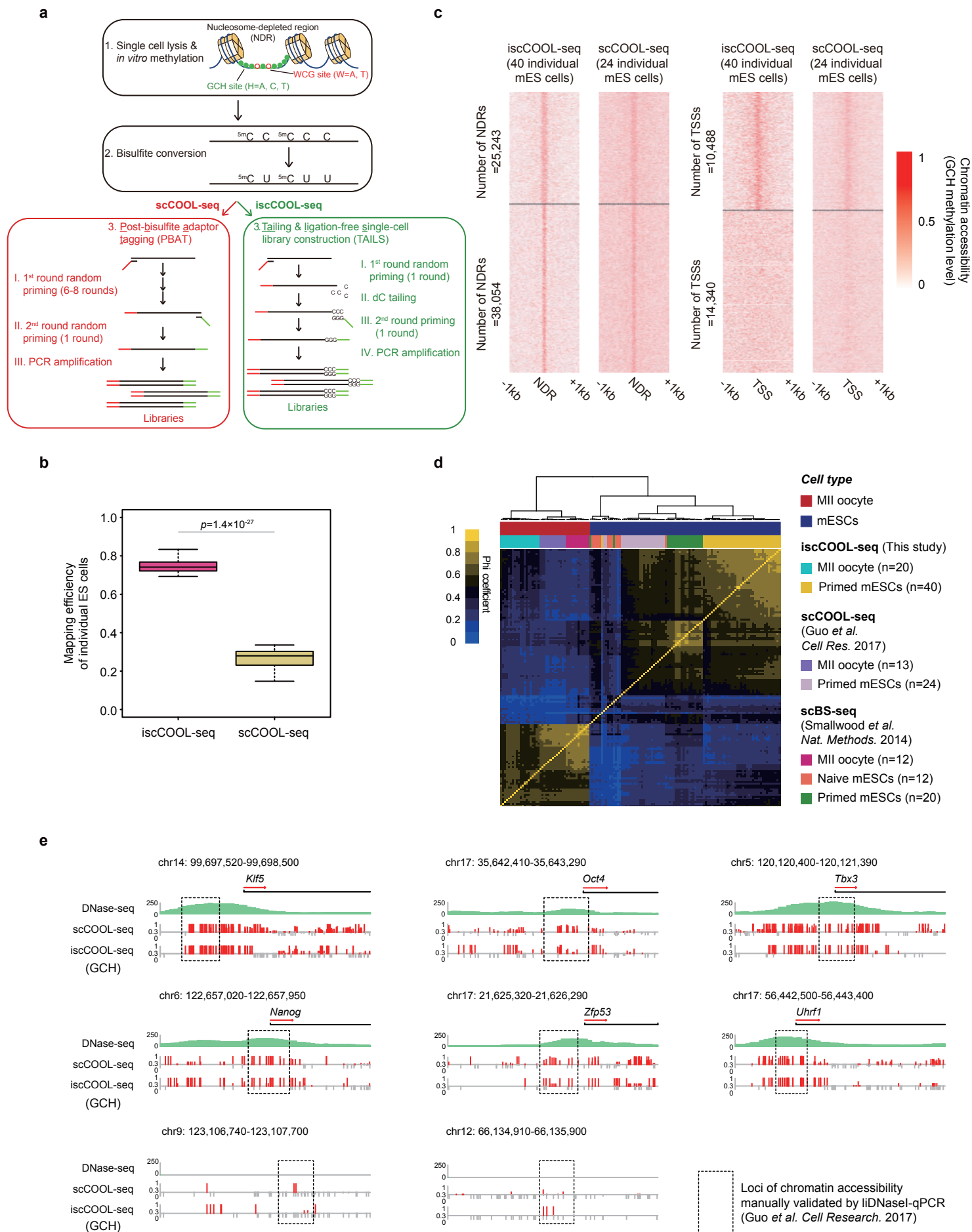




Supplementary information, Fig. S1 Sensitivity and accuracy of the iscCOOL-seq method. **(a)** Diagram of the improved single-cell COOL-seq method by using the TAILS strategy. **(b)** Comparison of mapping efficiency of individual mESCs between iscCOOL-seq and scCOOL-seq. **(c)** A heatmap showed that both the chromatin accessibility of regions around NDRs (± 1 kb) and TSSs (± 1 kb) detected by scCOOL-seq in mouse ESCs can be reproduced in iscCOOL-seq. **(d)** A heatmap showed the phi coefficients of digital DNA methylation level of individual mouse MII oocytes and ES cells performed by iscCOOL-seq, scCOOL-seq (Guo *et al. Cell Research*. 2017) or scBS-seq (Smallwood *et al. Nature Methods*. 2014). **(e)** Representative loci showed that the open regions (*Klf5*, *Oct4*, *Tbx3*, *Nanog*, *Zfp53* and *Uhrf1*) and closed regions (chr9: 123,106,740-123,107,700 and chr12: 66,134,910-66,135,900) in mouse ES cells, confirmed by liDNaseI-qPCR and scCOOL-seq (Guo *et al. Cell Research*. 2017), could be reproduced by iscCOOL-seq. P-values were defined by the two-tailed Student's *t*-test.