

Supplementary Materials

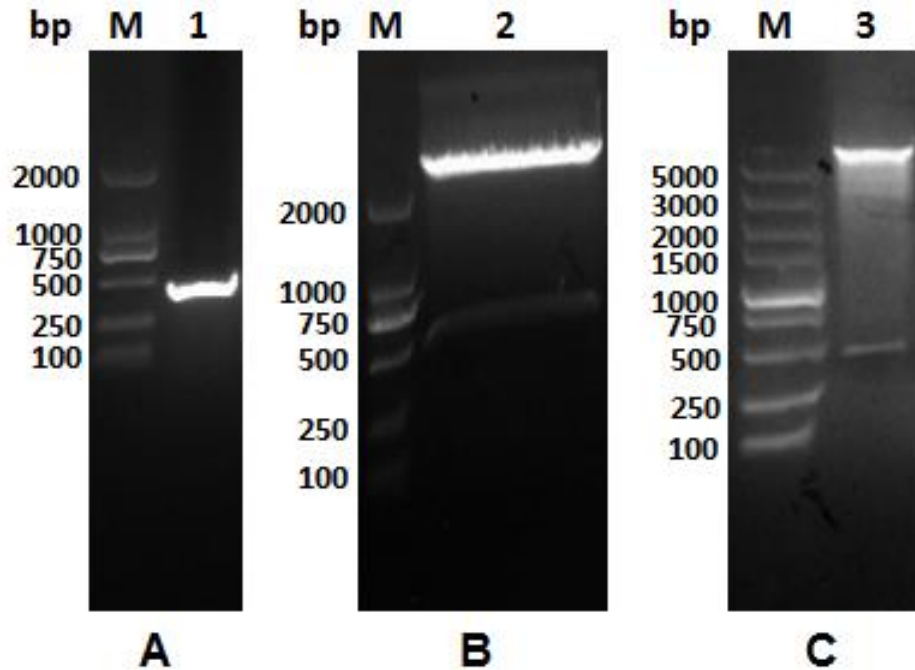


Figure S1. PCR amplification and recombinant plasmids confirmation for HcES-15 gene. M: Molecular weight marker. PCR product for HcES-15 (A), cloned into pMD-19T vector (B) and pET32a vector (C), confirmed by restriction enzyme digestion with *Bam*HI and *Eco*RI.

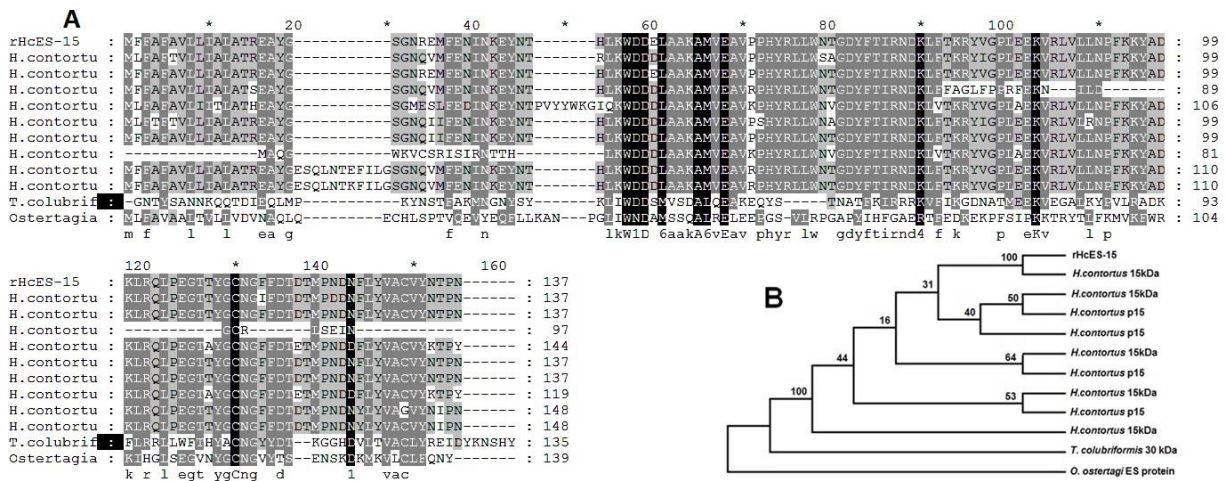


Figure S2. Multiple sequence alignment of amino acid for HcES-15. (A): The protein sequence of HcES-15 aligned with *H. contortus* ES antigens reported in the NCBI database, *H. contortus* 15 kDa excretory/secretory protein AAV84000.1 (100%), CDJ84355.1 (92%), O18518.1 (89%), CDJ84539.1 (85%) and CDJ84626.1 (81%), *H. contortus* p15 CDJ85218.1 (97%), CDJ85217.1 (92%), AEG76953.1 (88%) and CDJ84625.1 (83%), *O. ostertagi* putative L3 ES protein CAH23216.1 (26%), *T. colubriformis* 30 kDa antigenic glycoprotein O97391.1 (38%). (B): Phylogenetic relationship of deduced amino acid sequences of HcES-15 with other known sequences. The values on branches indicate bootstraps for 1000 replicates.

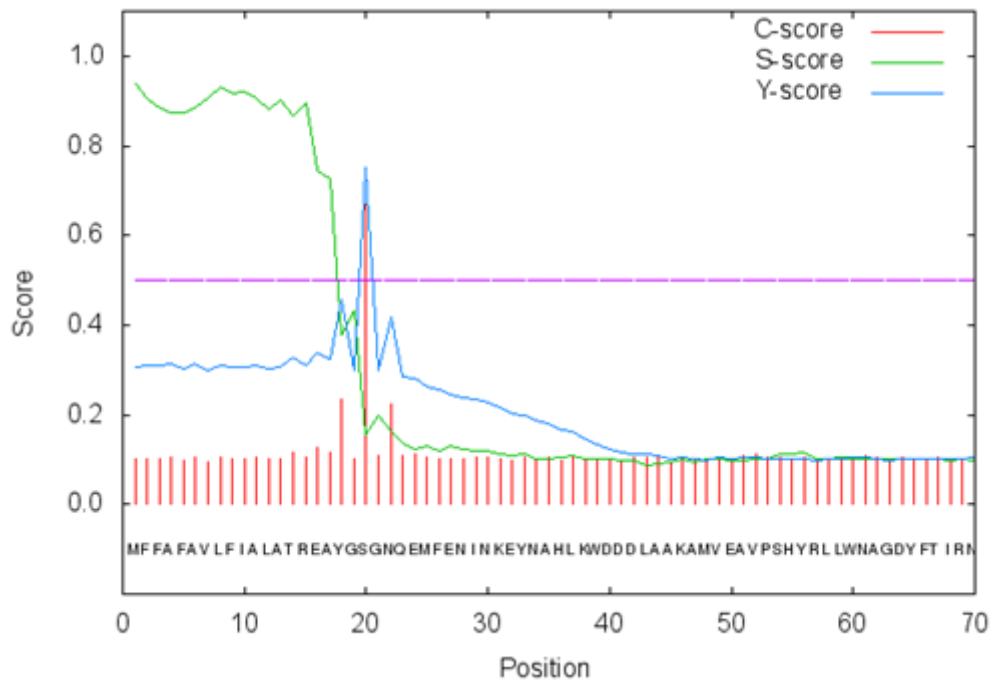


Figure S3. N-terminal signal peptide prediction. The amino acid sequences of HcES-15 (NCBI accession numbers: AY821552.1) was used to predict N-terminal signal peptides by SignalP 4.1 Server (<http://www.cbs.dtu.dk/services/SignalP/>).

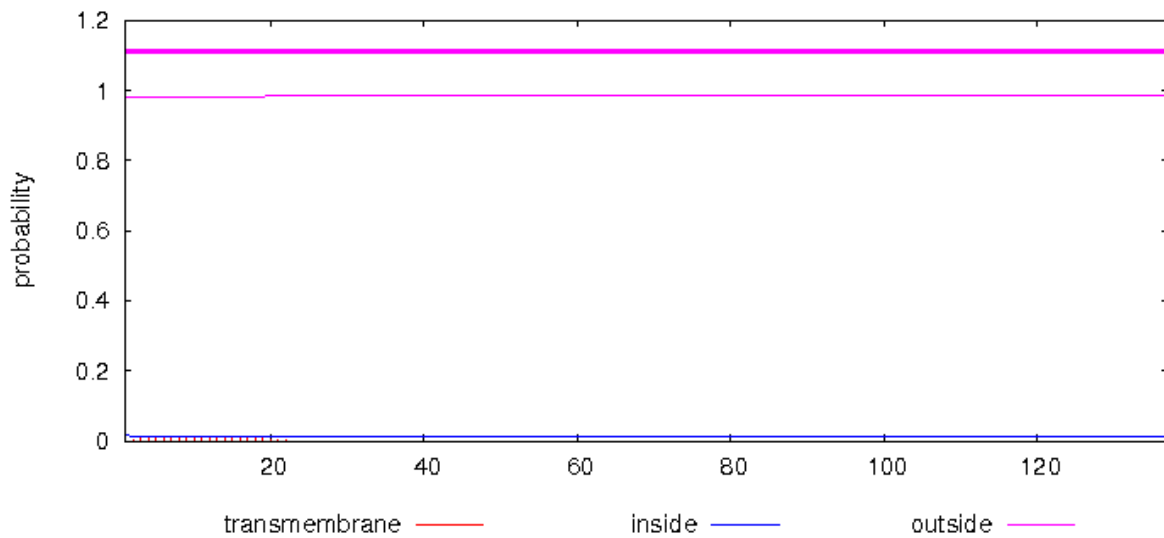


Figure 4. Membrane protein prediction using TMHMM Server v.2.0. The amino acid sequences of HcES-15 (NCBI accession numbers: AY821552.1) was analyzed to predict transmembrane structures using TMHMM Server v.2.0. There were no transmembrane domains was predicted in this protein structure. <http://www.cbs.dtu.dk/services/TMHMM/>.