

Table1 Suppl. Real-time quantitative PCR primer sequences and their amplicon characteristics of ten candidate reference genes under abiotic stress in peanut.

Name	Accession No.	Primer sequences (5'→3')	Amplicon length [bp]	Amplification efficiency[%]	r ²
<i>UBQ10R</i>	EG030441	F:CGCACACTCGCTGACTACAAC R:CACGGAGACGGAGGACAAGG	64	107.3	0.989
<i>ADH3</i>	EG529529	F:GCTTCAAGAGCAGGTCACAAGT R:GAGACATCCTCCTTCGTGCATA	143	108.6	0.986
<i>MTP</i>	GO265464	F:CGAGGTGGTGGCAGATGAAAG R:ACTCCTTGCTCTCTTGGTCCTATTCC	185	95.0	0.995
<i>GAPDH</i>	Not available	F:CAACAACGGAGACATCAACG R:ATCACTGCCACCCAGAAAAC	190	96.8	0.999
<i>60S</i>	EH042095.1	F:TGGAGTGAGAGGTGCATTG R:TCTTTTGACGACCAGGGAAC	155	96.0	0.999
<i>CYP</i>	GO340500	F:TCCTCCTTCCACCGTGTCAATC R:GACCCGCATTGCGCATCG	163	92.7	0.997
<i>EF1b</i>	GO339841	F:GCTGCTGCTGCTGATGACG R:TGCCTTCTTATCCTCCTCTGTCTC	66	105.5	0.996
<i>TUA5</i>	GO264294	F:CTGATGTCGCTGTGCTCTTGG R:CTGTTGAGGTTGGTGTAGGTAGG	94	95.8	0.998
<i>ACT2</i>	GO326795.1	F:GAGCTGAAAGATTCCGATGC R:GCAATGCCTGGGAACATAG	178	91.9	0.990
<i>TUB4</i>	GO335391	F:GATGTTGTTAGGAAGGAGGCTGAG R:CACTTTGGGCGAAGGGAATACC	174	105.8	0.993

Table 2 Suppl. Stable value and ranking of data analysis by *NormFinder* algorithm. Best combination: *UBAQ10R* + *ACT2* (expression stability value M = 0.216)

Name	Al-sensitive cv. ZH2						Al-tolerant cv. 99-1507					
	root rank	M	stem rank	M	leaf rank	M	root rank	M	stem rank	M	Leaf rank	M
<i>TUA5</i>	3	0.360	7	0.299	8	0.572	9	0.486	9	0.522	9	1.208
<i>UBQ10R</i>	1	0.278	1	0.171	1	0.247	1	0.158	1	0.101	1	0.214
<i>ACT2</i>	2	0.305	9	0.338	6	0.392	3	0.191	2	0.103	5	0.431
<i>TUB4</i>	8	0.930	10	0.781	10	1.094	10	0.822	10	0.792	10	1.221
<i>ADH3</i>	5	0.543	6	0.266	3	0.325	7	0.334	8	0.459	2	0.275
<i>60S</i>	9	1.180	5	0.231	4	0.337	5	0.280	4	0.159	3	0.295
<i>GAPDH</i>	7	0.820	2	0.187	5	0.357	6	0.331	6	0.225	7	0.582
<i>EF1b</i>	4	0.421	3	0.221	2	0.286	4	0.246	7	0.243	4	0.428
<i>CYP</i>	6	0.558	8	0.314	7	0.488	2	0.178	3	0.145	6	0.486
<i>MTP</i>	10	1.285	4	0.223	9	0.572	8	0.367	5	0.207	8	0.883

Table 3 Suppl. Stable value and ranking of data analysis by *BestKeeper* algorithm (SD - standard deviation).

Name	Al-sensitive cv. ZH ₂						Al-tolerant cv. 99-1507					
	root rank	SD	stem rank	SD	leaf rank	SD	root rank	SD	stem rank	SD	leaf rank	SD
<i>TUA5</i>	2	1.126	1	0.186	1	0.659	1	0.281	1	0.128	5	1.094
<i>UBQ10R</i>	8	1.832	6	0.760	2	0.686	8	1.091	6	0.746	1	0.255
<i>ACT2</i>	7	1.689	2	0.353	7	1.345	2	0.391	2	0.252	8	1.549
<i>TUB4</i>	10	2.329	10	1.574	10	1.613	10	1.991	10	1.589	10	2.336
<i>ADH3</i>	6	1.476	7	0.826	5	1.073	5	0.651	7	0.921	3	1.044
<i>60S</i>	4	1.196	8	1.160	9	1.506	9	1.551	9	1.258	6	1.164
<i>GAPDH</i>	3	1.185	9	1.276	6	1.142	6	0.933	8	1.181	7	1.401
<i>EF1b</i>	5	1.413	3	0.633	8	1.492	7	0.966	3	0.407	9	2.111
<i>CYP</i>	1	0.960	4	0.661	3	0.847	4	0.421	4	0.679	2	0.752
<i>MTP</i>	9	1.921	5	0.693	4	0.913	3	0.386	5	0.689	4	1.053

Table 4 Suppl. ReFinder ranking of the candidate reference genes with respect to their expression stability under different experimental conditions (GM – geometric mean).

Name	Al-sensitive cv. ZH ₂						Al-tolerant cv. 99-1507						Entire	
	root rank	GM	stem rank	GM	leaf rank	GM	root rank	GM	stem rank	GM	leaf rank	GM	rank	GM
<i>TUA5</i>	2	2.884	4	3.826	4	4.160	4	3.979	4	4.327	9	7.399	3	4.079
<i>UBQ10R</i>	1	2.000	1	1.817	1	1.260	1	2.000	1	1.817	1	1.442	1	1.000
<i>ACT2</i>	3	3.037	6	5.451	9	6.649	3	3.107	2	2.289	6	5.848	4	4.243
<i>TUB4</i>	9	8.618	10	10.000	10	10.000	10	10.000	10	10.000	10	10.000	9	9.826
<i>ADH3</i>	7	5.646	7	5.518	5	4.217	7	5.944	9	7.652	2	1.817	5	5.601
<i>60S</i>	8	6.868	9	6.214	7	5.241	6	5.130	7	5.241	3	3.302	7	6.316
<i>GAPDH</i>	6	5.278	5	4.481	3	3.915	9	6.604	8	6.952	8	7.000	6	6.106
<i>EF1b</i>	5	3.915	2	3.000	2	3.634	5	4.820	6	5.013	5	5.241	2	3.798
<i>CYP</i>	4	3.107	8	6.073	6	5.013	2	2.520	3	2.884	4	4.160	3	4.079
<i>MTP</i>	10	9.655	3	3.420	8	6.604	8	6.000	5	5.000	7	6.350	8	6.376

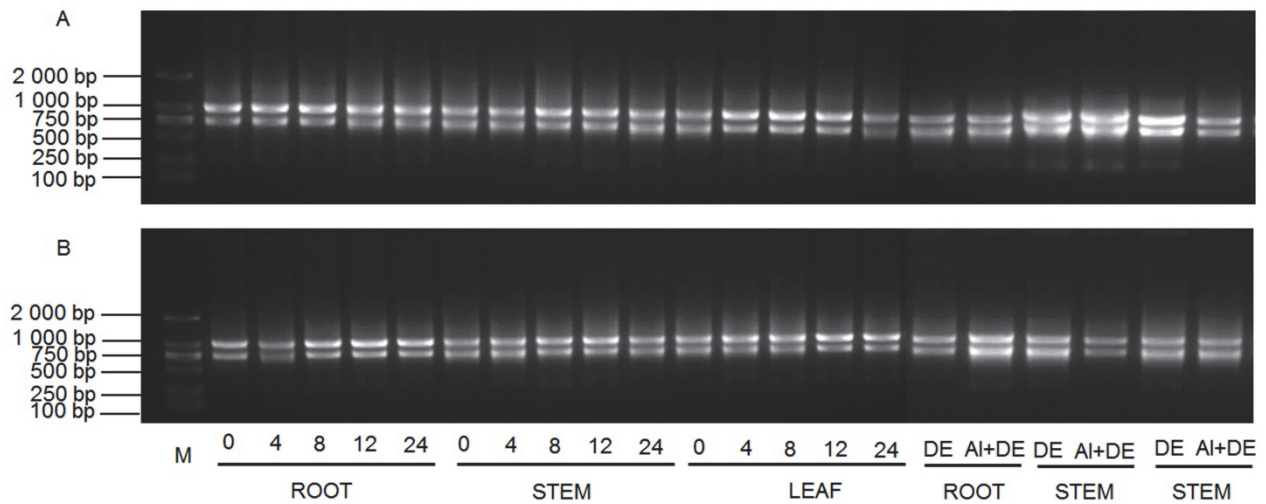


Fig. 1. Suppl. Agarose gel electrophoresis analysis of total RNA extracted from each sample. M - marker; lane 0 - control; lane 4 - 100 μ M AlCl₃ for 4 h; lane 8 - 100 μ M AlCl₃ for 8 h; lane 12 - 100 μ M AlCl₃ for 12 h; lane 24 - 100 μ M AlCl₃ for 24 h; Lane DE – 50 μ M acetyl-Asp-Glu-Val-Asp-aldehyde (Ac-DEVD-CHO) for 2 h; lane Al +DE - 50 μ M Ac-DEVD-CHO treatment for 2 h prior to 100 μ M AlCl₃ for 8 h.

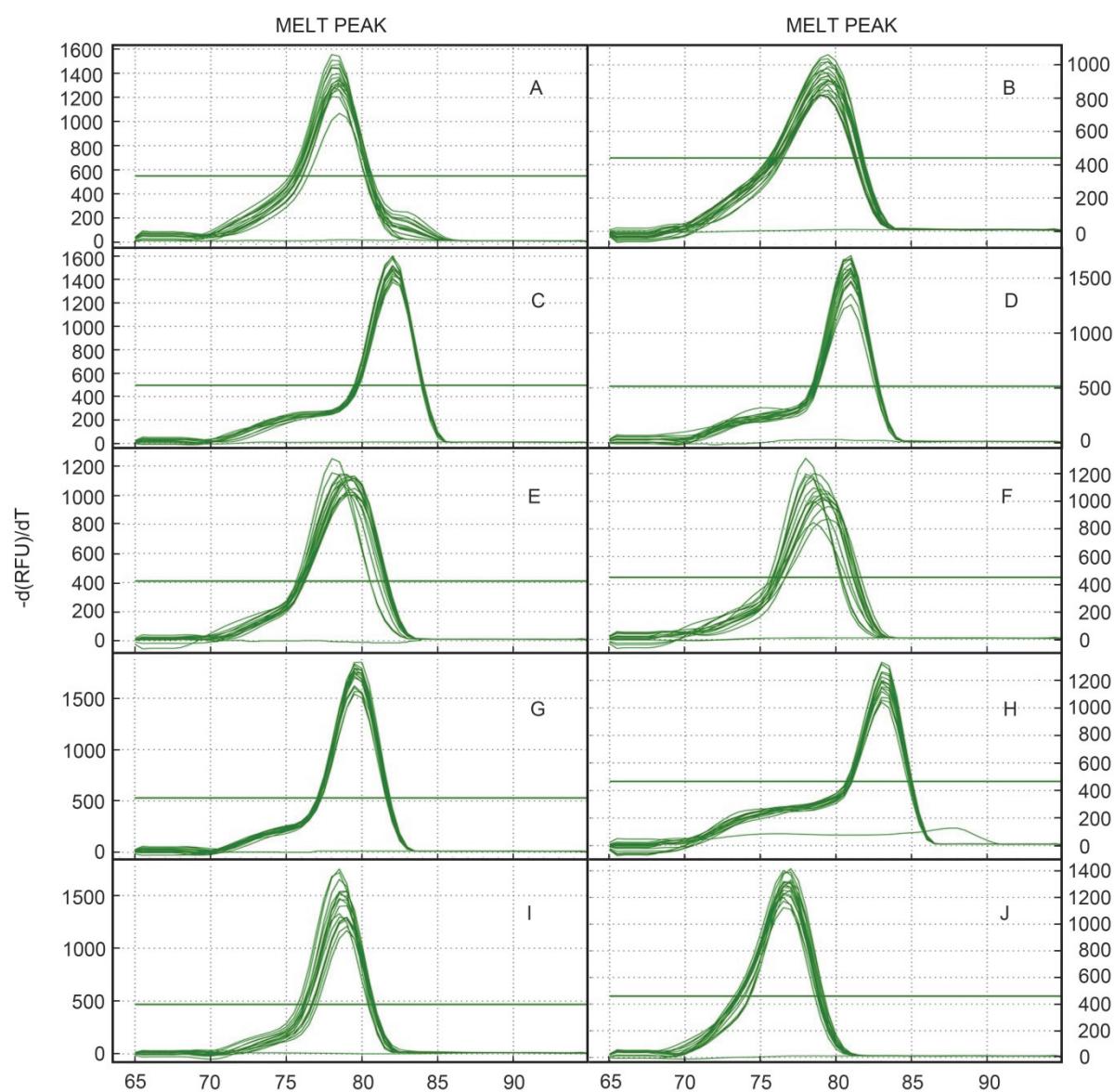


Fig. 2. Suppl. Melting curves of ten candidate reference genes showed a single peak, including *UBQ10R* (A), *MTP* (B), *GAPDH* (C), *TUB4* (D), *60S* (E), *TUA5* (F), *ADH3* (G), *CYP* (H), *ACT2* (I), *EF1b* (J).