

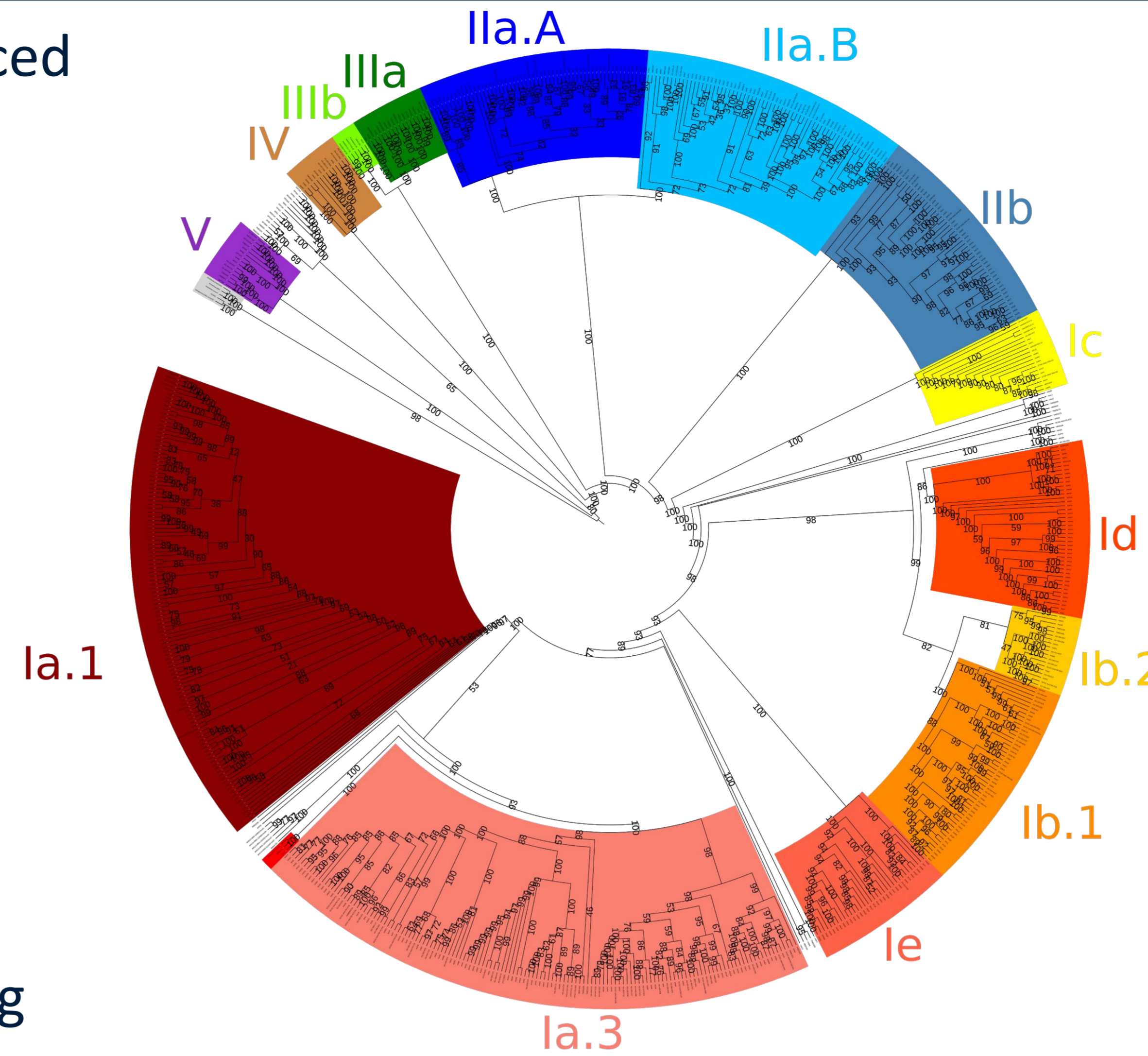


Background

- 90% of the ocean's biomass is comprised of marine microorganisms^[3]
- SAR11 bacteria are the most ubiquitous^[4]
- Complete SAR11 genomes are relatively rare due to difficulty in culturing^[5]
- Single-cell Amplified Genomes provide an alternative to culturing and metagenomic based genomic studies

1 Phylogenetics

- Where do newly sequenced SAR11 SAGs exist within current ecotypes?
- Phylogenetic tree from bacterial single-copy marker genes
- Confirmation of branch structure by Average Amino-acid Identity
- Ecological niche determination by metagenomic mapping



2 Viral Signatures

- What viral signatures are present?
- 21 phage genomes identified
- Gene sharing network provide phage identity
- Gene ortholog search for taxonomic and protein coding region identity
- Ecological niche determination by metagenomic mapping

Single-cell Amplified Genomes provide clade-wide insights in hard-to-culture marine microorganisms

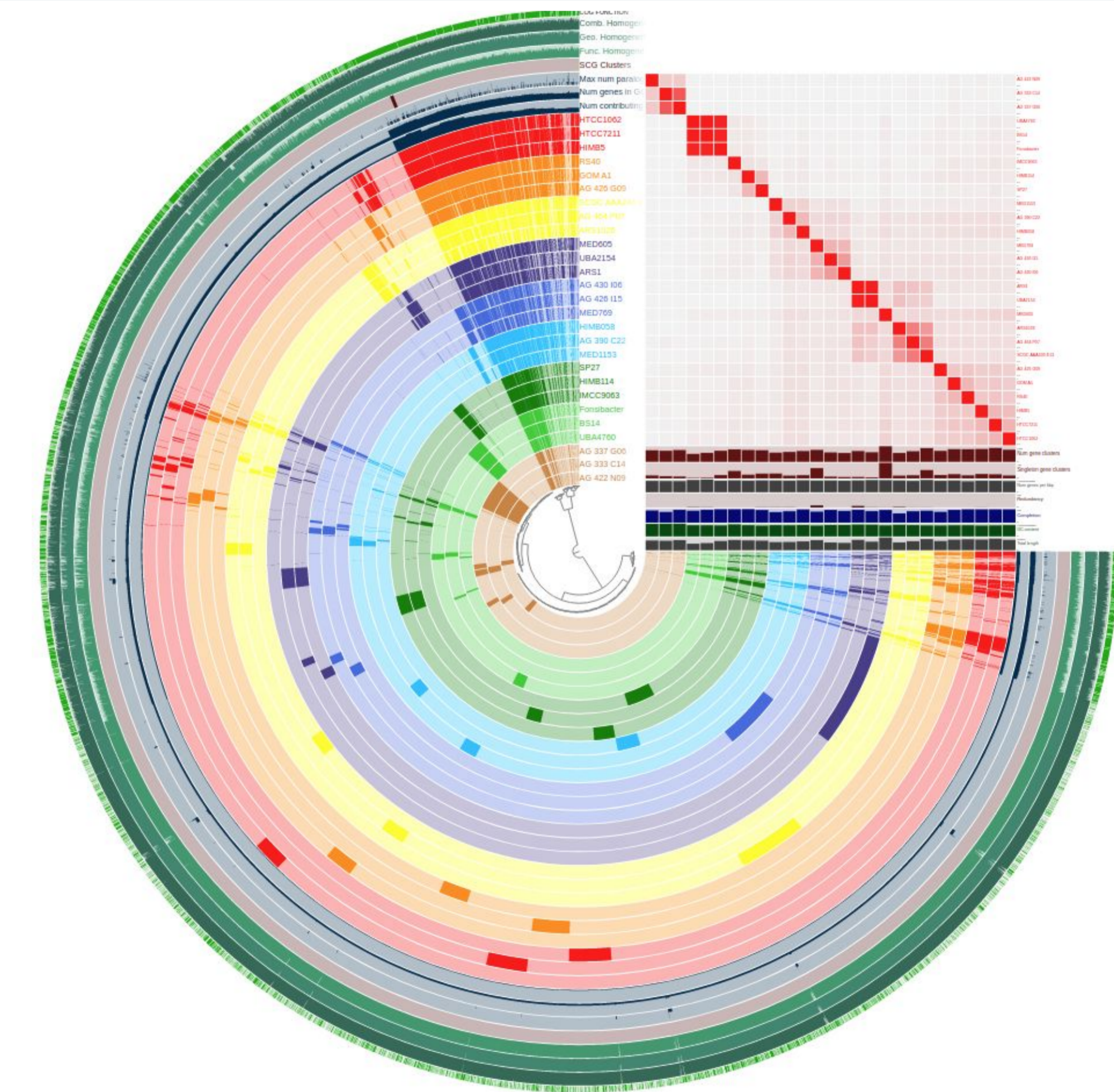


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3 Hypervariable Regions

- Regions undergoing higher evolutionary rates
- What advantages do HVRs provide?
- Gene clustering and coverage distribution reveal clade-wide HVRs
- SAR11 HVRs contain genes conferring advantages in nutrient uptake or phage defense



Discussion

- Phylogenetic analysis confirms new SAR11 clades
- New phage genomes identified
- All SAR11 HVRs contain nutrient uptake or phage defense genes