



Figure S4. Multiple-sequence alignment of NpCysRPs and other orthologous sequences. **A.** NpCysRP1, **B.** NpCysRP2 and **C.** NpCysRP3. Partial protein sequences were aligned using Jalview software and the Tcofee method. The conserved cysteine residues are highlighted in yellow. The blue shading intensity reflects the level of amino acid identity at each position. The access numbers of each sequence are: **A.** *N. parvum* (EOD50423.1), *L. theobromae* (KAB2569989.1), *D. corticola* (XP_020126718.1), *D. seriata* (KKY27788.1), *S. luteus* (KIK46160.1), *C. laeve* (TFK32468.1), *B. bassiana* (PQK10211.1), *C. sidae* (TEA07484.1), *A. leporis* (KAB8069877.1), *R. solani* (CUA75287.1), *C. confragosa* (OAA70963.1). **B.** *N. parvum* (EOD50922.1), *L. theobromae* (KAB2578904.1), *D. corticola* (XP_020125849.1), *D. seriata* (KKY21900.1), *F. avenaceum* (KIL85060.1), *T. thermophilus* (XP_003666291.1), *A. terreus* (XP_001217394.1), *P. musae* (KXT13283.1) *T. terrestris* (XP_003656631.1), *P. tritici-repentis* (XP_001934627.1), *C. nymphaeae* (KXH38321.1), *M. mycetomatis* (KXX77126.1), *T. citrinoviride* (XP_024746670.1), *C. epimyces* (XP_007733601.1), *T. longibrachiatum* (PTB72285.1), *T. reesei* (XP_00696324.1), *E. mesophila* (RVX68508.1), *T. parareesei* (A9Z42_0055550), *A. lentulus* (KKO98531.1), *T. harzianum* (XP_024771023.1), *T. guizhouense* (PB44849.1), *A. neoniger* (XP_025474954.1), *C. asianum* (KAF0319766.1), *C. orchidophilum* (XP_022481280.1), *B. panamericana* (XP_007680904.1). **C.** *N. parvum* (EOD5288.1), *M. phaseolina A* (EKG20686.1), *M. phaseolina B* (EKG22346.1), *M. phaseolina C* (EKG22347.1), *F. euwallaceae* (RTE68176.1), *F. kuroshium* (RMI89680.1), *Fusarium* sp. AF-3 (RSL38373.1), *F. avenaceum* (KIL83641.1), *F. oxysporum* (EXK86396.1), *C. fioriniae* (EXF77634.1), *C. fructicola* (XP_031888108), *C. spinosum* (TDZ33147).