Supporting Information Figure S3. Distribution of genome content in *Clonostachys*. Genomes were annotated using a MAKER-based pipeline. The annotations from MAKER was used to classify the genome sequences into functional categories, including exons, introns, intergenic regions, dispersed repeats, simple repeats and low complexity regions. Strains included were *C. solani* 1703, *C. byssicola* CBS 245.78, *C. rhizophaga* CBS 906.72A, *C. chloroleuca* CBS 570.77, *Clonostachys* sp. CBS 192.96 and *C. rosea* IK726.