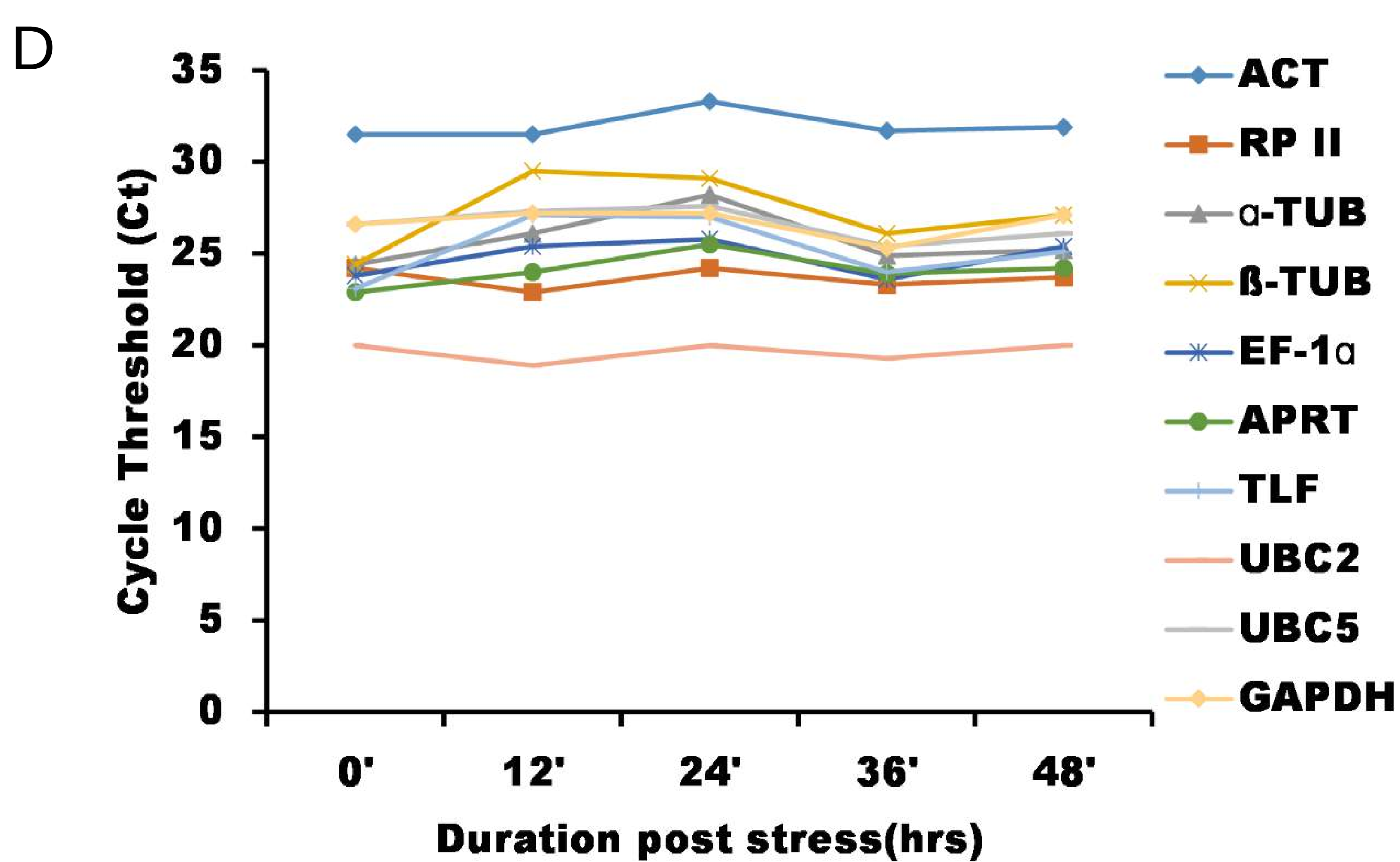
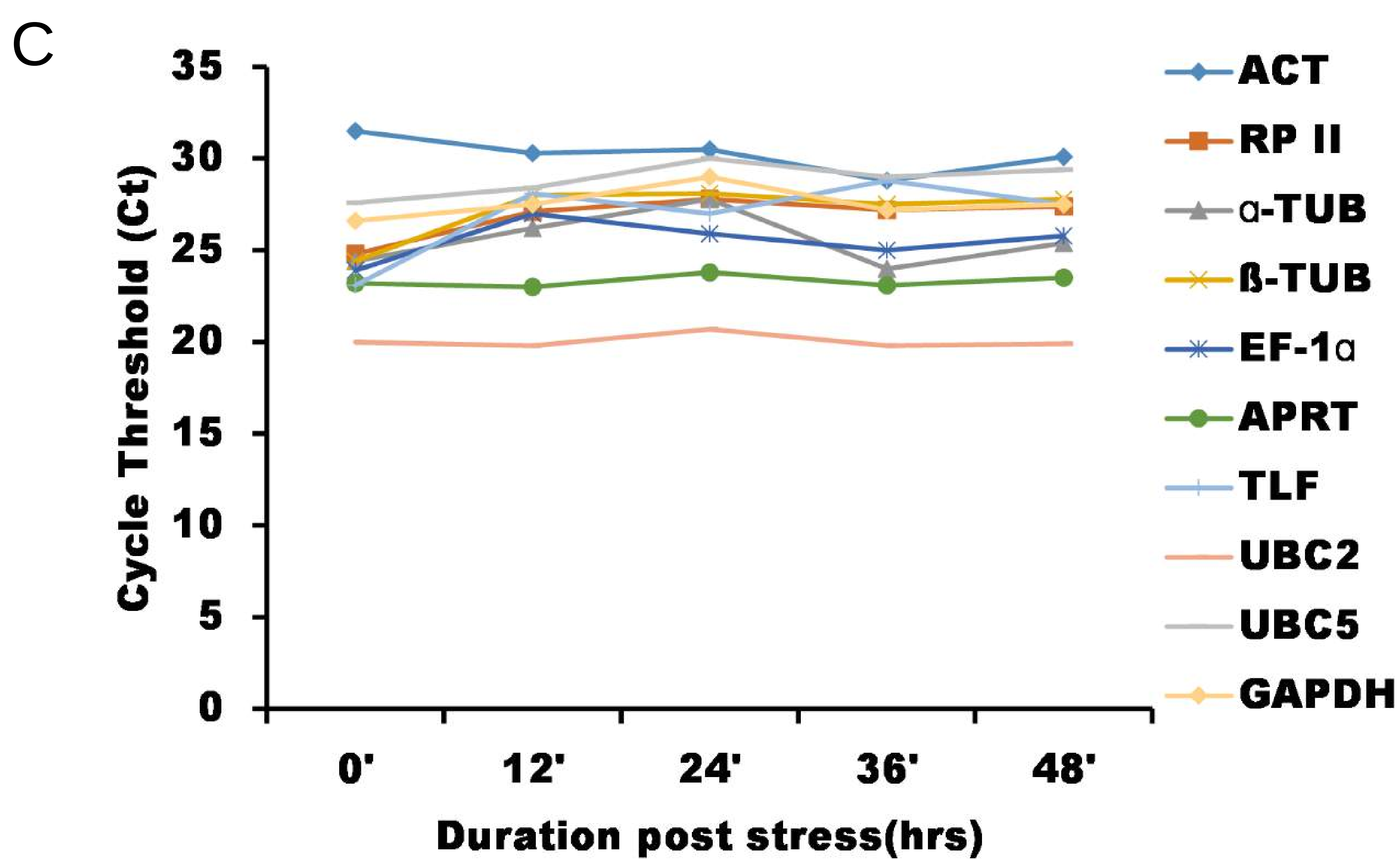
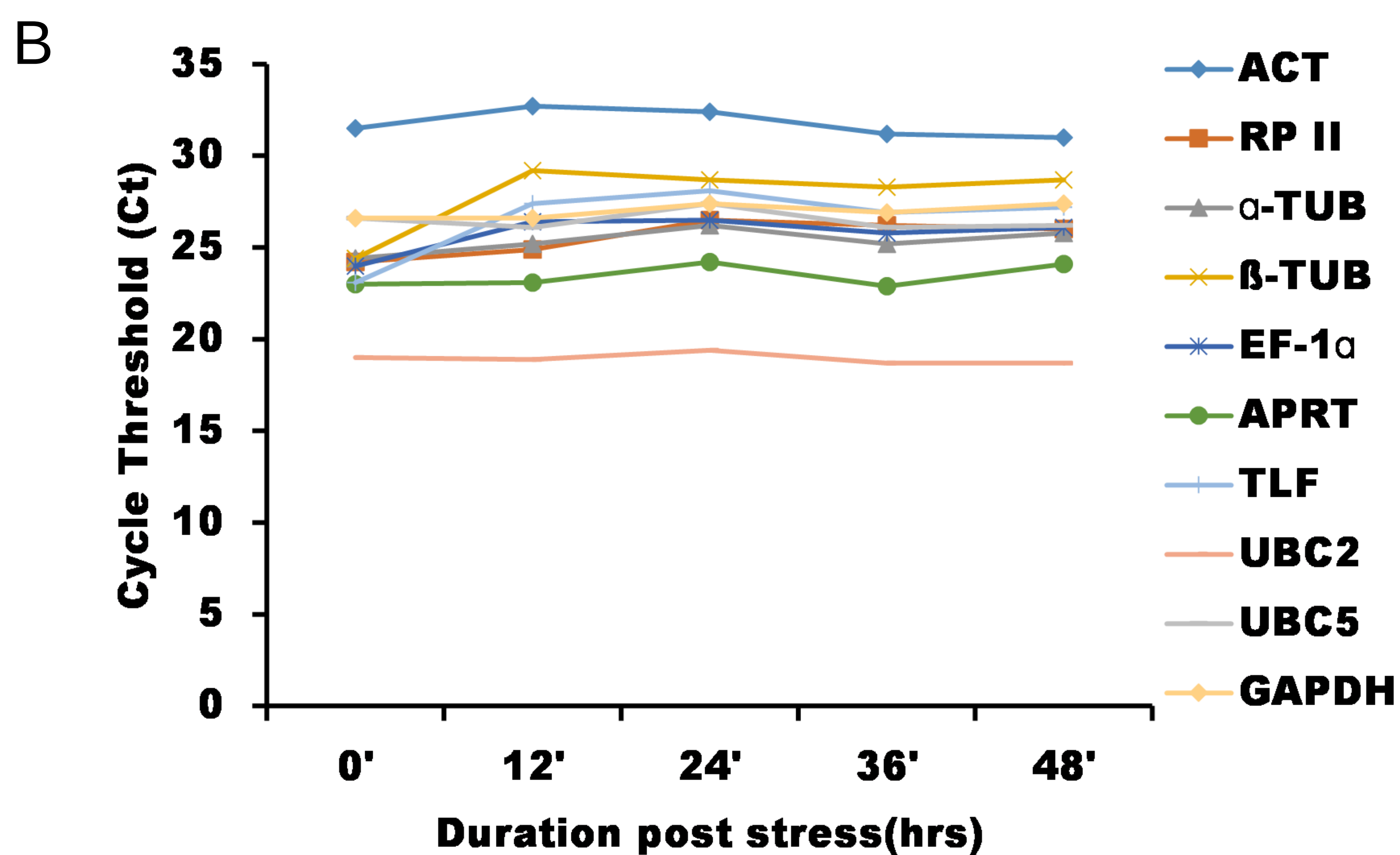
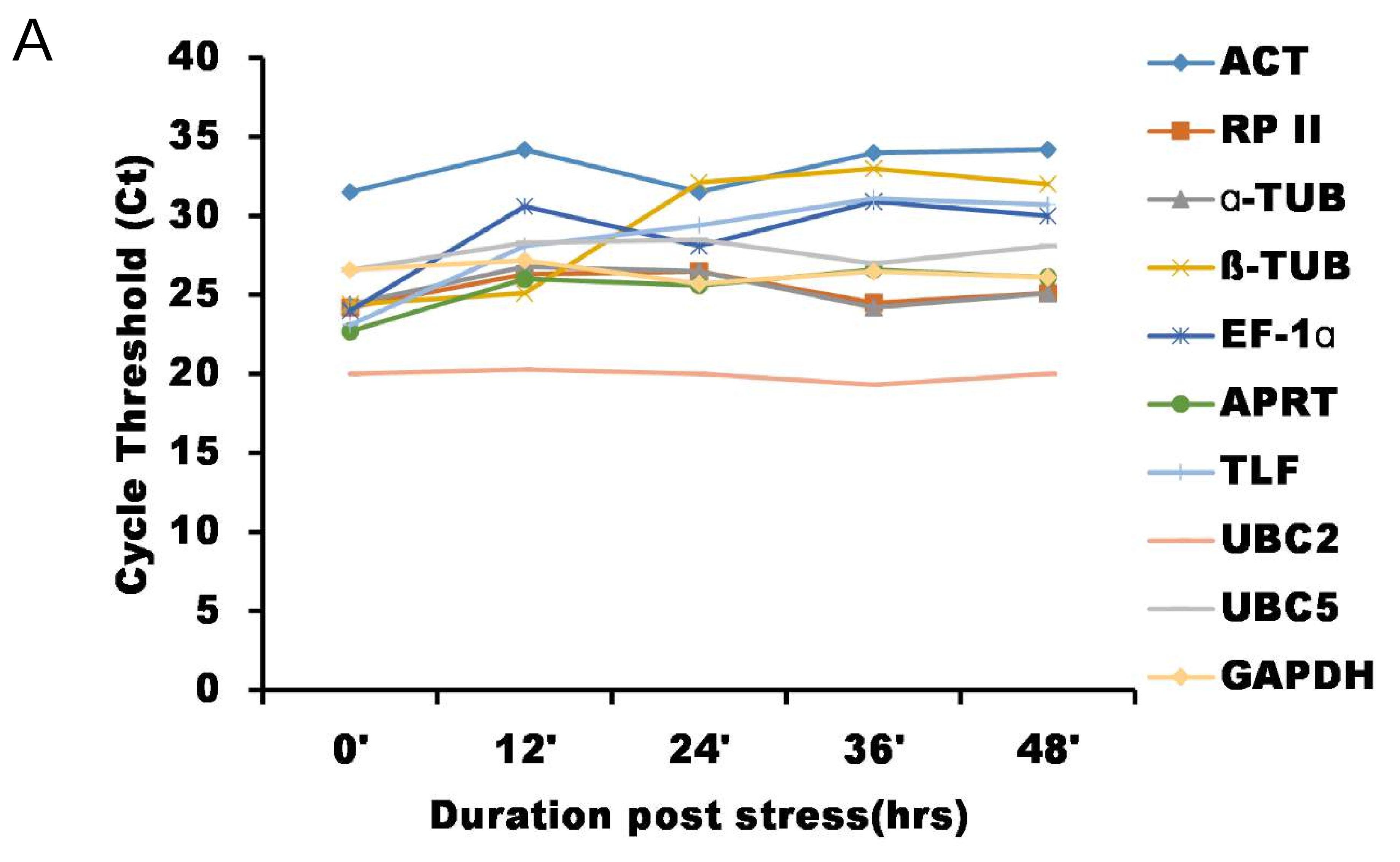


**Selection and validation of reliable reference genes for quantitative real-time PCR in
Barnyard millet (*Echinochloa* spp.) under varied abiotic stress conditions**

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Supplementary Fig. s1. The mean Ct/Cq values of 10 candidate reference tested under (A) Drought, (B) Salinity, (C) Cold, and (D) Hot conditions at different time points.

Supplementary Table s1. Details of CDS sequences of *Echinochloa* spp. used for designing qRT-PCR primers

S. No	Gene Name	Location	Sequence/source
1	<i>ACT</i>	scaffold50.371	ATGGCTGACGGCGAAGACATCCAGCCGCTTGTGTGTGACAATGGGACCGGCATGGTCA AGGCTGGTTTTGCTGGTGATGATGCACCAAGGGCTGTTTTCCCAAGTATTGTTGGGCGT CCCCGTCACACTGGTGTGATGGTTGGCATGGGGCAGAAGGATGCGTATGTTGGTGATG AGGCCCAGTCCAAGAGGGGTATCCTGACCTTGAAGTACCCGATCGAGCATGGTATTGTT AGCAACTGGGATGATATGGAGAAGATCTGGCACCACACCTTCTACAATGAACTACGTG TTGCACCTGAGGAGCACCTGTGCTGCTGACTGAAGCCCCACTCAACCCCAAGGCTAAC AGGGAGAAGATGACCCAGATCATGTTTGAGACCTTCAATGTTCCCTGCCATGTATGTTGC CATCCAGGCTGTGCTTTCTTGTATGCCAGTGGACGGACAACCTGGTATCGTTTTGGACT CTGGTGATGGTGTGTCAGCCACACTGTGCCAATCTATGAAGGTTATGCCCTTCCTCATGCC ATCCTCCGTCTTGACCTTGCTGGGCGTGACCTGACTGACAGCCTGATGAAGATTCTCAC TGAGAGAGGTTACTCCTTCACCACCACTGCTGAACGGGAAATCGTAAGGGACATCAAG GAAAAGCTCGCGTATGTGGCTCTTGACTACGAGCAGGAGCTGGAGAATGCGAAGACCA GCTCATCTGTGGAGAAAAGCTACGAGCTGCCTGATGGTCAGGTGATCACCATTGGGGC AGAGAGGTTTAGATGCCCTGAGGTCCTCTTCCAGCCTTCCATCATTGGTATGGAAGCTC CTGGCATCCATGAGACCACCTACAACCTCCATTATGAAGTGTGATGTGGATATTAGGAAG GACTTGTATGGTAACATTGTGCTCAGTGGTGGCACGACCATGTTCCCTGGTATCGCGGA CCGTATGAGCAAGGAGATCACTGCCCTTGACCCGAGCAGCATGAAAATTAAGGTGGTG GCACCACCTGAAAGGAAATACAGTGTCTGGATAGGAGGGTCCATCCTTGCCTCACTTA GCACCTTCCAACAGATGTGGATATCAAAGGCGGAGTACGATGAGTCGGGGCCAGCAAT TGTTACCGGAAGTGCTTCTAA
2	<i>RP II</i>	scaffold377.22	ATGGACCGTCCGGCGGCCGCGCGTTCGTACCAGCGCTTCCCCCGCGTGAAGATCCGCG ACCTCAAGGACGACTTCGCCAAGTTCGAGCTCCGCGACACCGACGCCAGCATGGCCAA CGCCCTCCGCGCGTTCATGATCGCGGAGGTCCCCACCGTCGCCATCGACCTCGTCGAGA TCGAGGTCAACTCCTCCGTCCTCAACGACGAGTTCATCGCGCACCGCCTGGGGCTCATC CCCCTCACCTCCTCCGCGCCATGCAAATGCGATTCTCCCGGGACTGCGACGCCTGCGA CGGTGACGGCTCCTGCGAGTTCTGCTCCGTCGAGTTCAACCTCCACGCGCGCGCCGAAT CCGACCAGACGCTCGAGGTCACATCCAACGACCTGAGGTCCTTGGACCCCAAGGTATG CCCCGTCGACCAGGCACGCGCCTACCAGCAGGCGCTCGGTGGCGCTGACGGCTTTGAC CCCAACGAGCAGAGGCAAGTCATCCTTCATTTACACGATAGGGATGAAGAAGCATGGG GAATACTTATTGTAAAGCTGCGTCGGGGGCAAGAACTGAGGCTTCGTGCCATTGCTAG GAAGGGAATCGGCAAGGACCATGCCAAATGGTCACCAGCTGCTACCGTGACTTTCATG TATGAGCCTGACATACGTATCAATGAAGAACTCATGGATACATTGACGCTTGATGAGA

			AAAGAAGCTGGATCGAAAGCAGCCCTACAAAAGTATTTGAGCTTGATAATGTTACCCA GCAGGTGACGGTGGTTGACAATGGTGAGGCATACACCTATGACGATGAGGTGATCAAG AAGGCGGAGGCCATGGGAAAGCCGGGCTTAGTGAGATCAATGCGAAGGAGGACAGC TTCATCTTCACCGTGGAACGACGGGCGCCATCACGGCCTACGAGCTGATCATGAACG CCATCACGGTCCTGAGGCAGAAGCTGGATGCCGTCCGCCTCCAGGACGACGACAGCGA CCTTGCGGAGCTCGGCGCCCATCTCGGTGGA
3	<i>a-TUB</i>	scaffold2.684	ATGAGAGAGATCATCAGCATCCACATCGGCCAGGCCGGGATCCAGGTGCGCAACTCCT GCTGGGAGCTCTACTGCCTCGAGCACGGCATCGAGCCCGATGGCACCATGCCAAGTGA TACCTCGGTTGGCGTCGCACATGATGCCTTCAACACCTTCTTCAGTGAGACCGGCTCTG GCAAGCATGTGCCGAGGGCCATCTTTGTTGACCTTGAGCCCACTGTCATCGATGAGGTG CGCACTGGCTCATACCGCCAGCTCTTCCACCCAGAGCAGCTCATCTCTGGGAAGGAGG ATGCGGCTAACAACCTTTGCCCGTGGCCACTACACTGTTGGAAGGAGATTGTCGATCTC TGCCTGGACCGCGTGCGCAAGCTAGCAGACAATTGCACTGGGCTGCAGGGATTCTTGG TGTTCAATGCTGTTGGTGGTGGTACTGGCTCTGGACTTGGTTCACTGCTGTTGGAGCGC CTCTCAGTTGATTACGGCAAGAAGTCTAAGCTCGGCTTCACCATTTATCCGTCCCCACA GGTGTCAACAGCTGTTGTAGAGCCATACAACAGTGTCTCTCTACCCACTCCCTGCTTG AGCACACAGATGTTGCAGTCCTCCTGGACAATGAGGCAATCTATGACATATGCCGGAG GTCCCTTGACATTGAAAGGCCAACCTACACCAACTTGAACAGGCTGATCTCACAGATCA TATCTTCGCTTACCACCTCCCTGAGATTTGATGGTGCTATCAACGTGGATGTTACAGAG TTCCAGACCAACCTTGTTCCATACCCACGCATCCATTTTCATGCTTTCATCATATGCCCT GTAATCTCTGCCGAGAAGGCCTACCATGAGCAGCTCTCTGTGCCCGAAATCACCAATGC TGTCTTTGAGCCCTCAAGCATGATGGCCAAGTGTGACCCAAGGCATGGGAAGTACATG GCTTGCTGCTTGATGTACCGTGGTGTGTTGTTCCCAAGGATGTCAATGCTGCCGTTGC AACCATCAAGACCAAGAGAACTGTCCAGTTTGTGGACTGGTGCCCCACTGGATTCAAG TGTGGCATCAACTACCAGCCACCCTCTGTTGTCCCTGGAGGCGACCTGGCAAAGGTCCA GCGTGCCGTGTGCATGATCAGCAACAACACAGCCGTTGCTGAGGTGTTCTCGCGCATCG ACCACAAGTTCGACCTGATGTATGCTAAGCGTGCCTTCGTGCACTGGTACGTTGGTGAG GGTATGGAGGAAGGCGAGTTCTCAGAGGCCCGTGAGGACTTGGCTGCCCTTGAGAAGG ACTACGAGGAGGTTGGCGCAGAGGGCGCAGACGACGAAGGTGACGAGGGAGAAGACT ATTGA

4	<i>β-TUB</i>	scaffold3.941	ATGAGGGAGATCCTACACATCCAGGGCGGGCAGTGCGGGAACCAGATCGGCGCCAAGT TCTGGGAGGTGATCTGCGACGAGCACGGCATCGACGCCACGGGCCGCTACGCGGGGGA CTCGGACCTCCAGCTCGAGCGCATCAACGTCTACTACAACGAGGCCAGCGGGGGCCGG TTCGTGCCGCGCGCCGTGCTCATGGACCTCGAGCCCGGGACCATGGACTCCGTCCGCTC CGGCCCCCTTCGGCCAGATCTTCCGCCCCGACAACCTTCGTCTTCGGCCAGTCCGGCGCCG GCAACAACCTGGGCCAAGGGACACTACACCGAGGGCGCCGAGCTCATCGACTCCGTCTCT CGACGTTCGTCCGCAAGGAGGCCGAGAACTGCGACTGCCTCCAGGGTTTCCAAGTTTGC CATTCTTGGGAGGAGGCACTGGTTCTGGCATGGGCACCCTTCTTATTTCTAAGATCAG GGAGGAGTACCCTGATAGAATGATGTTGACCTTCTCCGTATTCCCATCACCAAAGGTTT CAGATACTGTTGTGGAGCCATACAATGCTACACTTTCGGTTTACCAACTTGTGAGAAT GCTGATGAATGTATGGTGCTTGACAATGAAGCTCTGTATGACATCTGCTTCCGCACACT AAAGCTTGCCACCCCTACCTTTGGTGACCTGAACCATCTTATCTCTGCTACCATGAGTG GCGTCACGTGCTGCCTGAGGTTCCCTGGTCAGCTCAACTCCGACCTGCGCAAGCTTGCC GTGAACCTCATCCCATTCCCTCGTCTCCATTTCTTCATGGTTCGGCTTTGCGCCGCTGACC TCACGTGGATCGCAGCAGTACCGCGCCCTCACTGTCCCTGAGCTGACCCAGCAGATGTG GGATGCCAAGAACATGATGTGTGCCGCTGACCCCGCCACGGCCGTTACCTCACGGCCT CCGCCATGTTCCGTGGGAAGATGAGCACCAAGGAGGTGGACGAGCAGATGCTCAACGT CCAGAACAAAGAACTCGTCTTACTTCGTGGAGTGGATCCCGAACAAATGTCAAGTCCAGT GTGTGCGACATCCCACCCAAGGGTCTGAAGATGGCGGGTACCTTCGTGCGGAACTCCA CCTCCATTACAGGAGATGTTCCGCAGGGTGAGCGAGCAGTTCACGGCCATGTTACGGCG CAAGGCCTTCTTGCACTGGTACACCGGCGAGGGGATGGACGAGATGGAGTTCACCGAA GCTGAGAGCAACATGAATGACCTGGTTGCGGAGTACCAGCAGTACCAGGACGCCACCG CCGACGAGGAGTATGAGGACGAGGAGGAAGAGGAGGAGGCGGCCGAATAA
5	<i>EF-1a</i>	scaffold8.559	ATGGGTAAGGAGAAGTCCCACATCAACATCGTGGTCATTGGCCACGTCGACTCTGGCA AGTCGACCACCACTGGCCACCTGATCTACAAGCTTGAGAGTATTGACAAGCGTGTGATC GAGAGGTTTCGAGAAGGAGGCTGCTGAGATGAACAAGCGGTCCTTCAAATACGCGTGGG TGCTTGACAAGCTCAAGGCTGAGCGTGAGAGAGGTATCACCATTGATATCGCCCTGTG GAAGTTCGAGACCACCAAGTACTACTGCACTGTGATTGACGCCCTGGACACCGTGACT TCATCAAGAACATGATCACTGGTACCTCCCAGGCTGACTGTGCTGTCTTATCATTGAC TCCACCACTGGTGGTTTTGAGGCTGGTATCTCCAAGG
6	<i>APRT</i>	scaffold29.598	ATGCTGCCCCCCTGCGGTTCCAGCCTCGCCTCGGCCTCGGCCTCCCGTCGTCAGCAGC AGCAGCAGCGTCGGCGCCGCCGCCGCTTTTCTCCGCGCGGGCCCCGCCGCCACCACCA CCGGCGTCTCCGTGCGCGGCGCGAGACCCAGCGCGCGTGTACCGGCGGGAGGCGGGCG AGGGCCGGCGGTGGCGATGGCGTCCGGCGACGCGCGCGTGGCGGGGATCGCGTCCTCC ATCCGCGTCATCCCCGACTTCCCCAAGCCAGGAATCATGTTTCAGGATATCACGACATT GCTCCTCGATCCGAAGGCGTTCCGTGACACGATCGACCTCTTTGTTGAGCGCTACAAGG

			ACCAAGGGATCACCGTAGTTGCTGGTGTGAAGCTAGGGGTTTTATCTTTGGCCCTCCT ATTGCTTTAGCCATAGGTGCAAAATTTGTACCTTTGAGAAAGCCAAAAAAGTTGCCAGG CGAGGTGATCTCTGAAGAATATTCTTTGGAATATGGCACCGACAAAATAGAAATGCAT GTTGGAGCTGTGGAGGCCAATGATCGAGCACTTGTTGTCGATGATCTCATTGCCACTGG TGGAACACTATGTGCAGCTGTCAAACCTTCTCGAGCGTGTTGGAGCAAAGGTGGTTGAGT GTGCTTGTGTCATTGAATTGCCAGAATTGAAGGGCCGGGACAAGCTAGGGGACAGGCC CGTTTTCGTCCTTGTG
7	TLF	scaffold89.132	ATGGTGAAGTTCACGGCGGAAGAGCTCCGTGGCATCATGGACAAAAAGAACAACATTC GTAATATGTCCGTTATTGCTCATGTGGACCATGGCAAGTCTACCCTTACAGATTCCTTG TGGCAGCTGCTGGTATCATTGCCCAGGAAGTTGCTGGTGATGTTTCGCATGACTGATACT CGTGCAGATGAAGCAGAGCGTGGTATTACAATCAAATCCACTGGTATATCTCTTTACTA TGAGATGACTGAGGAGTCACTGAAGAATTACAAGGGTGAGAGAGATGGTAGCGAATA CTTGATCAACCTTATTGACTCACCTGGGCACGTTGATTTTTCTTCGGAAGTCACAGCTGC TCTTCGTATCACCGATGGTGCTCTAGTTGTGGTTGACTGTATTGAAGGTGTCTGTGTGCA AACTGAAACTGTGCTCCGCCAGGCTCTTGTTGAGAGGATTAGGCCAGTCCTTACTGTGA ACAAGATGGACAGGTGCTTCCTTGAGCTTCAGGTTGAGGGTGAGGAAGCCTACCAGAC TTTCTCCCGTGTCAATTGAGAATGCCAATGTCATTATGGCTACATATGAAGATAAGCTCC TAGGTGATGTCCAAGTCTACCCAGAGAAGGGAAGTGTGCTTTCTCTGCTGGTCTGCAT GGCTGGGCCTTCACCCTCACCAACTTTGCCAAGATGTATGCATCCAAGTTTGGAGTTGA TGAATCTAAGATGATGGAGAGGCTCTGGGGTGAGAAGTTTTTTGACCCAGCCACAAAG AAGTGGAACACGAAGAACACAGGCTCTGCTACCTGCAAGAGAGGATTTGTTTCAGTTCT GCTATGAGCCAATCAAGCAAATCATCAACACCTGCATGAATGACCAGAAGGATAAGTT GTGGCCCATGCTTCAAAGCTTAATGTTACCATGAAGGCTGATGAGAAGGAATTGGTT GGCAAGGCTTTGATGAAGCGTGTTATGCAAACCTGGCTCCCAGCCAGTACTGCCCTACT TGAGATGATGATATTCCACCTCCCTTCCCCATCAAAGGCACAAAAGTATCGTGTGGAGA ACTTGTACGAGGGACCCCTTGATGATATCTATGCTACTGCTATCAGGAAGTGTGATCCA GAGGGTCCTCTTATGCTGTATGTTCAAAGATGATTCCAGCATCTGACAAAGGCAGGTT CTTTGCCTTCGGTCGTGTCTTCTCAGGGAAGGTCGCTACTGGTATGAAGGTTTGAATCA TGGGTCCCAACTATGTCCCTGGCCAGAAGAAGGATCTATATGTCAAGAGTGTCCAGCGT ACTGTTATCTGGATGGGAAAGAAACAAGAGTCAGTTGAGGATGTTCCCTTGTGGTAACA CTGTTGCTATGGTTGGTCTGGATCAGTTCATCACAAAGAATGCTACACTCACTAATGAG AAGGAGGTTGATGCATGCCAATCAGAGCAATGAAGTTCTCTGTCTCCCCTGTTGTGCG TGTTGCTGTTTCAGTGCAAGGTTGCCTCTGACCTACCCAAGCTAGTTGAAGGTTTGAAGC GTCTCGCAAAGTCTGATCCTATGGTCCTCTGTACAATTGAAGAATCTGGTGAGCATATT ATTGCTGGAGCTGGTGAGCTTCATCTGGAGATTTGCCTGAAGGATCTGCAGGAAGACTT CATGGGTGGTGCTGAGATTATTGTTTCCCCGCCTGTTGTCTCTTCCGTGAAACTGTTCT

			TGAGAAATCCTGCCGAACAGTCATGAGTAAGTCCCCAACAAGCACAACCGTCTTTAC ATGGAAGCCCCGCCCTTGGAAGAGGGTCTTGCTGAGGCCATTGATGAAGGTCGCATTG GTCCACGTGATGATCCCAAGGTGCGCTCCAAGATCCTCTCTGAGGAGTTCGGCTGGGAC AAGGATCTTGCCAAGAAGATTTGGTGCTTTGGACCTGAGACCACCGGCCCGAACATGG TTGTTGATATGTGTAAGGGAGTGCAGTACCTCAATGAAATCAAGGATTCTGTGGTGGCT GGTTTCCAGTGGGCCTCAAAGGAGGGTGCGCTAGCTGAGGAGAACATGCGTGGAATTT GCTTTGAGGTCTGTGATGTTGTTCTTCACGCTGATGCAATTCACAGGGGTGGTGGCCAG GTCATTCCAAGTCCAGGAGGGTCATTTATGCTTCTCAGCTGACGGCCAAGCCAAGGCT GCTCGAGCCAGTTTACCTTGTGGAGATCCAGGCCCCAGAAAATGCACTTGGTGGTATCT ATGGTGTTCTGAACCAGAAGAGAGGGGCACGTGTTTGAGGAGATGCAGAGGCCGGGGAC CCCGCTCTACAACATCAAGGCTTACCTCCCTGTCATCGAGTCATTTGGGTTCTCAAGCC AATTGAGGGCTGCAACCTCTGGCCAGGCGTTCCCCCAGTGTGTGTTTGACCACTGGGAC ATGATGGGCTCTGATCCTCTGGAGGCTGGCTCCAGGCCGCTCAGCTGGTGTGGATAT CCGCAAGAGGAAGGGTCTCAAGGAACAGATGACCCCTCTTTCTGAGTTCGAGGACAAG CTCTAA
8	UBC2	<i>E.frumentacea</i> mRNA GWHTBDNQ043355	https://ngdc.cncb.ac.cn/gwh/Assembly/21453/show
9	UBC5	<i>E.frumentacea</i> mRNA GWHTBDNQ048013	https://ngdc.cncb.ac.cn/gwh/Assembly/21453/show
10	GAPDH	<i>E.frumentacea</i> mRNA GWHTBDNQ085699	https://ngdc.cncb.ac.cn/gwh/Assembly/21453/show
11	SOD1	<i>E.frumentacea</i> mRNA GWHTBDNQ090839	https://ngdc.cncb.ac.cn/gwh/Assembly/21453/show

Supplementary Table s2. Details of primer sequences and amplicon characteristics of candidate reference and target genes

S. No	Gene	Genome location	Primer sequences (5'3')	Amplicon size (bp)	Tm (°C)	E (%)	R ²
			Forward/Reverse				
Reference genes							
1	Actin (ACT)	E.crus-galli Scaffold50.371	F: CAAGGCTAACAGGGAGAAGATG	120	62	93.7	0.97
			R: TCCACTGGCATACAAGGAAAG				
2	RNA polymerase II (RP II)	E.crus-galli mRNA	F: TGTTGTGAGGAAGGAAGCTG	110	62	95.4	0.98
			R: GTGGCATTGTATGGCTCAAC				
3	Tubulin- <i>a</i> (<i>a</i> -TUB)	E.frumentacea mRNA Scaffold2.684	F: CCATACAACAGTGTCTCTCTAC	96	62	110.1	0.97
			R: CCTCCGGCATATGTCATAGATT				
4	Tubulin-β (β-TUB)	E.crus-galli Scaffold3.941	F: TCCGTATTCCCATCACCAAAG	116	62	102.4	0.99
			R: GCTTCATTGTCAAGCACCATAC				
5	Elongation factor -1 <i>a</i> (EF-1 <i>a</i>)	E.crus-galli Scaffold8.559	F: AGGCCCGTTATGATGAGATTG	97	62	102.1	0.99
			R: AAACCAGAGATTGGGACGAAG				
6	Adenine phosphoribosyltransferase (APRT)	E.crus-galli Scaffold29.598	F: TGGTGGAACACTATGTGCAG	97	62	100.7	0.98
			R: GCCCTTCAATTCTGGCAATTC				
7	TATA-Binding Protein (TBP)-Like Factor (TLF)	E.crus-galli Scaffold89.132	F: GCTACCTGCAAGAGAGGATTT	101	62	105.6	0.99
			R: AGCATGGGCCACAACCTTAT				
8	Ubiquitin-conjugating enzyme 2 (UBC2)	E.frumentacea mRNA GWHTBDNQ043355	F: CTTCTATTCAGTCCCTGCTGTG	95	62	99.4	0.99
			R: GTTGTACTCCCGCTTGTCT				
9	Ubiquitin-conjugating enzyme E2 5 (UBC5)	E.frumentacea mRNA GWHTBDNQ048013	F: CCTTGCACAAATACCTCGTAATG	101	62	105.2	0.98
			R: GCGGAGAGTCCTGATTTCTTAG				
10	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	E.frumentacea mRNA GWHTBDNQ085699	F: TGAAGGATTGGAGAGGAGGA	103	62	91.2	0.99
			R: TTTCCGTTCAAGCTCAGGTAAG				
Target gene							
1	Cu/Zn-binding superoxide dismutase (SOD1)	E.frumentacea mRNA GWHTBDNQ090839	F: GGACCACATTTCAACCCAAAC	117	62	106.3	0.99
			R: AATGGTTGCCTCAGCTACTC				

Supplementary Table s3. Cq values of reference gene under time intervals of varied stress treatment

Treatment	Post duration hours	Replicates	<i>ACT</i>	<i>RP II</i>	<i>α-TUB</i>	<i>β-TUB</i>	<i>EF-1a</i>	<i>APRT</i>	<i>TLF</i>	<i>UBC2</i>	<i>UBC5</i>	<i>GAPDH</i>
PEG 6000	0'	RI	31.6	24.2	24.4	24.4	24.0	22.7	23.1	20.0	26.6	26.6
		RII	31.5	24.3	24.3	24.6	24.0	23.3	23.0	20.0	26.5	26.7
		RIII	31.5	24.2	25.0	24.2	23.8	22.8	23.1	20.1	26.6	26.4
	12'	RI	34.2	26.3	26.8	25.1	30.6	26.0	28.1	20.3	28.3	27.2
		RII	34.2	26.5	26.0	26.3	30.8	26.1	28.1	20.8	28.7	27.1
		RIII	34.2	26.0	26.2	26.6	30.4	25.8	28.4	20.1	28.1	27.2
	24'	RI	31.5	26.5	26.5	32.1	28.1	25.6	29.4	20.0	28.5	25.7
		RII	31.4	26.5	26.6	32.0	28.1	25.5	29.1	20.0	28.4	25.6
		RIII	31.6	26.6	26.3	32.0	28.1	25.3	29.5	20.0	28.3	25.6
	36'	RI	34.0	24.5	24.2	33.0	30.9	26.6	32.1	19.3	27.0	26.5
		RII	34.4	23.5	23.9	32.9	30.6	26.6	30.5	19.2	27.8	26.5
		RIII	33.7	24.1	24.4	32.5	30.6	26.5	31.4	19.3	27.2	26.4
	48'	RI	34.2	25.1	25.1	32.0	30.0	26.1	30.5	20.0	28.1	26.1
		RII	33.8	24.4	24.9	32.2	30.5	26.4	30.1	19.8	28.0	26.7
		RIII	34.1	24.5	25.4	33.1	30.8	27.1	31.0	20.1	28.2	26.3
NaCl 250mM	0'	RI	31.5	24.2	24.4	24.4	24.0	23.0	23.1	20.0	26.6	26.6
		RII	31.6	24.3	24.5	24.6	23.9	22.8	23.0	20.0	26.8	26.7
		RIII	31.4	24.2	24.4	26.5	24.2	23.7	23.0	20.0	26.4	26.4
	12'	RI	32.7	24.9	25.2	29.2	26.4	25.1	27.4	18.9	26.1	26.6
		RII	32.4	25.1	25.2	29.4	26.6	25.2	27.9	19.2	26.4	26.5
		RIII	33.2	24.8	25.3	28.7	26.1	25	26.9	19.5	26.3	26.7
	24'	RI	32.4	26.5	26.2	28.7	26.5	24.8	28.1	19.4	27.4	27.4
		RII	32.6	26.5	26.4	28.4	26.9	24.5	28.1	19.2	27.7	27.4
		RIII	32.7	26.6	26.1	28.2	26.1	24.9	28.0	19.2	27.3	27.5
	36'	RI	30.0	26.2	25.2	28.3	25.8	22.9	26.9	18.7	26.1	26.9
		RII	29.1	26.1	25.2	28.1	25.7	22.9	26.5	18.3	26.5	26.7
		RIII	29.8	26.3	25.1	28.4	25.5	22	26.2	18.3	25.8	27.0

	48'	RI	31.0	26.0	25.8	28.7	26.1	24.1	27.2	18.7	26.2	27.4
		RII	31.1	26.2	25.3	28.5	26.1	24.8	27.1	19.2	26.1	27.2
		RIII	31.4	26.1	25.9	28.5	26.6	24.3	27	18.3	26.3	27.1
Cold	0'	RI	31.5	24.8	24.4	24.4	23.9	23.2	23.1	20.0	27.6	26.6
		RII	31.6	24.3	24.3	24.6	24.0	23.0	23.0	20.0	27.8	26.7
		RIII	31.5	24.3	24.6	24.2	23.8	22.8	23.1	20.1	27.0	26.4
	12'	RI	30.3	27.1	26.2	28.0	27.0	23.0	28.1	19.8	28.4	27.5
		RII	29.8	26.6	26.4	28.6	27.0	23.6	28.2	19.3	28.4	27.2
		RIII	30.5	27.9	26.0	28.1	27.0	23.0	28.2	19.7	28.6	27.7
	24'	RI	30.5	27.8	27.8	28.1	25.9	23.8	27.0	20.7	30.0	29.0
		RII	30.7	27.7	26.1	28.2	25.7	23.2	26.5	20.8	31.0	29.0
		RIII	30.3	28.0	27.0	28.0	25.1	24.0	27.4	20.4	30.4	30.0
	36'	RI	28.8	27.2	24.2	27.5	25.0	23.1	28.8	19.8	29.0	27.2
		RII	28.9	26.9	24.7	27.6	25.3	23.2	28.6	19.6	29.2	27.1
		RIII	28.8	27.3	23.9	27.4	25.0	23.2	28.8	19.9	29.2	27.4
	48'	RI	30.1	27.4	25.4	27.8	25.8	23.5	27.5	19.9	29.4	27.5
		RII	29.8	28.1	24.6	27.5	24.9	23.10	27.40	19.7	29.0	27.1
		RIII	29.7	27.0	25.0	27.6	25.0	24.00	26.80	20.0	29.0	27.3
Hot	0'	RI	31.5	24.2	24.4	24.4	23.8	22.9	23.1	20.0	26.6	26.6
		RII	31.4	24.3	24.4	24.6	23.8	23.2	23.0	20.0	26.8	27.1
		RIII	31.6	24.2	24.3	24.2	24.0	24.0	23.0	20.4	26.4	26.0
	12'	RI	31.5	22.9	26.1	29.5	25.4	24.0	27.1	18.9	27.3	27.2
		RII	31.7	22.8	26.2	29.2	25.4	24.1	27.0	18.6	27.6	27.8
		RIII	31.4	23.1	26.2	28.6	25.5	24.0	27.1	19.0	27.1	28.0
	24'	RI	33.3	24.2	28.2	29.1	25.8	25.5	27.0	20.0	27.6	27.2
		RII	33.2	24.1	27.8	29.1	25.4	25.1	26.4	19.8	27.2	27.4
		RIII	32.8	24.1	28.6	28.5	25.7	25.8	26.1	20.2	27.6	26.7
	36'	RI	31.7	23.3	24.9	26.1	23.6	23.9	24.0	19.3	25.4	25.3
		RII	31.7	23.4	25.1	26.1	23.9	24.0	24.0	19.2	25.6	26.4
		RIII	30.6	23.1	25.0	26.1	23.4	23.8	24.1	19.3	26.5	26.7

	48'	RI	31.9	23.7	25.2	27.1	25.4	24.2	25.1	20.0	26.1	27.1
		RII	30.7	23.1	24.8	26.3	25.3	24.8	24.8	20.2	26.6	26.7
		RIII	30.6	23.4	25.0	26.6	24.8	24.0	24.1	20.0	25.3	27.0