



Figure S5. Predicted proteoforms of NpCysRP2 and other orthologous sequences. **A.** Multiple-sequence alignment of NpCysRP2 with *L. theobromae* and *D. corticola* orthologous sequences. **A.** Partial protein sequence of *N. parvum* (EOD50922.1) was aligned with full sequences of *L. theobromae* (KAB2578904.1) and *D. corticola* (XP_020125849.1) using Jalview software and the Tcoffee method. The blue shading intensity reflects the level of amino acid identity at each position. **B** and **C.** Predicted transmembrane topology were obtained with PROTTER software for orthologous of NpCysRP2 in *L. theobromae* and *D. corticola* (B) and for other 24 orthologous (C). The predicted signal peptide and the cysteine residues are colored in red and yellow, respectively.