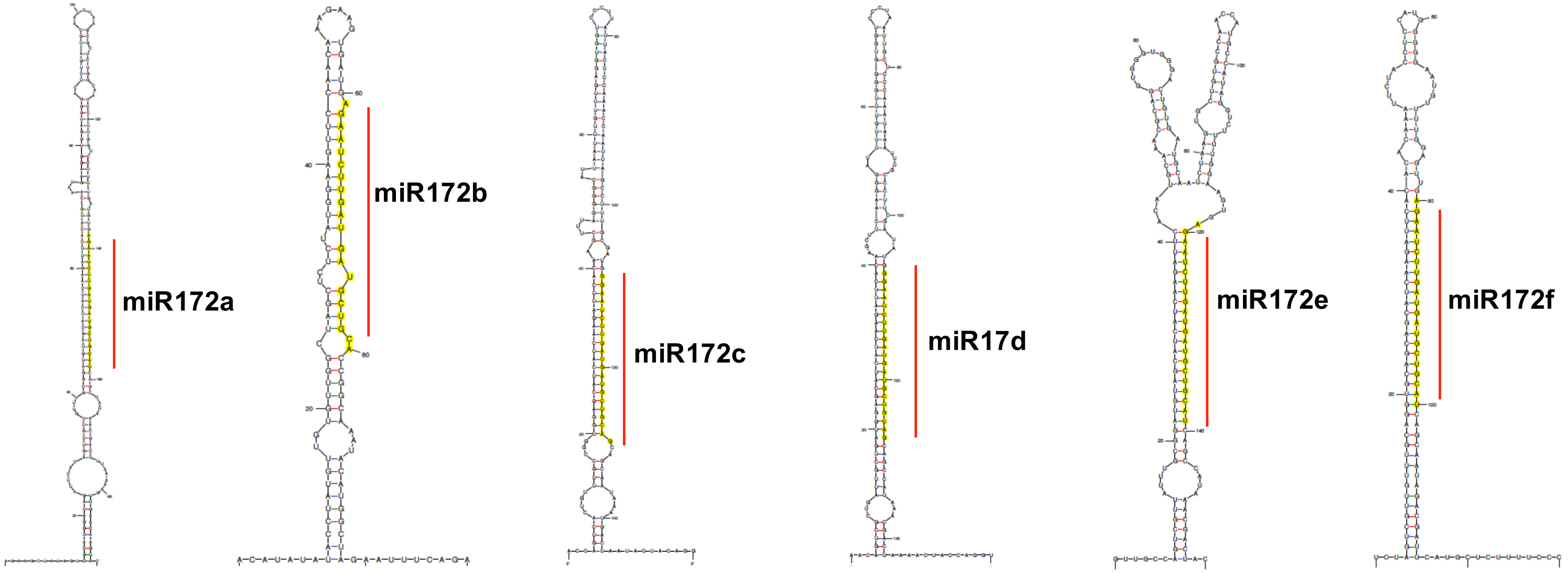
This work	Pelaez et al., 2012	Sequence	*P. vulgaris* genome mapping
miR172a (miR172a/e/f)	ath-miR172a	AGAAUCUUGAUGAUGCUGCA (20nt)	Chr. 5 pos. 35,820,612-631
miR172b	zma-miR172a	AGAAUCUUGAUGAUGCUGCAU (21nt)	Chr. 5 pos. 37,407,928-947
miR172c (miR172c/d)	ptc-miR172g	GGAAUCUUGAUGAUGCUGCAG (21nt)	Chr. 1 pos. 49,411,375-395
miR172d	ptc-miR172g	GGAAUCUUGAUGAUGCUGCAG (21nt)	Chr. 8 pos. 49,749,706-726
miR172e	ath-miR172a	AGAAUCUUGAUGAUGCUGCA (20nt)	Chr. 11 pos. 7,868,006-025
miR172f	ath-miR172a	AGAAUCUUGAUGAUGCUGCA (20nt)	Chr. 7 pos. 10,358,575-594



Supplemental Figure S1. miR172 isoforms encoded in the *Phaseolus vulgaris* genome and the most stable secondary structures predicted for their precursors. Data from analysis of the *P. vulgaris* genome sequence (Schmutz et al., 2014; www.phytozome.net V.1.0). The previous designation of each miR172 isoform according to Peláez et al. 2012 is provided. The most stable secondary structure predicted for each pre-miR172 using Mfold is shown, mature miR172 sequence are highlighted with red lines and yellow boxes.