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Invitation to review a manuscript for BMC Medical Genomics

1 message

BioMed Central Editorial <editorial@biomedcentral.com> Tue, May 12, 2015 at 9:59 AM
Reply-To: BioMed Central Editorial <editorial@biomedcentral.com>
To: Dr Shicheng Guo <scguo@ucsd.edu>

Dear Dr Guo,

We invite you to review a manuscript that has been submitted to BMC Medical Genomics by Juan Pablo Lopez and colleagues. The title, authors and abstract of the manuscript are at the foot of this e-mail. This journal has a policy of open peer review (as detailed below) and we ask reviewers to return their reports within 14 days. If you need longer, please contact us as we may be able to arrange an alternative deadline for your review.

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We do hope you are able to help. If, however, you cannot review, we would be most grateful if you could suggest alternative reviewers by accessing the website at the link above; you will not need to register. If you have any difficulties with the system, or have any queries, please reply to this email.

I look forward to hearing from you within the next few days.

With best wishes,

Dr. Jen-Tsan Ashley Chi

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Title: Biomarker discovery: Quantification of microRNAs and other small non-coding RNAs using next generation sequencing
Journal: BMC Medical Genomics
Type of article: Technical advance

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Abstract:

Background: Small ncRNAs (sncRNAs) offer great hope as biomarkers of disease and response to treatment. This has been highlighted in the context of several medical conditions such as cancer, liver disease, cardiovascular disease, and central nervous system disorders, among many others. Here we assessed several steps involved in the development of an ncRNA biomarker discovery pipeline, ranging from sample preparation to bioinformatic processing. At each stage, we evaluated the pros and cons of different techniques that may be suitable for different experimental designs. Evaluation methods included quality of data output in relation to hands-on laboratory time, cost, and efficiency of processing.

Results: Our results show that good quality sequencing libraries can be prepared from small amounts of total RNA and that varying degradation levels in the samples do not have a significant effect on the overall quantification of sncRNAs via NGS. In addition, we describe the strengths and limitations of three commercially available library preparation methods: (1) Novex TBE PAGE gel; (2) Pippin Prep automated gel system; and (3) AMPure XP beads. We describe our bioinformatics pipeline, provide recommendations for sequencing coverage, and describe in detail the expression and distribution of all sncRNAs in four human tissues: whole-blood, brain, heart and liver.

Conclusions: Ultimately this study provides tools and outcome metrics that will aid researchers and clinicians in choosing an appropriate and effective high-throughput sequencing quantification method for various study designs, and overall generating valuable information that can contribute to our understanding of small ncRNAs as potential biomarkers and mediators of biological functions and disease.