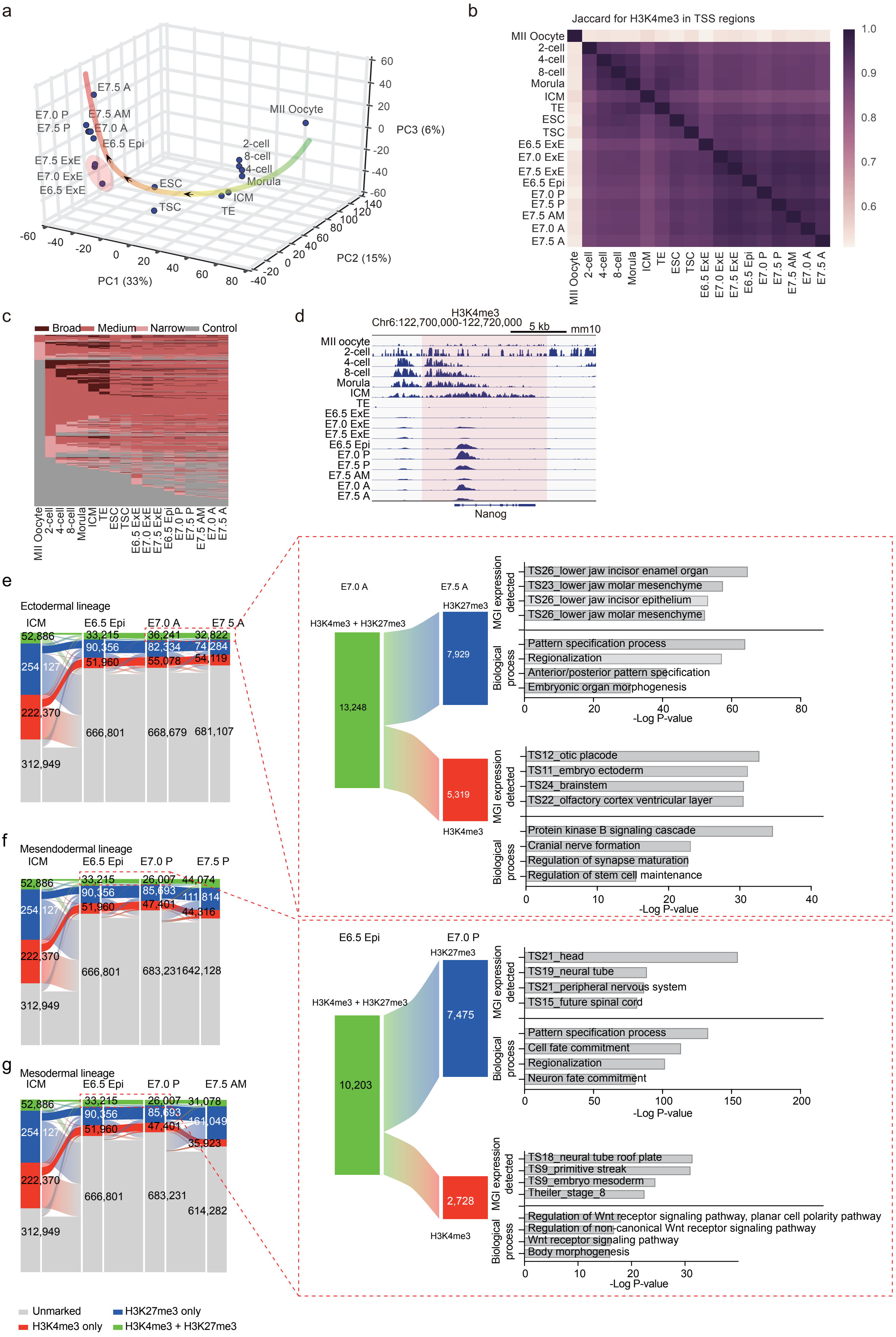

Supplementary information, Fig. S3 The dynamics of promoter-related histone modifications during early mouse embryogenesis.

Fig. S3 The dynamics of promoter-related histone modifications during early mouse embryogenesis. a Three-dimensional principal component analysis based on H3K4me3 and H3K27me3 data from pre-implantation embryo and the mouse gastrula. **b** Clustering analysis based on Pearson correlations of H3K4me3 modification patterns between samples from pre-implantation embryos and gastrula. **c** Dynamics of the H3K4me3 domain length on all of the RefSeq promoters following the developmental process from the pre-implantation to gastrulation stage. The promoters were classified according to the breadth of H3K4me3 peak: broad (> 5 kb, dark red), medium (1-5 kb, red), narrow (200 bp-1 kb, pink) and null (grey). **d** Representative genome browser snapshot of H3K4me3 enrichment at the range of *Nanog*. **e-g** Alluvial plots depicting the dynamics of bivalent domains (H3K4me3 + H3K27me3) during mouse early embryogenesis. **e**, ectoderm; **f**, mesendoderm; **g**, mesoderm. Genomic regions with both H3K4me3 and H3K27me3 modifications in E7.0 A but resolved into H3K4me3 (5,319) or H3K27me3 (7,929) in E7.5 A, and genomic regions with both H3K4me3 and H3K27me3 modifications in E6.5 Epi but resolved into H3K4me3 (2,728) or H3K27me3 (7,475) in E7.0 P were then subjected to GREAT analysis. The published data of H3K4me3 and H3K27me3 enrichment in pre-implantation embryos[11] and H3K27me3 in the gastrula[20] were used in these analyses.