



Supplementary Figure S2 The *hslU* and *hslIV* genes in *L. biflexa* strains and analysis data of AAA+ chaperone-peptidase complex domains. **(A)** The *hslU* gene segments amplified from *L. biflexa* strains by PCR. Lane M: DNA marker. Lanes 1 and 2: amplicons of the *hslU* genes from *L. biflexa*, serogroup Samaranga serovar Patoc strain Patoc 1 and serogroup Andamana serovar andamana strain CH-11, respectively. **(B)** The *hslIV* gene segments amplified from *L. biflexa* strains by PCR. The legend is the same as in **A** but for the *hslIV* gene detection. **(C)** Predictive chaperone domains in the HslU from *L. biflexa* strain Patoc 1. The Walker A and B motifs function as nucleotide phosphate- and Mg²⁺-binding sites, respectively. The arginine finger is responsible for sensing ATP binding and hydrolysis and conformational change. **(D)** Predictive peptidase domains in the HslV from *L. biflexa* strain Patoc 1. **(E)** Comparison of domains in HslU proteins from strains of *L. interrogans* and *L. biflexa*. **(F)** Comparison of domains in HslV proteins from strains of *L. interrogans* and *L. biflexa*. “*”, “#” and “Δ” indicate the enzymatic active, polypeptide substrate-binding and HslU subunit interaction sites, respectively.