

Erratum to: A metagenomics study for the identification of respiratory viruses in mixed clinical specimens: an application of the iterative mapping approach

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Unfortunately, the accession numbers under “NGS data analysis pipeline in Materials and methods” section was incorrectly published in the original article and the corrected version should read as:

“Six genomes obtained in this study were deposited in GenBank, including HPeV-1 (accession number KY460516), human parainfluenza virus 4a (HPIV-4a, KY460515), HRV-A101 (KY460514), and HRV-C3 (KY460513) detected in NGS 1, and HPIV-4a (KY460518) and RSV (KY460517) detected in NGS 2. ...”

The online version of the original article can be found under doi:[10.1007/s00705-017-3367-4](https://doi.org/10.1007/s00705-017-3367-4).

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