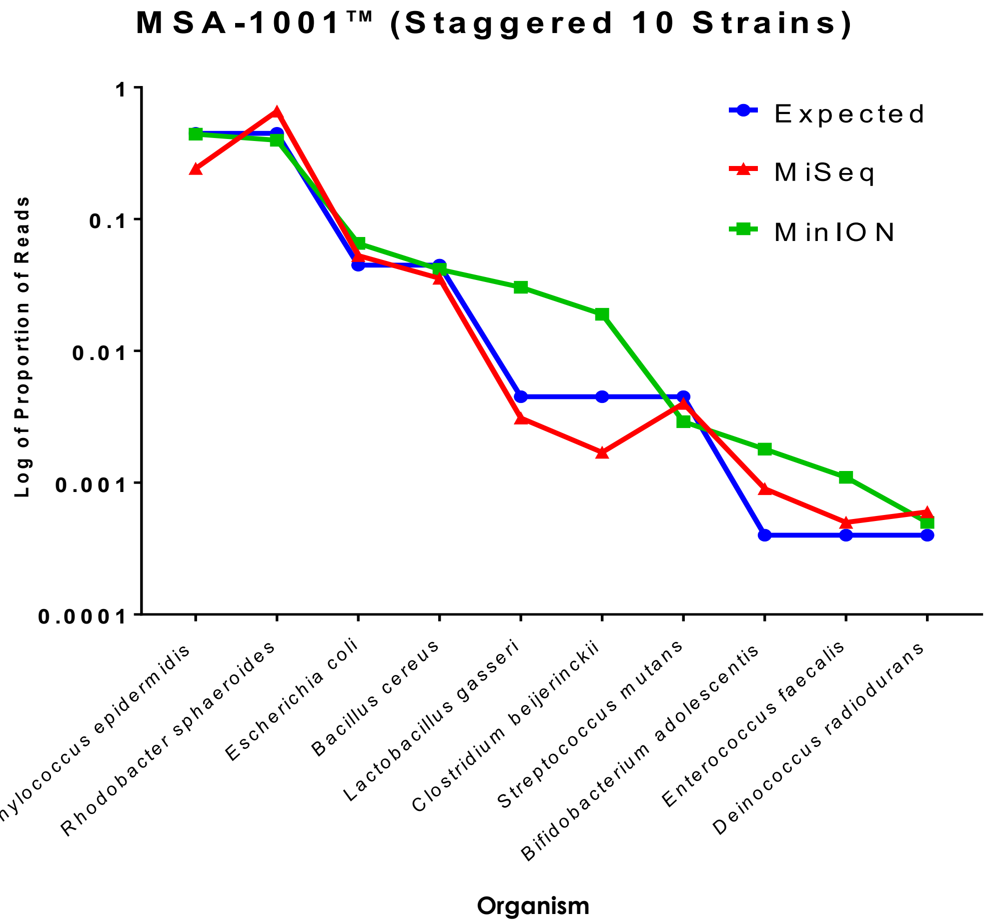
ATCC® quality control score (One Codex)

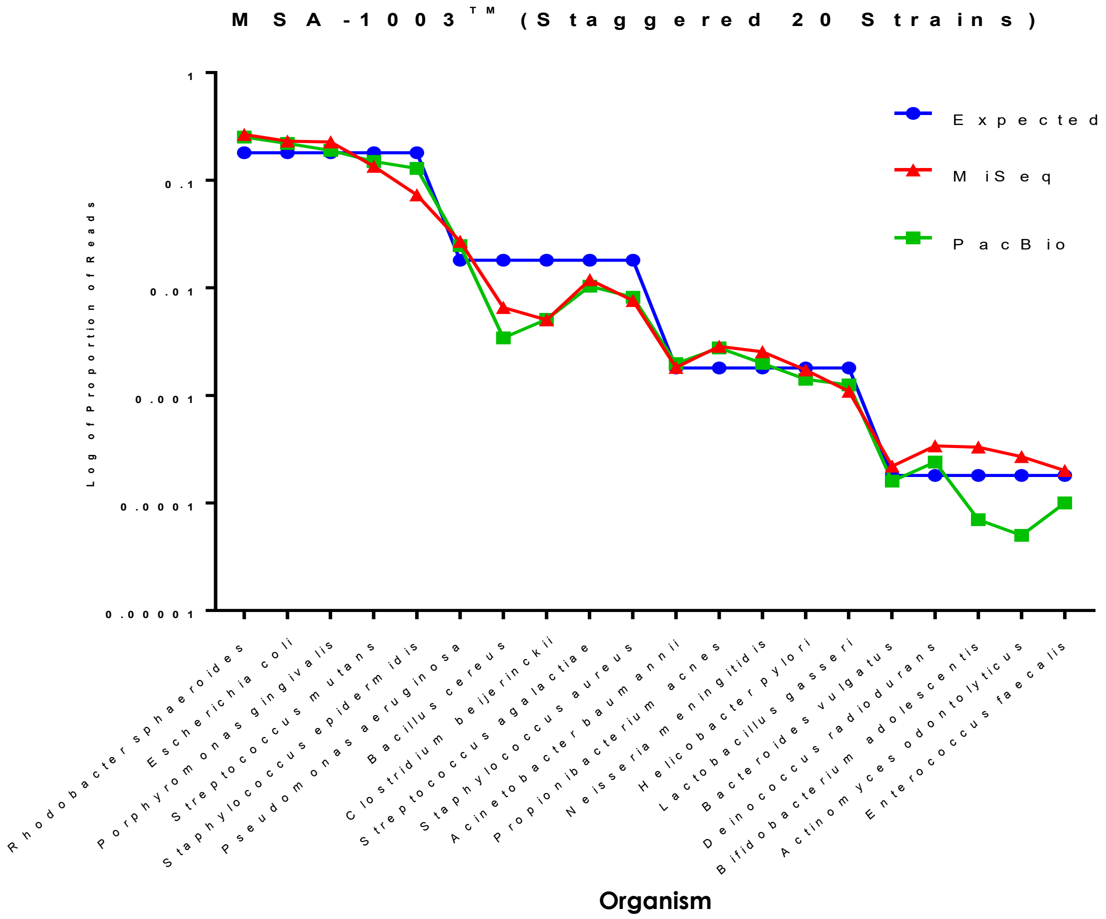
One Codex Analysis	16S rRNA run 1	16S rRNA run 2	Shotgun run 1	Shotgun run 2
True positives	100%	100%	100%	100%
Relative abundance	95%	95%	97%	97%
False positives	0%	0%	12%	16%
Overall score	98%	98%	95%	95%

Data courtesy of Dr. Joan Wong, PACBIO®

Shotgun Metagenomic Analysis: Short vs Long Reads

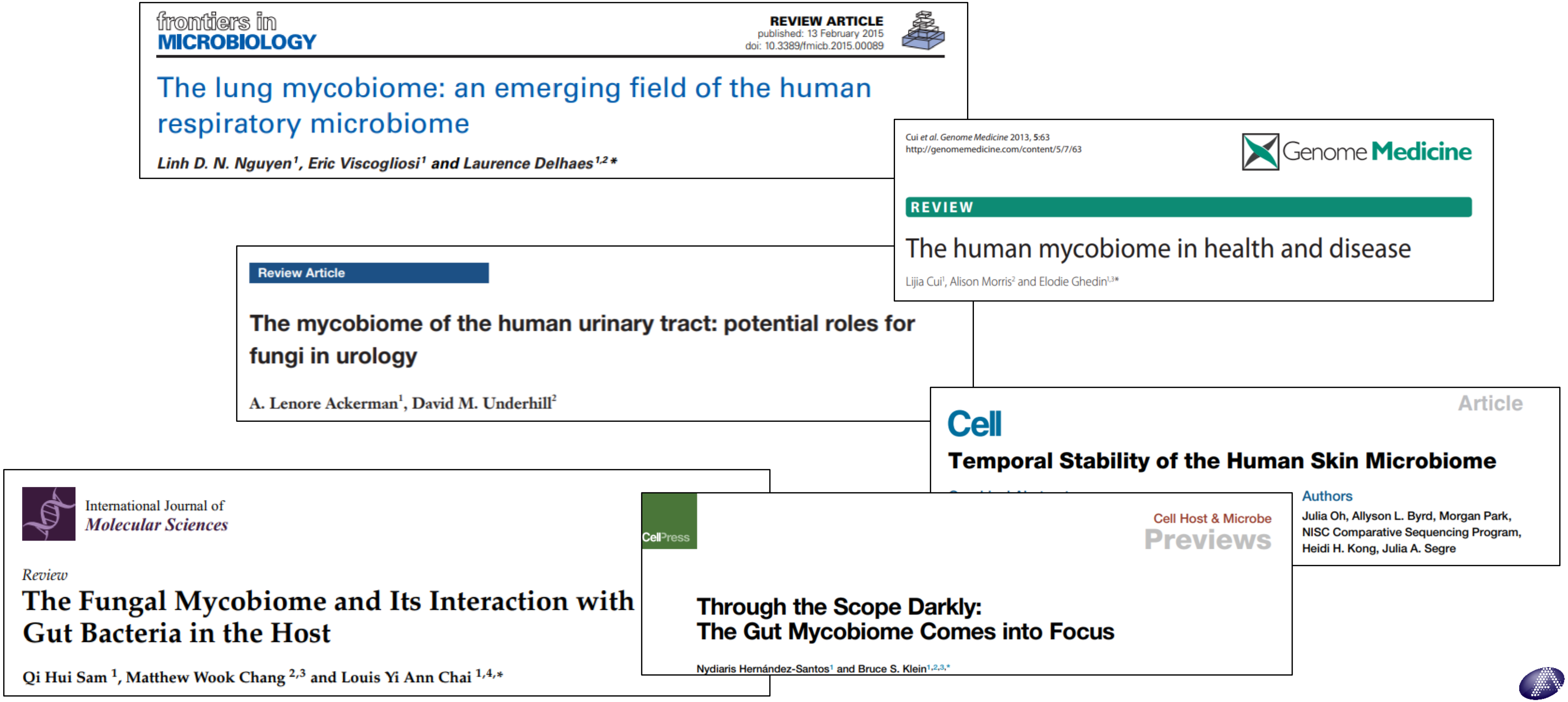
ATCC® NGS Standards are technology agnostic





Fungal Mock Community Standards for Mycobiome Studies

Mycobiome Research: An Emerging Need for Reference Material



frontiers in MICROBIOLOGY

REVIEW ARTICLE
published: 13 February 2015
doi: 10.3389/fmicb.2015.00089

The lung mycobiome: an emerging field of the human respiratory microbiome

Linh D. N. Nguyen[1], *Eric Viscogliosi*[1] *and Laurence Delhaes*[1,2]*

Cui *et al. Genome Medicine* 2013, 5:63
http://genomemedicine.com/content/5/7/63

Genome Medicine

REVIEW

The human mycobiome in health and disease

Lijia Cui[1], Alison Morris[2] and Elodie Ghedin[1,3]*

Review Article

The mycobiome of the human urinary tract: potential roles for fungi in urology

A. Lenore Ackerman[1], David M. Underhill[2]

Cell

Article

Temporal Stability of the Human Skin Microbiome

Authors

Julia Oh, Allyson L. Byrd, Morgan Park, NISC Comparative Sequencing Program, Heidi H. Kong, Julia A. Segre

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International Journal of *Molecular Sciences*

Review

The Fungal Mycobiome and Its Interaction with Gut Bacteria in the Host

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CellPress

Cell Host & Microbe
Previews

Through the Scope Darkly: The Gut Mycobiome Comes into Focus

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Mycobiome Composition: Fungal Mock Community

Fungi strains selection attributes and clinical relevance

ATCC® No.	Species Name	Genome Size (Mb)	Relevancy
MYA-4609™	***Aspergillus fumigatus***	28.8	Opportunistic, airborne pathogen that is responsible for 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***	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	Bakers' and brewers' yeast originating in food. Emerging pathogen in immunocompromised patients.
9533™	***Trichophyton interdigitale***	21.9	Can infect skin and nails to cause chronic infections such as athlete's foot and ringworm.
204094™	***Cutaneotrichosporon dermatis (Trichosporon dermatis)***	23.3	Emerging opportunistic agent of invasive fungal infections, particularly in severely immunocompromised patients.
10106™	***Penicillium chrysogenum***	32.5	Spore-former, less prevalent, but can be responsible for intestinal infection in immunosuppressed patients.
36031™	***Fusarium keratoplasticum*** **(*F. solani* complex)**	48.6	Filamentous, opportunistic pathogen that causes fungal keratitis.

ATCC® Mycobiome NGS Standards

Product description, research use, and applications

Standard	ATCC® Catalog No.	Preparation	Description
Mycobiome	**MSA-2010™**	Whole cell	Even mixture of whole cells comprising 10 fungal strains (2 × 10^6 cells of each organism)
	MSA-1010™	Genomic DNA	Even mixture of genomic DNA comprising 10 fungal strains (2 × 10^6 genome copies of each organism)

Sample Collection → Sequencing → Data Analysis

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

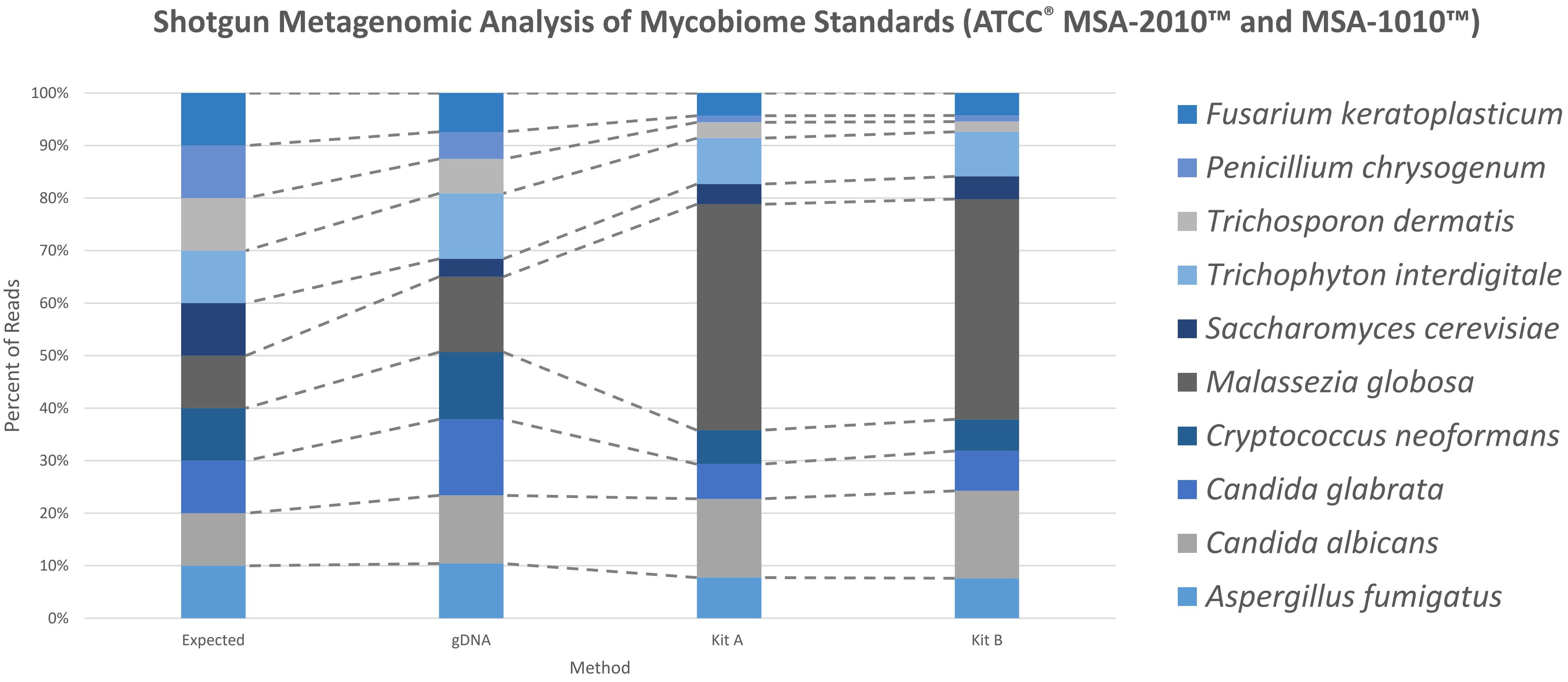
ITS and Shotgun
- Choice method
- Choice of primers
- Library preparation
- Platform

Bioinformatics
- NGS quality
- Depth and coverage
- Pipelines & Algorithm
- Database

MYCOBIOME WORKFLOW

Mycobiome Standards: Evaluation of DNA Extraction kits

Challenges with the development of whole cell standards and fungal DNA extraction methods

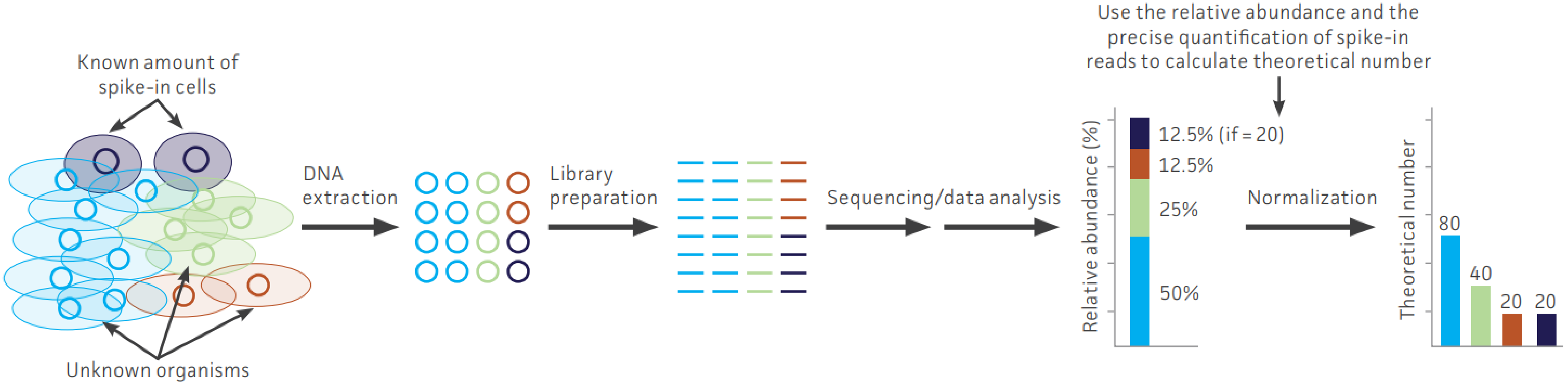


Conclusions about the ATCC® Mycobiome Standards

- Whole cell standards can help identify biases introduced during DNA extraction and can be used as full-process controls
- Genomic DNA standards can be used for comparing various library preparation methods and sequencing platforms
- The data analysis for mycobiome profiling is challenging due to the lack of complete fungal reference genomes and the limited availability of analyses pipelines

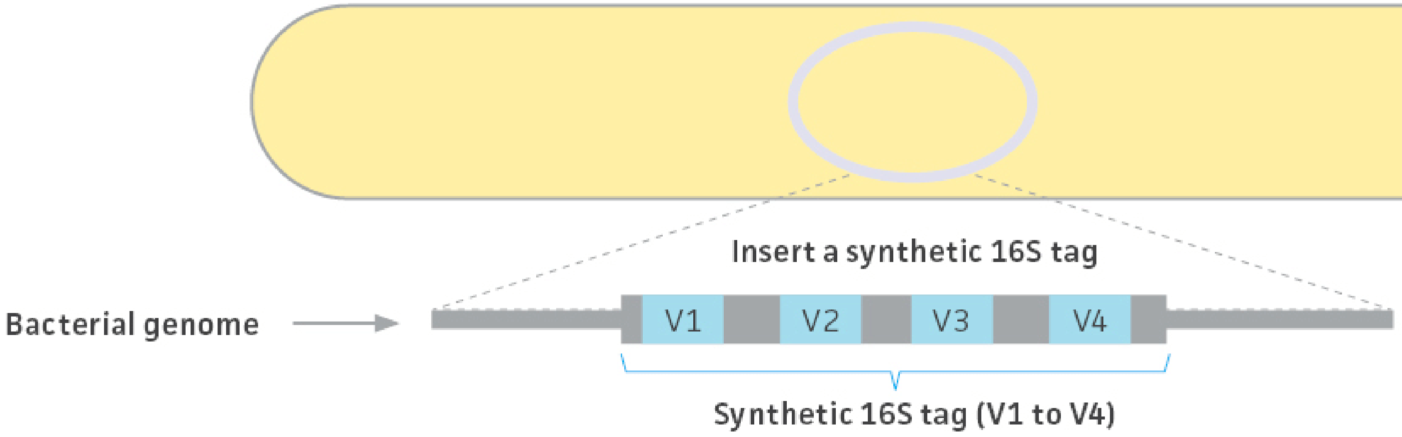
Spike-in Internal Controls: Synthetic 16S Tagged Strains

The Output of a Metagenomic Data is a Relative Abundance

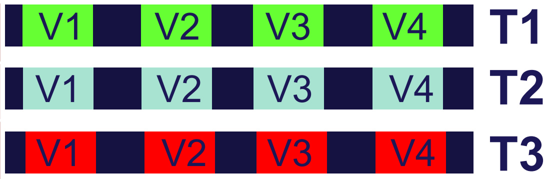


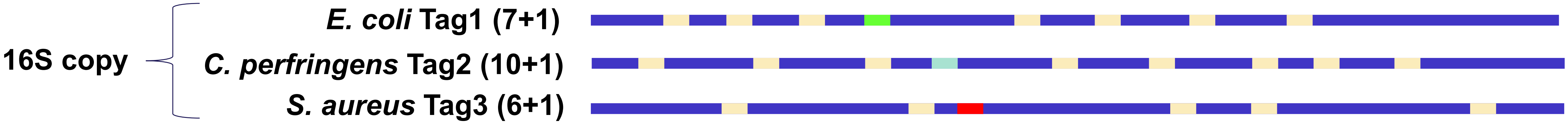
Relative abundance does not reflect the quantity of the microbial community and the inter-sample differences among taxa.

Engineering Synthetic 16S Tag Into Bacterial Genome



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





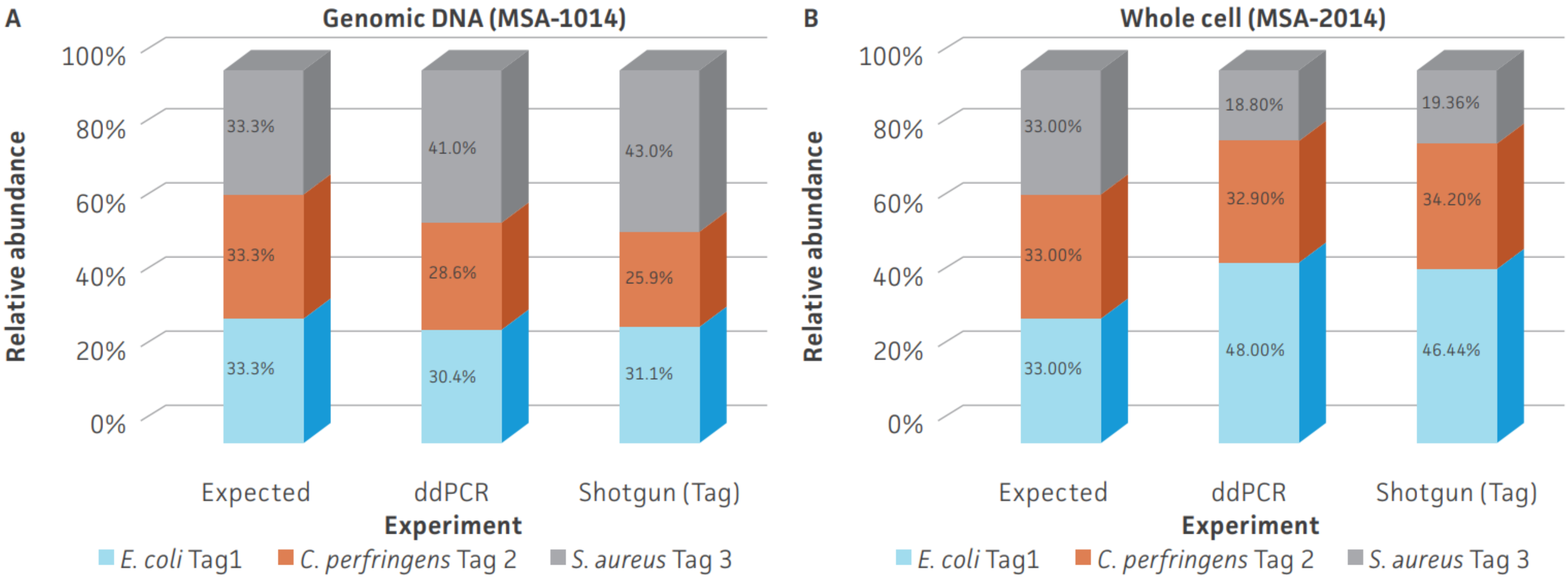
Spike-in Standards (3 Strain Tagged Mix)

ATCC® Catalog No.	Preparation	Specification	Importance
MSA-1014™	Genomic DNA	6 × 10^7 genomes copies/vial ± 1 log	▪ Microbiome measurements and data normalization ▪ 16S rRNA and shotgun assay verification, validation, and quality control
MSA-2014™	Whole cells	6 × 10^7 cells/vial ± 1 log	

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 × 10^7
***Clostridium perfringens* Tag2**	Positive	3.25	799	29.0	10	1	2 × 10^7
***Staphylococcus aureus* Tag3**	Positive	2.70	833	32.8	6	1	2 × 10^7

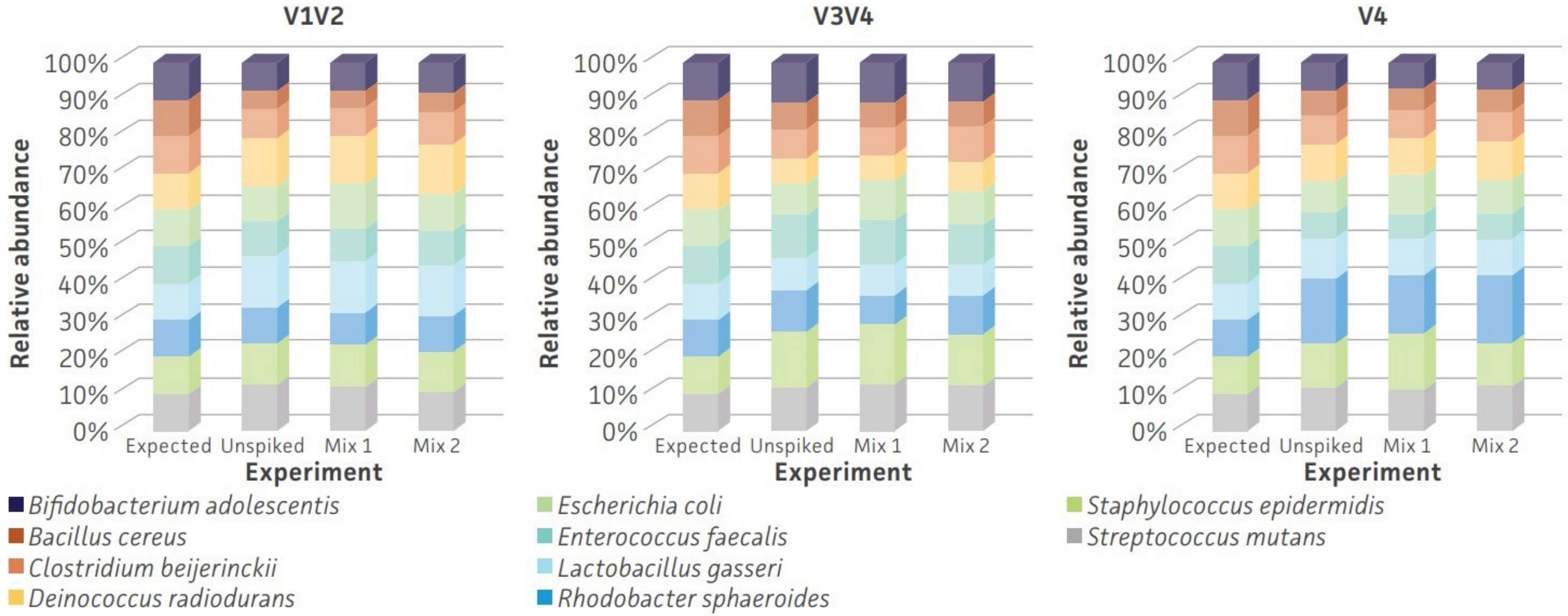
Development of Spike-in Standards and Quality Control



Relative abundance of the genomic DNA and whole cell spike-in standards

Relative Abundance of a Mock Community with Spike-in

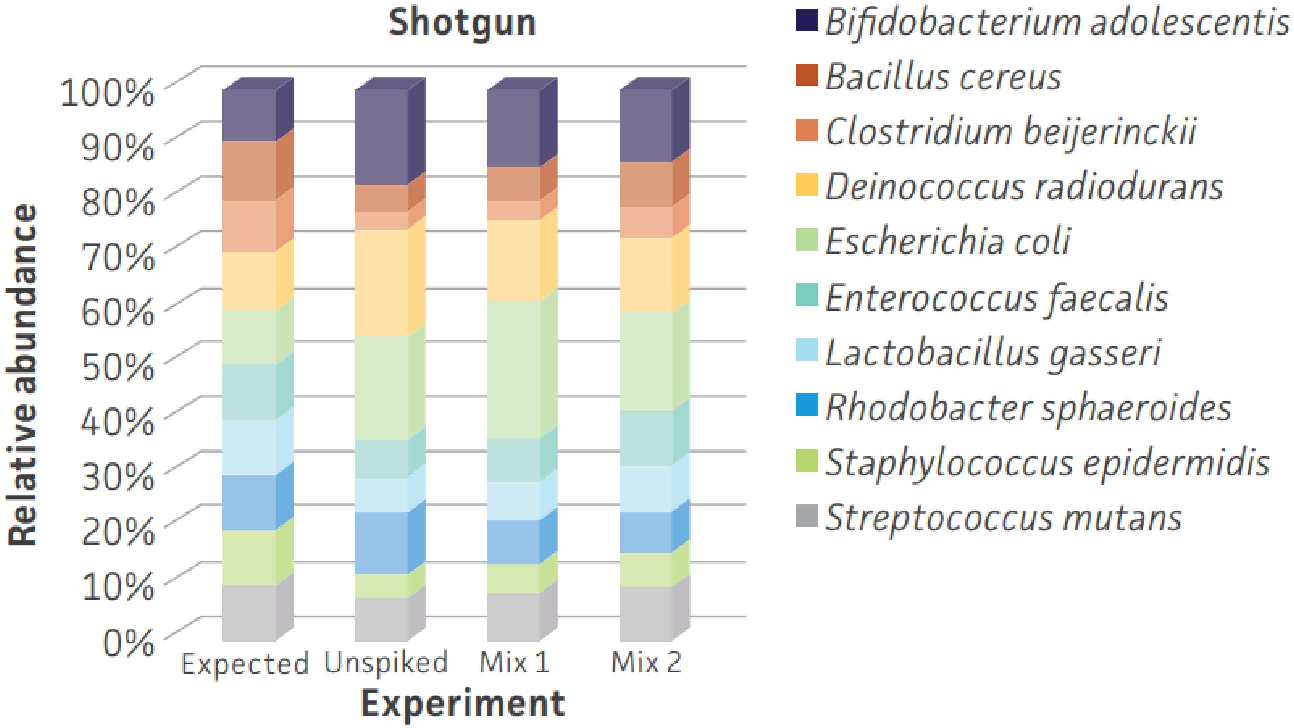
The spike-in doesn't have obvious impact on 16S relative abundance



ATCC® MSA-1014™ was mixed with ATCC® MSA-1000™ at ~ 1:10 and ~1:100

Relative Abundance of a Mock Community with Spike-in

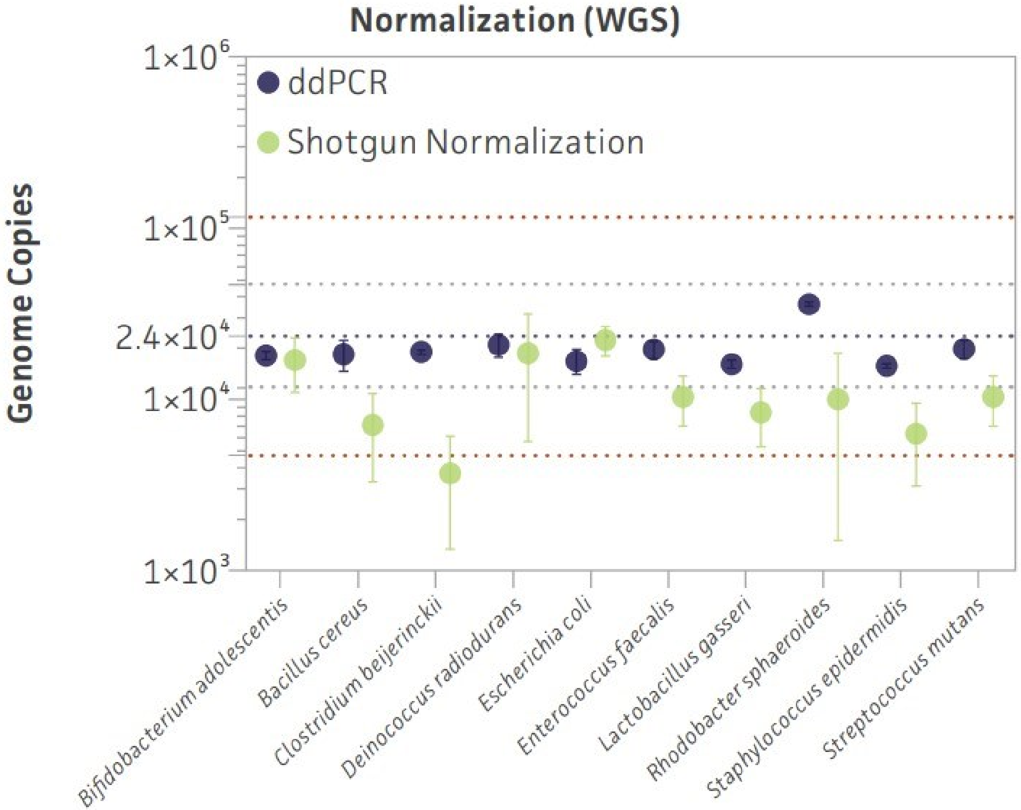
The spike-in doesn't have an obvious impact on whole genome shotgun analysis



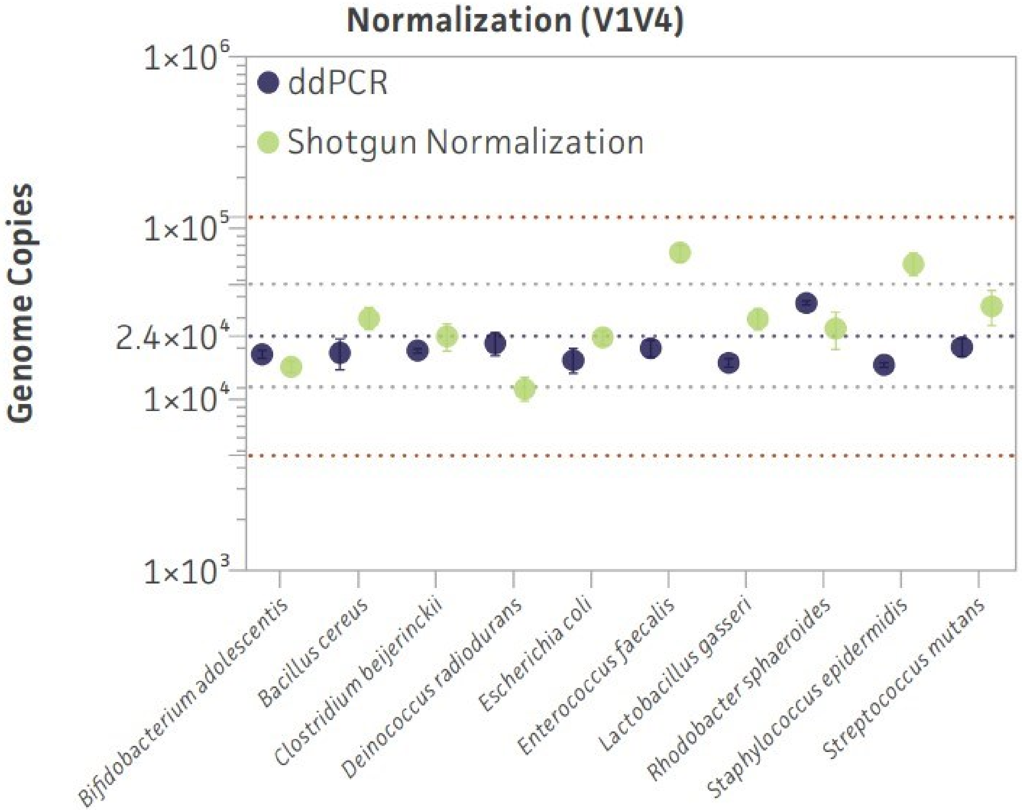
ATCC® MSA-1014™ was mixed with ATCC® MSA-1000™ at ~ 1:10 and ~1:100

Comparison of Absolute Quantitation by ddPCR and Normalized WGS

Three tagged genomic DNA mixed with 10 even genomic DNA (ATCC® MSA-1000™)



Normalization (WGS)



Normalization (V1V4)

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

Virome and Mycobiome Standards

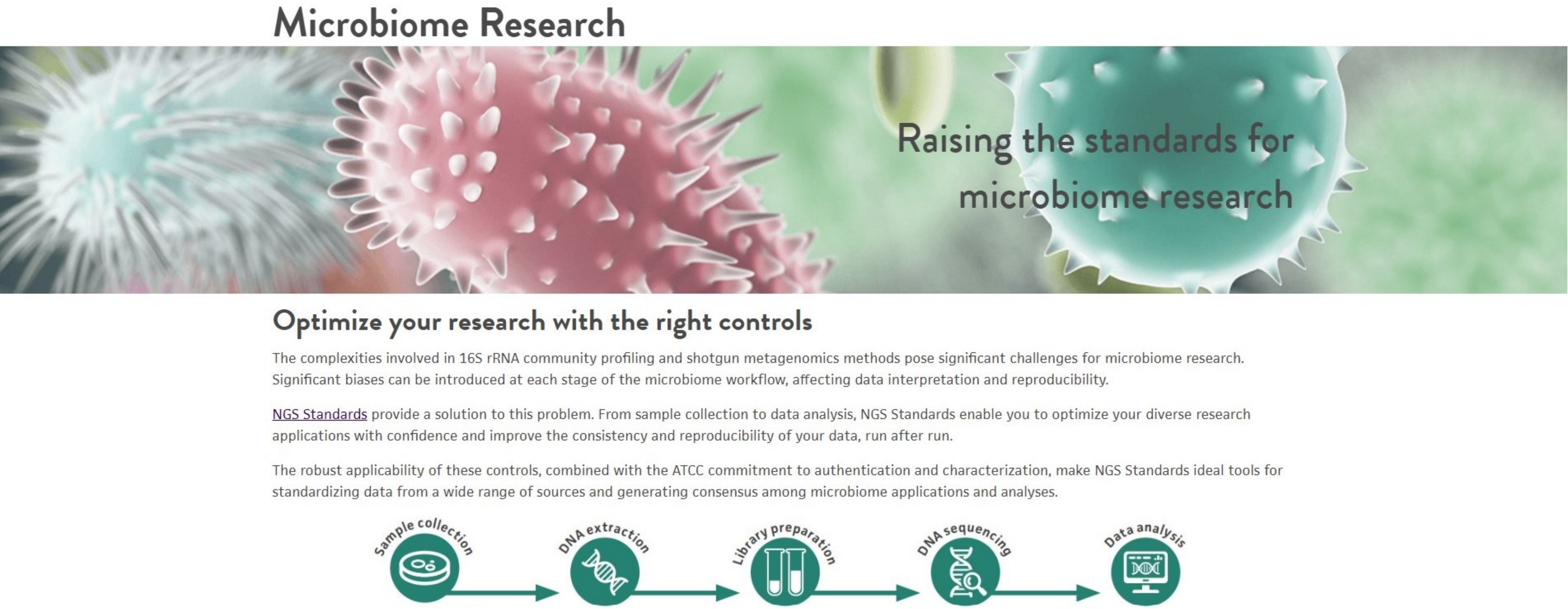
- Genomic DNA and whole cell standards comprising diverse and clinically relevant strains
- Even mixtures of 6-10 strains

Bundled with data analysis on the One Codex platform

1. UPLOAD YOUR DATA
2. SELECT YOUR NGS STANDARD
3. ENTER YOUR METADATA
4. REVIEW YOUR RESULTS

ATCC NGS Standards for Microbiome Research

www.atcc.org/Microbiome



Microbiome Research

Raising the standards for microbiome research

Optimize your research with the right controls

The complexities involved in 16S rRNA community profiling and shotgun metagenomics methods pose significant challenges for microbiome research. Significant biases can be introduced at each stage of the microbiome workflow, affecting data interpretation and reproducibility.

NGS Standards provide a solution to this problem. From sample collection to data analysis, NGS Standards enable you to optimize your diverse research applications with confidence and improve the consistency and reproducibility of your data, run after run.

The robust applicability of these controls, combined with the ATCC commitment to authentication and characterization, make NGS Standards ideal tools for standardizing data from a wide range of sources and generating consensus among microbiome applications and analyses.

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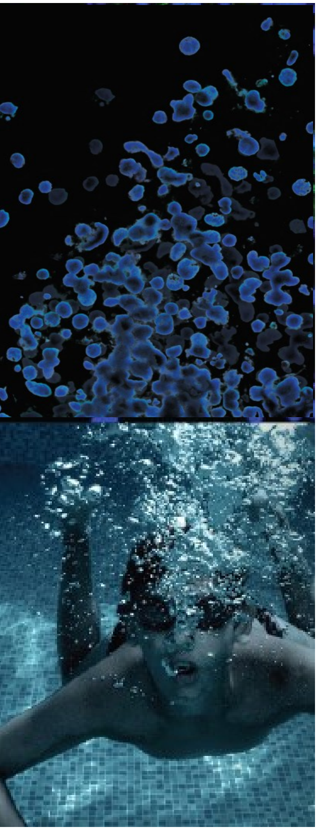

Questions?

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