

Subject	222				251				
Sample type	OP				NP / OP				
Sample day	1	1	4	4	1	1	3	3	3
Replicate	1	2	1	2	1	2	1	2	3

241 intergenic	704	576	741	729	241 intergenic	1303	4964	2277	575	584
1059 orf1ab T265I	5162	562	2877	675	1918 orf1ab silent	1449	4334	1728	1347	515
3037 orf1ab silent	3513	716	1527	671	3037 orf1ab silent	2589	1542	1850	278	887
8782 orf1ab silent	283	489	281	219	8782 orf1ab silent	2305	230	1900	107	316
11916 orf1ab S3884L	2366	258	946	118	14408 orf1ab P314L	2062	64	3791	186	206
14408 orf1ab P314L	3229	474	1252	120	18060orf1absilent	2529	478	1816	184	302
18060 orf1ab silent	3162	412	1151	261	18877 orf1ab silent	4242	175	4399	753	745
18998 orf1ab A1844V	248	394	324	137	21625 S silent	1529	16	529	38	81
21526 orf1ab I2687V	36	31	36	16	23230 S silent	2075	3342	3509	1050	488
23403 S D614G	1948	1034	1824	1065	23403 S D614G	2573	4155	4784	1276	579
25563 orf3a Q57H	4793	822	2629	1069	25563 orf3a Q57H	1375	4101	1487	487	365
28144 orf8 S84L	928	328	626	214	28144 orf8 S84L	1034	115	3792	508	465
29540 intergenic	757	374	265	316						

Base change

Expected	C
A	G
T	Ins/Del

Figure 2. Longitudinal variation detected in SARS-CoV-2 genomes from our inpatient cohort. Each column represents a single sample, defined by subject, sample type, and days after initiation of sampling. Base substitutions are shown relative to USA-WA1-2020 reference. Tile color indicates the observed base change; tiles with more than one color indicate the presence of minor variants. Each tile also shows the number of sequence reads obtained.