Table 1. Suppl. A summary of spectrophotometric estimation of total RNA isolated from three different biological replicates from few representative tissues used in this study.

Species name	Tissue	Biological replicates	Concentration [μg cm^{-3}]	$A_{260/280}$
Bambusa balcooa	Young leaf	1	596.3	1.87
		2	635.1	1.96
		3	861.7	2.03
B. bambos	Internode	1	746.7	2.01
		2	625.6	1.96
		3	567.3	1.92
B. vulgaris	Root	1	634.5	1.95
		2	587.8	1.90
		3	686.8	2.01
B. tulda	Cum sheath	1	2106.2	2.05
		2	749.6	2.01
		3	836.3	2.02
B. tulda	Early staged inflorescence bud	1	435.3	1.95
		2	524.0	1.91
		3	517.3	1.89

Table 2. Suppl. A summary of 10 candidate reference genes and 2 genes selected for data validation. Abbreviations used: bp- base pair, Ct- threshold cycle, SE- standard error, E- efficiency of PCR, F- forward, R- reverse.

Gene names	Gene descriptions	Accession numbers/locus IDs	Source Organisms	Primer sequences (5'-3')	Tm [°C]	Amplicon length [bp]	Ct	E [%]
NTB	*nucleotide tract-binding protein*	gi|242381788	*Phyllostachys edulis*	F-AGCTTATGGATATGTGGAGAA R-CTTCTTGGCGTGATTGATACT	55	111	26.15±0.26	104.93
		Os05g36120	*Oryza sativa*					
		Bradi2g24150	*Brachypodium distachyon*					
		TAE45871G003	*Triticum aestivum*					
		Zm00001d010173	*Zea mays*					
		Seita.3G228300	*Setaria italica*					
CAC	*clathirin adaptor complexes medium subunit*	gi|242375393	*P. edulis*	F-TTTCTTCAGCAATGTGTGT R-CCCTTTTGCTTGTTTCTTGA	55	110	22.18±0.07	101.95
		Os12g10560	*O. sativa*					
		Bradi4g40287	*B. distachyon*					
		TAE04243G001	*T. aestivum*					
		Zm00001d007270	*Z. mays*					
		Seita.3G098000	*S. italica*					
CYP	*peptidyl prolyl cis-trans isomerase/cyclophilin*	gi|242381616	*P. edulis*	F-TTTACGGCGCCAAGTTCG R-TGGGAGCCGTTGGTGTTG	55	100	25.86±0.21	106.61
		Os09g39780	*O. sativa*					
		Bradi4g38880	*B. distachyon*					
		TAE04698G001	*T. aestivum*					
		Zm00001d016660	*Z. mays*					
		Seita.2G137800	*S. italica*					
18S	*18s ribosomal rna*	gi|242375117	*P. edulis*	F-GCAACTATGGTGCCTCTATG R-GCGACACCAGCAATCACCCA	55	105	24.38±0.12	105.16
		Os01g42480	*O. sativa*					
		Bradi2g43200	*B. distachyon*					
		TAE28272G001	*T. aestivum*					
		Zm00001d011325	*Z. mays*					
		Seita.5G222700	*S. italica*					
UBQ3	*polyubiquitin 3*	AY954394.1	*O. sativa*	F-GAAGGAGTCCACCCTGCACCT R-CTGGATCTTGGCCTTCACGTT GTC	55	136	17.76±0.24	94.50
		PH01000093G1330	*P. edulis*					
		Bradi3g04730	*B. distachyon*					
		TAE23060G001	*T. aestivum*					
		Zm00001d015327	*Z. mays*					
		Seita.4G259900	*S. italica*					
ACT7	*actin 7*	XP_015641450	*O. sativa*	F-GGATTGGTGGTTCTATTTTGGC R-CACTTCATATGGACAATGCC	55	103	26.95±0.3	89.54
		GU434145	*P. edulis*					
		Bradi2g56000	*B. distachyon*					
		TAE46567G001	*T. aestivum*					
		Zm00001d012277	*Z. mays*					
		Seita.5G393000	*S. italica*					
eEF1α	*eukaryotic elongation factor 1α*	AK061464	*O. sativa*	F-CGTGTGATTGAGAGGTTCGAGAA R- AGGTACCCGTGATCATGTTCT	55	211	22.15±0.32	94.06
		PH01001781G0230	*P. edulis*					
		Bradi4g12750	*B. distachyon*					
		TAE11753G001	*T. aestivum*					
		Zm00001d037905	*Z. mays*					
		Seita.3G265500	*S. italica*					
eIF4α	*eukaryotic initiation factor 4α*	XP_015626460	*O. sativa*	F-ATGCTCTCCCGTGGTTTCAAG R-CAAGGGTAAGCTCATCTCTCTT CAC	55	172	22.92±0.31	91.42
		PH01002192G0160	*P. edulis*					
		Bradi1g34170	*B. distachyon*					
		TAE05656G001	*T. aestivum*					
		Zm00001d015251	*Z. mays*					
		Seita.1G089900	*S. italica*					
GAPDH	*glyceraldehyde-3-phosphate dehydrogenase*	XP_015650130	*O. sativa*	F-CCACAAACTGCCTTGCTCC R-CCCTGCCACCCCTCCAG	55	144	22.71±0.32	96.99
		PH01003320G0070	*P. edulis*					
		Bradi3g14040	*B. distachyon*					
		TAE53137G001	*T. aestivum*					
		Zm00001d049641	*Z. mays*					
		Seita.6G079600	*S. italica*					
UBQ5	*ubiquitin 5*	AK061988	*O. sativa*	F-ATCACGCTGGAGGTGGAGT	55	213	22.32±0.22	109.47

		PH01001122G0410 Bradi2g34750 TAE04445G002 Zm00001d053838 Seita.7G270700	*P. edulis* *B. distachyon* *T. aestivum* *Z. mays* *S. italica*	R-CTTCTTCTTGCGCTTCTTGGC				
TOC1	*timing of cab expression1*	KY249524	*Bambusa tulda*	F-AGGAACAAGGAACTGCGCCAC ATC R-GTCTTCGCCGCCACACATG	55	168	23.01±0.88	99.37
MADS14	*Mads14*	KX186751	*B. tulda*	F-TCGTGGAGAAGCAGAAGGTC R-CTGCTGCGTCCTCTGCCCT	55	163	24.97±0.59	95.03

Table 3. Suppl. The predicted stability ranking of 10 candidate reference genes using expression data obtained from 4 species *(Bambusa tulda*, *B. bambos*, *B. vulgaris*, and *B. balcooa*), 9 organs, and 3 developmental stages. This analysis was done using the *NormFinder* (NF) and *RefFinder* (RF) programs. The values within *brackets* indicate the ranking order of the candidate reference genes in NF and RF analyses.

Species			*B. tulda, B. balcooa, B. bambos, B vulgaris*			*B. tulda*	*B. tulda*		
Experimental sets			leaf	internode	rhizome	young leaves from flowering and non flowering culms, flag leaf, possible flag leaf, culm sheath, internode, root, rhizome, early staged inflorescence bud	leaf (tip, middle, base)	internode (tip, middle, base)	inflorescence bud (early, middle, late)
Reference genes	*ACT7*	NF	0.77 (6)	0.61 (6)	2.41 (10)	0.93 (7)	0.02 (1)	0.69 (10)	0.81 (10)
		RF	6.00 (6)	5.33 (5)	10.00 (10)	5.24 (5)	2.21 (1)	8.80 (10)	7.40 (10)
	GAPDH	NF	0.92 (7)	0.68 (8)	0.54 (2)	1.12 (9)	0.34 (6)	0.51 (6)	0.61 (8)
		RF	7.65 (7)	5.66 (6)	3.83 (4)	9.00 (10)	6.45 (7)	6.22 (8)	6.70 (8)
	UBQ3	NF	0.37 (4)	0.71 (9)	0.81 (5)	0.65 (4)	0.56 (9)	0.53 (7)	0.27 93)
		RF	2.99 (4)	7.77 (9)	6.12 (8)	4.86 (4)	8.97 (10)	6.96 (9)	3.98 (4)
	UBQ5	NF	0.10 (2)	0.46 (4)	0.59 (3)	0.63 (3)	0.06 (2)	0.46 (4)	0.26 (2)
		RF	2.00 (2)	4.28 (4)	2.91 (3)	2.21 (2)	2.51 (2)	3.46 (4)	1.86 (1)
	18S	NF	1.07 (9)	0.67 (7)	0.98 (7)	1.31 (10)	0.65 (10)	0.64 (9)	0.63 (9)
		RF	8.45 (9)	7.04 (8)	4.92 (6)	5.62 (8)	5.62 (6)	5.20 (6)	5.20 (6)
	CAC	NF	0.10 (1)	0.13 (1)	1.07 (8)	0.89 (6)	0.26 (4)	0.61 (8)	0.32 (4)
		RF	1.57 (1)	1.41 (1)	4.76 (5)	5.29 (6)	2.63 (3)	5.66 (7)	4.00 (5)
	CYP	NF	1.45 (10)	0.59 (5)	0.75 (4)	0.54 (2)	0.30 (5)	0.46 (5)	0.13 (1)
		RF	9.74 (10)	5.73 (7)	2.38 (2)	4.05 (3)	2.66 (4)	5.01 (5)	2.78 (2)
	NTB	NF	0.96 (8)	0.77 (10)	0.28 (1)	0.80 (5)	0.45 (8)	0.25 (2)	0.56 (7)
		RF	8.00 (8)	9.15 (10)	1.50 (1)	5.32 (7)	7.67 (9)	2.78 (2)	7. 27 (9)
	eIF4α	NF	0.30 (3)	0.33 (2)	0.94 (6)	0.54 (1)	0.40 (7)	0.14 (1)	0.44 (6)
		RF	2.45 (3)	2.00 (2)	5.96 (7)	1.41 (1)	7.45 (8)	2.00 (1)	5.42 (7)
	eEF1α	NF	0.47 (5)	0.44 (3)	1.36 (9)	0.95 (8)	0.18 (3)	0.34 (3)	0.44 (6)
		RF	4.40 (5)	2.91 (3)	9.00 (9)	6.62 (9)	4.21 (5)	2.82 (3)	3.64 (3)

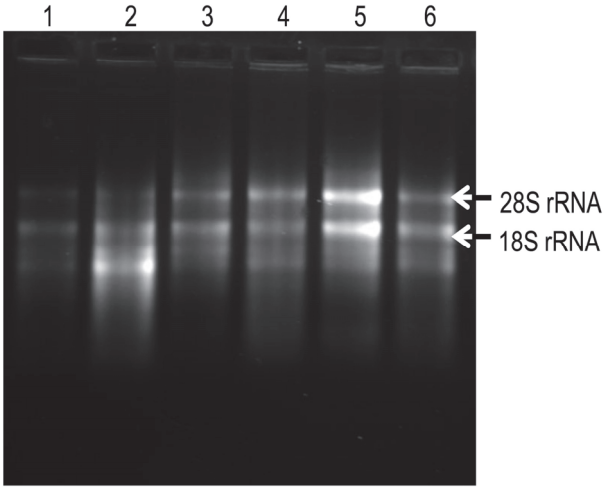


Fig. 1. Suppl. Assessment of quality of RNA isolated from a few of representative tissues used for this study. Representative agarose-formamide gel electrophoresis (1 %, m/v) of total RNA isolated from middle staged inflorescence bud (*lane* 1), root (*lane* 2), culm sheath (*lane 3*), rhizome (*lane* 4), leaf from non flowering culm (*lane* 5), and internode (*lane* 6) of *Bambusa tulda.*

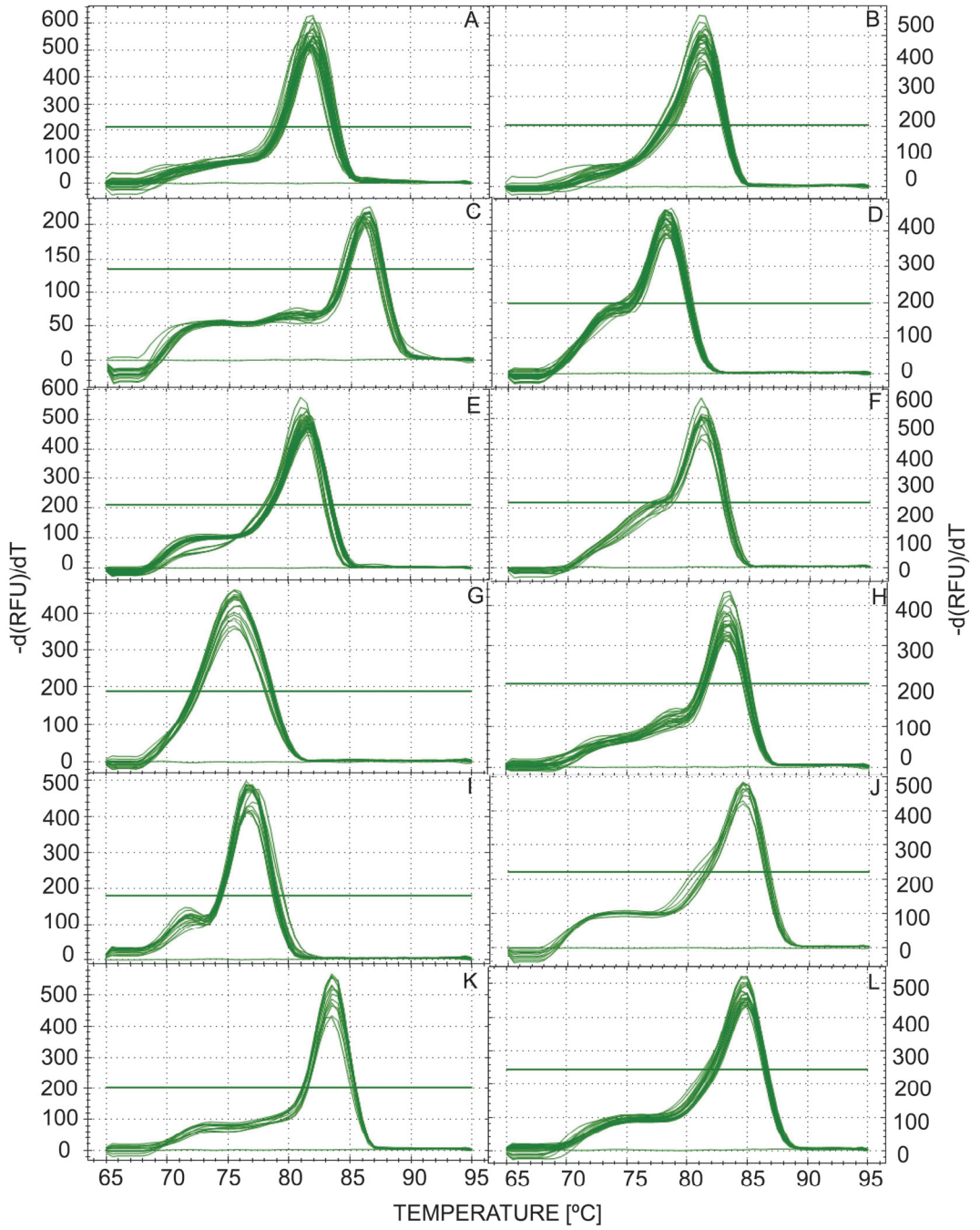
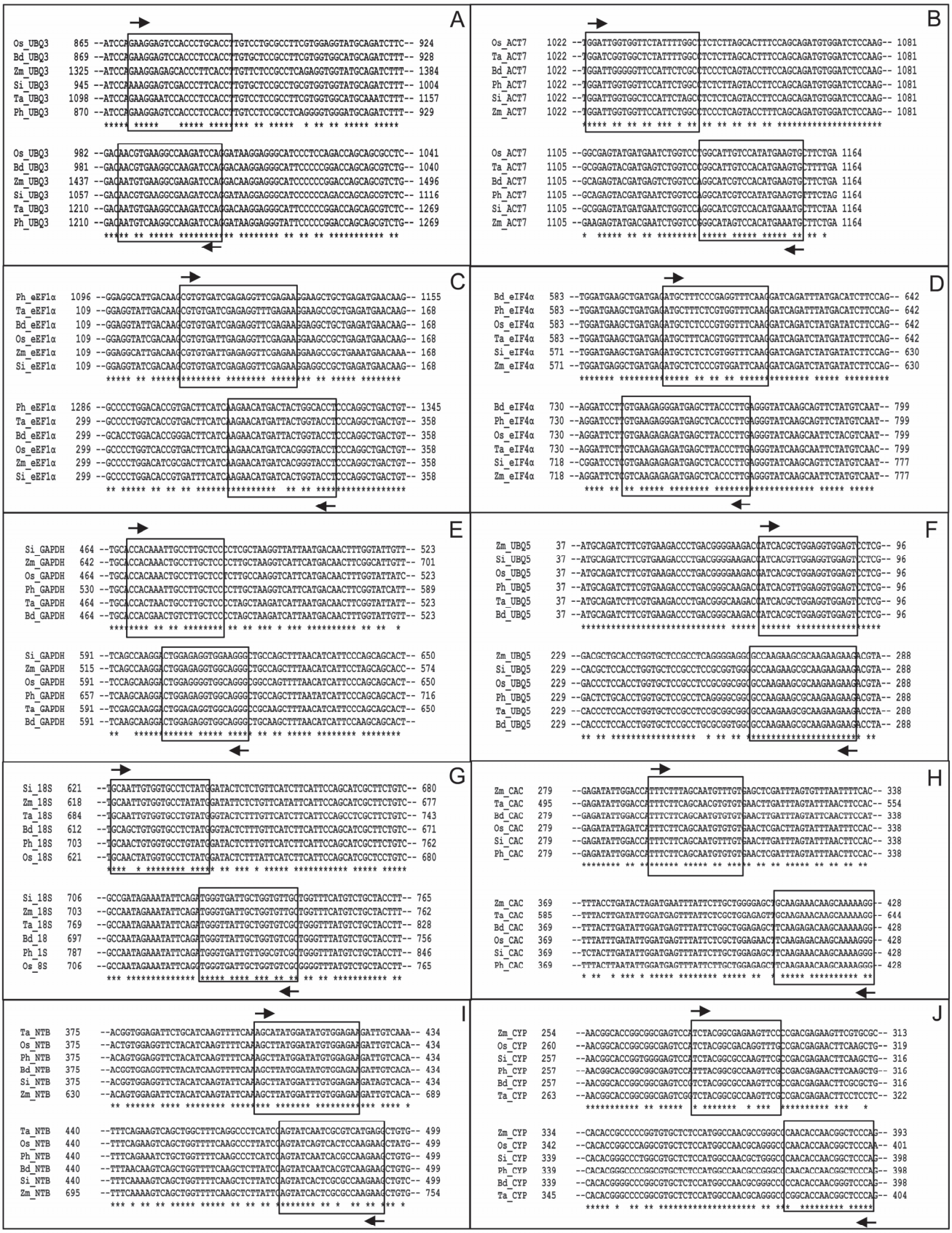


Fig. 2. Suppl. Melting curve analyses of 10 candidate reference genes *GAPDH* (*A*), *eIF4α* (*B*), *UBQ5* (*C*), *NTB* (*D*), *UBQ3* (*E*), *ACT7* (*F*), *CAC* (*G*), *eEF1α* (*H*), *CYP* (*I*), and *18S* (*J*), and two target genes *MADS14* (*K*) and *TOC1* (*L*) to verify primer specificity during real time PCR amplification. This analyses were performed in the *CFX* manager program (*Bio-Rad*, Hercules, USA) by observing the change in fluorescence as a consequence of increasing temperature [-d(RFU)/dT].


A
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Bd_UBQ3 869 --ATCCAGAAGGAGTCCACCCTCCACCTTGTGCTCCGCCTTCGTGGTGGCATGCAGATCTTT-- 928
Zm_UBQ3 1325 --ATCCAGAAGGAGAGCACCCTTCACCTTGTTCTCCGCCTCAGAGGTGGTATGCAGATCTTT-- 1384
Si_UBQ3 945 --ATCCAAAAGGAGTCGACCCTTCACCTTGTGCTCCGCCTGCGTGGTGGTATGCAGATCTTT-- 1004
Ta_UBQ3 1098 --ATCCAGAAGGAATCCACCCTCCACCTTGTCCTCCGCCTTCGTGGTGGCATGCAAATCTTT-- 1157
Ph_UBQ3 870 --ATCCAGAAGGAGTCCACCCTCCACCTTGTCCTCCGCCTCAGGGGTGGGATGCAGATCTTT-- 929
Os_UBQ3 982 --GACAACGTGAAGGCCAAGATCCAGGATAAGGAGGGCATCCCTCCAGACCAGCAGCGCCTC-- 1041
Bd_UBQ3 981 --GACAACGTGAAGGCCAAGATCCAGGACAAGGAGGGCATTCCCCCGGACCAGCAGCGTCTG-- 1040
Zm_UBQ3 1437 --GACAATGTGAAGGCGAAGATCCAGGACAAGGAGGGCATCCCCCCGGACCAGCAGCGTCTG-- 1496
Si_UBQ3 1057 --GACAACGTGAAGGCGAAGATCCAGGATAAGGAGGGCATCCCCCCAGACCAGCAGCGTCTC-- 1116
Ta_UBQ3 1210 --GACAATGTGAAGGCCAAGATCCAGGACAAGGAGGGCATTCCCCCGGACCAGCAGCGTCTC-- 1269
Ph_UBQ3 1210 --GACAATGTCAAGGCCAAGATCCAGGATAAGGAGGGTATTCCCCCGGACCAGCAGCGTCTG-- 1269
B
Os_ACT7 1022 --TGGATTGGTGGTTCTATTTTGGCTTCTCTTAGCACTTTCCAGCAGATGTGGATCTCCAAG-- 1081
Ta_ACT7 1022 --TGGATCGGTGGCTCTATTTTGGCTTCTCTTAGCACTTTCCAGCAGATGTGGATCTCCAAG-- 1081
Bd_ACT7 1022 --TGGATTGGGGGTTCCATTCTCGCTTCCCTCAGTACCTTCCAGCAGATGTGGATCTCCAAG-- 1081
Ph_ACT7 1022 --TGGATTGGTGGTTCCATTCTGGCTTCTCTTAGTACCTTCCAGCAGATGTGGATCTCCAAG-- 1081
Si_ACT7 1022 --TGGATTGGTGGCTCCATTCTAGCTTCTCTCAGTACCTTCCAGCAGATGTGGATCTCCAAG-- 1081
Zm_ACT7 1022 --TGGATTGGTGGTTCCATTCTGGCTTCCCTCAGTACCTTTCAGCAGATGTGGATCTCCAAG-- 1081
Os_ACT7 1105 --GGCGAGTATGATGAATCTGGTCCTGGCATTGTCCATATGAAGTGCTTCTGA 1164
Ta_ACT7 1105 --GCGGAGTACGATGAGTCTGGTCCTGGCATTGTCCACATGAAGTGCTTTTGA 1164
Bd_ACT7 1105 --GCAGAGTACGATGAGTCTGGTCCAGGCATCGTCCACATGAAGTGCTTCTGA 1164
Ph_ACT7 1105 --GCAGAGTACGATGAATCTGGTCCAGGCATCGTCCATATGAAGTGTTTCTAG 1164
Si_ACT7 1105 --GCGGAGTATGATGAATCTGGTCCAGGCATCGTCCACATGAAATGCTTCTAA 1164
Zm_ACT7 1105 --GAAGAGTATGACGAATCTGGTCCGGGCATAGTCCACATGAAATGCTTCTGA 1164
C
Ph_eEF1α 1096 --GGAGGCATTGACAAGCGTGTGATCGAGAGGTTCGAGAAGGAAGCTGCTGAGATGAACAAG-- 1155
Ta_eEF1α 109 --GGAGGTATTGACAAGCGTGTGATCGAGAGGTTTGAGAAGGAAGCCGCTGAGATGAACAAG-- 168
Bd_eEF1α 109 --GGAGGTATTGACAACGTGTGATCGAGAGGTTCGAGAAGGAGGCTGCTGAGATGAACAAG-- 168
Os_eEF1α 109 --GGAGGTATCGACAACGTGTGATTGAGAGGTTCGAGAAGGAAGCCGCTGAGATGAACAAG-- 168
Zm_eEF1α 109 --GGAGGCATTGACAAGCGTGTGATTGAGAGGTTCGAGAAGGAAGCCGCTGAAATGAACAAA-- 168
Si_eEF1α 109 --GGAGGTATCGACAACGTGTGATCGAGAGGTTCGAGAAGGAGGCCGCTGAGATGAACAAG-- 168
Ph_eEF1α 1286 --GCCCCTGGACACCGTGACTTCATCAAGAACATGACTACTGGCACCTCCCAGGCTGACTGT-- 1345
Ta_eEF1α 299 --GCCCCTGGTCACCGTGACTTCATCAAGAACATGATTACTGGTACCTCCCAGGCTGACTGT-- 358
Bd_eEF1α 299 --GCACCTGGACACCGGGACTTCATCAAGAACATGATTACTGGTACCTCCCAGGCTGACTGT-- 358
Os_eEF1α 299 --GCCCCTGGTCACCGTGACTTCATCAAGAACATGATCACGGGTACCTCCCAGGCTGACTGT-- 358
Zm_eEF1α 299 --GCCCCTGGACATCGCGACTTCATCAAGAACATGATCACGGGTACCTCCCAGGCTGACTGT-- 358
Si_eEF1α 299 --GCCCCTGGACACCGTGATTTCATCAAGAACATGATCACTGGTACCTCCCAGGCTGACTGT-- 358
D
Bd_eIF4α 583 --TGGATGAAGCTGATGAGATGCTTTCCCGAGGTTTCAAGGATCAGATTTATGACATCTTCCAG-- 642
Ph_eIF4α 583 --TGGATGAAGCTGATGAGATGCTTTCTCGTGGTTTCAAGGATCAGATTTATGACATCTTCCAG-- 642
Os_eIF4α 583 --TGGATGAAGCTGATGAGATGCTCTCCCGTGGTTTCAAGGATCAGATCTATGATATCTTCCAG-- 642
Ta_eIF4α 583 --TGGATGAAGCTGATGAGATGCTTTCACGTGGTTTCAAGGATCAGATCTATGATATCTTCCAG-- 642
Si_eIF4α 571 --TGGATGAAGCTGATGAGATGCTCTCTCGTGGTTTCAAGGATCAGATCTATGATATCTTCCAG-- 630
Zm_eIF4α 571 --TGGATGAGGCTGATGAGATGCTCTCCCGTGGATTCAAGGATCAGATCTATGATATCTTCCAG-- 630
Bd_eIF4α 730 --AGGATCCTTGTGAAGAGGGATGAGCTTACCCTTGAGGGTATCAAGCAGTTCTATGTCAAT-- 799
Ph_eIF4α 730 --AGGATCCTTGTGAAGAGGGATGAGCTCACCCTTGAGGGTATCAAGCAGTTCTATGTCAAT-- 799
Os_eIF4α 730 --AGGATTCTTGTGAAGAGAGATGAGCTTACCCTTGAGGGTATCAAGCAATTCTACGTCAAT-- 799
Ta_eIF4α 730 --AGGATTCTTGTCAAGAGAGATGAGCTTACCCTTGAGGGTATCAAGCAATTCTATGTCAAC-- 799
Si_eIF4α 718 --CGGATCCTTGTGAAGAGAGATGAGCTCACCCTTGAGGGTATCAAGCAGTTCTATGTCAAT-- 777
Zm_eIF4α 718 --AGGATTCTTGTCAAGAGAGATGAGCTCACCCTTGAGGGTATCAAGCAATTCTATGTCAAT-- 777
E
Si_GAPDH 464 --TGCACCACAAATTGCCTTGCTCCCCTCGCTAAGGTTATTAATGACAACTTTGGTATTGTT-- 523
Zm_GAPDH 642 --TGCACCACAAACTGCCTTGCTCCCCTTGCTAAGGTCATTCATGACAACTTCGGCATTGTT-- 701
Os_GAPDH 464 --TGCACCACAAACTGCCTTGCTCCCTTGCTAAGGTCATTCATGACAACTTTGGTATTATC-- 523
Ph_GAPDH 530 --TGCACCACAAATTGCCTTGCTCCCCTTGCTAAGGTCATTCATGACAACTTCGGTATCATT-- 589
Ta_GAPDH 464 --TGCACCACTAACTGCCTTGCTCCCCTAGCTAAGATCATTAATGACAACTTCGGTATTATT-- 523
Bd_GAPDH 464 --TGCACCACGAACTGTCTTGCTCCCCTAGCTAAGATCATTAATGACAACTTTGGTATTGTT-- 523
Si_GAPDH 591 --TCAGCCAAGGACTGGAGAGGTGGAAGGCTGCCAGCTTTAACATCATTCCCAGCAGCACT-- 650
Zm_GAPDH 515 --TCAGCCAAGGACTGGAGAGGTGGCAGGGCTGCCAGCTTTAACATCATTCCTAGCAGCACC-- 574
Os_GAPDH 591 --TCCAGCAAGGACTGGAGGGGTGGCAGGGCGGCCAGTTTTAACATCATTCCCAGCAGCACT-- 650
Ph_GAPDH 657 --TCAAGCAAGGACTGGAGAGGTGGCAGGGCTGCCAGCTTTAATATCATTCCCAGCAGCACT-- 716
Ta_GAPDH 591 --TCGACCAAGGACTGGAGAGGTGGCAGGGCCGCAAGCTTTAACATCATTCCCAGCAGCACT-- 650
Bd_GAPDH 591 --TCAAGCAAGGACTGGAGAGGTGGCAGGGCTGCAAGCTTTAACATCATTCCAAGCAGCACT--
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Si_UBQ5 37 --ATGCAGATCTTCGTGAAGACCCTGACGGGGAAGACCATCACGTTGGAGGTGGAGTCCTCG-- 96
Os_UBQ5 37 --ATGCAGATCTTCGTGAAGACCCTGACGGGCAAGACCATCACGTTGGAGGTGGAGTCCTCG-- 96
Ph_UBQ5 37 --ATGCAGATCTTCGTGAAGACCCTGACGGGCAAGACCATCACGTTGGAGGTGGAGTCCTCG-- 96
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Bd_UBQ5 37 --ATGCAGATCTTCGTGAAGACCCTGACGGGCAAGACCATCACGCTGGAGGTGGAGTCCTCG-- 96
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Si_UBQ5 229 --CACGCTCCACCTGGTGCTCCGCCTCCGCGGTGGCGCCAAGAAGCGCAAGAAGAAGACGTA-- 288
Os_UBQ5 229 --GACCCTCCACCTGGTGCTCCGCCTCCGCGGCGGCGCCAAGAAGCGCAAGAAGAAGACGTA-- 288
Ph_UBQ5 229 --GACTCTGCACCTGGTGCTCCGCCTCAGGGGCGGCGCCAAGAAGCGCAAGAAGAAGACGTA-- 288
Ta_UBQ5 229 --CACCCTCCACCTGGTGCTCCGCCTCCGCGGCGGCGCCAAGAAGCGCAAGAAGAAGACCTA-- 288
Bd_UBQ5 229 --CACCCTCCACCTGGTGCTCCGCCTGCGCGGTGGCGCCAAGAAGCGCAAGAAGAAGACCTA-- 288
G
Si_18S 621 --TGCAATTGTGGTGCCTCTATGGATACTCTCTGTTCATCTTCATTCCAGCATCGCTTCTGTC-- 680
Zm_18S 618 --TGCAATTGTGGTGCCTATATGGATATTCTCTGTTCATATTCATTCCAGCATCGCTTCTGTC-- 677
Ta_18S 684 --TGCAATTGTGGTGCCTGTATGGGTACTCTTTGTTCATCTTCATTCCAGCCTCGCTTCTGTC-- 743
Bd_18S 612 --TGCAGCTGTGGTGCCTCTATGGGTACTCTTTGTTCATCTTCATTCCAGCATCGCTTCTGTC-- 671
Ph_18S 703 --TGCAACTGTGGTGCCTGTATGGATACTCTTTGTTCATCTTCATTCCAGCATCGCTTCTGTC-- 762
Os_18S 621 --TGCAACTATGGTGCCTCTATGGATACTCTTTATTCATCTTCATTCCAGCATCGCTCCTGTC-- 680
Si_18S 706 --GCCGATAGAAATATTCAGATGGGTGATTGCTGGTGTTGCTGGTTTCATGTCTGCTACCTT-- 765
Zm_18S 703 --GCCAATAGAAATATTCAGATGGGTGATTGCTGGTGTTGCTGGTTTCATGTCTGCTACTTT-- 762
Ta_18S 769 --GCCAATAGAAATATTCAGATGGGTTATTGCTGGTGTCGCTGGGTTTATGTCTGCTACCTT-- 828
Bd_18 697 --GCCAATAGAAATATTCAGATGGGTTATTGCTGGTGTCGGTTGGTTTATGTCTGCTACCTT-- 756
Ph_1S 787 --GCCAATAGAAATATTCAGATGGGTGATTGTTGGCGTCGCTGGGTTTATGTCTGCTACCTT-- 846
Os_8S 706 --GCCAATAGAAATATTCAGCTGGGTGATTGCTGGTGTCGCGGGGTTTATGTCTGCTACCTT-- 765
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Ta_CAC 495 --GAGATATTGGACCATTTCTTCAGCAACGTGTGTGAACTTGATTTAGTATTTAACTTCCAC-- 554
Bd_CAC 279 --GAGATATTGGACCATTTCTTCAGCAATGTGTGTGAACTTGATTTAGTATTCAACTTCCAT-- 338
Os_CAC 279 --GAGATATTAGATCATTTCTTCAGCAATGTGTGTGAACTCGACTTAGTATTTAATTTCCAC-- 338
Si_CAC 279 --GAGATATTGGACCATTTCTTCAGCAATGTTTGTGAACTTGATTTAGTATTTAACTTCCAC-- 338
Ph_CAC 279 --GAGATATTGGACCATTTCTTCAGCAATGTGTGTGAACTCGATTTAGTATTTAACTTCCAC-- 338
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Ta_CAC 585 --TTTACTTGATATTGGATGAGTTTATTCTCGCTGGAGAGTTGCAAGAAACAAGCAAAAAGG-- 644
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Os_CAC 369 --TTTATTTGATATTGGATGAGTTTATTCTCGCTGGAGAACTTCAAGAGACAAGCAAAAGGG-- 428
Si_CAC 369 --TCTACTTGATATTGGATGAGTTTATTCTTGCTGGAGAGCTTCAAGAAACAAGCAAAAGGG-- 428
Ph_CAC 369 --TTTACTTAATATTGGATGAGTTTATTCTTGCTGGAGAGCTTCAAGAAACAAGCAAAAGGG-- 428
I
Ta_NTB 375 --ACGGTGGAGATTCTGCATCAAGTTTTCAAAGCATATGGATATGTGGAGAAGATTGTCAAA-- 434
Os_NTB 375 --ACTGTGGAGGTTCTACATCAAGTTTTCAAAGCTTATGGATATGTGGAGAAGATTGTCACA-- 434
Ph_NTB 375 --ACAGTGGAGGTTCTACATCAAGTTTTCAAAGCTTATGGATATGTGGAGAAGATTGTCACA-- 434
Bd_NTB 375 --ACGGTGGAGGTTCTACATCAAGTTTTCAAAGCTTATGGATATGTGGAGAAGATTGTCACA-- 434
Si_NTB 375 --ACGGTGGAGGTTCTACATCAAGTATTCAAAGCTTATGGATTTGTGGAGAAGATAGTCACA-- 434
Zm_NTB 630 --ACAGTGGAGATTCTACATCAAGTATTCAAAGCTTATGGATTTGTGGAGAAGATTGTCACA-- 689
Ta_NTB 440 --TTTCAGAAGTCAGCTGGCTTTCAGGCCCTCATCCAGTATCAATCGCGTCATGAGCCTGTG-- 499
Os_NTB 440 --TTTCAGAAGTCAGCTGGTTTTCAAGCCCTTATCCAGTATCAGTCACTCCAAGAAGCTATG-- 499
Ph_NTB 440 --TTTCAGAAATCTGCTGGTTTTCAAGCCCTCATCCAGTATCAATCACGCCAAGAAGCTGTG-- 499
Bd_NTB 440 --TTTAACAAGTCAGCTGGTTTTCAAGCTCTTATCCAGTATCAATCACGTCAAGAAGCTGTG-- 499
Si_NTB 440 --TTTCAAAAGTCAGCTGGTTTTCAAGCTCTTATCCAGTATCACTCGCGCCAAGAAGCTGTC-- 499
Zm_NTB 695 --TTTCAAAAGTCAGCTGGTTTTCAAGCTCTTATTCAGTATCACTCGCGCCAAGAAGCTGTG-- 754
J
Zm_CYP 254 --AACGGCACCGGCGGCGAGTCCATCTCTACGGCGAGAAGTTCCCCGACGAGAAGTTCGTGCGC-- 313
Os_CYP 260 --AACGGCACCGGCGGCGAGTCCATCTCTACGGCGACAGGTTTGCCGACGAGAACTTCAAGCTG-- 319
Si_CYP 257 --AACGGCACCGGTGGGGAGTCCATCTACGGCGCCAAGTTCGCCGACGAGAACTTCAAGCTG-- 316
Ph_CYP 257 --AACGGCACCGGCGGCGAGTCCATTTACGGCGCCAAGTTCGCCGACGAGAACTTCAAGCTG-- 316
Bd_CYP 257 --AACGGCACCGGCGGCGAGTCCGTCTACGGCGCCAAGTTCGCCGACGAGAACTTCGCGCTG-- 316
Ta_CYP 263 --AACGGCACCGGCGGCGAGTCCGTCTACGGCGCCAAGTTCGCCGACGAGAACTTCCTCCTC-- 322
Zm_CYP 334 --CACACCGCCCCCGGTGTGCTCTCCATGGCCAACGCCGGGCCCAACACCAACGGCTCCCAG-- 393
Os_CYP 342 --CACACCGGCCCAGGCGTGCTCTCCATGGCCAACGCAGGGCCCAACACCAACGGCTCCCAA-- 401
Si_CYP 339 --CACACGGGCCCTGGCGTGCTCTCCATGGCCAACGCTGGGCCCAACACCAACGGCTCCCAG-- 398
Ph_CYP 339 --CACACGGGCCCCGGCGTGCTCTCCATGGCCAACGCCGGGCCCAACACCAACGGCTCCCAG-- 398
Bd_CYP 339 --CACACGGGCCCCGGCGTGCTCTCCATGGCCAACGCGGGGCCCCCACACCAACGGGTCCCAG-- 398
Ta_CYP 345 --CACACGGGCCCCGGCGTGCTCTCCATGGCCAACGCAGGGCCCGGCACCAACGGCTCCCAG-- 404

Fig. 3. Suppl. Multiple sequence alignment of homologous sequences of 10 candidate reference genes *UBQ3* (*A*), *ACT7* (*B*), *eEF1α* (*C*), *eIF4α* (*D*), *GAPDH* (*E*), *UBQ5* (*F*), *18S* (*G*), *CAC* (*H*), *NTB* (*I*), and *CYP* (*J*), obtained from sequenced monocot species. The *black boxes* indicate conserved regions used for primer designing. The *arrows* indicate direction of polymerization in PCR. *Os- Oryza sativa*, *Zm- Zea mays*, *Ta- Triticum aestivum*, *Si- Setaria italica*, *Bd- Brachypodium distachyon*, *Ph- Phyllostachys heterocycla*.

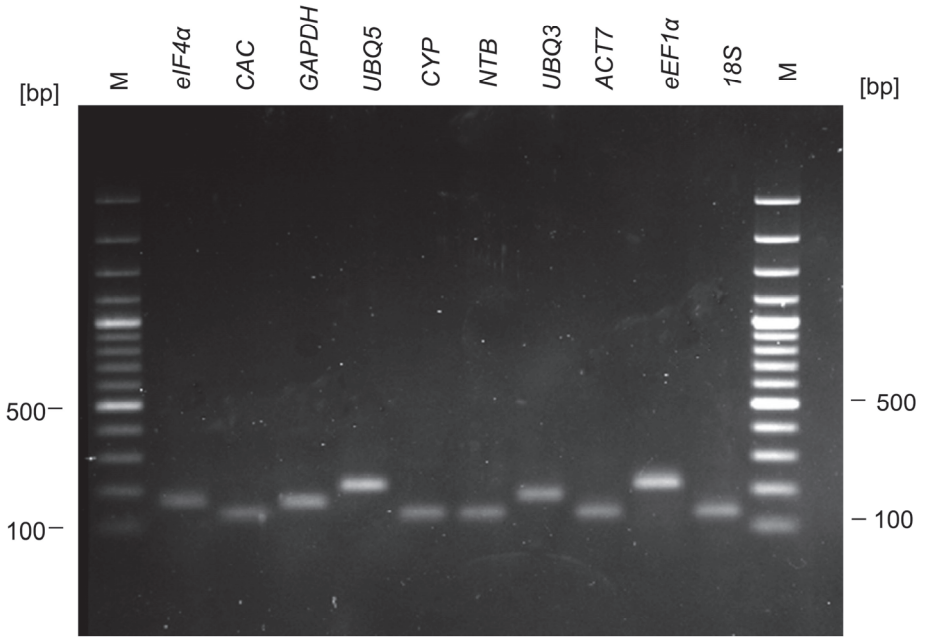

Fig. 4. Suppl. An agarose gel (2.5 %, m/v) showing a specific PCR amplification of selected 10 candidate reference genes of desired length from a cDNA library. M- molecular marker.