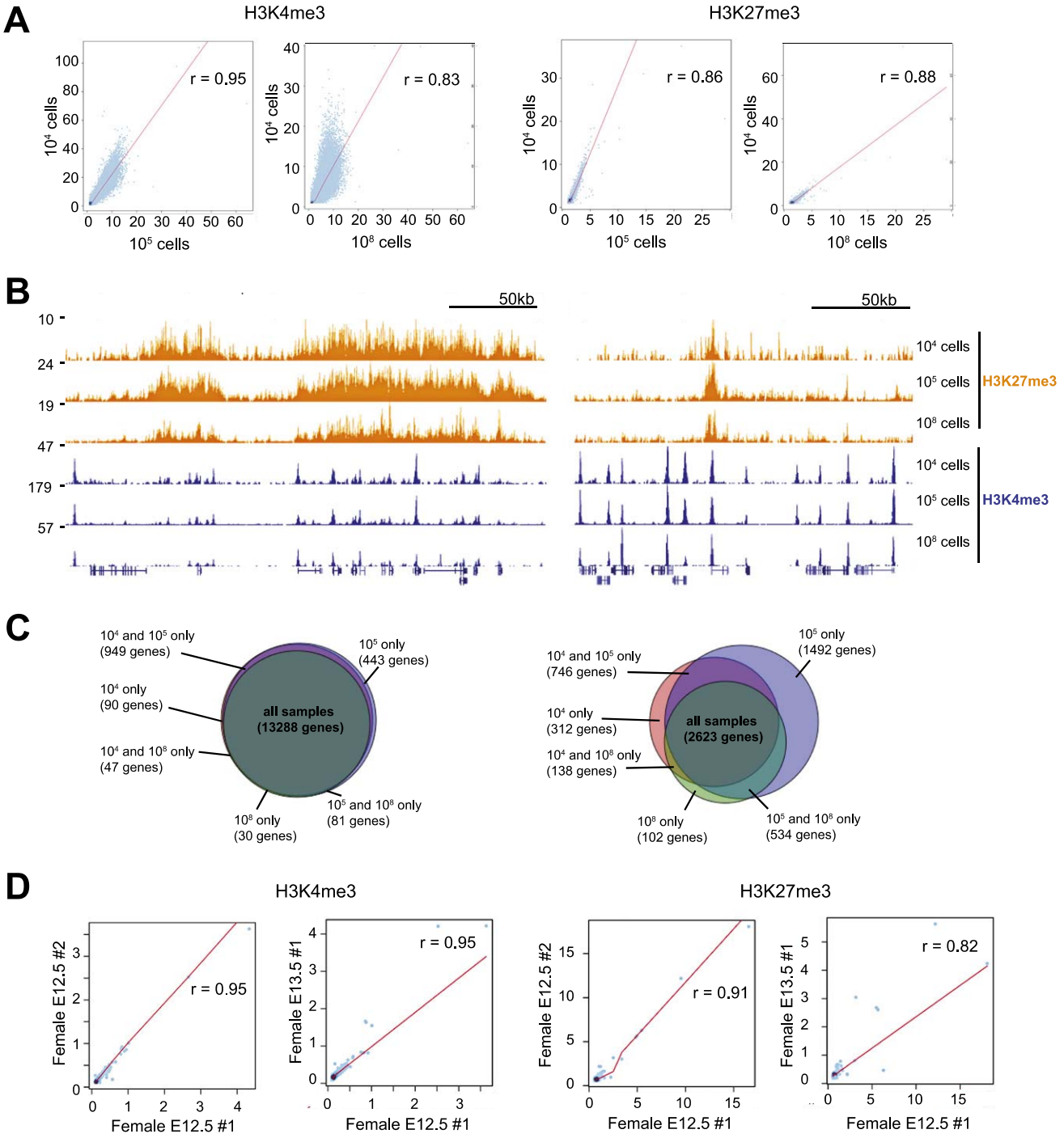

Fig. S2. Validation of small-scale ChIP-seq protocol using mouse embryonic stem cells (mESCs). (*A*) Pearson correlations between datasets for H3K4me3 or H3K27me3 ChIP datasets. (*Left*) ChIP performed on 2×10^4 vs. 1×10^5 cells grown in the same dish. (*Right*) ChIP performed on 2×10^4 cells vs. $\sim 1 \times 10^8$ cells; 1×10^8 cell dataset from Mikkelsen et al. (1). (*B*) Sample gene tracks for data from 2×10^4, 1×10^5, or 1×10^8 cells at the HoxB cluster (*Left*) and at a gene-rich region on chromosome 19 (chr19:3,922,435-4,515,456) (*Right*). (*C*) Overlap between genes associated with H3K4me3 or H3K27me3 in ChIP-seq from 2×10^4, 1×10^5, or $\sim 1 \times 10^8$ cells. (*D*) Pearson correlation between biological replicates in fetal germ cells. Shown are scatter-plots for median signal in 50-kb windows for replicates from female E12.5 germ cells, where ChIP was performed on different days, and female E12.5 compared with female E13.5 germ cells where ChIP was performed on the same day.

1. Mikkelsen TS, et al. (2007) Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. *Nature* 448(7153):553–560.