



slides: [goo.gl/xxxxx](https://goo.gl/xxxxx)



@MadsAlbertsen85

# Why metagenomics is broken

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CAMI

25-08-2014

ISME15, Seoul, South Korea



# Critical Assessment of Metagenome Interpretation

Showcase potentials and limitations



# Critical Assessment of Metagenome Interpretation

Showcase potentials and limitations

The implication of lack of reference genomes on  
taxonomic classification

The impact of micro-diversity on  
assembly and  
genome completeness metrics

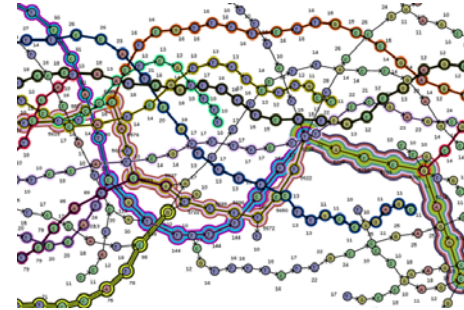
**More visualisations, please.**



Sequence



Assemble



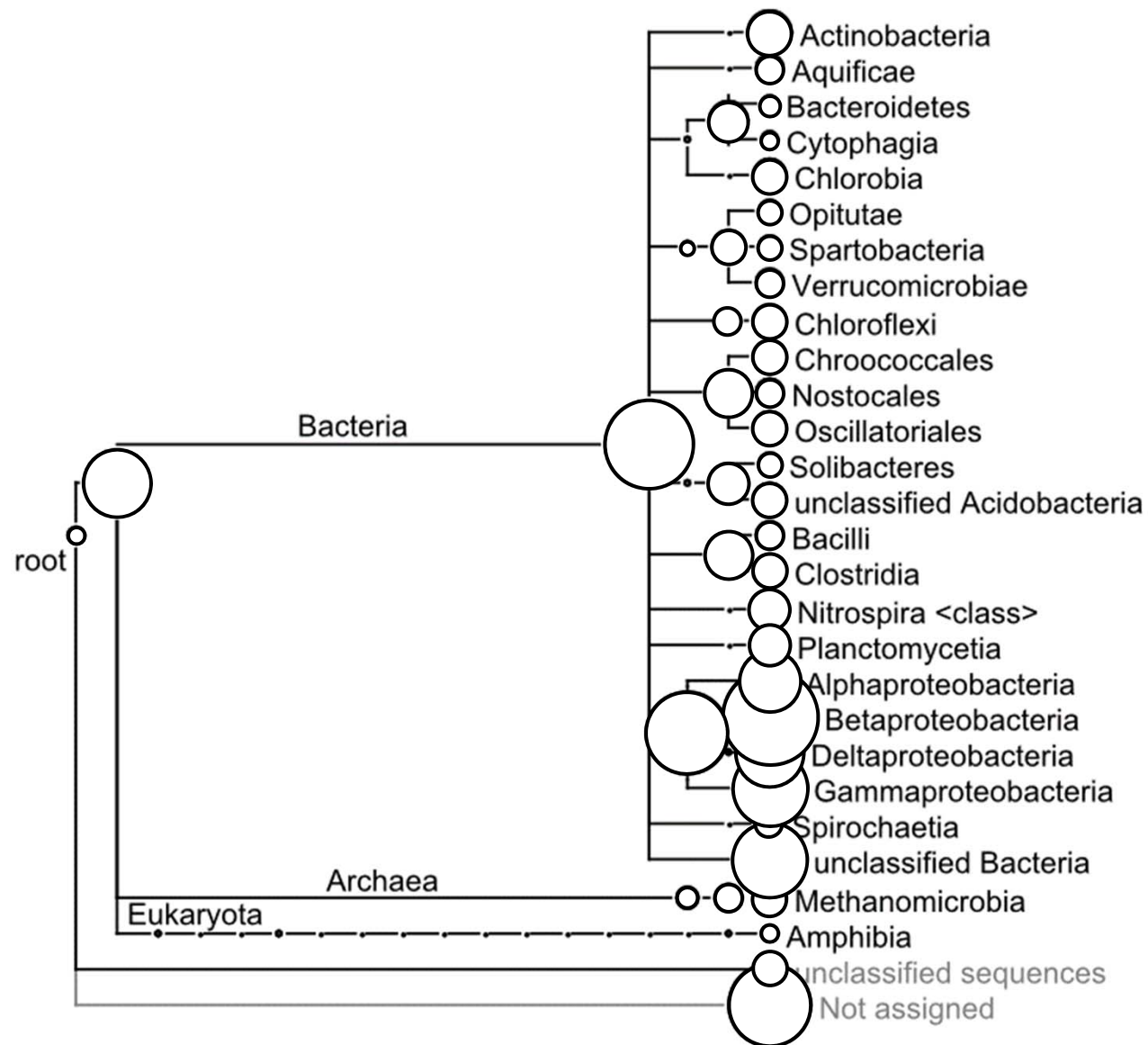
Compare to database

(BLAST vs. NCBI RefSeq)

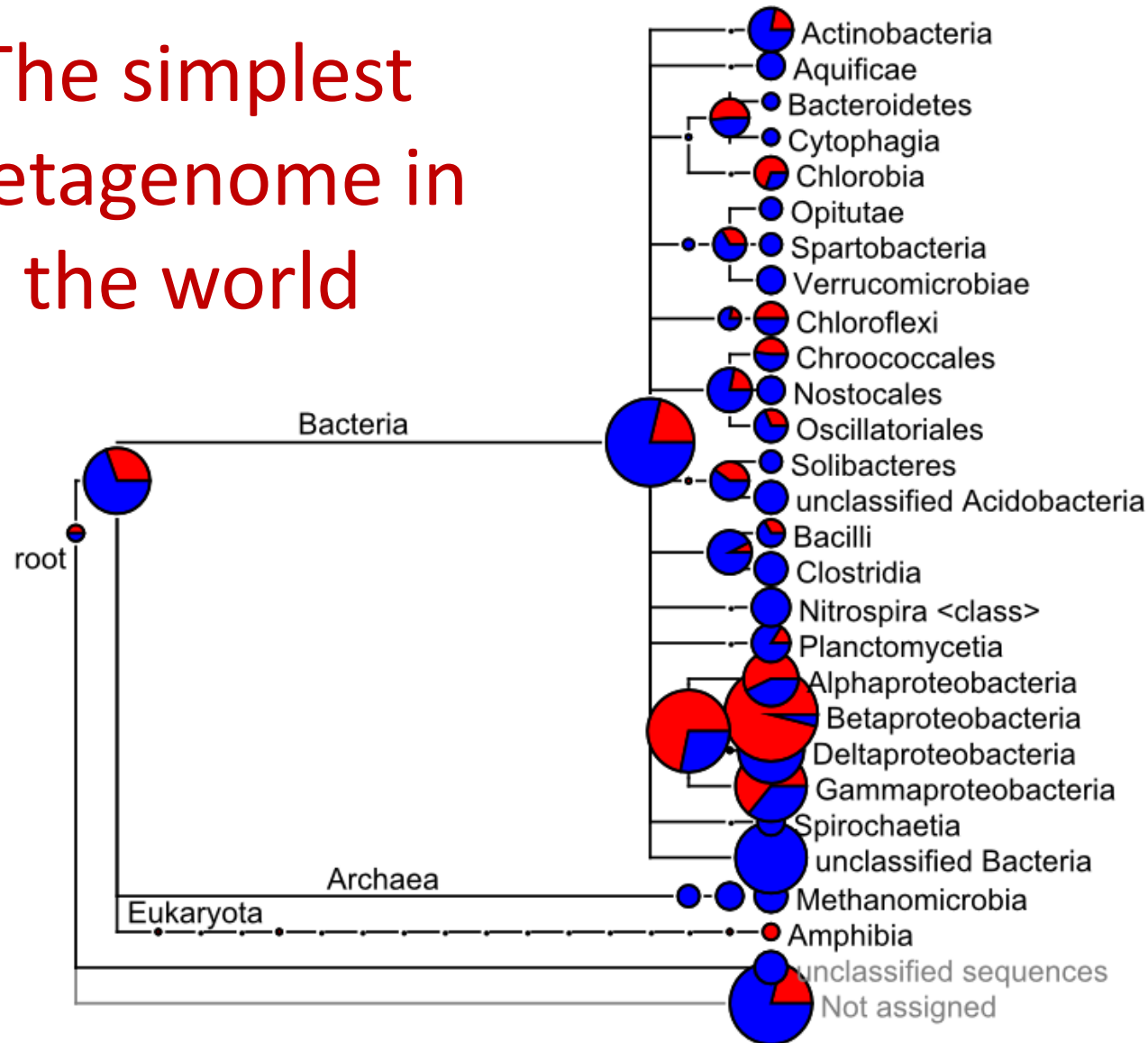


Taxonomic Classification

(MEGAN)



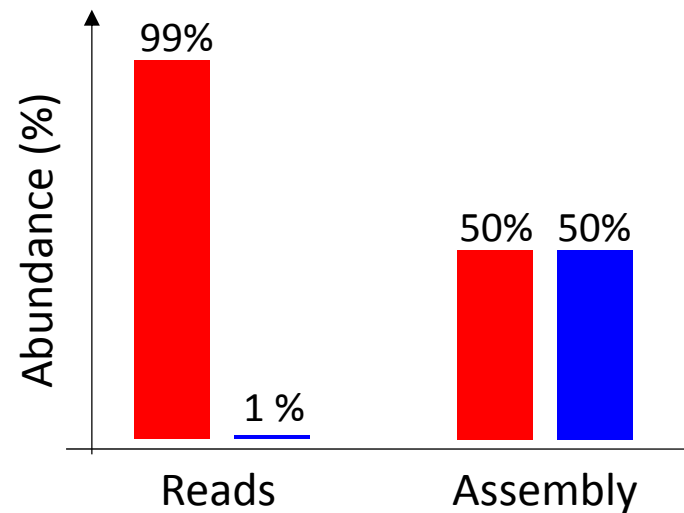
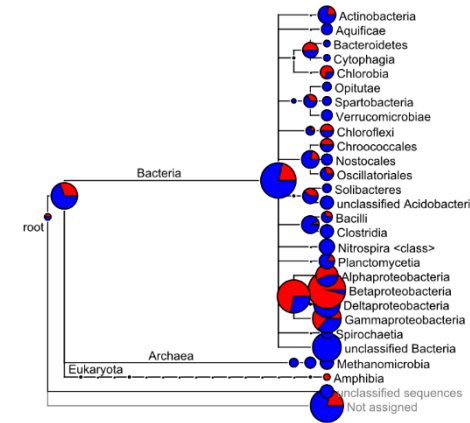
# The simplest metagenome in the world



*Accumulibacter* (Class Betaproteobacteria)

*Nitrospira* (Class Nitrospira)

# The simplest metagenome in the world



Remember to correct for read abundance

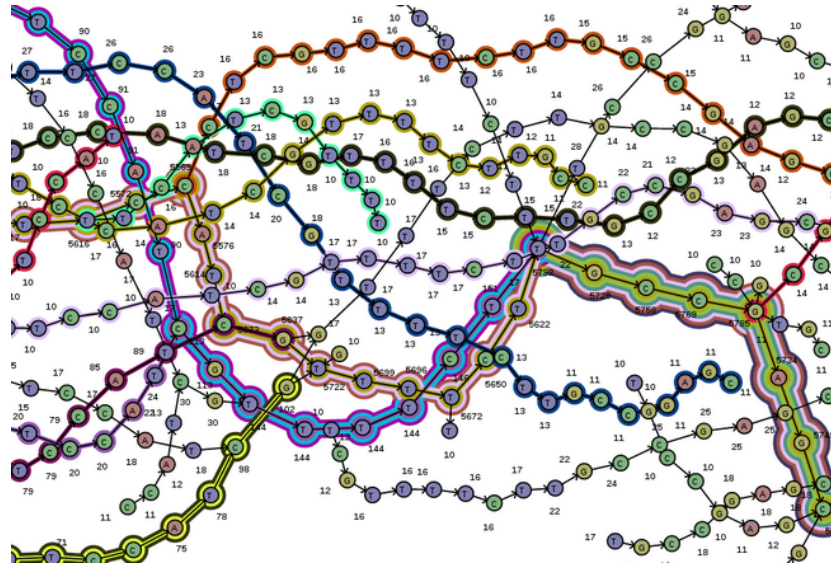
*Accumulibacter* (Class Betaproteobacteria)

*Nitrospira* (Class Nitrospira)



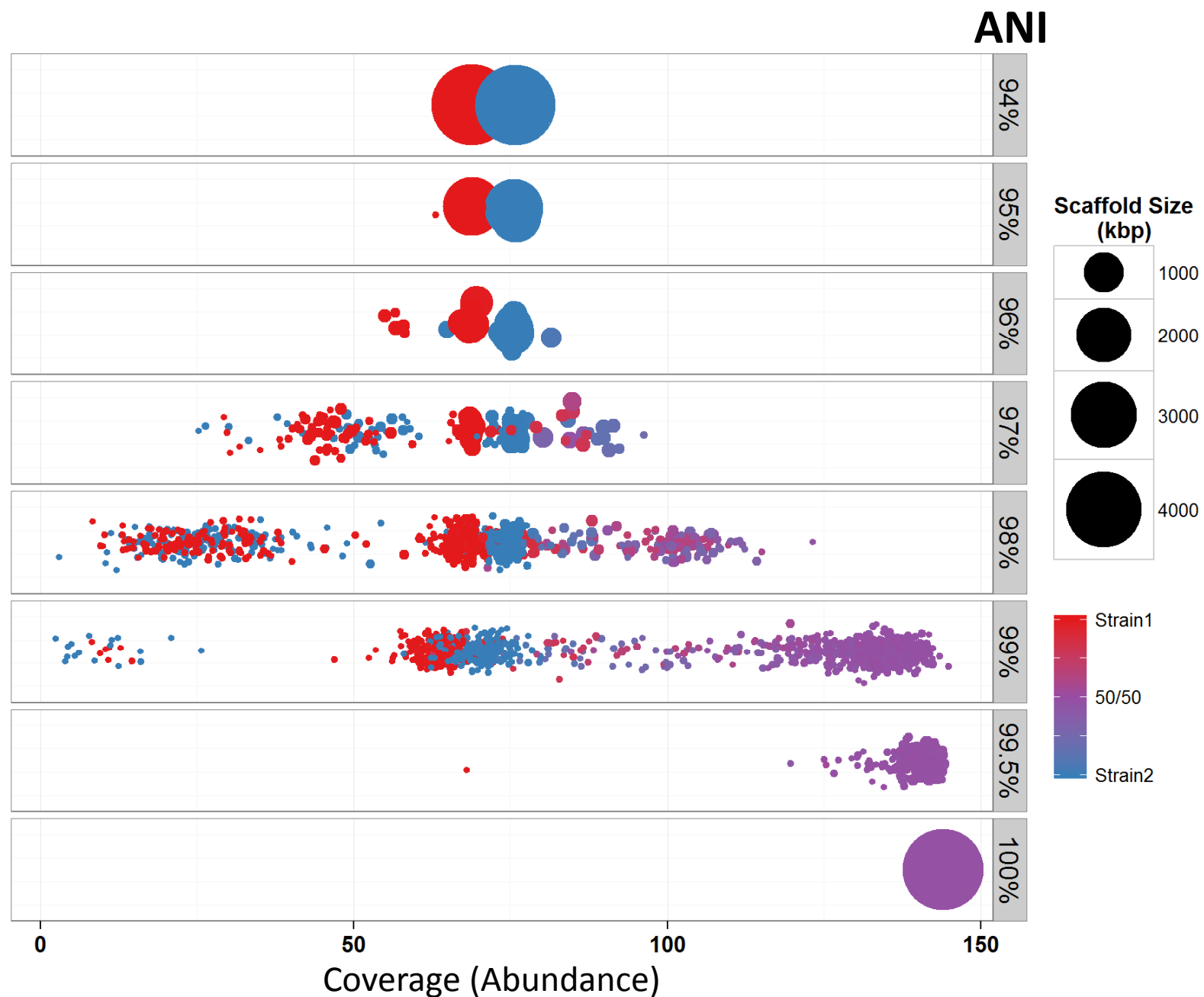


# Assembly



*... of the simplest  
metagenome in the world*







Sequencing



Assembly



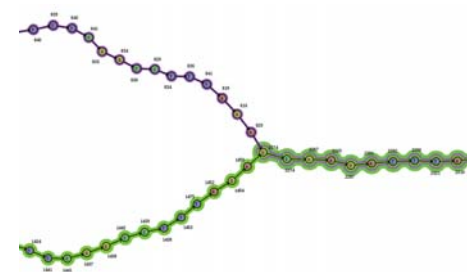
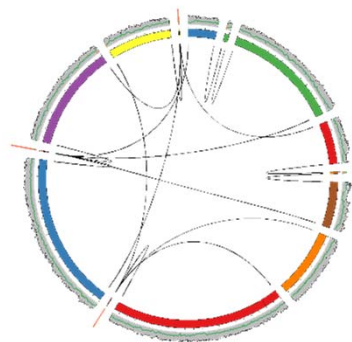
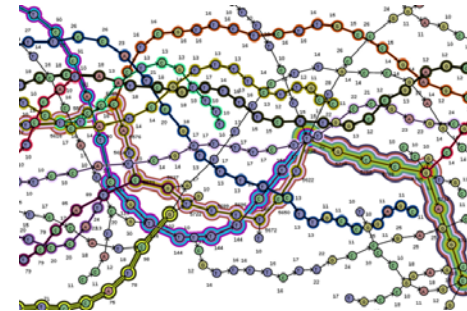
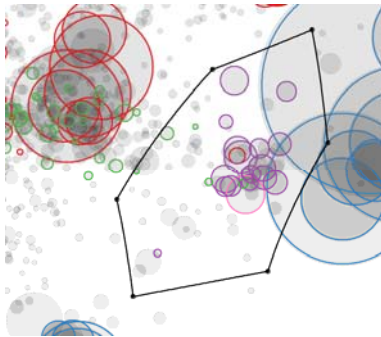
**Genome Binning**

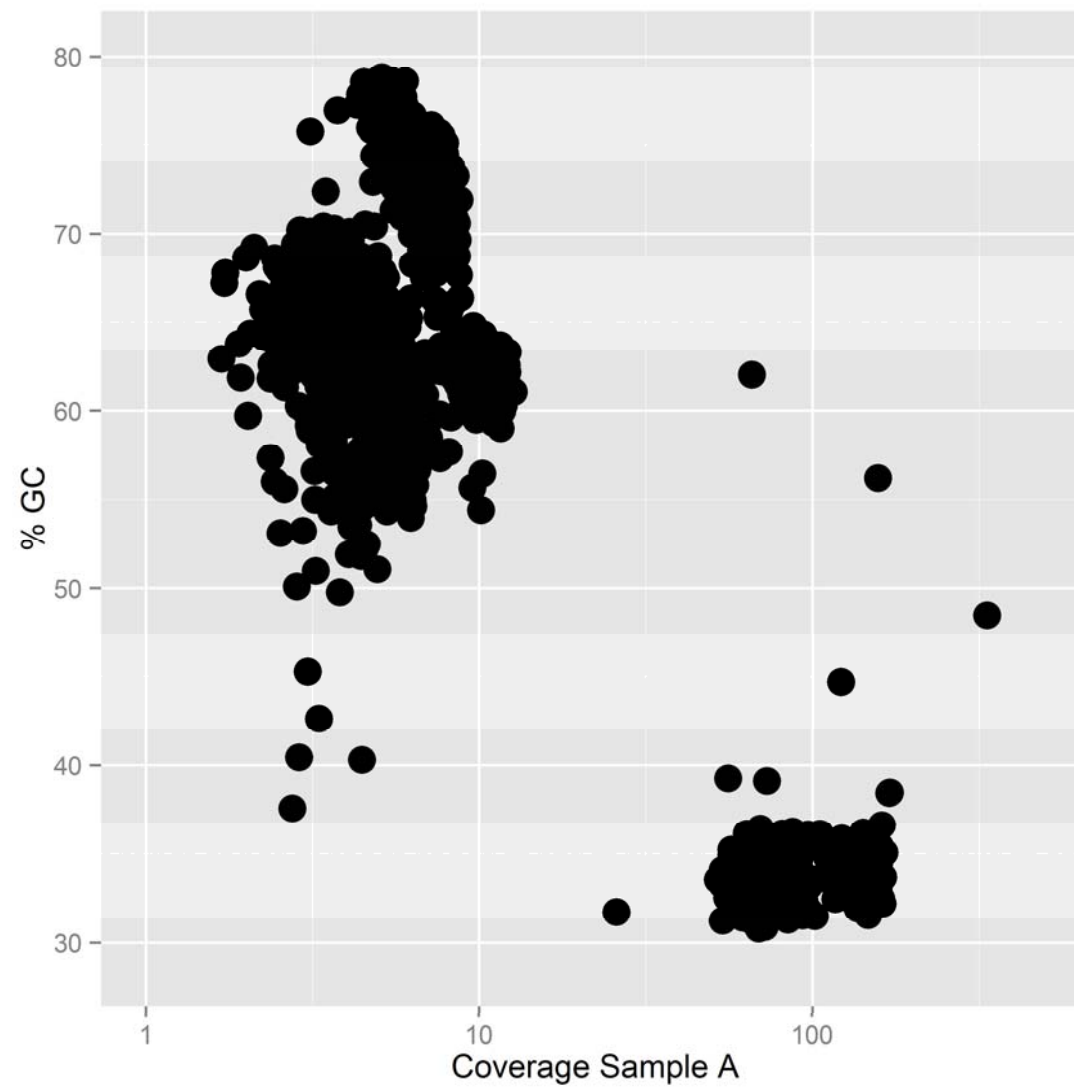


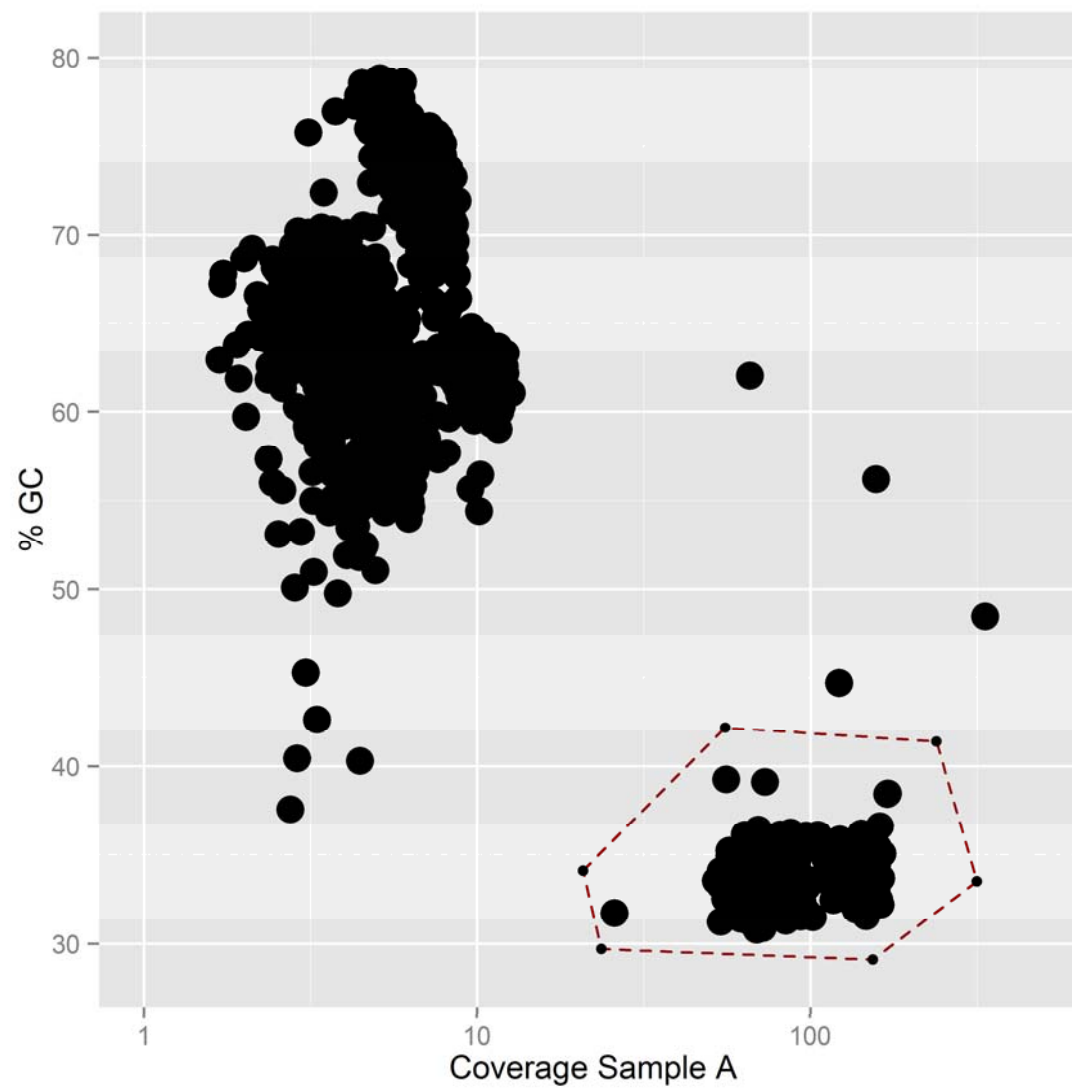
Re-assembly



Manual curation







#### Assembly statistics

# Scaffolds	447
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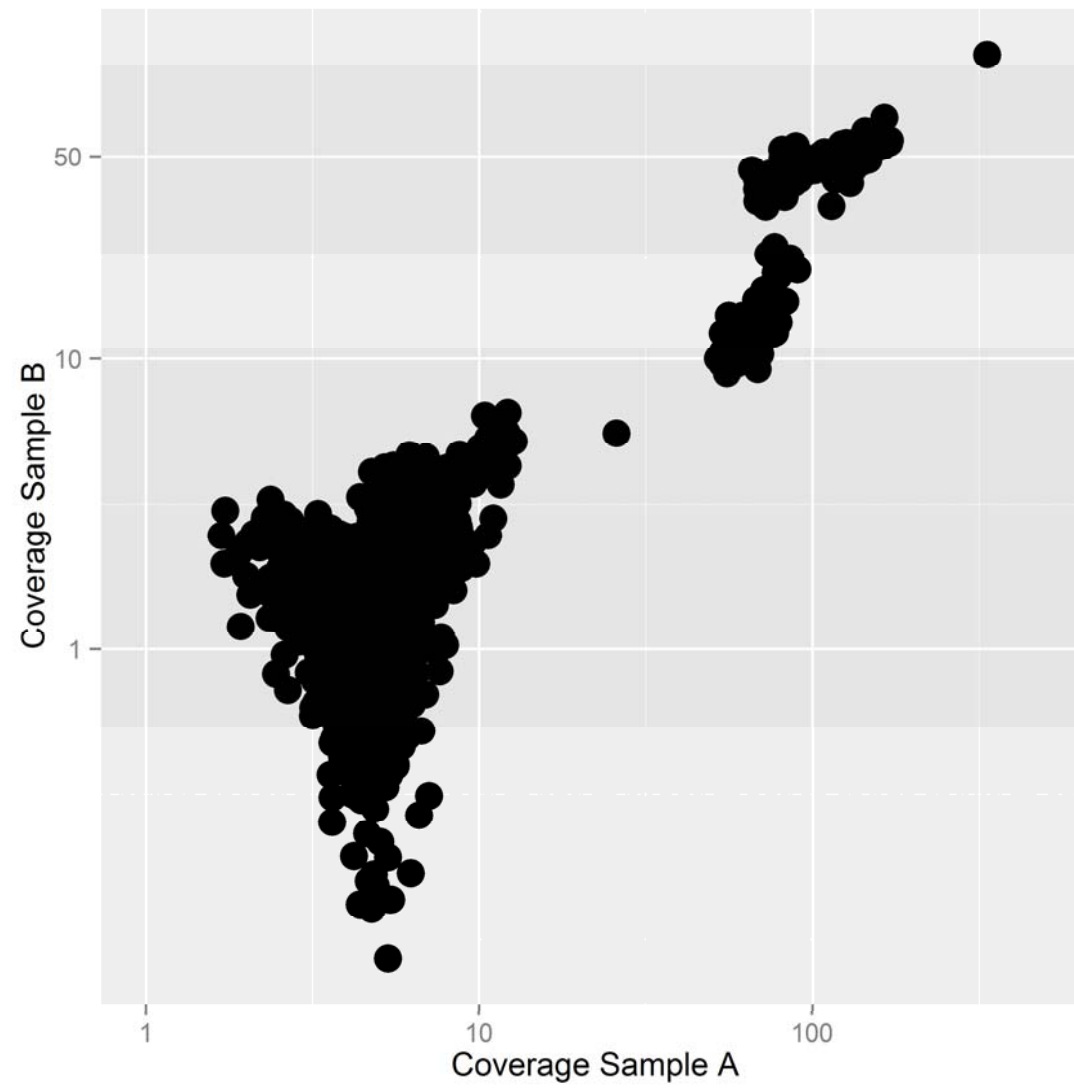
Total Mbp	4.46
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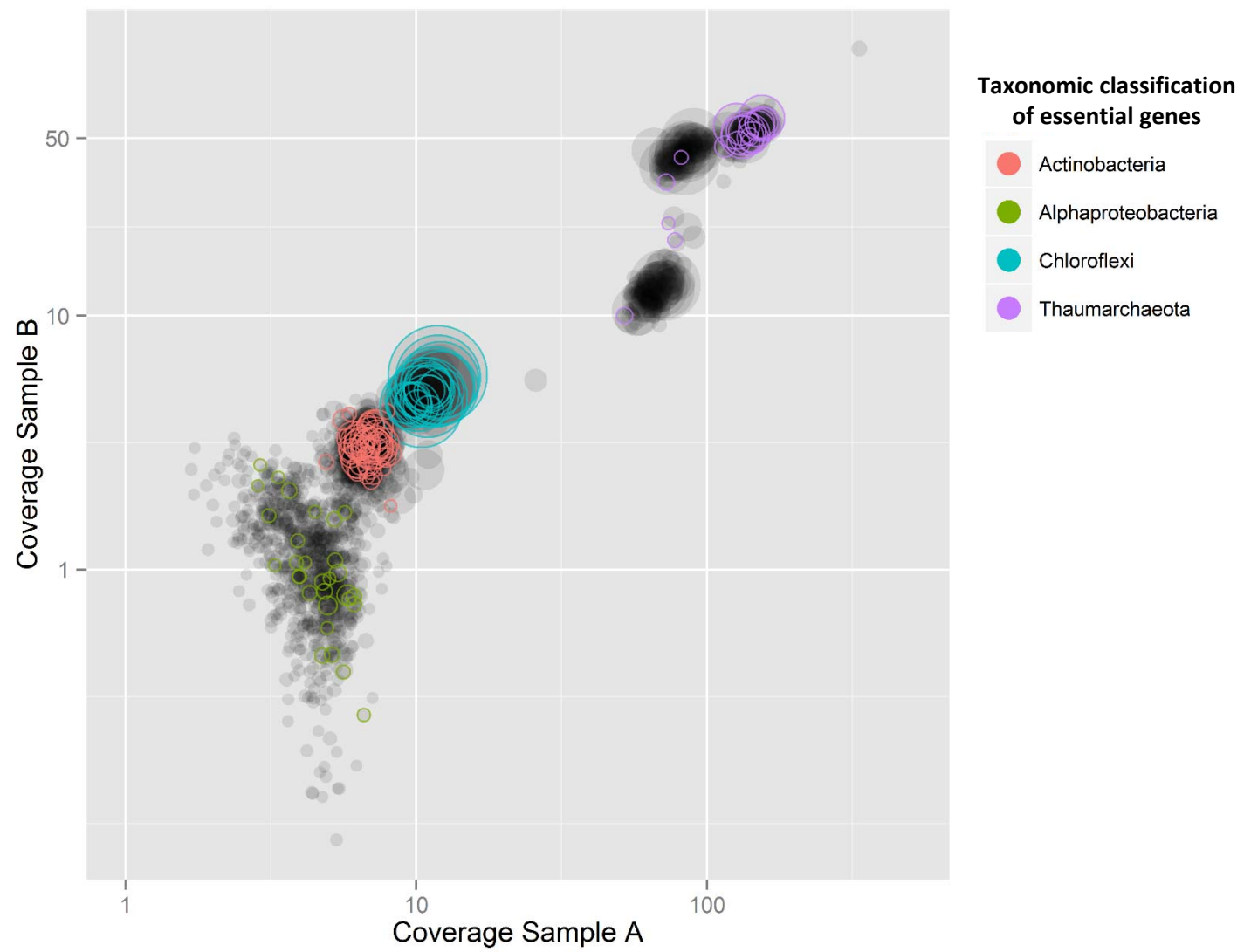
% GC	33.7
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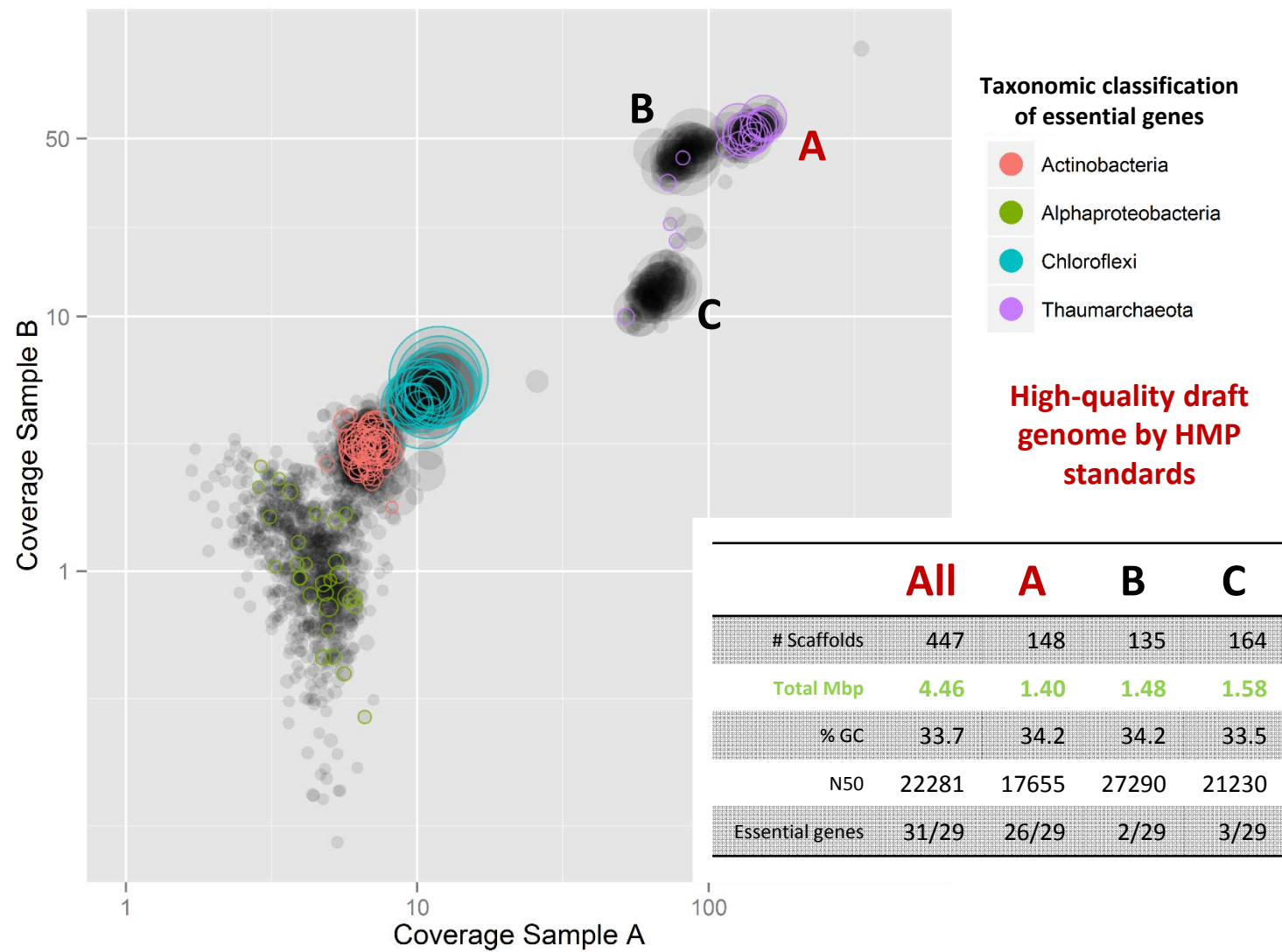
N50	22281
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Essential genes	31/29
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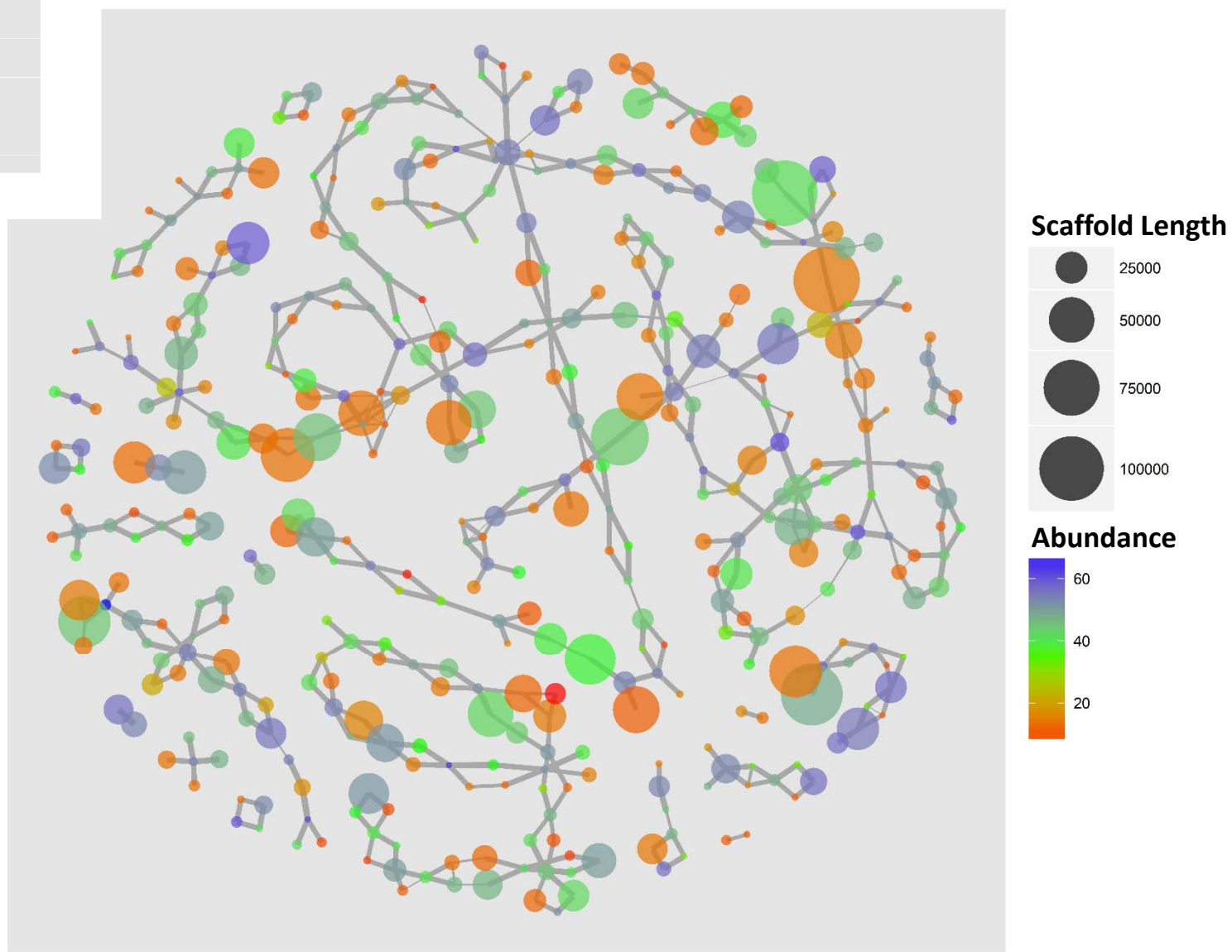
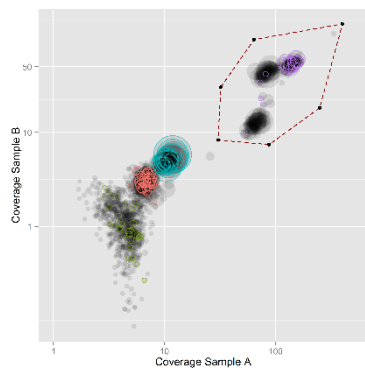
**High-quality draft genome by HMP standards**

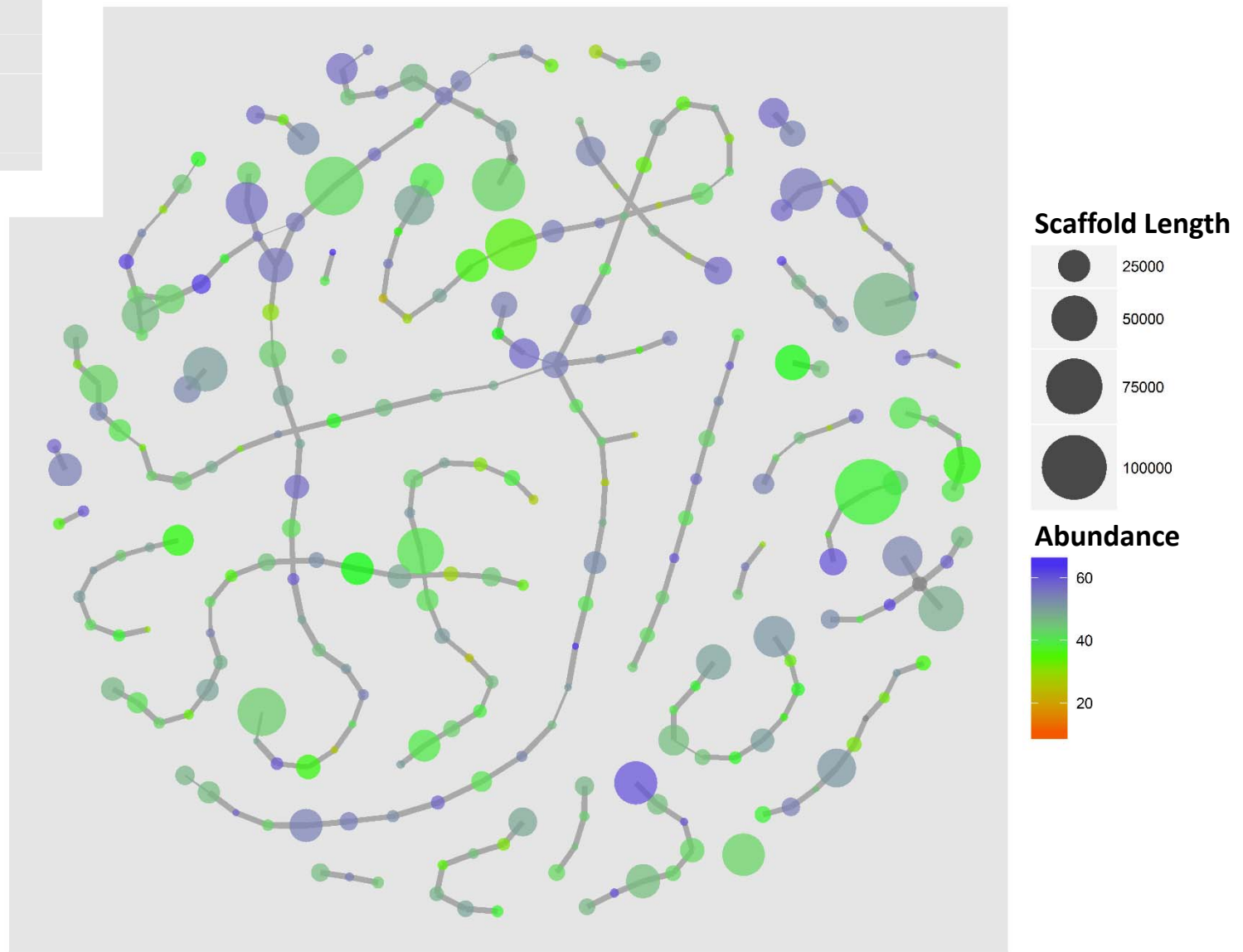
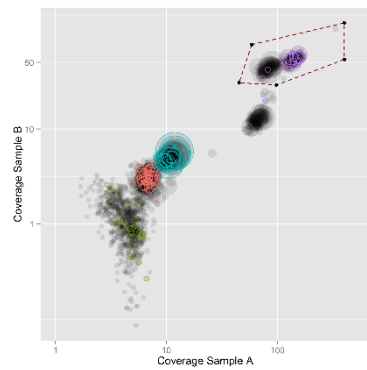


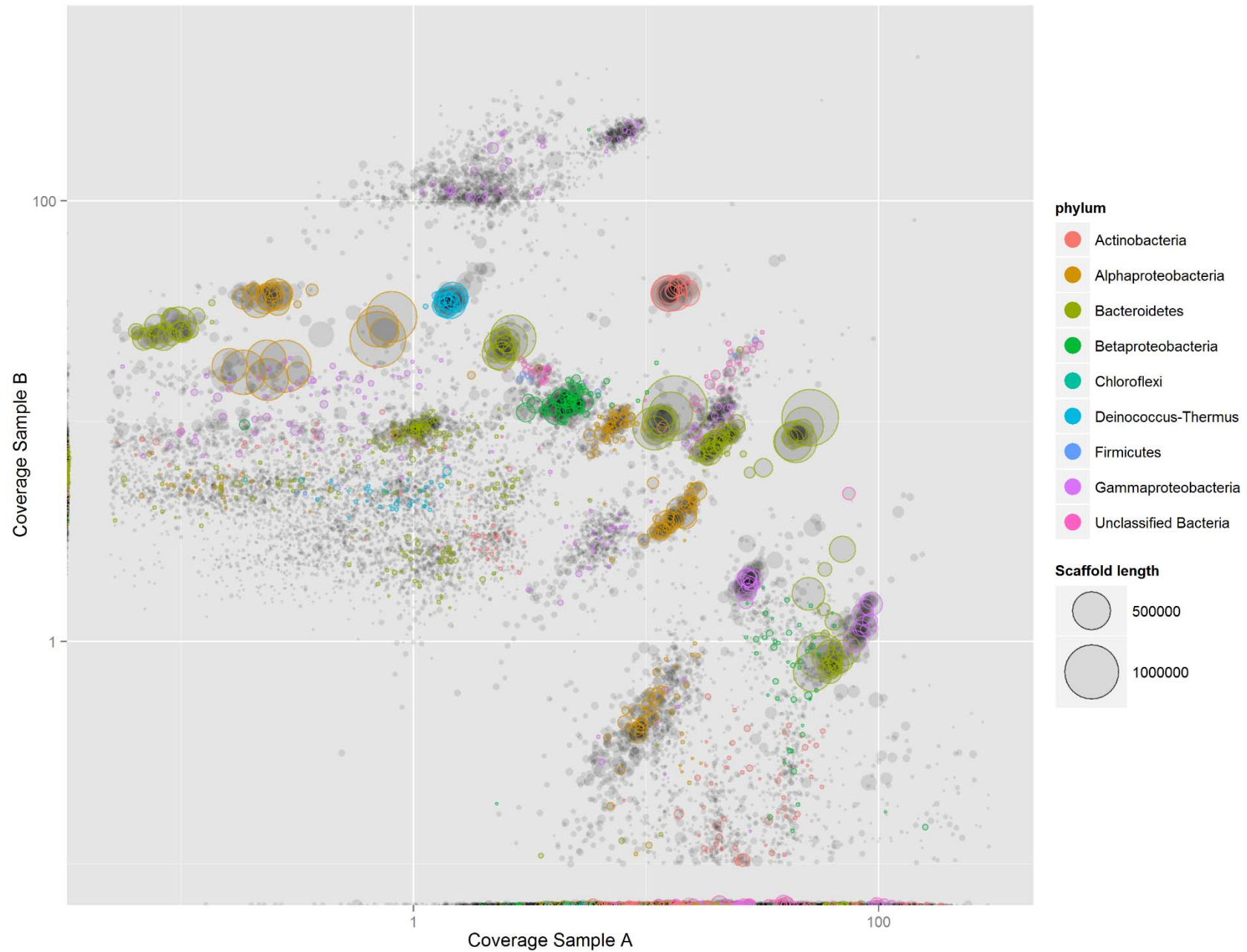


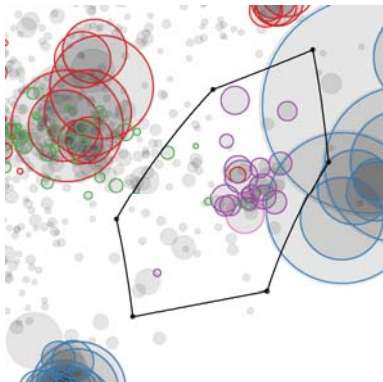
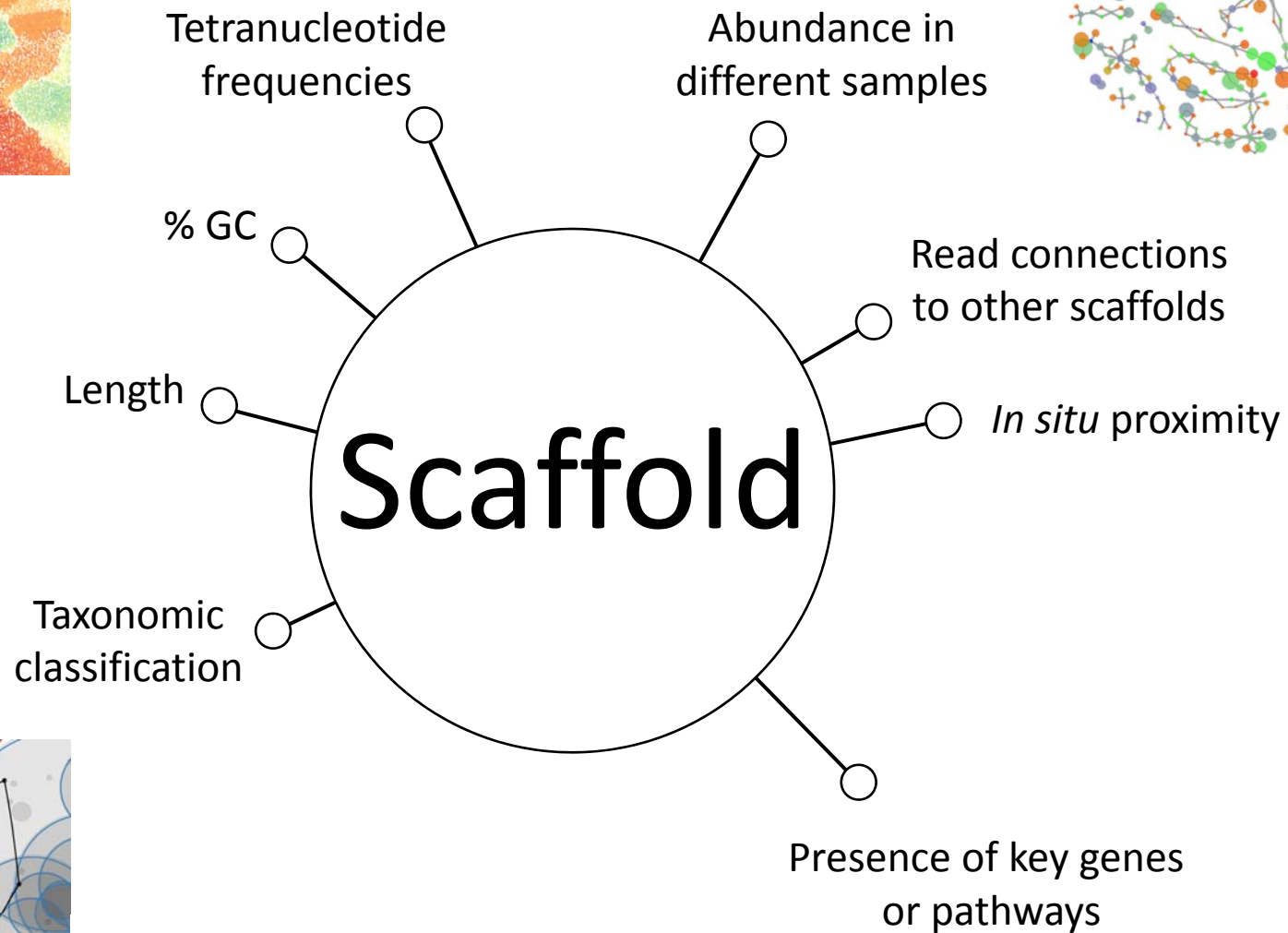
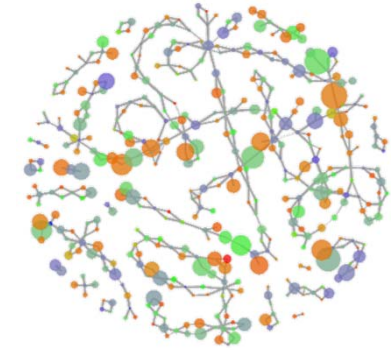
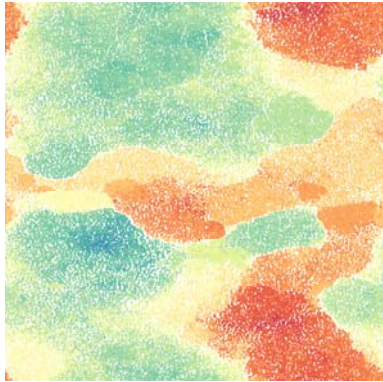












The logo for mmgenome, featuring the text 'mmgenome' in a sans-serif font. The 'mm' is green and the 'genome' is white, all set against a light gray rectangular background.

mmgenome

A toolbox for reproducible genome  
extraction from metagenomes



MadsAlbertsen/mmgenome

[goo.gl/ohCVPg](https://goo.gl/ohCVPg)



# Unknown unknowns

*“We **pray** that micro-diversity didn’t compromise the assembly and **hope** our key genes are present.”*



# Acknowledgements



**Per H. Nielsen**  
Søren M. Karst  
Rasmus H. Kirkegaard  
Simon J. McIlroy



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**mmgenome**

A toolbox for reproducible genome  
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C. Dorringer



H. Daims



A. Loy



M. Wagner



F. Moeller



J. Neufeld  
L. Sauder



KØBENHAVNS UNIVERSITET



M. Kuhl  
L. Behrendt



G.W. Tyson



P. Hugenholtz



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