



Figure 4—figure supplement 2. ECT2/ECT3 targets are co-expressed with ECT2/3 in highly dividing root cells. (A) t-SNE plot for scRNA-seq data in roots from Denyer et al. (2019), with cells coloured according to their cell-type cluster definitions described on the right side (<https://www.zmbp-resources.uni-tuebingen.de/timmermans/plant-single-cell-browser-arabidopsis-root-atlas/> and personal communication with Thomas Denyer). Dashed-enclosed region indicates clusters that contain meristematic cells. **(B)** Temporal reference map derived from pseudotime analysis of cells (Denyer et al., 2019) illustrates the progressive maturation of cells from the meristem core (reproduced with permission from Ma et al. (2020)). **(C)** Violin plot showing *ECT2* and *ECT3* single cell expression levels in the different clusters defined in A. These plots and their corresponding grey-red shaded t-SNE plots in Figure 4B (centre panels) were obtained from the above-mentioned website (Ma et al., 2020). **(D)** Box plot showing the proportion of marker genes from Denyer et al. (2019), which are targets of ECT2 or ECT3 in roots. These values were used to obtain the corresponding grey-orange shaded t-SNE plot shown in Figure 4B (right panel).