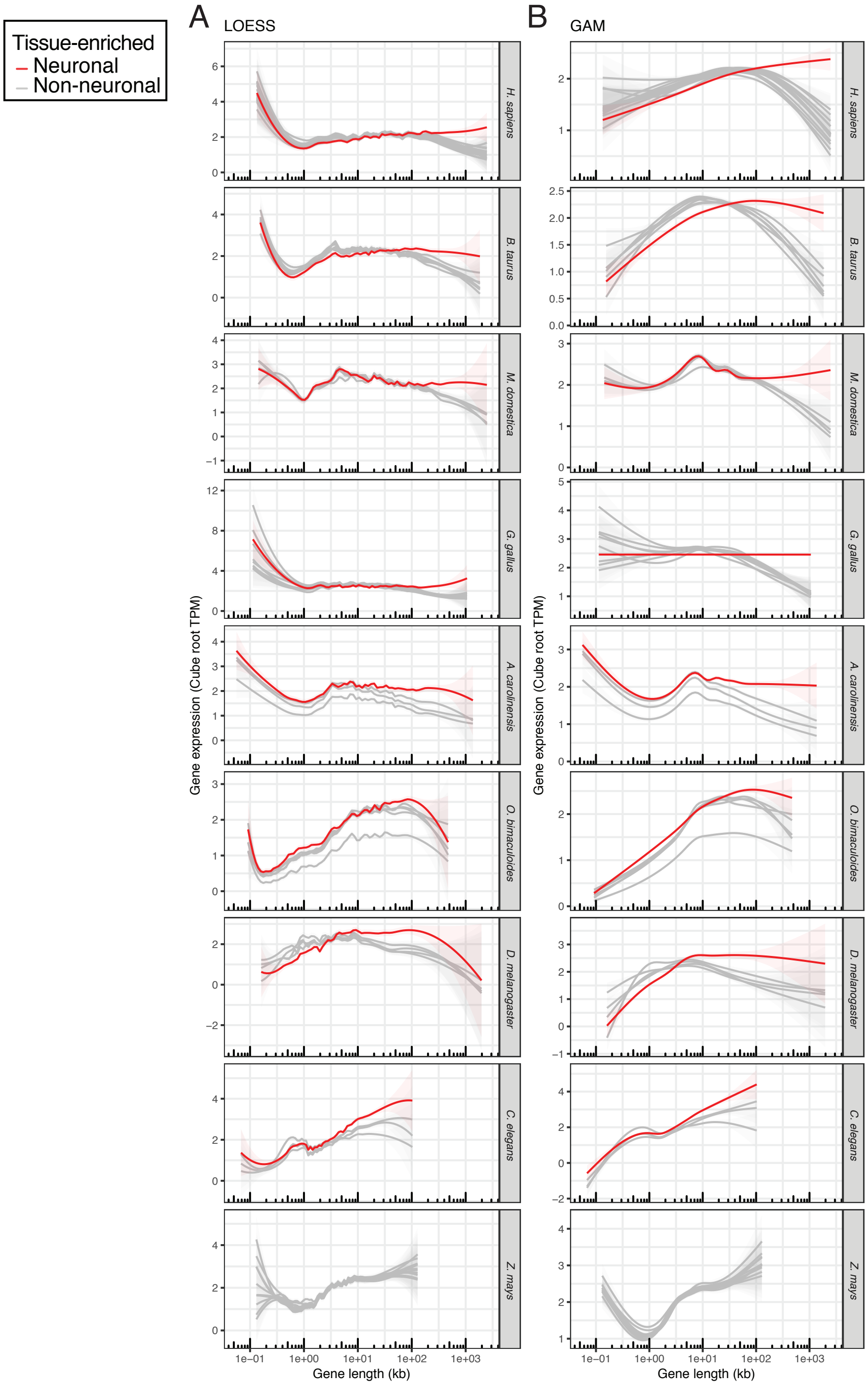

Figure S5. Smooth-quantile-normalized gene expression conditional on gene length. Each plot shows transcriptome data across multiple tissues from species presented in Fig. 1. Neuronal tissues or cells are shown in red and all other tissues and cell types are shown in grey, and transparent ribbons show 95% confidence intervals. (A) Loess smoothing of gene expression conditional on gene length (kb). (B) Generalized additive model of gene expression conditional on gene length (kb).