

# Single cell sequencing reveal depth-associated biogeography and conserved phage defence in ubiquitous marine bacteria

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## 1 Background

- 90% of the ocean's biomass is comprised of marine microorganisms<sup>[3]</sup>
- SAR11 bacteria are the most ubiquitous<sup>[4]</sup>
- King-of-the-mountain ecological strategy enables high SAR11 abundance despite high phage abundance and predation<sup>[5]</sup>
- Complete SAR11 genomes are relatively rare due to difficulty in culturing<sup>[6]</sup>
- Single-cell Amplified Genomes provide an alternative to culturing and metagenomic based genomic studies

## 2 Hypervariable region

- What advantages do HVRs provide?
- Region undergoing higher evolutionary rates
- Gene clustering and coverage distribution reveal clade-wide HVRs
- SAR11 HVRs contain genes conferring advantages in phage defense
- Homologous recombination of phage defense genes allow SAR11s to retain high abundance

## 3 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

## 4 Phylogenetics

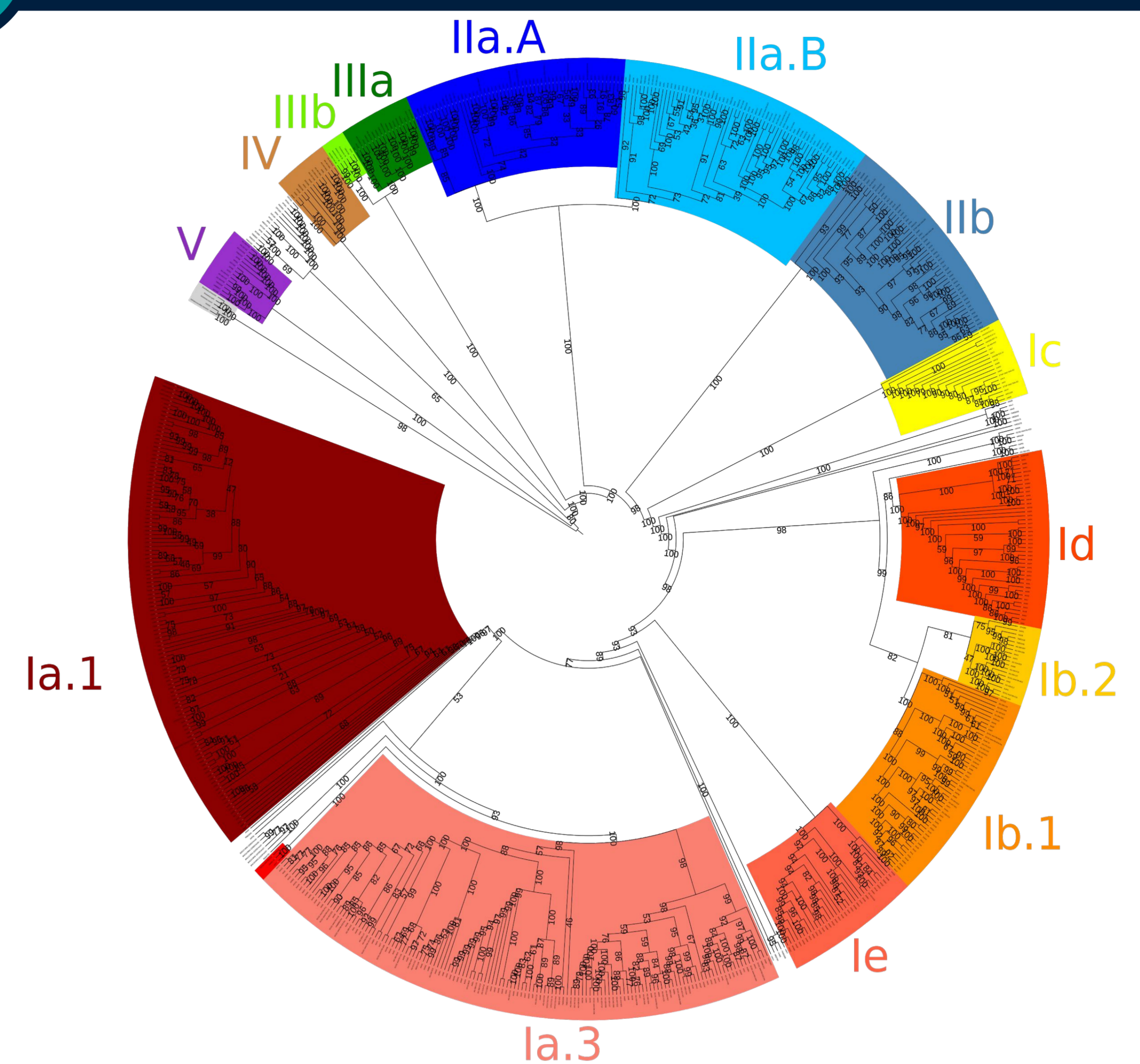


Fig 1. Phylogenetic tree of 451 SAR11 SAGs and reference genomes. 120 bacterial marker genes are used to infer tree structure. Clades Ib.2, Id and Ie are previously undescribed clades.

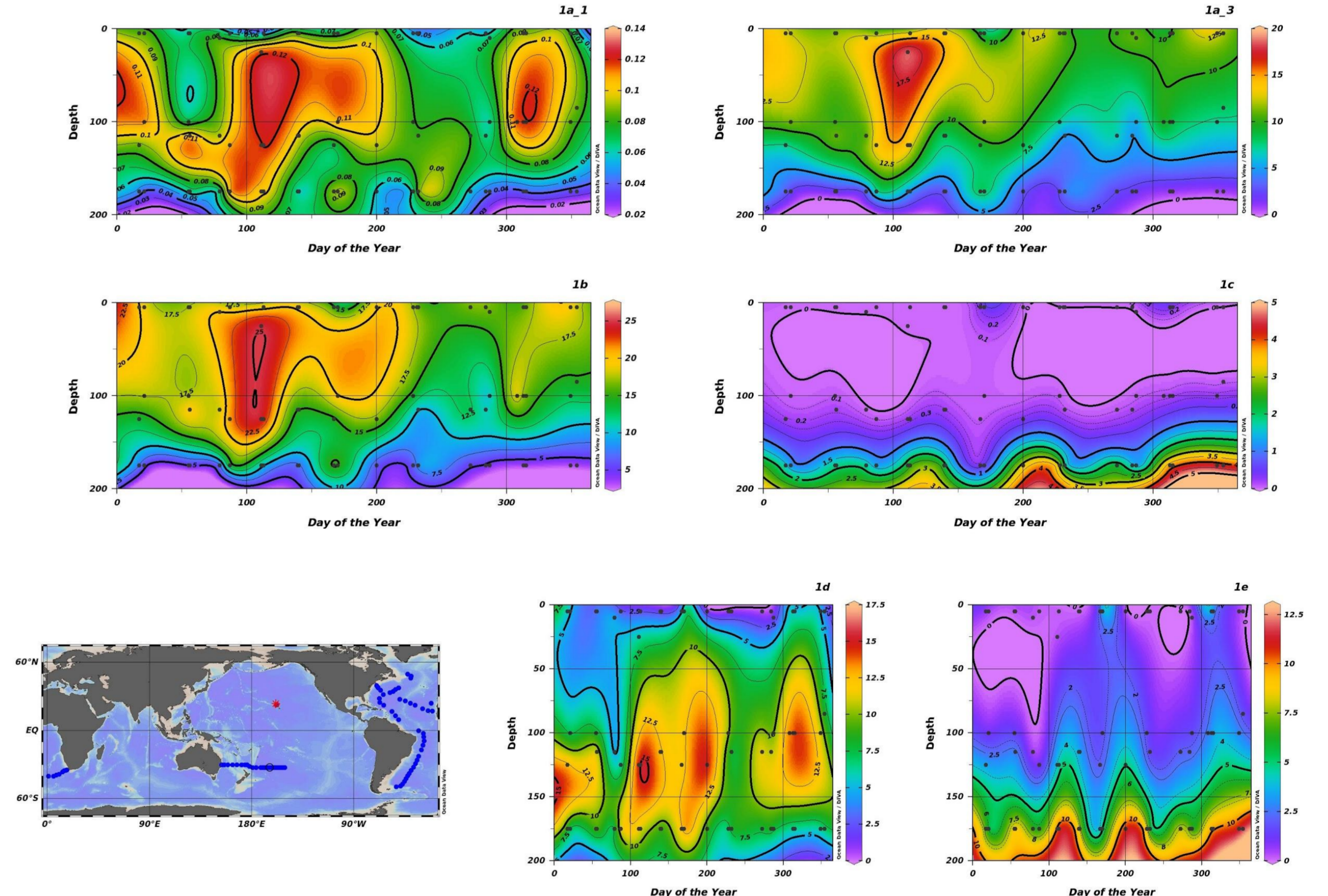
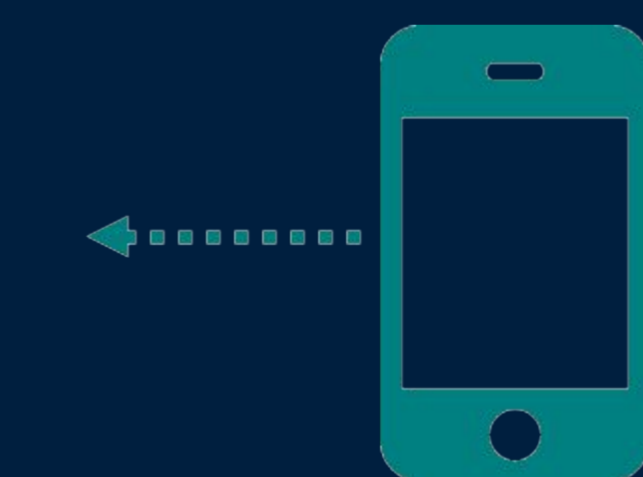


Fig 2. Heatplots of SAR11 clade presence/absence at the Hawaii Ocean Time-series against depth and day of the year. Abundance is in percentage clade coverage at differing spatial and temporal points compared to extracted metagenomic data.

- 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 of SAR11 clade genome coverage

## 5 Discussion

- Phylogenetics and ecological mapping confirms novel SAR11 clades
- Identified phages coincide with SAR11 abundance
- Evolutionary pressure for phage defense genes is conserved across all SAR11 clade HVRs



Take a picture and follow the link to find out more!

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