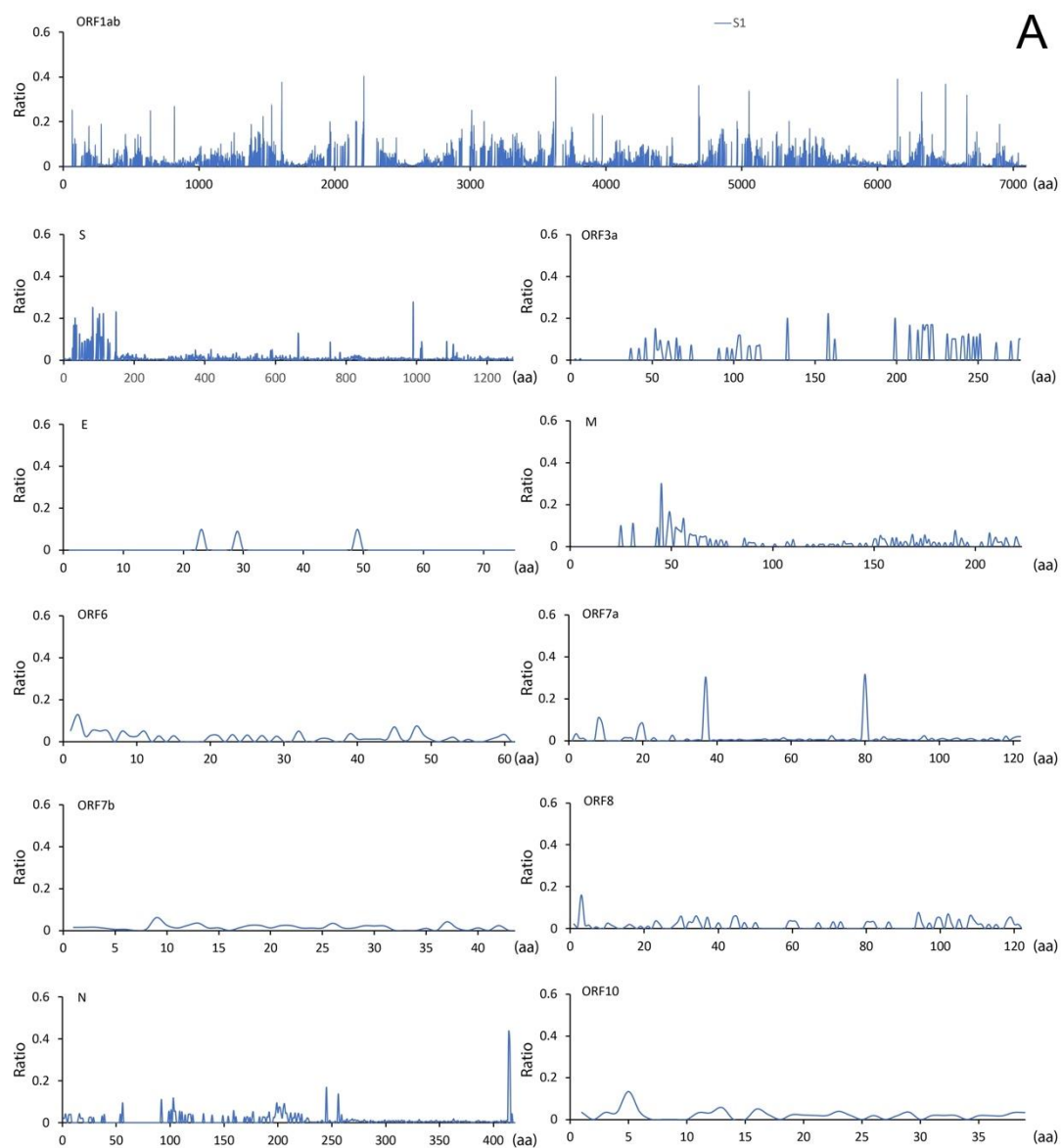
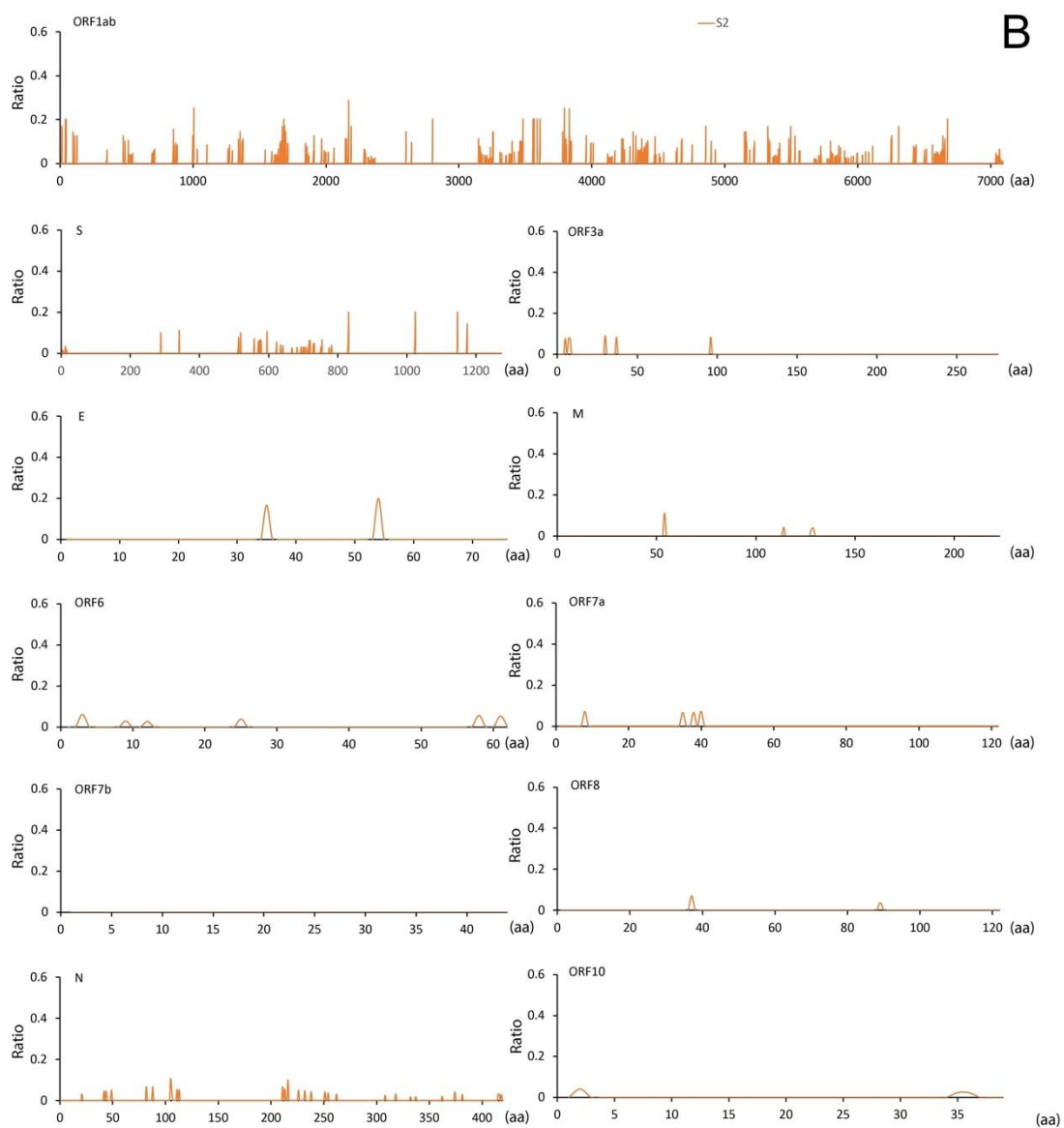
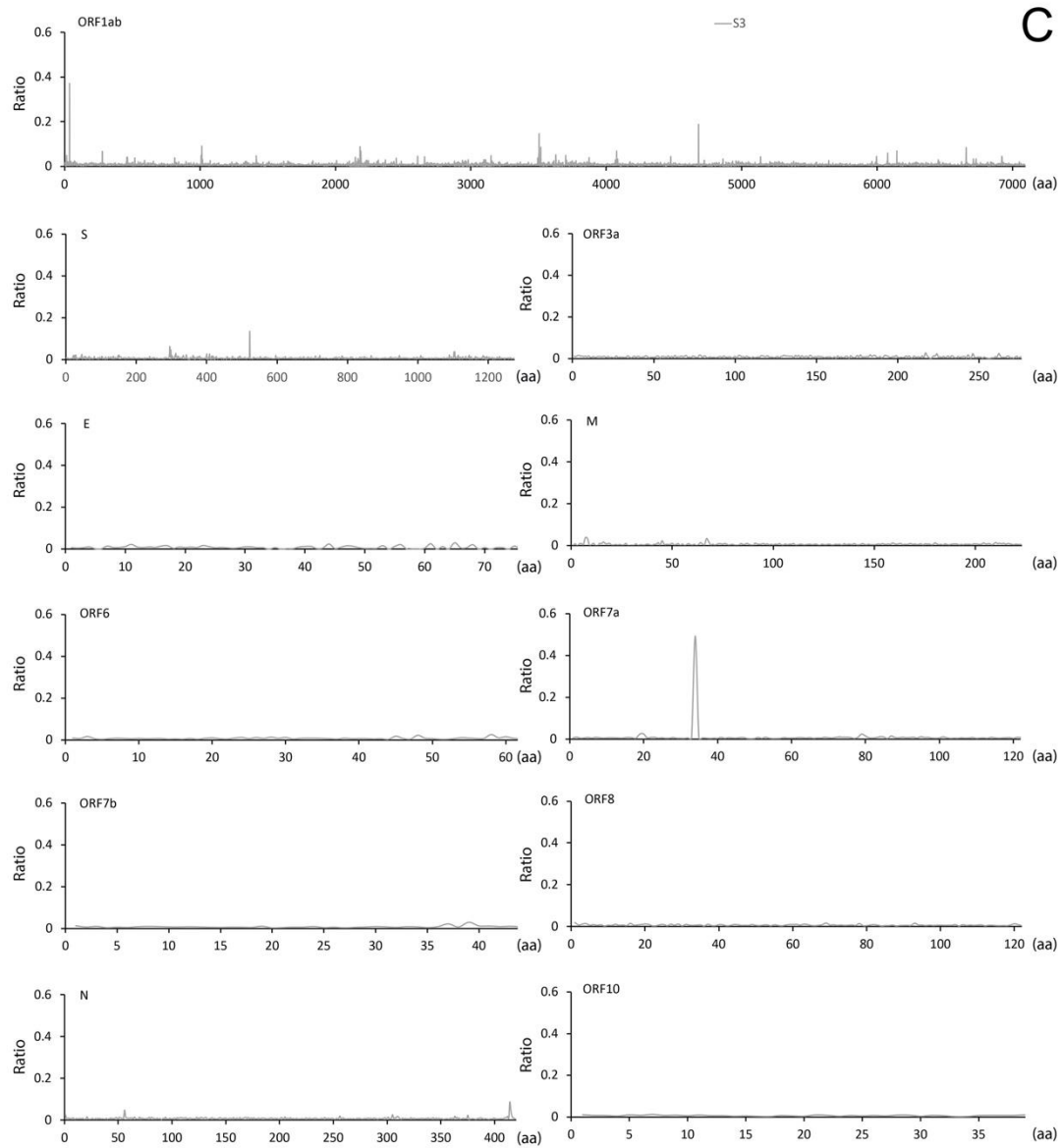


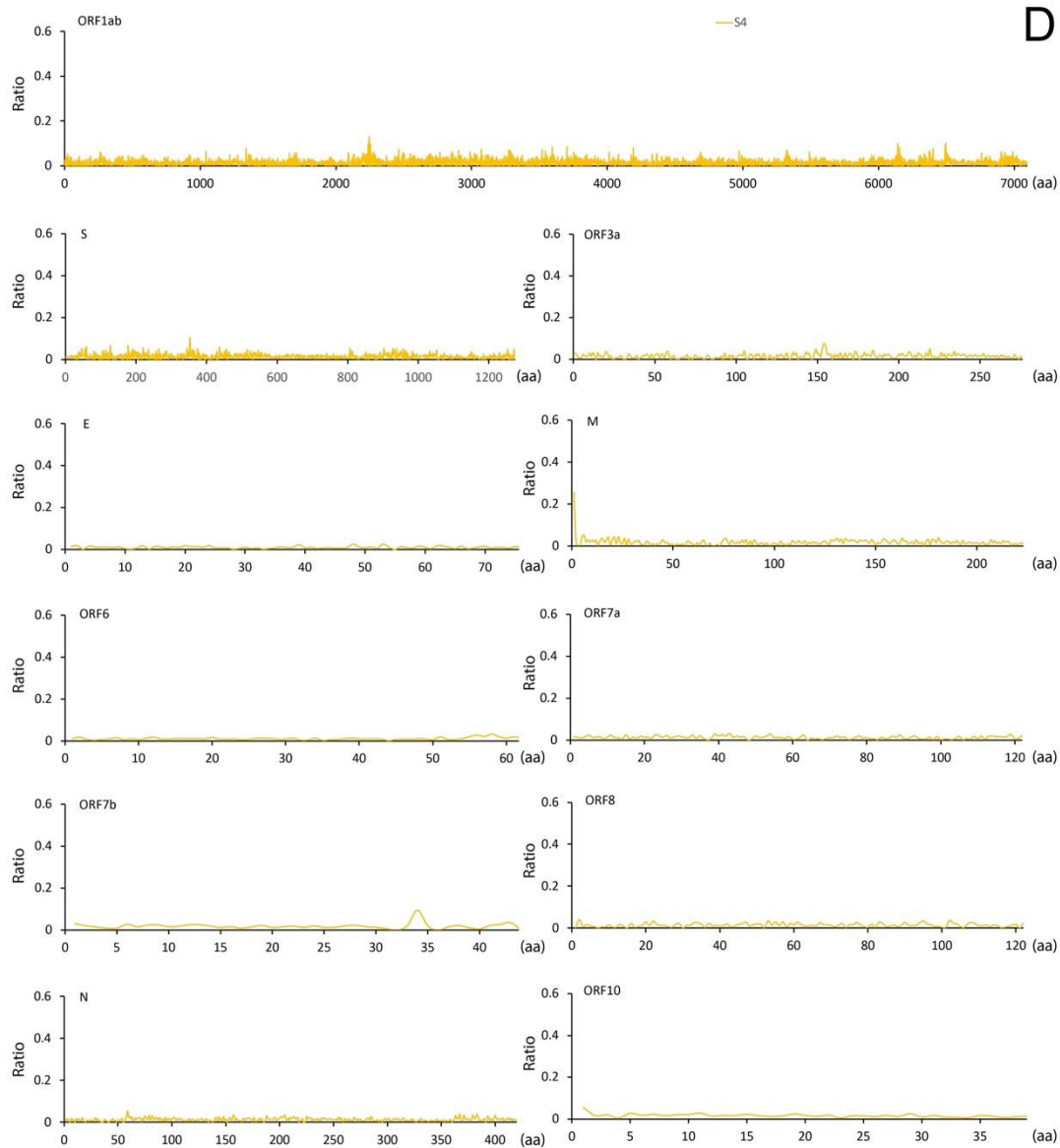
Supplementary information

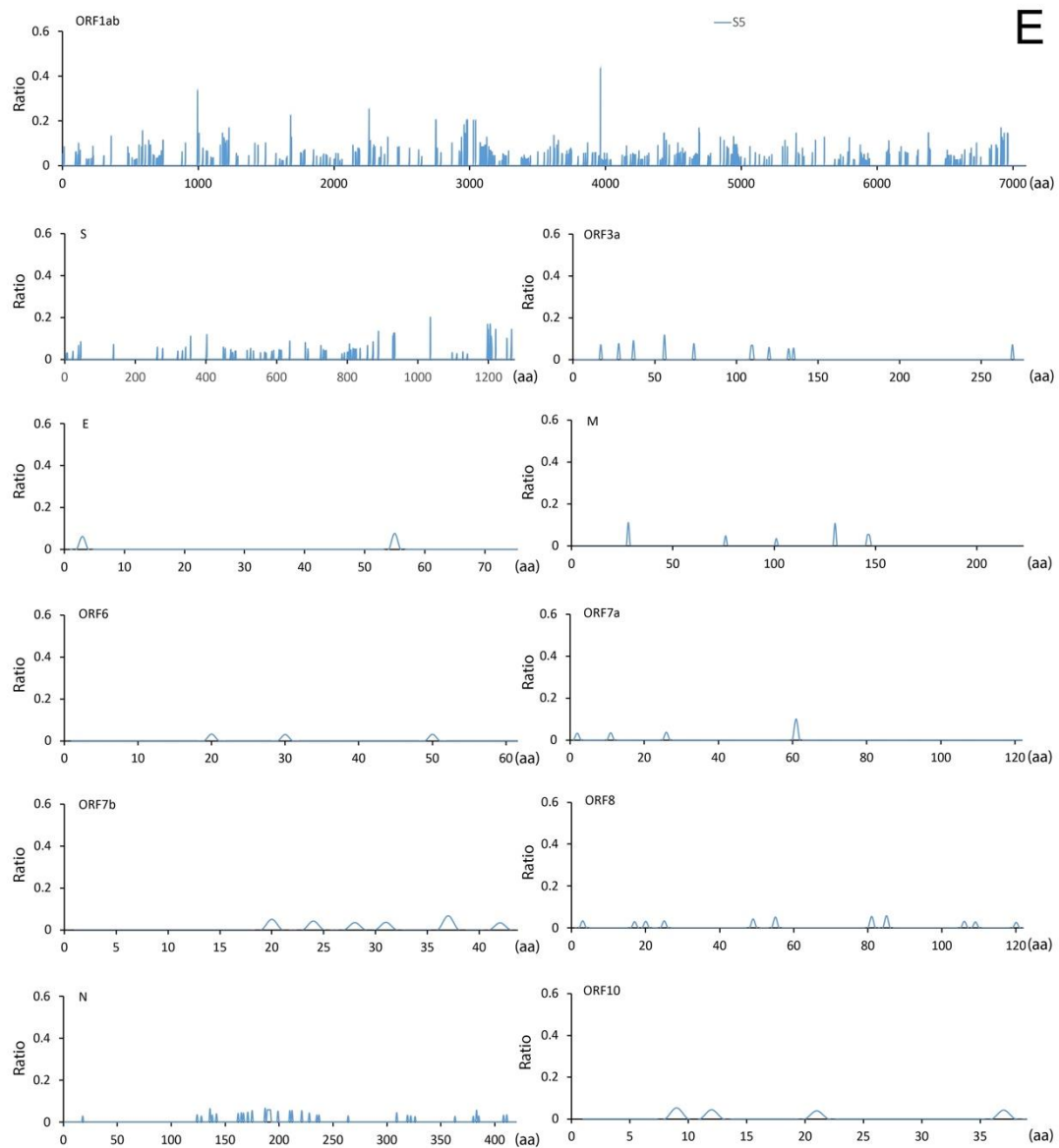
Fig. S1-S5

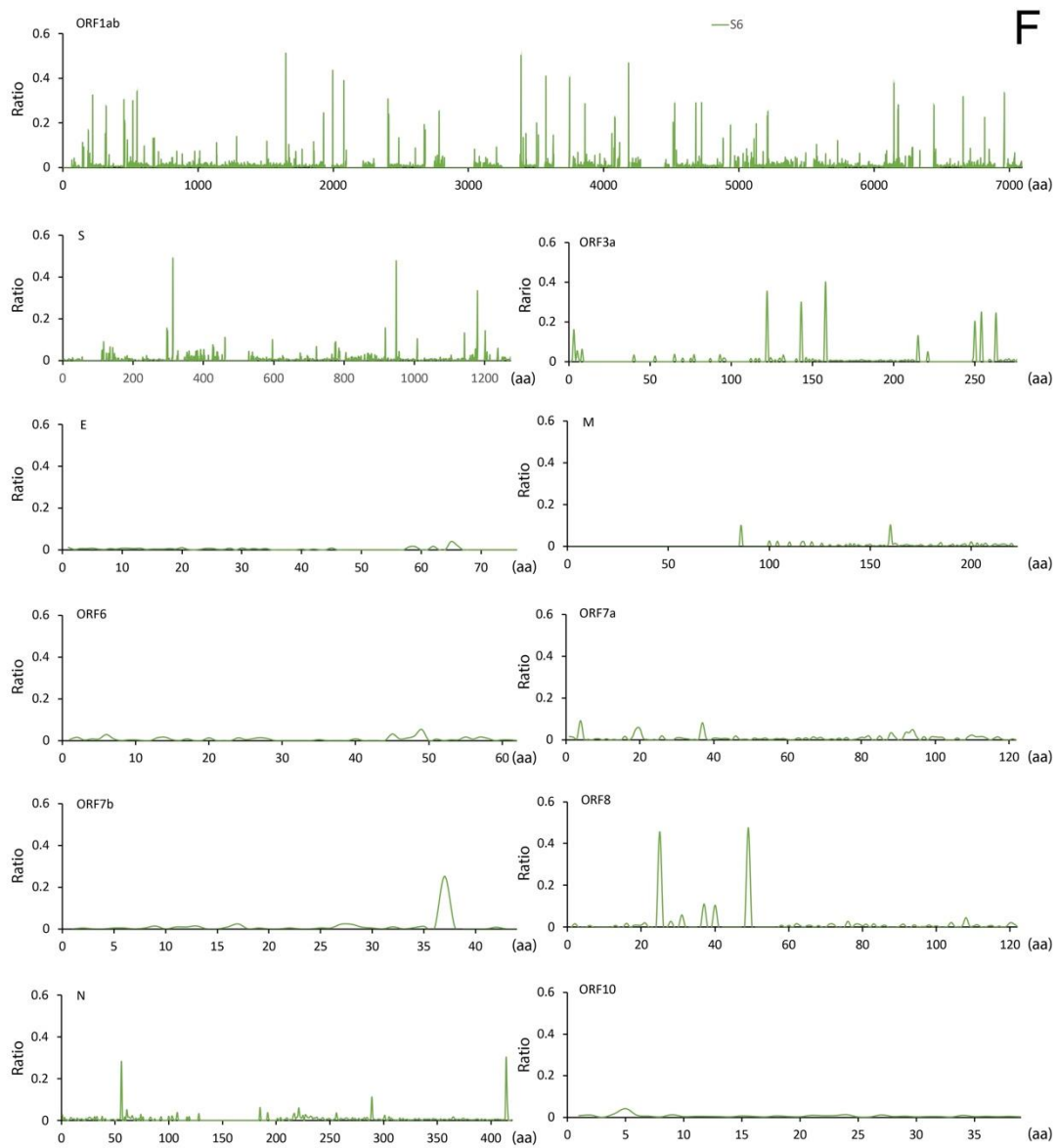


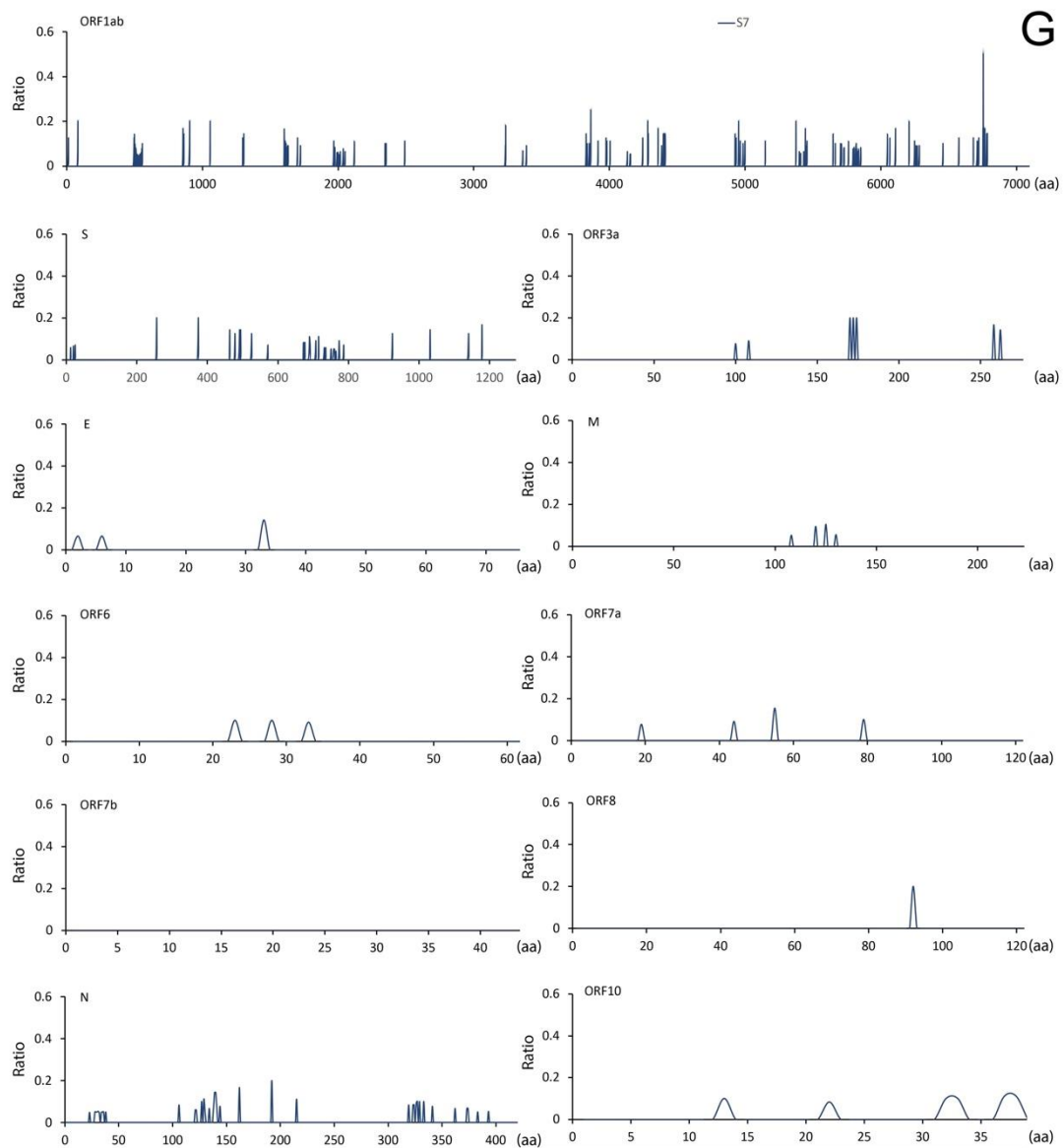


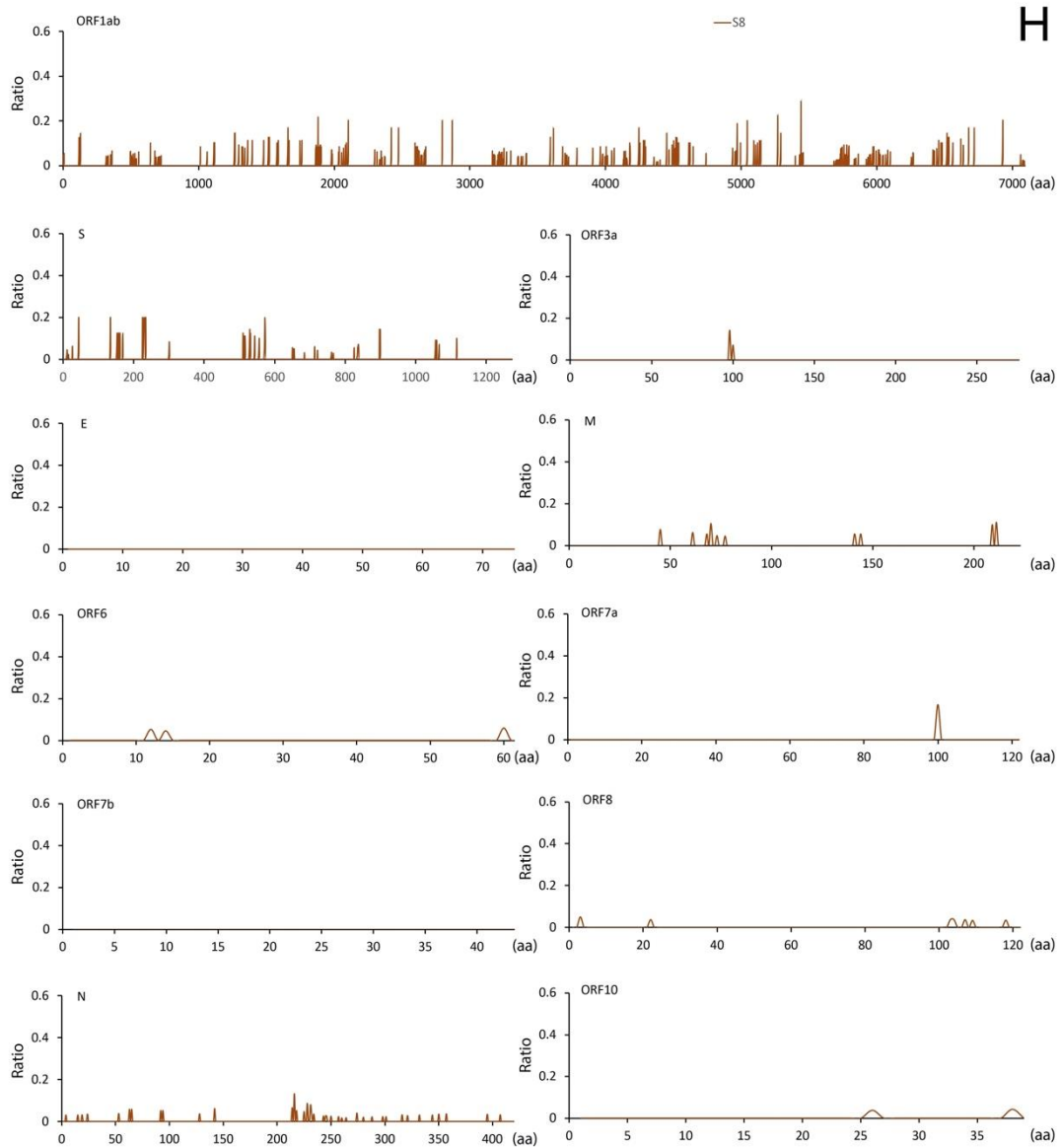


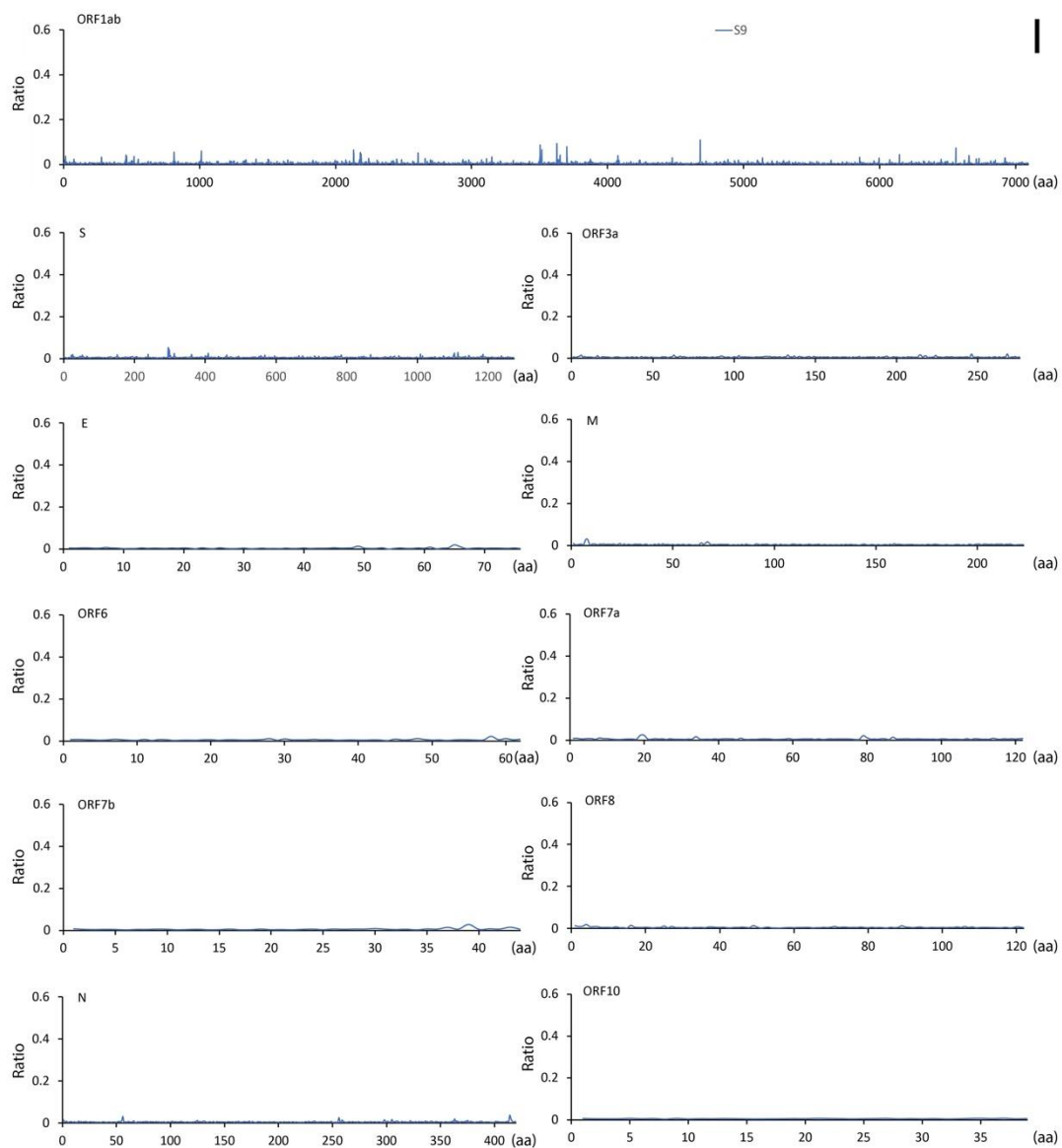


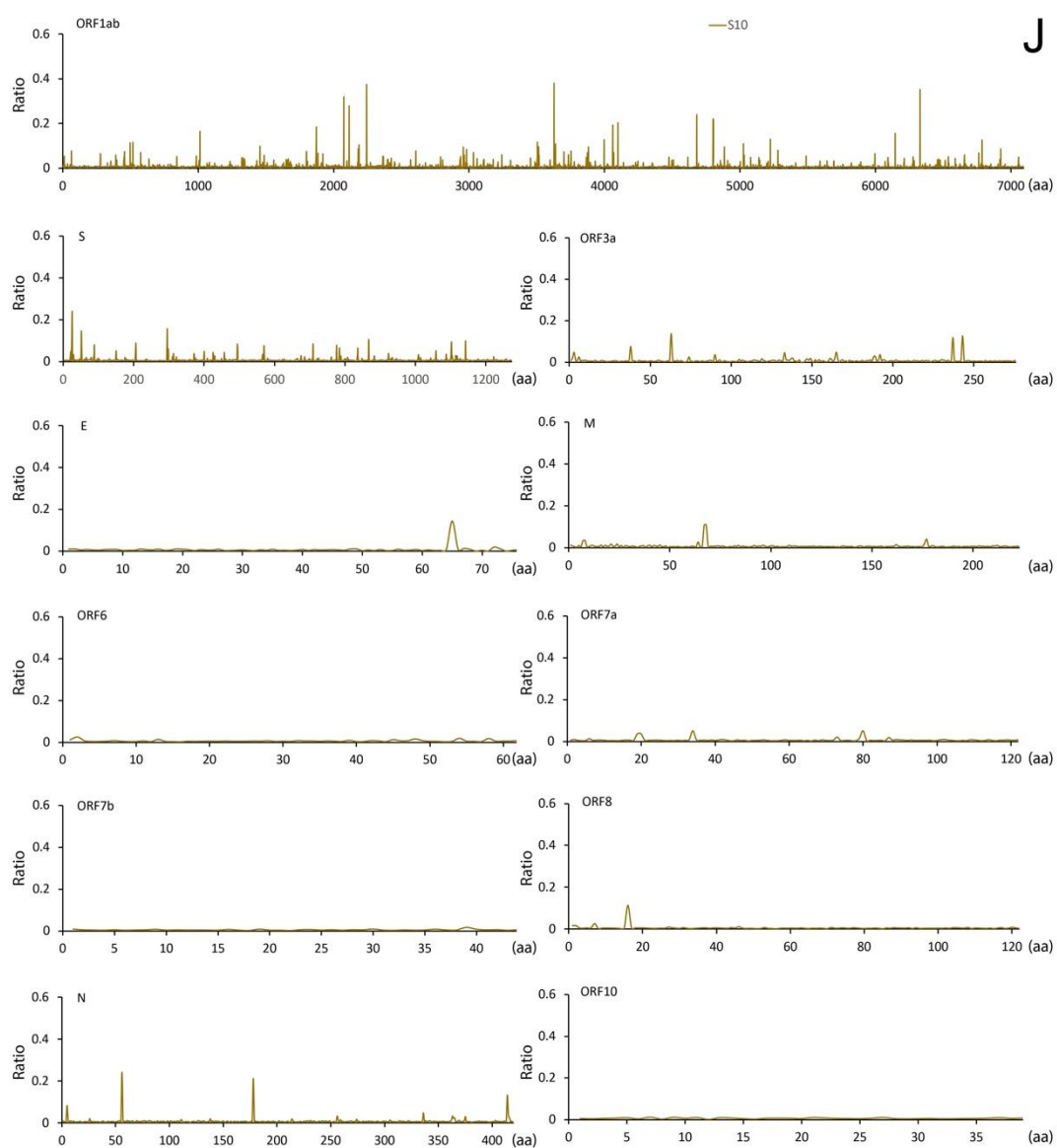


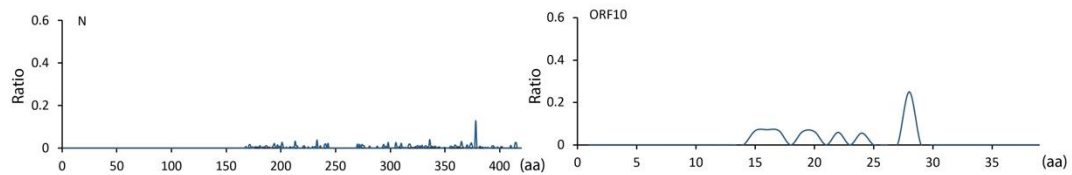
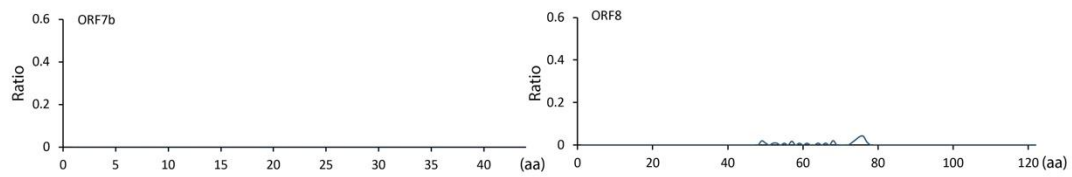
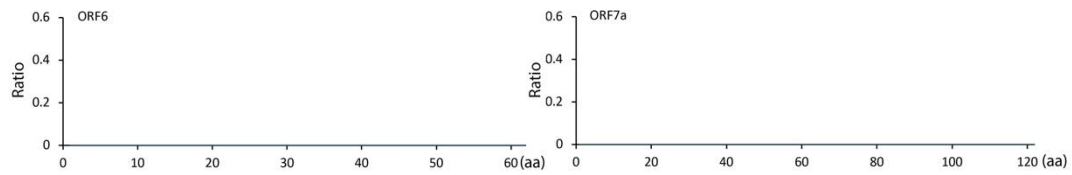
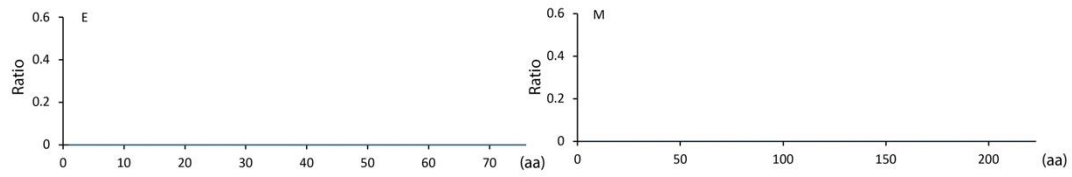
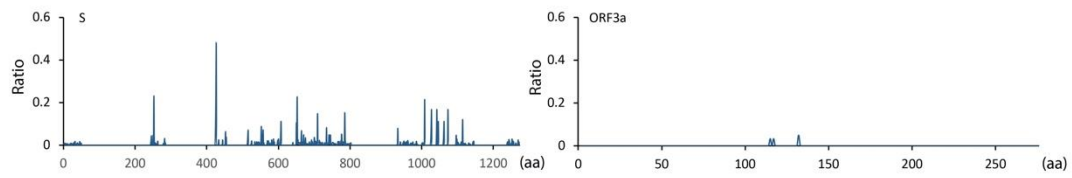
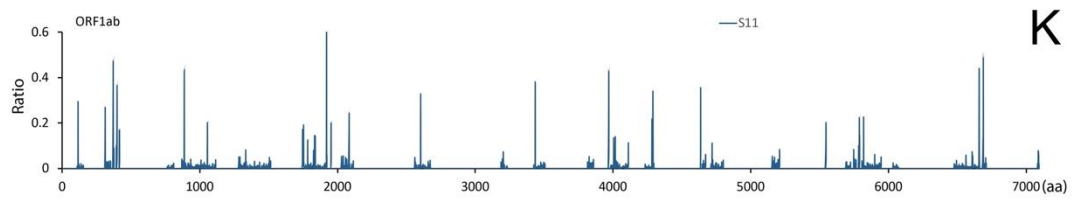


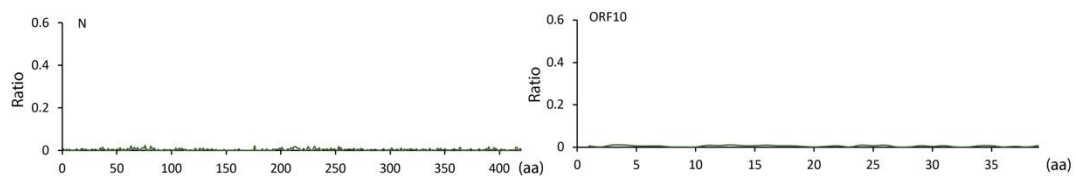
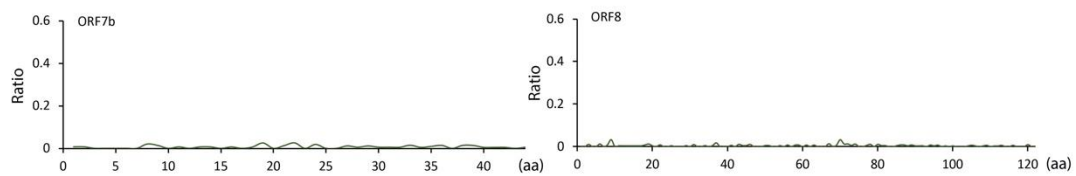
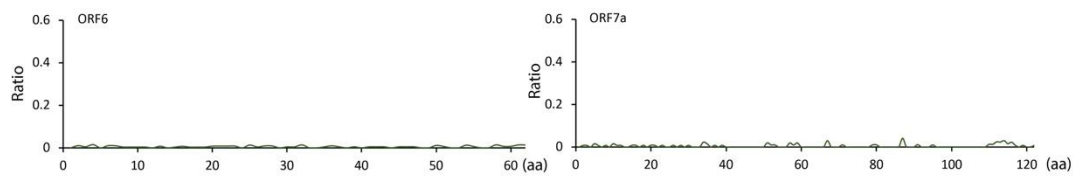
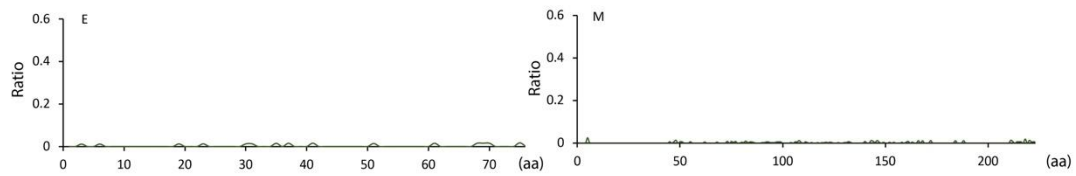
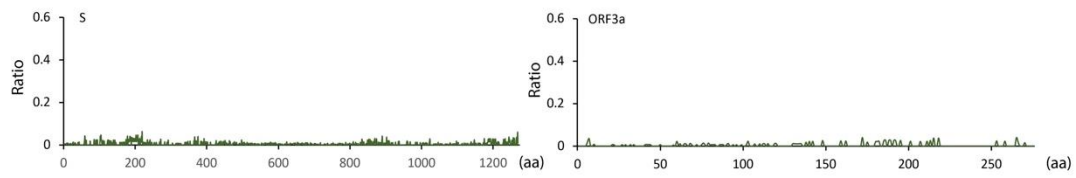
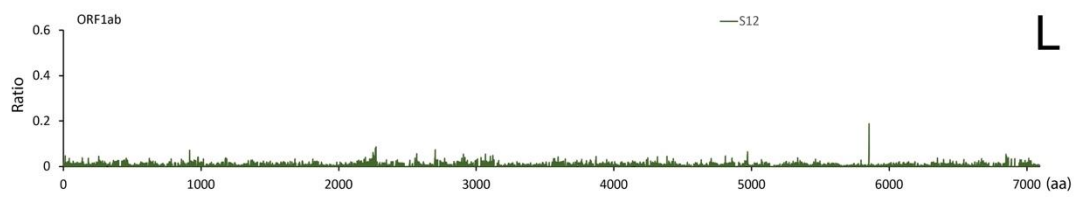


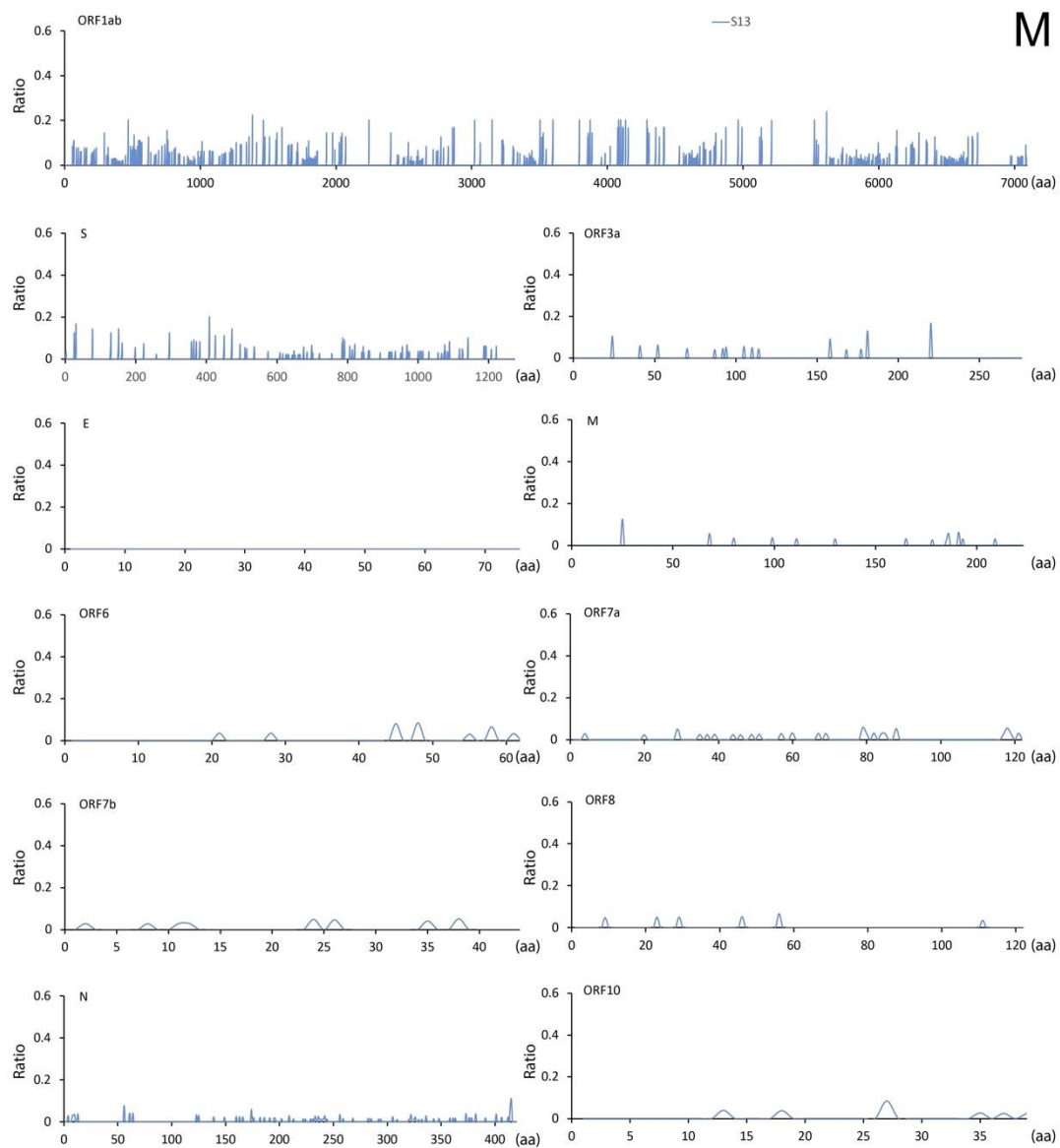


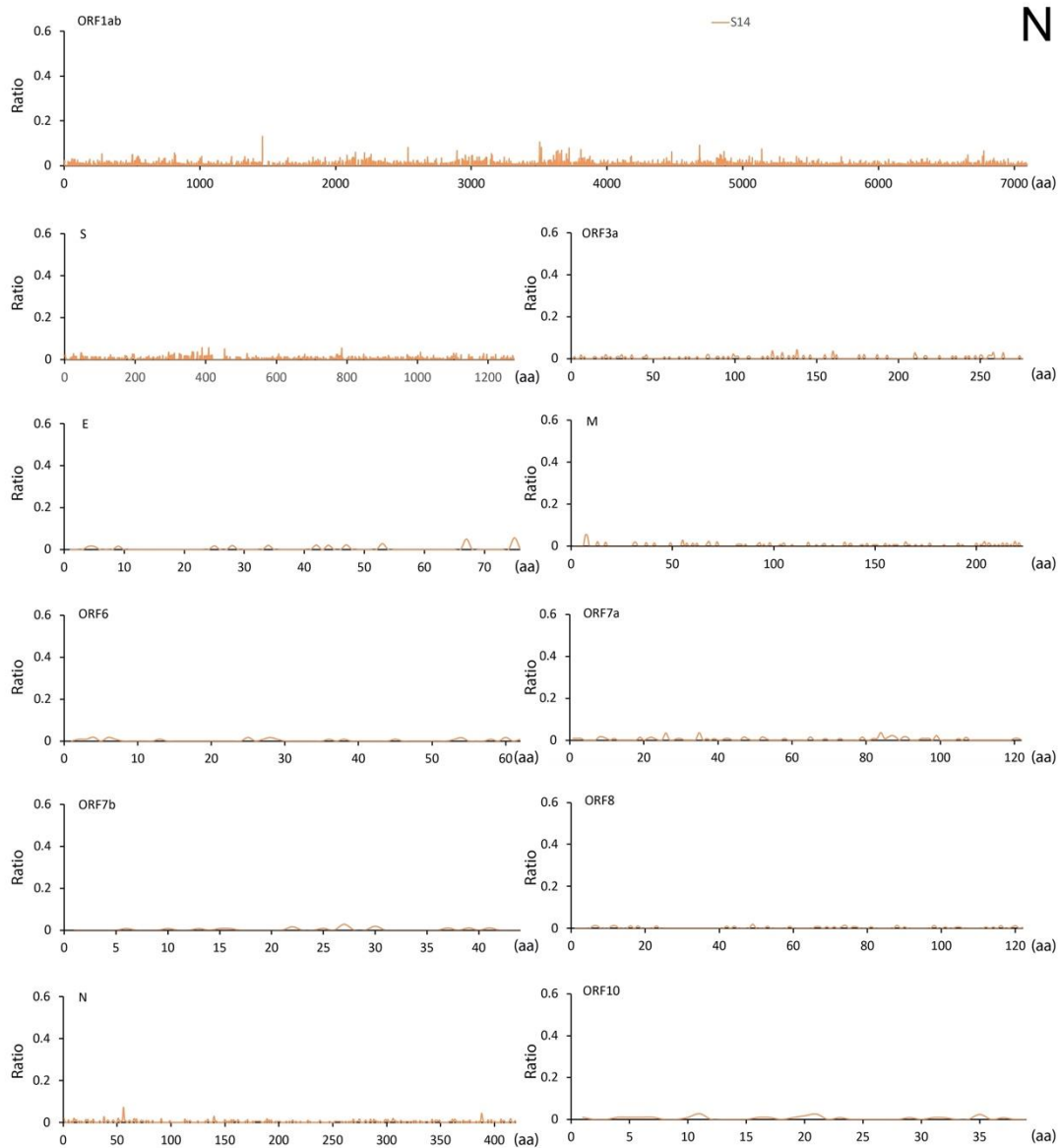


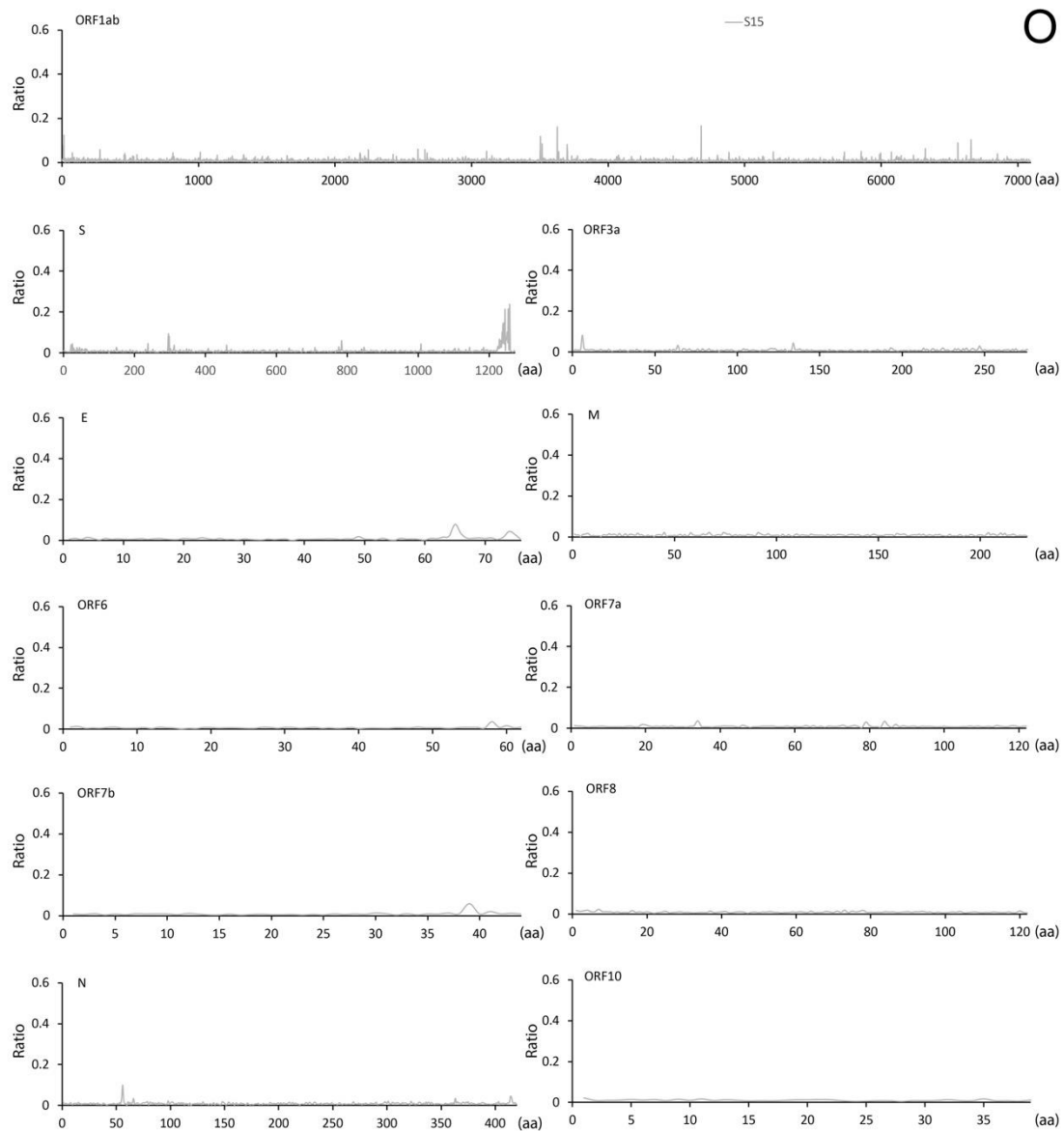












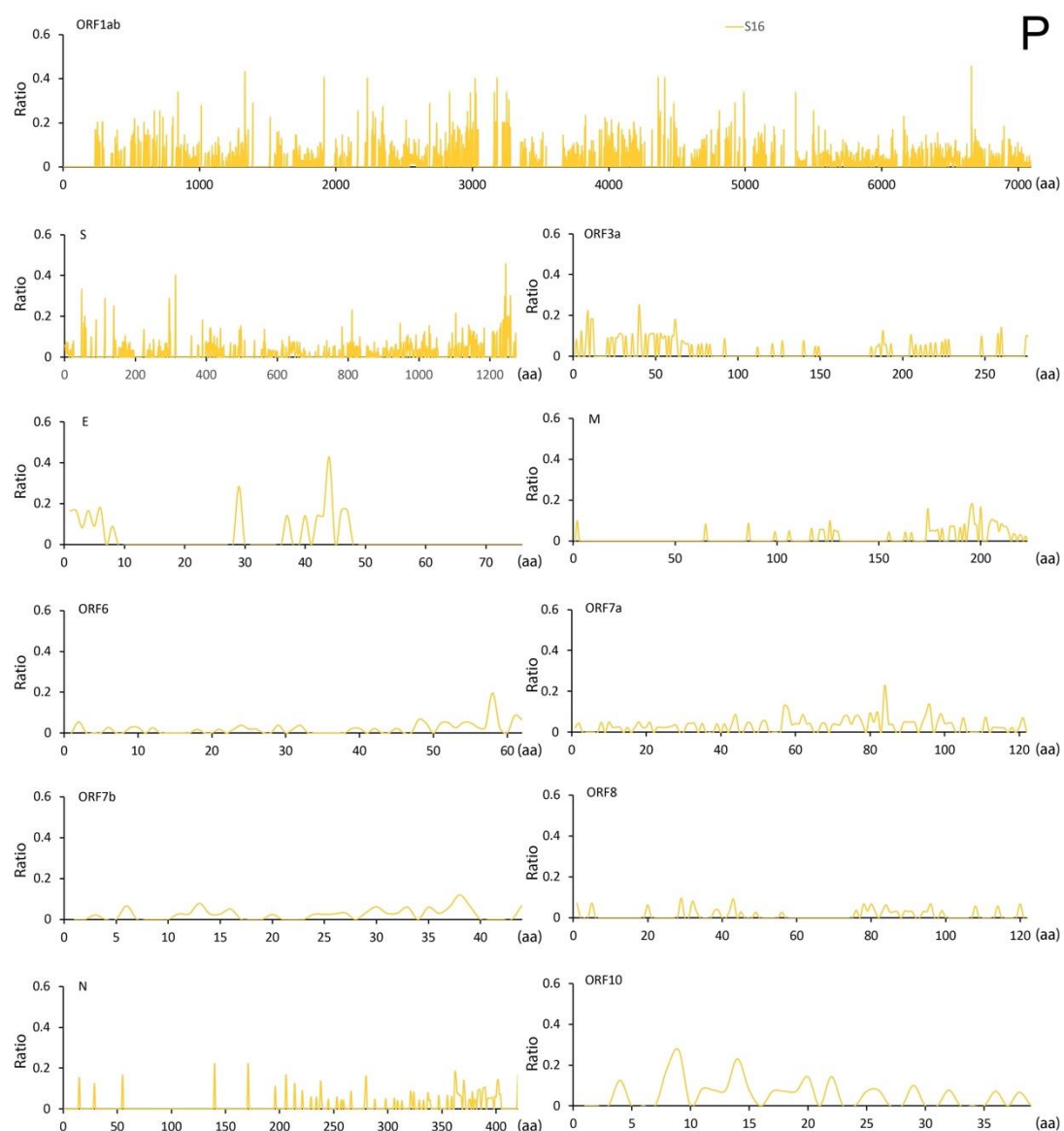


Fig. S1. Individual map of minor variant genomes across the SARS-CoV-2 genome for S1 (A), S2 (B), S3 (C), S4 (D), S5 (E), S6 (F), S7 (G), S8 (H), S9 (I), S10 (J), S11 (K), S12 (L), S13 (M), S14 (N), S15 (O), and S16 (P) in Fig. 1. The amino acid site with coverage ≥ 10 were showed.

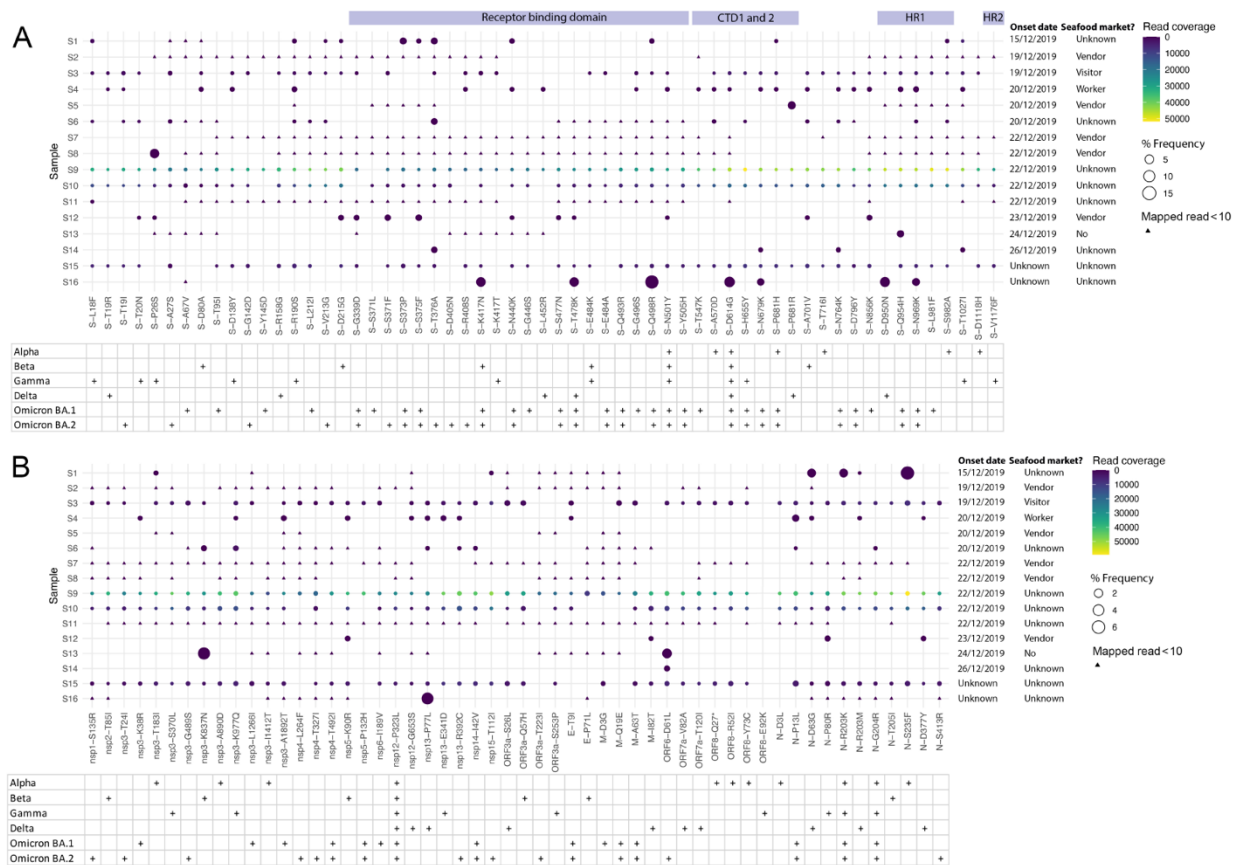


Fig. S2. Non-synonymous substitutions in the minor genomic variants of SARS-CoV-2 from each of the 16 down selected patients focusing on sites that define VoCs (<https://covariants.org/variants>) in the spike protein (A) and other regions of the genome (B). The amino acid site with coverage ≥ 10 were showed.



Fig. S3. Non-synonymous substitutions in the minor genomic variants of SARS-CoV-2 from each of the 16 down selected patients focusing on sites that define VoCs (<https://covariants.org/variants>) in the spike protein (A) and other regions of the genome (B). The amino acid site with coverage ≥ 100 were showed.

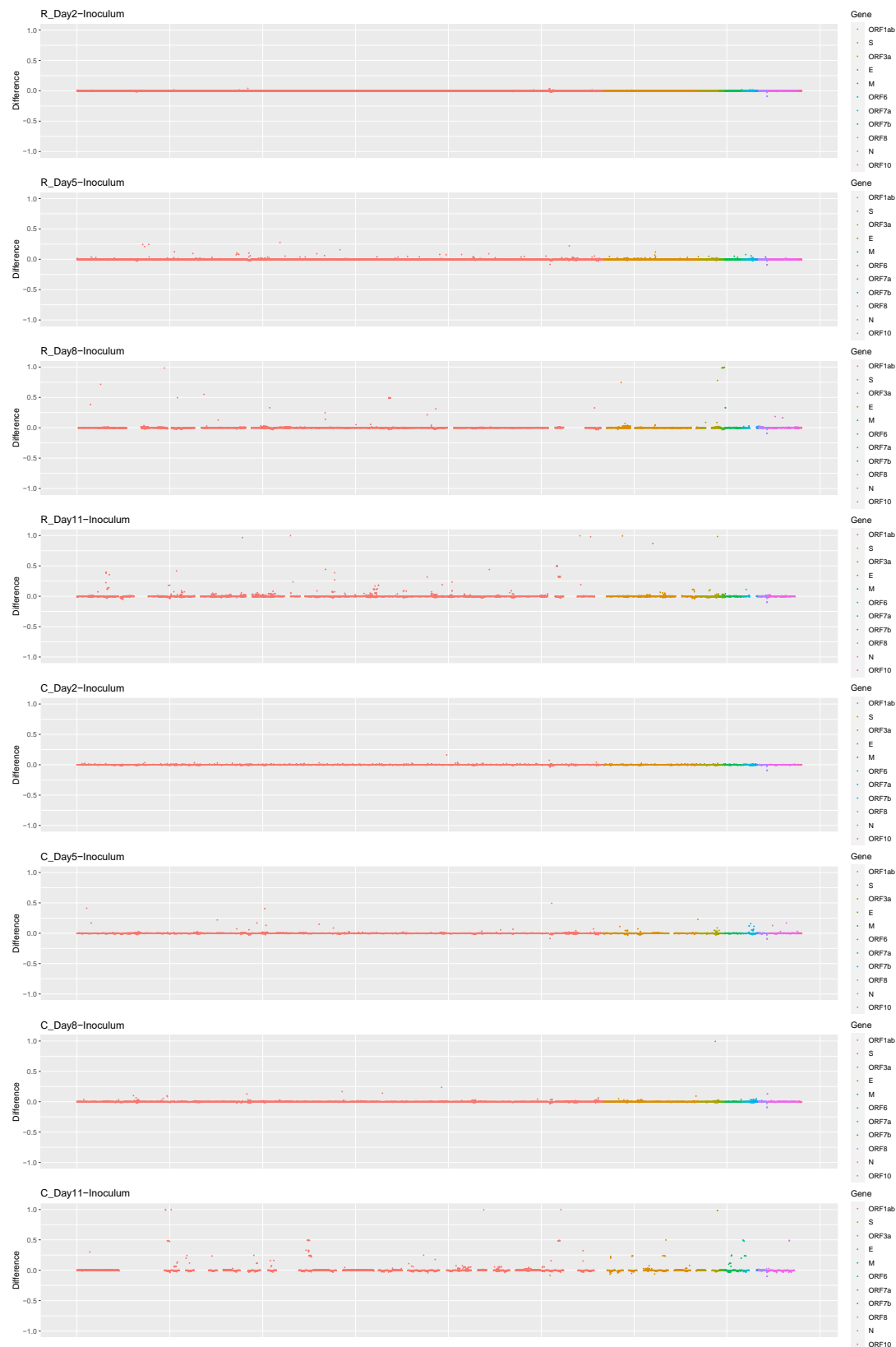


Fig. S4. The difference in non-synonymous mutation frequencies between the inoculum and the days post-infection was examined in two non-human primate models: rhesus (R) and cynomolgus (C) macaques. Each dot represents an amino acid site. Positive values indicate an increase in mutation frequencies compared to the inoculum during the days post-infection. The data were extracted from a published paper (DOI: 10.1186/s13059-023-02881-5).

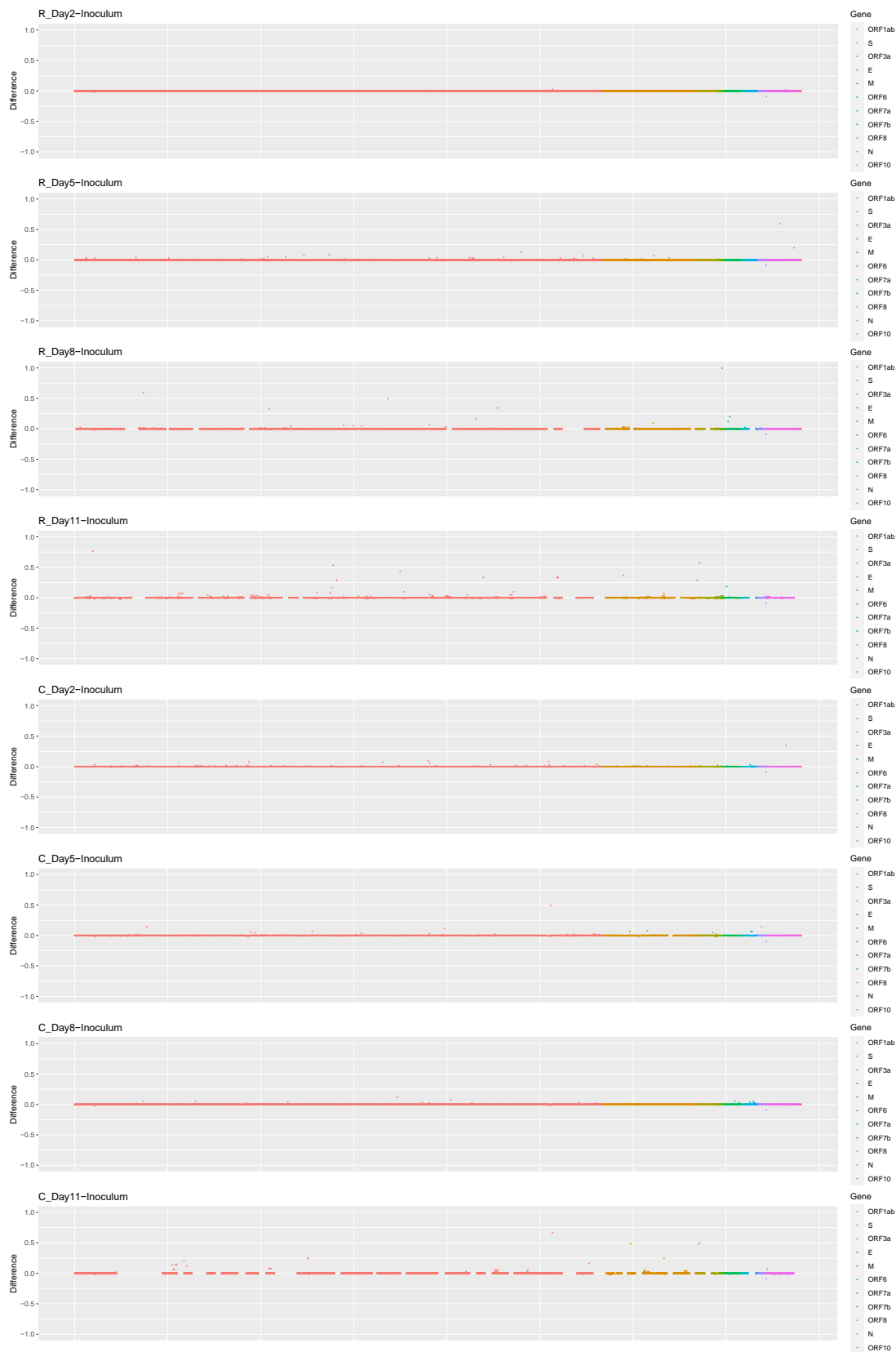


Fig. S5. The difference in synonymous mutation frequencies between the inoculum and the days post-infection was examined in two non-human primate models: rhesus (R) and cynomolgus (C) macaques. Each dot represents an amino acid site. Positive values indicate an increase in mutation frequencies compared to the inoculum during the days post-infection. The data were extracted from a published paper (DOI: 10.1186/s13059-023-02881-5).