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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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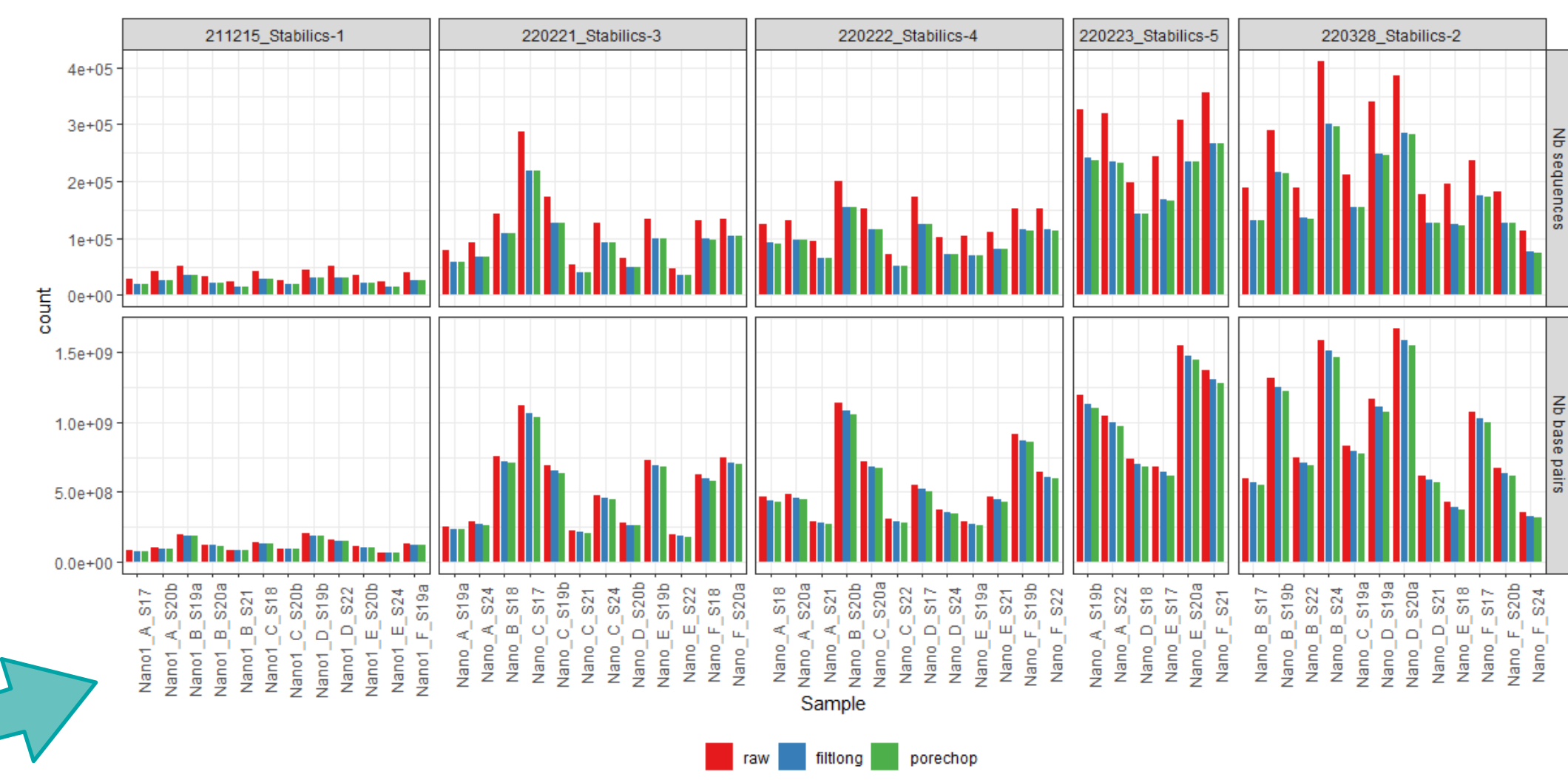
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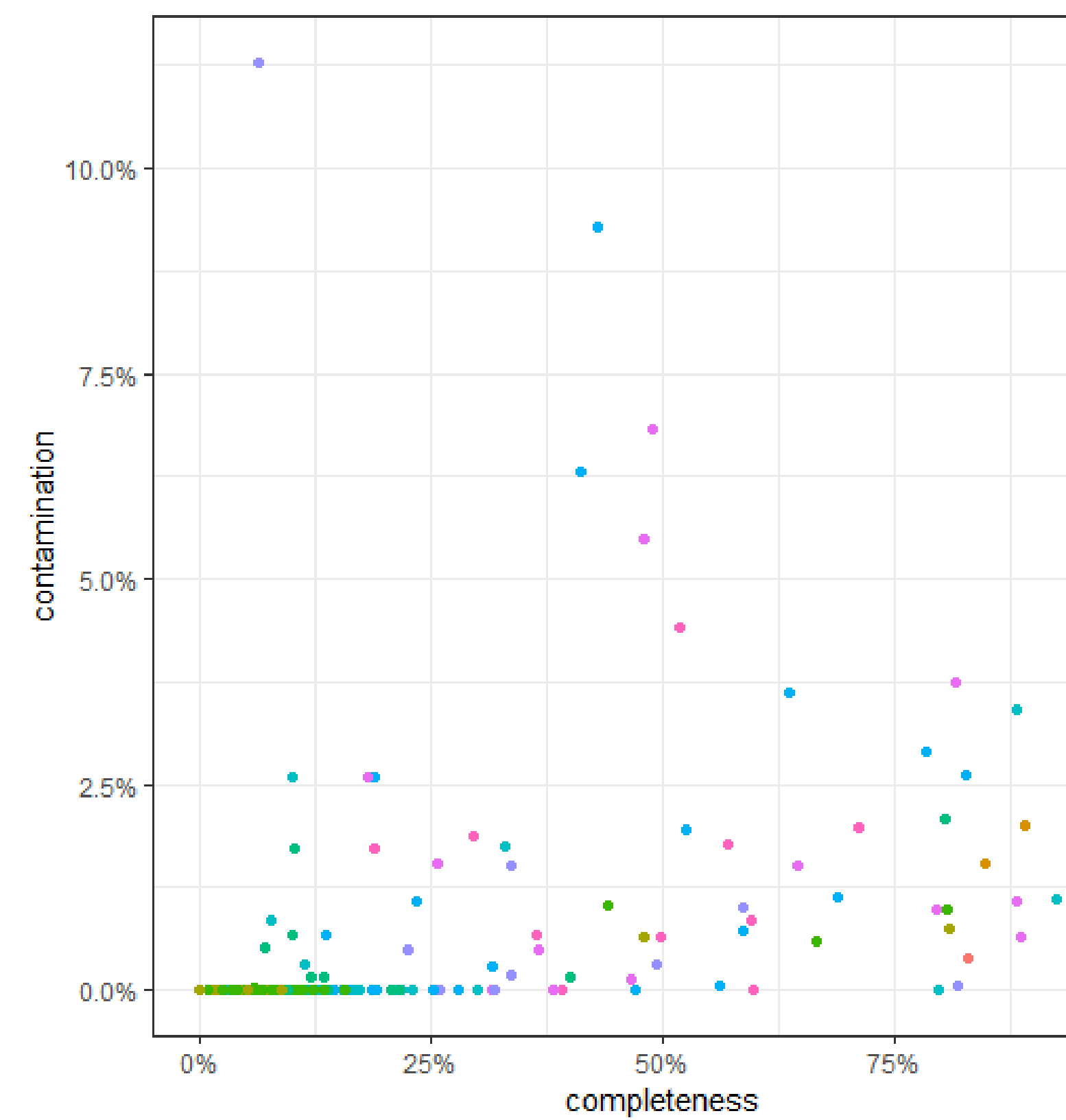
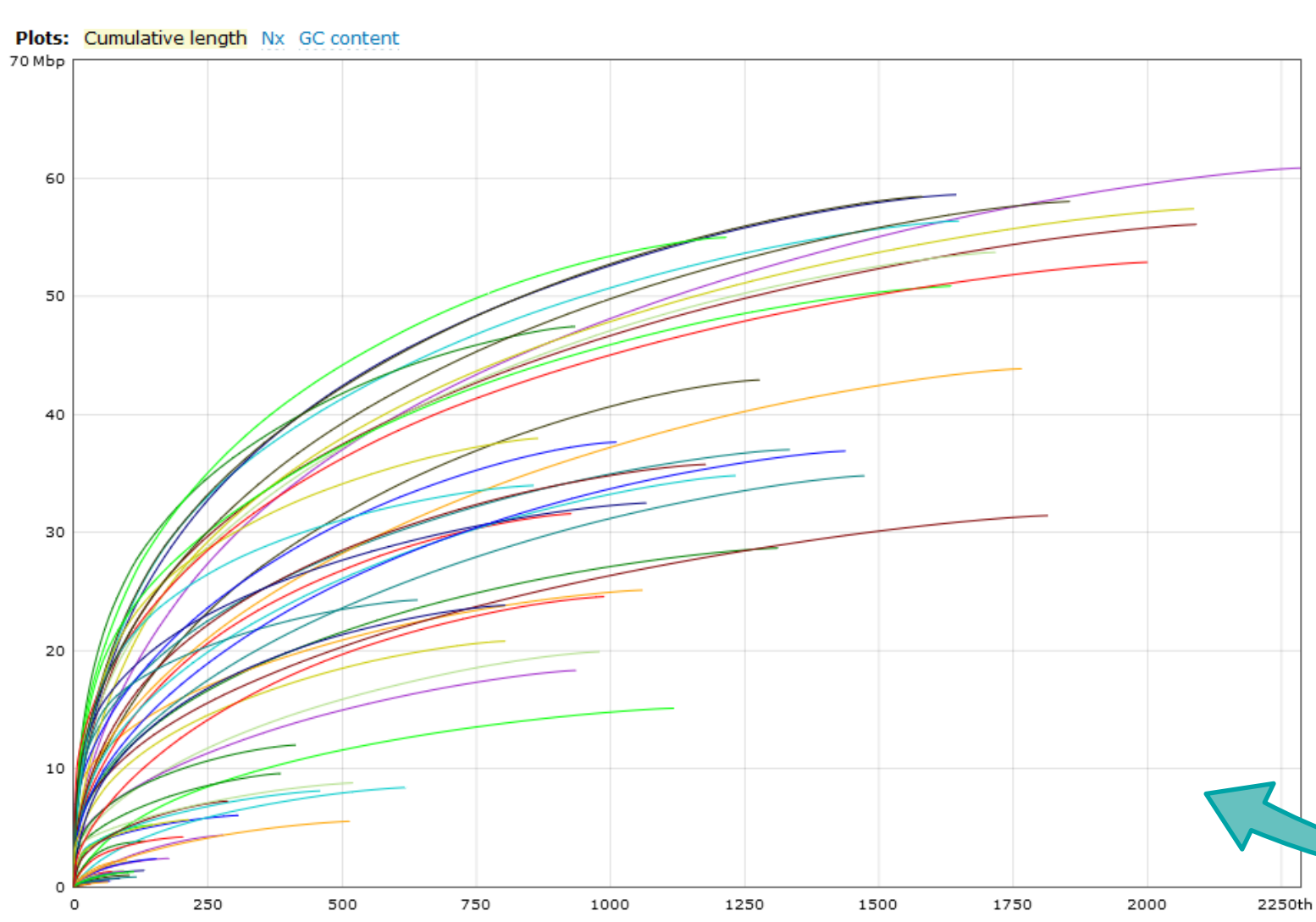
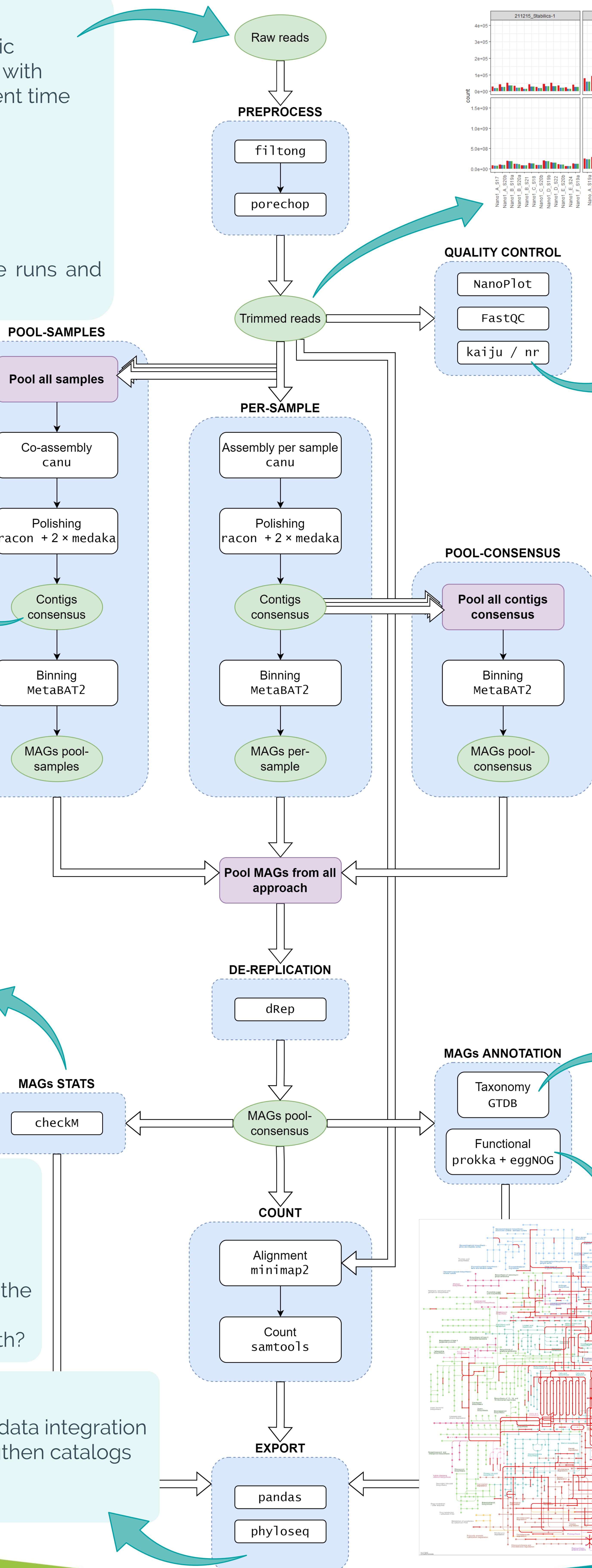
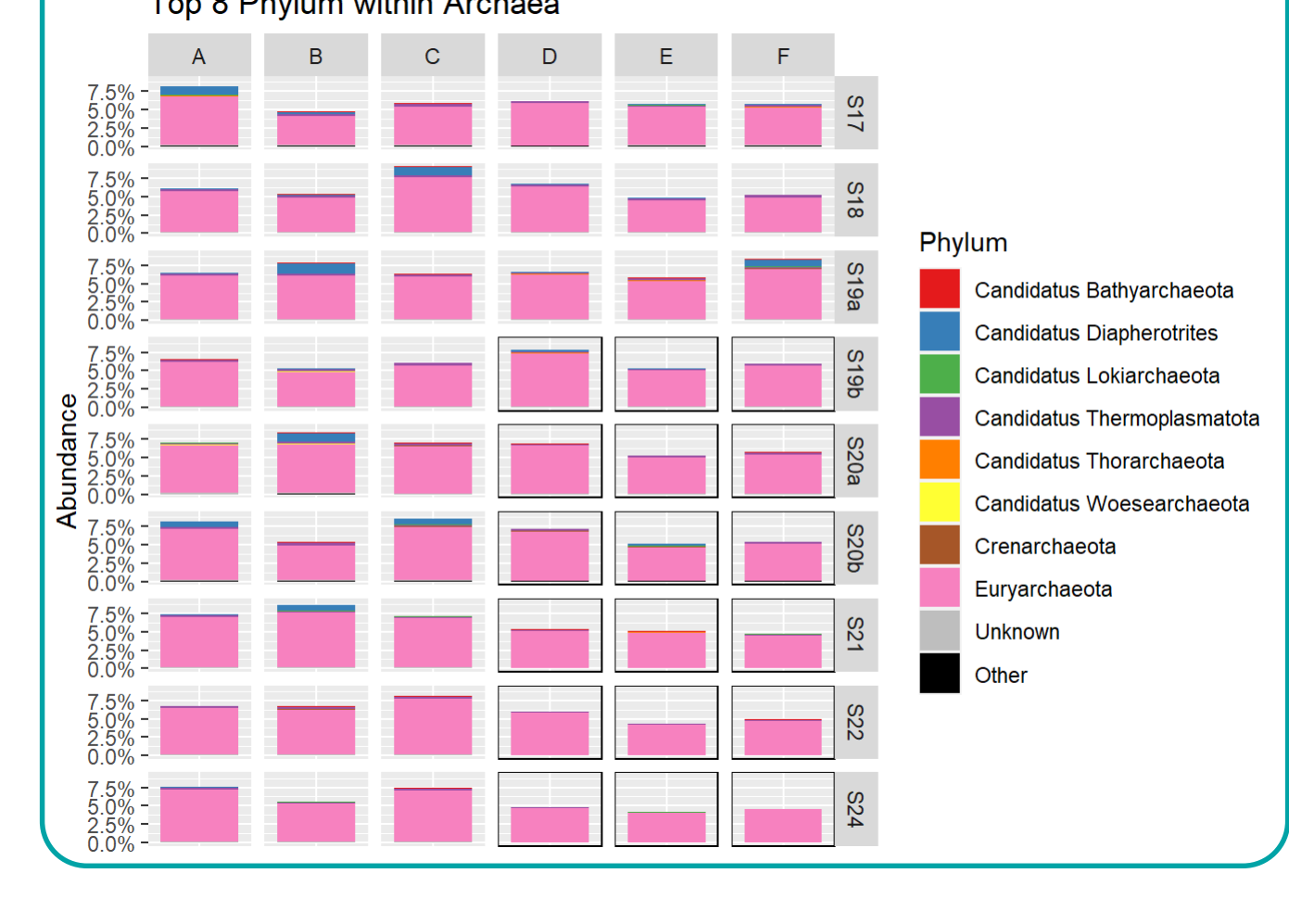
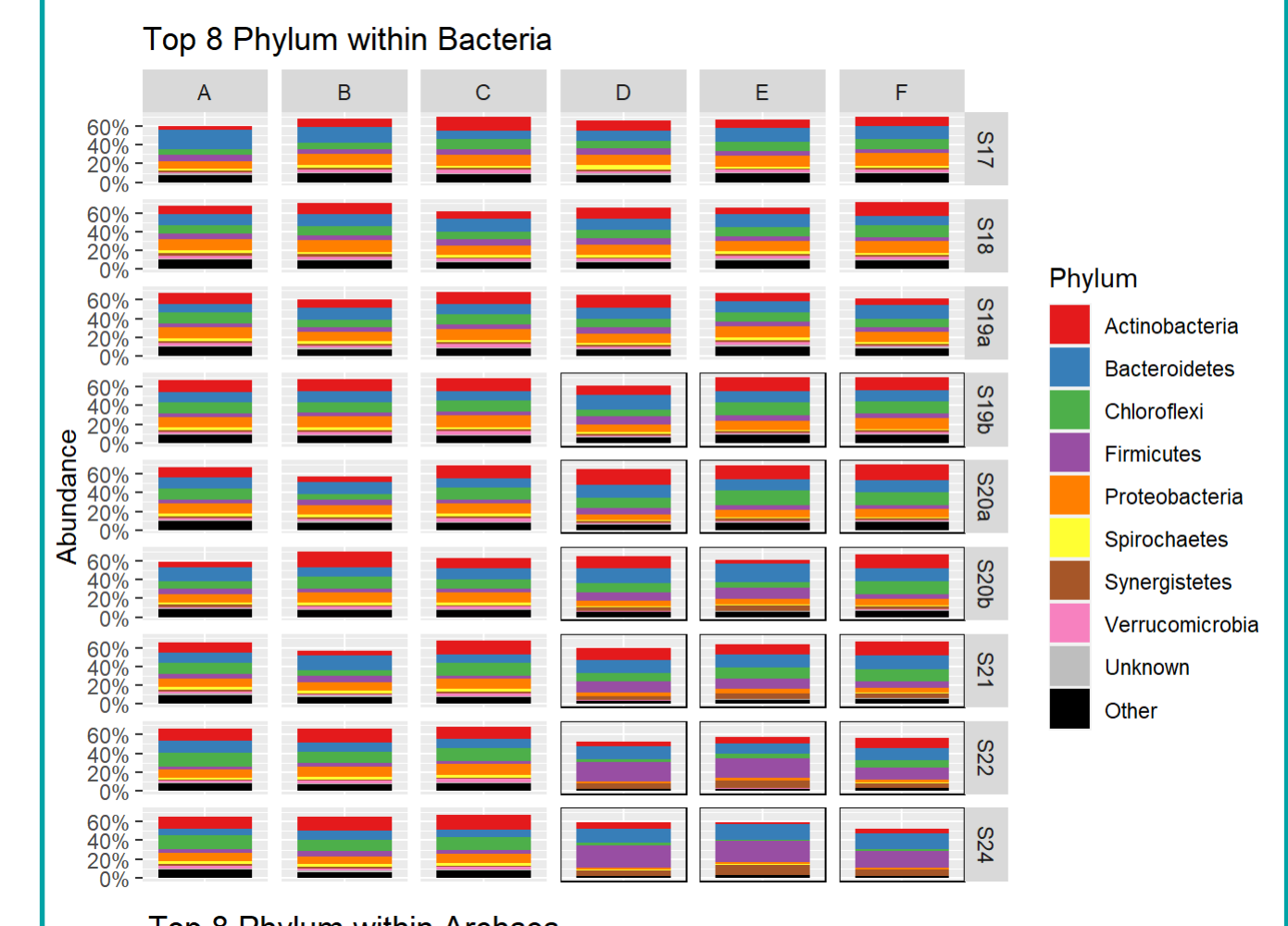
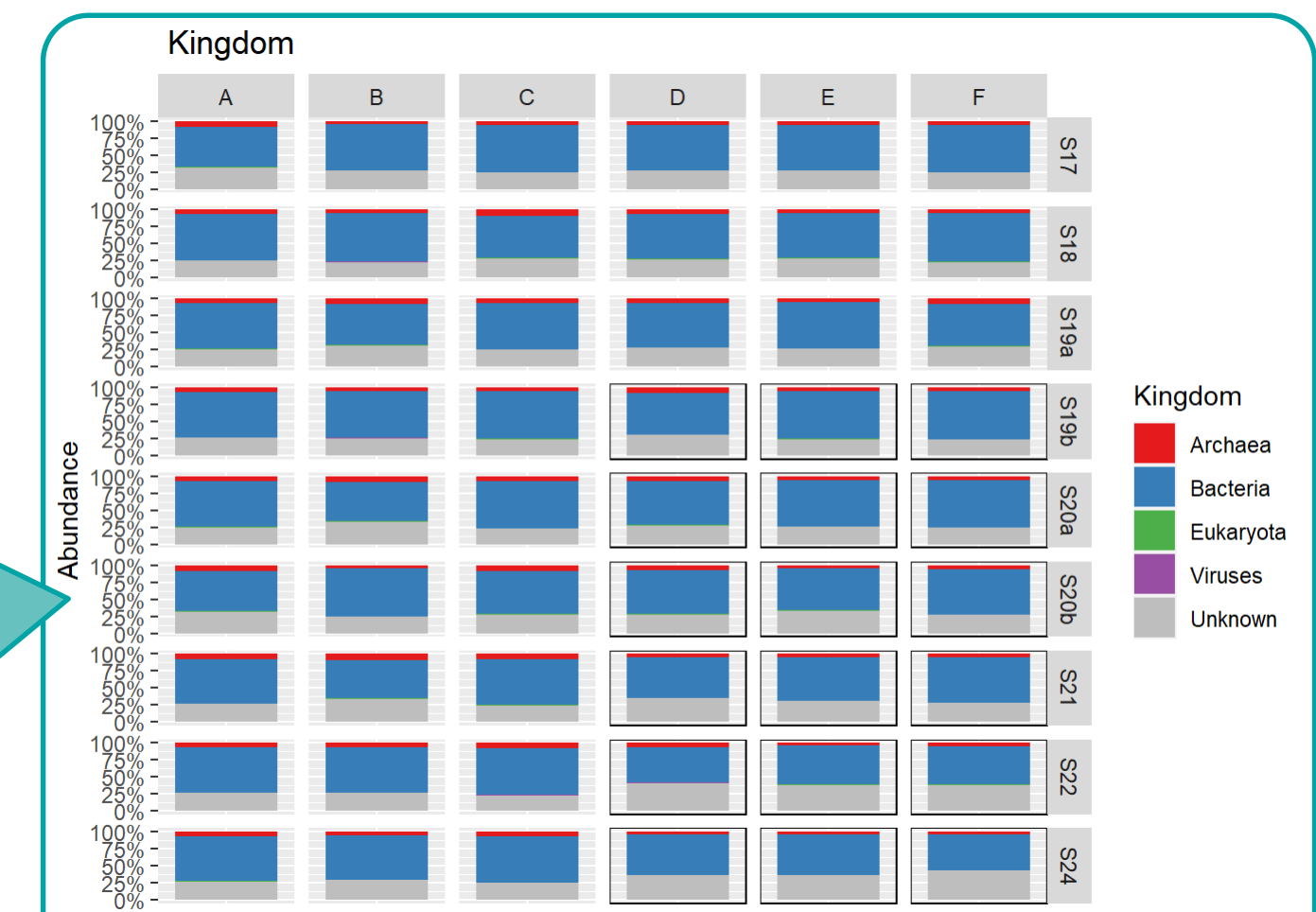
➤ Data

- 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



QUALITY CONTROL

- NanoPlot
- FastQC
- kaiju / nr



- MAGs STATS**
- Nb contigs: [1,4], [9,16], [25,36], [49,64], [81,100], [4,9], [16,25], [36,49], [64,81], [100,Inf]

➤ 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 ...

