Resource Table

RESOURCE	SOURCE	ID
Deposited Data		
Embryonic Stem Cell (ESC) Markers	https://www.gsea-msigdb.org/gsea/ (BHATTACHARYA_EMBRYONIC_STEM_CELL [1])	BHATTACHARYA_EMBRYONIC_STEM_CELL
PhyloP score (100way, hg38)	UCSC (hg38, 100-way, PhyloP) [2]	https://hgdownload.soe.ucsc.edu/goldenPath/hg38/phyloP100way/
PhyloP score (100way, hg19)	UCSC (hg19, 100-way, PhyloP) [2]	https://hgdownload.soe.ucsc.edu/goldenPath/hg19/phyloP100way/
Human Frontal Cortex (scATAC, hg19, generated by liftOver, hg38 to hg19)	Zhang et al. [3]	GSE184462
Human Frontal Cortex (scHiC, hg19)	Lee et al. [4] and Luo et al. [5]	GSE130711
Human Cerebral Cortex (single-cell multiome, scRNA and scATAC, hg38)	Zhu et al. [6]	GSE204684
Human Retina (scATAC, hg38)	Finkbeiner et al. [7]	GSE184386
Human Adult atlas (scATAC, hg38)	Zhang et al. [3]	GSE184462
Human Fetal atlas (scATAC, hg38, generated by liftOver, hg19 to hg38)	Domcke et al. [8]	https://descartes.brotmanbaty.org/
Human Hepatic Organoid (scATAC, hg19)	Kim et al. [9]	GSE159557
Human ESC & Teratoma (scATAC, hg19)	Liu et al. [10]	GSE216323
Processed Data	This study	https://github.com/jumphone/InferC
Software and Algorithms		
MACS2 (2.2.6)	Zhang et al. [11] and Feng et al. [12]	https://github.com/macs3-project/MACS/
FitHiC (2.0.8)	Kaul et al. [13] and Ay et al. [14]	https://github.com/ay-lab/fithic
UCSC Genome Browser (hg38)	Nassar et al. [15]	https://genome.ucsc.edu/
UCSC Tools (e.g. bigWigAverageOverBed, liftOver)	Nassar et al. [15]	https://genome.ucsc.edu/util.html
R (4.2.0)	R Core Team	https://www.r-project.org/
Seurat (4.3.0)	Hao et al. [16], Stuart et al. [17], Butler et al. [18], and Satija et al. [19]	https://satijalab.org/seurat/
Signac (1.9.0)	Stuart et al. [20]	https://stuartlab.org/signac/
Cicero (1.16.1)	Pliner et al. [21]	https://cole-trapnell-lab.github.io/cicero-release/
EpiTrace (0.0.1.3)	Xiao et al. [22]	https://github.com/MagpiePKU/EpiTrace
ComplexHeatmap (2.14.0)	Gu et al. [23]	https://github.com/jokergoo/ComplexHeatmap
pROC (1.18.2)	Robin et al. [24]	https://web.expasy.org/pROC/
Inferloop (1.0.2)	Zhang et al. [25]	https://github.com/jumphone/InferLoop
FitDevo (1.2.1)	Zhang et al. [26]	https://github.com/jumphone/FitDevo
VECTOR (0.0.4)	Zhang et al. [27]	https://github.com/jumphone/Vector
This study	This study	https://github.com/jumphone/InferC

References:

1. Bhattacharya, B., et al., *Gene expression in human embryonic stem cell lines: unique molecular signature.* Blood, 2004. **103**(8): p. 2956-64.
2. Pollard, K.S., et al., *Detection of nonneutral substitution rates on mammalian phylogenies.* Genome Res, 2010. **20**(1): p. 110-21.
3. Han, X.P., et al., *Construction of a human cell landscape at single-cell level.* Nature, 2020. **581**(7808): p. 303-+.
4. Lee, D.S., et al., *Simultaneous profiling of 3D genome structure and DNA methylation in single human cells.* Nat Methods, 2019. **16**(10): p. 999-1006.
5. Luo, C., et al., *Single nucleus multi-omics identifies human cortical cell regulatory genome diversity.* Cell Genom, 2022. **2**(3).
6. Zhu, K., et al., *Multi-omic profiling of the developing human cerebral cortex at the single-cell level.* Sci Adv, 2023. **9**(41): p. eadg3754.
7. Finkbeiner, C., et al., *Single-cell ATAC-seq of fetal human retina and stem-cell-derived retinal organoids shows changing chromatin landscapes during cell fate acquisition.* Cell Rep, 2022. **38**(4): p. 110294.
8. Domcke, S., et al., *A human cell atlas of fetal chromatin accessibility.* Science, 2020. **370**(6518): p. 809-+.
9. Kim, J.H., et al., *Integrative analysis of single-cell RNA-seq and ATAC-seq reveals heterogeneity of induced pluripotent stem cell-derived hepatic organoids.* iScience, 2023. **26**(9): p. 107675.
10. Liu, D., et al., *Characterization of human pluripotent stem cell differentiation by single-cell dual-omics analyses.* Stem Cell Reports, 2023. **18**(12): p. 2464-2481.
11. Zhang, Y., et al., *Model-based Analysis of ChIP-Seq (MACS).* Genome Biology, 2008. **9**(9).
12. Feng, J., et al., *Identifying ChIP-seq enrichment using MACS.* Nat Protoc, 2012. **7**(9): p. 1728-40.
13. Kaul, A., S. Bhattacharyya, and F. Ay, *Identifying statistically significant chromatin contacts from Hi-C data with FitHiC2.* Nat Protoc, 2020. **15**(3): p. 991-1012.
14. Ay, F., T.L. Bailey, and W.S. Noble, *Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts.* Genome Res, 2014. **24**(6): p. 999-1011.
15. Nassar, L.R., et al., *The UCSC Genome Browser database: 2023 update.* Nucleic Acids Res, 2023. **51**(D1): p. D1188-D1195.
16. Hao, Y., et al., *Integrated analysis of multimodal single-cell data.* Cell, 2021. **184**(13): p. 3573-3587 e29.
17. Stuart, T., et al., *Comprehensive Integration of Single-Cell Data.* Cell, 2019. **177**(7): p. 1888-1902 e21.
18. Butler, A., et al., *Integrating single-cell transcriptomic data across different conditions, technologies, and species.* Nat Biotechnol, 2018. **36**(5): p. 411-420.
19. Satija, R., et al., *Spatial reconstruction of single-cell gene expression data.* Nat Biotechnol, 2015. **33**(5): p. 495-502.
20. Stuart, T., et al., *Single-cell chromatin state analysis with Signac.* Nat Methods, 2021. **18**(11): p. 1333-1341.
21. Pliner, H.A., et al., *Cicero Predicts cis-Regulatory DNA Interactions from Single-Cell Chromatin Accessibility Data.* Mol Cell, 2018. **71**(5): p. 858-871 e8.
22. Xiao, Y., et al., *Tracking single-cell evolution using clock-like chromatin accessibility loci.* Nat Biotechnol, 2024.
23. Gu, Z., R. Eils, and M. Schlesner, *Complex heatmaps reveal patterns and correlations in multidimensional genomic data.* Bioinformatics, 2016. **32**(18): p. 2847-9.
24. 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.
25. Zhang, F., et al., *InferLoop: leveraging single-cell chromatin accessibility for the signal of chromatin loop.* Brief Bioinform, 2023. **24**(3).
26. Zhang, F., et al., *FitDevo: accurate inference of single-cell developmental potential using sample-specific gene weight.* Brief Bioinform, 2022. **23**(5).
27. Zhang, F., X. Li, and W. Tian, *Unsupervised Inference of Developmental Directions for Single Cells Using VECTOR.* Cell Rep, 2020. **32**(8): p. 108069.