

1. Supplemental Material

1.1. Tables

Table S1. Verified substituted bases from the discovered strain 1 from SRR11092062, a “-” sign means the base is deleted.

Position	Bases in Reference Strain	Bases in WH Discovered Strain 1	Frequency	Segment Length	Change Status
348	T	C	1	156	non-synonymous
565	T	C	5	0	synonymous
1645	C	G	1	54	non-synonymous
1804	A	T	2	66	non-synonymous
2248	T	A	2	0	synonymous
2249	G	A	2	0	non-synonymous
2251	A	T	2	0	non-synonymous
2253	A	G	2	0	non-synonymous
2254	A	G	2	0	non-synonymous
2450	C	A	2	149	non-synonymous
2451	T	A	2	1	non-synonymous
2452	A	G	2	1	non-synonymous
2453	C	T	2	1	non-synonymous
2454	T	C	2	1	non-synonymous
2455	C	G	2	0	non-synonymous
2456	A	G	2	0	non-synonymous
2457	T	A	2	0	non-synonymous
2458	G	T	2	0	non-synonymous
2460	C	G	2	2	non-synonymous
2462	C	A	2	0	non-synonymous
2463	T	G	2	0	non-synonymous
3264	C	T	2	0	non-synonymous
3625	A	G	4	176	synonymous
3784	C	T	3	0	synonymous
3912	C	T	2	0	non-synonymous
4288	G	T	2	0	non-synonymous
5091	C	T	2	0	non-synonymous
6119	T	C	2	0	non-synonymous
6120	C	T	2	0	non-synonymous
6121	A	C	2	0	non-synonymous
6122	A	C	2	1	synonymous
6125	G	C	2	0	non-synonymous
6126	A	T	2	0	non-synonymous
6127	G	T	2	0	non-synonymous
6270	C	A	2	0	non-synonymous
6273	A	C	2	0	non-synonymous
6274	T	G	2	0	non-synonymous

Table S1. Cont.

Position	Bases in Reference Strain	Bases in WH Discovered Strain 1	Frequency	Segment Length	Change Status
6275	A	G	2	0	non-synonymous
6277	A	T	2	0	non-synonymous
7241	G	C	3	17	non-synonymous
7242	A	C	3	1	non-synonymous
7244	T	C	3	1	non-synonymous
7245	G	T	3	2	non-synonymous
7246	G	T	3	1	non-synonymous
7247	T	G	3	1	non-synonymous
7248	T	G	3	1	non-synonymous
7249	T	C	3	1	non-synonymous
7250	T	C	3	1	synonymous
7252	G	C	3	2	synonymous
7253	G	C	3	2	non-synonymous
7254	C	G	3	3	non-synonymous
7256	T	C	3	1	non-synonymous
7257	A	T	3	0	non-synonymous
7930	A	G	2	0	synonymous
7933	A	G	2	4	synonymous
7935	C	A	2	2	non-synonymous
7936	G	T	2	1	non-synonymous
7937	T	C	2	1	non-synonymous
7938	C	G	2	1	non-synonymous
8173	A	G	2	24	synonymous
8174	G	C	2	1	non-synonymous
8175	C	T	2	2	non-synonymous
8177	C	G	2	3	non-synonymous
8179	G	C	2	3	non-synonymous
8181	A	T	2	0	non-synonymous
8182	A	C	2	2	non-synonymous
8183	G	C	2	0	non-synonymous
8185	G	A	2	0	non-synonymous
8186	T	C	2	0	non-synonymous
9167	T	A	3	161	non-synonymous
10,009	T	A	2	0	synonymous
10,451	A	G	12	179	non-synonymous
10,933	T	-	2	0	non-synonymous
12506	A	-	2	0	non-synonymous
12,847	T	A	2	118	synonymous
13,529	T	C	2	0	non-synonymous
13,927	T	C	3	0	synonymous

Table S1. *Cont.*

Position	Bases in Reference Strain	Bases in WH Discovered Strain 1	Frequency	Segment Length	Change Status
15,060	T	C	2	0	non-synonymous
15,771	T	C	3	150	non-synonymous
15,957	G	A	2	137	non-synonymous
16,333	C	A	2	0	synonymous
16,335	T	G	2	0	non-synonymous
16,757	C	A	2	51	non-synonymous
16,759	C	G	2	2	non-synonymous
16,760	C	T	2	1	non-synonymous
16,761	A	C	2	1	non-synonymous
16,762	C	G	2	3	non-synonymous
16,763	T	G	2	1	non-synonymous
16,764	T	A	2	1	non-synonymous
16,765	A	T	2	1	non-synonymous
16,766	A	C	2	1	non-synonymous
16,767	C	G	2	0	non-synonymous
17,458	C	A	3	0	non-synonymous
17,459	C	G	3	1	non-synonymous
17,460	A	T	3	0	non-synonymous
17,650	T	G	2	175	synonymous
17,825	C	T	7	1	non-synonymous
18,022	A	G	3	0	synonymous
18,024	T	C	3	0	non-synonymous
18,025	G	T	3	0	non-synonymous
18,597	G	A	2	0	non-synonymous
19,050	T	A	2	9	non-synonymous
19,817	T	A	2	80	non-synonymous
19,819	C	G	2	0	non-synonymous
19,820	C	T	2	0	non-synonymous
19,821	A	C	2	1	non-synonymous
19,823	A	G	2	2	non-synonymous
19,824	G	A	2	0	non-synonymous
19,825	G	T	2	1	non-synonymous
19,826	T	C	2	0	non-synonymous
19,828	A	T	2	3	non-synonymous
19,830	A	G	2	0	non-synonymous
19,831	A	C	2	0	non-synonymous
19,832	T	C	2	3	non-synonymous
20,136	A	C	3	0	non-synonymous
21,587	C	T	2	0	non-synonymous
22,114	T	G	2	0	synonymous

Table S1. *Cont.*

Position	Bases in Reference Strain	Bases in WH Discovered Strain 1	Frequency	Segment Length	Change Status
22,274	T	C	2	0	non-synonymous
22,990	T	A	3	0	synonymous
23,364	G	A	2	0	non-synonymous
23,366	A	G	2	0	non-synonymous
23,367	C	T	2	0	non-synonymous
23,368	A	C	2	0	non-synonymous
23,369	A	G	2	0	non-synonymous
23,605	T	C	4	206	synonymous
23,859	C	G	1	56	non-synonymous
24,108	T	A	1	177	non-synonymous
24,259	T	A	1	155	synonymous
24,653	G	C	2	0	non-synonymous
24,654	A	T	2	1	non-synonymous
24,655	G	C	2	0	non-synonymous
24,656	T	C	2	0	non-synonymous
24,658	T	A	2	0	non-synonymous
24,659	G	C	2	0	non-synonymous
24,661	A	T	2	0	non-synonymous
24,804	T	A	2	0	non-synonymous
24,805	T	G	2	2	non-synonymous
24,807	G	C	2	2	non-synonymous
24,808	T	G	2	0	non-synonymous
24,809	C	G	2	0	non-synonymous
25,046	C	G	2	0	non-synonymous
25,518	T	C	2	3	synonymous
25,519	T	C	2	0	non-synonymous
25,522	G	C	2	3	non-synonymous
25,525	T	C	2	0	non-synonymous
25,526	G	T	2	1	non-synonymous
25,527	G	T	2	0	non-synonymous
25,669	C	A	2	1	non-synonymous
25,670	A	G	2	0	non-synonymous
25,671	C	T	2	0	non-synonymous
25,673	T	G	2	0	non-synonymous
25,674	T	G	2	0	non-synonymous
25,675	T	A	2	0	non-synonymous
25,677	G	C	2	2	non-synonymous
26,354	T	A	1	163	non-synonymous
26,836	G	T	2	40	non-synonymous
26,838	A	G	2	0	non-synonymous

Table S1. Cont.

Position	Bases in Reference Strain	Bases in WH Discovered Strain 1	Frequency	Segment Length	Change Status
26,839	C	G	2	1	non-synonymous
26,840	G	C	2	2	non-synonymous
26,842	G	T	2	2	non-synonymous
26,843	T	C	2	0	non-synonymous
26,844	T	C	2	1	non-synonymous
26,845	C	G	2	0	non-synonymous
26,846	C	A	2	1	non-synonymous
26,847	A	C	2	0	non-synonymous
26,849	G	T	2	5	non-synonymous
27,017	T	A	4	158	synonymous
27,372	A	G	3	0	synonymous
27,885	T	G	3	2	non-synonymous
28,293	A	G	3	151	non-synonymous
28,510	T	C	3	1	synonymous
28,777	A	C	2	0	synonymous
29,066	A	C	3	0	non-synonymous
29,456	C	T	3	0	non-synonymous
29,840	T	A	3	142	synonymous
29,843	G	C	3	3	synonymous
29,844	A	G	3	162	synonymous
29,845	T	G	3	162	synonymous
29,846	T	A	3	1	synonymous

Table S2. Verified substituted bases from discovered strain 2 of SRR11092062, a “-” sign means the base is deleted.

Position	Bases in Reference Strain	Bases in WH Discovered Strain 2	Frequency	Segment Length	Change Status
3625	A	C	3	153	synonymous
4291	A	T	2	0	synonymous
6160	T	A	2	0	synonymous
6161	G	A	2	0	non-synonymous
6162	A	G	2	0	non-synonymous
6163	T	A	2	11	non-synonymous
6164	G	C	2	11	non-synonymous
6165	T	C	2	11	non-synonymous
6167	G	C	2	11	non-synonymous
6169	G	T	2	11	non-synonymous
6171	C	G	2	1	non-synonymous
6172	T	C	2	11	non-synonymous

Table S2. *Cont.*

Position	Bases in Reference Strain	Bases in WH Discovered Strain 2	Frequency	Segment Length	Change Status
6173	A	C	2	2	non-synonymous
6175	T	C	2	3	non-synonymous
6176	G	C	2	3	non-synonymous
6177	A	G	2	3	non-synonymous
6178	T	A	2	9	non-synonymous
6179	T	C	2	4	non-synonymous
6180	A	T	2	3	non-synonymous
7305	T	A	2	159	non-synonymous
10,451	A	C	6	214	non-synonymous
13,392	G	T	2	56	non-synonymous
13,950	T	A	2	50	non-synonymous
13,951	A	G	2	0	non-synonymous
13,953	A	C	2	2	non-synonymous
13,954	T	G	2	1	non-synonymous
13,955	T	G	2	2	non-synonymous
13,957	C	T	2	0	non-synonymous
13,958	G	C	2	1	non-synonymous
13,959	C	G	2	1	non-synonymous
13,960	G	T	2	1	non-synonymous
13,961	T	A	2	0	non-synonymous
15,882	T	A	1	176	non-synonymous
16,469	C	A	2	129	non-synonymous
16,470	C	A	2	150	non-synonymous
16,471	A	G	2	150	non-synonymous
16,473	T	C	2	1	non-synonymous
16,474	A	G	2	1	non-synonymous
17,374	A	G	2	157	synonymous
17,709	A	G	4	233	non-synonymous
17,886	T	C	3	153	non-synonymous
18,108	A	G	2	1	non-synonymous
19,150	G	A	2	145	non-synonymous
19,151	C	A	2	1	non-synonymous
19,152	C	G	2	1	non-synonymous
19,153	A	T	2	2	non-synonymous
19,155	A	G	2	2	non-synonymous
19,156	C	G	2	2	non-synonymous
19,159	T	C	2	1	synonymous
19,160	C	G	2	2	non-synonymous
19,162	G	A	2	3	non-synonymous
19,163	A	G	2	3	non-synonymous

Table S2. *Cont.*

Position	Bases in Reference Strain	Bases in WH Discovered Strain 2	Frequency	Segment Length	Change Status
19,165	A	C	2	2	non-synonymous
19,167	A	T	2	1	non-synonymous
19,168	T	G	2	3	non-synonymous
19,171	A	G	2	4	synonymous
19,172	C	T	2	4	non-synonymous
19,173	A	T	2	1	non-synonymous
19,174	G	C	2	0	non-synonymous
19,175	A	T	2	1	non-synonymous
19,176	T	G	2	1	non-synonymous
19,177	G	T	2	0	non-synonymous
19,896	T	C	2	0	non-synonymous
21,486	T	A	2	0	non-synonymous
21,487	A	C	2	0	non-synonymous
21,488	A	T	2	3	non-synonymous
21,489	A	T	2	2	non-synonymous
21,638	C	A	2	143	non-synonymous
21,639	C	A	2	143	non-synonymous
21,640	T	G	2	143	non-synonymous
21,641	G	T	2	143	non-synonymous
21,643	A	G	2	143	non-synonymous
21,644	T	G	2	143	non-synonymous
22,114	T	C	2	160	synonymous
23,280	C	T	1	52	non-synonymous
23,281	T	C	1	12	non-synonymous
23,590	T	C	2	207	synonymous
28,240	T	C	2	1	non-synonymous
28,242	G	T	2	1	non-synonymous
28,243	T	G	2	1	non-synonymous
28,245	T	A	2	1	non-synonymous
28,246	T	G	2	2	non-synonymous
28,248	G	T	2	3	non-synonymous
28,249	A	C	2	1	non-synonymous
28,251	T	G	2	1	non-synonymous
28,253	C	T	2	2	non-synonymous
28,254	A	C	2	1	non-synonymous
29,177	C	T	2	0	non-synonymous
29,377	T	A	2	21	synonymous
29,542	A	G	2	139	synonymous
29,543	G	A	2	1	synonymous
29,544	A	C	2	2	synonymous

Table S2. *Cont.*

Position	Bases in Reference Strain	Bases in WH Discovered Strain 2	Frequency	Segment Length	Change Status
29,546	C	G	2	0	synonymous
29,547	A	C	2	1	synonymous
29,548	C	T	2	1	synonymous
29,549	A	T	2	0	synonymous
29,550	C	G	2	1	synonymous
29,551	A	G	2	1	synonymous
29,552	A	C	2	3	synonymous
29,553	G	C	2	0	synonymous
29,554	G	T	2	0	synonymous
29,556	A	C	2	0	synonymous
29,559	T	C	2	0	synonymous
29,560	G	T	2	0	synonymous
29,561	G	T	2	3	synonymous
29,724	C	A	2	50	synonymous
29,725	A	G	2	4	synonymous
29,727	T	C	2	2	synonymous
29,728	T	G	2	1	synonymous
29,729	T	G	2	0	synonymous
29,730	C	A	2	1	synonymous
29,731	A	T	2	2	synonymous
29,733	C	G	2	2	synonymous
29,734	G	T	2	1	synonymous
29,737	G	C	2	4	synonymous
29,739	C	A	2	2	synonymous
29,740	A	T	2	1	synonymous
29,741	C	G	2	1	synonymous
29,742	G	T	2	0	synonymous
29,745	G	T	2	2	synonymous

Table S3. Verified substituted bases from the MR discovered strain 1, a “-” sign in original strain means the base is inserted in MR discovered strain 1, and the “-” sign in MR discovered strain 1 means the base is deleted.

Position	Bases in Assembled Contig	Bases in MR Discovered Strain 1	Frequency	Segment Length	Change Type
289	G	T	4	0	unavailable
1413	T	C	17	129	non-synonymous
1659	A	C	2	0	non-synonymous
1766	T	G	20	77	synonymous
2938	C	G	1	58	non-synonymous
3270	A	G	27	117	non-synonymous

Table S3. *Cont.*

Position	Bases in Assembled Contig	Bases in MR Discovered Strain 1	Frequency	Segment Length	Change Type
5611	C	T	2	0	non-synonymous
6725	-	T	3	1	non-synonymous
7535	A	C	5	0	non-synonymous
7749	C	A	3	0	non-synonymous
8111	G	A	18	0	non-synonymous
8367	A	T	2	2	non-synonymous
9111	G	A	1	104	non-synonymous
10,347	C	T	25	0	non-synonymous
10,433	T	A	1	93	non-synonymous
10,925	A	T	4	0	synonymous
11,840	C	A	3	0	synonymous
11,944	T	C	20	103	non-synonymous
12,168	A	G	1	118	non-synonymous
13,328	-	A	2	4	non-synonymous
14,363	G	T	2	0	unavailable
14,833	C	T	16	0	unavailable
15,082	T	-	2	0	unavailable
15,795	T	G	2	51	unavailable
16,288	C	T	3	0	unavailable
16,592	G	T	3	6	unavailable
16,687	T	-	2	0	unavailable
17,542	T	C	4	0	unavailable
18,452	A	G	13	0	unavailable
18,803	C	A	1	88	unavailable
18,888	C	T	2	0	unavailable
19,867	T	A	1	88	unavailable
20,011	C	T	2	66	unavailable
20,145	C	G	2	0	unavailable
21,083	G	A	3	0	unavailable
21,332	C	T	23	0	unavailable
22,208	G	A	2	0	synonymous
22,946	G	A	2	0	synonymous
23,071	C	T	2	35	non-synonymous
23,259	A	-	2	0	non-synonymous
23,276	C	T	2	12	synonymous
24,597	A	T	2	0	non-synonymous
24,773	C	T	23	0	synonymous
25,220	A	-	3	0	non-synonymous
25,701	T	A	1	114	unavailable
25,736	C	T	3	3	unavailable

Table S3. Cont.

Position	Bases in Assembled Contig	Bases in MR Discovered Strain 1	Frequency	Segment Length	Change Type
25,935	G	T	20	0	unavailable
27,086	A	G	2	0	unavailable
27,379	T	A	1	106	unavailable
27,754	A	C	2	85	unavailable
27,755	C	T	2	1	unavailable
27,756	T	A	2	0	unavailable
27,898	G	T	3	7	unavailable
27,992	C	T	26	0	unavailable
28,115	T	C	14	140	unavailable
28,243	-	T	4	1	unavailable
28,500	C	T	19	0	unavailable
28,813	T	A	1	81	unavailable
28,897	C	T	37	0	unavailable
29,028	G	T	5	36	unavailable
29,080	-	A	5	57	unavailable
29,524	A	T	1	128	unavailable
29,609	T	C	3	9	unavailable

Table S4. Verified substituted bases from MR discovered train 2.

Position	Bases in Assembled Contig	Bases in MR Discovered Strain 2	Frequency	Segment Length	Change Type
1558	A	T	1	134	non-synonymous
5598	A	G	2	0	non-synonymous
7471	T	C	2	0	non-synonymous
10,724	T	A	1	163	non-synonymous
13,378	G	T	2	0	non-synonymous
15,099	T	A	3	0	unavailable
15,350	A	T	1	140	unavailable
15,855	A	T	1	133	unavailable
17,156	T	C	1	89	unavailable
17,483	G	A	1	138	unavailable
17,589	G	T	2	0	unavailable
18,476	A	G	2	0	unavailable
21,277	G	A	2	0	unavailable
21,622	T	A	1	105	non-synonymous
22,283	A	G	2	0	non-synonymous
27,778	G	A	2	10	unavailable
28,851	T	G	2	0	unavailable

Table S5. Substituted bases of strain 1 from FMDV sample. The consensus sequence doesn't contain the first 350 bases in the reference genome sequence EU448639.1, so the positions are adjusted when determining the synonymity. The non-synonymous/synonymous ratio is 3.56. There are 178 changes in total.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 1	Frequency	Change Type
64	A	C	2	unavailable
158	G	A	2	unavailable
233	T	C	3	unavailable
243	A	G	21	unavailable
299	C	A	2	unavailable
413	A	G	81	unavailable
426	T	G	2	unavailable
455	A	C	11	unavailable
538	T	G	10	unavailable
562	A	G	2	unavailable
593	A	G	2	unavailable
645	T	C	4	unavailable
767	T	A	20	non-synonymous
799	A	C	5	non-synonymous
853	T	C	13	non-synonymous
863	A	C	63	non-synonymous
942	C	T	5	synonymous
973	A	G	2	non-synonymous
1009	C	T	2	non-synonymous
1063	A	C	115	non-synonymous
1123	T	G	3	non-synonymous
1175	T	G	5	non-synonymous
1189	A	C	23	non-synonymous
1262	T	G	2	non-synonymous
1342	T	A	8	non-synonymous
1394	T	A	31	non-synonymous
1398	C	A	2	non-synonymous
1419	T	C	4	synonymous
1480	T	C	8	non-synonymous
1483	A	C	56	non-synonymous
1563	T	G	7	synonymous
1622	G	A	3	non-synonymous
1639	A	C	27	non-synonymous
1640	A	C	49	non-synonymous
1690	T	A	7	non-synonymous
1710	T	C	2	synonymous
1765	T	G	2	non-synonymous

Table S5. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 1	Frequency	Change Type
1820	A	C	49	non-synonymous
1901	A	G	53	non-synonymous
1912	A	C	33	non-synonymous
1984	A	G	27	non-synonymous
2034	A	G	2	synonymous
2081	A	C	44	non-synonymous
2135	T	G	130	non-synonymous
2142	T	C	26	synonymous
2157	T	C	4	synonymous
2220	T	G	3	synonymous
2282	T	G	116	non-synonymous
2312	T	C	2	non-synonymous
2330	A	C	15	non-synonymous
2405	G	A	453	non-synonymous
2417	A	G	528	non-synonymous
2468	T	C	2	non-synonymous
2486	C	T	2	non-synonymous
2539	T	A	4	non-synonymous
2605	A	G	81	non-synonymous
2689	T	G	9	non-synonymous
2714	T	C	49	non-synonymous
2720	A	C	96	non-synonymous
2788	A	G	808	non-synonymous
2856	T	G	102	synonymous
2872	A	G	109	non-synonymous
2932	A	C	303	non-synonymous
2993	T	C	3	non-synonymous
3046	A	G	87	non-synonymous
3103	T	C	4	non-synonymous
3120	T	C	2	synonymous
3199	A	C	19	non-synonymous
3266	A	C	128	non-synonymous
3320	T	G	2	non-synonymous
3338	A	G	5	non-synonymous
3400	A	G	163	non-synonymous
3475	G	A	2	non-synonymous
3524	T	C	119	non-synonymous
3564	A	G	92	synonymous
3644	A	C	32	non-synonymous

Table S5. Cont.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 1	Frequency	Change Type
3645	G	C	18	non-synonymous
3671	A	C	3	non-synonymous
3725	T	G	72	non-synonymous
3759	A	C	1302	non-synonymous
3848	T	A	524	non-synonymous
3886	A	C	23	non-synonymous
3947	T	C	8	non-synonymous
3963	A	C	11	synonymous
4037	C	T	10	non-synonymous
4056	A	C	58	synonymous
4106	T	G	2390	non-synonymous
4169	T	G	66	non-synonymous
4170	C	G	39	non-synonymous
4171	A	C	8	non-synonymous
4223	A	C	12	non-synonymous
4276	T	G	421	non-synonymous
4292	A	C	384	non-synonymous
4381	T	A	237	non-synonymous
4419	A	G	3	synonymous
4441	A	C	123	non-synonymous
4450	A	C	706	non-synonymous
4510	A	C	230	non-synonymous
4565	A	T	6	non-synonymous
4629	T	A	49	synonymous
4663	A	C	33	non-synonymous
4735	G	T	3226	non-synonymous
4788	C	T	2709	synonymous
4868	T	G	670	non-synonymous
4896	G	T	282	non-synonymous
4946	T	G	124	non-synonymous
4983	C	T	5	synonymous
5033	A	T	3	non-synonymous
5085	C	T	28	synonymous
5118	A	C	6	non-synonymous
5177	T	C	5	non-synonymous
5228	T	C	3	non-synonymous
5278	T	G	5	non-synonymous
5299	A	C	4	non-synonymous
5394	T	C	28	synonymous
5419	T	C	22	non-synonymous

Table S5. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 1	Frequency	Change Type
5469	C	T	2	synonymous
5478	A	C	64	synonymous
5544	T	C	4	synonymous
5552	A	G	3	non-synonymous
5621	T	G	12	non-synonymous
5624	A	G	2	non-synonymous
5625	G	A	6	synonymous
5679	T	G	8	synonymous
5720	C	A	664	non-synonymous
5780	T	G	8	non-synonymous
5832	C	A	3	non-synonymous
5846	A	C	6	non-synonymous
5851	A	G	44	non-synonymous
5860	A	C	308	non-synonymous
5922	A	T	4	synonymous
5923	G	T	4	non-synonymous
5945	A	C	36	non-synonymous
5996	G	A	8	non-synonymous
6010	A	C	24	non-synonymous
6066	T	G	16	synonymous
6112	A	C	169	non-synonymous
6165	A	G	553	synonymous
6236	T	G	8	non-synonymous
6270	T	C	2	synonymous
6338	T	G	9	non-synonymous
6396	T	G	43	synonymous
6399	G	T	51	synonymous
6400	T	A	78	non-synonymous
6459	T	G	130	synonymous
6479	T	A	24	non-synonymous
6543	T	G	22	non-synonymous
6561	A	C	70	synonymous
6624	T	G	14	synonymous
6629	A	G	10	non-synonymous
6680	T	C	50	non-synonymous
6683	A	G	4	non-synonymous
6740	T	G	226	non-synonymous
6760	A	C	2	non-synonymous
6793	A	C	71	non-synonymous
6852	T	C	3	synonymous

Table S5. Cont.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 1	Frequency	Change Type
6857	A	G	21	non-synonymous
6930	C	A	4	non-synonymous
6953	C	T	4	non-synonymous
7004	T	C	5839	non-synonymous
7091	T	G	136	non-synonymous
7148	T	G	17	non-synonymous
7197	A	G	324	synonymous
7254	C	A	5	non-synonymous
7262	A	C	56	non-synonymous
7344	T	G	49	non-synonymous
7350	T	C	125	synonymous
7401	C	A	3	synonymous
7405	A	C	16	non-synonymous
7461	C	A	2	synonymous
7478	A	C	187	non-synonymous
7531	A	C	30	non-synonymous
7612	T	C	110	non-synonymous
7671	A	G	3	synonymous
7708	G	T	2	non-synonymous
7777	T	G	52	unavailable
7828	-	A	33	unavailable
7829	-	A	12	unavailable

Table S6. Substituted bases of strain 2 from FMDV sample. The consensus sequence doesn't contain the first 350 bases in the reference genome sequence EU448639.1, so the positions are adjusted when determining the synonymity. The non-synonymous/synonymous ratio is 3.68. There are 166 changes in total.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 2	Frequency	Change Type
93	A	C	2	unavailable
165	A	G	2	unavailable
188	G	A	2	unavailable
225	A	G	2	unavailable
258	A	C	20	unavailable
323	A	G	2	unavailable
394	T	G	203	unavailable
413	A	G	25	unavailable
473	T	C	10	unavailable
495	G	A	3	unavailable

Table S6. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 2	Frequency	Change Type
548	A	G	2	unavailable
607	A	G	2	unavailable
768	C	A	4	synonymous
804	A	G	37	synonymous
853	T	C	24	non-synonymous
910	T	C	2	non-synonymous
936	G	A	2	non-synonymous
974	T	C	2	non-synonymous
1026	T	C	2	synonymous
1063	A	C	4	non-synonymous
1075	A	C	34	non-synonymous
1131	T	C	2	synonymous
1201	T	G	13	non-synonymous
1229	A	T	2	non-synonymous
1347	T	C	5	synonymous
1402	T	A	18	non-synonymous
1440	G	A	6	synonymous
1495	T	C	9	non-synonymous
1498	A	C	17	non-synonymous
1575	T	C	2	synonymous
1603	A	C	3	non-synonymous
1654	T	C	10	non-synonymous
1693	G	A	2	non-synonymous
1795	A	C	9	non-synonymous
1865	T	C	10	non-synonymous
1867	A	C	8	non-synonymous
1919	T	G	130	non-synonymous
1942	T	G	2	non-synonymous
1985	A	C	2	non-synonymous
2067	C	T	55	synonymous
2142	T	C	35	synonymous
2163	T	G	2	synonymous
2214	C	T	2	synonymous
2274	T	G	49	synonymous
2338	C	G	10	non-synonymous
2339	G	C	4	non-synonymous
2404	C	T	298	non-synonymous
2417	A	G	237	non-synonymous
2456	T	G	5	non-synonymous
2492	A	G	2	non-synonymous

Table S6. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 2	Frequency	Change Type
2522	C	T	3	non-synonymous
2558	T	C	2	non-synonymous
2577	A	G	3	synonymous
2662	T	C	13	non-synonymous
2706	T	C	2	synonymous
2746	A	C	73	non-synonymous
2799	T	A	2	non-synonymous
2841	A	T	15	synonymous
2892	T	G	17	synonymous
2930	T	C	54	non-synonymous
2932	A	C	54	non-synonymous
3023	T	G	3	non-synonymous
3063	G	A	3	synonymous
3107	C	T	2	non-synonymous
3157	A	C	8	non-synonymous
3235	A	C	26	non-synonymous
3294	T	G	5	synonymous
3296	A	G	2	non-synonymous
3297	G	A	2	non-synonymous
3362	T	C	3	non-synonymous
3409	A	G	6	non-synonymous
3482	A	C	4	non-synonymous
3557	T	C	125	non-synonymous
3566	A	G	5	non-synonymous
3617	T	C	18	non-synonymous
3668	A	G	3	non-synonymous
3680	A	G	3	non-synonymous
3744	T	G	92	synonymous
3768	C	A	384	non-synonymous
3867	T	G	357	synonymous
3895	G	T	4	non-synonymous
3968	T	C	9	non-synonymous
3972	G	T	6	synonymous
4057	C	A	7	non-synonymous
4106	T	G	853	non-synonymous
4111	C	A	853	non-synonymous
4171	A	C	8	non-synonymous
4172	C	T	2	non-synonymous
4177	A	G	5	non-synonymous
4234	T	A	16	non-synonymous

Table S6. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 2	Frequency	Change Type
4250	A	G	101	non-synonymous
4310	T	C	21	non-synonymous
4364	T	G	138	non-synonymous
4381	T	A	12	non-synonymous
4419	A	C	53	synonymous
4478	A	C	185	non-synonymous
4549	G	A	18	non-synonymous
4594	T	C	10	non-synonymous
4649	T	A	7	non-synonymous
4684	A	C	38	non-synonymous
4735	G	T	140	non-synonymous
4762	T	G	140	non-synonymous
4807	A	C	7	non-synonymous
4868	T	G	250	non-synonymous
4871	A	G	250	non-synonymous
4899	C	A	545	non-synonymous
4958	T	G	22	non-synonymous
4984	C	T	3	non-synonymous
5066	C	T	3	non-synonymous
5115	C	T	7	synonymous
5172	A	G	7	synonymous
5258	T	G	4	non-synonymous
5325	G	A	4	synonymous
5335	A	G	2	non-synonymous
5394	T	G	12	synonymous
5423	A	G	10	non-synonymous
5475	A	C	42	synonymous
5528	A	G	7	non-synonymous
5591	T	C	15	non-synonymous
5604	A	C	7	synonymous
5676	T	G	3	non-synonymous
5685	A	C	82	synonymous
5744	A	G	24	non-synonymous
5801	T	C	4	non-synonymous
5843	T	G	7	non-synonymous
5851	A	G	90	non-synonymous
5907	A	G	5	synonymous
5947	C	T	8	non-synonymous
6026	T	G	12	non-synonymous
6099	T	C	326	synonymous

Table S6. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 2	Frequency	Change Type
6173	T	G	117	non-synonymous
6185	A	C	16	non-synonymous
6243	C	A	8	non-synonymous
6252	C	T	2	synonymous
6298	G	A	3	non-synonymous
6328	A	T	9	non-synonymous
6398	T	G	22	non-synonymous
6408	C	G	30	synonymous
6409	G	A	72	non-synonymous
6459	T	C	53	synonymous
6500	A	G	24	non-synonymous
6559	T	C	16	non-synonymous
6569	A	C	54	non-synonymous
6668	T	C	60	non-synonymous
6752	T	C	229	non-synonymous
6793	A	G	35	non-synonymous
6844	A	G	26	non-synonymous
6896	T	C	10	non-synonymous
6960	T	G	88	synonymous
6994	A	G	10	non-synonymous
7031	A	G	10	non-synonymous
7129	T	G	91	non-synonymous
7197	A	G	6	synonymous
7248	C	A	4	non-synonymous
7253	A	C	29	non-synonymous
7350	T	C	1116	synonymous
7399	A	C	60	non-synonymous
7445	A	C	59	non-synonymous
7499	C	A	3	non-synonymous
7512	A	C	23	non-synonymous
7607	T	C	131	non-synonymous
7652	A	G	2	non-synonymous
7695	T	C	2	synonymous
7726	T	C	4	unavailable
7784	T	C	200	unavailable
7790	G	T	180	unavailable

Table S7. Substituted bases of strain 3 from FMDV sample. The consensus sequence doesn't contain the first 350 bases in the reference genome sequence EU448639.1, so the positions are adjusted when determining the synonymity. The non-synonymous/synonymous ratio is 4.0. There are 170 changes in total.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 3	Frequency	Change Type
246	A	C	15	unavailable
376	A	G	2	unavailable
436	T	C	15	unavailable
451	A	C	19	unavailable
521	T	G	5	unavailable
588	C	T	2	unavailable
649	A	G	2	unavailable
727	A	G	2	non-synonymous
785	T	C	4	non-synonymous
792	A	C	8	synonymous
844	A	C	23	non-synonymous
918	A	G	2	synonymous
961	A	G	4	non-synonymous
1030	C	T	2	non-synonymous
1061	A	C	16	non-synonymous
1113	T	G	2	synonymous
1149	T	C	2	synonymous
1204	T	G	4	non-synonymous
1253	A	G	4	non-synonymous
1319	G	T	2	non-synonymous
1372	T	A	18	non-synonymous
1409	T	C	2	non-synonymous
1461	T	G	5	non-synonymous
1489	A	C	12	non-synonymous
1543	G	A	2	non-synonymous
1606	A	C	3	non-synonymous
1648	A	C	9	non-synonymous
1778	A	C	5	non-synonymous
1830	A	C	4	non-synonymous
1878	T	C	138	synonymous
1942	T	G	34	non-synonymous
2016	T	C	2	synonymous
2051	C	T	2	non-synonymous
2071	G	T	14	non-synonymous
2132	T	G	4	non-synonymous
2220	T	C	4	synonymous
2279	T	C	15	non-synonymous

Table S7. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 3	Frequency	Change Type
2331	C	-	58	non-synonymous
2398	T	G	9	non-synonymous
2456	T	G	11	non-synonymous
2503	A	C	2	non-synonymous
2552	T	C	4	non-synonymous
2581	A	C	3	non-synonymous
2643	A	C	10	synonymous
2706	T	C	2	synonymous
2714	T	C	5	non-synonymous
2720	A	C	13	non-synonymous
2725	T	C	42	non-synonymous
2850	T	G	26	non-synonymous
2856	T	G	3	synonymous
2867	A	G	12	non-synonymous
2924	A	T	8	non-synonymous
2932	A	C	8	non-synonymous
2976	G	A	2	synonymous
3029	C	A	3	non-synonymous
3061	C	T	2	non-synonymous
3122	A	G	2	non-synonymous
3155	T	C	2	non-synonymous
3202	A	C	3	non-synonymous
3256	A	C	12	non-synonymous
3319	G	A	2	non-synonymous
3350	T	C	2	non-synonymous
3401	T	C	4	non-synonymous
3433	C	A	3	synonymous
3509	A	G	110	non-synonymous
3559	G	A	8	non-synonymous
3560	C	T	2	non-synonymous
3573	G	T	2	non-synonymous
3626	T	A	10	non-synonymous
3627	G	T	2	synonymous
3678	T	C	3	synonymous
3716	C	T	2	non-synonymous
3766	T	A	10	non-synonymous
3767	A	C	37	non-synonymous
3823	T	G	275	non-synonymous
3836	T	G	13	non-synonymous
3839	T	C	2	non-synonymous

Table S7. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 3	Frequency	Change Type
3889	T	C	13	non-synonymous
3936	G	A	4	synonymous
3990	A	G	85	synonymous
4059	T	G	7	synonymous
4106	T	G	51	non-synonymous
4111	C	A	51	non-synonymous
4112	T	A	51	non-synonymous
4114	A	T	12	non-synonymous
4187	T	G	11	non-synonymous
4258	G	C	575	non-synonymous
4287	C	G	375	non-synonymous
4373	G	C	53	non-synonymous
4381	T	A	6	non-synonymous
4389	G	T	3	non-synonymous
4441	A	C	428	non-synonymous
4494	C	A	3	non-synonymous
4510	A	G	83	non-synonymous
4571	C	T	3	non-synonymous
4614	A	G	7	synonymous
4660	A	C	16	non-synonymous
4726	T	G	274	non-synonymous
4785	C	A	5	non-synonymous
4797	A	C	8	synonymous
4868	T	G	32	non-synonymous
4869	T	G	32	non-synonymous
4908	A	C	139	non-synonymous
4976	T	G	12	non-synonymous
5015	C	T	2	non-synonymous
5076	C	A	3	non-synonymous
5085	C	T	8	synonymous
5137	T	C	6	non-synonymous
5181	G	T	3	non-synonymous
5265	T	C	4	synonymous
5316	T	C	3	synonymous
5362	A	C	10	non-synonymous
5412	C	A	3	non-synonymous
5417	A	C	2	non-synonymous
5463	A	C	39	synonymous
5520	A	C	4	synonymous
5584	G	A	4	non-synonymous

Table S7. *Cont.*

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 3	Frequency	Change Type
5612	A	G	4	non-synonymous
5668	A	G	4	non-synonymous
5689	A	C	38	non-synonymous
5745	C	G	22	non-synonymous
5808	T	C	2	synonymous
5810	A	C	23	non-synonymous
5860	A	C	76	non-synonymous
5904	A	G	2	synonymous
5924	A	G	7	non-synonymous
6009	C	T	57	synonymous
6064	G	C	3	non-synonymous
6081	C	G	4	non-synonymous
6082	A	G	4	non-synonymous
6145	A	C	100	non-synonymous
6196	A	C	5	non-synonymous
6252	C	T	13	synonymous
6325	G	A	3	non-synonymous
6344	A	G	2	non-synonymous
6396	T	C	8	synonymous
6404	A	C	49	non-synonymous
6467	T	C	14	non-synonymous
6541	T	C	6	non-synonymous
6554	A	C	48	non-synonymous
6604	A	C	2	non-synonymous
6654	T	A	5	non-synonymous
6657	A	C	26	synonymous
6707	T	C	14	non-synonymous
6758	T	C	87	non-synonymous
6830	T	A	6	non-synonymous
6831	A	G	13	synonymous
6884	A	G	16	non-synonymous
6956	T	G	14	non-synonymous
6998	A	C	5	non-synonymous
7056	C	A	3	non-synonymous
7085	A	G	8	non-synonymous
7136	T	C	27	non-synonymous
7163	C	T	5	non-synonymous
7227	C	A	4	synonymous
7262	A	C	31	non-synonymous
7306	A	C	9	non-synonymous

Table S7. Cont.

Position	Bases in Assembled Contig	Bases in FMDV Discovered Strain 3	Frequency	Change Type
7370	T	C	15	non-synonymous
7379	A	C	16	non-synonymous
7432	T	C	3	non-synonymous
7462	A	C	27	non-synonymous
7512	A	G	6	synonymous
7563	T	G	91	synonymous
7627	T	A	54	non-synonymous
7648	T	C	2	non-synonymous
7685	T	C	2	non-synonymous
7733	G	C	2	unavailable
7734	A	G	2	unavailable
7783	C	T	267	unavailable
7784	T	C	267	unavailable

1.2. Sequences

1.3. SRR11092062 Discovered Strain 1 Spike Protein Sequence

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1 MFVFLVLLSLVSSQCVNLTT RTQLPPAYTNSFTRGVYYPD KVFRRSVLHSTQDLFLPFFS NVTWFHAIHVSGTNGTKRFD NPVLPFNDGVYFASTEKSNI 100
101 IRGWIFGTTLDSTQSKLLIV NNATNVVIKVCQFQCNDFP LGVYYHKNNKSWMESEFRVY SSANNCTFEYVSQPFLMDLE GKQGNFKNLREFVFNIDGY 200
201 FKITYSKHTPINLVRDLPGQF SALEPLVDLPIGINITRLQT LLALHRSYLTGPDSSSGWTA GAAAYYVGYLQPRFTLLKYN ENGTITDAVDCALDPLSETK 300
301 CTLKSFTVEKGYQTSNFRV QPTESIVRFPNITNLCPEGE VFNATRFASVYAWNRKRISN CVADYSVLVNSASFSTFKCY GVSPTKLNDLCFTNVYADSF 400
401 VIRGDEVRLQIAPGQTGIAD YNYKLDDFTGCVIAWNSNN LDSKVGNGNYLYRLFRKSN LKPFERDISTEYQAGSTPC NGVEGFNCYFPLQSYGFQPT 500
501 NGVGYQPYRVVLSFELLHA PATVCGPKKSTNLVKNKCVN FNFNGLTGTGVLTESNKKFL PFQQFGRDIADTTDAVRDPQ TLEILDITPCSGGVSITP 600
601 EVDTSNQVAVLYQDVNCTEV PVAIHADQLTPTWRVYSTGS NVFQTRAGCLIGAEHVNNSY ECDIPIGAGICASYQTQNS PRRARSVASQSIAYTMSLG 700
701 AENSVAYSNNISAIPTNFTI SVTTEILPVSMTKTSVDCTM YICGDSTECNLLLYQGSFC TQLNRGLTGLAVEQDKNTQE VFAQVKQIYKTPPIKDFGGF 800
801 NFSQILPDPSPKSKRSIED LLFNKVTADAGFIKQYQDC LGDIAARDHICAQKFNGLTV LPPLTDEMIAQYTSALLAG TITSGWTFGAGAALQIPFAM 900
901 QMAYRFNGIGVGTQNVLYENQ KLIANQFNSAIGIKQDSLSS TASALGKLQDVVNQNAQALN TLVKQLSSNFGAISSVLNDI LSRLDKVEAEVQIDRLITGR 1000
1001 LQSLQTYVTQQLIRAAEIRA SANLAATKMSLRLLGQSKRV DFCGKGYHLSFPQSAPHGV VFLHVTYVPAQEKNFTTAPA KSDDGKAHFPREGVFSNGT 1100
1101 HWFVTQRNFYEPQIITDNT FVSGNCDVIGIVNNVTYDP LQPELDSFKELDKYFKNHT SADVDLGDISGINASVNIQ KEIDRLNEVAKNLNESLIDL 1200
1201 QELGKYEYQIKWPWYIWLGF IAGLIAIVMTILCCMTSC CSCLKGCCSCGSCCKFDEDD SEPVLKGVKLHYT SEPVLKGVKLHYT 1273

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1.4. Difference of SRR11092062 Discovered Strain 1 Spike Protein Sequence and SARS-CoV-2 Spike Protein Sequence

The format of EMBOSS Needle is that each three lines followed an empty line, the first in the three lines is 50 amino acid bases of SARS-CoV-2 original strain spike protein, the second line is the matching status, and the third line is 50 amino acid bases of discovered strain 1. | means the two bases at the position in the first protein sequence and the second protein sequence are the same, other signs mean the two bases are different. The figure is located at [1](#) and [1](#).

1.5. SRR11092062 Discovered Strain 2 Spike Protein Sequence

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1 MFVFLVLLSLVSSQCVNLTT RTQLPKSDTNSFTRGVYYPD KVFRRSVLHSTQDLFLPFFS NVTWFHAIHVSGTNGTKRFD NPVLPFNDGVYFASTEKSNI 100
101 IRGWIFGTTLDSTQSKLLIV NNATNVVIKVCQFQCNDFP LGVYYHKNNKSWMESEFRVY SSANNCTFEYVSQPFLMDLE GKQGNFKNLREFVFNIDGY 200
201 FKITYSKHTPINLVRDLPGQF SALEPLVDLPIGINITRFQT LLALHRSYLTGPDSSSGWTA GAAAYYVGYLQPRFTLLKYN ENGTITDAVDCALDPLSETK 300
301 CTLKSFTVEKGYQTSNFRV QPTESIVRFPNITNLCPEGE VFNATRFASVYAWNRKRISN CVADYSVLVNSASFSTFKCY GVSPTKLNDLCFTNVYADSF 400
401 VIRGDEVRLQIAPGQTGIAD YNYKLDDFTGCVIAWNSNN LDSKVGNGNYLYRLFRKSN LKPFERDISTEYQAGSTPC NGVEGFNCYFPLQSYGFQPT 500
501 NGVGYQPYRVVLSFELLHA PATVCGPKKSTNLVKNKCVN FNFNGLTGTGVLTESNKKFL PFQQFGRDIADTTDAVRDPQ TLEILDITPCSGGVSITP 600
601 GTNTSNQVAVLYQDVNCTEV PVAIHADQLTPTWRVYSTGS NVFQTRAGCLIGAEHVNNSY ECDIPIGAGICASYQTQNS PRRARSVASQSIAYTMSLG 700
701 AENSVAYSNNISAIPTNFTI SVTTEILPVSMTKTSVDCTM YICGDSTECNLLLYQGSFC TQLNRALTGLAVEQDKNTQE VFAQVKQIYKTPPIKDFGGF 800
801 NFSQILPDPSPKSKRSIED LLFNKVTADAGFIKQYQDC LGDIAARDLICAQKFNGLTV LPPLTDEMIAQYTSALLAG TITSGWTFGAGAALQIPFAM 900

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901 QMAYRFNGIGVTQNVLYENQ KLIANQFNSAIGKIQDSLSS TASALGKLQDVVNQNAQALN TLVKQLSSNFGAISSVLNDI LSRLDKVEAEVQIDRLITGR 1000

1001 LQSLQTYTVQQLIRAAEIRA SANLAATKMSECVLQGSQKRV DFCGKGHYLMSFPQSAHPGV VFLHVTVYVPAQEKNFTTAPA ICHDGKAHFPREGVFSVNGT 1100

1101 HWFVTQRNFYEPQIHTDNT FVSGNCDVVGIVNNTVYDP LQPELDSFKEELDKYFKNHT SPDVDLGDISGINASVVNIQ KEIDRLNEVAKNLNESLIDL 1200

1201 QELGKYEQYIKWPWYIWLGF IAGLIAIVMTIMLCCMTSC CSCLKGCCSCGSCCKFDEDD SEPVLKGVKLHYT 1273

1.6. Difference of Discovered Strain 2 Spike Protein Sequence and SARS-CoV-2 Spike Protein Sequence

The format of EMBOSS Needle is that each three lines followed an empty line, the first in the three lines is 50 amino acid bases of SARS-CoV-2 original strain spike protein, the second line is the matching status, and the third line is 50 amino acid bases of discovered strain 2. | means the two bases at the position in the first protein sequence and the second protein sequence are the same, other signs mean the two bases are different.The figure is located at [2](#) and [2](#).

1.7. SRR11092062 Discovered Strain 1 Nucleotide Sequence

1 ATTAAAGGTTTATACCTTCC CAGTAAACAACAACCAAC TTTCGATCTCTTGTAGATCT GTTCTCTAAACGAACTTTAA AATCTGTGTGGCTGCACTC 100

101 GCGTCGATGCTTAGTGCACT CACGCAGTATAATTAATAC TAATTACTGTCGTTGACAGG ACACGAGTAACCTCGTCTATC TTCTGCAGGCTGCTTACGGT 200

201 TTCTGCGGTGTTGCAGCCGA TCATCAGCACATCTAGGTTT CGTCCGGGTGTGACCGAAAG GTAAGATGGAGAGCCTTGTG CCTGTTTTCAACGAGAAAAAC 300

401 ACACGTCCAACCTCAGTTTGC CTGTTTTACAGGTTCCGCAC GTGCTCGCAGCTGGCTTTGG AGACTCCGTGGAGGAGGTCT TATCAGAGGCACGTCAACAT 400

401 CTTAAGAGTGGCACTTGTGG CTGTAGAGAAGTTGAAAG GGTGTTGCTGCTCAACTGAA CAGCCCTATGTGTTCATCA ACGTTGGATGCTCGAAGT 500

501 CACCTCATGTGTCATGTTATG GTTAGAGCTGTGAGCAAGT CGAAGGCATTACGTACGGTC GTAGCCGTGAGACACTGGT GTCCTTGCCCTCATGTGGG 600

601 CGAAATACCACTGGCTTACC GCAAGGTTCTTCTGTGAAG AACGGTAATAAAGGAGCTGG TGCCCATAGTTACGGGCCG ATCTAAAGTCATTTGACTTA 700

701 GCGGACGAGCTTGGCAGCTGA TCCTTATGAAGATTTTCAAG AAGATCTGGAACACTAAACAT AGCAGTGGTGTTACCCGTGA ACTCATGCGTGAGCTTAACG 800

801 GAGGGCCTACACTCGCTATG CTGATAACAACITCTGTG CCTGATGGTCCCTCTGT AGTCATTAAGAAGCCTTCTA CCACTGTCTGGTAAAGCTT 900

901 ATGCACCTTGTCCGACAAC TGCACCTTATTTGACACTAAG AGGGGTGTATCTGCTGCCG TGAACATGAGCATGAAATTG CTTGGTACACGGAAAGCTT 1000

1001 GAAAAGAGCTATGAATTGA CACACCTTTTGAATTAATAT TGGCAAAGAAATTGACACC TTCAATGGGGAATGCCAAA TTTTGTATTTCCTTAAAT 1100

1101 CCATAATCAAGACTATTTCAA CCAAGGGTTGAAAAGAAAAA GCTTGATGGCTTATGGGTA GAATTCGATCTGTCTATCCA GTTGGCTGACCAAATGAAT 1200

1201 CAACCAAAATGTGCTTTTCAA CTCTCATGAAGTGTGATCAT TGTGTTGAAACTTCATGGCA CAGCGGCGAATTTGTAAAG CCATCTGCCGAATTTGTGGC 1300

1301 ACTGAGAAATTTGACTAAAGA AGGTGCCACTACTTGTGGTT ACTTACCCCAAAATGCTGTT GTTAAATTTATTTGTCAGC ATGTCACAATTCAGAAGTAG 1400

1401 GACCTGAGCATAGTCTTGCC GAATACCCATAATGAATCTGG CTGAAAACCAATCTTCTGTA AGGGTGGTGCACACTATTGCC TTGGAGGCTGTGTGTCTC 1500

1501 TTATGTGTGTTGCCATAACA AGTGTGCCATTGGGTTCCTA CGTGCTAGCCGCTAACATAGG TTGTAACCATACAGGTGTG TTGGAGAAGGTTCCGAAGGT 1600

1601 CTTAATGACAACTTCTTGA AATACTCCAAAAGAGAAAG TCAAGATCAATATTGTTGGT GACTTTAAACTTAATGAAGA GATCGCCATTATTTGGCAT 1700

1701 TCAATTTTCTCCGCACCTCT TGAACCTGCTCAAAATTC TG TCGGTGTTTTACAGAAGGCC GCTATAACAATACTAGATGG AATTTACAGTATTCACCTGA 2000

2001 GACTCATTTGATGTATGATG TTACATCTGATTGGCTAC TAACATCTAGTTGTAATGG CTTACATTAACAGGTGGTGT GTTCAGTTGACTTCGCAGTG 2100

2101 GCTAACTAACATCTTTGGCA CTGTTTTGAAAAAAGCTTCAA CCGTCTCTGATTGGCTTGA AGAGAAGTTTAAGGAAGGTG TAGAGTTTCTTAGAGACGGT 2200

2201 TGGGAAATTTGTAATTTAT CTCAACCTGTGCTTGTGAAA TTGTCGGAAGTCGGATTGTC ACCTGTGCAAAGGAAATTA GAGAGAGTGTTCAGACATCT 2300

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29801 CTAATGTGTAAAAATTAATTT TAGTAGTGCTATCCCCAAGT CGGATTAATAGCTTCTTAGG AGAATGACAAAAAAAAAAAAA AAAAAAAAA 29889

1.8. *SRR11092062 Discovered Strain 2 Nucleotide Sequence*

1 ATIAAAGGTTTATACCTTCC CAGGTAAACAACCAACCAAC TTTCGATCTCTGTAGATCT GTTCTCTAAACGAACTTAA AATCTGTGGCTGTCACTC 100
101 GCGTCGATGCTTAGTGCAC TACGACAGTATAATTAATAAC TAATACTGCTGCTTGACAGG ACACGAGTAACTCGTCTATC TTCTGCAGGCTGCTTACGGT 200
201 TTCGTCGGTGTTGCAGCCGA TCATCAGCACATCTAGGTTT CGTCCGGGTGTGACCGAAAG GTAAGATGGAGAGCCTTGTG CCTGGTTTCAACGAGAAAAAC 300
301 ACACGTCCAACCTAGTTTGC CTGTTTTACAGGTTTCGGAC GTGCTCGTACGTGGCTTTGG AGACTCCGTGGAGGAGTCT TATCAGAGGCACGTCAACAT 400
401 CTTAAAGATGGCACTTGTGG CTTAGTAGAAGTTGAAAAAG GCGTTTTGCCTCAACTTGAA CAGCCCTATGTGTTTCATCA ACGTTCGGATGCTCGAACTG 500
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29601 GTCTACTCTTGTGCAGAATG AATTCTCGTAACTACATAGC ACAAGTAGATGTAGTTAAT TTAATCTACATAGCAATCT TTAATCAGTGTGTAACATTA 29700

29701 GGGAGGACTTGAAAGACCA CCAAGTCGGATCGTAGCCAT GTCGTAGTAGCATCGAGTGT ACAGTGAAACAATGCTAGGA GAGTCGCATATGGAAGAG 29800

29801 CCCTAATGTGTAAATAAT TTAGTAGTGCTATCCCCAT GTGATTTTAATAGCTTCTTA GGAGAATGACAAAAAAAAA AAAAAAAAAA 29891

1.9. SRR12596175 Assembled Contig Spike Protein Sequence

1 MFLLTTRTMFVLVLLPLV SSQCVNLTRTQLPPAYTNS FTRGVYYPDKVFRSVLHST QDLFLPFFSNVTWFHAIHVS GTNGTKRFDNPVLPFNDGVY 100

101 FASTEKSNIIRGWIFGTTLD SKTQSLIIVNNATNVIVKVC EFQFCNDPFLGVYYHKNNKS WMESEFRVYSSANNCTFEYV SQPFLMDLEGKQGNFKNLRE 200

201 FVFKNIDGYFKIYSKHTPIN LVRLDPQGFSALEPLVDLPI GINITRFQTLALHRSYLTP GDSSSGWTAGAAAYVGYLQ PRFLFKYNENGTTTDAVDC 300

301 ALDPLSETCKTLKSFTVEKG IYQTSNFRVQPTESIVRFPN ITNLCPFGEVFNATREASVY AWRNRKRISNCVADYSVLNS ASFSTFKCYGVSPTKLNDLC 400

401 FTNVYADSFVIRGDEVQRQA PGQTGKIADYNYKLPDDFTG CVIAWNSNNLDSKVGGNYN YLYRLFRKSNLKPFERDISTE IYQAGSTPCNGVEGFNCYFP 500

501 LQSYGFQPTNGVGYQPYRVV VLSFELLHAPATVCGPKKST NLVKNKCVNFNFNGLTGTGV LTESNKKFLPFQQFGRDIAD TTDAVRDPQTLEILDITPCS 600

601 FGGVSVITPGTNTSNQVAVL YQGVNCTEVPVAIHADQLTP TWRVYSTGSNVFQTRAGCLI GAHVNNNSYECDIPIGAGIC ASYQTQTNSPRRARSVASQS 700

701 IIAYMSLGAENSVAYSNNS IAIPTNFTISVTTEILPVSM TKTSVDCTMYICGDSSTECN LLLQYGSFCTQLNRALTGIA VEQDKNTQEVFAQVKQIYKT 800

801 PPIKDFGGFNFSQILPDPSK PSKRSHEDLLFNKVTLADA GFIKQYGDCLGDIAARDLIC AQKFNGLTVLPPLTDEMIA QYTSALLAGTTTSGWTFGAG 900

901 AALQIPFAMQAYRFNGIGV TQNVLYENQKLIANQFNSAI GKIQDSLSTASALGKLQDV VNQNAQALNTLVKQLSSNFG AISSVLNDILSRDKVEAEV 1000

1001 QIDRLITGRQLSQTYVTYQG LIRAAEIRASANLAATKMSE CVLGQSKRVDFCGKGYHLMS FPQSAPHGVVFLHVTYVPAQ EKNFTTAPAICHGKAHFPR 1100

1101 EGVFVSNTHGWFTVQRNFYE PQIITDNTFVSGNCDVVIG IVNNTVYDLPQPELDSFKEE LDKYFKNHTSPVDLGDISG INASVVNIQKEIDRLNEVAK 1200

1201 NLNESLIDLQELGKYEQYIK WPWYIWLGFIAGLIAIVMT IMLCCMTSCCCLKGCCSCG SCCKFDEDDSEPVLKGVKLH YT 1282

1.10. SRR12596175 Discovered Strain 1 Possible Spike Protein Sequence

1 MFLLTTRTMFVLVLLPLV SSQCVNLKSRTQLPPAYTNS FTRGVYYPGKVFRRSVLHST QDLFLPFFSNVTWFHAIHVS GTIGTKRFDNPVLPFNDGVY 100

101 FASTEKSIIIRGWIFGTTLD SKTQSLIIVNNSTNVIVKVC EFQFCNDPFLGVYYHKNNKS WMESEFRVYSSANNCTFE-V SQPFLMDLEGKQGNFKNLRE 200

201 FVFKNIDGYFKIYSKHTPIN LVRLDPQGFSALEPLVDLPI GINITRFQIILSLHRSYLTP GDSSSGWTAGAAAYVGYLQ PRSFLFKYNENGTTTDAVDC 300

```
301 ALDPLSGTKCTLKSFTVEKG IYQTSNFRVQPTESIVRFPN IKYLCPFGEVFNATRFASVY AWRNKRISNCVADYSVLYNS VPSTFKCYGVSPTKLNDLC 400
401 FTNVYADSFVIRGDEVRLQA PGQTGKIADYNYKLPDDFTG CVIAWNSNNLDSKVGGNYN YLYRFRKSNLKPFEERDISTE IYQAGSTPCNGVEGFNCYFL 500
501 LQLYGFQPTNGVGYPYRVV VLSFELLHAPATVCASKKST NLVKNKCVNFNFNGLTGTGV LTESNKSFCLENNLAETLLT LLMLSEVHRHLRFLTLHHVL 600
601 LVVSVL-RQEQILLTRLLFF IRVSTAQKSLLLFMQINLLL LGVFILQVLKFLKHVQAV- GLNMSTTHMSVTPYPLVQVYA LVIRLSLILGGHVV-LVNP 700
701 SLHSLCHLVQKIQLLTLTL LPYPQILLVLVLPQKYQCL- PRHQ-IVQCTFGMIQLNAAI YCCNMAVVFHN-TVL-LE-L LNKTKTPKKFVHKSNNKFTKH 800
801 HQLKILVVLIFHK-FQIHQN QARGHLLKIYFSTK-HLQLL ASSNNMVIALVILLLEPSFV HKSLTALLFCHLCSQIR-LL NTLLHC-RVLSLVGGLVQV 900
901 LHYYKHYVLCKWIGLGMVLEL HRMPMSRMTKN-LPTNLIVLL AKFKTHFLPQQANLENFKMW STKMHL-TRLLNNLAPILV QFQVF-MISFHVLTCLRKCC 1000
1001 KLIG-SQADFNVCRRH-LNN -LELQKSELLILLLLNCQS VYLDNQKELIFVERAIIICP SLSQHLMV-FSCM-LMSLHK KRTSQLLLLPFVMMME-HTFLV 1100
1101 KVSFLQMAHTGL-HKGIFMN HKSLLQTTHLCIVTVML-E VSTTQFMILCNLN-THSRRS -INILRIIHHQMLI-VTSLA LMLQL-TYKKKLTASMLQ- 1200
1201 F-MNLSSISKNLSESSI-M AMVHLARFYSWLDCHSNGDN YALLYDQLL-LSQGLLFLGI LLQI-RRL-ASAQRSQITL HI 1282
```

1.11. Difference of SRR11092062 Discovered Strain 1 Spike Protein Sequence and SARS-CoV-2 Spike Protein Sequence

The format of EMBOSS Needle is that each three lines followed an empty line, the first in the three lines is 50 amino acid bases of SARS-CoV-2 original strain spike protein, the second line is the matching status, and the third line is 50 amino acid bases of discovered strain 1. | means the two bases at the position in the first protein sequence and the second protein sequence are the same, other signs mean the two bases are different. The figure is located at [1](#) and [1](#).

1.12. SRR12596175 Discovered Strain 2 Possible Spike Protein Sequence

```
1 MFLTTKRTMFVFLVLLPLD SSQCVNLTRTQLPPAYTNS FTRGVYYPDKVFRSSVLHST QDLFLPFSNVTWFHAIHVS GTNGTKRFDNPVLPFNDGVY 100
101 FASTEKSNIRGWFPGTTLD SKTQSLILVNATNVIVKVC EFQFCNDPFLGVYHHKNNKS WMESEFRVYSSANNCTFEYV SQPFLMDLEGKQGNFKNLR 200
201 VFVKNDIDGYFKIYKHTPIN LVRLDLPQGSFALEPLVDLPM GINTRFQTLALHRSYLTG GDSSSGWTAGAAAYVGYLQ PRTFLKYNENGTTTDAVDC 300
301 ALDPLSETKCTLKSFTVEKG IYQTSNFRVQPTESIVRFPN ITNLCPFGEVFNATRFASVY AWRNKRISNCVADYSVLYNS ASFSTFKCYGVSPTKLNDLC 400
401 FTNVYADSFVIRGDEVRLQA PGQTGKIADYNYKLPDDFTG CVIAWNSNNLDSKVGGNYN YLYRFRKSNLKPFEERDISTE IYQAGSTPCNGVEGFNCYFP 500
501 LQSYGFQPTNGVGYPYRVV VLSFELLHAPATVCGPKKST NLVKNKCVNFNFNGLTGTGV LTESNKKFLPQQFGRDIAD TTDVAVRDPQTLEILDITPCS 600
601 FGGVSVITPGTNSNQAVL YQGVNCTEVPVAIHADQLTP TWRVYSTGSNVQTRAGCLI GAHVNNNSYECIDIPIGAGIC ASYQTQTNSPRRARSVASQS 700
701 IIAYTMSLGAENSVAYSNNS IAIPNTFTISVTTEILPVSM TKTSVDCTMYICGDSCECSN LLLQYGSFCTQLNRALTGIA VEQDKNTQEVFAQVKQIYKT 800
801 PPIKDFGFGNFSQILPDPK PSKRSFIEDLLFNKVTLADA GFIKQYGDCLGDIAARDLIC AQKFENGLTVLPPLTDEMIA QYTSALLAGTTTSGWTFGAG 900
901 AALQIPFAMQAYRNGVIG TQNVLYENQKLIANQFNSAI GKIQDSLSTASALGKLQDV VNQNAQALNTLVKQLSSNFG AISSVLNDILSRDKVEAEV 1000
1001 QIDRLITGRLQSLQTYVTQQ LIRAAEIRASANLAATKMSE CVLGQSKRVDPCGKGHYHLS FPQSAPHGVVFLHVTYVPAQ EKNFTTAPAICHDGKAHFPR 1100
1101 EGVFVSNGTWFWFTQRNFYE PQIHTDNTFVSGNCDVVG IVNNTVYDPLQPELDSFKEE LDKYFKNHTSPDVLGDISG INASVNIQKEIDRLNEVAK 1200
1201 NLNESLIDLQELGKYEQYIK WPWYIWLGIAGLIAIVMVT IMLCCMTSCCCLKGCCSCG SCCKFDEDDSEPVKGVKLH YT 1282
```

1.12.1. Difference of Discovered Strain 2 Spike Protein Sequence and SARS-CoV-2 Spike Protein Sequence

The format of EMBOSS Needle is that each three lines followed an empty line, the first in the three lines is 50 amino acid bases of SARS-CoV-2 original strain spike protein, the second line is the matching status, and the third line is 50 amino acid bases of discovered strain 2. | means the two bases at the position in the first protein sequence and the second protein sequence are the same, other signs mean the two bases are different. The figure is located at [2](#) and [2](#).

1.13. SRR12596175 Assembled Contig Nucleotide Sequence

```
1 GTGTCATCCCCATGTGATT TTTTGTGTCATTCTCTAA GAAGCATATAAAATCACATG GGGATAGCACTACTAAAATT AATTTTACACATTAGGGCTC 100
101 TTCCATATAGGCAGCTCTCC CTAGCATTTGTCACGTGACA CTCGATCGTACTCCGCGTGG CCTCGTGAAAATGTGGTGG CTCCTTCAAGTCCTCCCTAA 200
201 TGTATACACTGATTAAGA TGTGATGTGAGATTAAGT TAACTACATCTACTGTGCT ATGTAGTTACGAGAATTCAT TCTGCACAAGAGTAGACTAT 300
301 ATATCGTAAACGGAAAAGCG AAAACGTTTATATAGCCCAT CTGCGTGTGTGGTCTGCAT GAGTTTAGGCCTGAGTTGAG TCAGCACTGCTCATGGATTG 400
401 TTGCAATTGTTGGAGAAAT CATCCAAATCTGCAGCAGGA AGAAGAGTACAGTTTGCTG TTTCTTCTGTCTCTGCGGTA AGGCTTGAGTTTCATCAGCC 500
501 TTTCTTTTGTGCTCTTTT AGGCTCTGTGGTGGGAATG TTTGTATGCGTCAATATGC TTATTCAGCAAATGACTTG ATCTTTGAAATTTGGATCTT 600
601 GTGTCACCAATTGTATGGCA CCTGTGTAGGTCAACCACGT TCCCGAAGGTGTGACTTCCA TGCCAATGCGCGACATCCG AAGAAGCTGAAGCGCTGGG 700
701 GGCAAATGTGCAATTGCG GCCAATGTTGTAATCAGTT CTTGTCTGATAGTCTCTG GTCCCCAAAATTCCTTGGG TTGTCTTGAGACCAGCTCTG 800
801 CCGAAAGCTGTGTACATT GTATGCTTAGTGCGAGTAC GTTTTGCCGAGGCTTCTTA GAAGCCTCAGCAGCAGATT CTTAGTGACAGTTTGGCCTT 900
901 GTTGTGTGTGGCCTTTACCA GACATTTTGCTCTCAAGCTG GTTCAATCTGTCAAGCAGCA GCAAAGCAAGAGCAGCATCA CCGCCATTGCCAGCCATTCT 1000
1001 AGCAGGAGAAGTCCCTTAC TGCTGCCTGGAGTTGAATTT CTTGAATCTGTGCGACTACG TGATGAGGAACGAGAAGAGG CTTGACTGCCGCCTCTGCTC 1100
1101 CCTTCTGCGTAGAAGCCTTT TGGCAATGTTGTTCTTGAG GAAGTTGTAGCAGCATTGCA GCATTGTAGCAGCATTGCG GGTGCCAATGTGATCTTTTG 1200
1201 GTGTATTCAAGGCTCCCTCA GTTGCAACCATATGATGCC GTCTTTGTAGCACCATAGG GAAGTCCAGCTTCTGGCCCA GTTCTAGGTAGTAGAAATA 1300
```

1301 CCATCTTGGACTGAGATCTT TCATTTTACCGTCACCACCA CGAATTCGTCTGGTAGCTCT TCGGTAGTAGCCAATTTGGT CATCTGGACTGCTATTGGTG 1400

1401 TTAATTGGAACGCCTTGTCC TCGAGGGAATTTAAGGTCTT CCTTGCCATTGTGAGTGAGA GCGGTGAACCAAGACGCAGT ATTATTGGGTAAACCTTGGG 1500

1501 GCCGACGTTGTTTGATCGC GCCCCACTGCGTTCCTCATT CTGGTTACTGCCAGTTGAAT CTGAGGGTCCACCAAACGTA ATGCGGGGTGCATTTCGCTG 1600

1601 ATTTTGGGGTCCATTATCAG ACATTTTAGTTTGTTCGTTT AGATGAAATCTAAAAACA CGAACGTCATGATACTCTAA AAAGTCTTCATAGAACGAAC 1700

1701 AACGCACTACAAGACTACCC AATTAGGTTCTTGGAATT AATTGTAAGGTAAACAGG AAAGTGTATAATTACCGATA TCGATGTACTGAATGGGTGA 1800

1801 TTAGAACCAACCTCATCCA CGCACAATTCAATTAAGGT GCTGATTTTCTAGCTCCTAC TCTAATATACCATTAGAAT AGAAGTGAATAGGACACGGG 1900

1901 TCATCAACTACATATGGTTG ATGTTGAGTACATGACTGTA AACTACATTCTTGGTGAAAT GCAGTACAGTTGTGATGAT TCCTAAGAAAAAAGAAATT 2000

2001 TCATGTTCGTTTAGGCGTGA CAAGTTTCATTATGATCTG CAGTTCAGTGAGAACCCAA AGATAATAAGCATAATTAACAAAGGAATAGCAGAAAGGC 2100

2101 TAAAAAGCACAAATAGAAAGT CAATTATGAAAGTTCAATC ATTCTGTCTTCTTTTGAAGT GTGAAGCAAAGTGTATTAAC CACTATTGCCGCAACAATAA 2200

2201 GAAAAATTGGAGAGTAAAGT TCTTGAACCTCTCTTGTCT GATGAACAGTTTAGGTGAAA CTGATCTGGCAGCTAACTGA TAGACGTGTTTTACGCCGTC 2300

2301 AGGACAAGCAAAAGCAAATT GAGTGTAAAGCAAGTCAGT GCAAAATTGTTATCAGCTAG AGGATGAAATGGTGAAATGC CCTCGTATGTTCCAGAAGAG 2400

2401 CAAGGTTCTTTTAAAGTAC TGTGTACCTCTAACACACT CTTGCTAGTGATAAAGTCA CAAGTAGCGAGTGTATCAG TGCCAAGAAAAGAATAATT 2500

2501 TCATGTTCGTTTAAATCAAT TCCATTGGTTGCTCTTCATC TAATTGAGAATATTTATCT CAGTTAGTGAAGTATAGATAA TTTTAAATATGAGGTTTAT 2600

2601 GATGTAATCAAGATTCCAAA TGGAAACTTTAAAGTCCTC ATAATAATTAGTAATATCTC TGCTATAGTAACCTGAAAGT CAACGAGATGAAACATCTGT 2700

2701 TGTCACTTACTGTACAAGCA AAGCAATATTGTCACTGCTA CTGGAATGGTCTGTGTTAA TTTATAGTTGCCAATCCTGT AGCGACTGTATGCAGCAAAA 2800

2801 CCTGAGTCACCTGTACACG CTGCGAAGCTCCCAATTTGT AATAAGAAAGCGTTCGTGAT GTAGCAACAGTGATTCTTT AGGCAGGTCCTTGATGTCAC 2900

2901 AGCGTCCTAGATGGTGCCA GCAATACGAAGATGCCAGG AAGGATCACAGCTCCGATTA CGAGTTCACTTTCTAGAAGC GGTCTGGTCAGAATAGTGCC 3000

3001 ATGGAGTGGCAGCTTGAGAA GAATGTTAGTTTCTGGATTG AATGACCACATGGAACCGGT ACGCGCAACAGCTGTAAGG AAGCAATGAAGTAGCTGAGC 3100

3101 CACATCAAGCTACAAGACA AGCCATTGCGATAGCAATTC CACCGGTGATCCAATTTATT CTGTAACAGCAGCAAGCAC AAAACAAGCTAAAGTTACTG 3200

3201 GCCATAACAGCCAGAGGAAA ATTAACTTAATTATATACAA AAACCTATTCTGTTGGCAT AGGCAAAATGTAGAAGACAA ATCCATGTAAGGAATAGGAA 3300

3301 ACCTATTACTAGTTCCATT GTTCAAGGAGCTTTTAAAGC TCTTCAACGTAATAGTACC GTTGAATCTGCCATGCTA AAATTAAGTTCCAACAGA 3400

3401 AAAACTAATATAATTTAG TTCGTTTAGACCAGAAGATC AGGAACTCTAGAAGAATTCA GATTTTAAACAGAGAGTAA ACGTAAAAAGAAGGTTTAC 3500

3501 AAGACTCAGTTAACAATAT TGCAGCAGTACGCACACAAT CGAAGCGCAGTAAGGATGGC TAGTGTAAGTACGAAGAATA CCACGAAAGCAAGAAAAAGA 3600

3601 AGTAGCTATTAAGTATTAAGTACCTGTCTCTCCGAAA CGAATGAGTACATAAGTTCG TACTCATCAGCTTGTGCTTA CAAAGGCACGCTAGTAGTCG 3700

3701 TCGTCGGTTATCATAAATT GGTTCATTACTGGATTAAC AACTCCGGATGAACCGTCGA TTGTGTGAATTTGGACATGT TCTCAGGCTCATCAACAAT 3800

3801 TTTATTGTAGTGAAGAAGG TAACATGTTCAACACCAAGT TCTGTACTCAATTGAGTTGA GTACAGCTGGTAATAGTCTG AAGTGAAGTAACTGTGTAAT 3900

3901 ACAACACAGTCTTTTACTCC AGATTCCCAATTTTTCAGTAT AACCACCAATCTGGTAGTCA TGTTCAGAAATAGGACTTGT TGTGCCATCACCTGAAGTAA 4000

4001 TGACAATTGAAGAAGTTACA CTATTGTAAGGTATACAATA GTCGTAACAATTAGTATGCC AGCAAGAAAAATAGTTGGCA TCATAAGTAATGGGTTTTT 4100

4101 GGAACGCGATTTCAGCAAA GCCAAAGCCTCATTATTATT CTTACAAAGTTTACTCTG CAAGAAGTAGACTAAAGCAT AAAGATAGAGAAAAGGGCT 4200

4201 TCAAGGCGCAGCAACGAG CAAAAGGTGTGAGTAAAGTCTTACAACAACAACAGCAAG TTGCAAAACAAAGTGAACACC CTTGAGAGTGCTAGTTGCC 4300

4301 ATCTCTTTTGAAGGTTATG ATTTTGGAAGCGCTATGAAA AACAGCAAGAAGTGCAACGC CAACAATAAGCCATCCGAAA GGGAGTGAGGCTTGATCGG 4400

4401 TATCTGTGAGTAGCGCGAA CAAAATCTGAAGGAGTAGCA TCCTTGATTTCACCTTGCTT CAAAGTTACAGTTCCAATTG TGAAGATTCTCATAAACAAA 4500

4501 TCCATAAGTTTCGTTATGTG TAAATGTAATTGACTCCTTT GAGCACTGGCTCAGATCGT CTTTCATCAAATTTGCAGCAG GATCCACAAGAACACAGCC 4600

4601 CTTGAGACAACTACAGCAAC TGGTCATACAGCAAAAGCATA ATTGTCACCATTACTATGGC AATCAAGCCAGCTATAAAAC CTAGCCAAATGTACCATGGC 4700

4701 CATTTTATATACTGCTCATA CTTTCCAAGTTCTTGAGAT CGATGAGAGATTCAATTAAA TTCTTGGAACCTCATTGAG GCGGTCAATTTCTTTTTGAA 4800

4801 TGTTTACAACCTGAAGCATT AATGCCAGAGATGTCACCTAA ATCAACATCTGGTGATGAT GATTCTTAAATATTATCT AACTCTCCTTGAATGATC 4900

4901 TAATTGAGTTGCAAGGAT CATAAATCTGTGTTGACA ATTCTATTACAACATCACA GTTACCAGACACAATGTGT TGCTGTAGTAATGATTGT 5000

5001 GGTTTCATAAAATTCCTTG TGTTACAACACAGTGTGTGC CATTGAAACAAGACACCT TCACGAGGAAAGTGTGCTTT TCCATCATGACAAATGGCAG 5100

5101 GAGCAGTTGTGAAGTCTTT TCTTGTGACGGACATAAGT CACATGCAAGAAGACTACAC CATGAGGTGCTGACTGAGGG AAGGACATAAGATGATAGCC 5200

5201 CTTTCCACAAAATCAACTC TTTTGTATGTCCAAGTACA CACTCTGACATTTTAGTAGC AGCAAGATTAGCAGAAGCTC TGATTTCTGCAGCTCTAAT 5300

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5401 CATTTAAACACTTGAAATT GCACAAAATTTGGAGCTAAG TTGTTTAAACAGCGTGTTA AAGCTTGTGATTTTGGTIG ACCACATCTGAAGTTTCC 5500

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5601 GTAACCTCAATACCATTAAC CTTAAGCCATTGTCATAG CAAATGGTATTGTGAATGCA GCACCTGCACCAAGGTCCA ACCAGAAGTGATTGTACCCG 5700

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5901 GGTTTGATGGATCTGGTAA TATTGTGAAAAATTAAC CACCAAAATCTTTAATGGT GGTGTTTGTAAAATTTGTTT GACTGTGCAAAAACCTCTT 6000

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6201 ATAGAGTTATTAGAGTAAGC AACTGAATTTTCTGCACCAA GTGACATAGTGTAGGCAATG ATGGATTGACTAGCTACACT ACGTCCCGCCGAGGAGAAT 6300

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6401 TGTTTGAACAAATAGAAC CTGTAGAATAAACACGCCAA GTAGGAGTAAGTTGATCTGC ATGAATAGCAACAGGACTT CTGTGAGTTAACACCCTGA 6500

6501 TAAAGAACAGCAACCTGGTT AGAAGTATTGTTCCTGGTG TTATAACACTGACACCACCA AAAGAACATGGTGTAATGTC AAGAATCTCAAGTGTCTGTG 6600

6601 GATCACGGACAGCATCAGTA GTGTCAGCAATGTCTCTGCC AAATTGTGGAAGGCAGAA ACTTTTGTAGACTCAGTA AGAACACCTGTGCTGTAA 6700

6701 ACCATTGAAGTTGAAATTGA CACATTGTTTTTAACCAA TTAGTAGACTTTTTAGGTCC ACAACAGTTGCTGGTGCAT GTAGAAGTTCAAAAGAAAGT 6800

6801 ACTACTACTCTGTATGGTTG GTAACCAACACCATTAGTGG GTTGGAAACCATATGATTGT AAAGGAAAGTAACAATTAAA ACCTTCAACACCATTACAAG 6900

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7101 GGAGCGATTGTCTGACTTC ATCACCTCTAATTACAAATG AATCTGCATAGACATTAGTA AAGCAGAGATCATTAAATTT AGTAGGAGACACTCCATAAC 7200

7201 ACTTAAAGTGGAATATGAT GCGGAATTATATAGGACAGA ATAATCAGCAACACAGTTGC TGATTCTCTTCTGTTCCAA GCATAAACAGATGCAAACT 7300

7301 GGTGGCGTAAAAAAGTTTCA CAAAAGGGCACAAGTTTGTG ATATTAGGAAATCTAACAAT AGATTCTGTGTGGTGGACTC TAAAGTTAGAAGTTGATAG 7400

7401 ATTCCTTTTCTACAGTGAA GGATTTCAACGTACACTTTG TTTCTGAGAGAGGGTCAAGT GCACAGTCTACAGCATCTGT AATGGTTCCATTTTCATTAT 7500

7501 ATTTTAATAGAAAAGTCCTA GGTGTGAAGATAACCCACATA ATAAGCTGCAGCACCAGCTG TCCAACCTGAAGAAGAATCA CCAGGAGTCAAAACTTCT 7600

7601 ATGTAAAGCAAGTAAAGTTT GAAACCTAGTGATGTTAATA CCTATTGGCAAATCTACCAA TGGTCTAAAGCCGAAAAAC CCTGAGGGAGATCAGCACT 7700

7701 AAATTAATAGGCGTGTGCTT AGAATATATTTTAAATAAC CATCAATATTTCTTAAACACA AATTCCTTAAGATTTTGTAA ATTACCTGTTTTCTCTCAA 7800

7801 GGTCCATAAGAAAAGGCTGA GAGACATATTCAAAGTGCA ATTATTGCGACTAGATAAAA CTCTGAACCTCACTTTCCATC CAATCTTGTGTTTTGTG 7900

7901 GTAATAAACCCCAAAATGAT CATTACAAAATTGAAAT TCACAGACTTTAATAACAAC ATTAGTAGCGTTATTAAACA TAAGTAGGGACTGGGTCTC 8000

8001 GAATCTAAAGTAGTACCAAA AATCCAGCCTCTTATTATGT TAGACTTCTCAGTGAAGCA AAATAAACACCATCATIAAA TGGTAGGACAGGGTATCAA 8100

8101 ACCTCTTAGTACCATTTGGTC CCAGAGACATGTATAGCATG GAACCAAGTAACATTGGAAA AGAAAGGTAAGAACAAGTCC TGAGTTGAATGAAAACTGA 8200

8201 GGATCTGAAAACCTTTGTCAG GGTAATAAACACCACGTGTG AAGAATTAGTGTATGCAGG GGGTAATTGAGTTCTGGTTG TAAGATTAAACACTGACTA 8300

8301 GAGACTAGTGGCAATAAAAC AAGAAAAACAACATTGTTC GTTAGTTGTIAACAAGAAC ATCACTAGAAAATAACAAC TCATTGTTTTCTCTAATTATA 8400

8401 AGTCTACCTTTACTAAGAAG AGATAAAATCATATCAATTG TTAGCTCTCTTTTAAAGAC ATAACAGCAGTACCCCTTAA TTAAAGGGAAATTTACTCA 8500

8501 TGTCAAATAAAGAATAGGAA GACAACTGAATTGGATTGT ATCTCTCAAAATATGTAAT TTGCATGCATGACATAACCA TCTATTTGTCGCGTGGTT 8600

8601 GCCAAGATAATTACATCCAA TTAATAATGCTTCAGATGAT GACGCTTACATTAGTAAC AAAGGCTGTCCACCATGCCA AGTGCCCATGAGCTTATAA 8700

8701 AGATCAGCATTTCAAGAATG TTTCTGTATCTTTATAGCCA CGGAACCTCCAAGAGTAGC TTTGTGTATAAACCCACA AATGTAAGTAAAAAACCT 8800

8801 CTTTAGAGTCAATTTCTTTT GTAACATTTTAGTCTTAGG GTCGTACATACACTAATAA TGAGATCCCATTTATTAGCT GTATGTACAGTTGCACAATC 8900

8901 ACCAATCAAAGTTGAATCTG CATCAGAGACAAAGTCATTA AGATCTGAATCGACAAGCAG CGTACCCGTAGGCAACCACT GTCTTAAACAGCTGTACCT 9000

9001 GGTGCAACTCCTTTATCAGA ACCAGCACCAAAATGTATAA CTCTCATATTATAGGTACA GCTAATGTTAATGTGTTAA ATATTGACACAGTTGAGTAT 9100

9101 ATTTTGCAGACTTCATCAAT ATGCTTTAGGTAATGTTCG ACTATCACCATAATTTTGAA GGTACACTTTTCTAATAGC ATTCTTGCATTTTGTAAAG 9200

9201 ATTAGCATAGCAACACCCG GTTGCCACGCTTGACTAGAT TGTAATTTGGGTAATATGT TTCTACATGCCATCTTAC ACCAAAGCATAAATGAAATT 9300

9301 TCTGTATAGTCAATAGTCAC TTTGACAACCTTAGAACTA CAGATAAATCTTGGGATTTT ATTATTCAACAAATCATC AAGTAATAAATCAATAACAG 9400

9401 AACACACACACTIAGATGAA CCTGTTTGCATCTGTTAT GAAATAGTTTTTAACTGTAC TGCCATAGGAATAAAATCT TCTAATTCAAAAGGTGATTC 9500

9501 CTTAAACAGTTIAGCTAGTC CAATCAGTAGATGTAAACCA CTAACCTGACTATGACTAAA ATCTCCATAAACGATAATGTT CGAAGGCATAGCCTTCTAAT 9600

9601 TTATACCGTCAATGAATTC ATCCATAGCTAATTCTAAGA AATCAATTTCCATTGTACTC CTGGGTTTAAATCTGTAA ATTCTACTCTGAGTAAAGT 9700

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1.14. SRR12596175 Discovered Strain 1 Nucleotide Sequence

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1.15. SRR12596175 Discovered Strain 2 Nucleotide Sequence

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26601 TGAACAATGGAACCTAGTAA TAGGTTTCTTATCTTACATA TGGATTGTCTTCTACAAAT TGCTATGCCAACAGGAATA GGTTTTGTATATAATTAAG 26700

26701 TTAATTTTCTCTGGCTGTT ATGCCAGTAACCTTAGCTT GTTTGTGCTTGTGCTGTTT TACAGAATAAATTGGATCAC CGGTGGAATTGCTATCGCAA 26800

26801 TGGCTTGTCTGTAGGCTTG ATGTGGCTCAGCTACTTCAT TGCTTCTTCAGACTGTTTG CGGTACGCGTTCATGTGG TCATTCAATCCAGAACTAA 26900

26901 CATTCTTCTCAACGTGCCAC TCCATGGCACTATTCTGACC AGACCGCTTCTAGAAAGTGA ACTCGTAATCGGAGCTGTGA TCCTTCGTGGACATCTTCGT 27000

27001 ATTGCTGGACACCATCTAGG ACGCTGTGACATCAAGGACC TGCCTAAAGAAATCACTGTT GCTACATCACGAACGCTTTC TTATTACAAATGGGAGCTT 27100

27101 CGCAGCGTGTAGCAGGTGAC TCAGGTTTTGCTGCATACAG TCGCTACAGGATTGGCAACT ATAAATTAAACACAGACCAT TCCAGTAGCAGTGACAATAT 27200

27201 TGCCTTGCTGTACAGTAAG TGACAACAGATGTTTCATCT CGTTGACTTTCAGGTTACTA TAGCAGAGATATTACTAATT ATTATGAGGACTTTTAAAGT 27300

27301 TTCCATTGGGAATCTTGATT ACATCATAAACCTCATAATT AAAAATTTATCTAAGTCACT AACTGAGAATAAATATTCTC AATTAGATGAAGAGCAACCA 27400

27401 ATGGAGATTGATIAAACGAA CATGAAAATTATCTTTTCT TGGCACTGATAACACTCGCT ACTTGTGAGCTTTATCACTA CCAAGAGTGTGTAGAGGTA 27500

27501 CAACAGTACTTTTAAAGAA CCTTGCTCTTCTGGAACATA CGAGGGCAATTCACCATTTT ATCCTCTAGCTGATAACAAA TTGCACTGACTTGCTTTAG 27600

27601 CACTCAATTTGCTTTTGCTT GTCTGACGGCGTAAACAC GTCTATCAGTTACGTGCCAG ATCAGTTTCACCTAACTGT TCATCAGACAAGAGGAAGTT 27700

27701 CAAGAACTTACTCTCCAAT TTTTCTTATTGTTGCGGCAA TAGTGTTTATAACACTTTGC TTCACACTCAAAGAAAAAC AGAATGATTGAACTTTCATT 27800

27801 AATTGACTTCTATTGTGCT TTTAGCCTTTCTGCTATTC CTGTGTTTAATTATGCTTAT TAICTTTTGGTTCTCACTTG AACTGCAAGATCATAATGAA 27900

27901 ACTTGTACGCGCTAAACGAA CATGAAATTTCTTGTTTTCT TAGGAATCATCACAACGTGA GCTGCATTTACCAAGAATG TAGTTTACAGTCATGTACTC 28000

28001 AACATCAACCATATGTAGTT GATGACCCGTGCTCATTCA CTCTATTCTAAATGGTATA TTAGAGTAGGAGCTAGAAAA TCAGCACCTTTAATTGAATT 28100

28101 GTGCGTGGATGAGGTTGGTT CTAATCACCCATTCACTAG ATCGATATCGGTAATTATAC AGTTTCCTGTTTACCTTTTA CAATTAATTGCCAGGAACCT 28200

28201 AAATTGGGTAGTCTTGTAGT GCGTGTGCTGCTTATGAAG ACTTTTATAGATATCATGAC GTTCGTGTTGTTTAGAATT CATCTAAACGAACAACTAA 28300

28301 AATGTCTGATAATGGACCCC AAAATCAGCGAAATGCACCC CGCATTCAGTTTGGTGGACC CTCAGATTCAACTGGCAGTA ACCAGAATGGAGAACGCAGT 28400

28401 GGGGCGCGATCAAAACAACG TCGGCCCAAGGTTTACCCA ATAATACTGCTCTTGTTGTC ACCGCTCTCACTCAACATGG CAAGGAAGACCTTAAATTCC 28500

28501 CTCGAGGACAAGGCGTTCCA ATTAACACCAATAGCAGTCC AGATGACCAAATTTGGTACT ACCGAAGAGCTACCAGACGA ATTCGTGGTGGTGACGGTAA 28600

28601 AATGAAGATCTCAGTCCAA GATGGTATTCTACTACCTA GGAAGTGGGCAGAAAGCTGG ACTTCCTATGGTGCTAACA AAGACGGCATCATATGGGTT 28700

28701 GCAACTGAGGGAGCCTTGAA TACACCAAAAGATCACATTG GCACCCGAATCTGCTAAC AATGCTGAATCGTGCTACA ACTTCCTCAAGGAACAACAT 28800

28801 TGCCAAAAGGCTTCTACGCA GAAGGGAGCAGAGGCGGAG TCAAGCCTCTGCTGCTTCT CATCACGTAGTCGCAACAGT TCAAGAAATCAACTCCAGG 28900

28901 CAGCAGTAGGGAACTTCTC CTGCTAGAATGGCTGGCAAT GCGCGTGATGCTGCTCTTGC TTTGCTGCTGCTTGACAGAT TGAACCACTTGAGAGCAA 29000

29001 ATGCTCTGTTAAAGGCCAACA ACAACAAGGCCAACTGTCA CTAAGAAATCTGCTGCTGAG GCTTCTAAGAAGCCTCGGCA AAAACGTACTGCCACTAAAG 29100

29101 CATACAATGTAACACAAGCT TTCGGCAGACGTGGTCCAGA ACAAAACCAAGGAAATTTTG GGGACCAGGAACTAATCAGA CAAGGAACTGATTACAAACA 29200

29201 TTGGCCGCAAAATGCACAA TTTGCCCCAGCGCTTCAGCG TTCTTCGGAATGTCGCGCAT TGGCATGGAAGTCACACCTT CGGGAACGTGGTTGACCTAC 29300

29301 ACAGGTGCCATCAAATTGGA TGACAAAGATCCAAATTTCA AAGATCAAGTCATTTTGCTG AATAAGCATATTGACGCATA CAAAACATTCCCACCAACAG 29400

29401 AGCCTAAAAAGGACAAAAAG AAGAAGGCTGATGAAACTCA AGCCTTACCGCAGAGACAGA AGAAACAGCAAACCTGTGACT CTTCTTCTGCTGCAGATTT 29500

29501 GGATGATTTCTCAAACAAT TGACAACAATCCATGAGCAGT GCTGACTCAACTCAGGCCTA AACTCATGCAGACCACACAA GGCAGATGGGCTATATAAAC 29600

29601 GTTTTCGCTTTTTCGTTTAC GATATATAGTCTACTCTTGT GCAGAATGAATTTCTGTAAC TACATAGCACAAGTAGAATG AGTTAACTTTAATCTCATAT 29700

29701 AGCAATCTTTAATCAGTGTG TAACATTAGGGAGGACTTGA AAGAGCCACCACATTTTTCAC CGAGGCCACGCGAGTACGA TCGAGTGTACAGTGAACAAT 29800

29801 GCTAGGGAGAGCTGCCTATA TGAAGAGCCCTAATGTGTA AAATTAATTTTAGTAGTGCT ATCCCCATGTGATTTTAATA GCTTCTTAGGAGATGACAA 29900

29901 AAAAAAATCACATGGGGAT AGCAC 29925

EMBOSS_001	1	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHS	50
EMBOSS_001	1	MFVFLVLLSLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHS	50
EMBOSS_001	51	TQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSNI	100
EMBOSS_001	51	TQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSNI	100
EMBOSS_001	101	IRGWIFGTTLDSTQSLIVNNATNVVIKVFCEQFCNDPFLGVYYHKNNK	150
EMBOSS_001	101	IRGWIFGTTLDSTQSLIVNNATNVVIKVFCEQFCNDPFLGVYYHKNNK	150
EMBOSS_001	151	SWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGY	200
EMBOSS_001	151	SWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFKNIDGY	200
EMBOSS_001	201	FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	250
EMBOSS_001	201	FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRLQTLALHRSYLT	250
EMBOSS_001	251	PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK	300
EMBOSS_001	251	PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK	300
EMBOSS_001	301	CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV	350
EMBOSS_001	301	CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV	350
EMBOSS_001	351	YAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADSF	400
EMBOSS_001	351	YAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADSF	400
EMBOSS_001	401	VIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGNGYN	450
EMBOSS_001	401	VIRGDEVQRQIAPGQTGKIADYNYKLPPDFTGCVIAWNSNNLDSKVGNGYN	450
EMBOSS_001	451	YLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
EMBOSS_001	451	YLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
EMBOSS_001	501	NGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG	550
EMBOSS_001	501	NGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG	550
EMBOSS_001	551	VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP	600
EMBOSS_001	551	VLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP	600

Figure S1. Difference of discovered strain 1 spike protein sequence and original strain spike protein sequence

EMBOSS_001	601	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL	650
EMBOSS_001	601	..:	650
EMBOSS_001	601	EVDTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL	650
EMBOSS_001	651	IGAETHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLG	700
EMBOSS_001	651		700
EMBOSS_001	651	IGAETHVNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLG	700
EMBOSS_001	701	AENSVAYSNNISAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSSTCS	750
EMBOSS_001	701		750
EMBOSS_001	701	AENSVAYSNNISAIPTNFTISVTTEILPVSMKTSTVDCTMYICGDSSTCS	750
EMBOSS_001	751	NLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF	800
EMBOSS_001	751	.	800
EMBOSS_001	751	NLLLQYGSFCTQLNRGLTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF	800
EMBOSS_001	801	NFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLI	850
EMBOSS_001	801	.	850
EMBOSS_001	801	NFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDHI	850
EMBOSS_001	851	CAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAAALQIPFAM	900
EMBOSS_001	851		900
EMBOSS_001	851	CAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAAALQIPFAM	900
EMBOSS_001	901	QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD	950
EMBOSS_001	901		950
EMBOSS_001	901	QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD	950
EMBOSS_001	951	VVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGR	1000
EMBOSS_001	951		1000
EMBOSS_001	951	VVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGR	1000
EMBOSS_001	1001	LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM	1050
EMBOSS_001	1001	. ..:	1050
EMBOSS_001	1001	LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM	1050
EMBOSS_001	1051	SFPQSAPHGVVFLHVTYVPAQEKNFTTAPACHDGAHFPREGVFSNGT	1100
EMBOSS_001	1051	. ..:	1100
EMBOSS_001	1051	SFPQSAPHGVVFLHVTYVPAQEKNFTTAPAKSDDGAHFPREGVFSNGT	1100
EMBOSS_001	1101	HWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE	1150
EMBOSS_001	1101		1150
EMBOSS_001	1101	HWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE	1150
EMBOSS_001	1151	ELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	1200
EMBOSS_001	1151	.	1200
EMBOSS_001	1151	ELDKYFKNHTSADVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	1200
EMBOSS_001	1201	QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMTSCCSCCLKGCCSC	1250
EMBOSS_001	1201		1250
EMBOSS_001	1201	QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMTSCCSCCLKGCCSC	1250
EMBOSS_001	1251	GSCCKFDEDDSEPVLGKVKLHYT	1273
EMBOSS_001	1251		1273
EMBOSS_001	1251	GSCCKFDEDDSEPVLGKVKLHYT	1273

Figure S1. Difference of discovered strain 1 spike protein sequence and original strain spike protein sequence

EMBOSS_001	1	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYYPDKVFRSSVLHS	50
EMBOSS_001	1	MFVFLVLLPLVSSQCVNLTTRTQLPKSDTNSFTRGVVYYPDKVFRSSVLHS	50
EMBOSS_001	51	TQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTSEKSN	100
EMBOSS_001	51	TQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTSEKSN	100
EMBOSS_001	101	IRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNK	150
EMBOSS_001	101	IRGWIFGTTLDSTQSLIVNNATNVVIVKCEFCNDPFLGVVYHKNNK	150
EMBOSS_001	151	SWMESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGY	200
EMBOSS_001	151	SWMESEFRVYSSANNCTFEYVSQPFMDLEGKQGNFKNLREFVFNIDGY	200
EMBOSS_001	201	FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	250
EMBOSS_001	201	FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYLT	250
EMBOSS_001	251	PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK	300
EMBOSS_001	251	PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK	300
EMBOSS_001	301	CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV	350
EMBOSS_001	301	CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASV	350
EMBOSS_001	351	YAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADSF	400
EMBOSS_001	351	YAWNRRKISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADSF	400
EMBOSS_001	401	VIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNLDLSDKVGNNY	450
EMBOSS_001	401	VIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNLDLSDKVGNNY	450
EMBOSS_001	451	YLRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
EMBOSS_001	451	YLRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPT	500
EMBOSS_001	501	NGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG	550
EMBOSS_001	501	NGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTG	550
EMBOSS_001	551	VLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP	600
EMBOSS_001	551	VLTESNKKFLPFQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP	600
EMBOSS_001	601	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL	650
EMBOSS_001	601	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCL	650
EMBOSS_001	651	IGAHEVNNSEYCDIPIGAGICASYQTQTNSPRRARSVASQSIAYTMSLG	700
EMBOSS_001	651	IGAHEVNNSEYCDIPIGAGICASYQTQTNSPRRARSVASQSIAYTMSLG	700

Figure S2. Difference of discovered strain 2 spike protein sequence and original strain spike protein sequence

EMBOSS_001	701	AENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC	750
EMBOSS_001	701	AENSVAYSNNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTEC	750
EMBOSS_001	751	NLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF	800
EMBOSS_001	751	NLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGF	800
EMBOSS_001	801	NFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLI	850
EMBOSS_001	801	NFSQILPDPSKPSKRSFIEDLLFNKVTADAGFIKQYGDCLGDIARDLI	850
EMBOSS_001	851	CAQKFNGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM	900
EMBOSS_001	851	CAQKFNGLTVLPPLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM	900
EMBOSS_001	901	QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD	950
EMBOSS_001	901	QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQD	950
EMBOSS_001	951	VVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGR	1000
EMBOSS_001	951	VVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGR	1000
EMBOSS_001	1001	LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM	1050
EMBOSS_001	1001	LQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLM	1050
EMBOSS_001	1051	SFPQSAPHGVVFLHVTYVPAQEKNF TTAPAICHDGKAHFPREGVFVSNGT	1100
EMBOSS_001	1051	SFPQSAPHGVVFLHVTYVPAQEKNF TTAPAICHDGKAHFPREGVFVSNGT	1100
EMBOSS_001	1101	HWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE	1150
EMBOSS_001	1101	HWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKE	1150
EMBOSS_001	1151	ELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	1200
EMBOSS_001	1151	ELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	1200
EMBOSS_001	1201	QELGKYEQYIKWPWYIWLGF IAGLIAIVMVTIMLCMTSCCCLKGCCSC	1250
EMBOSS_001	1201	QELGKYEQYIKWPWYIWLGF IAGLIAIVMVTIMLCMTSCCCLKGCCSC	1250
EMBOSS_001	1251	GSCCKFDEDDSEPVLKGVKLHYT	1273
EMBOSS_001	1251	GSCCKFDEDDSEPVLKGVKLHYT	1273

Figure S2. Difference of discovered strain 2 spike protein sequence and original strain spike protein sequence

EMBOSS_001	1	MFLTTKRTMFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVVYPDK	50
EMBOSS_001	1	MFLTTIIRTMFVFLVLLPLVSSQCVNLKSRQLPPAYTNSFTRGVVYPGK	50
EMBOSS_001	51	VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSQNGTKRFDNPVLPFNDGVY	100
EMBOSS_001	51	VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSQIGTKRFDNPVLPFNDGVY	100
EMBOSS_001	101	FASTEKSNIIRGWIFGTTLDSKTQSLIVNNATNVVIKVEFCQFCNDPFL	150
EMBOSS_001	101	FASTEKSIIIRGWIFGTTLDSKTQSLIVNNSTNVVIKVEFCQFCNDPFL	150
EMBOSS_001	151	GVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLEGKQGNFKNLRE	200
EMBOSS_001	151	GVYYHKNNKSWMESEFRVYSSANNCTFE-VSQPFLLMDLEGKQGNFKNLRE	199
EMBOSS_001	201	FVFKNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQTL	250
EMBOSS_001	200	FVFKNIDGYFKIYSKHTPINLVRDLPGGFSALEPLVDLPIGINITRFQII	249
EMBOSS_001	251	LALHRSYLTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDC	300
EMBOSS_001	250	LSLHRSYLTPGDSSSGWTAGAAAYVGYLQPRSFLLKYNENGTITDAVDC	299
EMBOSS_001	301	ALDPLSEKCTLKSTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEV	350
EMBOSS_001	300	ALDPLSGKCTLKSTVEKGIYQTSNFRVQPTESIVRFPNIKYLCPFGEV	349
EMBOSS_001	351	FNATRFASVYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLC	400
EMBOSS_001	350	FNATRFASVYAWNRKRISNCVADYSVLVNSVPFSTFKCYGVSPTKLNDLC	399
EMBOSS_001	401	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNL	450
EMBOSS_001	400	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNL	449
EMBOSS_001	451	DSKVGGNVNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFP	500
EMBOSS_001	450	DSKVGGNVNYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFL	499
EMBOSS_001	501	LQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	550
EMBOSS_001	500	LQLYGFQPTNGVGYQPYRVVLSFELLHAPATVCASKKSTNLVKNKCVNF	549
EMBOSS_001	551	NFNGLTGTGVLTESNKKFLPFQFGRDIADT-----TDAVRDPQTLEI	593
EMBOSS_001	550	NFNGLTGTGVLTESNKSFLF----NNLAETLLTLLMLSEVHRHLRFTL	595
EMBOSS_001	594	LDITPCSFGGVSVITP-----GTNTSNQVAVLYQGVNCTEVPV	631
EMBOSS_001	596	HHVLLV----VSVLRQEQLLTRLLFFIRVSTAQKSLLLFMQINLLLLGV	641
EMBOSS_001	632	AIHADQLTPTWRVYSTGSMVFQTRAGCLIGAHEVMNSYECDIPIGAGICA	681
EMBOSS_001	642	FI-LQVLKFLKHVQAVGLNMSTT-----HMSVTY----PL-----	671
EMBOSS_001	682	SYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISV	731
EMBOSS_001	672	-VQVYALVIRLSLILLGGHVVLNPSL---HSLCHLVQKIQLLTLITLLP	717

Figure S3. Difference of MR discovered strain 1 spike protein sequence and the MR assembled contig spike protein sequence

EMBOSS_001	732	TTEILPVSMTK-----TSVDCT-----MYICGDSTECNLLLL	763
EMBOSS_001	718	YPQILLLLVLPQKFYQCLPRHQIVQCTFGMIQLNAAIYCCNMAVFNHTVL	767
EMBOSS_001	764	QYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK-----QIYKTPP-	802
EMBOSS_001	768	-----LELLNKTPTPKKFVHKSNKFTKHHQLKILVVLIFHKFQIHQNQAR	812
EMBOSS_001	803	---IKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDC	849
EMBOSS_001	813	GHLKIKYFSTKHLQLL-----ASSNNMVIALV---ILLLEPSFVHK----	850
EMBOSS_001	850	LGDIAARDLICAQKFNGLTVLPPLLTDEMIAYQTSALLAGTITS-----	893
EMBOSS_001	851	----SLTALLFCHLCSQIRLLNTLLHCRVL-----SLLVGPLVQVLHYKY	891
EMBOSS_001	894	----GWTFGAGA-ALQIPFAMQ-----MAYRFNGIGVTQMWLYEN	928
EMBOSS_001	892	HVLCKWLIGLVMVLELHRMFSMRTKNLPTNLIVLLAKFKTHFLPQQANLEN	941
EMBOSS_001	929	QKLIANQFNISAIGKIQDSLSTASALGKLDQVNVNQAQALNTLVKQLSSN	978
EMBOSS_001	942	FKM---WSTKMHKLTRLNNLAPILVQFQ-----	967
EMBOSS_001	979	FGAISSVLNDILSRDLKVEAEVQIDRLITGRQLSLQTY-VTQQLIRAAEI	1027
EMBOSS_001	968	---VFMISFHVLTKL-----RLCKKLIGSQADFNVCRHMLNNLEL	1004
EMBOSS_001	1028	RASANLAATKMSEC---VLGQSKRVDFCGKGYHLMSPQASAPHGVWF---	1071
EMBOSS_001	1005	QKSELLILLLLLCNSQSVYLDNQKELIFVERA---IILCPSLSQHLMMFSCM	1052
EMBOSS_001	1072	---LH-----VTYVPAQEKNFITAPAI---CHDGKAHFPREGVFSN	1107
EMBOSS_001	1053	LMSLHKKRTSQLLLPFV-MMEHTFLVKVSLFQMAHTGL----HKGIFMNH	1097
EMBOSS_001	1108	-----GTHWF-----VTQRNFYEPQIITTDNTFVSGNCDVVIGIVNN-	1144
EMBOSS_001	1098	KSLLQTTHLCVTVMLLEVSTTQF---MILCNLNTHSRRSIN-ILRIIHQ	1143
EMBOSS_001	1145	-TVYDPLQPELD-SFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEI	1192
EMBOSS_001	1144	MLIVTSLALMLQLTYKKKL-----TASMRLQI	1170
EMBOSS_001	1193	DRLNEVAKNLN--ESLIDLQELGK-----YEQYIKWPW	1223
EMBOSS_001	1171	MNLSSISKNLSESMSSIMAMVHLARFYSWLDCHSNGDNYALLYDQLLSQG	1220
EMBOSS_001	1224	YIWLGFIAGLIAIV----MVTIMLCMTSCCSCCLKGCCSCGSCCKFDED	1268
EMBOSS_001	1221	LLFLGILLQIRRLASAQRSQITLHI-----	1245
EMBOSS_001	1269	DSEPVLKGVKLHYT	1282
EMBOSS_001	1246		1245

EMBOSS_001	1	MFLTTKRTMFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDK	50
EMBOSS_001	1	MFLTTKRTMFVFLVLLPLDSSQCVNLTTRTQLPPAYTNSFTRGVYYPDK	50
EMBOSS_001	51	VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVY	100
EMBOSS_001	51	VFRSSVLHSTQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVY	100
EMBOSS_001	101	FASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKVFCEQFCNDPFL	150
EMBOSS_001	101	FASTEKSNIIRGWIFGTTLDSTQSLIVNNATNVVIVKVFCEQFCNDPFL	150
EMBOSS_001	151	GVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF LMDLEGKQGNFKNLRE	200
EMBOSS_001	151	GVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPF LMDLEGKQGNFKNLRE	200
EMBOSS_001	201	FVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTL	250
EMBOSS_001	201	FVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTL	250
EMBOSS_001	251	LALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDC	300
EMBOSS_001	251	LALHRSYLT PGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDC	300
EMBOSS_001	301	ALDPLSEKCTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEV	350
EMBOSS_001	301	ALDPLSEKCTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEV	350
EMBOSS_001	351	FNATRFASVYAHNRKRISNCVADYSVLVNSASFSTFKCYGVSPKLNCLC	400
EMBOSS_001	351	FNATRFASVYAHNRKRISNCVADYSVLVNSASFSTFKCYGVSPKLNCLC	400
EMBOSS_001	401	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNL	450
EMBOSS_001	401	FTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNL	450
EMBOSS_001	451	DSKVGGNMYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFP	500
EMBOSS_001	451	DSKVGGNMYLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNCYFP	500
EMBOSS_001	501	LQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	550
EMBOSS_001	501	LQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF	550
EMBOSS_001	551	NFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCS	600
EMBOSS_001	551	NFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTL EILDITPCS	600
EMBOSS_001	601	FGGVSVITPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSN	650
EMBOSS_001	601	FGGVSVITPGTNTSNQVAVLYQGVNCTEVPVAIHADQLTPTWRVYSTGSN	650
EMBOSS_001	651	VFQTRAGCLIGAHEVMNSYECDIPIGAGICASYQTQTNSPRRARSVASQS	700
EMBOSS_001	651	VFQTRAGCLIGAHEVMNSYECDIPIGAGICASYQTQTNSPRRARSVASQS	700
EMBOSS_001	701	IIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMY	750
EMBOSS_001	701	IIAYTMSLGAENSVAYSNNIAIPTNFTISVTTEILPVSMKTSTVDCTMY	750

Figure S4. Difference of MR discovered strain 2 spike protein sequence and MR assembled contig spike protein sequence

EMBOSS_001	751	ICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKT	800
EMBOSS_001	751		800
EMBOSS_001	751	ICGDSTECSNLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKT	800
EMBOSS_001	801	PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCL	850
EMBOSS_001	801		850
EMBOSS_001	801	PPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCL	850
EMBOSS_001	851	GDIAARDLICAQKFNGTLVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG	900
EMBOSS_001	851		900
EMBOSS_001	851	GDIAARDLICAQKFNGTLVLPPLLTDEMIAQYTSALLAGTITSGWTFGAG	900
EMBOSS_001	901	AALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSST	950
EMBOSS_001	901		950
EMBOSS_001	901	AALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDLSST	950
EMBOSS_001	951	ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEV	1000
EMBOSS_001	951		1000
EMBOSS_001	951	ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEV	1000
EMBOSS_001	1001	QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1050
EMBOSS_001	1001		1050
EMBOSS_001	1001	QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVD	1050
EMBOSS_001	1051	FCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPR	1100
EMBOSS_001	1051		1100
EMBOSS_001	1051	FCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHGDKAHFPR	1100
EMBOSS_001	1101	EGVFVSNQTHWVFVTRNFYEPQIITDNTFVSGNCDVWIGIVNNTVYDPL	1150
EMBOSS_001	1101		1150
EMBOSS_001	1101	EGVFVSNQTHWVFVTRNFYEPQIITDNTFVSGNCDVWIGIVNNTVYDPL	1150
EMBOSS_001	1151	QPELDSFKEELDKYFKNHTSPDVLGDISGINASVNIQKEIDRLNEVAK	1200
EMBOSS_001	1151		1200
EMBOSS_001	1151	QPELDSFKEELDKYFKNHTSPDVLGDISGINASVNIQKEIDRLNEVAK	1200
EMBOSS_001	1201	NLNEIDLQELGKYEQYIKWPWYIWLGFIAGLIAIMVTIMLCCMTSCC	1250
EMBOSS_001	1201		1250
EMBOSS_001	1201	NLNEIDLQELGKYEQYIKWPWYIWLGFIAGLIAIMVTIMLCCMTSCC	1250
EMBOSS_001	1251	SCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT	1282
EMBOSS_001	1251		1282
EMBOSS_001	1251	SCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT	1282

Figure S4. Difference of MR discovered strain 2 spike protein sequence and MR assembled contig spike protein sequence