

Table S1(a) Parameters used for *de novo* assembly of the *Buchnera Aphis glycines* strain genome using the CLC Genomics Workbench.

Word Size	54
Bubble Size	650
Minimum Contig Length	250
Mismatch Cost	2
Insertion Cost	3
Deletion Cost	3
Length Fraction	0.9
Similarity Fraction	0.95

Table S1(b) Mapping parameters used for coverage analysis of the *Buchnera Aphis glycines* strain genome using the CLC Genomics Workbench.

Mismatch Cost	2
Insertion Cost	3
Deletion Cost	3
Length Fraction	0.8
Similarity Fraction	0.95
Auto-detect paired distances	Yes