Reviewer's report

Title: A sequenced-based approach to identify reference genes for gene expression analysis

Version: 2 Date: 24 March 2010

Reviewer: xing xie

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1. Finally, which genes could be used for normalization in gene expression studies of lung cancer? the authors should make the results and conclusion more clearly in the abstract.

2. author chose only 4 genes for further validation, why not the total 15 genes? It is really not a huge task.

3. the authors should state more details about PCR validation, such as cDNA dilution, amplification curves, dissolution curves,

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:

I declare that I have no competing interests