

## Supplementary Table

**Supplementary Table 1. Resource Table**

RESOURCE		SOURCE	ID
<b>Deposited Data</b>			
<b>Training dataset</b>  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
<b>Testing dataset</b>  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
<b>Deconvolution analysis</b>	scRNA-seq	Foreskin Epidermis Human, Wang <i>et al.</i> [3]	GSE147482
	Bulk expression	Epidermal regeneration, Lopez-Pajares <i>et al.</i> [4]	GSE52651
<b>Spatial data analysis</b>	Hearts	Mantri <i>et al.</i> [5]	GSE149457
	Intestines	Fawcner-Corbett <i>et al.</i> [6]	GSE158328
<b>Breast cancer analysis</b>	scRNA-seq	Wu <i>et al.</i> [7]	<a href="https://singlecell.broadinstitute.org/single_cell/study/SCP1039">https://singlecell.broadinstitute.org/single_cell/study/SCP1039</a>
	TCGA bulk	UCSC XENA (GDC TCGA Breast Cancer)	<a href="https://xenabrowser.net/datapages/">https://xenabrowser.net/datapages/</a>
Multiple Alignments		UCSC (hg19, 100-way, Amino Acid)	<a href="http://hgdownload.cse.ucsc.edu/goldenPath/hg19/multiz100way">http://hgdownload.cse.ucsc.edu/goldenPath/hg19/multiz100way</a>
Human Cell Landscape		Han <i>et al.</i> [8]	<a href="https://figshare.com/articles/HCL_DGE_Data/7235471">https://figshare.com/articles/HCL_DGE_Data/7235471</a>
<b>Software and Algorithms</b>			
CCAT		Teschendorff <i>et al.</i> [2]	<a href="https://github.com/aet21/SCENT">https://github.com/aet21/SCENT</a>
CytoTRACE		Gulati <i>et al.</i> [1]	<a href="https://cytotrace.stanford.edu/">https://cytotrace.stanford.edu/</a>
SCENT		Teschendorff <i>et al.</i> [9]	<a href="https://github.com/aet21/SCENT">https://github.com/aet21/SCENT</a>
StemID		Grun <i>et al.</i> [10]	<a href="https://github.com/dgrun/StemID">https://github.com/dgrun/StemID</a>
cmEntropy		Kannan <i>et al.</i> [11]	<a href="https://github.com/skannan4/cm-entropy-score">https://github.com/skannan4/cm-entropy-score</a>
SLICE		Guo <i>et al.</i> [12]	<a href="https://research.cchmc.org/pbge/slice.html">https://research.cchmc.org/pbge/slice.html</a>
Seurat		Stuart <i>et al.</i> [13-16]	<a href="https://satijalab.org/seurat/">https://satijalab.org/seurat/</a>
CIBERSORTx		Newman <i>et al.</i> [17]	<a href="https://cibersortx.stanford.edu/">https://cibersortx.stanford.edu/</a>
ComplexHeatmap		Gu <i>et al.</i> [18]	<a href="https://github.com/jokergoo/ComplexHeatmap">https://github.com/jokergoo/ComplexHeatmap</a>
pROC		Robin <i>et al.</i> [19]	<a href="https://web.expasy.org/pROC/">https://web.expasy.org/pROC/</a>
DESeq2		Love <i>et al.</i> [20]	“DESeq2” package in R
Combat		Johnson <i>et al.</i> [21]	“sva” package in R
BEER		Zhang <i>et al.</i> [22]	<a href="https://github.com/jumphone/BEER">https://github.com/jumphone/BEER</a>
clusterProfiler		Yu <i>et al.</i> [23]	“clusterProfiler” package in R
This study		This study	<a href="https://github.com/jumphone/fitdevo">https://github.com/jumphone/fitdevo</a>

## 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. Fawcner-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.