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Table #	Abbreviated Title	Full Title	Caption
1	RNAseq Summary, by Sample	RNAseq Summary, by Sample	Summary of the RNA-seq processing (FASTQ trimming and alignment) for each dataset. bbdup and HISAT2 were used for trimming and alignment, respectively. The trimming parameters for each dataset were as follows: Carpenter, ftm = 5 ref=adapters.fa ktrim=r k=21 mink=11 hdist=2 tbo tpe qtrim=rl trimq=20 minlen=75 maq=20; Walker, ftm = 5 ref=adapters_overrepresented.fa ktrim=r k=21 mink=11 hdist=2 qtrim=rl trimq=20 minlen=50 maq=20; Powell, ref=adapters.fa ktrim=r k=21 mink=11 hdist=2 qtrim=rl trimq=20 minlen=75 maq=20.
2	Overall DE Summary	Overall Differential Expression Summary	Summary of gene and differential expression results related to dispersion and fold change. and Dispersion and fold change values are rounded to 4 and 2 decimal places, respectively.
3-5	Diff. Exp. {Study}	Differential Expression Results for {Study}	Differential expression results for the 3 studies - Carpenter (Supplementary Table S2), Walker (Supplementary Table S3), and Powell (Supplementary Table S4) - including the log2 fold change of each gene and empirical Bayes statistics. Only genes that passed the filter thresholds were included in the final analysis. Limma voom models were used to calculate the results, as described in the main text. Some genes are unnamed in the Ensembl genomes, and just their IDs are used to identify them.
6	Craving Genes Summary	Craving Genes and Homologs Summary	Summary of shared Craving genes and their human, mouse, and rat homologs. The datasets that identified them as DEGs (Carpenter, Walker, and/or Powell) are listed, along with whether they are up- or down-regulated in the high craving condition (Carpenter - C28, Walker - S30, Powell - C21) relative to the control/low-craving condition (Carpenter - S28, Walker - S30, Powell - C1). ^ The human gene FTH1 is homologous with mouse, and the mouse gene Fth1 is homologous with rat, but the rat gene Fth1 is not homologous with human FTH1.
7	Sex by Tissue ANOVAs	Sex:Tissue ANOVAs for Shared "Craving" genes	Full results for 2-way, type III ANOVAs analyzing main effects of Sex and Tissue and Sex:Tissue interactions across brain tissues in the Gene-Tissue Expression (GTEx) database. F statistic, ges, and P value are rounded to 4 decimals. * indicates significant main effect or interaction (P < 0.05). Calculations were performed using age-matched samples from males and females >= 55 years of age the GTEx database of human RNA-sequencing data, with gene expression measured in transcripts per million (TPM). +CELF6 is a paralog of another Craving gene that corresponds to a poorly annotated novel transcript, ENSG00000273025, which was excluded from the analyses.
8	Tissue Tukey's, Contrasts	Tukey's Tests Comparing Expression between Tissues	Results of post-hoc Tukey tests comparing expression between brain tissues in the Gene-Tissue Expression (GTEx) database. * indicates significant difference between male and female expression in a tissue. For Tukey statistics for individual tissues, including summary data in the form of compact letter displays (CLDs), see Supplementary Table S6. Calculations were performed using age-matched samples from males and females >= 55 years of age the GTEx database of human RNA-sequencing data, with gene expression measured in transcripts per million (TPM).
9	Tissue Tukey's, CLD	Tukey's Statistics Comparing Expression across Tissues, Using Compact Letter Displays	Post-hoc Tukey statistics comparing expression across brain tissues in the Gene-Tissue Expression (GTEx) database. Compact letter displays (CLDs) for each gene summarize the differences between tissues. Tissues are assigned letter(s) to reflect their expression relative to other tissues, with tissues that have similar expression levels assigned the same letter(s). For an individual gene, "a" indicates the tissue(s) with the highest expression, then "b", "c", and so on. See Supplementary Table S5 for tissue comparisons that informed these CLDs. Calculations were performed using age-matched samples from males and females >= 55 years of age the GTEx database of human RNA-sequencing data, with gene expression measured in transcripts per million (TPM). +CELF6 is a paralog of another Craving gene that corresponds to a poorly annotated novel transcript, ENSG00000273025, which was excluded from the analyses.
10	Sex by Tissue Tukey's	Tukey's tests for Significant Sex:Tissue Interactions.	Full results for post-hoc Tukey tests comparing sex differences in expression across brain tissues in the Gene-Tissue Expression (GTEx) database. Analyses were only performed for genes with a significant Sex:Tissue interaction (see Supplementary Table S7). Estimate, lower and upper confidence intervals, and P value are rounded to 4 decimals. * indicates significant difference between male and female expression in a tissue. Calculations were performed using age-matched samples from males and females >= 55 years of age the GTEx database of human RNA-sequencing data, with gene expression measured in transcripts per million (TPM). +CELF6 is a paralog of another Craving gene that corresponds to a poorly annotated novel transcript, ENSG00000273025, which was excluded from the analyses.