

The CM Human Microbiome Profiler (CHAMP™) : beyond the gut

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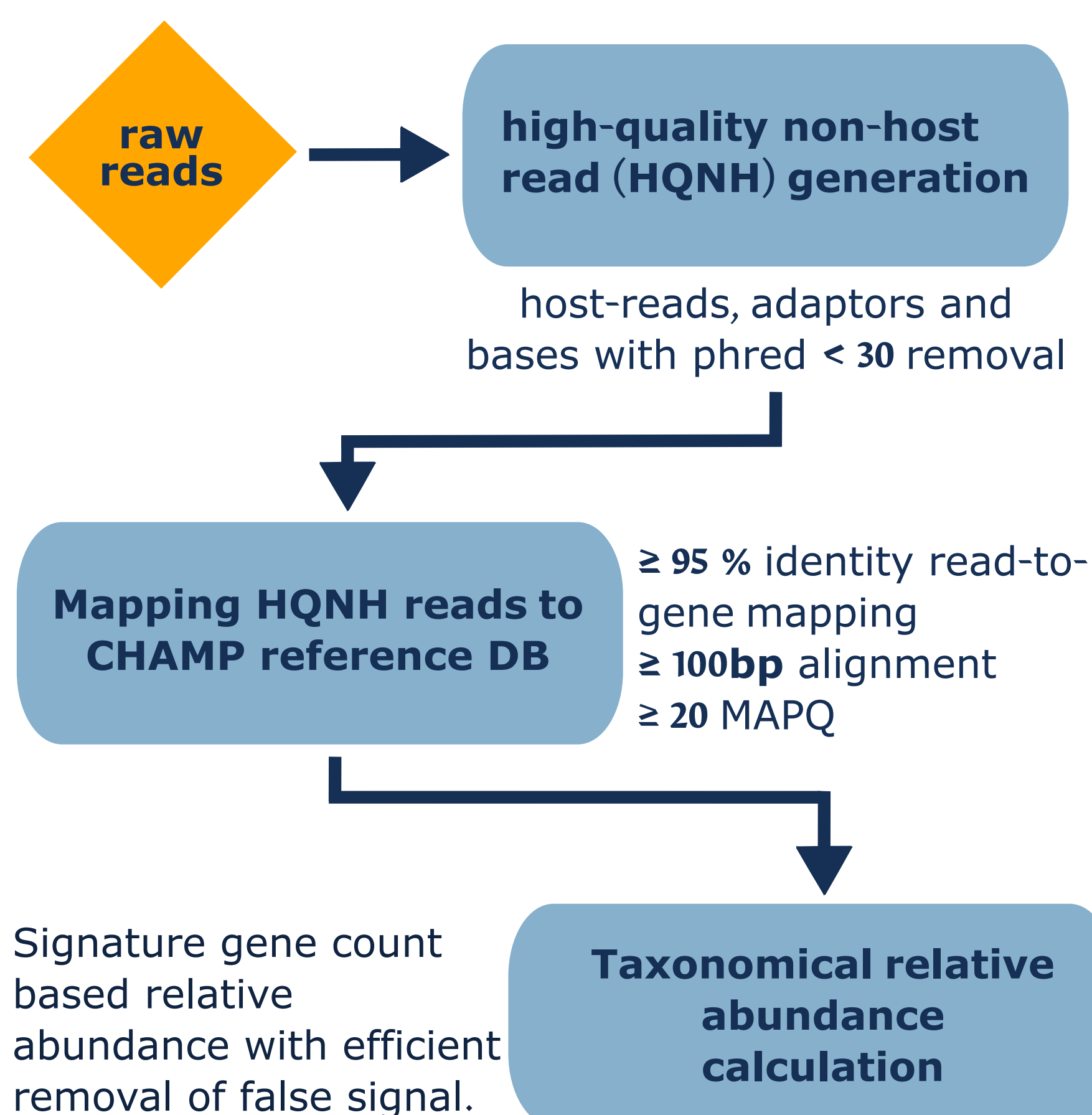
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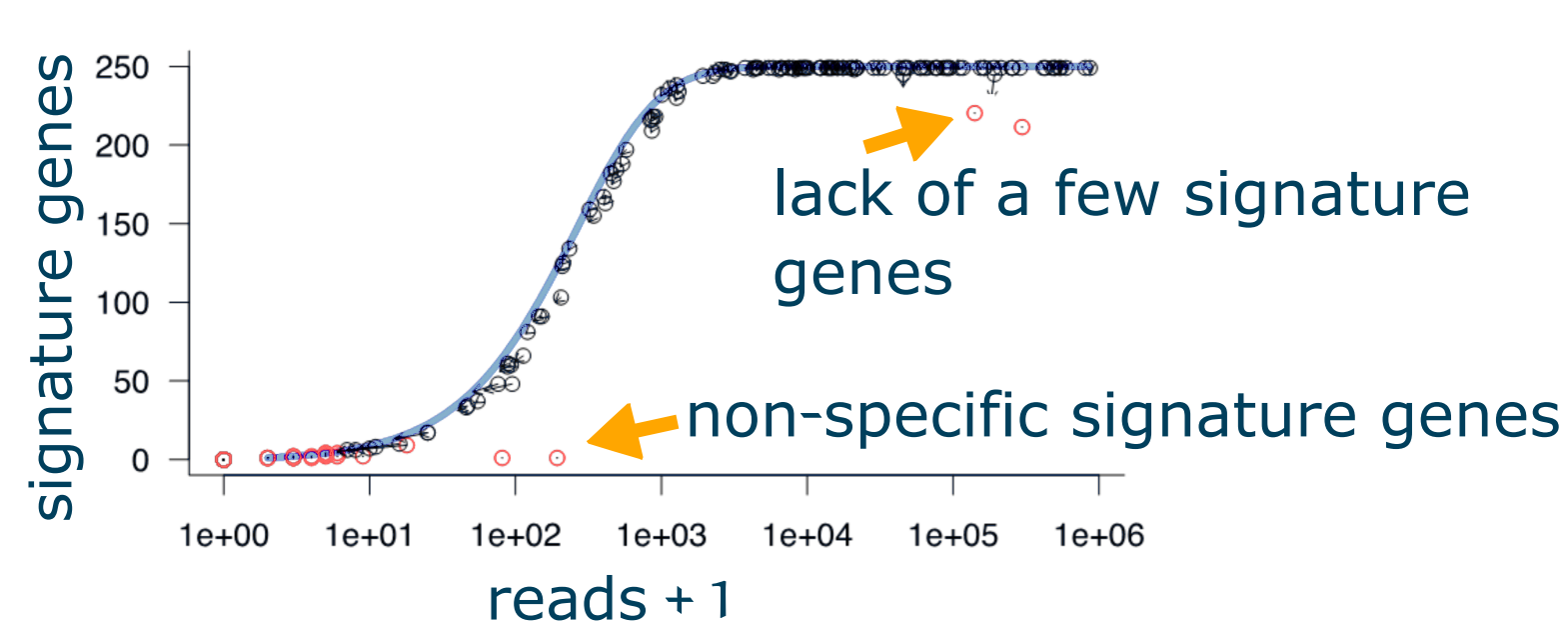
1. Introduction

- Validity of the numerous association studies between the human microbiome composition and health-related outcomes depends on accurate taxonomic profiling.
- Taxonomic profiling refers to the identification and relative abundance quantification of microorganisms in biological samples.
- Here, we present and benchmark the **CM HumAn Microbiome Profiler 2.0 (CHAMP)**, a signature (marker) gene-based short-read human microbiome-tailored taxonomic profiler.

3. Algorithm



mapped signature genes of strain



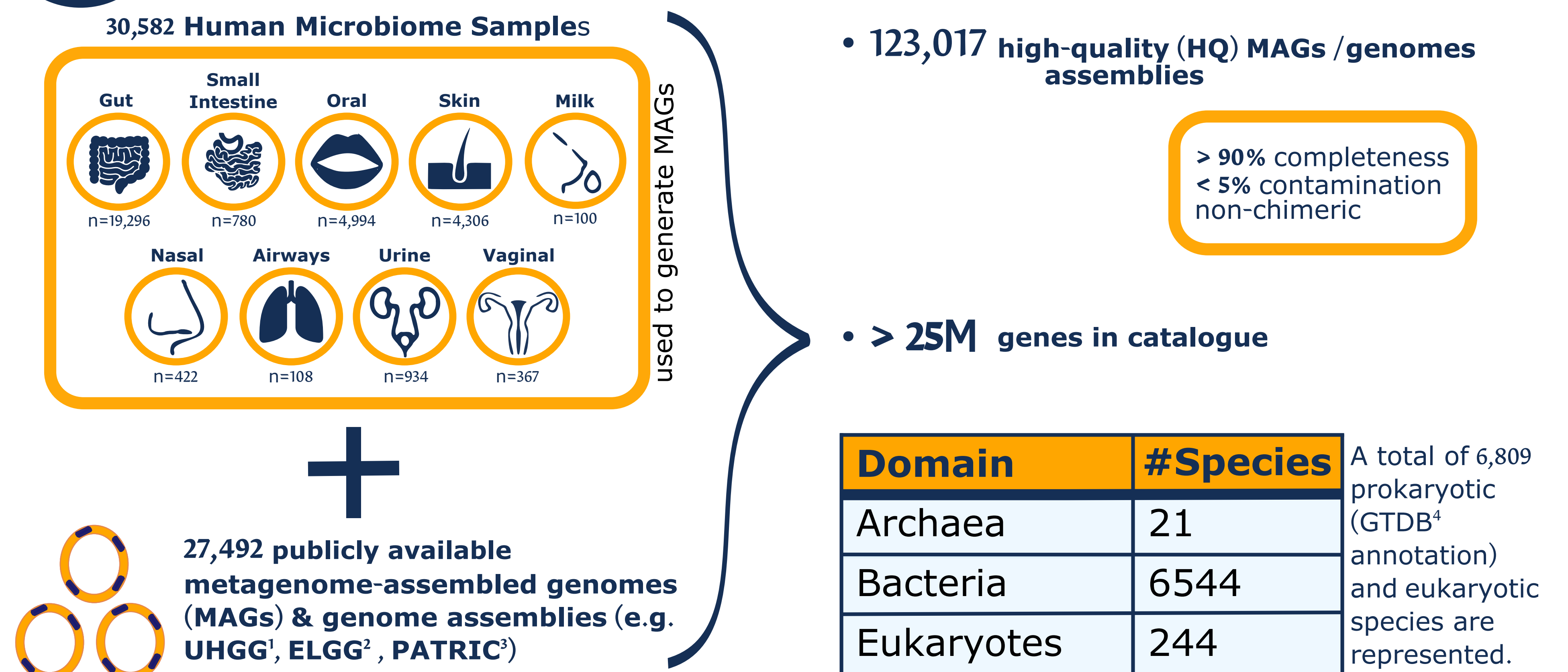
5. Conclusion

CHAMP is a human microbiome-tailored profiler that benefits from a comprehensive database of human-derived genomes and MAGs. Evaluation of CHAMP with DNA mock communities and *in silico* data showed it supersedes other profilers across benchmarking metrics. It outperforms particularly well in recall and false positive relative abundance (FPRA).

6. References

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2. CHAMP Reference Database



4. Benchmark Results

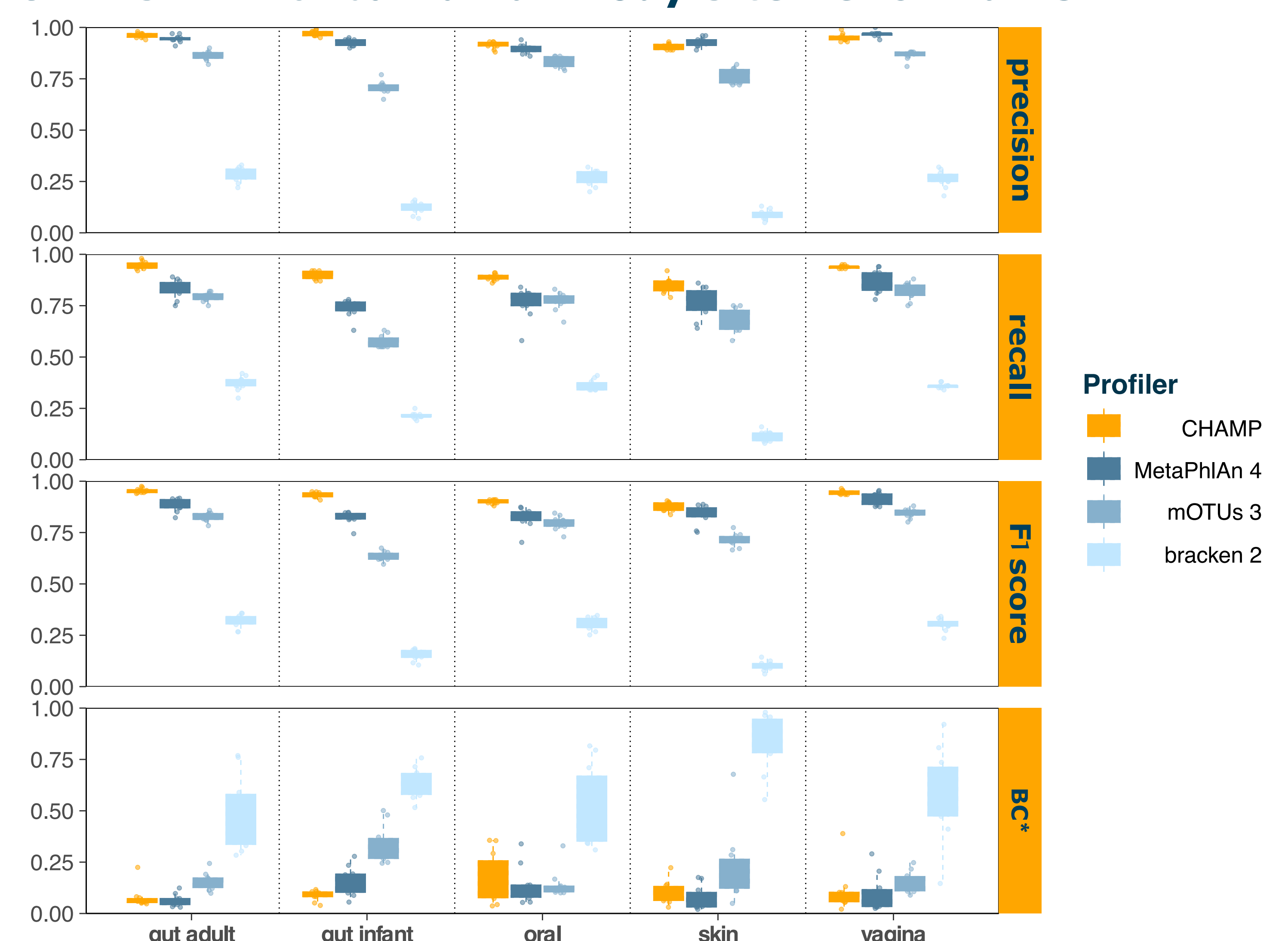
NIBSC DNA Reference Reagents Benchmarks

Profiler	Sen	FPRA	Div	Sim
Kraken	74	4	95	66
Bracken 2	74	5	87	64
Centrifuge	74	3	37	52
MetaPhlAn 4	90	6	19	70
CHAMP	96	0.01	20	72
groundtruth	100	0	20	100

Sen - sensitivity; FPRA - false positive relative abundance Div - Diversity; Sim - Similarity

On the left, benchmarking data corresponds to 2 National Institute for Biological Standards and Control (NIBSC)⁵ DNA mock communities composed of 20 common gut microbiome species. 5 replicates for each mock community, of staggered and even compositions, respectively.

CAMISIM *In silico* Human Body Site Benchmarks



On the right, benchmarking data consists of 10 *in silico* simulated metagenomes per human body site. Knowledge on body site native species was collated from previous literature for the adult gut⁶, infant gut⁷, oral⁶, skin⁸ and vagina⁶, respectively. CHAMP has been benchmarked against Bracken 2⁹, mOTUs 3¹⁰, and MetaPhlAn 4¹¹. BC* stands for Bray-Curtis dissimilarity.

