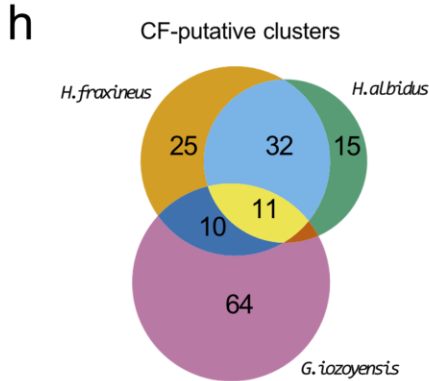
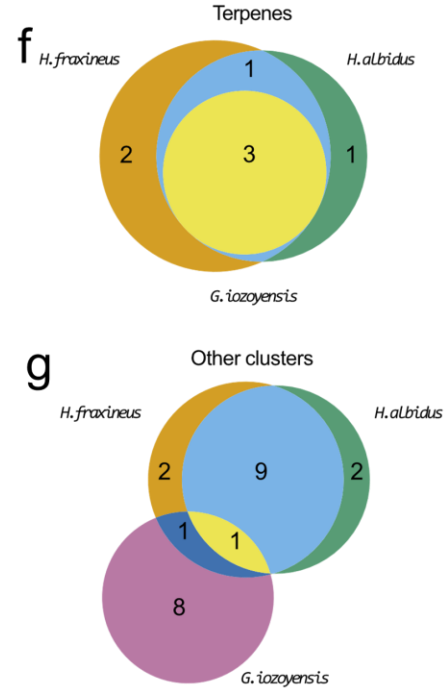
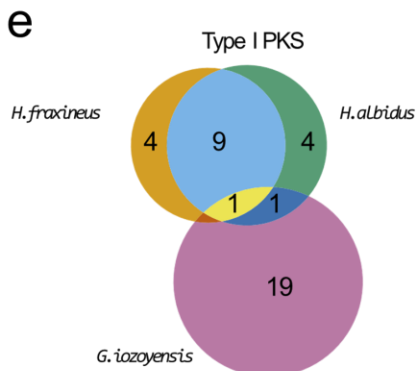
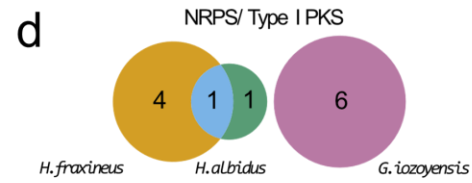
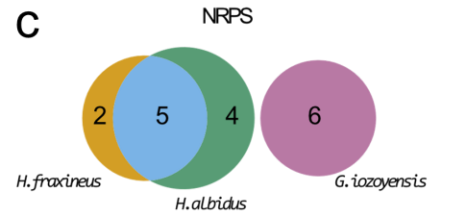
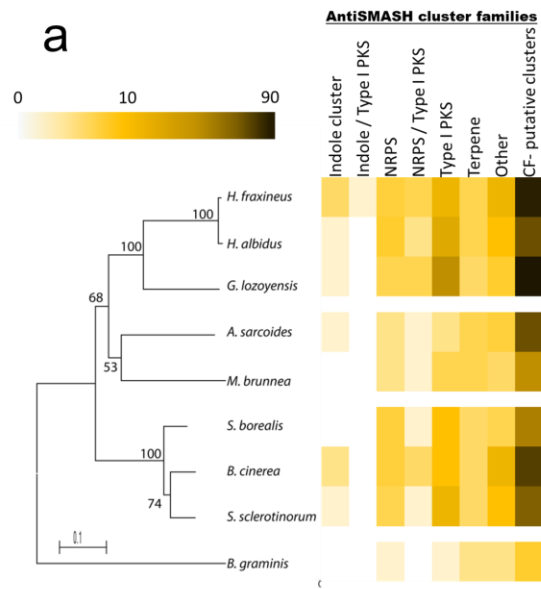




Supporting figure S1: Biosynthetic gene clusters (BGCs) predicted by AntiSMASH. a.) A heat-map of the number BGCs predicted in selected AntiSMASH families in *Hymenoscyphus fraxineus*, *Hymenoscyphus albidus*, *Glarea iozoyensis*, *Ascochyta sarcoides*, *Marssonina brunnea*, *Sclerotinia borealis*, *Botrytis cinerea*, *Sclerotinia sclerotiorum* and *Blumeria graminis* genomes annotated by our MAKER pipe-line. The Venn diagram in b-h show the overlap in identified clusters between *H. fraxineus*, *H. albidus*, *G. iozoyensis* in different AntiSMASH families. For a cluster to be considered to be overlapping in any species comparison species at least three genes in the clusters must be orthologous between species.