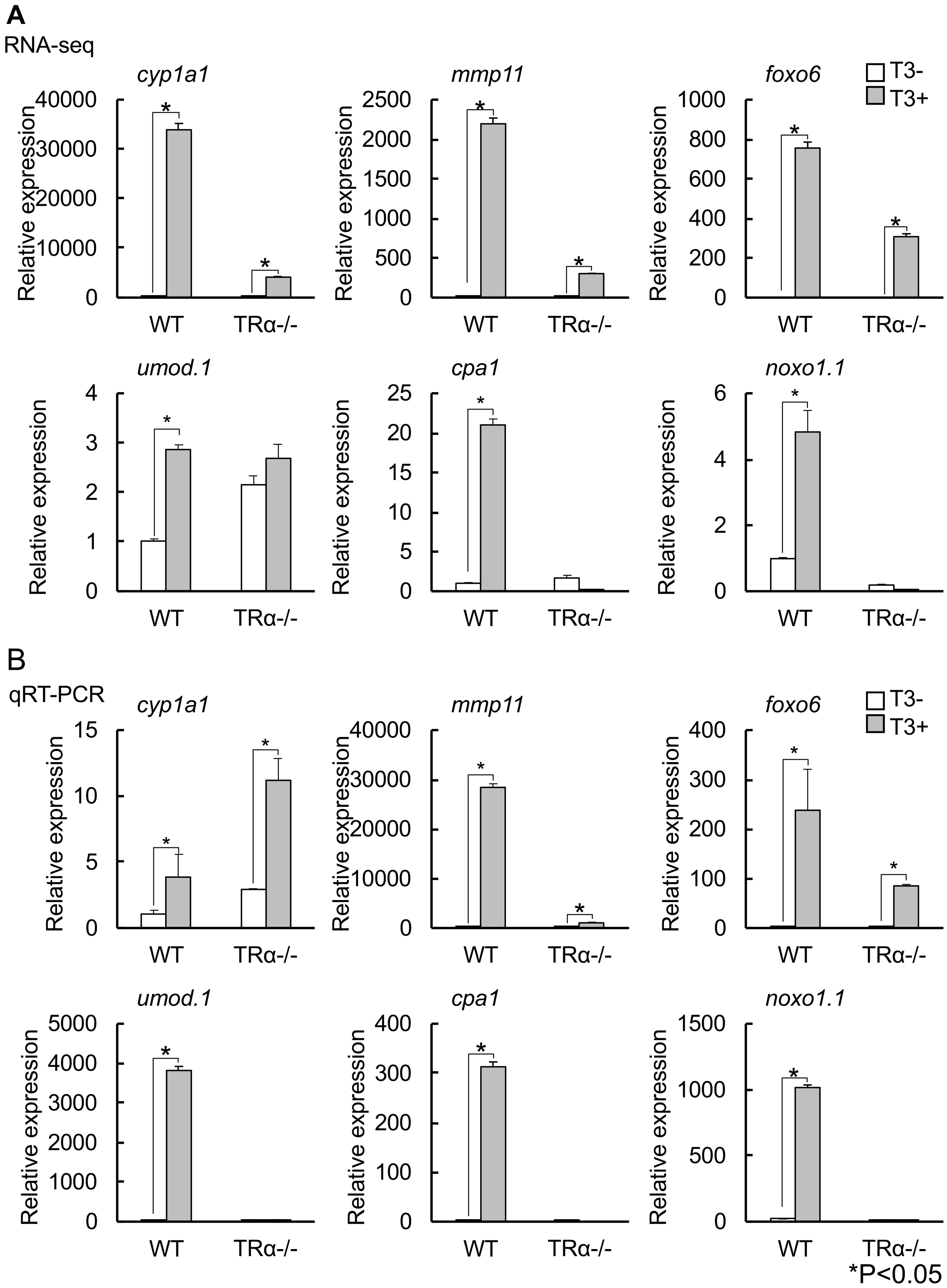

Supplemental Figure 3. Independent confirmation of RNA-seq data by qRT-PCR data for selected genes.

(A) Three genes (*cyp1a1*, *mmp11*, *foxo6*, Top) upregulated by T3 in both wild-type and $TR\alpha^{-/-}$ tadpoles and three genes (*umod.1*, *cpa1* and *noxo1.1*, Bottom) upregulated by T3 only in wild type tadpoles as identified from RNA-seq. Each bar represents the mean plus S.E. and the asterisk (*) indicates a significant difference between the T3 − and T3+ samples (padj<0.05).

(B) RT-PCR analyses confirms the regulation as found by RNA-seq for the 6 genes in (A). *X. tropicalis* tadpoles at stage 54 were treated with or without 10 nM T3 for 18 hours. RNA was isolated from the intestine and subjected to RT-PCR analysis for the 6 genes in (A). Note that the same regulation patterns were found for all genes as by RNA-seq (A). The asterisk (*) indicates a significant difference between the T3 − and T3+ samples (P<0.05). Each bar represents the mean plus S.E.