Table S4. Frequency of different substitutions types in the SARS-CoV-2 lineages and among the virus variants identified in a single individual

substitution	A>C [%]		A>G [%]		A>U [%]		C>A [%]		C>G [%]		C>U [%]		G>A [%]		G>C [%]		G>U [%]		U>A [%]		U>C [%]		U>G [%]		total [%]	
	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa	GL	Pa
nonsynonymous	0.0	0.0	5.9	7.0	2.2	3.0	3.7	2.0	0.0	0.0	20.7	19.0	5.9	14.0	3.7	4.0	10.4	13.0	2.2	2.0	2.2	5.0	0.7	2.0	57.8	71.0
synonymous	0.0	0.0	1.5	0.0	0.7	0.0	0.7	1.0	0.7	0.0	22.2	14.0	1.5	0.0	0.7	1.0	2.2	2.0	0.0	0.0	6.7	6.0	0.0	1.0	37.0	25.0
UTR	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	1.5	0.0	0.7	0.0	0.0	1.0	0.7	1.0	0.0	0.0	0.0	0.0	0.0	0.0	3.7	2.0
stop	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	1.0	0.0	0.0	0.0	0.0	0.7	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	2.0
total	0.0	0.0	7.4	7.0	3.0	3.0	5.2	3.0	0.7	0.0	45.2	34.0	8.1	14.0	4.4	6.0	14.1	17.0	2.2	2.0	8.9	11.0	0.7	3.0	100.0	100.0

GL - Global pattern; Pa - virus variants identified in the course of medical treatment of a single individual