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Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in Europe is driven by nosocomial spread

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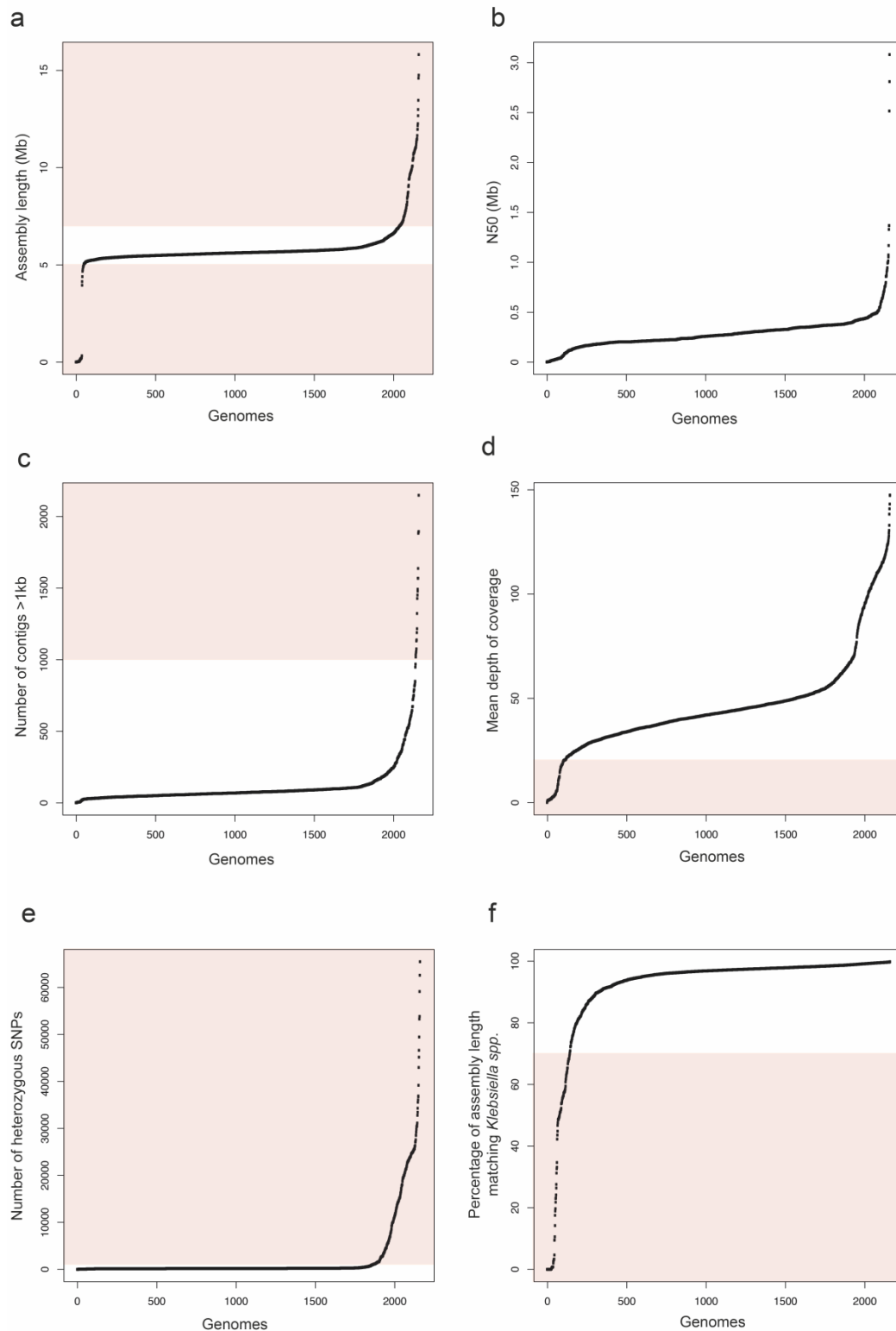
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Supplementary Information of

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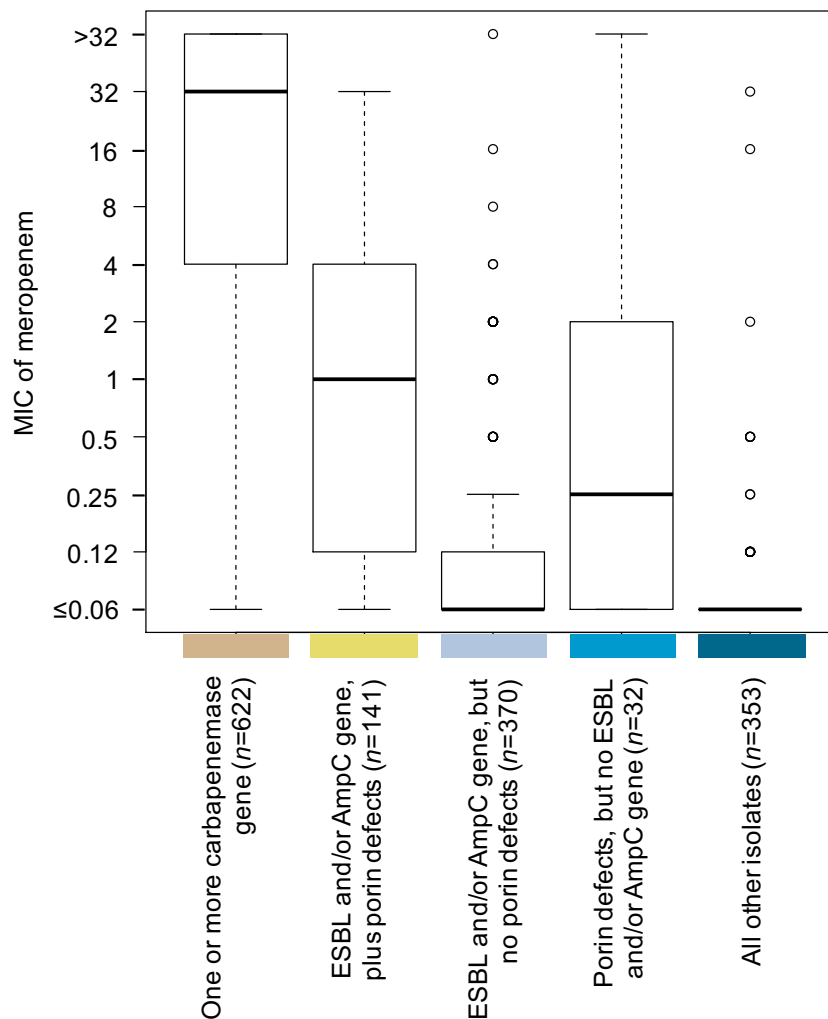
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Supplementary Figures

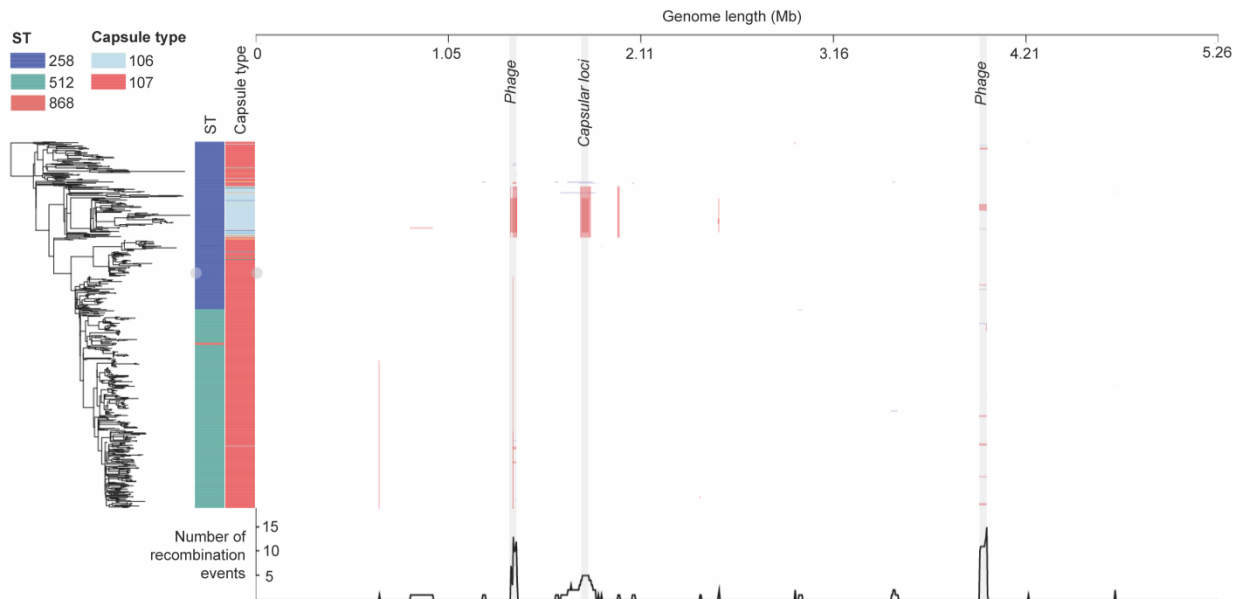


Supplementary Figure 1. Quality control (QC) data for all 2162 sequenced isolates submitted as *K. pneumoniae*. Plots show the assembly length (a), N50 values of the assemblies (b), the number of contigs per assembly over 1kb (c), the mean depth of coverage (d), the number of

heterozygous SNPs called by mapping reads to a reference (e), and the percentage of the assembly length matching *Klebsiella spp.* using MASH (f).



Supplementary Figure 2. Boxplots show minimum inhibitory concentration (MIC) values for meropenem obtained by centralised re-testing of 1518/1649 *K. pneumoniae sensu stricto* isolates that are divided according to the beta-lactam resistome groupings. The y-axis values are treated as if they increment equally. The boxes represent the interquartile range of values in each category and the bold line within each box shows the median value. Whiskers show the upper and lower values that are still within 1.5x the value of the interquartile range above and below the third and first quartiles, respectively. Outliers, represented by small circles, are values outside of these ranges. The boxplots from left to right represent 622, 141, 370, 32 and 353 values.



Supplementary Figure 3. Recombination events in the ST258/512 lineage. Phylogenetic tree of 651 isolates belonging to ST258, ST512 and ST868, and the predicted recombined regions, as visualised in Phandango. Genomic regions predicted to have been involved in at least five recombination events are highlighted. Only isolates with a capsule (K-) type of 106 or 107 (which constitute the majority) are labelled in the key.

Supplementary Tables

Supplementary Tables 2, 3, 4 and 6 are provided separately due to their large size.

Supplementary Table 1. Summary of the quality control (QC) results for all sequenced isolates submitted as *K. pneumoniae*.

Criteria	No. (and %) of <i>K. pneumoniae</i> passed from total of 2162
Assembly length (5-7Mb)	2045 (94.6%)
No. of SPAdes contigs (>1000bp) < 1000	2141 (99.0%)
90% assembly length in contigs > 1000bp	2095 (96.9%)
Correct species match using MASH (raw reads)	2099 (97.1%)
Correct species match using MASH (SPAdes assembly)	2062 (95.4%)
Correct species match using MASH (individual SPAdes contigs)	2106 (97.4%)
Percentage length of individual SPAdes contigs with top match to correct taxa > 70	2020 (93.4%)
No. of heterozygous SNPS < 1000	1863 (86.2%)
Mean depth of coverage > 20x	2058 (95.2%)
All criteria fulfilled	1717 (79.4%)

Supplementary Table 5. Concordance between the PCR results obtained by the national expert laboratories (NELs) and *in silico* results from the genome sequencing data for each of the four major carbapenemase genes (*bla*_{KPC-like}, *bla*_{NDM-like}, *bla*_{VIM-like} and *bla*_{OXA-48-like}). Results are shown for the 944 isolates submitted as carbapenem-non-susceptible only (PCR was not performed on isolates submitted as susceptible). False positive and negative results are calculated for the PCR results with the *in silico* results being the reference.

Carbapenemase gene	<i>bla</i>_{KPC-like}	<i>bla</i>_{NDM-like}	<i>bla</i>_{VIM-like}	<i>bla</i>_{OXA-48-like}
No. isolates positive <i>in silico</i>	305	76	53	238
No. isolates negative <i>in silico</i>	639	868	891	706
No. isolates positive <i>in silico</i> but negative with PCR	5	5	2	8
No. isolates negative <i>in silico</i> but positive with PCR	6	9	7	8
False negative rate (%)	1.64	6.58	3.77	3.36
False positive rate (%)	0.94	1.04	0.79	1.13
Total no. (and %) of concordant isolates	933 (98.8%)	930 (98.5%)	935 (99.0%)	928 (98.3%)

Supplementary Table 7. URLs to phylogenetic analysis and corresponding metadata of isolates submitted by each of the participating countries, available using Microreact. Data for countries that contributed a minimum of 5 isolates to the collection analysed here are included.

Country	URL
Austria	https://microreact.org/project/EuSCAPE_Austria
Belgium	https://microreact.org/project/EuSCAPE_Belgium
Croatia	https://microreact.org/project/EuSCAPE_Croatia
Czech Republic	https://microreact.org/project/EuSCAPE_CzechRepublic
Denmark	https://microreact.org/project/EuSCAPE_Denmark
Estonia	https://microreact.org/project/EuSCAPE_Estonia
France	https://microreact.org/project/EuSCAPE_France
Germany	https://microreact.org/project/EuSCAPE_Germany
Greece	https://microreact.org/project/EuSCAPE_Greece
Hungary	https://microreact.org/project/EuSCAPE_Hungary
Ireland	https://microreact.org/project/EuSCAPE_Ireland
Israel	https://microreact.org/project/EuSCAPE_Israel
Italy	https://microreact.org/project/EuSCAPE_Italy
Lithuania	https://microreact.org/project/EuSCAPE_Lithuania
Luxembourg	https://microreact.org/project/EuSCAPE_Luxembourg
Malta	https://microreact.org/project/EuSCAPE_Malta
Montenegro	https://microreact.org/project/EuSCAPE_Montenegro
Norway	https://microreact.org/project/EuSCAPE_Norway
Poland	https://microreact.org/project/EuSCAPE_Poland
Portugal	https://microreact.org/project/EuSCAPE_Portugal
Romania	https://microreact.org/project/EuSCAPE_Romania
Serbia	https://microreact.org/project/EuSCAPE_Serbia
Slovakia	https://microreact.org/project/EuSCAPE_Slovakia
Slovenia	https://microreact.org/project/EuSCAPE_Slovenia
Spain	https://microreact.org/project/EuSCAPE_Spain
Turkey	https://microreact.org/project/EuSCAPE_Turkey
United Kingdom	https://microreact.org/project/EuSCAPE_UK

Supplementary Note

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