CORRECTION

Correction: PaCBAM: fast and scalable processing of whole exome and targeted sequencing data

Samuel Valentini[1], Tarcisio Fedrizzi[2], Francesca Demichelis[2] and Alessandro Romanel[1*]

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The wrong Supplementary file was originally published with this article [1]; it has now been replaced with the correct file.

The correct Additional file 1 is also included in this Correction and the original article has been updated.

Supplementary Information

> **Additional file 1: Figure S1.** Genomic region mean coverage computation. **Figure S2.** Cumulative coverage distribution report. **Figure S3.** Variant allelic fraction distribution report. **Figure S4.** SNP allelic fraction distribution report. **Figure S5.** Alternative bases distribution report. **Figure S6.** Strand bias distribution report. **Figure S7.** Genomic regions depth of coverage distribution report. **Figure S8.** Genomic regions GC content distribution report. **Figure S9.** Run time comparison at 150X depth of coverage. **Figure S10.** Run time comparison at 230X depth of coverage. **Figure S11.** Run time comparison at 300X depth of coverage. **Figure S12.** Memory usage comparison at 150X depth of coverage.

> **Figure S13.** Memory usage comparison at 230X depth of coverage. **Figure S14.** Memory usage comparison at 300X depth of coverage. **Figure S15.** Memory usage comparison among PaCBAM pileup and pileup module of ASEQ. **Figure S16.** Comparison of PaCBAM duplicates filtering strategy to Sambamba markdup and Picard MarkDuplicates modules. **Figure S17.** Performance of PaCBAM duplicated reads filtering. **Table S1.** Mean depth of coverage and target sizes of all BAM files used to test PaCBAM performance. **Table S2.** Time and memory usage of duplicates filtering performance analyses. **Table S3.** Versions of the tools used in performance evaluation analysis.

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Reference
1. Valentini, et al. PaCBAM: fast and scalable processing of whole exome and targeted sequencing data. BMC Genomics. 2019;20:1018. https://doi.org/10.1186/s12864-019-6386-6.

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*Correspondence:
Alessandro Romanel
alessandro.romanel@unitn.it
[1] Laboratory of Bioinformatics and Computational Genomics, Department of Cellular, Computational and Integrative Biology (CIBIO), University of Trento, Trento, Italy
[2] Laboratory of Computational and Functional Oncology, Department of Cellular, Computational and Integrative Biology (CIBIO), University of Trento, Trento, Italy