

Supplementary Materials

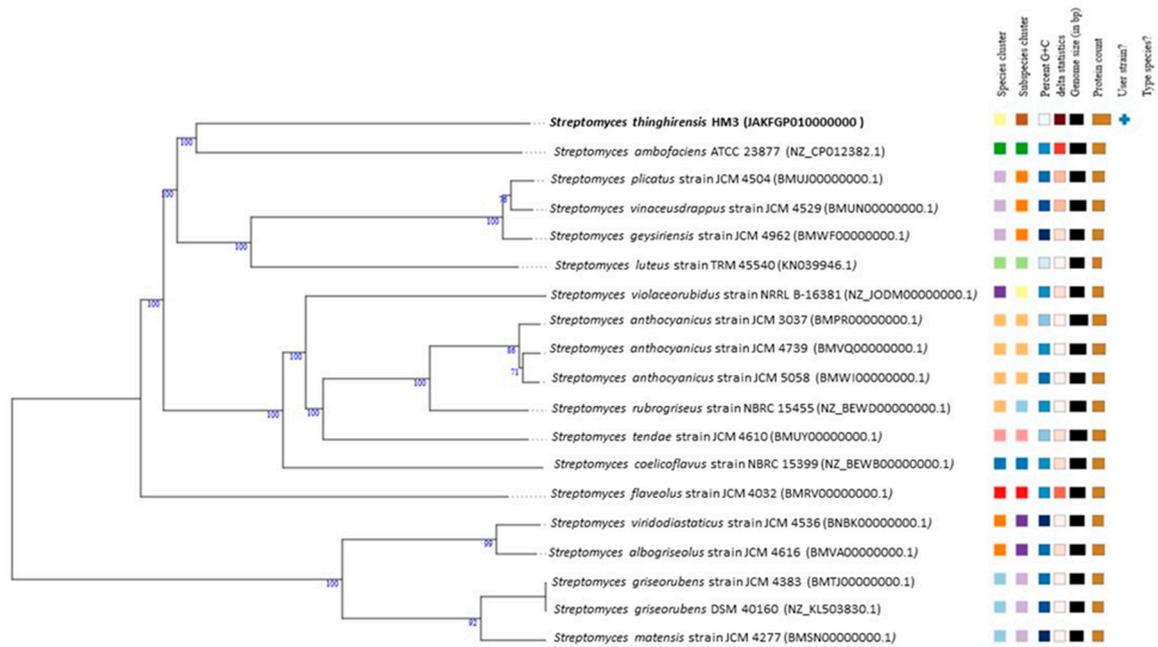
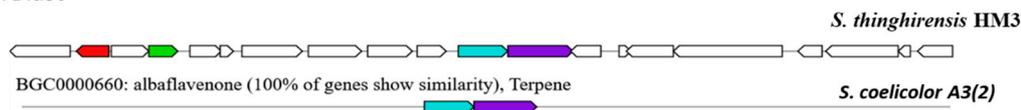


Figure S1: Tree inferred with FastME 2.1.6.1 in TYGS database from GBDP distances calculated from genome sequences (NCBI GenBank accession ID JAKFGP000000000) showing the phylogenetic relationships between strain HM3 and the most closely related type strains of the genus *Streptomyces*. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 92.2 %.

KnownClusterBlast



ClusterBlast

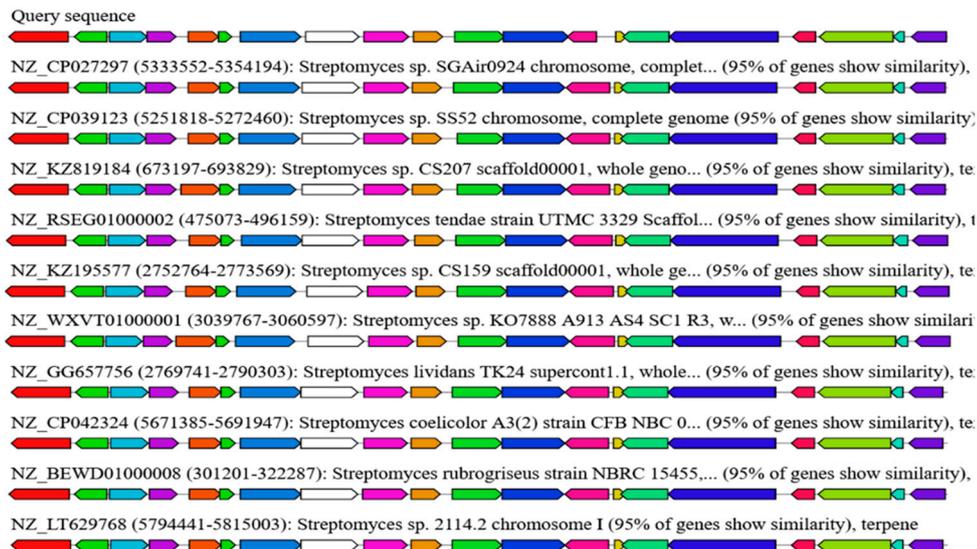
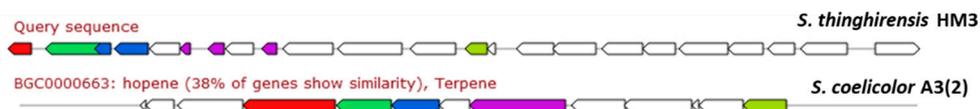


Figure S2. Terpene (albaflavenone), KnownClusterBlast and ClusterBlast.

KnownClusterBlast



ClusterBlast

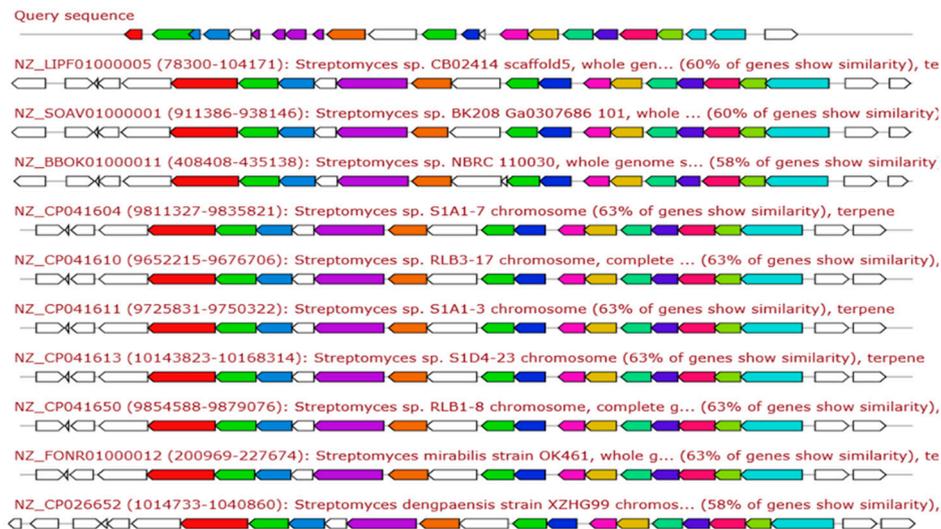
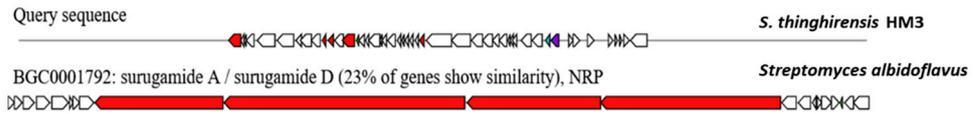


Figure S3: Terpene (hopene), KnownClusterBlast and ClusterBlast

KnownClusterBlast



ClusterBlast

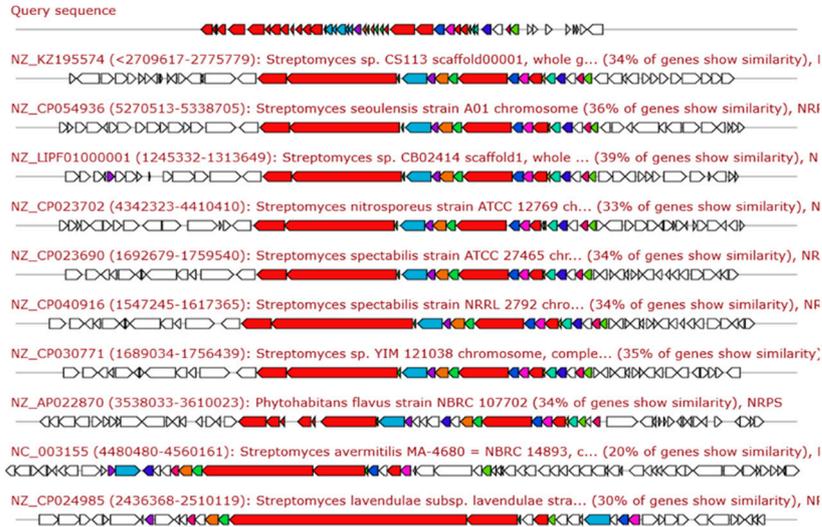
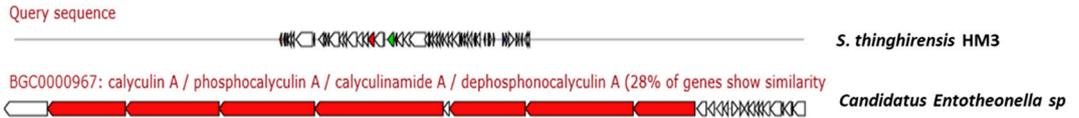


Figure S4: Non-ribosomal peptide synthetase cluster (NRPS), KnownClusterBlast and ClusterBlast

KnownClusterBlast



ClusterBlast

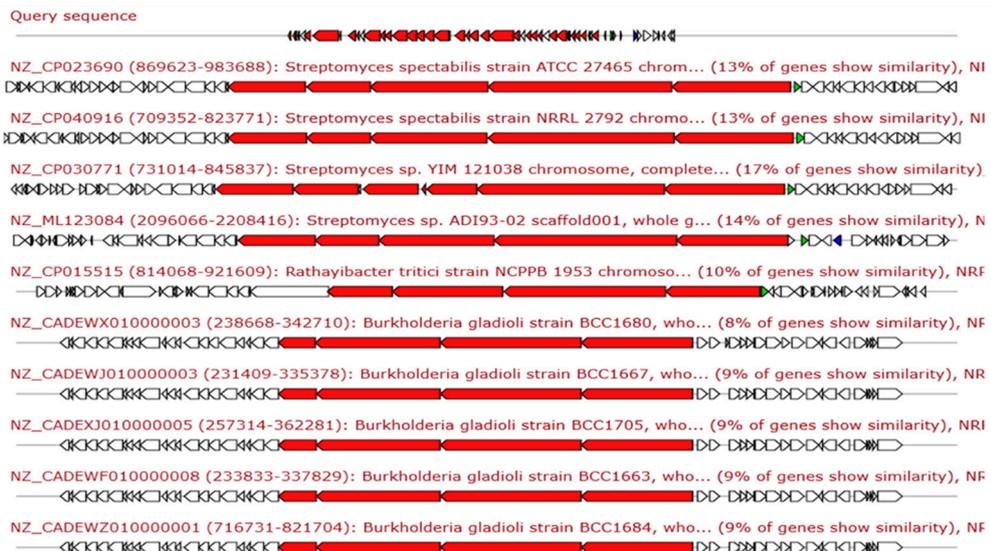


Figure S5: NRPS-like fragment/transAT-PKS-like, KnownClusterBlast and ClusterBlast

KnownClusterBlast



Pfam domains

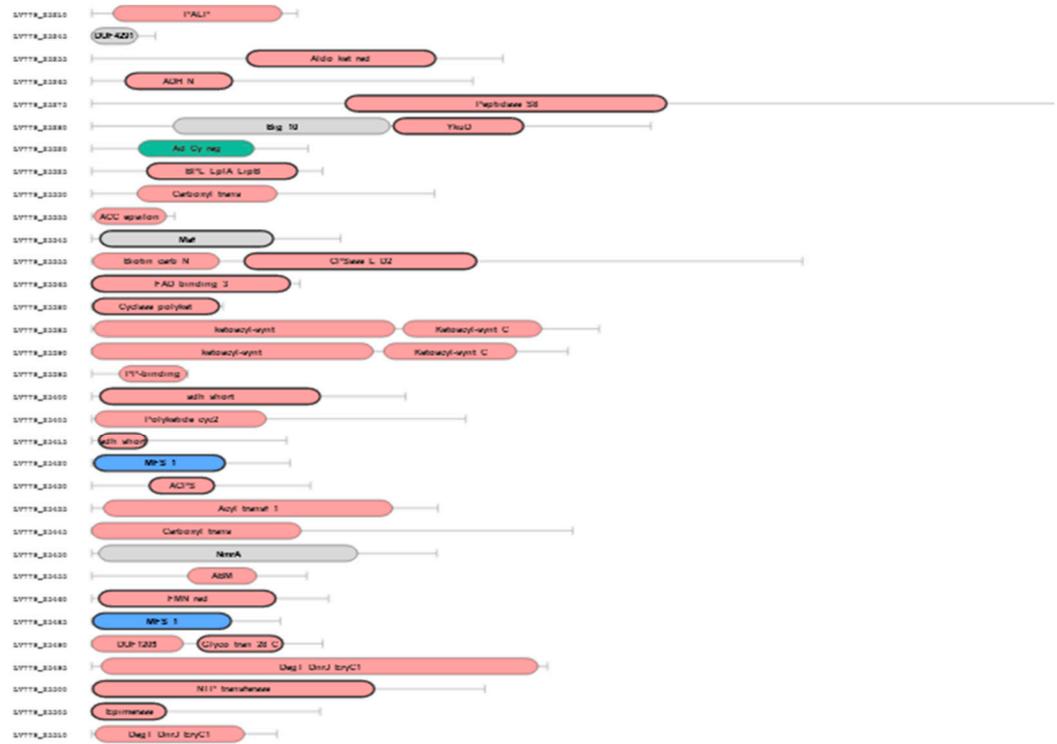


Figure S6: Type II PKS BCG based on KnownClusterBlast and Pfam domains.

KnownClusterBlast

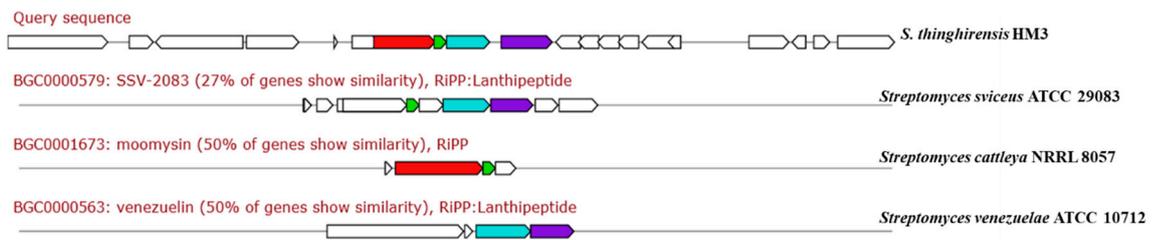


Figure S7: Ribosomally synthesised and post-translationally modified peptide product (RiPP) cluster/Lanthipeptide, KnownClusterBlast

KnownClusterBlast

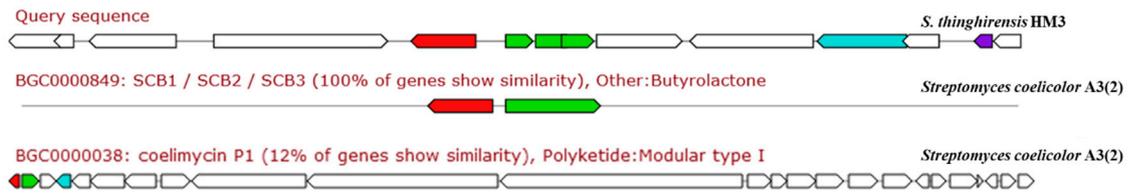


Figure S8: Butyrolactone cluster, KnownClusterBlast

KnownClusterBlast

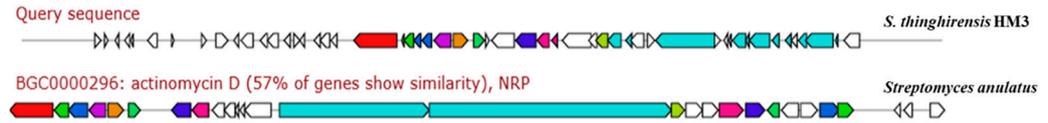


Figure S9: Other, Cluster containing a secondary metabolite-related protein that does not fit into any other category (actinomycin D), KnownClusterBlast