

Figure S2. Genetic organization and conservation of fusarubin/oxyjavanicin BGC across the FSSC genomes and *F. fujikuroi*. Each color represents a different gene and the core biosynthetic gene *PKS3* is indicated.

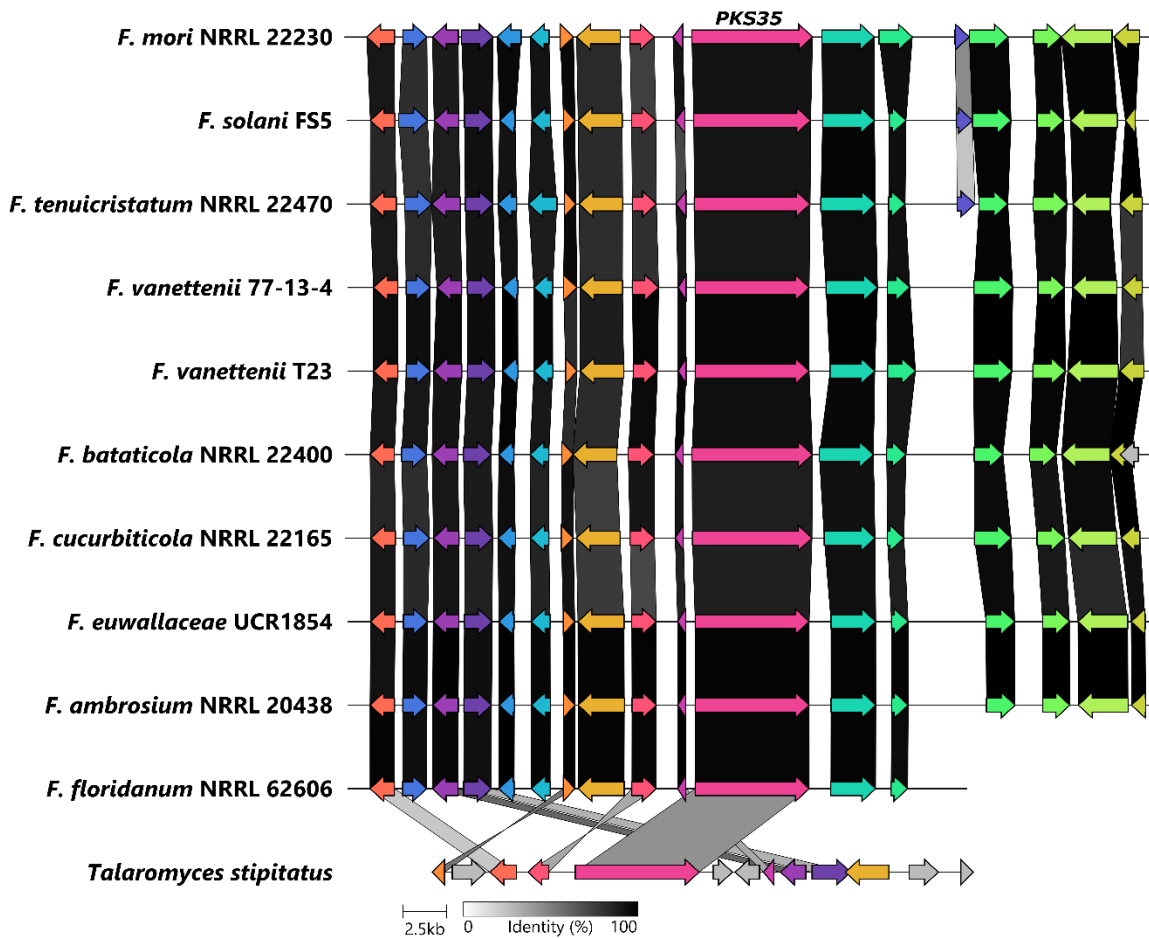


Figure S3. Genetic organization and conservation of the red pigment BGC across the FSSC genomes and *Talaromyces stipitatus*. Each color represents a different gene and the core biosynthetic gene *PKS35* is indicated.

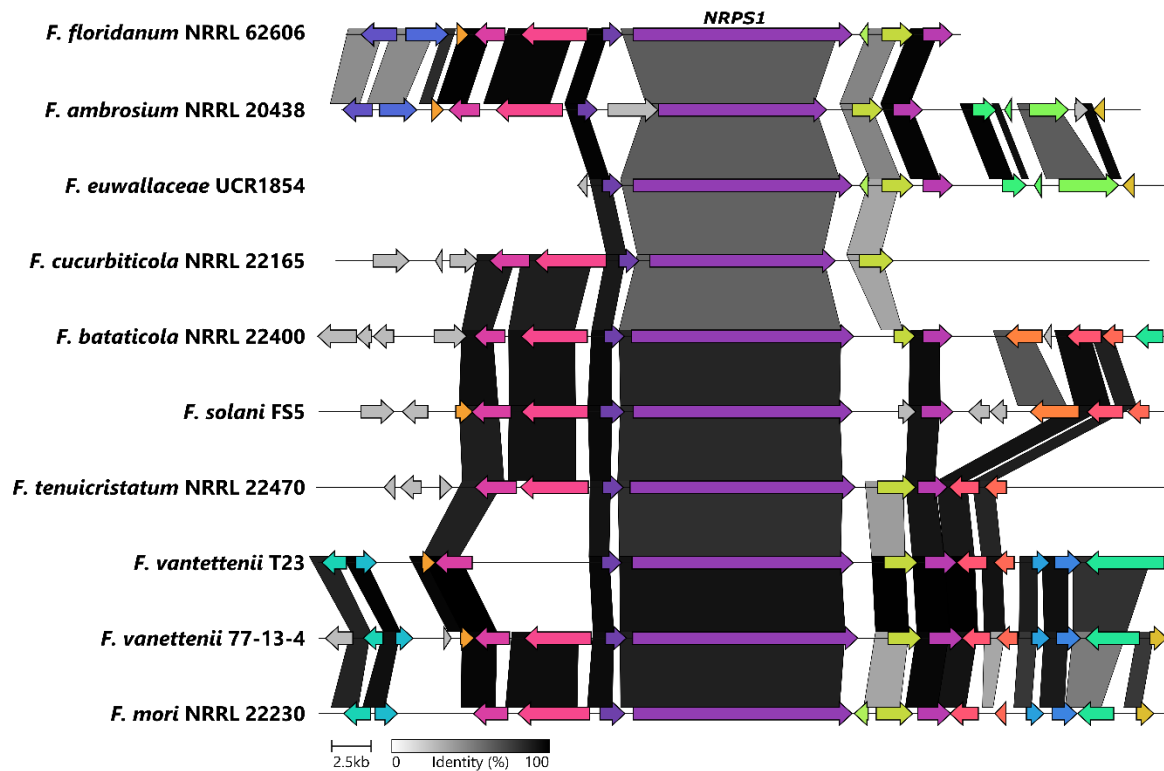


Figure S4. Genetic organization and conservation of the malonichrome BGC across the FSSC genomes. Each color represents a different gene and the core biosynthetic gene *NRPS1* is indicated.

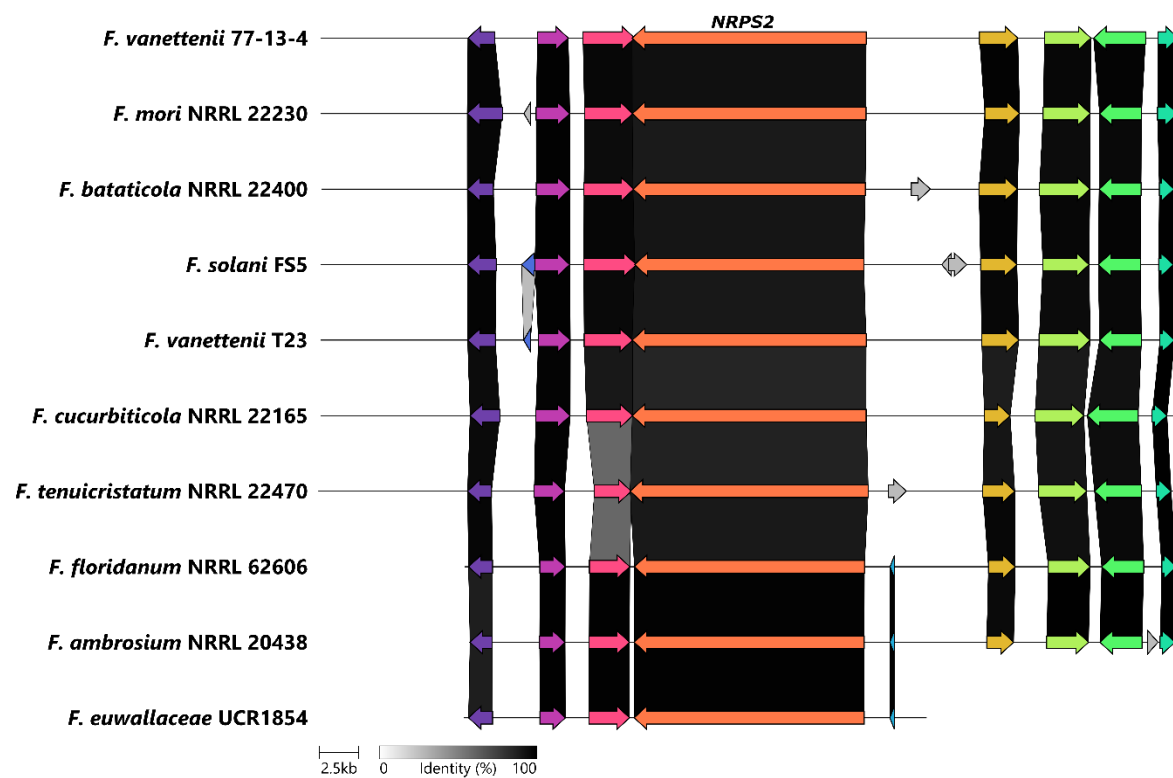


Figure S5. Genetic organization and conservation of the ferricrocin BGC across the FSSC genomes. Each color represents a different gene and the core biosynthetic gene *NRPS2* is indicated.

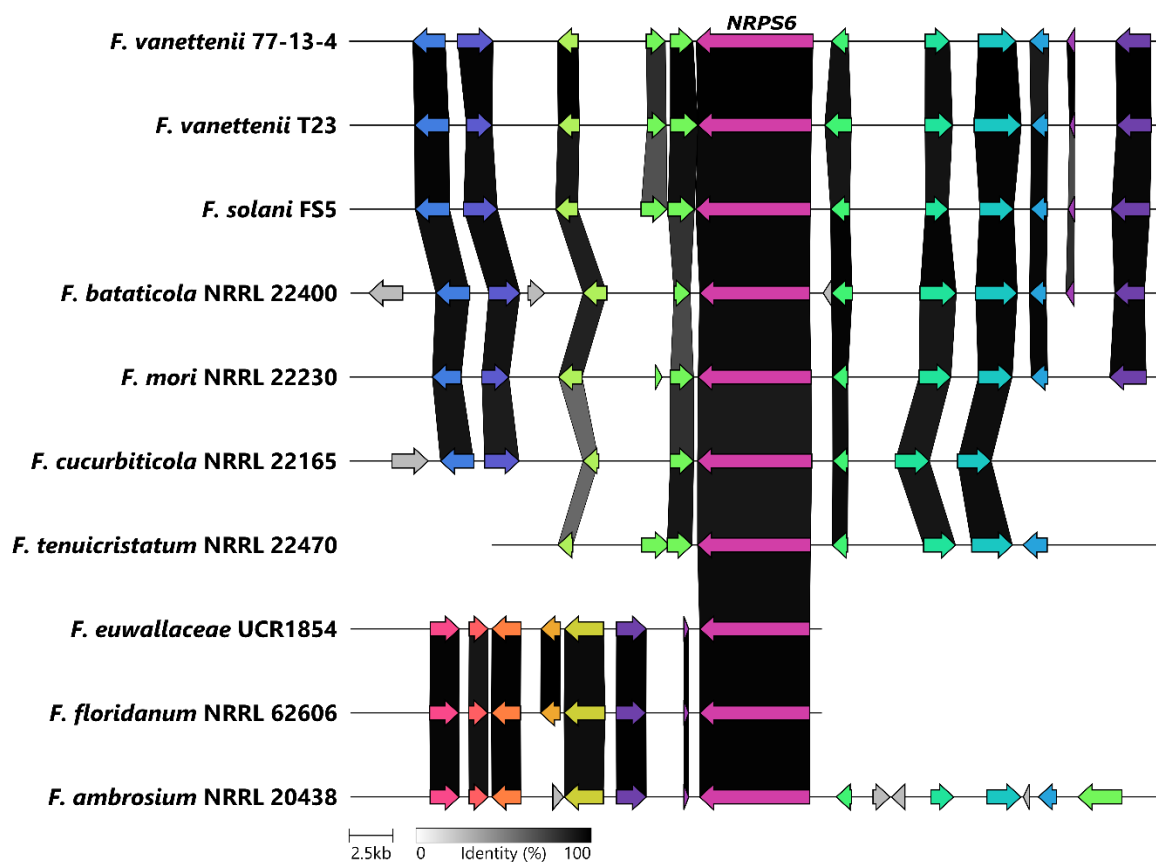


Figure S6. Genetic organization and conservation of the triacetylfusarinine/fusarinine BGC across the FSSC genomes. Each color represents a different gene and the core biosynthetic gene *NRPS6* is indicated.

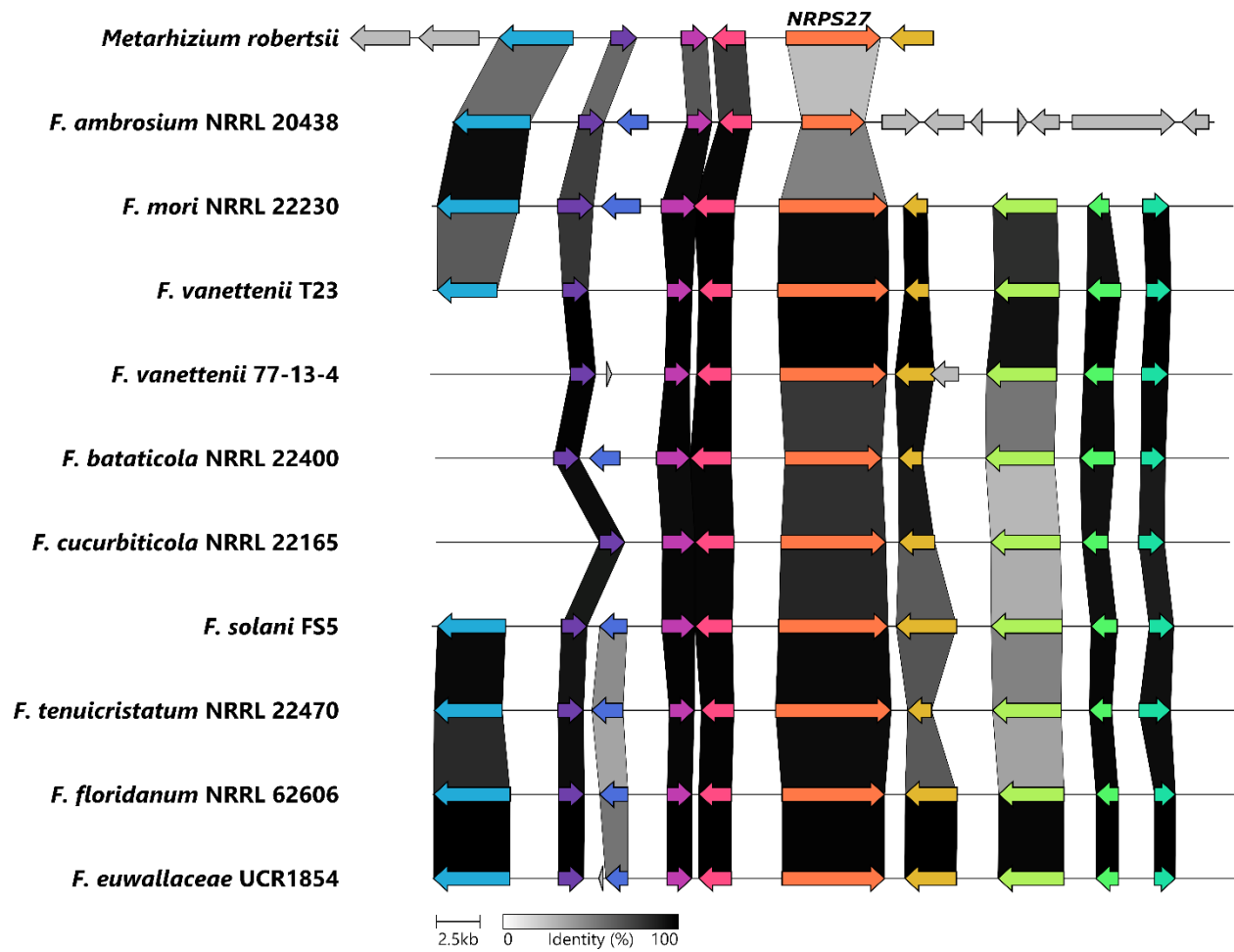
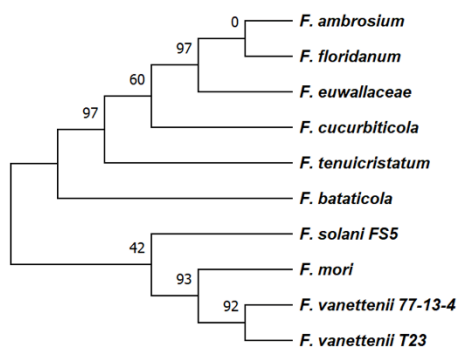
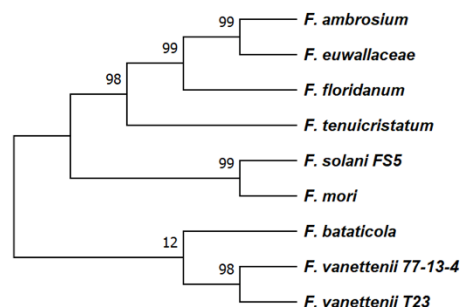


Figure S7. Genetic organization and conservation of the putative metachelin BGC across the FSSC genomes and *Metarhizium robertsii*. Each color represents a different gene and the core biosynthetic gene *NRPS27* is indicated.

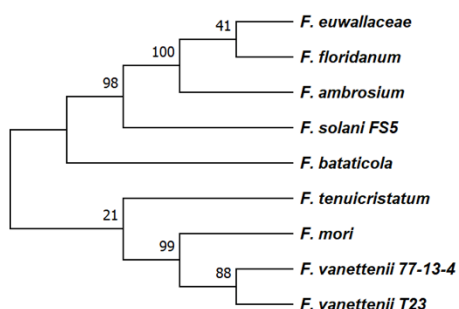
T-GCF1



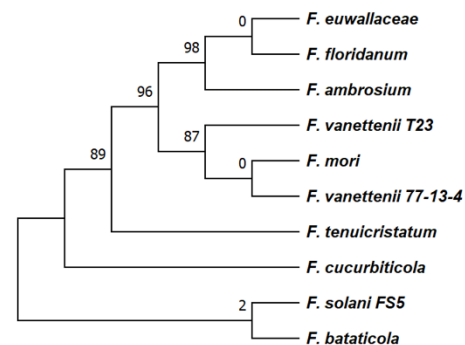
T-GCF2



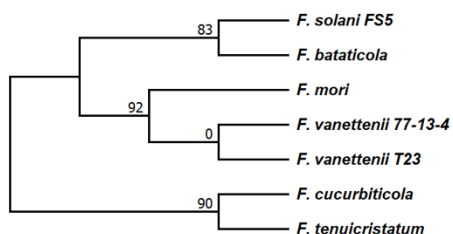
T-GCF3



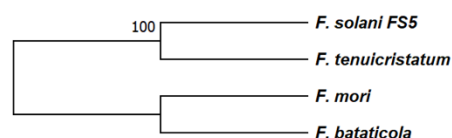
T-GCF4



T-GCF5



T-GCF6



T-GCF7

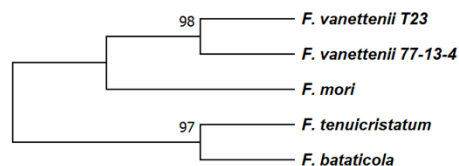
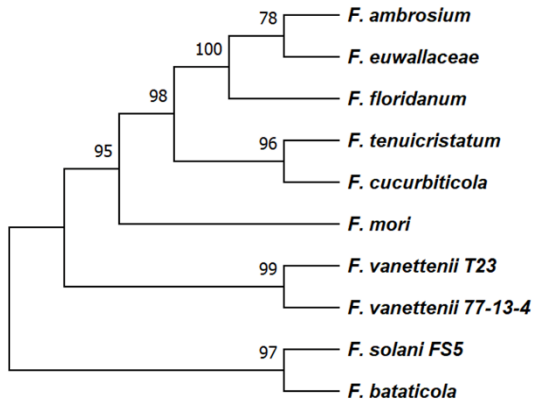


Figure S8. The multi-locus phylogenetic analysis of the terpene GCFs generated by BiG-SCAPE. Only the T-GCFs shared by at least three members of FSSC isolates are shown. T-GCF4, T-GCF5, and T-GCF6 are predicted to produce squalstatin S1, lanosterol/clavaric acid, and aspterric acid, respectively.

I-GCF1



I-GCF2

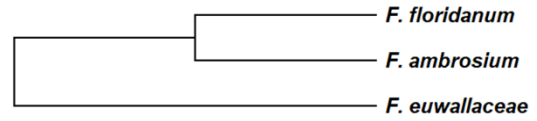


Figure S9. The multi-locus phylogenetic analysis of the indole GCFs generated by BiG-SCAPE. Only the I-GCFs shared by at least three members of FSSC isolates are shown.

P-GCF1

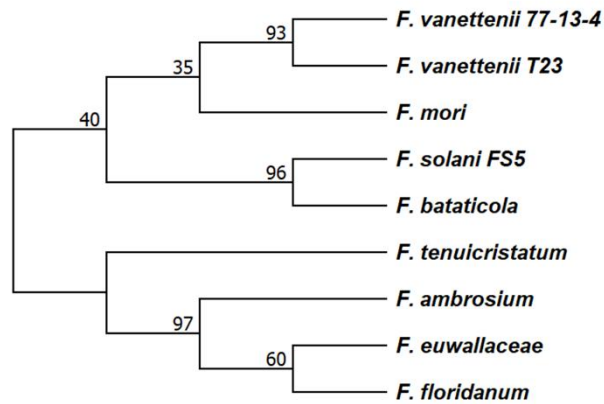


Figure S10. The multi-locus phylogenetic analysis of the phosphonate GCFs generated by BiG-SCAPE. Only the P-GCFs shared by at least three members of FSSC isolates are shown.