**CORRECTION**

# Correction to: Single-Cell RNA Sequencing of the Adult Mammalian Heart – State of the Art and Future Perspectives

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**Correction to: Current Heart Failure Reports 2021.**
https://doi.org/10.1007/s11897-021-00504-3

After the publication of the original article, we noticed that we need a correction in Fig. 2. In the part of the table containing human studies, in Nomura et al. (2018), in the column indicating the type of samples, sham and TAC was now correctly replaced with healthy and DCM. Please see below the corrected version. We apologize for any inconvenience that this may have caused.

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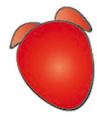2 Department of Medical Biology, Amsterdam University Medical Center, Amsterdam, The Netherlands

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**mouse**

| study | living cells vs frozen nuclei | healthy vs diseased | platform | application |
|---|---|---|---|---|
| Gladka et al.(2018) Circulation | living cells CM | sham IR | FACS | cellular heterogeneity |
| Skelly et al.(2018) Cell Reports | living cells non-CM | healthy | FACS | cellular communication |
| Nomura et al.(2018) Nat. Comm. | living cells CM | sham TAC | manual pickup | network and trajectory analysis |
| Kretzschmar et al. (2018) PNAS | living cells | sham IR and MI | FACS | Identification of rare cells |
| Ren et al. (2020) Circulation | living cells | sham TAC | ICELL8 | network and trajectory analysis |
| Yekelchyk et al. (2019) Basic Res. Cardiol. | living cells CM | sham TAC | ICELL8 | cellular heterogeneity |
| Wang et al. (2020) Nat. Comm. | living cells | healthy | ICELL8 | network and trajectory analysis |
| Vidal et al. (2019) JCI Insights | nuclei | healthy and aging | 10x Genomics | cellular heterogeneity |
| Zhang et al. (2019) Cell Discov. | nuclei | healthy and MI | 10x Genomics | Identification of rare cells |
| See et al.(2017) Nat.Comm. | nuclei CM | sham TAC | IFC system | network and trajectory analysis |
| Li et al. (2019) Eur. Heart J. | living cells non-CM | healthy and MI | 10x Genomics | cellular heterogeneity |
| Farbehi et al. (2019) Elife | living cells non-CM | healthy and MI | 10x Genomics | cellular communication |

**Adult mammalian heart**

**human**

| study | living cells vs frozen nuclei | healthy vs diseased | platform | application |
|---|---|---|---|---|
| Nomura et al. (2018) Nat. Comm. | living cells CM | healthy DCM | manual pickup | network and trajectory analysis |
| Wang et al. (2020) Nat. Cell Biology | living cells all cells | healthy, HF and LVAD | ICELL8 | cellular heterogeneity and network analysis |
| Selewa et al. (2020) Sci. Rep. | nuclei CM | healthy | DropNuc-seq | cellular heterogeneity |
| See et al.(2017) Nat.Comm | nuclei CM | non-failing DCM | IFC system | network and trajectory analysis |
| Litvinukova et al. (2020) Nature | living cells nuclei | healthy | 10x Genomics FACS | cellular heterogeneity and communication |
| Tucker et al. (2020) Circulation | nuclei | healthy | 10x Genomics | cellular heterogeneity |

**Fig. 2** Overview of single-cell sequencing studies applied to adult healthy and diseased mouse or human heart. CM cardiomyocytes, IR ischemia/reperfusion, MI myocardial infarction, TAC transaortic constriction, HF heart failure, LVAD left ventricular assist device, DCM dilated cardiomyopathy