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**Supplemental information**

**Remdesivir-induced emergence of SARS-CoV2  
variants in patients with prolonged infection**

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**Supplementary Material:**

**Supplementary Figures:**

**Supplementary Figure S1:** Nucleotide variant (NV) filtering and classification scheme.

**Supplementary Figure S2:** Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P03, P13, P05 and P06.

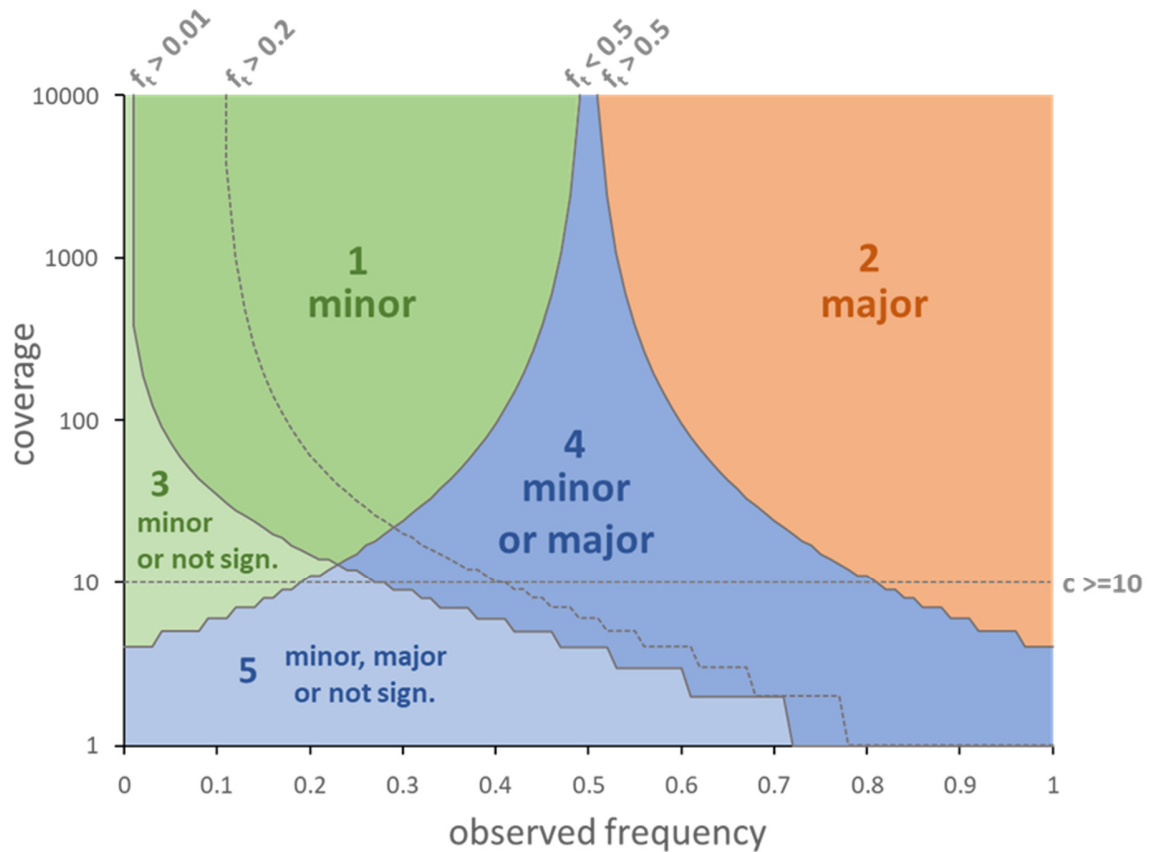
**Supplementary Figure S3:** Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P07, P08 and P09.

**Supplementary Figure S4:** Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P14, P15 and P16.

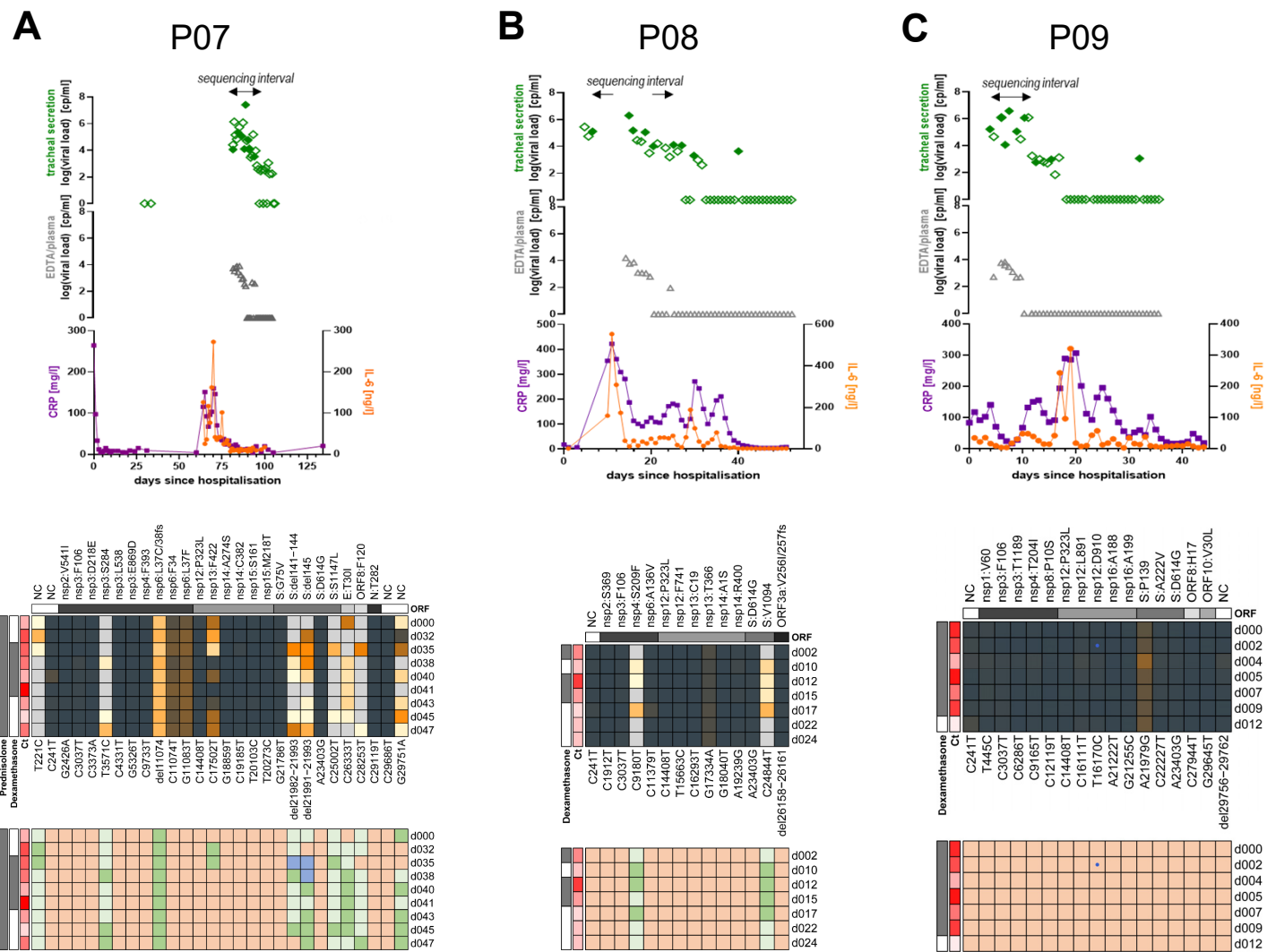
**Supplementary Figure S5:** Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P17, P18 and P10.

**Supplementary Figure S1: Nucleotide variant (NV) filtering and classification scheme.**

Solid grey lines indicate the minimum coverage required to differentiate observed frequency values from the threshold frequency values indicated at the top. Colored and labeled areas denote the classification of a given NV according to the observed coverage/frequency values. Dotted lines indicate additional cutoffs used for variant filtering. Data points with coverage values below 10 were generally not considered for downstream analysis.

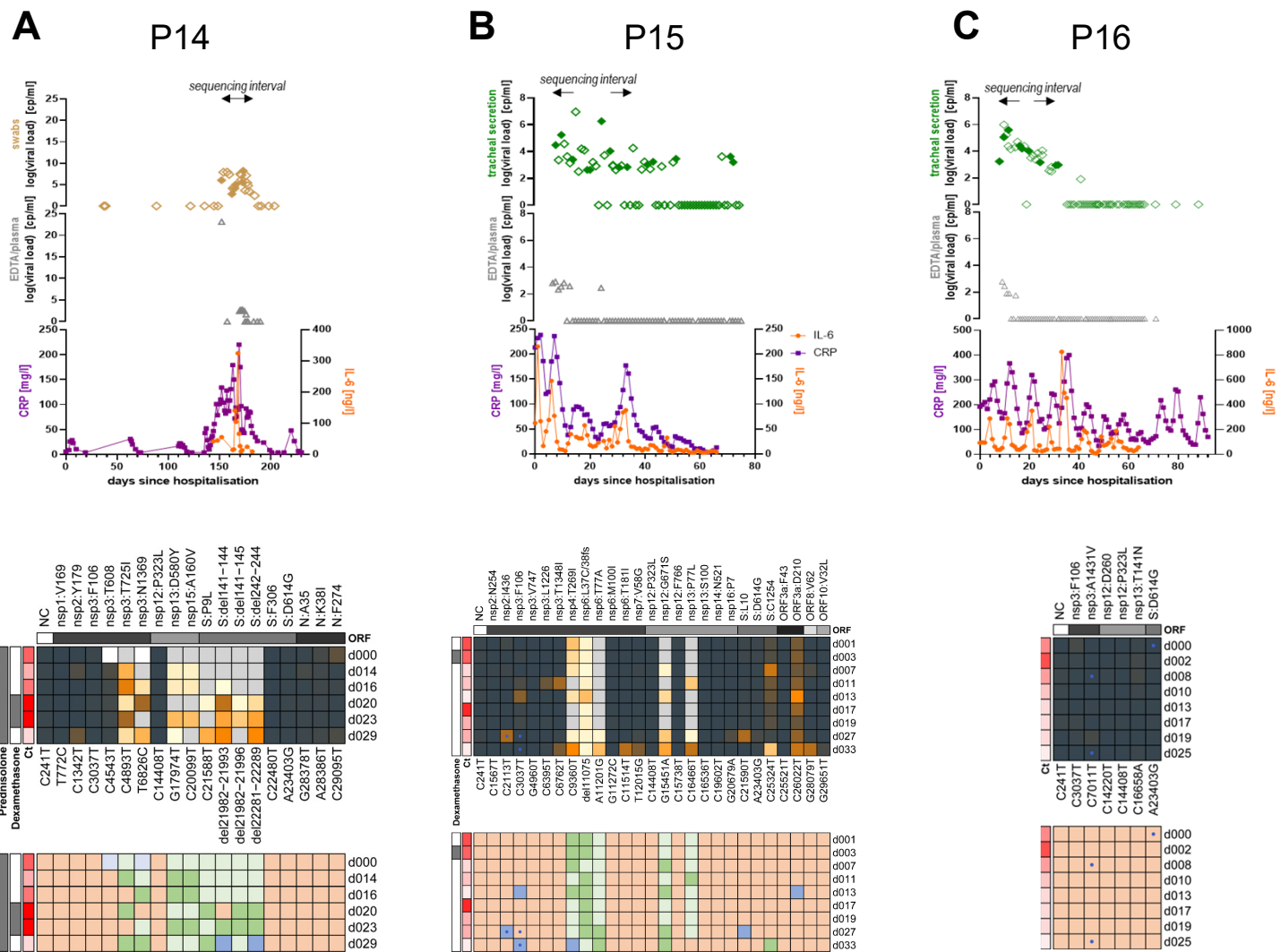






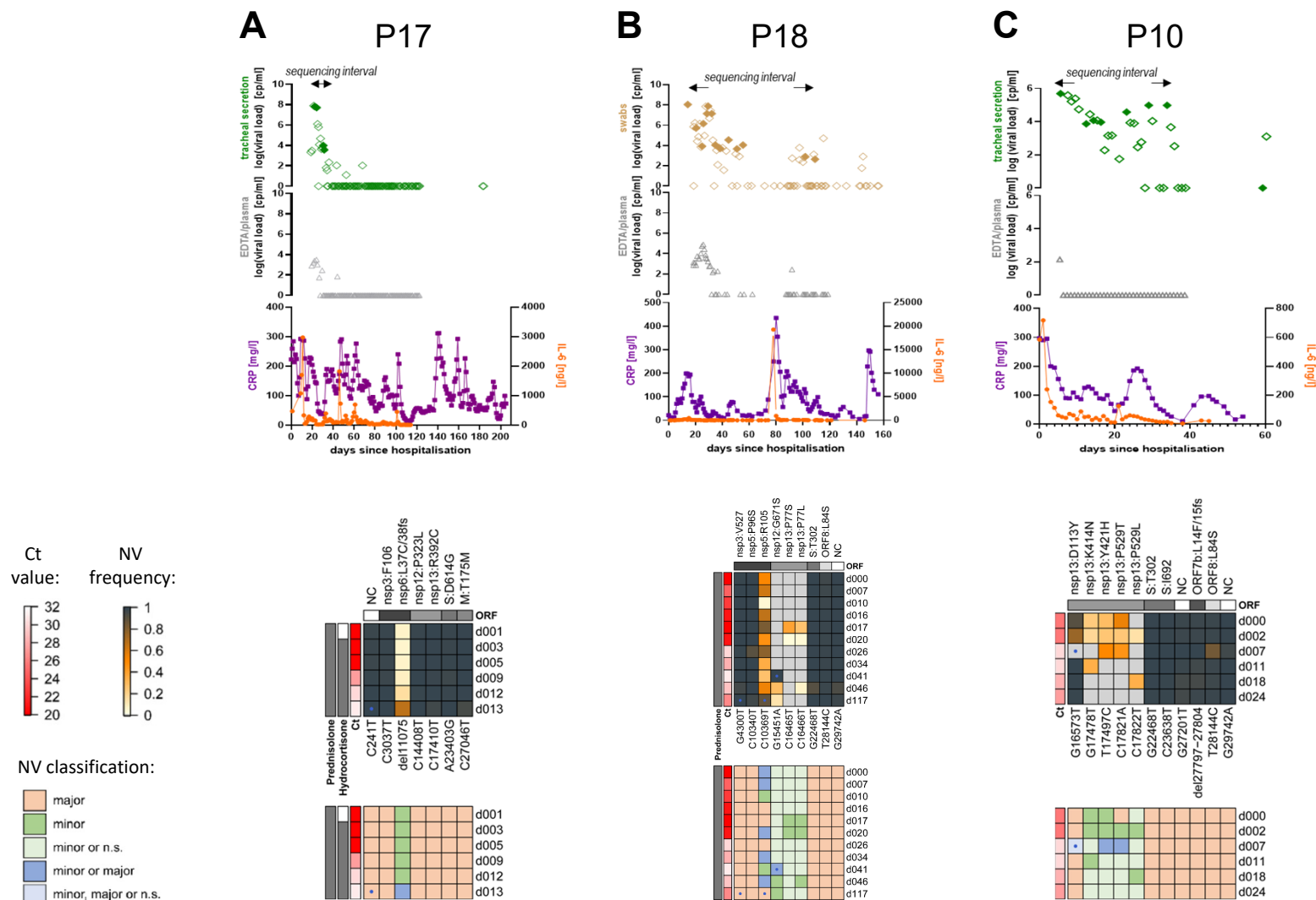
**Supplementary Figure S3: Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P07, P08 and P09.**

Upper plots in each panel show timeline of clinical and laboratory findings in patients with prolonged SARS-CoV-2 infection. Viral loads are shown separately for respiratory and (where available) blood samples. Respiratory samples subjected to SARS-CoV-2 genome sequencing are indicated by filled symbols. CRP and IL-6 values are indicated by purple and orange line plots, respectively. Heat maps in the center of each panel depict the frequency of nucleotide variants (NVs) in sequenced samples. Ct values and treatment regimen are shown to the left of the maps (see legends at left for Ct value and NV frequency color scales). The lowermost map in each panel shows classification of NVs according to the color scheme shown in the legend (n.s.: not significant; see main text and methods section for further information). Samples with coverage levels below 10 are shown with a blue dot in each map.



**Supplementary Figure S4: Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants in samples from patients P14, P15 and P16.**

Upper plots in each panel show timeline of clinical and laboratory findings in patients with prolonged SARS-CoV-2 infection. Viral loads are shown separately for respiratory and (where available) blood samples. Respiratory samples subjected to SARS-CoV-2 genome sequencing are indicated by filled symbols. CRP and IL-6 values are indicated by purple and orange line plots, respectively. Heat maps in the center of each panel depict the frequency of nucleotide variants (NVs) in sequenced samples. Ct values and treatment regimen are shown to the left of the maps (see legends at left for Ct value and NV frequency color scales). The lowermost map in each panel shows classification of NVs according to the color scheme shown in the legend (n.s.: not significant; see main text and methods section for further information). Samples with coverage levels below 10 are shown with a blue dot in each map.



**Supplementary Figure S5: Timeline of clinical and laboratory findings and maps of SARS-CoV-2 nucleotide variants detected in samples from patients P17, P18 and P10.**

Upper plots in each panel show timeline of clinical and laboratory findings in patients with prolonged SARS-CoV-2 infection. Viral loads are shown separately for respiratory and (where available) blood samples. Respiratory samples subjected to SARS-CoV-2 genome sequencing are indicated by filled symbols. CRP and IL-6 values are indicated by purple and orange line plots, respectively. Heat maps in the center of each panel depict the frequency of nucleotide variants (NVs) in sequenced samples. Ct values and treatment regimen are shown to the left of the maps see legends at left for Ct value and NV frequency color scales). The lowermost map in each panel shows classification of NVs according to color scheme shown in the legend (n.s.: not significant; see main text and methods section for further information). Samples with coverage levels below 10 are shown with a blue dot in each map.