We appreciate the feedback from both reviewers and feel that their suggestions have significantly improved the quality of the manuscript. As will be apparent below, we struggled with adding to the text while respecting the scope of MRA and the formatting guidelines to limit manuscripts to 500 words. The manuscript is currently at ~520 words. In the responses below we refer to the line numbers of the marked up version of the manuscript.

**Reviewer #1 (Comments for the Author (Required)):**

**l. 37: Please briefly describe the protocol used for RNA extraction and library preparation, as well as the sequencing (platform & read length)**

The data used in this study was originally published in Jenior *et al.* 2017 and Jenior *et al.* 2018 (see line 15) and has been publicly available online for at least 2 years. Given the 500 word limit on this paper and that the methods used have already been published elsewhere, we do not believe they should be included here.

**l. 39: Please indicate which tool was used for the RdRP screening (Blast ? Hmmsearch ?) and which reference sequence/model was used (i.e. was this all RdRP from Viral RefSeq ? All RdRP from specific viral groups ?).**

Contigs were screened for the presence of RdRP coding sequences using Blast v2.9.0 against a database containing all Viral RefSeq protein sequences annotated as RdRP. The database used in screening is publicly available and can be found here:

<https://github.com/SchlossLab/Stough_Mouse_RNA_Virome_MRA_2019/blob/master/data/references/rdrp_bait.fasta>

We have edited the text to include these details (see lines 24-26).

**l. 47 & 50: Please briefly indicate how it was determined that the genomes were "complete" (as indicated in the title). Otherwise, the contigs should be referred to as "coding-complete".**

Thank you for bringing this to our attention. As these genomes appear to be linear, more work is required to validate the true end sequences of the genomes. We have changed the text to state that genomes are coding-complete.

**l. 51: "46.2" should be "46.2%"**

Thank you for bringing this to our attention, the text has been edited accordingly.

**Fig. 1: Please highlight the new virus genomes on both tree so that a reader can easily identify where they branch**

Thank you for bringing this to our attention, we have edited the figure accordingly.

**## Reviewer #2:**

**A few more suggestions:**

**Please be careful with the use of "microbiome", "microbiota", "microbe", etc. It is often not very clear if the entire ecosystem or only bacteria are referred to. Please rephrase were appropriate.**

Thank you for bringing this to our attention. We have examined the text accordingly.

**The names of the novel sequences (as used in the tree) should be mentioned in the text.**

Thank you for bringing this to our attention. We have edited the text accordingly.

**L16: I am not sure if RNA viruses are still been ignored. This could have been said 10 years ago, but not anymore in my opinion. I would suggest rephrasing along the lines of e.g. "RNA viruses remain understudied".**

Thank you for bringing this to our attention. We have edited the text accordingly.

**L23 "infection" of what?**

Infection of mammals.

**L26-27: By now, there are numerous manuscripts in literature investigating RNA viruses in the gut and many other samples types. Please rephrase.**

The current literature is still dominated by efforts to describe DNA virus populations. While RNA virus studies do exist, this does not mean the field is not “focused on using DNA metagenomics” as described here.

**L37: Was any quality trimming performed on the reads before assembly?**

RNA sequences from each sample were trimmed of adapter sequences and low-quality bases using Trimmomatic v0.39. The text has been edited to include this information.

**L41: indicate the length range of these 29 contigs.**

As these contigs are not part of the resource being announced here, we do not believe it is appropriate to include the requested information.

**L42: "Almost all RNA viruses"? Are there RNA viruses without an RdRp?**

Retroviruses do not encode RdRP.

**L44: "...using IQ-TREE v1.6.12 and relevant reference sequences selected based on XXX (10)."**

Thank you for bringing this to our attention, we have edited the text accordingly.

**L47: provide family and genus (both in Italic) the astrovirus belongs to.**

Thank you for bringing this to our attention, we have edited the text accordingly.

**L48: Figure 1A should be described. What were the most closely related known viruses and their hosts, etc... How close was their similarity?**

As we only have 500 words to describe the context surrounding these virus genomes, we do not believe this extra detail is relevant given the scope of a Microbiology Resource Announcement. The code used to generate these analyses, and the results are freely available online as described in the Data Availability section.

**L52: Narnaviridae should be in Italic, and provide some more information about this family of viruses (eg. Hosts etc...). It should be added that mice are most likely not the host of this virus... More likely fungi…**

The scope of a Microbiology Resource Announcement does not allow for speculation of host for these viruses.

**L52: Figure 1B should be described. What were the most closely related known viruses and their hosts, etc... How close was their similarity?**

As we only have 500 words to describe the context surrounding these virus genomes, we do not believe this extra detail is relevant given the scope of a Microbiology Resource Announcement. The code used to generate these analyses, and the results are freely available online as described in the Data Availability section.