Figure S2 - Bayesian phylogenetic tree of 81 HyPRPs from soybean and three other plant species. The Bayesian analysis was done using MrBayes v.3.1.2 after alignment of the conserved 8CM domain of HyPRPs using Muscle software, as described in Material and Methods, except for two independent runs of 5,000,000 generations each. The unrooted cladogram was edited using FigTree v.1.3.1. Nodal support is given by the posteriori probability values shown next to the corresponding nodes. Bootstraps from neighbor-joining analysis have been omitted since they were less reliable than the Bayesian method. The scale bar indicates the estimated number of amino acid substitutions per site. The soybean pathogen responsive genes analyzed in a time-course real time RT-qPCR experiment are underlined in black. The names of the HyPRP-encoding genes are identified by their locus ID in Phytozome: Cucsa - *Cucumis sativus*, Glyma - *Glycine max*, AC or Medtr - *Medicago truncatula* and ppa - *Prunus persica*.