



# Newly assembled bacteria and their associations with common diseases



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## EstMB cohort

### Estonian Microbiome Cohort

- 2509 oral, stool & plasma samples short reads deep sequencing (in average 56 mln reads per sample)
- + NMR metabolites data
- + Electronic Health records (EHR)

## Research goals

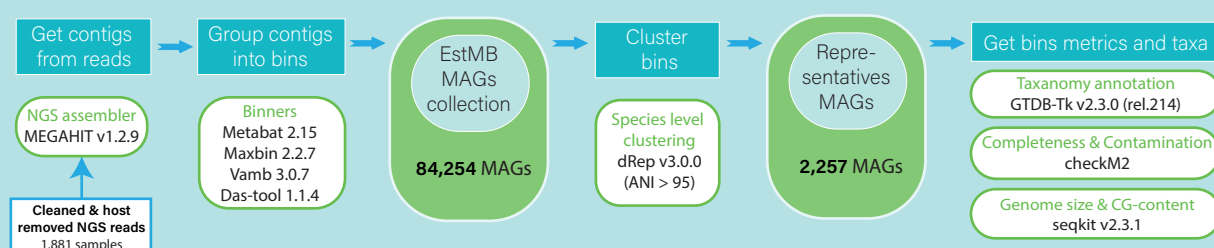
- Create a database of MAGs from the Estonian population
- Evaluate the added value of de-novo assembled MAGs compared to existing human gut databases.
- Investigate the association between the microbiome and common diseases.

## Why MAG?

### MAG - Metagenome-Assembled Genomes

Assembling microbial genomes de novo within a population cohort allows for the discovery of population-specific and new species, leading to more accurate predictions.

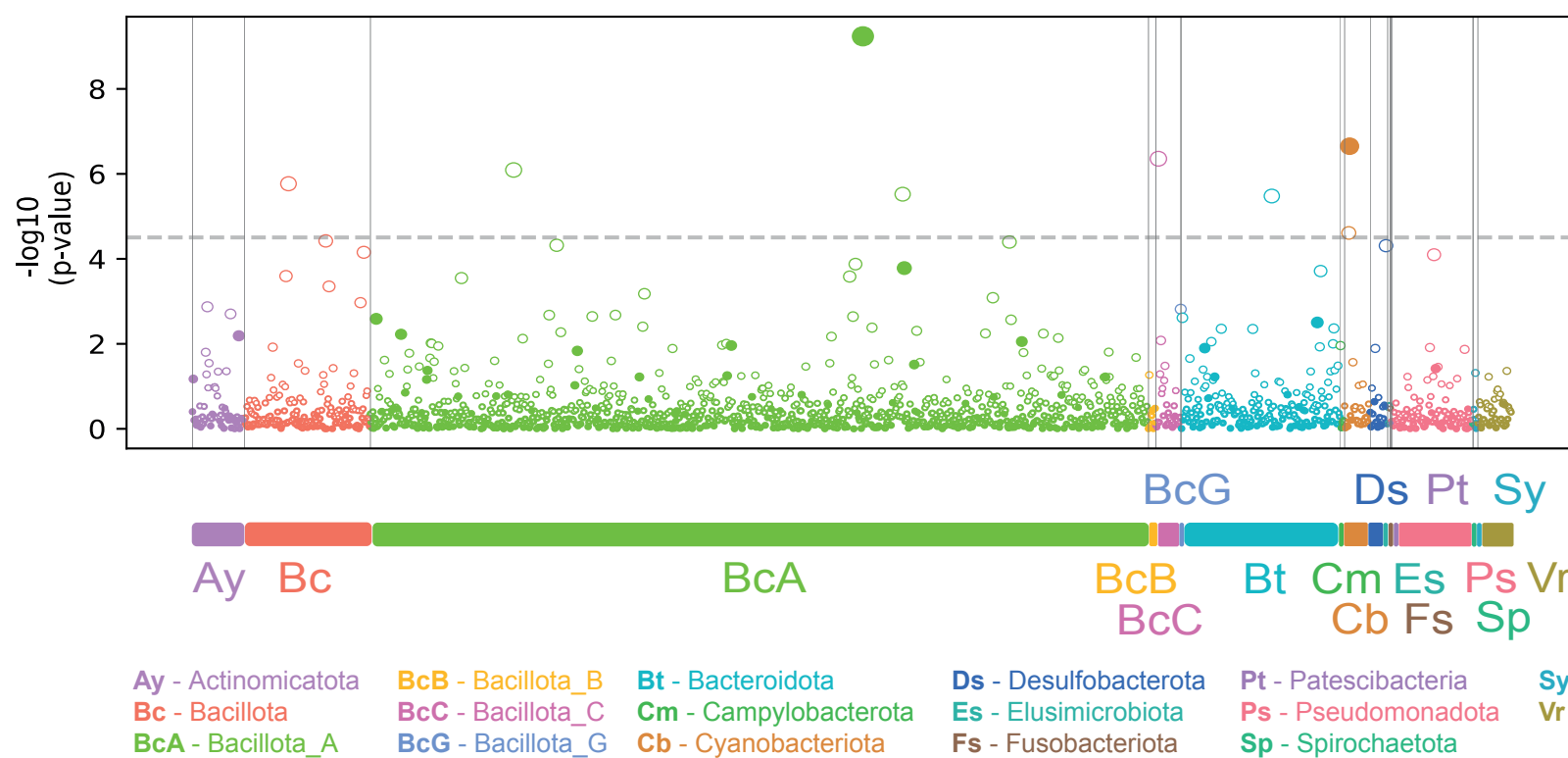
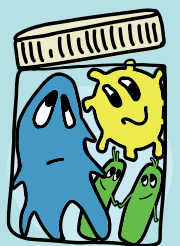
## Pipeline



## EstMB MAGs db

1881 human gut samples

- 84 254 MAGs
- 2 257 species including 353 new species



**Heart failure**  
(ICD10 code I50)  
cases: 102  
controls: 1768

Results: Metagenome-wide association between the abundance of gut bacterial species and Heart failure disease

## Conclusion

- Here we present a collection of MAGs retrieved from 1,881 samples of the Estonian population (EstMB MAGs db)
- We have assembled 84,254 MAGs representing 2,257 species. This population-specific reference set contains 353 MAGs (15,6%) of potentially new species.
- We demonstrated the value of de novo assembly of bacterial genomes by performing associations with diseases and found 44 significant associations with 15 phenotypes for 41 unique bacterial species (including 9 new species).

## Call for actions

Interested in learning more about this research?  
**Check out my GitHub:**  
[https://github.com/Chartiza/EstMB\\_MAGs\\_db\\_paper](https://github.com/Chartiza/EstMB_MAGs_db_paper)

Have a microbiome cohort and want to collaborate?  
**Reach me at:** Email: [pantiukh@ut.ee](mailto:pantiukh@ut.ee)  
Twitter: @KPantiukh

Curious about other work from our group?  
Look for posters with the **Tartu Microbiome logo!**