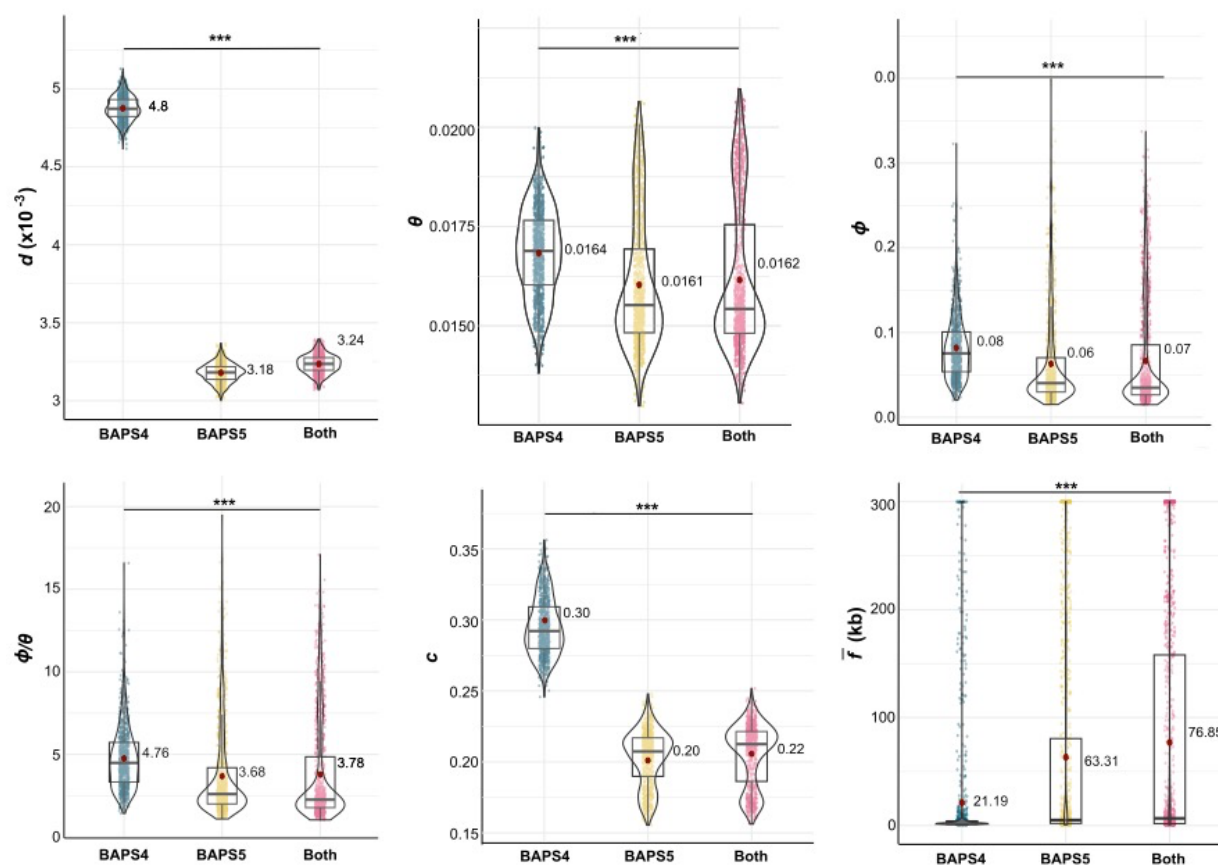


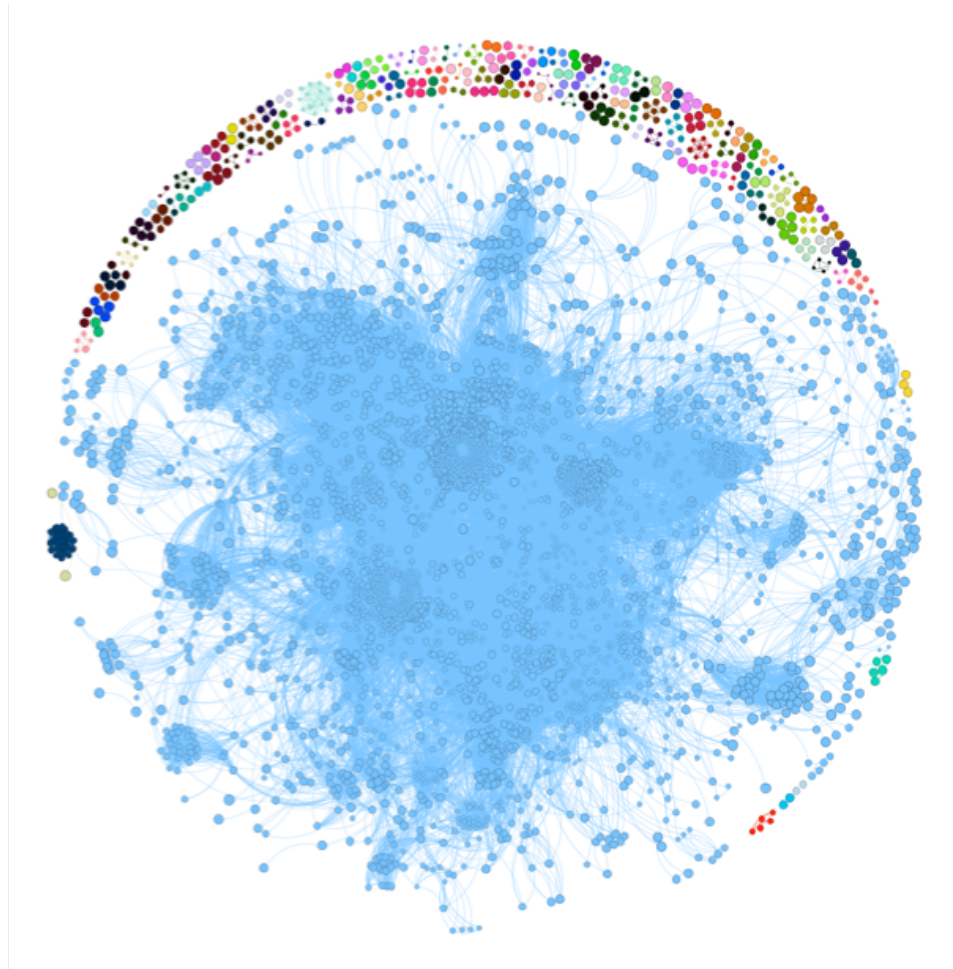
## Supplementary figures

### Heterogeneity in recombination rates and accessory gene co-occurrence distinguish *Pseudomonas aeruginosa* phylogroups

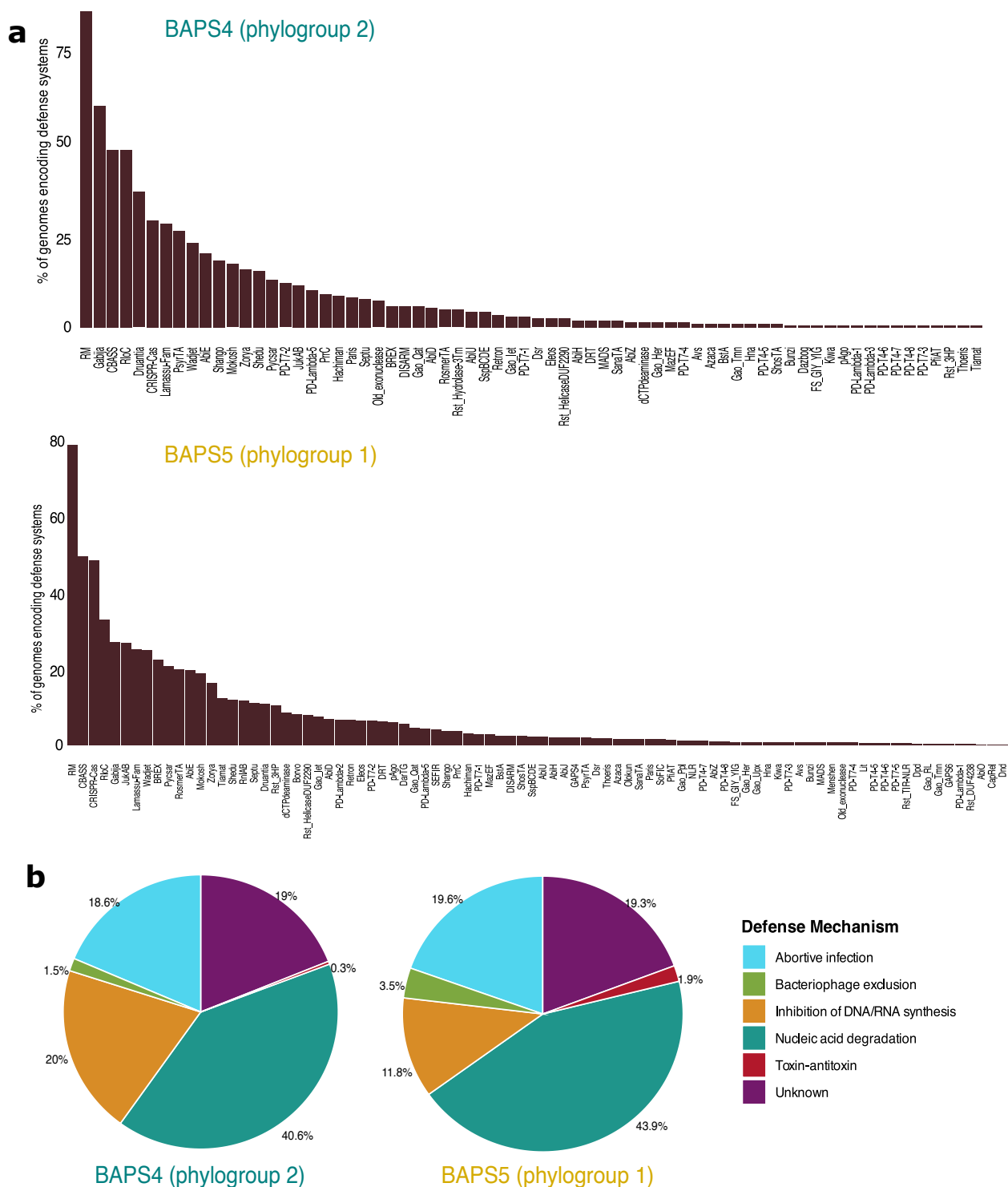
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Supplementary Figure S1. Comparison of recombination parameters in phylogroup 1 (BAPS5) only, phylogroup 2 (BAPS4) only, and combined BAPS5+BAPS4. Parameters were calculated using Mcorr.



Supplementary Figure S2. Co-occurrence network of shared accessory genes in the combined dataset of BAPS4 (phylogroup 2) and (b) BAPS5 (phylogroup 1).



Supplementary Figure S3. Defense systems detected in *P. aeruginosa* genomes identified using DefenseFinder (reference 34). Frequency and types of defense systems in sequence clusters (a) BAPS4 (phylogroup 2) and (b) BAPS5 (phylogroup 1). A genome may contain more than one defense system. Classification of the defense mechanisms and their proportion in sequence clusters (c) BAPS4 (phylogroup 2) and (d) BAPS5 (phylogroup 1).