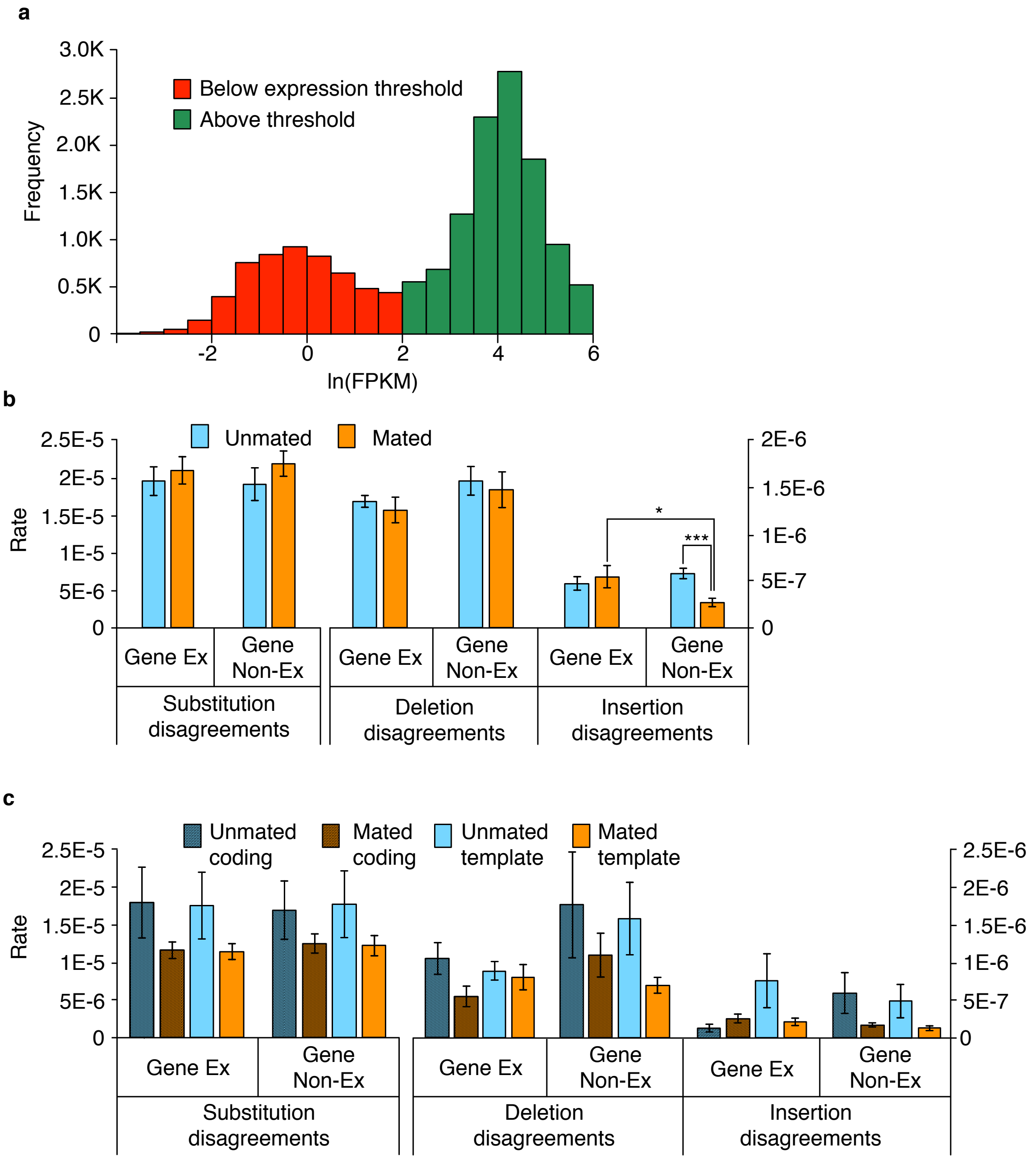

Supplemental Fig S12. Duplex disagreement rates as a function of gene expression.
(**a**) Gene expression levels in MZs (data pooled from mated and unmated worms). Colors show threshold chosen to distinguish between expressed and non-expressed genes (same thresholds used in b-c). (**b-c**) Gene (b) or coding or template (c) duplex disagreements broken down by thresholded gene expression status. Error bars give SEM (standard error of the mean), while stars denote significance of pairwise differences computed using bootstrapped confidence intervals (*: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$), with p-values corrected using Hochberg's step-up procedure with a 5% false discovery rate.