

SUPPLEMENTARY FIGURE 4 LEGEND

Panel A: Maximum likelihood phylogenetic tree of 22 *Neisseria gonorrhoeae* sequences after filtering for recombination. All major nodes had >70% bootstrap support. Isolates from the same couple are numbered on the tree, along with in silico molecular typing data for the two-gene multiantigen sequence typing (NG-MAST) and the seven-gene multilocus sequence typing (MLST) schemes. The same NG-MAST or MLST types are represented by the same colours.

Of note, couples 2 and 5 have close genomic relatedness, as do couples 7 and 10, raising the possibility of direct gonorrhoea transmission between these couples. We reviewed these cases and found that the genomically-related couples presented to the clinic more than six months apart (i.e. the men in these couples presented on the same day, but the couples presented more than six months apart), making direct transmission between the couples unlikely.

Panel B: Box plots illustrating the median and interquartile range (IQR) for pairwise SNP distances between paired isolates from couples either within the same (median 6 SNPs; IQR 2-8 SNPs) or different (median 1476 SNPs; IQR 811-1593 SNPs) sexual partnerships, after filtering for recombination. Whiskers represent the highest and lowest values within $1.5 \times \text{IQR}$ of the upper and lower quartiles, and dots represent pairwise SNP distances. When interpreting pairwise SNP distances, data should be interpreted in the context of known epidemiological associations. However, for reference, a previous paper suggested that a pairwise SNP threshold of 11 SNPs was indicative of transmission, in their local context.¹

REFERENCES

1. De Silva D, Peters J, Cole K, et al. Whole-genome sequencing to determine transmission of *Neisseria gonorrhoeae*: an observational study. *The Lancet Infectious diseases* 2016;16(11):1295-303. doi: 10.1016/S1473-3099(16)30157-8 [published Online First: 2016/10/30]