**Supplemental Figure 1.** Quantitative analysis of histone 2A, 2B and histone 4 modifications during mESC lineage commitment

Proteomic analysis of H2A, H2AZ and H2B peptides in mESCs and A. neuroectoderm and B. endoderm committed wild-type cells. Proteomic analysis of the H4 peptides in mESCs and C. neuroectoderm and D. endoderm committed wild-type cells. The abundance of each modified peptide was normalized to H3K4me0 peptide in that particular cell type. The results of two biological replicates are shown.

**Supplemental Figure 2.** Expression level of H3K36 demethylases

Expression levels of histone demethylases for H3K36 methylation during neuroectoderm differentiation time-course measured by RT-qPCR analysis. Results are normalized to β-actin levels. The error bars represent SEM of at least three biological replicates. Statistical analysis (Student’s t-test) was done using GraphPad Prism software. \*: p-value<0.05. Nonsignificant values are not shown.

**Supplemental Figure 3.** Expression level of H3K36me2 and H3K36me3 readers

Expression levels of readers for H3K36me2 and H3K36me3 during neuroectoderm differentiation time-course measured by RT-qPCR analysis. Results are normalized to β-actin levels. The error bars represent SEM of at least three biological replicates. Statistical analysis (Student’s t-test) was done using GraphPad Prism software. \*: p-value<0.05; \*\*: p-value<0.01. Nonsignificant values are not shown.

**Supplemental Figure 4.** Expression level of selected genes during endoderm differentiation

Expression profile changes of A. pluripotency genes Oct4 (Pou5f1), Sox2, Nanog and Klf4,

B. endoderm differentiation related genes (Foxa2, Gsc, Sox17, Gata6, Gata4 and Hnf4a)

C. selected H3K36 methyltransferases (Nsd1, Nsd2, Nsd3, Setd2, Setd5), demethylase

(Kdm4c) and readers (Dnmt3a, Dnmt3b, Msh6, Zmynd11, Psip, Mrg15) during the course of

endoderm differentiation visualized by Integrative Genome Viewer (Robinson et al., 2011)

using the reference genome Mus musculus 10 (GRCm38/mm10). The results are representative of three biological replicates. For easy comparison purposes, all time points have the same scale on the y-axis for each gene. D. Relative expression level of selected genes. Genes with |(fold change (FC))| ≥ 1.5 (|logFC| ≥ 0.58) and false discovery rate (FDR) < 0.05 are significantly altered during differentiation (highlighted). Fold changes were calculated as mESC/days of endoderm differentiation.