

Supplementary Table 5. Results of the pairwise comparison of recovered ACDCT and MLST genes from the WGS data for each *T. pallidum* specimen

Specimen ID	MLST and other Typing genes recovered with $\geq$ 70% coverage to the reference gene	Percentage of sequence similarity <sup>a</sup> compared to the reference gene (MLST allele <sup>b</sup> )
OS-12-CSF	<i>rpsA</i>	100%
	<i>tp0136</i>	X <sup>c</sup>
	<i>tp0548</i>	100% (1)
	<i>tp0705</i>	100% (1)
OS-12-VF	<i>rpsA</i>	99.96%
	<i>tprG</i>	99.91%
	16S rRNA	100%
	23S rRNA	100%
	<i>tp0136</i>	100% (19)
	<i>tp0548</i>	100% (1)
	<i>tp0705</i>	100% (1)
OS-4-B	16S rRNA	100%
	23S rRNA	100%
	<i>tp0548</i>	100% (3)
OS-18-VF	<i>tprJ</i>	100%
	16S RNA	100%
	<i>tp0136</i>	99.89% (6 <sup>d</sup> )
	<i>tp0548</i>	100% (3)
	<i>tp0705</i>	100% (1)

Abbreviations: ACDCT, augmented CDC typing system; B, blood; CSF, cerebrospinal; VF, vitreous fluid.

<sup>a</sup>Sequence percent similarity was determined from the *de novo* assemblies using BLAST

<sup>b</sup>MLST alleles were determined by SRSRT2 using *T. pallidum* short read sequences

<sup>c</sup>MLST allelic profile for *tp0136* could not be determined

<sup>d</sup>Closest match for *tp0136* was to allele 6 with 1 indel mutation