

Detection of co-infection events and the emergence of novel SARS-CoV-2 recombinants in the epidemiological surveillance of Andalusia (Spain)

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INTRODUCTION

Since the beginning of the pandemic, Andalusia has been running a genomic study project of SARS-CoV-2 sequencing, the Genomic Surveillance Circuit of Andalusia, a systematic genomic surveillance program in coordination with the Ministry of Health in which the Microbiology Services of the Virgen del Rocio Hospital in Seville and San Cecilio Hospital in Granada participate together with the Computational Medicine Platform. This study analyses the cases of SARS-CoV-2 infection with no clear lineage assignment that occurred in the first five months of 2022, a period of high viral circulation.

METHODS

The study comprised 90 SARS-CoV-2 positive samples with >90% coverage with no clear clade or lineage assignment (Nexstrain/Pangolin) from approximately 7,722 genomes sequenced within the Andalusian Genomic Surveillance Circuit in the period January-May 2022, a period of high circulation of Delta and Omicron variants.

Procedure for the detection of co-infection and recombinant events: use of mutation frequency plots, using different labels for the mutations specific to lineages and another label for the common mutations. Mutations specific to lineages are retrieved from LAPIS (Lightweight API for Sequences)

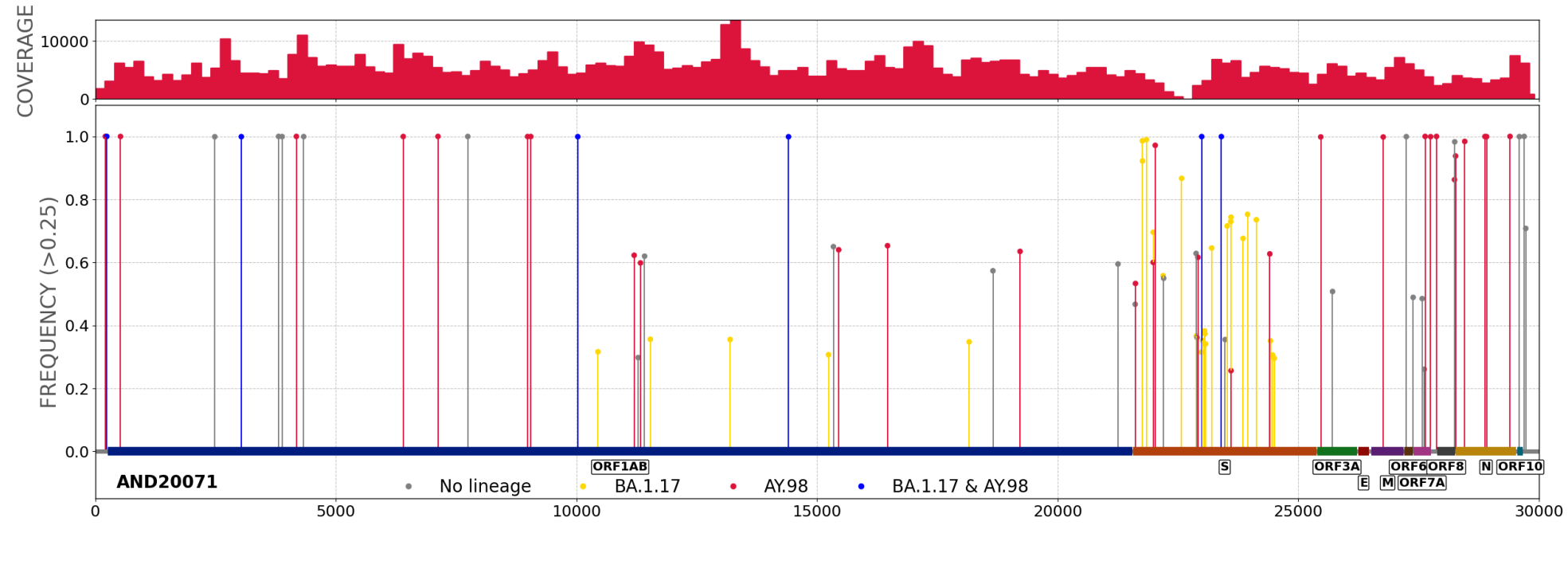
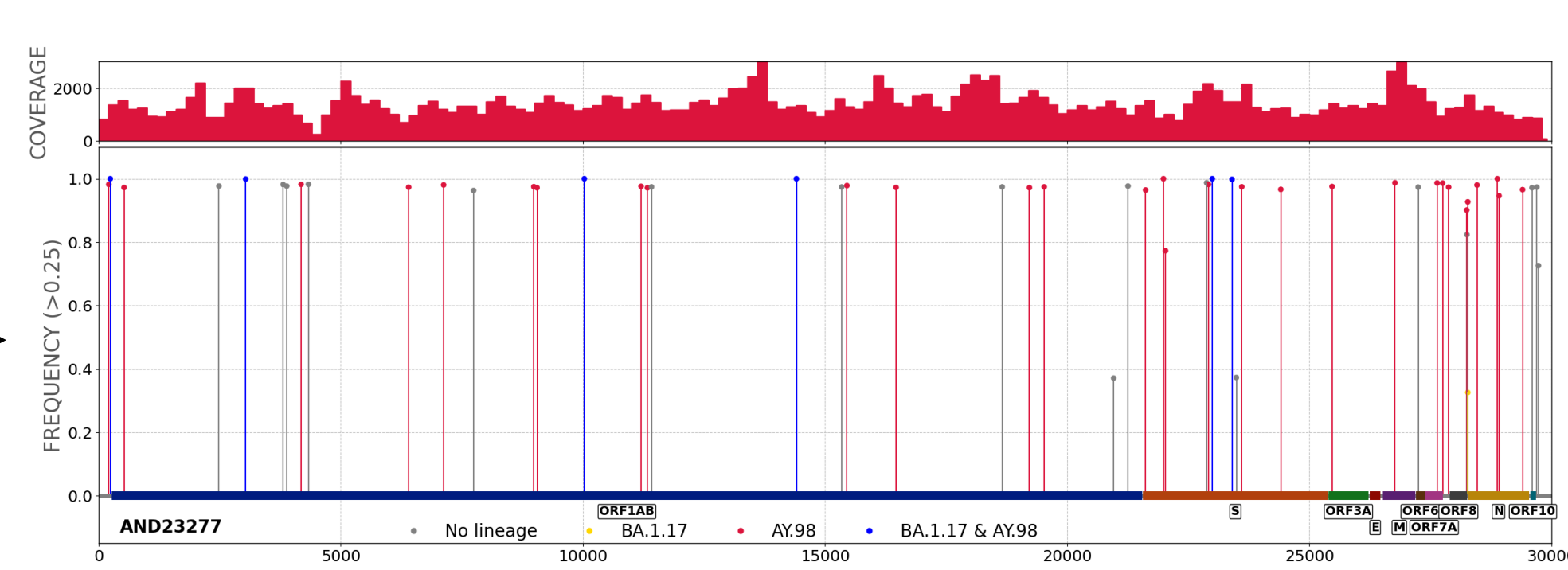
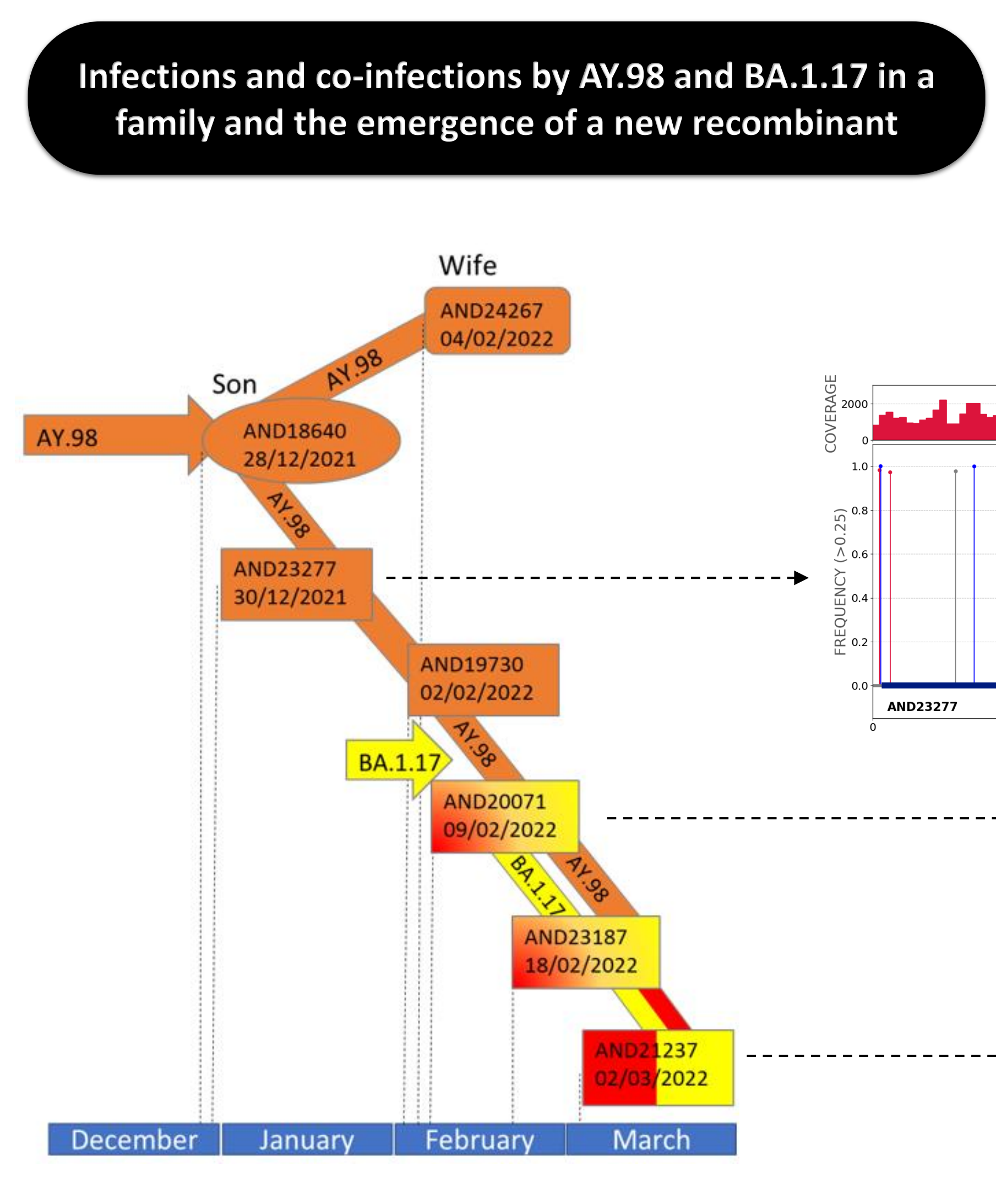
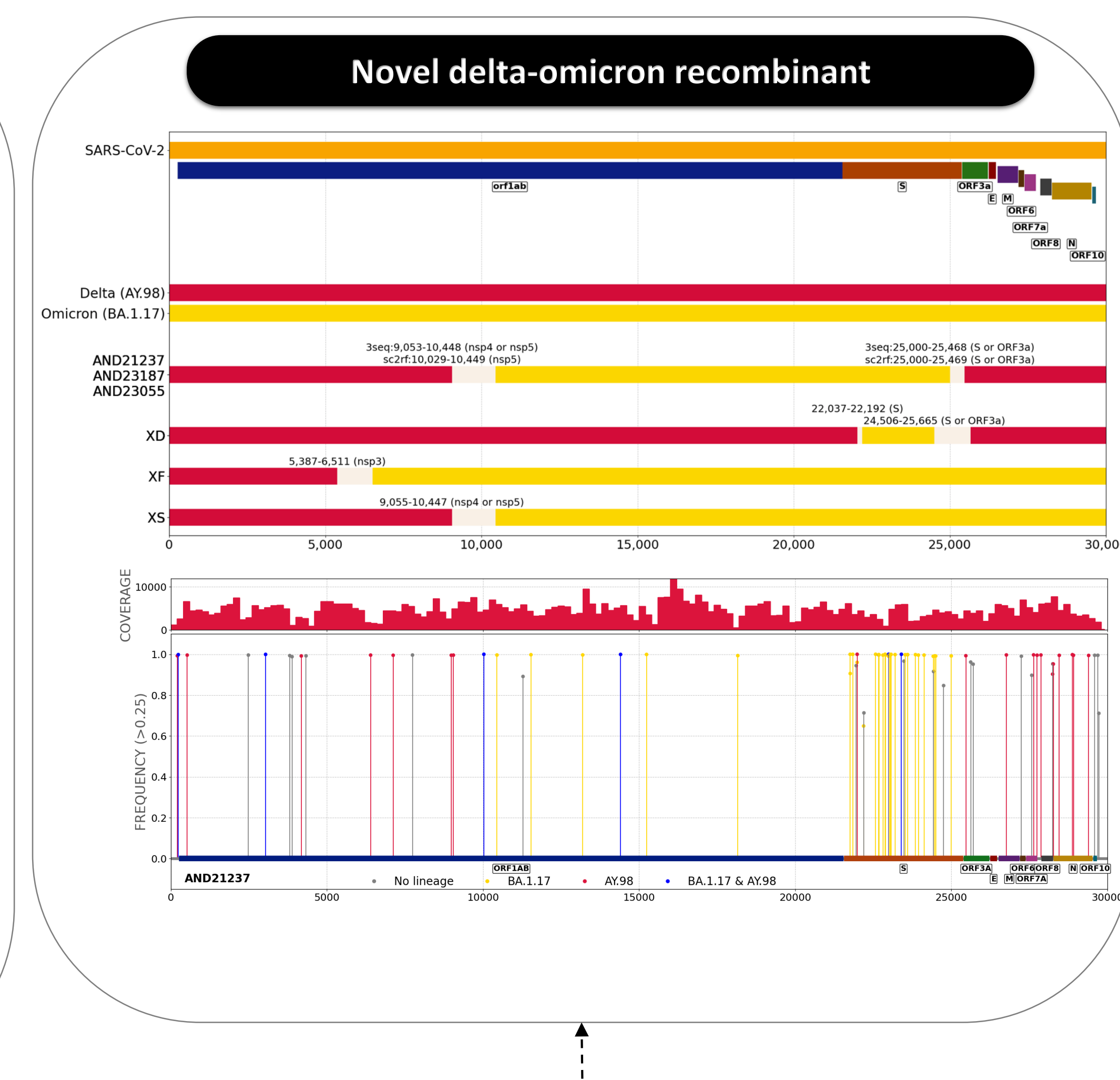
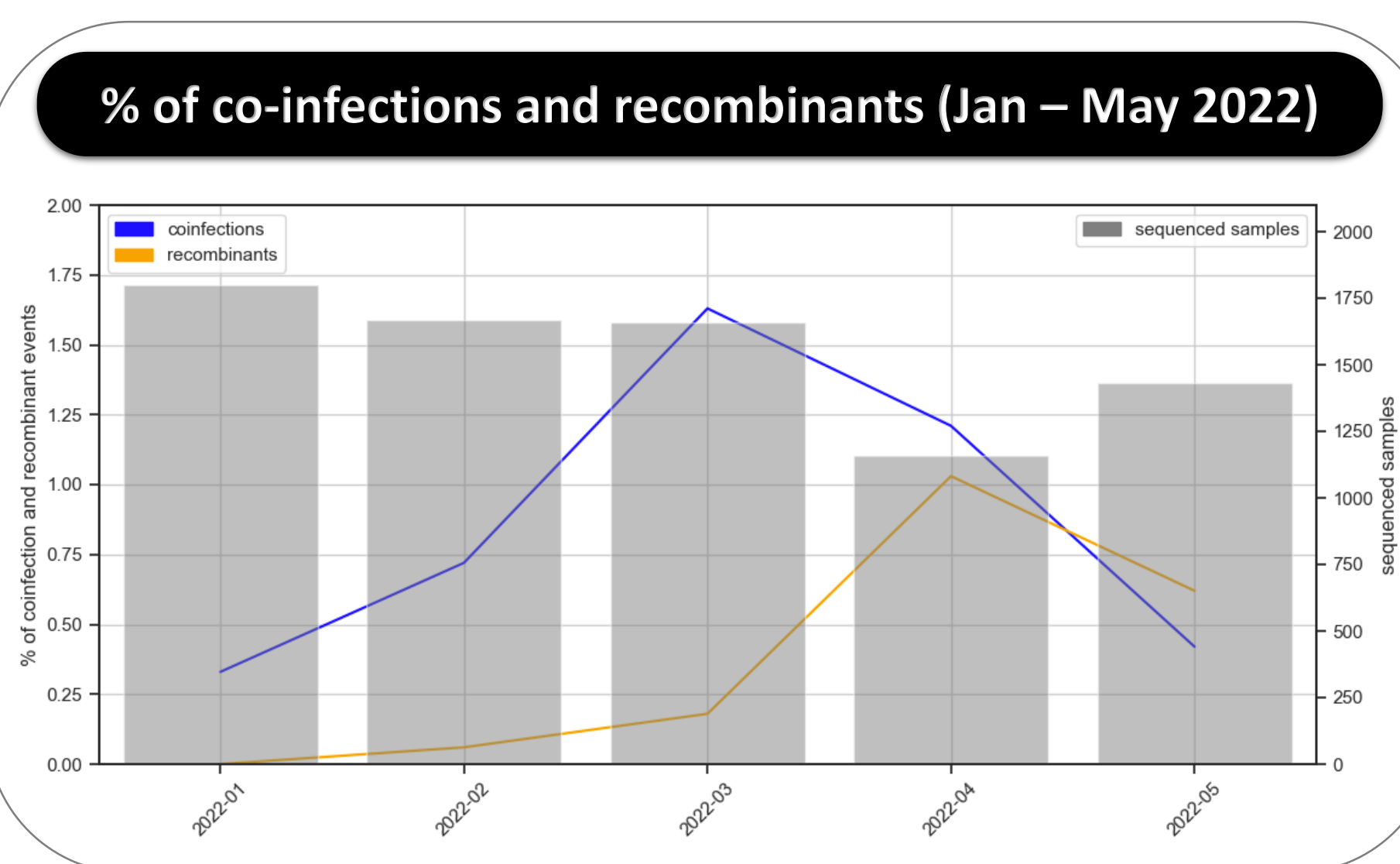
co-infection event

when the common mutations are in the 100% range but the lineage-specific ones are in complementary proportions (e.g. 50-50, 60-40, etc)

recombinant event

when all the mutations are in the range of 100%, and lineage-specific mutations are located in non-overlapping regions. Known recombinants are detected using Nextclade and unknown ones are identified by means of 3seq and sc2rf tools

RESULTS



CONCLUSIONS

1. Co-infection events are occurring, a significant percentage of which have led to recombination between variants and/or lineages of SARS-CoV-2.
2. Surveillance efforts and real-time analyses to detect recombinants should be maintained to monitor the circulation and potential spread of recombinant high-fitness genotypes.
3. Immunocompromised individuals and those around them may play a key role in the evolution of new viruses/strains

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