



Fig. S1.

**Fig. S1.** NbrRPL10 protein architecture and the response of *NbrRPL10* silenced *N. benthamiana* to host and to nonhost pathogens. (A) Conserved domain architecture of NbrRPL10 protein showing the L16-L10 motif. The conserved domain in NbrRPL10 is predicted using NCBI-CDD tool (<https://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml>). (B) *NbrRPL10* gene segments used for VIGS were predicted using *PssRNAit* webserver (<https://plantgrn.noble.org/pssRNAit/>) and primer locations used to amplify the gene fragments is shown as arrows. The green arrow shows primers that amplify conserved region of *NbrRPL10A* and *NbrRPL10B* and this fragment when used for VIGS should silence both the genes. The purple arrow indicates primers that amplify a gene fragment that is specific to *NbrRPL10A* and when used for VIGS should silence only *NbrRPL10A*. Similarly, the red arrows amplify a gene fragment that is specific to *NbrRPL10B*. (C) Transcript levels of *NbrRPL10A* and *NbrRPL10B* in VIGS silenced lines. The total RNA from 4-week old silenced plants was isolated and converted to cDNA for expression studies using RT-qPCR. The error bars indicate the expression from three biological replicates. (D) Response of *NbrRPL10s* VIGS plants to *pDSKGFPuv* expressing host (*P. syringae* pv. *tabaci*) and nonhost (*P. syringae* pv. *tomato* T1) pathogens. Three weeks after TRV inoculation, *N. benthamiana* plants were vacuum infiltrated with host or nonhost pathogen at  $1 \times 10^4$  cfu mL<sup>-1</sup> concentration. Photographs were taken 3 days after pathogen infection under UV light.