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Dear Editor,

We are submitting our manuscript “Viral genetic determinants of prolonged human orthopneumovirus infection”.

In this manuscript we tackle an observation which is of great interest in our field but not yet reported. The content is in-line with the journal’s aims, the data and analysis is public, and our work is reproducible.

We performed surveillance of 2,093 infants with natural quasi random infection of respiratory syncytial virus (RSV) which included monitoring by RT-qPCR, serology, and sequencing. We performed viral genetic association testing to detect variants that contribute to prolonged infection. We identified viral genetic variants that associated with prolonged infection which we assessed in depth.

As a disease which causes significant morbidity and mortality, each advance in preventative measures can have lasting consequences for global health.

Your Sincerely,

Dylan Lawless, PhD, and
Tina V. Hartert, MD, MPH