Supplemental Materials for

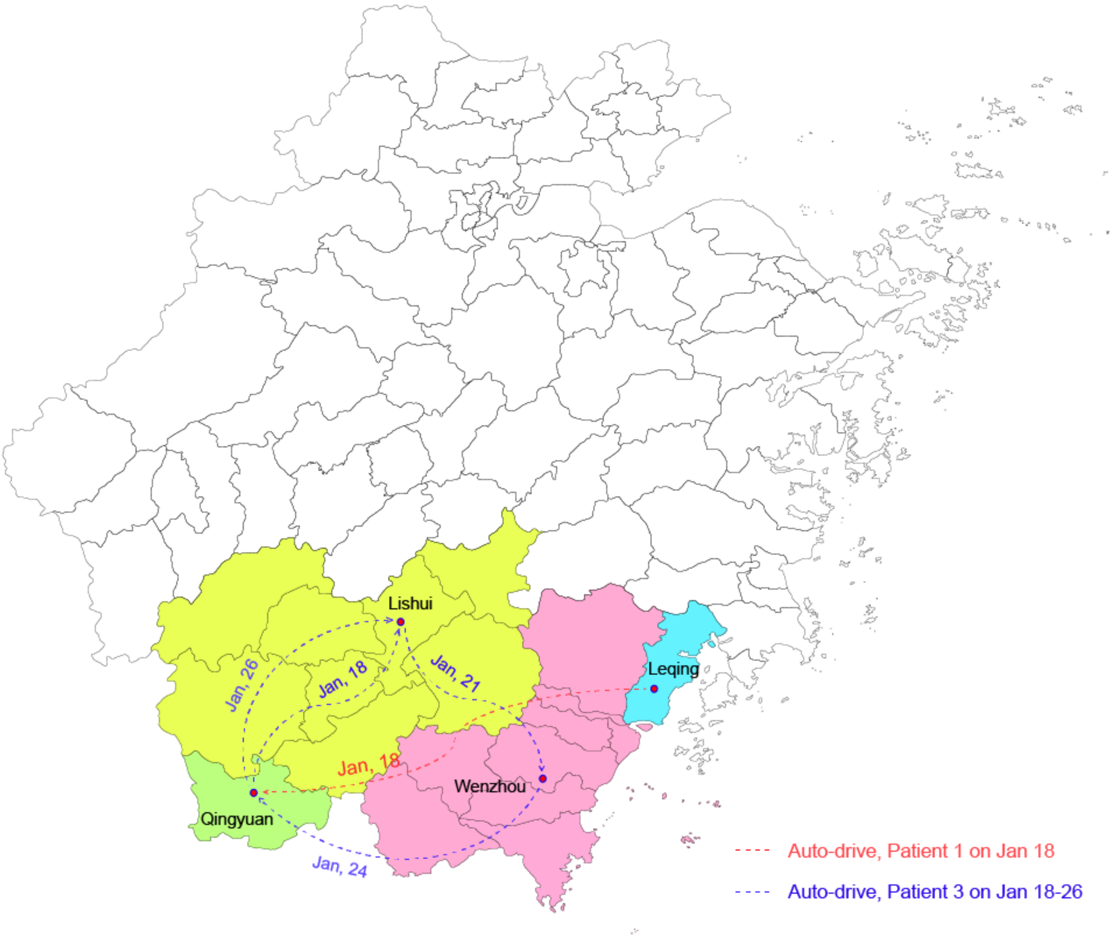

Fig. S1 Tracking the movement of Patient 1 and the contact Patient 3, prior to the onset of COVID-19 symptoms

On Jan 18, 2020, Patient 1 returned from Leqing County to hometown Qingyuan County for a dinner party. Of note, Patient 3 was also attended this party.

On Jan 18, 2020, Patient 3 auto-drove back home in Lishui City, visited Wenzhou City, on Jan 21 of 2020, passed by Qingyuan County on Jan 24 of 2020, and finally returned Lishui City on Jan 26 of 2020. The movement tracks of the two COVID-19 patients were recorded with arrowed/dashed lines (red for patient 1, and blue for patient 3).

The map of Zhejiang province is given with Adobe Illustrator, and the cities/counties where patients visited are colored.

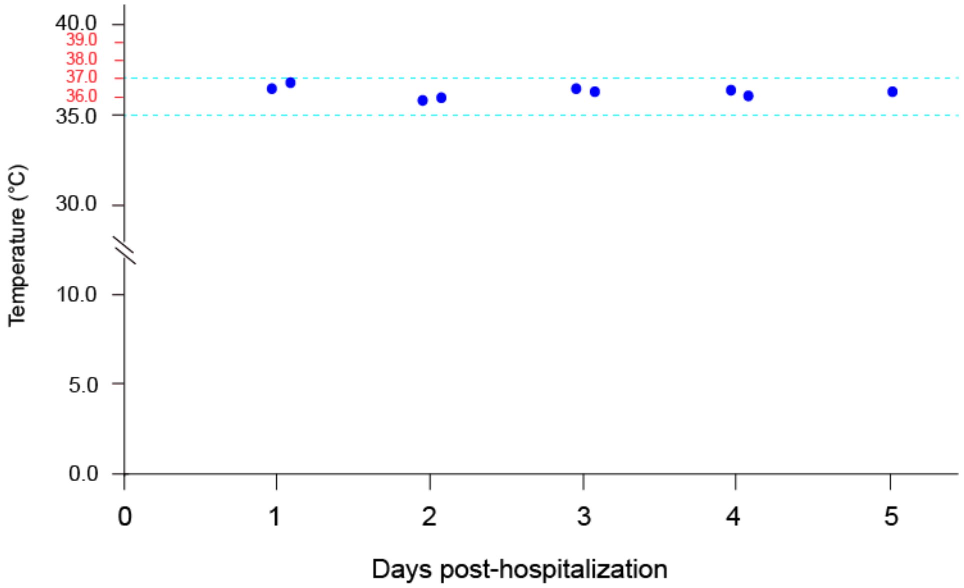

Fig. S2 Patient 3 has no fever in the 5 days post-hospitalization

The body temperature remains at the normal level (varying from 35.8°C to 36.8°C)

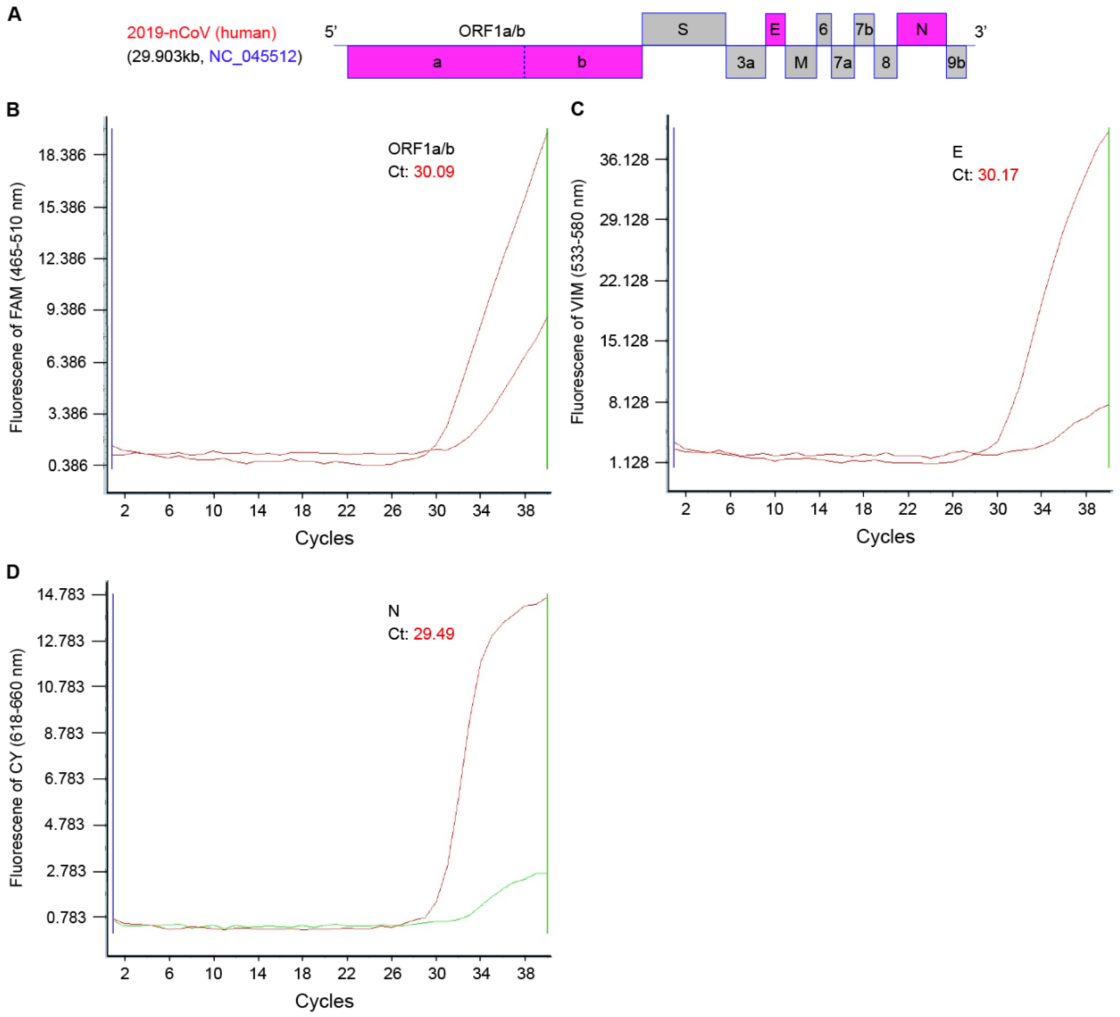

Fig. S3 Real-time quantitative PCR detection of the patient 3 with influenza-like illness

A. Cartoon scheme for 2019-nCoV (renamed as SARS-CoV-2) genome

The three target genes (highlighted in magenta), refer to ORF1a/b, E, and N, respectively.

B. Real-time qPCR detection (FAM) for the ORF1a/b-specific locus of 2019-nCoV (SARS-CoV-2)

C. qPCR detection (VIM) of 2019-nCoV (SARS-CoV-2) with specific primer against E protein-encoding gene

D. Real-time qPCR detection (CY) for the nucleocapsid (N) protein-specific locus of 2019-nCoV (SARS-CoV-2)

The values of Ct (cycle threshold) are 30.09 for ORF1a/b, 30.17 for E, and 29.49 for N, respectively.

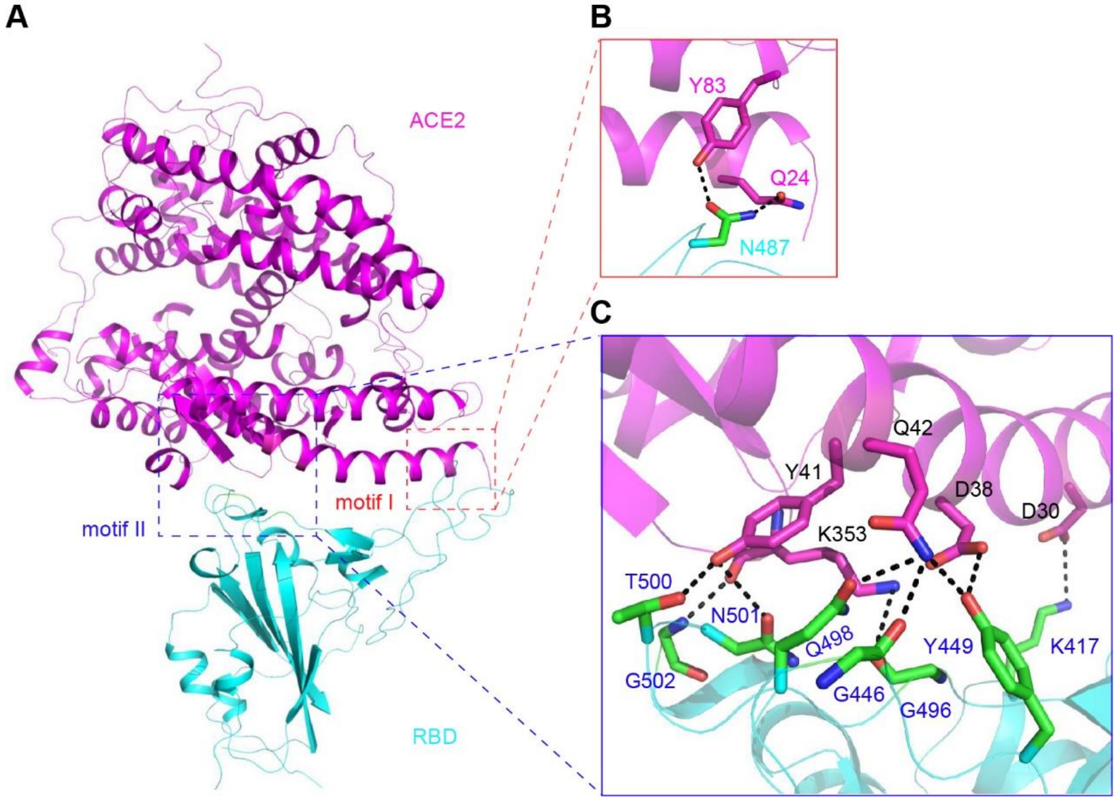

Fig. S4 Structural insights into the binding of 2019-nCoV to cellular receptor ACE2

A. Ribbon representation of complex structure of 2019-nCoV RBD and the N-terminal peptidase domain of ACE2 receptor

Presumably, two motifs (motif 1& 2) contributed to the maintenance of the stable interface between the cellular receptor ACE2 and RBD of 2019-nCoV spiker protein. Motif 1 is squared with blue dashed line, and motif 2 is squared with red dashed line. ACE2 is colored magenta, and RBD of 2019-nCoV is indicated in cyan.

B. Structural snapshot of motif 1 with contact residues labeled

N487 of RBD is suggested to interact with the two residues (Q24 and Y83) of cellular receptor ACE2.

C. Enlarged view of motif 2 of the RBD-ACE2 interface

Five residues of ACE2 (D30, D38, Y41, Q42 & K353) are contact residues interacting with the eight residues of RBD of 2019-nCoV surface protein (K417, G446, Y449, G496, Q498, T500, N501, and G502).

Structural re-analysis was conducted on the basis of the PDB information of RBD/ACE2 reported by Lan *et al.* [1].

Supplemental references

1. Lan, J. *et al.* Crystal structure of the 2019-nCoV spike receptor-binding domain bound with the ACE2 receptor. *bioRxiv* (2020).