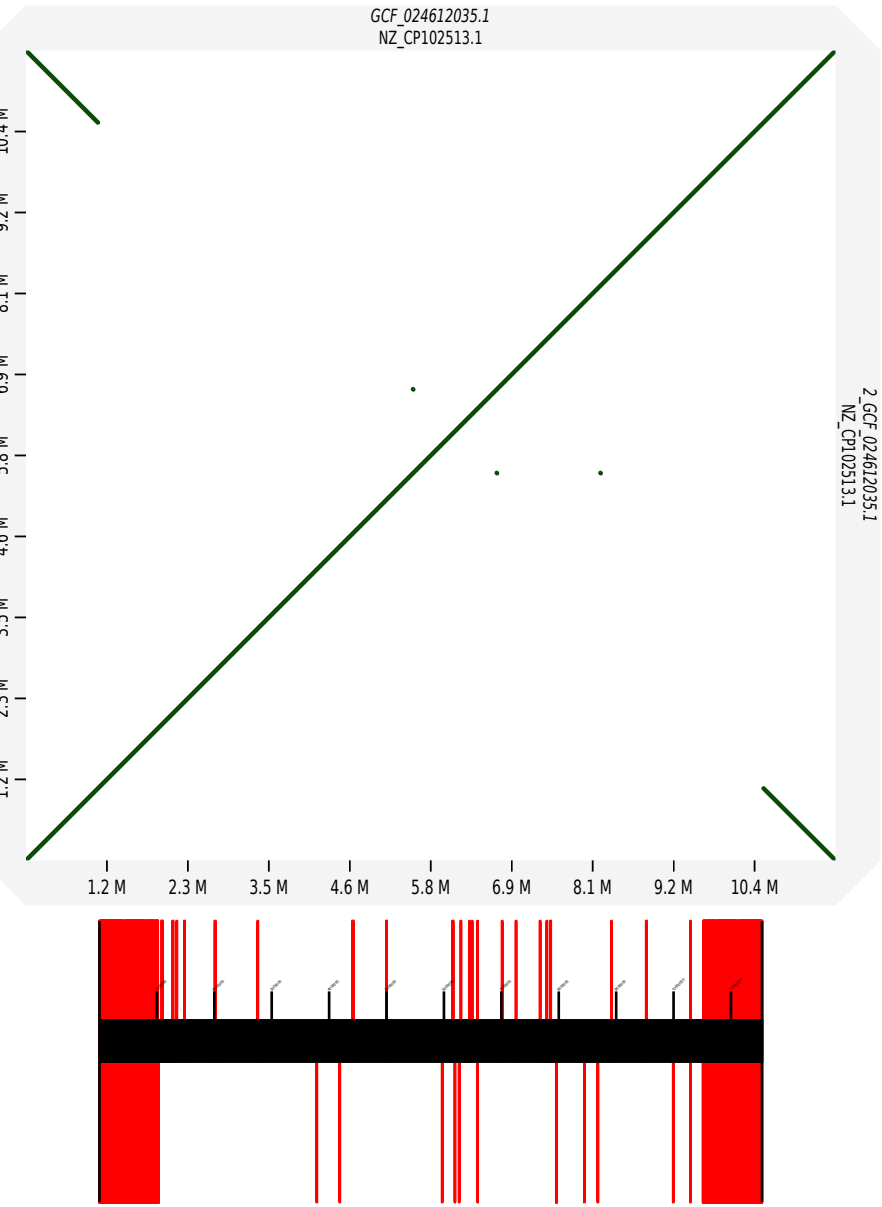


Supplementary figure 5: Recent gene duplications in eight *Streptomyces* genomes

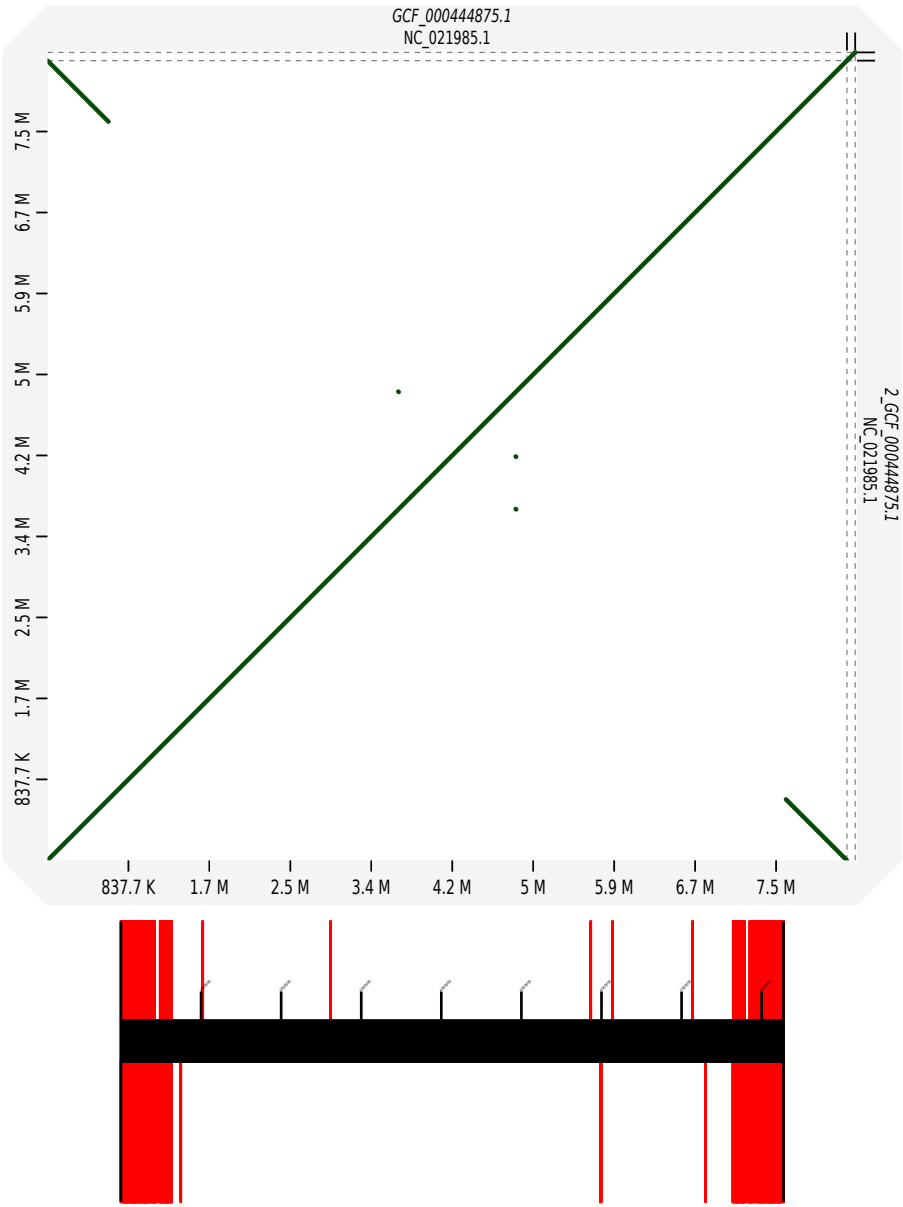
In order to investigate very recent and extensive lineage-specific expansions of certain *Streptomyces* species, genome-scale dotplots of each of the genomes against itself were performed with the D-genies software (default parameters) and the Minimap2 v2.24 aligner.

Below each genome dotplot we show the genome diagrams with the recent paralogues. Recent paralogues were calculated using the 91-100% aminoacid identity cut-off and are shown in red color. Vertical bars above the diagram are genes located on the positive strand, while vertical bars below are genes located on the negative strand. The diagrams were created using the Biopython library.

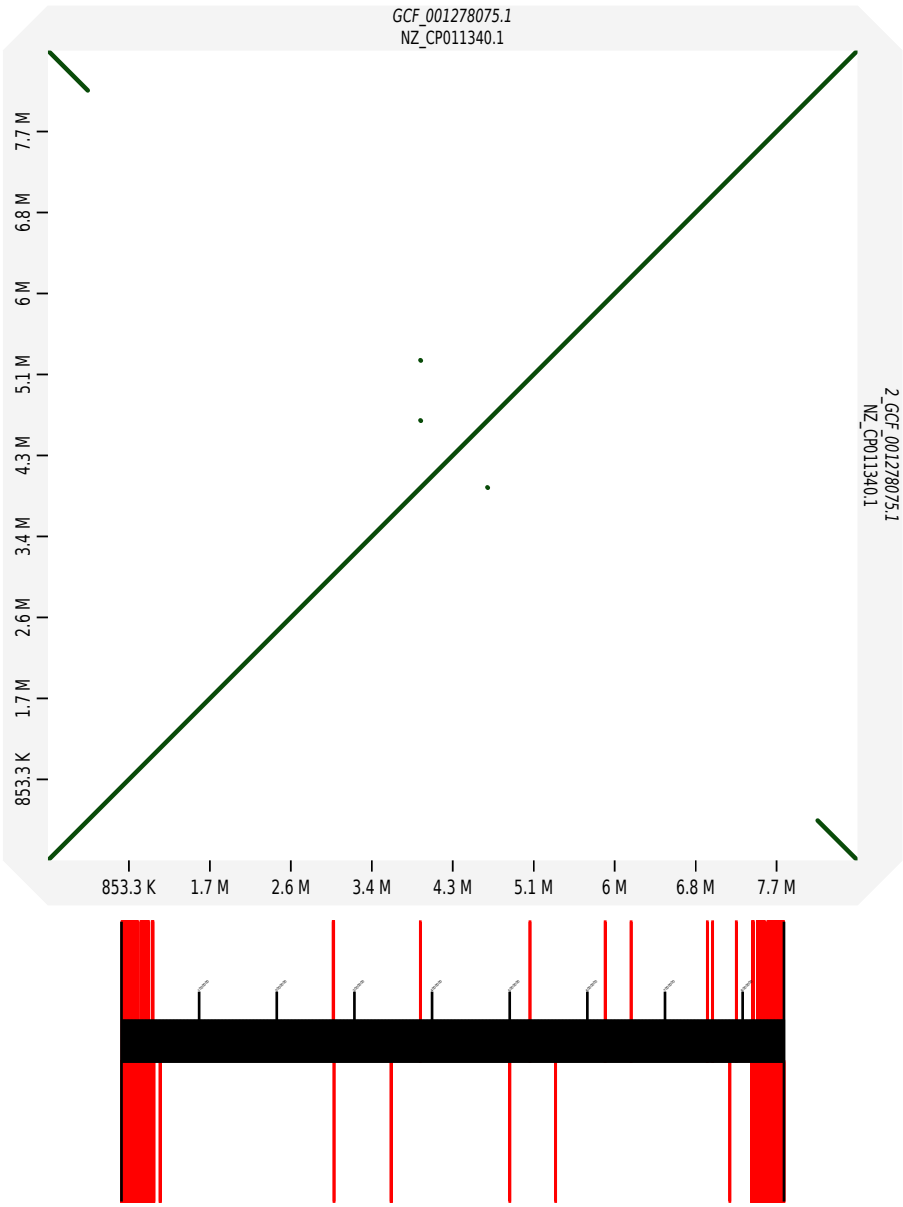
I) *Streptomyces* sp. DSM 40750; C74



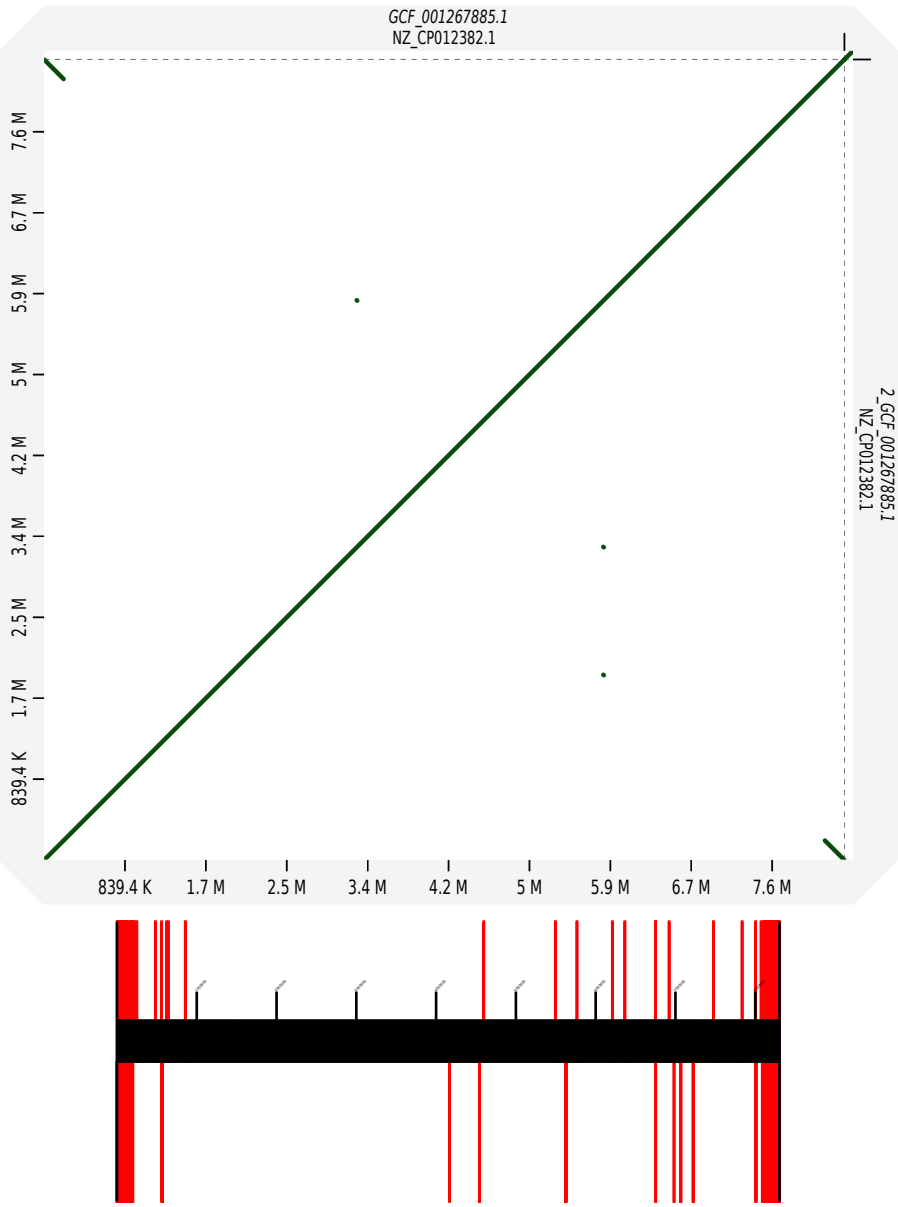
II) *S. collinus*; C19



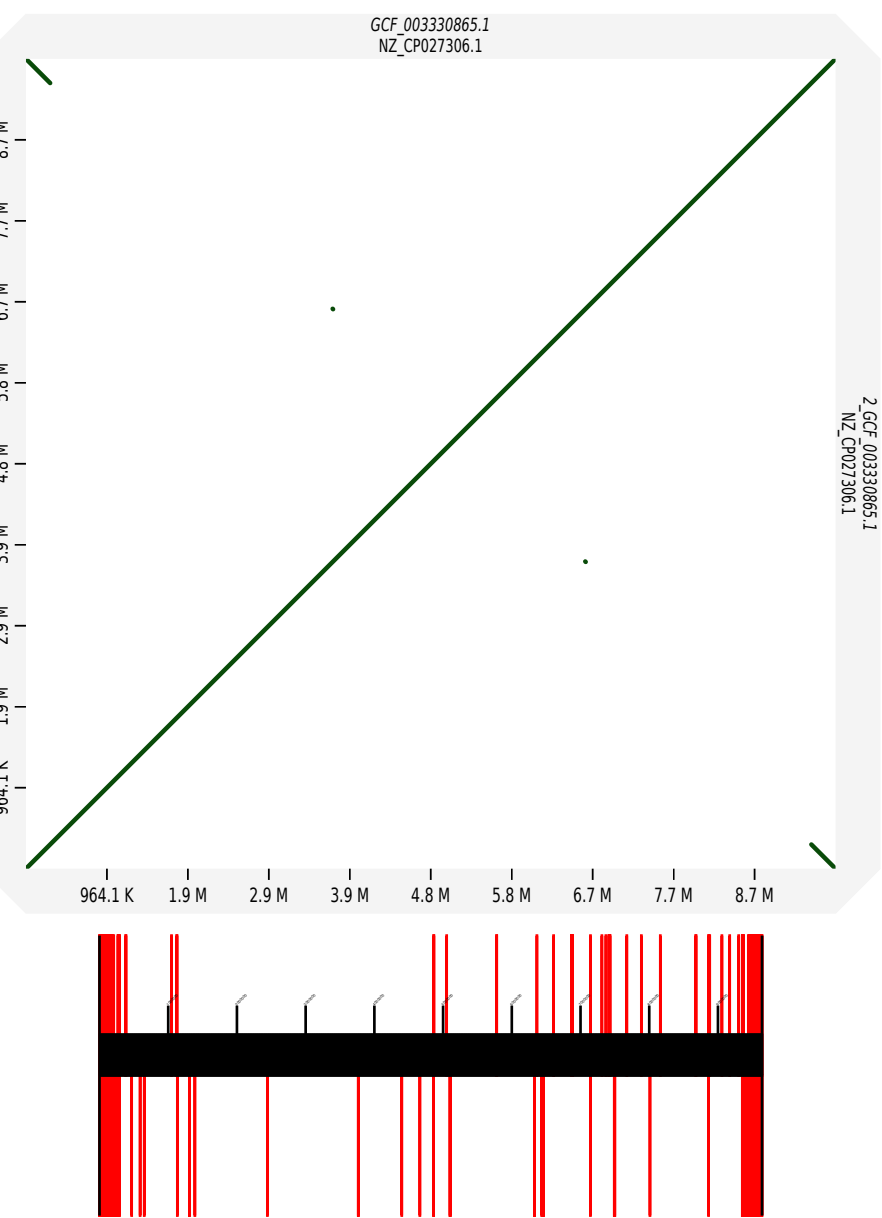
III) *S. pristinaespiralis*; C42



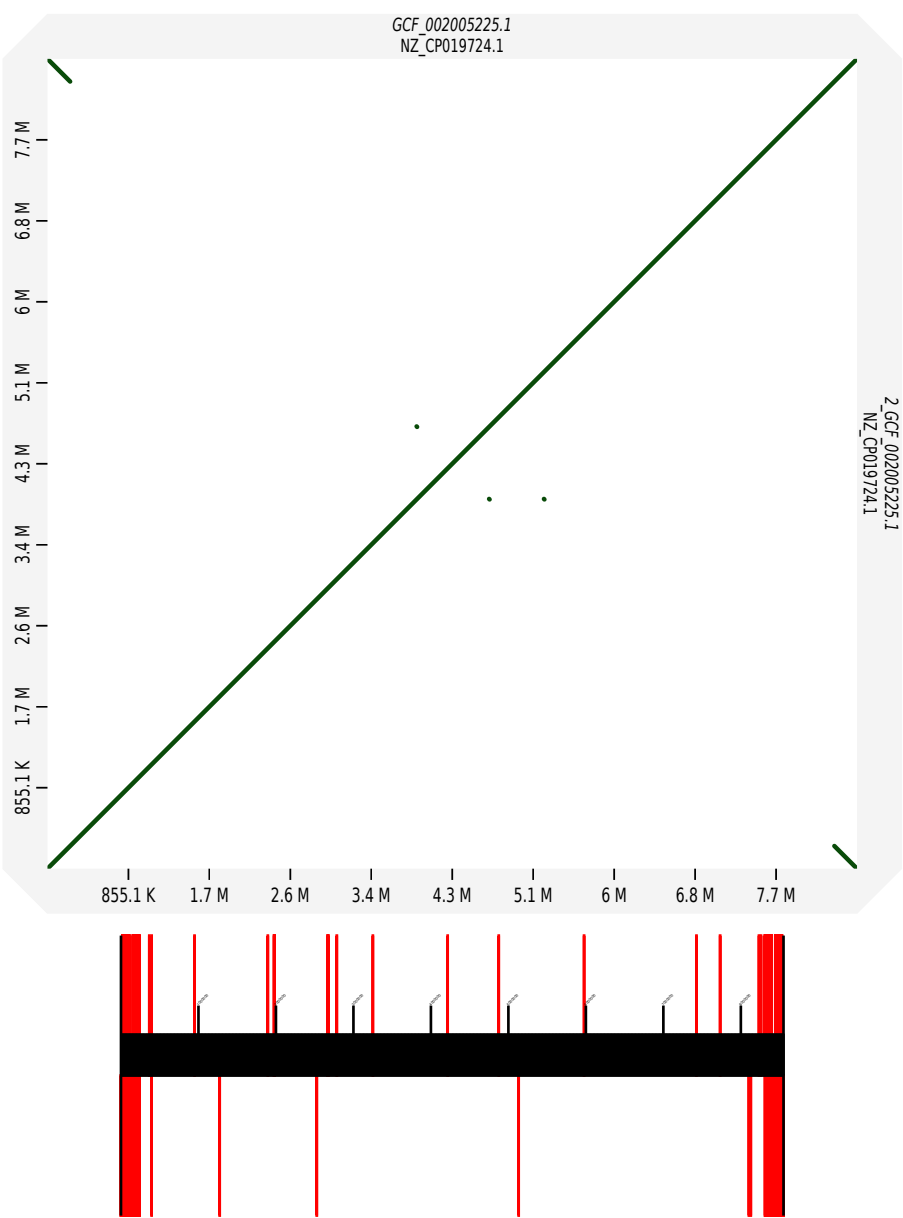
IV) *S. ambofaciens*; C32



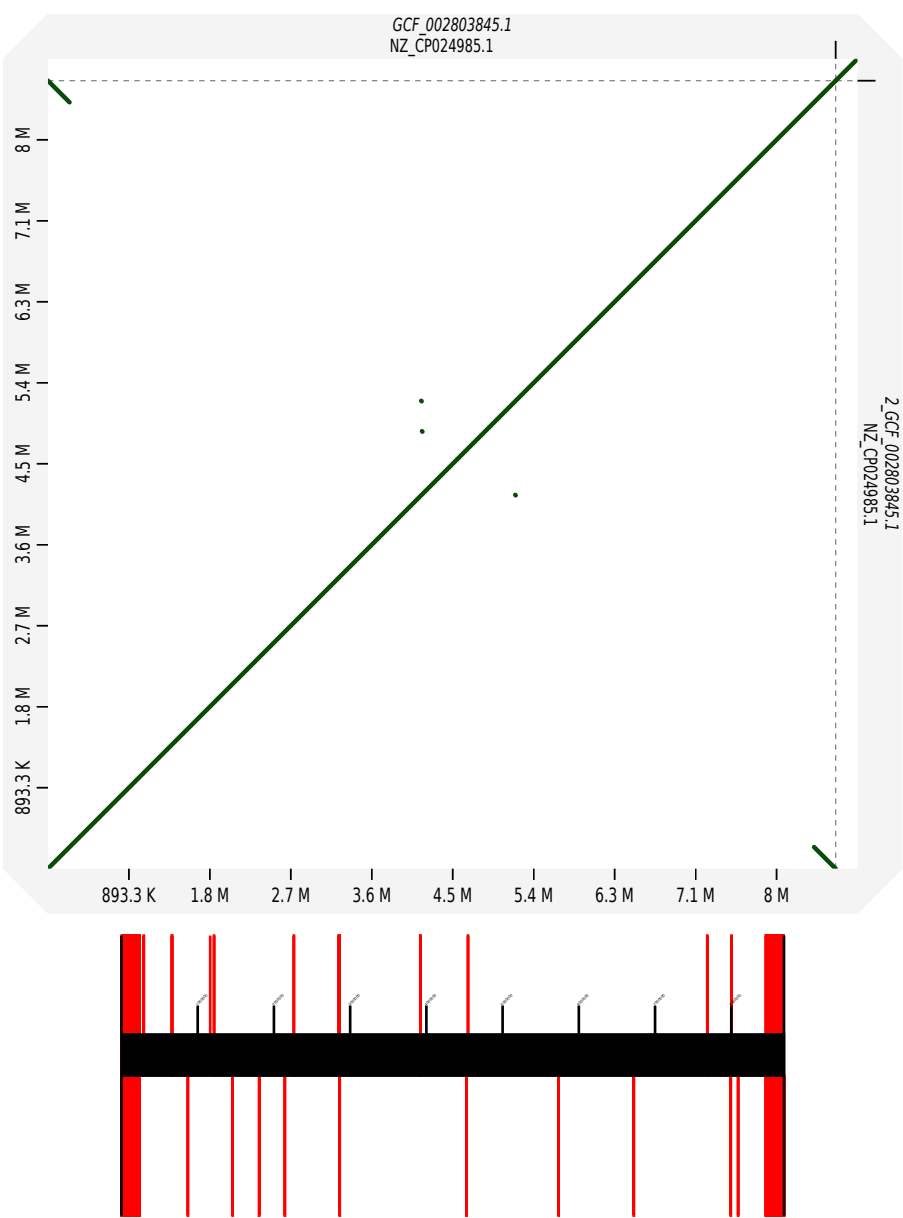
V) *S. atratus*; C153



VI) *S. pactum*; C102



VII) *S. lavendulae*; C47



VII) *Streptomyces* sp. TN58; C177

