



Figure 1—figure supplement 2. Characteristics of ECT3-HyperTRIBE editing sites relative to target expression levels. (A-C) Number of significant editing sites (A), maximum or average editing proportions (B), and significance of editing sites according to either minimum or average $-\log_{10}(\text{adjusted } p\text{-value})$ per gene (C) in ECT3-HT targets split according to their expression levels (mean $\log_2(\text{TPM}+1)$ over the five ECT3-HT control samples)), in both aerial and root tissues.