



Supplementary Materials:

Table S1. The Predicted Subcellular Localization of Zm-6&1-FEH2.

Program	Apoplast	ER	Golgi	CHL	MT	Other
PSORT	0.814 ^a	0.2	NA	NA	NA	0.178
TargetP	0.274	NA	NA	0.141	0.377	0.018
SignalP	0.923 ^a	NA	NA	NA	NA	NA

The three intracellular targeting prediction programs used were PSORT (<http://psort.hgc.jp/>), Target P (<http://www.cbs.dtu.dk/services/TargetP/>), and SIGNAL P (<http://www.cbs.dtu.dk/Services/SignalP/>). CHL, chloroplast; ER, endoplasmic reticulum; Golgi, Golgi body; MT, mitochondria; NA, not applicable. ^a The higher the value, the higher the probability of localization in the indicated subcellular compartment.

Table S2. Oligonucleotides used for PCR amplification and cloning. Included are primers for full length constructs (full); partial cDNAs for qPCR (qPCR); for heterologous expression of mature proteins for *P. pastoris* overexpression (pPICZ).

cDNA	Comment	Primer name	Primer sequence (5'-3')
<i>Zm-6&1-FEH2</i>	Full gateway +/-Stop codon	FEHGw-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGGCCATGGC CATGGCCCCGA
		FEHGw-R+	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCATCCCTTGTTA ACCTGTGC
		FEHGw-R-	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCCTTGTTAACC TGTGC
	qPCR	FEHq-F	GCTGTACGCGTTCAACAAT
		FEHq-R	TAATTCATGTGCCCATGCTC
	pPICZαA	FEHpP-F	GACTAGTCTAGACCTCCCTTGTTAACCTGTGC
		FEHpP-R	GACTAGTCTAGACCCAGTGGATCCGCACGGTCGTC
<i>Zm-INVINH1</i>	Full gateway -Stop codon	Inh1Gw-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGAAGCTTCT GCAAGCTCTGT
		Inh1Gw-R-	GGGGACCACTTTGTACAAGAAAGCTGGGTCCAACGCGGCCGT TACAGACAGC
<i>Zm-ubiquitin</i>	qPCR	UbiquPCR-F	GCTCTGACACCATCGACAACGTGAA
		UbiquPCR-R	GCTGCTTGCCGGCGAAGATC
<i>Zm-β-tubulin</i>	qPCR	TubuqPCR-F	CCTATAACGCCACGCTCTCTGT
		TubuqPCR-R	CATTGTCCAGCACCATGCA