

**Table S1.** Results from CiiiDER transcription factor enrichment analysis to analyze shared transcription factors (TFs) between the sexes during hibernation. The enriched TF binding site columns denote the number of over- and under-represented transcription factor binding sites revealed in the enrichment analysis, with either upregulated or downregulated differentially expressed (DE) genes used as input. Overlapped TFs represent the number of shared transcription factors between males and females at late hibernation (LH) vs. early hibernation (EH). Red lettering indicates the TFs whose binding site is significantly over-represented in DE genes relative to the background set. Black lettering indicates the TF whose binding site is significantly under-represented and contains binding sites more frequently in the background set relative to DE genes.

Group	Number of enriched TF binding sites for upregulated DE genes	Number of shared TF binding sites between groups	Identity of TF with enriched binding site	Number of enriched TF binding sites for downregulated DE genes	Number of shared TF binding sites between groups	Identity of TF with enriched binding site
Male LH vs. EH	118	25	<i>Emx1, Mix-A, Foxc1, Fev, Emx2, Meox1, Lmx1a, Fli1, Alx4, Arx, Dmbx1, Phox2a, Gcm2, Vsx1, Dlx1, Vsx2, Ets1, Alx1, Wt1, Dmrt1, Pou6f2, Prrx2, Rhox11, Elk2</i>	60	10	<i>Hoxc11, Nfic, Hoxd12 Hoxd11, Hoxc12, Spi1, Tfap2a, Zfp42, Hoxa11, Hoxd10</i>
Female LH vs. EH	76			97		