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# Identification of genomic regions for high-resolution taxonomic profiling using long-read sequencing technology

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## Taxonomic profiling: who is in the community?

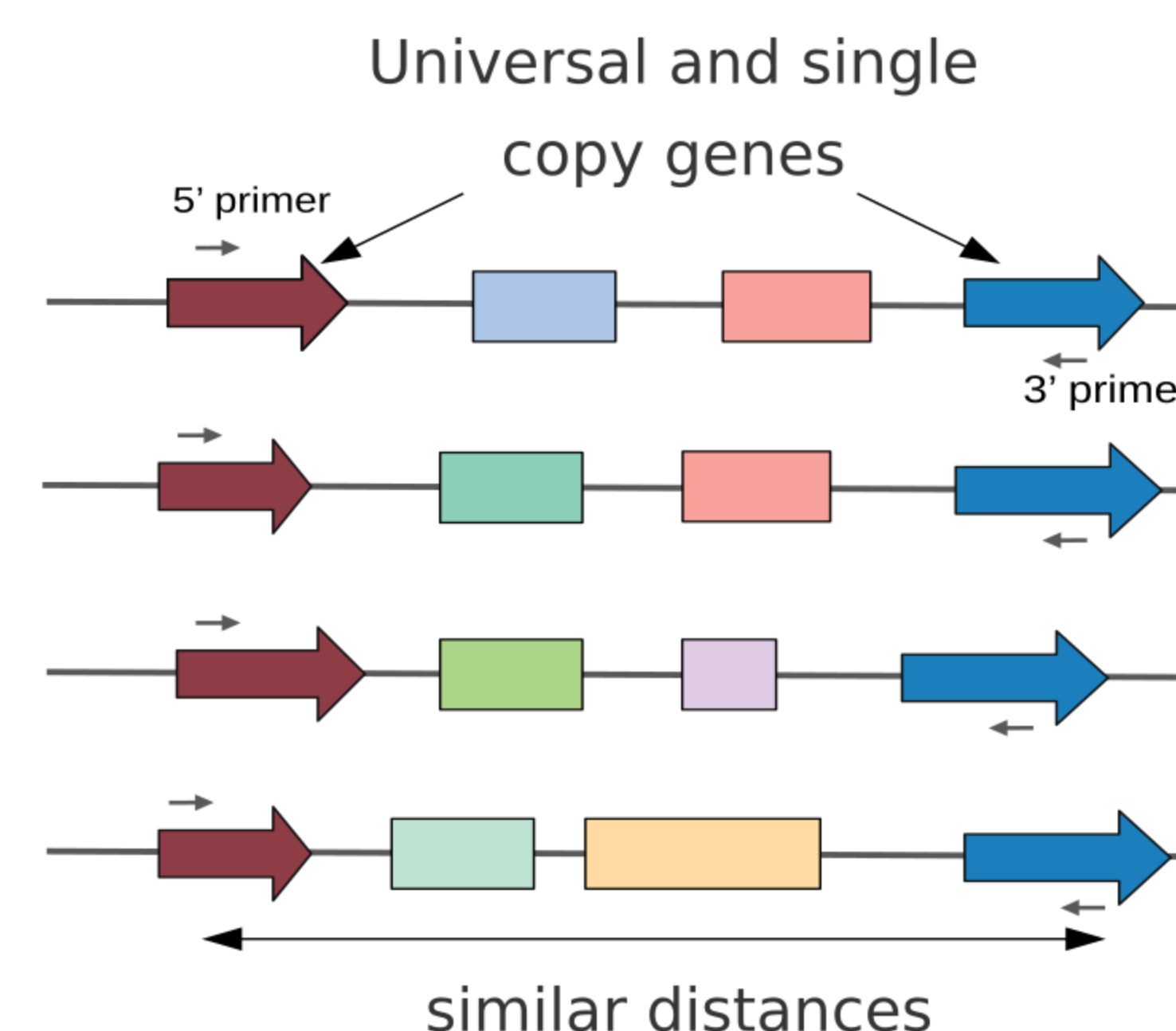


**The widespread MiSeq illumina amplicon sequencing approach:** Target a small part of the 16S RNA gene or alternative markers (rpoB, recA and gyrB) [1].

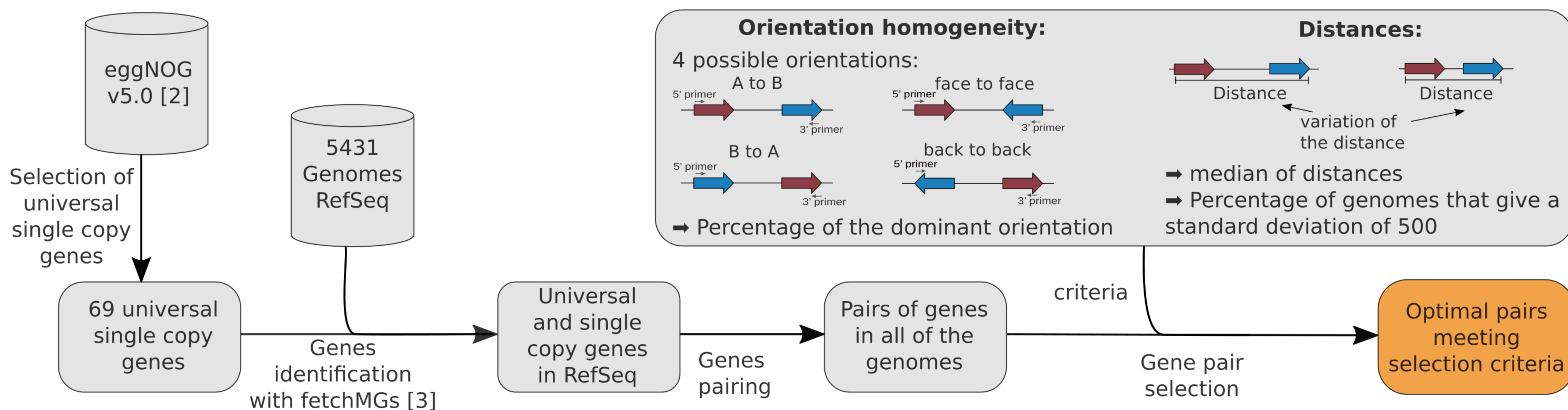
**Limits of the approach:**

- Amplicon size of around 450pb
- Poor resolution for closely related organisms
- Multicopy affects the abundance estimation

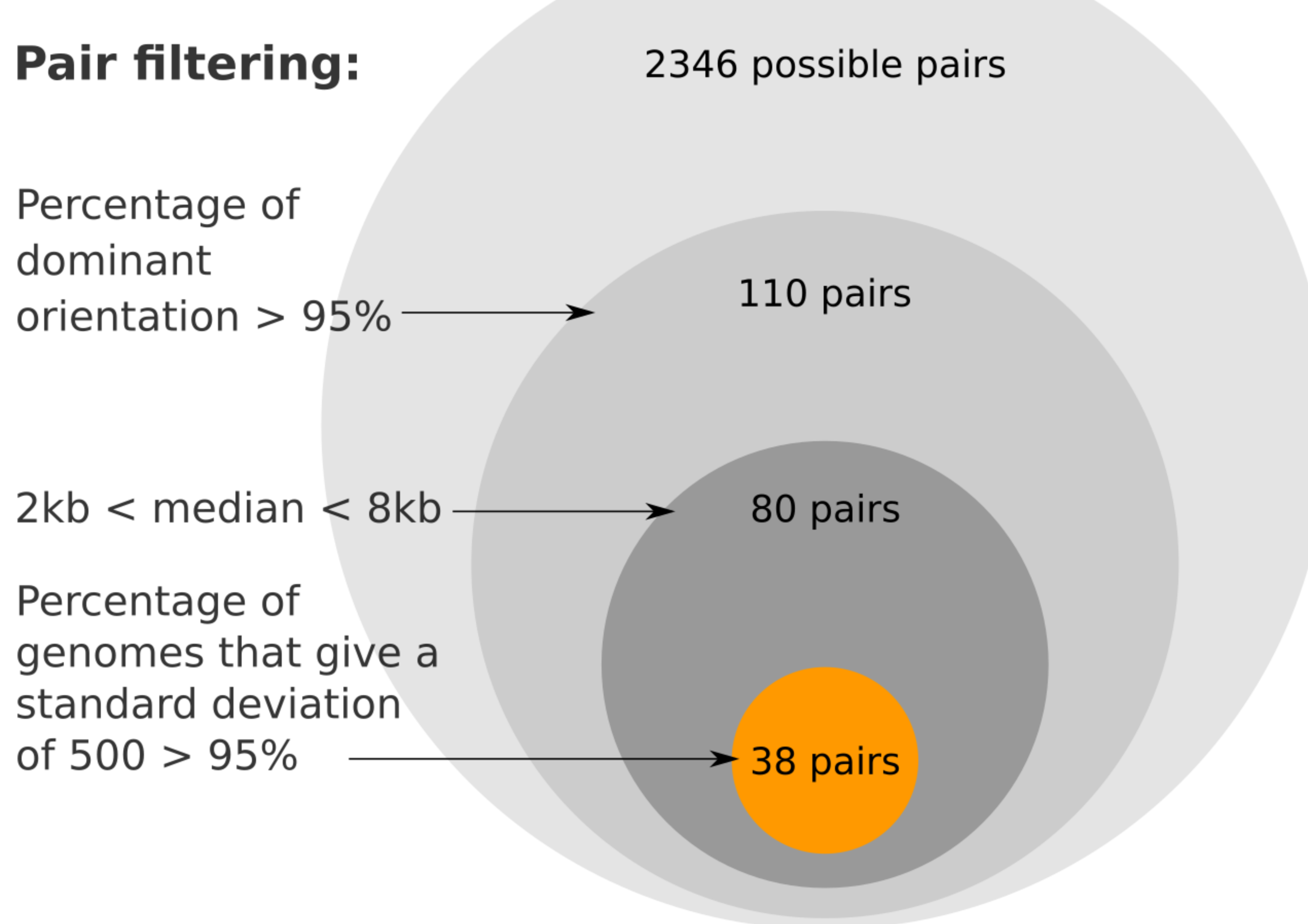
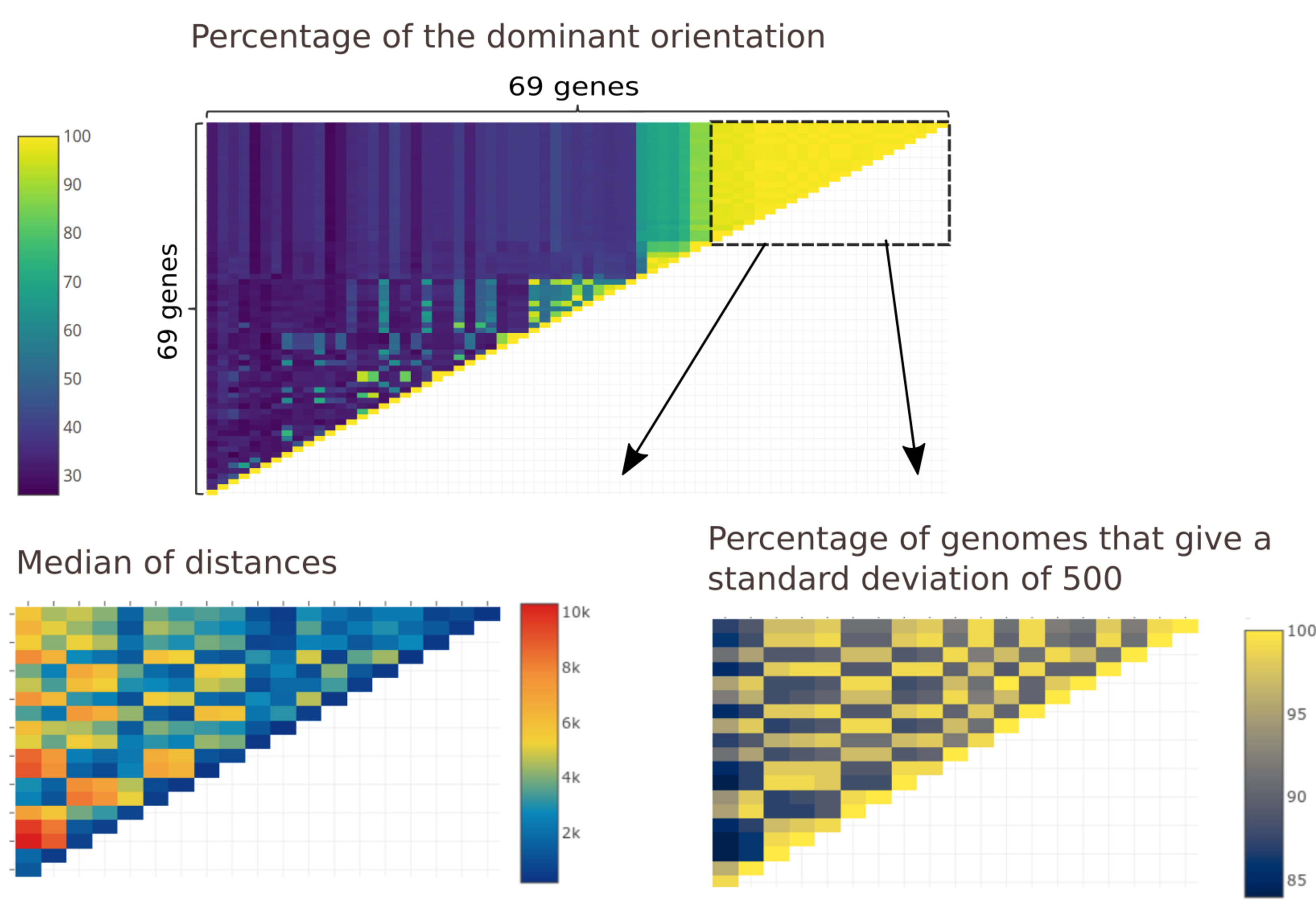
**Our strategy using long read approach with Oxford Nanopore Technologies:** Identify genomic regions bounded by two universal and single copy genes.



## Genomic regions identification workflow



## Optimal pair selection



## Conclusion and perspectives

Our approach enables the identification of several pairs of genes found in **single copy** and displaying **consistent distances and orientations** across bacterial genomes. These pairs are very promising targets to enhance taxonomic profiling with long read sequencing technologies.

**The next steps of the project are:**

- ➔ Investigate how well these regions can discriminate closely related organisms.
- ➔ Design primers in order to amplify the chosen regions.
- ➔ Test out the chosen regions in a wet lab experiment on a real microbial community.

[1] Poirier, Simon, et al. "Deciphering intra-species bacterial diversity of meat and seafood spoilage microbiota using gyrB amplicon sequencing: A comparative analysis with 16S rDNA V3-V4 amplicon sequencing." PloS one 13.9 (2018): e0204629.  
 [2] Huerta-Cepas, Jaime, et al. "eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses." Nucleic acids research 47.D1 (2018): D309-D314.  
 [3] Milanese, Alessio, et al. "Microbial abundance, activity and population genomic profiling with mOTUs2." Nature communications 10.1 (2019): 1014.