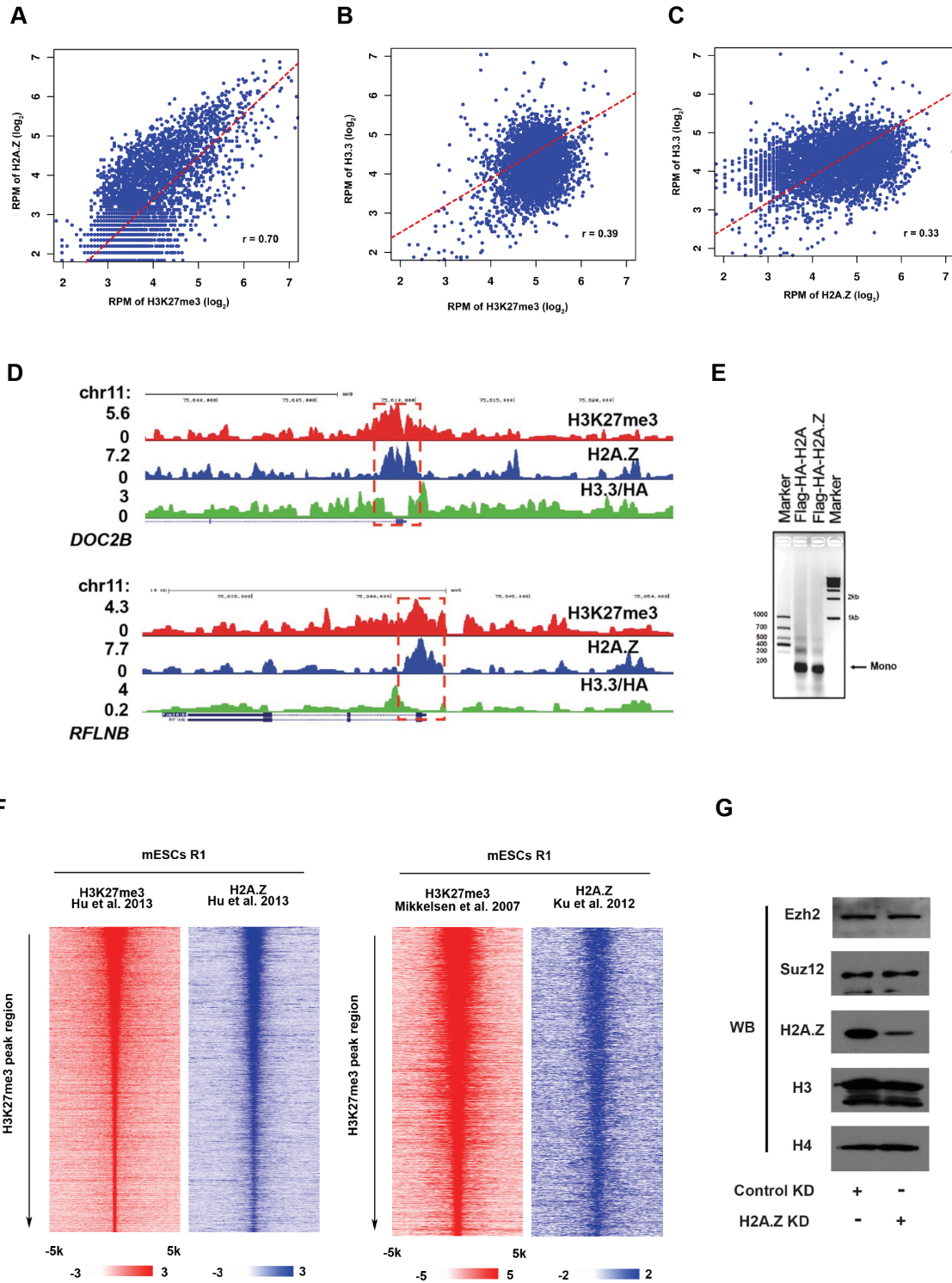




Additional file1: Fig.S1. H2A.Z is required for the proper genome-wide distribution of H3K27me3 in mES cells.

- A.** Scatterplot comparing the mean of the H3K27me3 and H2A.Z ChIP-seq signals on H3K27me3 peak regions. Both signals of H3K27me3 and H2A.Z are normalized with RPM. The coefficient of determination (r) is indicated.
- B.** Scatterplot comparing the mean of the H3K27me3 and H3.3 ChIP-seq signals on H3K27me3 peak regions. Both signals of H3K27me3 and H2A.Z are normalized with RPM. The coefficient of determination (r) is indicated.
- C.** Scatterplot comparing the mean of the H2A.Z and H3.3 ChIP-seq signals on H3K27me3 peak regions. Both signals of H3K27me3 and H2A.Z are normalized with RPM. The coefficient of determination (r) is indicated.
- D.** H3K27me3, H2A.Z and H3.3 occupancy in specific gene loci (from top to bottom: *DOC2B*, *RFLNB* respectively) in wild-type mES cells.
- E.** DNA electrophoresis used to check the quality of H2A- or H2A.Z-containing mono-nucleosomes in mono-nucleosomes immune-precipitation (Mono-IP) assay.
- F.** Heat-map for distributions of H3K27me3, H2A.Z at the H3K27me3 enriched regions in mES cells. ChIP-seq data was cited from Ku M. et al., 2012 and Hu G. et al., 2013 correspondingly.
- G.** Western blot to analyze the dynamic changes of Ezh2 or Suz12 protein level upon knockdown of H2A.Z in mES cells.