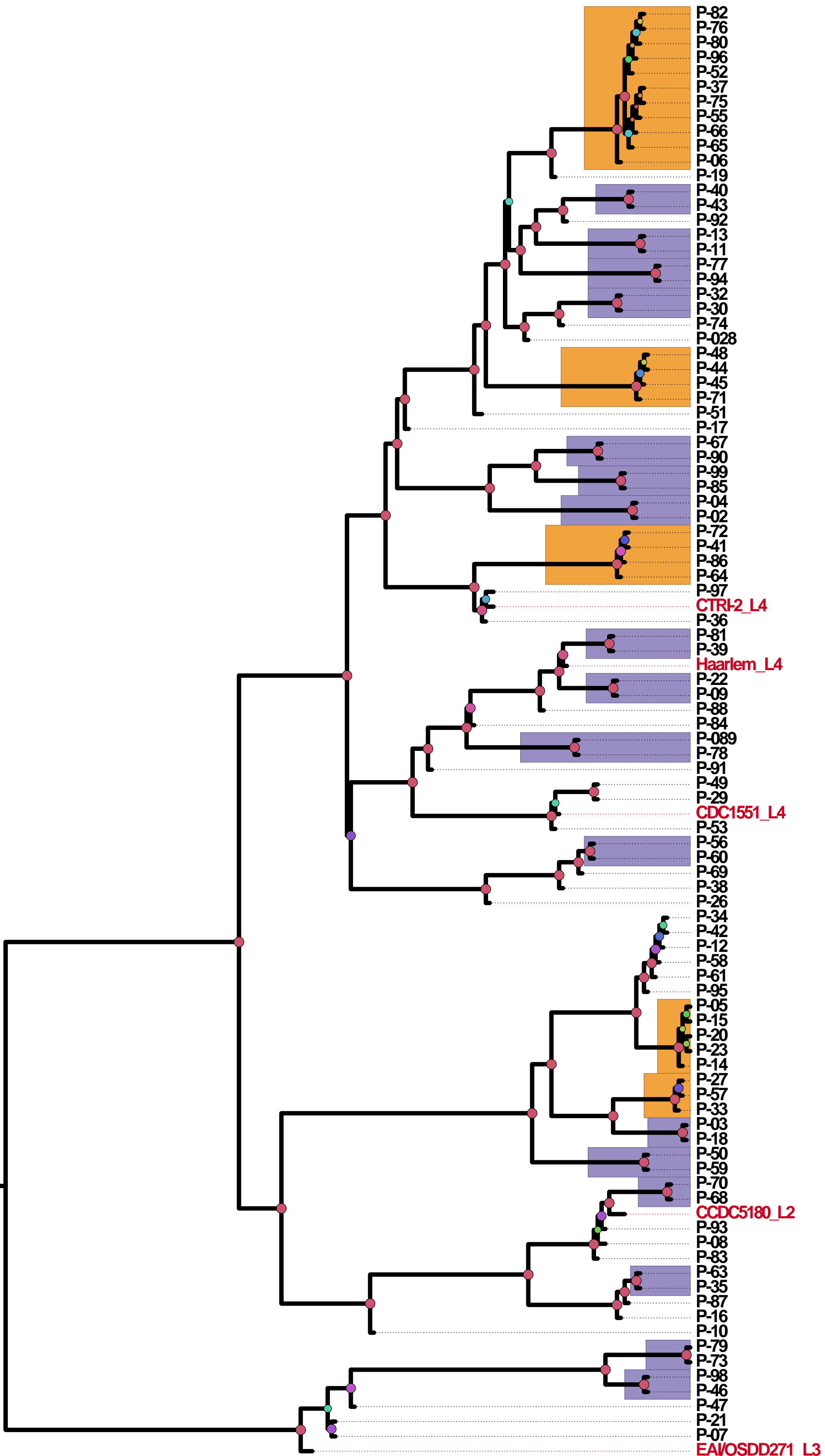


## **Transmission dynamics study of tuberculosis isolates with whole genome sequencing in southern Sweden**

Nader Alaridah<sup>1</sup>, Erika Tång Hallbäck<sup>5</sup>, Jeanette Tångrot<sup>4</sup>, Niclas Winqvist<sup>2,3</sup>, Erik Sturegård<sup>3</sup>, Kerstin Florén-Johansson<sup>5</sup>, Bodil Jönsson<sup>5</sup>, Erik Tenland<sup>1</sup>, Christina Welinder-Olsson<sup>5</sup>, Patrik Medstrand<sup>6</sup>, Bertil Kaijser<sup>5</sup>, Gabriela Godaly<sup>1</sup>

<sup>1</sup>Laboratory medicine, Department of Microbiology, Immunology and Glycobiology, Lund University, Lund, Sweden. <sup>2</sup>Regional Office for Infectious Disease Control and Prevention, Malmö, Sweden. <sup>3</sup>Translational Medicine, Clinical Infection medicine, Lund University, Sweden, <sup>4</sup>National Bioinformatics Infrastructure Sweden (NBIS), SciLifeLab, Department of Molecular Biology, Computational Life Science Cluster, Umeå University, Sweden, <sup>5</sup>Department of Infectious Diseases, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden. <sup>6</sup>Translational medicine, Department of Clinical Virology, Lund University, Malmö, Sweden.

**Supplemented Figure 1.** Phylogenetic tree showing that four of the seven main global lineages of *M. tuberculosis* circulated in Scania county during the time of the sampling. 62 % of the isolates belonged to lineage 4 (Europe, America and Africa) and 30 % belonged to lineage 2 (East Asia), with lesser representation from lineage 3 (8 %, India and East Africa).



5.0E-5