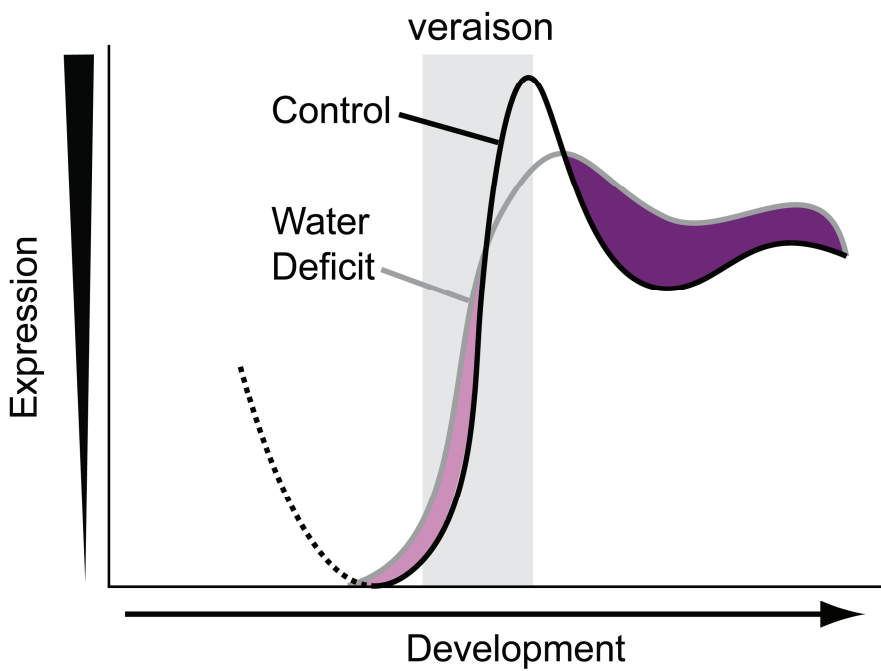
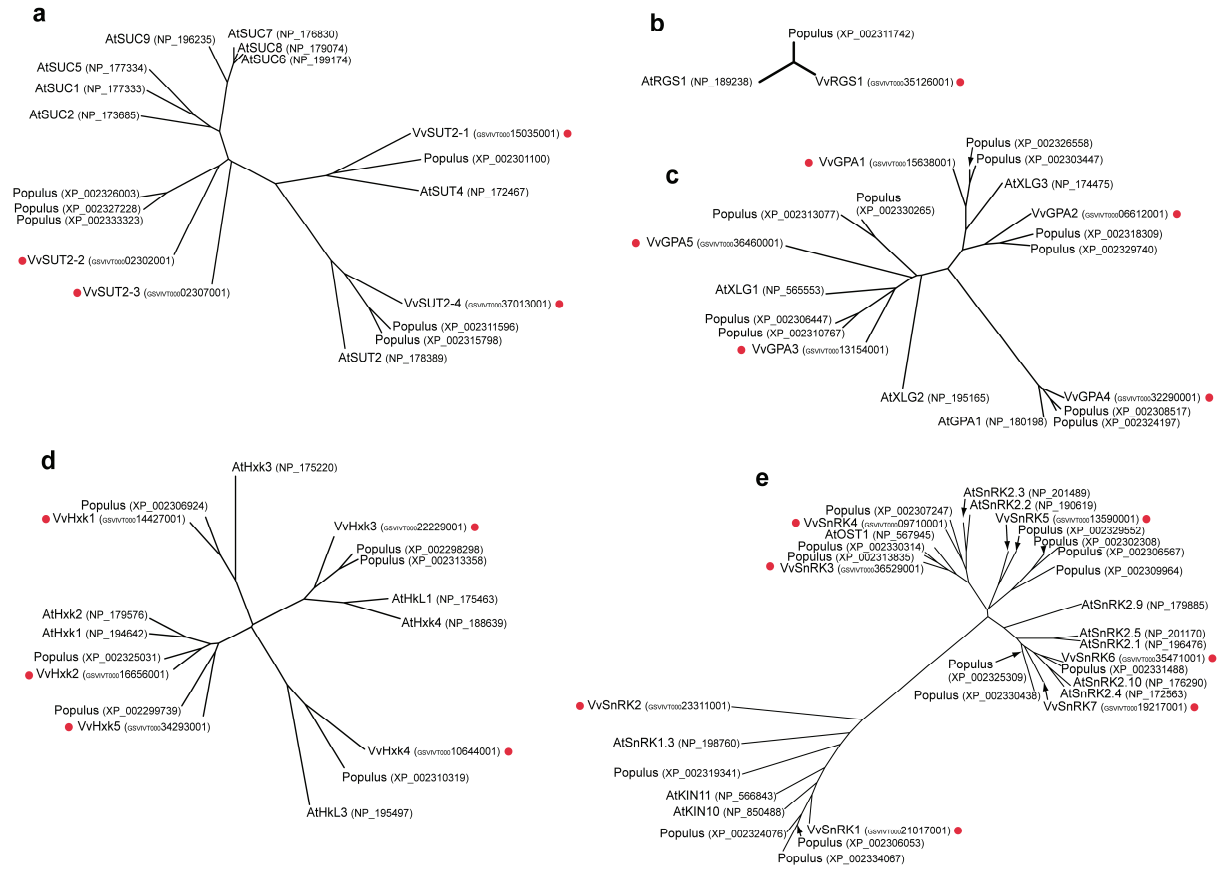


Supplemental Figures

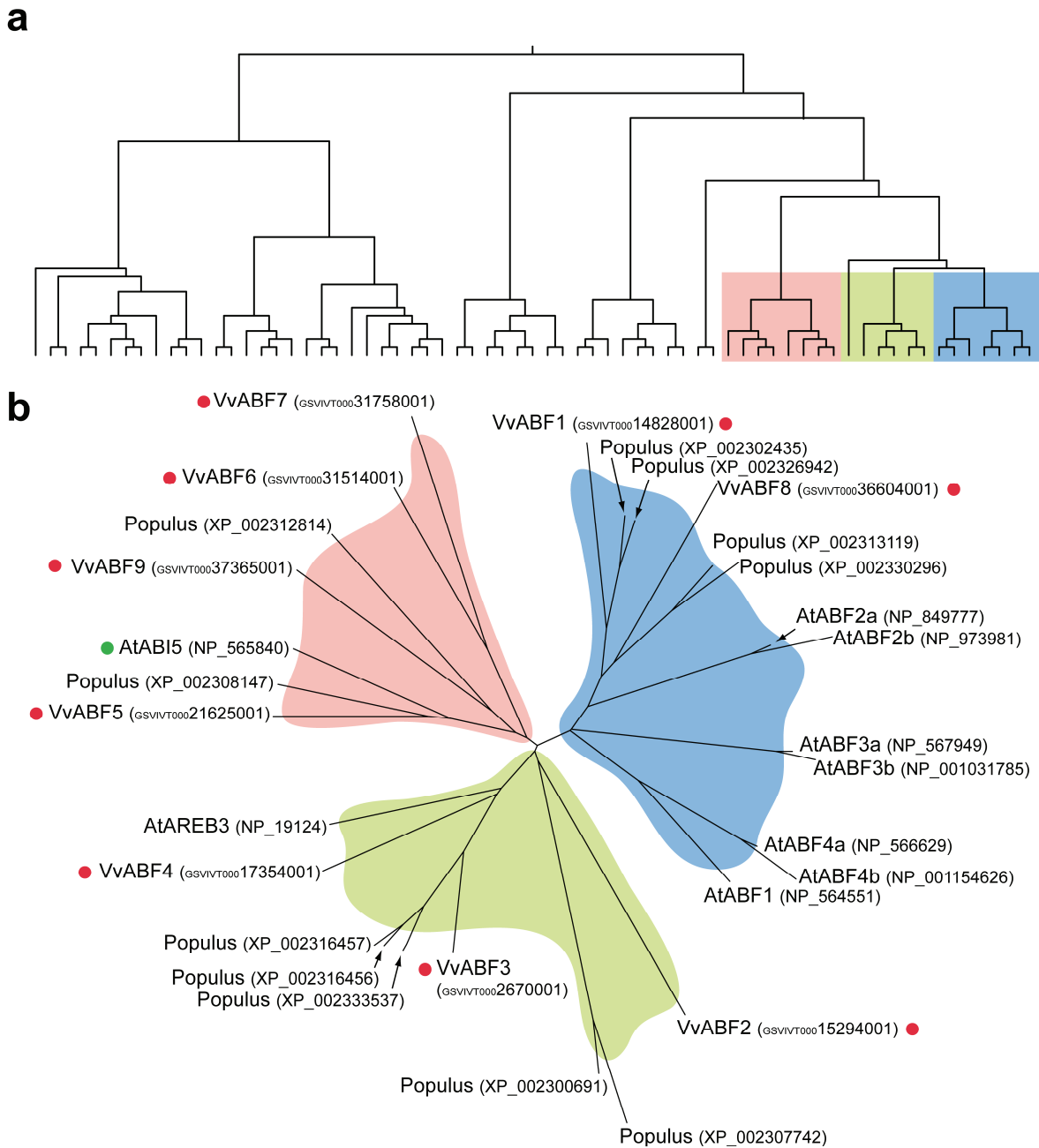


Suppl. Fig. 1 Characteristic changes in the expression of core flavonoid and anthocyanin specific genes in response to water deficit from Castellarin et al. 2007a

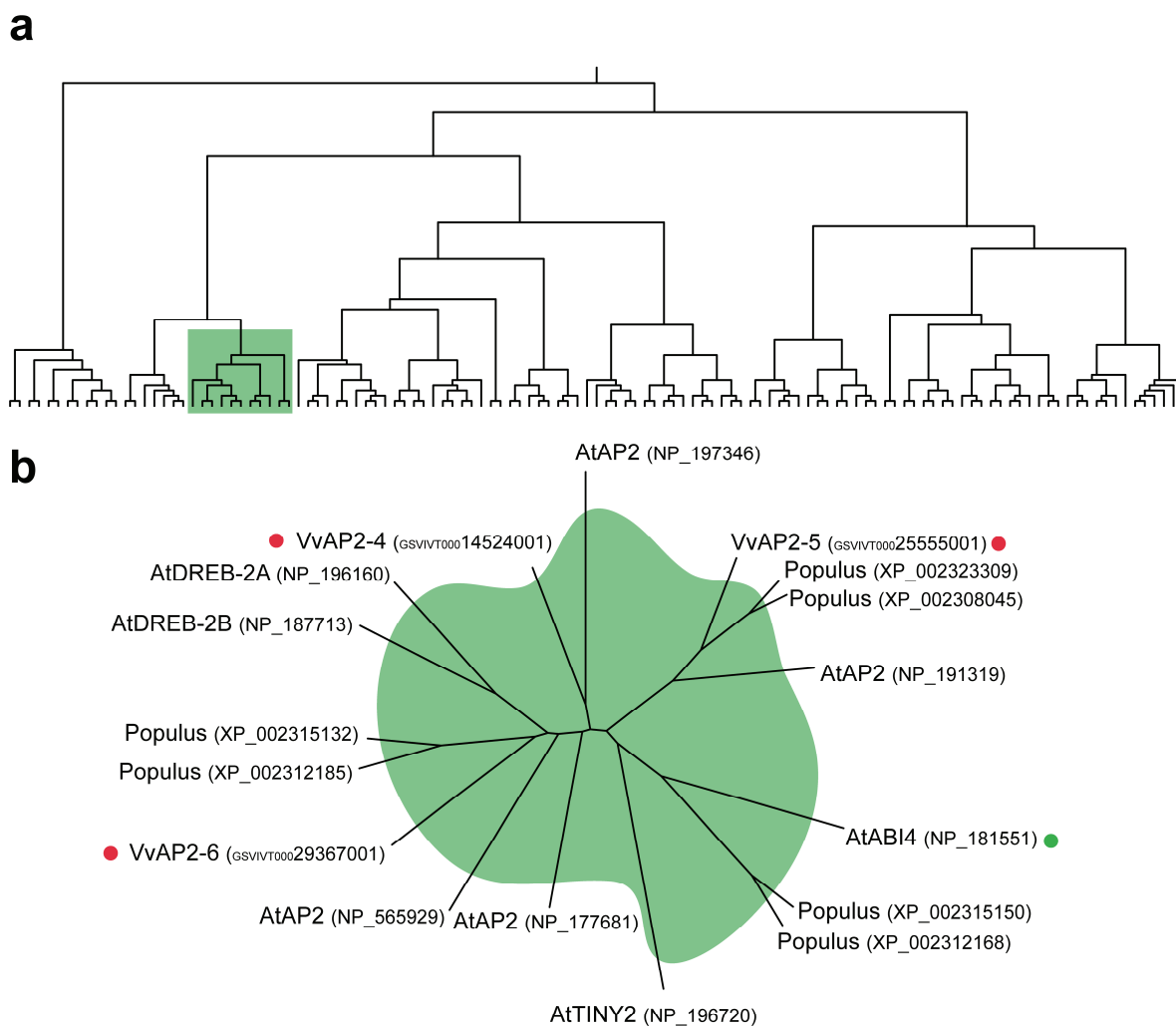
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Suppl. Fig. 2 Unrooted dendrograms of the SUC (a), RGS1 (b) and GPA1 (c), Hxk (d), and SnRK (e) protein families with *Vitis vinifera* (red dots), Arabidopsis, and *Populus trichocarpa* orthologs included. NCBI and *Vitis* Genoscope accessions are given



Suppl. Fig. 3 *Vitis vinifera* orthologs of the ABA related ABF transcription factors. **(a)** Rooted dendrogram of the entire Arabidopsis ABF family with nested grape orthologs. Sub-groups containing the ABA insensitive mutant *abi5* are colored. **(b)** Unrooted dendrogram of clustering *AtABI5* (green dot) and other *Vitis vinifera* (red dots), Arabidopsis, and *Populus trichocarpa* orthologs. NCBI and *Vitis* Genoscope accessions are given



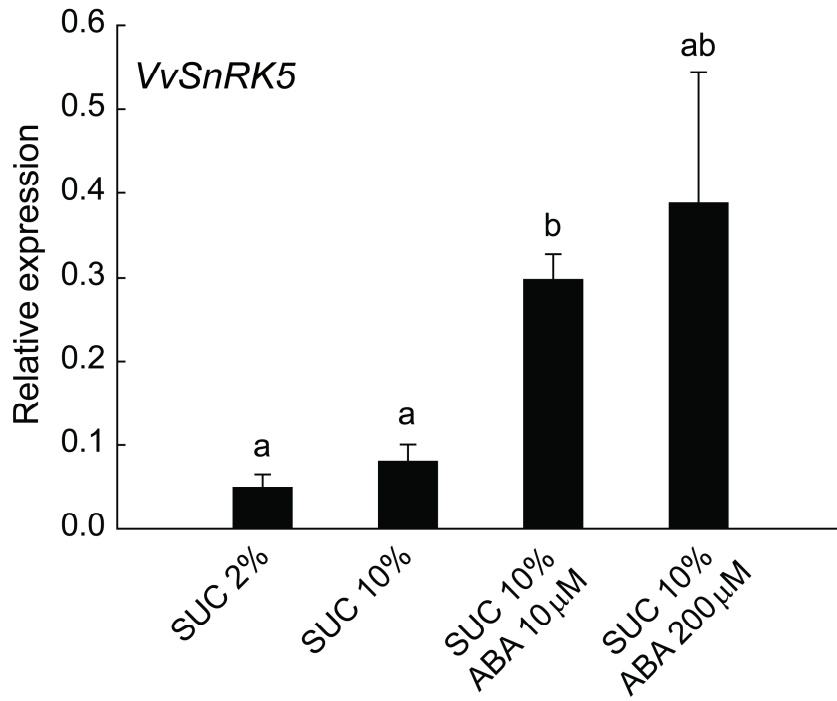
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Suppl. Fig. 4 *Vitis vinifera* orthologs of the ABA related AP2 transcription factors. **(a)** Rooted dendrogram of the entire Arabidopsis AP2 family with nested grape orthologs. Sub-group containing the ABA insensitive mutant *abi4* is colored. **(b)** Unrooted dendrogram of clustering AtABI4 (green dot) and other *Vitis vinifera* (red dots), Arabidopsis, and *Populus trichocarpa* orthologs. NCBI and *Vitis* Genoscope accessions are given



Suppl. Fig. 5 Exploding berries. 200 μM ABA alone and 2% sucrose + ABA treatments were not included in our analyses because of a phenomenon where the berries exploded reproducibly (shown here). Berries cultured on 2% sucrose + 200 μM ABA had average weight gains during the culture experiment of 45%, over double that of the healthy 2% sucrose controls

For Peer Review



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Suppl. Fig. 6 *VvSnRK5* expression in berry culture under various treatments. Values are means with bars representing SE. Different letters denote significant differences ($P < 0.05$; Tukey's HSD, $n = 3$)

Supplemental File 1

Expression (log₂ copies/ng RNA) of all genes during berry ripening in control (C) and water deficit (ED) treatments.

Family Number	Gene	Treatment	Developmental time [#]						P*
			I		II		III		
Stage	Description	Dates	33 DAA	57 DAA	OR green	OR red	81 DAA	123 DAA	
I	Prior to the onset of ripening	33 and 57 DAA							
II	OR, The Onset of Ripening (50% veraison)	C. 74 DAA; ED, 67 DAA							
III	After the onset of ripening	81 and 123 DAA							
1	Sut2-1	C	7.22	6.10	8.58	8.74	9.41	10.54	0.0054
		ED	5.94	6.43	8.69	8.81	8.46	10.19	0.0075
1	Sut2-2	C	7.61	6.71	6.23	4.75	4.73	2.88	0.0003
		ED	6.65	7.66	6.42	4.81	4.18	2.77	0.0022
1	Sut2-3	C	5.55	6.11	5.79	5.49	5.51	4.99	ns
		ED	5.96	6.43	5.78	4.86	5.96	6.41	ns
1	Sut2-4	C	6.81	5.69	7.33	8.04	8.83	9.34	0.0001
		ED	5.24	6.08	7.42	7.53	8.52	9.24	0.0269
2	GPA1	C	7.40	6.32	7.89	7.79	8.63	9.24	ns
		ED	7.11	6.80	8.58	8.74	7.53	9.08	ns
2	GPA3	C	5.18	4.53	7.25	7.48	8.69	9.91	0.0009
		ED	4.37	4.98	8.18	8.64	8.17	8.05	ns
2	GPA4	C	5.54	4.45	6.61	7.14	7.59	7.52	0.0111
		ED	4.75	5.20	7.54	7.49	6.86	7.14	ns
3	RGS1	C	5.66	5.30	6.82	7.46	7.88	8.27	0.0060
		ED	5.32	5.89	7.31	7.62	7.38	8.20	ns
4	Hxk1	C	7.52	5.97	7.13	7.22	7.65	8.07	0.0287
		ED	6.60	6.54	8.07	7.17	7.00	7.45	ns
4	Hxk2	C	8.34	7.44	9.04	9.62	10.25	11.63	0.0006
		ED	7.12	7.83	10.02	9.99	9.65	11.87	0.0099
4	Hxk3	C	5.64	4.51	5.62	6.04	7.01	7.55	0.0033
		ED	4.25	5.30	5.75	5.62	6.19	7.78	0.0293
4	Hxk4	C	4.79	4.21	3.75	4.02	4.05	3.66	ns
		ED	3.94	4.50	2.99	2.53	3.38	4.62	ns
5	PP2C-1	C	5.37	3.92	5.19	4.96	6.01	6.63	ns
		ED	3.84	4.19	5.62	4.80	4.77	6.21	ns
5	PP2C-3	C	7.54	6.58	9.06	10.12	10.52	11.76	0.0000
		ED	6.72	7.88	10.81	10.84	9.85	12.08	0.0028
5	PP2C-5	C	7.46	6.93	8.14	7.49	8.95	9.79	ns
		ED	5.26	5.72	7.97	9.05	7.26	7.77	ns
5	PP2C-6	C	5.16	4.66	8.01	7.74	8.09	9.22	0.0052
		ED	4.28	4.68	8.69	8.34	6.44	8.45	0.0391
5	PP2C-7	C	6.37	4.12	6.11	5.54	6.95	7.41	0.0292
		ED	5.40	4.91	7.46	6.71	6.21	7.23	ns
5	PP2C-9	C	6.50	4.85	7.55	7.32	8.72	9.01	0.0035
		ED	4.92	5.38	8.28	7.76	7.45	8.81	0.0350
6	SnRK1	C	8.37	7.22	8.49	8.88	9.59	11.49	0.0015
		ED	7.01	7.51	9.09	8.18	8.99	11.04	0.0198
6	SnRK3	C	5.95	5.30	6.30	6.92	7.99	9.07	0.0048
		ED	4.67	4.82	6.68	6.95	6.92	9.29	0.0077
6	SnRK4	C	5.06	4.48	4.95	4.71	5.52	5.83	ns
		ED	3.45	4.68	4.82	3.77	4.58	5.42	ns

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2	6	SnRK5	C	6.66	5.97	7.79	8.01	8.26	9.50	0.0001
3			ED	6.00	5.79	8.95	8.93	7.08	10.37	0.0127
4	6	SnRK6	C	7.40	6.62	8.27	8.73	9.18	10.51	0.0063
5			ED	6.87	7.84	9.66	9.74	8.98	10.26	ns
6	6	SnRK7	C	6.50	4.90	7.64	7.50	8.76	7.53	0.0083
7			ED	6.25	4.92	8.09	8.36	7.68	7.20	ns
8	7	WRKY1	C	7.10	7.01	7.86	8.20	8.78	9.10	ns
9			ED	5.84	8.69	8.48	8.32	8.24	9.46	ns
10	7	WRKY2	C	4.73	5.32	6.02	6.18	6.10	5.97	ns
11			ED	4.12	6.28	5.53	5.02	5.27	6.27	ns
12	7	WRKY3	C	5.98	4.52	5.98	6.03	8.02	8.26	0.0408
13			ED	5.04	5.98	7.16	6.05	7.86	8.85	0.0303
14	7	WRKY5	C	4.40	3.75	5.37	6.16	6.99	7.35	0.0069
15			ED	2.50	4.70	6.60	6.17	6.50	8.03	0.0021
16	7	WRKY6	C	3.83	2.25	4.95	5.00	6.10	6.63	0.0160
17			ED	2.69	3.31	5.73	5.61	4.92	6.71	0.0079
18	7	WRKY16	C	0.89	0.00	0.79	2.32	3.04	2.36	ns
19			ED	0.00	0.00	2.79	2.87	2.45	3.07	ns
20	7	WRKY18	C	5.81	4.39	6.75	4.32	8.28	7.37	ns
21			ED	5.22	5.79	8.49	7.79	7.64	8.12	ns
22	7	WRKY19	C	8.43	6.45	7.95	7.62	9.01	9.04	ns
23			ED	7.24	7.33	8.80	8.91	7.87	9.11	ns
24	8	HB2	C	8.16	7.38	8.06	8.24	7.04	5.76	ns
25			ED	6.33	7.35	8.55	8.59	4.95	4.88	0.0205
26	8	HB3	C	8.49	8.10	9.64	8.84	11.05	9.63	ns
27			ED	7.14	7.87	9.96	8.79	9.47	10.22	ns
28	8	HB4	C	6.38	4.90	8.23	8.69	9.56	9.09	0.0012
29			ED	3.99	4.48	8.28	7.57	7.91	9.03	0.0037
30	8	HB8	C	5.37	3.18	7.85	8.35	8.44	2.94	0.0001
31			ED	4.23	6.03	8.16	7.95	6.85	7.37	ns
32	9	ABF1	C	6.34	5.93	8.77	8.47	8.72	9.38	0.0002
33			ED	4.98	5.95	9.94	9.21	7.89	8.97	0.0066
34	10	AP2-6	C	4.53	3.14	5.95	5.50	6.95	7.04	0.0293
35			ED	2.12	3.93	5.78	4.96	5.72	6.47	0.0193

for expression summary in Figs. 1 and 2 values in each stage (I, II, III) were averaged

* P values for ANOVAs of expression with time

red type denotes significant differences between treatments ($P < 0.05$; Tukey's HSD)

Supplemental File 1

Family	Gene	Genoscope accession	Primer	Sequence
1	SUT2-1	GSVIVT00015035001	forward	taggtcaagggttatcaatgggtg
			reverse	ctacaagtcactggcgaatgctg
1	SUT2-2	GSVIVT00002302001	forward	tgtgcttggcactgacggta
			reverse	tggaatgctgtaggtgatcgcaa
1	SUT2-3	GSVIVT00002307001	forward	gcagctcgttgatgggtggg
			reverse	tggaggcatcaagcttctgc
1	SUT2-4	GSVIVT00037013001	forward	gctggttgggcatgagca
			reverse	aggaaagccaagaagagcaaacac
2	GPA1-1	GSVIVT00015638001	forward	ctacctgatgatcgtagtcca
			reverse	acacagaacactacagctcga
2	GPA1-2	GSVIVT00006612001	forward	agtcaactcagagcaatggtcttcg
			reverse	agccatttgacccatcatgca
2	GPA1-3	GSVIVT00013154001	forward	tggcaggaatttgaagcca
			reverse	tatcaacggcccgtccaagaa
2	GPA1-4	GSVIVT00032290001	forward	gcaagaattcgtacaacaggtgctc
			reverse	ggtcactcgttaatagcagcac
2	GPA1-5	GSVIVT00036460001	forward	gaggtatgcattgttcagcgca
			reverse	agcatttgagagcatttcccagg
3	RGS1-1	GSVIVT00035126001	forward	cctggcaaaggattactggtcgtc
			reverse	tgaaggatgttctcgtggaagg
4	HXK-1	GSVIVT00014427001	forward	tgaccatctggatgctgttga
			reverse	tggagaatccctacaatgcctgca
4	HXK-2	GSVIVT00016656001	forward	gtgtgatattgtgctactcgtgg
			reverse	ttgaggggtcctccaagcag
4	HXK-3	GSVIVT00022229001	forward	ccccgaattgatggaagtgcga
			reverse	ttcaggatcccaacaatgcctg
4	HXK-4	GSVIVT00010644001	forward	taaggtcacctgatatggctgc
			reverse	aagacgagctccacgttctgca
4	HXK-5	GSVIVT00034293001	forward	agtttctggcatgtattggcgca
			reverse	gactgatgtgcatgatgcatgg
5	VvPP2C-1	GSVIVT00016515001	forward	tgtgtcgtggaaaagtacctgtgc
			reverse	aacgccacatacacgtaagccgtc
5	VvPP2C-2	GSVIVT00016669001	forward	atgaagttggagaggtggctcg
			reverse	gtctgagctatttctcccgtatgc
5	VvPP2C-3	GSVIVT00018423001	forward	atggtcagtggagctgaattgc
			reverse	atcaggcttgggtcggatgacag
5	VvPP2C-4	GSVIVT00006760001	forward	tctgaagccatagtgacccccaa
			reverse	gcatttctcacaatctgcagg
5	VvPP2C-5	GSVIVT00024072001	forward	gtggaggatgagagagacgggta
			reverse	tttgaccaccatgccatcaa
5	VvPP2C-6	GSVIVT00024235001	forward	ccaaaccacgaatggctcgcacta
			reverse	gcatttctcaacctgactccgta
5	VvPP2C-7	GSVIVT00032224001	forward	gagtgattcccttcagtgac
			reverse	cacactacgaacaagtgtccac
5	VvPP2C-8	GSVIVT00038525001	forward	agccctgaagaggtgcttcag
			reverse	tcagtggtgataatagccacc
5	VvPP2C-9	GSVIVT00034142001	forward	ggtcaaattgtgctaaggcga
			reverse	gcagatgcctcaaatcagaccca
5	VvPP2C-10	GSVIVT00034305001	forward	agtgcacttacgccgctgagga
			reverse	ccgttactccattcatcaccac
6	SnRK-1	GSVIVT00021017001	forward	gttgagaatgatggtgttccagg
			reverse	tgagcaaggaaagctgcacaa

	Family	Gene	Genoscope accession	Primer	Sequence
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Family	Gene	Genoscope accession	Primer	Sequence
8	VvATHB-9	GSVIVT00027741001	forward	tgaggcttctagagacaagcttcg
			reverse	gtcaagctccaagttctgcgctc
8	VvATHB-10	GSVIVT00037197001	forward	agtcggatagtaagcttgaggcga
			reverse	gcatcgtagctagctctgagtg
9	VvABF-1	GSVIVT00014828001	forward	atggaattggaagcagaggttgca
			reverse	tcagtgtgcgctcaagcaacg
9	VvABF-2	GSVIVT00015294001	forward	tttcgagggctccagccattgag
			reverse	ctcatctgaaaaccagcgctcc
9	VvABF-3	GSVIVT00002670001	forward	ggaaaagagtttcccaagagga
			reverse	cagacgtgaaactttgttctccag
9	VvABF-4	GSVIVT00017354001	forward	aagactgttgaaaggcggcta
			reverse	aagctggtactttggtctgtcga
9	VvABF-5	GSVIVT00021625001	forward	gcaacatcagtagcgggtgtacca
			reverse	acggtcgcactcattgccaacgctc
9	VvABF-6	GSVIVT00031514001	forward	agttactggcgctggaagagg
			reverse	accagcgactctagctcaactg
9	VvABF-7	GSVIVT00031758001	forward	gggatttgcgtttgatcccggtg
			reverse	agccgccttatccaagggctccaa
9	VvABF-8	GSVIVT00036604001	forward	agctcgggtaatggtgggctacag
			reverse	ttaaacacataaggagcaggcga
9	VvABF-9	GSVIVT00037365001	forward	tgggttgggaattctccgcttcac
			reverse	atctacgctgtcgacgctcca
10	VvAP2-4	GSVIVT00014524001	forward	gtgcactataaaaggagttcgcca
			reverse	gtccctaaccagagacgagcac
10	VvAP2-5	GSVIVT00025555001	forward	tcgtggtgtaggcaaagaacc
			reverse	ttctcggcagtcgcaaaagagc
10	VvAP2-6	GSVIVT00029367001	forward	tgggttgctgagattcgggagcca
			reverse	tcagcttcgtcatatgcaagagc

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