**Reviewer Comments:**

**Reviewer 1  
This manuscript represents a valuable contribution to the field and is suitable for publication with minor revision. Here are somme comments to be addressed**

We are very grateful to the reviewer for this suggestion. The manuscript is improved by the feedback.

**1- Expanding the discussion to explore the potential functional implications of the identified transcripts and splicing patterns, particularly regarding viral replication and immunosuppression, would strengthen the manuscript.**

We appreciate the reviewer for this suggestion. We have addressed this by including “*These new potential proteins and isoforms significantly extend the repertoire of THEV gene products than predicted, adding a hefty number of proteins of undefined function to the previously predicted five (See* ***Figure 1****). These new potential proteins and isoforms of unknown functions may mediate or contribute to viral replication efficiency, or the immunosuppression associated with THEV. Hence, further studies of these potential proteins is urgently needed*” on line 476-481 of the discussion.

We have included “*The potential new proteins identified in our work adds to the number of proteins with undefined functions in THEV; these may have roles in viral replication efficiency, or the immunosuppression associated with THEV. Hence, further studies of these proteins and other predicted proteins of unknown function should be useful in elucidating THEV-induced immunosuppression*” and “*More importantly, this work characterizing the splicing of THEV mRNAs will allow researchers to accurately clone any THEV gene(s) of interest to study its potential role in inducing immunosuppression or other functions*” on lines 534-538 and 540-542 of the conclusion section, respectively. We have also included a condensed version of this idea in the abstract on line 50-52: “*Studies of the newly identified potential proteins should be urgently performed as these proteins may have roles in THEV-induced immunosuppression.*”

**2- While some limitations are mentioned, the authors should consider expanding the challenges posed by overlapping transcripts and the potential for false positives/negatives in transcript assembly.**

We have addressed this by discussing more limitations and elaborating on some of those previously stated. In the third paragraph of the discussion section (on lines 441-457) of the manuscript, we have written this: “*Short read deep sequencing effectively reconstructs full AdV mRNA structures, particularly mapping splice sites (18). However, the substantial overlapping nature of AdV mRNAs and fragmentation during library preparation make it challenging to map the exact TSS, TTS, and PASs of assembled transcripts. As AdVs make heavy use of alternative polyadenylation, short read RNA-seq is ill-equipped to discriminate mRNA variants of the same gene produced via alternative polyadenylation. Thus, shorter variants of alternatively polyadenylated mRNAs may potentially be incorporated into the longer variants during transcript assembly, significantly diminishing the diversity of mRNA in the transcriptome. Also, independent transcripts with significant overlaps may be assembled as a single, longer mRNA, since the short reads alone do not provide enough context for the transcript assembler (StringTie) to distinguish them. Such fusions may affect the transcript expression level estimations by inflating or deflating the expression levels of the transcripts involved, affecting the proper understanding of the temporal gene expression regulation and also the diversity of the transcriptome. Transcripts that have reads mistakenly fused with them would have inflated expression levels while those whose reads are counted elsewhere would show false lower expression levels. In our case, since we used other independent methods to validate the splice junctions, we believe these drawbacks to be minimized.*”

**Also, here are some limitations that should also be stated:  
- The study focused on a specific strain of THEV (the VAS vaccine strain), and findings may not be generalizable to other strains or variants of THEV.**

We are grateful to the reviewer for suggesting this important point. We have included “*We also note that although THEV genomic sequences show minimal differences between strains (12), the transcriptomes may have significant variations; hence, our results may vary from other THEV strains*” on line 531-533 to communicate this.

**- The study primarily used in vitro experiments with a turkey B-cell line, and the relevance of these findings to in vivo infections or other cell types may be limited.**

We are grateful to the reviewer for suggesting this important point. We have included “*Also, performing the study in vivo or with primary turkey cells may show different results*” on line 533-534.

**- The comparison of THEV gene expression patterns to those of human adenoviruses may introduce biases due to differences in viral biology and host interactions.**

Unfortunately, our study is the first of its kind for this genus of adenovirus (Siadenoviruses); hence there is no prior study or a more closely related virus to make comparisons but the human adenoviruses which are the best studied.We acknowledge that there may be substantial differences in viral biology and host interactions; however, the comparisons we make are only to note similarities or differences between THEV and the human adenoviruses that may suggest a similar biology or process or difference worthy of investigation.

**- The study's conclusions are based on the data obtained from a single experiment, and additional studies or replication of the findings would strengthen the reliability of the results.**

Since our work is the first transcriptomic study for THEV I’m not sure what the reviewer is requiring us to do here?

**- The challenges or limitations faced during the study, which could provide a more balanced perspective on the study's outcomes, should be stated.**

We have addressed this by including a more elaborate challenges. In the first paragraph of the discussion section (on lines 421-427) of the manuscript, we write these two challenges: “*Furthermore, in our case, no prior transcriptomic studies for THEV exist; hence, assembling the transcripts without any prior experimentally-derived annotation of THEV splicing using only short illumina reads proved difficult. Lastly, we had initially planned to sequence RNA from another time point (8 hpi); however, all the RNA samples from 8 hpi and one replicate sample from 12 hpi got too degraded during the library preparation steps to be yield any useful data. We believe that these would have contributed to better insights into the temporal expression levels and splicing.*” **3- The manuscript should be English edited  
- The first definition mentions MOI in line 119 and then abbreviates only at line 482**

We have addressed this by spelling out the full definition of MOI on line 146 and abbreviating it on the second mention on line 569.

**- transcription unit, start codon, turkey hemorrhagic enteritis virus should be abbreviated in all manuscripts after first definition**

We are grateful to the reviewer for pointing this out. We have addressed this comment by abbreviating the words/terms stated by the reviewer throughout the manuscript after their first definition. The changes were made for transcription unit on lines 431, 595, 767, 781, and 809; for start codon on lines 277, 492, 811, 832, 844, and 856; and for turkey hemorrhagic enteritis virus on line 629.