



Figure S1: Phylogenetic analysis of LysM modules. LysM module protein sequences were aligned using Muscle (Edgar, 2004) and phylogenetic analysis was performed using maximum likelihood methods implemented in MEGA ver. 6 (Tamura et al., 2013). Statistical support for branches was assessed by 1000-iteration bootstrap resampling. Branch support values (bootstrap proportions  $\geq 70\%$ ) are associated with nodes. The LysM modules from *Clonostachys rosea* are highlighted in rectangle. The number in parenthesis indicates the position of LysM module within the LysM protein.

Accession number of proteins: *Cladosporium Fulvum* Ecp6: PDB: 4B9H\_A; *Magnaporthe oryzae* slp1: EHA51101.1; *Magnaporthe oryzae* slp2: EHA50138.1; *Mycosphaerella graminicola* Mg3LysM: XP\_003850050.1; *Mycosphaerella graminicola* Mg1LysM (Marshall et al., 2011); *Colletotrichum higginsianum* ChELP1 and ChELP2 (Takahara et al., 2016); *Colletotrichum graminicola* CgELP1: EFQ32497.1; *Colletotrichum graminicola* CgELP2: EFQ27803.1; *Colletotrichum lindemuthianum* ClCiH1: CAA04765.1; *Trichoderma atroviride* Tal6: XP\_013947368.1; *Verticillium dahliae* Vd2LysM: XP\_009653211.1; *Verticillium dahliae* Vd4LysM: XP\_009648083.1; *Verticillium dahliae* Vd5LysM: XP\_009652680.1; *Verticillium dahliae* Vd6LysM: XP\_009654198.1; *Beauveria bassiana* Blys2: XP\_008596457.1; *Beauveria bassiana* Blys4: XP\_008599172.1; *Beauveria bassiana* Blys5: XP\_008601921.1; *Beauveria bassiana* Blys6: XP\_008602072.1; *Beauveria bassiana* Blys7: XP\_008602298.1; *Beauveria bassiana* Blys8: XP\_008602669.1; *Penicillium expansum* PeLysM1: XP\_016599271.1; *Penicillium expansum* PeLysM2: XP\_016600130.1; *Penicillium expansum* PeLysM3: XP\_016600884.1; *Penicillium expansum* PeLysM4: XP\_016594789.1; *Clonostachys rosea* LYSM1: MT037001; *Clonostachys rosea* LYSM2: MT037002; *Clonostachys rosea* CHIC2: MT037003.

Takahara H, Hacquard S, Kombrink A, Hughes HB, Halder V, Robin GP, et al. *Colletotrichum higginsianum* extracellular LysM proteins play dual roles in appressorial function and suppression of chitin-triggered plant immunity. *New Phytol.* 2016; 211:1323-1337.

Marshall R, Kombrink A, Motteram J, Loza-Reyes E, Lucas J, Hammond-Kosack KE, et al. Analysis of two in planta expressed LysM effector homologs from the fungus *Mycosphaerella graminicola* reveals novel functional properties and varying contributions to virulence on wheat. *Plant Physiol.* 2011; 156:756-769.