

**Molnupiravir  
N=10**

**Paxlovid  
N=9**

**Drug Naïve  
N=5**

**7  
complete  
follow-up**

**3  
not complete  
follow-up**

**6  
complete  
follow-up**

**3  
not complete  
follow-up**

**1  
complete  
follow-up**

**4  
not complete  
follow-up**

- One patient with undetectable viral load at all time points

- One patient without Day 7 (ID 12)
- One patient without Day 7 and undetectable viral load at Day 5 (ID13)
- One patient without Day 5 and 7

- One patient without Day 2 (ID 7)
- One patient without Day 7 and for which sequencing failed at the remaining time-points
- One patient without Day 2, 5 and 7

- Patient with SARS-CoV-2 RNA load undetectable at Day 7

- Two patients without Day 2 (ID17 and ID21)
- One patient without Day 2 and undetectable viral load at Day 7 (ID19)
- One patient without Day 5 (ID20)



**6 patients included  
in the final analysis**

**ID12 and ID13  
included in the final  
analysis**

**All included in the  
final analysis**

**ID7 included in the  
final analysis**

**Patient included in  
the final analysis**

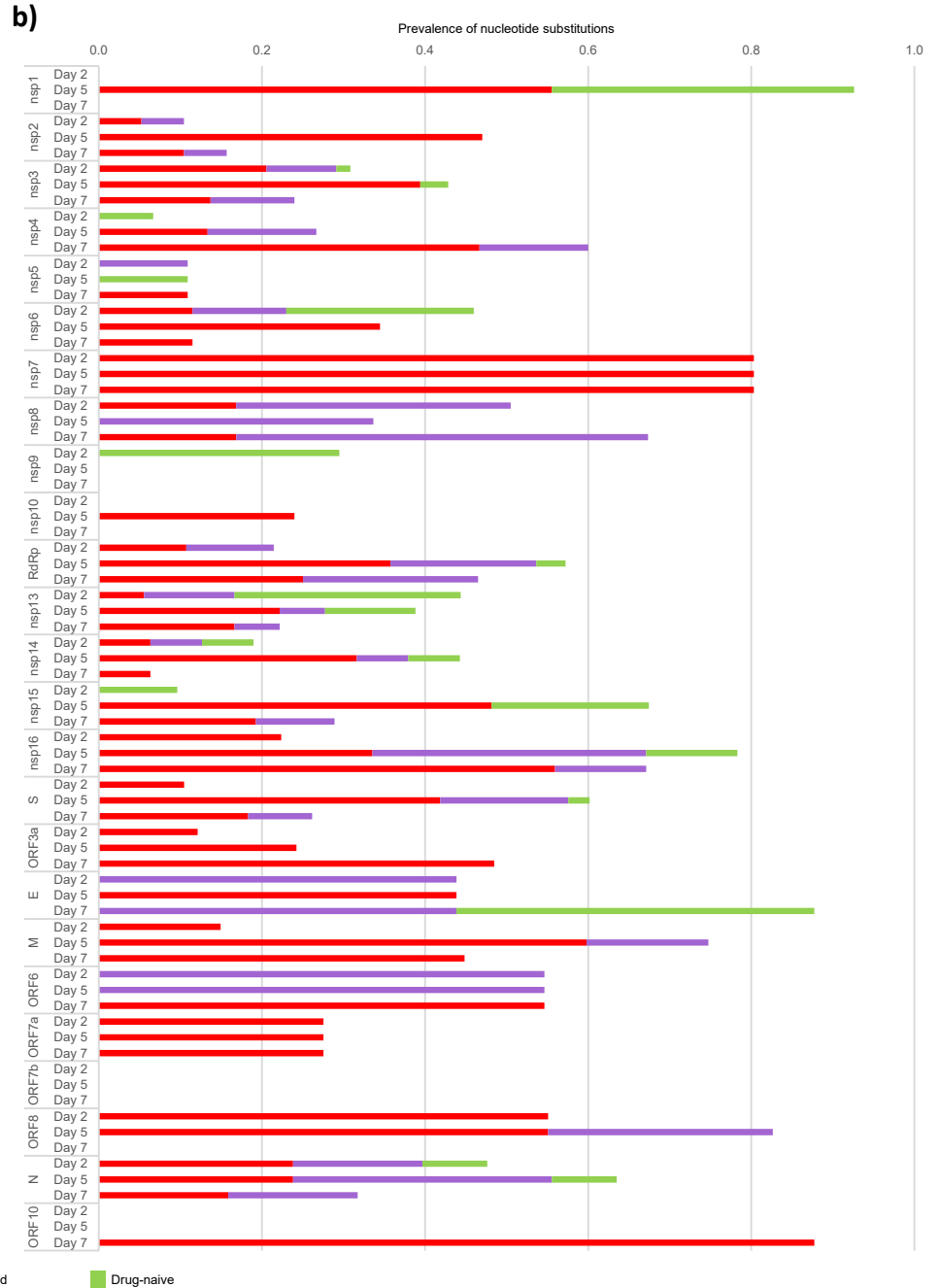
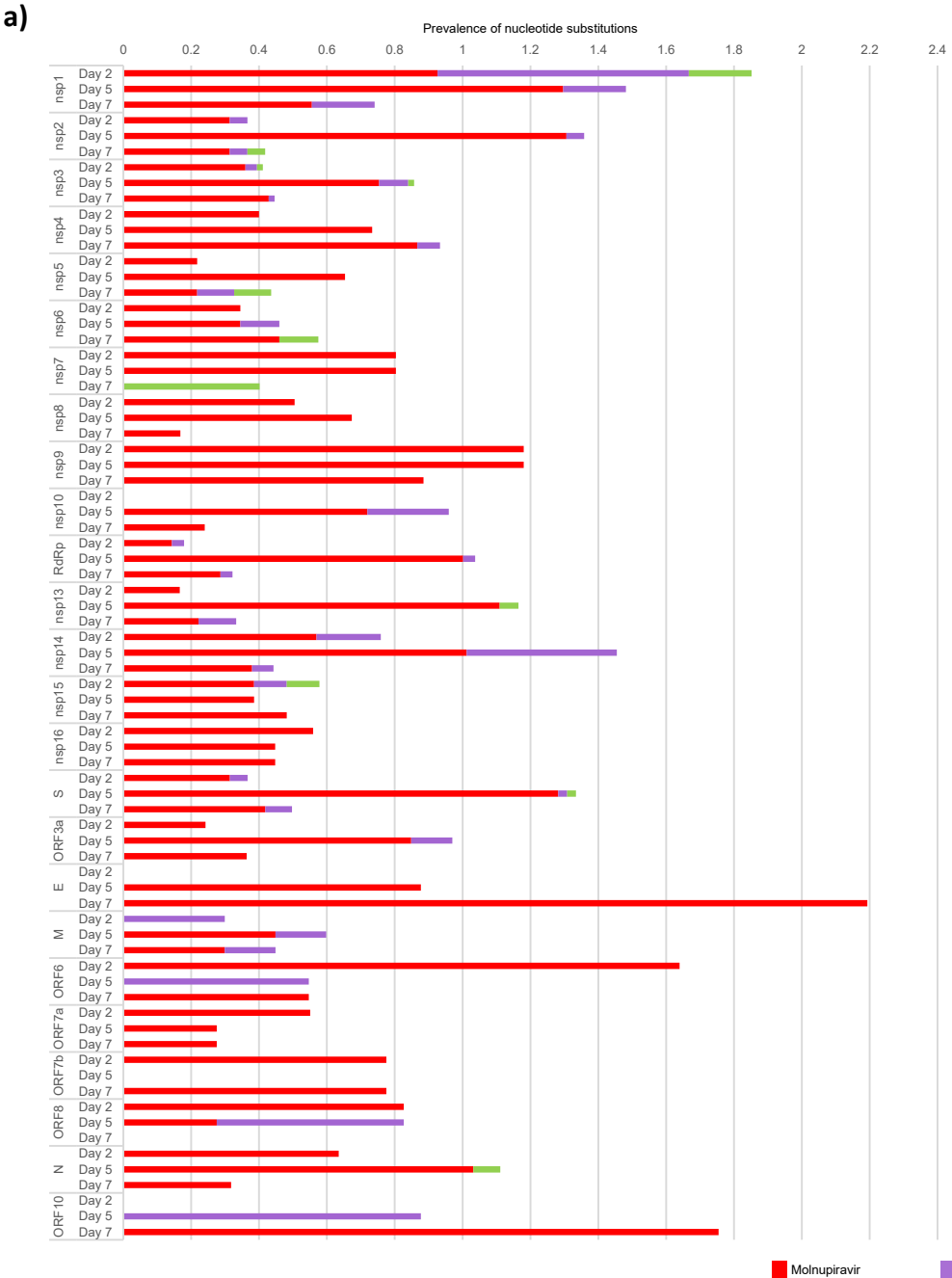
**All included in the  
final analysis**

**TOTAL NUMBER OF MOLNUPIRAVIR  
TREATED PATIENTS: 8**

**TOTAL NUMBER OF PAXLOVID TREATED  
PATIENTS: 7**

**TOTAL NUMBER OF DRUG NAIVE  
PATIENTS: 5**

**Supplementary Figure 1. Selection criteria for the 20 SARS-CoV-2 infected patients included in the final analyses.**



**Supplementary Figure 2. Prevalence of C to T and G to A transitions (a) and other nucleotide substitutions (b) per site divided by nucleotide sequence length. Graph bars are colored based on study group.**

**Supplementary Table 1: Genetic distance between different time-points according to study groups.**

	Genetic distance, median (IQR) ( $\times 10^{-4}$ )			P-value*	P-value**
	Day 0 - Day 2	Day 2 - Day 5	Day 5 - Day 7		
<b>Molnupiravir treated</b>	8.5 (0.0-9.6)	16.2 (8.5-32.9)	20.9 (8.5-29.2)	0.043	0.144
<b>Paxlovid treated</b>	2.1 (0.0-3.4)	3.1 (0.9-5.5)	3.1 (0.4-9.0)	0.686	0.600
<b>Drug Naive</b>	3. (0.8-6.0)	3.4	2.1 (0.4-3.4)	NA	0.155

Genetic distance is expressed as nucleotide substitutions per site. P-values were calculated by Wilcoxon test; NA: not available. \*P-values comparing genetic distance observed at Day0-Day2 and at Day2-Day5. \*\*P-values comparing genetic distance observed at Day2-Day5 and at Day5-Day7.