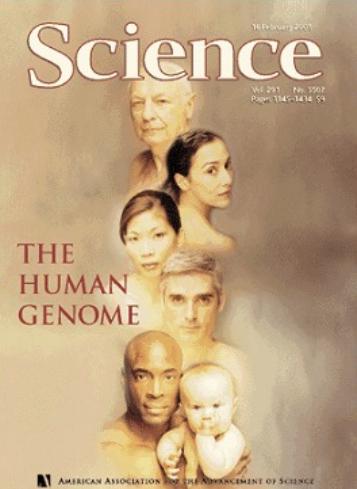
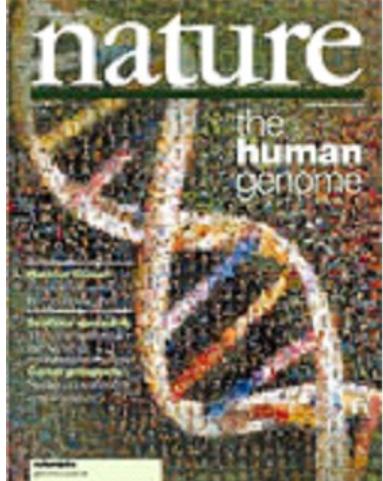
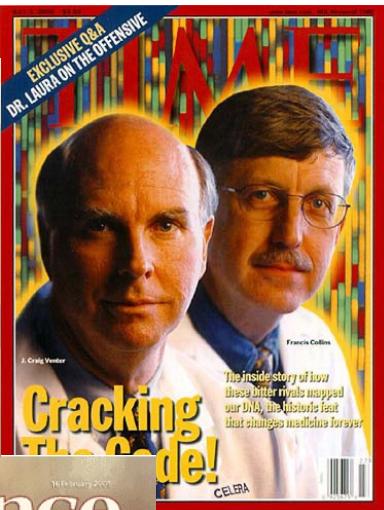




- Unassembled meta-omes are very valuable (arguably most valuable)...
- ...but their interpretation requires suitable reference genomes

## Using SAGs as reference databases

# Sequencing of the first human genome, year 2000



## Effort:

- Thousands of scientists
- >10 years
- >\$5,000,000,000

## Impact on human health:

- Deeper understanding of biology
- Diagnosis of rare disorders
- Emerging gene therapies

## Science fields ignited:

- Geno-, transcript-, prote-(meta)omics
- Next-gen sequencing
- Large-scale bioinformatics

RESEARCH ARTICLE

Nurk *et al.*, *Science* **376**, 44–53 (2022)

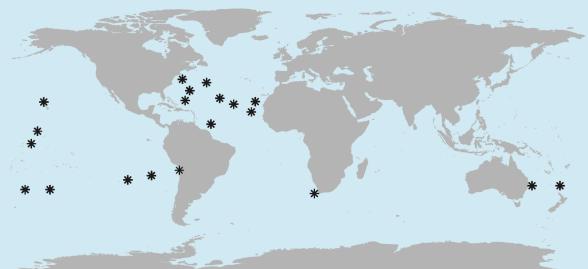
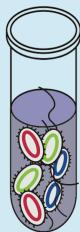
1 April 2022

HUMAN GENOMICS

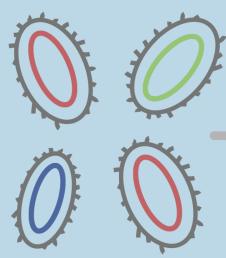
The complete sequence of a human genome

# Global Ocean Reference Genomes (GORG) - Tropics

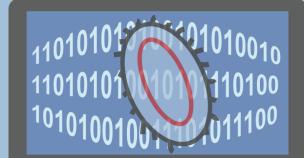
28 water samples from tropical and subtropical Atlantic and Pacific oceans



Randomized genomic sequencing of 12,715 individual cells of prokaryoplankton



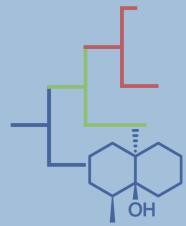
Reference genome database



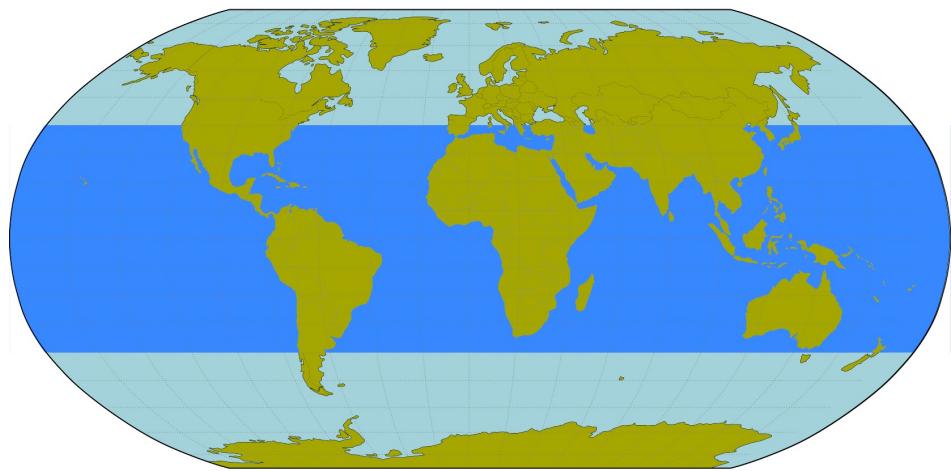
Global patterns of variation



Lineage-resolved metabolism



From: Pachiadaki et al., 2019, Cell



# Classifiers of unassembled metagenomes



## ARTICLE

Received 26 Nov 2015 | Accepted 7 Mar 2016 | Published 13 Apr 2016

DOI: 10.1038/ncomms11257

OPEN

## Fast and sensitive taxonomic classification for metagenomics with Kaiju

Peter Menzel<sup>1</sup>, Kim Lee Ng<sup>1</sup> & Anders Krogh<sup>1</sup>

Wood and Salzberg *Genome Biology* 2014, **15**:R46  
<http://genomebiology.com/2014/15/3/R46>

Ounit *et al.* *BMC Genomics* (2015) 16:236  
DOI 10.1186/s12864-015-1419-2



## RESEARCH ARTICLE

Open Access

## CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative $k$ -mers

Rachid Ounit<sup>1</sup>, Steve Wanamaker<sup>2</sup>, Timothy J Close<sup>2</sup> and Stefano Lonardi<sup>1\*</sup>



## METHOD

Open Access

## Kraken: ultrafast metagenomic sequence classification using exact alignments

Derrick E Wood<sup>1,2\*</sup> and Steven L Salzberg<sup>2,3</sup>

Bigelow | Laboratory for Ocean Sciences

ARTICLE

Received 26 Nov 2015 | Accepted 7 Mar 2016 | Published 13 Apr 2016

DOI: 10.1038/ncomms11257

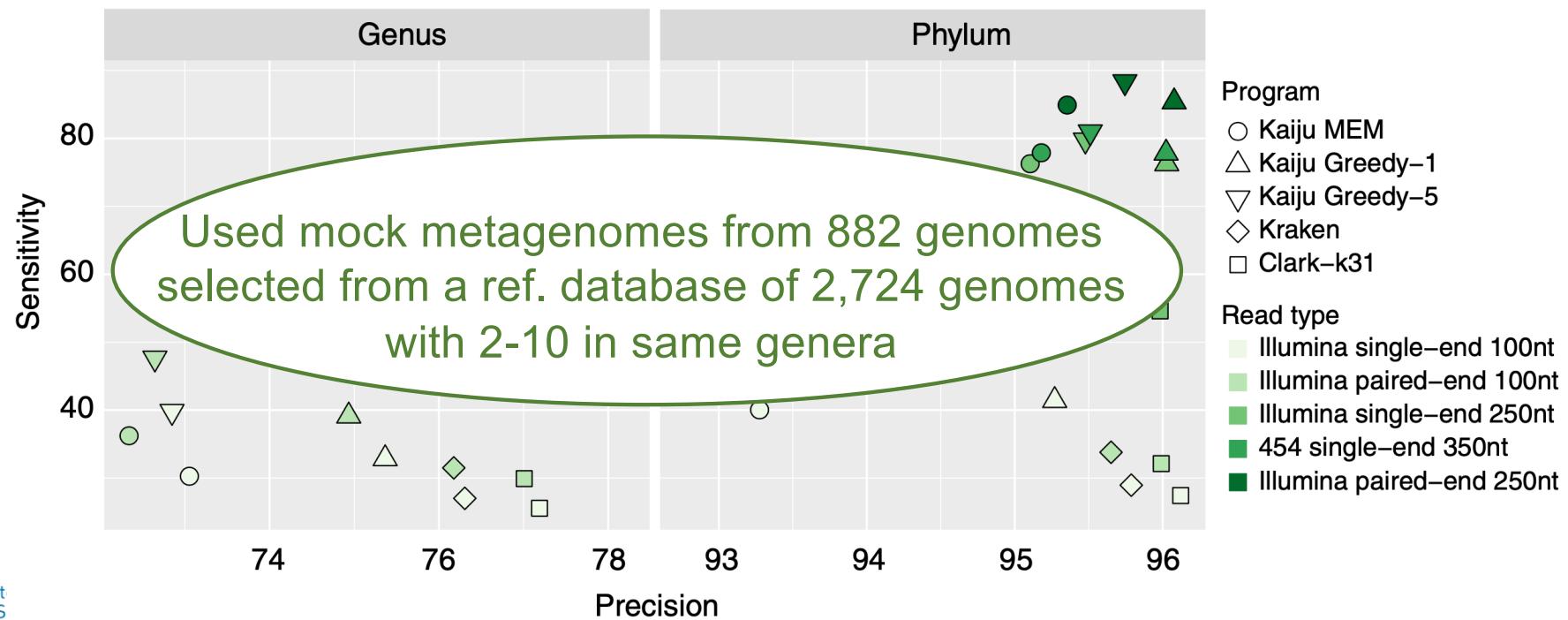
OPEN

## Fast and sensitive taxonomic classification for metagenomics with Kaiju

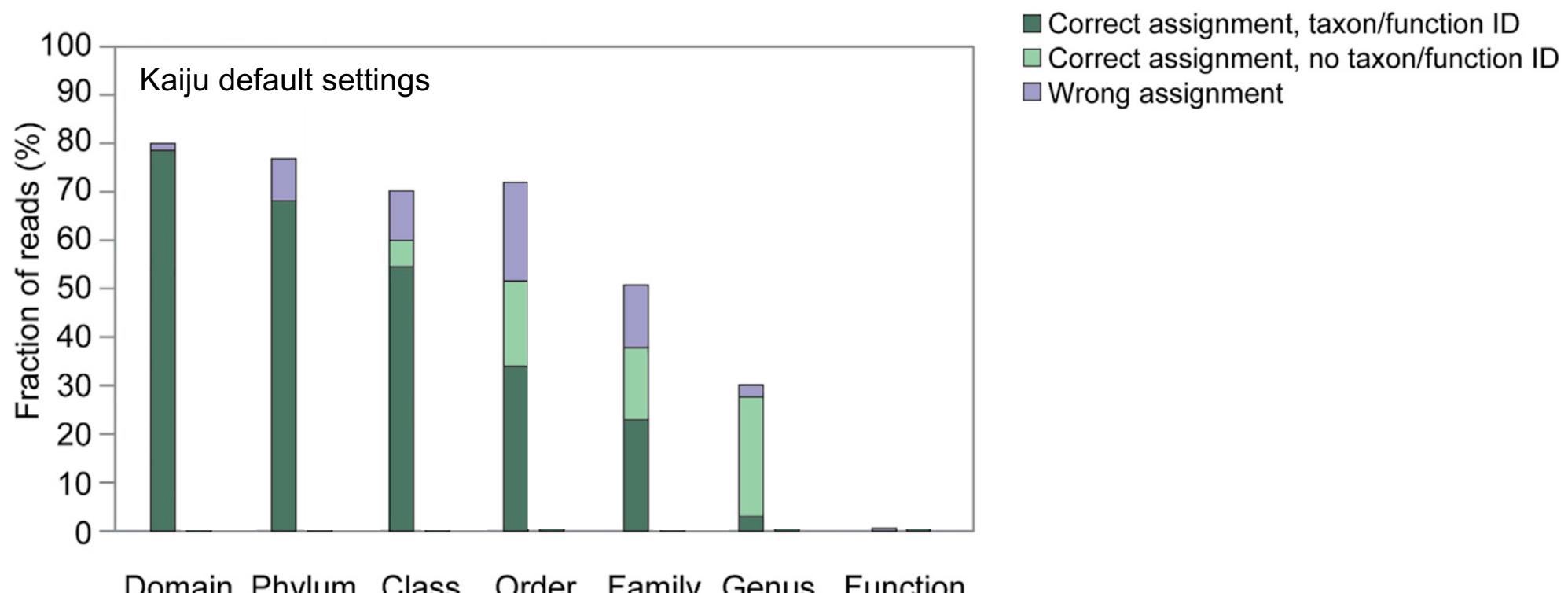
Peter Menzel<sup>1</sup>, Kim Lee Ng<sup>1</sup> & Anders Krogh<sup>1</sup>

### Advantages relative to other read classifiers:

- Both taxonomic and functional assignment
- Built-in LCA for hierarchical taxonomy assignment
- Higher sensitivity
- Fairly extensive validation

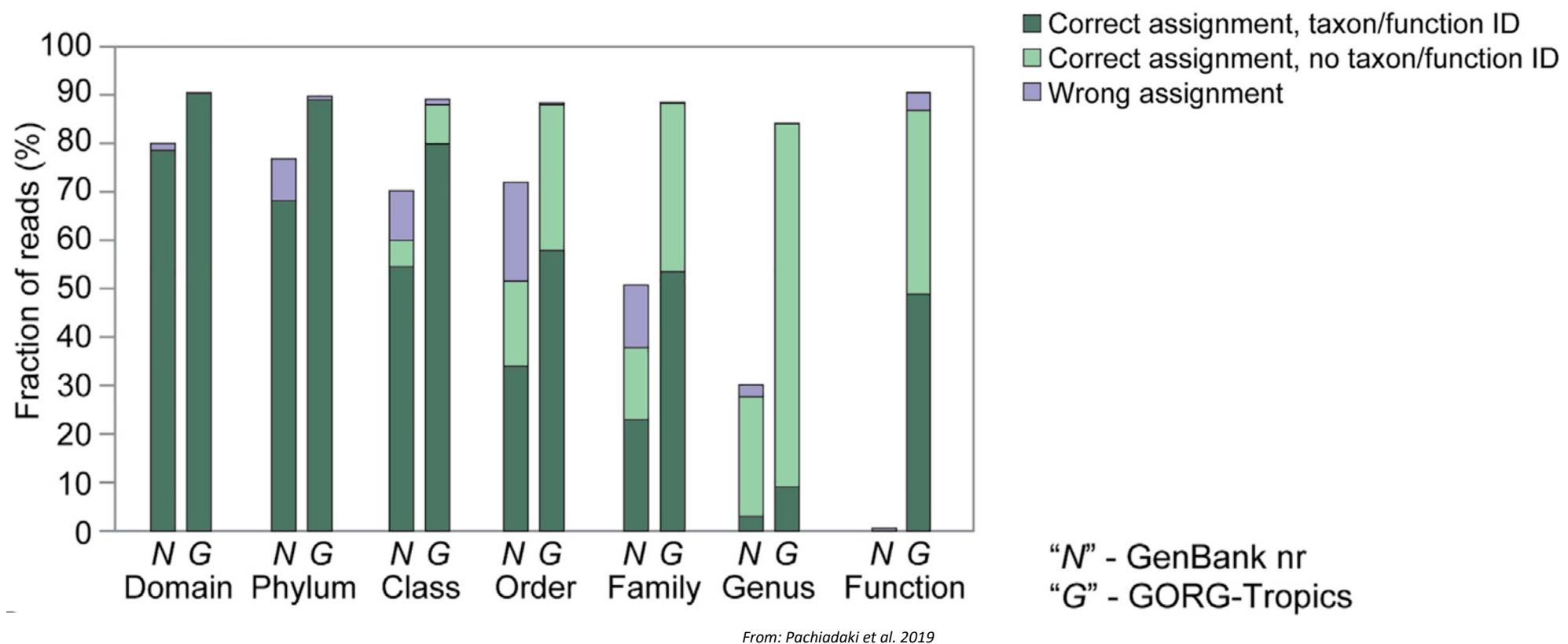


# Kaiju annotation of a tropics mock metagenome

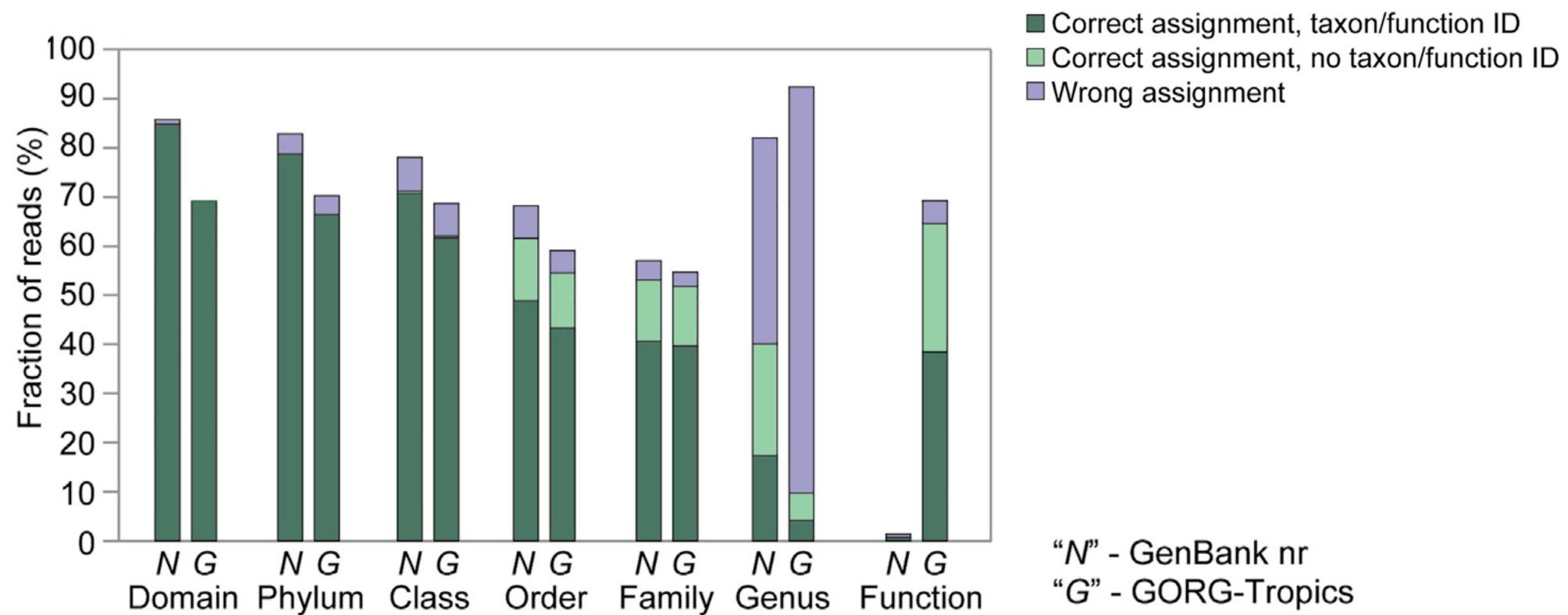


From: Pachiadaki et al. 2019

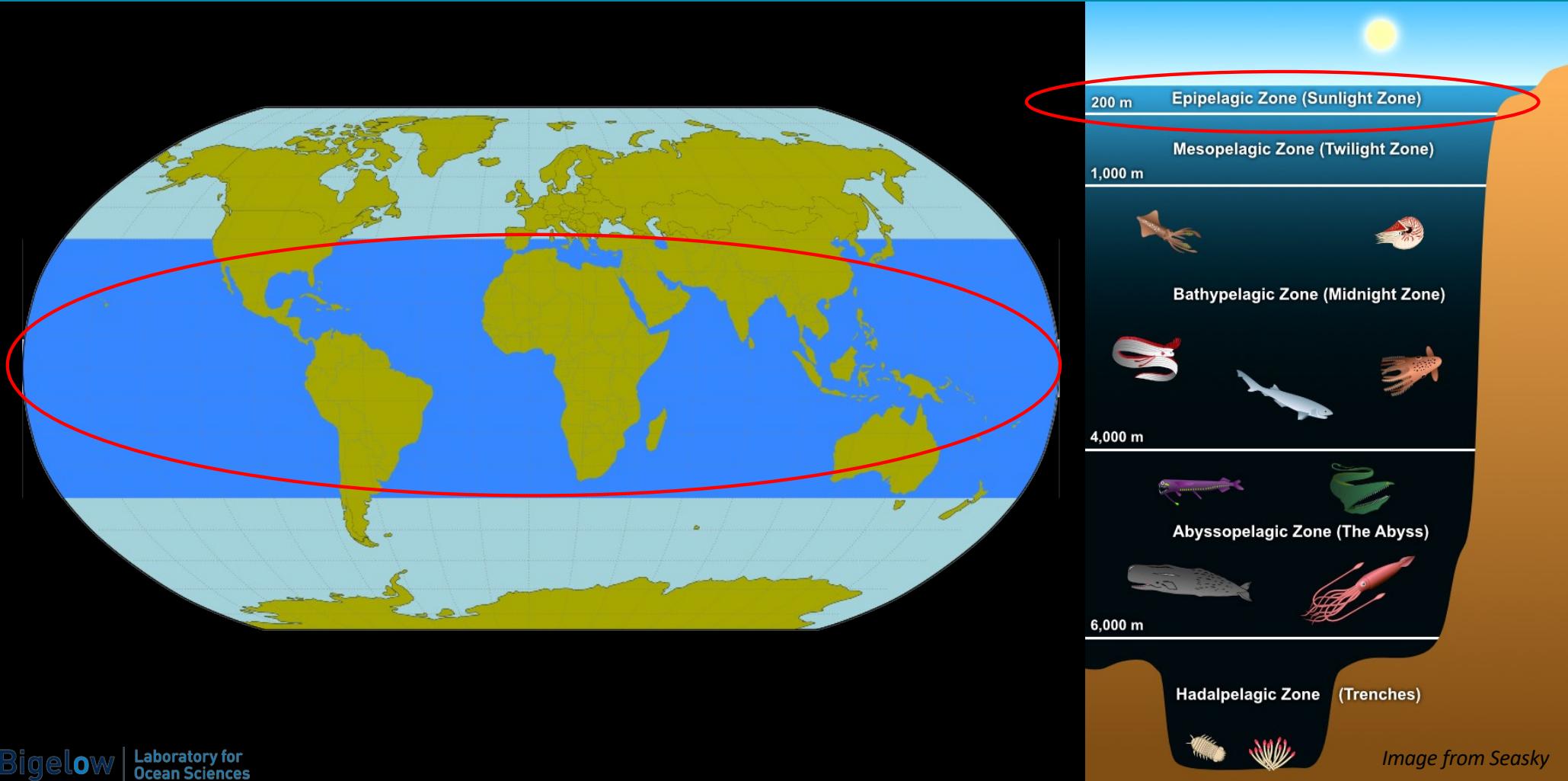
# Kaiju annotation of a tropics mock metagenome



# Kaiju annotation of a temperate mock metagenome



# GORG-Tropics coverage



# Next: GORG-Dark

