

Sup. Material for: Visual linkage and interactive features of Evidente for an enhanced analysis of SNP-based phylogenies

M. Witte Paz¹, T. Harbig¹, D. Varga¹, E. Kränzle¹, and K. Nieselt¹

¹ University of Tübingen, Institute for Bioinformatics and Medical Informatics, Tübingen, Germany

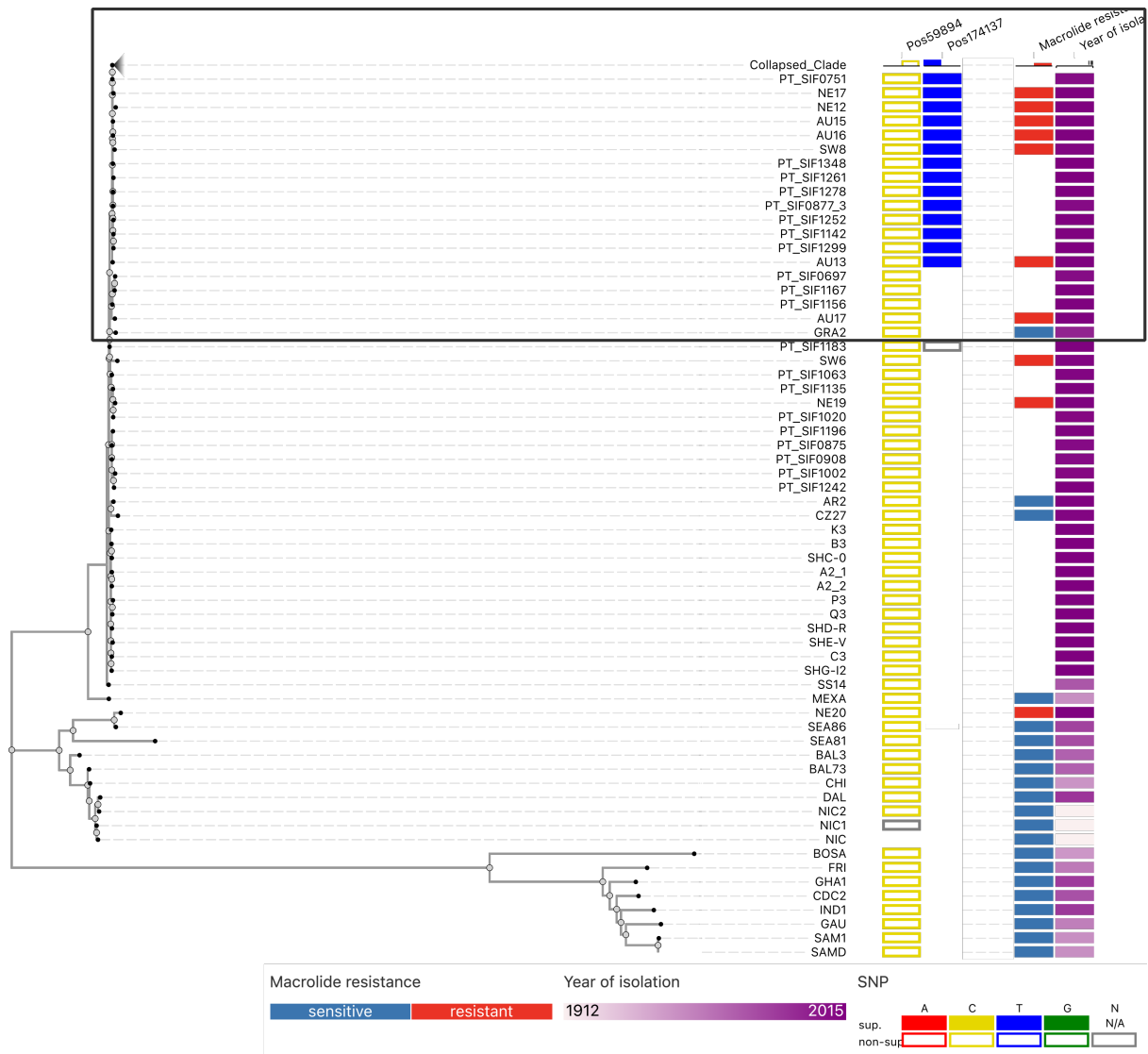


Figure S1: Genomic data of *Treponema pallidum* [PDSBG*22] visualized in Evidente. It also visualizes the SNPs found in two genomic positions as well as two metadata columns (macrolide resistance and year of isolation). The black rectangle shows the area where Figure 2 was zoomed into.

References

- [PDSBG*22] PLA-DÍAZ M., SÁNCHEZ-BUSÓ L., GIACANI L., ŠMAJS D., BOSSHARD P. P., BAGHERI H. C., SCHUENEMANN V. J., NIESELT K., ARORA N., GONZÁLEZ-CANDELAS F.: Evolutionary processes in the emergence and recent spread of the syphilis agent, *Treponema pallidum*. *Molecular biology and evolution* 39, 1 (2022), msab318. [1](#)