Table 4. List of all SNVs in *S* genes with multiple occurrences

Sequence alignments were generated by the method described in *Materials and Methods* as well as in the Table 2 legend. The names of the genomic sequences (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). All of the palm civet sequences were shaded with light green.

Characteristics of the SNVs observed are listed in the top rows. From the top of the rows, they include the predicted tertiary location of the corresponding amino acid residues with respect to the computer-simulated 3D structure of the Spike (S) protein, the variant nucleotides observed at the loci, the affected codon, the resulting amino acid switches, the amino acid coordinate of the S protein, and the nucleotide coordinate of the *S* gene and of the genome [based on GZ02 (1)], respectively.

All 49 SNVs that are observed in more than one of the 103 S CDS sequences, i.e., two more SNVs observed than that using whole genome sequences (Table 2) are listed because more sequences were added for the analysis. One of them (nucleotide 22220) causes synonymous variation in the amino acid residue 243D, which is predicted to be partially exposed at the top of the S1 domain, whereas the other (nucleotide 23163) causes a nonsynonymous variation of amino acid residue 558F/I, which is predicted to be exposed at the side of S1 domain but not involved in receptor binding.

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 printed with pink, and the undetermined nucleotides (N) were shaded with orange.

SNVs that contribute to the grouping of genotypes based on the predominant clustering criteria previously described (1) were further highlighted in the rows with different color shading and bolding of the letters as described for Table 2, except:

1. The 3-nt loci in the *S* gene 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), 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 those 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. Compared with Table 2, nucleotides 23719 and 23785 were excluded, because the addition of more PC04 samples showed the variations within the category.

4. The SNVs distinguishing the SARS-CoV of the palm civet (PC03 and PC04) and the 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.

5. Compared with Table 2, nucleotide 23485 was excluded, because the addition of the GZ03-03 sample of the HP04 group showed the variation within the category.

6. Some special SNVs are illustrated:

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

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

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

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

Predicted tertiary location of AA with respect to computer simulated 3D structure		Partially exposed side	Exposed top	Exposed top	Exposed top	Exposed top	Exposed top	Exposed top	Exposed top	Exposed side	Partially exposed side	Partially exposed side	Buried	Buried	Exposed side	Exposed top	Partially exposed side	Partially exposed side	Exposed top	Exposed side	Exposed side	Exposed side		480 Exposed side	487 Exposed side	558 Exposed side	561 Partially exposed side	577 Buried, interface S1-S1	596 Buried	607 Exposed side down	609 Buried, interface S1-S2		613 Exposed side down	665 Buried, interface S1-S2	end of S1 domain	701 Not modelled	743 Partially exposed side		748 Partially exposed side	754 Partially exposed	765 Partially exposed	778 Buried	894 Exposed side	964 Exposed side	1001 Exposed side	1025 Exposed side	1148 Exposed down	1163 Buried	1180 Not modelled	1208 Not modelled	1247 Not modelled
SNV		tg	ct	ac	cg	ag	ct	ag	ct	ca	tc	ct	ct	ca	ga	ga	ga	ct	tc	ct	tc	ag	ta	ag	cg	ta	ct	tg	tc	tc	gt	ct	ta	tc		ct	ag	cg	ag	ct	ct	gt	ag	gt	gt	ct	ct	ga	tc	ct	ct
Codon		gct3	tca2	cca3	acg2	gac2	gct2	cag2	ccc3	aac3	tta2	gac3	act2	aca2	gga1	agg3	aga2	tct2	ttt2	tcc3	ctt2	aat aga aaa		gat2	act2	ttc1	tcc3	tct1	gtt3	tct1	gca tta		gat3	tta2	gtg	tca2	aca1	aca2	gca3	gct2	gct2	gat1	acc1	tcg3	agg2	tgt3	ctt1	gaa1	att3	gcc2	ctc1
AA switch		A-A	S-L	P-P	T-R	D-G	A-V	Q-R	P-P	N-K	L-S	D-D	T-I	T-K	G-R	R-R	R-K	S-F	F-S	S-S	L-P	N,R,K		D-G	T-S	F-I	S-S	S-A	V-V	S-P	A-L		D-E	L-S	V	S-L	T-A	T-R	A-A	A-V	A-V	D-Y	T-A	S-S	R-M	C-C	L-F	E-K	I-I	A-V	L-F
AA residue #		27	49	61	75	77	139	147	218	227	239	243	244	261	311	342	344	353	360	461	472	479		480	487	558	561	577	596	607	609		613	665	675	701	743		748	754	765	778	894	964	1001	1025	1148	1163	1180	1208	1247
nt coordinate for S		81	146	183	224	230	416	440	654	681	716	729	731	782	931	1026	1031	1058	1079	1383	1415	1436	1437	1439	1460	1672	1683	1729	1788	1819	1825	1826	1839	1994		2102	2227	2228	2244	2261	2294	2332	2680	2892	3002	3075	3442	3487	3540	3623	3739
nt coordinate for genome	Host/Phase	21572	21637	21674	21715	**21721**	**21907**	**21931**	22145	22172	22207	**22220**	**22222**	22273	22422	22517	22522	22549	**22570**	22874	**22906**	**22927**	**22928**	**22930**	**22951**	**23163**	23174	23220	23279	23310	**23316**	**23317**	23330	**23485**		23593	23718	**23719**	23735	23752	**23785**	**23823**	24171	24383	24493	24566	24933	24978	25031	25114	25230
GZ03-01	HP04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
GD03T13	HP04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
GZ03-02	HP04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	G	C	T	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
GZ03-03	HP04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	N	N	N	N	N	N	T	C	T	T	T	T	T	A	T		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
PC4-227	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	T	G	C	C	G	C	C	C
PC4-115	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
PC4-13	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	G	A	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
PC4-136	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	G	A	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
PC4-127	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	G	A	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	T	G	C	C	G	C	C	C
PC4-205	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	G	A	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	G	G	C	C	G	C	C	C
PC4-199	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	G	A	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	C	G	A	G	G	C	C	G	C	C	C
PC4-137	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	A	G	G	T	C	T	T	T	T	T	T	C		C	A	G	A	C	C	G	A	T	G	C	C	G	C	C	C
PC4-145	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	G	A	C	T	G	A	T	G	C	C	G	C	C	C
PC4-241	PC04	T	C	A	C	A	T	G	T	C	C	C	C	C	G	G	G	C	C	T	C	A	T	G	G	T	C	T	T	T	T	T	A	C		C	A	C	A	C	T	G	A	T	G	C	C	G	C	C	C
SZ16	PC03	T	C	A	C	A	C	A	T	A	T	T	C	A	G	G	G	C	C	C	T	A	A	A	G	T	C	T	T	C	G	C	T	C		T	G	C	A	T	C	G	G	T	G	C	C	G	T	C	C
SZ3	PC03	T	C	A	C	A	C	A	T	A	T	C	C	A	G	G	G	C	C	C	T	A	A	A	G	T	C	T	T	C	G	C	T	C		T	G	C	A	T	C	G	G	G	G	C	C	G	T	C	C
SZ1	PC03	T	C	A	C	A	C	A	T	A	T	T	C	A	G	G	G	C	C	C	T	A	A	A	G	A	C	T	T	C	G	C	T	C		T	G	C	A	T	C	G	G	T	G	T	C	G	T	C	C
SZ13	PC03	T	C	A	C	A	C	A	T	A	T	T	C	A	G	G	G	C	C	C	T	A	A	A	G	A	C	T	T	C	G	C	T	C		T	G	C	A	T	C	G	G	T	G	C	C	G	T	C	C
GZ02	HP03E	T	C	A	C	A	C	A	C	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	G	T	C	C
GD01	HP03E	T	C	A	C	A	C	A	C	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	A	T	C	C
HGZ8L1-A	HP03E	T	C	A	G	A	C	A	T	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	A	T	C	C
ZS-C	HP03E	T	C	A	G	A	C	A	T	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	A	T	C	C
ZS-B	HP03E	T	C	A	G	A	C	A	T	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	A	T	C	C
ZS-A	HP03E	T	C	A	G	A	C	A	T	C	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	C	C	A	T	C	C
HSZ-A	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	G	T	C	C
HSZ-Bb	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	G	T	C	C
HSZ-BC	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	G	T	C	C
HSZ-CC	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	G	T	C	T
HSZ-Cb	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	G	T	C	T
HGZ8L1-B	HP03E	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
GZ50	HP03M	T	T	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	A	T	C	C
GZ-A	HP03M	T	T	A	C	A	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	A	T	C	C
JMD	HP03M	T	C	A	G	A	N	N	N	N	T	C	C	C	A	G	G	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	G	A	G	G	T	C	A	T	C	C
BJ03	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
BJ02	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	A	G	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
BJ01	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-W1	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-Bb	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HSZ2-A	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-D	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-E	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-C	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	T	A	T	C	C
HGZ8L2	HP03M	T	C	A	C	A	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-Fb	HP03M	T	C	A	C	G	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HZS2-FC	HP03M	T	C	A	C	G	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
BJ04	HP03M	T	C	C	C	G	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	T	T	C	A	T	C	C
NS-1	HP03M	T	C	C	C	G	C	A	T	C	C	C	C	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	T	T	C	A	T	C	C
FRA	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	T	A	T	C	C
SOD	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	T	A	T	C	C
ShanghaiQXC1	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	G	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
GZ-B	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
GZ-C	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TOR2	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	G	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TC1	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TC2	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TC3	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
URBANI	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
AS	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
WHU	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
HSR	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-SU10	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
FRANKFURT	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	T	A	T	C	C
HKU-39849	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-AG01	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-AG02	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-AG03	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW1	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW2	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW3	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW4	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW5	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW6	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW7	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW8	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW9	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW10	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TW11	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWC	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWH	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWJ	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWK	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWS	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
TWY	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
GD69	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SINO3-11	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SINO1-11	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN850	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN847	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN845	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN852	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	C	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN849	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN848	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
SIN2774	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN2748	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN2677	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN2500	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN3765V	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	T	T	C	T	A	T	A	C	T	T	T	C	T	G	C	T	T		C	A	C	G	C	C	T	A	G	G	T	C	A	T	C	C
PUMC01	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
PUMC02	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
PUMC03	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
SIN2679	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	T	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-LC1	HP03L	T	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	C	C
CUHK-LC2	HP03L	G	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	T	C
CUHK-LC3	HP03L	G	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	T	C
CUHK-LC4	HP03L	G	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	T	C
CUHK-LC5	HP03L	G	C	A	C	G	C	A	T	C	C	C	T	C	G	A	A	C	T	C	T	A	T	A	C	T	C	T	T	T	G	C	T	T		C	A	C	A	C	C	T	A	G	G	T	C	A	T	T	C