

Table S4. Significantly enriched transcription factors (TFs) from CiiiDER enrichment analysis. The enriched TF column denotes the over-represented enriched TF within a sex at the planned comparison (group column). Differentially expressed (DE) target columns denote the predicted DE genes that the TF contains enriched binding sites in, at each comparison.

Group	Enriched TF within a sex	LH vs. EH DE gene targets	LH DE gene targets
Upregulated DE genes in males at LH vs. EH & upregulated in males vs. females at LH	<i>Srebf1</i>	<i>Ccdc177, Tyrobp, Sgsh, Qprt, Cdca5, Tspo</i>	<i>Coro2a, Foxg1, Aebp1, Dkk1, Phlda2</i>
Upregulated DE genes in females at LH vs. EH & upregulated in females vs. males at LH	<i>Maf</i>	<i>Cnga3, Slc24a4</i>	<i>Adamts13, Slc24a4, Capb2, Nrep, Vwa3a</i>
	<i>Gcm1</i>	<i>Ccdc177, Slc16a2, Slc24a4</i>	<i>Fsip1, Neurog2, Rorb, Slc24a4, Cabp2, Rax</i>
	<i>Mef2b</i>	<i>Cnga3</i>	<i>Angpt1, Vwa3a</i>