

Table S1. Distribution of the main phylogenetic *Mycobacterium tuberculosis* lineages according to molecular clusters involving either non-European-born tuberculosis (TB) cases only, European-born TB cases only, or mixed clusters involving both non-European-born and European-born TB cases.

Cluster category	No. of clusters	No. of patients	No. of patients (%) ¹				
			Lineage 1	Lineage 2	Lineage 3	Lineage 4	HIV-infected ²
Non-EU-born only	16	38	5 (13.2)	6 (15.8)	5 (13.2)	22 (57.9)	12 (31.6)
Mixed	8	26	0	0	0	26 (100)	5 (19.2)
EU-born only	11	26	0	0	0	26 (100)	4 (15.4)

P values by Fisher's exact test: ¹ $p < 0.0001$ across lineages and cluster categories; ² $p = 0.34$ across HIV status and cluster categories

EU, European

Lineage 1: Indo-Oceanic lineage; Lineage 2: East-Asian lineage (includes Beijing strains); Lineage 3: Delhi/CAS; Lineage 4: Euro-American lineage