

Published datasets used in this study

	Data Source	Reference
F123 <i>in situ</i> Hi-C	GSE86150	5
sNMseq	GSE97179	6
Chromatin states in mESCs	https://github.com/gireeshkbogu/chromatin_states_chromHMM_mm9	2
Single cell Methylome in serum and 2i mESCs	GSE56879	7
Single cell Hi-C	GSE94489	3
Single cell Hi-C	GSE84920	8

Supplementary References

1. DeMaere, M.Z. & Darling, A.E. Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. *GigaScience* **7**(2017).
2. Bogu, G.K. *et al.* Chromatin and RNA Maps Reveal Regulatory Long Noncoding RNAs in Mouse. *Molecular and Cellular Biology* **36**, 809 (2016).
3. Nagano, T. *et al.* Cell-cycle dynamics of chromosomal organization at single-cell resolution. *Nature* **547**, 61-67 (2017).
4. Yang, T. *et al.* HiCRep: assessing the reproducibility of Hi-C data using a stratum- adjusted correlation coefficient. *Genome Research* (2017).
5. Fang, R. *et al.* Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq. *Cell Research* **26**, 1345 (2016).
6. Luo, C. *et al.* Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. *Science* **357**, 600 (2017).
7. Smallwood, S.A. *et al.* Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. *Nature Methods* **11**, 817 (2014).
8. Ramani, V. *et al.* Massively multiplex single-cell Hi-C. *Nat Methods* **14**, 263-266 (2017).