

Electronic Supplementary Material

Genetic Analysis of an Emerging GII.P2-GII.2 Norovirus Associated With a 2016 Outbreak of Acute Gastroenteritis in China

Yuanyun Ao¹, Xiaolu Xie², Xiaogen Dong³, Miao Jin¹, Zhaojun Duan¹✉

1. National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 102206, China;

2. Graduate School, Peking Union Medical College, Beijing 100730, China;

3. Fengtai District Center for Disease Control and Prevention, Beijing 100071, China

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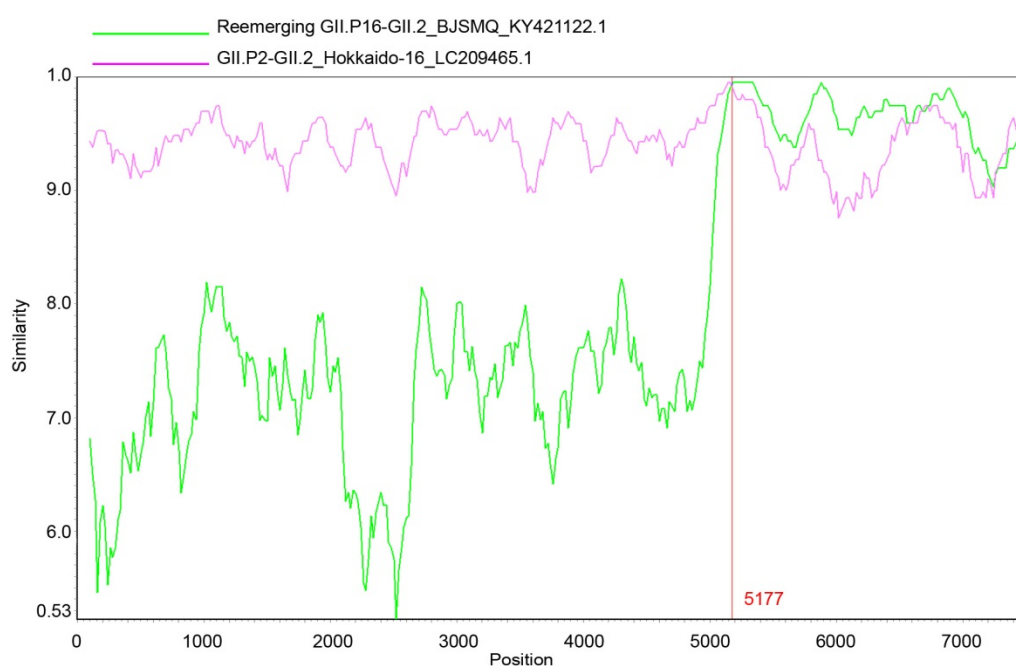


Fig. S1 SimPlot analysis of the complete genomic sequence of the emerging GII.P2/GII.2 strain for recombination. SimPlot analysis was reconstructed with a slide window width of 200 bp and a step size of 20 bp. The query sequence of the emerging GII.P2-GII.2 strain BJFTJYX was aligned with the two reference strains as shown at the windows. The X-axis indicates the nucleotide positions of the NoV sequences, while the Y-axis indicates nucleotide similarity (%) between the emerging GII.P2-GII.2 strain and the reference strains.