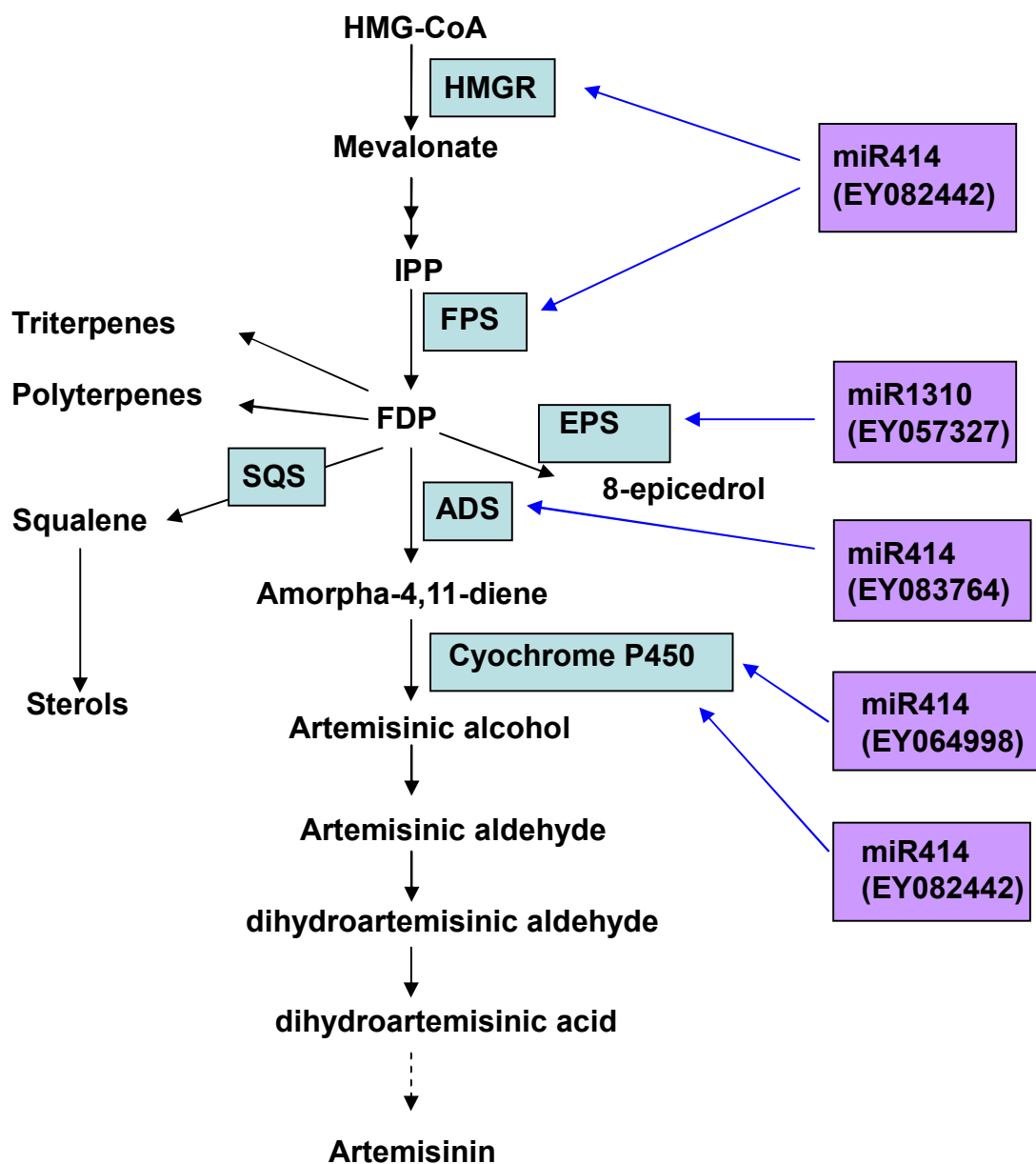


## Supplementary Material

Pani, A., *et al.* 2011. Computational identification of sweet wormwood (*Artemisia annua*) microRNA and their mRNA targets. *Genomics Proteomics Bioinformatics* 9(6): 200-210.

DOI: 10.1016/S1672-0229(11)60023-5

Figures S1



**Figure S1** Diagram for pathways related to artemisinin biosynthesis and the predicted miRNAs in *A. annua*. Enzymes that catalyze different reactions are highlighted in green while the predicted miRNAs are highlighted in purple. Both ADS and EPS are SQC. HMGR, HMG-coA reductase; IPP, isopentenyl diphosphate; FPS, farnesyl diphosphate synthase; FDP, farnesyl diphosphate; SQC, sesquiterpene cyclase; SQS, squalene synthase; EPS, epi-cedrol synthase; ADS, amorpha-4,11-diene synthase.