

Table S1. Information of the six *Ginkgo biloba* accessions.

Genotype	Full name	Origin
FS	Guilin 7	Institute of Forestry Science and Technology in Guilin
YZ	Yezi ginkgo	Yiyuan, Shandong
XY	Xiaoyuanzi	Huayuan, Tancheng
YL	Yuanling-13	Shandong Agricultural University
CL	Cao-1	Caolou, Gangshang
NJ	Nanjing	Nanjing Forestry University

Table S2. FPKM values of 12 reference genes covering 14 transcriptomes data of *G. biloba*.

Gene	Gene_id	Normal 5	Normal 6	Normal 7	Normal 8	Normal 9	Normal 10	CV		
<i>RP II</i>	Gb_40102	77.89182	105.7834	132.898	92.906	99.071	125.719	0.195		
<i>ADSS</i>	Gb_32787	1890.109	1175.536	1798.322	1607.015	1663.152	2390.148	0.226		
<i>ACT</i>	Gb_00790	126.752	218.1323	207.566	141.750	147.6534	164.3615	0.221		
<i>TUB</i>	Gb_02392	65.434	113.209	75.871	78.897	75.87138	129.3459	0.282		
<i>UBI</i>	Gb_24579	175.654	143.737	169.851	197.134	137.604	153.163	0.137		
Gene	Gene_id	IF	IL	MF	ML	MS	OS	RT	ST	CV
<i>HYP</i>	Gb_05998	82.45	60.03	83.523	83.033	85.526	88.753	89.003	94.556	0.123
<i>HAS28</i>	Gb_13272	141.433	131.476	128.26	175.356	121.6	158.933	152.233	156.553	0.125
<i>H2A</i>	Gb_34906	514.056	370.093	413.453	443.676	373.686	453.853	465.313	355.52	0.130
<i>EIF4E</i>	Gb_08649	128.853	108.326	127.646	116.78	105.653	133.126	86.903	113.17	0.132
<i>EIF3I</i>	Gb_07392	118.99	83.5433	124.77	70.526	102.13	144.66	77.496	96.786	0.250
<i>ACA</i>	Gb_36873	107.013	99.83	104.94	86.056	64.31	91.566	92.093	77.34	0.159
<i>EF1</i>	Gb_08439	161.866	149.270	243.276	109.390	79.563	196.63	120.246	229.103	0.361

Note: Coefficient of variation (CV) was calculated for every gene and listed last. Data (Normal 5-10) are unpublished. IL: immature leaf, IF: immature fruit, MF: mature fruit, ML: mature leaf, MS: microstrobilus, OS: ovulate strobilus, RT: root, ST: stem

Table S3. Ranking of the potential reference genes of *G. boliba* by NormFinder (The tabulated data of Figure 4a).

Rank	Different genotypes	Different developmental stages	Different tissues	MeJA treatment	Heat stress	Cold stress	All samples
1	<i>EF1</i> (0.157)	<i>HAS28</i> (0.072)	<i>EIF3I</i> (0.248)	<i>RP II</i> (0.083)	<i>HAS28</i> (0.03)	<i>EIF4E</i> (0.047)	<i>HYP</i> (0.332)
2	<i>UBI</i> (0.25)	<i>HYP</i> (0.168)	<i>RP II</i> (0.291)	<i>ACA</i> (0.09)	<i>GAPDH</i> (0.104)	<i>RP II</i> (0.049)	<i>HAS28</i> (0.364)
3	<i>HYP</i> (0.263)	<i>UBI</i> (0.201)	<i>ADSS</i> (0.301)	<i>TUB</i> (0.116)	<i>ACA</i> (0.106)	<i>UBI</i> (0.06)	<i>ADSS</i> (0.616)
4	<i>ACA</i> (0.266)	<i>RP II</i> (0.205)	<i>HAS28</i> (0.33)	<i>HAS28</i> (0.173)	<i>UBI</i> (0.18)	<i>ACA</i> (0.066)	<i>ACT</i> (0.725)
5	<i>RP II</i> (0.289)	<i>H2A</i> (0.276)	<i>EIF4E</i> (0.509)	<i>EIF4E</i> (0.18)	<i>HYP</i> (0.272)	<i>ACT</i> (0.159)	<i>TUB</i> (0.831)
6	<i>H2A</i> (0.308)	<i>ACA</i> (0.282)	<i>TUB</i> (0.584)	<i>ACT</i> (0.203)	<i>EIF3I</i> (0.373)	<i>HYP</i> (0.175)	<i>EF1</i> (0.931)
7	<i>EIF3I</i> (0.369)	<i>EIF3I</i> (0.418)	<i>H2A</i> (0.591)	<i>HYP</i> (0.205)	<i>TUB</i> (0.469)	<i>HAS28</i> (0.209)	<i>ACA</i> (1.006)
8	<i>EIF4E</i> (0.48)	<i>ACT</i> (0.462)	<i>ACT</i> (0.754)	<i>EIF3I</i> (0.252)	<i>ADSS</i> (0.608)	<i>TUB</i> (0.249)	<i>EIF3I</i> (1.042)
9	<i>ACT</i> (0.565)	<i>EIF4E</i> (0.463)	<i>EF1</i> (0.898)	<i>UBI</i> (0.267)	<i>EIF4E</i> (0.64)	<i>EIF3I</i> (0.269)	<i>UBI</i> (1.153)
10	<i>GAPDH</i> (0.655)	<i>EF1</i> (0.487)	<i>HYP</i> (0.919)	<i>GAPDH</i> (0.328)	<i>ACT</i> (0.659)	<i>GAPDH</i> (0.405)	<i>RP II</i> (1.368)
11	<i>ADSS</i> (0.666)	<i>GAPDH</i> (0.489)	<i>ACA</i> (1.411)	<i>ADSS</i> (0.433)	<i>RP II</i> (0.693)	<i>ADSS</i> (0.441)	<i>EIF4E</i> (1.571)
12	<i>TUB</i> (0.732)	<i>TUB</i> (0.696)	<i>UBI</i> (1.52)	<i>H2A</i> (0.09)	<i>H2A</i> (0.845)	<i>EF1</i> (1.054)	<i>H2A</i> (1.675)
13	<i>HAS28</i> (0.864)	<i>ADSS</i> (1.143)	<i>GAPDH</i> (2.347)	<i>EF1</i> (1.265)	<i>EF1</i> (1.094)	<i>H2A</i> (1.171)	<i>GAPDH</i> (1.815)

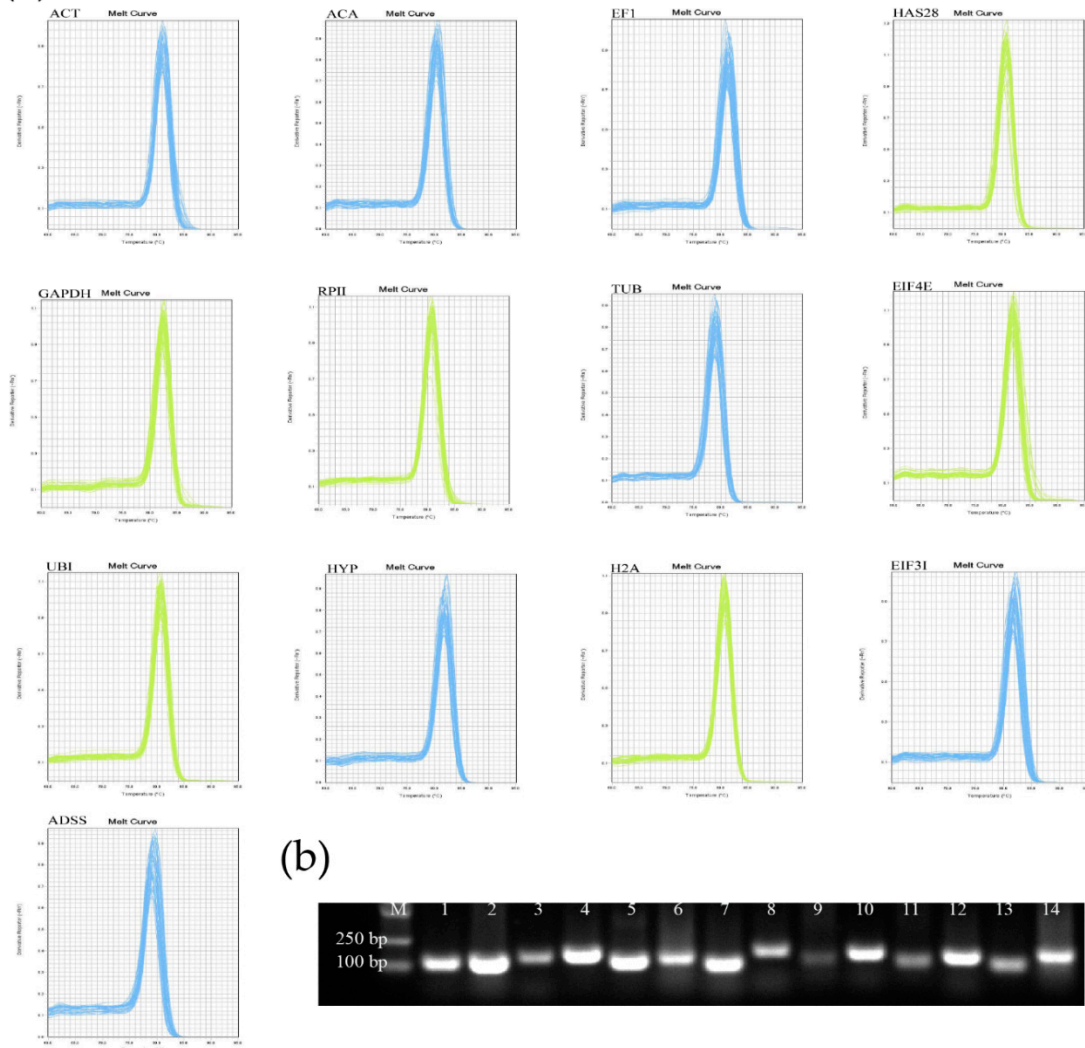
Table S4. Ranking of the potential reference genes of *G. boliba* by Bestkeeper (The tabulated data of Figure 4b).

Rank	Different genotypes	Different developmental stages	Different tissues	MeJA treatment	Heat stress	Cold stress	All samples
1	<i>EF1</i>	<i>H2A</i>	<i>EIF3I</i>	<i>EIF3I</i>	<i>ACA</i>	<i>GAPDH</i>	<i>HAS28</i>
SD	0.33	0.25	0.23	0.11	0.06	0.17	0.41
2	<i>ACT</i>	<i>UBI</i>	<i>RP II</i> /0.25	<i>ACA</i>	<i>HYP</i>	<i>RP II</i>	<i>HYP</i>
SD	0.38	0.26		0.15	0.12	0.19	0.43
3	<i>ADSS</i>	<i>RP II</i>	<i>ADSS</i>	<i>ACT</i>	<i>UBI</i>	<i>ACA</i>	<i>ADSS</i>
SD	0.39	0.28	0.29	0.16	0.21	0.21	0.57
4	<i>H2A</i>	<i>HAS28</i>	<i>HAS28</i>	<i>HAS28</i>	<i>HAS28</i>	<i>HYP</i>	<i>ACT</i>
SD	0.42	0.39	0.32	0.17	0.25	0.23	0.61
5	<i>RP II</i>	<i>ACA</i>	<i>EIF4E</i>	<i>UBI</i>	<i>GAPDH</i>	<i>ADSS</i>	<i>TUB</i>
SD	0.42	0.4	0.42	0.17	0.27	0.25	0.61
6	<i>TUB</i>	<i>EIF4E</i>	<i>ACT</i>	<i>HYP</i>	<i>EIF3I</i>	<i>EIF4E</i>	<i>ACA</i>
SD	0.42	0.43	0.43	0.2	0.37	0.27	0.69
7	<i>UBI</i>	<i>EF1</i>	<i>H2A</i>	<i>ADSS</i>	<i>RP II</i>	<i>UBI</i>	<i>UBI</i>
SD	0.42	0.44	0.54	0.28	0.41	0.28	0.81
8	<i>ACA</i>	<i>GAPDH</i>	<i>TUB</i>	<i>RP II</i>	<i>TUB</i>	<i>EIF3I</i>	<i>EF1</i>
SD	0.44	0.44	0.54	0.33	0.42	0.29	0.82
9	<i>HYP</i>	<i>HYP</i>	<i>HYP</i>	<i>EIF4E</i>	<i>EIF4E</i>	<i>ACT</i>	<i>EIF3I</i>
SD	0.49	0.45	0.66	0.38	0.43	0.3	1.02
10	<i>EIF3I</i>	<i>ACT</i>	<i>EF1</i>	<i>GAPDH</i>	<i>ADSS</i>	<i>HAS28</i>	<i>RP II</i>
SD	0.54	0.46	0.79	0.38	0.45	0.36	1.09
11	<i>HAS28</i>	<i>EIF3I</i>	<i>ACA</i>	<i>TUB</i>	<i>H2A</i>	<i>TUB</i>	<i>EIF4E</i>
SD	0.55	0.52	0.89	0.38	0.52	0.38	1.21
12	<i>EIF4E</i>	<i>TUB</i>	<i>UBI</i>	<i>H2A</i>	<i>ACT</i>	<i>H2A</i>	<i>H2A</i>
SD	0.58	0.64	1.12	0.94	0.53	0.61	1.45
13	<i>GAPDH</i>	<i>ADSS</i>	<i>GAPDH</i>	<i>EF1</i>	<i>EF1</i>	<i>EF1</i>	<i>GAPDH</i>
SD	0.78	0.93	1.96	1.02	0.72	0.92	1.54

Table S5. Ranking of the potential reference genes of *G. boliba* by Delta CT (The tabulated data of Figure 4c).

Rank	Different genotypes	Different developmental stages	Different tissues	MeJA treatment	Heat stress	Cold stress	All samples
1	<i>UBI</i>	<i>HAS28</i>	<i>EIF3I</i>	<i>ACA</i>	<i>GAPDH</i>	<i>EIF4E</i>	<i>HAS28</i>
SD	0.46	0.47	0.83	0.41	0.51	0.047	1.16
2	<i>EF1</i>	<i>HYP</i>	<i>HAS28</i>	<i>ACT</i>	<i>HAS28</i>	<i>RP //</i>	<i>HYP</i>
SD	0.47	0.47	0.85	0.44	0.51	0.049	1.18
3	<i>RP //</i>	<i>RP //</i>	<i>RP //</i>	<i>HAS28</i>	<i>ACA</i>	<i>UBI</i>	<i>ADSS</i>
SD	0.48	0.5	0.85	0.45	0.53	0.06	1.27
4	<i>ACA</i>	<i>UBI</i>	<i>ADSS</i>	<i>HYP</i>	<i>UBI</i>	<i>ACA</i>	<i>ACT</i>
SD	0.49	0.5	0.89	0.45	0.55	0.066	1.29
5	<i>H2A</i>	<i>ACA</i>	<i>EIF4E</i>	<i>RP //</i>	<i>HYP</i>	<i>ACT</i>	<i>TUB</i>
SD	0.5	0.51	0.9	0.45	0.6	0.159	1.34
6	<i>HYP</i>	<i>H2A</i>	<i>TUB</i>	<i>EIF3I</i>	<i>EIF3I</i>	<i>HYP</i>	<i>EF1</i>
SD	0.52	0.52	0.97	0.46	0.63	0.175	1.42
7	<i>EIF3I</i>	<i>EIF3I</i>	<i>H2A</i>	<i>UBI</i>	<i>TUB</i>	<i>HAS28</i>	<i>ACA</i>
SD	0.53	0.57	1.05	0.46	0.66	0.209	1.45
8	<i>EIF4E</i>	<i>ACT</i>	<i>ACT</i>	<i>TUB</i>	<i>EIF4E</i>	<i>TUB</i>	<i>EIF3I</i>
SD	0.62	0.61	1.08	0.47	0.76	0.249	1.47
9	<i>ACT</i>	<i>EIF4E</i>	<i>EF1</i>	<i>EIF4E</i>	<i>ACT</i>	<i>EIF3I</i>	<i>UBI</i>
SD	0.73	0.62	1.2	0.51	0.78	0.269	1.58
10	<i>GAPDH</i>	<i>EF1</i>	<i>HYP</i>	<i>GAPDH</i>	<i>ADSS</i>	<i>GAPDH</i>	<i>RP //</i>
SD	0.76	0.63	1.33	0.54	0.79	0.405	1.64
11	<i>ADSS</i>	<i>GAPDH</i>	<i>ACA</i>	<i>ADSS</i>	<i>RP //</i>	<i>ADSS</i>	<i>EIF4E</i>
SD	0.78	0.65	1.68	0.6	0.8	0.441	1.8
12	<i>TUB</i>	<i>TUB</i>	<i>UBI</i>	<i>H2A</i>	<i>H2A</i>	<i>EF1</i>	<i>H2A</i>
SD	0.83	0.82	1.77	1.25	0.93	1.054	1.92
13	<i>HAS28</i>	<i>ADSS</i>	<i>GAPDH</i>	<i>EF1</i>	<i>EF1</i>	<i>H2A</i>	<i>GAPDH</i>
SD	0.94	1.2	2.48	1.3	1.15	1.171	2.05

(a)



(b)

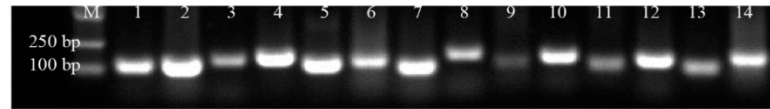


Figure S1. The primer specificity and amplification products of thirteen candidate reference genes. (a) Melting curves with a single peak; (b) Agarose gel electrophoresis (1%) of normal PCR. M: 2000 bp marker. 1-14: *ACT*, *ACA*, *EF1*, *HAS28*, *GAPDH*, *RPII*, *EIF4E*, *H2A*, *UBI*, *HYP*, *TUB*, *EIF3I*, *ADSS*, and *CHS*, respectively.