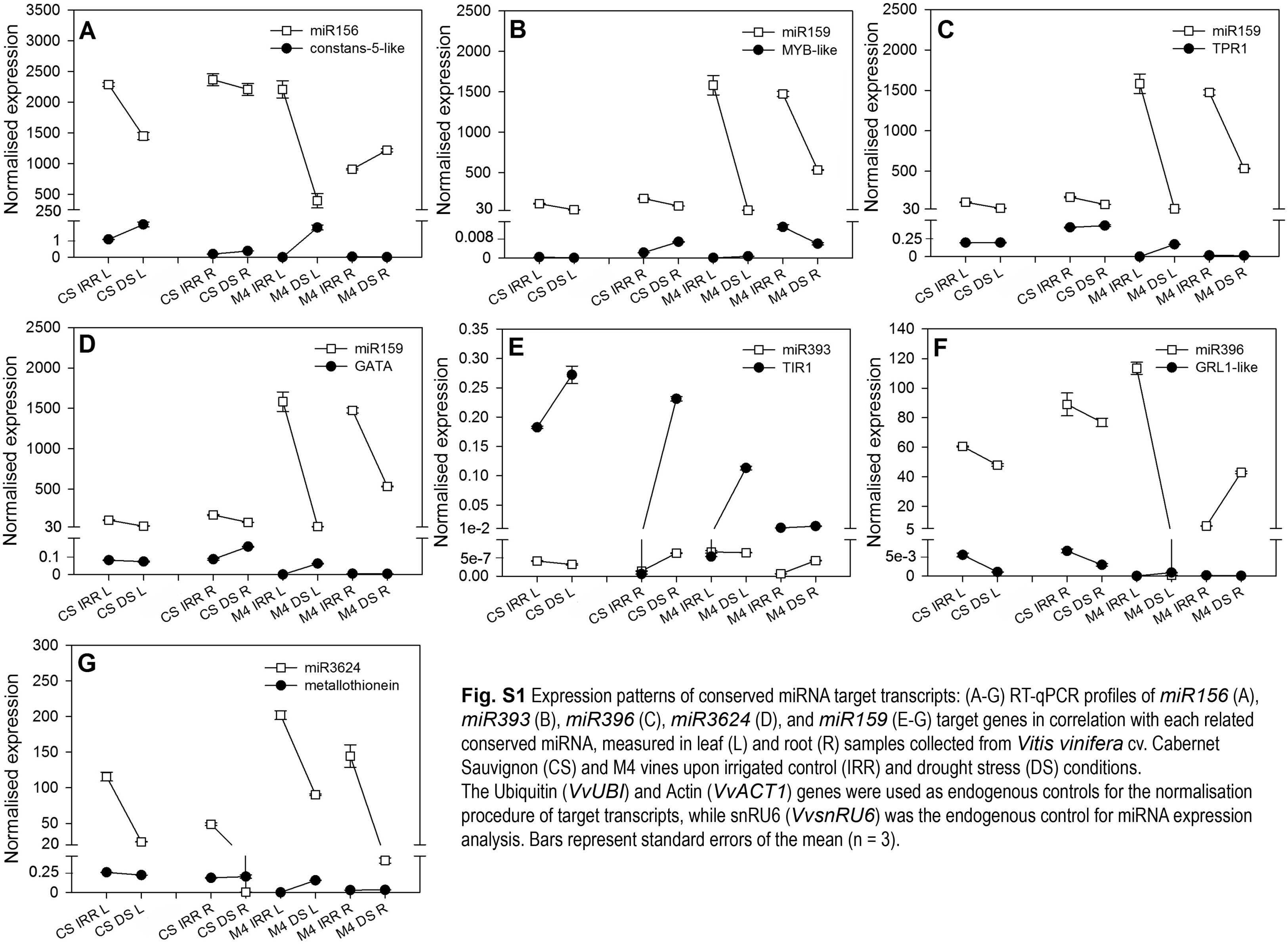

**Fig. S1** Expression patterns of conserved miRNA target transcripts: (A-G) RT-qPCR profiles of *miR156* (A), *miR393* (B), *miR396* (C), *miR3624* (D), and *miR159* (E-G) target genes in correlation with each related conserved miRNA, measured in leaf (L) and root (R) samples collected from *Vitis vinifera* cv. Cabernet Sauvignon (CS) and M4 vines upon irrigated control (IRR) and drought stress (DS) conditions.
The Ubiquitin (*VvUBI*) and Actin (*VvACT1*) genes were used as endogenous controls for the normalisation procedure of target transcripts, while snRU6 (*VvsnRU6*) was the endogenous control for miRNA expression analysis. Bars represent standard errors of the mean (n = 3).