Author’s response to reviews

Title: Identification of single nucleotide variants using position-specific error estimation in deep sequencing data

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Dear BMC Medical Genomics Editor,

Thank you for informing us that our manuscript is potentially acceptable for publication, subject to some revisions. We have now made the necessary corrections as requested. In particular

1) We have formatted the abstract into Background, Methods, Results, and Conclusions. The 'Results' section in the older version has been split into 'Methods' and 'Results'. No other changes made in the abstract.

2) We have organised the main text into Background, Methods, Results, Discussion and Conclusions as per submission guidelines. We have made the following changes: (i) ‘Results and Discussion’ in the old version is now ‘Results’; (ii) ‘Conclusions’ in the old version is now ‘Discussion’ (we have also removed the very last sentence 'In general we believe that the use of
models with position-specific error estimates, as described here, could improve SNV detection especially at low VAF.’); (iii) We have added a ‘Conclusions’ section.

(3) The manuscript does not contain any tracked changes, comments, highlights, strikethroughs or text in different colours. All relevant tables/figures/additional files are also clean versions.

We hope that in its present revised form you will find the manuscript suitable for publication in BMC Medical Genomics.

Yours sincerely,

Stefano Lise