

A

		Repeat R2	
GmMYB29A2	MVRAPCCEKMG	LKKGPWTPPEEDQILMSYIQKHGHGNWRALPKLAGLLRCGKSCRLRWINY	60
VvMYB14	MGRAPCCEKMG	LKKGPWTPPEEDQILVNYIHLYGHGNWRALPKQAGLLRCGKSCRLRWITNY	60
		* *****:***:***:*****	
		Repeat R3	
GmMYB29A2	LRPDIKRGNFSEEEETIIKMHELLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL	LNNSD	120
VvMYB14	LRPDIKRGNFTSEEEETIIELHERLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL	KHNH	120
		*****:***** **:*	
GmMYB29A2	IQKRVSKPRIKRSDSNSSTLTQLEPTSSA-----CT-----TSLSDFSSFSE---	162	
VvMYB14	ATPPPKRHSLDASQ---VEKQQNPINSATNSRSESLGYGPVLSPPQPSFSDISSAATTTT	176	
		.: .: *: . :* :*	
GmMYB29A2	--GTKNMMDMIKSEDIESVETIMPPIDESFWSEATVDYESSTMMTSNSWTISNELAPPQY	220	
VvMYB14	TTTTATMSDITTPCIKVDSPEDFPEMDENFWSEVLSSNKSGAAG-----DLPGAASGPQL	231	
		* .*: . . :* :*:****. . :*: : . : *	
GmMYB29A2	QFNSVESFQQQSVDYNGSNDDHDGMDFWYDIFIKSGESIELPEF	264	
VvMYB14	QFPFSPRAVIGSSPY--STYDMDMEFWYNIFTRSGELHELSEI	272	
		** * . . .*:***:* :*** ** *:	

Percent identity: 49.65

Percent similarity: 54.58

B

		Repeat R2	
GmMYB29A2	LKKGPWTPPEEDQILMSYIQKHGHGNWRALPKLAGLLRCGKSCRLRWINY	LRPDIKRGNFS	60
VvMYB14	LKKGPWTPPEEDQILVNYIHLYGHGNWRALPKQAGLLRCGKSCRLRWITNY	LRPDIKRGNFT	60
		*****:***:***:*****	
		Repeat R3	
GmMYB29A2	SEEEETIIKMHELLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL		105
VvMYB14	SEEEETIIELHERLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRL		105
		***** **:*	

Percent identity: 88.57

Percent similarity: 89.52

Supplemental Figure S2. Similarity and identity among GmMYB29A2 and VvMYB14 amino acid sequences. (A) Full-length amino acid sequences. (B) R2 R3 putative DNA-binding domain sequences. '*' indicates identical amino acids, ':' amino acids with similar biochemical features.