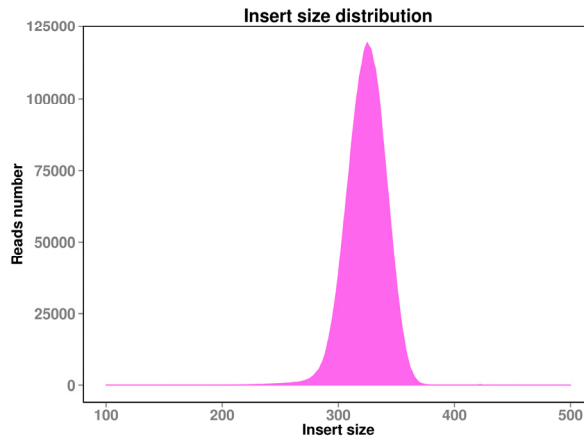


## Supplemental Figures and Tables

**Table S1.** Comparison statistics with reference genome Bt LLP29.

Sample	Total-Reads	Mapped (%)	Properly-Mapped (%)
LLP29-M19	14,602,840	98.45	98.04

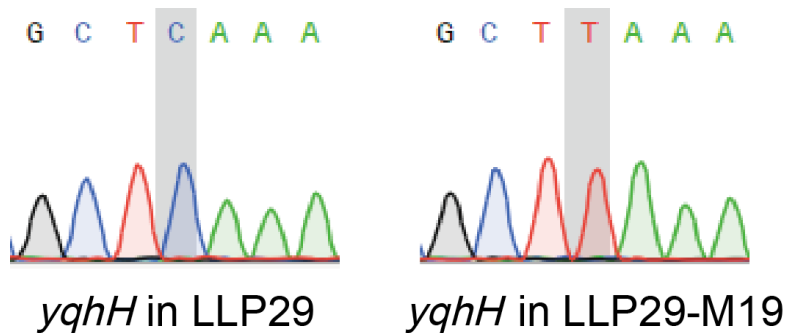
Total-Reads: The number of Clean Reads; Mapped (%): The percentage of Clean Reads mapped to the reference genome in all Clean Reads; Properly-mapped (%): The paired-end sequencing sequences are mapped to the reference genome and the distance conforms to the length distribution of sequencing fragments.



**Figure S1.** Distribution of Bt LLP29-M19 inserts. The abscissa is the length of the inserted fragment, and the ordinate is the number of corresponding reads.

**Table S2.** Statistics of SNPs detected by Bt LLP29-M29 and the reference genome.

SNP Number	Transition	Transversion	Ti/Tv	Heterozygosity	Homozygosity	Het-Ratio
1318	889	429	2.07	1085	233	0.17%



**Figure S2.** Sequence alignment of *yqhH* gene.

**Table S3.** Primers for vector construction, knockout and complementation, and validation of helicase activity.

<i>yqhH</i> -F	CGGGATCCATGAATGTCGATATTTCCGTAGATCG
<i>yqhH</i> -R	GGAATTCATGTTGCTGCATAGCCTTGC
5'H-A	H-GCACTGGCCGTCGTTTTACGGTCGTGACTGGGAAAACCCTGGCG
3'F-B	TTTTTTTTTTTTTTTTTTTTTCCAAGTAAAACGACGGCCAGTGC-F
<i>yqhH</i> -A1	CTAGAAGCTTCTGCAGACGCGTCGACGCTCCTTCTAAAGCAGAAGG
<i>yqhH</i> -A2	CACCTCAAATGGTTCGCTGCAAGAAATTTTCGCGCAATC

<i>yqhH</i> -B1	GAGCGCCTACGAGGAATTTTCGATCTACGGAAATATCGAC
<i>yqhH</i> -B2	GCCTCGCGTCGGGCGATATCGGATCCCATGACTTGCTAACCATTCCG
<i>yqhH</i> -K1	GATTGCGCGAAAATTTCTTGCAGCGAACCATTGAGGTG
<i>yqhH</i> -K2	GTCGATATTTCCGTAGATCGAAATTCCTCGTAGGCGCTC
<i>yqhH</i> -F1	ATGTGAGCGAGTAAGAGTGG
<i>yqhH</i> -R1	GATGGAGTGAAAGAGCCT
<i>yqhH</i> -F2	TGAAACCCAGGACAATAA
<i>yqhH</i> -R2	CCTCTTCTGCTCCAACTTCA
<i>yqhH</i> -R-F1*	TGTGAGCGAGTAAGAGTGCC
<i>yqhH</i> -R-R1*	GAATGGTAAAGCGATTCTAGC
<i>yqhH</i> -R-F2*	GAACAGGAGTAGCGGTTAGT
<i>yqhH</i> -R-R2*	CGAAAGATTCCACACATTCA

F: fluorescein, H: hexachlorofluorescein.