Table S3. Single nucleotide variants and their frequencies (%) in each studied specimen (Table S1), relative to MN908947.3 reference genome.
Position genome position (MN908947.3 coordinates); *ref* reference base; *alt* alternative base; *aa* amino acid mutation and corresponding codon position (MN908947.3 coordinates); *ND* not detected.

position	ref	alt	gene	aa	13	14	15	16	42	43	44	46	52	53	54	55	56	62	63	64	65	66
670	T	G	nsp1	S135R	ND	ND	ND	ND	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
694	T	A	nsp1	F143L	ND	ND	ND	ND	99.7	99.5	99.6	89.7	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
1027	T	C	nsp2	P74P	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.8	ND	ND
1150	C	T	nsp2	G115G	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.9	ND	ND
1627	C	T	nsp2	L274L	ND	ND	ND	ND	ND	ND	ND	ND	99.9	100.0	99.9	100.0	100.0	99.9	73.8	92.4	ND	99.8
2388	C	T	nsp2	T528I	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	17.6	15.5	100.0	ND
2422	G	T	nsp2	K539N	ND	ND	ND	ND	ND	ND	ND	ND	5.2	ND	ND	ND	ND	ND	ND	ND	ND	ND
2470	C	T	nsp2	A555A	100.0	99.9	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
2524	A	G	nsp2	T573T	ND	ND	ND	3.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
2790	C	T	nsp3	T24I	ND	ND	ND	ND	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
2832	A	G	nsp3	K38R	99.9	99.9	99.8	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
3037	C	T	nsp3	F106F	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
3648	T	C	nsp3	I310T	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.5	ND
3859	A	G	nsp3	Q380Q	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.3
4184	G	A	nsp3	G489S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0
4321	C	T	nsp3	A534A	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	99.9	100.0	100.0
4358	C	T	nsp3	Q547*	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	4.6	ND	ND
4925	G	T	nsp3	D736Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.0	ND	ND
5386	T	G	nsp3	A889A	99.8	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
5549	C	A	nsp3	L944I	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
5803	T	G	nsp3	Y1028*	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.1	ND
6041	G	C	nsp3	D1108H	ND	ND	ND	ND	ND	ND	ND	ND	4.1	ND	ND	ND	ND	ND	ND	ND	ND	ND
6354	C	T	nsp3	S1212L	ND	ND	ND	ND	ND	ND	ND	ND	3.4	ND	ND	ND	ND	ND	ND	ND	ND	ND
6515	T	A	nsp3	L1266I	99.7	99.6	99.8	99.8	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
6675	C	T	nsp3	T1319I	ND	ND	ND	ND	100.0	100.0	99.7	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
6822	C	T	nsp3	T1368I	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.2
7312	G	T	nsp3	L1531F	ND	ND	ND	ND	ND	ND	ND	ND	3.5	ND	ND	ND	ND	ND	ND	ND	ND	ND
8302	A	G	nsp3	K1861K	ND	ND	ND	ND	ND	ND	9.6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
8354	C	T	nsp3	R1879C	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.2	ND	ND	ND	ND	ND	ND
8393	G	A	nsp3	A1892T	100.0	100.0	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
9196	A	G	nsp4	T214T	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.5	ND	ND
9344	C	T	nsp4	L264F	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0
9424	A	G	nsp4	V290V	ND	ND	ND	ND	99.9	100.0	99.9	100.0	ND	ND	ND	ND	ND	100.0	100.0	100.0	99.9	99.9

9534	C	T	nsp4	T327I	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9
9893	C	T	nsp4	L447F	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	98.5	71.3	92.6	ND	100.0
9950	G	C	nsp4	A466P	ND	ND	ND	ND	ND	ND	ND	ND	3.0	ND	ND	ND	ND	ND	ND	ND	ND	ND
10029	C	T	nsp4	T492I	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9
10198	C	T	nsp5ab	D48D	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	99.9	100.0	100.0	100.0	100.0
10278	T	A	nsp5ab	L75H	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	8.0	ND	ND	ND	ND	ND	ND
10439	G	C	nsp5ab	A129P	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	4.0	ND	ND
10447	G	A	nsp5ab	R131R	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.8	100.0
10448	C	T	nsp5ab	P132S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	25.5	4.1	100.0	ND
10449	C	A	nsp5ab	P132H	100.0	99.9	100.0	99.9	100.0	99.9	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
10848	G	T	nsp5ab	C265F	ND	ND	ND	ND	ND	ND	ND	ND	3.2	ND	ND	ND	ND	ND	ND	ND	ND	ND
11075	T	C	nsp6	F35L	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.0	ND	ND
11130	C	T	nsp6	S53F	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.9	ND
11288	T	A	nsp6	S106T	ND	ND	ND	ND	ND	ND	ND	ND	96.2	100.0	94.4	100.0	100.0	92.9	100.0	100.0	100.0	100.0
11291	G	A	nsp6	G107S	99.9	99.5	100.0	99.5	ND	ND	ND	ND	99.9	100.0	99.8	100.0	99.9	100.0	99.9	99.8	100.0	100.0
11296	T	G	nsp6	F108L	ND	ND	ND	ND	ND	ND	ND	ND	99.6	99.9	99.8	99.9	99.8	99.8	99.9	99.8	100.0	99.9
11537	A	G	nsp6	I189V	99.9	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
11948	C	T	nsp7	H36Y	ND	ND	ND	ND	ND	ND	6.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
12049	C	T	nsp7	N69N	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.3	3.4	ND	ND	ND	ND	ND	ND	ND
12160	G	A	nsp8	E23E	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
12499	C	T	nsp8	N136N	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	100.0	77.8	79.6	ND	100.0
12880	C	T	nsp9	I65I	ND	ND	ND	ND	99.9	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	99.9	100.0
12921	C	T	nsp9	T79I	ND	ND	ND	ND	ND	ND	ND	ND	3.9	ND	ND	ND	ND	ND	ND	ND	ND	ND
13195	T	C	nsp10	V57V	99.9	100.0	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
13299	T	C	nsp10	L92S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.4	ND	ND	ND	ND
13386	G	T	nsp10	G121V	ND	ND	ND	ND	34.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
13749	G	T	nsp12	K103N	ND	ND	ND	ND	7.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
13874	T	C	nsp12	I145T	ND	ND	ND	ND	ND	ND	ND	ND	3.7	ND	ND	ND	ND	ND	ND	ND	ND	ND
13922	A	T	nsp12	D161V	ND	ND	ND	ND	ND	ND	7.1	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
14408	C	T	nsp12	P323L	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0
14625	C	T	nsp12	C395C	ND	ND	ND	ND	ND	ND	ND	ND	3.2	ND	ND	ND	ND	ND	ND	ND	ND	ND
15007	G	A	nsp12	D523N	5.7	4.4	5.8	4.1	ND	ND	ND	ND	4.9	3.8	5.6	5.3	6.4	5.2	5.2	5.5	6.5	6.4
15009	T	C	nsp12	D523D	6.3	4.8	8.4	5.9	ND	ND	ND	ND	8.0	8.8	8.4	5.9	7.4	6.8	6.5	7.1	9.1	6.8
15100	G	T	nsp12	A554S	ND	ND	ND	ND	ND	ND	ND	ND	5.3	ND	ND	ND	ND	ND	ND	ND	ND	ND
15216	C	T	nsp12	S592S	ND	ND	ND	ND	ND	ND	ND	ND	ND	8.0	ND	41.1	ND	ND	ND	ND	ND	ND
15237	C	T	nsp12	H599H	ND	3.1	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
15240	C	T	nsp12	N600N	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
15303	A	G	nsp12	K621K	ND	ND	ND	ND	9.4	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

15377	G	T	nsp12	C646F	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.4	ND	ND
15472	G	C	nsp12	G678R	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.0	ND	ND
15629	G	A	nsp12	C730Y	ND	ND	ND	ND	8.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
15714	C	T	nsp12	L758L	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0
16206	G	T	nsp12	E922D	ND	ND	ND	ND	ND	ND	ND	ND	3.0	ND	ND	ND	ND	ND	ND	ND	ND	ND
16977	T	C	nsp13	V247V	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	24.4	ND	
17020	T	C	nsp13	F262L	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.8	ND	ND	ND	ND	ND	ND	ND	ND
17104	C	T	nsp13	H290Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	98.6	72.8	91.4	10.4	99.8
17130	C	T	nsp13	Y298Y	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	8.4	ND	
17410	C	T	nsp13	R392C	ND	ND	ND	ND	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
18160	G	A	nsp14	D41N	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	20.1	ND	
18163	A	G	nsp14	I42V	98.9	99.7	96.3	100.0	100.0	100.0	99.9	100.0	100.0	100.0	99.9	100.0	100.0	100.0	99.9	100.0	99.9	100.0
18163	A	T	nsp14	I42L	ND	ND	3.6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
18416	A	G	nsp14	D126G	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	21.5	ND	
18685	T	G	nsp14	C216G	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.3	ND	ND
19024	C	T	nsp14	L329F	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.5	ND	ND
19955	C	T	nsp15	T112I	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	99.7	100.0	100.0	100.0	100.0	100.0	100.0	100.0
20055	A	G	nsp15	E145E	ND	ND	ND	ND	ND	ND	ND	ND	98.8	100.0	99.5	98.6	96.8	ND	ND	ND	ND	ND
20933	G	T	nsp16	G92V	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.3	ND	ND
21077	C	T	nsp16	T140I	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	97.5	78.8	89.8	ND	99.9
21381	C	A	nsp16	S241S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	5.9	ND	ND
21595	C	T	S12	V11V	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
21618	C	T	S12	T19I	ND	ND	ND	ND	100.0	100.0	99.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
21641	G	T	S12	A27S	ND	ND	ND	ND	ND	ND	ND	ND	99.8	98.5	100.0	99.7	99.8	99.4	98.3	100.0	100.0	99.4
21762	C	T	S12	A67V	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
21770	G	A	S12	V70I	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	100.0	98.9	94.7	100.0	100.0	98.7	100.0	100.0
21846	C	T	S12	T95I	100.0	100.0	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
21869	G	T	S12	G103C	ND	ND	ND	ND	ND	ND	ND	ND	3.8	ND	ND	ND	ND	ND	ND	ND	ND	ND
21987	G	A	S12	G142D	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0
22200	T	G	S12	V213G	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0
22578	G	A	S12	G339D	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	99.9	100.0	100.0	99.9	99.9
22599	G	A	S12	R346K	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
22673	T	C	S12	S371P	99.9	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
22674	C	T	S12	S371F	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0
22679	T	C	S12	S373P	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
22686	C	T	S12	S375F	99.9	99.9	99.7	100.0	100.0	99.6	100.0	99.9	100.0	99.9	100.0	100.0	99.9	99.9	99.9	99.9	100.0	99.9
22688	A	G	S12	T376A	ND	ND	ND	ND	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0
22775	G	A	S12	D405N	ND	ND	ND	ND	100.0	100.0	100.0	100.0	99.7	100.0	100.0	99.9	100.0	99.6	100.0	100.0	100.0	99.7

22786	A	C	S12	R408S	ND	ND	ND	ND	100.0	99.7	99.4	99.9	99.9	100.0	99.9	99.9	99.9	99.9	99.8	99.9	99.9	99.9
22801	G	A	S12	G413G	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	7.3	ND	ND	ND	ND	ND	ND
22813	G	T	S12	K417N	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
22882	T	G	S12	N440K	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
22898	G	A	S12	G446S	99.9	99.9	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
22992	G	A	S12	S477N	100.0	99.9	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
22995	C	A	S12	T478K	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23013	A	C	S12	E484A	100.0	99.9	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23040	A	G	S12	Q493R	99.9	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23048	G	A	S12	G496S	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23055	A	G	S12	Q498R	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23063	A	T	S12	N501Y	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23075	T	C	S12	Y505H	100.0	100.0	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23202	C	A	S12	T547K	100.0	100.0	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
23243	C	T	S12	P561S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	3.7	ND	ND
23403	A	G	S12	D614G	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0
23525	C	T	S12	H655Y	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0
23599	T	G	S12	N679K	99.7	99.9	99.9	99.9	100.0	99.9	100.0	99.9	100.0	99.9	99.9	100.0	99.9	100.0	99.8	99.9	99.9	99.9
23604	C	A	S12	P681H	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
23854	C	A	S12	N764K	100.0	99.9	99.8	99.9	ND	ND	ND	ND	100.0	99.9	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0
23948	G	T	S12	D796Y	100.0	100.0	100.0	100.0	ND	ND	ND	ND	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0
23997	C	T	S12	P812L	ND	ND	ND	ND	ND	ND	ND	ND	3.7	ND	ND	ND	ND	ND	ND	ND	ND	ND
24130	C	A	S12	N856K	100.0	99.9	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
24424	A	T	S12	Q954H	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	99.9	100.0	100.0	100.0	100.0
24469	T	A	S12	N969K	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	99.8	100.0	100.0	100.0	100.0	100.0
24503	C	T	S12	L981F	100.0	100.0	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
24763	T	C	S12	Y1067Y	ND	ND	ND	ND	ND	ND	ND	ND	4.3	ND	ND	ND	ND	ND	ND	ND	ND	ND
24794	G	T	S12	A1078S	ND	ND	ND	ND	ND	ND	ND	ND	4.1	ND	ND	ND	ND	ND	ND	ND	ND	ND
25000	C	T	S12	D1146D	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0
25139	T	G	S12	L1193V	3.5	4.2	5.2	73.3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
25157	G	T	S12	D1199Y	ND	ND	ND	ND	ND	ND	ND	ND	3.2	ND	ND	ND	ND	ND	ND	ND	ND	ND
25174	A	G	S12	G1204G	ND	ND	ND	ND	ND	ND	9.4	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
25441	C	T	ORF3a	Q17*	ND	ND	ND	ND	ND	ND	ND	ND	3.3	ND	ND	ND	ND	ND	ND	ND	ND	ND
25555	G	T	ORF3a	V55F	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
25584	C	T	ORF3a	T64T	99.9	100.0	99.9	99.9	100.0	99.9	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0
25621	G	A	ORF3a	V77I	ND	ND	ND	7.3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26060	C	T	ORF3a	T223I	ND	ND	ND	ND	100.0	99.9	99.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	99.9	100.0	100.0
26270	C	T	E	T9I	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0

26374	T	C	E	C44R	ND	ND	ND	ND	3.8	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26529	G	A	M	D3N	ND	ND	ND	ND	ND	ND	ND	ND	100.0	99.9	100.0	99.9	100.0	99.9	100.0	100.0	99.9	100.0
26530	A	G	M	D3G	99.9	100.0	100.0	99.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26577	C	G	M	Q19E	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
26709	G	A	M	A63T	100.0	100.0	100.0	99.9	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
26858	C	T	M	F112F	ND	ND	ND	ND	99.9	100.0	99.8	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
26885	C	T	M	N121N	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	99.0	56.3	92.9	ND	99.9
26895	C	T	M	H125Y	ND	ND	ND	3.5	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
27038	A	G	M	T172T	ND	ND	ND	ND	ND	ND	ND	ND	100.0	100.0	100.0	100.0	99.9	99.3	54.3	91.8	ND	99.8
27259	A	C	ORF6	R20R	99.9	99.9	99.9	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
27438	T	C	ORF7a	C15C	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	34.0	21.5	99.9	ND
27605	T	C	ORF7a	V71A	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	97.6	56.9	85.1	ND	99.9
27697	C	T	ORF7a	L102F	ND	ND	ND	ND	ND	ND	ND	ND	5.1	3.1	ND	ND	ND	ND	ND	ND	ND	ND
27807	C	T	ORF7b	L18L	100.0	100.0	100.0	100.0	ND	ND	ND	ND	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0
27969	A	T	ORF8	T26S	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	8.6	ND
28311	C	T	N	P13L	100.0	100.0	99.9	99.9	100.0	100.0	100.0	100.0	100.0	99.6	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
28330	A	G	N	G19G	ND	ND	ND	ND	ND	ND	ND	ND	100.0	99.7	100.0	99.9	100.0	99.0	60.2	84.9	ND	99.9
28363	A	T	N	G30G	99.4	100.0	99.4	99.4	ND	ND	ND	ND	99.4	100.0	99.4	100.0	100.0	ND	ND	ND	ND	ND
28370	A	G	N	S33G	99.2	99.4	99.8	99.8	ND	ND	ND	ND	98.7	100.0	99.8	ND	99.6	100.0	99.9	99.7	100.0	100.0
28378	G	A	N	A35A	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
28628	G	C	N	A119P	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	4.9	ND	ND
28636	T	G	N	L121L	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	6.3	ND	ND	ND	ND	ND	ND
28637	C	G	N	P122A	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	4.5	ND	ND	ND	ND	ND	ND
28724	C	T	N	P151S	ND	ND	ND	ND	100.0	100.0	100.0	100.0	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
28881	G	A	N	R203K	100.0	99.8	99.9	99.9	99.9	99.9	99.9	100.0	99.9	100.0	100.0	100.0	100.0	99.9	99.9	100.0	100.0	99.9
28882	G	A	N	R203R	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
28883	G	C	N	G204R	100.0	99.9	99.9	100.0	100.0	100.0	100.0	100.0	99.9	100.0	99.9	100.0	100.0	100.0	100.0	99.9	99.9	99.9
29510	A	C	N	S413R	ND	ND	ND	ND	100.0	100.0	99.9	100.0	100.0	100.0	100.0	99.9	100.0	100.0	100.0	100.0	100.0	100.0
29514	C	T	N	A414V	ND	ND	ND	ND	3.6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
29517	A	G	N	D415G	6.8	ND	7.9	5.8	14.4	5.6	ND	7.8	12.6	10.3	9.2	10.6	7.6	6.8	8.2	11.8	6.4	10.1
29518	C	G	N	D415E	3.7	ND	3.7	ND	4.6	ND	ND	ND	4.1	3.1	3.5	4.0	ND	ND	ND	4.1	ND	3.2
29518	C	T	N	D415D	4.7	ND	3.5	ND	4.6	ND	ND	ND	3.7	3.4	4.9	4.7	3.7	ND	3.4	5.2	ND	4.3
29580	C	T	ORF10	A8V	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	4.8	ND	ND	ND	ND
29666	C	T	ORF10	L37F	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	46.3	15.2	100.0	ND