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**Supplementary Data**

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

**Griphin Ochieng Ocholaa,b,c,d, Bei Lia, Vincent Obandae, Sheila Ommehf, Harold Ochiengc, Xing-Lou Yanga,b, Samson Omondi Onyuoka,c , Zheng-Li Shia,b, Bernard Agwandac\*, Ben Hua,b\***

*a CAS Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, 430071, China*

*b Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan, 430074, China*

*c Mammalogy Section, National Museums of Kenya, Nairobi, 40658-00100, Kenya*

*d University of Chinese Academy of Sciences, Beijing, 100049, China*

*e Veterinary Services Department, Kenya Wildlife Service, Nairobi, 40241-00100, Kenya*

*f Institute of Biotechnology Research, Jomo Kenyatta University of Science and Technology, Nairobi, 62000-00200, Kenya*

\*Corresponding authors,

benrisky@gmail.com (B. Agwanda); huben@wh.iov.cn (B. Hu)

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 1440bp |
| Adeno-pol-R | GCHACCATYAGCTCCAACTC |
| Adeno-pol-nF | GGGCTCRTTRGTCCAGCA |  Round 2260bp |
| Adeno-pol-nR | TAYGACATCTGYGGCATGTA |
| Adeno-associated virus | AAV-F | CTGCCCACCTACAACAACCA | *cap* gene | 447bp |
| AAV-R | GTAYTCBAGGCAGTAGAAGG |
| Bocavirus | panBOV-F1 | TAATGCAYCARGAYTGGGTIGANCC | *NS1* gene | Round 1293bp |
| panBOV-R1 | GTACAGTCRTAYTCRTTRAARCACCA |
| panBOV-F2 | GCAYCARGAYTGGGTIGANCCWGC | Round 2290bp |
| panBOV-R1 | GTACAGTCRTAYTCRTTRAARCACCA |
| Hepadnavirus | HBV-pol-F1 | TAGACTSGTGGTGGACTTCTC | polymerase | Round 1590bp |
| HBV-pol-R1 | CATATAASTRAAAGCCAYACAG |
| HBV-pol-F2 | TGCCATCTTCTTGTTGGTTC | Round 2260bp |
| HBV-pol-R2 | AGTRAAYTGAGCCAGGAGAAAC |
| Herpesvirus | TS-TERM\_707s | TTGTGGACGAGRSIMAYTTYAT | terminase  | Round 1519bp |
| TS-TERM\_707as | ACAGCCACGCCNGTICCIGAIGC |
| TS-TERM\_708s | GCAAGATCATNTTYRTITCITC | Round 2419bp |
| TS-TERM\_708as | TGTTGGTCGTRWAIGCIGGRT |
| Polyomavirus | VP1/1f | CCAGACCCAACTARRAATGARAA | *VP1* gene | Round 1829-1137bp |
| VP1/1r | AACAAGAGACACAAATNTTTCCNCC |
| VP1/2f | ATGAAAATGGGGTTGGCCCNCTNTGYAARG | Round 2249-273bp |
| 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).