**Response to Reviewers**

We would like to thank the editor and reviewers for their comments.

**NGSANE: A Lightweight Production Informatics Framework for High Throughput Data Analysis**

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We have corrected grammar, punctuation and affiliation section. We also notice that the GATK reference was not conform to the URL-referencing guideline and changed it to now be a URL in the main body of the text. Furthermore, we revised the Funding and Acknowledgement section to adhere to the guidelines (extended abbreviations and split into funding and acknowledgment) to now read

*Funding*: F.A.B, H.J.F and S.J.C were funded by the National Health and Medical Research Council [1051757, 1010620 and 1063559 to S.J.C]; the Cancer Institute of New South Wales [11/REG/1-10 to Dr Warren Kaplan] and the National Breast Cancer Foundation [program grant to S.J.C.]. Additional funding was received from the Commonwealth Scientific and Industrial Research Organisation's Transformational Capability Platform (D.C.B.), Science and Industry Endowment Fund (D.C.B. and S.J.C) and Information Management and Technology Services.

*Acknowledgements*: Piotr Szul with AMI and StarCluster usage.

These changes extended the document above two pages. We therefore re-worded three sentences (pg 1, para 8)

*HPC and parallel execution.* NGSANE supports Sun Grid Engine (SGE) and Portable Batch System (PBS) job scheduling and can be operated in different modes for development and production, thus enabling ~~efficient and~~ flexible processing of NGS data.

and sentence (pg1, para 9)

This allows different existing modules, parameter settings, or software versions to be executed by changes to the project specific configuration file rather than ~~requiring changes~~ the software code itself (hot swapping).

as well as the following sentence to (pg2, para 7)

*Knowledge transfer.* NGSANE provides a unified framework (i.e. ~~defined~~ folder structure) for processing ~~raw~~ data from different experimental protocols. This allows co-investigators and reviewers to easily understand and reproduce work ~~using~~ from NGSANE's log and report files.

In addition, we introduced the acronyms “Next Generation Sequencing Analysis for Enterprises” and “High Performance Computing” in the smaller font sized abstract.

In the supplementary, we added a caption to figure 1 and table 1 as well as a reference anchor for them to the main text of the supplementary manuscript. We also included the missing SeqWare reference in the table.