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## Implementation of a Nanopore metagenomic workflow for time-series of complex microbial communities: MAG catalog and functional annotation.

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### ► To cite this version:

Cédric Midoux, Chrystelle Bureau, Baptiste Quentin, Olivier Chapleur. Implementation of a Nanopore metagenomic workflow for time-series of complex microbial communities: MAG catalog and functional annotation.. MICROBES symposium, Sep 2022, Orsay, France. . hal-03765009

**HAL Id: hal-03765009**

**<https://hal.inrae.fr/hal-03765009>**

Submitted on 1 Sep 2022

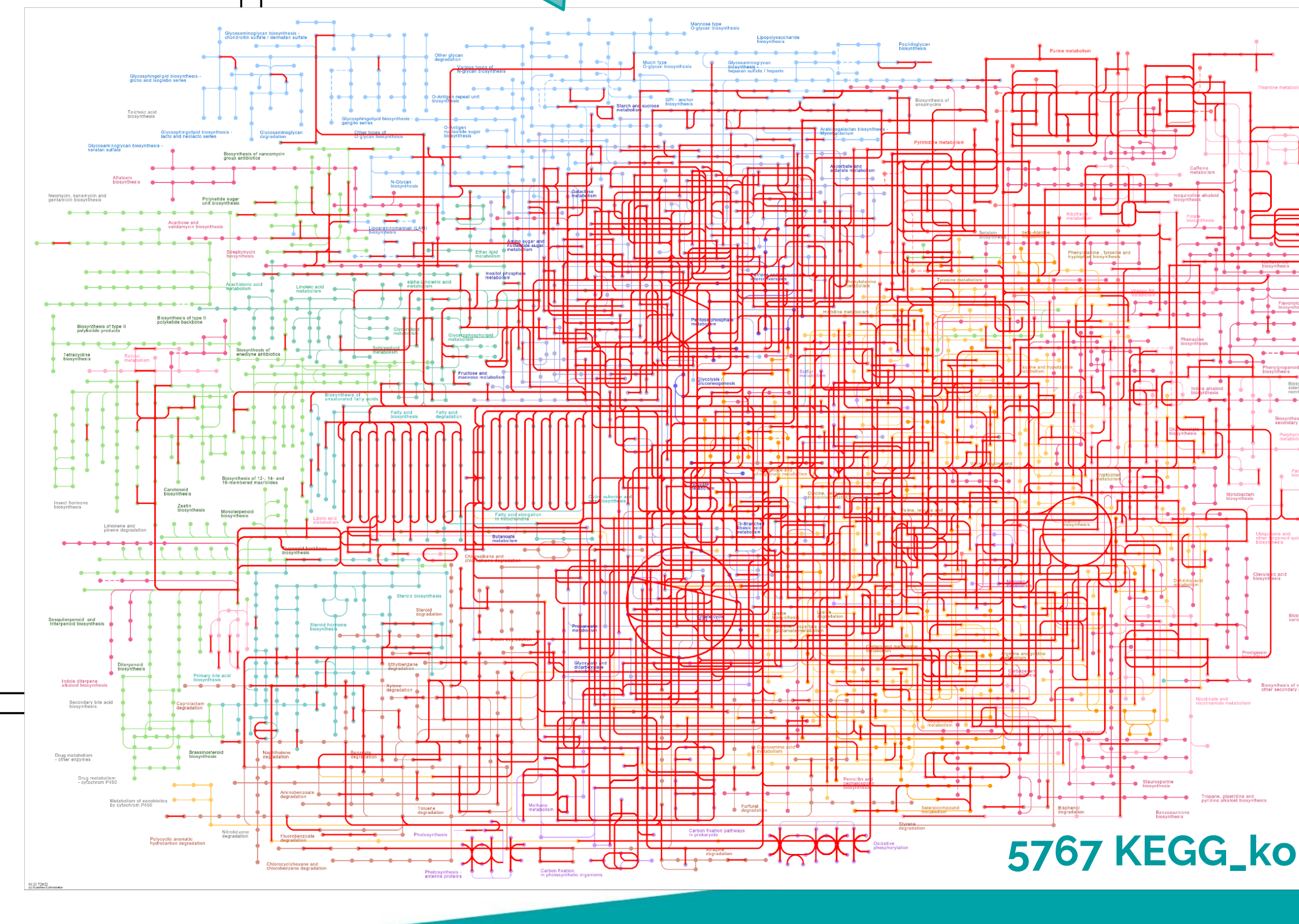
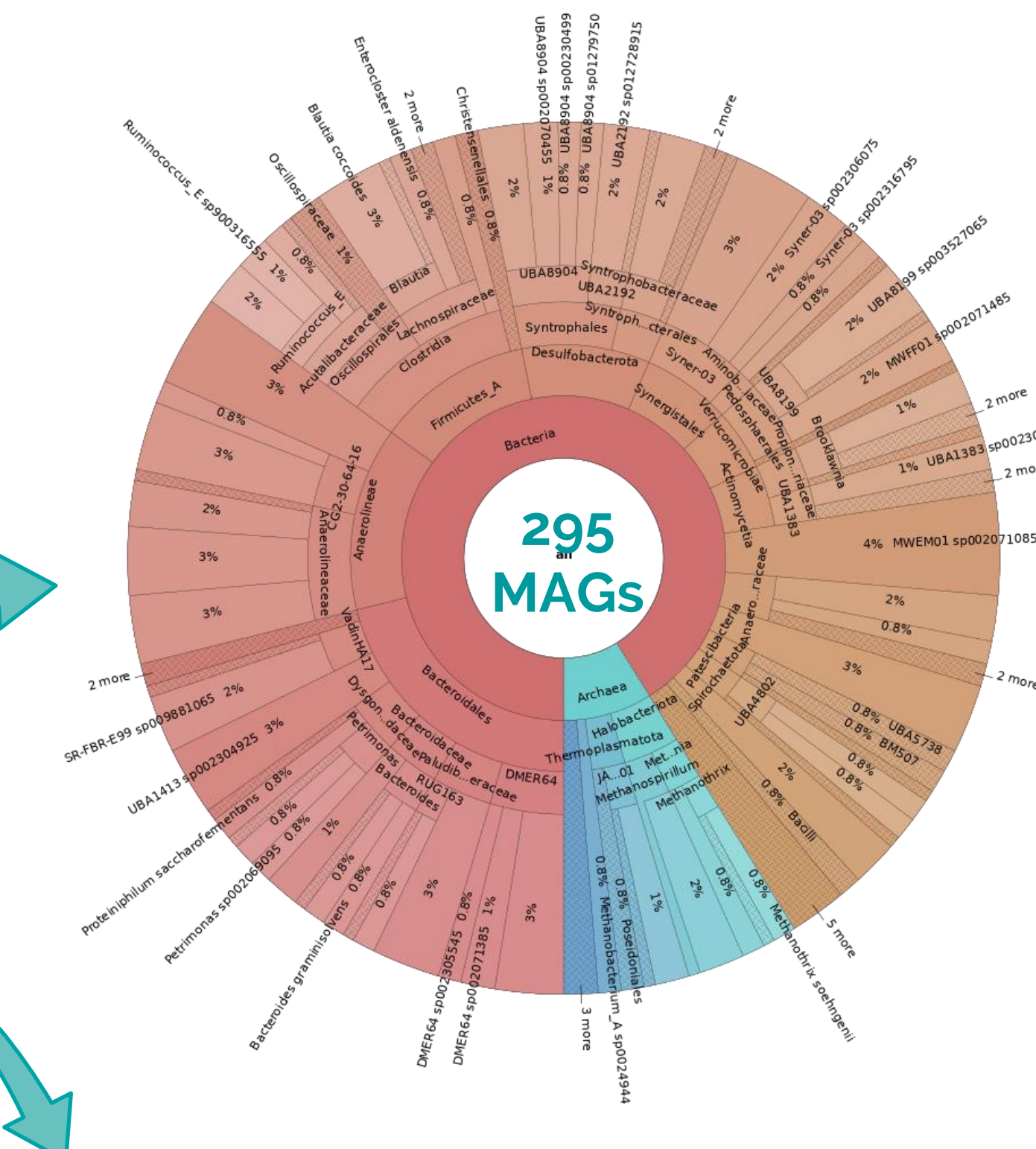
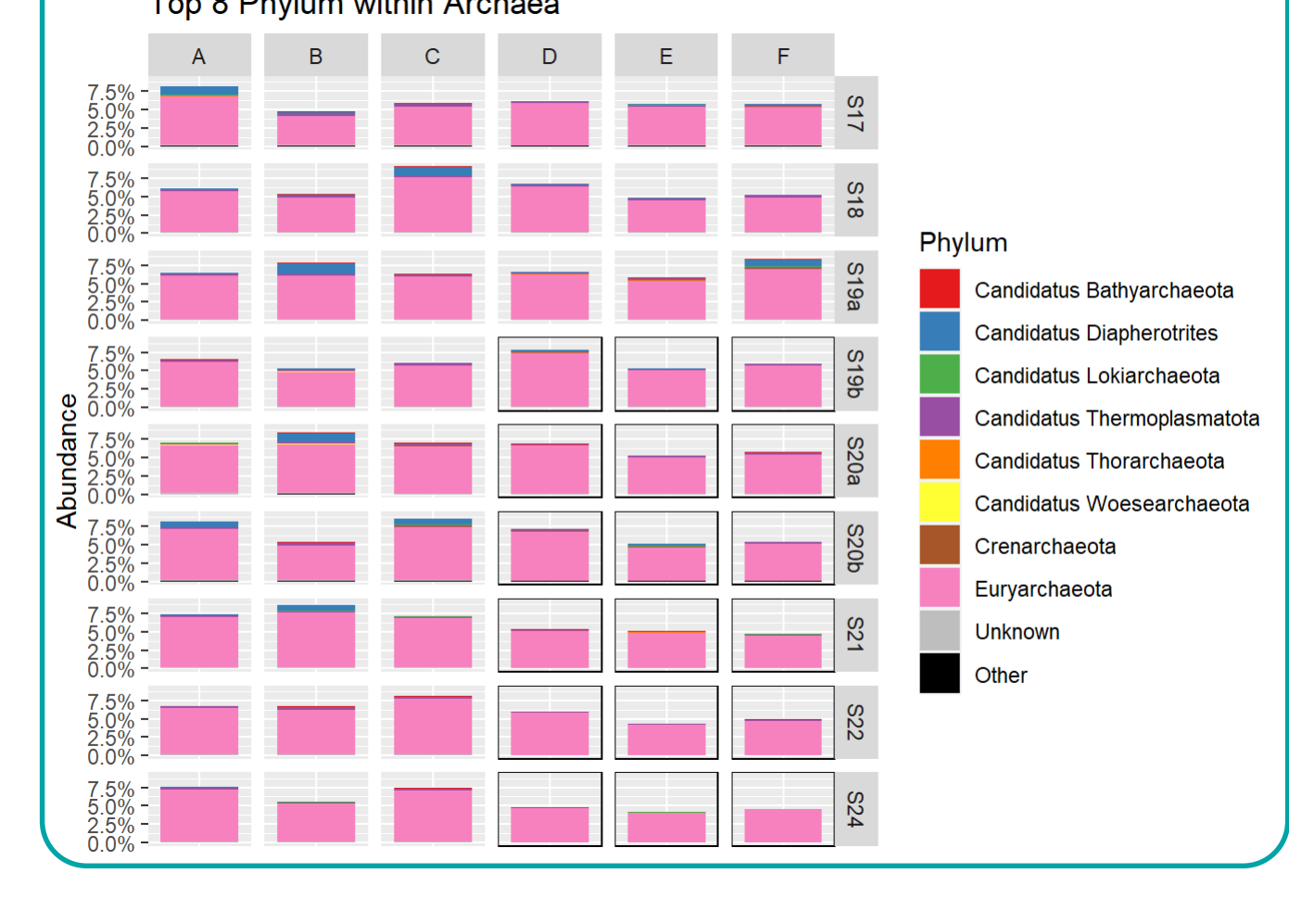
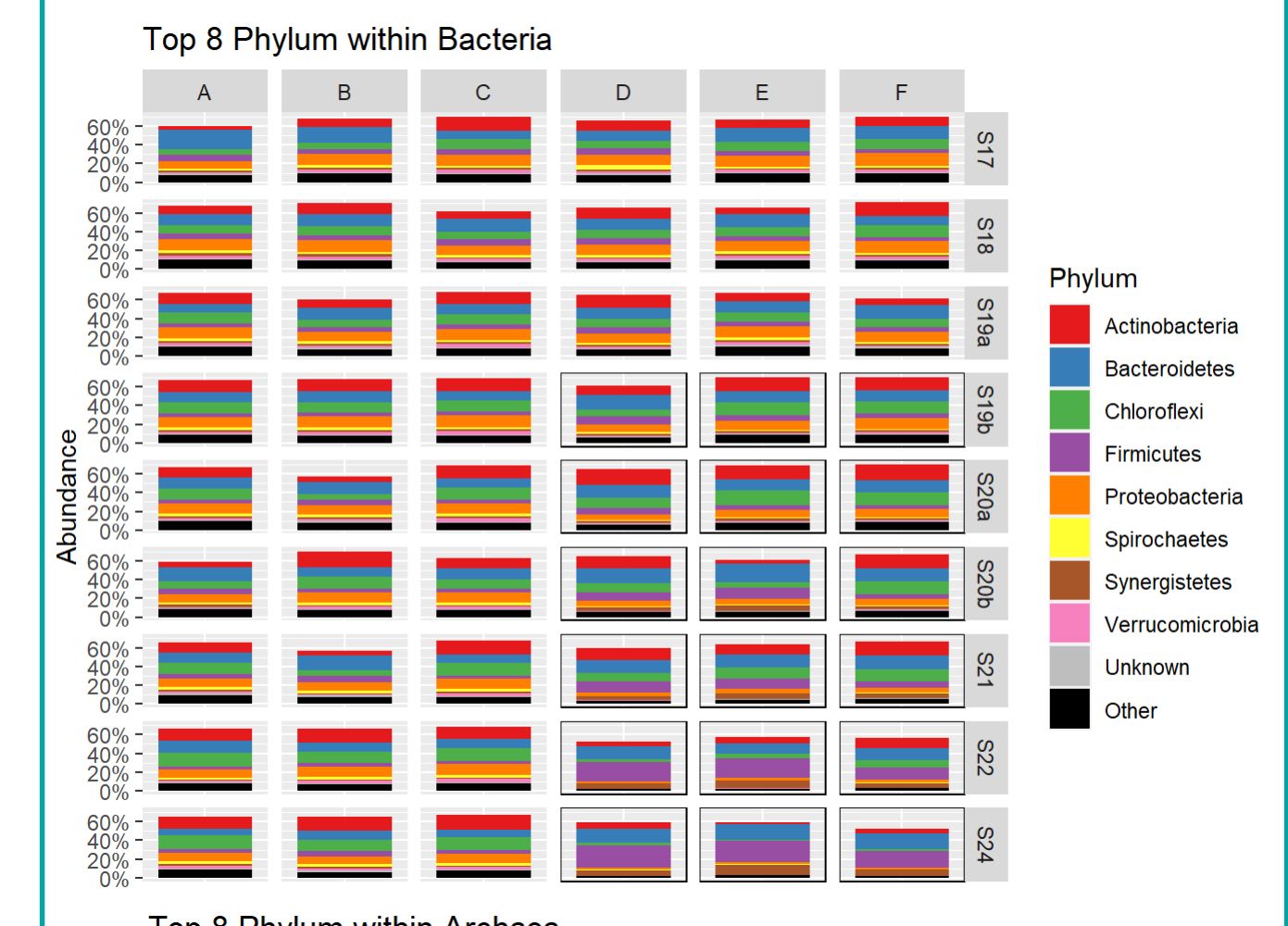
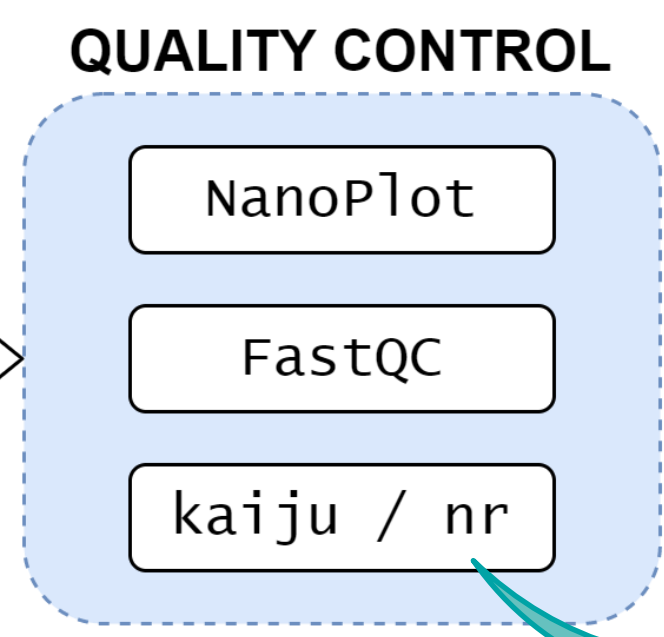
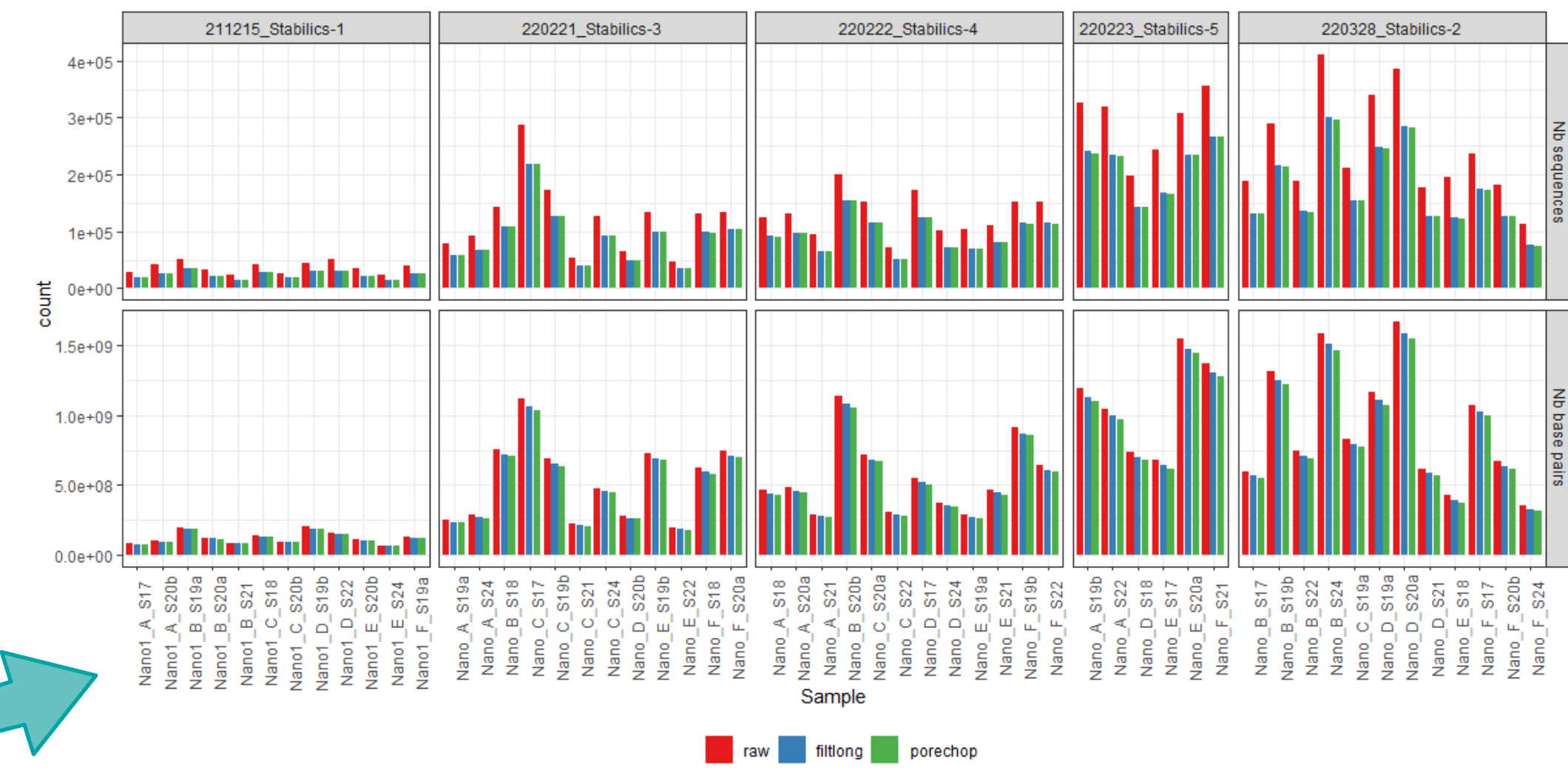
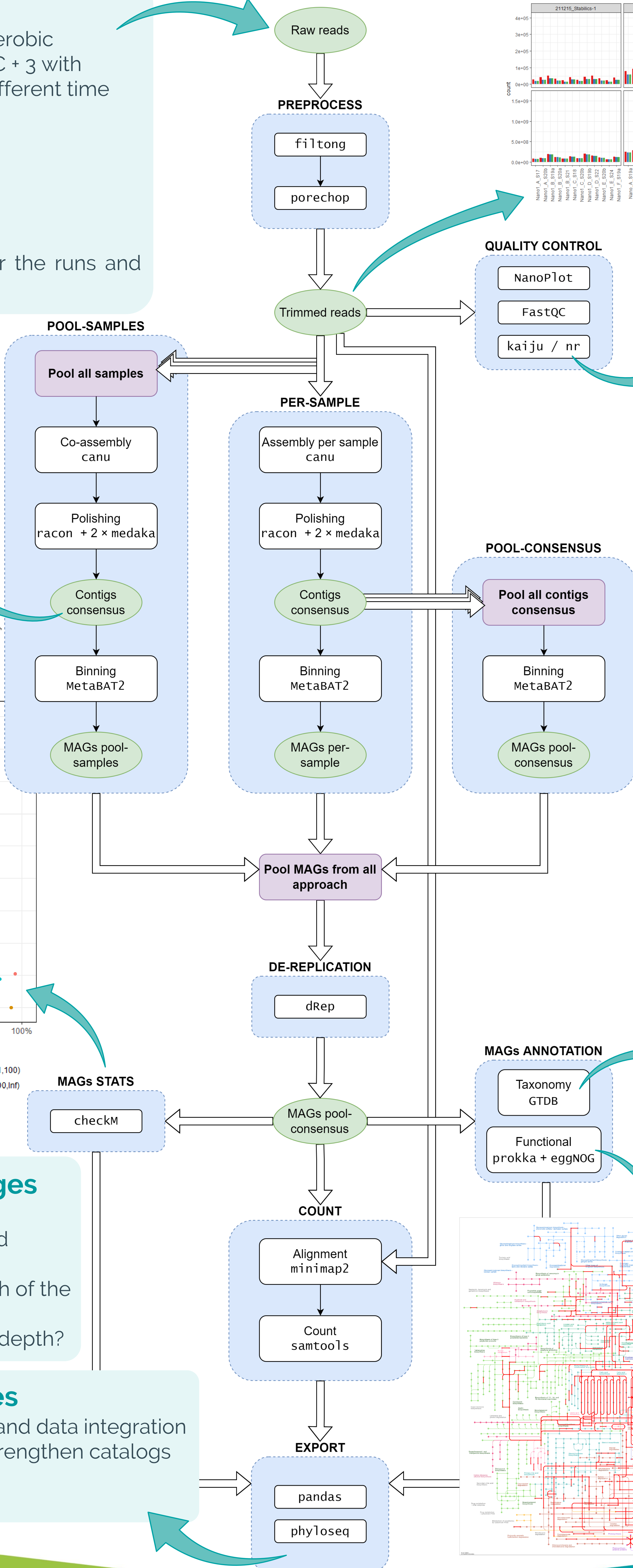
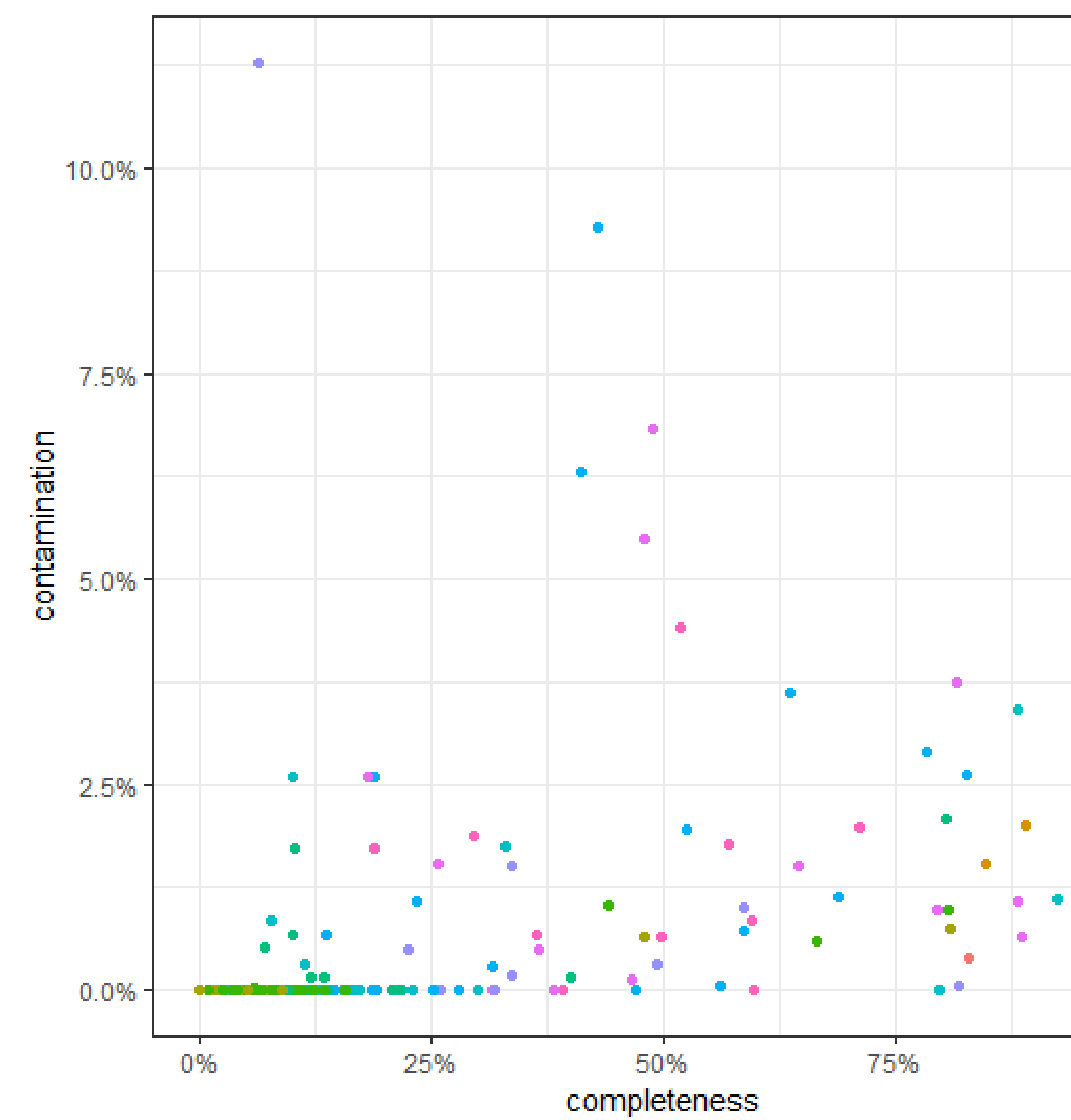
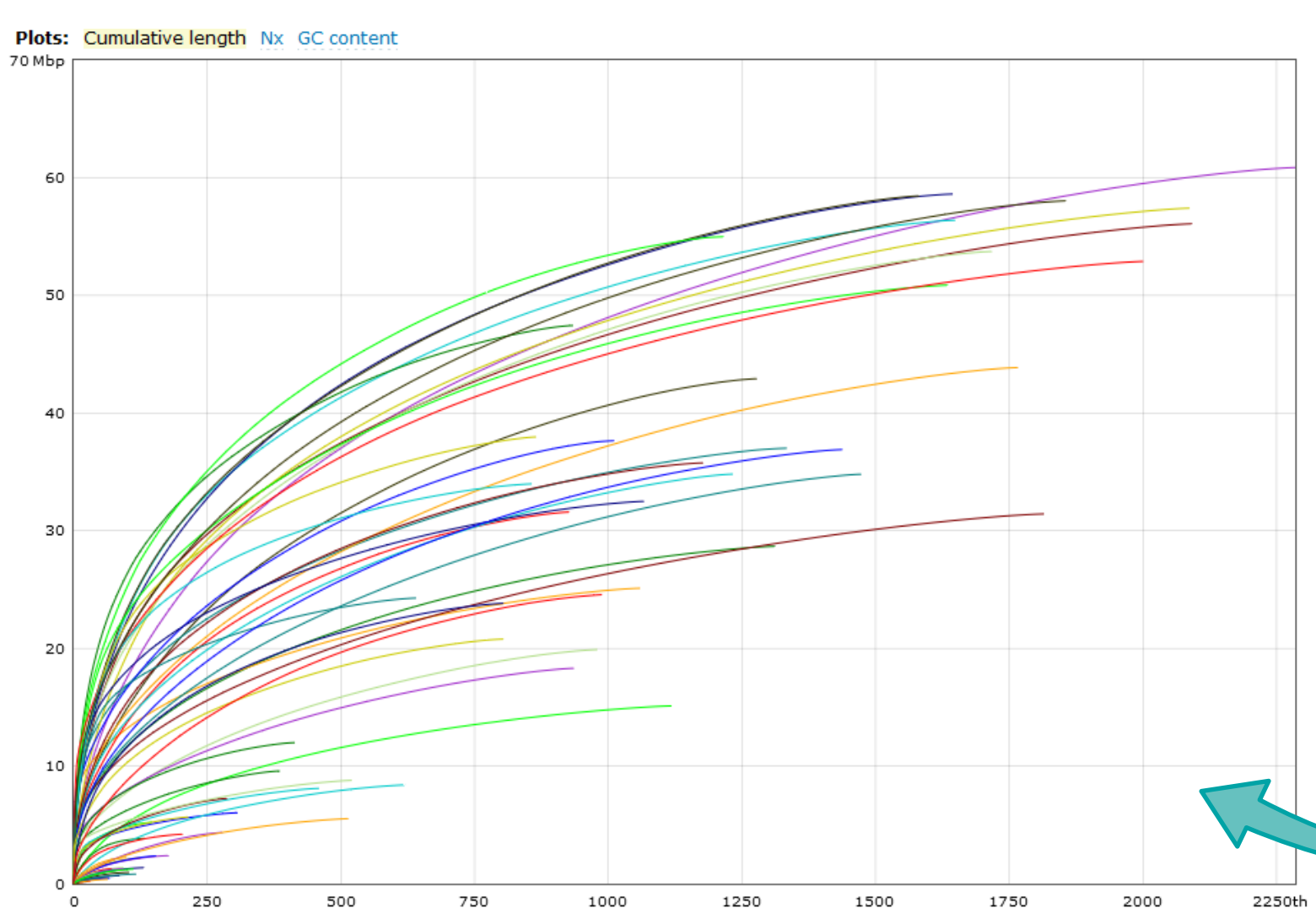
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## ➤ Data

- Samples come from 6 anaerobic digesters (3 controls: A, B, C + 3 with perturbation: D, E, F) at 9 different time points (n = 54)
- Lab-made sequencing :
  - MinION Mk1C
  - Flow-cells R9.4.1
  - Rapid Barcoding Kit
  - Multiplexing
- Throughput increases over the runs and our experience



## ➤ Statistical Challenges

- How to normalize count?
- Are reads correctly distributed between MAGs?
- Should we consider the length of the reads for normalization?
- Which effects of sequencing depth?

## ➤ Perspectives

- Statistical analysis and data integration
- Add new data to strengthen catalogs
- Workflow sharing
- Publications ...

