

**Table S3.** Results from CiiiDER transcription factor enrichment analysis to analyze sex-specific transcription factors (TFs) across hibernation. The enriched TFs column denotes the number of over- and under-represented transcription factor binding sites revealed in the enrichment analysis, with upregulated differentially expressed (DE) genes used as input. 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
Male LH vs. EH	118	14	<i>Pbx1, Elk1, Hsf1, Stat6, Fli1, Etv3, Sreb1, Hsf2, Etv6, Etv2, Hsf4, Erf, Etv5, Elk3</i>
Males vs. females at LH	63		
Female LH vs. EH	76	12	<i>Mef2a, Meox1, Mef2c, Fli1, Alx4, Gcm1, Lmx1b, Ets1, Maf, Mef2b, Fos12::Jun, Meis2</i>
Females vs. males at LH	90		