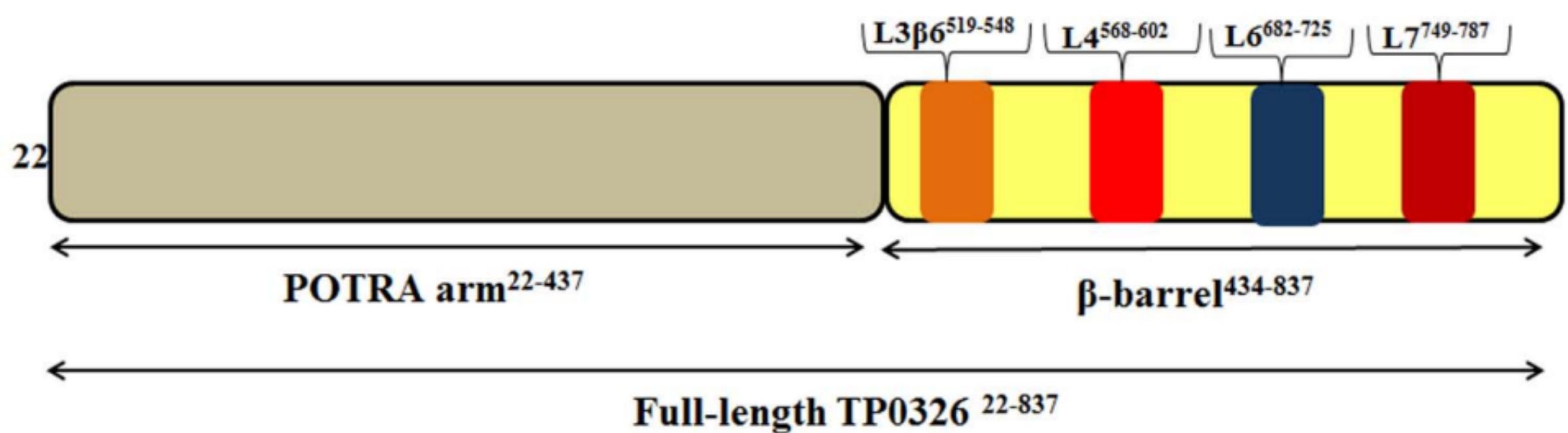
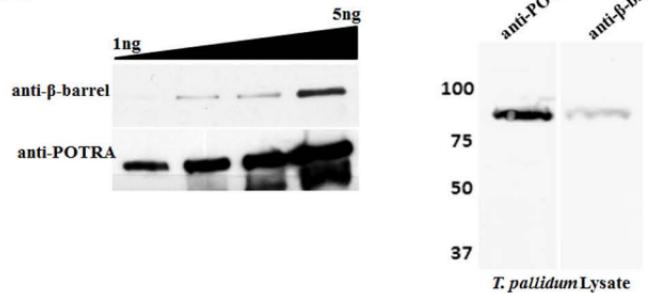
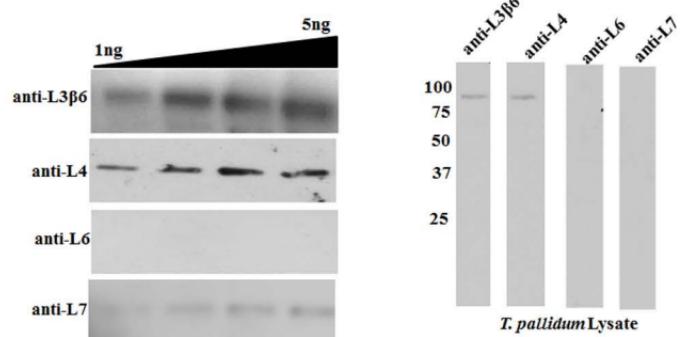
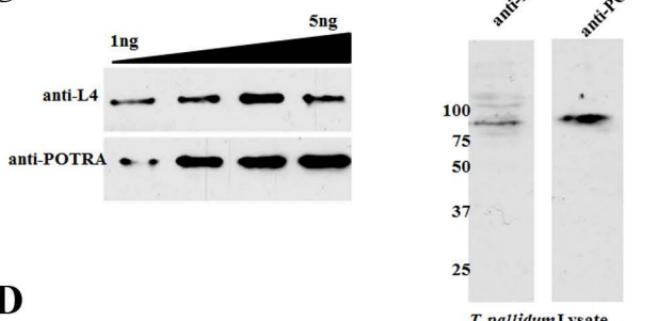
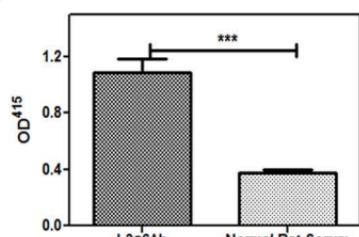


**Supplemental Table . List of constructs and primers**

Primer	Description	Sequence
Full length TP0326-F	amplification of <i>TP0326</i>	AAAGCTAGCATGCAGGCAAACGACAATTGGTAC
Full length TP0326-R	amplification of <i>TP0326</i>	GGGAAGCTCAAATTATTACCGTGAACGACAACACAA
L3β6-F	amplification of <i>L3β6</i>	AAAGGATCCATGGCAACGGGCTG
L3β6-R	amplification of <i>L3β6</i>	CCCCTGAG GCGGAATACTTGAG
L4-F	amplification of <i>L4</i>	AAAGGATCCAT ATTAGGGTGAAC
L4-R	amplification of <i>L4</i>	CCCCTGAGCGTCCAAAACGA
L6-F	amplification of <i>L6</i>	AAAGGATCCATGGTTCAAACGTATTAT
L6 <sup>Ab</sup> -F	amplification of L6 <sup>Ab</sup>	AAAGGATCCATGGACGGAGGAAAAGCGAA
L6 & L6 <sup>Ab</sup> -R	amplification of L6 & L6 <sup>Ab</sup>	CCCCTCGAGGTCTCCGGTGTTTTT
L7-F	amplification of <i>L7</i>	AAAGGATCCATGGATGCGGCAATGGTGTAC
L7-R	amplification of <i>L7</i>	CCCCTGAG CAGTCCTCAGAGCT
326 <sup>Pel</sup> -F	amplification of 326 <sup>Pel</sup>	AAAGGATCCCATGCAGGCAAACGACAATTGG
326 <sup>Pel</sup> -R	amplification of 326 <sup>Pel</sup>	GGGAAGCTCAAATTATTACCGTGAACGACAACACAA
POTRA-F	amplification of <i>POTRA</i>	CCCGCTAGCATGCAGGCAAACGACAATTGGTAC
POTRA-R	amplification of <i>POTRA</i>	CCCAAGCTTCTGCTCCTCACATTCA
β-barrel-F	amplification of <i>β-barrel</i>	AAAGCTAGCATGAACGTTGAAGAACAAATCG
β-barrel-R	amplification of <i>β-barrel</i>	TTTAAGCTTCAGATTGTTAACGGTAAA
β-barrel-F1	amplification of <i>β-barrel</i> from Cali-77 and Cali-84	AATGTGGAGGAGCAGTCGACG
β-barrel-R1	amplification of <i>β-barrel</i> from Cali-77 and Cali-84	CTACAAATTATTACCGTGAAC
L4 <sup>Gln593</sup> (+)	Mutagenesis of <i>L4</i>	CAGCCCTCGACCAGACCGTAAAGAG
L4 <sup>Gln593</sup> (-)	Mutagenesis of <i>L4</i>	TCTTTACGGTCTGGTCGAAGGGCTG
Skp of <i>E. coli</i> -F	amplification of <i>skp</i>	GATAGCTAGCGCTGACAAATTGCAATCGTC
Skp of <i>E. coli</i> -R	amplification of <i>skp</i>	GATAAAGCTTTAACCTGTTCACTACGTCG

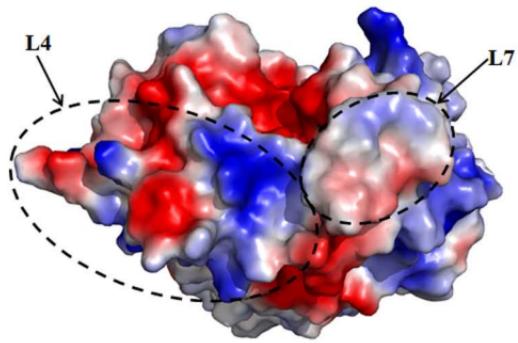
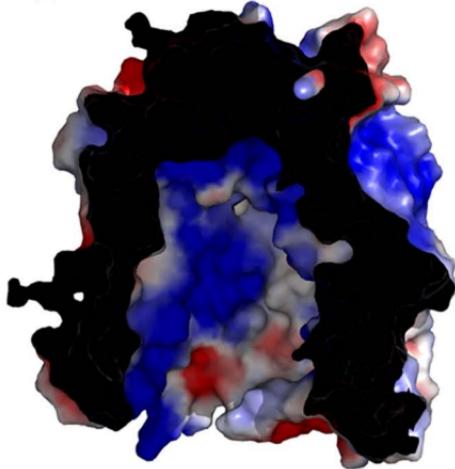
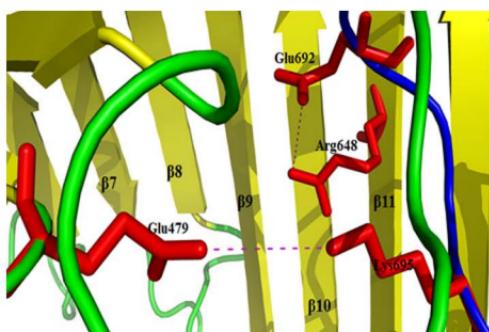


**Supplemental Figure1.** Schematic representation of TP0326 recombinant constructs utilized in this study.

**A****B****C****D**

**Supplemental Figure 2. Sensitivity and specificity of antisera.** (A) Immunoblot reactivity of rat anti- $\beta$ -barrel and -POTRA antisera against graded amounts of recombinant full-length TP0326 and *T. pallidum* whole cell lysates (1  $\times$  10<sup>8</sup> *Tp* per lane). (B) Immunoblot reactivity of rat anti-L3 $\beta$ 6, L4, L6, and -L7 antisera against graded amounts of recombinant  $\beta$ -barrel and *T. pallidum* whole cell lysates (1  $\times$  10<sup>8</sup> *Tp* per lane). (C) Immunoblot reactivity of rabbit anti-L4 and anti-POTRA against recombinant full-length TP0326 and *T. pallidum* whole cell lysates (1  $\times$  10<sup>8</sup> *Tp* per lane). (D) Reactivity of rat anti- L3 $\beta$ 6 and normal rat antisera against L3 peptide.

**Supplemental Figure 3.** Sequence alignment of the  $\beta$ -barrel domains of *T. pallidum* (Tp), *N. gonorrhoeae* (Ng), *H. ducreyi* (Hd) and *E. coli* (Ec) BamA. The multiple sequence alignment was performed using the ClustalW server (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>). Identical positions are indicated by asterisks, while strongly homologous residues are denoted by colons. Weakly homologous residues are marked by single dots. The  $\beta$ -1 and  $\beta$ -16 strands of the TP0326  $\beta$ -barrel are indicated by yellow arrows. The residues essential for lateral opening of *E. coli* BamA are highlighted in red. The L4, L6 and L7 loops of TP0326 are depicted by black lines, whereas the corresponding loops in Ng, Hd, and Ec BamAs are within the blue box.

**A****B****C**

**Supplemental Figure 4.** Electrostatic potential of the TP0326 β-barrel viewed from the extracellular face (A) and inside the β-barrel (B). (C) Salt bridges (dashed lines) predicted by ModWeb to stabilize L6 to L3 and β11.

# Supplemental Figure 5A

Nichols	1	MLKKASAFLIASCCVMSLAWAQANDNWYEGKPIASAISFEGLEYIARGQOLDTIFSQYKGQK
SS14	1	MLKKASAFLIASCCVMSLAWAQANDNWYEGKPIASAISFEGLEYIARGQOLDTIFSQYKGQK
Dal-1	1	MLKKASAFLIASCCVMSLAWAQANDNWYEGKPIASAISFEGLEYIARGQOLDTIFSQYKGQK
Chicago	1	MLKKASAFLIASCCVMSLAWAQANDNWYEGKPIASAISFEGLEYIARGQOLDTIFSQYKGQK
Mexico	1	MLKKASAFLIASCCVMSLAWAQANDNWYEGKPIASAISFEGLEYIARGQOLDTIFSQYKGQK

Nichols	61	WTYELYLEILQKVVDLEYFSEVSPKAVENTDPEYQYVMLQFTVKERPSVKGIKMVGNSQIR
SS14	61	WTYELYLEILQKVVDLEYFSEVSPKAVENTDPEYQYVMLQFTVKERPSVKGIKMVGNSQIR
Dal-1	61	WTYELYLEILQKVVDLEYFSEVSPKAVENTDPEYQYVMLQFTVKERPSVKGIKMVGNSQIR
Chicago	61	WTYELYLEILQKVVDLEYFSEVSPKAVENTDPEYQYVMLQFTVKERPSVKGIKMVGNSQIR
Mexico	61	WTYELYLEILQKVVDLEYFSEVSPKAVENTDPEYQYVMLQFTVKERPSVKGIKMVGNSQIR

Nichols	121	SGDLLSKILLKKGDIYNEVKMKVQESLRRHYLDQGYAAVKISCEAKTEAGGGVVVQFTIQ
SS14	121	SGDLLSKILLKKGDIYNEVKMKVQESLRRHYLDQGYAAVKISCEAKTEAGGGVVVQFTIQ
Dal-1	121	SGDLLSKILLKKGDIYNEVKMKVQESLRRHYLDQGYAAVKISCEAKTEAGGGVVVQFTIQ
Chicago	121	SGDLLSKILLKKGDIYNEVKMKVQESLRRHYLDQGYAAVKISCEAKTEAGGGVVVQFTIQ
Mexico	121	SGDLLSKILLKKGDIYNEVKMKVQESLRRHYLDQGYAAVKISCEAKTEAGGGVVVQFTIQ

Nichols	181	EGKQTVVVSRIQFKGNKAFTESVLKKVLSTQEARFLTSGVFKENALEADKAAVHSYYAERG
SS14	181	EGKQTVVVSRIQFKGNKAFTESVLKKVLSTQEARFLTSGVFKENALEADKAAVHSYYAERG
Dal-1	181	EGKQTVVVSRIQFKGNKAFTESVLKKVLSTQEARFLTSGVFKENALEADKAAVHSYYAERG
Chicago	181	EGKQTVVVSRIQFKGNKAFTESVLKKVLSTQEARFLTSGVFKENALEADKAAVHSYYAERG
Mexico	181	EGKQTVVVSRIQFKGNKAFTESVLKKVLSTQEARFLTSGVFKENALEADKAAVHSYYAERG

Nichols	241	YIDARVEGVAKTVDKKTDASRNLVTLTYTVVEGEQYRYGGVTIVGNQIFSTEELQAKIRL
SS14	241	YIDARVEGVAKTVDKKTDASRNLVTLTYTVVEGEQYRYGGVTIVGNQIFSTEELQAKIRL
Dal-1	241	YIDARVEGVAKTVDKKTDASRNLVTLTYTVVEGEQYRYGGVTIVGNQIFSTEELQAKIRL
Chicago	241	YIDARVEGVAKTVDKKTDASRNLVTLTYTVVEGEQYRYGGVTIVGNQIFSTEELQAKIRL
Mexico	241	YIDARVEGVAKTVDKKTDASRNLVTLTYTVVEGEQYRYGGVTIVGNQIFSTEELQAKIRL

Nichols	301	KRGAIMNMVAFEQGFQALADAYFENGYSNYLNKEEHRDTAEKTLTSFKITVVERERSHVE
SS14	301	KRGAIMNMVAFEQGFQALADAYFENGYSNYLNKEEHRDTAEKTLTSFKITVVERERSHVE
Dal-1	301	KRGAIMNMVAFEQGFQALADAYFENGYSNYLNKEEHRDTAEKTLTSFKITVVERERSHVE
Chicago	301	KRGAIMNMVAFEQGFQALADAYFENGYSNYLNKEEHRDTAEKTLTSFKITVVERERSHVE
Mexico	301	KRGAIMNMVAFEQGFQALADAYFENGYSNYLNKEEHRDTAEKTLTSFKITVVERERSHVE

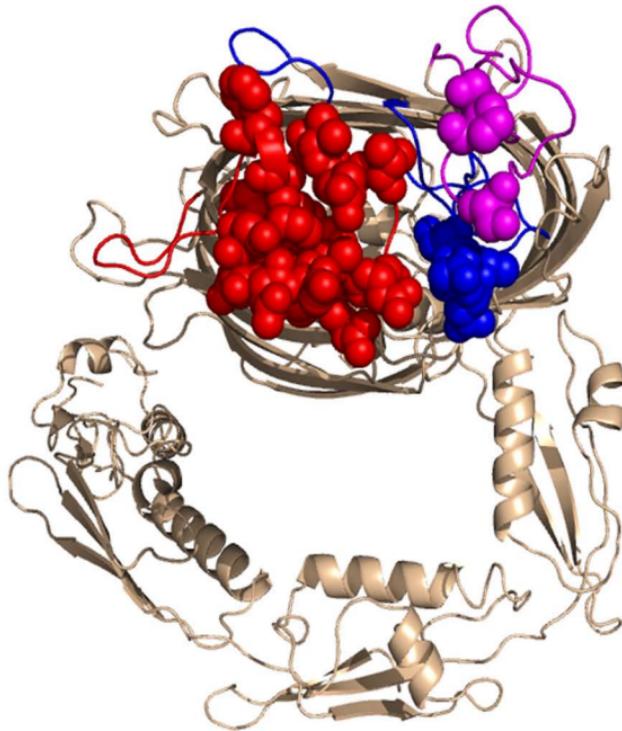
Nichols	361	HIIIKGTKNTKDEVILREMLLKPGDVFSKSFKTDSLRLNLFNLRYFSSLVPDVRPGSEQDL
SS14	361	HIIIKGTKNTKDEVILREMLLKPGDVFSKSFKTDSLRLNLFNLRYFSSLVPDVRPGSEQDL
Dal-1	361	HIIIKGTKNTKDEVILREMLLKPGDVFSKSFKTDSLRLNLFNLRYFSSLVPDVRPGSEQDL
Chicago	361	HIIIKGTKNTKDEVILREMLLKPGDVFSKSFKTDSLRLNLFNLRYFSSLVPDVRPGSEQDL
Mexico	361	HIIIKGTKNTKDEVILREMLLKPGDVFSKSFKTDSLRLNLFNLRYFSSLVPDVRPGSEQDL

Nichols	421	VDIIL
SS14	421	VDIIL
Dal-1	421	VDIIL
Chicago	421	VDIIL
Mexico	421	VDIIL

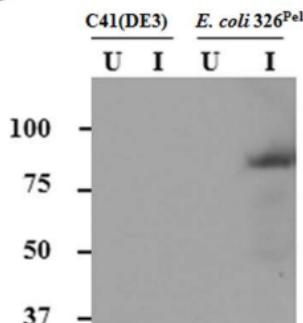
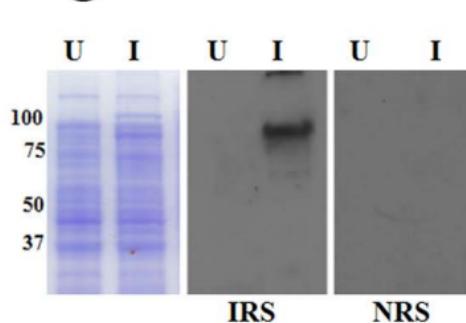
## Supplemental Figure 5B

**Supplemental Figure 5.** Multiple sequence alignment of POTRA arm (A) and  $\beta$ -barrel (B)

sequences from geographically diverse *T. pallidum* strains. Identical residues are highlighted in red. Accession numbers: Nichols (AAC65313); Chicago (ADD72452); SS14 (ACD70752); Dallas-1 (ABW94728); Mexico A (ABW94735); Cali84 (KP713716); Cali77 (KP713715).



**Supplemental Figure 6.** Predicted conformational B cell epitopes in TP0326 are shown as spheres. The predicted three large extracellular loops L4, L6 and L7 are shown in red, blue and magenta, respectively.

**A****B****C**

**Supplemental Figure 7. Construction and expression of 326<sup>pel</sup> in *E. coli*.** (A) Orientation of the 326<sup>pel</sup> construct in pET26b. Shown are the positions of PelB leader sequence, hexahistidine-tag and restriction sites used for cloning. (B) Immunoblot analysis of un-induced (U) and IPTG-induced (I) C41(DE3) or *E. coli*<sup>326pel</sup> cells with rat anti-POTRA antiserum. (C) Immunoblot analysis of un-induced (U) and IPTG-induced (I) *E. coli*<sup>326pel</sup> with C41(DE3)-adsorbed IRS and NRS. In panels B and C, molecular mass standards (kDa) are indicated on the right.