SUPPLEMENTARY TABLE S1 - Table showing the number of genes expressed in each CNS region

Region	No. of genes expressed		
CRBL	16,653		
FCTX	15,213		
HIPP	14,830		
НҮРО	14,956		
MEDU	14,388		
ОСТХ	15,274		
PUTM	15,036		
SNIG	14,392		
SPCO	14,506		
тстх	15,310		
THAL	14,599		
WHMT	14,078		

SUPPLEMENTARY TABLE S2 - Canonical pathways with evidence of sex-biased expression in at least one CNS region

Canonical Pathway	Enrichment	CNS Region	p-value
BIOCARTA_STRESS_PATHWAY	F>M	HIPP, WHMT	0.001, 0.009
KEGG_LYSOSOME	F>M	WHMT	0.016
KEGG_INSULIN_SIGNALING_PATHWAY	F>M	WHMT	0.039
REACTOME_COMPLEMENT_CASCADE	F>M	WHMT	0.04
KEGG_CHEMOKINE_SIGNALING_PATHWAY	F>M	WHMT	0.022
KEGG_LYSOSOME	M>F	CRBL	0.006
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	M>F	SNIG	0.006

Significant sex-biased enrichment in at least one region (p-value < 0.05, where enrichment p-values were estimated using an empirical permutation-based procedure) was detected for 12 canonical pathways of which 7 could be considered independent.

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