

**Supplementary Table 1.** Primer sequences for PCR analysis of *Kmr* and *pdeF* gene

Primer name	Sequence (5' → 3')	Base count	T <sub>m</sub> (°C)	Amplicon length (bp)
Kmr-F	CGCGATTAATTCACATGGATGCT	26	61.9	490
Kmr-R	TTCAACAGGCCAGCCATTACGCTCGT	26	67.8	490
pde-F	GAGCATGTCCGACAACCTGCAGCGCA	25	60.9	2,313 (wild type), 4,414 (MT16)
pde-R	ATGCCATACAATAGTCGGTTACAAT	25	59.3	2,313 (wild type), 4,414 (MT16)

PCR, polymerase chain reaction; T<sub>m</sub>, melting temperature; MT, mutant.

**Supplementary Table 2.** Summary of genome sequencing data using Illumina short-read sequencing method

Sample ID	Total bases (bp)	Total reads	GC (%)	Q20 (%)	Q30 (%)
MT3	1,088,276,932	7,207,132	53.8	96.4	91.6
MT4	1,113,376,454	7,373,354	53.7	96.8	92.4
MT5	1,174,768,826	7,779,926	53.3	96.7	92.2
MT6	1,124,713,534	7,448,434	53.8	96.9	92.5
MT12	1,268,666,666	8,401,766	53.8	97.0	92.7
MT13	1,271,973,566	8,423,666	53.6	96.8	92.3
MT16	1,059,333,554	7,015,454	53.8	96.9	92.4

MT, mutant.