Objectives
The aim is to identify new HEV animal reservoirs that could contribute to viral zoonotic transmissions. This will give us a better understanding for viral zoonosis, evolutionary history and preparedness for preventive measures.

Introduction
Hepatitis E virus (HEV):
• ~7.2 kb positive ssRNA virus member to the genus Hepevirus in the Hepeviridae family. The HEV genome is organized with three open reading frames (ORFs1-3).

Material and Method
Moose (Alces alces) is the largest species in the deer family and also hunted for human consumption. Here we report for the first time a novel HEV isolate detected in a Swedish Moose.

Result
• qPCR screening assay is both positive for HEV RdRp and capsid region (C_r-value of 33 respectively 34).
• The percentage sequence identity for each Hepevirus compared to the Moose HEV sequence is illustrated below.

Conclusion
The amplified ORF1-ORF2/ORF3 sequence are very useful for HEV analysis to expand our understanding of HEV. Low sequence identity to other HEVs demonstrates that Moose HEV is a potential new genotype or forms a separate genus. Diverged ORF3 might reflect host adaptation, which is also seen in Hepeviruses like Bat HEV [3]. Moose HEV expands the HEV reservoir and could contribute a potential zoonotic route to the human population. Therefore it is important to identify new types of HEVs.

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References