

Evaluation indicators	Results
CEGMA	95.16% Completeness
Reads	98.84% Mapping rate; 92.98% Coverage
Qv	23.0487

Table S1. Genome assembly quality assessment for *E. corni*. Includes mapping rates, coverage, heterozygosity, and base-level accuracy (Qv) to evaluate completeness, consistency, and sequence accuracy.

Chromosome	Best-hit species	Phylum	Class	Order	E-value	Identity (%)
Chr1	<i>Eretmocerus</i> sp. WTT-2016	Arthropoda	Insecta	Hymenoptera	0.0	95.31
Chr2	<i>Nasonia vitripennis</i>	Arthropoda	Insecta	Hymenoptera	0.0	81.02
Chr3	<i>Phlogophora meticulosa</i>	Arthropoda	Insecta	Hymenoptera	0.0	81.12
Chr4	<i>Trichogramma pretiosum</i>	Arthropoda	Insecta	Hymenoptera	0.0	79.63

Table S2. Taxonomic assignment of the four major chromosomes based on BLASTN against NCBI nt database. All four chromosomes showed best hits to insect species (Hymenoptera or Lepidoptera), with no evidence of prokaryotic or non-insect metazoan contamination.

Category	Number of BUSCOs
Complete BUSCOs (C)	1121
Complete and single-copy BUSCOs (S)	1090
Complete and duplicated BUSCOs (D)	31
Fragmented BUSCOs (F)	104
Missing BUSCOs (M)	142
C: 82.0% [S: 79.7%, D: 2.3%], F: 7.6%, M: 10.4%	1367

Table S3. BUSCO assessment of *E. corni* gene models (longest transcript per gene). Analysis performed using the insecta_odb10 reference database. Statistics include percentages of complete, single-copy, duplicated, fragmented, and missing BUSCO genes.