

**Table S1.** Bracovirus-related sequences flanking Hel\_C35 insertion.

| Conserved sequences | Distance from Hel_c35 | BV with > 70% sequence identity hits |
|---------------------|-----------------------|--------------------------------------|
| Upstream            |                       |                                      |
|                     | 16.9 kb               | CcBV, CsBV                           |
|                     | 9.5 kb                | CvBV, CcBV, CsBV, GiBV, GfBV, MmBV   |
|                     | 1.18 kb               | CcBV, CsBV                           |
|                     | 0 kb                  | CsBV, CvBV*, CcBV*, GiBV*            |
| Downstream          |                       |                                      |
|                     | 2.5 kb                | CcBV, CsBV                           |
|                     | 3.5 kb                | CvBV, CcBV, CsBV,                    |
|                     | 5.1 kb                | CvBV, CcBV, CsBV                     |

\* Hits retrieved from adjacent sequences (see text)

Abbreviations: CcBV, *Cotesia congregata* bracovirus; CsBV, *Cotesia sesamiae* bracovirus; CvBV, *Cotesia vestalis* bracovirus; MmBV, *Microplitis mediator* bracovirus; GiBV, *Glyptapanteles indiensis* bracovirus; GfBV, *Glyptapanteles flavicoxis* bracovirus.