

How Genome Detective assigns SARS-CoV-2 (the virus that causes COVID-19 disease)

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**SEQUENCE ASSIGNMENT**

**Name**

hCoV-19TurkeyCTF\_00012021|EPI\_


**Length**

29879

**ASSIGNMENT**

**Type**

Severe acute respiratory syndrome-related coronavirus (Taxonomy ID: 694009 (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=694009>))

 Continue to the cov typing tool (</app/typingtool/cov/blast-job/panviral/1.132/fc0352c0-be18-4ec5-a78a-6bf94be7a098/sequence/0>) to get a more specific assignment.

**Reference Genome**

NC\_045512.2 ([https://www.ncbi.nlm.nih.gov/nuccore/NC\\_045512.2](https://www.ncbi.nlm.nih.gov/nuccore/NC_045512.2)) (Length: 29903bp)

**Host(s)**

Homo sapiens / Paguma larvata (host info (<http://www.genome.jp/virushostdb/694009>))

**NT Identity (%)**

99.8694

**AA Identity (%)**

99.8118

**Number of stop codons**

15

**Number of CDS**

15

**ALIGNMENT**

**Alignment score**

59512 (NT) + 118524 (AA) = 178036

**Concordance (%)**

99.7781

### Alignment method

Global, seeded, nucleotide + amino acids (AGA)

### NT Alignment

Download alignment (FASTA) (/app/typingtool/virus/nt-alignment.fasta;jsessionid=8DA826779EC8C7EBDC4889C19B93F0AB?wtd=8DA826779EC8C7EBDC4889C19B93F0AB&request=resource&resource=oc8e45fe5&rand=795710)

### CDS Alignments

Download CDS alignments (FASTA) (/app/typingtool/virus/cds-alignment.fasta;jsessionid=8DA826779EC8C7EBDC4889C19B93F0AB?wtd=8DA826779EC8C7EBDC4889C19B93F0AB&request=resource&resource=oc8e45fe8&rand=795712)

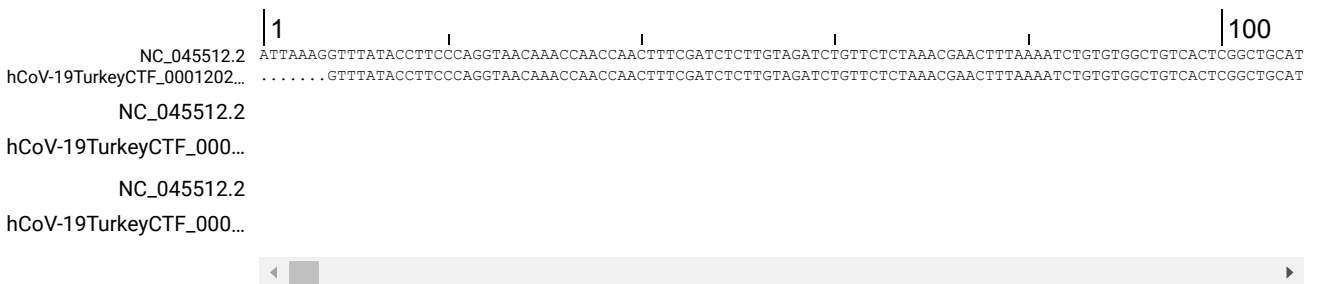
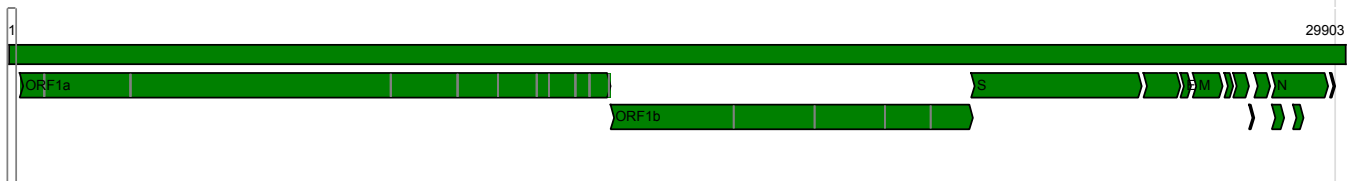
### PHYLOGENETIC ANALYSIS

Continue to the cov typing tool (/app/typingtool/cov/blast-job/panviral/1.132/fc0352c0-be18-4ec5-a78a-6bf94be7a098/sequence/0) to get a more specific assignment.

## ALIGNMENT DETAILS

### ALIGNMENT

Using **NC\_045512.2** (Severe acute respiratory syndrome coronavirus 2 (taxon:2697049)) as reference for alignment, numbering and genome annotations.



### GENETIC DIVERSITY ANALYSIS

HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
<b>NT</b>	8	29903	99.9%	59512	99.7%	29852 (99.9%)	29817 (99.8%)	4/21	

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
Mutations:	241C>T, 733T>C, 1278A>G, 2749C>T, 3037C>T, 3828C>T, 5147C>T, 6319A>G, 6613A>G, 11288_11296delTCTGGTTTT, 12778C>T, 13860C>T, 14408C>T, 14925C>T, 17259G>T, 18647C>A, 21614C>T, 21621C>A, 21638C>T, 21974G>T, 22132G>T, 22812A>C, 23012G>A, 23063A>T, 23403A>G, 23525C>T, 24642C>T, 25088G>T, 26149T>C, 28167G>A, 28269_28270insAAAC, 28512C>G, 28877A>T, 28878G>C, 28881G>A, 28882G>A, 28883G>C, 29859_29870delTAGGAGAATGAC								
<b>CDS</b>									
ORF1ab	1	7097	99.9%	49475	99.9%	7086 (99.9%)	7080 (99.9%)	0/3/0/0	1
Protein mutations:	K338R (1278A>G), S1188L (3828C>T), R1628C (5147C>T), S3675_F3677del (11288_11296delTCTGGTTTT), P4715L (14408C>T), E5665D (17259G>T), P6128H (18647C>A)								
Codon mutations:	GAT156GAC (733T>C), AAA338AGA (1278A>G), GAC828GAT (2749C>T), TTC924TTT (3037C>T), TCA1188TTA (3828C>T), CGT1628TGT (5147C>T), CCA2018CCG (6319A>G), GTA2116GTG (6613A>G), TCT3675_TTT3677del (11288_11296delTCTGGTTTT), TAC4171TAT (12778C>T), GAC4532GAT (13860C>T), CCT4715CTT (14408C>T), GTC4887GTT (14925C>T), GAG5665GAT (17259G>T), CCT6128CAT (18647C>A)								
ORF1a	1	4406	99.8%	30185	99.9%	4395 (99.9%)	4392 (99.9%)	0/3/0/0	1
Protein mutations:	K338R (1278A>G), S1188L (3828C>T), R1628C (5147C>T), S3675_F3677del (11288_11296delTCTGGTTTT)								
Codon mutations:	GAT156GAC (733T>C), AAA338AGA (1278A>G), GAC828GAT (2749C>T), TTC924TTT (3037C>T), TCA1188TTA (3828C>T), CGT1628TGT (5147C>T), CCA2018CCG (6319A>G), GTA2116GTG (6613A>G), TCT3675_TTT3677del (11288_11296delTCTGGTTTT), TAC4171TAT (12778C>T)								
ORF1b	1	2696	100%	19318	99.9%	2696 (100%)	2693 (99.9%)	0/0/0/0	1
Protein mutations:	P314L (14408C>T), E1264D (17259G>T), P1727H (18647C>A)								
Codon mutations:	GAC131GAT (13860C>T), CCT314CTT (14408C>T), GTC486GTT (14925C>T), GAG1264GAT (17259G>T), CCT1727CAT (18647C>A)								
S	1	1274	100%	8898	99.0%	1274 (100%)	1262 (99.1%)	0/0/0/0	1
Protein mutations:	L18F (21614C>T), T20N (21621C>A), P26S (21638C>T), D138Y (21974G>T), R190S (22132G>T), K417T (22812A>C), E484K (23012G>A), N501Y (23063A>T), D614G (23403A>G), H655Y (23525C>T), T1027I (24642C>T), V1176F (25088G>T)								
Codon mutations:	CTT18TTT (21614C>T), ACC20AAC (21621C>A), CCT26TCT (21638C>T), GAT138TAT (21974G>T), AGG190AGT (22132G>T), AAG417ACG (22812A>C), GAA484AAA (23012G>A), AAT501TAT (23063A>T), GAT614GGT (23403A>G), CAT655TAT (23525C>T), ACT1027ATT (24642C>T), GTT1176TTT (25088G>T)								
ORF3a	1	276	100%	1950	99.7%	276 (100%)	275 (99.6%)	0/0/0/0	1
Protein mutations:	S253P (26149T>C)								
Codon mutations:	TCC253CCC (26149T>C)								
E	1	76	100%	474	100%	76 (100%)	76 (100%)	0/0/0/0	1
M	1	223	100%	1538	100%	223 (100%)	223 (100%)	0/0/0/0	1
ORF6	1	62	100%	400	100%	62 (100%)	62 (100%)	0/0/0/0	1

## HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
ORF7a	1	122	100%	846	100%	122 (100%)	122 (100%)	0/0/0/0	1
ORF7b	1	44	100%	316	100%	44 (100%)	44 (100%)	0/0/0/0	1
ORF8	1	122	100%	914	99.6%	122 (100%)	121 (99.2%)	0/0/0/0	1
Protein mutations: E92K (28167G>A)									
Codon mutations: GAA92AAA (28167G>A)									
N	1	420	100%	2839	99.0%	420 (100%)	417 (99.3%)	0/0/0/0	1
Protein mutations: P80R (28512C>G), R203K (28881G>A 28882G>A), G204R (28883G>C)									
Codon mutations: CCA80CGA (28512C>G), AGT202TCT (28877A>T 28878G>C), AGG203AAA (28881G>A 28882G>A), GGA204CGA (28883G>C)									
ORF10	1	39	100%	269	100%	39 (100%)	39 (100%)	0/0/0/0	1
ORF9b	1	98	100%	612	99.0%	98 (100%)	97 (99.0%)	0/0/0/0	1
Protein mutations: Q77E (28512C>G)									
Codon mutations: CAG77GAG (28512C>G)									
ORF14	1	74	100%	490	97.6%	74 (100%)	72 (97.3%)	0/0/0/0	1
Protein mutations: V49L (28878G>C), G50N (28881G>A 28882G>A 28883G>C)									
Codon mutations: GCA48GCT (28877A>T), GTA49CTA (28878G>C), GGG50AAC (28881G>A 28882G>A 28883G>C)									
<b>Proteins</b>									
ORF1ab polyprote...	1	7097	99.9%	49475	99.9%	7086 (99.9%)	7080 (99.9%)	0/3/0/0	1
Protein mutations: K338R (1278A>G), S1188L (3828C>T), R1628C (5147C>T), S3675_F3677del (11288_11296delTCTGGTTTT), P4715L (14408C>T), E5665D (17259G>T), P6128H (18647C>A)									
Codon mutations: GAT156GAC (733T>C), AAA338AGA (1278A>G), GAC828GAT (2749C>T), TTC924TTT (3037C>T), TCA1188TTA (3828C>T), CGT1628TGT (5147C>T), CCA2018CCG (6319A>G), GTA2116GTG (6613A>G), TCT3675_TTT3677del (11288_11296delTCTGGTTTT), TAC4171TAT (12778C>T), GAC4532GAT (13860C>T), CCT4715CTT (14408C>T), GTC4887GTT (14925C>T), GAG5665GAT (17259G>T), CCT6128CAT (18647C>A)									
leader protein (YP...	1	180	100%	1231	100%	180 (100%)	180 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: GAT156GAC (733T>C)									
nsp2 (YP_009725...	1	638	100%	4399	99.9%	638 (100%)	637 (99.8%)	0/0/0/0	0
Protein mutations: K158R (1278A>G)									
Codon mutations: AAA158AGA (1278A>G)									

## HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
nsp3 (YP_009725...	1	1945	100%	13184	99.9%	1945 (100%)	1943 (99.9%)	0/0/0/0	0
Protein mutations: S370L (3828C>T), R810C (5147C>T)									
Codon mutations: GAC10GAT (2749C>T), TTC106TTT (3037C>T), TCA370TTA (3828C>T), CGT810TGT (5147C>T), CCA1200CCG (6319A>G), GTA1298GTG (6613A>G)									
nsp4 (YP_009725...	1	500	100%	3529	100%	500 (100%)	500 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: none									
3C-like proteinase...	1	306	100%	2230	100%	306 (100%)	306 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: none									
nsp6 (YP_009725...	1	290	97.2%	1944	99.6%	279 (98.9%)	279 (98.9%)	0/3/0/0	0
Protein mutations: S106_F108del (11288_11296delTCTGGTTTT)									
Codon mutations: TCT106_TTT108del (11288_11296delTCTGGTTTT)									
nsp7 (YP_009725...	1	83	100%	511	100%	83 (100%)	83 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: none									
nsp8 (YP_009725...	1	198	100%	1235	100%	198 (100%)	198 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: none									
nsp9 (YP_009725...	1	113	100%	764	100%	113 (100%)	113 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: TAC31TAT (12778C>T)									
nsp10 (YP_00972...	1	139	100%	1075	100%	139 (100%)	139 (100%)	0/0/0/0	0
Protein mutations: none									
Codon mutations: none									
RNA-dependent R...	1	932	100%	6723	99.8%	932 (100%)	931 (99.9%)	0/0/0/0	0
Protein mutations: P323L (14408C>T)									
Codon mutations: GAC140GAT (13860C>T), CCT323CTT (14408C>T), GTC495GTT (14925C>T)									
helicase (YP_009...	1	601	100%	4237	99.9%	601 (100%)	600 (99.8%)	0/0/0/0	0

## HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
Protein mutations:	E341D (17259G>T)								
Codon mutations:	GAG341GAT (17259G>T)								
3'-to-5' exonuclea...	1	527	100%	3982	99.7%	527 (100%)	526 (99.8%)	0/0/0/0	0
Protein mutations:	P203H (18647C>A)								
Codon mutations:	CCT203CAT (18647C>A)								
endoRNAse (YP_0...	1	346	100%	2364	100%	346 (100%)	346 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
2'-O-ribose methyl...	1	298	100%	2066	100%	298 (100%)	298 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
ORF1a polyprotei...	1	4406	99.8%	30185	99.9%	4395 (99.9%)	4392 (99.9%)	0/3/0/0	1
Protein mutations:	K338R (1278A>G), S1188L (3828C>T), R1628C (5147C>T), S3675_F3677del (11288_11296delTCTGGTTTT)								
Codon mutations:	GAT156GAC (733T>C), AAA338AGA (1278A>G), GAC828GAT (2749C>T), TTC924TTT (3037C>T), TCA1188TTA (3828C>T), CGT1628TGT (5147C>T), CCA2018CCG (6319A>G), GTA2116GTG (6613A>G), TCT3675_TTT3677del (11288_11296delTCTGGTTTT), TAC4171TAT (12778C>T)								
leader protein (YP...	1	180	100%	1231	100%	180 (100%)	180 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	GAT156GAC (733T>C)								
nsp2 (YP_009742...	1	638	100%	4399	99.9%	638 (100%)	637 (99.8%)	0/0/0/0	0
Protein mutations:	K158R (1278A>G)								
Codon mutations:	AAA158AGA (1278A>G)								
nsp3 (YP_009742...	1	1945	100%	13184	99.9%	1945 (100%)	1943 (99.9%)	0/0/0/0	0
Protein mutations:	S370L (3828C>T), R810C (5147C>T)								
Codon mutations:	GAC10GAT (2749C>T), TTC106TTT (3037C>T), TCA370TTA (3828C>T), CGT810TGT (5147C>T), CCA1200CCG (6319A>G), GTA1298GTG (6613A>G)								
nsp4 (YP_009742...	1	500	100%	3529	100%	500 (100%)	500 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
3C-like proteinase...	1	306	100%	2230	100%	306 (100%)	306 (100%)	0/0/0/0	0

## HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F	Stop Codons
Protein mutations:	none								
Codon mutations:	none								
nsp6 (YP_009742...	1	290	97.2%	1944	99.6%	279 (98.9%)	279 (98.9%)	0/3/0/0	0
Protein mutations:	S106_F108del (11288_11296delTCTGGTTTT)								
Codon mutations:	TCT106_TTT108del (11288_11296delTCTGGTTTT)								
nsp7 (YP_009742...	1	83	100%	511	100%	83 (100%)	83 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
nsp8 (YP_009742...	1	198	100%	1235	100%	198 (100%)	198 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
nsp9 (YP_009742...	1	113	100%	764	100%	113 (100%)	113 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	TAC31TAT (12778C>T)								
nsp10 (YP_00974...	1	139	100%	1075	100%	139 (100%)	139 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
nsp11 (YP_00972...	1	13	100%	82	100%	13 (100%)	13 (100%)	0/0/0/0	0
Protein mutations:	none								
Codon mutations:	none								
surface glycoprot...	1	1274	100%	8898	99.0%	1274 (100%)	1262 (99.1%)	0/0/0/0	1
Protein mutations:	L18F (21614C>T), T20N (21621C>A), P26S (21638C>T), D138Y (21974G>T), R190S (22132G>T), K417T (22812A>C), E484K (23012G>A), N501Y (23063A>T), D614G (23403A>G), H655Y (23525C>T), T1027I (24642C>T), V1176F (25088G>T)								
	D614G (common variant; produces more infectious particles when pseudotyped on VSV ex vivo; increases viral load in hamster upper respiratory tract)								
Codon mutations:	CTT18TTT (21614C>T), ACC20AAC (21621C>A), CCT26TCT (21638C>T), GAT138TAT (21974G>T), AGG190AGT (22132G>T), AAG417ACG (22812A>C), GAA484AAA (23012G>A), AAT501TAT (23063A>T), GAT614GGT (23403A>G), CAT655TAT (23525C>T), ACT1027ATT (24642C>T), GTT1176TTT (25088G>T)								
ORF3a protein (Y...	1	276	100%	1950	99.7%	276 (100%)	275 (99.6%)	0/0/0/0	1
Protein mutations:	S253P (26149T>C)								
Codon mutations:	TCC253CCC (26149T>C)								

## HIDE MUTATIONS

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
envelope protein (...)	1	76	100%	474	100%	76 (100%)	76 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								
membrane glycop...	1	223	100%	1538	100%	223 (100%)	223 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								
ORF6 protein (YP_...	1	62	100%	400	100%	62 (100%)	62 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								
ORF7a protein (Y...	1	122	100%	846	100%	122 (100%)	122 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								
ORF7b (YP_00972...	1	44	100%	316	100%	44 (100%)	44 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								
ORF8 protein (YP_...	1	122	100%	914	99.6%	122 (100%)	121 (99.2%)	0/0/0/0	1
Protein mutations:	E92K (28167G>A)								
Codon mutations:	GAA92AAA (28167G>A)								
nucleocapsid pho...	1	420	100%	2839	99.0%	420 (100%)	417 (99.3%)	0/0/0/0	1
Protein mutations:	P80R (28512C>G), R203K (28881G>A 28882G>A), G204R (28883G>C)								
Codon mutations:	CCA80CGA (28512C>G), AGT202TCT (28877A>T 28878G>C), AGG203AAA (28881G>A 28882G>A), GGA204CGA (28883G>C)								
ORF10 protein (Y...	1	39	100%	269	100%	39 (100%)	39 (100%)	0/0/0/0	1
Protein mutations:	none								
Codon mutations:	none								

\*: Inserts / Deletes / Misaligned / Frameshifts



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