



CORRECTION

Correction to: Discrimination of False Negative Results in RT-PCR Detection of SARS-CoV-2 RNAs in Clinical Specimens by Using an Internal Reference

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Published online: 21 September 2020
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Correction to: *Virologica Sinica* (2020)

<https://doi.org/10.1007/s12250-020-00273-8>

In the original version of Fig. 4I and 4J, the cutoff lines were accidentally shifted during figure layout. Figures 4I and 4J are re-drawn and provided below.

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The original article can be found online at <https://doi.org/10.1007/s12250-020-00273-8>.

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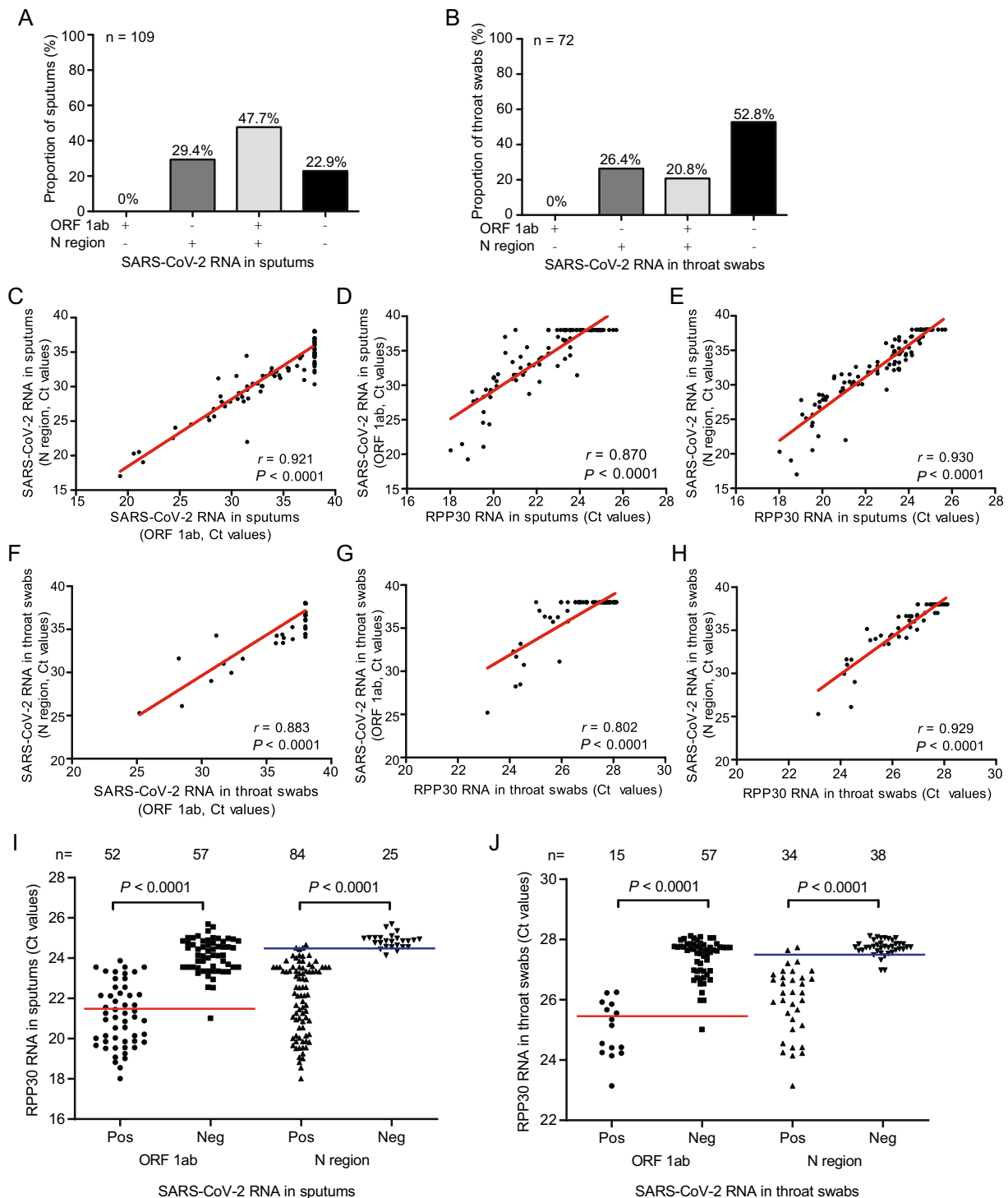


Fig. 4 The RT-PCR detection of SARS-CoV-2 RNAs in 181 sputum and throat swab specimens from 20 patients with conflicting RT-PCR results. 109 paired sputum (A) and 72 throat swab (B) specimens were collected and subjected to SARS-CoV-2 specific RT-PCR assays targeting the *ORF1ab* and *N* regions. +: RT-PCR positive; -: RT-PCR negative. Pearson correlation coefficients for the levels of detected SARS-CoV-2 RNA (based on the assays for *ORF1ab* and *N* region) and *RPP30* RNAs in patient samples were calculated. For sputum specimens: C *ORF1ab* and *N* region; D *ORF1ab* and *RPP30*; E *N* region and *RPP30*. For throat swab specimens: F *ORF1ab* and *N* region; G *ORF1ab* and *RPP30*; H *N* region and *RPP30*. The Ct values of *RPP30* RT-PCR were used to analyze the positive and negative results of *ORF1ab* and *N*-specific RT-PCR assays with 109 sputum (I) and 72 throat swab (J) specimens. Pos: positive results; Neg: negative results. The negative RT-PCR results of SARS-CoV-2 detection correspond to high Ct values for RT-PCR for *RPP30* RNAs. Red lines: cutoffs for *ORF1ab* RT-PCR; blue lines: cutoffs for *N* specific RT-PCR. The results were tested for significance by using the Mann-Whitney test (I, J). A *P* value of < 0.05 is considered as significant.