

Figure S4 Alignment (MEGA-X, Muscle) of the predicted protein sequences of 23 *D. carota* *FAD2s* [5] and seven newly identified carrot *FAD2s* (*DcFAD2-25* to *DcFAD2-31*, this study). Three putative His boxes are underlined in blue. The position of the G/A residues putatively promoting acetylenase activity is marked by a black arrow. Residues indicating divergent *FAD2* function (according [5]) are marked with red arrows. The putative ER localization motif at the C-terminus is underlined in black.