

Supplementary Table 1. Performance of hypothalamus tissue gene expression prediction models built using GTEx data.

Prediction performance (R ²)	All	Protein	lncRNAs	miRNAs	Others ^a
0.01	7584	5518	1896	45	125
0.04	4666	3365	1195	22	84
0.09	2497	1748	685	10	54
0.16	1187	808	347	6	26
≥ 0	10807	7953	2621	67	166

Abbreviations: *Protein*, protein coding genes; *lncRNAs*, long non-coding RNAs; *miRNAs*, microRNAs.

^a Including processed transcripts, immunoglobulin genes, and T cell receptor genes.

Supplementary Table 2. Performance of ovary tissue gene expression prediction models built using GTEx data.

Prediction performance (R ²)	All	Protein	lncRNAs	miRNAs	Others ^a
0.01	8580	5969	2331	96	184
0.04	5521	3869	1492	50	110
0.09	3049	2138	827	20	64
0.16	1480	1035	403	8	34
≥ 0	11,921	8,302	3,226	139	254

Abbreviations: *Protein*, protein coding genes; *lncRNAs*, long non-coding RNAs; *miRNAs*, microRNAs.

^a Including processed transcripts, immunoglobulin genes, and T cell receptor genes.

Supplementary Table 3. Functional pathway analysis and relevant functions for TWAS-identified genes associated with age at natural menopause.

Top diseases and functions in networks	Molecules in network	ANM-associated molecules	Score ^a
Embryonic Development, Organ Development, Organismal Development	BAG6, CBY1, CCNB1, CEBPA, CKAP2, CSNK2B, CTNNB1, CYP2B6, DPEP1, EPHB3, EPHX1, FDFT1, FGFR4, FOXO1, FXR2, GLIPR1, HMGCS1, LSS, MGEA5, NAA10, NOTCH4, NUSAP1, PFKM, PRIM1, RAB5C, RAD23A, RELA, SEMA3C, SNRK, TCF19, TP53, TPD52L1,	BAG6, CBY1, CSNK2B, EPHX1, FGFR4, NOTCH4, NUSAP1, PRIM1, RAB5C, TCF19	23
Inflammatory Disease, Neurological Disease, Skeletal and Muscular Disorders	P-TEFb, PRRC2A	PRRC2A	3
Developmental Disorder, Hereditary Disorder, Metabolic Disease	NUPR1, SUOX	SUOX	3
Cancer, Cell Cycle, Cellular Development	GPRIN1, MITF	GPRIN1	3
Cancer, Cell Death and Survival, Cellular Assembly and Organization	ILF3, NR3C1, ZNF346	ZNF346	3
		<i>P</i> value	overlapped genes (%)
Top canonical pathways	Sulfite oxidation IV	1.24E-03	1/1 (100)
	Clathrin-mediated endocytosis signaling	1.77E-03	3/196 (1.5)
	IL-2 signaling	2.83E-03	2/64 (3.1)
	EGF signaling	3.19E-03	2/68 (2.9)
	PI3K/AKT signaling in the pathogenesis of influenza	3.66E-03	2/73 (2.7)
		<i>P</i> value	# molecules
Diseases and disorders	Infectious disease	3.04E-02 - 2.76E-04	5
	Endocrine system disease	3.17E-02 - 3.33E-04	8
	Gastrointestinal disease	4.49E-02 - 3.33E-04	21
	Immunological disease	4.84E-02 - 3.33E-04	8
	Inflammatory disease	4.49E-02 - 3.33E-04	6
		<i>P</i> value	# molecules
Molecular and cellular functions	Cellular compromise	1.24E-03 - 1.24E-03	1
	Lipid metabolism	1.96E-02 - 1.24E-03	4
	Small molecule biochemistry	1.96E-02 - 1.24E-03	4
	Cellular growth and proliferation	4.84E-02 - 2.48E-03	2
	cell cycle	1.72E-02 - 3.71E-03	2

^a The score is the negative Log of the *P* value for network association testing.

Supplementary Figure 1.

