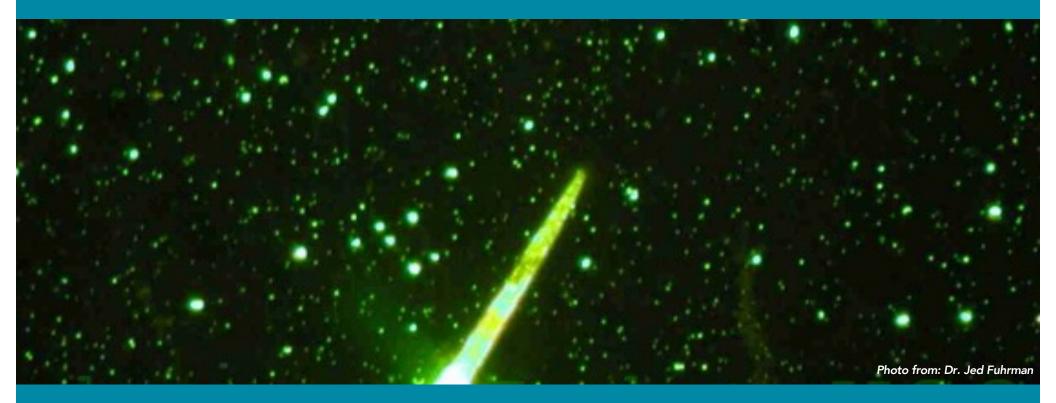
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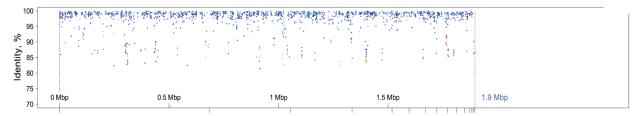
SAGs as references for meta-omics

## Metagenome fragment recruitment

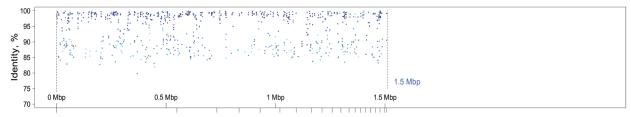


## Metagenome recruitment on first two SAGs sequenced

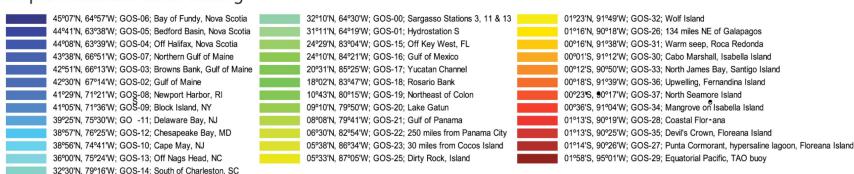
#### Flavobacteria bacterium MS024-2A



#### Flavobacteria bacterium MS024-3C



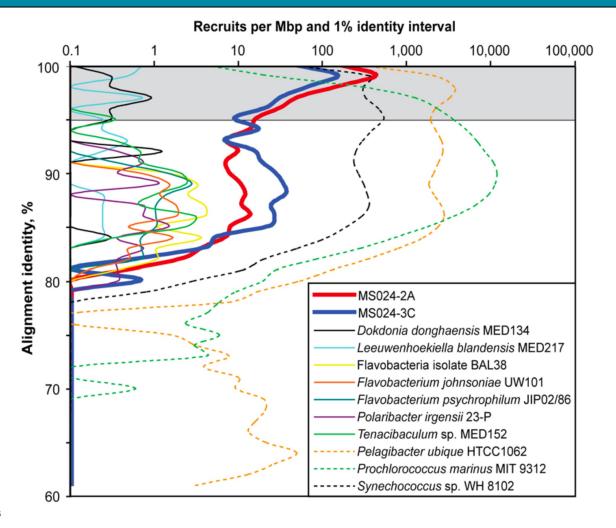
### Sample Metadata Color Coding



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From: Woyke et al. 2009

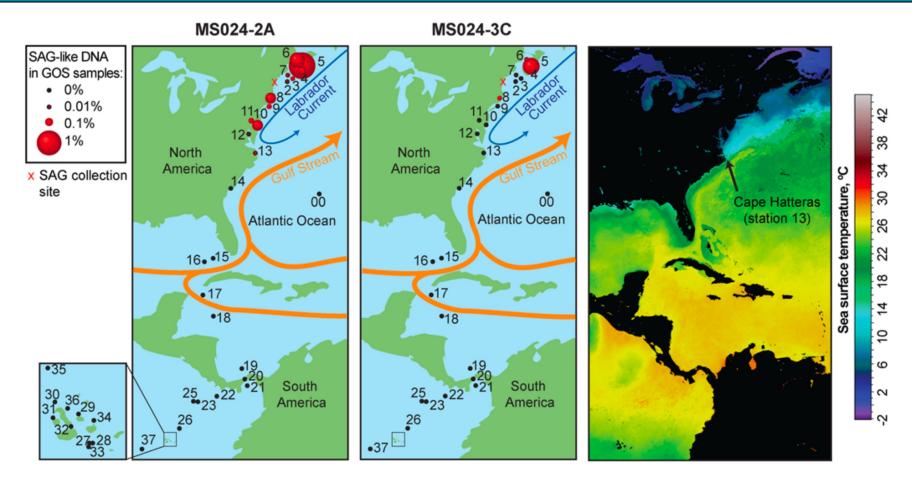
## Metagenome recruitment on first two SAGs sequenced





From: Woyke et al. 2009

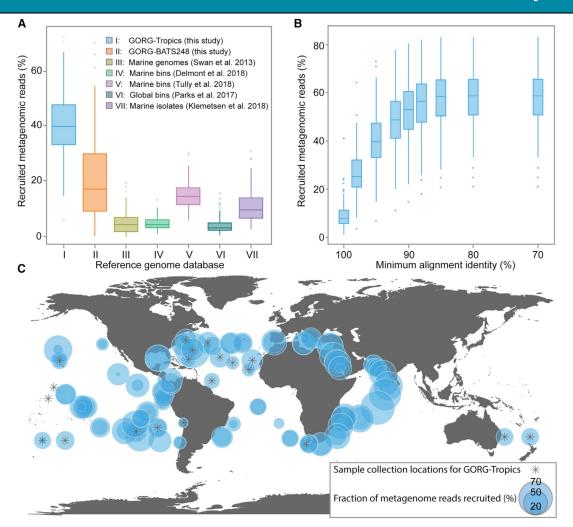
## Metagenome recruitment on first two SAGs sequenced





From: Woyke et al. 2009

## Recruitment on GORG-Tropics



From: Pachiadaki et al. 2019



### Read classifiers

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



METHOD Open Access

# Kraken: ultrafast metagenomic sequence classification using avact alignments

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

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

Genome Biology

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

**SHORT REPORT** 

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## Improved metagenomic analysis with Kraken 2

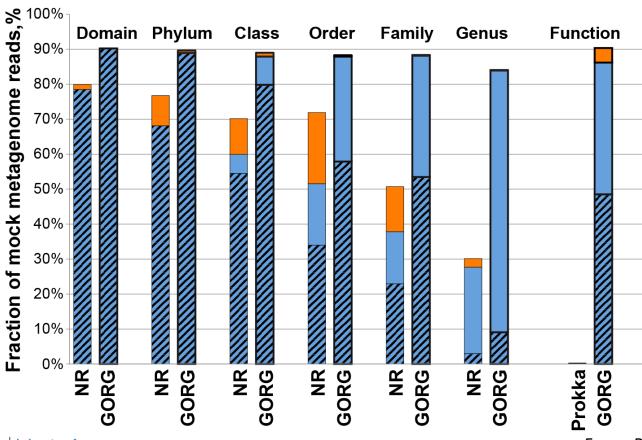


Derrick E. Wood<sup>1,2</sup>, Jennifer Lu<sup>2,3</sup> and Ben Langmead<sup>1,2\*</sup>



### Accuracy of Kaiju, default versus GORG-Tropics databases





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From: Pachiadaki et al. 2019

## Use of GORG Classifier to quantify per-genus gene expression

