

**SUPPLEMENTAL DATA FILE**  
**Genome Summaries and Coverage Maps (related to Figure 2)**

**Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China**

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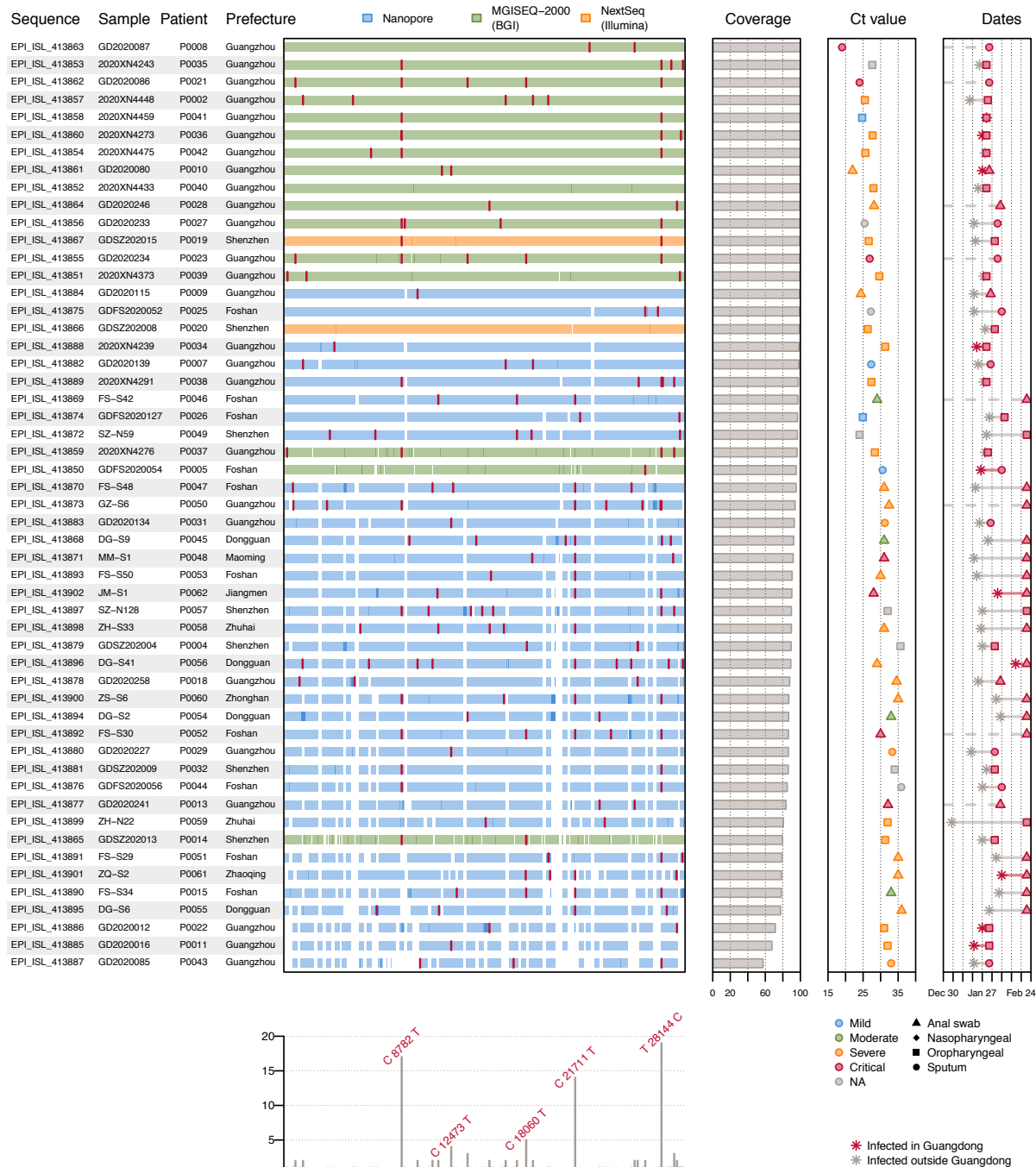
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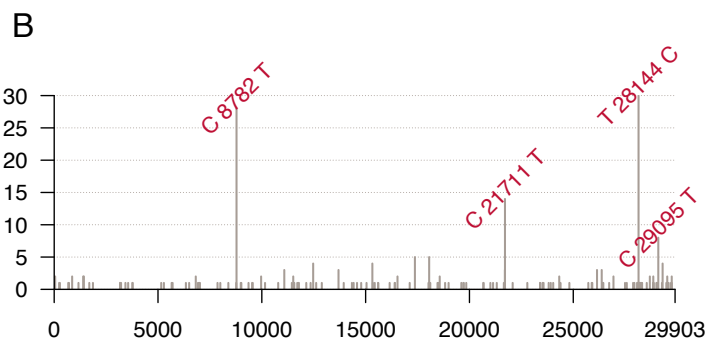
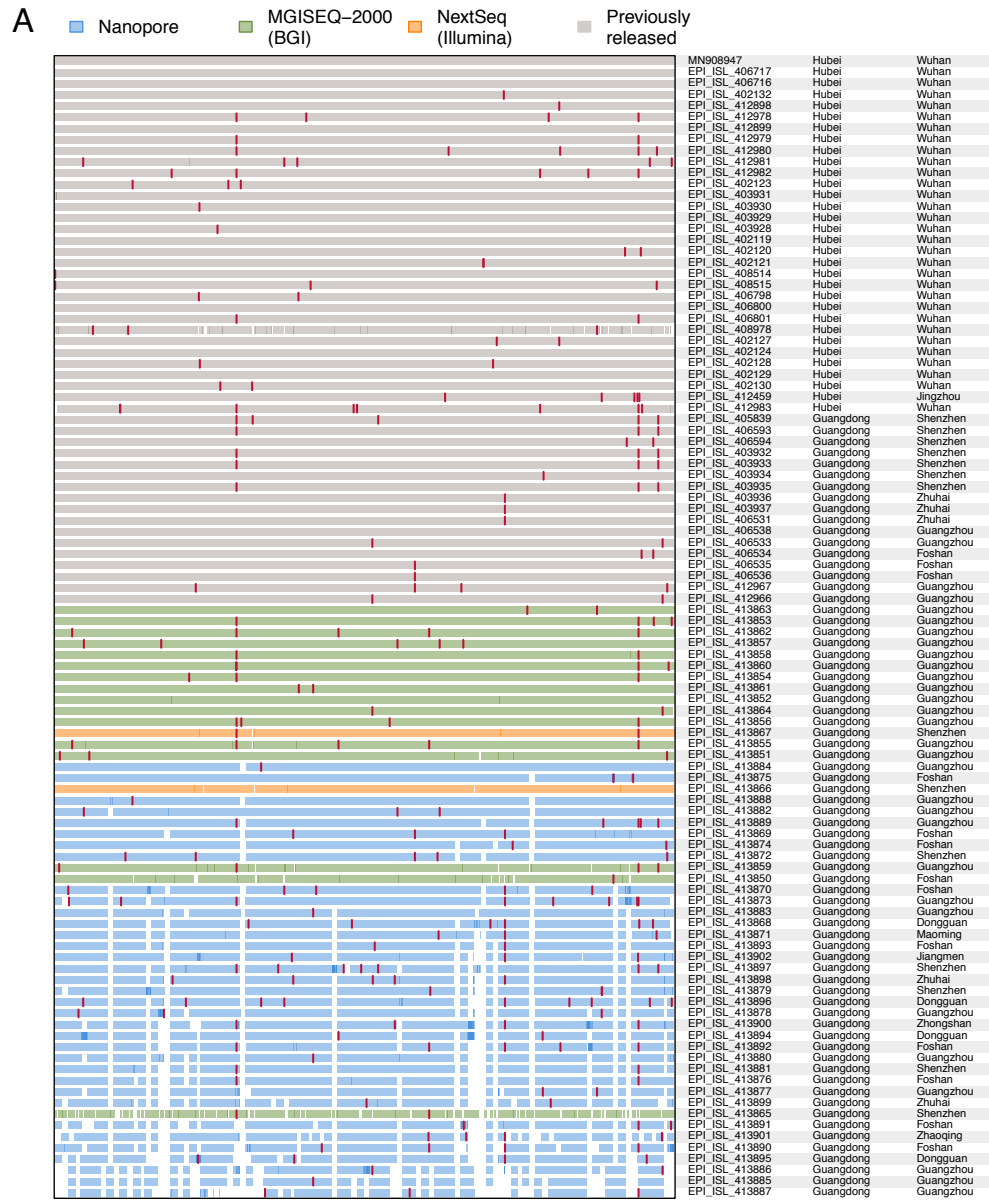
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**Data S1.1: Detailed summary of the 53 genomes reported here.**

The figure shows from left to right: (i) GISAID accessions; (ii) sample codes; (iii) patient codes; (iv) prefecture; (v) genome coverage map and locations of SNPs (with respect to the reference genome MN908947.3), coloured by sequencing platform, with the frequency of SNPs shown below; (vi) genome coverage; (vii) RT-PCR Ct value, coloured by disease severity and (viii) the symptom onset (asterisks) and collection dates (see legend for the sample types). Where the date of symptom onset is unknown a dashed line is drawn.



**Data S1.2: Genome coverage map for genomes reported here and 49 previously reported genomes from Hubei and Guangdong.**

Single nucleotide polymorphisms (with respect to MN908947.3) are coloured in red. Each of the 53 genomes reported here is coloured according to sequencing approach. GISAID accession numbers and sampling locations (province and prefecture) are displayed on the right. (B) Genomic location and frequency of single nucleotide polymorphisms (with respect to the reference genome MN908947.3) among the 102 genomes in panel A.