

Supplementary data 2. Genome sequence variations occurred in 14 SARS-CoV isolates

Genome position	Singapore cases					Overseas cases									variation frequency	ORF / protein	AA change
	Index	Primary	Primary	Primary	Secondary	Canada	Hanoi	HK	HK	S. China	N. China	N. China	N. China	N. China			
	SIN2500 29711	SIN2748 29706	SIN2774 29711	SIN2677 29705	SIN2679 29711	TOR2 29712	URBANI 29727	HKU3984 29727	CUHKW1 29712	GZ01 29429	BJ01 28920	BJ02 29430	BJ03 29291	BJ04 24774			
17564	T	T	T	T	T	T	T	T	<b>G</b>	<b>G</b>	<b>G</b>	<b>G</b>	<b>G</b>	<b>G</b>	6	nsp10	D-->E
27827	T	T	T	T	T	T	T	T	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	6	non-coding	
9404	T	T	T	T	T	T	T	T	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	-	5	nsp1	V-->A
22222	T	T	T	T	T	T	T	T	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	<b>C</b>	N	5	spike	I-->T
19084	<b>T</b>	<b>T</b>	<b>T</b>	<b>T</b>	C	C	C	C	C	C	C	C	C	C	4	nsp11	I-->T
19834	A	A	A	A	A	A	A	A	A	A	<b>G</b>	<b>G</b>	<b>G</b>	<b>G</b>	4	nsp12	silent
9854	C	C	C	C	C	C	C	C	C	C	<b>T</b>	<b>T</b>	<b>T</b>	-	3	nsp1	A-->V
27243	C	C	C	C	C	C	C	C	C	C	<b>T</b>	<b>T</b>	N	<b>T</b>	3	putative protein	P-->L
2601	T	T	T	T	T	<b>C</b>	T	<b>C</b>	T	T	T	T	T	-	2	MHV p65	silent
7919	C	C	C	C	C	C	<b>T</b>	C	C	C	C	<b>T</b>	C	C	2	nsp1	A-->V
8559	T	T	T	T	T	T	T	T	T	<b>C</b>	T	T	T	<b>A</b>	2	nsp1	Y-->*
8572	G	G	G	G	G	G	G	G	G	<b>T</b>	G	<b>T</b>	G	G	2	nsp1	V-->L
9479	T	T	T	T	T	T	T	T	<b>C</b>	<b>C</b>	T	T	T	-	2	nsp1	V-->A
19064	A	A	A	A	A	A	<b>G</b>	A	<b>G</b>	A	A	A	A	A	2	nsp11	silent
21721	G	G	G	G	G	G	G	G	<b>A</b>	-	-	<b>A</b>	-	-	2	spike	G-->D
29279	A	A	A	A	A	A	A	A	<b>C</b>	A	<b>C</b>	A	A	A	2	non-coding	
508	G	G	G	G	G	G	G	G	G	<b>T</b>	G	G	G	G	1	leader	G-->C
1206	T	T	T	T	T	T	T	T	T	T	T	T	T	-	1	MHV p65	silent
1476	A	A	A	<b>G</b>	A	A	A	A	A	A	A	A	A	A	1	MHV p65	silent
3626	T	T	T	T	T	T	T	T	T	<b>C</b>	T	T	T	T	1	nsp1	I-->T
4220	A	A	A	A	A	A	A	A	A	<b>G</b>	A	A	A	A	1	nsp1	K-->R
4952	T	T	T	T	T	T	T	T	T	T	<b>A</b>	T	-	-	1	nsp1	M-->K
5251	C	C	C	C	C	C	C	C	C	<b>A</b>	C	C	C	-	1	nsp1	L-->I
5773	A	A	A	A	A	A	A	A	A	N	A	<b>C</b>	A	-	1	nsp1	K-->Q
6612	G	G	G	G	G	G	G	G	G	<b>T</b>	G	-	G	N	1	nsp1	L-->F
6929	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	1	nsp1	C-->Y
7746	G	G	G	G	G	G	G	G	<b>T</b>	G	G	G	G	G	1	nsp1	silent
7930	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	G	G	1	nsp1	D-->N
8124	T	T	T	T	T	T	T	T	T	T	T	<b>A</b>	T	T	1	nsp1	D-->E
8387	G	G	G	G	G	G	G	<b>C</b>	G	G	G	G	G	G	1	nsp1	S-->T
8417	G	G	G	G	G	G	G	<b>C</b>	G	G	G	G	G	G	1	nsp1	R-->T
8502	T	T	T	T	T	T	T	T	T	<b>G</b>	T	T	T	T	1	nsp1	C-->W
8580	A	A	A	A	A	A	A	A	A	<b>T</b>	A	A	A	A	1	nsp1	silent
8946	T	T	T	T	T	T	T	T	T	<b>A</b>	T	T	T	N	1	nsp1	silent
9095	C	C	C	C	C	C	C	C	C	<b>T</b>	C	C	C	C	1	nsp1	T-->I
9176	T	T	T	T	T	T	T	T	T	<b>C</b>	T	T	T	T	1	nsp1	V-->A
10029	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	G	-	1	nsp2	silent
10550	A	A	A	A	A	A	A	A	A	A	<b>C</b>	A	-	-	1	nsp2	Q-->P
10921	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	N	-	1	nsp3	V-->K
10922	T	T	T	T	T	T	T	T	T	<b>A</b>	T	T	N	-	1	nsp3	V-->K
10923	T	T	T	T	T	T	T	T	T	<b>G</b>	T	T	N	-	1	nsp3	V-->K
10926	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	N	-	1	nsp3	G-->I
10927	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	N	-	1	nsp3	G-->I
10928	G	G	G	G	G	G	G	G	G	<b>T</b>	G	G	N	-	1	nsp3	G-->I
10929	C	C	C	C	C	C	C	C	C	<b>T</b>	C	C	C	-	1	nsp3	silent
10930	A	A	A	A	A	A	A	A	A	<b>G</b>	A	A	A	-	1	nsp3	T-->A
11664	G	G	G	G	G	G	G	G	G	N	G	<b>A</b>	N	-	1	nsp3	M-->I
11811	G	G	G	G	G	G	G	G	G	G	-	G	<b>A</b>	-	1	nsp4	silent
11815	T	T	T	T	T	T	T	T	T	T	-	T	<b>G</b>	-	1	nsp4	S-->A
11818	G	G	G	G	G	G	G	G	G	G	-	G	<b>A</b>	-	1	nsp4	V-->I
11971	G	G	G	G	G	G	G	G	G	G	N	<b>A</b>	G	G	1	nsp4	D-->N
11974	A	A	A	A	A	A	A	A	A	A	N	<b>T</b>	A	A	1	nsp4	I-->F
13494	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	G	G	1	nsp9 RdRp	V-->S
13495	T	T	T	T	T	T	T	<b>G</b>	T	T	T	T	T	T	1	nsp9 RdRp	V-->S
15807	T	T	T	T	T	T	T	T	T	T	T	<b>G</b>	-	-	1	nsp9 RdRp	C-->G
16521	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	1	nsp10	D-->N
16622	C	C	C	C	C	C	<b>T</b>	C	C	C	C	C	C	C	1	nsp10	silent
17131	T	T	T	T	T	T	T	T	T	<b>C</b>	T	T	T	T	1	nsp10	L-->S
17846	C	C	C	C	C	C	C	C	<b>T</b>	C	C	C	C	-	1	nsp10	silent
18065	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	G	-	1	nsp11	silent
18176	C	C	C	C	C	C	C	C	C	<b>T</b>	C	C	C	C	1	nsp11	silent
18282	C	C	C	C	<b>A</b>	C	C	C	C	C	C	C	C	C	1	nsp11	L-->I
18965	T	T	<b>A</b>	T	T	T	T	T	T	T	T	T	T	T	1	nsp11	silent
19183	T	T	T	T	T	T	<b>C</b>	T	T	T	T	T	T	T	1	nsp11	V-->A
20363	G	G	G	G	G	G	G	G	G	G	G	G	<b>T</b>	G	1	nsp12	M-->I
20596	A	A	A	A	A	<b>G</b>	A	A	A	A	A	A	A	N	1	nsp13	Q-->R
20699	A	A	A	A	A	A	A	A	A	A	N	<b>C</b>	A	-	1	nsp13	silent
20704	G	<b>N</b>	G	G	G	G	G	G	G	G	N	G	G	-	1	nsp13	G-->E
20910	G	G	G	G	G	<b>T</b>	G	G	G	G	G	G	G	-	1	nsp13	D-->Y
20992	G	G	G	G	G	G	G	G	G	<b>A</b>	G	G	G	G	1	nsp13	R-->K
21403	A	A	A	A	A	A	A	A	A	N	N	A	N	<b>T</b>	1	nsp13	silent
21404	T	T	T	T	T	T	T	T	T	N	N	T	N	<b>C</b>	1	nsp13	silent

Supplementary data 2. continue

Genome position	Singapore cases					Oversea cases										variation frequency	ORF / protein	AA change
	Index	Primary	Primary	Primary	Secondary	Canada	Hanoi	HK	HK	S. China	N. China	N. China	N. China	N. China	N. China			
	SIN2500 29711	SIN2748 29706	SIN2774 29711	SIN2677 29705	SIN2679 29711	TOR2 29712	URBANI 29727	HKU3984 29727	CUHKW1 29712	GZ01 29429	BJ01 28920	BJ02 29430	BJ03 29291	BJ04 24774				
21405	T	T	T	T	T	T	T	T	T	N	N	T	N	A	1	nsp13	S->K	
21406	C	C	C	C	C	C	C	C	C	N	N	C	N	A	1	nsp13	S->K	
21407	T	T	T	T	T	T	T	T	T	N	N	T	N	A	1	nsp13	S->K	
21408	C	C	C	C	C	C	C	C	C	N	N	C	N	T	1	nsp13	L->C	
21409	T	T	T	T	T	T	T	T	T	N	N	T	N	G	1	nsp13	L->C	
21411	C	C	C	C	C	C	C	C	C	N	N	C	N	T	1	nsp13	L->C	
21412	T	T	T	T	T	T	T	T	T	N	N	T	N	G	1	nsp13	L->C	
21413	G	G	G	G	G	G	G	G	G	N	N	G	N	T	1	nsp13	L->C	
21414	G	G	G	G	G	G	G	G	G	N	N	G	N	C	1	nsp13	E->P	
21415	A	A	A	A	A	A	A	A	A	N	N	A	N	C	1	nsp13	E->P	
21416	A	A	A	A	A	A	A	A	A	N	N	A	N	G	1	nsp13	E->P	
21417	A	A	A	A	A	A	A	A	A	N	N	A	N	T	1	nsp13	silent	
21418	A	A	A	A	A	A	A	A	A	N	N	A	N	G	1	nsp13	silent	
22145	T	T	T	T	T	T	T	T	T	C	T	T	T	N	1	spike	silent	
22207	C	C	C	C	C	C	C	C	C	T	C	C	C	N	1	spike	S->L	
22422	G	G	G	G	G	G	G	G	G	A	G	G	G	G	1	spike	G->R	
22466	T	T	T	T	T	T	T	T	T	T	N	G	T	T	1	spike	F->L	
22479	A	A	A	A	A	A	A	A	A	A	N	A	T	A	1	spike	N->Y	
22517	A	A	A	A	A	A	A	A	A	G	N	A	A	A	1	spike	silent	
22522	A	A	A	A	A	A	A	A	A	G	N	A	A	A	1	spike	K->R	
22634	T	T	T	T	T	T	T	T	T	T	T	T	A	T	1	spike	N->K	
23174	C	C	C	C	T	C	C	C	C	C	C	C	C	C	1	spike	silent	
23220	T	T	T	T	T	G	T	T	T	T	T	T	T	T	1	spike	S->A	
23792	C	C	T	C	C	C	C	C	C	C	C	C	C	N	1	spike	silent	
23823	T	T	T	T	T	T	T	T	T	G	T	T	T	N	1	spike	Y->D	
24566	T	T	T	T	T	T	T	T	T	C	T	T	T	T	1	spike	silent	
24872	T	T	T	T	T	T	C	T	T	T	T	T	T	T	1	spike	silent	
24978	A	A	A	A	A	A	A	A	A	G	A	A	A	A	1	spike	K->E	
25299	G	G	G	G	G	G	G	G	G	G	A	G	G	G	1	putative protein	G->E	
25569	T	T	T	T	T	T	T	A	T	T	T	-	T	T	1	putative protein	M->K	
25779	A	A	A	A	A	A	A	A	A	C	A	A	A	A	1	putative protein	E->A	
25844	A	A	A	A	A	A	A	A	A	T	A	A	A	A	1	putative protein	R->W	
25984	C	C	C	C	C	C	C	C	C	C	C	T	C	C	1	putative protein	silent	
26186	G	G	G	G	G	G	G	G	G	A	G	G	G	G	1	protein E	V->M	
26428	A	G	G	G	G	G	G	G	G	G	G	G	G	G	1	protein M	K->E	
26586	T	T	T	T	T	T	T	T	T	C	T	T	T	T	1	protein M	silent	
26600	C	C	C	C	C	C	C	T	C	C	C	C	C	C	1	protein M	silent	
26857	T	T	T	T	T	T	C	T	T	T	T	T	T	T	1	protein M	S->P	
27012	A	A	A	A	A	A	A	A	A	N	A	A	A	G	1	protein M	silent	
27013	A	A	A	A	A	A	A	A	A	N	A	A	A	T	1	protein M	N->Y	
27016	A	A	A	A	A	A	A	A	A	N	A	A	A	G	1	protein M	T->G	
27017	C	C	C	C	C	C	C	C	C	N	C	C	C	G	1	protein M	T->G	
27019	G	G	G	G	G	G	G	G	G	N	G	G	G	A	1	protein M	D->N	
27022	C	C	C	C	C	C	C	C	C	N	C	C	C	T	1	protein M	H->Y	
27024	C	C	C	C	C	C	C	C	C	N	C	C	C	T	1	protein M	H->Y	
27025	G	G	G	G	G	G	G	G	G	N	G	G	G	A	1	protein M	A->K	
27026	C	C	C	C	C	C	C	C	C	N	C	C	C	A	1	protein M	A->K	
27027	C	C	C	C	C	C	C	C	C	N	C	C	C	A	1	protein M	A->K	
27028	G	G	G	G	G	G	G	G	G	N	G	G	G	T	1	protein M	G->L	
27029	G	G	G	G	G	G	G	G	G	N	G	G	G	T	1	protein M	G->L	
27030	T	T	T	T	T	T	T	T	T	N	T	T	T	A	1	protein M	G->L	
27032	G	G	G	G	G	G	G	G	G	N	G	G	G	A	1	protein M	S->N	
27033	C	C	C	C	C	C	C	C	C	N	C	C	C	T	1	protein M	S->N	
27111	A	A	A	G	A	A	A	A	A	A	A	A	A	A	1	putative protein	E->G	
28089	C	C	C	C	C	C	C	C	C	T	C	C	C	N	1	non-coding		
variations	2	2	3	3	2	4	6	9	9	46	7	19	16	35	163			
		deletion		deletion														
		27794-27798		27760-27765														

Note: The first 16 are recurrent variations. The rest occur only in single isolates