

**Table S7:** List of simple repeat sequences identified in the first 100 000 bp of chromosome 3 of *Fusarium circinatum*.

Repeat motif	Orientation of repeat	Begin (bp)	End (bp)	Score <sup>a</sup>	Deletion (%) <sup>b</sup>	Insertion (%) <sup>c</sup>
(TTTCCT)n	+	1247	1278	16	0	3,2
(TTAA)n	+	917	1958	17	6,5	3,8
(TA)n	+	1959	1987	15	6,9	0
(TTAA)n	+	1988	1993	17	6,5	3,8
(ATA)n	+	2117	2166	19	0	8,7
(TAATA)n	+	6736	6798	15	3,2	4,8
(TTTCT)n	+	6843	6881	29	5,1	0
(TA)n	+	8231	8265	15	2,9	2,9
(TAATAC)n	+	8292	8374	16	7,2	2,3
(CTAT)n	+	9294	9356	18	3,2	3,2
(TA)n	+	10826	10851	17	3,9	0
(TACT)n	+	11819	11881	12	4,8	6,5
(TAGTAT)n	+	12097	12141	16	2,2	9,5
(CTG)n	+	22570	22594	12	8	3,9
(AATTA)n	+	35150	35191	13	0	5
(GCGAC)n	+	49266	49291	13	3,9	3,9
(CGCCCAT)n	+	63441	63483	13	0	4,9
(TGTCC)n	+	71676	71702	12	3,7	0
(GTC)n	+	72429	72461	14	0	0

<sup>a</sup> Alignment score of the repeated sequences based on the overall average in matches, mismatches, insertions and deletions between repeated sequences located within the index.

<sup>b</sup> Average percentage of deletions between repeat copies overall.

<sup>c</sup> Average percentage of insertions between repeat copies overall.