

Supplementary References:

100. G. Finak, A. McDavid, M. Yajima, J. Deng, V. Gersuk, A. K. Shalek, C. K. Slichter, H. W. Miller, M. J. McElrath, M. Prlic, P. S. Linsley, R. Gottardo, MAST: a flexible statistical framework for assessing transcriptional changes and characterizing heterogeneity in single-cell RNA sequencing data. *Genome Biology* **16**, 1-13 (2015).
101. J. X. Binder, S. Pletscher-Frankild, K. Tsafou, C. Stolte, S. I. O'Donoghue, R. Schneider, L. J. Jensen, COMPARTMENTS: unification and visualization of protein subcellular localization evidence. *Database: the journal of biological databases and curation* **2014**, bau012 (2014).
102. B. Li, C. N. Dewey, RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics* **12**, 323 (2011).