

Genetic diversity of European flat oyster (*Ostrea edulis*) populations by UMI-tagged amplicon sequencing

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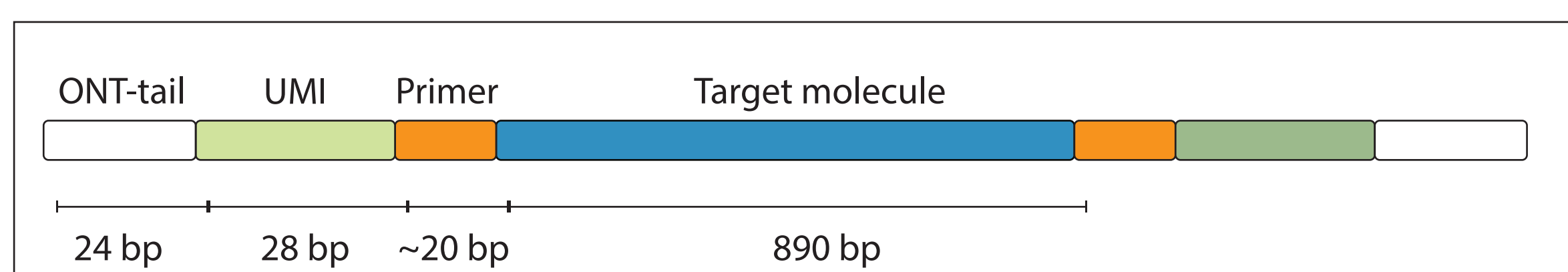
Genetic diversity of the European flat oyster

The European flat oyster (*Ostrea edulis*) is a bivalve species native to the North Sea. Continuous exposure to overexploitation, habitat destruction, and the spread of diseases have led to massive declines in population stocks. Despite efforts to restore flat oyster beds, the impact of restoration efforts on the genetic diversity remains unknown.

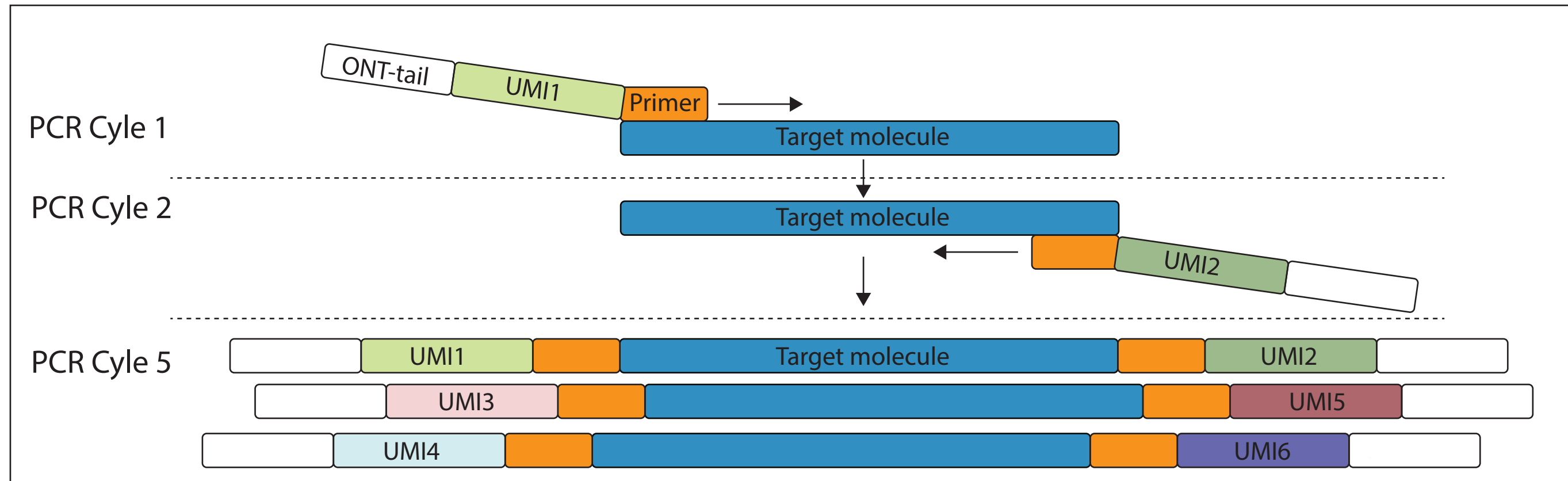
Four mitochondrial genetic haplogroups have been identified within Dutch flat oyster populations. These haplogroups are distinguished by limited, spread out SNPs. To better study genetic diversity in Dutch flat oyster populations, we combine tagging of molecules with unique molecular identifiers (UMIs) with ONT sequencing.

UMI-tagging

a) UMI-tagged molecule



b) Tagging molecules with UMIs



c) Amplification of tagged molecules with EXP-PBC096 Barcoding expansion kit

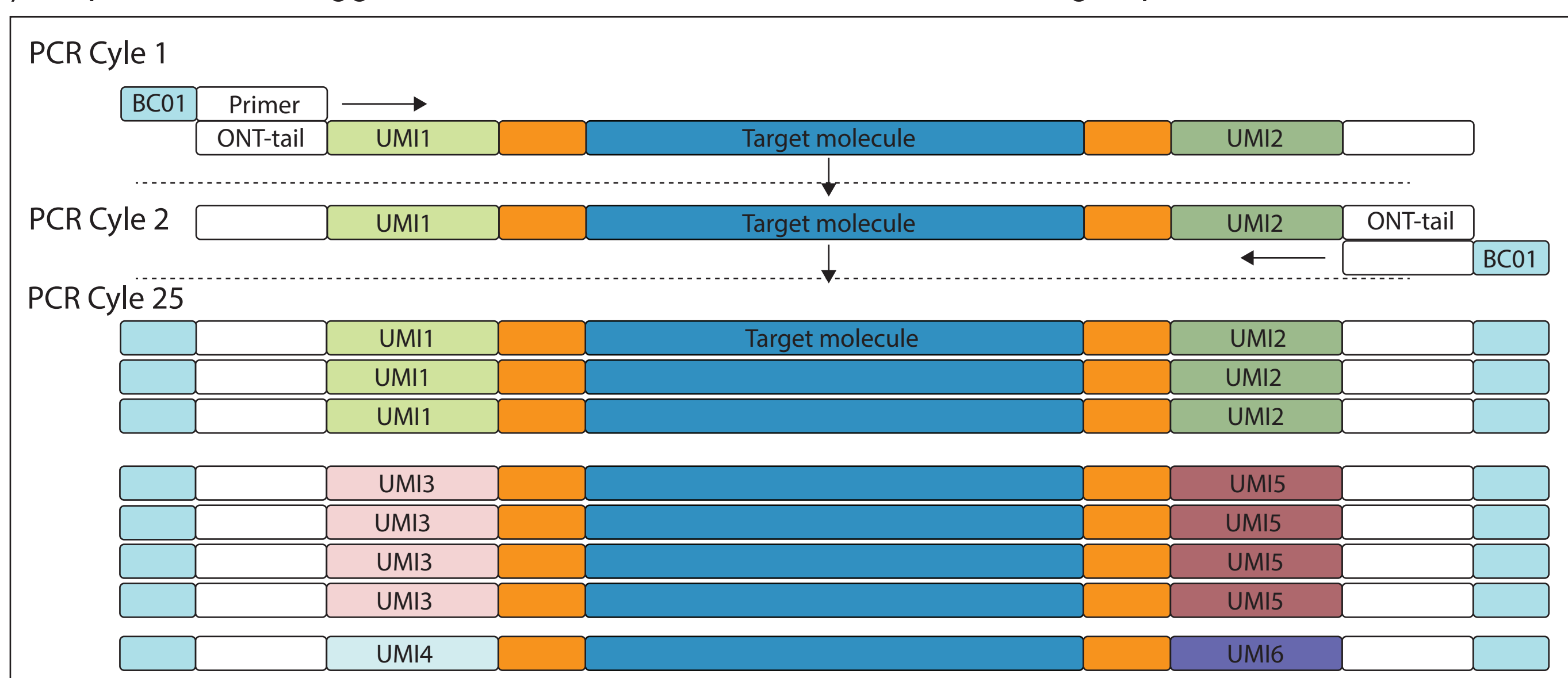


Fig 1. UMI-tagging workflow

Bioinformatics analysis

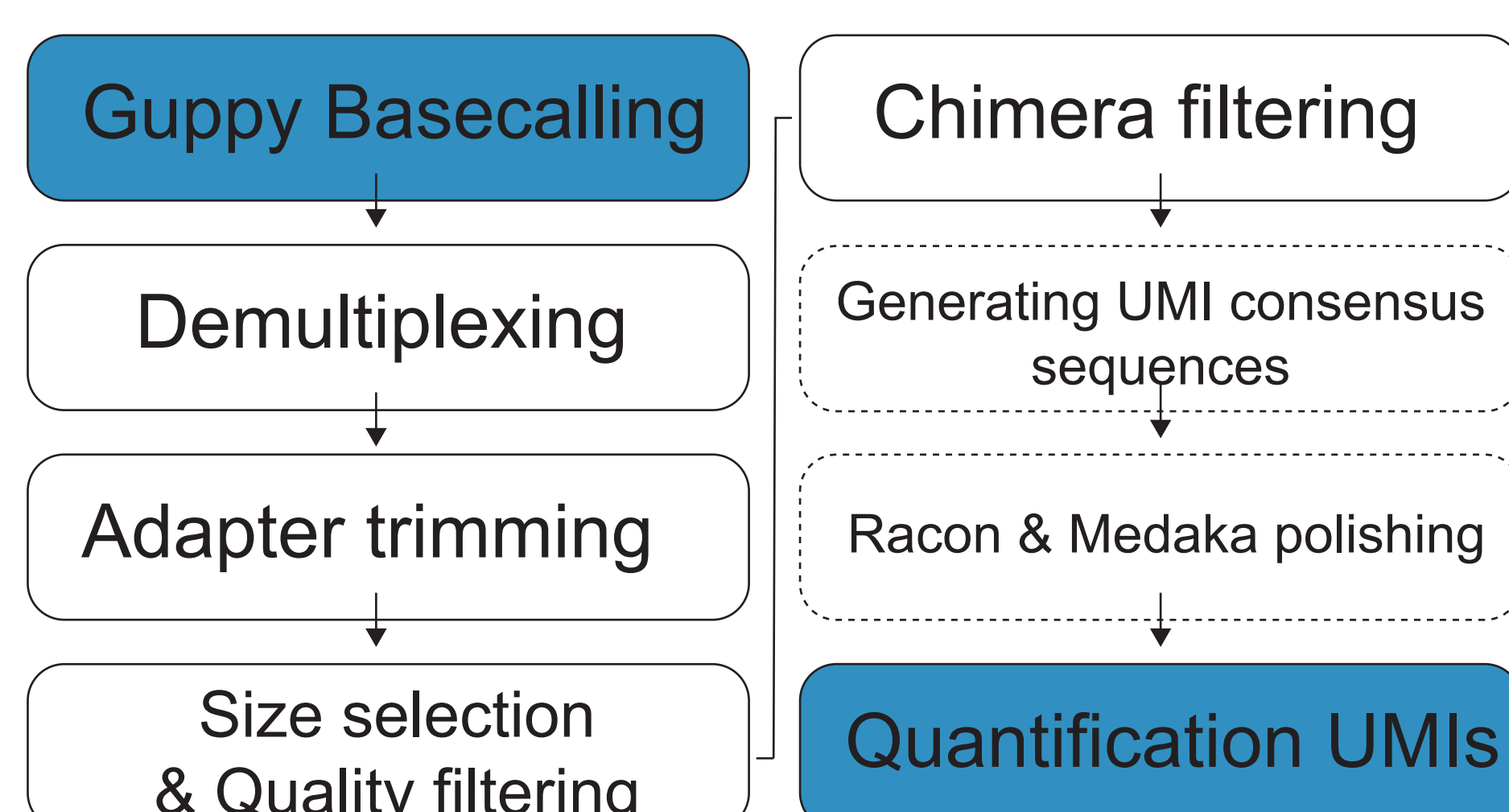


Fig 2. Bioinformatics analysis workflow: from raw reads to UMI-consensus sequences

Phylogenetic tree of UMIs within a sample

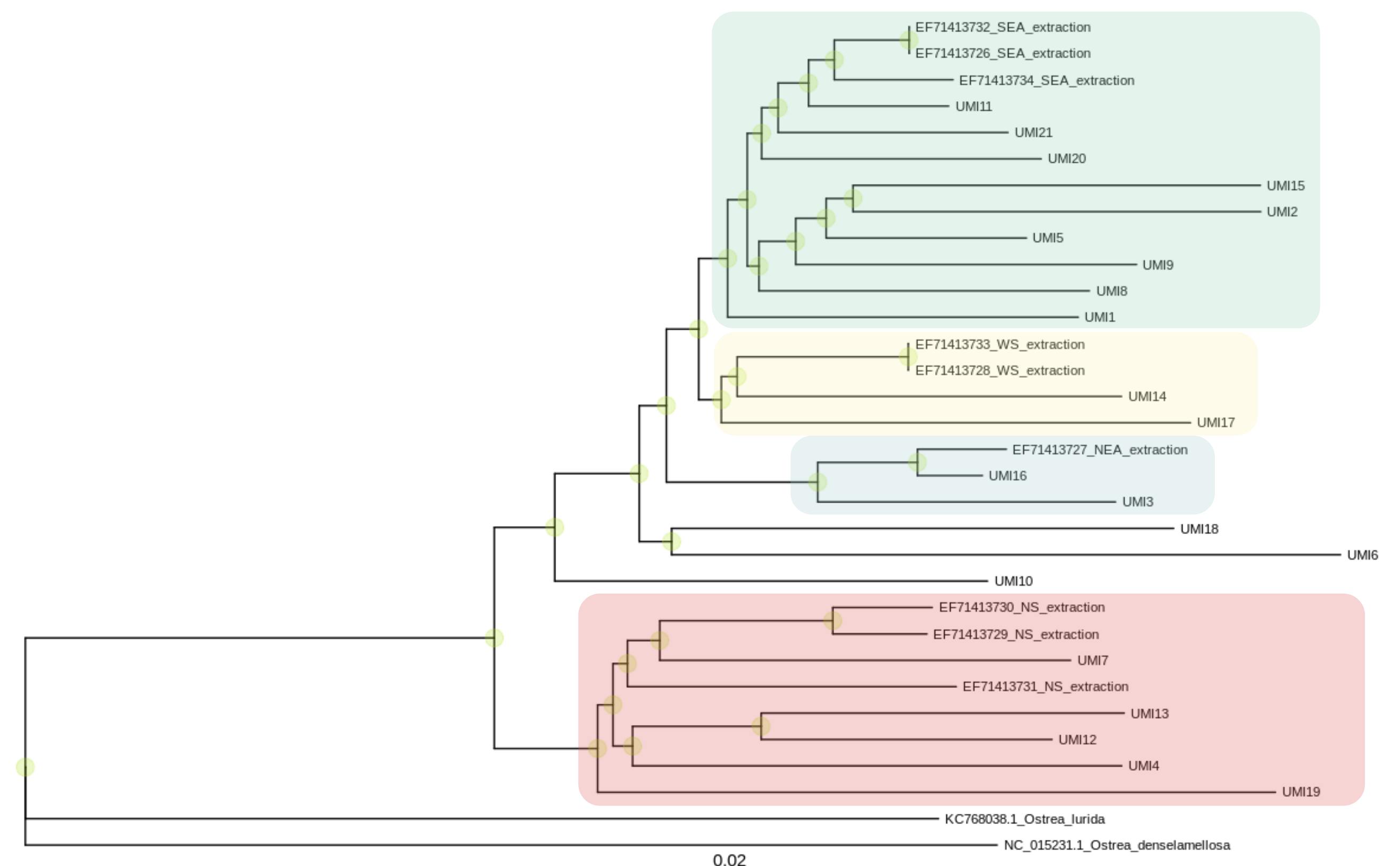
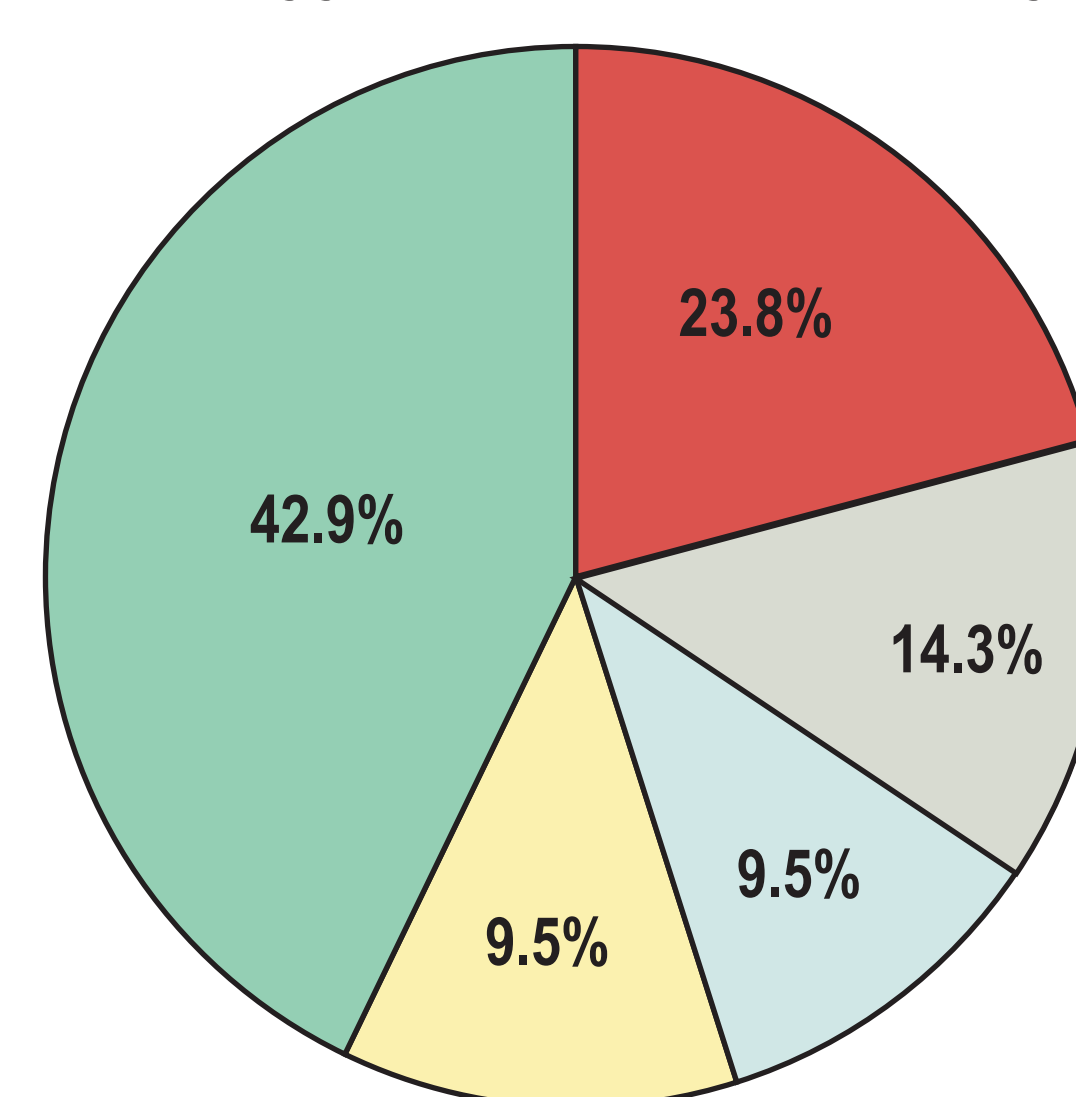


Fig 3. Phylogenetic tree construction of all unique UMIs within one sample and reference sequences of used haplogroups

Haplogroup contribution

a) Haplogroup contribution derived by UMI-tagged amplicon sequencing



b) Ground-truth haplogroup contribution

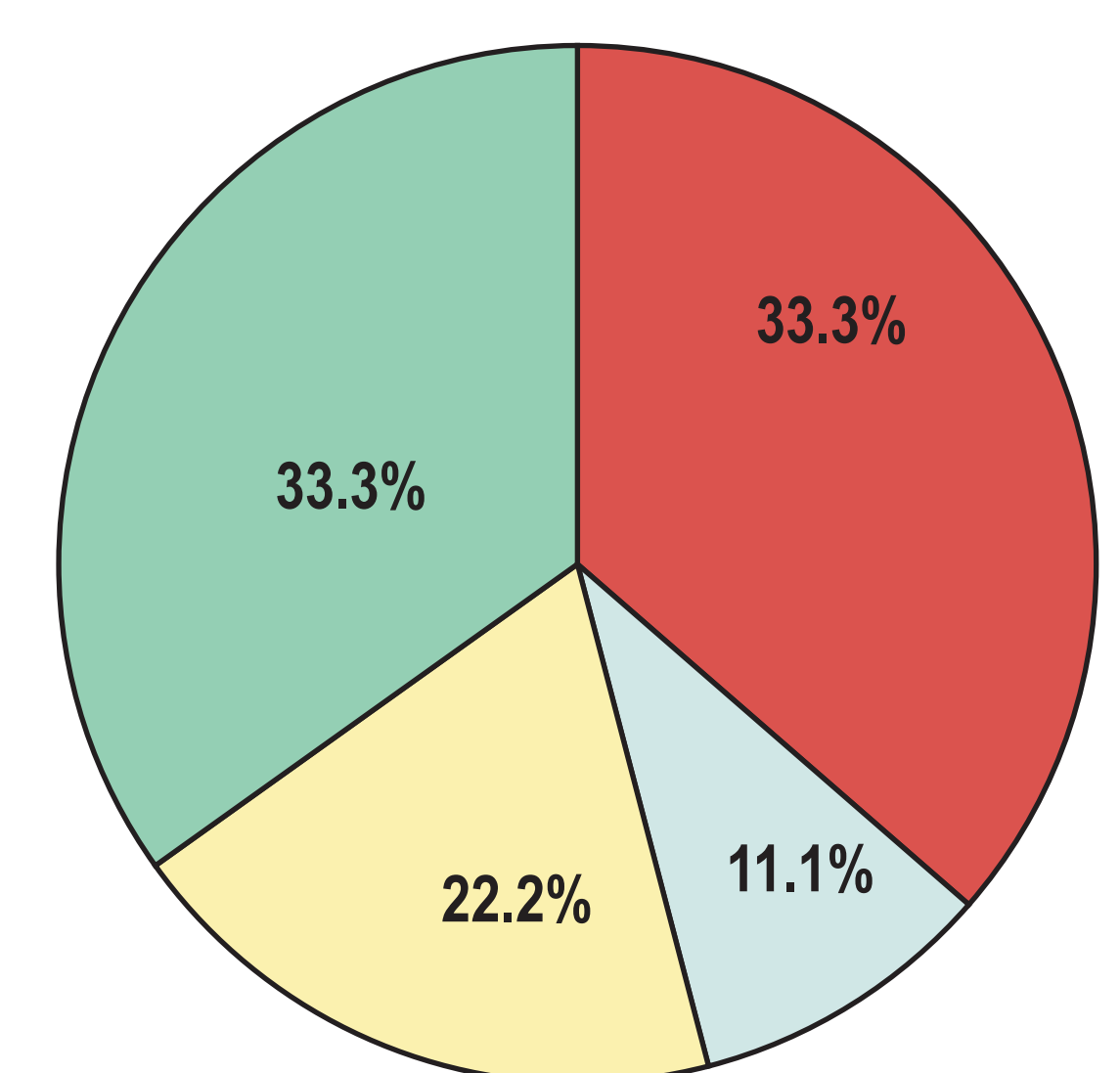
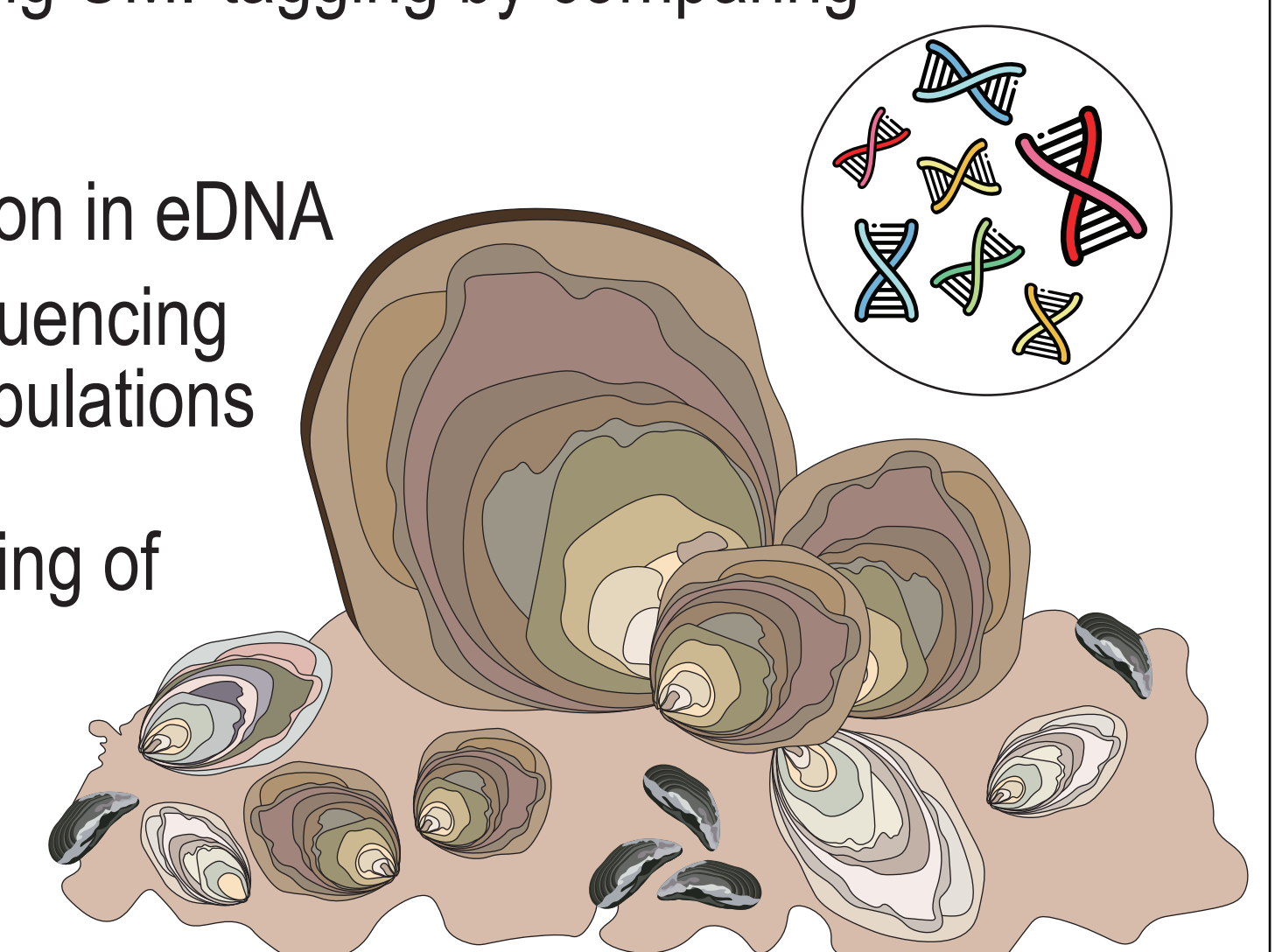


Fig 4. Haplogroup contribution within a sample derived by UMI-tagged amplicon sequencing compared to the ground-truth haplogroup contribution of the mock sample.

Future perspective

- 1) Validation of quantification method using UMI-tagging by comparing quantification to RT-PCR.
- 2) Quantification of haplogroup contribution in eDNA samples using UMI-tagged amplicon sequencing
 - Study genetic diversity in oyster populations non-invasively
 - Enable less labor-intensive monitoring of population genetics



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