



Figure S1. Expression pattern of *MeSWEET10a* in vegetative tissues. (Supports Figure 1)

Y-axis: Fragments per Kilobase of transcript per Million mapped reads (FPKM) values.

X-axis: tissue types included in tissue-specific RNA-seq data (Wilson et al., 2017). OES: organized embryogenic structures, FEC: friable embryogenic callus, SAM: shoot apical meristem, RAM: root apical meristem. Graph was produced using the available online Cassava Atlas tool (http://shiny.danforthcenter.org/cassava_atlas).