

Figure S4. (A). Homology model of N-terminal domain (NTD) of spike protein from SARS-related coronavirus BtKY72 showing the locations of three CSIs specific for the *Sarbecovirus*-lineage 3. The homology models are based on available experimental structure of SARS coronavirus BJ012 spike protein (PDB: 5x58). The location of identified 1 aa deletion is highlighted. Detailed species distribution information for the 1 aa deletion in Figure 8C. (B). Homology model of RBD of SARS-related coronavirus BtKY72 spike protein (Acc no: APO40579) based on available experimental structure of SARS coronavirus BJ012 spike protein (PDB: 5x58). The receptor binding domain (RBD) domain is highlighted as green and extended C-terminal region as pale green. The locations of identified signature indels are highlighted red and labelled. Detailed species distribution information for the 1 aa insert and 2 aa insert in RBD in Figure 8A and 8B.

S3 Fig. A multiple sequence alignment of the spike protein from pangolin-CoV_MP789 and representative CoV strains from SARS-CoV-2 and CoVZC clusters showing the chimeric nature of MP789 sequence. In this alignment, the polymorphic positions where the sequence of pangolin-CoV_MP789 is identical to that of CoVZC cluster of viruses are highlighted in yellow, whereas the polymorphic positions where the sequence of pangolin-CoV_MP789 is similar to SARS-CoV-2 viruses are highlighted in blue.

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YP_009724390_SARS-COV-2/ Wuhan-      -MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLH
QHS34546_SARS-CoV-2/ human/ IND/     -MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVVYPDKVFRSSVLH
QJA16794_SARS-CoV-2/ human/ ID-U     -MFVFLVLLPLVSSQCVNLTTRTQLPPSYTNSFTRGVVYPDKVFRSSVLH
QIG55945.1_Pangolin_CoV_MP789        MLLFFFLHFALVNSQCVNLTGRAAIQPSFTNSSQRGVYYPDTIFRSNTLV
AVP78031_Bat-SARS-like-CoVZC45       MLFFLFLQFALVNSQCVNLTGRTPLNPNYTNSSQRGVYYPDTIYRSDTLV
AVP78042_Bat-SARS-like_CoVZXCC       MLFFLFLQFALVNSQCD-LTGRTPLNPNYTNSSQRGVYYPDTIYRSDTLV
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YP_009724390_SARS-COV-2/ Wuhan-      STQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSN
QHS34546_SARS-CoV-2/ human/ IND/     STQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSN
QJA16794_SARS-CoV-2/ human/ ID-U     STQDLFLPFFSNVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSN
QIG55945.1_Pangolin_CoV_MP789        LSQGYFLPFYSNVSWYYALT-KTNSAEKRDNPVLDKDGIFYAAATEKSN
AVP78031_Bat-SARS-like-CoVZC45       LSQGYFLPFYSNVSWYYSLT-TNNAATKRTDNPILDKDGIFYAAATEHSN
AVP78042_Bat-SARS-like_CoVZXCC       LSQGYFLPFYSNVSWYYSLT-TNNAATKRTDNPILDKDGIFYAAATEHSN
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YP_009724390_SARS-COV-2/ Wuhan-      IIRGWIFGTTLDSTQSLIVNNAATNVVIVKCEFCNDPFLGVYHKN
QHS34546_SARS-CoV-2/ human/ IND/     IIRGWIFGTTLDSTQSLIVNNAATNVVIVKCEFCNDPFLGVYHKN
QJA16794_SARS-CoV-2/ human/ ID-U     IIRGWIFGTTLDSTQSLIVNNAATNVVIVKCEFCNDPFLGVYHKN
QIG55945.1_Pangolin_CoV_MP789        IIRGWIFGTTLDNTSQSLIVNNAATNVIKVCNFDYDPYLSGYHNN-
AVP78031_Bat-SARS-like-CoVZC45       IIRGWIFGTTLDNTSQSLIVNNAATNVIKVCNFDYDPYLSGYHNN-
AVP78042_Bat-SARS-like_CoVZXCC       IIRGWIFGTTLDNTSQSLIVNNAATNVIKVCNFDYDPYLSGYHNN-
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YP_009724390_SARS-COV-2/ Wuhan-      KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNKIDG
QHS34546_SARS-CoV-2/ human/ IND/     KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNKIDG
QJA16794_SARS-CoV-2/ human/ ID-U     KSWMESEFRVYSSANNCTFEYVSQPFLMDXEGKQVFNKLNREFVFNKIDG
QIG55945.1_Pangolin_CoV_MP789        KTWSIREFAVYSSYANCTFEYVSKSFMLDIAGKSGLFDTLREFVFRNV
AVP78031_Bat-SARS-like-CoVZC45       KTWSIREFAVYSSYANCTFEYVSKSFMLDIAGKSGLFDTLREFVFRNV
AVP78042_Bat-SARS-like_CoVZXCC       KTWSIREFAVYSSYANCTFEYVSKSFMLDIAGKSGLFDTLREFVFRNV
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YP_009724390_SARS-COV-2/ Wuhan-      YFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYL
QHS34546_SARS-CoV-2/ human/ IND/     YFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYL
QJA16794_SARS-CoV-2/ human/ ID-U     YFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLALHRSYL
QIG55945.1_Pangolin_CoV_MP789        YFKIYSKYTPVNVNSNLPVIGFSALEPLVEIPAGINITKFRLLTIHRGDP
AVP78031_Bat-SARS-like-CoVZC45       HFKIYSKFTPVNLRGLPTGLSVLQPLVELPVSINITKFRLLTIHRGDP
AVP78042_Bat-SARS-like_CoVZXCC       HFKIYSKFTPVNLRGLPTGLSVLQPLVELPVSINITKFRLLTIHRGDP
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YP_009724390_SARS-COV-2/ Wuhan-      TPGDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSET
QHS34546_SARS-CoV-2/ human/ IND/     TPGDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSET
QJA16794_SARS-CoV-2/ human/ ID-U     TPGDSSSGWTAGAAAYVGYLQPRFTLLKYNENGTITDAVDCALDPLSET
QIG55945.1_Pangolin_CoV_MP789        MPNN--GWTVFAAAYVGYLAPRTFMLNENGTITDAVDCALDPLSEA
AVP78031_Bat-SARS-like-CoVZC45       MPNN--GWTAFSAAYFVGYLKPRTFMLKYNENGTITDAVDCALDPLSET
AVP78042_Bat-SARS-like_CoVZXCC       MSNN--GWTAFSAAYFVGYLKPRTFMLKYNENGTITDAVDCALDPLSET
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YP_009724390_SARS-COV-2/ Wuhan-      KCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFAS
QHS34546_SARS-CoV-2/ human/ IND/     KCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFAS
QJA16794_SARS-CoV-2/ human/ ID-U     KCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFAS
QIG55945.1_Pangolin_CoV_MP789        KCTLKSLTVQKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFAS
AVP78031_Bat-SARS-like-CoVZC45       KCTLKSLTVQKGIYQTSNFRVQPTQSVVRFNITNLCPFHVKVFNATRFPS
AVP78042_Bat-SARS-like_CoVZXCC       KCTLKSLVQKGIYQTSNFRVQPTQSVVRFNITNLCPFHVKVFNATRFPS
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YP_009724390_SARS-COV-2/ Wuhan-      VYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADS
QHS34546_SARS-CoV-2/ human/ IND/     VYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADS
QJA16794_SARS-CoV-2/ human/ ID-U     VYAWNRKRISNCVADYSVLVNSASFSTFKCYGVSPTKLNDLCFTNVYADS
QIG55945.1_Pangolin_CoV_MP789        VYAWNRKRISNCVADYSVLVNSTSFSTFKCYGVSPTKLNDLCFTNVYADS
AVP78031_Bat-SARS-like-CoVZC45       VYAWERTKISDCIADYTVFYNSTSFSTFKCYGVSPSKLIDLCTFSVYADT
AVP78042_Bat-SARS-like_CoVZXCC       VYAWERTKISDCIADYTVFYNSTSFSTFKCYGVSPSKLIDLCTFSVYADT
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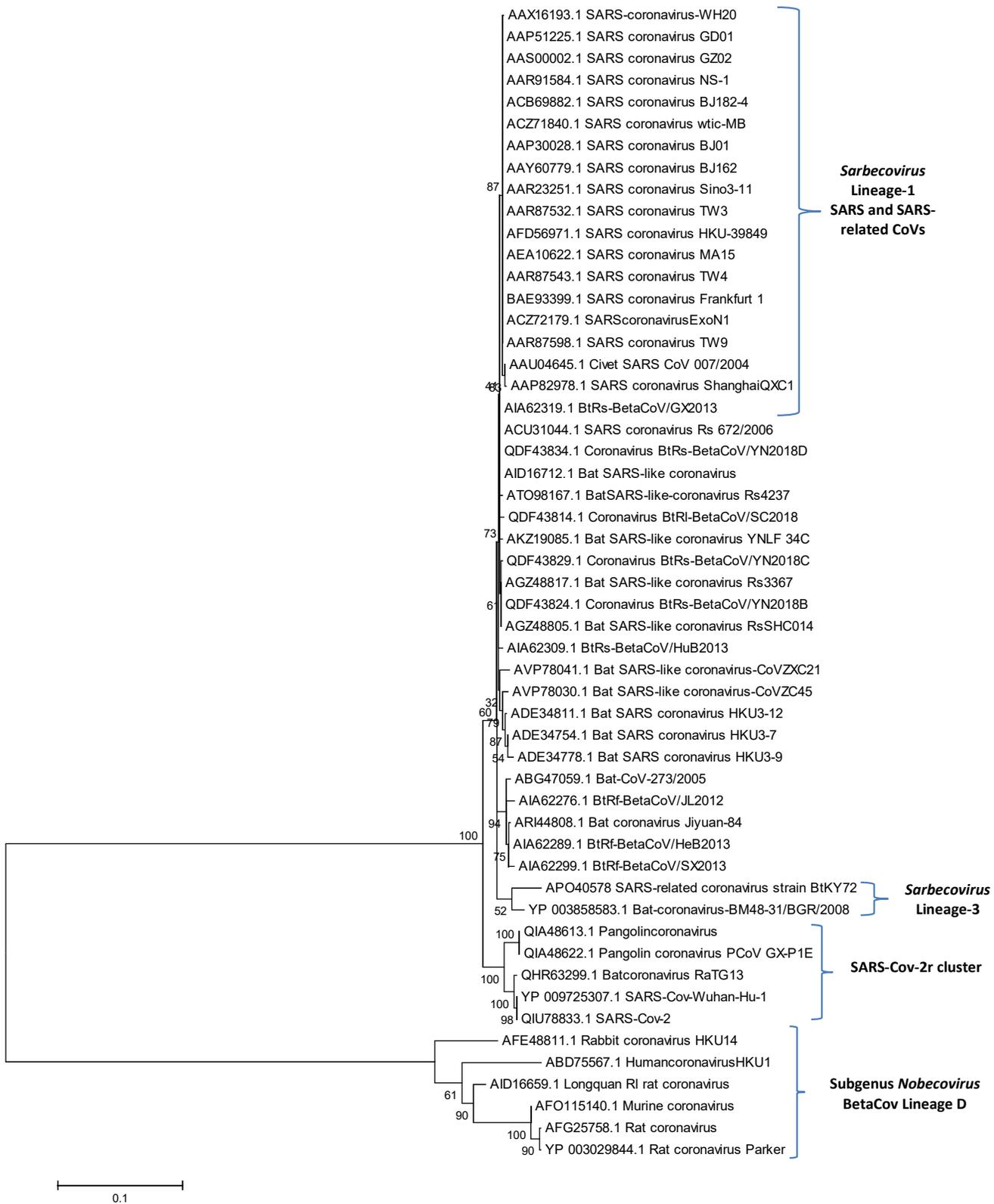


Figure S2. A maximum likelihood tree based on RNA dependent RNA polymerase protein sequences showing branching of different strains of Sarbecoviruses

