

Supplementary Materials:

Supplementary Tables

Table S1: The acquired protein sequences from the BLAST result including the reference protein sequences for MERS, SARS-CoV and SARS-CoV-2 coronavirus strains are as follows:

Virus Type	Accession number (S proteins)	Accession number (E proteins)	Accession number (M proteins)
MERS	ATG84756.1	AGV08472.1	AGV08396.1
	ASU90340.1	ASU90554.1	AHI48589.1
	ALJ54448.1	AHZ65623.1	AVN89358.1
	AKI29255.1	ALR69646.1	ANI69895.1
	AHI48572.1	ANF29266.1	AGV08590.1
SARS-CoV	AFR58672.1	NP_828854.1	AAP33701.1
	ABD72984.1	AAP51230.1	BAE93405.1
	AAR23250.1	ACB69908.1	AFR58704.1
	AAR07630.1	ACZ72023.1	AFR58690.1
	AAP33697.1	AAR23255.1	ABF65840.1
SARS-CoV-2	YP_009724390.1	YP_009724392.1	YP_009724393.1

	QIO04367.1	QHZ00381.1	QII87843.1
	QII87830.1	QIS60608.1	QIQ49785.1
	QII57278.1	QID88859.1	QIS60561.1
	QHU79173.2	QIS30357.1	QIS60981.1

Table S2: Accession number of common human coronavirus protein sequences obtained from the BLAST results for S, E and M proteins.

Common human coronavirus strains	Accession number (S proteins)	Accession number (E proteins)	Accession number (M proteins)
Human coronavirus 229E	APT69856.1	CAA46114.1	AAA45461.1
	ARU07601.1	AOG74785.1	APT69865.1
	APT69883.1	AGW80935.1	AST12967.1
	APT69849.1	AFR79252.1	AFR79253.1
	ARK08642.1	NP_073554.1	NP_073555.1
Human coronavirus NL63	AFV53148.1	BBL54111.1	YP_003770.1
	YP_003767.1	APD51493.1	ARE29965.1
	AFD98785.1	APD51485.1	AGT51369.1

	AFD98806.1	AAV67329.1	ABD34826.1
	AFD98834.1	YP_003769.1	ABC87313.1
Human coronavirus OC43	AAR01015.1	QEG03816.1	YP_009555244.1
	CAA79896.1	YP_009555243.1	AGT51484.1
	AAB27260.2	AMK59679.1	AGT51633.1
	YP_009555241.1	AAX85680.1	AGT51405.1
	AAT84362.1	AAX85671.1	AGT51454.1
Human coronavirus HKU1	BBA20986.1	AGT17765.1	ABD75596.1
	ABD75617.1	AGT17760.1	ABD75532.1
	AGT17758.1	BBA20987.1	ABD75500.1
	ABD75625.1	Q0ZME5.1	YP_173241.1
	ABD75505.1	-	ABD75588.1

Table S3: Accession number of SARS-CoV-2 protein sequences obtained from the BLAST results for S, E and M proteins.

SARS-CoV-2 proteins	Accession number
S protein	QII57278.1; YP_009724390.1 ; QIO04367.1 ; QHU79173.2; QII87830.1; QIA98583.1 ; QIA20044.1 ; QIK50427.1 ; QHR84449.1 ; QIJ96493.1 ; QIC53204.1 ; QHZ00379.1 ; QHS34546.1 ; 6VSB_A Chain A; 6VXX_A Chain A ; 6VYB_A Chain A
E protein	QHZ00381.1 ; QID88859.1 ; QIS30357.1 ; QIS30397.1 ; QIS30527.1 ; QIS60608.1 ; QIU81371.1 ; QIU81527.1 ; YP_009724392.1
M protein	YP_009724393.1 ; QII87843.1 ; QIU81888.1; QIQ49785.1 ; QIU81660.1 ; QIU81036.1 ; QIS60561.1 ; QIS60981.1 ; QIG55988.1 ; QIS61257.1 ; QIS60897.1 ; QIS30228.1 ; QIS61389.1 ; QIQ68477.1 ; QIS30507.1 ; QIU81372.1 ; QIS30358.1 ; QIS30638.1 ; QIS30528.1 ; QIS30398.1 ; QIS60609.1 ; QIS30188.1 ; QIU78870.1 ; QHR93621.1

Table S4. Predicted epitopes for CD8+ T-cell along with their interacting MHC class I alleles with affinity < 500 nM.

Protein	Epitope	Position	Antigenicity (Vaxigen v2.0)	MHC class I allele with total score having IC50 values < 500 nM
S	WTAGAAA YY	258-266	Probable antigen(0.5371)	HLA-A*01:01(25.27), HLA-A*01:07(34.48), HLA-A*01:02(34.85), HLA-A*01:21(44.76), HLA-A*01:21(112.68) HLA-A*25:02(144.23), HLA-A*25:04(168.61), HLA-A*26:02(4.31), HLA-A*26:04(13.51), HLA-A*26:01(14.63), HLA-A*26:03(176.4), HLA-A*29:02(6.57), HLA-A*29:04(8,82), HLA-A*30:02(17.68), HLA-A*30:03(22.83), HLA-A*34:06(33.88), HLA-A*68:05(67.26), HLA-B*15:17(5.59), HLA-B*15:15(78.1) HLA-B*15:08(79.29), HLA-B*35:10(13.94), HLA-B*35:07(22.65), HLA-B*35:07(23.62) HLA-C*02:03(234.76), HLA-C*02:05(317.47), HLA-C*03:01(37.99), HLA-C*03:02(37.99,) HLA-C*05:04(81.16), HLA-C*12:04(280), HLA-C*12:05(283.13).

	KIADYNY KL	417-425	Probable antigen(1.6639)	HLA-A*02:02(5.74), HLA-A*02:05(10.51), HLA-A*02:01(11.35), HLA-A*02:01(228.25), HLA-A*30:06(228.25) HLA-A*32:05(30), HLA-A*32:06(63.32), HLA-A*32:02(69), HLA-B*39:02(319.38) HLA-C*02:03(50), HLA-C*05:04(411.22) HLA-C*15:02(312.72), HLA-C*15:06(315.22).
E	YVYSRVK NL	57-65	Probable antigen(0.7020)	HLA-A*02:01(348.45) HLA-A*02:02(264.44), HLA-A*02:03(27.56),HLA-A*02:06(314.41), HLA-A*02:11(44.60), HLA-A*02:13(349.43), HLA-A*02:14(408.68),HLA-A*02:21(240.69), HLA-A*26:02(359.95),HLA-A*26:03(484.69), HLA-A*32:07(497.98),HLA-A*34:01(377.61), HLA-A*68:23(80.87), HLA-B*07:34(250.99), HLA-B*07:54(497.90),HLA-B*08:01(116.20), HLA-B*08:04(308.30), HLA-B*08:05(82.40), HLA-B*08:07(205.49), HLA-B*08:10(38.25), HLA-B*08:11(103.48), HLA-B*08:13(39.61), HLA-B*15:17(104.28),HLA-B*15:29(454.66), HLA-B*39:17(420.38),HLA-B*42:07(239.11), HLA-C*01:12(403.25), HLA-C*01:21(84.79),

				HLA-C*02:05(253.04),HLA-C*02:12(416.56), HLA-C*02:16(405.44), HLA-C*03:01(21.02), HLA-C*03:02(21.02), HLA-C*06:02(187.05), HLA-C*06:03(147.22),HLA-C*06:05(294.93), HLA-C*07:01(205.07),HLA-C*07:03(145.68), HLA-C*08:09(234.76),HLA-C*08:11(234.76), HLA-C*12:02(56.67), HLA-C*12:03(12.24), HLA-C*12:06(12.98), HLA-C*14:02(45.82), HLA-C*14:03(92.38), HLA-C*15:02(177.20), HLA-C*15:04(88.76)HLA-C*16:04(38.33), HLA-C*16:01(85.37).
M	GTITVE ELK	6-14	Prob able antigen(1.0976)	HLA-A*11:01(32.06),HLA-A*68:01(35.92), HLA-A*03:12(223.83), HLA-A*11:64(34.92), HLA-A*11:60(36.36), HLA-A*03:72(302), HLA-A*03:50(335.69),HLA-A*30:26(184.37), HLA-A*31:03(319.02),HLA-A*31:06(317.70), HLA-A*68:04(289.14), HLA-A*68:10(17.15).

Supplementary Figures

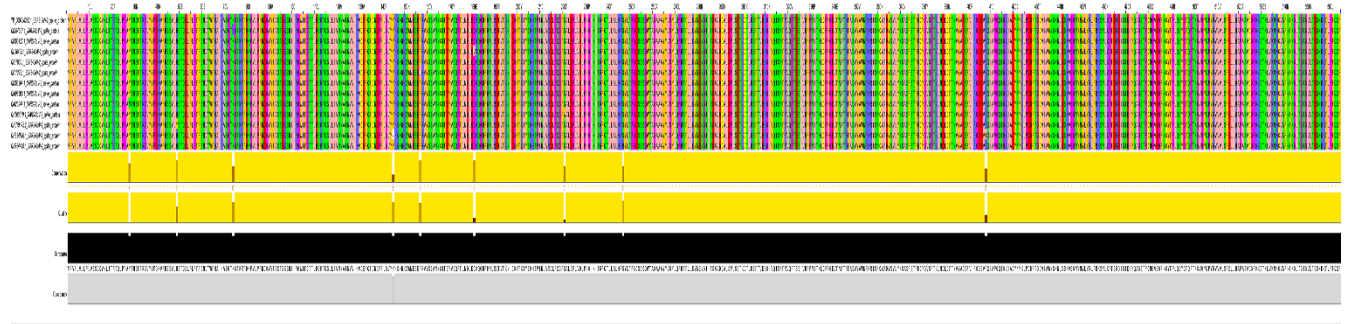


Figure S1: Multiple sequence alignment of the conserved sequences of S protein visualized by Jalview.

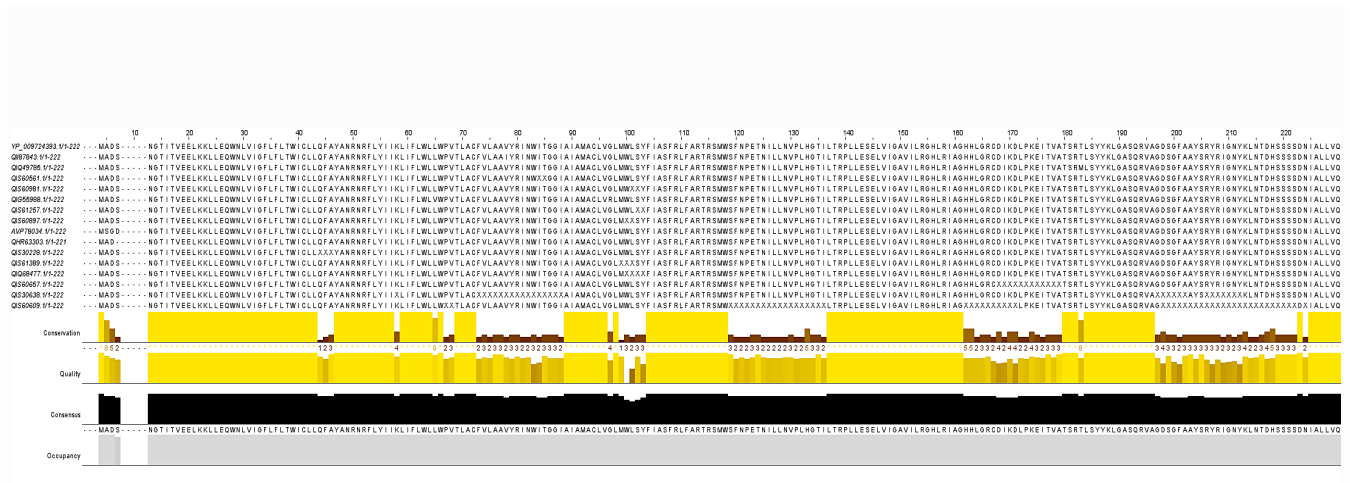


Figure S2: Multiple sequence alignment of the conserved sequences of M protein visualized by Jalview.

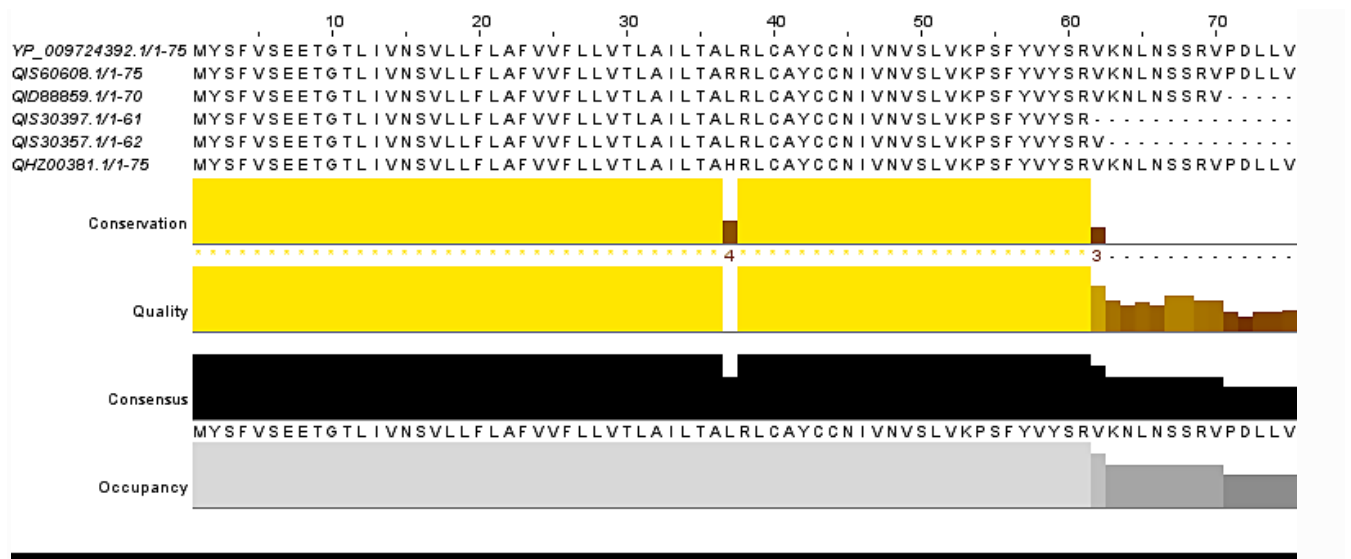


Figure S3: Multiple sequence alignment of the conserved sequences of E protein visualized by Jalview.

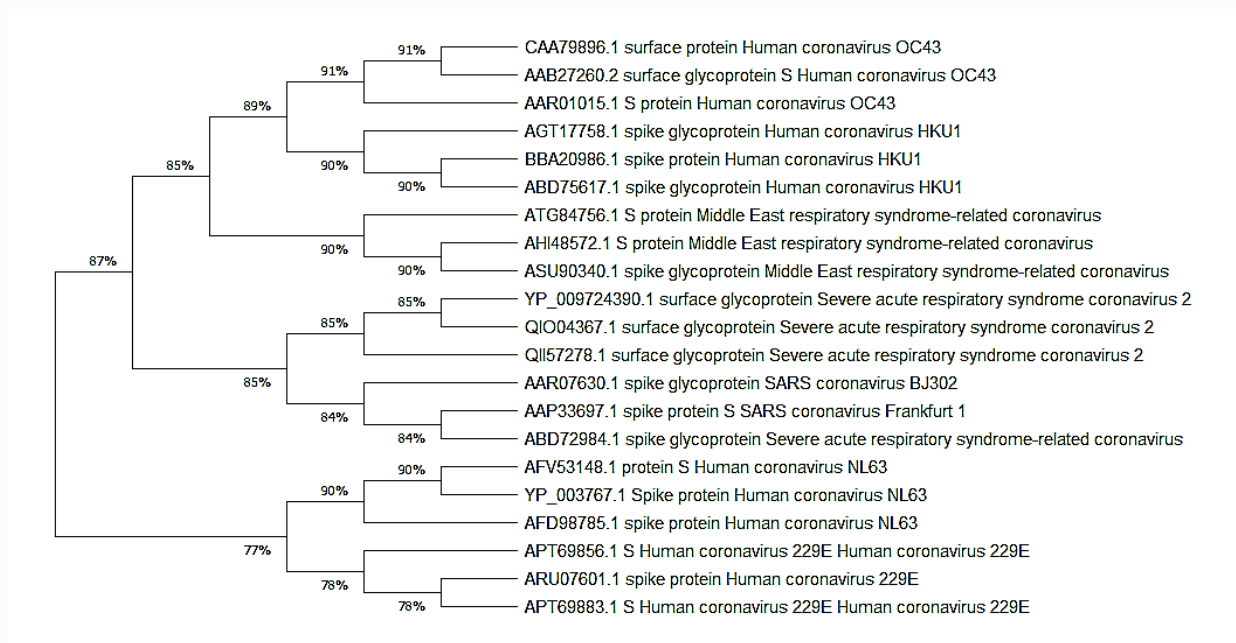


Figure S4: Phylogenetic relationship on account of S protein sequences of MERS, SARS-CoV, SARS-CoV-2 and Human coronavirus strains.

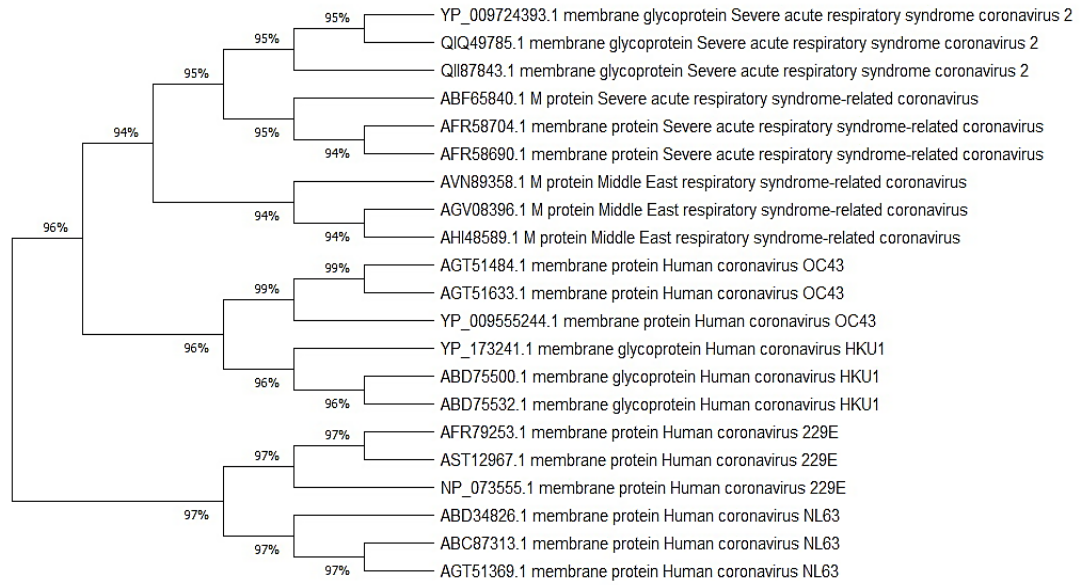


Figure S5: Phylogenetic relationship on account of M protein sequences of MERS, SARS-CoV, SARS-CoV-2 and Human coronavirus strains.

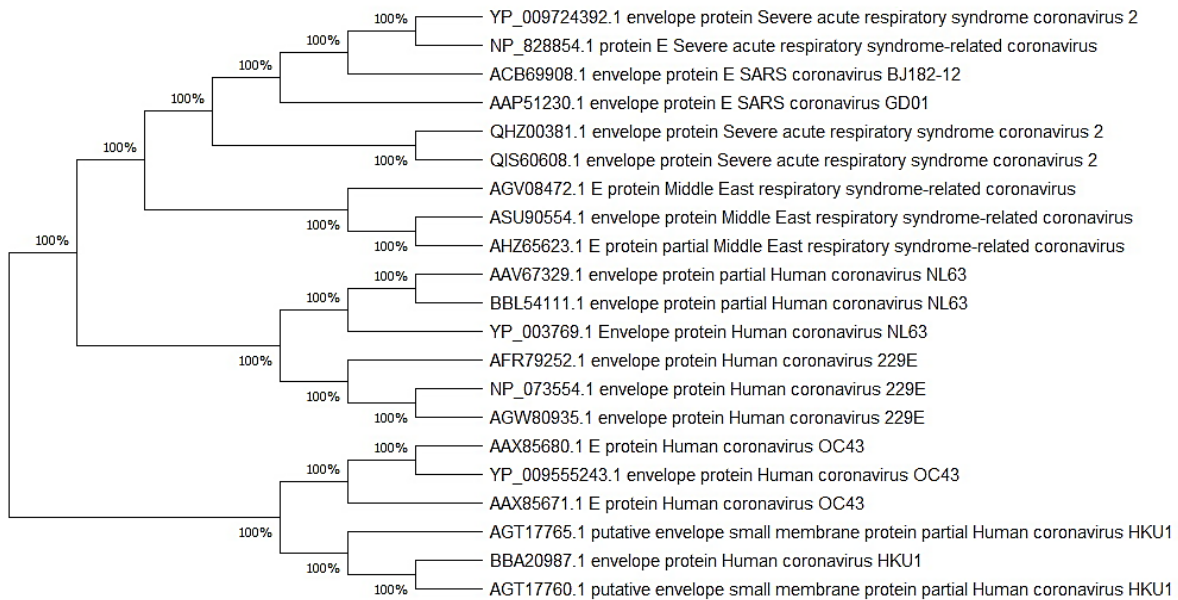


Figure S6: Phylogenetic relationship on account of E protein sequences of MERS, SARS-CoV, SARS-CoV-2 and Human coronavirus strains.

List of abbreviations

NCBI National Centre for Biotechnology Information

PDB Protein Data Bank

RBD Receptor-Binding Domain

NTD N-Terminal Domain

MHC Major Histo-compatibility Complex