Table S2. Conservation of M23 peptidase domain-bearing peptides predicted from *T. pallidum* and *T. denticola* genomes. *T. pallidum* proteins were identified by BLAST analyses using the amino acid sequence of Tp0155 against the *T. pallidum* genome (TIGR Comprehensive Microbial Resource). % identity of corresponding *T. pallidum* and *T. denticola* genes is included. TDE1136 was omitted from analysis as no similar truncated sequence is present in the *T. pallidum* genome.

T. denticola **protein**	**Most similar *T. pallidum* protein**	**LysM domains**	**M23 peptidase domain**	**% identity**
TDE2318	Tp0155	2	1	42.7
TDE1738	Tp0706	1	1	50
TDE2753	Tp0864	2	1	31.6
TDE0110	Tp0049	0	1	47.1
TDE1297	Tp0444	2	1	32.1
TDE2189	Tp0702	0	1	21.6

Fig. S4. Dose-dependent binding to matrix (♦) or plasma fibronectin (■), or to BSA blocked wells alone (Δ) of recombinant *T. denticola* peptides with homology to *T. pallidum* Tp0155. (a) rTDE2318 (b) rTDE2753 (c) rTDE1738 (d) rTDE1297 (e) rTDE1136. Matrix or plasma fibronectin (0 or 5 μg), coated onto plastic wells, was incubated with increasing concentrations of recombinant *T. denticola* proteins and binding was detected with anti tetra His and HRP conjugated secondary antibodies and then color reagent *o*-phenylenediamine (A_{490}). Error bars indicate ± SD of the mean from triplicates of a representative experiment.

Supplemental data Fig. S4 (b/w)