



**Figure S1.** Phylogenetic tree and genotypes of 284 *T. asahii* clinical isolates inferred by the Neighbor-joining method. Reference sequences GenBank accession numbers G1: AB066386, G2: AB072606, G3: AB066397, G4: AB180191, G5: AB071387, G6: AB180192, G7: AB180194, G8: AB439002, G9: AB439003, G10: EU441158, G11: EU441160, G12: JF412789, G13: KJ176993, G14: KJ176992 and G15: KJ176995.

**Footnotes:** In total, 485 nucleotides were studied and 72 variable sites were found after excluding gaps position (haplotype diversity of 0.4525). Were found: (i) 216 clinical isolates that aligned with the G1 reference sequence (GenBank accession number: AB066386) and the putative G11 reference sequence (GenBank accession number: EU441160), (ii) 28 clinical isolates that aligned with the G3 reference sequence (GenBank accession number: AB066397); (iii) eight clinical isolates that aligned with the G4 reference sequence (GenBank accession number: AB180191); (iv) 21 clinical isolates that aligned with the G5 reference sequence (GenBank accession number: AB071387); (v) 11 clinical isolates that aligned with the G7 reference sequence (GenBank accession number: AB180194). Notably, no clinical isolate tested in our collection grouped with the reference sequences for GenBank accession nos. G2: AB072606, G6: AB180192, G8: AB439002, G9: AB439003, G10: EU441158, G12: JF412789, G13: KJ176993, G14: KJ176992 and G15: KJ176995.