

Supplementary

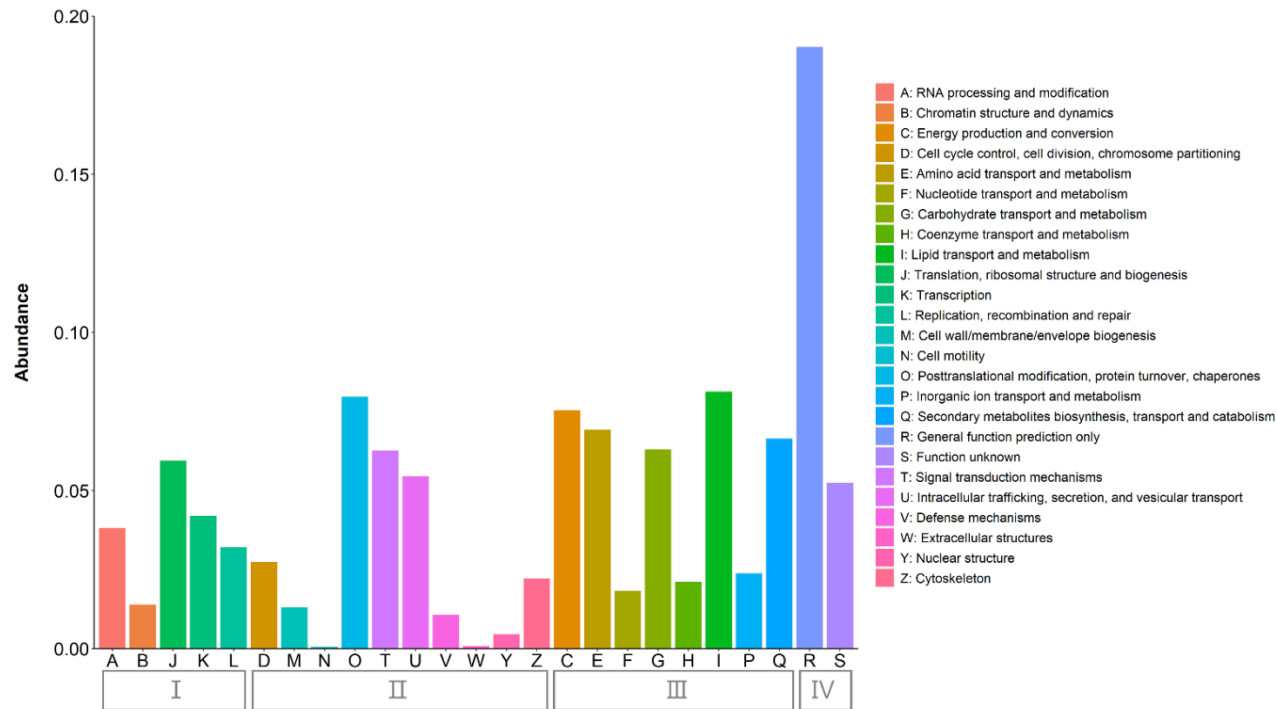


Figure S1. Histogram of KOG distribution of predicted proteins from *A. terreus* ATCC 20541.

A total of 3,191 KOG groups were assigned to 6,689 *A. terreus* proteins using the webMGA tool with a cut-off e-value of $1e^{-5}$. KOG function classification was divided into 26 classes (A-Z), which were assigned to four major groups including classification information storage and processing (I), cellular processes and signaling (II), metabolism (III), and function poorly characterized proteins (IV).

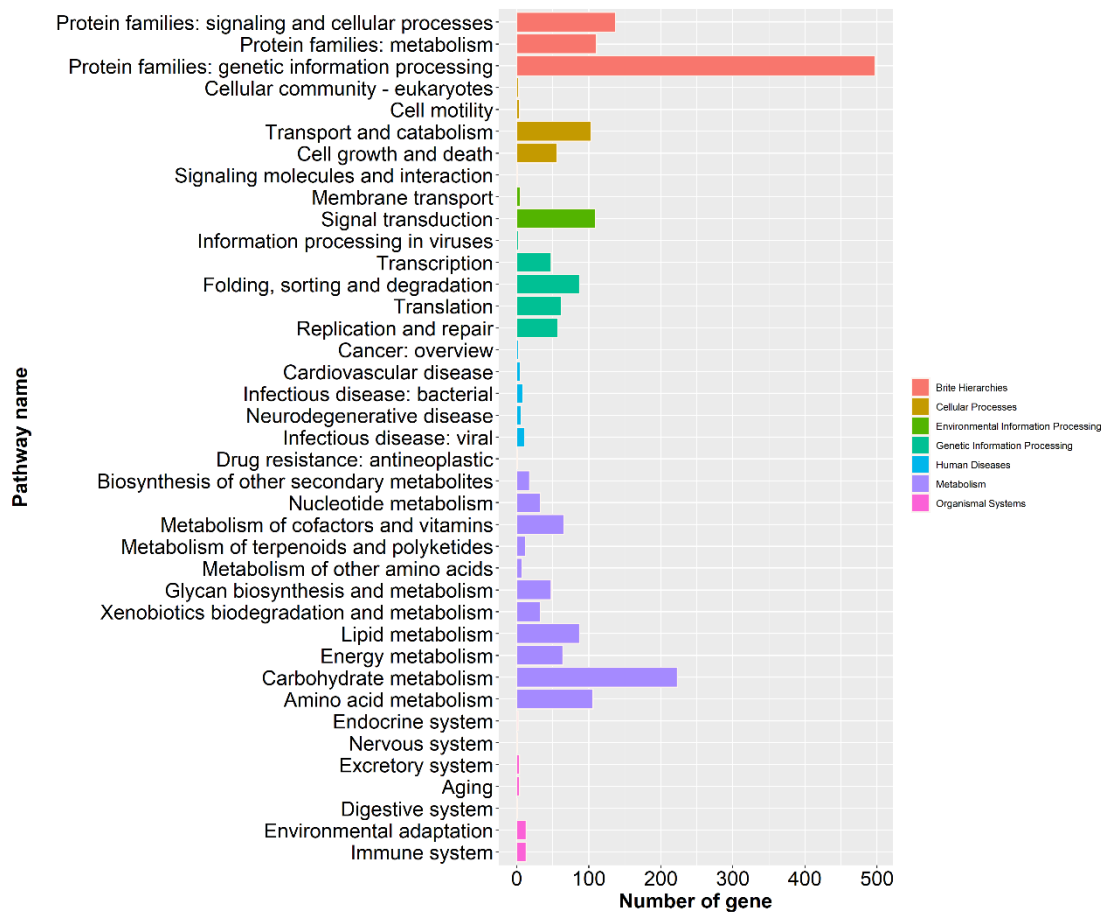


Figure S2. KEGG pathway analysis of *A. terreus* ATCC 20541 genome.

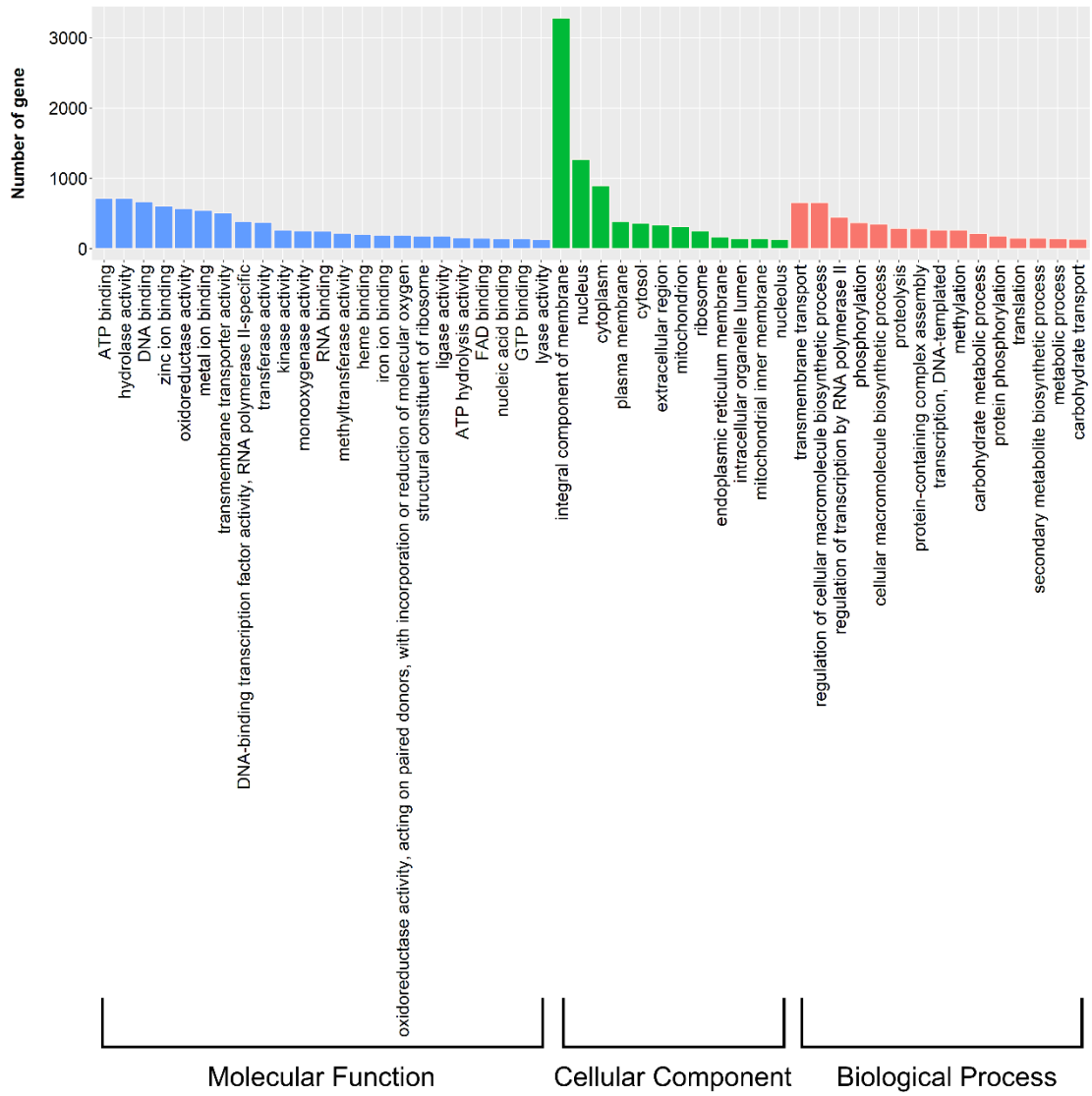


Figure S3. GO analysis of *A. terreus* ATCC 20541 genome (top 50).

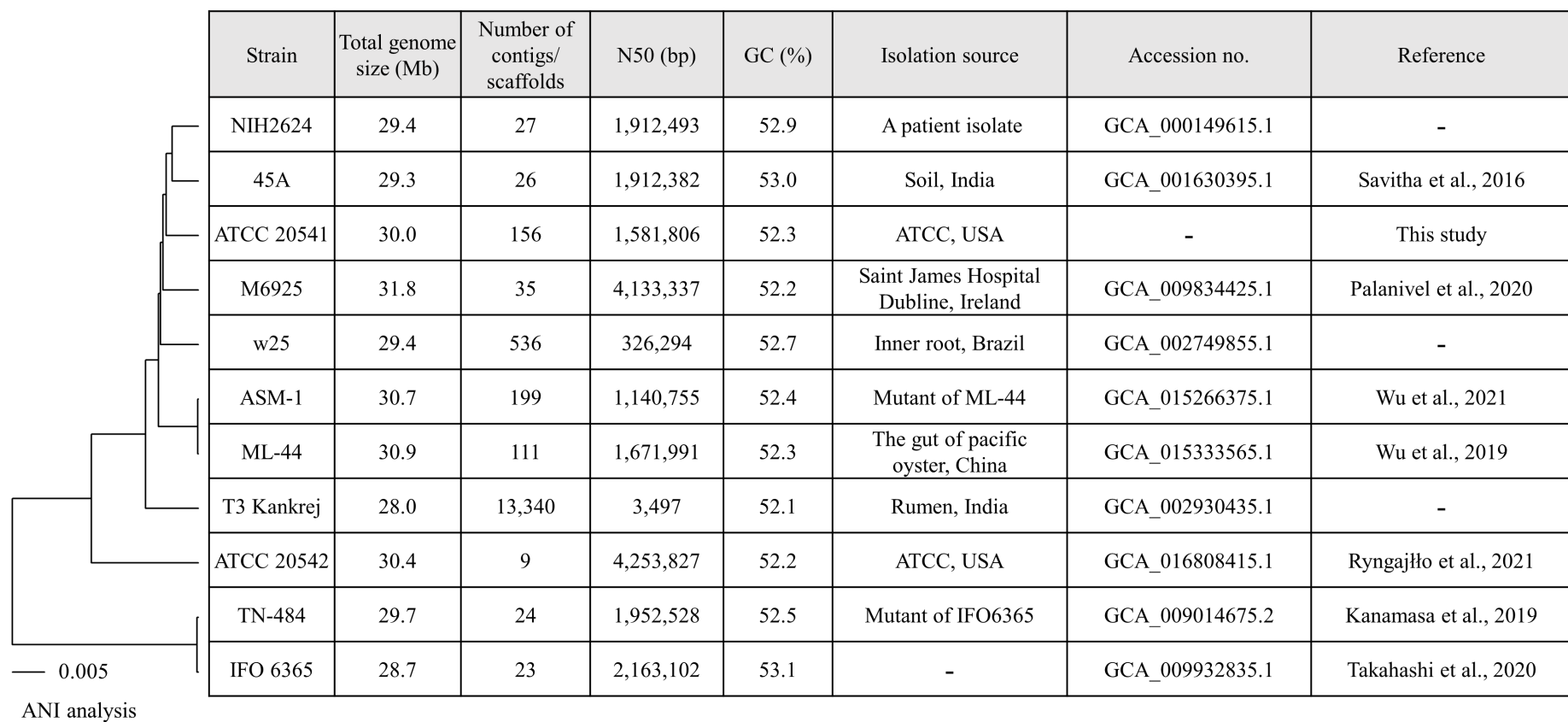


Figure S4. Characteristics of complete *A. terreus* genomes deposited at the NCBI database.

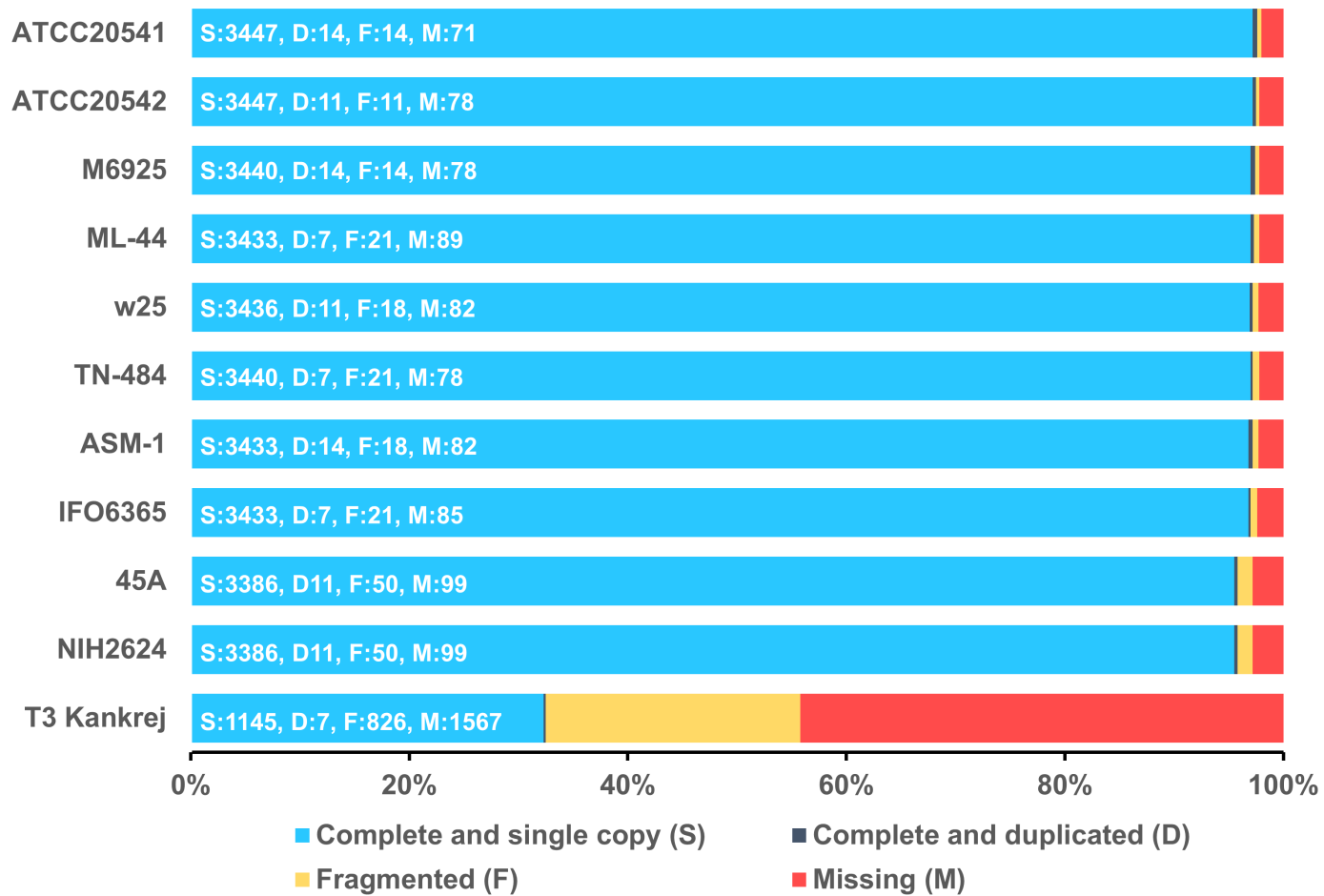


Figure S5. Genome BUSCO assessments for eleven *A. terreus* strains.

S: Complete and single-copy BUSCOs; D: Complete and duplicated BUSCOs; F: Fragmented BUSCOs; M: Missing BUSCOs.



Figure S6. Comparison of the orthologous secondary metabolism in *A. terreus* strains.

Heatmap represents the presence (pink) or absence (gray) matrix of orthologous SM proteins predicted by antiSMASH v. 6.0.1 (fungal version) (Blin et al., 2021). The dendrogram was generated based on hierarchical clustering analysis. X-axis: orthologous SM proteins; Y-axis: strain clustering.

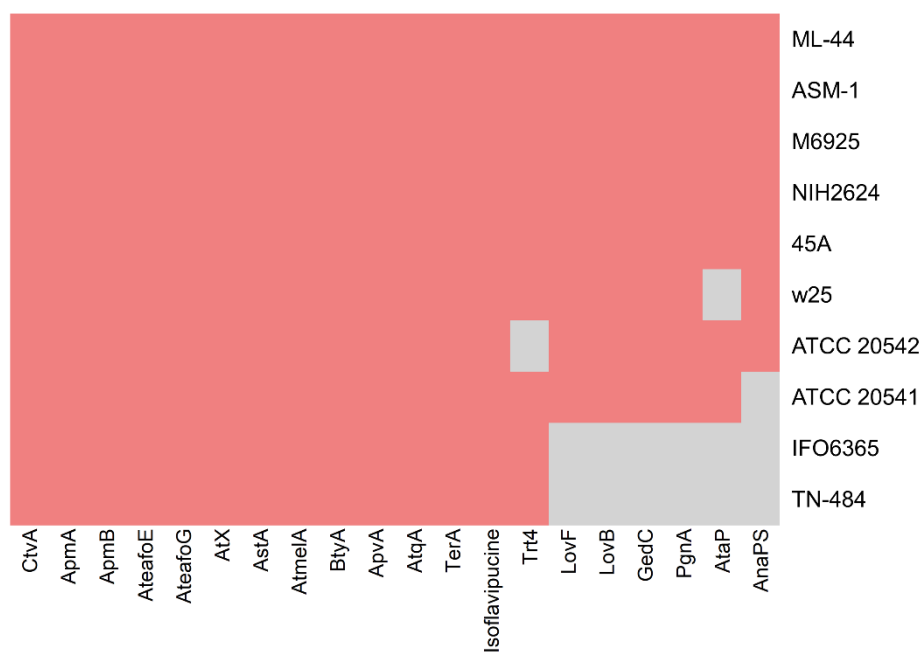


Figure S7. Comparison of the core SM proteins in *A. terreus* strains. Heatmap represents the presence (pink) or absence (gray) matrix of orthologous *A. terreus* NIH2624 core biosynthetic proteins associated with SMs in *A. terreus* strains. X-axis: orthologous *A. terreus* NIH2624 core SM proteins (Romsdahl and Wang, 2019); Y-axis: strains.

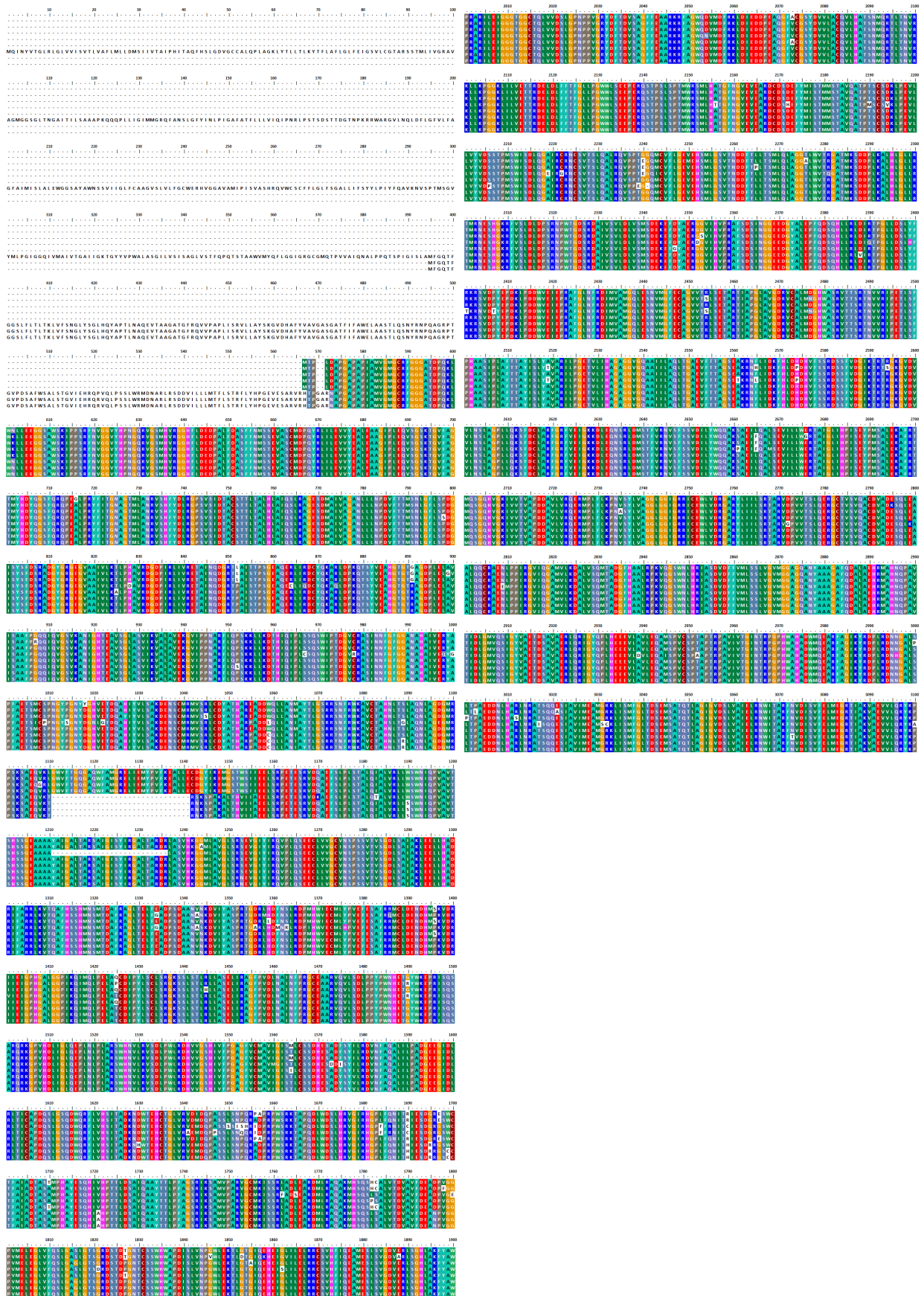


Figure S9. Sequence alignment of the *lovF* gene in *A. terreus* strains.