Supplementary Table S2 Statistical summary of high-throughput sequencing data.

Sample	Clean reads	Clean bases	GC content	%≥Q30
CT5-10-1	24,683,787	7,386,057,914	50.36%	98.30%
CT5-10-2	23,183,722	6,942,706,155	50.58%	98.24%
CT5-10-3	24,452,608	7,317,413,851	50.50%	98.58%
CT5-5-1	21,665,573	6,481,458,067	50.49%	98.67%
CT5-5-2	20,347,725	6,088,854,918	50.35%	98.66%
CT5-5-3	21,160,070	6,327,403,466	50.45%	98.49%

Note: (1) Clean reads: total number of pair-end Reads in Clean Data; (2) Clean bases: Clean Data total bases; (3) ≥Q30% : Clean Data The percentage of bases with a mass value greater than or equal to 30.