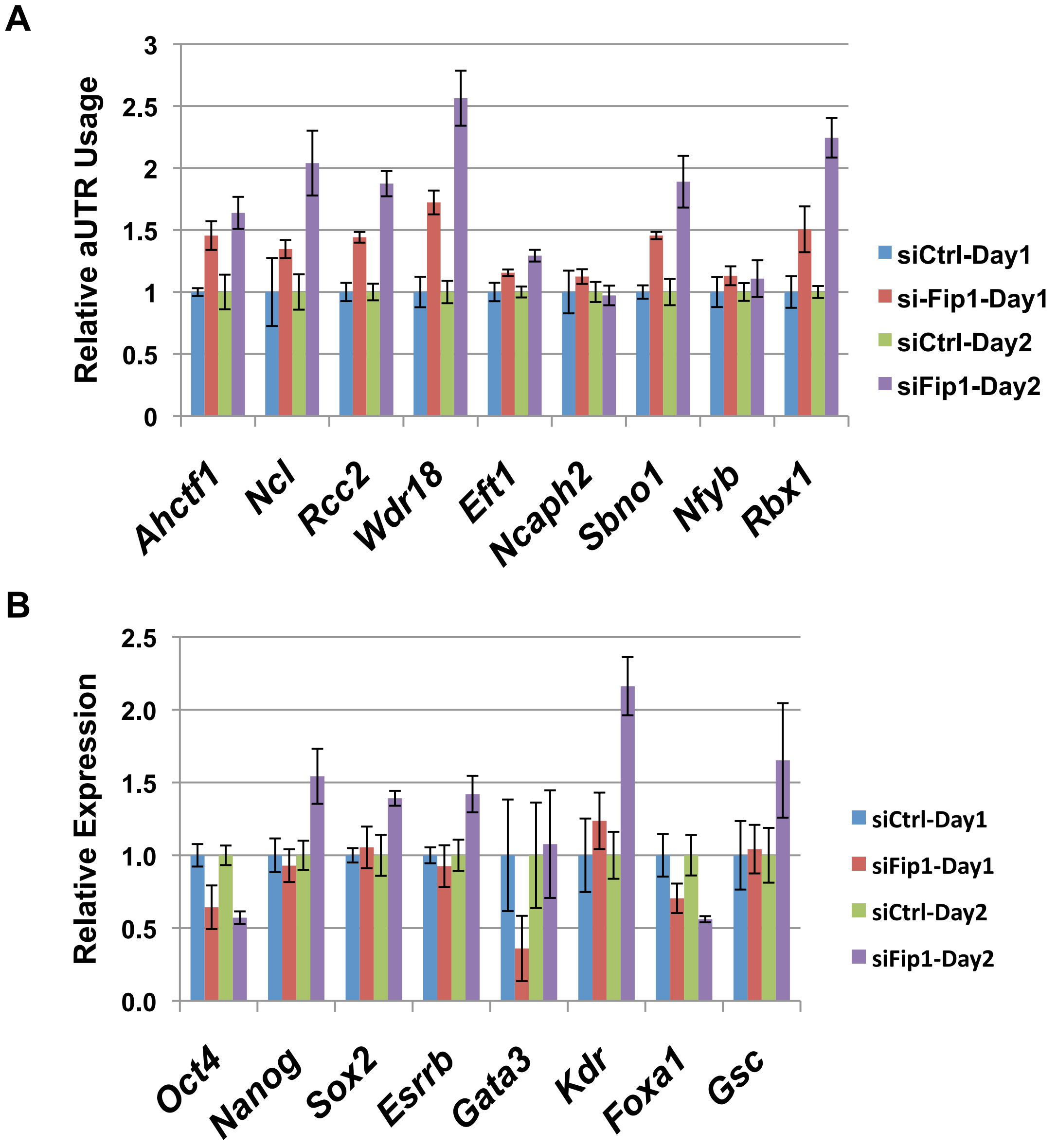

Figure S10. APA changes precede differentiation after Fip1 knockdown. (A) RT-qPCR quantification of relative aUTR usage (aUTR/common region) are normalized to the corresponding siCtrl sample and plotted as mean ± SEM (n=3). (B) RT-qPCR analyses of the expression levels of the specified marker genes. Their levels in siFip1 samples are normalized to the corresponding siCtrl and plotted as mean ± SEM (n=3).