



Supplemental Figure S4. Special and temporal characterization of BELD genes. (A) BELD genes are enriched in module M16 of the co-expression networks generated by Parishak et al. 2013. P , P value, one-tailed Fisher's exact test. *ns*, not significant, $P > 0.05$. (B) Heatmap presentation of expression profiles of BELD genes in 13 tissues. The FPKM values were obtained from Shen et al. (C-E) Comparisons of H3K27ac (C), H3K4me1 (D), and ATAC-seq (E) signals in gene bodies between BELD genes and non-BELD control genes. P , P value, one-tailed t -test. (F) Comparisons of mCG and hmCG levels in CG and CH contexts between BELD and non-BELD control genes in their gene body regions and surrounding regions (± 50 kb). (G) Heatmaps of normalized signals of H3K27ac across the gene bodies and surrounding regions (± 100 kb) of the BELD and non-BELD control genes at ten developmental time points. The profiles at embryonic time points, P0, and P56 were obtained from the ENCODE project (Consortium 2012), and the profiles at P14 were obtained from a recent study (Stroud et al, 2017).