**Table S1.** Average nucleotide composition (%) of Cer-SERV genomes.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Nucleotide** | **Complete genome** | **LTR** | **Gag-pro-pol** | **Env** | **SRV** (type D retrovirus)[1] |
| A | 31.4 | 22.6 | 33.3 | 29.7 | 33.3 |
| T/U | 26.0 | 27.2 | 25.7 | 27.5 | 25.8 |
| C | 23.9 | 33.2 | 21.9 | 24.3 | 22.8 |
| G | 18.7 | 17.0 | 19.1 | 18.5 | 18.2 |

1. Berkhout, B.; Grigoriev, A.; Bakker, M.; Lukashov, V.V. Codon and amino acid usage in retroviral genomes is consistent with virus-specific nucleotide pressure. *AIDS research and human retroviruses* **2002**, *18*, 133-141, doi:10.1089/08892220252779674.