

Subject	Sample type	211				Sample type	251			
		ETA		OP			ETA		NP / OP	
		1	1	1			1	1	2	3
241 intergenic		1120	944	990		241 intergenic	1422	2277	575	584
1059orf1ab T265I		1394	640	2642		1918orf1ab silent	1605	1728	1347	515
3037orf1ab silent		1287	591	1690		3037orf1ab silent	1227	1850	278	887
4113orf1ab A1283V		1326	1237	1753		8782orf1ab silent	1129	1900	107	316
6285orf1ab T2007I		2512	920	129		14408orf1ab P314L	2583	3791	186	206
8782orf1ab silent		1353	435	120		18060orf1ab silent	1249	1816	184	302
9615orf1ab T3117I		1061	321	660		18877orf1ab silent	3374	4399	753	745
11916orf1ab S3884L		1239	568	1283		21625S silent	264	529	38	81
14408orf1ab P314L		1492	517	1631		23230S silent	2725	3509	1050	488
17443orf1ab A1326T		710	376	1536		23403S D614G	3810	4784	1276	579
18060orf1ab silent		1198	567	1633		25563orf3a Q57H	1114	1487	487	365
18998orf1ab A1844V		1291	665	106		26333E T30I	1331	1975	281	271
21792S K77I		1159	461	1931		28144orf8 S84L	2363	3792	508	465
21793S K77I		1156	464	1939						
23403S D614G		1441	2056	1532						
24197S A879S		1204	538	2322						
25563orf3a Q57H		1361	645	2480						
28144orf8 S84L		1044	558	386						
29540intergenic		1648	351	419						

#### Base change



**Figure 3.** Site-specific variation detected in SARS-CoV-2 genomes from our inpatient cohort. Each column represents a single sample from subjects from whom two sample types were collected on the same day. 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.