

Description of additional supplementary files

Title: Supplementary Data 1

Description: Marker peaks identified in each cluster.

Title: Supplementary Data 2

Description: Marker genes identified in each cluster.

Title: Supplementary Data 3

Description: Marker genes showing both cell type-specific accessibility (scATAC-seq) and gene expression (scRNA-seq) of root.

Title: Supplementary Data 4

Description: Marker genes identified in endodermis sub-type 1, using expression levels predicted from nearest scRNA-seq neighbors in co-embedding.

Title: Supplementary Data 5

Description: Marker genes identified in endodermis sub-type 2, using expression levels predicted from nearest scRNA-seq neighbors in co-embedding.

Title: Supplementary Data 6

Description: Marker genes identified in endodermis sub-type 3, using expression levels predicted from nearest scRNA-seq neighbors in co-embedding.

Title: Supplementary Data 7

Description: Peaks significantly associated with *TTG2* expression level, derived from linear regression of *TTG2* expression levels with accessibility levels of each peak in epidermis cells.