



Figure 1—figure supplement 1. Identification of ECT3 targets using HyperTRIBE (extended data). (A) Expression levels of *ECT3-FLAG-ADAR* or *FLAG-ADAR* in apices (aerial tissues) or root tips of 10-day-old seedlings of the 5+5 independent transgenic lines (L1-L5) used for the experiment. (B) Consensus motif identified at significant editing sites of *ect3-1/ECT3-FLAG-ADAR* lines. (C) Scatterplot of the editing proportions (E.P. = $G/(A+G)$) of potential and significant editing sites (E.S.) of *ect3-1/ECT3-FLAG-ADAR* lines compared to the *FLAG-ADAR* controls. N.S., not significant. (D) Principal component analysis of editing proportions at significant editing sites in *ECT3-HT*. (E) Distribution of the correlations between editing proportions and ADAR expression (TPM) for significant editing sites in *ect3-1/ECT3-FLAG-ADAR* lines. Background correlations are based on randomly shuffling ADAR expression for each site.