

Supplementary Material

Distinct Hormonal and Morphological Control of Dormancy and Germination in *Chenopodium album* Dimorphic Seeds

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Research Topic "Molecular Basis of Seed Germination and Dormancy"

Supplementary Figure 1 | Population-based thermal-time threshold modelling of *C. album* dimorphic seeds.

Supplementary Figure 2 | Effect of light and hormones on the germination of *C. album* dimorphic seeds.

Supplementary Figure 3 | Gibberellin metabolite contents in dry and imbibed *C. album* dimorphic seeds.

Supplementary Figure 4 | BLAST analysis of *C. quinoa* GA and ABA metabolism gene transcripts.

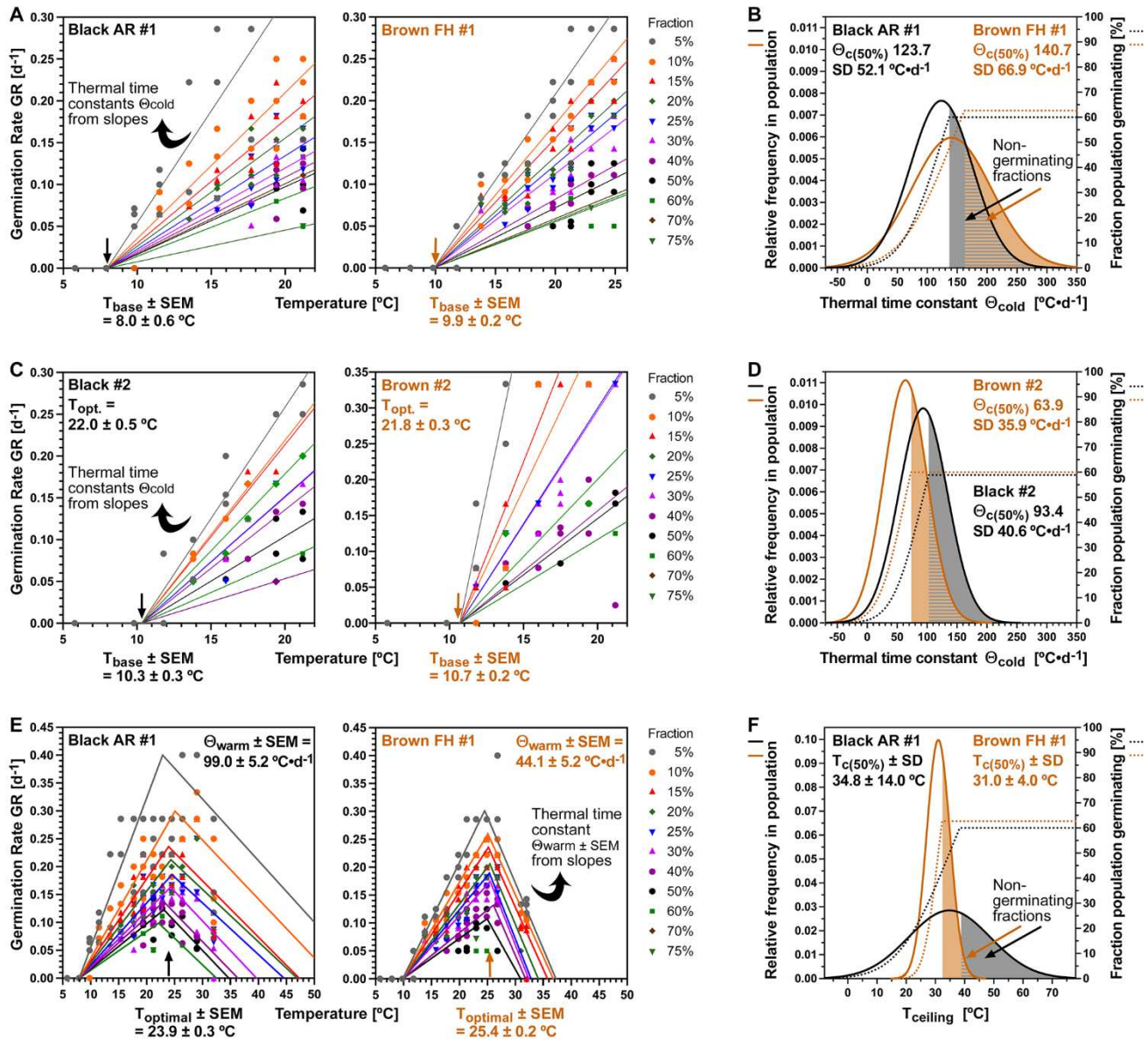
Supplementary Figure 5 | Transcript expression patterns of GA and ABA metabolism genes during *C. quinoa* seed germination.

Supplementary Figure 6 | BLAST analysis of identified sequences of *C. album* GA and ABA metabolism genes.

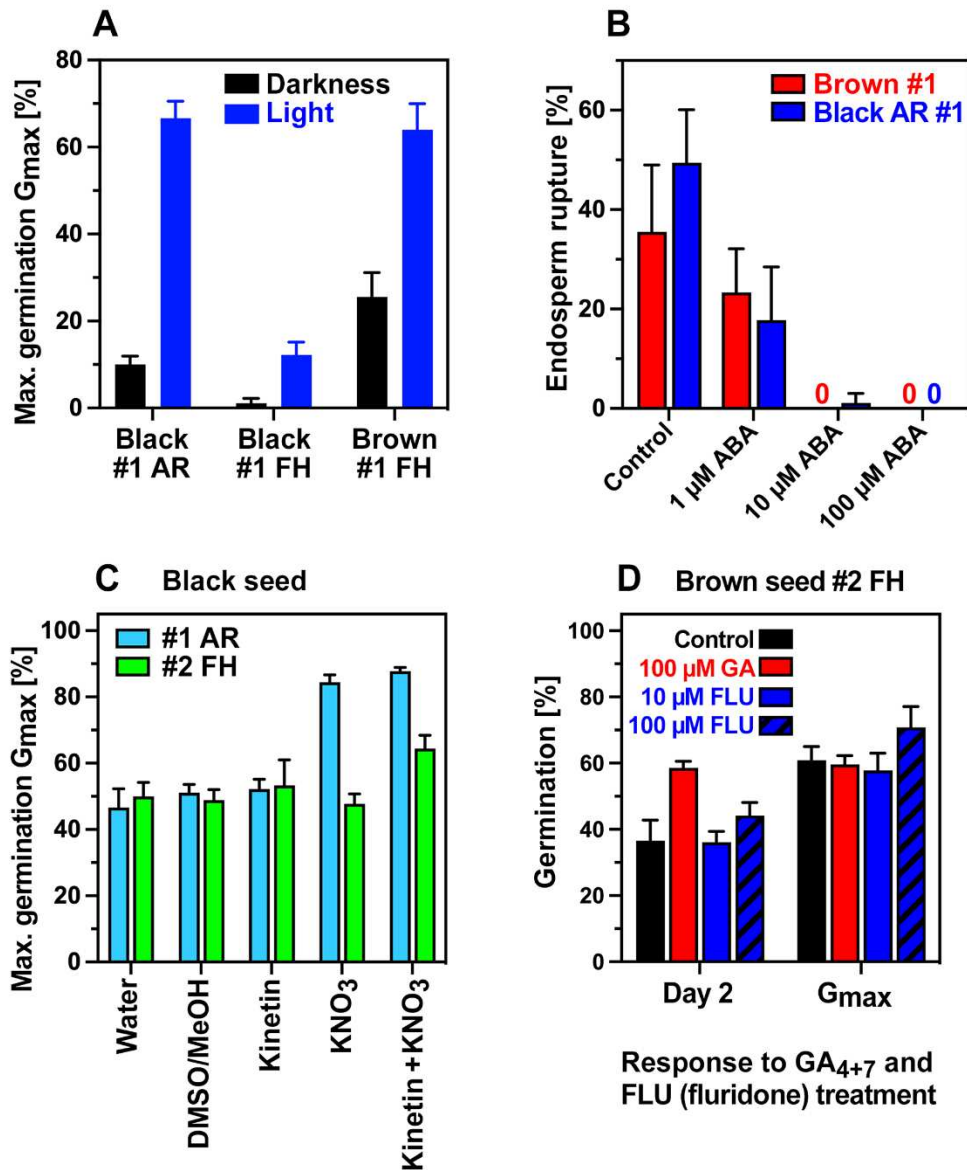
Supplementary Table 1 | Primer sequences used for PCR cloning of *C. album* sequences.

Supplementary Table 2 | Primer sequences used for the *C. album* RT-qPCR analysis.

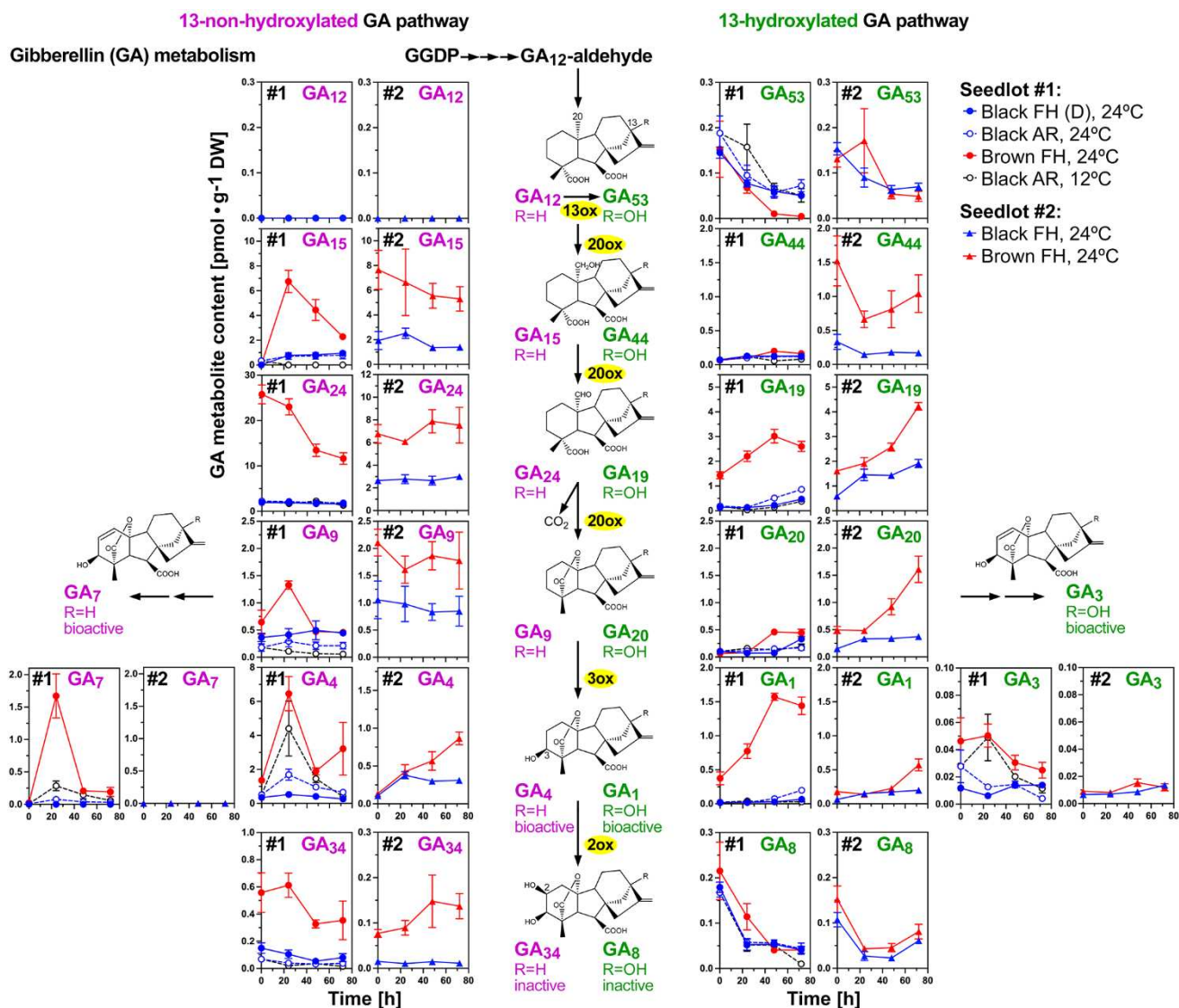
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Supplementary Figure 1 | Population-based thermal-time threshold modeling of *Chenopodium album* dimorphic seeds. (A) Germination rates (GR_g), i.e. the inverse of time to germination for a given percentage of the population ($1/t_g$), of after-ripened (AR) black and freshly harvested (FH) brown seeds of seedlot #1 were calculated from the germination kinetics (Figure 1D), and plotted against the temperatures. Single-plate values for the sub-optimal (colder) temperature range for the different percentage fractions are presented and were used in linear regression analysis with GraphPad Prism v7 to calculate regression lines and to estimate base temperatures (T_{base} , derived from intercepts with x-axis) and thermal-time constants ($\Theta_{cold(g)}$; derived from different slopes). (B) Frequency distribution of $\Theta_{cold(g)}$ and in the seed populations calculated from the standard deviations (SD) of the thermal-time constant at 50% germination ($\Theta_{cold(50\%)}$); the non-germinating seed fraction populations are indicated. (C,D) The corresponding analysis for seedlot #2. (E) Full thermal-time analysis of seedlot #1 including in the supra-optimal (warmer) temperature range, estimated optimal temperatures ($T_{opt.}$) and thermal-time constants $\Theta_{warm} \pm SEM$ (slopes are similar in the supra-optimal temperature range). (F) Estimated ceiling temperatures (T_c) which are normal distributed around $T_{c(50\%)}$.



Supplementary Figure 2 | Effect of light and hormones on the germination of *Chenopodium album* dimorphic seeds. (A) Effects of continuous darkness and white light ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$) on the maximal germination percentages (G_{max}) of after-ripened (AR) and freshly harvested (FH) mature seeds of seedlot #1 imbibed at 24°C for 20 days. **(B)** Endosperm rupture of FH brown and AR black seeds imbibed for 10 days in the absence or presence of abscisic acid (ABA) at the concentrations indicated. **(C)** The effect of kinetin ($40 \mu\text{M}$), KNO_3 (10mM), DMSO (0.1%) and MeOH (0.1%) on the G_{max} of imbibed black seeds at 24°C for 20 days. **(D)** The effect of GA_{4+7} (GA) and fluridone on the germination of brown seeds of seedlot #2. Mean \pm SEM values are presented.



Supplementary Figure 3 | Gibberellin metabolite contents in dry and imbibed *Chenopodium album* dimorphic seeds. Temporal GA metabolite content comparison in seedlots #1 and #2 at 24°C, and AR #1 black seeds at 12°C; Mean ± SEM values are presented. The 13-non-hydroxylated and the 13-hydroxylated GA biosynthesis and catabolic pathways with key enzymes (GA 20- oxidases, GA 3- oxidases, GA2-oxidases) are indicated. For further details, methods and references see the main text.

A BLAST analysis of GA20ox genes to identify *Chenopodium quinoa* sequences as templates for primer design

Arabidopsis thaliana gene identifier	Gene	Protein length (aa)	BlastN vs predicted (Phytozome website)	Score	E-value	BlastX vs <i>Chenopodium quinoa</i> transcripts (Phytozome website)	Score	E-value
AT4G25420	GA20ox1	377	jgi:C_Quinoa_Scaffold_1783_392_Cquinoa 392 v1.0	207	1.0E-50	jgi:36311734_C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20...	494	9.0E-174
			jgi:C_Quinoa_Scaffold_4250_392_Cquinoa 392 v1.0	204	1.0E-49	jgi:36288619_C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20...	491	1.0E-172
			jgi:C_Quinoa_Scaffold_2608_392_Cquinoa 392 v1.0	204	1.0E-49	jgi:36318333_C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20...	489	6.0E-172
			jgi:C_Quinoa_Scaffold_3256_392_Cquinoa 392 v1.0	194	7.0E-47	jgi:36292046_C_quinoa_v1_0 392 AUR62013454-RA AUR62013454-RA GA20...	373	7.0E-127
			jgi:C_Quinoa_Scaffold_3429_392_Cquinoa 392 v1.0	105	3.0E-20	jgi:36285550_C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20...	369	3.0E-126
AT5G51810	GA20ox2	378	jgi:C_Quinoa_Scaffold_4250_392_Cquinoa 392 v1.0	199	2.0E-48	jgi:36318333_C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20...	473	2.0E-165
			jgi:C_Quinoa_Scaffold_2608_392_Cquinoa 392 v1.0	199	2.0E-48	jgi:36288619_C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20...	471	9.0E-165
			jgi:C_Quinoa_Scaffold_1783_392_Cquinoa 392 v1.0	184	1.0E-43	jgi:36311734_C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20...	461	8.0E-161
			jgi:C_Quinoa_Scaffold_3256_392_Cquinoa 392 v1.0	160	1.0E-36	jgi:36319174_C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20...	358	6.0E-122
			jgi:C_Quinoa_Scaffold_2088_392_Cquinoa 392 v1.0	123	3.0E-25	jgi:36292046_C_quinoa_v1_0 392 AUR62013454-RA AUR62013454-RA GA20...	356	6.0E-120
AT5G07200	GA20ox3	380	jgi:C_Quinoa_Scaffold_1783_392_Cquinoa 392 v1.0	157	2.0E-35	jgi:36311734_C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20...	489	2.0E-171
			jgi:C_Quinoa_Scaffold_4250_392_Cquinoa 392 v1.0	149	3.0E-33	jgi:36318333_C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20...	488	8.0E-171
			jgi:C_Quinoa_Scaffold_2608_392_Cquinoa 392 v1.0	145	3.0E-32	jgi:36288619_C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20...	487	2.0E-170
			jgi:C_Quinoa_Scaffold_3256_392_Cquinoa 392 v1.0	143	1.0E-31	jgi:36292046_C_quinoa_v1_0 392 AUR62013454-RA AUR62013454-RA GA20...	357	1.0E-119
			jgi:C_Quinoa_Scaffold_2088_392_Cquinoa 392 v1.0	115	6.0E-23	jgi:36319174_C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20...	347	7.0E-117
AT1G60980	GA20ox4	385	jgi:C_Quinoa_Scaffold_1783_392_Cquinoa 392 v1.0	154	4.0E-35	jgi:36311734_C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20...	468	4.0E-165
			jgi:C_Quinoa_Scaffold_2608_392_Cquinoa 392 v1.0	148	7.0E-33	jgi:36288619_C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20...	462	7.0E-163
			jgi:C_Quinoa_Scaffold_3256_392_Cquinoa 392 v1.0	145	2.0E-32	jgi:36318333_C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20...	459	1.0E-161
			jgi:C_Quinoa_Scaffold_2088_392_Cquinoa 392 v1.0	115	6.0E-23	jgi:36319174_C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20...	338	9.0E-116
			jgi:C_Quinoa_Scaffold_1611_392_Cquinoa 392 v1.0	100	4.0E-18	jgi:36285550_C_quinoa_v1_0 392 AUR62007685-RA AUR62007685-RA GA20...	316	3.0E-104

plus direct search for *C. quinoa* sequences (Phytozome)

Verification of *C. quinoa* GA20ox genes and transcript sequences ← Identified potential *C. quinoa* GA20ox sequences

Primer design for PCR cloning of *C. album* sequences (Supplementary Table 1)

Sanger sequencing of *C. album* sequences and verification via BLAST analysis (Supplementary Figure 6) and phylogenetic trees (Figure 5A)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

Phytozome <i>Chenopodium quinoa</i> gene ID	Phytozome <i>Chenopodium quinoa</i> transcript	BLAST back to TAIR (BlastX using <i>Chenopodium quinoa</i> phytozome cds)	Score	E-value	DEG in <i>Chenopodium quinoa</i> seed transcriptome	Subgroup and name in phylogeny (Figure 6A)
AUR62007685	AUR62007685-RA	AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	333	5.0E-113	no	A1 - CqGA20ox1-like
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	332	1.0E-112		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	317	2.0E-106		
		AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	313	4.0E-105		
		AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	297	9.0E-99		
AUR62013454	AUR62013454-RA	AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	372	4.0E-128	yes (Figure S5)	A1 - CqGA20ox1-like
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	371	1.0E-127		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	356	2.0E-121		
		AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	348	2.0E-118		
		AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	331	1.0E-111		
AUR62006843	AUR62006843-RA	AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	261	1.0E-85		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	261	1.0E-81		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	293	1.0E-97	yes (Figure S5)	A2 - CqGA20ox1-like
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	292	2.0E-97		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	290	1.0E-96		
AUR62000497	AUR62000497-RA	AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	277	3.0E-91		
		AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	275	2.0E-90		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	186	5.0E-57		
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	182	2.0E-55		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	293	1.0E-97	no	A2 - CqGA20ox1-like
AUR62033388	AUR62033388-RA	AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	493	4.0E-175	no	B1 - CqGA20ox1-like
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	487	8.0E-173		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	480	6.0E-170		
		AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	467	7.0E-165		
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	369	2.0E-127		
AUR62004269	AUR62004269-RA	AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	367	1.0E-128	no	B1 - CqGA20ox1-like
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	369	7.0E-128		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	358	1.0E-124		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	357	2.0E-123		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	347	3.0E-119		
AUR62016064	AUR62016064-RA	AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	338	4.0E-116		
		AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	239	4.0E-77		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	493	3.0E-175	yes (Figure S5)	B2 - CqGA20ox2-like
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	490	5.0E-174		
		AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	487	8.0E-173		
AUR62021271	AUR62021271-RA	AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	462	8.0E-163		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	370	4.0E-128		
		AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	363	3.0E-125		
		AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	344	2.0E-116		
		AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	494	2.0E-175	yes (Figure S5)	B2 - CqGA20ox2-like
AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	488	2.0E-173				
AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	483	4.0E-171				
AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	454	1.0E-159				
AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	370	4.0E-128				
AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	359	2.0E-123				
AT1G44090.1 Symbols: GA20OX5, ATGA20OX5 ARABIDOPSIS THALIANA ...	340	1.0E-114				

Figure S4 continued next page...

B BLAST analysis of GA3ox genes to identify *Chenopodium quinoa* sequences as templates for primer design

Arabidopsis thaliana gene identifier	Gene	Protein length (aa)	BlastN vs predicted (Phytozome website)	Score	E-value	BlastX vs <i>Chenopodium quinoa</i> transcripts (Phytozome website)	Score	E-value
AT1G15550	GA3ox1	358	gi C:Quinoa_Scaffold_3333_392:Quinoa 392 v1.0	92.4	6.0E-16	gi 36308453 C. quinoa_v1_0 392 AUR62011599-RAJ AUR62011599-RALE:...	395	1.0E-134
			gi C:Quinoa_Scaffold_4087_392:Quinoa 392 v1.0	50.9	2.0E-03	gi 36305840 C. quinoa_v1_0 392 AUR62032368-RAJ AUR62032368-RALE:...	298	2.0E-97
			gi C:Quinoa_Scaffold_3876_392:Quinoa 392 v1.0	47.3	2.3E-02	gi 36284702 C. quinoa_v1_0 392 AUR62024851-RAJ AUR62024851-RALE:...	290	3.0E-94
AT1G80340	GA3ox2	347	gi C:Quinoa_Scaffold_3333_392:Quinoa 392 v1.0	68	7.0E-09	gi 36308453 C. quinoa_v1_0 392 AUR62011599-RAJ AUR62011599-RALE:...	384	2.0E-130
			gi C:Quinoa_Scaffold_3514_392:Quinoa 392 v1.0	50.9	2.0E-03	gi 36284702 C. quinoa_v1_0 392 AUR62024851-RAJ AUR62024851-RALE:...	299	7.0E-98
			gi C:Quinoa_Scaffold_4383_392:Quinoa 392 v1.0	46.4	2.2E-02	gi 36305840 C. quinoa_v1_0 392 AUR62032368-RAJ AUR62032368-RALE:...	299	1.0E-97
AT4G21690	GA3ox3	349	gi C:Quinoa_Scaffold_1516_392:Quinoa 392 v1.0	58.1	9.0E-06	gi 36308453 C. quinoa_v1_0 392 AUR62011599-RAJ AUR62011599-RALE:...	320	2.0E-107
						gi 36284702 C. quinoa_v1_0 392 AUR62024851-RAJ AUR62024851-RALE:...	305	4.0E-102
						gi 36305840 C. quinoa_v1_0 392 AUR62032368-RAJ AUR62032368-RALE:...	298	2.0E-99
AT1G80330	GA3ox4	355	gi C:Quinoa_Scaffold_3333_392:Quinoa 392 v1.0	129	2.0E-27	gi 36308453 C. quinoa_v1_0 392 AUR62011599-RAJ AUR62011599-RALE:...	360	5.0E-123
			gi C:Quinoa_Scaffold_3514_392:Quinoa 392 v1.0	111	5.0E-22	gi 36284702 C. quinoa_v1_0 392 AUR62024851-RAJ AUR62024851-RALE:...	291	1.0E-96
			gi C:Quinoa_Scaffold_1516_392:Quinoa 392 v1.0	66.2	2.0E-08	gi 36305840 C. quinoa_v1_0 392 AUR62032368-RAJ AUR62032368-RALE:...	286	2.0E-94
						gi 36294241 C. quinoa_v1_0 392 AUR62038693-RAJ AUR62038693-RALE:...	256	4.0E-83
						gi 36294257 C. quinoa_v1_0 392 AUR62038694-RAJ AUR62038694-RAJACO2:...	186	2.0E-56

plus direct search for *C. quinoa* sequences (Phytozome)

Verification of *C. quinoa* GA3ox genes and transcript sequences ← Identified potential *C. quinoa* GA3ox sequences

Phytozome <i>Chenopodium quinoa</i> gene ID	Phytozome <i>Chenopodium quinoa</i> transcript	BLAST back to TAIR (BlastX using <i>Chenopodium quinoa</i> phytozome cds)	Score	E-value	DEG in <i>Chenopodium quinoa</i> seed transcriptome	Subgroup and name in phylogeny (Figure 6B)
AUR62011599	AUR62011599-RA	AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	393	4.0E-136	yes (Figure S5)	C - CqGA3ox1-like
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	363	2.0E-124		
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	360	6.0E-123		
		AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	298	3.0E-99		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	296	1.0E-98		
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	286	2.0E-94		
AT1G78240.1 Symbols: OSU1, TSD2, QUA2 TUMOROUS SHOOT DEVELOPM...	934	0.0E+00				
AUR62016415	AUR62016415-RA	AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	152	4.0E-45	yes (Figure S5)	C - CqGA3ox1-like
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	144	4.0E-42		
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	127	7.0E-36		
		AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	127	1.0E-35		
		AT1G78550.1 Symbols: no symbol available no full name availab...	63	8.0E-12		
AUR62038694	AUR62038694-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	193	2.0E-59	no	D3 - CqGA3ox4-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	186	1.0E-56		
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	177	5.0E-53		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	159	3.0E-46		
		AT4G25420.2 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	105	2.0E-28		
		AT4G25420.1 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	106	6.0E-28		
AT1G17020.1 Symbols: ATSRG1, SRG1 SENESCENCE-RELATED GENE 1, ...	104	1.0E-25				
AUR62038695	AUR62038695-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	142	1.0E-41	no	D3 - CqGA3ox4-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	130	6.0E-37		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	127	1.0E-35		
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	118	4.0E-32		
		AT2G38240.1 Symbols: JOX4, JA04 JASMONATE-INDUCED OXYGENASE4...	73	1.0E-15		
		AT4G25420.2 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	69	5.0E-14		
AT4G25420.1 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	69	7.0E-14				
AUR62038693	AUR62038693-RA	AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	256	6.0E-83	no	D3 - CqGA3ox1-like
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	256	1.0E-82		
		AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	255	1.0E-82		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	236	3.0E-75		
		AT1G17020.1 Symbols: ATSRG1, SRG1 SENESCENCE-RELATED GENE 1, ...	152	7.0E-43		
		AT2G38240.1 Symbols: JOX4, JA04 JASMONATE-INDUCED OXYGENASE4...	152	1.0E-42		
AT4G25300.1 Symbols: no symbol available no full name availab...	145	2.0E-40				
AUR62032075	AUR62032075-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	137	2.0E-39	no	D3 - CqGA3ox1-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	125	6.0E-35		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	112	4.0E-30		
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	105	3.0E-27		
		AT4G25420.2 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	68	6.0E-14		
AUR62032673	AUR62032673-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	142	2.0E-40	no	D3 - CqGA3ox1-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	134	3.0E-37		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	117	8.0E-31		
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	108	1.0E-27		
		AT4G25420.2 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	71	4.0E-14		
		AT4G25420.1 Symbols: ATGA20X1, AT2301, GA5, GA20X1 ARABIDOP...	71	6.0E-14		
AT2G38240.1 Symbols: JOX4, JA04 JASMONATE-INDUCED OXYGENASE4...	69	2.0E-13				
AUR62032368	AUR62032368-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	298	3.0E-99	no	D4 - CqGA3ox1-like
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	296	1.0E-98		
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	286	2.0E-94		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	281	1.0E-92		
		AT1G78550.1 Symbols: no symbol available no full name availab...	176	8.0E-52		
AUR62024851	AUR62024851-RA	AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	305	5.0E-102	no	D4 - CqGA3ox1-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	291	9.0E-97		
		AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	291	2.0E-96		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	281	1.0E-92		
		AT1G78550.1 Symbols: no symbol available no full name availab...	173	1.0E-50		
AUR62032076	AUR62032076-RA	AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	137	5.0E-39	no	D4 - CqGA3ox1-like
		AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	133	7.0E-38		
		AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	131	4.0E-37		
		AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	124	2.0E-34		
		AT4G25310.1 Symbols: no symbol available no full name availab...	114	2.0E-30		
		AT1G78550.2 Symbols: no symbol available no full name availab...	108	7.0E-29		
AT4G25300.2 Symbols: no symbol available no full name availab...	107	1.0E-28				

Primer design for PCR cloning of *C. album* sequences (Supplementary Table 1)

Sanger sequencing of *C. album* sequences and verification via BLAST analysis (Supplementary Figure 6) and phylogenetic trees (Figure 5B)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

Figure S4 continued next page...

C BLAST analysis of GA2ox genes to identify *Chenopodium quinoa* sequences as templates for primer design

Arabidopsis thaliana gene identifier	Gene	Protein length (aa)	BlastN vs predicted (Phytozome website)	Score	E-value	BlastX vs <i>Chenopodium quinoa</i> transcripts (Phytozome website)	Score	E-value
AT1G78440.1	GA2ox1	329	gi C_Quinoa_Scaffold_1747_392_Cquinoa 392 v1.0	125	3.0E-26	gi 36301611 C. quinoa_v1_0 392 AUR62002752-RA AUR62002752-RA GA2O...	371	7.0E-127
			gi C_Quinoa_Scaffold_1000_392_Cquinoa 392 v1.0	125	3.0E-26	gi 36311284 C. quinoa_v1_0 392 AUR62011753-RA AUR62011753-RA GA2O...	280	2.0E-91
			gi C_Quinoa_Scaffold_1611_392_Cquinoa 392 v1.0	49.1	6.0E-03	gi 36310380 C. quinoa_v1_0 392 AUR62024597-RA AUR62024597-RA GA2O...	248	4.0E-78
						gi 36304895 C. quinoa_v1_0 392 AUR62030199-RA AUR62030199-RA GA2O...	169	6.0E-50
AT1G30040	GA2ox2	341	gi C_Quinoa_Scaffold_1000_392_Cquinoa 392 v1.0	124	1.0E-25	gi 36301611 C. quinoa_v1_0 392 AUR62002752-RA AUR62002752-RA GA2O...	379	1.0E-127
			gi C_Quinoa_Scaffold_1747_392_Cquinoa 392 v1.0	117	2.0E-23	gi 36311284 C. quinoa_v1_0 392 AUR62011753-RA AUR62011753-RA GA2O...	281	7.0E-90
			gi C_Quinoa_Scaffold_3799_392_Cquinoa 392 v1.0	53.6	2.0E-04	gi 36310380 C. quinoa_v1_0 392 AUR62024597-RA AUR62024597-RA GA2O...	250	3.0E-77
						gi 36304895 C. quinoa_v1_0 392 AUR62030199-RA AUR62030199-RA GA2O...	190	1.0E-56
AT2G34555	GA2ox3	335	gi C_Quinoa_Scaffold_1000_392_Cquinoa 392 v1.0	107	7.0E-21	gi 36301611 C. quinoa_v1_0 392 AUR62002752-RA AUR62002752-RA GA2O...	338	6.0E-114
			gi C_Quinoa_Scaffold_1747_392_Cquinoa 392 v1.0	103	3.0E-19	gi 36311284 C. quinoa_v1_0 392 AUR62011753-RA AUR62011753-RA GA2O...	266	3.0E-96
			gi C_Quinoa_Scaffold_1611_392_Cquinoa 392 v1.0	52.7	5.0E-04	gi 36310380 C. quinoa_v1_0 392 AUR62024597-RA AUR62024597-RA GA2O...	234	3.0E-73
						gi 36304895 C. quinoa_v1_0 392 AUR62030199-RA AUR62030199-RA GA2O...	167	2.0E-49
AT1G47990	GA2ox4	321	gi C_Quinoa_Scaffold_1747_392_Cquinoa 392 v1.0	51.8	4.0E-04	gi 36311284 C. quinoa_v1_0 392 AUR62011753-RA AUR62011753-RA GA2O...	304	4.0E-101
			gi C_Quinoa_Scaffold_3670_392_Cquinoa 392 v1.0	46.4	1.8E-02	gi 36310380 C. quinoa_v1_0 392 AUR62024597-RA AUR62024597-RA GA2O...	275	4.0E-89
			gi C_Quinoa_Scaffold_3378_392_Cquinoa 392 v1.0	46.4	1.8E-02	gi 36301611 C. quinoa_v1_0 392 AUR62002752-RA AUR62002752-RA GA2O...	268	9.0E-87
						gi 36308110 C. quinoa_v1_0 392 AUR62011417-RA AUR62011417-RA SRG1...	145	1.0E-39

plus direct search for *C. quinoa* sequences (Phytozome)

Verification of *C. quinoa* GA2ox genes and transcript sequences

Identified potential *C. quinoa* GA2ox sequences

Primer design for PCR cloning of *C. album* sequences (Supplementary Table 1)

Sanger sequencing of *C. album* sequences and verification via BLAST analysis (Supplementary Figure 6) and phylogenetic trees (Suppl. Figure 7)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

Phytozome <i>Chenopodium quinoa</i> gene ID	Phytozome <i>Chenopodium quinoa</i> transcript	BLAST back to TAIR (BlastX using <i>Chenopodium quinoa</i> phytozome cds)	Score	E-value	DEG in <i>Chenopodium quinoa</i> seed transcriptome	Subgroup and name in phylogeny (Suppl. Figure S7)
AUR62002752	AUR62002752-RA	AT1G30040.1 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	384	1.0E-133	yes (Figure S5)	C19 - CqGA2ox-like
		AT1G78440.1 Symbols: GA2OX1, ATGA2OX1 gibberellin 2-oxidase 1...	370	4.0E-128		
		AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	354	1.0E-121		
		AT1G02400.1 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	279	2.0E-92		
AUR62030199	AUR62030199-RA	AT1G30040.2 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	191	7.0E-61	no	C19 - CqGA2ox-like
		AT1G30040.1 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	191	5.0E-60		
		AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	183	8.0E-57		
		AT1G78440.1 Symbols: GA2OX1, ATGA2OX1 gibberellin 2-oxidase 1...	168	3.0E-51		
		AT1G02400.2 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	138	4.0E-40		
		AT1G02400.1 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	137	2.0E-39		
AUR62011753	AUR62011753-RA	AT1G02400.1 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	337	2.0E-115	yes (Figure S5)	C19 - CqGA2ox2-like
		AT1G47990.1 Symbols: ATGA2OX4, GA2OX4 Arabidopsis thaliana gi...	303	3.0E-102		
		AT1G30040.1 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	284	2.0E-94		
		AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	281	2.0E-93		
AUR62024597	AUR62024597-RA	AT1G02400.1 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	313	5.0E-105	no	C19 - CqGA2ox2-like
		AT1G47990.1 Symbols: ATGA2OX4, GA2OX4 Arabidopsis thaliana gi...	275	3.0E-100		
		AT1G30040.1 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	253	2.0E-81		
		AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	249	2.0E-80		
		AT1G78440.1 Symbols: GA2OX1, ATGA2OX1 gibberellin 2-oxidase 1...	246	3.0E-79		
		AT1G02400.2 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	232	2.0E-74		
AUR62022014	AUR62022014-RA	AT4G21200.1 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	236	1.0E-77	yes (Figure S5)	C20 - CqGA2ox8-like
		AT1G50960.1 Symbols: GA2OX7, ATGA2OX7 ARABIDOPSIS THALIANA GI...	147	3.0E-43		
		AT4G10490.1 Symbols: DL O2 DIM8-LIKE OXYGENASE 2 chr4:648390...	105	5.0E-27		
		AT5G58660.1 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	99	1.0E-24		
		AT5G07200.1 Symbols: ATGA2OX3, YAP169, GA2OX3 gibberellin 2...	99	2.0E-24		
		AT3G47190.1 Symbols: GA2ox10 Gibberellin 2-oxidase 10 chr3:...	97	6.0E-24		
AUR62022015	AUR62022015-RA	AT5G51810.1 Symbols: AT2353, ATGA2OX2, GA2OX2 gibberellin 2...	94	2.0E-22		
		AT4G21200.1 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	402	3.0E-140	no	C20 - CqGA2ox8-like
		AT1G50960.1 Symbols: GA2OX7, ATGA2OX7 ARABIDOPSIS THALIANA GI...	266	4.0E-87		
		AT5G58660.1 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	159	1.0E-45		
		AT4G21200.3 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	150	4.0E-44		
		AT4G25420.1 Symbols: ATGA2OX1, AT2301, GA5, GA2OX1 ARABIDOP...	155	1.0E-43		
AUR62001627	AUR62001627-RA	AT5G58660.2 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	205	3.0E-65	no	C20 - CqGA2ox8-like
		AT5G58660.1 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	205	3.0E-64		
		AT3G47190.1 Symbols: GA2ox10 Gibberellin 2-oxidase 10 chr3:...	197	3.0E-61		
		AT4G21200.1 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	113	3.0E-29		
		AT4G25300.1 Symbols: no symbol available no full name availab...	107	8.0E-27		
		AT1G50960.1 Symbols: GA2OX7, ATGA2OX7 ARABIDOPSIS THALIANA GI...	103	1.0E-25		
AUR62020152	AUR62020152-RA	AT1G17020.1 Symbols: ATSRG1, SRG1 SENESCENCE-RELATED GENE 1, ...	103	2.0E-25		
		AT5G58660.2 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	204	2.0E-64	no	C20 - CqGA2ox8-like
		AT5G58660.1 Symbols: GA2ox9 Gibberellin 2-oxidase 9 chr5:23...	202	7.0E-63		
		AT3G47190.1 Symbols: GA2ox10 Gibberellin 2-oxidase 10 chr3:...	185	2.0E-56		
		AT4G21200.1 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	115	7.0E-30		
		AT1G50960.1 Symbols: GA2OX7, ATGA2OX7 ARABIDOPSIS THALIANA GI...	103	3.0E-25		

Figure S4 continued next page...

D BLAST analysis of NCED genes to identify *Chenopodium quinoa* sequences as templates for primer design

Arabidopsis thaliana gene identifier	Gene	Protein length (aa)	BlastN vs predicted (Phytozome website)	Score	E-value	BlastX vs <i>Chenopodium quinoa</i> transcripts (Phytozome website)	Score	E-value
AT3G63520	NCED2	583	jgi:C_Quinoa_Scaffold_1747_392_Cquinoa392/v1.0	547	4.0E-153	jgi:36303079 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	682	0.0E+00
			jgi:C_Quinoa_Scaffold_1000_392_Cquinoa392/v1.0	497	7.0E-138	jgi:36306192 C_ quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA-RAINED...	679	0.0E+00
			jgi:C_Quinoa_Scaffold_2370_392_Cquinoa392/v1.0	489	1.0E-135	jgi:36301918 C_ quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA-RAINED...	655	0.0E+00
					jgi:36304873 C_ quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA-RAINED...	624	0.0E+00	
					jgi:36292536 C_ quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA-RAINED...	572	0.0E+00	
					jgi:36318712 C_ quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA-RAINED...	479	3.0E-162	
AT3G14440	NCED3	599	jgi:C_Quinoa_Scaffold_1770_392_Cquinoa392/v1.0	713	0.0E+00	jgi:36306192 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	781	0.0E+00
			jgi:C_Quinoa_Scaffold_2674_392_Cquinoa392/v1.0	710	0.0E+00	jgi:36303079 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	774	0.0E+00
			jgi:C_Quinoa_Scaffold_1747_392_Cquinoa392/v1.0	564	6.0E-158	jgi:36301918 C_ quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA-RAINED...	711	0.0E+00
					jgi:36304873 C_ quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA-RAINED...	684	0.0E+00	
					jgi:36292536 C_ quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA-RAINED...	616	0.0E+00	
					jgi:36318712 C_ quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA-RAINED...	571	0.0E+00	
AT1G30100	NCED5	589	jgi:C_Quinoa_Scaffold_1747_392_Cquinoa392/v1.0	579	2.0E-162	jgi:36303079 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	803	0.0E+00
			jgi:C_Quinoa_Scaffold_1000_392_Cquinoa392/v1.0	521	5.0E-145	jgi:36306192 C_ quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA-RAINED...	801	0.0E+00
			jgi:C_Quinoa_Scaffold_2674_392_Cquinoa392/v1.0	519	2.0E-144	jgi:36301918 C_ quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA-RAINED...	773	0.0E+00
					jgi:36304873 C_ quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA-RAINED...	725	0.0E+00	
					jgi:36292536 C_ quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA-RAINED...	670	0.0E+00	
					jgi:36318712 C_ quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA-RAINED...	557	0.0E+00	
AT3G24220	NCED6	577	jgi:C_Quinoa_Scaffold_2888_392_Cquinoa392/v1.0	400	1.0E-108	jgi:36303079 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	639	0.0E+00
			jgi:C_Quinoa_Scaffold_3458_392_Cquinoa392/v1.0	394	5.0E-107	jgi:36318712 C_ quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA-RAINED...	634	0.0E+00
			jgi:C_Quinoa_Scaffold_1770_392_Cquinoa392/v1.0	185	4.0E-44	jgi:36306192 C_ quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA-RAINED...	632	0.0E+00
					jgi:36301918 C_ quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA-RAINED...	604	0.0E+00	
					jgi:36304873 C_ quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA-RAINED...	575	0.0E+00	
					jgi:36292536 C_ quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA-RAINED...	521	0.0E+00	
AT1G78390	NCED9	657	jgi:C_Quinoa_Scaffold_2674_392_Cquinoa392/v1.0	505	4.0E-140	jgi:36306192 C_ quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA-RAINED...	754	0.0E+00
			jgi:C_Quinoa_Scaffold_1770_392_Cquinoa392/v1.0	477	6.0E-132	jgi:36303079 C_ quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA-RAINED...	753	0.0E+00
			jgi:C_Quinoa_Scaffold_1747_392_Cquinoa392/v1.0	453	2.0E-124	jgi:36301918 C_ quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA-RAINED...	724	0.0E+00
					jgi:36304873 C_ quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA-RAINED...	681	0.0E+00	
					jgi:36292536 C_ quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA-RAINED...	613	0.0E+00	
					jgi:36318712 C_ quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA-RAINED...	564	0.0E+00	

plus direct search for *C. quinoa* sequences (Phytozome)

Verification of *C. quinoa* NCED genes and transcript sequences

Identified potential *C. quinoa* NCED sequences

Primer design for PCR cloning of *C. album* sequences (Supplementary Table 1)

Sanger sequencing of *C. album* sequences and verification via BLAST analysis (Supplementary Figure 6) and phylogenetic trees (Figure 6A)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

Phytozome <i>Chenopodium quinoa</i> gene ID	Phytozome <i>Chenopodium quinoa</i> transcript	BLAST back to TAIR (BlastX using <i>Chenopodium quinoa</i> phytozome cds)	Score	E-value	DEG in <i>Chenopodium quinoa</i> seed transcriptome	Subgroup and name in phylogeny (Figure 7A)
AUR62002735	AUR62002735-RA	AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	772	0.0E+00	no	2/5 - CqNCED1
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	747	0.0E+00		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	740	0.0E+00		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT ...	729	0.0E+00		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	604	0.0E+00		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	329	2.0E-105		
AUR62030185	AUR62030185-RA	AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	744	0.0E+00	no	2/5 - CqNCED1
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	726	0.0E+00		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT ...	725	0.0E+00		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	723	0.0E+00		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	586	0.0E+00		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	302	5.0E-96		
AUR62003579	AUR62003579-RA	AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	670	0.0E+00	no	2/5 - CqNCED2
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	645	0.0E+00		
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	635	0.0E+00		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT ...	635	0.0E+00		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	520	0.0E+00		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	302	5.0E-96		
AUR62037951	AUR62037951-RA	AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	802	0.0E+00	no	3/9 - CqNCED1
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT ...	795	0.0E+00		
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	778	0.0E+00		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	758	0.0E+00		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	633	0.0E+00		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	381	8.0E-125		
AUR62043087	AUR62043087-RA	AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT...	801	0.0E+00	no	3/9 - CqNCED1
		AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	798	0.0E+00		
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	779	0.0E+00		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	753	0.0E+00		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	629	0.0E+00		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	375	9.0E-123		
AUR62015113	AUR62015113-RA	AT3G63520.1 Symbols: ATNCED1, ATCCD1, CCD1, NCED1 carotenoid ...	346	3.0E-112		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	634	0.0E+00	yes (Figure S5)	6 - CqNCED6
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	588	0.0E+00		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT ...	584	0.0E+00		
		AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	557	0.0E+00		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	553	0.0E+00		
AUR62017576	AUR62017576-RA	AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	501	2.0E-175	yes (Figure S5)	6 - CqNCED6
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT...	461	1.0E-159		
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	459	3.0E-158		
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	438	6.0E-151		
		AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	436	5.0E-150		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	253	1.0E-78		
AUR62017575	AUR62017575-RA	AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	121	9.0E-33	no	6*
		AT4G18350.1 Symbols: ATNCED2, NCED2 NINE-CIS-EPOXYCAROTENOID ...	113	7.0E-30		"short sequence, not included in phylogeny
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	110	1.0E-28		
		AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	103	2.0E-26		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT...	96	1.0E-23		
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	79	7.0E-18		
AUR62025811	AUR62025811-RA	AT3G63520.1 Symbols: ATNCED1, ATCCD1, CCD1, NCED1 carotenoid ...	877	0.0E+00	yes (Figure S5)	1/4 - CqCCD1
		AT4G19170.1 Symbols: NCED4, CCD4 carotenoid cleavage dioxygen...	330	6.0E-106		
		AT1G30100.1 Symbols: NCED5, ATNCED5 nine-cis-epoxycarotenoid ...	323	4.0E-103		
		AT3G24220.1 Symbols: NCED6, ATNCED6 nine-cis-epoxycarotenoid ...	322	6.0E-103		
		AT1G78390.1 Symbols: ATNCED9, NCED9 NINE-CIS-EPOXYCAROTENOID ...	320	3.0E-101		
		AT3G14440.1 Symbols: SIS7, ATNCED3, NCED3, STO1 SALT TOLERANT...	310	4.0E-98		

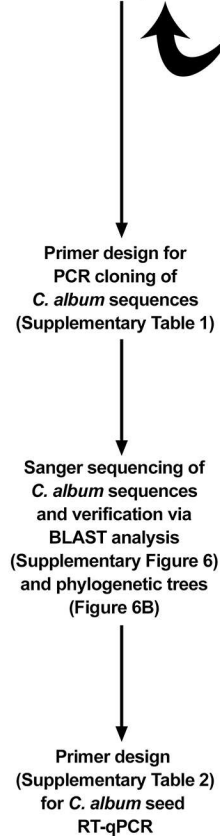
Figure S4 continued next page...

E BLAST analysis of CYP707A genes to identify *Chenopodium quinoa* sequences as templates for primer design

Arabidopsis thaliana gene identifier	Gene	Protein length (aa)	BlastN vs predicted (Phytozome website)	Score	E-value	BlastX vs <i>Chenopodium quinoa</i> transcripts (Phytozome website)	Score	E-value
AT4G19230	CYP707A1	484	g C_Quinoa_Scaffold_3973_392_Cquinoa 392 v1.0	233	1.0E-58	g 36319720_C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP7...	684	0.0E+00
			g C_Quinoa_Scaffold_1280_392_Cquinoa 392 v1.0	224	5.0E-56	g 36294192_C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP7...	665	0.0E+00
			g C_Quinoa_Scaffold_2493_392_Cquinoa 392 v1.0	126	4.0E-26	g 36321619_C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP7...	533	0.0E+00
AT2G29090	CYP707A2	482	g C_Quinoa_Scaffold_2716_392_Cquinoa 392 v1.0	187	1.0E-44	g 36321619_C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP7...	618	0.0E+00
			g C_Quinoa_Scaffold_2493_392_Cquinoa 392 v1.0	159	2.0E-36	g 36319720_C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP7...	529	0.0E+00
			g C_Quinoa_Scaffold_4480_392_Cquinoa 392 v1.0	96	7.0E-17	g 36294192_C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP7...	523	0.0E+00
AT5G45340	CYP707A3	463	g C_Quinoa_Scaffold_3973_392_Cquinoa 392 v1.0	211	1.0E-51	g 36292451_C_quinoa_v1_0 392 AUR62003877-RA AUR62003877-RA CYP7...	392	2.0E-121
			g C_Quinoa_Scaffold_1280_392_Cquinoa 392 v1.0	201	6.0E-49	g 36319720_C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP7...	716	0.0E+00
			g C_Quinoa_Scaffold_2493_392_Cquinoa 392 v1.0	159	2.0E-36	g 36294192_C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP7...	699	0.0E+00
AT3G19270	CYP707A4	443	g C_Quinoa_Scaffold_2493_392_Cquinoa 392 v1.0	94	2.0E-16	g 36319720_C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP7...	507	7.0E-178
			g C_Quinoa_Scaffold_2716_392_Cquinoa 392 v1.0	90	2.0E-15	g 36321619_C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP7...	495	1.0E-173
			g C_Quinoa_Scaffold_3973_392_Cquinoa 392 v1.0	86	2.0E-14	g 36294192_C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP7...	490	2.0E-171
						g 36292451_C_quinoa_v1_0 392 AUR62003877-RA AUR62003877-RA CYP7...	448	3.0E-145
						g 36289290_C_quinoa_v1_0 392 AUR62001933-RA AUR62001933-RA CYP7...	321	1.0E-107

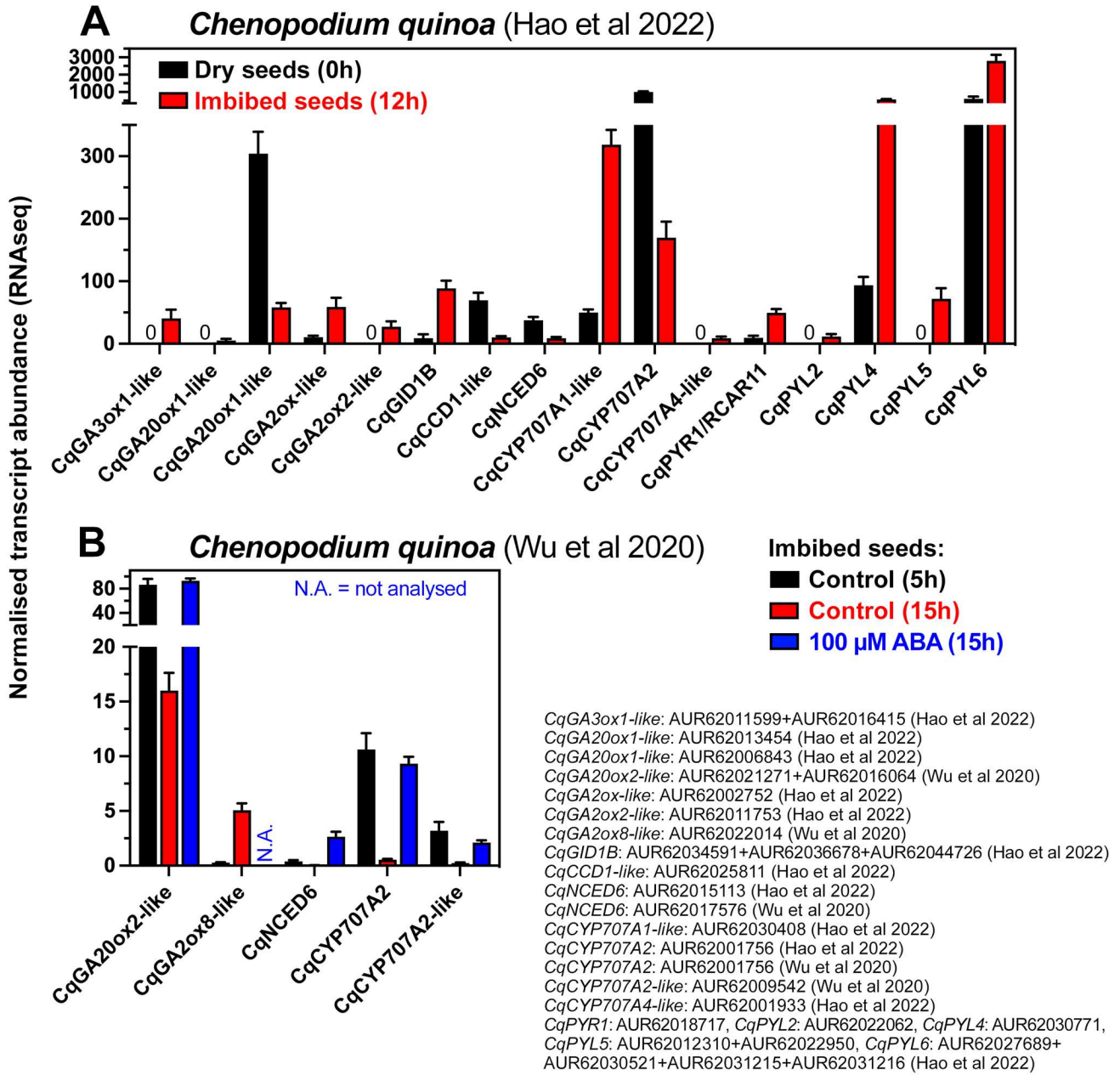
plus direct search for *C. quinoa* sequences (Phytozome)

Verification of *C. quinoa* CYP707A genes and transcript sequences ← Identified potential *C. quinoa* CYP707A sequences



Phytozome <i>Chenopodium quinoa</i> gene ID	Phytozome <i>Chenopodium quinoa</i> transcript	BLAST back to TAIR (BlastX using <i>Chenopodium quinoa</i> phytozome cds)	Score	E-value	DEG in <i>Chenopodium quinoa</i> seed transcriptome	Subgroup and name in phylogeny (Figure 7B)
AUR62030408	AUR62030408-RA	AT4G19230.1 Symbols: CYP707A1 *cytochrome P450, family 707, s...	716	0.0E+00	yes (Figure S5)	1/3 - CqCYP707A1-like
		AT5G45340.1 Symbols: CYP707A3 *cytochrome P450, family 707, s...	705	0.0E+00		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	673	0.0E+00		
		AT5G45340.2 Symbols: CYP707A3 *cytochrome P450, family 707, s...	658	0.0E+00		
		AT2G29090.2 Symbols: CYP707A2 *cytochrome P450, family 707, s...	532	0.0E+00		
		AT2G29090.1 Symbols: CYP707A2 *cytochrome P450, family 707, s...	532	0.0E+00		
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	526	0.0E+00		
		AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	498	9.0E-175		
AUR62010485	AUR62010485-RA	AT4G19230.1 Symbols: CYP707A1 *cytochrome P450, family 707, s...	708	0.0E+00	no	1/3 - CqCYP707A1-like
		AT5G45340.1 Symbols: CYP707A3 *cytochrome P450, family 707, s...	699	0.0E+00		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	665	0.0E+00		
		AT5G45340.2 Symbols: CYP707A3 *cytochrome P450, family 707, s...	652	0.0E+00		
		AT2G29090.2 Symbols: CYP707A2 *cytochrome P450, family 707, s...	533	0.0E+00		
		AT2G29090.1 Symbols: CYP707A2 *cytochrome P450, family 707, s...	533	0.0E+00		
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	519	0.0E+00		
		AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	491	3.0E-172		
AUR62009542	AUR62009542-RA	AT2G29090.2 Symbols: CYP707A2 *cytochrome P450, family 707, s...	630	0.0E+00	yes (Figure S5)	2 - CqCYP707A2-like
		AT2G29090.1 Symbols: CYP707A2 *cytochrome P450, family 707, s...	630	0.0E+00		
		AT4G19230.1 Symbols: CYP707A1 *cytochrome P450, family 707, s...	565	0.0E+00		
		AT2G29090.3 Symbols: CYP707A2 *cytochrome P450, family 707, s...	552	0.0E+00		
		AT5G45340.1 Symbols: CYP707A3 *cytochrome P450, family 707, s...	550	0.0E+00		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	533	0.0E+00		
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	527	0.0E+00		
		AT5G45340.2 Symbols: CYP707A3 *cytochrome P450, family 707, s...	518	0.0E+00		
		AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	496	1.0E-174		
AUR62001756	AUR62001756-RA	AT2G29090.4 Symbols: CYP707A2 *cytochrome P450, family 707, s...	286	6.0E-95	yes (Figure S5)	2 - CqCYP707A2
		AT2G29090.2 Symbols: CYP707A2 *cytochrome P450, family 707, s...	286	3.0E-93		
		AT2G29090.1 Symbols: CYP707A2 *cytochrome P450, family 707, s...	286	3.0E-93		
		AT2G29090.3 Symbols: CYP707A2 *cytochrome P450, family 707, s...	275	8.0E-90		
		AT4G19230.1 Symbols: CYP707A1 *cytochrome P450, family 707, s...	246	1.0E-77		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	246	2.0E-77		
		AT5G45340.1 Symbols: CYP707A3 *cytochrome P450, family 707, s...	241	8.0E-76		
		AT5G45340.2 Symbols: CYP707A3 *cytochrome P450, family 707, s...	238	1.0E-74		
		AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	234	2.0E-73		
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	234	6.0E-73		
		AT5G14400.2 Symbols: CYP724A1 *cytochrome P450, family 724, s...	139	2.0E-37		
AUR62001933	AUR62001933-RA	AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	322	1.0E-108	yes (Figure S5)	4 - CqCYP707A4-like
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	321	4.0E-108		
		AT4G19230.1 Symbols: CYP707A1 *cytochrome P450, family 707, s...	279	1.0E-91		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	279	2.0E-91		
		AT5G45340.2 Symbols: CYP707A3 *cytochrome P450, family 707, s...	276	5.0E-91		
		AT5G45340.1 Symbols: CYP707A3 *cytochrome P450, family 707, s...	277	6.0E-91		
		AT2G29090.3 Symbols: CYP707A2 *cytochrome P450, family 707, s...	234	5.0E-75		
		AT2G29090.2 Symbols: CYP707A2 *cytochrome P450, family 707, s...	233	1.0E-73		
		AT2G29090.1 Symbols: CYP707A2 *cytochrome P450, family 707, s...	233	1.0E-73		
		AT2G29090.4 Symbols: CYP707A2 *cytochrome P450, family 707, s...	182	2.0E-55		
AUR62003877	AUR62003877-RA	AT3G19270.1 Symbols: CYP707A4 *cytochrome P450, family 707, s...	429	4.0E-138	no	4 - CqCYP707A4-like
		AT3G19270.2 Symbols: CYP707A4 *cytochrome P450, family 707, s...	429	8.0E-138		
		AT3G09040.4 Symbols: MEF12 mitochondrial RNA editing factor 1...	412	9.0E-125		
		AT3G09040.1 Symbols: MEF12 mitochondrial RNA editing factor 1...	412	9.0E-125		
		AT3G09040.3 Symbols: MEF12 mitochondrial RNA editing factor 1...	413	1.0E-124		
		AT3G09040.2 Symbols: MEF12 mitochondrial RNA editing factor 1...	413	1.0E-124		
		AT1G16480.1 Symbols: no symbol available no full name availab...	394	6.0E-119		
		AT4G19230.2 Symbols: CYP707A1 *cytochrome P450, family 707, s...	377	5.0E-118		

Supplementary Figure 4 | BLAST analysis of *Chenopodium quinoa* GA and ABA metabolism gene transcripts. To identify *Chenopodium* sequences the *C. quinoa* genome was mined and BLAST analyses conducted with the *A. thaliana* and *C. quinoa* transcript sequences via TAIR and Phytozome as presented in the workflow and tables. For further details and references see the main text.



Supplementary Figure 5 | Transcript expression patterns of GA and ABA metabolism genes during *Chenopodium quinoa* seed germination. Differentially expressed genes from the published transcriptomes of Hao et al. (2022) and Wu et al. (2020) are presented. For further details and the references see the main text. Presented mean \pm SEM values are the cumulative transcript abundances for the corresponding *C. quinoa* genes listed in the table. See Figures 5, 6, S4 and S7 for BLAST analyses and phylogenies of the *C. quinoa* sequences.

A BLAST analysis against *Chenopodium quinoa* of *Chenopodium album* sequences used as templates for RT-qPCR primer design

Verification of *C. album* sequences via BLAST analysis (this table) and phylogenetic trees (Figures 5, 6 and S7)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

Chenopodium album seed RT-qPCR (Figures 7)

<i>C. album</i> gene name (sequence name)	Genebank accession number	Length (bp)*	BLASTX vs Phytozome (<i>Chenopodium album</i> versus <i>Chenopodium quinoa</i>)	Score	E-value	RT-qPCR results
CalGA20ox1 (EL36)	OQ360684	650	jgi:36319174 C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20ox...	227	1.0E-74	none
			jgi:36311734 C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20ox...	226	6.0E-73	
			jgi:36318333 C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20ox...	182	8.0E-56	
			jgi:36288619 C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20ox...	179	1.0E-54	
			jgi:36292046 C_quinoa_v1_0 392 AUR62013454-RA AUR62013454-RA GA20ox...	142	1.0E-40	
			jgi:36285500 C_quinoa_v1_0 392 AUR62007685-RA AUR62007685-RA GA20ox...	141	2.0E-40	
CalGA20ox2 (EL39)	OQ351935	374	jgi:36288619 C_quinoa_v1_0 392 AUR62016064-RA AUR62016064-RA GA20ox...	196	2.0E-62	Figure 7
			jgi:36318333 C_quinoa_v1_0 392 AUR62021271-RA AUR62021271-RA GA20ox...	193	1.0E-61	
			jgi:36319174 C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20ox...	118	2.0E-33	
			jgi:36311734 C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20ox...	120	2.0E-33	
			jgi:36302756 C_quinoa_v1_0 392 AUR62006843-RA AUR62006843-RA GA20ox...	96	1.0E-24	
			jgi:36298246 C_quinoa_v1_0 392 AUR62000497-RA AUR62000497-RA GA20ox...	96	2.0E-24	
CalGA20ox3 (EL37)	OQ351936	311	jgi:36292046 C_quinoa_v1_0 392 AUR62013454-RA AUR62013454-RA GA20ox...	217	3.0E-69	Figure 7
			jgi:36285500 C_quinoa_v1_0 392 AUR62007685-RA AUR62007685-RA GA20ox...	147	1.0E-42	
			jgi:36311734 C_quinoa_v1_0 392 AUR62033388-RA AUR62033388-RA GA20ox...	92	2.0E-21	
			jgi:36319174 C_quinoa_v1_0 392 AUR62004269-RA AUR62004269-RA GA20ox...	91	2.0E-21	
			jgi:36302756 C_quinoa_v1_0 392 AUR62006843-RA AUR62006843-RA GA20ox...	90	5.0E-21	
			jgi:36298246 C_quinoa_v1_0 392 AUR62000497-RA AUR62000497-RA GA20ox...	87	5.0E-20	
CalGA3ox1/2 (EL51)	OQ360685	654	jgi:36290230 C_quinoa_v1_0 392 AUR62016415-RA AUR62016415-RA LE: GA3c...	196	7.0E-64	Figure 7
			jgi:36308453 C_quinoa_v1_0 392 AUR62011599-RA AUR62011599-RA LE: GA3c...	193	5.0E-60	
			jgi:36305840 C_quinoa_v1_0 392 AUR62032368-RA AUR62032368-RA LE: GA3c...	119	9.0E-32	
			jgi:36284702 C_quinoa_v1_0 392 AUR62024851-RA AUR62024851-RA LE: GA3c...	117	5.0E-31	
			jgi:36294240 C_quinoa_v1_0 392 AUR62038695-RA AUR62038695-RA GA3ox...	110	3.0E-30	
			jgi:36307459 C_quinoa_v1_0 392 AUR62032673-RA AUR62032673-RA GA3ox...	112	3.0E-30	
CalGA3ox3/4 (EL12)	OQ351937	224	jgi:36302364 C_quinoa_v1_0 392 AUR62032075-RA AUR62032075-RA GA3ox...	116	5.0E-35	Figure 7
			jgi:36307459 C_quinoa_v1_0 392 AUR62032673-RA AUR62032673-RA GA3ox...	111	4.0E-32	
			jgi:36294240 C_quinoa_v1_0 392 AUR62038695-RA AUR62038695-RA GA3ox...	92	2.0E-25	
			jgi:36294241 C_quinoa_v1_0 392 AUR62038693-RA AUR62038693-RA LE: GA3c...	94	1.0E-24	
			jgi:36305840 C_quinoa_v1_0 392 AUR62032368-RA AUR62032368-RA LE: GA3c...	92	7.0E-24	
			jgi:36294257 C_quinoa_v1_0 392 AUR62038694-RA AUR62038694-RA ACO2...	88	9.0E-23	
CalGA3ox1/4 (EL13)	OQ351938	184	jgi:36320333 C_quinoa_v1_0 392 AUR62032076-RA AUR62032076-RA LE: GA3c...	126	7.0E-39	Figure 7
			jgi:36284702 C_quinoa_v1_0 392 AUR62024851-RA AUR62024851-RA LE: GA3c...	104	1.0E-28	
			jgi:36305840 C_quinoa_v1_0 392 AUR62032368-RA AUR62032368-RA LE: GA3c...	103	2.0E-28	
			jgi:36294241 C_quinoa_v1_0 392 AUR62038693-RA AUR62038693-RA LE: GA3c...	102	7.0E-28	
			jgi:36294257 C_quinoa_v1_0 392 AUR62038694-RA AUR62038694-RA ACO2...	79	2.0E-19	
			jgi:36301471 C_quinoa_v1_0 392 AUR62035812-RA AUR62035812-RA SRG1...	70	5.0E-16	
CalGA20x2 (EL45)	OQ360686	180	jgi:36301611 C_quinoa_v1_0 392 AUR62002752-RA AUR62002752-RA GA20ox...	100	4.0E-27	Figure 7
			jgi:36304895 C_quinoa_v1_0 392 AUR62030199-RA AUR62030199-RA GA20ox...	93	2.0E-25	
			jgi:36310380 C_quinoa_v1_0 392 AUR62024597-RA AUR62024597-RA GA20ox...	44	7.0E-07	
			jgi:36311284 C_quinoa_v1_0 392 AUR62011753-RA AUR62011753-RA GA20ox...	44	2.0E-06	
CalNCED3 (EL02)	OQ351932	1053	jgi:36303079 C_quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA NCED...	425	7.0E-146	Figure 7
			jgi:36306192 C_quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA NCED...	420	6.0E-144	
			jgi:36304873 C_quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA NCED...	318	3.0E-140	
			jgi:36301918 C_quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA NCED...	281	8.0E-136	
			jgi:36318712 C_quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA NCED...	266	9.0E-109	
			jgi:36291573 C_quinoa_v1_0 392 AUR62017576-RA AUR62017576-RA NCED...	266	1.0E-86	
CalNCED5 (EL49)	OQ360683	981	jgi:36304873 C_quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA NCED...	621	0.0E+00	Figure 7
			jgi:36301918 C_quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA NCED...	613	0.0E+00	
			jgi:36292536 C_quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA NCED...	506	1.0E-179	
			jgi:36306192 C_quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA NCED...	500	8.0E-176	
			jgi:36303079 C_quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA NCED...	492	2.0E-172	
			jgi:36318712 C_quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA NCED...	411	3.0E-142	
CalNCED6A (EL07)	OQ351933	821	jgi:36291573 C_quinoa_v1_0 392 AUR62017576-RA AUR62017576-RA NCED...	449	7.0E-160	Figure 7
			jgi:36318712 C_quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA NCED...	439	3.0E-154	
			jgi:36304873 C_quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA NCED...	293	3.0E-97	
			jgi:36306192 C_quinoa_v1_0 392 AUR62043087-RA AUR62043087-RA NCED...	292	2.0E-95	
			jgi:36303079 C_quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA NCED...	292	2.0E-95	
			jgi:36301918 C_quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA NCED...	261	9.0E-84	
CalNCED6B (EL16)	OQ351934	307	jgi:36291595 C_quinoa_v1_0 392 AUR62017575-RA AUR62017575-RA NCED...	205	5.0E-70	Figure 7
			jgi:36318712 C_quinoa_v1_0 392 AUR62015113-RA AUR62015113-RA NCED...	91	1.0E-22	
			jgi:36301918 C_quinoa_v1_0 392 AUR62002735-RA AUR62002735-RA NCED...	74	2.0E-16	
			jgi:36304873 C_quinoa_v1_0 392 AUR62030185-RA AUR62030185-RA NCED...	72	6.0E-16	
			jgi:36292536 C_quinoa_v1_0 392 AUR62003579-RA AUR62003579-RA NCED...	70	3.0E-15	
			jgi:36303079 C_quinoa_v1_0 392 AUR62037951-RA AUR62037951-RA NCED...	68	2.0E-14	
CalCYP707A1/3 (EL61)	OQ351929	411	jgi:36319720 C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP707...	135	2.0E-38	Figure 7
			jgi:36321619 C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP707...	115	4.0E-31	
			jgi:36294192 C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP707...	111	1.0E-29	
			jgi:36314201 C_quinoa_v1_0 392 AUR62001756-RA AUR62001756-RA CYP707...	88	3.0E-21	
			jgi:36292451 C_quinoa_v1_0 392 AUR62003877-RA AUR62003877-RA CYP707...	78	2.0E-17	
			jgi:36310554 C_quinoa_v1_0 392 AUR62019994-RA AUR62019994-RA KAO1...	68	5.0E-14	
CalCYP707A2 (EL65)	OQ351930	465	jgi:36321619 C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP707...	247	1.0E-81	Figure 7
			jgi:36319720 C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP707...	140	4.0E-40	
			jgi:36294192 C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP707...	126	7.0E-35	
			jgi:36292451 C_quinoa_v1_0 392 AUR62003877-RA AUR62003877-RA CYP707...	114	1.0E-29	
			jgi:36314201 C_quinoa_v1_0 392 AUR62001756-RA AUR62001756-RA CYP707...	97	2.0E-24	
			jgi:36289290 C_quinoa_v1_0 392 AUR62001933-RA AUR62001933-RA CYP707...	89	6.0E-22	
CalCYP707A4 (EL67)	OQ351931	511	jgi:36289290 C_quinoa_v1_0 392 AUR62001933-RA AUR62001933-RA CYP707...	340	2.0E-120	Figure 7
			jgi:36292451 C_quinoa_v1_0 392 AUR62003877-RA AUR62003877-RA CYP707...	349	5.0E-113	
			jgi:36319720 C_quinoa_v1_0 392 AUR62030408-RA AUR62030408-RA CYP707...	146	6.0E-42	
			jgi:36294192 C_quinoa_v1_0 392 AUR62010485-RA AUR62010485-RA CYP707...	137	9.0E-39	
			jgi:36321619 C_quinoa_v1_0 392 AUR62009542-RA AUR62009542-RA CYP707...	127	4.0E-35	
			jgi:36293993 C_quinoa_v1_0 392 AUR62010642-RA AUR62010642-RA CYP8...	83	8.0E-19	

* Length of deposited *C. album* sequence in Genebank

Figure S6 continued next page...

B BLAST analysis against *Arabidopsis thaliana* of *Chenopodium album* sequences used as templates for RT-qPCR primer design

Verification of *C. album* sequences via BLAST analysis (this table) and phylogenetic trees (Figures 5, 6 and S7)

Primer design (Supplementary Table 2) for *C. album* seed RT-qPCR

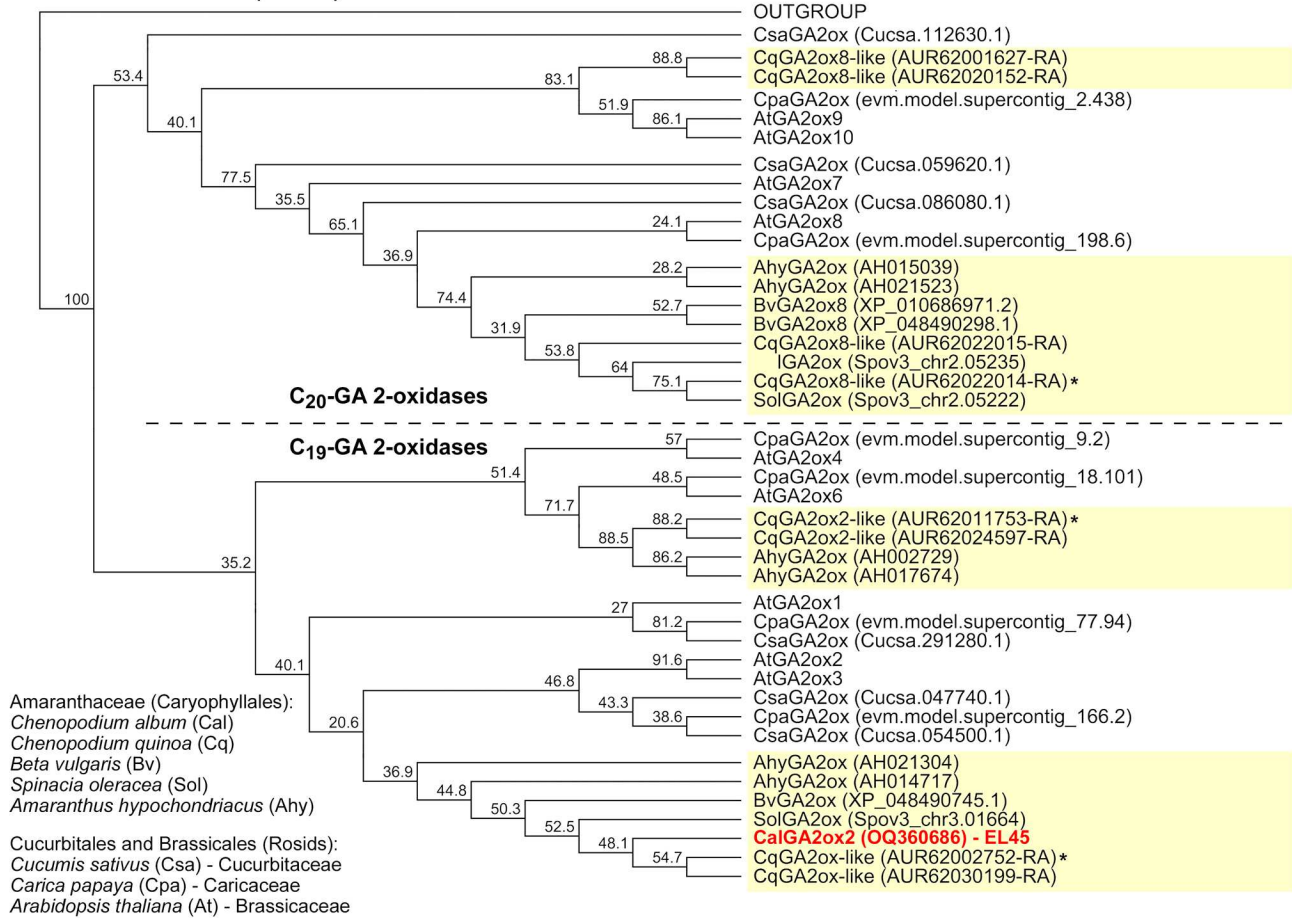
Chenopodium album seed RT-qPCR (Figures 7)

<i>C. album</i> gene name (sequence name)	Genebank accession number	Length (bp)*	BLASTX vs TAIR (<i>Chenopodium album</i> versus <i>Arabidopsis thaliana</i>)	Score	E-value	RT-qPCR results
CalGA20ox1 (EL36)	OQ360684	650	AT4G25420.2 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	197	2.0E-62	none
			AT5G51810.2 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	194	2.0E-61	
			AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	196	3.0E-61	
			AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	192	1.0E-59	
			AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	180	6.0E-55	
			AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	169	8.0E-51	
CalGA20ox2 (EL39)	OQ351935	374	AT5G51810.2 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	137	1.0E-40	Figure 7
			AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	137	6.0E-40	
			AT4G25420.2 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	123	5.0E-35	
			AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	123	2.0E-34	
			AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	113	1.0E-30	
			AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	112	2.0E-30	
CalGA20ox3 (EL37)	OQ351936	311	AT4G25420.2 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	96	5.0E-23	Figure 7
			AT4G25420.1 Symbols: ATGA20OX1, AT2301, GA5, GA20OX1 ARABIDOP...	96	1.0E-22	
			AT5G51810.2 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	90	4.0E-21	
			AT5G51810.1 Symbols: AT2353, ATGA20OX2, GA20OX2 gibberellin 2...	90	1.0E-20	
			AT5G07200.1 Symbols: ATGA20OX3, YAP169, GA20OX3 gibberellin 2...	78	2.0E-16	
			AT1G60980.1 Symbols: GA20OX4, ATGA20OX4 gibberellin 20-oxidas...	76	2.0E-15	
CalGA3ox1/2 (EL51)	OQ360685	654	AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	123	2.0E-33	Figure 7
			AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	117	3.0E-31	
			AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	110	2.0E-28	
			AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	106	5.0E-27	
			AT1G78550.1 Symbols: no symbol available no full name availab...	61	7.0E-11	
			AT1G17010.1 Symbols: no symbol available no full name availab...	60	3.0E-10	
CalGA3ox3/4 (EL12)	OQ351937	224	AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	52	3.0E-09	Figure 7
			AT1G80340.1 Symbols: GA4H, GA3OX2, ATGA3OX2 ARABIDOPSIS THALI...	45	7.0E-07	
			AT4G21690.1 Symbols: ATGA3OX3, GA3OX3 ARABIDOPSIS THALIANA GI...	44	1.0E-06	
			AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	44	2.0E-06	
			AT3G19010.2 Symbols: no symbol available no full name availab...	37	4.0E-04	
			AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	37	6.0E-04	
CalGA3ox1/4 (EL13)	OQ351938	184	AT1G80330.1 Symbols: GA3OX4, ATGA3OX4 gibberellin 3-oxidase 4...	73	4.0E-17	Figure 7
			AT4G25310.1 Symbols: no symbol available no full name availab...	72	7.0E-17	
			AT1G17020.1 Symbols: ATSRG1, SRG1 SENESCENCE-RELATED GENE 1, ...	71	4.0E-16	
			AT4G21200.1 Symbols: ATGA2OX8, GA2OX8 gibberellin 2-oxidase 8...	70	6.0E-16	
			AT1G15550.1 Symbols: GA4, ATGA3OX1, GA3OX1 ARABIDOPSIS THALIA...	70	7.0E-16	
			AT4G25300.2 Symbols: no symbol available no full name availab...	69	9.0E-16	
CalGA2ox2 (EL45)	OQ360686	180	AT1G30040.2 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	57	3.0E-11	Figure 7
			AT1G30040.1 Symbols: ATGA2OX2, GA2OX2 gibberellin 2-oxidase, ...	57	3.0E-11	
			AT2G34555.1 Symbols: GA2OX3, ATGA2OX3 gibberellin 2-oxidase 3...	52	9.0E-10	
			AT1G78440.1 Symbols: GA2OX1, ATGA2OX1 gibberellin 2-oxidase 1...	52	1.0E-09	
			AT1G02400.2 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	51	3.0E-09	
			AT1G02400.1 Symbols: ATGA2OX6, DTA1, ATGA2OX4, GA2OX6 Arabido...	51	3.0E-09	
CalNCED3 (EL02)	OQ351932	1053	AT1G30100.1 Symbols: NCEd5, ATNCEd5 nine-cis-epoxycarotenoid ...	325	8.0E-154	Figure 7
			AT3G14440.1 Symbols: SIS7, ATNCEd3, NCEd3, STO1 SALT TOLERANT...	334	1.0E-151	
			AT1G78390.1 Symbols: ATNCEd9, NCEd9 NINE-CIS-EPOXYCAROTENOID ...	325	3.0E-147	
			AT4G18350.1 Symbols: ATNCEd2, NCEd2 NINE-CIS-EPOXYCAROTENOID ...	320	4.0E-143	
			AT3G24220.1 Symbols: NCEd6, ATNCEd6 nine-cis-epoxycarotenoid ...	280	2.0E-112	
			AT4G19170.1 Symbols: NCEd4, CCD4 carotenoid cleavage dioxygen...	169	6.0E-64	
CalNCED5 (EL49)	OQ360683	981	AT3G14440.1 Symbols: SIS7, ATNCEd3, NCEd3, STO1 SALT TOLERANT...	523	0.0E+00	Figure 7
			AT1G30100.1 Symbols: NCEd5, ATNCEd5 nine-cis-epoxycarotenoid ...	512	2.0E-180	
			AT1G78390.1 Symbols: ATNCEd9, NCEd9 NINE-CIS-EPOXYCAROTENOID ...	513	4.0E-180	
			AT4G18350.1 Symbols: ATNCEd2, NCEd2 NINE-CIS-EPOXYCAROTENOID ...	504	1.0E-177	
			AT3G24220.1 Symbols: NCEd6, ATNCEd6 nine-cis-epoxycarotenoid ...	415	2.0E-142	
			AT3G63520.1 Symbols: ATNCEd1, ATCCD1, CCD1, NCEd1 carotenoid ...	224	5.0E-69	
CalNCED6A (EL07)	OQ351933	821	AT3G24220.1 Symbols: NCEd6, ATNCEd6 nine-cis-epoxycarotenoid ...	322	4.0E-107	Figure 7
			AT3G14440.1 Symbols: SIS7, ATNCEd3, NCEd3, STO1 SALT TOLERANT...	310	4.0E-102	
			AT1G78390.1 Symbols: ATNCEd9, NCEd9 NINE-CIS-EPOXYCAROTENOID ...	303	5.0E-99	
			AT4G18350.1 Symbols: ATNCEd2, NCEd2 NINE-CIS-EPOXYCAROTENOID ...	298	1.0E-97	
			AT1G30100.1 Symbols: NCEd5, ATNCEd5 nine-cis-epoxycarotenoid ...	284	4.0E-92	
			AT3G63520.1 Symbols: ATNCEd1, ATCCD1, CCD1, NCEd1 carotenoid ...	164	6.0E-47	
CalNCED6B (EL16)	OQ351934	307	AT3G24220.1 Symbols: NCEd6, ATNCEd6 nine-cis-epoxycarotenoid ...	73	3.0E-16	Figure 7
			AT4G18350.1 Symbols: ATNCEd2, NCEd2 NINE-CIS-EPOXYCAROTENOID ...	69	1.0E-14	
			AT1G78390.1 Symbols: ATNCEd9, NCEd9 NINE-CIS-EPOXYCAROTENOID ...	68	1.0E-14	
			AT1G30100.1 Symbols: NCEd5, ATNCEd5 nine-cis-epoxycarotenoid ...	66	1.0E-13	
			AT3G14440.1 Symbols: SIS7, ATNCEd3, NCEd3, STO1 SALT TOLERANT...	58	5.0E-11	
			AT4G19170.1 Symbols: NCEd4, CCD4 carotenoid cleavage dioxygen...	46	7.0E-07	
CalCYP707A1/3 (EL61)	OQ351929	411	AT5G45340.2 Symbols: CYP707A3 "cytochrome P450, family 707, s...	125	9.0E-35	Figure 7
			AT5G45340.1 Symbols: CYP707A3 "cytochrome P450, family 707, s...	125	1.0E-34	
			AT4G19230.1 Symbols: CYP707A1 "cytochrome P450, family 707, s...	121	3.0E-33	
			AT2G29090.3 Symbols: CYP707A2 "cytochrome P450, family 707, s...	120	4.0E-33	
			AT4G19230.2 Symbols: CYP707A1 "cytochrome P450, family 707, s...	120	1.0E-32	
			AT2G29090.2 Symbols: CYP707A2 "cytochrome P450, family 707, s...	119	3.0E-32	
CalCYP707A2 (EL65)	OQ351930	465	AT2G29090.3 Symbols: CYP707A2 "cytochrome P450, family 707, s...	158	2.0E-47	Figure 7
			AT2G29090.2 Symbols: CYP707A2 "cytochrome P450, family 707, s...	158	2.0E-46	
			AT2G29090.1 Symbols: CYP707A2 "cytochrome P450, family 707, s...	158	2.0E-46	
			AT4G19230.1 Symbols: CYP707A1 "cytochrome P450, family 707, s...	151	5.0E-44	
			AT4G19230.2 Symbols: CYP707A1 "cytochrome P450, family 707, s...	151	5.0E-44	
			AT5G45340.2 Symbols: CYP707A3 "cytochrome P450, family 707, s...	146	2.0E-42	
CalCYP707A4 (EL67)	OQ351931	511	AT3G19270.1 Symbols: CYP707A4 "cytochrome P450, family 707, s...	200	6.0E-63	Figure 7
			AT3G19270.2 Symbols: CYP707A4 "cytochrome P450, family 707, s...	200	1.0E-62	
			AT4G19230.1 Symbols: CYP707A1 "cytochrome P450, family 707, s...	163	2.0E-48	
			AT4G19230.2 Symbols: CYP707A1 "cytochrome P450, family 707, s...	163	2.0E-48	
			AT5G45340.2 Symbols: CYP707A3 "cytochrome P450, family 707, s...	161	7.0E-48	
			AT5G45340.1 Symbols: CYP707A3 "cytochrome P450, family 707, s...	161	9.0E-48	

*Length of deposited *C. album* sequence in Genebank

Supplementary Figure 6 | BLAST analysis of identified *Chenopodium album* GA and ABA metabolism gene sequences against *Chenopodium quinoa* (A) and *Arabidopsis thaliana* (B). PCR cloned *C. album* sequences EL36 (*CalGA20ox1*), EL39 (*CalGA20ox2*), EL37 (*CalGA20ox3*), EL51 (*CalGA3ox1/2*), EL12 (*CalGA3ox3/4*), EL13 (*CalGA3ox1/4*), EL45 (*CalGA2ox2*), EL02 (*CalNCED3*), EL02 (*CalNCED3*), EL49 (*CalNCED5*), EL07 (*CalNCED6A*), EL16 (*CalNCED6B*), EL61 (*CalCYP707A1/3*), EL65 (*CalCYP707A2*), EL67 (*CalCYP707A4*) with *Chenopodium album* Genbank accession numbers (BankIt sequence submissions #2664064 and #2668656). Naming of *C. album* GA-oxidase sequences was according to their top BLAST results for *A. thaliana* (Figure 5 and Supplementary Figure 7) which is not necessarily related to their subgroup in the phylogenetic trees (Supplementary Figure 6B). Naming of *C. album* NCED and CYP707A sequences was according to the subgroup in the phylogenetic trees (Figure 6) and their top BLAST results for *A. thaliana* (Supplementary Figure 6B). Note that *CalNCED6B* and its putative *C. quinoa* ortholog AUR62017575 are both short sequences which are according to BLAST analyses NCED6 homologs (Supplementary Figures 4D and 6). For further details and references see the main text.

Gibberellin 2-oxidases (GA2ox)



Supplementary Figure 7 | Phylogenetic tree of the predicted amino acid sequences of GA 2-oxidases (GA2ox). Known and putative amino acid NCED (A) and CYP707A (B) sequences of *Chenopodium quinoa*, *Chenopodium album* and other Amaranthaceae plus selected Brassicales and Cucurbitales species (as indicated) were aligned using ClustalW and Neighbor-Joining trees were built as described in methods. *Chenopodium quinoa* (Supplementary Figure 4) and the *C. album* (Supplementary Figure 6) sequence (*CalGA2ox2* - EL45) representing the C₁₉-GA 2-oxidase and C₂₀-GA 2-oxidase subgroups were identified. An * indicates identified DEGs during *C. quinoa* seed germination (Supplementary Figure 5).

Supplementary Table 1 | Primers used for PCR cloning of *Chenopodium album* sequences.

Name of amplified <i>C. album</i> sequence	Primer type	Primer sequence (5'-3')	Genbank accession number ^b
EL23 (<i>PUB33-like</i>) ^a	Forward	GTCATATCCCGGCACAAGA	OQ360687
	Reverse	TAAGCCTCCTCCTTAGCGGT	
EL25 (<i>ACT7-like</i>) ^a	Forward	GTCATGGTTGGTATGGGCCA	OQ360688
	Reverse	GTGAAGGCTGGAAGAGGACC	
EL27 (<i>CDC27B</i>) ^a	Forward	TTTTCAGCGAGCTGTGCAAC	OQ360689
	Reverse	GCAACTTTTCAATGGCAGCC	
EL02	Forward	CTTGACTCTCCAAAGAAAGCTTCA	OQ351932
	Reverse	AAGCTTGACTGTCGCAACCA	
EL49	Forward	ACAAGCTCTCCCTGTAAGCG	OQ360683
	Reverse	TCGCCCTAGTAAGTTCCGGT	
EL07	Forward	TGCACCGGTTTCAGGAACATC	OQ351933
	Reverse	CCTCATTTTCCTCCCATGCATTC	
EL16	Forward	GGAGCCGTGGCCTAAATGTA	OQ351934
	Reverse	AGGAACCCTTGAAGGCATGC	
EL61	Forward	AGAGAATCCCTCACCGACGA	OQ351929
	Reverse	TTGCCAGTTCATTGCCAGGA	
EL65	Forward	GCCCCTAAATTTCCCGGAA	OQ351930
	Reverse	CTGCGCAATGGTGAATGCTT	
EL67	Forward	TACTTTGGATTTCGTGGGCCG	OQ351931
	Reverse	TGCTGGCCATCCTTAAGCTC	
EL51	Forward	CGTGCTCAGTTGAGTCAGGT	OQ360685
	Reverse	GGTGGGTGGCATCAATGAGA	
EL12	Forward	CCTGAATCGCATAACATGGGC	OQ351937
	Reverse	TGGGGCTCGTAAAACCTTCA	
EL13	Forward	ACTGCCTTCCCTCTGAGACA	OQ351938
	Reverse	GCAAGCAATCATGAACCGCA	
EL36	Forward	CGGGTTCGATTTCGATGCAAC	OQ360684
	Reverse	CTAGGTCGAACAGCTTGCCA	
EL37	Forward	AGAAACTCGACGCCCAATT	OQ351936
	Reverse	GCATCATTGCGAGGTTTCGAC	
EL39	Forward	AAGCCTCATTGACCCGGAAG	OQ351935
	Reverse	CACTTTGTCCTTGCTTGGGC	
EL45	Forward	ACAGCTGGAAGACGAAGCTC	OQ360686
	Reverse	TCCTTCCGCCATTGTTTCCA	

^a Reference gene. ^b *Chenopodium album* BankIt sequence submissions #2664064 and #2668656.

Supplementary Table 2 | Primer sequences used for the *Chenopodium album* RT-qPCR analysis.

<i>C. album</i> gene name (sequence name)	Primer type	Primer sequence (5'-3')	Amplicon length (bp) ^b
<i>CalPUB33-like</i> (EL23) ^a	Forward	TGCTTTCTGCCACATCTGGT	142
	Reverse	ACACAGTCCAAGGATGCAGG	
<i>CalACT7-like</i> (EL25) ^a	Forward	GTCTCGTGGATACCTGCAGC	168
	Reverse	AGCTGAGAGATTCCGTTGCC	
<i>CalCDC27B</i> (EL27) ^a	Forward	CATGTATGATAAGGCCATGTTGCAT	117
	Reverse	GCAAGAAGTTACCTTTATGGTGGC	
<i>CalNCED3</i> (EL02)	Forward	CGTGATTGCGAAATCGTGCA	168
	Reverse	GCGCATCCTAAGGTAGACCC	
<i>CalNCED5</i> (EL49)	Forward	GTGATGGGATGGTCCATGCA	153
	Reverse	CAATCCCCGAATGTCCGTGA	
<i>CalNCED6A</i> (EL07)	Forward	GGAGTGGCTAATGCTGGTGT	159
	Reverse	GTGTGCAATCAACGGGCAAT	
<i>CalNCED6B</i> (EL16)	Forward	ACAAAGCATGGTTCCCCACC	108
	Reverse	GGAGCCGTGGCCTAAATGTA	
<i>CalCYP707A1/3</i> (EL61)	Forward	GGGTACCTAATTCCTAAAGGGTGG	97
	Reverse	AAGGGTCAAACCTTCTCAGGCTC	
<i>CalCYP707A2</i> (EL65)	Forward	AAGGAAGCTTCTAAATGGGGACAT	194
	Reverse	GCAGTAGTATCATGAGCAGCGA	
<i>CalCYP707A4</i> (EL67)	Forward	GGCAACAAAGGACCTTCTTGGA	117
	Reverse	GCTGTATCTTGAGCAGCAAACAGAA	
<i>CalGA3ox1/2</i> (EL51)	Forward	TGGTGTACGGGTTATGGCC	114
	Reverse	GGCCAAAGTTGACGAGCATG	
<i>CalGA3ox3/4</i> (EL12)	Forward	TTGCAATCCCGTGGTTTGTG	131
	Reverse	TGCCAATGAGAAGTCGCTGT	
<i>CalGA3ox1/4</i> (EL13)	Forward	CTCATATCCACCGTGCCCTG	108
	Reverse	TGGAGGCCACTTACATTGCC	
<i>CalGA20ox3</i> (EL37)	Forward	ACGTTGTCTTTCCCTCACCG	72
	Reverse	GCCTAAAGCCGAGGTGAAGT	
<i>CalGA20ox2</i> (EL39)	Forward	CTAGTGGGTGAGGCTTGCC	81
	Reverse	GGCATCCCTAACCAACTCGG	
<i>CalGA20ox2</i> (EL45)	Forward	CGTAATGGCGACGTTGGTTG	139
	Reverse	ACAGAGGAAAACAGAGTAGAGCG	

^a Reference gene. ^b Amplicon length based on *C. album* sequences verified by gel electrophoresis.