

Virological Surveillance and Molecular Characterization of Human Parainfluenzavirus Infection in Children with Acute Respiratory Illness: Germany, 2015-2019

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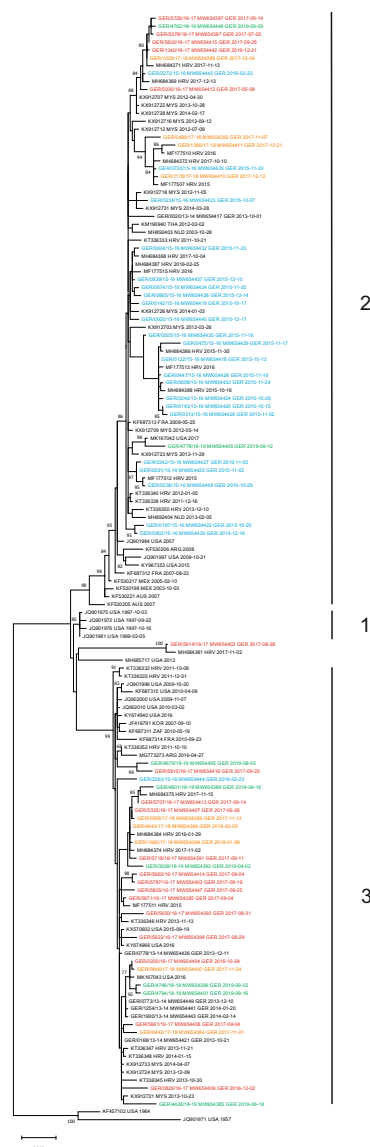


Figure S3: Maximum likelihood tree of partial HN gene of HPIV-1. German sequences of this study are coloured by epidemic season: 2015/16 in blue, 2016/17 in red, 2017/18 in orange, and 2018/19 in green. Clades are indicated on the right. Only bootstrap values greater or equal 80% are displayed at the branch nodes.