

## Erratum to: Bat origin of a new human coronavirus: there and back again

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We miscalculated identities of several genes, and the corrected [Table 1](#) should be as follows:

**Table 1** Sequence identities of 2019-nCoV compared with bat SARSr-CoV RaTG13 and SARS-CoV BJ01 (nt/aa%)<sup>a)</sup>

	BatCoV RaTG13	SARS-CoV BJ01
ORF1ab	96.5/98.6	81.4/86.1
S	92.9/97.4	74.6/76.1
NS3	96.3/97.8	75.5/72.4
E	99.6/100	93.5/94.7
M	95.5/99.6	85.5/90.5
NS6	98.4/100	76.2/ 67.2
NS7a	95.6 /97.5	82.1/85.2
N	96.9/99.0	88.2/90.5
Whole genome	96.1/-	80.2/-

a) This table demonstrates identities of 2019-nCoV WIV04 (GenBank Accession No. MN996528.1) compared with bat SARSr-CoV RaTG13 (GenBank Accession No. MN996532.1) and SARS-CoV BJ01 (GenBank Accession No. AY278488.2). Identities were calculated by using nucleotide sequences and amino acid sequences and expressed by ‘nucleotide sequence identity/amino acid sequence identity’. The nucleotide sequence identities were computed by online blastn and the amino acid identities were computed by online blastp. S, spike glycoprotein; E, envelope small membrane protein; M, membrane protein; N, nucleoprotein.

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