**Reviewer #1**: *The authors addressed most of my previous concerns, however there are some issues, which require more detail/precision in the manuscript.*

*In the order of appearance in the text:*

*- "we used an in-house developed R pipeline." -> Here, they should include the link to the github repository. The link in the data availability section is not working though.*

A

*- "The CAGEfightR [35] package was used to determine TSS positions. The TSS clusters within a 10 nucleotides window were termed identical." Does TSS cluster refer to the TSS positions outputted by CAGEfightR or are these the clusters obtained after merging TSS within 10 nt.*

A

*- "Reference transcript counting": It is unclear what is compared against the reference annotation here. The reads from dcRNA-seq? This needs to be clarified.*

A

*- nucleotide vs. nt-s: The authors use both terms, but should only use one consistently*

We use “nucleotide” in the revised version of the manuscript.

*- "The clusters were merged with the dcDNA-Seq dataset" -> The TSS clusters?*

A

*- ". , which contains transcript identities based on the alignment of 5′-ends" -> I don't understand what this is supposed to mean or refer to. The TSSs or the dcRNA-seq, if the latter why would only the 5'end be aligned. This needs to be rephrased to be unclear*

A

*- "Transcripts were reconstructed by pairing validated TSS peaks": what are validated TSS peaks? peaks confirmed by dcRNA-seq in the previous paragraph? But this already merged transcripts (from dcRNA-seq? unclear) with TSS, why do you need to do it again? Also transcripts are from the dcRNA-seq data or where do they come from?*

A

*- "their 3′-ends overlapped a known TES" -> known means from the previous annotation?*

A

*- "This approach enabled the integration of the CAGE-Seq and dcDNA-Seq datasets to annotate TSSs."-> but you did this already in the previous section? Why did you do this again?*

A

*- "Newly assembled transcripts were integrated with our prior annotation"-> how?*

A

*- "Validated transcripts"-> when is a transcript considered validated?*

A

*- "To further filter TSS transcripts" -> what are TSS transcripts, it has not been defined to which transcripts this term refers to.*

A

*- "To identify groups of TSSs, TESs, and transcripts with similar temporal expression patterns, we performed de novo clustering on normalized gene expression data. [..] For gene clustering, .." -> gene clustering aims to identify groups of transcripts with similar temporal expression patterns? If not how are these groups of transcripts identified. This needs to be clarified.*

A

*- "Our findings reinforced that ORF64 is the sole IE gene in EHV-1" -> It needs to be explicitly mentions that ORF64 is the only gene with significant expression levels after CHX treatment.*

A

*- "Among the examined transcripts, 251 received the highest level of support (\*\*\*) - indicating robust validation - while 47 had medium support (\*\*) and 51 showed the lowest level of support (\*) (see Methods for details)." -> Methods only talks about assigning confidence to TSS. Are you talking about TSS here? You need to be more precise with your terms!*

A

*- OriS = Oris? If yes, please use a consistent notation, if not explain.*

We defined OriS.

*- Supplementary Figure S1 needs to indicate the location of raRNA, Ori-L and the other genes/mRNAs mentioned in this section, otherwise it cannot be understood.*

A

*- noir = NOIR? If yes, please use a consistent notation, if not explain.*

We now use “NOIR” throughout the manuscript.

*- Legend to Supplementary Figure S2 and Supplementary Figure S5 need to state the scale of the y-axis is determined independently for each time-point*

A

*- Supplementary Figure S4 should be before Supplementary Figure S3 und referenced in the previous paragraph, which discusses the traditional kinetic clusters*

A

*- Figure 7 should be a Supplementary Figure as it is too large for the main manuscript. The text will be unreadable if it is scaled to fit in the main manuscript.*

A

*- "By integrating multiple data sources (dcDNA-Seq, dRNA-Seq, and CAGE-Seq) and using different tools - including LoRTIA for dcDNA-Seq libraries and NAGATA for dRNA-Seq data" -> where is the dRNA-seq data integrated? This did not become clear in the methods (see also my above questions).*

A

*- "The R codes used to perform the analysis and generate the plots are available at: https://github.com/Balays/EHV-1-dynamic" -> the link does not exist.*

A