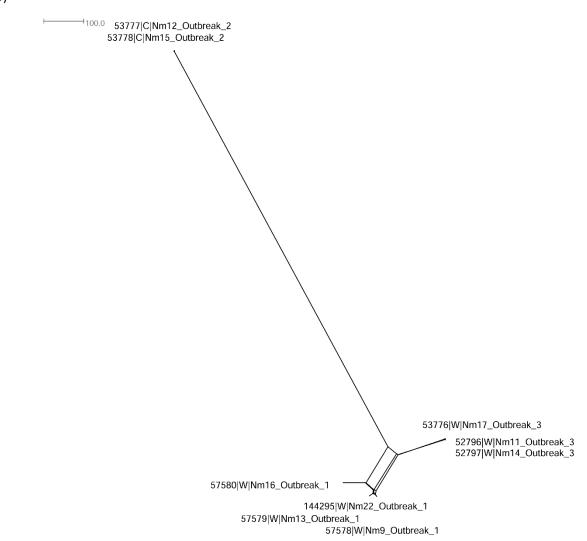


a)



Supplementary Figure 1. *Neisseria meningitidis* genome comparison. Neighbornet network showing the genomic relatedness of a) all isolates and b) outbreak isolates in 1,422 core loci of *Neisseria meningitidis* v2 (Jolley KA, Bray JE, Maiden MCJ. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Res. 2018;3:124). PubMLST ID, capsule group, alias and outbreak designation (if any) is shown for each node.