**Supplementary Fig. 1: Anatomical representation of regions extracted via micropunch** (obtained by approaching the regions of interest caudally and punching rostrally). For each animal, one pair of bilateral caudal (1) and one pair of bilateral rostral (2) punches were made, each 1.00 mm in depth and 1.00 mm in diameter. All four punches, which collectively comprised the entire amygdala, were combined prior to RNA extraction.

**Supplementary Fig. 2: Unsupervised Principal Component Analyses (PCA) for RNASeq Data.** Two-dimensional representation of the first two principal components of all datasets (A), male datasets (B), and female datasets (C). Clustering by exposure was strongest in females.

**Supplementary Table 1.** Maletranscriptomic datasets (normalized to male vehicle; adjusted p-value ≤ 0.05).

**Supplementary Table 2.** Femaletranscriptomic datasets (normalized to female vehicle; adjusted p-value ≤ 0.05).

**Supplementary Table 3.** Significant (adjusted p-value ≤ 0.05) sex-differences in gene expression identified by RNAseq (female vehicle compared to male vehicle).