The *Citrus* ABA-signalosome: Identification and transcriptional regulation during sweet orange fruit ripening and leaf dehydration

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Supplementary Material

Table S1. Colour evolution (*a/b* ratio) of ‘Navelate’ and ‘Pinalate’ fruits during ripening.

		***a/b* ratio**	
	Month	**Navelate**	**Pinalate**
Immature green (IG)	July	-0.89 ± 0.01	-0.89 ± 0.01
Mature green I (MI)	September	-0.72 ± 0.01	-0.72 ± 0.01
Mature green II (MII)	October	-0.41 ± 0.01	-0.50 ± 0.01
Breaker (Bk)	October	-0.13 ± 0.01	-0.31 ± 0.01
Coloured (C)	November	0.49 ± 0.01	0.10 ± 0.01
Full coloured (FC)	February	0.63 ± 0.01	0.12 ± 0.01

Values are mean of three replicates ± SD.

Table S2. Primers designed for gene expression analyses by quantitative RT-PCR (qRT-PCR).

***Citrus* gene**	**Homologous in *A. thaliana***	**Forward / Reverse**	**Sequence 5' → 3'**	**Amplicon size (bp)**
CsPYR1	AT4G17870;	F	CCGGGGTAACTCAGGACGAG	198
	Pyrabactin Resistance 1	R	CGGAGACGGAACAGCTCTTG	
CsPYL2	AT2G26040;	F	GGCCTATCATCGAAAGATACC	209
	PYR1-Like protein 2	R	CGATACAACCGTCACTTCTC	
CsPYL4	AT2G38310;	F	CGAACGAAGACACCTGCGTG	168
	PYR1-Like protein 4	R	CGAGAACAGAACATGACCTG	
CsPYL5	AT5G05440;	F	GCCCGGCGGTACATCACAAA	184
	PYR1-Like protein 5	R	GCCCGCAGCTAACAGCACG	
CsPYL8	AT4G27920;	F	GCGGTGCATTTTGGACGCTTC	111
	PYR1-Like protein 8	R	GGCAAAGCCTTAGCAGAATCG	
CsPYL9	AT1G01360;	F	CGGAGATCATCGACGGGAGA	166
	PYR1-Like protein 9	R	CGGTCCTGCACCGCCATCC	
CsABI1	AT4G26080;	F	GGTGACTGCAAAAGCACGAT	129
	ABA-insensitive 1	R	GGGGCAACAGGTTCACCTCC	
CsAHG1	AT5G51760;	F	CGGGTAATGCGAATGCGGG	170
	ABA-hypersensitive germination 1	R	CCCAACGCTCCCACACGCGCACG	
CsAHG3	AT3G11410;	F	GGGATGACTTCAGTTTGCGGTA	227
	ABA-hypersensitive germination 3	R	CGGAGCTCTTCACTTTAATGGC	
CsHAB1	AT1G72770;	F	CCGGAGTGTCTTCGAGGTGG	173
	Hypersensitive to ABA 1	R	GGCCATTCAAACAGTGGCTC	
CsHAI3	AT5G59220;	F	GCCCCTGGCGGCCACTCC	245
	Highly ABA-induced 3	R	GGCCCACACATATAGAAACC	
CsSnRK2.2	AT3G50500;	F	CTGTTCCAGACACTAATCCA	165
	SNF1-related protein kinase 2.2	R	GGCTACTCATAGTCTTTTCATCC	
CsSnRK2.6	AT4G33950;	F	GAGCCAAAGAACTTCCGCAA	139
	SNF1-related protein kinase 2.6	R	GGGTTTCGGATCTCGGGTAT	
CsALDH3	AT1G44170;	F	GGAGTGAGGAGGAGACGAAGA	188
	Aldehyde Dehydrogenase 3 H1	R	ACGAAGAGCGTCGACGATGTC	
CsHVA22E	AT5G50720;	F	GCGGCATGGCTGGTTCTGC	178
	Abscisic acid induced-like protein	R	GCCTCGTGCTCCCCTTTCTT	
CsACT	AT5G09810;	F	TTAACCCCAAGGCCAACAGA	176
	Actin7. Structural constituent	R	TCCCTCATAGATTGGTACAGTATGAGA	
CsGAPDH	AT1G13440;	F	CGTCCCTCTGCAAGATGACTCT	204
	Glyceraldehyde-3P dehydrogenase	R	GGAAGGTCAAGATCGGAATCAA	
CsTUB	AT1G75780;	F	GCATCTTGAACCCGGTAC	158
	Tubulin1. Structural constituent	R	ATCAATTCGGCGCCTTCAG	

Table S3. Similarity matrix between *Citrus* and *Arabidopsis* PYR/PYL/RCAR proteins based on deduced amino acid and sequences alignment.

	AtPYR1	**AtPYL1**	**AtPYL2**	**AtPYL3**	**AtPYL4**	**AtPYL5**	**AtPYL6**	**AtPYL7**	**AtPYL8**	**AtPYL9**	**AtPYL10**	**AtPYL11**	**AtPYL12**	**AtPYL13**	**CsPYR1**	**CsPYL2**	**CsPYL4**	**CsPYL5**	**CsPYL8**	**CsPYL9**
AtPYR1	100																			
AtPYL1	77.50	100																		
AtPYL2	39.00	35.80	100																	
AtPYL3	35.20	31.70	56.50	100																
AtPYL4	51.40	44.00	39.20	31.10	100															
AtPYL5	39.70	33.20	36.40	28.70	45.40	100														
AtPYL6	46.90	42.00	37.60	27.00	57.20	40.90	100													
AtPYL7	31.10	30.70	27.80	27.20	31.70	31.20	29.80	100												
AtPYL8	42.10	41.00	31.70	30.20	48.40	37.10	41.70	41.80	100											
AtPYL9	30.00	28.90	31.30	28.70	32.00	32.70	30.10	81.30	44.00	100										
AtPYL10	40.80	39.60	32.60	27.70	47.70	34.70	42.90	39.80	70.30	42.00	100									
AtPYL11	36.40	36.50	38.80	30.10	39.50	38.50	39.70	36.30	33.60	36.30	35.30	100								
AtPYL12	36.80	34.40	37.30	29.20	37.70	39.20	38.70	34.50	32.50	34.50	32.90	81.10	100							
AtPYL13	36.20	32.50	32.70	27.80	34.00	33.60	36.40	34.70	29.30	34.70	32.50	63.10	66.00	100						
CsPYR1	73.40	65.20	37.00	34.00	48.20	33.50	43.50	32.60	43.90	33.50	43.40	37.50	36.20	33.80	100					
CsPYL2	43.00	38.50	66.70	63.60	41.30	39.40	36.10	32.00	37.80	33.00	34.30	39.70	39.20	36.10	43.30	100				
CsPYL4	50.80	45.60	36.80	29.10	68.30	46.00	56.70	29.40	47.80	31.90	43.30	41.10	39.30	36.90	46.60	39.30	100			
CsPYL5	52.10	46.90	41.30	34.40	65.50	46.20	55.20	36.00	45.50	36.20	44.80	43.60	40.00	37.60	47.40	46.40	68.70	100		
CsPYL8	29.00	28.80	30.10	26.50	31.70	29.70	28.30	37.30	52.70	45.20	48.50	34.20	33.10	32.20	29.90	32.10	29.70	32.40	100	
CsPYL9	32.00	32.90	35.20	31.70	38.40	33.30	32.30	45.20	50.30	52.40	47.90	37.90	35.30	34.10	37.10	38.40	32.80	37.00	80.00	100

Table S4. Similarity matrix between *Citrus* and *Arabidopsis* clade-A PP2C proteins based on deduced amino acid and sequences alignment.

	AtABI1	**AtABI2**	**AtAHG1**	**AtAHG3**	**AtHAB1**	**AtHAB2**	**AtHAI1**	**AtHAI2**	**AtHAI3**	**CsABI1**	**CsAHG1**	**CsAHG3**	**CsHAB1**	**CsHAI3**
AtABI1	100													
AtABI2	79.30	100												
AtAHG1	39.00	37.60	100											
AtAHG3	44.30	47.80	43.30	100										
AtHAB1	45.50	52.20	36.70	36.80	100									
AtHAB2	51.40	57.30	39.50	41.40	71.30	100								
AtHAI1	40.50	45.10	39.60	55.70	37.10	39.70	100							
AtHAI2	42.00	44.50	38.60	55.30	37.80	39.70	59.10	100						
AtHAI3	46.20	46.30	43.10	59.80	40.40	42.40	66.60	66.50	100					
CsABI1	54.20	58.70	39.50	40.80	43.70	50.40	40.40	39.80	42.70	100				
CsAHG1	40.80	45.30	41.90	65.20	36.20	40.60	52.60	53.40	61.40	40.80	100			
CsAHG3	40.50	45.30	41.80	65.30	36.60	41.10	52.80	53.40	61.40	41.00	97.80	100		
CsHAB1	53.90	58.20	40.70	38.80	55.10	58.50	40.20	37.70	42.90	61.00	39.50	39.90	100	
CsHAI3	42.50	42.40	37.90	60.10	41.10	40.90	63.60	55.20	64.70	40.70	57.70	57.70	40.80	100

Table S5. Similarity matrix between *Citrus* and *Arabidopsis* subclass III SnRK2 proteins based on deduced amino acid and sequences alignment.

	AtSnRK2.2	**AtSnRK2.3**	**AtSnRK2.6**	**CsSnRK2.2**	**CsSnRK2.6**
AtSnRK2.2	100				
AtSnRK2.3	88.40	100			
AtSnRK2.6	74.40	75.50	100		
CsSnRK2.2	81.50	79.40	78.10	100	
CsSnRK2.6	74.70	85.30	88.90	82.00	100

Table S6. Absolute gene expression analysis by qRT-PCR of the ABA-signalosome components in 'Navelate' and 'Pinalate' varieties during fruit ripening and leaf dehydration. Values correspond to number of copies of each gene per μg of total RNA. Values are means of three biological replicates for each sampling period and variety.

			PYR/PYL/RCAR						**PP2CA**					**SnRK2**	
		Ripening Stage	**PYR1**	**PYL2**	**PYL4**	**PYL5**	**PYL8**	**PYL9**	**ABI1**	**AHG1**	**AHG3**	**HAB1**	**HAI3**	**SnRK2.2**	**SnRK2.6**
Fruit	**Navelate**	**IG**	9	n.d.	1566	1101	24	12757	692	267	3976	8714	806	16256	139325
		M1	11	n.d.	710	1239	16	7274	410	205	3897	5415	1385	2172	48701
		M2	12	n.d.	1548	2167	20	10136	452	227	5780	5649	386	993	10790
		BK	5	n.d.	656	772	22	7393	910	515	5805	6409	4217	1329	21883
		C	5	n.d.	691	440	17	7035	1755	685	14247	8034	8474	975	18380
		FC	10	n.d.	1386	1777	16	4633	517	455	7029	4707	2473	1362	17485
	Pinalate	**IG**	16	n.d.	1289	1313	23	16294	951	627	3005	8842	1081	9523	114626
		M1	10	n.d.	827	1323	17	7921	448	190	2590	6018	1000	2338	45145
		M2	12	n.d.	1271	2240	18	7959	293	211	3756	5669	570	2553	25048
		BK	7	n.d.	228	754	19	5599	724	153	5041	5424	3150	2823	73697
		C	5	n.d.	636	236	17	4575	1246	1170	7237	4482	6083	992	27681
		FC	15	n.d.	1694	2461	17	3890	278	243	2784	3253	1191	878	13993
		Time (h)	**PYR1**	**PYL2**	**PYL4**	**PYL5**	**PYL8**	**PYL9**	**ABI1**	**AHG1**	**AHG3**	**HAB1**	**HAI3**	**SnRK2.2**	**SnRK2.6**
Leaf	**Navelate Control**	**0**	2	14285	n.d.	60	n.d.	9701	941	78	5792	10897	1404	2081	89249
		0.5	3	15739	n.d.	19	n.d.	5438	994	74	5303	5543	2617	3188	80093
		1	3	26296	n.d.	34	n.d.	23444	1265	147	21048	12786	1721	7058	88636
		3	5	6959	n.d.	19	n.d.	17770	12915	575	17871	6708	8004	7915	226187
		6	7	9551	n.d.	7	n.d.	9128	14860	993	23212	32122	31092	7614	280793
		24	6	12976	n.d.	12	n.d.	7536	9828	273	27177	15686	7099	2477	173883
	Navelate Dehydrated	**0.5**	4	9502	n.d.	10	n.d.	5471	1303	159	7421	8349	2041	10075	116749
		1	3	13953	n.d.	20	n.d.	6409	1941	333	18297	6591	4435	1767	123039
		3	4	9016	n.d.	13	n.d.	10582	27461	1177	45915	11233	24000	3520	197336
		6	6	2834	n.d.	2	n.d.	11275	24788	1636	39621	10851	30651	5186	385560
		24	3	4713	n.d.	2	n.d.	4011	20881	1257	28182	13576	11416	2296	98070
	Pinalate Control	**0**	3	10088	n.d.	47	n.d.	7903	1225	84	8043	18094	1889	1658	91632
		0.5	5	6931	n.d.	19	n.d.	4243	757	60	6156	6784	2008	2464	106470
		1	5	43144	n.d.	36	n.d.	1548	4148	477	25649	35083	8803	5519	178654
		3	10	14910	n.d.	24	n.d.	20635	5914	329	10905	6800	9468	6457	361168
		6	11	5060	n.d.	8	n.d.	17515	15664	772	14101	15016	21672	6257	232467
		24	10	8800	n.d.	9	n.d.	9555	13371	300	21100	13213	21028	5650	166202
	Pinalate Dehydrated	**0.5**	3	8659	n.d.	18	n.d.	5579	858	87	4227	12878	3402	8018	153159
		1	5	6180	n.d.	32	n.d.	7428	961	104	9189	6770	1709	1934	106777
		3	9	9079	n.d.	14	n.d.	9139	24848	1262	26478	9791	26066	2160	377740
		6	10	3609	n.d.	2	n.d.	10084	26187	1470	31848	17913	24384	6420	236768
		24	4	5351	n.d.	1	n.d.	2968	23933	1359	26266	7678	27236	6948	302733

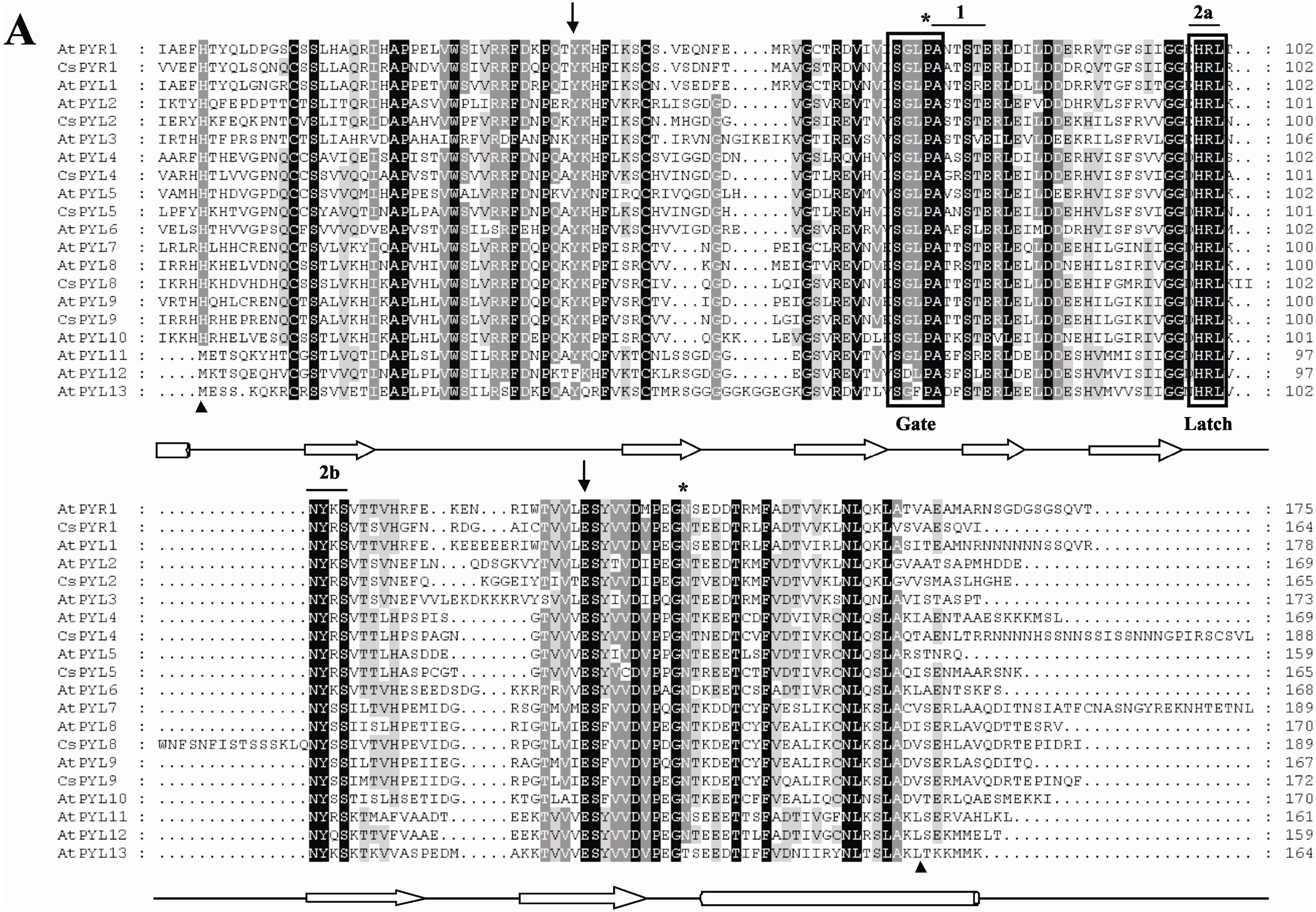
n.d. not detected

Supplemental Figure Legends

Figure S1. Multiple sequence alignment of the *Arabidopsis thaliana* and *Citrus sinensis* ABA signalling core components. (A) START-like domain of the ABA-receptors, delimited by black triangles below the alignment. ABA-binding sites are indicated by arrows and PP2Cs interaction sites by asterisks. Boxes indicate *Gate* and *Latch* loops. Horizontal lines (1 and 2) above the alignment delimit the two ABA-binding regions. Line 2 is divided in 2a and 2b due to the insertion of 17 amino acid residues in CsPYL8 protein. (B) PP2C-like domain of the clade-A PP2Cs proteins, delimited by black triangles below the alignment. Metal-binding sites are pointed out by asterisks and phosphatase activity regulatory sequences are underlined. (C) Subclass III SnRK2s full protein sequences. Black triangles below the alignment delimit protein kinase domain, asterisk indicate ATP binding site and plus symbol highlights the proton acceptor active site. Horizontal lines are numbered as follows: 1, ATP binding region; 2, activation loop; 3, osmotic stress response domain I; and 4, ABA response and ABI1 binding domain II. Predicted secondary structures of AtPYR1 (A), AtABI1 (B) and AtSnRK2.6 (C) are reported below the corresponding alignment with alpha-helices as tubes, beta-strands as arrows and coiled regions as lines, as estimated by PSIPRED software. Dots indicate gaps in the amino acid sequences when compared with others for obtaining optimal alignments. Amino acids are numbered to the right of each line. Identical residues are in black, highly conservative are in dark grey and less conserved are in light grey.

Figure S2. Predicted tertiary structure model of the ABA-signalosome components of *Citrus* by using the *Arabidopsis* available crystallographic structure of homologous proteins as templates in I-Tasser program (left). Overlay of the predicted structure with the corresponding *Arabidopsis* homologous (right). Query structures are shown in cartoon, while templates are displayed using purple trace. (A-D) PYR/PYL/RCAR ABA-receptors. (E) PP2CA. (F) SnRK2.

Figure S3. Gene expression analysis by RT-qPCR of *Citrus HVA22E* (upper panel) and *ALDH* (lower panel) in ‘Navelate’ (black) and ‘Pinalate’ (white) fruits during development and ripening stages (Immature Green, IG; Mature Green I, MI; Mature Green II, MII; Breaker, Bk; Coloured, C; Full Coloured, FC). Expression values are relative to transcript levels obtained in MI ‘Navelate’ fruits. Values are mean ratios ± SE from three biological samples for each sampling period and variety, and analyzed in duplicate. Significant differences ($p \leq 0.05$) in gene expression between ‘Navelate’ and ‘Pinalate’ flavedo samples for the same maturity stage are indicated by an asterisk.



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AtPYR1  : IAEFHTYQLDPGSCSSLHAQRIHAPPELVWSIVRRFDKPQTYKHFIKSCS.VEQNFE....MRVGCTRDVIVISGLPANTSTERLDILDDERRVTGFSIIGGEHRLT.. : 102
CsPYR1  : VVEFHTYQLSQNQCSSLLAQRIRAPNDVVWSIVRRFDQPQTYKHFIKSCS.VSDNFT....MAVGSTRDVNVISGLPAATSTERLDILDDDRQVTGFSIIGGEHRLR.. : 102
AtPYL1  : IAEFHTYQLGNGRCSSLLAQRIHAPPETVWSVVRRFDRPQIYKHFIKSCN.VSEDFE....MRVGCTRDVNVISGLPANTSRERLDLLDDDRRVTGFSITGGEHRLR.. : 102
AtPYL2  : IKTYHQFEPDPTTCTSLITQRIHAPASVVWPLIRRFDNPERYKHFVKRCRLISGDGD......VGSVREVTVISGLPASTSTERLEFVDDDHRVLSFRVVGGEHRLK.. : 101
CsPYL2  : IERYHKFEQKPNTCVSLITQRIDAPAHVVWPFVRRFDNPQKYKHFIKSCN.MHGDGG......VGSIREVTVVSGLPASTSTERLEILDDEKHILSFRVVGGEHRLN.. : 100
AtPYL3  : IRTHHTFPRSPNTCTSLIAHRVDAPAHAIWRFVRDFANPNKYKHFIKSCT.IRVNGNGIKEIKVGTIREVSVVSGLPASTSVEILEVLDEEKRILSFRVLGGEHRLN.. : 106
AtPYL4  : AARFHTHEVGPNQCCSAVIQEISAPISTVWSVVRRFDNPQAYKHFLKSCSVIGGDGDN.....VGSLRQVHVVSGLPAASSTERLDILDDERHVISFSVVGGDHRLS.. : 102
CsPYL4  : VARHHTLVVGPNQCCSSVVQQIAAPVSTVWSVVRRFDNPQAYKHFVKSCHVINGDGD......VGTLREVHVISGLPAGRSTERLEILDDERHVISFSVIGGDHRLA.. : 101
AtPYL5  : VAMHHTHDVGPDQCCSSVVQMIHAPPESVWALVRRFDNPKVYKNFIRQCRIVQGDGLH.....VGDLREVMVVSGLPAVSSTERLEILDEERHVISFSVVGGDHRLK.. : 102
CsPYL5  : LPFYHKHTVGPNQCCSYAVQTINAPLPAVWSVVRRFDNPQAYKHFLKSCHVINGDGH......VGTLREVHVISGLPAANSTERLEILDDEHHVLSFSVIGGDHRLN.. : 101
AtPYL6  : VELSHTHVVGPSQCFSVVVQDVEAPVSTVWSILSRFEHPQAYKHFVKSCHVVIGDGRE.....VGSVREVRVVSGLPAAFSLERLEIMDDDRHVISFSVVGGDHRLM.. : 102
AtPYL7  : LRLRHLHHCRENQCTSVLVKYIQAPVHLVWSLVRRFDQPQKYKPFISRCTV...NGD....PEIGCLREVNVKSGLPATTSTERLEQLDDEEHILGINIIGGDHRLK.. : 100
AtPYL8  : IRRHHKHELVDNQCSSTLVKHINAPVHIVWSLVRRFDQPQKYKPFISRCVV...KGN....MEIGTVREVDVKSGLPATRSTERLELLDDNEHILSIRIVGGDHRLK.. : 100
CsPYL8  : IKRHHKHDVHDHQCSSSLVKHIKAPVHLVWSLVRRFDQPQKYKPFVSRCIV...QGD....LQIGSVREVNVKSGLPATTSTERLELLDDEEHIFGMRIVGGDHRLKII : 102
AtPYL9  : VRTHHQHLCRENQCTSALVKHIKAPLHLVWSLVRRFDQPQKYKPFVSRCTV...IGD....PEIGSLREVNVKSGLPATTSTERLELLDDEEHILGIKIIGGDHRLK.. : 100
CsPYL9  : IRRHHRHEPRENQCTSALVKHIRAPVHLVWSLVRRFDQPQKYKPFVSRCVV...NGD....LGIGSVREVNVKSGLPATTSTERLELLDDEEHILGIKIVGGDHRLR.. : 100
AtPYL10 : IKKHHRHELVESQCSSTLVKHIKAPLHLVWSIVRRFDEPQKYKPFISRCVV...QGKK...LEVGSVREVDLKSGLPATKSTEVLEILDDNEHILGIRIVGGDHRLK.. : 101
AtPYL11 : ....METSQKYHTCGSTLVQTIDAPLSLVWSILRRFDNPQAYKQFVKTCNLSSGDGG......EGSVREVTVVSGLPAEFSRERLDELDDESHVMMISIIGGDHRLV.. :  97
AtPYL12 : ....MKTSQEQHVCGSTVVQTINAPLPLVWSILRRFDNPKTFKHFVKTCKLRSGDGG......EGSVREVTVVSDLPASFSLERLDELDDESHVMVISIIGGDHRLV.. :  97
AtPYL13 : ....MESS.KQKRCRSSVVETIEAPLPLVWSILRSFDKPQAYQRFVKSCTMRSGGGGKGGEGKGSVRDVTLVSGFPADFSTERLEELDDESHVMVVSIIGGNHRLV.. : 102

AtPYR1  : ...............NYKSVTTVHRFE..KEN...RIWTVVLESYVVDMPEGNSEDDTRMFADTVVKLNLQKLATVAEAMARNSGDGSGSQVT................ : 175
CsPYR1  : ...............NYRSVTSVHGFN..RDG...AICTVVLESYVVDVPEGNTEEDTRLFADTVVKLNLQKLVSVAESQVI.......................... : 164
AtPYL1  : ...............NYKSVTTVHRFE..KEEEEERIWTVVLESYVVDVPEGNSEEDTRLFADTVIRLNLQKLASITEAMNRNNNNNNSSQVR................ : 178
AtPYL2  : ...............NYKSVTSVNEFLN...QDSGKVYTVVLESYTVDIPEGNTEEDTKMFVDTVVKLNLQKLGVAATSAPMHDDE...................... : 169
CsPYL2  : ...............NYRSVTSVNEFQ.....KGGEIYTIVTESYVVDIPEGNTVEDTKMFVDTVVKLNLQKLGVVSMASLHGHE....................... : 165
AtPYL3  : ...............NYRSVTSVNEFVVLEKDKKKRVYSVVLESYIVDIPQGNTEEDTRMFVDTVVKSNLQNLAVISTASPT........................... : 173
AtPYL4  : ...............NYRSVTTLHPSPIS........GTVVVESYVVDVPPGNTKEETCDFVDVIVRCNLQSLAKIAENTAAESKKKMSL................... : 169
CsPYL4  : ...............NYRSVTTLHPSPAGN.......GTVVVESYVVDVPPGNTNEDTCVFVDTIVKCNLQSLAQTAENLTRRNNNNHSSNNSSISSNNNGPIRSCSVL : 188
AtPYL5  : ...............NYRSVTTLHASDDE........GTVVVESYIVDVPPGNTEEETLSFVDTIVRCNLQSLARSTNRQ............................. : 159
CsPYL5  : ...............NYRSVTTLHASPCGT.......GTVVVESYVCDVPPGNTREETCTFVDTIVRCNLQSLAQISENMAARSNK....................... : 165
AtPYL6  : ...............NYKSVTTVHESEEDSDG...KKRTRVVESYVVDVPAGNDKEETCSFADTIVRCNLQSLAKLAENTSKFS......................... : 168
AtPYL7  : ...............NYSSILTVHPEMIDG.....RSGTMVMESFVVDVPQGNTKDDTCYFVESLIKCNLKSLACVSERLAAQDITNSIATFCNASNGYREKNHTETNL : 189
AtPYL8  : ...............NYSSIISLHPETIEG.....RIGTLVIESFVVDVPEGNTKDETCYFVEALIKCNLKSLADISERLAVQDTTESRV................... : 170
CsPYL8  : WNFSNFISTSSSKLQNYSSIVTVHPEVIDG.....RPGTLVIESFVVDVPDGNTKDETCYFVEALIKCNLKSLADVSEHLAVQDRTEPIDRI................. : 189
AtPYL9  : ...............NYSSILTVHPEIIEG.....RAGTMVIESFVVDVPQGNTKDETCYFVEALIRCNLKSLADVSERLASQDITQ...................... : 167
CsPYL9  : ...............NYSSIMTVHPEIIDG.....RPGTLVIESFVVDVPEGNTKDETCYFVQALIRCNLKSLADVSERMAVQDRTEPINQF................. : 172
AtPYL10 : ...............NYSSTISLHSETIDG.....KTGTLAIESFVVDVPEGNTKEETCFFVEALIQCNLNSLADVTERLQAESMEKKI.................... : 170
AtPYL11 : ...............NYRSKTMAFVAADT......EEKTVVVESYVVDVPEGNSEEETTSFADTIVGFNLKSLAKLSERVAHLKL........................ : 161
AtPYL12 : ...............NYQSKTTVFVAAE.......EEKTVVVESYVVDVPEGNTEEETTLFADTIVGCNLRSLAKLSEKMMELT......................... : 159
AtPYL13 : ...............NYKSKTKVVASPEDM.....AKKTVVVESYVVDVPEGTSEEDTIFFVDNIIRYNLTSLAKLTKKMMK........................... : 164
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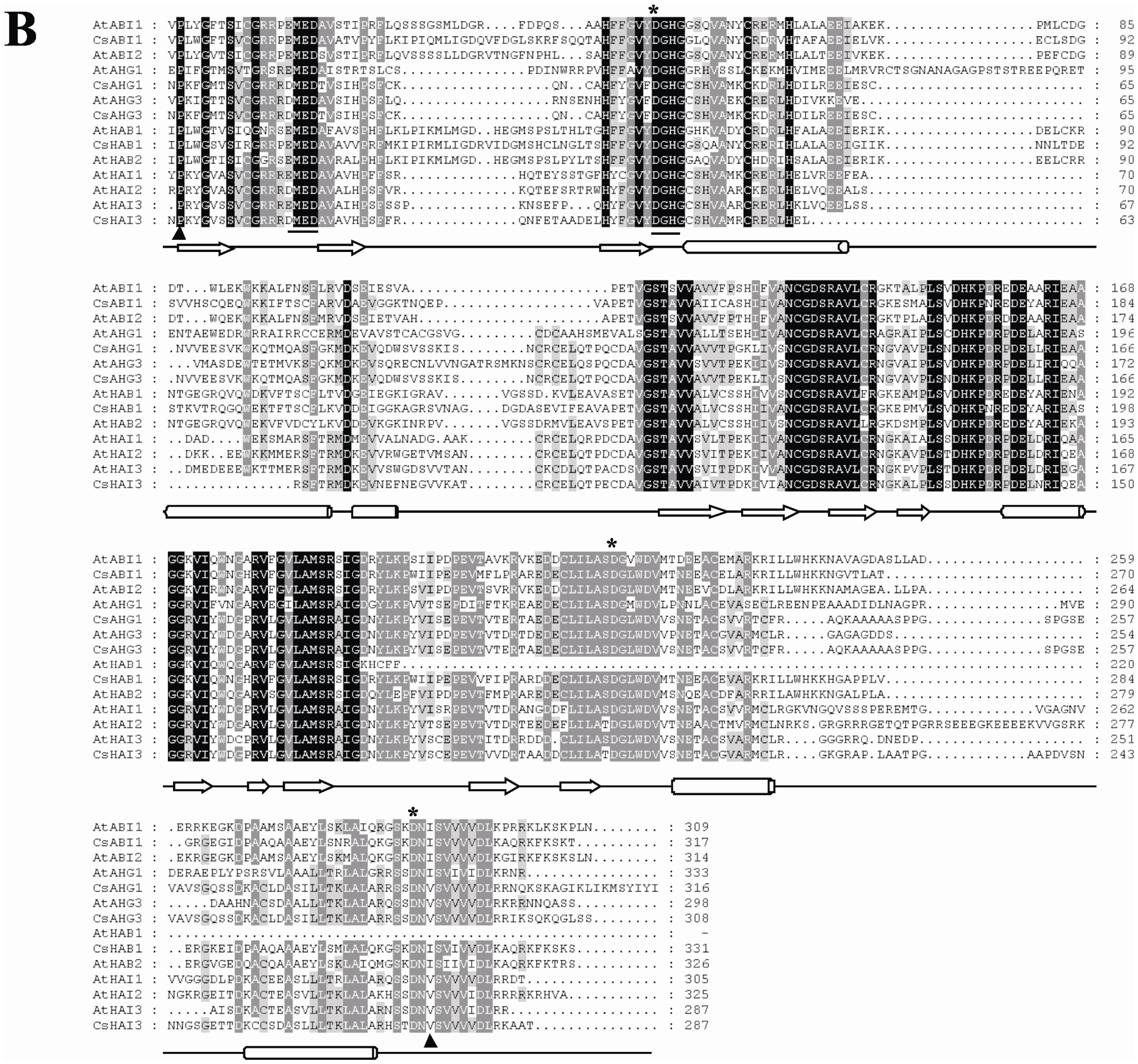
Figure S1A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AtABI1 : VPLYGFTSICGRRPEMEDAVSTIPRFLQSSSGSMLDGR....FDPQS...AAHFFGVYDGHGGSQVANYCRERMHLALAEEIAKEK.................PMLCDG : 85
CsABI1 : VPLWGFTSVCGRRPEMEDAVATVPYFLKIPIQMLIGDQVFDGLSKRFSQQTAHFFGVYDGHGGLQVANYCRDRVHTAFAEEIELVK.................ECLSDG : 92
AtABI2 : VPLYGVTSICGRRPEMEDSVSTIPRFLQVSSSSLLDGRVTNGFNPHL...SAHFFGVYDGHGGSQVANYCRERMHLALTEEIVKEK.................PEFCDG : 89
AtAHG1 : EPIFGTMSVTGRSREMEDAISTRTSLCS...............PDINWRRPVHFFAVYDGHGGRHVSSLCKEKMHVIMEEELMRVRCTSGNANAGAGPSTSTREEPQRET : 95
CsAHG1 : NEKFGMTSVCGRRRDMEDTVSIHPSFCK..................QN..CAHFYGVFDGHGCSHVAMKCKDRLHDILREEIESC........................ : 65
AtAHG3 : NEKIGTTSVCGRRRDMEDAVSIHPSFLQ.................RNSENHHFYGVFDGHGCSHVAEKCRERLHDIVKKEVE......................... : 65
CsAHG3 : NEKFGMTSVCGRRRDMEDTVSIHPSFCK..................QN..CAHFYGVFDGHGCSHVAMKCKDRLHDILREEIESC........................ : 65
AtHAB1 : IPLWGTVSIQGNRSEMEDAFAVSPHFLKLPIKMLMGD..HEGMSPSLTHLTGHFFGVYDGHGGHKVADYCRDRLHFALAEEIERIK.................DELCKR : 90
CsHAB1 : IPLWGSVSIRGRRPEMEDAVAVVPRFMKIPIRMLIGDRVIDGMSHCLNGLTSHFFGVYDGHGGSQAANYCRERIHLALAEEIGIIK.................NNLTDE : 92
AtHAB2 : IPLWGTISICGGRSEMEDAVRALPHFLKIPIKMLMGD..HEGMSPSLPYLTSHFFGVYDGHGGAQVADYCHDRIHSALAEEIERIK.................EELCRR : 90
AtHAI1 : YPKYGVASVCGRRREMEDAVAVHPFFSR.............HQTEYSSTGFHYCGVYDGHGCSHVAMKCRERLHELVREEFEA........................ : 70
AtHAI2 : RPRYGVASVCGRRRDMEDAVALHPSFVR.............KQTEFSRTRWHYFGVYDGHGCSHVAARCKERLHELVQEEALS........................ : 70
AtHAI3 : .PRYGVSSVCGRRREMEDAVAIHPSFSSP............KNSEFP...QHYFGVYDGHGCSHVAARCRERLHKLVQEELSS........................ : 67
CsHAI3 : NPKYGVSSVCGRRRDMEDAVAVHPSFR.............QNFETAADELHYFGVYDGHGCSHVAMRCRERLHEL............................... : 63
AtABI1 : DT...WLEKWKKALFNSFLRVDSEIESVA.......................PETVGSTSVVAVVFPSHIFVANCGDSRAVLCRGKTALPLSVDHKPDREDEAARIEAA : 168
CsABI1 : SVVHSCQEQWKKIFTSCFARVDAEVGGKTNQEP.................VAPETVGSTAVVAIICASHIIVANCGDSRAVLCRGKESMALSVDHKPNREDEYARIEAA : 184
AtABI2 : DT...WQEKWKKALFNSFMRVDSEIETVAH.....................APETVGSTSVVAVVFPTHIFVANCGDSRAVLCRGKTPLALSVDHKPDRDDEAARIEAA : 174
AtAHG1 : ENTAEWEDRWRRAIRRCCERMDEVAVSTCACGSVG.........CDCAAHSMEVALSGSTAVVALLTSEHIIVANCGDSRAVLCRAGRAIPLSCDHKPDRPDELARIEAS : 196
CsAHG1 : .NVVEESVKKTKQTMQASFGKMDKEVQDWSVSSKIS........NCRCELQTPQCDAVGSTAVVAVVTPGKLIVSNCGDSRAVLCRNGVAVPLSNDHKPDRPDELLRIEAA : 166
AtAHG3 : ...VMASDEMTETMVKSFQKMDKEVSQRECNLVVNGATRSMKNSCRCELQSPQCDAVGSTAVVSVVTPEKIIVSNCGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQQA : 172
CsAHG3 : .NVVEESVKKTKQTMQASFGKMDKEVQDWSVSSKIS........NCRCELQTPQCDAVGSTAVVAVVTPEKLIVSNCGDSRAVLCRNGVAVPLSNDHKPDRPDELLRIEAA : 166
AtHAB1 : NTGEGRQVQWDKVFTSCFLTVDGEIEGKIGRAV.......VGSSD.KVLEAVASETVGSTAVVALVCSSHIVVSNCGDSRAVLFRGKEAMPLSVDHKPDREDEYARIENA : 192
CsHAB1 : STKVTRQGQWEKTFTSCFLKVDDEIGGKAGRSVNAG....DGDASEVIFEAVAPETVGSTAVVALVCSSHIIVANCGDSRAVLCRGKEPMVLSVDHKPNREDEYARIEAS : 198
AtHAB2 : NTGEGRQVQWEKVFVDCYLKVDDEVKGKINRPV.......VGSSDRMVLEAVSPETVGSTAVVALVCSSHIIVSNCGDSRAVLLRGKDSMPLSVDHKPDREDEYARIEKA : 193
AtHAI1 : ..DAD....WEKSMARSFTRMDMEVVALNADG.AAK........CRCELQRPDCDAVGSTAVVSVLTPEKIIVANCGDSRAVLCRNGKAIALSSDHKPDRPDELDRIQAA : 165
AtHAI2 : ..DKK..EEWKKMMERSFTRMDKEVVRWGETVMSAN........CRCELQTPDCDAVGSTAVVSVITPEKIIVANCGDSRAVLCRNGKAVPLSTDHKPDRPDELDRIQEA : 168
AtHAI3 : ..DMEDEEEWKTTMERSFTRMDKEVVSWGDSVVTAN........CKCDLQTPACDSVGSTAVVSVITPDKIVVANCGDSRAVLCRNGKPVPLSTDHKPDRPDELDRIEGA : 167
CsHAI3 : ...............RSFTRMDKEVNEFNEGVVKAT........CRCELQTPECDAVGSTAVVAIVTPDKIVIANCGDSRAVLCRNGKALPLSSDHKPDRPDELNRIQEA : 150
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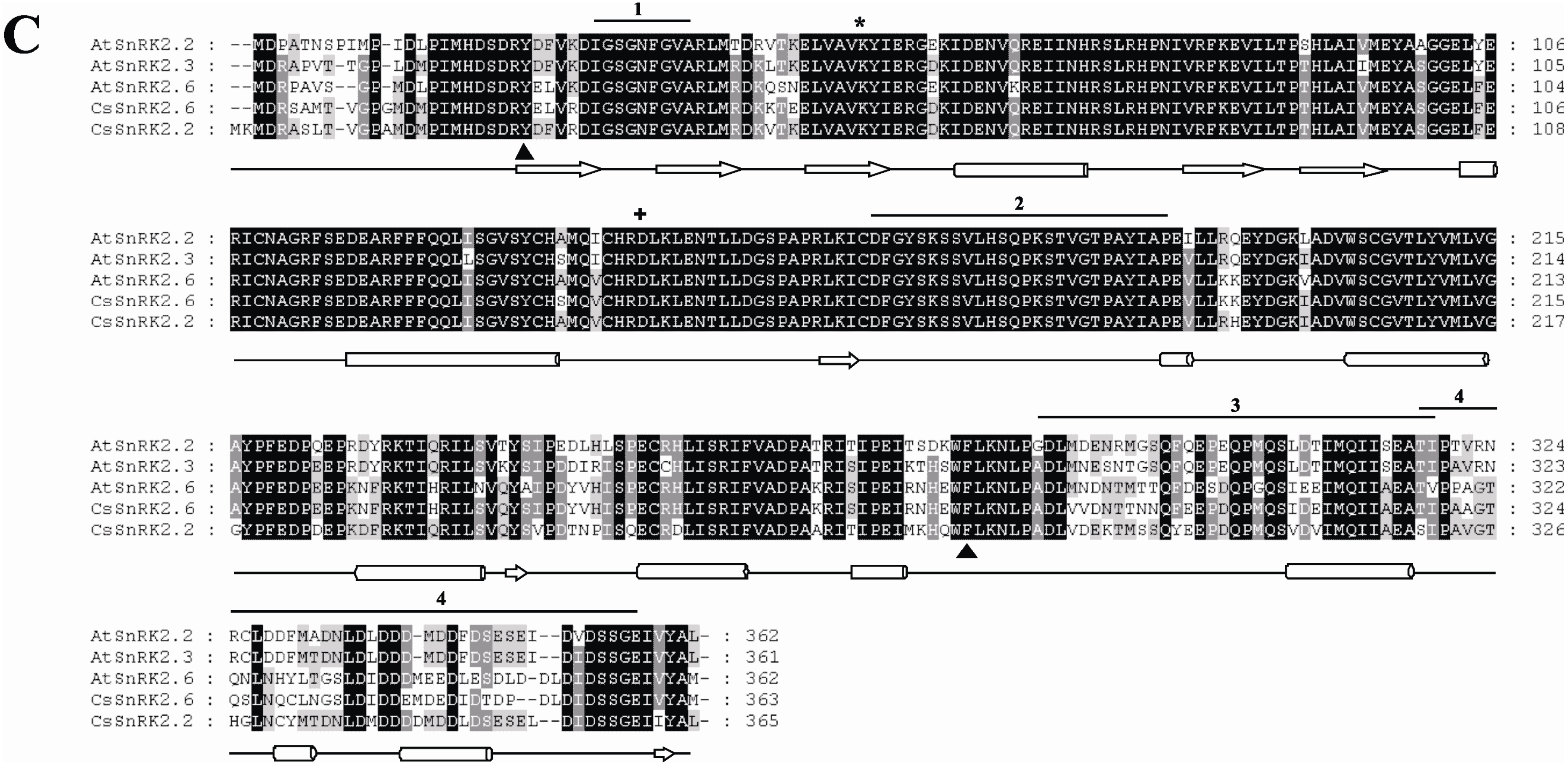
AtABI1 : GGKVIQWNGARVFGVLAMSRSIGDRYLKPSIIPDPEVTAVKRVKEDDCLILASDGVWDVMTDEEACEMARKRILLWHKKNAVAGDASLLAD.................. : 259
CsABI1 : GGKVIQWNGHRVFGVLAMSRSIGDRYLKPWIIPEPEVMFLPRAREDECLILASDGLWDVMTNEEACELARKRILLWHKKNGVTLAT........................ : 270
AtABI2 : GGKVIRWNGARVFGVLAMSRSIGDRYLKPSVIPDPEVTSVRRVKEDDCLILASDGLWDVMTNEEVCDLARKRILLWHKKNAMAGEA.LLPA.................. : 264
AtAHG1 : GGRVIFVNGARVEGILAMSRAIGDKYLKPVVTSEPDITFTKREAEDECLILASDGMWDVLPNNLACEVASECLREENPEAAADIDLNAGPR...............MVE : 290
CsAHG1 : GGRVIYWDGPRVLGVLAMSRAIGDNYLKPYVISEPEVTVTERTAEDECLILASDGLWDVVSNETACSVVRTCFR.....AQKAAAAASPPG.............SPGSE : 257
AtAHG3 : GGRVIYWDGARVLGVLAMSRAIGDNYLKPYVIPDPEVTVTDRTDEDECLILASDGLWDVVPNETACGVARMCLR.....GAGAGDDS....................... : 254
CsAHG3 : GGRVIYWDGPRVLGVLAMSRAIGDNYLKPYVISEPEVTVTERTAEDECLILASDGLWDVVSNETACSVVRTCFR.....AQKAAAAASPPG.............SPGSE : 257
AtHAB1 : GGKVIQWQGARVFGVLAMSRSIGKHCFF... : 220
CsHAB1 : GGKVIQWNGHRVFGVLAMSRSIGDRYLKPWIIPEPEVVFIPRARDDECLILASDGLWDVMTNEEACEVARKRILLWHKKHGAPPLV........................ : 284
AtHAB2 : GGKVIQWQGARVSGVLAMSRSIGDQYLEPFVIPDPEVTFMPRAREDECLILASDGLWDVMSNQEACDFARRRILAWHKKNGALPLA.......................... : 279
AtHAI1 : GGRVIYWDGPRVLGVLAMSRAIGDNYLKPYVISRPEVTVTDRANGDDFLILASDGLWDVVSNETACSVVRMCLRGKVNGQVSSSPEREMTG............VGAGNV : 262
AtHAI2 : GGRVIYWDGARVLGVLAMSRAIGDNYLKPYVTSEPEVTVTDRTEEDEFLILATDGLWDVVTNEAACTMVRMCLNRKS.GRGRRRGETQTPGRRSEEEGKEEEEKVVGSRK : 277
AtHAI3 : GGRVIYWDCPRVLGVLAMSRAIGDNYLKPYVSCEPEVTITDRRDDD.CLILASDGLWDVVSNETACSVARMCLR...GGGRRQ.DNEDP................... : 251
CsHAI3 : GGRVIYWDGPRVLGVLAMSRAIGDNYLKPYVSCEPEVTVVDRTAADDCLILATDGLWDVVSNETACGVARMCLR....GKGRAP.LAATPG...........AAPDVSN : 243
*
AtABI1 : .ERRKEGKDPAAMSAAEYLSKLAIQRGSKDNISVVVVDLKPRRKLKSKPLN........ : 309
CsABI1 : ..GRGEGIDPAAQAAAEYLSNRALQKGSKDNISVVVVDLKAQRKFKSKT.......... : 317
AtABI2 : .EKRGEGKDPAAMSAAEYLSKMALQKGSKDNISVVVVDLKGIRKFKSKSLN........ : 314
AtAHG1 : DERAEPLYPSRSVLAAALLTRLALGRRSSDNISVIVIDLKRNR................ : 333
CsAHG1 : VAVSGQSSDKACLDASILLTKLALARRSSDNVSVVVVDLRRNQKSKAGIKLIKMSYIYI : 316
AtAHG3 : .....DAAHNACSDAALLLTKLALARQSSDNVSVVVVDLRKRRNNQASS.......... : 298
CsAHG3 : VAVSGQSSDKACLDASILLTKLALARRSSDNVSVVVVDLRRIKSQKQGLSS........ : 308
AtHAB1 : .... : -
CsHAB1 : ..ERGKEIDPAAQAAAEYLSMLALQKGSKDNISVIVVDLKAQRKFKSKS.......... : 331
AtHAB2 : ..ERGVGEDQACQAAAEYLSKLAIQMGSKDNISIIVIDLKAQRKFKTRS.......... : 326
AtHAI1 : VVGGGDLPDKACEEASLLLTRLALARQSSDNVSVVVVDLRRDT................ : 305
AtHAI2 : NGKRGEITDKACTEASVLLTKLALAKHSSDNVSVVVIDLRRRRKRHVA........... : 325
AtHAI3 : .....AISDKACTEASVLLTKLALARNSSDNVSVVVIDLRR.................. : 287
CsHAI3 : NNGSGETTDKCCSDASLLLTKLALARHSTDNVSVVVVDLRKAAT............... : 287

Figure S1B



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AtSnRK2.2 : --MDPATNSPIMP-IDLPIMHDSDRYDFVKDIGSGNFGVARLMTDRVTKELVAVKYIERGEKIDENVQREIINHRSLRHPNIVRFKEVILTPSHLAIVMEYAAGGELYE : 106
AtSnRK2.3 : --MDRAPVT-TGP-LDMPIMHDSDRYDFVKDIGSGNFGVARLMRDKLTKELVAVKYIERGDKIDENVQREIINHRSLRHPNIVRFKEVILTPTHLAIIMEYASGGELYE : 105
AtSnRK2.6 : --MDRPAVS--GP-MDLPIMHDSDRYELVKDIGSGNFGVARLMRDKQSNELVAVKYIERGEKIDENVKREIINHRSLRHPNIVRFKEVILTPTHLAIVMEYASGGELFE : 104
CsSnRK2.6 : --MDRSAMT-VGPGMDMPIMHDSDRYELVRDIGSGNFGVARLMRDKKTEELVAVKYIERGDKIDENVQREIINHRSLRHPNIVRFKEVILTPTHLAIVMEYASGGELFE : 106
CsSnRK2.2 : MKMDRASLT-VGPAMDMPIMHDSDRYDFVRDIGSGNFGVARLMRDKVTKELVAVKYIERGDKIDENVQREIINHRSLRHPNIVRFKEVILTPTHLAIVMEYASGGELFE : 108

AtSnRK2.2 : RICNAGRFSEDEARFFFQQLISGVSYCHAMQICHRDLKLENTLLDGSPAPRLKICDFGYSKSSVLHSQPKSTVGTPAYIAPEILLRQEYDGKLADVWSCGVTLYVMLVG : 215
AtSnRK2.3 : RICNAGRFSEDEARFFFQQLLSGVSYCHSMQICHRDLKLENTLLDGSPAPRLKICDFGYSKSSVLHSQPKSTVGTPAYIAPEVLLRQEYDGKIADVWSCGVTLYVMLVG : 214
AtSnRK2.6 : RICNAGRFSEDEARFFFQQLISGVSYCHAMQVCHRDLKLENTLLDGSPAPRLKICDFGYSKSSVLHSQPKSTVGTPAYIAPEVLLKKEYDGKVADVWSCGVTLYVMLVG : 213
CsSnRK2.6 : RICNAGRFSEDEARFFFQQLISGVSYCHSMQVCHRDLKLENTLLDGSPAPRLKICDFGYSKSSVLHSQPKSTVGTPAYIAPEVLLKKEYDGKIADVWSCGVTLYVMLVG : 215
CsSnRK2.2 : RICNAGRFSEDEARFFFQQLISGVSYCHAMQVCHRDLKLENTLLDGSPAPRLKICDFGYSKSSVLHSQPKSTVGTPAYIAPEVLLRHEYDGKIADVWSCGVTLYVMLVG : 217

AtSnRK2.2 : AYPFEDPQEPRDYRKTIQRILSVTYSIPEDLHLSPECRHLISRIFVADPATRITIPEITSDKWFLKNLPGDLMDENRMGSQFQEPEQPMQSLDTIMQIISEATIPTVRN : 324
AtSnRK2.3 : AYPFEDPEEPRDYRKTIQRILSVKYSIPDDIRISPECCHLISRIFVADPATRISIPEIKTHSWFLKNLPADLMNESNTGSQFQEPEQPMQSLDTIMQIISEATIPAVRN : 323
AtSnRK2.6 : AYPFEDPEEPKNFRKTIHRILNVQYAIPDYVHISPECRHLISRIFVADPAKRISIPEIRNHEWFLKNLPADLMNDNTMTTQFDESDQPGQSIEEIMQIIAEATVPPAGT : 322
CsSnRK2.6 : AYPFEDPEEPKNFRKTIHRILSVQYSIPDYVHISPECRHLISRIFVADPAKRISIPEIRNHEWFLKNLPADLVVDNTTNNQFEEPDQPMQSIDEIMQIIAEATIPAAGT : 324
CsSnRK2.2 : GYPFEDPDEPKDFRKTIQRILSVQYSVPDTNPISQECRDLISRIFVADPAARITIPEIMKHQWFLKNLPADLVDEKTMSSQYEEPDQPMQSVDVIMQIIAEASIPAVGT : 326

AtSnRK2.2 : RCLDDFMADNLDLDDD-MDDFDSESEI--DVDSSGEIVYAL- : 362
AtSnRK2.3 : RCLDDFMTDNLDLDDD-MDDFDSESEI--DIDSSGEIVYAL- : 361
AtSnRK2.6 : QNLNHYLTGSLDIDDDMEEDLESDLD-DLDIDSSGEIVYAM- : 362
CsSnRK2.6 : QSLNQCLNGSLDIDDEMDEDIDTDP--DLDIDSSGEIVYAM- : 363
CsSnRK2.2 : HGLNCYMTDNLDMDDDDMDDLDSESEL--DIDSSGEIIYAL- : 365
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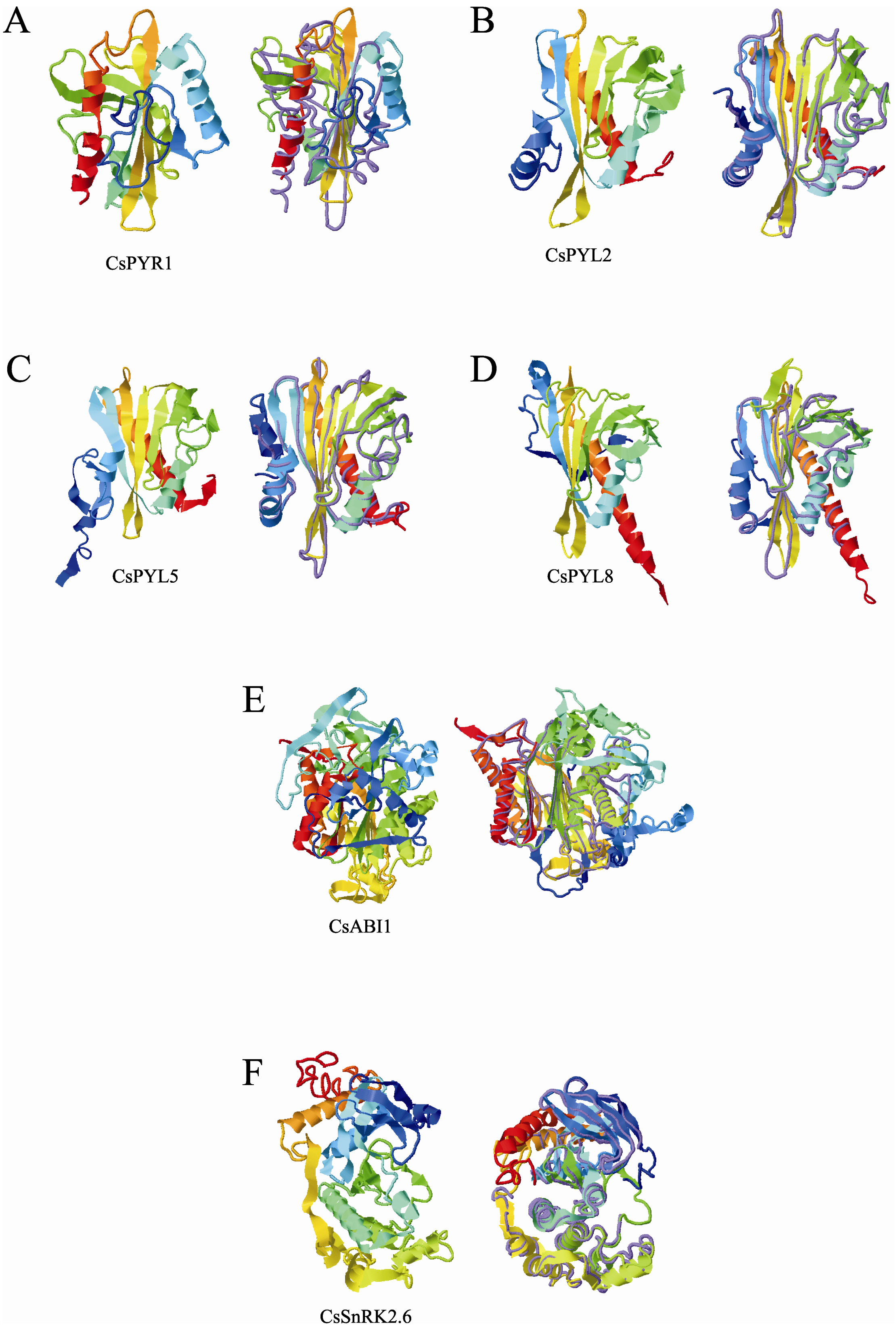
Figure S1C



CsPYR1

CsPYL2

CsPYL5

CsPYL8

CsABI1

CsSnRK2.6

Figure S2

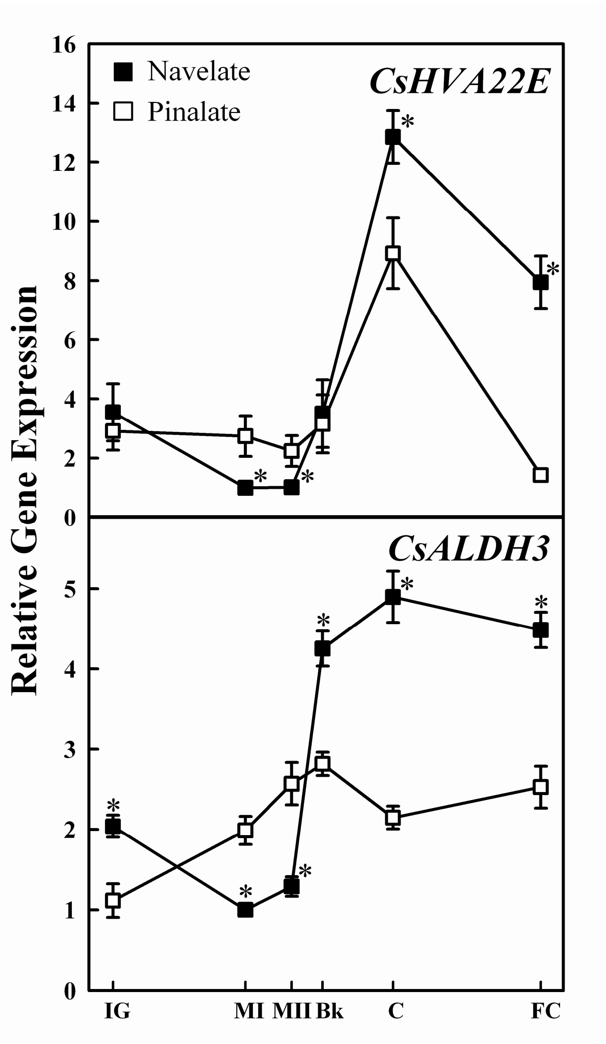

Relative Gene Expression
■ Navelate
□ Pinalate
CsHVA22E
CsALDH3
16
14
12
10
8
6
4
2
0
5
4
3
2
1
0
*
IG
MI
MII
Bk
C
FC

Figure S3