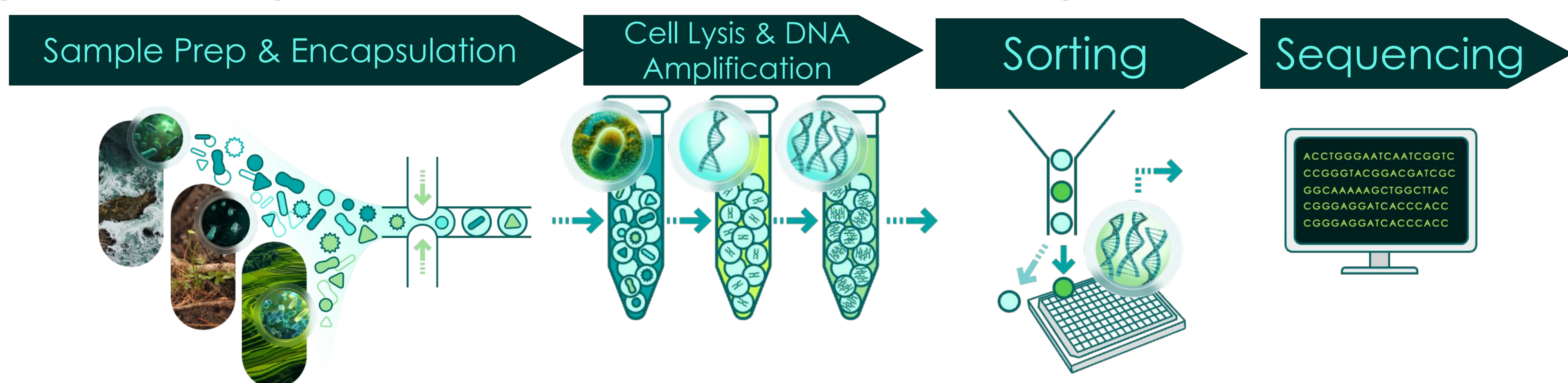


bit-MAP[®]

Microbial Single-Cell Genome Analysis Service

• Diverse samples • No need for cultivation • High-quality data

High-quality genomic information from a single cell



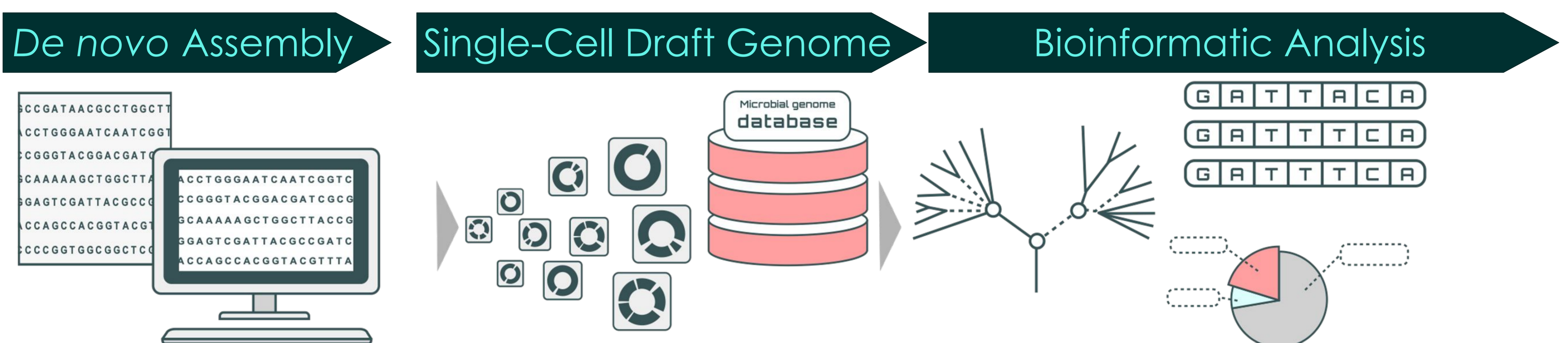
Using microfluidics to isolate individual microbes from a sample

Multi-step biochemical reactions performed within hydrogel capsules

Sort capsules using FACS, sequence microbial whole genomes and construct libraries

Bioinformatic analysis at single-cell resolution

Chijiwa, et al. Microbiome (2020), Nishikawa, et. al. ISME commu (2022)



Assemble raw reads obtained from NGS to construct contigs

Integrate single cell derived genomics data into individual draft genomes

Analyze individual genomics data for phylogenetic classification and functional analysis

Our single-cell genomics analysis technology delivers deeper insights than existing methods

	16S rRNA metagenomics	Shotgun metagenomics	bit-MAP [®] Single-cell genomics
Purpose	Microbiome Composition	Composition & Genome	Individual microbe function
Target	Partial 16S rRNA genes	Fragmented community genome	Individual genomes and plasmids
Length of sequence	400 base pairs (bp)	Tens~Tens of billions bp	Millions - Hundreds of millions × # of cells
Sequencing effort	Small	Large	Variable
Microbial composition	+++	+++	++
Gene composition	-	+++	++
Linking taxa and function	-	+	+++
Strain variant analysis	-	-	+++

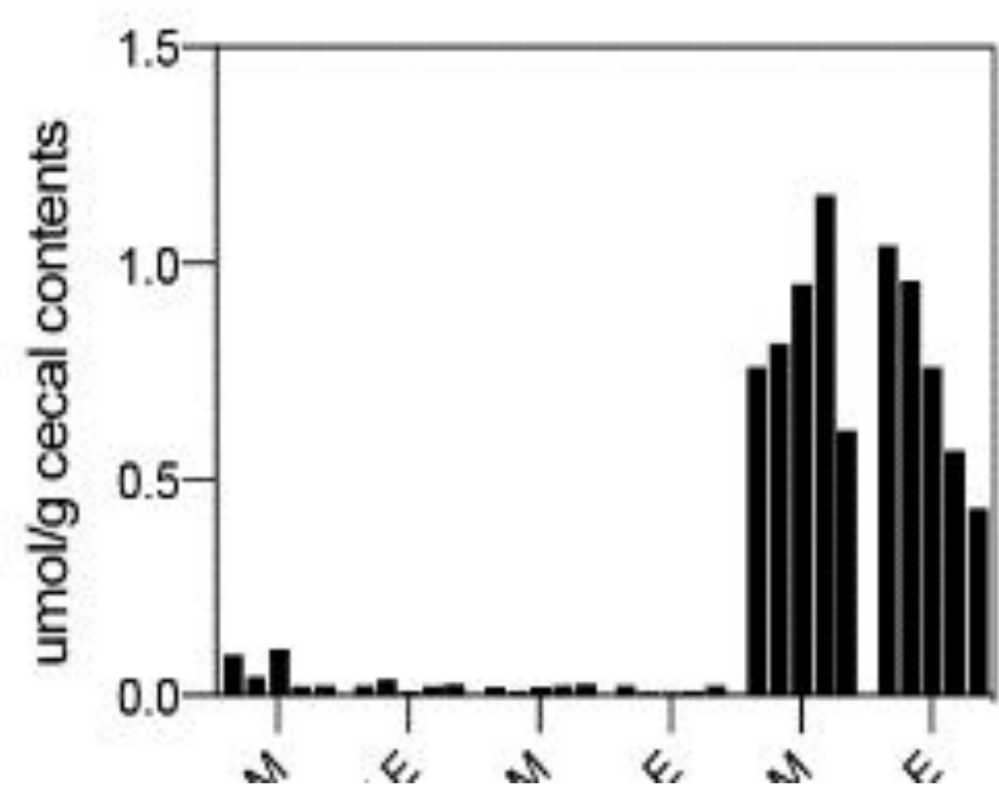
Identify bacteria of interest

Hosokawa et al., Microbiome 2020
<https://doi.org/10.1186/s40168-019-0779-2>



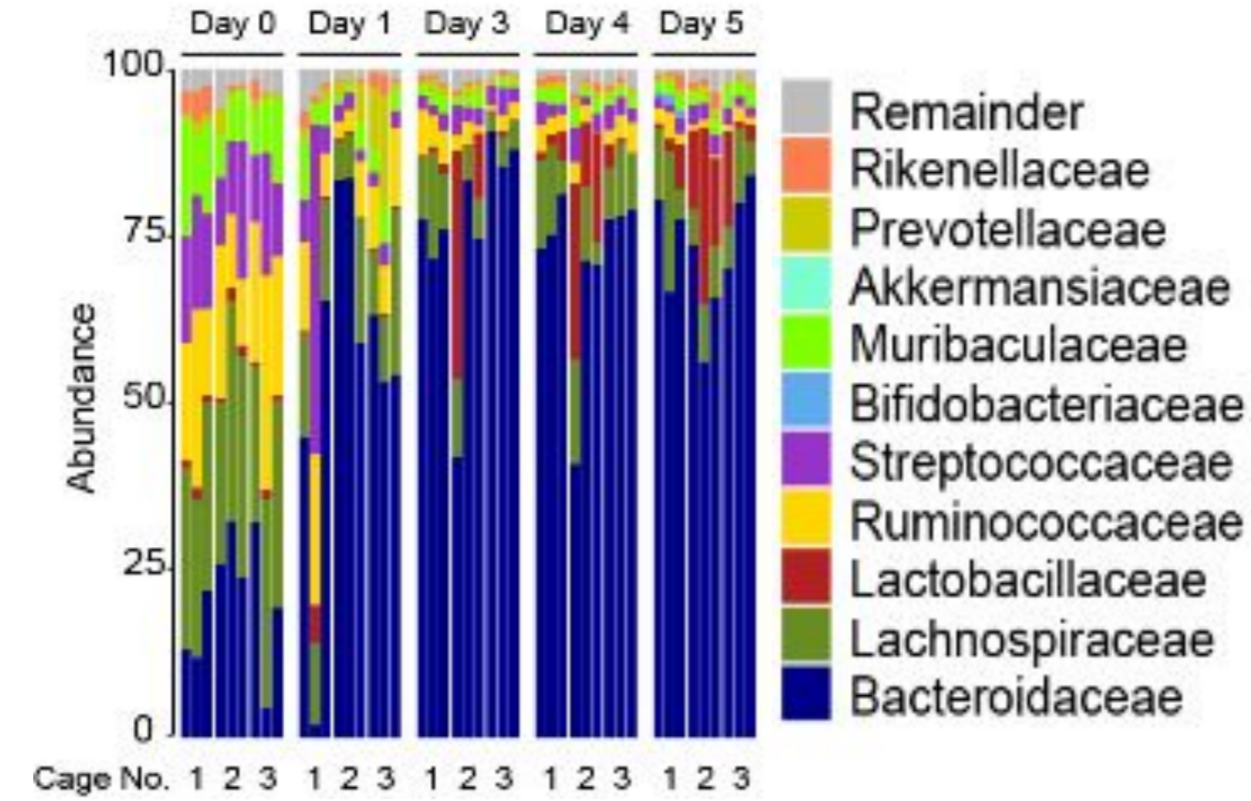
Inulin-supplemented diet for 2 weeks

Metabolomics

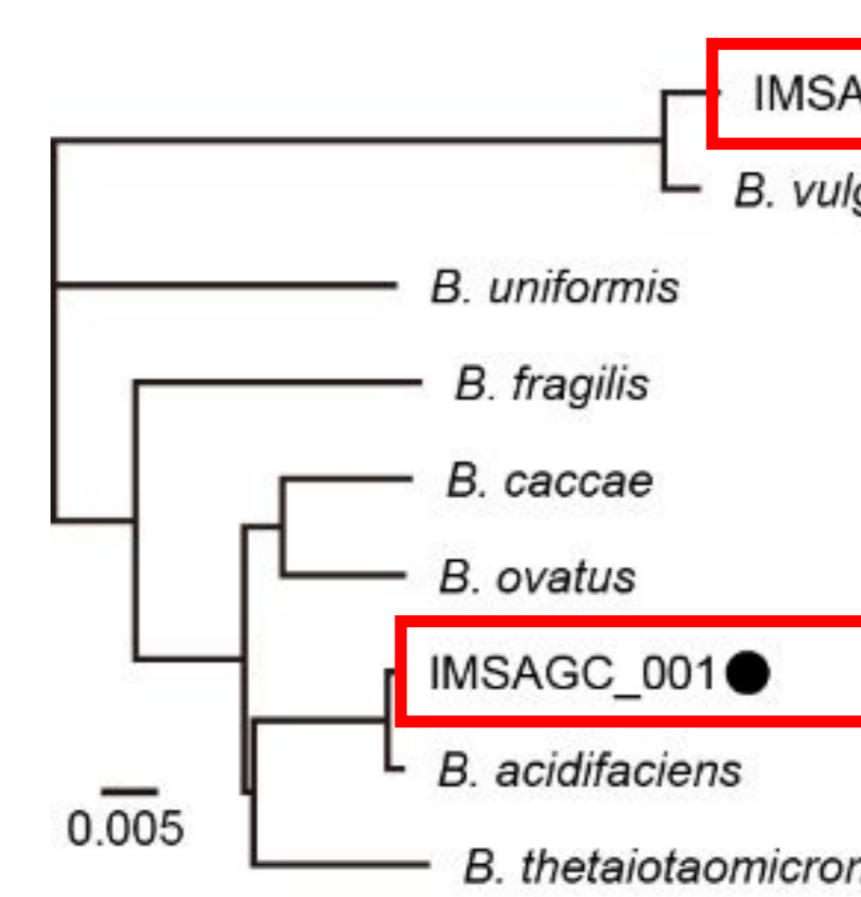


Increase of succinate in cecum

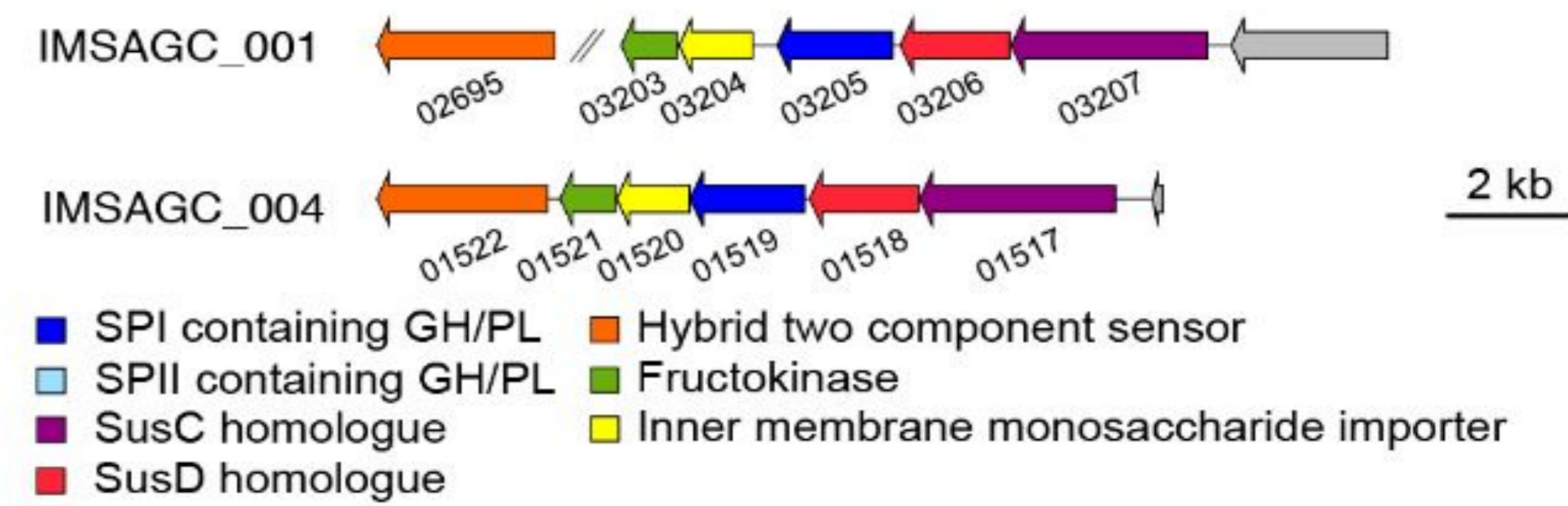
Metagenomics



Increase of *Bacteroides* sp.



Identification of inulin utilization gene cluster and succinate synthesis pathway from draft genomes of uncultured *Bacteroides* Sp.



Discover unknown bacteria

Nishikawa et al., ISME 2022,
<https://doi.org/10.1038/s43705-022-00179-4>

8 Environmental samples



Desert



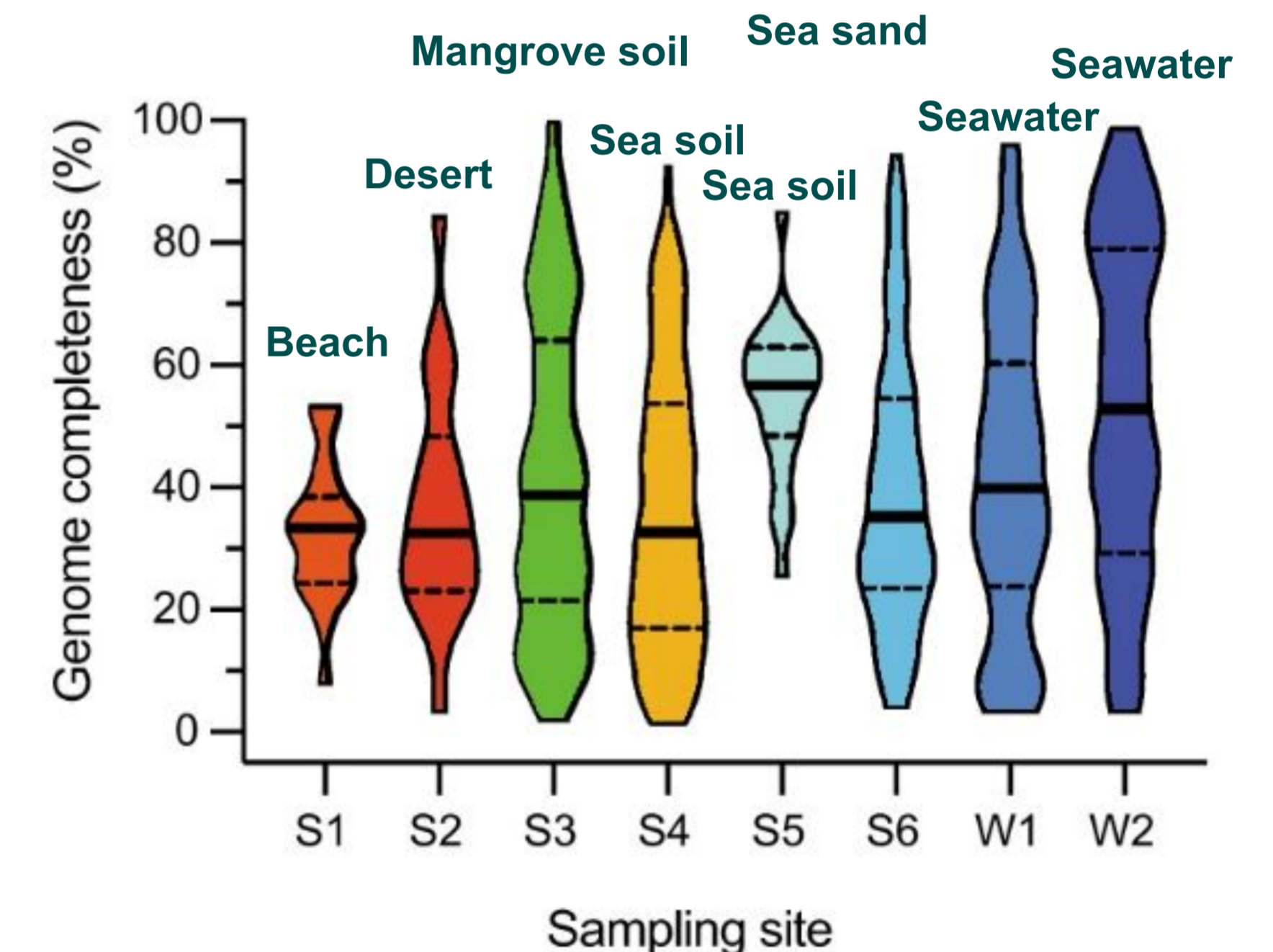
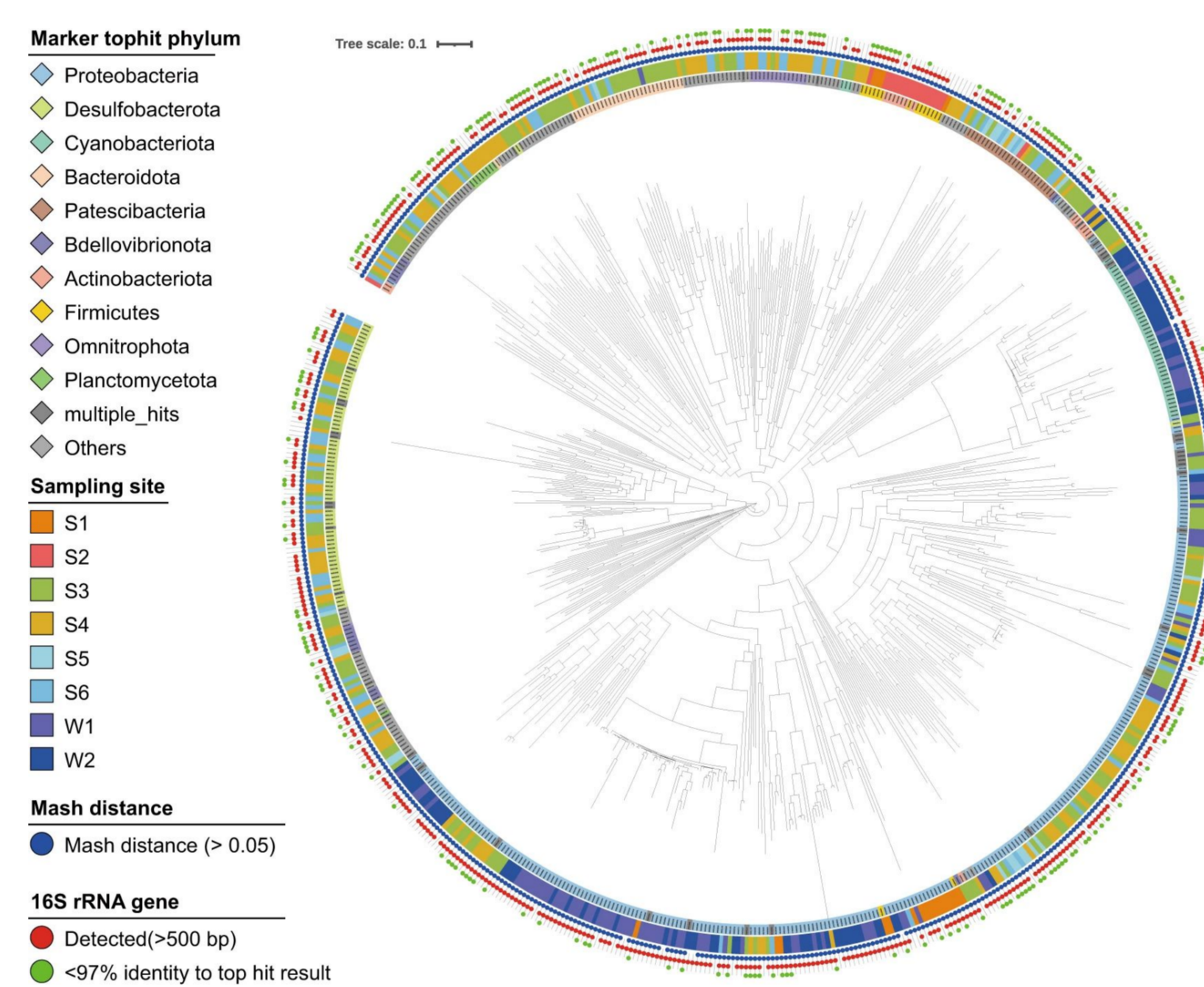
Mangrove



Beach



Sea water



Each single amplified genome (SAG) is nearly unique and 98.7% (228/231 species) of them were newly identified

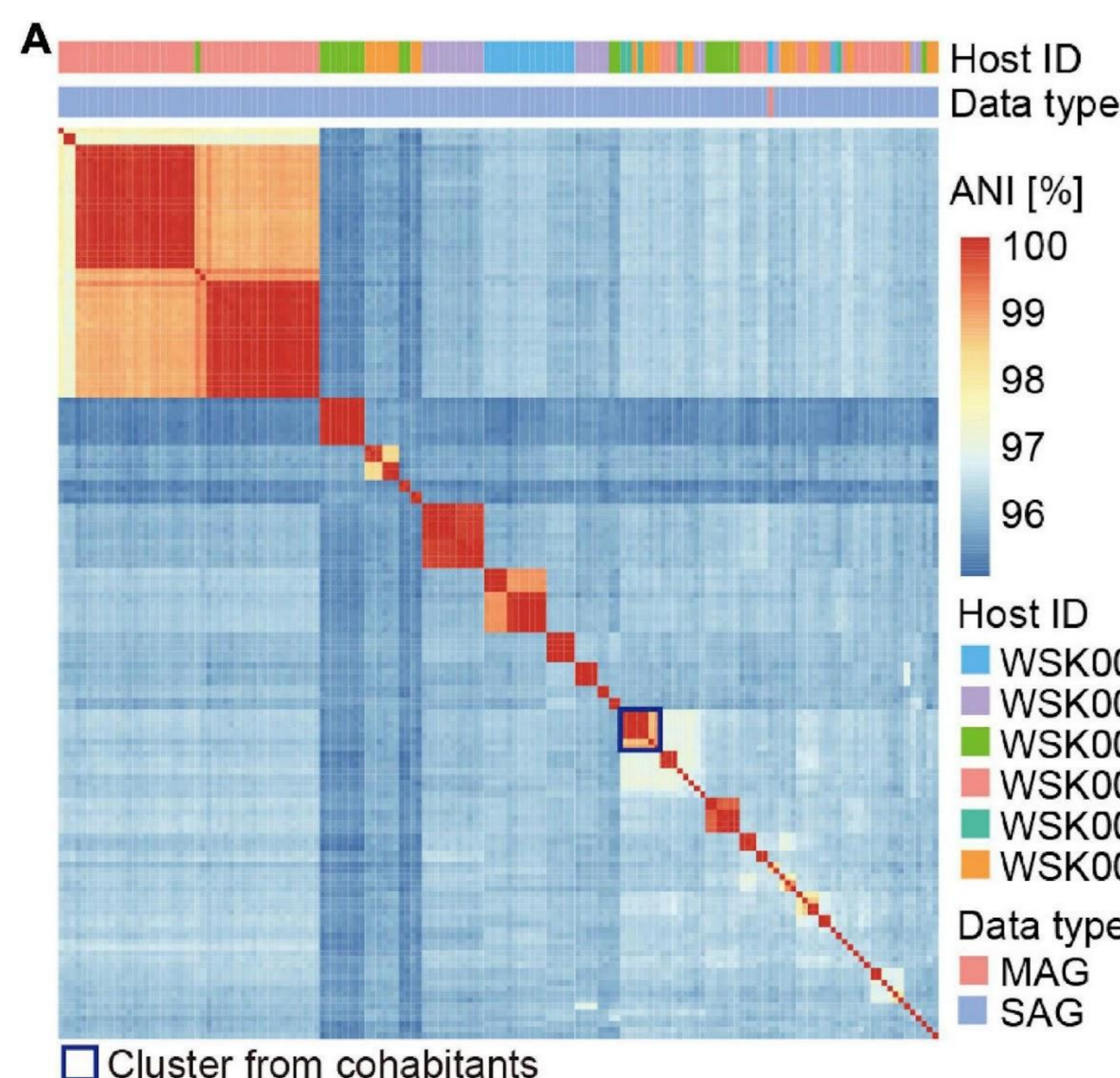
Compare genomes at strain-level

Ide, K et al., Front. Microbiol. 2022
<https://doi.org/10.3389/fmicb.2022.955404>

Skin microbiome



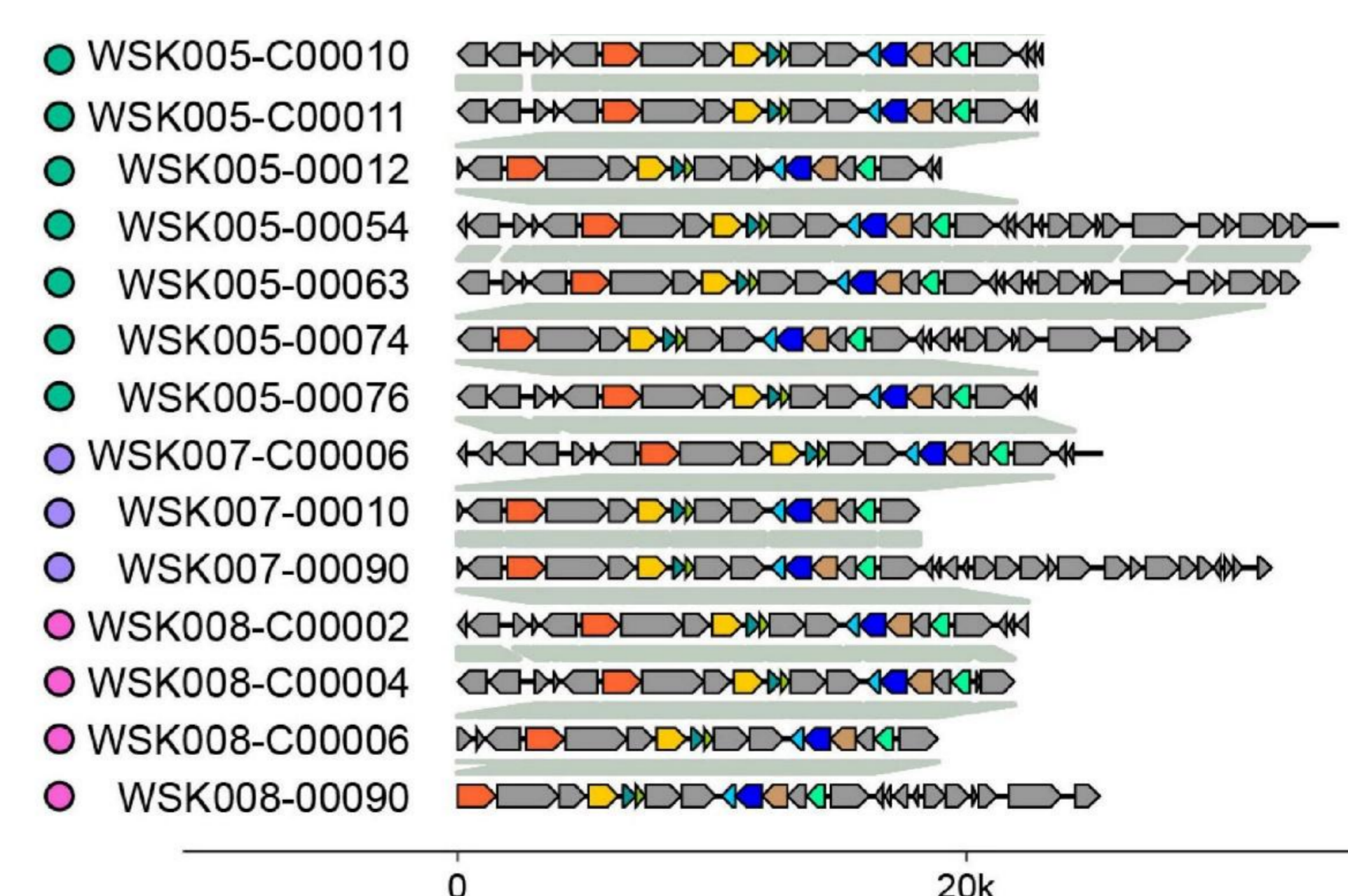
Collected from 8 hosts



Strain-resolved genomes for *Moraxella osloensis*

Host ID

Genes on plasmids



Plasmids found in *M. osloensis* HQ SAG

