



## Corrigendum: Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development

Michał Pawlak, Katarzyna Z. Kedzierska, Maciej Migdal, et al.

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## Corrigenda

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**Genome Research 29:** 2088–2103 (2019)

**Corrigendum: Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging**

Jacob C. Kimmel, Lolita Penland, Nimrod D. Rubinstein, David G. Hendrickson, David R. Kelley, and Adam Z. Rosenthal

The authors would like to correct an error in the Methods section of the above-mentioned article under the “Quality control” subheading. The corrected text is as follows and has been updated in the article online:

“Additionally, we filtered out cells with a high fraction of reads mapping to the mitochondrial genome (>10%) or the *Rn45s* repeat (>5%) as likely dead cells (Ilicic et al. 2016).”

The authors apologize for any confusion this may have caused.

doi: 10.1101/gr.259820.119

**Genome Research 29:** 506–519 (2019)

**Corrigendum: Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development**

Michal Pawlak, Katarzyna Z. Kedzierska, Maciej Migdal, Karim Abu Nahia, Jordan A. Ramilowski, Lukasz Bugajski, Kosuke Hashimoto, Aleksandra Marconi, Katarzyna Piwocka, Piero Carninci, and Cecilia L. Winata

The authors would like to correct an omission in the Methods section of the above-mentioned article under the “CM collection by fluorescence-activated cell sorting (FACS)” subheading. The corrected text is as follows and has been updated in the article online:

“Cell suspension was prepared from 500 embryos and larvae as previously described (Winata et al. 2013), omitting the fixation step and directly resuspending cells in FACSmix Cell Dissociation Solution (AMS Biotechnology) for cell sorting.”

The authors apologize for any confusion this may have caused.

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