

Additional file 1: Table S1

Name	Type of gene	Amplification efficiency [%]	Tm [°C]	Forward primer sequence	Reverse primer sequence	Reference
<i>ACT1</i>	Constitutive	105	57	GGTGCTCCCTGCTGTATGAA	AGGCAACACGTTACACCAGT	Sekhon <i>et al.</i> (2011)
<i>GPA1</i>	Constitutive	82	58	GGCGTTAATGCCGACCAGTA	TAGGAGTGGGTGGTGGTCAT	Sekhon <i>et al.</i> (2011)
<i>TUB</i>	Constitutive	80	57	ATCTATGACATCTGCCGCCG	GGAGCGTAGGACGAAAGCAT	Sekhon <i>et al.</i> (2011)
<i>EF1A</i>	Constitutive	82	57	AAGTATGCGTGGGTGCTTGA	GGTCTCGAACTTCCACAGGG	Sekhon <i>et al.</i> (2011)
<i>MEP</i>	Constitutive	106	57	GCCAAGATCTTCTGCTGGGT	GAACGAGAAGGAACAGCCCA	Manoli <i>et al.</i> (2012)
<i>FGP1</i>	Constitutive	97	58	AGTGATACGCCGCTCGAAAT	GGCACCAATAAGCAAGCACC	Manoli <i>et al.</i> (2012)
<i>UBI</i>	Constitutive	85	58	CCCATGGATGGTGCTGTCTT	GCGGTCGCACGATAGTTTTG	Sekhon <i>et al.</i> (2011)
<i>LUG</i>	Constitutive	107	58	AGTGCTACAGGGAAGGTTGC	TCATGTGCGTCATGTGGTCA	Manoli <i>et al.</i> (2012)
<i>CUL</i>	Constitutive	92	57	GCAGGAAGATTGCCATCCCA	ACCTTGCCTGATTGGTGGTT	Manoli <i>et al.</i> (2012)
<i>UCE</i>	Constitutive	104	57	CCGACAGGGCCAAGTATGAG	CCGGCACATTACACAGTTTG	Sekhon <i>et al.</i> (2011)
<i>ICE1</i>	Candidate	91	57	CAACCCATCAACACCGAC	GCAAAGCCATTGAAGCAG	Hu <i>et al.</i> (2011)
<i>DREB1</i>	Candidate	117	57	CCAGCGGTAGTTGTTGAC	TGTTCCCGTTACATTCGT	Hu <i>et al.</i> (2011)
<i>CDKA1</i>	Candidate	107	57	CTGCCCCGGAGTTTGCTAAGA	CGCAACACCGTGAGTATCT	Rymen <i>et al.</i> (2007)
<i>CYCA3</i>	Candidate	103	57	ACCAGGCATTCTCTTGCTGT	CACGAGTAAAGTATCCACGCA	Rymen <i>et al.</i> (2007)
<i>KRP1</i>	Candidate	96	57	CGTCGTACGGGGAGAACAT	GTGGACCCAGGAGTGCTAGT	Rymen <i>et al.</i> (2007)
<i>EXPA4</i>	Candidate	101	57	TGTGTTAGAGGGTGGTGGGT	AGGACCTGGACCTGGGATTA	Muller <i>et al.</i> (2007)
<i>EXPB2</i>	Candidate	97	57	ATACTACGGCGGAACGGAAC	CCAAGAGACGCCTCAACCTT	Muller <i>et al.</i> (2007)
<i>GGR</i>	Candidate	111	58	ATCGACTGGATTCTGACGCC	AACCAGAACGGGGGAGTTTC	Tanaka <i>et al.</i> (1999)
<i>CAB1</i>	Candidate	91	57	AGAACCTCGCTGACCACATC	AGACACACATGCATCTCGCA	Caffarri <i>et al.</i> (2005)
<i>psbS</i>	Candidate	104	57	GGGATCGGTTTCACCAAGGA	CCGGTAATGGCCTCTCCAAG	Reviewed in Baker (2008)
<i>VDE</i>	Candidate	102	57	AGTGGCTTAAACCCGACGTT	TGCGGACTCTCCATGTGATG	Reviewed in Baker (2008)

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<i>PEPC</i>	Candidate	98	57	CGAAGAGCTCCACAGTTCGT	GCTTGTCCCTTACATGGCCT	Naidu <i>et al.</i> (2003)
<i>PPDK</i>	Candidate	108	57	CTTTCATGGCCTGGGTGGAT	CCTTGTGCCCCATTGTTTCG	Naidu <i>et al.</i> (2003)
<i>rbcS</i>	Candidate	105	57	AGTAGCTAGTGCCATGCGTC	CAAGCAAGCAAAGGGTACGG	Naidu <i>et al.</i> (2003)