

Table S3. Summary statistics of MGISEQ2000 paired-end (2×150) read sequence data and *de novo* assembly of the *Cacopsylla jukyungi* genome.

Sequencing data Summary	
Platform	MGISEQ 2000
Library type	Paired-end
Read length	150
Number of reads	266,128,190
Total bp	39,919,228,500
Assembled Genome Summary	
Number of scaffolds	967,146
N50	1,506
N80	524
N90	351
Longest (shortest) scaffold, in bp	179,525 (200)
GC level	38.29
Total scaffolds bp	874,354,878
Average scaffold length	904.06