Supporting information for Ravanel *et al.* (2001) *Proc. Natl. Acad. Sci. USA* **98** (26), 15360–15365. (10.1073/pnas.261585098)

Table 2. Properties of the cDNAs characterized in this study

Properties	**AtDFA**	**AtDFB**	**AtDFC**	**AtDFD**
GenBank accession no.	AJ250872	AJ250873	AJ271786	AJ292545
cDNA, bp	1725	1830	2336	1616
ORF: residues	530	571	625	492
kDa	56.8	63.3	68.9	55.1
***Arabidopsis* ESTs** (location of the match)	AV441280/AV532931 (3') AV442646 (5')	AV526762 (5') AV520446 (3')	AV521153/AV527830 (3')	BE039115 (5')
Gene sequence	AB006707	AB071060	ATAC009400/ATAC010927	ATF1I16
Chromosome location	V	V	III	III
Cell localization*				
Mitochondrial score	0.36/0.66	0.79/0.64	0.98/0.46	0.00/0.14
Plastid score	0.34/0.41	0.02/0.12	0.04/0.18	0.11/0.05

*The prediction software PREDOTAR (http://www.inra.fr/Internet/produits/Predotar) and TARGETP [Emanuelsson, O., Nielsen, H., Brunak, S. & von Heijne, G. (2000) *J. Mol. Biol.* **300,** 1005–1016] were used to identify putative mitochondrial and plastid targeting sequences. Scores (PREDOTAR/TARGETP) were obtained by using default cutoffs.