**Supplementary Table**

**Supplementary Table 1. Resource Table**

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| --- | --- | --- | --- |
| **RESOURCE** | | **SOURCE** | **ID** |
| **Deposited Data** | | | |
| **Training dataset**  See Supp. Table 1 of CytoTRACE [1] for details. | 1 | HSCs\_Smartseq2\_Mouse | GSE59114 |
| 2 | Blastocyst\_timepoints\_SC3seq\_Macaque | GSE74767 |
| 3 | Cortical\_interneurons\_C1\_Mouse | GSE90860 |
| 4 | Dentate\_gyrus\_timepoints\_10x\_Mouse | GSE95753 |
| 5 | Embryonic\_HSCs\_Tang\_et\_al\_Mouse | GSE67123 |
| 6 | Endometrium\_CEL\_seq\_Mouse | GSE98451 |
| 7 | Germ\_cells\_Smartseq2\_Human | GSE86146 |
| 8 | Hepatoblast\_Smartseq2\_Mouse | GSE90047 |
| 9 | Invitro\_NPCs\_C1\_Human | GSE102066 |
| 10 | Lung\_development\_C1\_Mouse | GSE52583 |
| 11 | Medial\_ganglionic\_eminence\_C1\_Mouse | GSE94641 |
| 12 | mESC\_invitro\_ramDAseq\_Mouse | GSE98664 |
| 13 | Neural\_stem\_cells\_Dropseq\_Mouse | GSE107122 |
| 14 | Oligodendrocytes\_timepoints\_C1\_Mouse | GSE75330 |
| 15 | Pancreatic\_alpha\_cell\_Smartseq2\_Mouse | GSE87375 |
| 16 | Pancreatic\_beta\_cell\_Smartseq2\_Mouse | GSE87375 |
| 17 | Thymus\_Dropseq\_Mouse | GSE107910 |
| \*Zebrafish | Early\_development\_Dropseq\_Zebrafish | GSE106587 |
| **Testing dataset**  See Supp. Table 1 of CCAT [2] for details. | 1 | Embryo\_hESC\_C1\_Human | GSE75748 |
| 2 | Embryo\_0h\_C1\_Human | GSE75748 |
| 3 | Skeletal\_muscle\_myblast\_C1\_Human | GSE52529 |
| 4 | Pancreas\_Smartseq2\_Mouse | GSE115931 |
| 5 | Lung\_epithelial, C1\_Mouse | GSE52583 |
| 6 | Neural\_precursor\_D1, C1\_Human | GSE102066 |
| 7 | Neural\_precursor\_D3, C1\_Human | GSE102066 |
| 8 | Hepatoblast\_Smartseq2\_Mouse | GSE90047 |
| 9 | Brain\_D0D26\_CELseq\_Human | GSE86977 |
| 10 | Brain\_D0D40\_CELseq\_Human | GSE86977 |
| 11 | Brain\_D0D54\_CELseq\_Human | GSE86977 |
| 12 | Brain\_InDrop\_Mouse | GSE97390 |
| 13 | Neural\_stem\_Dropseq\_Mouse | GSE107122 |
| 14 | Intestine\_CELseq\_Mouse | GSE76408 |
| 15 | Brain\_10x\_Mouse | GSE95315 |
| 16 | Embryo\_Stem\_ramDAseq\_Mouse | GSE98664 |
| 17 | Embryo\_Scl\_C1\_Human | GSE85066 |
| 18 | Embryo\_Lat\_C1\_Human | GSE85066 |
| 19 | Pan.\_alpha&beta\_Smartseq2\_Mouse | GSE87375 |
| 20 | Blood\_C1\_Mouse | GSE60783 |
| 21 | Cort.\_interneurons\_C1\_Mouse | GSE90860 |
| 22 | Blastocyst\_SC3seq\_Mouse | GSE74767 |
| 23 | Thymus\_Dropseq\_Mouse | GSE107910 |
| 24 | Muscle\_Microwellseq\_Human | GSE134355 |
| 25 | Pancreas\_Microwellseq\_Human | GSE134355 |
| 26 | Hear\_Microwellseq\_Human | GSE134355 |
| 27 | AdrenalGland\_Microwellseq\_Human | GSE134355 |
| 28 | Embryo\_sciRNAseq3\_Mouse | GSE119945 |
| **Deconvolution analysis** | scRNA-seq | Foreskin Epidermis Human, Wang *et al.* [3] | GSE147482 |
| Bulk expression | Epidermal regeneration, Lopez-Pajares *et al.* [4] | GSE52651 |
| **Spatial data analysis** | Hearts | Mantri *et al.* [5] | GSE149457 |
| Intestines | Fawkner-Corbett *et al.* [6] | GSE158328 |
| **Breast cancer analysis** | scRNA-seq | Wu *et al.* [7] | https://singlecell.broadinstitute.org/single\_cell/study/SCP1039 |
| TCGA bulk | UCSC XENA (GDC TCGA Breast Cancer) | https://xenabrowser.net/datapages/ |
| Multiple Alignments | | UCSC (hg19, 100-way, Amino Acid) | http://hgdownload.cse.ucsc.edu/goldenPath/hg19/multiz100way |
| Human Cell Landscape | | Han *et al.* [8] | https://figshare.com/articles/HCL\_DGE\_Data/7235471 |
| **Software and Algorithms** | |  |  |
| CCAT | | Teschendorff *et al.* [2] | https://github.com/aet21/SCENT |
| CytoTRACE | | Gulati *et al.* [1] | https://cytotrace.stanford.edu/ |
| SCENT | | Teschendorff *et al.* [9] | https://github.com/aet21/SCENT |
| StemID | | Grun *et al.* [10] | https://github.com/dgrun/StemID |
| cmEntropy | | Kannan *et al.* [11] | https://github.com/skannan4/cm-entropy-score |
| SLICE | | Guo *et al.* [12] | https://research.cchmc.org/pbge/slice.html |
| Seurat | | Stuart *et al.* [13-16] | https://satijalab.org/seurat/ |
| CIBERSORTx | | Newman *et al.* [17] | https://cibersortx.stanford.edu/ |
| ComplexHeatmap | | Gu *et al.* [18] | https://github.com/jokergoo/ComplexHeatmap |
| pROC | | Robin *et al.* [19] | https://web.expasy.org/pROC/ |
| DESeq2 | | Love *et al.* [20] | “DESeq2” package in R |
| Combat | | Johnson *et al.* [21] | “sva” package in R |
| BEER | | Zhang *et al.* [22] | https://github.com/jumphone/BEER |
| clusterProfiler | | Yu *et al.* [23] | “clusterProfiler” package in R |
| This study | | This study | https://github.com/jumphone/fitdevo |

**References**

1. Gulati, G.S., et al., *Single-cell transcriptional diversity is a hallmark of developmental potential.* Science, 2020. **367**(6476): p. 405-411.

2. Teschendorff, A.E., et al., *Ultra-fast scalable estimation of single-cell differentiation potency from scRNA-Seq data.* Bioinformatics, 2021. **37**(11): p. 1528-1534.

3. Wang, S., et al., *Single cell transcriptomics of human epidermis identifies basal stem cell transition states.* Nat Commun, 2020. **11**(1): p. 4239.

4. Lopez-Pajares, V., et al., *A LncRNA-MAF:MAFB transcription factor network regulates epidermal differentiation.* Dev Cell, 2015. **32**(6): p. 693-706.

5. Mantri, M., et al., *Spatiotemporal single-cell RNA sequencing of developing chicken hearts identifies interplay between cellular differentiation and morphogenesis.* Nat Commun, 2021. **12**(1): p. 1771.

6. Fawkner-Corbett, D., et al., *Spatiotemporal analysis of human intestinal development at single-cell resolution.* Cell, 2021. **184**(3): p. 810-826 e23.

7. Wu, S.Z., et al., *A single-cell and spatially resolved atlas of human breast cancers.* Nat Genet, 2021. **53**(9): p. 1334-1347.

8. Han, X.P., et al., *Construction of a human cell landscape at single-cell level.* Nature, 2020. **581**(7808): p. 303-+.

9. Teschendorff, A.E. and T. Enver, *Single-cell entropy for accurate estimation of differentiation potency from a cell's transcriptome.* Nat Commun, 2017. **8**: p. 15599.

10. Grun, D., et al., *De Novo Prediction of Stem Cell Identity using Single-Cell Transcriptome Data.* Cell Stem Cell, 2016. **19**(2): p. 266-277.

11. Kannan, S., et al., *Transcriptomic entropy benchmarks stem cell-derived cardiomyocyte maturation against endogenous tissue at single cell level.* PLoS Comput Biol, 2021. **17**(9): p. e1009305.

12. Guo, M., et al., *SLICE: determining cell differentiation and lineage based on single cell entropy.* Nucleic Acids Res, 2017. **45**(7): p. e54.

13. Hao, Y., et al., *Integrated analysis of multimodal single-cell data.* Cell, 2021. **184**(13): p. 3573-3587 e29.

14. Stuart, T., et al., *Comprehensive Integration of Single-Cell Data.* Cell, 2019. **177**(7): p. 1888-1902 e21.

15. Butler, A., et al., *Integrating single-cell transcriptomic data across different conditions, technologies, and species.* Nat Biotechnol, 2018. **36**(5): p. 411-420.

16. Satija, R., et al., *Spatial reconstruction of single-cell gene expression data.* Nat Biotechnol, 2015. **33**(5): p. 495-502.

17. Newman, A.M., et al., *Determining cell type abundance and expression from bulk tissues with digital cytometry.* Nat Biotechnol, 2019. **37**(7): p. 773-782.

18. Gu, Z., R. Eils, and M. Schlesner, *Complex heatmaps reveal patterns and correlations in multidimensional genomic data.* Bioinformatics, 2016. **32**(18): p. 2847-9.

19. Robin, X., et al., *pROC: an open-source package for R and S+ to analyze and compare ROC curves.* BMC Bioinformatics, 2011. **12**: p. 77.

20. Love, M.I., W. Huber, and S. Anders, *Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2.* Genome Biol, 2014. **15**(12): p. 550.

21. Johnson, W.E., C. Li, and A. Rabinovic, *Adjusting batch effects in microarray expression data using empirical Bayes methods.* Biostatistics, 2007. **8**(1): p. 118-27.

22. Zhang, F., Y. Wu, and W. Tian, *A novel approach to remove the batch effect of single-cell data.* Cell Discovery, 2019. **5**(1).

23. Yu, G., et al., *clusterProfiler: an R package for comparing biological themes among gene clusters.* OMICS, 2012. **16**(5): p. 284-7.