

Table S8: Summary of tandem repeat sequences identified in the first 100 000 bp of chromosome 3 of *Fusarium circinatum*.

Indices ^A	Consensus repeat size	Copy number	Matches (%) ^B	Indels ^C	Score ^D
6812-6839	14	2	100	0	56
6843-6881	5	8	83	11	55
6842-6881	9	4	87	3	53
6843-6881	14	3	92	0	60
72425-72468	12	4	96	0	79

^A Genomic region in which repeated sequences are located (bp).

^B Average percentage of matches between copies repeated sequences within the index.

^C Average percentage of copies of the repeated sequence containing a insertion or a deletion.

^D Alignment score of the repeated sequences based on the overall average in matches, mismatches, insertions and deletions between repeated sequences located within the index.