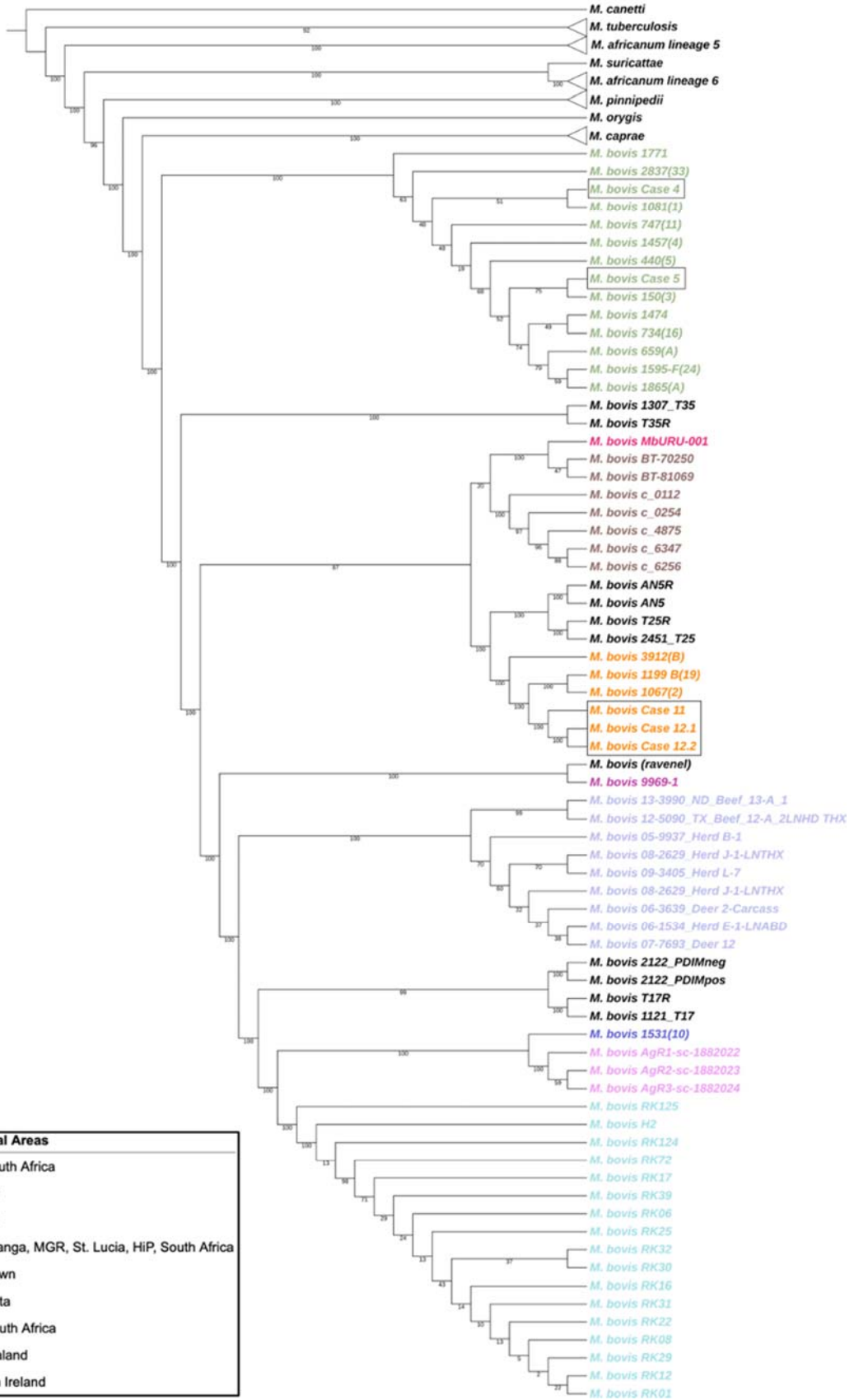


Free scale: 0.1



Geographical Areas	
■	KNP, South Africa
■	Uruguay
■	Panama
■	Mpumalanga, MGR, St. Lucia, HiP, South Africa
■	Cape Town
■	Minnesota
■	KZN, South Africa
■	New Zealand
■	Northern Ireland

Figure S1: Molecular phylogenetic analysis by maximum likelihood method with 1000 bootstrap replicates showing the relationship of the five wild dog *M. bovis* isolates to the 108 other *Mycobacterium* isolates from different animal hosts. The bootstrap values are shown next to the nodes. The phylogenetic tree was produced by RaxML and based on variable sites identified when compared to the *M. tuberculosis* H37Rv reference sequence (Stamatakis, 2006, 2015).