Table 2. List of all single-nucleotide variations (SNVs) with multiple occurrences

Sequence alignments were generated by using CLUSTALW Ver. 1.83 with the default DNA weight matrix for the 96 severe acute respiratory syndrome-coronavirus (SARS-CoV) genomic sequences analyzed in this study (91 human SARS-CoV and 5 palm civet SARS-like-CoV sequences). The names of the genomic sequences (as from INSD/GenBank) are listed on the first column based on clusters determined by our scoring algorithm (1). All of these sequences are further divided by colored lines into subgroups (defined in the text and Fig. 1) based on their host species (human vs. palm civet) and epidemiological phases (year and early, middle, and late phases of the 2002/2003 epidemic).

Characteristics of the SNVs observed are listed in the top rows. From the top, they include the relevant coding DNA sequences (CDSs) and/or predicted ORFs, the variant nucleotides observed at the loci, the affected codon, the resultant amino acid switches, the amino acid coordinate of the CDSs/ORFs, and the nucleotide coordinate of the genome [based on GZ02 (1)], respectively.

All of the 202 SNVs that are observed in more than one of the 99 genomic sequences are listed. Except for the two variations located outside of the coding sequences, 128 out the 200 SNVs within the CDSs were predicted to cause amino acid changes (nonsynonymous variations). Different characters of the amino acid switches were labeled with different-color shadings in the corresponding row: light pink for synonymous variations, yellow for nonsynonymous variations causing amino acid switches in the same physical-chemical group, and greenish yellow for nonsynonymous variations causing drastic amino acid switches. In the rows for individual sequences, the minor forms of the SNVs were shaded with pink, the deletions were shaded with blue, and the undetermined nucleotides (N) were

shaded with yellowish pink.

SNVs that contribute to the grouping of genotypes based on the predominant clustering criteria (1) were further highlighted in the top characteristic rows with different-color shading and bolding of the letters:

1. The positions of the 5-nt motif used to classify the major genotypes of the 2002-2003 epidemic human SARS-CoV (HP03) are shaded as reported (1), including the two loci external to the *S* gene (17564 and 27827, shaded in grey) and the three loci in the *S* gene, namely positions 21721 (yellow), 22222 (blue), and 23823 (green). These variations are all emphasized with bold face.

2. The SNVs distinguishing the SARS-CoVs of the 2003-2004 epidemic (PC04 and HP04) from that of the 2002-2003 epidemic (PC03 and HP03) are shaded in light pink, of which those causing nonsynonymous variations are emphasized with bold face.

3. The SNVs distinguishing the SARS-CoV of the palm civet (PC03 and PC04) and human patient of the 2003-2004 epidemic (HP04) from human patients of the 2002-2003 epidemic (HP03) are shaded in light blue. Because all of them cause nonsynonymous variations, they are all emphasized with bold face.

4. A few special SNVs need illustration:

(*i*) SNVs in nucleotides 2759 and 2760 cause amino acid switches in the same residue, 832 of Orf1ab. Although they both cause nonsynonymous variations, one change is within the same physical-chemical group (W-F). This group of variation is shaded with dark greenish yellow.

(*ii*) The SNV in nucleotide 6295 causes residue 2011C of Orf1ab (nsp3) switching to a stop codon. This amino acid switching was presented in red and shaded with dark greenish

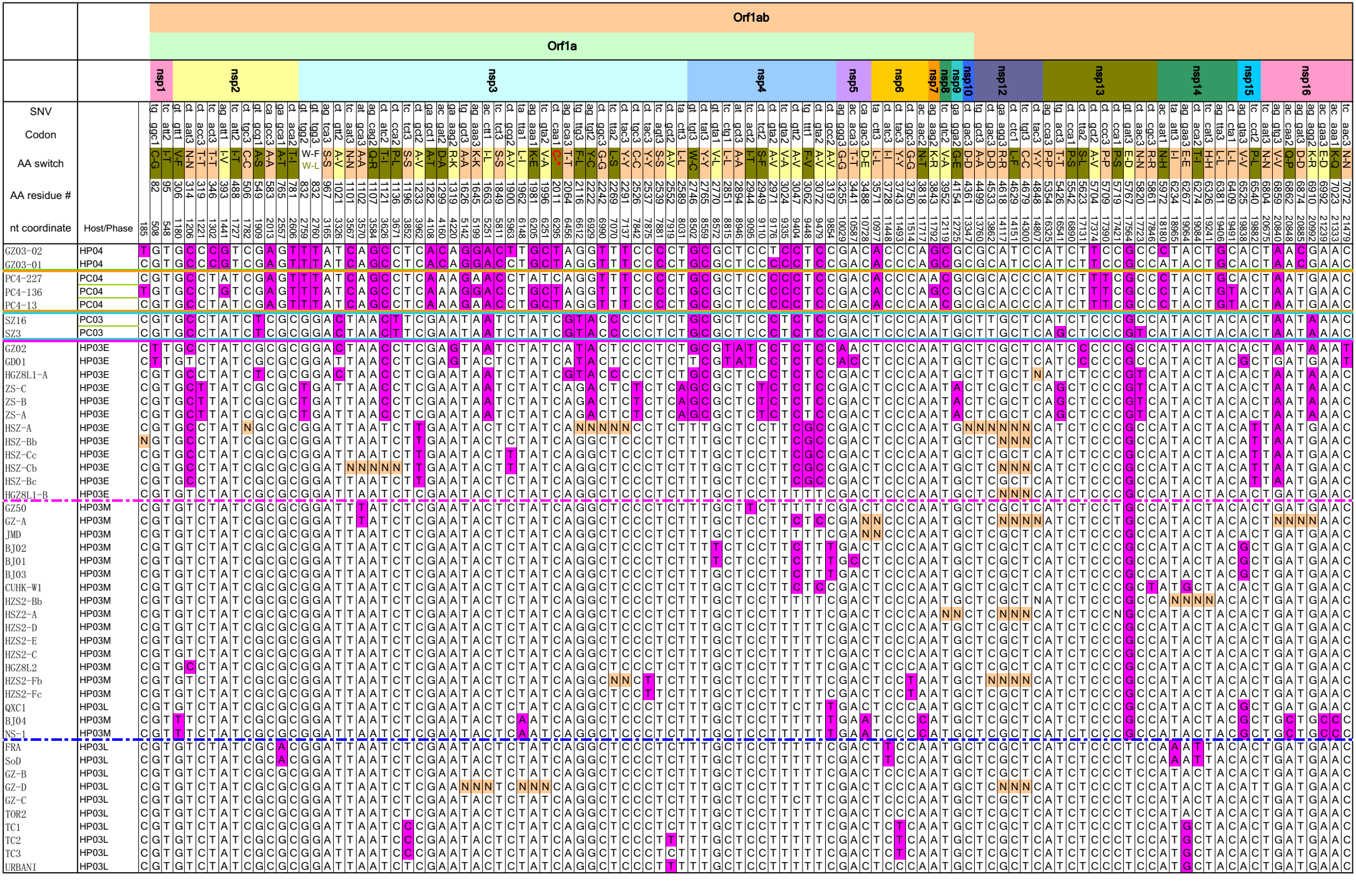
yellow.

(*iii*) SNVs in nucleotides 22927 and 22928 cause nonsynonymous amino acid switches in the same residue, 479 of S. This group of variations is emphasized with bold face and shaded with dark greenish yellow.

(*iv*) SNVs in nucleotides 23316 and 23317 cause the same nonsynonymous amino acid switches in the same residue, 609 of S. This group of variations is emphasized with bold face and shaded with dark greenish yellow.

(*v*) SNVs in nucleotides 23718 and 23719 cause nonsynonymous amino acid switches in the same residue, 743 of S. This group of variation is emphasized with bold face and shaded with dark greenish yellow.

1. The Chinese SARS molecular epidemiology consortium (2004) *Science* **303**, 1666-1669.


Orf1ab
Orf1a
nsp1
nsp2
nsp3
nsp4
nsp5
nsp6
nsp7
nsp8
nsp9
nsp10
nsp12
nsp13
nsp14
nsp15
nsp16
SNV
Codon
AA switch
AA residue #
nt coordinate
Host/Phase
W-F
W-L
GZ03-02 HP04
GZ03-01 HP04
PC4-227 PC04
PC4-136 PC04
PC4-13 PC04
SZ16 PC03
SZ3 PC03
GZ02 HP03E
GD01 HP03E
HGZ8L1-A HP03E
ZS-C HP03E
ZS-B HP03E
ZS-A HP03E
HSZ-A HP03E
HSZ-Bb HP03E
HSZ-Cc HP03E
HSZ-Cb HP03E
HSZ-Bc HP03E
HGZ8L1-B HP03E
GZ50 HP03M
GZ-A HP03M
JMD HP03M
BJ02 HP03M
BJ01 HP03M
BJ03 HP03M
CUHK-W1 HP03M
HZS2-Bb HP03M
HSZ2-A HP03M
HZS2-D HP03M
HZS2-E HP03M
HZS2-C HP03M
HGZ8L2 HP03M
HZS2-Fb HP03M
HZS2-Fc HP03M
QXC1 HP03L
BJ04 HP03M
NS-1 HP03M
FRA HP03L
SoD HP03L
GZ-B HP03L
GZ-D HP03L
GZ-C HP03L
TOR2 HP03L
TC1 HP03L
TC2 HP03L
TC3 HP03L
URBANI HP03L

			Orf1ab																																																																																																	
			Orf1a																																																																																																	
			nsp1		nsp2											nsp3																																		nsp4													nsp5			nsp6					nsp7	nsp8	nsp9	nsp10	nsp12						nsp13										nsp14							nsp15		nsp16							
SNV			tg	tc	gt	ct	ct	tc	ag	tc	ct	gt	ca	ga	ct	gt	gt	ag	ct	tc	at	ag	ct	ct	tc	ct	ga	ac	ga	tg	ag	ac	tc	ct	ta	ag	tc	ct	ag	tg	ag	ct	tc	ct	ct	ct	tc	ct	ta	gt	ct	gt	tc	at	tc	ct	ct	tc	ct	tg	ct	ct	ag	ac	ca	ta	ct	ct	ct	ac	ag	tc	ga	ct	tg	ct	ga	ct	tc	ct	ag	tg	ct	ct	ct	ct	ct	gt	ct	ct	ac	ta	ag	ct	tc	ag	ct	ag	tc	tc	ag	ac	ag	ag	ac	ac	tc
Codon			ggc1	att2	gtt1	aat3	acc3	act3	att1	att2	tgc3	gcg1	gcc3	gca1	aca2	tgg2	tgg3	tca3	gtt2	aat3	gca3	cag2	atc2	cca2	tct3	gct2	gct1	gat2	aag2	gct3	aaa3	ctt1	tct3	gcg2	tta1	aaa1	gta2	caa1	aca3	ttg3	tgt2	ggc3	tta2	tac3	tgc3	tac3	agt3	gct2	ctt3	tgt3	tat3	gta1	ctg1	gct3	act2	tct2	gta2	gta2	gtt2	ttt1	gta2	gcc2	ggg3	aca3	gac3	ctt3	atc3	tac3	ggc3	aac2	aag2	gtc2	gga2	gac3	gct3	gac3	agg3	ctc1	tgt3	tac3	cca3	act3	cca1	tta2	gct2	ccc3	cca1	gat3	aac3	cgc3	aat1	att3	gaa3	aca2	cat3	tta3	cta1	gta3	cct2	aat3	gtg3	caa2	gat3	agg2	gaa3	aaa1	aac3
AA switch			C-G	I-T	V-F	N-N	T-T	T-T	I-V	I-T	C-C	A-S	A-A	A-T	T-I	W-F	W-L	S-S	A-V	N-N	A-A	Q-R	T-I	P-L	S-S	A-V	A-T	D-A	R-K	A-A	K-K	I-L	S-S	A-V	L-I	K-E	V-A	C-*	T-T	F-L	Y-C	G-G	L-S	Y-Y	C-C	Y-Y	S-S	A-V	L-L	W-C	Y-Y	V-L	L-L	A-A	I-T	S-F	A-V	V-A	A-V	F-V	A-V	A-V	G-G	T-T	D-E	L-L	I-I	Y-Y	G-G	N-T	K-R	V-A	G-E	D-D	A-A	D-D	R-R	L-F	C-C	Y-Y	P-P	T-T	P-S	S-L	A-V	P-P	P-S	E-D	N-N	R-R	N-H	I-I	E-E	T-I	H-H	L-L	L-L	V-V	P-L	N-N	V-V	Q-P	D-D	K-R	E-D	K-Q	N-N
AA residue #			82	95	306	314	319	346	393	488	506	549	583	765	781	832	832	967	1021	1101	1102	1107	1121	1136	1196	1233	1282	1299	1319	1626	1645	1663	1849	1900	1962	1981	1996	2011	2064	2116	2222	2242	2269	2291	2526	2537	2539	2552	2589	2746	2765	2770	2851	2894	2944	2949	2971	3024	3047	3062	3072	3197	3255	3441	3488	3571	3728	3743	3750	3818	3843	3952	4154	4361	4499	4533	4618	4629	4679	4848	5354	5426	5542	5623	5704	5709	5719	5767	5820	5861	5972	6234	6267	6274	6326	6381	6409	6525	6540	6804	6859	6862	6874	6910	6992	7023	7072
nt coordinate		185	508	548	1180	1206	1221	1302	1441	1727	1782	1909	2013	2557	2606	2759	2760	3165	3326	3567	3570	3584	3626	3671	3852	3962	4108	4160	4220	5142	5199	5251	5811	5963	6148	6205	6251	6295	6456	6612	6929	6990	7070	7137	7842	7875	7881	7919	8031	8502	8559	8572	8815	8946	9095	9110	9176	9335	9404	9448	9479	9854	10029	10587	10728	10977	11448	11493	11514	11717	11792	12119	12725	13347	13760	13862	14117	14151	14300	14807	16325	16541	16890	17131	17374	17390	17421	17564	17723	17846	18180	18965	19064	19084	19241	19406	19491	19838	19882	20675	20840	20848	20885	20992	21239	21333	21479
AS	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
WHU	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	G	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
CUHK-SU10	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	T	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
FRANKFURT	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	A	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	T	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	A	A	T	T	A	C	A	C	T	G	A	T	G	A	A	C
HKU-39849	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
CUHK-AG01	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
CUHK-AG02	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
CUHK-AG03	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW1	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	G	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW2	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	G	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW3	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	G	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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TW5	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW6	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW7	HP03L	C	G	T	G	T	C	T	A	T	T	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TW8	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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TW10	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	T	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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TWC	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	G	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TWH	HP03L	C	G	T	G	T	C	T	A	T	T	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TWJ	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TWK	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TWS	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
TWY	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	T	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
GD69	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	C	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	T	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
HSR	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sino1-11	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	T	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sino3-11	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sin850	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sin849	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sin847	HP03L	C	G	C	G	T	C	T	A	C	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	T	T	C	G	C	T	T	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
Sin848	HP03L	C	G	C	G	T	C	T	A	C	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	T	T	C	G	C	T	T	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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Sin3765V	HP03L	C	G	C	G	T	C	T	A	C	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	T	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	C	A	C	A	C	T	G	A	T	G	A	A	C
SIN2774	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	A	A	T	T	A	C	A	C	T	G	A	T	G	A	A	C
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PUMC01	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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CUHK-LC1	HP03L	C	G	T	G	T	C	T	A	T	C	G	C	G	C	G	G	A	T	T	A	A	T	C	T	C	G	A	A	T	A	C	T	C	T	A	T	C	A	G	G	C	T	C	C	C	T	C	T	T	T	G	C	T	C	C	T	T	T	T	T	C	G	A	C	T	C	C	C	A	A	T	G	C	T	C	G	C	T	C	A	T	C	T	C	C	C	T	C	C	A	T	A	C	T	A	C	A	C	T	G	A	T	G	A	A	C
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S
Sars3a
Sars3b
E
M
Sars6
Sars7a
Sars8a
Sars8b
N
sars9b
SNV
Codon
AA switch
AA residue #
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PC4-13
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SZ3
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HSZ-Cc
HSZ-Cb
HSZ-Bc
HGZ8L1-B
GZ50
GZ-A
JMD
BJ02
BJ01
BJ03
CUHK-W1
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HSZ2-A
HZS2-D
HZS2-E
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HZS2-Fc
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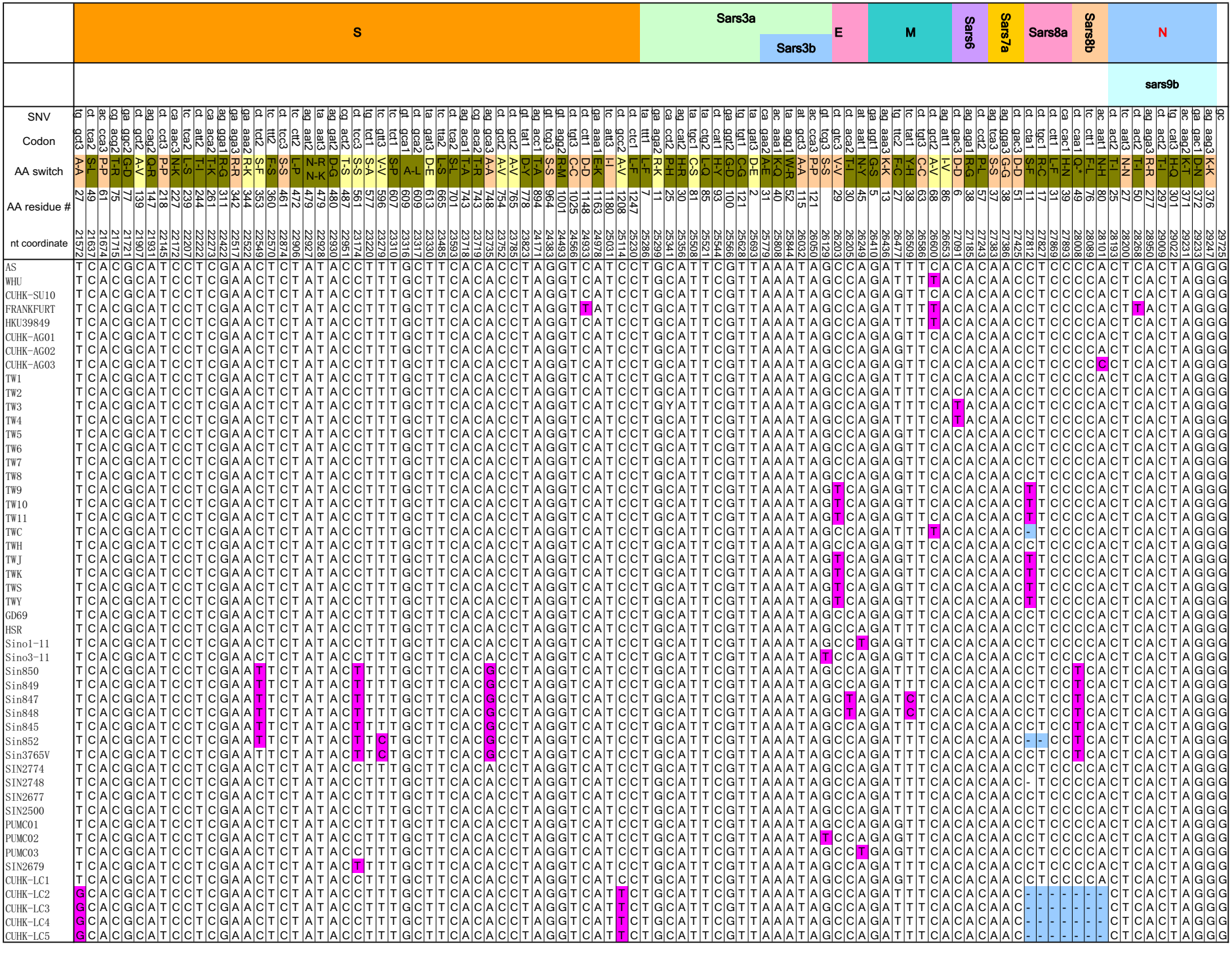
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N
sars9b
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AA switch
AA residue #
nt coordinate
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