

# a short story about long reads -- for metagenome assembly

Celia Diezel

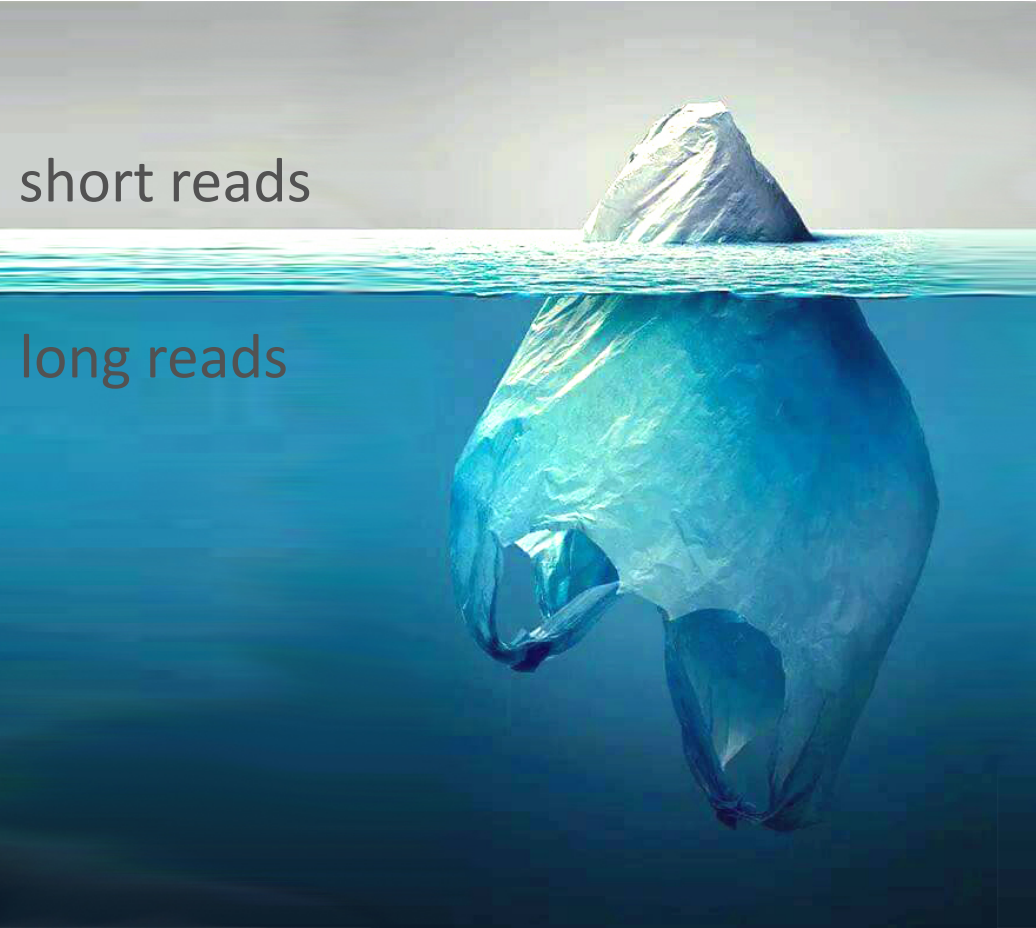
Friedrich-Schiller-University, Jena

RNA bioinformatics and high throughput sequencing

Prof. Manja Marz

# Why long reads?

reconstructing genomes



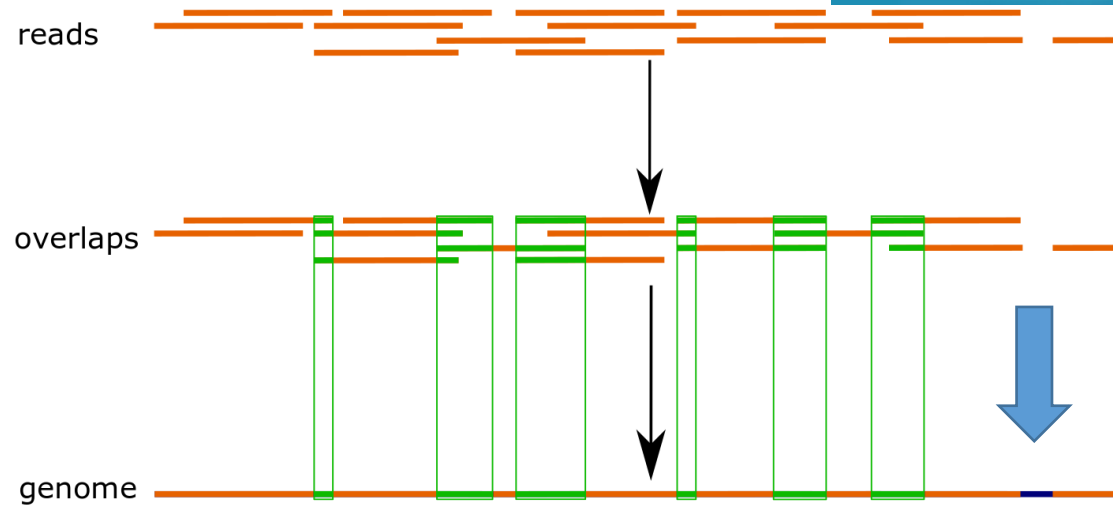
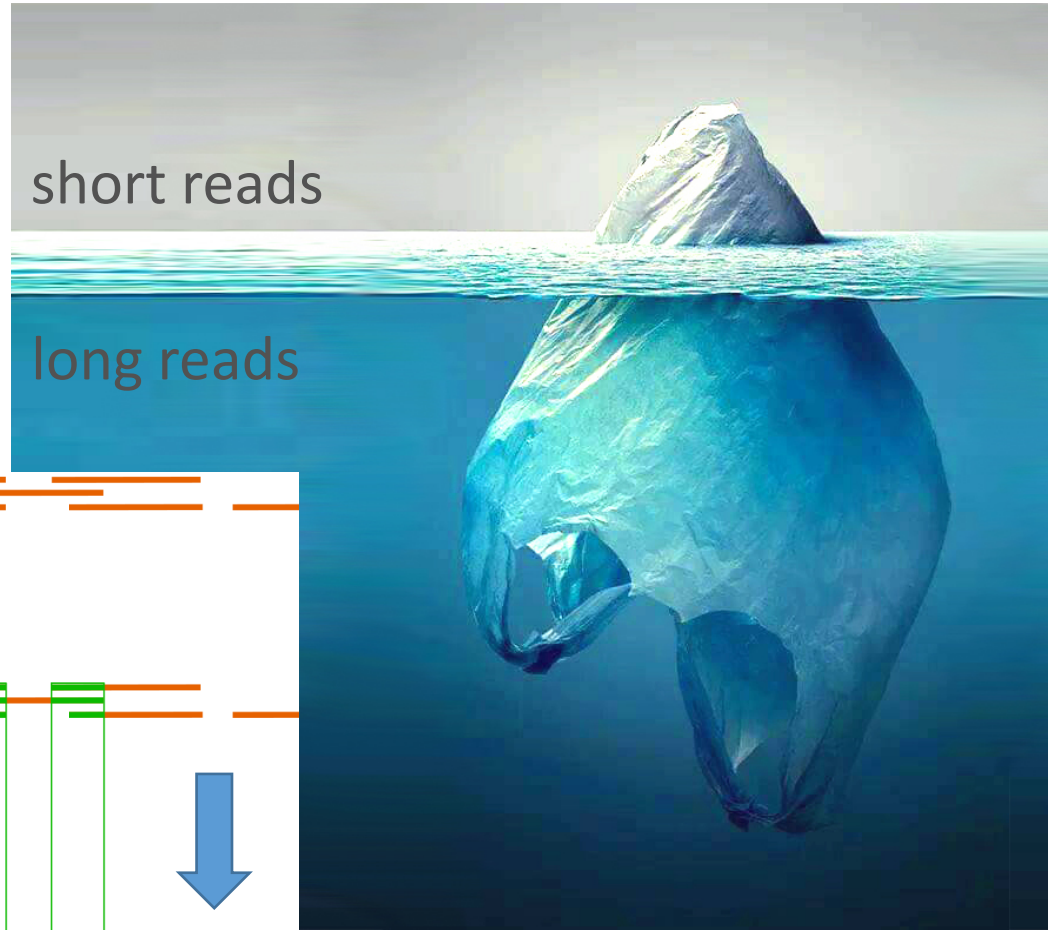
short reads

The image shows a blue-tinted scene of an iceberg floating in water. The water surface is a horizontal line. Above the surface, a small, sharp peak of the iceberg is visible, representing 'short reads'. Below the surface, the much larger, rounded, and crumpled part of the iceberg is submerged, representing 'long reads'. The text 'short reads' is positioned to the left of the visible peak, and 'long reads' is positioned to the left of the submerged part.

long reads

# Why long reads?

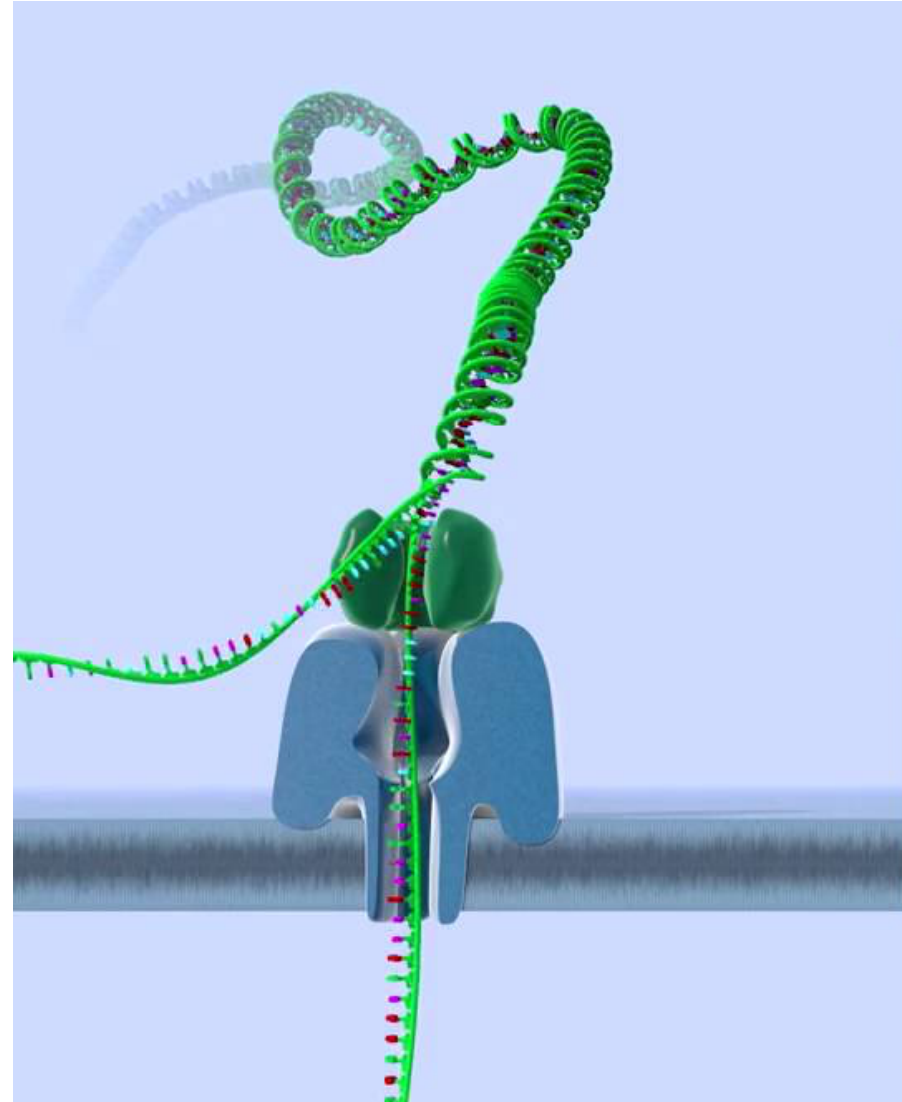
reconstructing genomes



long reads can span missing overlaps and repeats

# Nanopore sequencing

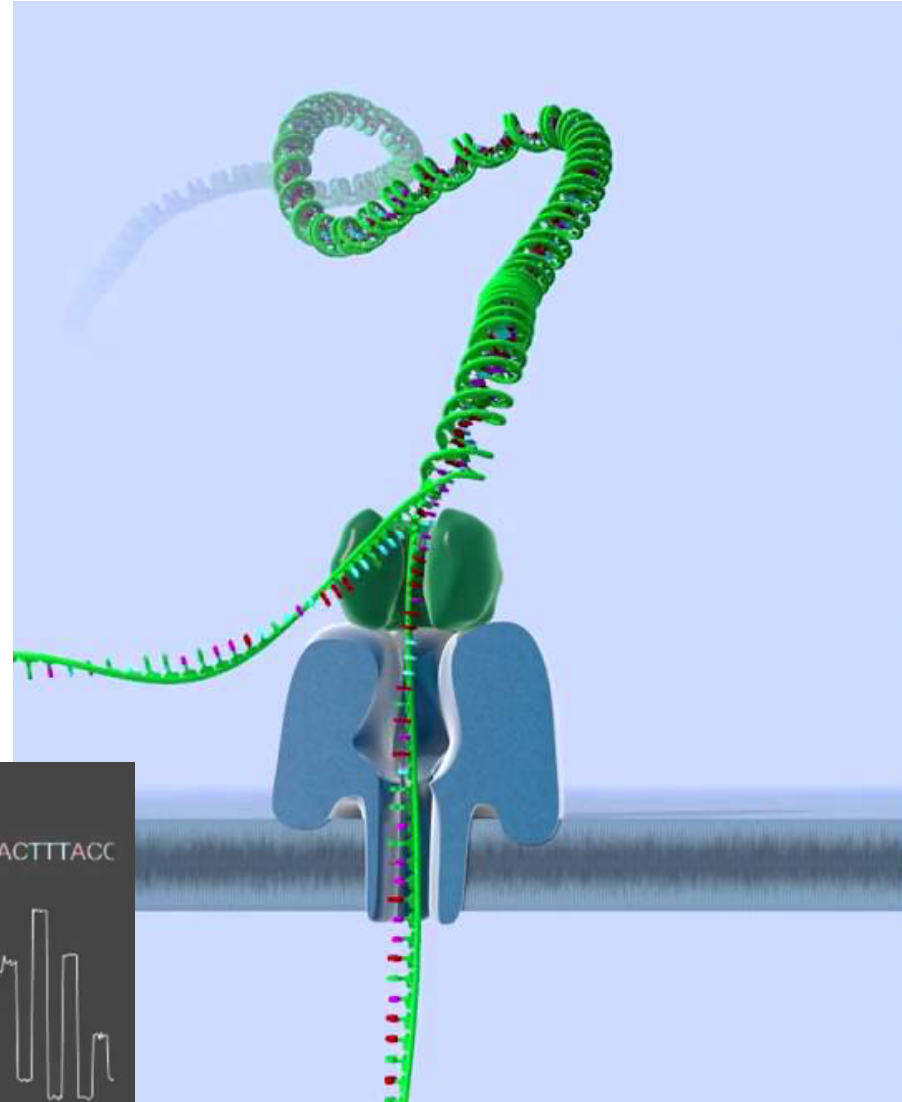
## Principle: MinION





# Nanopore sequencing

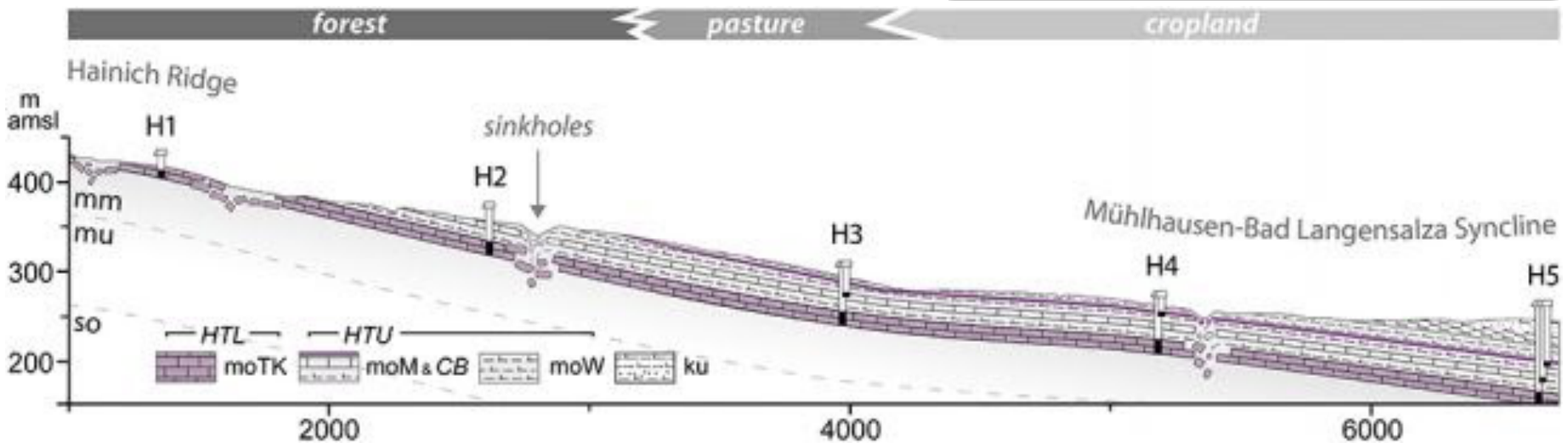
## Principle: MinION



# Aquadiva-Hainich National park

## Longitudinal characterization of microbes including viruses using metagenomic assembled genomes (MAGs)

- what biota live there?
- interactions?
- changes?

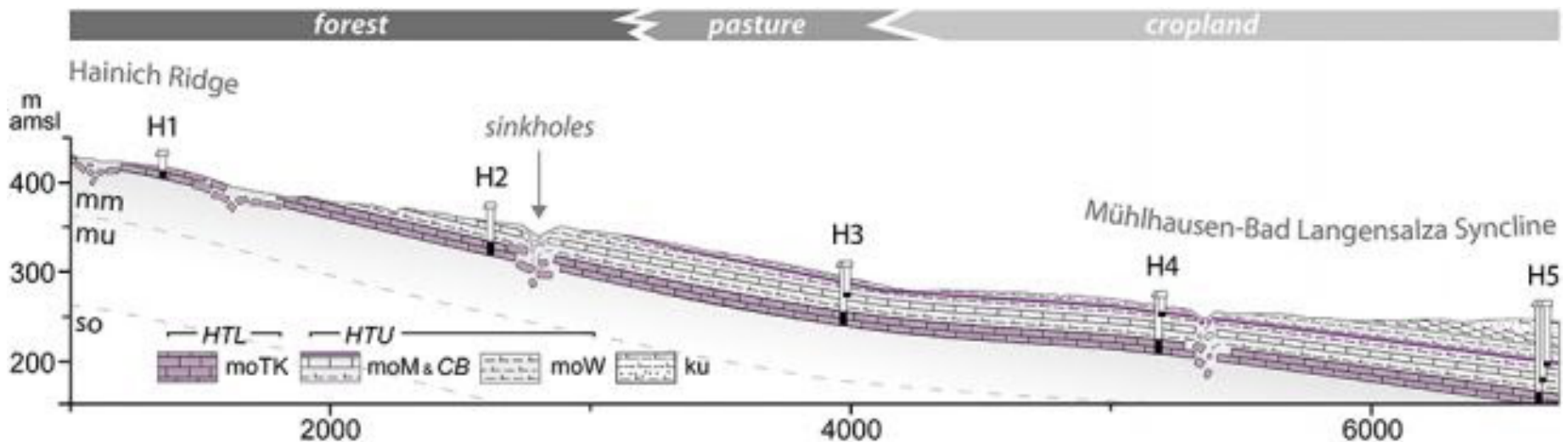


# Aquadiva-Hainich National park

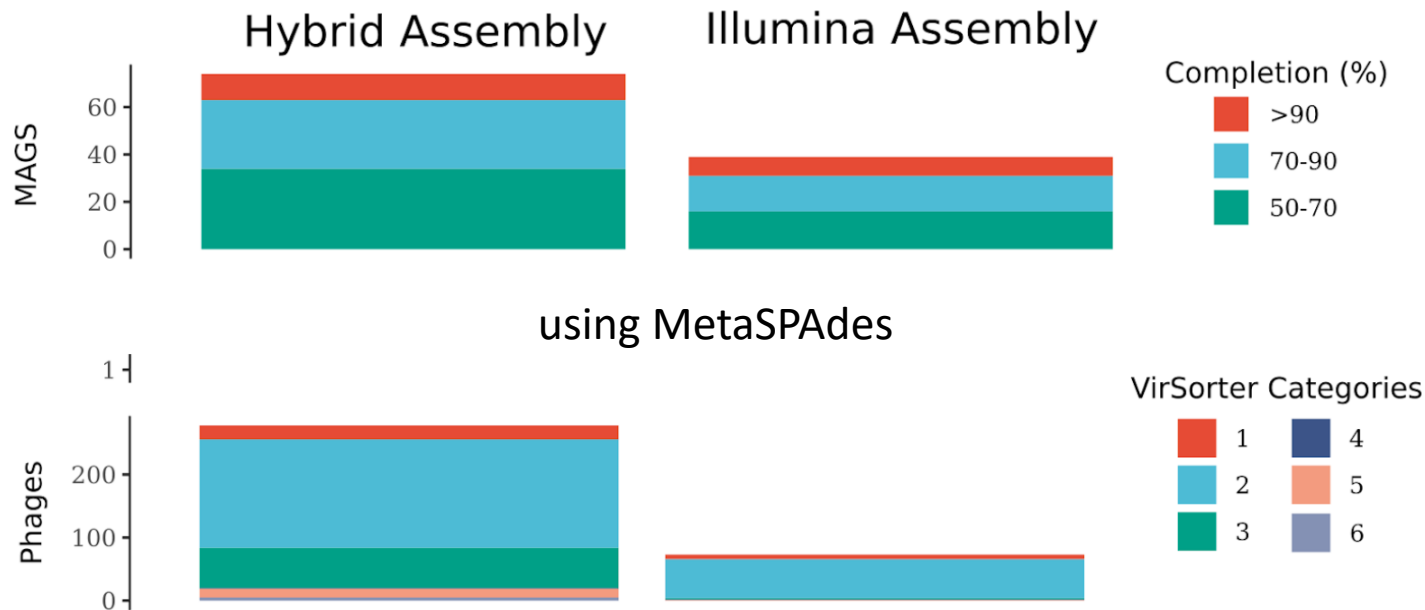
## Longitudinal characterization of microbes including viruses using metagenomic assembled genomes (MAGs)

- what biota live there?
- interactions?
- changes?

hybrid assembly



## Inclusion of ONT long reads improve MAGs and lead to the detection of more and complete viruses (and microbes)



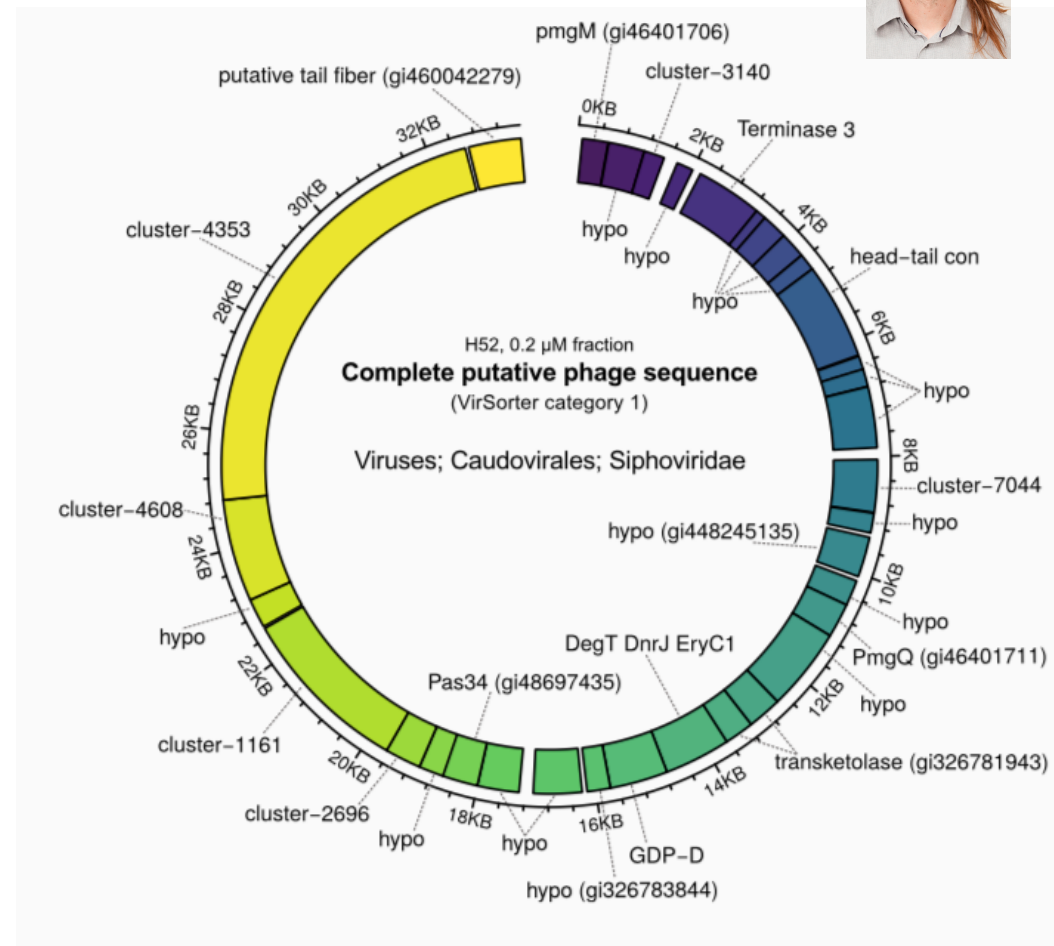
- more than doubled # of bacterial and archaeal MAGs
- four times more phages identified
- ten times more prophages



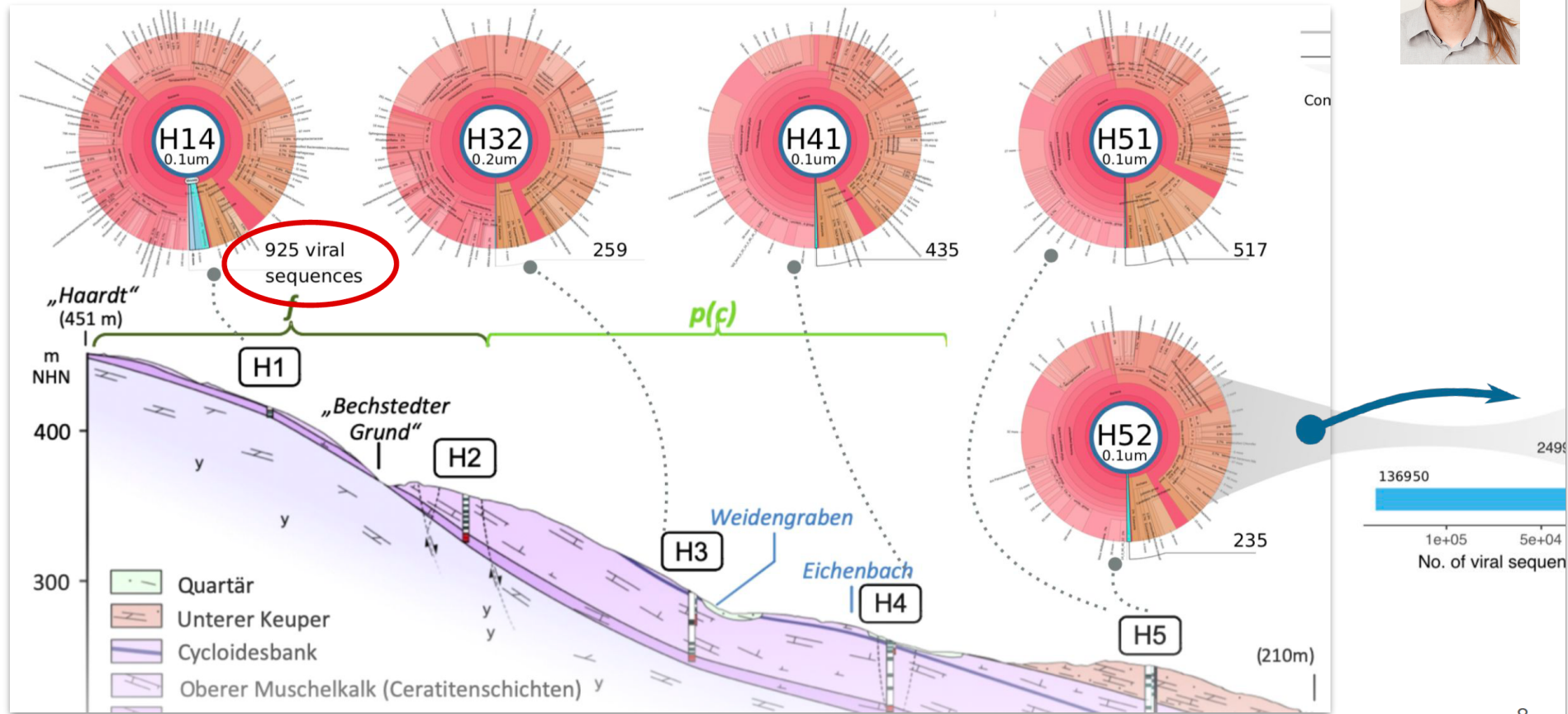
# Aquadiva

## assembly-free detection of complete viruses

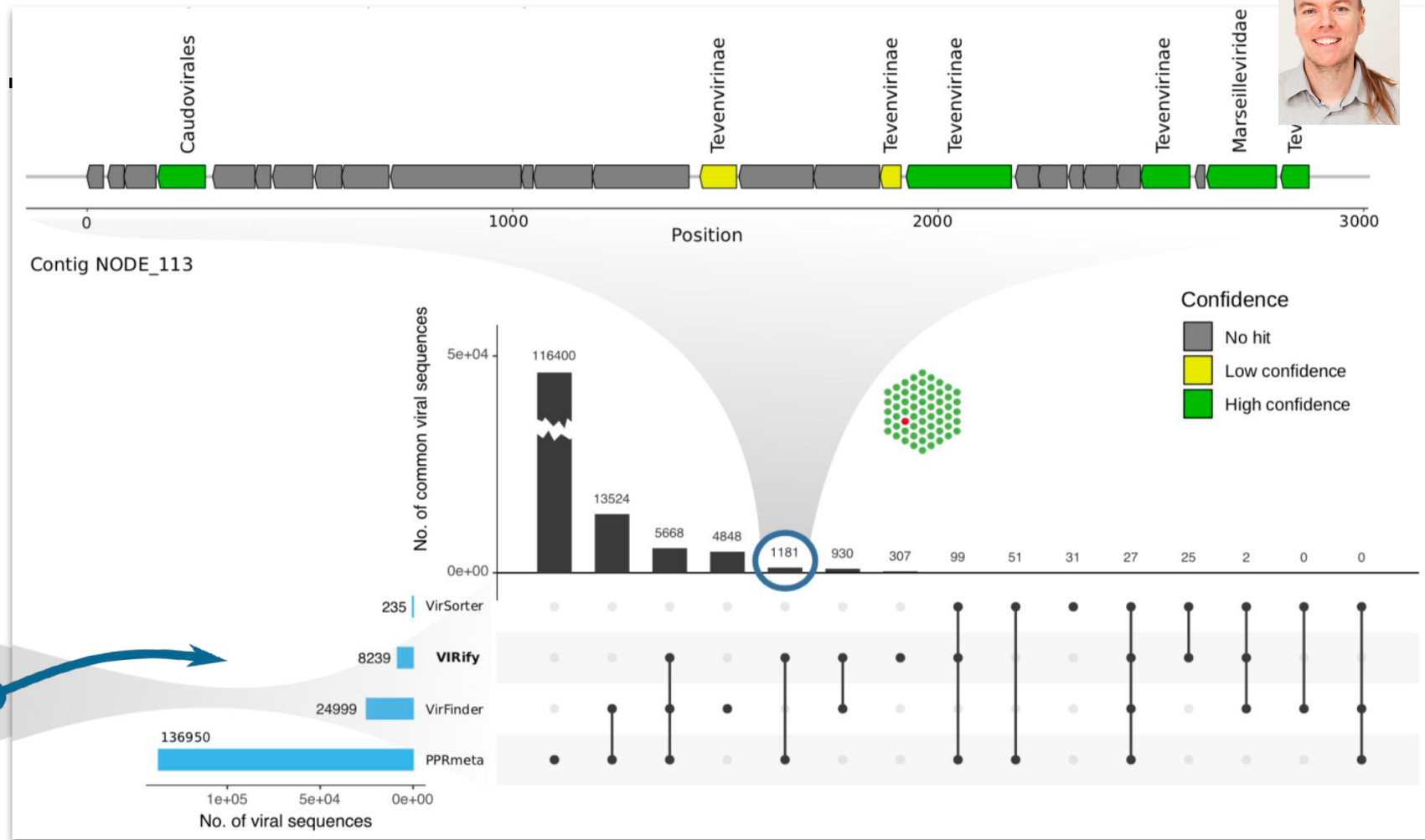
- a single nanopore read represents complete viral genome



## Longitudinal characterization of viruses using metagenome assemblies



## Specific models to confirm virus predictions





# Acknowledgements

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