|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Viral species | CcFV1 | CcFV2 | DmFV\* | EfFV | LbFV\* | LhFV | PcFV | PoFV |
| Data sources | Cotesia congregata MsT | Cotesia congregata CcC | Drosophila melanogaster | Encarsia formosa | Leptopilina boulardi | Leptopilina heterotoma | Psyttalia concolor | Platygaster orseoliae |
| Sequencing approach | Single end 454  3, 8 and 20 kb mate-pairs 454 +  paired end Illumina | PacBio Sequel | paired end Illumina | Illumina + Nanopore | 454 (type de 454?) +  paired end Illumina +  Minion Nanopore | Purification mais laquelle ? | Paired-end Illumina | Paired-end Illumina |
| Reference | Gauthier et al., 2021 and this study | This study | Wallace et al., 2021 | This study | Lepetit et al., 2017 | This study | This study | This study |
| Assembly parameters | ??? | ??? | ??? | ???Megahit + Porshop + Unicycler ? | ??? | ??? | ???UDBA | ???UDBA |
| Viral genome accession # |  |  | MT496832 to MT496840 |  | KY009685 |  |  |  |
| State | circular | circular | fractioned | circular | circular | fractioned | fractioned | fractioned |
| **Average coverage (wasp genome/virus genome)** | ??? | ??? | ??? | ??? | ??? | ??? | ??? | ??? |
| Cumulative size (bp) | 101,121 | 137,848 | 86,478 | 164,366 | 111,453 | 106,195 | 131,186 | 126,748 |
| # ORFs | 104 | 112 | 69 | 156 | 108$ | 110 | 122 | 128 |
| AT% | 59.8 | 74 | 66.5 | 58.6 | 78.7 | 66.5 | 67.1 | 71.8 |
| CD% | 92 | 81.5 | 86.1 | 79.9 | 80.7 | 90 | 82.5 | 82.7 |

$ from which nine were not confirmed when using the same method as the one used for the 6 new FV genome annotation (CD% = 79.2%), and to which the lef-5 homologous gene predicted using an alternative start codon should be added.

\*previously published