

Correction

Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity

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In the originally published version of this manuscript, Caroline Hendry was inadvertently excluded from the author list. Her contributions to the work included the following: the development of SOPs for the relatively novel Sendai virus infection method for reprogramming; the design and implementation of studies to assess the variation among lines derived from a single donor (which included up to 14 lines per donor and analyses at both the iPSC stage and post-differentiation); and, together with S.L.D. and P.C., contributing to the development of an optimized workflow for the characterization of a large library of human iPSC lines, the creation and isolation of iPSCs, the performance of quality control for pluripotency markers, the serial passaging of each line for at least 12 passages, the verification that said lines were Sendai-free, the freezing down of cells at every split, the active maintenance of databases to catalogue the large number of lines and splits, and the preparation of these cells for RNA-seq analysis to be performed by members of the E.E.S. lab. All of these studies were performed to optimize the workflow that underpinned the project, and hence, the paper.

All of the authors on the original author list, excluding those who are unable to be contacted and those who are deceased, have given their consent for Dr. Hendry's addition. The corrected author list is now included with this statement and the original manuscript online.