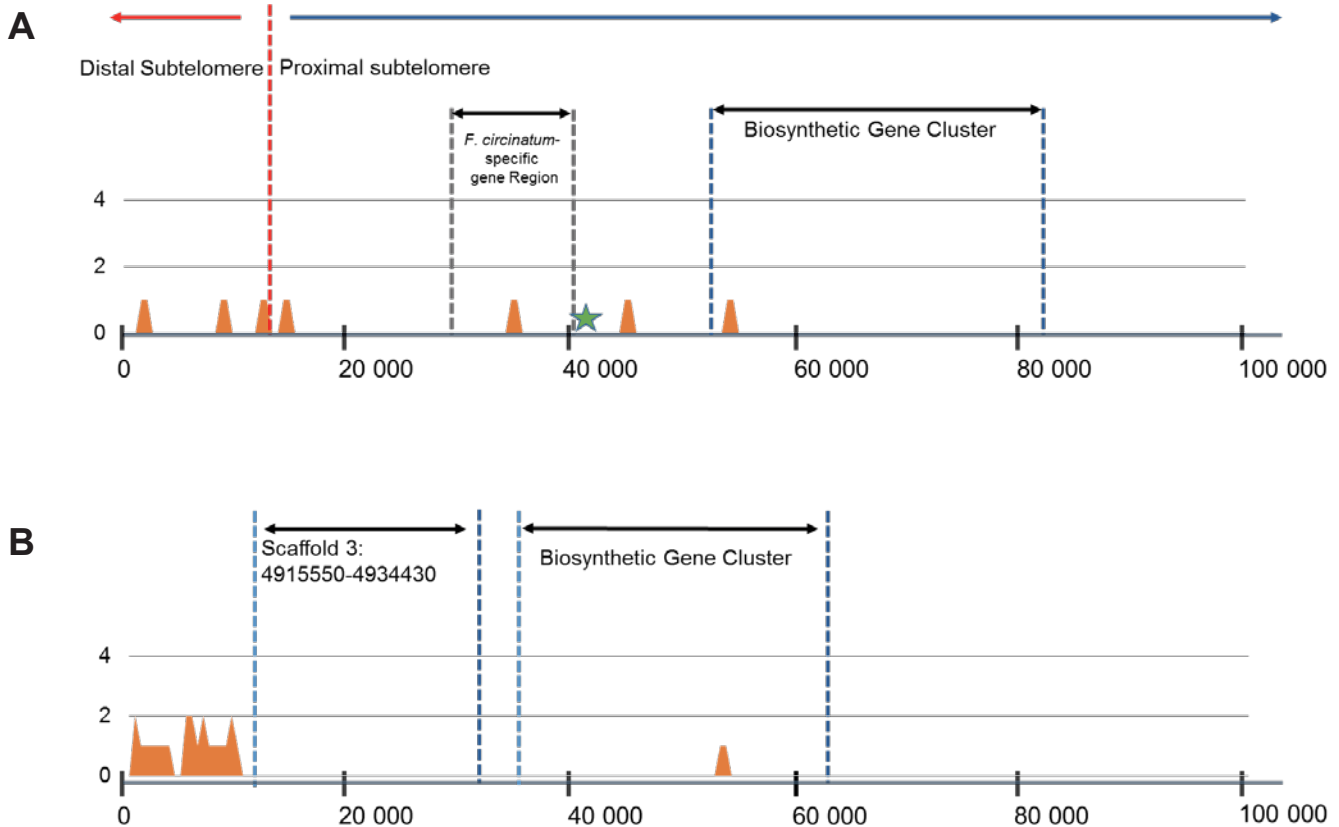
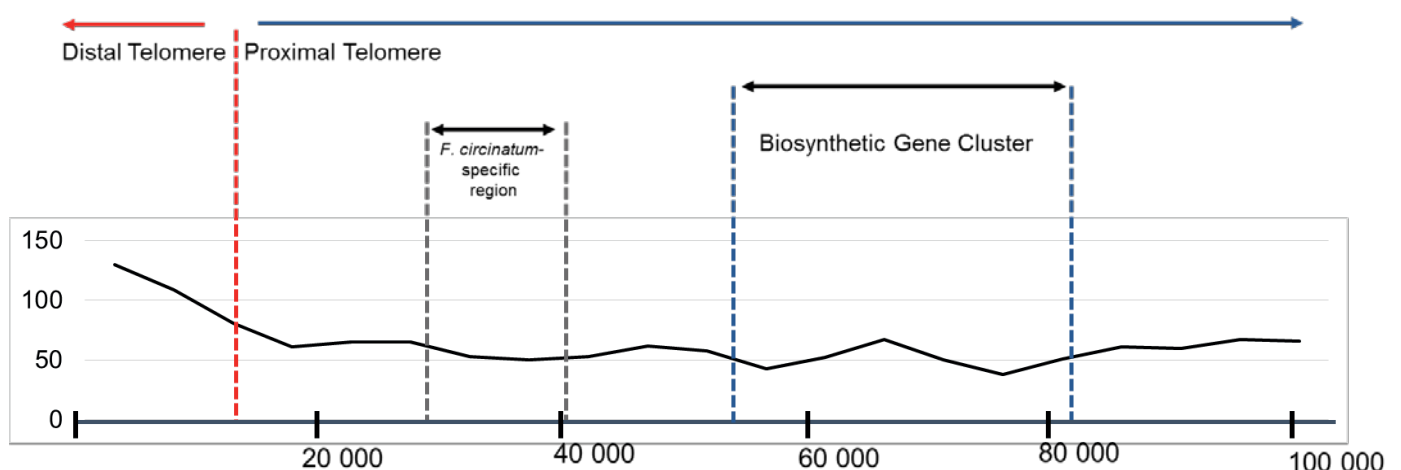


## Supplementary Figure S1



**Fig. S1.** Representation of homologous regions in *Fusarium circinatum* and *Fusarium temperatum*. (A) Schematic representation of the genomic organization of the first 100 000 bases of *F. circinatum* chromosome 3. Chart showing the count of transposable element repeat sequences in orange, determined using CENSOR-EMBL with a 1 000 bp sliding window and 500 bp increments. Transposable element repeat sequences are illustrated relative to the QTL marker, represented as a green star. (B) Schematic representation of the genomic organization the last 100 000 bases of *F. temperatum* scaffold three. The chart shows the count of transposable element repeat sequences in orange, determined using CENSOR-EMBL with a 1 000 p sliding window and 500 bp increments.

## Supplementary Figure S2



**Fig. S2.** Schematic representation of the genomic organization of the first 100 000 bp of chromosome 3 of *Fusarium circinatum*. Count of the "TTAGGG/CCCTAA" repeat motif across the first 100 000 bp of this region was determined using a 10 000 bp sliding window and 5000 bp increments.