Supplemental Table 1. Two-way ANOVA and the broad-sense heritability (h_B^2) of the four traits in the RILs grown in the Y12 and Y13 environments

Trait	Source	Sum of square	*df*	Mean square	*F* value	*P*	H_B^2 (%)
OC	Genotype	10589.86	180	58.83	9.69	< 0.01	78.8
	Environment	6162.12	1	6162.12	1015.35	< 0.01	
	Genotype × environment	1901.21	180	10.56	1.74	< 0.01	
	Error	4393.943	724	6.07			
SL	Genotype	277.44	169	1.64	23.99	< 0.01	89.4
	Environment	9.14	1	9.15	133.71	< 0.01	
	Genotype × environment	31.69	169	0.19	2.74	< 0.01	
	Error	46.53	680	0.07			
SS	Genotype	7800.40	174	44.83	9.96	< 0.01	78.5
	Environment	2086.10	1	2086.10	463.28	< 0.01	
	Genotype × environment	1563.91	174	8.99	2.00	< 0.01	
	Error	3152	700	4.50			
SW	Genotype	151.86	185	0.82	12.93	< 0.01	81.9
	Environment	0.92	1	0.92	14.42	< 0.01	
	Genotype × environment	28.74	185	0.16	2.45	< 0.01	
	Error	47.25	744	0.06			

OC oil content, SL silique length, SS seeds per silique, SW seed weight

Supplemental Table 2. Phenotypic correlation analyses for the four traits in three environments

		OC	SL	SS	SW
Y11	OC				
	SL	0.264*			
	SS	0.302**	0.534**		
	SW	0.300**	0.263*	-0.095	
Y12	OC				
	SL	0.279*			
	SS	0.331**	0.449**		
	SW	-0.003	0.274*	-0.272*	
Y13	OC				
	SL	0.337**			
	SS	0.381**	0.513**		
	SW	0.206*	0.211*	-0.224*	

OC oil content, SL silique length, SS seeds per silique, SW seed weight

* Indicates significant at level of $P<0.05$

** Indicates significant at level of $P < 0.01$.

Supplemental Table 3. Genetic correlations analyses for the four traits in two environments

		OC	SL	SS	SW
Y12	OC				
	SL	0.48**			
	SS	0.49**	0.48**		
	SW	0.31**	0.43**	-0.13*	
Y13	OC				
	SL	0.53**			
	SS	0.49**	0.58**		
	SW	0.35**	0.38**	-0.11*	

OC oil content, SL silique length, SS seeds per silique, SW seed weight

* Indicates significant at level of $P<0.05$

** Indicates significant at level of $P<0.01$

Supplemental Table 4. Summary of restriction site associated DNA (RAD) sequencing results from the 192 *B. napus* recombinant inbreed lines (RILs)

Item	Value
Total Illumina reads, $\times 10^6$	68.45
Total RAD tags, $\times 10^6$	15.16
RAD tags per inbred	39092 – 172934
Mean of tags per inbred	80631
Mean of reads per RAD tag	4.5
Median of reads per RAD tag	4.4
Total common RAD tags	96435
Total RAD loci	12786
Total polymorphisms	1700

Supplemental Table 5. quantitative trait loci (QTLs) detected in the recombinant inbreed line (RIL) population in three environments

QTL	Linkage group	Peak position (cM)	Confidence interval	LOD	Additive effect	R^2 (%)	Environment	QTL in Ref
*qOCA10.1**	A10	57.9	57.0–59.1	5.4	1.41	10.9	Y11	
*qSLA4.1**	A04	37.3	34.3–40.2	3.6	-0.19	7.7	Y11	
*qSLA6.1a**	A06	35.8	34.7–37.0	4.7	0.21	9.2	Y11	
*qSLA6.1b**	A06	41.5	39.1–41.9	4.8	0.21	9.2	Y11	
*qSSA6.1**	A06	5.5	4.5–6.2	3.6	-0.86	6.7	Y11	
*qSWC6.1**	C06	32.2	31.8–32.2	5.5	0.16	11.7	Y11	
qSLA1.1	A01	25.1	22.7 – 33.1	2.2	0.14	4.2	Y11	
qSWA3.1	A03	113.0	112.3 – 115.8	2.2	-0.10	4.6	Y11	
qSSC1.1	C01	25.8	25.4 – 26.6	3.0	0.87	6.4	Y11	
qSLC3.1	C03	104.3	103.8 – 104.8	2.4	0.15	4.7	Y11	*cqSLC3b* Yang *et al*. (2012)
*qOCA1.2a**	A01	15.6	8.1–16.9	3.2	0.68	5.1	Y12	
*qOCA1.2b**	A01	21.8	18.1–23.2	3.8	0.78	6.6	Y12	
*qOCA10.2a**	A10	47.3	47.0–48.9	4.1	0.84	7.6	Y12	
*qOCA10.2b**	A10	57.9	57.0–60.0	7.6	1.08	12.8	Y12	
*qOCC1.2**	C01	24.6	23.7–25.2	3.2	0.74	4.7	Y12	
*qOCC3.2**	C03	63.1	62.7–63.5	4.2	0.84	7.4	Y12	
*qOCC8.2a**	C08	31.9	31.3–34.8	3.4	0.78	6.6	Y12	*qOC-8-2* Wang *et al*. (2013)
*qOCC8.2b**	C08	37.5	36.2–41.3	4.5	0.83	7.4	Y12	
*qSLA1.2**	A01	26.1	24.3–32.6	4.1	0.16	7.4	Y12	
*qSLA4.2a**	A04	72.8	72.7–73.0	4.1	-0.15	7.1	Y12	
*qSLA4.2b**	A04	74.6	74.3–75.2	5.0	-0.17	8.4	Y12	

QTL	Linkage group	Peak position (cM)	Confidence interval	LOD	Additive effect	R^2 (%)	Environment	QTL in Ref
qSLA6.2*	A06	41.5	40.5–41.9	4.2	0.15	7.0	Y12	
qSSA3.2*	A03	24.1	16.1–30.0	4.0	-0.80	7.5	Y12	
qSSA6.2*	A06	6.3	5.7–7.1	3.9	-0.81	7.6	Y12	
qSSC2.2*	C02	38.4	37.0–41.6	3.6	0.81	6.6	Y12	
qSWA3.2*a	A03	109.4	106.2–112.3	4.8	-0.12	8.3	Y12	_qSL.N3-3_ Zhang _et al_. (2011)
qSWA3.2b*	A03	114.4	113.0–117.6	4.4	-0.11	7.8	Y12	
qSWA7.2*	A07	55.9	54.4–56.5	4.0	0.11	7.0	Y12	
qSSA1.2	A01	44.2	43.2 – 44.3	2.9	0.68	5.5	Y12	
qSWA6.2a	A06	24.6	19.5 – 28.0	2.8	0.09	4.1	Y12	
qSWA6.2b	A06	31.6	28.4 – 34.6	2.3	0.08	3.8	Y12	
qSSC1.2	C01	25.8	25.4 – 26.7	2.8	0.71	5.4	Y12	
qSLC3.2	C03	103.4	102.1 – 103.6	2.8	0.13	4.7	Y12	
qOCC4.2	C04	71.5	66.9 – 73.2	2.4	0.58	3.7	Y12	
qOCA7.3*	A07	49.9	49.5–51.4	5.7	1.32	10.7	Y13	_oilA7-1_ Jiang _et al_. (2014)
qOCA10.3*a	A10	47.3	45.6–50.4	6.8	1.37	11.9	Y13	
qOCA10.3b*	A10	57	55.8–58.8	5.3	1.24	9.8	Y13	
qOCC1.3*	C01	25.8	25.4–27.0	3.6	1.06	6.5	Y13	
qOCC2.3*	C02	38.4	34.4–47.0	3.4	1.00	5.6	Y13	_oilC2-3_ Jiang _et al_. (2014)
qSLC2.3*	C02	38.7	36.5–42.1	5.0	0.19	9.5	Y13	_cqSLC2_ Yang _et al_. (2012)
qSSA1.3a*	A01	33.9	30.3–35.1	3.8	0.83	6.7	Y13	
qSSA1.3b*	A01	43.2	40.0–44.2	3.6	0.80	6.3	Y13	
qSSA6.3a*	A06	36.8	35.8–38.7	4.3	-0.93	8.5	Y13	
qSSA6.3b*	A06	41.9	41.2–43.7	4.0	-0.86	7.1	Y13	
qSSC2.3*	C02	38.4	36.5–40.9	3.8	0.87	6.7	Y13	
qSWA3.3*	A03	24.1	14.8–25.4	3.8	0.11	7.2	Y13	

QTL	Linkage group	Peak position (cM)	Confidence interval	LOD	Additive effect	R^2 (%)	Environment	QTL in Ref
*qSWA7.3a**	A07	50.7	49.1–51.7	4.8	0.13	9.2	Y13	*TSWA7a-06* Fan *et al*. (2010)
*qSWA7.3b**	A07	56.3	55.6–56.5	4.1	0.11	6.7	Y13	
qOCA1.3	A01	20.8	17.6 – 23.4	2.5	0.82	4.2	Y13	
qSWA6.3a	A06	24.6	23.6 – 28.0	2.4	0.09	3.1	Y13	
qSWA6.3b	A06	31.6	29.5 – 34.6	2.4	0.09	4.2	Y13	
qSSC1.3	C01	25.8	25.5 – 27.0	3.1	0.79	5.6	Y13	
qOCC4.3	C04	71.5	67.6 – 71.8	2.6	0.81	4.1	Y13	
qOCC8.3	C08	38.2	38.1 – 43.7	2.2	0.74	3.5	Y13	

All QTLs were prefixed with "*q*", followed by the abbreviated trait name, mapped linkage group, a numerical code (1, 2, or 3) for one of the three environments, and a small alphabet (a, b, …) representing multiple QTLs if they are detected for the trait in the same linkage group and same environment. For example, *qOCA1.2a* is one of the two QTLs for oil content (OC) detected on linkage A1 in the environment in 2012 (Y12), and *qOCA1.2b* is another one.

Confidence interval: the flanking marker closest to the 95% confidence interval was used for significant QTLs; R^2: percentage of the phenotypic variation explained by the QTL

Additive effects indicate the effects of "M201" allele

* Indicates significant QTLs

QTL in Ref were the QTL detected in previous studies. The references for the QTL were also shown in the same column.

Supplemental Table 6. Candidate genes discovered underlying the QTL identified for A10 OC QTL (*cqOCA10b*)

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015344	A10	1897084	1905661	+	DNA-dependent DNA replication, sister chromatid cohesion	
Gene	Bra015345	A10	1894813	1896427	+	vesicle-mediated transport; Biological Process; integral to membrane; Cellular Component	
Gene	Bra015346	A10	1883582	1884778	+	cellular response to sulfur starvation, chloroplast organization	
Gene	Bra015347	A10	1871022	1873881	-	Putative endonuclease or glycosyl hydrolase	
Gene	Bra015348	A10	1868282	1870326	+	Ankyrin repeat family protein	
Gene	Bra015349	A10	1862605	1865057	-	RING/U-box superfamily protein; fatty acid beta-oxidation, protein import into peroxisome matrix	AT1G04790
Gene	Bra015350	A10	1861514	1862104	+	glycine-rich protein	
Gene	Bra015351	A10	1858421	1860649	+	Ypt/Rab-GAP domain of gyp1p superfamily protein; cytoplasm; FUNCTIONS IN: RAB GTPase activator activity	
Gene	Bra015352	A10	1850061	1852793	+	F-box and Leucine Rich Repeat domains containing protein	
Gene	Bra015353	A10	1847843	1849334	+	F-box and Leucine Rich Repeat domains containing protein	
Gene	Bra015354	A10	1843347	1844040	+	FLAVODOXIN-LIKE QUINONE REDUCTASE 1, FQR1;Encodes a flavin mononucleotide-binding flavodoxin-like quinone reductase that is a primary auxin-response gene	
Gene	Bra015355	A10	1836111	1837157	+	RNI-like superfamily protein;	
Gene	Bra015356	A10	1832558	1833928	+	Ypt/Rab-GAP domain of gyp1p superfamily protein	
Gene	Bra015357	A10	1821062	1827681	+	Tetratricopeptide repeat (TPR)-like superfamily protein	
Gene	Bra015358	A10	1818251	1820015	+	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain; FUNCTIONS IN: sequence-specific DNA binding transcription factor activity	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015359	A10	1813124	1814020	-	TRAF-like superfamily protein;	
Gene	Bra015360	A10	1805681	1807555	+	Intermediate filament protein	
Gene	Bra015361	A10	1799613	1802674	+	Encodes a twin-domain, kinase-GC signaling molecule that may function in biotic stress responses that is critically dependent on the second messenger cGMP	
Gene	Bra015362	A10	1794695	1797807	-	Protein of unknown function (DUF185); CONTAINS InterPro DOMAIN/s	
Gene	Bra015363	A10	1791651	1794224	+	O-fucosyltransferase family protein; CONTAINS InterPro DOMAIN/s: GDP-fucose protein O-fucosyltransferase	
Gene	Bra015364	A10	1786183	1789925	+	Encodes a protein with putative sucrose-phosphate synthase activity; galactolipid biosynthetic process, response to hypoxia, sucrose biosynthetic process	AT1G04920
Gene	Bra015365	A10	1783806	1785089	-	Putative uncharacterized protein	
Gene	Bra015366	A10	1779406	1781683	+	hydroxyproline-rich glycoprotein family protein	
Gene	Bra015367	A10	1777984	1778925	-	TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 20	
Gene	Bra015368	A10	1773936	1777526	+	TATA BOX ASSOCIATED FACTOR II 59	
Gene	Bra015369	A10	1766272	1768503	+	Protein of unknown function	
Gene	Bra015370	A10	1764626	1765733	+	Encodes a protein belonging to the mitochondrial carrier family and similar to animal mitoferrin but likely NOT to be located in the mitochondria, but rather in chloroplasts. It is likely to be involved in transporting iron into the chloroplast.	
Gene	Bra015371	A10	1761563	1763816	-	lipid-binding serum glycoprotein family protein; FUNCTIONS IN: lipid binding;	AT1G04970

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015372	A10	1759456	1760755	-	Encodes a Ca-dependent calmodulin binding protein. Sequence similarity to the WRKY transcription factor gene family	
Gene	Bra015373	A10	1755280	1756347	-	cysteine-type endopeptidase inhibitor	
Gene	Bra015374	A10	1748282	1750995	-	Encodes auxin response factor 9 (ARF9).	
Gene	Bra015375	A10	1739233	1741963	+	ARABIDOPSIS THALIANA PROTEIN DISULFIDE ISOMERASE 10, ATPDI10, ATPDIL2-2, PDI-LIKE 2-2, PDI10, PDIL2-2, PROTEIN DISULFIDE ISOMERASE	
Gene	Bra015376	A10	1736510	1738599	+	Zinc finger C-x8-C-x5-C-x3-H type family protein; FUNCTIONS IN: zinc ion binding, nucleic acid binding;	
Gene	Bra015377	A10	1736510	1737909	+	zinc finger (CCCH-type) family protein	
Gene	Bra015378	A10	1722786	1727170	+	Encodes a DNA glycosylase DEMETER (DME). Responsible for endosperm maternal-allele-specific hypomethylation at the MEDEA (MEA) gene. DME can excise 5-methylcytosine in vitro and when expressed in E. coli. DME establishes MEA imprinting by removing 5-methylcytosine to activate the maternal allele.	
Gene	Bra015379	A10	1714458	1717280	-	Encodes an atypical dual-specificity phosphatase	AT1G05000
Gene	Bra015380	A10	1712686	1713989	+	Encodes 1-aminocyclopropane-1-carboxylate oxidase	
Gene	Bra015381	A10	1705608	1707521	+	ENTH/ANTH/VHS superfamily protein; FUNCTIONS IN: phospholipid binding, clathrin binding, binding, phosphatidylinositol binding;	
Gene	Bra015382	A10	1702721	1704355	+	receptor like protein 20 (RLP20); FUNCTIONS IN: kinase activity; INVOLVED IN: signal transduction;	
Gene	Bra015383	A10	1692420	1692872	+	unknown protein	
Gene	Bra015384	A10	1688427	1690058	-	receptor like protein 20 (RLP20); FUNCTIONS IN: kinase activity; INVOLVED IN: signal transduction;	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015385	A10	1687498	1687731	+	Member of a large family of putative ligands homologous to the Clavata3 gene. Consists of a single exon.	
Gene	Bra015386	A10	1683789	1684750	+	unknown protein	
Gene	Bra015387	A10	1681177	1683502	-	dentin sialophosphoprotein-related	
Gene	Bra015388	A10	1670618	1671631	-	member of MEKK subfamily; activation of protein kinase activity, regulation of apoptotic process, regulation of mitotic cell cycle, stress-activated MAPK cascade	
Gene	Bra015389	A10	1665848	1669772	+	Helicase protein with RING/U-box domain; FUNCTIONS IN: helicase activity, DNA binding, zinc ion binding, ATP binding, nucleic acid binding;	
Gene	Bra015390	A10	1643145	1644134	-	ubiquitin carrier protein	
Gene	Bra015391	A10	1636359	1637645	-	Peptidase M50 family protein; FUNCTIONS IN: metalloendopeptidase activity;	
Gene	Bra015392	A10	1632191	1636110	+	Helicase protein with RING/U-box domain; FUNCTIONS IN: helicase activity, DNA binding, zinc ion binding, ATP binding, nucleic acid binding;	
Gene	Bra015393	A10	1629054	1631489	+	Calcium-binding tetratricopeptide family protein; FUNCTIONS IN: binding, zinc ion binding, calcium ion binding;	
Gene	Bra015394	A10	1625834	1628206	+	"CYTOCHROME P450, FAMILY 88, SUBFAMILY A, POLYPEPTIDE 3", ATKAO1, CYP88A3, ENT-KAURENOIC ACID OXYDASE 1, KAO1	
Gene	Bra015395	A10	1621610	1624875	+	Galactosyltransferase family protein; FUNCTIONS IN: transferase activity, transferring hexosyl groups, transferase activity, transferring glycosyl groups;	AT1G05170
Gene	Bra015396	A10	1609018	1611995	+	Encodes a subunit of the RUB1 activating enzyme that regulates the protein degradation activity of Skp1-Cullin-Fbox complexes, primarily, but not exclusively, affecting auxin responses. Acts alongside AS1 to exclude BP expression from leaves.	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015397	A10	1607137	1608298	+	embryo defective 2394 (emb2394); FUNCTIONS IN: structural constituent of ribosome, rRNA binding; INVOLVED IN: translation, embryo development ending in seed dormancy	
Gene	Bra015398	A10	1599853	1602929	-	Encodes a putative glutamate receptor GLR3 with dual localization in plastid and plasma membrane.	
Gene	Bra015399	A10	1598672	1599488	+	unknown protein	
Gene	Bra015400	A10	1597567	1598398	-	Transmembrane protein 97	
Gene	Bra015401	A10	1593110	1596759	+	Encodes a homeobox-leucine zipper family protein belonging to the HD-ZIP IV family. Mutants have trichomes that appear glass-like under a dissecting microscope as compared to the wild-type trichomes. The mutations do not affect trichome growth or branch number.	
Gene	Bra015402	A10	1585992	1587331	-	Encodes a cationic cell-wall-bound peroxidase homolog that is involved in the lignification of cell walls.	
Gene	Bra015403	A10	1582382	1583703	+	Encodes a cationic cell-wall-bound peroxidase homolog that is involved in the lignification of cell walls.	
Gene	Bra015404	A10	1578655	1580080	-	Encodes a cold-inducible cationic peroxidase that is involved in the stress response. In response to low temperature, RCI3 transcripts accumulate in the aerial part and in roots of etiolated seedlings but only in roots of light-grown seedlings.	
Gene	Bra015405	A10	1576054	1578342	+	TraB family protein; CONTAINS InterPro DOMAIN/s: Pheromone shutdown-related, TraB (InterPro:IPR002816);	
Gene	Bra015406	A10	1573945	1574433	-	Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3; FUNCTIONS IN: triglyceride lipase activity, carboxylesterase activity; INVOLVED IN: lipid catabolic process, lipid metabolic process;	AT3G14075

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015407	A10	1569148	1569501	+	TraB family protein; CONTAINS InterPro DOMAIN/s: Pheromone shutdown-related,	
Gene	Bra015408	A10	1567666	1568616	-	NAC domain protein. SMB, BRN1, and BRN2 act to regulate root cap maturation, in a partially redundant fashion.BRN1 and BRN2, control the cell wall maturation processes that are required to detach root cap layers from the root.	
Gene	Bra015409	A10	1561253	1563709	+	Protein of unknown function	
Gene	Bra015410	A10	1556441	1556692	+	TraB family protein; CONTAINS InterPro DOMAIN/s: Pheromone shutdown-related,	
Gene	Bra015411	A10	1545292	1547891	+	Protein of unknown function	
Gene	Bra015412	A10	1519558	1520400	+	unknown protein	
Gene	Bra015413	A10	1512016	1513223	+	CCT motif family protein; CONTAINS InterPro DOMAIN/s: CCT domain;regulation of transcription, DNA-templated	
Gene	Bra015414	A10	1493502	1495987	+	Nucleic acid-binding, OB-fold-like protein; CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold (InterPro:IPR012340), Nucleic acid-binding, OB-fold-like (InterPro:IPR016027); BEST Arabidopsis thaliana protein match is: F-box family protein	
Gene	Bra015415	A10	1457040	1466273	+	ZIP5; ZIP5; cation transmembrane transporter/ metal ion transmembrane transporter	
Gene	Bra015416	A10	1428665	1430223	+	Pectin lyase-like superfamily protein; FUNCTIONS IN: pectinesterase activity; INVOLVED IN: cell wall modification; LOCATED IN: endomembrane system, cell wall, plant-type cell wall	
Gene	Bra015417	A10	1421987	1424875	-	molecular_function unknown	
Gene	Bra015418	A10	1420811	1421335	-	unknown protein	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015419	A10	1417193	1417647	+	unknown protein	
Gene	Bra015420	A10	1411928	1414844	+	NAD(P)-binding Rossmann-fold superfamily protein; FUNCTIONS IN: binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, catalytic activity, cofactor binding; INVOLVED IN: metabolic process;	
Gene	Bra015421	A10	1397416	1403688	+	Sec14p-like phosphatidylinositol transfer family protein; CONTAINS InterPro DOMAIN/s: Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251), Phosphatidylinositol transfer protein-like, N-terminal (InterPro:IPR011074);	
Gene	Bra015422	A10	1374834	1376640	-	Protein of unknown function	
Gene	Bra015423	A10	1373100	1374498	+	unknown protein	
Gene	Bra015424	A10	1371257	1372550	+	C-8 sterol isomerases; FUNCTIONS IN: C-8 sterol isomerase activity; INVOLVED IN: ergosterol biosynthetic process; LOCATED IN: endoplasmic reticulum;	
Gene	Bra015425	A10	1369837	1370637	-	FUNCTIONS IN: DNA binding; INVOLVED IN: regulation of transcription, DNA-dependent;	
Gene	Bra015426	A10	1366071	1367207	-	Encodes a Protease inhibitor/seed storage/LTP family protein	
Gene	Bra015427	A10	1362513	1365797	+	Encodes a protein with similarity to RNA helicases. Mutants are defective in post-transcriptional gene silencing.	
Gene	Bra015428	A10	1355996	1358258	+	Encodes an inositol polyphosphate 5' phosphatase (5PTase) that is required for the proper recruitment of cells into developing vascular tissue in leaves and cotyledons. It is most similar to Type I 5PTases that are known to cleave a phosphate from IP3 or IP4. cvp2 mutants have elevated levels of IP3 and are hypersensitive to ABA in seed germination assays.	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015429	A10	1347584	1348936	+	one of Arabidopsis SKP1 homologues;DNA endoreduplication, proteasome assembly, proteasome-mediated ubiquitin-dependent protein catabolic process	
Gene	Bra015430	A10	1338748	1343684	+	chromatin remodeling 31 (chr31); FUNCTIONS IN: helicase activity, DNA binding, ATP binding, nucleic acid binding;	
Gene	Bra015431	A10	1333362	1337079	-	ARABIDOPSIS THALIANA SYNAPTOTAGMIN HOMOLOG E, ATSYTE, NTMC2T2.1, NTMC2TYPE2.1, SYNAPTOTAGMIN 5, SYNAPTOTAGMIN HOMOLOG E, SYT5, SYTE	
Gene	Bra015432	A10	1331868	1332828	-	Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds.	
Gene	Bra015433	A10	1323738	1325150	-	Protein of unknown function	
Gene	Bra015434	A10	1320225	1321339	-	unknown protein	
Gene	Bra015435	A10	1319282	1319998	+	A UDP-glucose transferase localized in the phragmoplast. It has been co-purified with the callose synthase complex and may transfer UDP-glucose from sucrose synthase to the callose synthase and thus help form a substrate channel for the synthesis of callose at the forming cell plate.	
Gene	Bra015436	A10	1307690	1317685	+	Encodes a callose synthase 1 catalytic subunit . Member of Glycosyltransferase Family- 48.	
Gene	Bra015437	A10	1305378	1305626	+	unknown protein	
Gene	Bra015438	A10	1296640	1304123	+	kelch repeat-containing F-box family protein	
Gene	Bra015439	A10	1295232	1296364	-	Encodes a gamma-secretase subunit. Associates with other subunits in intracellular membrane compartments	
Gene	Bra015440	A10	1288221	1293659	-	MA3 domain-containing protein; CONTAINS InterPro DOMAIN/s: Initiation factor eIF-4 gamma, MA3; response to ethylene, response to salt	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
						stress	
Gene	Bra015441	A10	1273310	1276177	+	unknown protein	
Gene	Bra015442	A10	1262689	1267016	+	member of Putative Na+/H+ antiporter family	
Gene	Bra015443	A10	1257619	1259136	-	Tetratricopeptide repeat (TPR)-like superfamily protein; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat	
Gene	Bra015444	A10	1254138	1256320	+	Encodes the small subunit of ADP-glucose pyrophosphorylase. The small subunit is the catalytic isoform responsible for ADP-glucose pyrophosphorylase activity. The presence of the small subunit is required for large subunit stability. Two isoforms of the small subunit (ApS1 and ApS2) have been described. ApS2 is a minor small subunit isoform present in all plant tissues tested.	AT1G05610
Gene	Bra015445	A10	1245447	1250315	-	Encodes an inositol polyphosphate 5-phosphatase with phosphatase activity toward only Ins(1,4,5)P3. Induced in response to ABA and wounding treatments. Expressed in young seedlings and flowers, while no transcripts were detectable in maturated roots, stems, and rosette leaves Modulates the development of cotyledon veins through its regulation of auxin homeostasis. Involved in blue light light－stimulated increase in cytosolic calcium ion.	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015446	A10	1242799	1244786	+	Pectin lyase-like superfamily protein; FUNCTIONS IN: polygalacturonase activity; INVOLVED IN: carbohydrate metabolic process; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Pectin lyase fold/virulence factor (InterPro:IPR011050), Pectin lyase fold (InterPro:IPR012334), Glycoside hydrolase, family 28 (InterPro:IPR000743), Parallel beta-helix repeat (InterPro:IPR006626); BEST Arabidopsis thaliana protein match is: Pectin lyase-like superfamily protein (TAIR:AT1G05660.1); Has 4025 Blast hits to 4009 proteins in 482 species: Archae - 4; Bacteria - 1133; Metazoa - 14; Fungi - 1282; Plants - 1474; Viruses - 2; Other Eukaryotes - 116	AT1G05650
Gene	Bra015447	A10	1239460	1240770	+	Pentatricopeptide repeat (PPR-like) superfamily protein; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat	
Gene	Bra015448	A10	1234249	1235828	+	Encodes a UDP-glucosyltransferase, UGT74E2, that acts on IBA (indole-3-butyric acid) and affects auxin homeostasis. The transcript and protein levels of this enzyme are strongly induced by H_2O_2 and may allow integration of ROS (reactive oxygen species) and auxin signaling. This enzyme can also transfer glycosyl groups to several compounds related to the explosive TNT when this synthetic compound is taken up from the environment.	AT1G05680
Gene	Bra015449	A10	1224561	1230577	-	Leucine-rich repeat transmembrane protein kinase protein; FUNCTIONS IN: kinase activity; INVOLVED IN: protein amino acid phosphorylation; ATP binding, kinase activity, protein serine/threonine kinase activity	
Gene	Bra015450	A10	1216923	1217712	-	basic helix-loop-helix (bHLH) DNA-binding superfamily protein; FUNCTIONS IN: sequence-specific DNA binding transcription factor activity; INVOLVED IN: response to ethylene stimulus, regulation of	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
						transcription;	
Gene	Bra015451	A10	1213098	1213994	+	Specifically restrict the long-distance movement of tobacco etch potyvirus (TEV) without involving either hypersensitive cell death or systemic acquired resistance	
Gene	Bra015452	A10	1210894	1211871	-	Got1/Sft2-like vescicle transport protein family	
Gene	Bra015453	A10	1206499	1210198	-	lipase class 3 family protein; FUNCTIONS IN: triglyceride lipase activity; INVOLVED IN: lipid metabolic process	AT1G05790
Gene	Bra015454	A10	1197888	1199309	-	Encodes a galactolipase. Located in the chloroplast. Involved in the initial step of jasmonic acid biosynthesis. Expressed in vegetative tissues and is necessary for the biosynthesis of basal-level JAs in vegetative tissues.	
Gene	Bra015455	A10	1184401	1185162	+	Arabidopsis thaliana telomere-binding protein, putative	
Gene	Bra015456	A10	1177878	1180605	-	basic helix-loop-helix (bHLH) DNA-binding superfamily protein; FUNCTIONS IN: DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription;	
Gene	Bra015457	A10	1167425	1169001	+	Encodes an endo chitinase-like protein AtCTL1. Essential for tolerance to heat, salt and drought stresses. Also involved in root hair development, cell expansion and response to cytokinin. Allelic to erh2. 11 alleles described in Hauser (1995). Mutant is defective in acquired thermotolerance, appears semidwarf throughout its life cycle and has extra lateral branches. There are two EMS alleles. Expression of AtHSP101 is not affected in the mutants.	
Gene	Bra015458	A10	1165587	1166566	-	unknown protein	
Gene	Bra015459	A10	1163760	1164402	+	Protein of unknown function	

Item	Name	Chromosome	Start	Stop	Strand	Annotations	Orthologous genes to *A. thaliana*
Gene	Bra015460	A10	1157877	1160540	-	Encodes ARI12 (ARIADNE 12). ARI12 belongs to a family of ‘RING between RING fingers' (RBR) domain proteins with E3 ligase activity. Expression of ARI12 is induced by UV-B exposure; cellular response to hypoxia, protein ubiquitination, response to UV-B, transcription factor import into nucleus	
Gene	Bra015461	A10	1154023	1157628	+	encodes a protein whose sequence is similar to a 2-oxoglutarate-dependent dioxygenase; metal ion binding, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	
Gene	Bra015462	A10	1148443	1150365	-	Encodes a member of the proline-rich extensin-like receptor kinase (PERK) family. This family consists of 15 predicted receptor kinases; plant-type cell wall modification, pollen tube development, pollen tube growth, protein autophosphorylation, regulation of unidimensional cell growth	
Gene	Bra015463	A10	1138842	1143350	-	zinc ion binding, nucleic acid binding;	
Gene	Bra015464	A10	1131509	1136920	-	cell division cycle protein 48-related / CDC48-related; FUNCTIONS IN: nucleoside-triphosphatase activity, nucleotide binding, ATP binding;	
Gene	Bra015465	A10	1130267	1130944	-	DNA binding; INVOLVED IN: regulation of transcription, DNA-dependent	
Gene	Bra015466	A10	1124637	1129429	+	ARM repeat superfamily protein; FUNCTIONS IN: binding;	
Gene	Bra015467	A10	1121510	1123796	+	RNA-binding (RRM/RBD/RNP motifs) family protein;	