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Dear Organizers,

We are pleased to submit our manuscript entitled, "An Ultra-Fast and Scalable Quantification Pipeline for Transposable Elements from Next Generation Sequencing Data," to be considered as a full-length paper in the "Challenges of Pattern Recognition in Biomedical Data" section of *Pacific Symposium on Biocomputing 2018*.

Transposable elements (TEs) are DNA sequences that can move from one location to another in the genome and represent a large proportion of the eukaryotic genomes. TEs in the genome had been considered as 'junk DNA', but recently it has been shown that they are important due to their functional roles in a variety of diseases such as cancer and neurodegenerative disease. The rapid development of RNA-sequencing technology has enabled us to study the activity of TEs at the systems level, but no efficient TE analysis tools are developed yet.

Here, we present SalmonTE, a fast and reliable pipeline for that quantification of TEs on the genome from NGS data. Our comparison results of SalmonTE in the various datasets have shown a big speed-up in computing time relative to previous tools and accurate quantification of TEs. This pipeline will enable the biomedical research community to re-analyze large amounts of data generated over the past years from the angle of TE expression. We also declare that this manuscript contains original, unpublished results, and is not currently under consideration elsewhere, and all co-authors concur with the contents of the paper.

We believe that this work would be of great interest to the broad community of biomedical research. We thank you for your consideration and look forward to hearing from you.

Sincerely,

Zhandong Liu, PhD
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