Review of: "CRSP: Comparative RNA-seq pipeline for species lacking both of sequenced genomes and reference transcripts"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

This manuscript describes a workflow for analyzing RNA-Seq data for organisms without genome reference, which is of great interest to the research community, since the vast majority of the species don't have a sequenced genome. The workflow was strung together by publicly available software tools, Although the authors designed this tool for species without sequenced genomes, only human RNA-Seq data were used for benchmarking. It is understandable that the sequences from species without a reference genome are not easy to evaluate due to the lack of a sequenced genome, perhaps additional data can be evaluated from other species, such as mouse. In addition, CRSP requires multiple transcriptome assemblies built previously for the species under investigation, which is not readily available for many species. Also, building de novo assemblies from RNA-Seq data is very computationally expensive. What if the researchers only have RNA-Seq data from one study and don't have the luxury of working with multiple pre-assembled transcriptomes?