

ERRATUM

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Erratum to: 'Reference-free inference of tumor phylogenies from single-cell sequencing data'

Ayshwarya Subramanian¹ and Russell Schwartz^{2*}

Unfortunately, the original version of this article [1] contained an error. Figures 2, 4 and 5 were incorrect and the captions for Figs. 4 and 5 were incorrect. Below are the correct figures and captions:

Author details

¹Department of Biostatistics, Harvard T.H. Chan School of Public Health, 655 Huntington Street, 02115 Boston, USA. ²Department of Biological Sciences and the Computational Biology Department, Carnegie Mellon University, 5000 Forbes Avenue, 15213 Pittsburgh, USA.

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Reference

1. Schwartz R, Subramanian A. Reference-free inference of tumor phylogenies from single-cell sequencing data'. *BMC Genomics*. 2015;16 Suppl 11:S7.

* Correspondence: russells@andrew.cmu.edu

²Department of Biological Sciences and the Computational Biology Department, Carnegie Mellon University, 5000 Forbes Avenue, 15213 Pittsburgh, USA

Full list of author information is available at the end of the article

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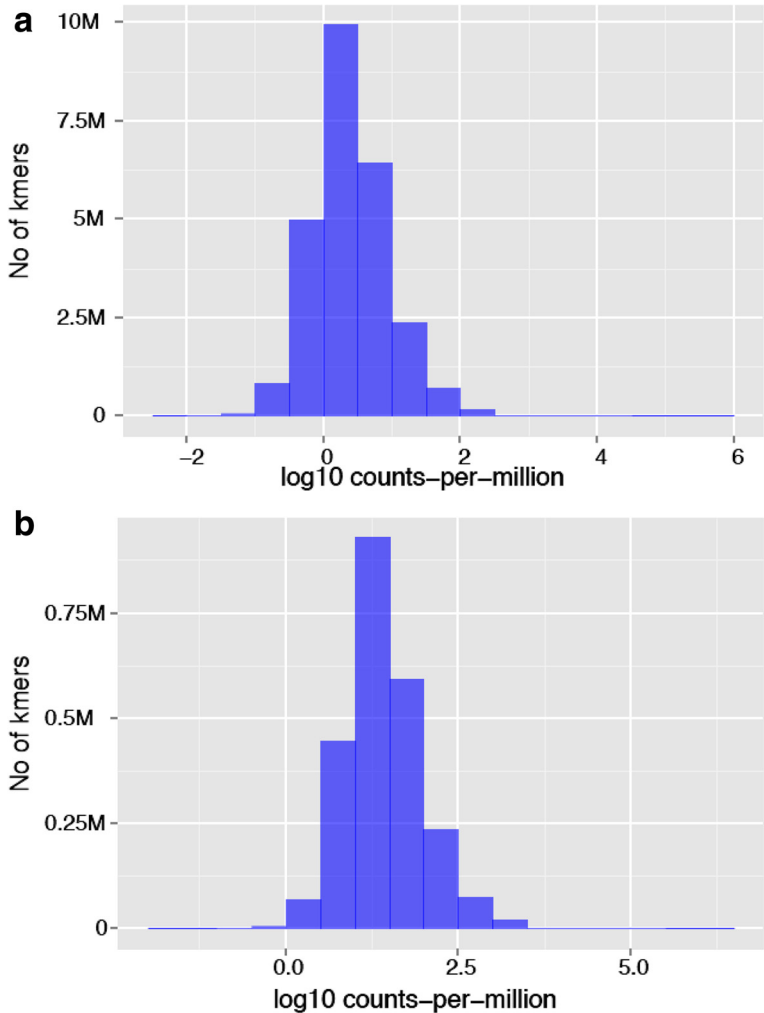


Fig. 2 Histogram of k-mer relative abundances. Both 20- and 25-mer relative abundance densities appear log-laplacian. These data included 20- and 25-mers found in all tumor cells. **a** Histogram of 20-mer relative abundances in log10 scale. **b** Histogram of 25-mer relative abundances in log10 scale

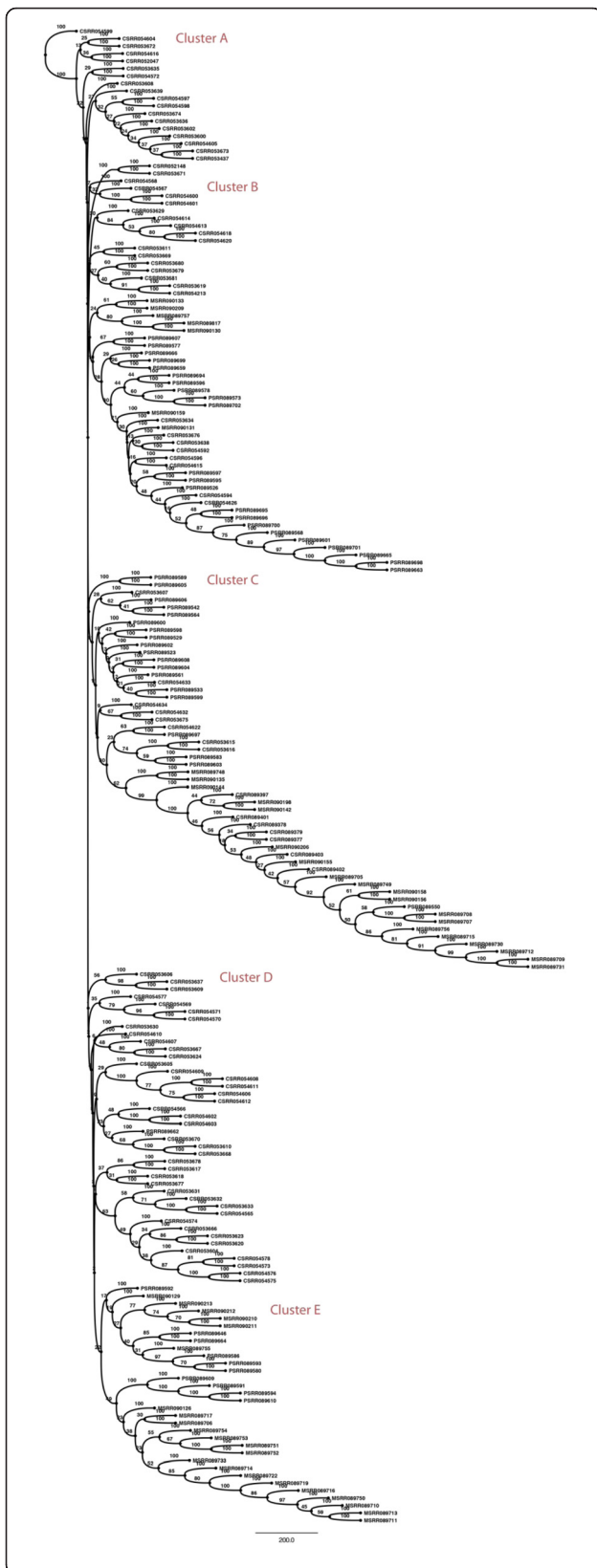


Fig. 4 20-mer bootstrap consensus neighbor-joining tree built from T10 primary breast tumor cells (prefix C), T16 primary (prefix P) and metastatic data (prefix M). Distinct groupings of cells are labeled as clusters

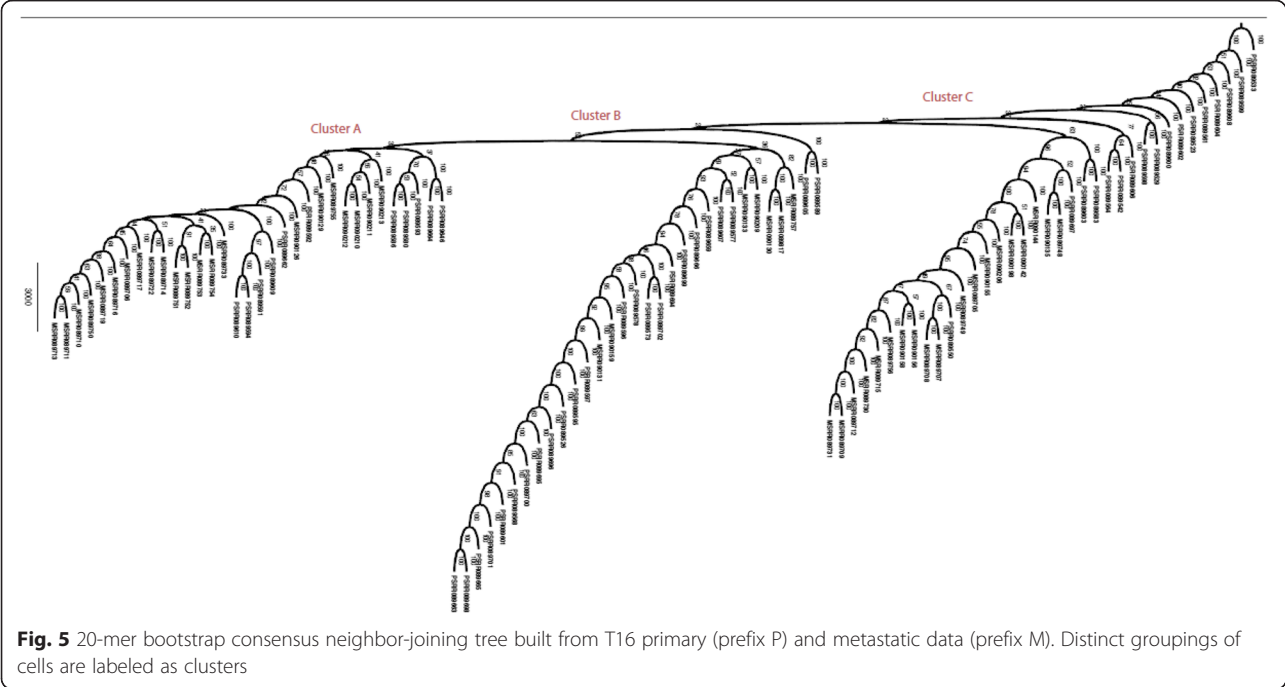


Fig. 5 20-mer bootstrap consensus neighbor-joining tree built from T16 primary (prefix P) and metastatic data (prefix M). Distinct groupings of cells are labeled as clusters