

Legends to supplementary materials

Supplementary Figure 1: Maximum likelihood tree of 164 Mbov strains built from 15,035 SNP positions, including the 131 strains from our study and 33 strains selected to reflect clades described previously (61). Scale bar indicates the likelihood of per-site substitution. Circles on nodes indicate resampling support of at least 90% (green circles) or at least 70% (black circles).

Supplementary Table 1: Sample metadata including host and year of isolation, WGS clusters, MIRU-VNTR types from miru-vntrplus.org, spoligotype data deduced from the SITVIT (IT) and mbovis.org (SB) databases, and ENA SRA archive accession numbers.

see supplementary Excel file

Supplementary Table 2: Number and host species of 131 animal and human Mbov strains investigated in the study by WGS and the collection used for MIRU-VNTR HGDI determination

Supplementary Table 3: Determination of MIRU-VNTR allelic heterogeneity (53) at each locus amongst 121 genetically unrelated Mbov strains isolated from animals and humans in Germany (1999 – 2017) including one Mbov BCG reference strain

Supplementary Table 4: Discriminatory power index (53) of 24 +1 MIRU/VNTR loci for a collection of 121 Mbov strains of human and animal origin (including one Mbov BCG reference strain)

Supplementary Table 5: Spoligotypes of 131 Mbov strains isolated in Germany from 1999 - 2017 and countries of isolation (ISO3166-1 alpha-3) already reported in SITVIT and mbovis.org databases, respectively

see supplementary Excel file

Supplementary Table 6: Mbov clades published previously (61) and corresponding d350 groups and strains from this study.

Supplementary Table 7: Comparison of Mbov clades published previously (61) and WGS d350 groups of the maximum likelihood phylogenetic tree formed with 131 German Mbov strains (present study)