

(A)

amiR-*SlBOP1-3* (*At miR-164b* backbone)

CTCGAGGAGAATGATGAAGGTGTGTGATGAGCAAGATCTAGCGGCTGAGAGTGTATtTTACTAGCTC
ATATATACACTCTCACCACAAATGCGTGTATATATGCGGAATTTTGTGATATAGATGTGTGTGTGTG
TTGAGTGTGATGATATGGATGAGTTAGTTCaTTACACTCTCttCCGCaAGATCATGACCACTCCACC
TTGGTGACGATGACGACGAGGGTTCAAGTGTACGCACGTGGGAATATACTTATATCGATAAACACA
CACGTGCGGGATCC

10	20	30	40	50	60	70						
	A	CU	UUUU	A	----	U	- -	A	G	A	A	
GAUCU	GCGG	GAGAGUGUA	ACUAGCUCAU	UAUA	CAC	CUCA	C	CACA	AUGCGU	UAUAU	UGC GG	A
CUAGA	CGCC	CUCUCACAU	UGAUUGAGUA	GUAU	GUG	GAGU	G	GUGU	UGUGUA	AUAUA	GUGUU	U
^	A	UU	UACU	G	AGUA	U	U	U	G	G	-	U
150	140	130	120	110	100	90	80					

(B)

Solyc04g040220/SlBOP1 5' GAUACACUCUCAGCCGCUAGA 3'
Solyc10g079460/SlBOP2 5' GAUACACUCUCAGCCGCUAGA 3'
Solyc10g079750/SlBOP3 5' GAUACACUCUCAGCCGCUAGA 3'
amiR-SlBOP1-3 3' UUAUGUGAGAGUCGGCGAUCU 5'

Supplementary Figure 1: (A) The pre-amiR-*Sl BOP1-3* sequence and predicted fold-back structure in the Arabidopsis (*At*) *miR-164b* backbone with the *amiR-SlBOP1-3* sequence highlighted in red. (B) An alignment of the *amiR-SlBOP1-3* sequence with the RNA target sequences of the *SlBOP1-3* genes. G-U wobbles between the *amiR-SlBOP1-3* and the target sequences are marked in blue.