

Table S8. Genes and primers for qRT-PCR in CK assays

			<i>Arabidopsis thaliana</i> best hits (BlastP) ¹				
Gene	Name	Primer pairs (5'>3')	Subject	Description	ID%	Pos%	E-value
<i>STMlike1</i>	<i>Prupe.3G212100</i>	Fw: GAAGTGGGTCTCCAGAAGAGGTTG Bw: GCTTCTGAGCTTCCGATGGATAGG	AT1G62360.1	STM SHOOT MERISTEMLESS	66	78	2.00E-107
<i>STMlike2</i>	<i>Prupe.4G015200</i>	Fw: GCAAGTACAGTGGATATCTGGGCAGT Bw: CAGAGCAATGTGCGAGAGATATC	AT1G62360.1	STM SHOOT MERISTEMLESS	83	89	9.00E-140
<i>KNOPE1</i>	<i>Prupe.1G416700</i>	Fw: GCTTGGCAACAATAATGCTCCTCC Bw: TCCAAGCCTGTCGACTCCGC	AT4G08150.1	KNAT1, BP KNOTTED-like from <i>Arabidopsis thaliana</i> , BREVIPEDI-CELLUS	66	79	1.00E-118
<i>KNOPE2</i>	<i>Prupe.1G249600</i>	Fw: CCTTCCGTGGGGAGCATC Bw: GGGTTCCTAATGGAGGAGGCG	AT1G23380.1	KNAT6 KNOTTED1-like homeobox gene 6	62	76	2.00E-130
<i>KNOPE2.1</i>	<i>Prupe.5G171100</i>	Fw: CGGATGCTGCTTCGGCTGTG Bw: CGTGCTCTTCGCCTGTTCTGTG	AT1G23380.1	KNAT6 KNOTTED1-like homeobox gene 6	60	68	4.00E-90
<i>KNOPE6</i>	<i>Prupe.6G312900</i>	Fw: ATGCTCTTGTTCAAACGGAGGG Bw: AGTCCAGCTGGTTTTTGGG	AT1G23380.1	KNAT6 KNOTTED1-like homeobox gene 6	56	70	3.00E-76
<i>KNOPE3</i>	<i>Prupe.1G486200</i>	Fw: GGATGAATGGAGAAAAGGAAACG Bw: GGAACCATGTCTCAGGTCATTG	AT5G25220.1	KNAT3 KNOTTED1-like homeobox gene	72	79	0.00E+00
<i>KNOPE4</i>	<i>Prupe.7G254700</i>	Fw: CTCTCTCTCTTTCTCTCAGC Bw: GCCATTACTTTGGTCTTTGC	AT5G11060.1	KNAT4 KNOTTED1-like homeobox gene 4	81	88	1.00E-149
<i>KNOPE7</i>	<i>Prupe.5G088100</i>	Fw: GCGCAAACTTCTGGTGACACTACTAC Bw: ACCGCCAAGGTACAAAAACAGC	AT1G62990.1	KNAT7 KNOTTED-like homeobox of <i>Arabidopsis thaliana</i> 7	85	91	9.00E-171
<i>KNOPEM</i>	<i>Prupe.5G236700</i>	Fw: GCTCACTTGGATTGTTTGAAGGTCG Bw: CGTTTGCTGCGGTTCTCTCCA	AT1G14760.2	KNATM KNOX <i>Arabidopsis thaliana</i> meinox	45	60	7.00E-21
<i>PpBEL1</i>	<i>Prupe.5G104600</i>	Fw: CAATGGTGGAGGCGTGTGCG Bw: ATTGAGCAGTGTTTCGCCTATCC	AT5G41410.1	BEL1, BELL 1	52	65	6.00E-142
<i>PpBLH1</i>	<i>Prupe.7G094300</i>	Fw: GCAGCAGGCAAGATTGAAGG Bw: GAAAAGCCAAGCACGAAGTACG	AT2G35940.3	BLH1 BEL1-like homeodomain 1	51	62	9.00E-168
<i>PpBLH2</i>	<i>Prupe.7G146900</i>	Fw: GCACAACTCCAACGCCTACA Bw: TCCTCGGAAGCCAGCCTATC	AT4G36870.2	SAW1, BLH2 BEL1-like homeodomain 2	82	90	4.00E-142
<i>PpBLH3</i>	<i>Prupe.1G373600</i>	Fw: ACAAGGTGGCTGGGAACGG Bw: TGAATATGCCCTCTGCTGTCTGA	AT1G75410.2	BLH3 BEL1-like homeodomain 3	49	63	9.00E-96
<i>PpBLH5</i>	<i>Prupe.6G144900</i>	Fw: TCCGCCTCCAACAACCCA Bw: TCACGCTCGGCAGGAAATG	AT2G35940.3	BLH1 BEL1-like homeodomain 1	43	56	3.00E-142
<i>PpBLH6</i>	<i>Prupe.8G089800</i>	Fw: TCTGAGAACGCACCTCAAACG Bw: CCTAAACACGCAGTCCAAAGC	AT4G34610.4	BLH6 BEL1-like homeodomain 6	65	73	8.00E-120
<i>PpBLH8</i>	<i>Prupe.6G105100</i>	Fw: TGGTTCATAAACCGCAGATGCG Bw: CCCCATCAGTCCACCGTCC	AT2G27990.1	BLH8, PNF BEL1-like homeodomain 8	42	54	3.00E-89
<i>PpCAT1</i>	<i>Prupe.5G011300</i>	Fw: CCATGAGATTGCGAGCGTTTG Bw: CCATAATCCCAATGACAATCCG	AT1G20630.1	CAT1 catalase 1	88	95	0.00E+00
<i>PpCAT2</i>	<i>Prupe.5G011400</i>	Fw: TCATCAGTAAGGCAGGGAAAGTACAC Bw: TGGGCAGGGTTAAACGCAAG	AT4G35090.2	CAT2 catalase 2	84	94	0.00E+00
<i>PpCKX6</i>	<i>Prupe.2G026700</i>	Fw: TATTGGTGGTACTCTGTCTAATGCTGG Bw: ATGATGCCAAACTGACCAAGCC	AT3G63440.1	CKX6 cytokinin oxidase/dehydrogenase 6	69	83	0.00E+00
<i>PpARR12</i>	<i>Prupe.1G391400</i>	Fw: GATTACCTGCTAAAACCGTCCG Bw: ATTTCCCGTGCCCGCTGA	AT2G25180.1	ARR12 response regulator 12	61	73	4.00E-130
<i>PpHK1</i>	<i>Prupe.7G170700</i>	Fw: CCTGTCACGGGTGAGAAGATAGGA Bw: GTAACACCCACAACAGCCACTATGC	AT2G17820.1	HK1 histidine kinase 1	66	79	0.00E+00
<i>PpRPII</i>	<i>Prupe.8G132000</i>	Fw: GGTCAAAATCCGTGAAATGCG Bw: GGATGAGTCCGAGCCTGTGGG	AT2G15430.1	NRPB3 Non-catalytic subunit of nuclear DNA-dependent RNA polymerases II, IV and V	81	92	0.00E+00

1, BlastP analysis against TAIR protein db. The percentages of identical residues (ID%), and of conservative substitutions (Pos%) were also reported.