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**Supplementary Data**

**Discovery of novel DNA viruses in small mammals from Kenya**

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Table S1 Sequences of primers used for PCR screening of DNA viruses

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Virus | Primer name | Primer sequence (5'-3') | Target gene | Amplicon size |
| Adenovirus | Adeno-pol-F | CAGCCKCKGTTRTGYAGGGT | polymerase | Round 1  440bp |
| Adeno-pol-R | GCHACCATYAGCTCCAACTC |
| Adeno-pol-nF | GGGCTCRTTRGTCCAGCA | Round 2  260bp |
| Adeno-pol-nR | TAYGACATCTGYGGCATGTA |
| Adeno-associated virus | AAV-F | CTGCCCACCTACAACAACCA | *cap* gene | 447bp |
| AAV-R | GTAYTCBAGGCAGTAGAAGG |
| Bocavirus | panBOV-F1 | TAATGCAYCARGAYTGGGTIGANCC | *NS1* gene | Round 1  293bp |
| panBOV-R1 | GTACAGTCRTAYTCRTTRAARCACCA |
| panBOV-F2 | GCAYCARGAYTGGGTIGANCCWGC | Round 2  290bp |
| panBOV-R1 | GTACAGTCRTAYTCRTTRAARCACCA |
| Hepadnavirus | HBV-pol-F1 | TAGACTSGTGGTGGACTTCTC | polymerase | Round 1  590bp |
| HBV-pol-R1 | CATATAASTRAAAGCCAYACAG |
| HBV-pol-F2 | TGCCATCTTCTTGTTGGTTC | Round 2  260bp |
| HBV-pol-R2 | AGTRAAYTGAGCCAGGAGAAAC |
| Herpesvirus | TS-TERM\_707s | TTGTGGACGAGRSIMAYTTYAT | terminase | Round 1  519bp |
| TS-TERM\_707as | ACAGCCACGCCNGTICCIGAIGC |
| TS-TERM\_708s | GCAAGATCATNTTYRTITCITC | Round 2  419bp |
| TS-TERM\_708as | TGTTGGTCGTRWAIGCIGGRT |
| Polyomavirus | VP1/1f | CCAGACCCAACTARRAATGARAA | *VP1* gene | Round 1  829-1137bp |
| VP1/1r | AACAAGAGACACAAATNTTTCCNCC |
| VP1/2f | ATGAAAATGGGGTTGGCCCNCTNTGYAARG | Round 2  249-273bp |
| VP1/2r | CCCTCATAAACCCGAACYTCYTCHACYTG |
| Poxvirus | rpo OPV-F1 | CTGTAGTTATAAACGTTCCGTGTG | polymerase | 204bp |
| rpo OPV-R1 | TTATCATACGCATTACCATTTCGA |

Table S2 Amino acid sequence identity of the major ORFs of *Lemniscomys striatus* polyomavirus KY187 and two most closely related polyomavirus species

|  |  |  |
| --- | --- | --- |
| ORFs | Related polyomavirus species | |
| *Glis glis* polyomavirus 1 | *Sciurus carolinensis* polyomavirus 1 |
| VP1 | 71.8% | 74.9% |
| VP2 | 47.3% | 46.1% |
| VP3 | 52.2% | 49.0% |
| LTAg | 58.8% | 59.7% |
| STAg | 46.7% | 44.6% |

\* The GenBank accession numbers of the two related polyomavirus genome sequences are: *Glis glis* polyomavirus 1 (MG701352), *Sciurus carolinensis* polyomavirus 1 (MK671101).