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PII: S0168-1702(17)30215-0
DOI: http://dx.doi.org/doi:10.1016/j.virusres.2017.05.003
Reference: VIRUS 97131

To appear in: *Virus Research*

Received date: 15-3-2017
Revised date: 5-5-2017
Accepted date: 5-5-2017

Please cite this article as: Qiu, Yuan, Chen, Ji-Ming, Wang, Tong, Hou, Guang-Yu, Zhuang, Qing-Ye, Wu, Run, Wang, Kai-Cheng, Detection of Viromes of RNA Viruses Using the Next Generation Sequencing Libraries Prepared by Three Methods.Virus Research http://dx.doi.org/10.1016/j.virusres.2017.05.003

Detection of Viromes of RNA Viruses Using the Next Generation Sequencing Libraries Prepared by Three Methods

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Highlights

- RNA-Seq libraries were constructed using three methods.
- RNA virome in ducks was detected.
- RNA virome in mink was detected.
- Various viruses in ducks or minks were possibly first identified.

Abstract: Virome (viral megagenomics) detection using next generation sequencing has been widely applied in virology, but its methods remain complicated and need optimization. In this study, we detected the viromes of RNA viruses of one mock sample, one pooled duck feces sample and one pooled mink feces sample on the Personal Genome Machine platform using the sequencing libraries prepared by three methods. The sequencing primers were added through random hybridization and ligation to fragmented viral RNA using a RNA-Seq kit in method 1, through random reverse transcription (RT) and polymerase chain reaction (PCR) in method 2 which was developed in our laboratory, and through hybridization and ligation to fragmented amplicons of random RT-PCR using a single primer in method 3. Although the results of these three samples (nine libraries) all showed that more classified viral families and genera were identified using methods 2 and 3 than using method 1, and more classified viral families and genera were identified using method 2 than using method 3, most of the differences were of no statistical significance. Moreover, 11 mammalian viral genera in minks were possibly identified for the first time through this study.