Table 1 Suppl. Details of candidate reference gene primers used in quantitative PCR.

Gene name	GeneBank acc. No.	Primer sequences (5′-3′)		Amplicon length [bp]	Efficiency factor
EF1a	KU886197	ATGCCCCAGTTCTTGACTGC	CAGAGAAAGTTTCCACCACCATT	180	1.94
UBQ	KU886196	GTCCACCCTTCACCTTGTTCTC	ACGGACCCACGACACTAAACG	86	1.95
ACT	KU886198	ACTGGTGTAATGGTTGGGATGG	CAATGCCGTGTTCAATTGGGTA	106	1.94
α-Tub	KU886199	CGATCCAAGGCACGGGAAAT	TTGGGCACCAGTCAACAAACT	131	1.94
β-Tub	KC505153	GCAGTTTACGGCCATGTTCA	TCCTCATCTGCAGTGGCATC	150	2.05
CYP38	KU886200	GTGTTCGGATTTGTGACGGA	GCAATCTTGTAGCTCGGGTTG	122	1.96
RTF	KU886201	AGAGGGCTGCTCTGAAATGC	TGAACTCGAACCTCGTCGTC	85	1.95
4-OH	KU886202	GGGAGTTACCGAAGCTGGTG	AAATGGTGCCACTCCTTGCT	199	2.00
VPS	KU886203	TGGACCAATGGCTCCTTTCTAC	TGGGCTATCAGGCATTGTGC	69	1.96

Table 2 Suppl. Pairwise analysis of candidate reference genes vs. *BestKeeper* index.

BestKeeper *vs*.	*EF1a*	*UBQ*	*ACT*	*α-Tub*	*β-Tub*	*CYP38*	*RTF*	*4-OH*	*VPS*
Pearson coeff. (r)	0.908	0.595	0.577	0.928	0.411	0.591	0.843	-0.001	0.791
P-value	0.001	0.019	0.024	0.001	0.127	0.020	0.001	1.000	0.001
BestKeeper *vs*.	*EF1a*			*α-Tub*			*RTF*		
Pearson coeff. (r)	0.961			0.987			0.879		
P-value	0.001			0.001			0.001		
BestKeeper *vs*.	*EF1a*			*α-Tub*					
Pearson coeff. (r)	0.972			0.987					
P-value	0.001			0.001					

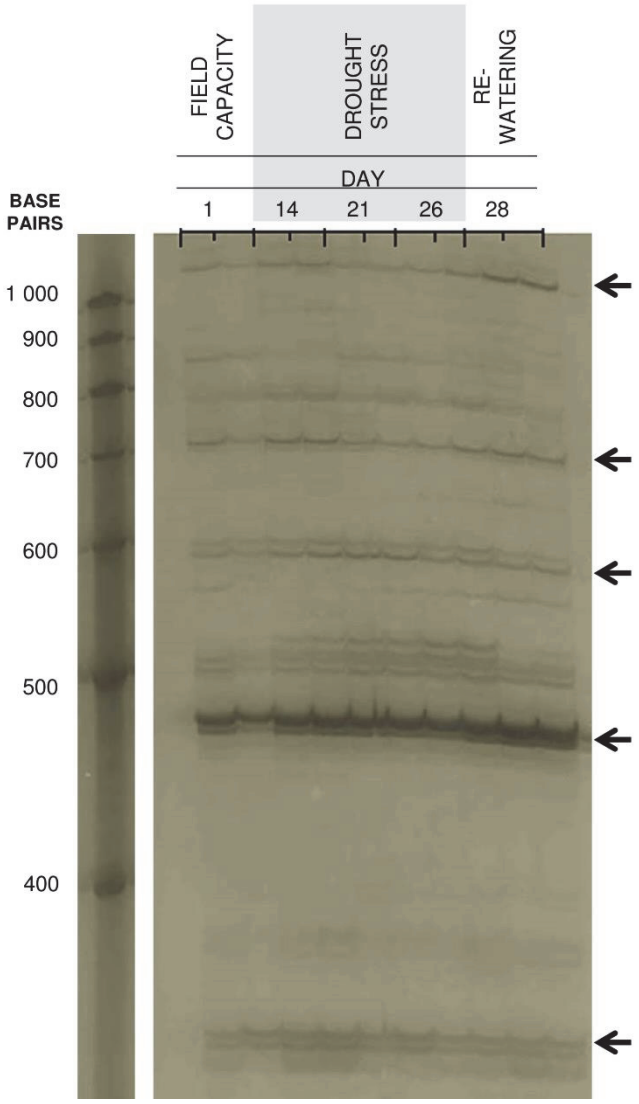

Fig. 1 Suppl. Polyacrylamide gel silver stained from a mRNA differential display assay. *Arrows* indicate the banding patterns with uniform intensity, which corresponds to transcript-derived fragments with stable expression when control plants (field capacity) and plants after re-watering are compared with drought-stressed plants.

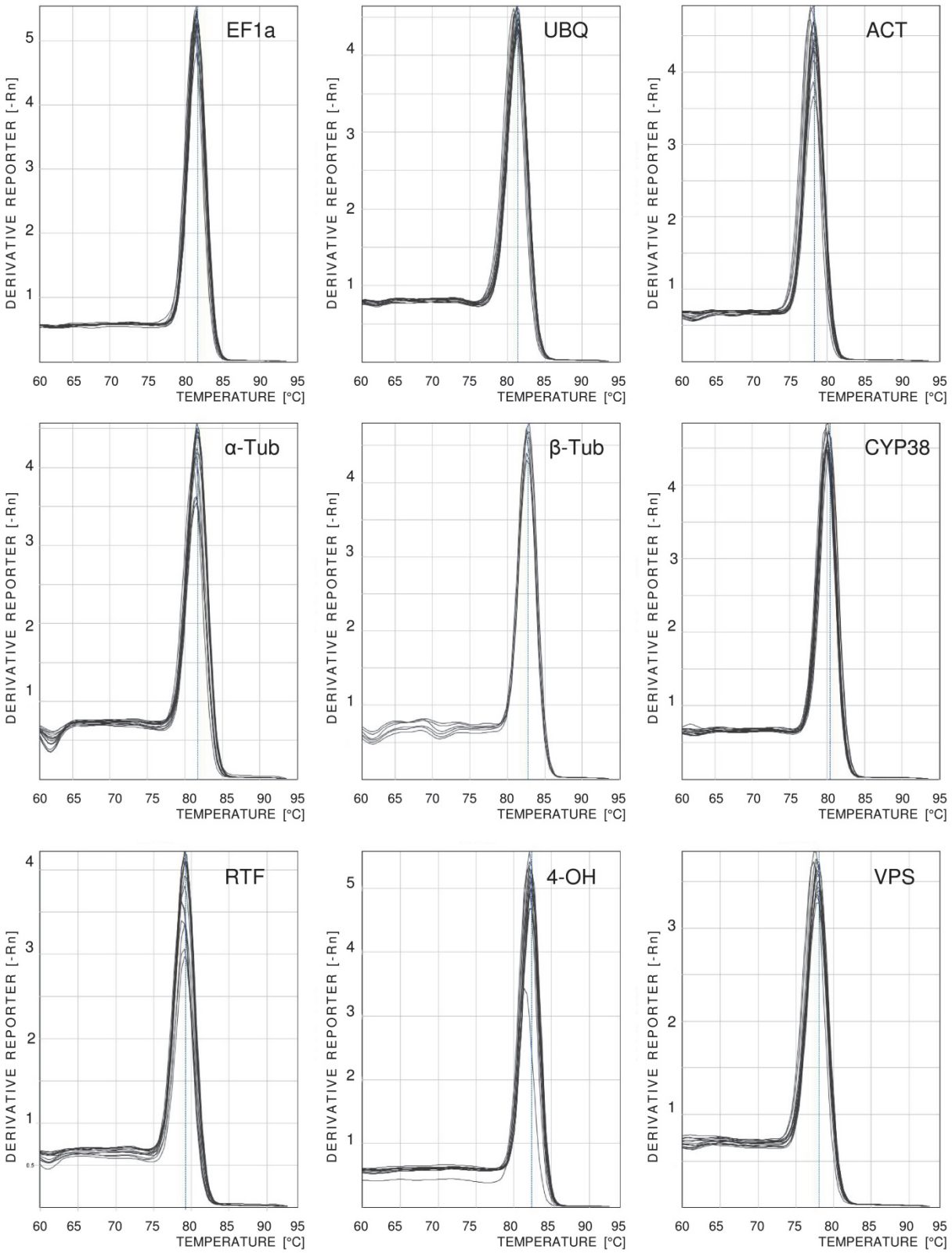

Fig. 2 Suppl. Specificity of primers using for quantitative PCR. The melting curve analysis shows a unique peak, confirming the specificity of the primer pairs used.