|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Contig #** | **Length (bp)** | **NCBI Accession No of Best hit** | **Best hit ID** | **e-Value** | **Max % ID** | **% Similarity to SSaDV** |
| V41\_94 | 1603 | ARI46484.1 | Ambidensovirus CaaDV1 VP4 | 8.00E-162 | 59 | 43 |
| V41-158 | 1565 | ARI46481.1 | Ambidensovirus CaaDV1 NS1 | 2.00E-68 | 63 | 54 |
| V42\_5549 | 929 | AIQ82698.1 | SSaDV VP4 | 1.00E-123 | 65 | 65 |
| V42\_6339 | 981 | ARI46481.1 | Ambidensovirus CaaDV1 NS1 | 3.00E-83 | 68 | 66 |
| V50\_5320 | 851 | ARI46483.1 | Ambidensovirus CaaDV1 VP3 | 3.00E-87 | 64 | n/a |

**Supplemental Table 13:** Similarity of 5 densovirus-like contiguous sequences derived from geographic samples. Max % Identity was determined by BLASTx against the non-redundant (nr) database at NCBI. % Similarity to SSaDV was determined based on BLASTn analysis against the SSaDV genome.