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Supplementary Materials: BrmiR828 targets *BrPAP1*, *BrMYB82* and *BrTAS4* Involved in the Light Induced Anthocyanin Biosynthetic Pathway in *Brassica rapa*

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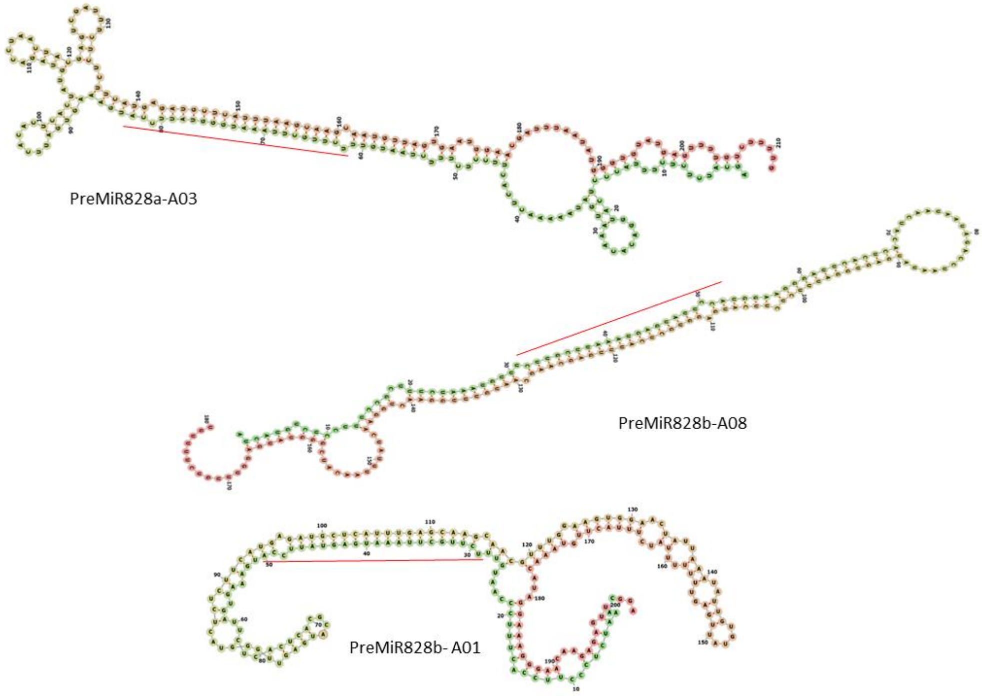
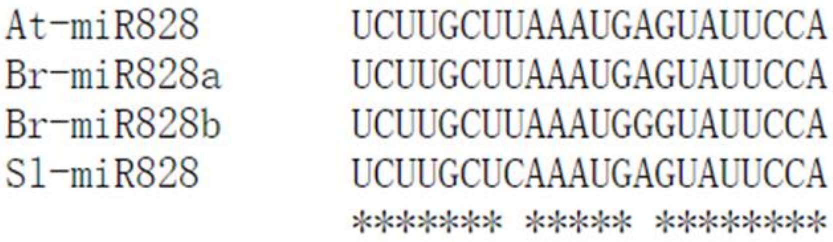


Figure S1. The prediction stem-loop structures of premiR828 homologs isolated in *Brassica rapa* by mfold [51]. The sequence designated by red line is mature miR828 sequence.



At-miR828	UCUUGCUUAAAUGAGUAUUCCA
Br-miR828a	UCUUGCUUAAAUGAGUAUUCCA
Br-miR828b	UCUUGCUUAAAUGGGUAUUCCA
Sl-miR828	UCUUGCUCAAAUGAGUAUUCCA
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Figure S2. Comparison of miR828 sequences in turnip, *Arabidopsis* and tomato.

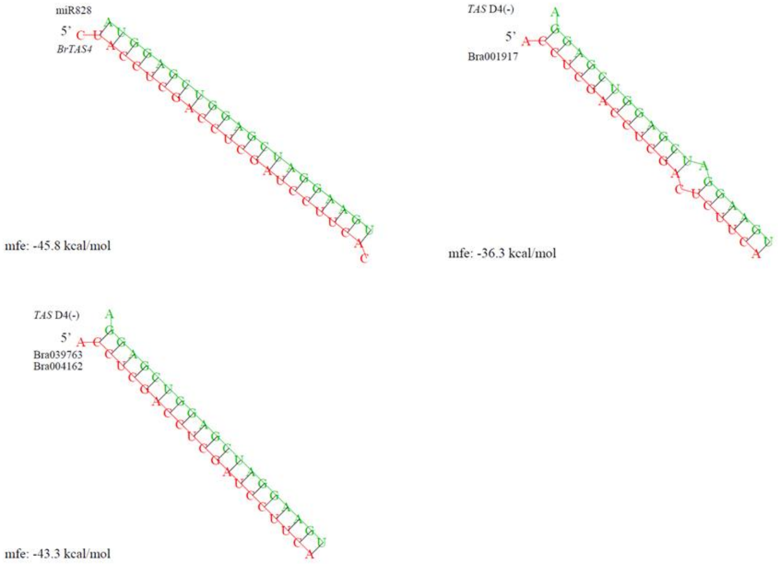

Figure S3. The complementarity binding profiles for BrmiR828 with BrTAS4 and for TAS4-D4 (-) with Bra001917 (BrPAP2), Bra039763 (BrPAP1) and Bra004162 (BrPAP2). Free energies of the duplex structures were calculated using RNA hybrid software (http://bibiserv.techfak.uni-bielefeld.de/rnahybrid, v2.1).

Table S1. Primers for premiR828, TAS4 and Real-time PCR primers for detected miR828 and targeted genes.

Gene ID	Forward primer (5′-3′)	Reverse primer (5′-3′)	Amplification length (nt)
BrTAS4	ATTCCGCGAAAGAGAGCAAGA	ATGCTTCCACCAGATTGTGACT	1150
BramiR828a-A03	AGCATCTCTCTTTACCCTCATGG	CAAAAGACAAAACTCATACACCCA	212
BramiR828b-A01	ACAATCTCCCTTCCACTTTCCC	TCCAACTCTCTTGTTCCCTTTC	203
BramiR828b-A08	ATCATGTCTCCTTTCCGCTTTCT	ACAAAAGACAAACCTCATACCCG	180
MiR828 Stem-loop primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTGGAAT		\
MiR828	CGCCGATCTTGCTTAAATGRGT	CCAGTGCAGGGTCCGAGGTA	65
Bra001917(PAP2)	CCTCCATGCCTTGGACTCAACAACAT	ACTATAAAGTTCATACTTCTCCCCAG	90
Bra004162(PAP2)	CCTCTATGCCTTGGACACAACGATAC	TTCTGGAAAGAGCGCAGCTGGATC	168
Bra039763(PAP1)	GAGCCAAGAACCAGTTGCGATTG	GTTCCACGGTCTCACCATCTAACAGA	113
Bra022602(MYB82)	GGAAGCCACTCCGTTGGTCG	CTATGCGGGCGAAGAAGTTG	128
Bra029113(MYB82)	AGTGGAAGCTCCTACCGACAAGA	GTGGTCGTCATAAGCCAAACAGT	130
BrTAS4-RT	TTCGCAGGTCGATACCAAGT	CCTGAATCTGCATTCACGGT	200
BrUBQ	TTGTAGTCAGCCAAGGTACGACCA	TGGAGAGTTCCGACACCATTGACA	130

Table S2. Nest primers for RLM 5′-RACE PCR used in this topic.

Gene ID	Primer name	Sequence (5′-3′)
Bra001917/ Bra004162/ Bra039763	Br-PAP1/2-RLM NP1	TCCAAAGTTGCTCAACGTCAAACG
	Br-PAP1/2-RLM NP2	TKGCTCTCMTCTAGCAAACT
	Br-PAP1/2-RLM NP3	AAGRRTCGAGGTCGAGGTTTGA
Bra022602/ Bra029113	Br-MYB82-RLM NP1	MMAAGAGTGTCTGKGTAATGAG
	Br-MYB82-RLM NP2	CTATGCGGGCGAAGAAGTTG
	Br-MYB82-RLM NP3	TCCTCCTCCATGGCTTCCTCT
BraTAS4	Br-TAS4-RLM NP1	TGCTTCCACCAGATTGTGACT
	Br-TAS4-RLM NP2	CCTTTTGCCAGTCCCCTTGA

5′ RACE Outer Primer：5′-CATGGCTACATGCTGACAGCCTA-3′. 5′ RACE Inner Primer：5′-CGCGGATCCACAGCCTACTGATGATCAGTCGATG-3′.

Table 3. Full-length amino acid sequences of MYBs from *Arabidopsis* and *Brassica rapa*.

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LSSLVMMNFASSDIEYCL
>ATMYB1
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