Suplementary table 1: Oligonucleotides designed to amplify putative novel viral sequences identified in salivary glands of mosquitoes from Pantanal, Brazil.

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| **Target** | **Genomic region** | **Primer sequence** | **Estimated size (bp)** | **Genome position** |
| Iflavirus-like | C-terminal | Ifla1F: AACACGTTCCTCCTGTTGGG | 300 | 7,285-7418 |
| Ifla1R: TGTTTAGACTTAGGCGGCGG |  |
| Iflavirus-like | C-terminal | Ifla2F: TGCGGAACAAATTCATTGCGAT | 1500 | 5,400-6,918 |
| Ifla2R: ACAACGAACGGAAACCATCTCT |  |
| Rhabdovirus-like | M-G\* | MGMF: TGGCTTGAAAACATCTATTCAGGC | 1000 | 1,319-1,980 |
| MGMR: TGCTACTACTGCAGTGAATCCG |  |
| Rhabdovirus-like | G-L | GLMF: ACAGCTTACGACCGACATC | 1000 | 1,900-2,810 |
| GLMR: GAAACTGCCTGATGGAGGGG |  |
| Circovirus-like | Rep-Cap\*\* | CircoF: AAATTTAATCGAGAAACCAGTAACTTTGAA | 1000 | 100-500 |
| CircoR: AATCTTGTTTTTCCGACTCCGCTT |  |  |

\*Region between M-G, G-L genes. \*\*Forward primer designed to Rep: Replication associated protein; reverse primer designed to Cap: Capsid protein (genome with circular topology).