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# Camelina seed transcriptome: a tool for meal and oil improvement and translational research

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## Summary

Camelina (*Camelina sativa*), a Brassicaceae oilseed, has received recent interest as a biofuel crop and production platform for industrial oils. Limiting wider production of camelina for these uses is the need to improve the quality and content of the seed protein-rich meal and oil, which is enriched in oxidatively unstable polyunsaturated fatty acids that are deleterious for biodiesel. To identify candidate genes for meal and oil quality improvement, a transcriptome reference was built from 2047 Sanger ESTs and more than 2 million 454-derived sequence reads, representing genes expressed in developing camelina seeds. The transcriptome of approximately 60K transcripts from 22 597 putative genes includes camelina homologues of nearly all known seed-expressed genes, suggesting a high level of completeness and usefulness of the reference. These sequences included candidates for 12S (cruciferins) and 2S (napins) seed storage proteins (SSPs) and nearly all known lipid genes, which have been compiled into an accessible database. To demonstrate the utility of the transcriptome for seed quality modification, seed-specific RNAi lines deficient in napins were generated by targeting 2S SSP genes, and high oleic acid oil lines were obtained by targeting *FATTY ACID DESATURASE 2 (FAD2)* and *FATTY ACID ELONGASE 1 (FAE1)*. The high sequence identity between *Arabidopsis thaliana* and camelina genes was also exploited to engineer high oleic lines by RNAi with *Arabidopsis FAD2* and *FAE1* sequences. It is expected that these transcriptomic data will be useful for breeding and engineering of additional camelina seed traits and for translating findings from the model *Arabidopsis* to an oilseed crop.

**Keywords:** camelina, transcriptome, seed, vegetable oil, meal, fatty acid, oleic acid.

## Introduction

*Camelina sativa* is an emerging Brassicaceae oilseed crop in the Great Plains of North America and Pacific Northwest of the United States. Archaeological excavations have uncovered evidence of camelina seed in agricultural use as early as 1500–400 BC, with more recent use as an oilseed crop in the 20th century in parts of Europe (Putnam *et al.*, 1993; Zubr, 1997). Several characteristics of camelina contribute to the rising interest in its use as an oilseed crop for both food and nonfood purposes. The oil content of camelina seeds ranges from 28% to 40% of the seed weight, with storage proteins making up an additional approximately 30% of the seed weight (Budin *et al.*, 1995; Marquard and Kuhlmann, 1986; Putnam *et al.*, 1993). In addition, camelina seed oil has received commercial interest for the nutraceutical value of its high omega-3 fatty acid content (Putnam *et al.*, 1993). Moreover, compared with that of other Brassicaceae species, camelina meal contains lower levels of glucosinolates, which can break down into toxic intermediates and limit the livestock feed value of the protein-rich meal (Pilgeram *et al.*, 2007; Zubr, 1997).

A number of agronomic attributes make camelina particularly attractive for production in geographic regions such as the Great Plains of North America. Camelina grows well on marginal land and has been shown to surpass yields of oilseed crops such as flax under drought-like conditions (Bramm *et al.*, 1990; Zubr, 1997). Furthermore, camelina has a moderate-to-low requirement for nutrients and a low seeding rate, making input costs low (Pilgeram *et al.*, 2007; Zubr, 1997). Because camelina reaches maturity in only 85–100 days, it can be used in double-cropping systems with crops such as winter wheat (Putnam *et al.*, 1993).

For research and technological development, camelina surpasses other oil crops in efficiency with respect to generation time and ease of transformation. Camelina is amenable to *Agrobacterium*-mediated transformation by simple floral dip infiltration under vacuum (Lu and Kang, 2008), a procedure commonly used in *Arabidopsis* research laboratories throughout the world. With this method, transgenic camelina lines can be generated 6–8 weeks after transformation. By contrast, soybean transformations typically require 6–10 months for the generation of transgenic seed following the initial biolistic or *Agrobacterium* delivery of genes to cells as well as extensive tissue culture

maintenance of plant material (Wang *et al.*, 2012). Because of these attributes, camelina can be quickly engineered for improved seed quality and agronomic traits with minimal technical expertise.

One target for biotechnological improvement is the fatty acid profile of camelina seed oil, which is not currently ideal for any single purpose. The high percentage of polyunsaturated fatty acids [35%–40%  $\alpha$ -linolenic acid (18 : 3) and 20%–25% linoleic acid (18 : 2)] in camelina oil makes it highly prone to oxidation and suboptimal for fuel and bio-based lubricant applications (Frohlich and Rice, 2005). Additionally, the potential negative impacts of the C20 and C22 fatty acid content of camelina oil for fuel and lubricant applications are still unclear and warrant further investigation (Kramer *et al.*, 1992). Transgenic approaches are beginning to show the effectiveness of single transgenes for seed composition modification. Using a single *FATTY ACID DESATURASE 2* (*FAD2*)-antisense suppression, construct to modify camelina resulted in the generation of mid-oleic acid (18 : 1 $\Delta$ 9) lines, but did not reduce levels of C20 and C22 fatty acids (Kang *et al.*, 2011).

Camelina agronomics and breeding programmes are emerging with hopes for the development of marketable traits, as have been successful over the past 20 years in canola (Putnam *et al.*, 1993). Initial genetic characterization of important agronomic traits by Gehringer *et al.* (2006) used AFLPs to construct a genetic map of camelina, with QTLs for seed yield, oil content, 1000-seed mass and plant height. In a recent molecular marker-based survey, Ghamkhar *et al.* (2010) evaluated four oil quality measures with respect to the geographic origins of 53 accessions, showing a strong association between environmental adaptation and oil content, and a high genetic diversity within the species that could be exploited in breeding. These efforts are currently limited by lack of publicly available sequence data.

A diploid inheritance of camelina traits was observed by Gehringer *et al.* (2006), while skewed segregation of some AFLP markers and extra amplification of Brassica-derived SSR markers suggested genomic duplication or polyploidy. Recent findings by Hutcheon *et al.* (2010) show that several genes known to be single copy in *Arabidopsis thaliana* and other diploids, including *FAD2* and *FATTY ACID ELONGASE 1* (*FAE1*), are present in three copies in the *C. sativa* genome, evidence that *C. sativa* may be allohexaploid, which has significant implications for camelina crop improvement through breeding.

Here, we present expressed gene sequences from *C. sativa* developing seeds. This report provides a detailed profile of transcripts for potential targets for seed quality improvement through biotechnology and breeding and represents an advance towards the development of camelina genomics tools. The 454 pyrosequencing combined with data from Sanger-based EST sequencing of developing camelina seeds was used to build a seed transcriptome reference. Sequence alignments showed high conservation in transcripts for genes associated with seed quality traits among camelina, *Arabidopsis* and canola taxa. Homology among genes acting in acyl lipid metabolism is presented, and a publicly available sequence catalogue was developed for camelina seed quality enhancement. We show further that highly abundant seed storage proteins (SSPs) patterns in these taxa are closely comparable. In addition, we demonstrate the value of the seed transcriptome for targeted suppression of genes that modify SSP compositions and oil quality traits for feed and biodiesel applications. Furthermore, data are presented highlighting the value of camelina for translation of *Arabidopsis*-based research.

## Results and discussion

### The transcriptome is a broad seed gene resource

Upon sequencing and assembly of >2 million 454 pyrosequencing reads from developing camelina seeds at 15–20 days after pollination (DAP) and 2047 Sanger reads of cloned ESTs, more than 60 000 camelina transcripts were identified (Table 1). The camelina transcriptome provided here includes both assembled transcripts (isotigs and unbroken contigs from the Newbler assembly) as well as singletons, and the dataset is trimmed for elements with a minimum length of 100 nucleotides. The data assembly is available as a BLAST database at [www.camelinagenome.org](http://www.camelinagenome.org) and additionally as unassembled reads at NCBI accessions SRA056520 (454 reads), JZ030844–JZ032890 (dbEST submission; LIBEST accession numbers 027979 and 027980), and NCBI BioProject PRJNA167924. A total of 103 276 searchable elements in the database were unified in the Newbler assembly into 22 597 isogroups and 43 060 singleton sequences that provide single-pass reference for additional transcripts (Table 1). With the expectation that at least some close paralogs and homeologs would be expressed together in seeds, we performed a survey of polymorphic transcripts by mapping back the original reads to the assembly and estimating variants for isogroups of greatest interest. The assembly reference as a whole, however, intentionally remains compressed with respect to possible homeologs, paralogs and alleles, that is, transcripts sharing >90% identity (40-bp overlap) remain assembled together. These were used for comparative functional genomics surveys below.

More than 95% of isogroups showed conservation with either TAIR10 or dbEST plant entries as evidenced by camelina tBLASTX hits with *E*-values <1 e<sup>-5</sup>. Of hits to TAIR10 proteins, 89% of isogroups (68.3% of individual transcripts) matched with *E*-values <1 e<sup>-10</sup>, and of those with TAIR10 hits of lower significance, half showed substantially higher significance in hits to NCBI dbEST entries representing other *Arabidopsis* data sets (*A. thaliana* or *A. lyrata*) or Brassica cDNA collections. About 16.7% of the camelina transcriptome data set did not significantly match *Arabidopsis* or Brassica protein sequences. Notwithstanding the fact that the vast majority of these (91%) were singletons and therefore less complete/accurate, based on NCBI NR database matches, many appear to be expressed portions of transposable elements conserved with those catalogued in the *A. thaliana* and *A. lyrata* genomes.

About half (45%) of all camelina BLASTX hits to TAIR10 showed  $\geq 90\%$  primary sequence identity to *Arabidopsis* proteins, with an average identity overall of 81%, suggesting very high conservation in seed functions. The majority of proteins involved in protein translation, folding and secretion, ubiquitination and proteolysis, among other highly conserved functions, were identical or nearly identical to those in *Arabidopsis*.

A high degree of transcriptome completeness was apparent when we surveyed a variety of measures. Full-length coding sequences made up a large proportion of the data set, evidenced by coverage of homologous *Arabidopsis* proteins. 10 647 camelina transcripts covered 100% of the length of TAIR10 representative gene model coding regions; 30 887 covered more than 80% of these lengths.

Our camelina seed sampling was limited to mid-developmental stages in which the embryo matures, cells expand and storage reserves accumulate, with similar morphology to *Brassica napus*



**Table 1** Summary of camelina transcript data sequenced and assembled

Data type	Reads sequenced			Data (nts)	Assembled database					
	<i>N</i> , quality filtered	<i>L</i> mean ± SD	<i>L</i> median		Total elements	Singleton 454 reads	Singleton ESTs	Isotigs	Transcript statistics	Isogroups
454 GS-FLX Titanium	2 013 672	373 ± 129	418	748 486 621	103 276	43 060	29	60 187	Mean isotig length ± SD 1492 ± 899 longest isotig length 23 135	22 597
Sanger EST clones	2047	555 ± 169	601	1 135 358					Mean reads coverage depth 14× single-isotig isogroups 10 764 (18%)	

seeds between 3 and 4 weeks of development (Hajdуч *et al.*, 2006). We were curious to estimate the extent to which our transcriptome represents a complete set of seed-expressed genes, although technically comparable data sets from other plants are not available. In a comprehensive profiling of transcripts using microarrays, genes expressed in *Arabidopsis* seeds from very early to late developmental stages were reported recently (Le *et al.*, 2010). After cleaning from this list currently obsolete TAIR10 gene models and accounting for redundancy in ATH1 probe hybridization, only 10 *Arabidopsis* genes, or 2.6% of the Le *et al.* *Arabidopsis* seed expression survey, appeared to lack homologues in our camelina sequenced data set.

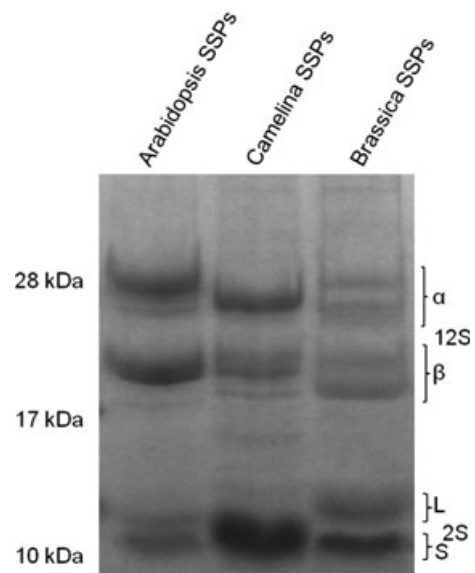
Overall, these results demonstrate that the transcriptome sequence reference presented here provides comprehensive representation of expressed genes in developing seed/embryos and will therefore broadly serve future studies aimed at camelina seed quality enhancement.

#### Developing camelina seeds contain abundant SSPs: potential targets for high-value protein production in *C. sativa*

The camelina developing seed transcriptome provides important information about SSP genes that can ultimately be used for meal improvement, as described below. Two types of SSPs occur in *Arabidopsis*, *B. napus* and other Brassicaceae crops: 12S globulins (referred to as cruciferins) and 2S albumins (referred to as napins; Herman and Larkins, 1999). SSPs are the main source of protein in meal and thus represent a potential target for modification (Schmidt and Herman, 2008). Whether it is increasing the protein content of the meal, replacing the SSPs with a more valuable protein, or decreasing the protein content to drive flux of energy reserve intermediates to a metabolic pathway of higher priority, SSP genes represent gainful targets for manipulation (Boothe *et al.*, 2010).

To compare SSPs found in camelina with *Arabidopsis* and *B. napus*, proteins were extracted from seeds and subjected to SDS-PAGE. Coomassie staining indicated that the predominant proteins in each species are similar in size (Figure 1). Mass spectrometry confirmed the presence of the large and small subunits of the 2S albumins and the  $\alpha$  and  $\beta$  subunits of the 12S globulins in all three species (data not shown).

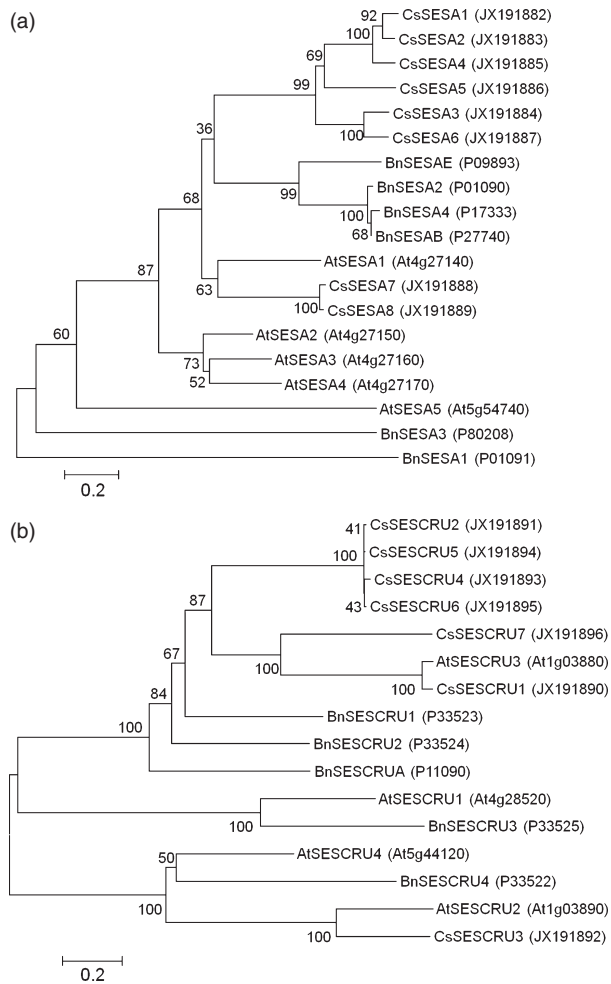
In *Arabidopsis*, the 2S albumins are encoded by five genes designated *SESA1-5* (Accession numbers P15457, P15458, P15459, P15460 and Q9FH31, respectively; Krebbers *et al.*, 1988; Van der Klei *et al.*, 1993). Interestingly, at least eight transcripts coding for 2S albumins in camelina were identified in



**Figure 1** Comparison between *Arabidopsis*, camelina and Brassica seed storage proteins. Equal loadings of protein extracts (12  $\mu$ L) from 100-mg seeds from each species were separated by 15% SDS-PAGE. Gels were stained with Coomassie for band detection. The  $\alpha$  and  $\beta$  subunits of the 12S and the large (L) and small (S) subunits of the 2S proteins are noted. Protein identities were confirmed by mass spectrometry (data not shown).

our assembly of EST and 454 reads and confirmed with the generation and sequencing of individual PCR products (Figure 2a and Figure S1). The camelina 2S protein sequences all share a high degree of identity among each other, ranging from 71% to 98%.

*SESCRU1-4* encodes *Arabidopsis* 12S globulins (Accession numbers Q96318, Q9ZWA9, P15456 and P15455, respectively; Pang *et al.*, 1988; Theologis *et al.*, 2000). Seven full-length genes and ten partial-length genes annotated as 12S-related proteins were identified in our camelina transcriptome (Figure 2b). Each of the full-length 12S proteins of camelina shows a higher degree of identity with homologues in *Arabidopsis* than with corresponding *B. napus* proteins. For example, *C. sativa* *SESCRU1* (*CsSESCRU1*) is 92% identical to the 12S *Arabidopsis* *SESCRU3* protein and only 84% identical to the 12S *SESCRU4* protein in *B. napus* (Figure S2). Additionally, *CsSESCRU6*, *CsSESCRU4* and *CsSESCRU5* all share 90% amino acid sequence identity to the



**Figure 2** Evolutionary relationship of camelina, Arabidopsis and Brassica 2S and 12S seed storage proteins (SSPs). 2S (a) and 12S (b) camelina contigs were aligned with Arabidopsis and Brassica homologues using ClustalW (Thompson *et al.*, 1994). Phylogenetic trees were built with the MEGA4 software, using the neighbour-joining method (Tamura *et al.*, 2007). The *Arabidopsis thaliana* and *Brassica napus* sequences used for (a) are AtSESA1–5 (Accession numbers P15457, P15458, P15459, P15460 and Q9FH31; respectively) and BnSESAE, BnSESA2, BnSESA4, BnSESA3, BnSESA1. The *A. thaliana* and *B. napus* sequences used for (b) are AtSESCR1–4 (Accession numbers Q96318, Q9ZWA9, P15456 and P15455, respectively), and BnSESCR1, BnSESCR2, BnSESCR3, BnSESCR4. Accession numbers for the camelina, and Brassica SSPs are shown in the trees.

AtSESCR4 protein and only about 80% identity to the *B. napus* SESCR1 protein (Figure S3).

### The camelina developing seed transcriptome can be used to modify SSP composition

To demonstrate the value of the transcriptome for seed quality modification, we sought to suppress camelina SSP expression based on our sequence information. Alteration in SSP composition can impact both livestock feed and industrial uses of the seed meal (Holding and Larkins, 2008). A chimeric hairpin construct was made using fragments of the camelina 2S *CsSESA7* and camelina 12S *CsSESCR3* sequences (Figure 3a) with the transgene under control of the strong seed-specific promoter for the soybean glycinin-1 gene. Knockdown of camelina 2S proteins

was nearly complete in eight individual  $T_1$  transgenic seeds based on SDS-PAGE analyses, compared with the wild-type control (Figure 3b). These results indicate that the hairpin sequence derived from *CsSESA7* may indeed recognize all of the camelina 2S transcripts.

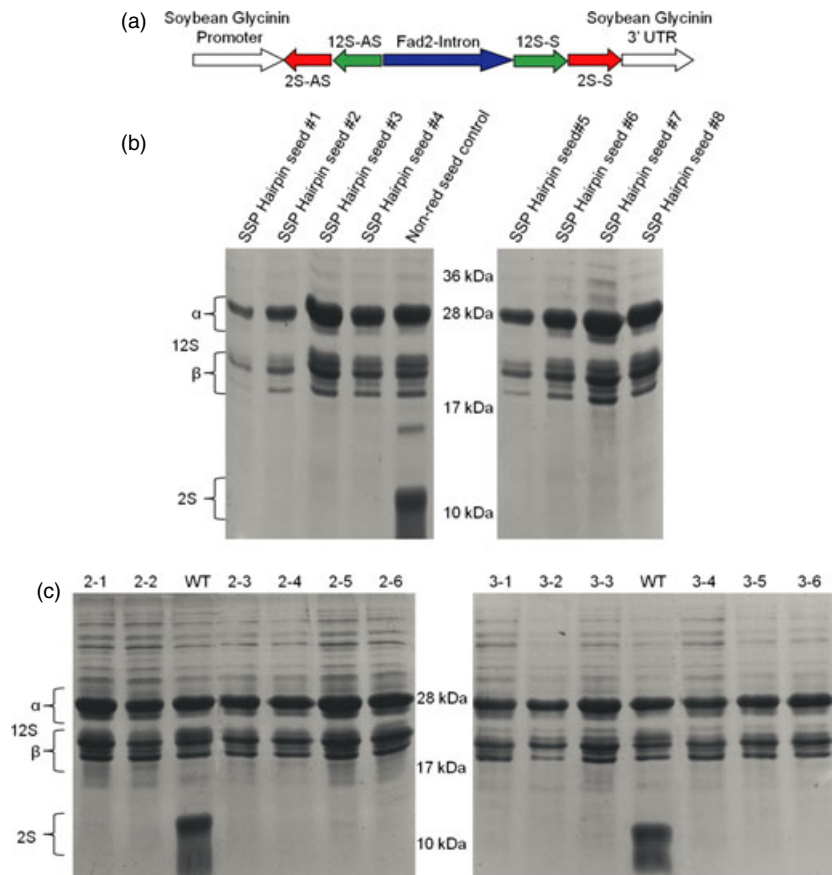
In contrast, our construct was not able to reduce overall 12S protein levels in seeds as evidenced from protein staining in SDS-PAGE, where little to no reduction is shown (Figure 3b,c). To further investigate the protein species present in these seeds, peptide analysis was carried out on gel-isolated camelina 12S  $\beta$  and  $\alpha$  subunits, revealing the best match among Arabidopsis proteins to be the subunits of SESCR4 (data not shown). The hairpin sequence used more closely matched the Arabidopsis SESCR2 protein (93%, as compared to 53% for SESCR4). We suspect that a camelina 12S hairpin sequence that more closely matches the Arabidopsis *SESCR4* sequence might lead to a more obvious knockdown effect on the camelina 12S proteins. An alignment of 12S protein sequences showed greater sequence divergence than that among 2S sequences (Figures S2 and S3). The hairpin derived from *CsSESCR3* is likely to have hybridized more selectively among camelina 12S transcripts. Our results show broad reduction in 2S SSPs and selective suppression of members of the 12S SSP family. It is likely that refining construct design using alternative 12S gene sequences would target the 12S proteins more broadly. It is also possible that seed development is more sensitive to overall 12S protein loss than to 2S loss and thus warrants further investigation.

Analysis of  $T_2$  seeds revealed that camelina 2S SSP suppression is stable (Figure 3c). Moreover, the suppression did not have any detrimental effects on seed germination under greenhouse conditions (results not shown). When total seed protein content and oil content were measured in the SSP RNAi lines, there was no significant difference between the content in wild-type seeds and two different homozygous RNAi lines, SSP RNAi 2 and SSP RNAi 3 (Figure S4). Lower expression of SSPs could lead to a change in the accumulation of other important components in the seed, including other proteins, oil and starch, which require more in-depth proteomic evaluation. In addition, introduction of high-value foreign proteins could make camelina seed meal a more attractive source of co-products for biofuel and industrial oil production.

### Genes related to fatty acid and oil synthesis are well-represented in the camelina developing seed transcriptome

Previously an acyl lipid metabolism gene database was developed for Arabidopsis (Beisson *et al.*, 2003), and this was recently expanded from deep transcriptional profiling of developing seeds of four different oilseed species (Troncoso-Ponce *et al.*, 2011). This significant endeavour resulted in detailed sequence information from more than 350 genes encoding for proteins involved in lipid metabolism and provides a useful resource for construction of additional oilseed lipid databases (<http://aralip.plantbiology.msu.edu/>).

To build a similar database for camelina, we queried the transcriptome assembly to predict camelina orthologs of Arabidopsis lipid metabolic pathway components using a reciprocal best-hits BLAST (RBH) approach. Protein sequences of the representative Arabidopsis gene model (AGI indicated) from the lipid metabolism database above were used to query the camelina transcriptome using tBLASTN, and in parallel, the camelina



**Figure 3** Seed storage protein (SSP) suppression in camelina. (a) Transgene of the double 2S and 12S camelina SSP hairpin used for RNAi suppression. Protein extracts (40  $\mu$ g) from eight different T<sub>1</sub> DsRed-positive individual seeds and one control seed (b) and six individual seeds from two different T<sub>2</sub> lines and controls (c) were separated by 15% SDS-PAGE. Gels were stained with Coomassie for band detection.

transcriptome was used with BLASTX to query the representative gene model proteins of TAIR10. For any given tBLASTN AGI hit, we retained the top hit of each camelina transcriptome element (reduced to isogroup or singleton), based firstly on bit score and secondly on *E*-value. RBH pairs are those tBLASTN AGI outputs that matched the AGI output of the top camelina to TAIR10 BLASTX hit. Both RBH pairs and members of likely co-orthologous groups are indicated in Table S1.

From 571 Arabidopsis genes related to lipid metabolism queried, 825 putative unique camelina genes or co-assembled homeologous gene sets were found. About 457 (80%) represented reciprocal best BLAST hits and therefore likely orthologs to 635 unique camelina isogroups.

Ninety-eight (17%) of the Arabidopsis queries matched camelina genes well but did not survive the RBH test. Camelina isogroups not already assigned a putative orthology in the RBH set but that aligned well to more than one Arabidopsis sequence along with remaining Arabidopsis queries that matched camelina genes already assigned in the RBH analysis, indicating lesser relative homology, are considered putative co-orthologs (Table S1). It is important to note that because our transcriptome contains only expressed genes of seeds rather than a whole-genome complement, accurate orthology cannot be determined. Figure 4b shows a portion of the database we prepared at [www.camelinagenome.org](http://www.camelinagenome.org).

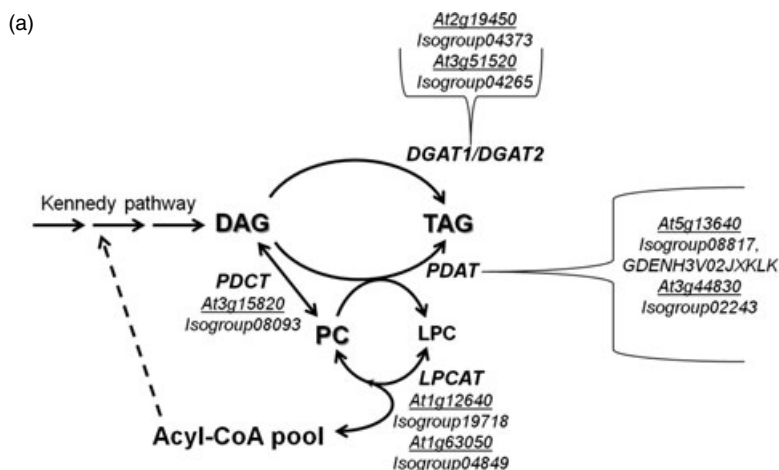
In the seed transcriptome presented here, transcripts for all plastid-localized *de novo* fatty acid biosynthetic pathway genes and all ER-associated triacylglycerol (TAG) synthesis enzymes were identified. Also found were several genes of current interest implicating a more complex route to TAG formation, including camelina homologues of At1g12640 and At1g63050, 1-acyl-

glycerol-3-phosphocholine acyltransferase (LPLAT/LPCAT) genes that are involved in phosphatidylcholine acyl editing (Bates *et al.*, 2012; Figure 4a). The acyl editing activity of LPCAT was shown to play an important role in phosphatidylcholine: diacylglycerol acyltransferase 1 (PDAT1) catalysed TAG biosynthesis in an Arabidopsis diacylglycerol acyltransferase 1 (DGAT1) mutant (Xu *et al.*, 2012; Figure 4a).

In addition to the acyl-CoA-dependent enzymes mentioned above, transcripts for acyl-CoA-independent phospholipid: diacylglycerol acyltransferase (PDAT) and phosphatidylcholine: diacylglycerol cholinephosphotransferase (PDCT/ROD1) were identified (Figure 4a). PDAT synthesizes TAG from phosphatidylcholine (PC) and diacylglycerol (DAG), and recently, it was shown to contribute along with DGAT1 to TAG biosynthesis (Dahlqvist *et al.*, 2000; Zhang *et al.*, 2009; Xu *et al.*, 2012). PDCT transfers a phosphocholine headgroup of PC to a DAG molecule at the *sn*-3 position (Lu *et al.*, 2009). This headgroup exchange allows 18 : 1 containing DAG molecules to be converted into PC for further desaturation or other modifications and for resulting modified fatty acids on PC to return to DAG molecules for TAG biosynthesis, thus modifying the fatty acid composition in TAG (Lu *et al.*, 2009; Hu *et al.*, 2012).

### SNPs in assembled transcripts estimate complexity in the camelina developing seed transcriptome

Use of a single set of overlap parameters does not allow for a separate assembly of all transcripts in a data set as complex as that of camelina. Sometimes transcripts from close paralogs, homeologs or alleles will be compressed into a single isotig when the entire reads set is used for a transcriptome assembly. Here, we subjected singletons to additional assembly (see Experimental



(b) Lipid Gene Database

- > Synthesis of Fatty Acids in Plastids
- > Synthesis of Membrane Lipids in Plastids
- > Synthesis of Membrane Lipids in Endomembrane System
- > Metabolism of Acyl-Lipids in Mitochondria
- > Synthesis and Storage of Oil
- > Lipid Signaling
- > Fatty Acid Elongation and Wax and Cutin Metabolism
- > Miscellaneous

Synthesis and Storage of Oil									
Function	TAIR10 AGI	Camelina isotig	Relationship to arabidopsis gene	Isotig length	Max variant count	Max reads fraction	Min variant count	Min reads fraction	Download
Acyl-CoA: Diacylglycerol Acyltransferase	At2g19450	g0437300003	RBH	1945	24	0.99	7	0.87	Isotigs Show Reads
Acyl-CoA: Diacylglycerol Acyltransferase	At3g51520	g0426900003	RBH	1332	3	0.77	1	0.19	Isotigs Show Reads

**Figure 4** Acyl-CoA-dependent and Acyl-CoA-independent routes to triacylglycerol (TAG) biosynthesis in camelina and the Camelina acyl lipid metabolism database. (a) Overview of acyl-CoA-dependent and acyl-CoA-independent flux between diacylglycerol (DAG) and TAG (b) Screenshot of the Camelina acyl lipid metabolism database. Abbreviations for (a): DGAT, diacylglycerol acyltransferase; PDAT, phosphatidylcholine: diacylglycerol acyltransferase; PDCT, phosphatidylcholine: diacylglycerol cholinephosphotransferase; LPCAT, 1-acyl-glycerol-3-phosphocholine acyltransferase; PC, phosphatidylcholine; LPC, lysophosphatidylcholine. Camelina candidate genes involved are shown in the pathway as isogroup number or singletons (a).

Procedures), potentially further combining slightly polymorphic transcripts into isotigs. The consensus sequence of a mixed-variant isotig is useful for the identification of functional homology, our primary goal in this study; however, lost are single-nucleotide polymorphisms (SNPs) present in the reads. These positions of variation would reveal evolutionary distance, functional and regulatory diversity in camelina genes and could be used for primer/probe design for further investigation. To add detail to the RBH analysis for lipid biosynthesis genes, therefore, we estimated variation within the isotigs listed in Table S1.

Briefly, reads that made up each assembled isotig were mapped back to its consensus sequence. With restrictions on quality and depth support for SNP identification and on overall length match to original isotig (Appendix S1), we counted the number of variants that could be formed from overlapping SNPs in the reads. Reads that disagreed with respect to any SNP(s) were used as evidence for other variant(s). Minimum variants and the fraction of reads supporting them are showing in Table S1, columns 18 and 19, respectively. In columns 16 and 17 of Table S1, we also indicate maximum number of variants that can be estimated from the data. In each case, variants contain no conflict among SNPs in overlapped regions. The minimum variant estimation requires all reads with nonconflicting polymorphism to assemble into a single variant, whereas the maximum variant estimation allows for all combination of reads that could possibly assemble based on sequence overlaps. The latter permits noise, reads combinations that are unlikely to be biologically real; however, we show this estimation to indicate that for some isotigs, there is evidence that given more sequencing depth and/or reassembly of reads, additional variants might be found. Each

isotig in our web database, [www.camelinagenome.org](http://www.camelinagenome.org), is linked to the reads that make up each isotig, found using the 'Show Reads' option within the camelina BLAST server. These are provided to selectively reassemble reads and/or design primers/probes for whole transcript validation.

The variant estimates in Table S1 provide a valuable starting point for further study of camelina lipid metabolism genes, while direct validation of transcripts and a whole-genome assembly of camelina will provide greater clarity for the separation of close paralogs, homeologs and expressed alleles. Figure S5 summarizes estimated transcript variation in the overall camelina lipid biosynthesis database with respect to the minimum variants calculated in the above analysis. 40% of the database is contained in isotigs that may be true single transcripts. Singletons make up 15% not subjected to variant analysis, leaving approximately 45% of available isotigs that may be expanded into additional individual transcript sequences upon further experimental analysis.

#### The camelina developing seed transcriptome is useful for oil modification and the close relationship between Arabidopsis and camelina allows for translational research for oil enhancement

In addition to its use for seed protein modification, the camelina developing seed transcriptome is a valuable resource for oil modification. More than 50% of camelina oil is composed of polyunsaturated fatty acids [35%–40%  $\alpha$ -linolenic acid (18 : 3) and 20%–25% linoleic acid (18 : 2)], rendering its use as a biofuel limited due to the high rates of oxidation of these fatty acids. A more ideal biodiesel blend, for example, would have high propor-



tions of the monoenoic oleic acid (18 : 1), which has greater oxidative stability than polyunsaturated fatty acids and better cold flow properties than saturated fatty acids (e.g. 16 : 0 and 18 : 0; Durrett *et al.*, 2008). *FAD2* encodes an ER membrane-bound desaturase catalysing conversion of oleic acid to linoleic acid, and *FAE1* encodes an enzyme that initiates the addition of 2 carbon units to 18 carbon fatty acyl-CoAs leading to the synthesis of very long-chain fatty acids. These two genes are consequently priority targets for genetic manipulation in camelina towards lowering the polyunsaturated fatty acid content and increasing the oleic acid content. Hutcheon *et al.* (2010) used Southern blot analyses and cloning to determine that there are three copies of each gene, with each copy showing more than 90% amino acid sequence identity to the Arabidopsis homologue. Seed-specific antisense suppression by Kang *et al.* (2011) of the camelina *FAD2* gene resulted in transgenic camelina lines with as high as approximately 50 wt% oleic acid content and a reduced 18 : 2 (6 wt%) and 18 : 3 (11 wt%) content compared with wild type, but no reduction in the content of C20 and C22 fatty acids.

According to our RBH analysis, camelina isogroup 03202 was orthologous to Arabidopsis *FAD2*. Upon inspection of the 132 454 reads that were assembled into this isogroup, we confirmed three variants closely resembling the cloned *FAD2-A*, *-B* and *-C* sequences previously reported (Hutcheon *et al.*, 2010), sharing  $\geq 98\%$  identity.

We amplified the *FAD2-C* cDNA for use in RNAi experiments (Figure 5a). Upon screening 24 *FAD2* RNAi lines, we were able to attain about 50 wt% oleic acid in camelina seed oil (Figure 5c). The 18 : 2 and 18 : 3 content was reduced to approximately 4.5 and 13 wt%, respectively, in the top-performing homozygous RNAi line. To further increase the oleic acid content in seed oil of camelina and reduce the content of C20 and C22 fatty acids, a camelina *FAE1* RNAi expression cassette was introduced into the same binary vector with the camelina *FAD2* RNAi cassette. The sequence amplified from a camelina seed cDNA library based on our reference set was identical to the previously reported *FAE1-A* gene (Hutcheon *et al.*, 2010). From 19 independent lines screened, we identified a line with as high as 70 wt% oleic acid (Figure 5a,c). The double *FAD2/FAE1* RNAi seeds contained only about 4 wt% 18 : 2 and 8 wt% 18 : 3 compared with 17 wt% 18 : 2 and 36 wt% 18 : 3 in wild-type seeds. In addition, C20 and C22 fatty acids were reduced from approximately 17 wt% of total fatty acids in wild-type seeds to approximately 4 wt% in *FAD2/FAE1* RNAi seeds. Of most significance, 20 : 1 levels were reduced from 12 wt% in wild-type seeds to 3 wt% in *FAD2/FAE1* RNAi seeds. We acknowledge that transgenic lines were not generated for *FAE1* RNAi suppression alone. However, the decrease in 20 : 1 and other very long-chain fatty acids and the corresponding increase in oleic acid content between the *FAD2/FAE1* RNAi and *FAD2* RNAi lines can be directly attributed to the *FAE1* suppression.

A nearly identical lipid profile phenotype was generated in camelina lines transformed with a seed-specific RNAi suppression construct using the Arabidopsis *FAD2* gene sequence as with the camelina *FAD2* sequence, demonstrating cross-utility of sequence references in oil engineering of these two closely related plants. Up to 50 wt% oleic acid was achieved in seeds of the top-performing lines, compared with approximately 12 wt% oleic acid in wild-type seeds (Figure 5d). Further studies using a double Arabidopsis *FAD2/FAE1* RNAi binary vector resulted in even higher levels of oleic acid in transgenic camelina seeds, up to approximately 66 wt% of total fatty acids (Figure 5d). The 18 : 2,

18 : 3, and C20 and C22 fatty acid components of the seed oil were also decreased in these lines to levels similar to those achieved with camelina homologues. Although the Arabidopsis *FAD2/FAE1* RNAi seeds did have significantly more total oil compared with wild-type seeds, total oil content levels were between 30% and 40% in all transgenic lines studied (Figure S4b).

Currently, no camelina genome sequence is available, and its complexity and polyploidy are expected to present hurdles on future attempts at oil engineering and other modification based on selective gene suppression, particularly through breeding. The results presented here show that it is possible to alter the fatty acid profile of camelina with limited genomic information, based on homology to equivalent Arabidopsis genes. The ability to achieve similar oil composition phenotypes in camelina using Arabidopsis homologues for gene suppression highlights the value of camelina for translating findings in Arabidopsis to a crop plant, which is desirable for showing agronomic relevance of discoveries in Arabidopsis. In addition, the high oleic acid phenotypes achieved here can serve as optimized oil platforms for more extensive metabolic engineering to achieve higher value traits, such as *sn*-3-acetyl TAGs or wax esters for drop-in biofuels or specialty lubricants (Carlsson *et al.*, 2011; Durrett *et al.*, 2010).

## Conclusions

In this study, *C. sativa* genomics tools were enhanced with detailed transcript analyses of developing seeds, including genes recognized as targets for meal and oil improvement. The sequences identified in this study were highly homologous to genes in Arabidopsis and *B. napus*. Camelina seed protein composition in transgenic plants was dramatically altered by SSP suppression based on sequence information from the seed transcriptome. The potential beneficial impacts of this genetic modification are yet to be explored: whether lowering protein content in the meal can increase oil content either directly or indirectly, or production of more valuable proteins can be achieved. Moreover, camelina oil composition was tailored towards a better biofuel and bio-based lubricant composition, with generation of transgenic lines with high oleic acid content and low polyunsaturated and very long-chain fatty acid content. This trait was achieved by means of RNAi suppression of genes for key enzymes involved in fatty acid modification, using not only camelina sequences identified in the transcriptomic data but also Arabidopsis sequences, showing the close relationship between the two species and the utility of camelina for translation of findings in Arabidopsis. Genes relevant to seed lipid metabolism in camelina, and their variants, were determined in a detailed sequence alignment survey and compiled into a publicly accessible database. This database will support future breeding and engineering efforts to modify camelina oil compositions for industrial or fuel purposes.

## Experimental procedures

### RNA isolation from developing seeds and cDNA library construction

Total RNA was isolated from *C. sativa* (cv. Sunesson) seeds removed from pods with seed coats intact at 10–13 and 15–20 DAP. Seeds were collected from greenhouse grown plants and immediately frozen in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  until use in RNA isolation.





7.5% of singletons mapped back to this assembly. Finally, 253 additional isotigs were assembled after subjecting the remaining singletons to another round of assembly as above.

The camelina transcriptome provided here includes both assembled transcripts (isotigs and unbroken contigs from the Newbler assembly) as well as singletons, and the data set is trimmed for elements with a minimum length of 100 nts.

### Phylogenetic tree building and sequence alignments

Phylogenetic trees were generated after ClustalW sequence alignment with the MEGA4 software neighbour-joining tree application and 1000 bootstrap replicates (Tamura *et al.*, 2007; Thompson *et al.*, 1994).

### Homology analysis and construction of the Camelina acyl lipid metabolism gene database

The camelina transcriptome assembly was matched by BLASTX (Altschul *et al.*, 1990), using BLOSUM62 scoring matrix and a word size of 3, to protein sequences of TAIR10 representative gene models ([www.arabidopsis.org](http://www.arabidopsis.org)) with an *E*-value limit of  $1 \times 10^{-5}$ . The top hit(s) for each query sequence was retained based on best bit score and *E*-value. Secondly TAIR10 models (above) were matched to camelina assembly elements (isotigs and singletons) using tBLASTN with an *E*-value limit of  $1 \times 10^{-5}$ . Candidate acyl lipid metabolism gene sequences were retrieved from the Arabidopsis Lipid Gene database (<http://lipids.plantbiology.msu.edu/>), and BLAST result sets above were trimmed to include only these genes. The best isotig for each isogroup was retained, trimming out putative alternative transcripts of the same gene.

The Camelina acyl lipid metabolism gene database ([www.camelinagenome.org](http://www.camelinagenome.org)) was constructed using Dreamweaver MX version 7.0.1 (Macromedia Inc., San Francisco, CA) and custom scripts written in PERL v5.10.1. The BLAST server uses NCBI BLAST 2.2.22.

### Analysis of lipid metabolism gene variants within isotigs

A custom Perl script was written to estimate variation within isotigs shown in Table S1. Briefly, reads were mapped back to the consensus isotig they comprised, and SNPs were determined. Putative transcript variations were called based on overlap of shared SNPs among reads, with one estimate (maximum variants) allowing for all possible reads overlap combinations and one estimate (minimum variants) restricting polymorphism into the minimum number of transcripts. The script and its full description are provided in [www.camelinagenome.org](http://www.camelinagenome.org), and see also Supporting information.

### SDS-PAGE analyses of SSPs

Briefly, crude SSPs were extracted from seeds by grinding 100 mg mature seeds in 200  $\mu$ L of extraction buffer [100 mM Tris-HCl, pH 8.0, 0.5% SDS (w/v), 10% glycerol (v/v) and 2%  $\beta$ -mercaptoethanol (v/v)]. Extracts were boiled for 3 min and centrifuged for 3 min at 16 300 *g*. The 12  $\mu$ L from each supernatant was subjected to 15% SDS-PAGE. Protein gels were stained with Coomassie Brilliant Blue R250 for 30 min and destained in 10% glacial acetic acid (v/v)/40% methanol (v/v) until bands were visualized. For the transgenic SSP camelina seed analyses, single seeds were ground in 100  $\mu$ L of extraction buffer, and 40  $\mu$ g protein from each supernatant was subjected to 15% SDS-PAGE. Total seed protein was measured as described in Supporting information.

### Mass spectrometry analyses

Mass spectrometry analyses were carried out by the Nebraska Center for Mass Spectrometry (NCMS) at the University of Nebraska-Lincoln using protein spot picking and mass spectrometry methods as described (Shevchenko *et al.*, 1996; Schweitzer *et al.*, 2012) with slight modifications described in Supporting information.

### Confirmation of individual camelina SSPs

To confirm the camelina 2S SSP transcripts represented distinct genes, specific primers for each gene were designed to PCR-amplify candidates from a camelina cDNA library (Table S2). PCR products were confirmed with sequencing.

### Preparation of RNAi suppression constructs for camelina SSP and FAD2/FAE1, and Arabidopsis FAD2/FAE1 genes

Detailed descriptions of the construction of RNAi suppression constructs for the preparation of camelina SSP and FAD2/FAE1, and Arabidopsis FAD2/FAE1 genes are provided in the Supporting information.

### Camelina transformation and selection of transformants

Camelina plants were grown under greenhouse conditions with 14-h day length (24–26 °C) and 8-h dark (18–20 °C) with natural and supplemental lighting at 400–500  $\mu$ moles/m<sup>2</sup>/s. Transgenic camelina lines were generated according to the *Agrobacterium*-mediated method of Lu and Kang (2008). DsRed-positive seeds were identified using a green LED flashlight with a red camera filter lens (Lu and Kang, 2008). For Basta-resistant lines, T<sub>1</sub> seeds were planted in flats, and the first true leaves were allowed to emerge. A 0.003% Basta solution was sprayed onto the surface of the leaves at 3- to 4-day intervals. Resistant young plants were transferred to individual pots and allowed to mature. For kanamycin-resistant lines, approximately 1 g of sterilized T<sub>1</sub> seeds was spread on a 15-cm plate containing 1  $\times$  MS with vitamins (pH 5.7) medium with 1% sucrose, 0.28% phytagar and 50  $\mu$ g/mL kanamycin. After 2 weeks of growth at room temperature under continuous light, resistant plants were planted and transferred to the greenhouse.

### Analysis of camelina seed fatty acid composition

Fatty acid methyl esters (FAMES) were prepared by transesterification with trimethylsulphonium hydroxide (TMSH; Butte, 1983). Single transgenic seeds were directly crushed in 50  $\mu$ L of TMSH in glass GC vials. Heptane (400  $\mu$ L) was added to each vial. After room temperature incubation with agitation for 30 min, FAMES were analysed by gas chromatography as described (Cahoon *et al.*, 2006). Total fatty acid content of seeds was measured as described in Supporting information.

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## Supporting information

Additional Supporting information may be found in the online version of this article:

**Figure S1** Sequence alignment of camelina, Arabidopsis and Brassica 2S seed storage proteins.

**Figure S2** Sequence comparison of camelina SESCOU1 to Arabidopsis SESCOU3 and Brassica SESCOU4 seed storage proteins.

**Figure S3** Sequence comparison of camelina SESCOU4, 5 and 6 to Arabidopsis SESCOU4 and Brassica SESCOU1 12S seed storage proteins.

**Figure S4** Protein and oil content in seed storage protein RNAi, and Arabidopsis and camelina *FAD2/FAE1* RNAi camelina seeds.

**Figure S5** Summary of estimated SNP-based variants within isotigs of the Camelina Lipid Biosynthesis Database.

**Table S1** Camelina lipid metabolism genes.

**Table S2** Primer sequences used to confirm seed storage protein candidates.

**Appendix S1** Experimental procedures.



Supplementary Figures

1	MANKLFLVCATLAVCFLLTNASIYRTVVEFDED-ATNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA1
1	MANKLFLVGATLALCFLLTNASIYRTVVEFDED-ATNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA2
1	MANKLFLVGATLALCFLLTNASIYRTVVEFDED-ATNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA3
1	MANKLFLVGATLALCFLLTNASIYRTVVEFDED-ATNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA4
1	MANKLFLVCATLALCFLLTNASIYRTVVEFDED-ATNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA5
1	MANKLFLVCATLALCFLLTNASIYRTVVEFDEE-TTNPMGPR--QRCQREFQQSQHLRAC	57	CsSESA6
1	MANKLFLVSATLALCFLLTNASIYRTVVEFEDDATNRQFRP-QQKQREFQQSQHLRAC	59	CsSESA7
1	MANKLFLVSATLALCFLLTNASIYRTVVEFEDDATNRQFRP-QQKQREFQQSQHLRAC	59	CsSESA8
1	MANKLFLVCATLALCFLLTNASIYRTVVEFEEDDASNPFVGRP--QRCQREFQQSQHLRAC	58	AtSESA3
1	MANKLFLVCATLALCFLLTNASIYRTVVEFEEDDASNPMGPR--QKCKQEFQQSQHLRAC	58	AtSESA2
1	MANKLFLVCAALALCFILTNASVYRTVVEFEEDDASNPIGPI--QKCKQEFQQSQHLRAC	58	AtSESA4
1	MANKLFLVCAALALCFLLTNASIYRTVVEFEEDDATNPIGPK-MRKCRKEFQKQHLRAC	59	AtSESA1
1	-MAKLIIVFATLALFILLANASIYRTVVEFEEDDVSNI---PQQGKQREFMKHQQLRGC	56	AtSESA5
1	MANKLFLVSATLALCFLLTNASIYRTVVEFEEDDATDSAGPFRI PKCRKEFQQSQHLRAC	60	BnSESA2
1	MANKLFLVSATLALCFLLTNASIYRTVVEFEEDDATNPAGPFRI PKCRKEFQQSQHLRAC	60	BnSESA4
1	-----PKCRKEFQQSQHLRAC	16	BnSESA1
1	MANKLFLVSATLALCFLLTNASVYRTVVEFEEDDATNPAGPFRI PKCRKEFQQSQHLRAC	60	BnSESAE
1	-----SAGPFRI PKCRKEFQQSQHLRAC	23	BnSESA3
1	MANKLFLVSATLALCFLLTNASIYRTVVEFEEDDATNPAGPFRI PKCRKEFQQSQHLRAC	60	BnSESA6
	:*::** :*::**		
58	QELMRRQMRQ--GRGG-----DEYDWEEDMEN-PQRR---QVLEQCCNELRQEDPAC	104	CsSESA1
58	QQFMRRQARQ--GRGG-----DEYDWEEDMET-SRRP---QQLLQCCNELRQEDPVC	104	CsSESA2
58	QQLMRRQMRQ--GRGD-----DEFLEDDMEN-PQRP---QQLLQCCNELRQEDPVC	105	CsSESA3
58	QQLMRSQMRQ--RGG-----DEYGLEDDMEN-PQRP---QQLLQCCNELRQEDPVC	104	CsSESA4
58	QQLMRRQMRQ--GRG-----DEYDWEEDMEN-PQRP---QQLLQCCNELRQEDPVC	103	CsSESA5
58	QELMRRQARQ--GRGG-----DEYDWEEDMEN-PQRR---QVLEQCCNELRQEDPAC	105	CsSESA6
60	QSWMRQSRQ--RSGP---ALDDEFDQDDIEN-PQRR---DPVLQCCNELQDQDPEC	111	CsSESA7
60	QSWMRQTRQ--RSGP---ALDDEFDQDDIEN-PQRR---HPVLQCCNELQDQDPEC	111	CsSESA8
59	QRWMSKMRQ--RGGG---SLDDEFDFE-----GPOQGYQLLQCCNELRQEE PVC	106	AtSESA3
59	QKLMRQMRQ--RGGG---SLDDEFLEDDIEN-PQGPQQGHQILQCCSELRQEE PVC	113	AtSESA2
59	QRWMRQMRQ--RGGG---SLDDEFMDIEN-PQR---RQLLQCCSELRQEE PVC	109	AtSESA4
60	QQMLLQARQ--RS-----DEFDFEDMEN-PQGGQEQQLFQCCNELRQEE PDC	108	AtSESA1
57	KQWIRKRAQQGRIGYEADDFELTLDVLEDD--ENPMGQQ--QSSLKMCNELRQVDRMC	113	AtSESA5
61	QQWLHKQAMQSG--GGP-SWILDGEFDFEDDMEN-PQGPQRRPPLLQCCNELHQEE PLC	116	BnSESA2
61	QQWLHKQAMQSG--SGP-SWILDGEFDFEDDMEN-PQGPQRRPPLLQCCNELHQEE PLC	116	BnSESA4
17	QQWLHKQAMQSG--GGP-SWILDGEFDFEDDMEN-PQGPQRRPPLLQCCNELHQEE PLC	71	BnSESA1
61	QQWLHKQAMQSG--GGP-SWILDGEFDFEDDMEN-PQGPQRRPPLLQCCNELHQEE PLC	119	BnSESAE
24	QQWLHKQAMQSG--SGP-----QGPQRRPPLLQCCNELHQEE PLC	62	BnSESA3
61	QQWLHKQAMQSG--SGP-SWILDGEFDFEDDMEN-PQGPQRRPPLLQCCNELHQEE PLC	116	BnSESA6
	: : : *		: *.**.* :
105	VCPTLQQAARSVSIQGGQGGQ-----QRQSARQVYQTAKHLNPNVCRIPQVDVCPFQ--	156	CsSESA1
105	VCPTLQQAARSVSIQGGQGGQ-----QRQSARQIYQTAKHLNPNVCRIPQVDVCPFQ--	156	CsSESA2
106	VCPTLRQAASVRLQGGH-----GPFQARKIYQTAKHLNPNVCRIPQVGVCPFQ--	153	CsSESA3
105	VCPTLRQAASVRLQGGH-----GPFQARKIYQTAKHLNPNVCRIPQVGVCPFQ--	152	CsSESA4
104	VCPTLQQAARSVSIQGGQGGQ-----QRQSARQIYQTAKHLNPNVCRIPQVDVCPFQ--	155	CsSESA5
106	VCPTLQQAARSVSIQGGQGGQ-----QRQSARQIYQTAKHLNPNVCRIPQVDVCPFQ--	157	CsSESA6
112	VCPTLQQAARSVRLQGGH-----GPFQASQILQTAKRLPNICNIPQVGVCPFRAS	161	CsSESA7
112	VCPTLQQAARSVRLQGGH-----GPFQASQILQTAKRLPNICNIPQVGVCPFRAS	161	CsSESA8
107	VCPTLQQAARSVSLQGG-H-----GPFQSRKIYQSAKYLPNICIKIQVGECPFQIT	156	AtSESA3
114	VCPTLRQAARSVSLQGG-H-----GPFQSRKIYQSAKYLPNICIKIQVGECPFQIT	163	AtSESA2
110	VCPTLRQAARSVRLQGGH-----GPFQSRKIYQSAKYLPNICIKIQVGECPFQIT	158	AtSESA4
109	VCPTLQQAARSVRLQGGH-----GPFQSRKIYQSAKYLPNICIKIQVGECPFQIT	156	AtSESA1
114	VCPTLQQAARSVRLQGGH-----GPFQSRKIYQSAKYLPNICIKIQVGECPFQIT	163	AtSESA5
117	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	172	BnSESA2
117	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	174	BnSESA4
72	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	127	BnSESA1
120	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	179	BnSESAE
63	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	120	BnSESA3
117	VCPTLKGASKAVKQIQQQGGQ--QGK--QQMVSRIYQTATHLKPVCNIPQVSVCPFQKT	172	BnSESA6
	*****: *::* * : : :*. **.* * * * *		
157	IPSGPSYY	164	CsSESA1
157	IPSGPSYY	164	CsSESA2
154	TIPSSPY	161	CsSESA3
153	TIPFSPY	160	CsSESA4
156	IPSGPSYY	163	CsSESA5
158	IPSGPSYY	165	CsSESA6
162	----PYY	164	CsSESA7
162	----PYY	164	CsSESA8
157	IPFPPPY	164	AtSESA3
164	IPFPPY-	170	AtSESA2
159	IPSIPSY	166	AtSESA4
157	IPSPSY	164	AtSESA1
164	P----Y-	165	AtSESA5
173	MPG-PSY-	178	BnSESA2
175	MPG-PSY-	180	BnSESA4
128	MPG-PSY-	133	BnSESA1
180	MPG-PGFY	186	BnSESAE
121	MPG-PS--	125	BnSESA3
173	MPG-PSY-	178	BnSESA6

**Supplementary Figure 1.** Sequence alignment of camelina, Arabidopsis and Brassica 2S SSPs. Camelina, Arabidopsis and Brassica 2S SSP protein sequences were aligned using ClustalW (Thompson et al., 1994). Accession numbers for CsSESA1-8: JX191882-JX191889, respectively; accession numbers for AtSESA1-5: P15457, P15458, P15459, P15460 and Q9FH31, respectively; accession numbers for BnSESA1, BnSESA2, BnSESA3, BnSESA4, BnSESA6 and BnSESAE: P01091, P01090, P80208, P17333, P27740 and P09893, respectively.

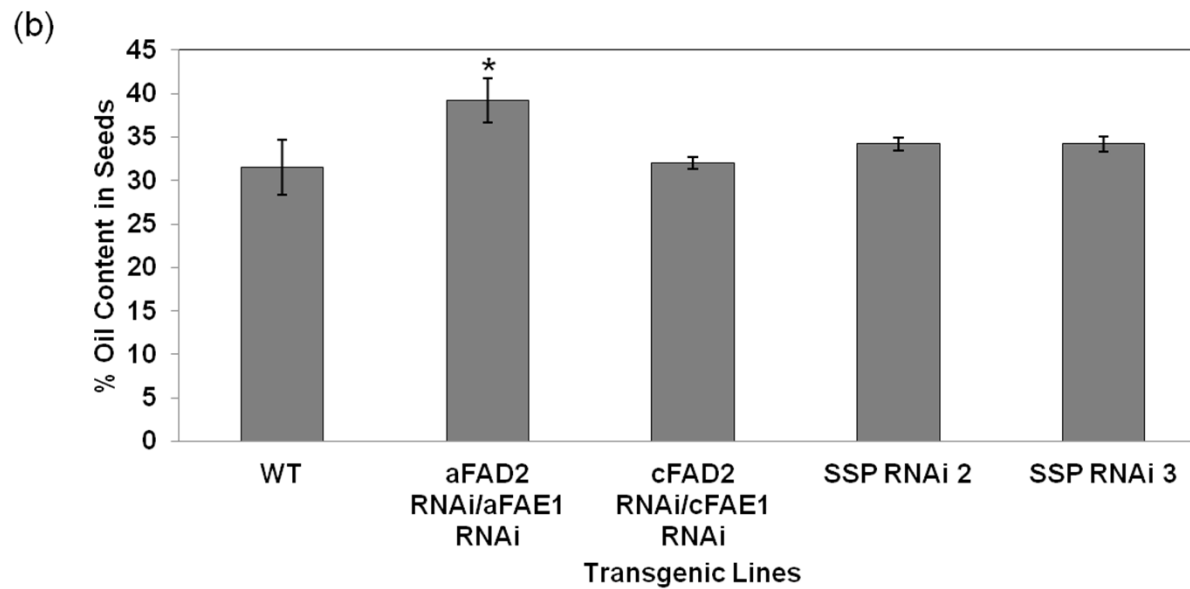
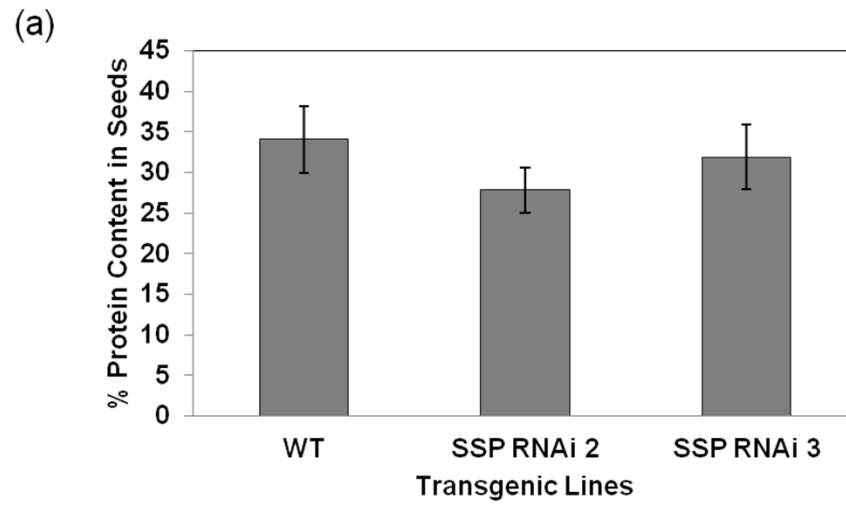






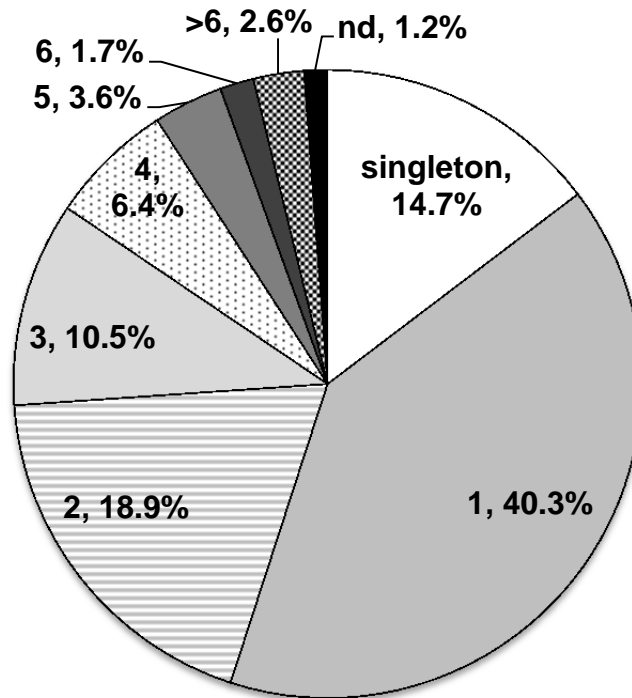






Supplementary Figure 4. Protein and oil content in SSP RNAi, and Arabidopsis and camelina FAD2/FAE1 RNAi camelina seeds. Total protein (a) was extracted and measured (Bradford, 1976) from seeds of wild type and homozygous SSP RNAi 2 and SSP RNAi 3 lines. Total oil content (b) in the SSP RNAi and Arabidopsis and camelina FAD2/FAE1 RNAi camelina seeds was determined by Bligh and Dyer (1959) extraction of total lipids, and transesterification to FAMES. The error bars represent the standard deviation of the average of 3-5 biological replicates of each sample. \*Student t-Test significance at  $p \leq 0.05$  compared to wild type.

**Supplementary Figure 5.**



**Supplementary Figure 5.** Summary of estimated SNP-based variants within isotigs of the Camelina Lipid Biosynthesis Database. Shown are proportions of isotigs with indicated number of Minimum variants according to Supplemental Table 1. Isotigs that were not retained after the variant analysis (*i.e.*, no single sequence, consensus or variant, could be determined by reads overlap within the parameters used) are indicated by *nd*, not determined.

Supplementary Table 1. Camelina lipid metabolism genes

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship Arabidopsis	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
Plastidial Homomeric Acetyl-CoA Carboxylase	At1g36180	isogroup07190	RH	AT1G36180	g07190000	94.19	5.00E-84	312	g07190000	AT1G36180	94.19	2.00E-83	304	468	1	0.71	1	0.71
Acyl-ACP Thioesterase FatA	At3g25110	isogroup09431	RH	AT3G25110	g09431000	94.57	0	739	g09431000	AT3G25110	94.57	0	687	1465	253	0.84	1	0.89
Acyl-ACP Thioesterase FatA	At4g13050	isogroup06800	RH	AT4G13050	g06800000	92.93	0	717	g06800000	AT4G13050	92.93	0	697	1292	11	0.86	3	0.69
Acyl-ACP Thioesterase FatB	At1g08510	isogroup05761	RH	AT1G08510	g05761000	96.55	0	774	g05761000	AT1G08510	96.39	0	806	1503	49	0.96	4	0.83
Plastidial Pyruvate Dehydrogenase E1alpha subunit	At1g01090	isogroup01655	RH	AT1G01090	g01655000	95.14	0	842	g01655000	AT1G01090	95.14	0	812	1577	162	0.82	7	0.62
		GDENH3V01AXRR	RH*	AT1G24180	GDENH3V01	79.31	1.00E-08	54.3	GDENH3V01	AT1G24180	85.19	8.00E-10	53.5	241	na	na	na	na
Plastidial Pyruvate Dehydrogenase E1alpha subunit	At1g24180	isogroup05798	RH	AT1G24180	g05798000	97.65	0	785	g05798000	AT1G24180	97.65	0	758	1209	15	0.87	6	0.82
		isogroup08993	RH	AT1G30120	g08993000	94.63	0	788	g08993000	AT1G30120	94.63	0	756	1569	9	1.00	2	0.98
Plastidial Pyruvate Dehydrogenase E1beta subunit	At1g30120	isogroup12774	RH*	AT1G30120	g12774000	95.52	0	787	g12774000	AT1G30120	95.52	0	761	1475	1	1.00	1	1.00
Plastidial Pyruvate Dehydrogenase E1beta subunit	At2g34590	isogroup02201	RH	AT2G34590	g02201000	94.2	0	775	g02201000	AT2G34590	94.74	0	764	1416	34	0.91	8	0.84
Plastidial Dihydropyruvate Acetyltransferase, pyruvate DH complex	At1g34430	isogroup11842	RH	AT1G34430	g11842000	95.48	0	811	g11842000	AT1G34430	95.48	0	845	1527	384	0.94	5	0.77
		GDENH3V02I0E0	RH*	AT1G54220	GDENH3V02	81.48	1.00E-06	46.2	GDENH3V02	AT1G54220	50	2.00E-07	50.4	377	na	na	na	na
Plastidial Dihydropyruvate Acetyltransferase, pyruvate DH complex	At1g54220	isogroup1855	RH	AT1G54220	g01855000	93.49	0	1044	g01855000	AT1G54220	93.49	0	1008	1864	55	0.88	3	0.71
		isogroup09187	RH*	AT1G54220	g09187000	71.43	3.00E-06	52	g09187000	AT1G54220	71.43	4.00E-07	50.4	442	1	1.00	1	1.00
Plastidial Dihydropyruvate Acetyltransferase, pyruvate DH complex	At3g13930	isogroup0452	RH*	AT3G13930	g0452000	94.43	0	1041	g0452000	AT3G13930	94.43	0	997	3592	3570	0.93	1	0.36
		GD75LV01WESL	RH*	AT3G25860	GD75LV01E	89.83	1.00E-45	182	GD75LV01E	AT3G25860	90	2.00E-77	179	477	na	na	na	na
Plastidial Dihydropyruvate Acetyltransferase, pyruvate DH complex	At3g25860	isogroup01768	RH	AT3G25860	g01768000	93.58	0	818	g01768000	AT3G25860	94.41	0	875	1714	450	0.94	3	0.71
		GDENH3V02HMK54	RH*	AT4G16155	GDENH3V02	75.24	5.00E-44	138	GDENH3V02	AT4G16155	75.24	6.00E-51	158	487	na	na	na	na
Plastidial Dihydropyruvate Dehydrogenase, pyruvate DH complex	At4g16155	isogroup03258	RH	AT4G16155	g03258000	95.58	0	977	g03258000	AT4G16155	95.58	0	964	1649	62	0.89	1	0.21
Plastidial Dihydropyruvate Dehydrogenase, pyruvate DH complex	At3g16950	isogroup01458	RH	AT3G16950	g01458000	94.57	0	1065	g01458000	AT3G16950	94.57	0	1050	2139	6	1.00	3	0.94
Plastidial Lipate Synthase	At5g08410	isogroup06022	RH	AT5G08410	g06022000	87.1	2.00E-83	305	g06022000	AT5G08410	87.1	4.00E-82	300	768	4	0.72	2	0.69
		isogroup02541	co-ortholog	AT4G31050	g02541000	35.48	1.00E-29	127	g02541000	AT4G31050	93.53	2.00E-126	448	982	2	0.64	2	0.64
Plastidial Lipoyltransferase	At4g31050	isogroup05427	co-ortholog	AT4G31050	g05427000	78.95	7.00E-126	447	g05427000	AT4G31050	84.34	9.00E-141	487	987	5	0.27	1	0.80
Acetyl-CoA carboxylase, alpha-carboxyl transferase	At2g38040	isogroup13550	RH	AT2G38040	g01355000	94.42	0	1382	g01355000	AT2G38040	94.42	0	1418	2807	8	0.83	5	0.82
Acetyl-CoA carboxylase, biotin carboxyl carrier protein	At5g15530	isogroup06920	RH	AT5G15530	g06920000	86.61	5.00E-118	421	g06920000	AT5G15530	87.01	1.00E-124	442	1142	5	0.73	3	0.79
		GDENH3V02BBK	RH*	AT5G16390	GDENH3V02	81.42	1.00E-34	144	GDENH3V02	AT5G16390	82.3	1.00E-39	158	427	na	na	na	na
Acetyl-CoA carboxylase, biotin carboxyl carrier protein	At5g16390	isogroup00509	RH	AT5G16390	g00509000	89.4	9.00E-117	417	g00509000	AT5G16390	89.4	2.00E-134	475	1804	2	0.65	2	0.65
Acetyl-CoA carboxylase, biotin carboxylase	At5g35360	isogroup04078	RH	AT5G35360	g04078000	95.41	0	1004	g04078000	AT5G35360	95.41	0	979	1664	57	0.94	4	0.84
Malonyl-CoA :ACP Malonyltransferase	At2g30200	isogroup04289	RH	AT2G30200	g04289000	94.42	0	669	g04289000	AT2G30200	94.42	0	703	1694	25	0.98	9	0.82
Ketoacyl-ACP Synthase I	At5g46290	isogroup15466	RH	AT5G46290	g15466000	92.07	0	713	g15466000	AT5G46290	93.09	0	708	1734	33	0.87	1	0.16
		GD75LV02D9805	RH*	AT1G74960	GD75LV02C	64.83	2.00E-46	185	GD75LV02C	AT1G74960	64.82	3.00E-45	177	487	na	na	na	na
Ketoacyl-ACP Synthase II	At1g74960	isogroup00725	RH	AT1G74960	g00725000	92.95	0	1004	g00725000	AT1G74960	92.95	0	1023	2491	1142	0.83	2	0.51
		isogroup00941	RH*	AT1G74960	g00941000	79.19	0	788	g00941000	AT1G74960	79.19	0	766	1818	75	0.94	3	0.62
Ketoacyl-ACP Synthase III	At1G62640	isogroup00346	RH	AT1G62640	g00346000	97.03	0	799	g00346000	AT1G62640	97.03	0	784	1759	65	0.91	7	0.89
Plastidial Ketoacyl-ACP Reductase	At1g24360	isogroup02055	RH	AT1G24360	g02055000	87.89	6.00E-161	562	g02055000	AT1G24360	87.89	2.00E-153	538	4963	2	0.85	2	0.85
		GDENH3V01D23FD	co-ortholog	AT1G62610	GDENH3V01	80.3	3.00E-57	219	GDENH3V01	AT3G55290	85.61	3.00E-60	226	419	na	na	na	na
		isogroup09618	co-ortholog	AT1G62610	g09618000	29.9	9.00E-09	58.9	g09618000	AT5G19290	11	3.00E-138	447	948	2	0.71	2	0.71
		isogroup09823	co-ortholog	AT1G62610	g09823000	29.84	1.00E-09	61.6	g09823000	AT3G09660	93.87	9.00E-171	596	1250	26	0.92	1	0.71
Plastidial Ketoacyl-ACP Reductase	At1g62610	isogroup00014	co-ortholog	AT1G62610	g00014000	90.43	2.00E-148	523	g00014000	AT3G09770	80.72	9.00E-175	570	2769	108	0.72	5	0.82
		isogroup02055	co-ortholog	AT1G62610	g02055000	34.12	6.00E-27	119	g02055000	AT1G24360	84.69	4.00E-147	517	4963	3	0.97	2	0.95
		isogroup04564	co-ortholog	AT1G62610	g04564000	25.2	6.00E-07	52.8	g04564000	AT1G24470	87.43	2.00E-154	304	1131	2	0.27	1	0.21
		isogroup05814	co-ortholog	AT1G62610	g05814000	31.27	2.00E-18	90	g05814000	AT3G12800	94.97	2.00E-163	572	1095	9	0.86	5	0.75
		isogroup10413	co-ortholog	AT1G62610	g10413000	33.33	5.00E-06	49.7	g10413000	AT1G01800	89.15	9.00E-147	516	1024	3	0.70	3	0.76
		isogroup10966	co-ortholog	AT1G62610	g10966000	27.04	2.00E-09	60.8	g10966000	AT1G67730	95.24	2.00E-174	498	1162	13	0.83	2	0.82
		isogroup11447	co-ortholog	AT1G62610	g11447000	31.42	1.00E-23	107	g11447000	AT5G06060	91.42	5.00E-137	483	1049	1	1.00	1	1.00
		isogroup11823	co-ortholog	AT1G62610	g11823000	31.15	2.00E-23	107	g11823000	AT5G06060	91.67	6.00E-139	490	1040	1	1.00	1	1.00
		isogroup21846	co-ortholog	AT1G62610	g21846000	31.96	2.00E-20	97.4	g21846000	AT5G06060	88.99	2.00E-108	387	667	1	1.00	1	1.00
		isogroup05667	co-ortholog	AT1G62610	g05667000	30.24	9.00E-14	75.5	g05667000	AT1G10310	95.45	4.00E-128	454	1037	6	0.59	3	0.44
		isogroup01189	co-ortholog	AT1G62610	g01189000	25.77	6.00E-10	62.8	g01189000	AT3G03330	91.46	7.00E-170	593	1841	7	0.91	3	0.91
		isogroup06190	co-ortholog	AT1G62610	g06190000	25.77	1.00E-09	61.6	g06190000	AT3G03330	93.92	4.00E-174	608	1993	7	0.62	2	0.55
		isogroup10437	co-ortholog	AT1G62610	g10437000	29.03	1.00E-19	95.1	g10437000	AT3G03980	91.25	1.00E-134	475	936	1	0.88	1	0.88
		isogroup13116	co-ortholog	AT1G62610	g13116000	30.54	5.00E-07	53.1	g13116000	AT3G03980	87.65	6.00E-76	279	488	1	1.00	1	1.00
		isogroup02730	co-ortholog	AT1G62610	g02730000	32.92	5.00E-10	63.2	g02730000	AT5G61830	90.21	3.00E-71	265	1140	1	0.39	1	0.39
		isogroup22262	co-ortholog	AT1G62610	g22262000	28.11	2.00E-12	70.5	g22262000	AT5G61830	93.67	4.00E-172	600	1124	1	0.98	1	0.98
		isogroup15501	co-ortholog	AT1G62610	g15501000	30.74	9.00E-21	98.6	g15501000	AT1G52340	90.21	1.00E-143	505	1131	1	1.00	1	1.00
		isogroup19097	co-ortholog	AT1G62610	g19097000	31.73	8.00E-21	99	g19097000	AT1G52340	90.21	2.00E-143	504	1002	1	1.00	1	1.00

Supplementary Table 1. Camelina lipid metabolism genes

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship		TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis				
			Arabidopsis	Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity	E-Value		bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
		isogroup10854	co-ortholog	AT1G62610	g10854r000c	28.93	9.00E-20	95.5	g10854r000c	AT3G51680	92.04	1.00E-148	522	965	6	0.84	3	0.84
		isogroup11092	co-ortholog	AT1G62610	e11092r000c	29.15	2.00E-20	97.4	e11092r000c	AT3G26770	93.42	2.00E-158	565	1133	6	1.00	2	1.00
		isogroup11256	co-ortholog	AT1G62610	g11256r000c	31.69	2.00E-09	61.2	g11256r000c	AT3G47360	90	3.00E-95	343	657	1	0.72	1	0.72
		isogroup12233	co-ortholog	AT1G62610	g12233r000c	27.72	2.00E-19	94.4	g12233r000c	AT1G54870	93.27	2.00E-175	611	1023	2	1.00	2	1.00
		isogroup13364	co-ortholog	AT1G62610	g13364r000c	24.9	4.00E-08	56.6	g13364r000c	AT2G24190	87.42	1.00E-147	519	996	2	0.82	2	0.82
		isogroup13381	co-ortholog	AT1G62610	e13381r000c	28.57	7.00E-06	49.3	e13381r000c	AT4G09750	94.71	8.00E-101	362	692	2	0.41	1	0.23
		isogroup16169	co-ortholog	AT1G62610	g16169r000c	28.88	7.00E-12	68.9	g16169r000c	AT5G65205	87.57	1.00E-106	290	715	2	0.82	2	0.82
		isogroup21115	co-ortholog	AT1G62610	g21115r000c	31.4	4.00E-12	70.1	g21115r000c	AT5G50600	93.14	0	661	1356	68	0.60	1	0.14
		isogroup22075	co-ortholog	AT1G62610	e22075r000c	30.36	1.00E-11	68.2	e22075r000c	AT5G10050	86.23	8.00E-79	289	589	1	1.00	1	1.00
		isogroup22390	co-ortholog	AT1G62610	e22390r000c	28.05	5.00E-17	86.3	e22390r000c	AT3G05260	97.13	2.00E-134	474	800	1	1.00	1	1.00
		GDENH3V01D23FD	co-ortholog	AT3G46170	GDENH3V01	81.82	8.00E-57	218	GDENH3V01	AT3G55290	85.61	3.00E-60	226	419	na	na	na	na
		isogroup09618	co-ortholog	AT3G46170	g09618r000c	29.53	1.00E-07	55.1	g09618r000c	AT5G19200	88.1	3.00E-138	447	948	2	0.71	2	0.71
		isogroup09823	co-ortholog	AT3G46170	g09823r000c	28.8	2.00E-08	57.4	g09823r000c	AT3G06060	93.87	9.00E-171	596	1250	26	0.83	5	0.71
		isogroup00014	co-ortholog	AT3G46170	r00014r000c	82.35	1.00E-137	484	r00014r000c	AT3G09770	80.72	9.00E-175	570	2769	108	0.92	5	0.82
		isogroup02055	co-ortholog	AT3G46170	g02055r000c	31.78	4.00E-22	103	g02055r000c	AT1G24360	87.81	2.00E-153	538	4963	4	0.71	4	0.71
		isogroup05814	co-ortholog	AT3G46170	g05814r000c	32.32	1.00E-15	82	g05814r000c	AT3G12800	94.97	2.00E-163	572	1095	9	0.80	5	0.75
		isogroup10413	co-ortholog	AT3G46170	e10413r000c	34.41	5.00E-06	49.7	e10413r000c	AT1G01800	89.15	9.00E-147	516	1024	3	0.76	3	0.76
		isogroup10966	co-ortholog	AT3G46170	g10966r000c	28.28	3.00E-09	60.8	g10966r000c	AT1G67730	95.24	2.00E-174	608	1162	13	0.83	2	0.82
		isogroup11440	co-ortholog	AT3G46170	e11440r000c	28.21	4.00E-21	99.8	e11440r000c	AT5G06060	91.92	5.00E-137	483	1049	2	0.76	2	0.76
		isogroup11823	co-ortholog	AT3G46170	g11823r000c	29.2	3.00E-21	100	g11823r000c	AT5G06060	91.67	6.00E-139	490	1040	1	1.00	1	1.00
		isogroup21846	co-ortholog	AT3G46170	g21846r000c	28.9	1.00E-16	85.1	g21846r000c	AT5G06060	88.99	2.00E-108	387	667	1	1.00	1	1.00
		isogroup05667	co-ortholog	AT3G46170	g05667r000c	30.57	2.00E-14	77.8	g05667r000c	AT1G10310	96.28	4.00E-129	457	1037	5	0.72	4	0.70
		isogroup01189	co-ortholog	AT3G46170	g01189r000c	27.6	1.00E-09	61.6	g01189r000c	AT3G03330	91.46	7.00E-170	593	1841	7	0.91	3	0.91
		isogroup05190	co-ortholog	AT3G46170	g05190r000c	26.61	1.00E-10	64.3	g05190r000c	AT3G03330	89.15	4.00E-174	608	1893	7	0.62	7	0.55
		isogroup10437	co-ortholog	AT3G46170	g10437r000c	27.04	4.00E-15	70.7	g10437r000c	AT3G03980	91.25	1.00E-134	475	936	1	0.88	1	0.88
		isogroup02730	co-ortholog	AT3G46170	g02730r000c	33.33	5.00E-09	59.7	g02730r000c	AT5G61830	90.21	3.00E-71	265	1140	1	0.39	1	0.39
		isogroup22262	co-ortholog	AT3G46170	g22262r000c	29.15	1.00E-12	72	g22262r000c	AT5G61830	93.67	4.00E-172	600	1124	1	0.98	1	0.98
		isogroup15501	co-ortholog	AT3G46170	g15501r000c	31.46	2.00E-21	100	g15501r000c	AT1G52340	90.21	1.00E-143	505	1131	1	1.00	1	1.00
		isogroup19097	co-ortholog	AT3G46170	g19097r000c	31.46	5.00E-21	99.8	g19097r000c	AT1G52340	90.21	2.00E-143	504	1002	1	1.00	1	1.00
		isogroup11558	co-ortholog	AT3G46170	g11558r000c	27.75	2.00E-06	51.2	g11558r000c	AT2G29360	90.96	2.00E-82	301	563	1	0.88	1	0.88
		isogroup03099	co-ortholog	AT3G46170	g03099r000c	28.19	9.00E-20	95.5	g03099r000c	AT3G29150	83.33	2.00E-124	442	1154	1	1.00	1	1.00
		isogroup21327	co-ortholog	AT3G46170	g21327r000c	29.01	2.00E-07	54.3	g21327r000c	AT2G29360	90.68	5.00E-78	286	500	1	0.88	1	0.88
		isogroup08739	co-ortholog	AT3G46170	g08739r000c	30	6.00E-13	72.8	g08739r000c	AT2G47140	91.88	4.00E-105	362	715	0	0	0	0
		isogroup13873	co-ortholog	AT3G46170	g13873r000c	29.45	3.00E-08	57	g13873r000c	AT2G47140	90.34	3.00E-69	256	481	1	1.00	1	1.00
		isogroup15024	co-ortholog	AT3G46170	g15024r000c	26.39	6.00E-09	59.3	g15024r000c	AT2G47120	83.91	1.00E-103	372	826	1	1.00	1	1.00
		isogroup19841	co-ortholog	AT3G46170	g19841r000c	30.77	1.00E-07	55.1	g19841r000c	AT3G29260	88.07	6.00E-86	312	533	1	1.00	1	1.00
		isogroup20992	co-ortholog	AT3G46170	g20992r000c	26.84	8.00E-10	62.4	g20992r000c	AT2G47130	86.76	5.00E-122	478	885	1	0.15	1	0.15
		isogroup02254	co-ortholog	AT3G46170	g02254r000c	26.61	6.00E-06	49.3	g02254r000c	AT3G29330	81.58	1.00E-116	372	1056	6	0.97	3	0.87
		isogroup08296	co-ortholog	AT3G46170	g08296r000c	28.09	8.00E-17	85.5	g08296r000c	AT2G29340	93.1	5.00E-140	493	970	9	0.97	3	0.87
		isogroup16196	co-ortholog	AT3G46170	e16196r000c	28.08	2.00E-09	60.8	e16196r000c	AT2G29330	90.15	3.00E-99	357	636	0	0	0	0
		isogroup18890	co-ortholog	AT3G46170	g18890r000c	28.24	1.00E-15	81.6	g18890r000c	AT2G29320	90.94	1.00E-129	458	758	1	1.00	1	1.00
		isogroup19897	co-ortholog	AT3G46170	g19897r000c	28.09	2.00E-14	77.4	g19897r000c	AT2G29340	82.76	8.00E-124	439	951	1	0.95	1	0.95
		isogroup00125	co-ortholog	AT3G46170	g00125r000c	28.29	7.00E-13	72.4	g00125r000c	AT5G10060	90.13	0	839	3385	88	0.73	1	0.42
		isogroup01137	co-ortholog	AT3G46170	g01137r000c	28.04	4.00E-10	63.5	g01137r000c	AT1G49670	87.73	0	1140	2131	131	0.94	1	0.14
		isogroup04429	co-ortholog	AT3G46170	g04429r000c	23.72	1.00E-08	72.8	g04429r000c	AT4G10260	95.17	0	634	1105	3	0.51	2	0.41
		isogroup04442	co-ortholog	AT3G46170	g04442r000c	28.9	2.00E-14	77.8	g04442r000c	AT4G03140	92.63	8.00E-161	563	1723	2	0.89	2	0.89
		isogroup04805	co-ortholog	AT3G46170	g04805r000c	25.87	4.00E-11	66.6	g04805r000c	AT2G20360	96.77	0	769	2696	1784	0.71	1	0.16
		isogroup04947	co-ortholog	AT3G46170	g04947r000c	24.42	1.00E-06	51.6	g04947r000c	AT5G04070	86.91	5.00E-153	472	1169	3	0.67	3	0.67
		isogroup05158	co-ortholog	AT3G46170	g05158r000c	29.21	2.00E-19	94.4	g05158r000c	AT1G07440	86.15	9.00E-130	459	948	1	0.97	1	0.97
		isogroup05354	co-ortholog	AT3G46170	g05354r000c	31.13	2.00E-29	127	g05354r000c	AT3G01980	78.38	4.00E-127	451	1143	3	1.00	3	1.00
		isogroup06007	co-ortholog	AT3G46170	g06007r000c	26.07	3.00E-09	60.5	g06007r000c	AT5G04990	91.95	0	637	1101	12	0.91	3	0.67
		isogroup06551	co-ortholog	AT3G46170	g06551r000c	30.29	3.00E-19	94	g06551r000c	AT5G18210	91.8	1.00E-121	432	787	1	0.41	1	0.41
		isogroup06575	co-ortholog	AT3G46170	g06575r000c	25.47	4.00E-08	56.6	g06575r000c	AT5G50770	88.89	1.00E-176	615	1268	2	0.99	2	0.99
		isogroup09115	co-ortholog	AT3G46170	g09115r000c	20.76	1.00E-06	52	g09115r000c	AT4G13250	93.61	0	918	1681	10	0.67	1	0.30
		isogroup09271	co-ortholog	AT3G46170	g09271r000c	26.97	8.00E-19	92	g09271r000c	AT3G26760	93.71	3.00E-156	547	1104	4	0.92	3	0.92
		isogroup09361	co-ortholog	AT3G46170	g09361r000c	26.64	5.00E-13	73.2	g09361r000c	AT2G29260	85.14	1.00E-151	532	1020	3	1.00	3	1.00
		isogroup10854	co-ortholog															

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis						
			Relationship	Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject		% identity	E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
.	.	isogroup2399	co-ortholog	AT3G55310	g20399f000	28.57	5.00E-21	99.4	g20399f000	AT2G29150	83.33	2.00E-124	442	1154	1	1.00	1	1.00
.	.	isogroup2132	co-ortholog	AT3G55310	e2123f000	30.52	5.00E-08	56.3	e2123f000	AT2G29260	90.68	5.00E-78	286	500	1	1.00	1	1.00
.	.	isogroup14460	co-ortholog	AT3G55310	g14460f000	33.33	7.00E-06	49.3	g14460f000	AT5G53090	95.02	7.00E-142	499	807	1	0.87	1	0.87
.	.	isogroup20851	co-ortholog	AT3G55310	g20851f000	34.21	3.00E-06	50.4	g20851f000	AT5G53090	93.13	1.00E-139	491	791	1	1.00	1	1.00
.	.	isogroup08739	co-ortholog	AT3G55310	g08739f000	30	1.00E-13	75.1	g08739f000	AT2G47140	91.88	4.00E-105	362	715	0	0	0	0
.	.	isogroup13873	co-ortholog	AT3G55310	e13873f000	30.82	8.00E-09	58.9	e13873f000	AT2G47140	90.34	3.00E-69	256	481	1	1.00	1	1.00
.	.	isogroup15024	co-ortholog	AT3G55310	g15024f000	25.35	1.00E-07	55.1	g15024f000	AT2G47120	83.91	1.00E-103	372	826	1	1.00	1	1.00
.	.	isogroup19841	co-ortholog	AT3G55310	g19841f000	29.85	5.00E-07	52.8	g19841f000	AT3G29260	88.07	6.00E-86	312	533	1	1.00	1	1.00
.	.	isogroup21292	co-ortholog	AT3G55310	e20992f000	27.94	1.00E-09	61.2	e20992f000	AT2G47130	86.76	5.00E-122	378	885	1	0.15	1	0.15
.	.	isogroup02542	co-ortholog	AT3G55310	e02542f000	29.56	1.00E-08	58.5	e02542f000	AT2G29330	80.7	2.00E-115	367	1056	4	1.00	2	0.99
.	.	isogroup08296	co-ortholog	AT3G55310	g08296f000	29.62	1.00E-18	91.7	g08296f000	AT2G29340	92.34	1.00E-138	488	970	6	0.97	2	0.94
.	.	isogroup16196	co-ortholog	AT3G55310	g16196f000	28.43	1.00E-12	71.6	g16196f000	AT2G29330	90.15	3.00E-99	357	636	0	0	0	0
.	.	isogroup18890	co-ortholog	AT3G55310	g18890f000	30.53	1.00E-18	91.7	g18890f000	AT2G29320	90.94	1.00E-129	458	758	1	1.00	1	1.00
.	.	isogroup19897	co-ortholog	AT3G55310	e19897f000	27.14	9.00E-17	85.5	e19897f000	AT2G29340	82.76	8.00E-124	439	951	1	0.95	1	0.95
.	.	isogroup01215	co-ortholog	AT3G55310	g01215f000	31.88	4.00E-17	86.7	g01215f000	AT5G10060	90.13	0	839	3385	88	0.73	1	0.42
.	.	isogroup01137	co-ortholog	AT3G55310	g01137f000	28.64	9.00E-13	87.2	g01137f000	AT1G49670	87.73	0	1140	2131	131	0.94	1	0.14
.	.	isogroup01694	co-ortholog	AT3G55310	g01694f000	32.26	4.00E-07	53.5	g01694f000	AT4G27760	94.41	0	719	1229	64	0.94	6	0.83
.	.	isogroup04292	co-ortholog	AT3G55310	g04292f000	27.27	1.00E-08	58.5	g04292f000	AT4G10020	95.17	0	634	1105	3	0.59	1	0.35
.	.	isogroup04442	co-ortholog	AT3G55310	e04442f000	30.94	6.00E-18	89.4	e04442f000	AT4G03140	92.63	8.00E-161	563	1723	2	0.89	2	0.89
.	.	isogroup04805	co-ortholog	AT3G55310	g04805f000	28.88	1.00E-07	55.1	g04805f000	AT2G20360	96.77	0	769	2696	1784	0.71	1	0.16
.	.	isogroup04947	co-ortholog	AT3G55310	g04947f000	28.21	1.00E-06	51.6	g04947f000	AT5G04070	86.91	5.00E-153	472	1169	3	0.67	3	0.67
.	.	isogroup05158	co-ortholog	AT3G55310	g05158f000	29.21	2.00E-20	97.8	g05158f000	AT1G07440	87.59	4.00E-135	477	948	5	0.51	1	0.38
.	.	isogroup05354	co-ortholog	AT3G55310	e05354f000	31.13	1.00E-28	124	e05354f000	AT3G01980	78.38	4.00E-127	451	1300	3	1.00	3	1.00
.	.	isogroup06007	co-ortholog	AT3G55310	e06007f000	25.13	1.00E-08	80.9	e06007f000	AT5G04900	91.95	0	637	1101	12	0.91	3	0.67
.	.	isogroup06551	co-ortholog	AT3G55310	g06551f000	27.69	7.00E-17	85.9	g06551f000	AT5G18210	91.8	1.00E-121	432	787	1	0.41	1	0.41
.	.	isogroup06575	co-ortholog	AT3G55310	g06575f000	24.41	3.00E-07	53.9	g06575f000	AT5G50770	88.89	1.00E-176	615	1268	2	0.99	2	0.99
.	.	isogroup09100	co-ortholog	AT3G55310	e09100f000	33.76	1.00E-08	58.5	e09100f000	AT4G23430	94.1	2.00E-170	595	1241	62	0.54	1	0.13
.	.	isogroup09115	co-ortholog	AT3G55310	g09115f000	21.7	7.00E-07	52.4	g09115f000	AT4G13250	93.61	0	918	1681	10	0.67	1	0.30
.	.	isogroup09271	co-ortholog	AT3G55310	g09271f000	27.04	1.00E-17	88.6	g09271f000	AT3G26760	93.71	3.00E-156	547	1104	4	0.92	3	0.92
.	.	isogroup09326	co-ortholog	AT3G55310	e09326f000	30.77	2.00E-06	51.2	e09326f000	AT4G11410	92.78	3.00E-146	514	938	5	0.73	1	0.32
.	.	isogroup10854	co-ortholog	AT3G55310	g10854f000	27.97	2.00E-15	80.9	g10854f000	AT3G29260	85.14	1.00E-151	522	1020	3	1.00	3	1.00
.	.	isogroup11092	co-ortholog	AT3G55310	g11092f000	28.57	2.00E-19	94	g11092f000	AT3G51680	92.04	1.00E-148	522	965	6	0.84	3	0.84
.	.	isogroup11256	co-ortholog	AT3G55310	g11256f000	29.14	6.00E-18	89.4	g11256f000	AT3G26770	93.42	2.00E-158	555	1133	6	1.00	2	1.00
.	.	isogroup12233	co-ortholog	AT3G55310	g12233f000	31.03	3.00E-10	63.9	g12233f000	AT3G47360	90	3.00E-95	343	657	1	0.72	1	0.72
.	.	isogroup13364	co-ortholog	AT3G55310	g13364f000	27.38	3.00E-18	90.1	g13364f000	AT1G54870	93.27	2.00E-175	611	1023	2	1.00	2	1.00
.	.	isogroup16169	co-ortholog	AT3G55310	g16169f000	35.79	3.00E-06	50.1	g16169f000	AT2G24190	87.42	1.00E-147	519	996	2	0.82	2	0.82
.	.	isogroup19189	co-ortholog	AT3G55310	g19189f000	29.26	1.00E-11	68.8	g19189f000	AT5G65205	87.57	1.00E-106	290	715	2	0.82	2	0.82
.	.	isogroup21115	co-ortholog	AT3G55310	e21115f000	29.68	2.00E-07	54.7	e21115f000	AT3G37540	88.46	4.00E-146	513	894	1	0.82	1	0.82
.	.	isogroup22075	co-ortholog	AT3G55310	e22075f000	30	5.00E-13	72.8	e22075f000	AT5G50600	93.14	0	661	1356	68	0.60	1	0.14
.	.	isogroup22390	co-ortholog	AT3G55310	e22390f000	31.95	4.00E-13	73.6	e22390f000	AT5G10050	86.23	8.00E-79	289	589	1	1.00	1	1.00
.	.	isogroup22390	co-ortholog	AT3G55310	g22390f000	29.28	6.00E-17	85.9	g22390f000	AT3G05260	97.13	2.00E-134	474	800	1	1.00	1	1.00
Plastidial Hydroxyacyl-ACP Dehydrase	At2g22230	isogroup11291	RH	AT2G22230	g11291f000	92.76	2.00E-103	373	g11291f000	AT2G22230	93.67	5.00E-116	414	979	2	0.87	2	0.87
Plastidial Hydroxyacyl-ACP Dehydrase	At5g10160	isogroup05468	RBH	AT5G10160	g05468f000	98.07	2.00E-115	412	g05468f000	AT5G10160	97.27	3.00E-116	414	931	2	0.58	1	0.08
Plastidial Enoyl-ACP Reductase	At2g05990	isogroup03067	RH	AT2G05990	g03067f000	96.92	0	771	g03067f000	AT2G05990	96.92	0	744	1418	12	0.83	3	0.75
Stearoyl-ACP Desaturase	At1g43800	isogroup00064	RH	AT1G43800	g00064f000	92.33	0	771	g00064f000	AT1G43800	92.33	0	729	1305	9	1.00	1	1.00
Stearoyl-ACP Desaturase	At2g43710	GD75LV02D2UA8	RH*	AT2G43710	GD75LV02I	98.73	1.00E-90	331	GD75LV02I	AT2G43710	98.73	8.00E-89	322	477	na	na	na	na
Stearoyl-ACP Desaturase	isogroup00948	RBH	AT2G43710	g00948f000	98	0	824	g00948f000	AT2G43710	98	0	801	1659	79	0.62	1	0.22	
Stearoyl-ACP Desaturase	At3g02610	isogroup14560	RBH	AT3G02610	e14560f000	92.51	0	790	e14560f000	AT3G02610	92.51	0	766	1338	1	0.98	1	0.98
Stearoyl-ACP Desaturase	GD75LV02D2UA8	co-ortholog	AT3G02620	GD75LV02I	77.85	5.00E-71	266	GD75LV02I	AT2G43710	98.73	8.00E-89	322	477	na	na	na	na	
Stearoyl-ACP Desaturase	isogroup00948	co-ortholog	AT3G02620	g00948f000	70.62	6.00E-150	528	g00948f000	AT2G43710	97.76	0	799	1659	57	0.64	1	0.18	
Stearoyl-ACP Desaturase	isogroup05860	co-ortholog	AT3G02620	g05860f000	76.59	0	655	g05860f000	AT5G16230	95.27	0	773	1386	1	0.83	1	0.83	
Stearoyl-ACP Desaturase	isogroup08599	co-ortholog	AT3G02620	e08599f000	65.17	4.00E-154	542	e08599f000	AT3G02630	97.22	0	786	1564	13	1.00	3	0.90	
Stearoyl-ACP Desaturase	isogroup08599	co-ortholog	AT3G02620	g08599f000	71.19	2.00E-153	540	g08599f000	AT5G16240	89.28	0	715	1430	6	0.98	3	0.98	
Stearoyl-ACP Desaturase	isogroup10062	co-ortholog	AT3G02620	g10062f000	59.1	6.00E-135	478	g10062f000	AT1G43800	92.33	0	729	1305	9	1.00	5	1.00	
Stearoyl-ACP Desaturase	isogroup14208	co-ortholog	AT3G02620	g14208f000	50	7.00E-16	83.2	g14208f000	AT5G16240	78.9	9.00E-40	157	353	1	1.00	1	1.00	
Stearoyl-ACP Desaturase	At3g02620	isogroup14560	co-ortholog	AT3G02620	g14560f000	87.62	0	740	g14560f000	AT3G02610	92.51	0	766	1338	1	0.98	1	0.98
Stearoyl-ACP Desaturase	At3g02630	isogroup06250	RBH	AT3G02630	e06250f000	96.97	0	809	e06250f000	AT3G02630	96.9							

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship Arabidopsis	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis							
				Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads	Fraction	Minimum	Min Reads	Fraction
Plastidial Linoleate Desaturase	A15g05580	GD75ULV03F56Z2	RHM*	GD75ULV03F	73.21	1.00E-46	161	GD75ULV03F	AT5G05580	73.21	9.00E-51	169	485	na	na	na	na	na	na	
Plastidial Phosphatidate Phosphatase	AT2g11810	isogroup14374	RH	AT2G01180	94.77	2.00E-160	562	g14374000C	AT2G01180	94.77	3.00E-161	564	1116	4	1.00	4	1.00	4	1.00	
Monogalactosyldiacylglycerol (MGDG) Synthase	AT4g31780	isogroup07447	RH	AT4G31780	93.88	0	650	g07447000C	AT4G31780	94.17	0	631	1516	5	0.87	2	0.42	2	0.42	
Monogalactosyldiacylglycerol (MGDG) Synthase	AT5g20410	GDENH3V02HC80V	RH	AT5G20410	87.23	3.00E-09	612	GDENH3V02I	AT5G20410	87.23	6.00E-18	85.5	146	na	na	na	na	na	na	
Monogalactosyldiacylglycerol (MGDG) Synthase	AT2g11810	isogroup18806	RH	AT2G11810	93.73	0	657	r18806000C	AT2G11810	93.73	0	668	1052	1	1.00	1	1.00	1	1.00	
MGDG Desaturase (palmitate-specific, FADS)	AT3g15850	isogroup05024	RH	AT3G15850	93.6	0	713	g05024000C	AT3G15850	93.6	0	742	1508	1	0.99	1	0.99	1	0.99	
Digalactosyldiacylglycerol (DGDG) Synthase	AT3g11670	isogroup09261	RH	AT3G11670	95.68	0	652	g09261000C	AT3G11670	95.68	0	640	2565	10	0.94	2	0.85	2	0.85	
Digalactosyldiacylglycerol (DGDG) Synthase	AT4g00550	isogroup08091	RH	AT4G00550	95.65	0	857	g08091000C	AT4G00550	94.47	0	838	1640	14	0.95	2	0.93	2	0.93	
UDP-Sulfolipinase Synthase	AT4g33030	isogroup05930	RH	AT4G33030	96.03	0	932	g05930000C	AT4G33030	96.03	0	919	1829	10	0.89	6	0.87	6	0.87	
Sulfolipid Synthase	AT5g01220	isogroup02345	RH	AT5G01220	89.59	0	877	g02345000C	AT5G01220	89.03	0	857	1617	36	0.82	2	0.57	2	0.57	
Permease-like Protein of Outer Chloroplast Envelope (TGD1)	AT1g19800	isogroup02203	RH	AT1G19800	89.84	4.00E-174	558	g02203000C	AT1G19800	90.16	2.00E-170	543	1341	4	0.45	4	0.45	4	0.45	
ER Dihydroxyacetone-Phosphate Reductase	AT2g41540	isogroup00673	RH	AT2G41540	96.85	0	803	g00673000C	AT2G41540	96.85	0	796	2159	14	0.90	3	0.81	3	0.81	
ER Dihydroxyacetone-Phosphate Reductase	AT3g07690	isogroup06558	RH	AT3G07690	94.27	0	909	g06558000C	AT3G07690	94.27	0	880	1653	44	0.94	2	0.66	2	0.66	
ER Dihydroxyacetone-Phosphate Reductase	AT2g40690	isogroup13300	RH	AT2G40690	96.9	0	838	g13300000C	AT2G40690	96.9	0	796	1345	3	0.81	2	0.81	2	0.81	
.	.	isogroup03521	co-ortholog	AT5G06090	g03521000C	98.44	1.00E-68	258	g03521000C	AT1G02390	95.94	0	779	1422	14	0.91	2	0.89	2	0.89
.	.	isogroup06735	co-ortholog	AT5G06090	g06735000C	47.44	1.00E-112	404	g06735000C	AT2G38110	95.39	0	964	1711	205	0.96	1	0.14	1	0.14
.	.	isogroup08047	co-ortholog	AT5G06090	g08047000C	46.11	4.00E-113	406	g08047000C	AT1G01610	96.42	0	968	1736	91	0.92	4	0.60	4	0.60
ER Glycerol-Phosphate Acyltransferase (GPAT)	AT5g06090	isogroup11777	co-ortholog	AT5G06090	e11777000C	91.35	0	350	e11777000C	AT3G11430	93.07	4.00E-102	368	1575	2	0.92	2	0.92	2	0.92
ER Glycerol-Phosphate Acyltransferase (GPAT)	isogroup12792	co-ortholog	AT5G06090	g12792000C	41.96	4.00E-70	263	g12792000C	AT4G00400	92.15	0	706	1310	1	1.00	1	1.00	1	1.00	
ER Glycerol-Phosphate Acyltransferase (GPAT)	AT3g11430	isogroup11777	RH	AT3G11430	93.07	1.00E-105	381	e11777000C	AT3G11430	93.07	4.00E-102	368	1575	2	0.92	2	0.92	2	0.92	
ER Glycerol-Phosphate Acyltransferase (GPAT)	AT1g01610	isogroup08047	RH	AT1G01610	g08047000C	96.42	0	962	g08047000C	AT1G01610	96.42	0	968	1736	91	0.92	4	0.60	4	0.60
ER 1-Acylglycerol-Phosphate Acyltransferase (LPAAT)	AT3g18850	isogroup00621	RH	AT3G18850	g00621000C	95	0	602	g13300000C	AT3G18850	95	0	597	3145	36	1.00	5	0.80	5	0.80
ER 1-Acylglycerol-Phosphate Acyltransferase (LPAAT)	isogroup05808	RHM*	AT3G18850	g19588000C	92.64	3.00E-86	312	g19588000C	AT3G18850	92.64	4.00E-87	317	760	1	1.00	1	1.00	1	1.00	
ER 1-Acylglycerol-Phosphate Acyltransferase (LPAAT)	AT1g75020	isogroup13207	RH	AT1G75020	93.57	0	711	g13207000C	AT1G75020	93.57	0	711	1257	2	0.85	2	0.85	2	0.85	
ER 1-Acylglycerol-Phosphate Acyltransferase (LPAAT)	AT1g51260	isogroup13078	RH	AT1G51260	g13078000C	95.07	4.00E-172	602	g13078000C	AT1G51260	95.07	3.00E-169	590	951	1	0.96	1	0.96	1	0.96
ER 1-Acylglycerol-Phosphate Acyltransferase (LPAAT)	AT3g7650	isogroup00657	RH	AT3G7650	g00657000C	96.14	0	773	g00657000C	AT3G7650	96.14	0	760	1382	152	0.99	5	0.65	5	0.65
ER Phosphatidate Phosphatase	AT1g15080	isogroup05039	RH	AT1G15080	g05039000C	94.12	2.00E-153	539	g05039000C	AT1G15080	94.12	2.00E-164	575	1195	11	1.00	4	1.00	4	1.00
ER Diacylglycerol Cholinephosphotransferase	AT3g25585	isogroup01306	RH	AT3G25585	g01306000C	98.46	0	796	g01306000C	AT3G25585	98.46	0	795	2464	4	0.92	2	0.92	2	0.92
ER Oleate Desaturase (FAD2)	AT3g12120	isogroup03202	RH	AT3G12120	g03202000C	96.35	0	770	g03202000C	AT3G12120	96.88	0	800	1402	64	0.80	4	0.80	4	0.80
ER Linoleate Desaturase (FAD3)	AT2g29980	isogroup09978	RH	AT2G29980	g09978000C	95.91	0	681	g09978000C	AT2G29980	95.91	0	704	1171	12	0.96	3	0.71	3	0.71
ER CDP-Diacylglycerol Synthetase	AT1g62430	isogroup05629	RH	AT1G62430	g05629000C	95.1	0	724	g05629000C	AT1G62430	95.1	0	727	1330	4	1.00	4	1.00	4	1.00
ER CDP-Diacylglycerol Synthetase	AT4g22340	isogroup05603	RH	AT4G22340	g05603000C	92.94	0	828	g05603000C	AT4G22340	92.94	0	815	1739	7	0.97	3	0.97	3	0.97
ER Phosphatidylglycerol-Phosphate Synthetase	AT3g55030	isogroup05547	RH	AT3G55030	g05547000C	92.77	9.00E-115	410	g05547000C	AT3G55030	93.62	4.00E-119	424	1226	1	0.90	1	0.90	1	0.90
Phosphatidylinositol Synthase	AT1g88000	isogroup09107	RH	AT1G88000	g09107000C	98.68	9.00E-130	460	g09107000C	AT1G88000	98.68	9.00E-128	452	977	5	0.86	4	0.84	4	0.84
Phosphatidylinositol Synthase	AT4g38570	isogroup09933	RH	AT4G38570	g09933000C	95.54	4.00E-116	394	g09933000C	AT4G38570	95.54	1.00E-114	389	1408	5	0.93	4	0.93	4	0.93
.	.	isogroup24613	RHM*	AT4G38570	g24613000C	55.17	2.00E-41	118	g24613000C	AT4G38570	51.46	2.00E-35	133	908	1	1.00	1	1.00	1	1.00
.	.	GD75ULV02D9URJ	RHM*	GD75ULV02D	75.17	6.00E-61	232	GD75ULV02D	AT4G09760	75.17	7.00E-61	226	511	na	na	na	na	na	na	
Choline Kinase	AT4g09760	isogroup10911	RH	AT4G09760	g10911000C	91.91	0	665	g10911000C	AT4G09760	91.91	0	660	1507	6	0.77	5	0.77	5	0.77
Choline Kinase	AT1g71697	isogroup05606	RH	AT1G71697	g05606000C	92.84	0	671	g05606000C	AT1G71697	92.84	0	668	1274	6	0.94	5	0.94	5	0.94
Choline Kinase	AT1g74320	isogroup11762	RH	AT1G74320	g11762000C	93.43	0	686	g11762000C	AT1G74320	93.43	0	675	1365	1	0.72	1	0.72	1	0.72
Ethanolamine Kinase	AT2g26830	isogroup11583	RH	AT2G26830	g11583000C	96.1	1.00E-178	563	g11583000C	AT2G26830	96.1	8.00E-180	552	1100	2	0.79	2	0.79	2	0.79
.	.	isogroup09812	RH	AT2G32260	g09812000C	93.11	2.00E-169	592	g09812000C	AT2G32260	93.11	2.00E-165	578	1016	42	0.96	6	0.93	6	0.93
CDP-Choline Synthetase	AT4g15130	isogroup11369	RH	AT4G15130	g11369000C	90.2	3.00E-162	568	g11369000C	AT4G15130	90.2	3.00E-158	554	1026	2	0.77	2	0.77	2	0.77
CDP-Ethanolamine Synthetase	AT2g38670	isogroup02987	RH	AT2G38670	g02987000C	96.44	0	682	g02987000C	AT2G38670	96.44	0	677	1475	6	0.87	6	0.87	6	0.87
.	.	GDENH3V02F9YVY	RHM*	AT4G25970	GDENH3V02I	41.43	5.00E-16	843	GDENH3V02I	AT4G25970	41.43	7.00E-16	79.3	428	na	na	na	na	na	
ER Phosphatidylserine Decarboxylase	AT4g25970	isogroup09552	RH	AT4G25970	g09552000C	95.88	0	1153	g09552000C	AT4G25970	95.88	0	1102	1898	60	0.97	7	0.91	7	0.91
.	.	isogroup10157	co-ortholog	AT5G57190	e10157000C	27.78	1.00E-09	63.5	e10157000C	AT4G16700	91.97	0	723	1199	1	0.21	1	0.21	1	0.21
ER Phosphatidylserine Decarboxylase	isogroup09552	co-ortholog	AT5G57190	GDENH3V02I	39.29	4.00E-14	78.2	GDENH3V02I	AT4G25970	41.43	7.00E-16	79.3	428	na	na	na	na	na		
.	.	GDENH3V02GQ0LZ	RHM*	AT1G15110	GDENH3V02I	41.73	2.00E-13	75.5	GDENH3V02I	AT1G15110	42.06	1.00E-13	72	414	na	na	na	na	na	
Phospholipid Base-Exchange	AT1g15110	isogroup09686	RH	AT1G15110	g09686000C	97.15	0	634	g09686000C	AT1G15110	97.15	0	655	1379	7	0.75	2	0.75	2	0.75
LCB1 subunit of Serine Palmitoyltransferase	AT4g36480	isogroup09563	RH	AT4G36480	g09563000C	94.78	0	935	g09563000C	AT4G36480	94.78	0	902	2108	68	0.98	2	0.83	2	0.83
LCB2 subunit of Serine Palmitoyltransferase	AT5g23670	GDENH3V02H643L	RHM*	AT5G23670	GDENH3V02I	100	3.00E-13	74.7	GDENH3V02I	AT5G23670	100	6.00E-14	72	352	na	na	na	na	na	
.	.	isogroup03597																		



Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
		isogroup05814	co-ortholog	AT1G66380	g05814000C	31.27	1.00E-19	94.7	g05814000C	AT3G12800	94.97	2.00E-163	572	1095	9	0.80	5	0.75
		isogroup01041	co-ortholog	AT1G66380	e10410000C	34.41	2.00E-07	54.3	e10410000C	AT1G01800	89.18	9.00E-147	516	1024	3	0.76	3	0.76
		isogroup10966	co-ortholog	AT1G66380	t10966000C	26.53	2.00E-09	61.2	t10966000C	AT1G67730	95.24	2.00E-174	608	1162	13	0.83	2	0.82
		isogroup11440	co-ortholog	AT1G66380	g11440000C	31.15	5.00E-24	109	g11440000C	AT5G06060	91.92	5.00E-137	483	1049	2	0.76	2	0.76
		isogroup11823	co-ortholog	AT1G66380	g11823000C	30.89	5.00E-24	109	g11823000C	AT5G06060	91.67	6.00E-139	490	1040	1	1.00	1	1.00
		isogroup21846	co-ortholog	AT1G66380	r21846000C	31.19	2.00E-20	97.8	r21846000C	AT5G06060	88.99	2.00E-108	387	667	1	1.00	1	1.00
		isogroup05667	co-ortholog	AT1G66380	g05667000C	29.76	4.00E-13	73.2	g05667000C	AT1G10310	95.45	4.00E-128	454	1037	6	0.59	3	0.44
		isogroup11889	co-ortholog	AT1G66380	g011889000C	26.8	2.00E-10	63.9	g011889000C	AT3G03330	91.46	7.00E-170	593	1841	7	0.91	3	0.91
		isogroup05190	co-ortholog	AT1G66380	g06190000C	26.8	5.00E-10	62.8	g06190000C	AT3G03330	93.92	4.00E-174	608	1993	7	0.62	2	0.55
		isogroup10437	co-ortholog	AT1G66380	r10437000C	29.04	3.00E-19	94	r10437000C	AT3G03980	91.25	1.00E-134	475	936	1	0.88	1	0.88
		isogroup13116	co-ortholog	AT1G66380	g13116000C	30.54	4.00E-08	56.6	g13116000C	AT3G03980	87.65	6.00E-76	279	488	1	1.00	1	1.00
		isogroup02730	co-ortholog	AT1G66380	g02730000C	33.33	2.00E-10	64.3	g02730000C	AT5G61830	90.21	3.00E-71	265	1140	1	0.39	1	0.39
		isogroup22262	co-ortholog	AT1G66380	g22262000C	28.11	1.00E-12	71.6	g22262000C	AT5G61830	93.67	4.00E-172	600	1124	1	0.98	1	0.98
		isogroup15501	co-ortholog	AT1G66380	r15501000C	30.97	2.00E-20	97.4	r15501000C	AT1G52340	90.21	1.00E-143	505	1031	1	1.00	1	1.00
		isogroup19097	co-ortholog	AT1G66380	g19097000C	31.97	3.00E-20	96.7	g19097000C	AT1G52340	90.21	2.00E-143	504	1102	1	1.00	1	1.00
		isogroup11558	co-ortholog	AT1G66380	g11558000C	30.52	4.00E-08	75.7	g11558000C	AT2G29360	90.96	2.00E-82	301	563	1	0.88	1	0.88
		isogroup20399	co-ortholog	AT1G66380	g20399000C	28.95	7.00E-22	102	g20399000C	AT2G29150	83.33	2.00E-124	442	1154	1	1.00	1	1.00
		isogroup21327	co-ortholog	AT1G66380	g21327000C	32.47	2.00E-09	61.2	g21327000C	AT2G29360	90.68	5.00E-78	286	500	1	1.00	1	1.00
		isogroup08739	co-ortholog	AT1G66380	r08739000C	30	4.00E-14	76.6	r08739000C	AT2G47140	91.88	4.00E-105	362	715	0	0	0	0
		isogroup13873	co-ortholog	AT1G66380	g13873000C	30.82	2.00E-10	64.7	g13873000C	AT2G47140	90.34	3.00E-69	256	481	1	1.00	1	1.00
		isogroup15024	co-ortholog	AT1G66380	g15024000C	28.3	1.00E-11	68.6	g15024000C	AT2G47120	83.91	1.00E-103	372	826	1	1.00	1	1.00
		isogroup19841	co-ortholog	AT1G66380	g19841000C	33.59	5.00E-19	59.7	g19841000C	AT3G29260	88.07	6.00E-86	312	533	1	1.00	1	1.00
		isogroup20992	co-ortholog	AT1G66380	r20992000C	30.73	2.00E-13	74.3	r20992000C	AT2G47130	86.76	5.00E-122	378	885	1	0.15	1	0.15
		isogroup01254	co-ortholog	AT1G66380	r01254000C	27.72	1.00E-06	49.7	r01254000C	AT3G29360	87.38	4.00E-116	372	1056	6	0.59	6	0.59
		isogroup08296	co-ortholog	AT1G66380	g08296000C	26.39	4.00E-15	80.1	g08296000C	AT2G29340	93.1	5.00E-140	493	970	9	0.97	3	0.87
		isogroup16196	co-ortholog	AT1G66380	g16196000C	29.06	2.00E-12	70.9	g16196000C	AT2G29330	90.15	3.00E-99	357	636	0	0	0	0
		isogroup18890	co-ortholog	AT1G66380	r18890000C	28.41	1.00E-15	81.3	r18890000C	AT2G29320	90.94	1.00E-129	458	758	1	1.00	1	1.00
		isogroup19897	co-ortholog	AT1G66380	g19897000C	27.04	7.00E-15	79	g19897000C	AT2G29340	82.76	8.00E-124	439	951	1	0.95	1	0.95
		isogroup00125	co-ortholog	AT1G66380	g00125000C	31.55	9.00E-18	89	g00125000C	AT5G10050	92.28	2.00E-140	493	3385	2	0.59	2	0.59
		isogroup04093	co-ortholog	AT1G66380	g04093000C	27.63	4.00E-14	76.6	g04093000C	AT4G36360	96.14	0	956	0	0	0	0	
		isogroup01137	co-ortholog	AT1G66380	g01137000C	28.04	1.00E-13	75.7	g01137000C	AT1G62970	87.73	0	1140	131	0.94	1	0.14	
		isogroup01694	co-ortholog	AT1G66380	g01694000C	30.65	9.00E-07	52.4	g01694000C	AT4G27760	94.41	0	719	1229	64	0.94	6	0.83
		isogroup04292	co-ortholog	AT1G66380	g04292000C	29.61	8.00E-11	65.5	g04292000C	AT4G10020	95.17	0	634	1105	3	0.59	1	0.35
		isogroup04442	co-ortholog	AT1G66380	g04442000C	29.48	7.00E-18	89.4	g04442000C	AT4G03140	92.63	8.00E-161	563	1723	2	0.89	2	0.89
		isogroup04805	co-ortholog	AT1G66380	g04805000C	28.19	1.00E-08	58.2	g04805000C	AT2G20360	96.77	0	769	2696	1784	0.71	1	0.16
		isogroup04947	co-ortholog	AT1G66380	g04947000C	29.3	1.00E-07	55.5	g04947000C	AT3G04070	86.91	5.00E-153	472	1169	3	0.67	3	0.67
		isogroup05158	co-ortholog	AT1G66380	g05158000C	29.32	1.00E-19	95.1	g05158000C	AT1G07440	86.84	6.00E-134	473	948	1	0.44	1	0.44
		isogroup05354	co-ortholog	AT1G66380	g05354000C	29.84	1.00E-27	121	g05354000C	AT3G01980	78.38	4.00E-177	451	1143	3	0.87	3	0.87
		isogroup05812	co-ortholog	AT1G66380	g05812000C	29.53	5.00E-07	53.1	g05812000C	AT3G59710	84.93	6.00E-104	374	1109	6	0.97	3	0.97
		isogroup06007	co-ortholog	AT1G66380	r06007000C	26.53	8.00E-11	65.5	r06007000C	AT5G04900	92.53	0	641	1101	9	0.77	3	0.77
		isogroup06551	co-ortholog	AT1G66380	g06551000C	30.04	2.00E-19	94.4	g06551000C	AT5G18210	91.8	1.00E-121	432	787	1	0.41	1	0.41
		isogroup06575	co-ortholog	AT1G66380	g06575000C	24.8	3.00E-06	50.4	g06575000C	AT5G50770	88.89	1.00E-176	615	1268	2	0.99	2	0.99
		isogroup07493	co-ortholog	AT1G66380	g07493000C	26.77	5.00E-11	66.2	g07493000C	AT3G04000	74.76	2.00E-119	426	1486	1	0.56	1	0.56
		isogroup09100	co-ortholog	AT1G66380	g09100000C	27.94	3.00E-09	60.5	g09100000C	AT4G23430	94.1	2.00E-170	595	1241	62	0.54	1	0.13
		isogroup09311	co-ortholog	AT1G66380	g09311000C	22.17	1.00E-07	53.1	g09311000C	AT4G13150	93.21	0	1681	309	0.78	1	0.75	
		isogroup09271	co-ortholog	AT1G66380	g09271000C	28.73	3.00E-21	100	g09271000C	AT3G26760	93.71	3.00E-156	547	1104	4	0.92	3	0.92
		isogroup09326	co-ortholog	AT1G66380	g09326000C	31.51	5.00E-06	49.7	g09326000C	AT4G11410	92.78	3.00E-146	514	938	5	0.73	1	0.32
		isogroup09361	co-ortholog	AT1G66380	r09361000C	29.01	1.00E-15	82	r09361000C	AT2G29260	85.14	1.00E-151	532	1020	3	1.00	3	1.00
		isogroup10854	co-ortholog	AT1G66380	g10854000C	29.29	7.00E-21	99	g10854000C	AT3G51680	92.04	1.00E-148	522	965	6	0.84	3	0.84
		isogroup11092	co-ortholog	AT1G66380	g11092000C	29.96	2.00E-21	100	g11092000C	AT3G26770	93.42	2.00E-158	555	1133	6	1.00	2	1.00
		isogroup11256	co-ortholog	AT1G66380	g11256000C	31.69	1.00E-10	64.7	g11256000C	AT3G47360	90	3.00E-95	343	657	1	0.72	1	0.72
		isogroup12233	co-ortholog	AT1G66380	r12233000C	28.41	2.00E-20	97.4	r12233000C	AT1G54870	93.27	2.00E-175	611	1023	2	1.00	2	1.00
		isogroup13364	co-ortholog	AT1G66380	g13364000C	26.24	6.00E-09	59.3	g13364000C	AT2G24190	87.42	1.00E-147	519	996	2	0.82	2	0.82
		isogroup13381	co-ortholog	AT1G66380	g13381000C	28.83	5.00E-07	53.1	g13381000C	AT4G09750	94.71	8.00E-101	362	692	2	0.41	1	0.23
		isogroup16169	co-ortholog	AT1G66380	g16169000C	28.88	3.00E-12	70.5	g16169000C	AT5G65205	87.57	1.00E-106	290	715	2	0.82	2	0.82
		isogroup21115	co-ortholog	AT1G66380	g21115000C	30.54	3.00E-13	73.9	g21115000C	AT5G50600	93.14	0	661	1356	68	0.60	1	0.14
		isogroup22075	co-ortholog	AT1G66380	r22075000C	30.36	4.00E-12	70.1	r22075000C	AT5G10050	86.23	8.00E-79	289	589	1	1.00	1	1.00
		isogroup22390	co-ortholog	AT1G66380	g22390000C	30.36	1.00E-18	91.7	g22390000C	AT3G05260	97.13	2.00E-134	474	800	1	1.00	1	1.00
		isogroup02541	RBH	AT1G04640	g02541000C	93.53	4.00E-129	458	g02541000C	AT1G04640	93.53	2.00E-126	448	982	2	0.64	2	0.64
Mitochondrial Lipoyltransferase	At1g47580	isogroup12827	RBH	AT1G47580	g12827000C	62.28	2.00E-26	113	g12827000C	AT1G47580	61.82	2.00E-25	110	502	1	1.00	1	1.00
Mitochondrial Phosphatidylglycerol-Phosphate Synthase	At4g04870	isogroup05317	RBH	AT4G04870	r05317000C	90.99	6.00E-173	604	r05317000C	AT4G04870	90.99	1.00E-179	625	1266	4	0.98	3	0.98
		isogroup00696	RBH	AT5G09300	g00696000C	89.24	0	859	g00696000C	AT5G09300	89.24	0	825	1952	71	0.79	1	0.09
α-Ketoacid Decarboxylase E1a of BC Ketoacid DH Complex	At1g21400	isogroup00131	RBH	AT1G21400	g00131000C	89.87	0	885	g00131000C	AT1G21400	89.87	0	852	2606	432			

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship Arabidopsis	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis							
				Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads	Fraction	Minimum	Min Reads	Fraction
Mitochondrial Acyl Carrier Protein	At2g44620	isogroup19844	RBH	AT1G244520	g19844000C	97.54	1.00E-65	245	g19844000C	AT2G44620	97.54	2.00E-63	238	530	1	1.00	1	1.00	1	1.00
Mitochondrial Acyl Carrier Protein	At1g55290	isogroup14894	RBH	AT1G55290	g04894000C	91.26	5.00E-64	239	g04894000C	AT1G55290	92.26	3.00E-61	231	716	0	0	0	0	0	0
Mitochondrial Acyl Carrier Protein	At5g47630	isogroup13594	RBH	AT5G47630	g13594000C	88.24	1.00E-46	155	g13594000C	AT5G47630	89.29	9.00E-45	151	598	1	1.00	1	1.00	1	1.00
Mitochondrial Phosphatidylserine Decarboxylase	At4g16700	isogroup10157	RBH	AT4G16700	g10157000C	91.19	0	702	g10157000C	AT4G16700	91.97	0	723	1199	1	0.21	1	0.21	1	0.21
Mitochondrial Glycerol-3-Phosphate Dehydrogenase	At3g10370	isogroup14863	RBH*	AT4G16700	g14863000C	93.38	1.00E-70	265	g14863000C	AT4G16700	93.38	7.00E-74	261	488	1	1.00	1	1.00	1	1.00
Mitochondrial Diacylglycerol Cholinephosphotransferase	At3g10370	isogroup18522	RBH	AT3G10370	g18522000C	97.56	0	508	g18522000C	AT3G10370	94.25	0	496	1720	5	1.00	3	1.00	3	1.00
Mitochondrial Diacylglycerol Cholinephosphotransferase	At1g13560	isogroup02341	RBH	AT1G13560	g02341000C	98.97	0	791	g02341000C	AT1G13560	98.97	0	795	1566	28	0.99	2	0.92	2	0.92
Acyl-CoA : Diacylglycerol Acyltransferase	At2g19450	isogroup04373	RBH	AT2G19450	g04373000C	91.65	0	949	g04373000C	AT2G19450	91.65	0	975	1945	24	0.99	7	0.87	7	0.87
Acyl-CoA : Diacylglycerol Acyltransferase	At4g26740	isogroup07110	RBH	AT4G26740	g0711000C	90.16	5.00E-162	569	g04265000C	AT3G55320	90.16	6.00E-168	587	1332	3	0.97	1	0.19	1	0.19
Calenin	At5g55240	isogroup06079	RBH	AT5G55240	g06079000C	93	3.00E-135	478	g06079000C	AT5G55240	93	2.00E-135	478	870	3	0.94	3	0.94	3	0.94
Calenin	isogroup11565	RBH	AT1G70670	g11565000C	95.38	5.00E-108	387	g11565000C	AT1G70670	95.38	2.00E-106	382	1005	4	0.90	3	0.90	3	0.90	
Calenin	isogroup18748	RBH*	AT1G70670	g18748000C	87.79	1.00E-64	243	g18748000C	AT1G70670	87.5	2.00E-65	244	560	1	1.00	1	1.00	1	1.00	
Calenin	isogroup20775	RBH*	AT1G70670	g20775000C	95.38	5.00E-108	387	g20775000C	AT1G70670	95.38	2.00E-106	382	994	1	1.00	1	1.00	1	1.00	
Calenin	isogroup11565	co-ortholog	AT1G70680	g11565000C	82.81	8.00E-90	327	g11565000C	AT1G70670	95.38	3.00E-106	381	1005	2	0.87	2	0.87	2	0.87	
Calenin	isogroup18748	co-ortholog	AT1G70680	g18748000C	80.3	2.00E-59	225	g18748000C	AT1G70670	87.5	2.00E-65	244	560	1	1.00	1	1.00	1	1.00	
Calenin	isogroup20775	co-ortholog	AT1G70680	g20775000C	82.29	5.00E-89	324	g20775000C	AT1G70670	95.38	2.00E-106	382	994	1	1.00	1	1.00	1	1.00	
Calenin	isogroup06079	co-ortholog	AT1G70680	g06079000C	43.21	4.00E-32	135	g06079000C	AT5G55240	93	2.00E-135	478	870	3	0.94	3	0.94	3	0.94	
Calenin	isogroup07110	co-ortholog	AT1G70680	g0711000C	44.58	8.00E-34	140	g0711000C	AT4G26740	97.96	2.00E-144	508	998	15	0.97	2	0.96	2	0.96	
Calenin	isogroup07717	co-ortholog	AT1G70680	g07717000C	43.11	2.00E-33	140	g07717000C	AT2G33380	91.56	4.00E-128	454	924	3	0.91	3	0.91	3	0.91	
Calenin	isogroup11565	co-ortholog	AT1G23240	g11565000C	63.39	2.00E-65	246	g11565000C	AT1G70670	95.38	2.00E-106	382	1005	4	0.90	3	0.90	3	0.90	
Calenin	isogroup18748	co-ortholog	AT1G23240	g18748000C	62.99	4.00E-44	175	g18748000C	AT1G70670	87.5	2.00E-65	244	560	1	1.00	1	1.00	1	1.00	
Calenin	isogroup20775	co-ortholog	AT1G23240	g20775000C	63.39	2.00E-65	246	g20775000C	AT1G70670	95.38	2.00E-106	382	994	1	1.00	1	1.00	1	1.00	
Calenin	isogroup06079	co-ortholog	AT1G23240	g06079000C	42.07	0	37	g06079000C	AT5G55240	88.89	2.00E-126	448	870	3	0.89	3	0.89	3	0.89	
Calenin	isogroup07110	co-ortholog	AT1G23240	g0711000C	42.86	4.00E-40	162	g0711000C	AT4G26740	97.96	2.00E-144	508	998	15	0.97	2	0.96	2	0.96	
Calenin	isogroup07717	co-ortholog	AT1G23240	g07717000C	43.48	7.00E-42	168	g07717000C	AT2G33380	91.56	4.00E-128	454	924	3	0.91	3	0.91	3	0.91	
Calenin	isogroup11565	co-ortholog	AT1G23250	g11565000C	54.67	7.00E-41	164	g11565000C	AT1G70670	95.38	2.00E-106	382	1005	4	0.90	3	0.90	3	0.90	
Calenin	isogroup18748	co-ortholog	AT1G23250	g18748000C	53.12	5.00E-24	102	g18748000C	AT1G70670	87.5	2.00E-65	244	560	1	1.00	1	1.00	1	1.00	
Calenin	isogroup20775	co-ortholog	AT1G23250	g20775000C	54.67	7.00E-41	164	g20775000C	AT1G70670	95.38	2.00E-106	382	994	1	1.00	1	1.00	1	1.00	
Calenin	isogroup06079	co-ortholog	AT1G23250	g06079000C	32.65	1.00E-18	90.9	g06079000C	AT5G55240	93	2.00E-135	478	870	3	0.94	3	0.94	3	0.94	
Calenin	isogroup07110	co-ortholog	AT1G23250	g0711000C	34.23	1.00E-19	93.3	g0711000C	AT4G26740	97.96	2.00E-144	508	998	15	0.97	2	0.96	2	0.96	
Calenin	isogroup07717	co-ortholog	AT1G23250	g07717000C	38.06	5.00E-23	105	g07717000C	AT2G33380	91.56	4.00E-128	454	924	3	0.91	3	0.91	3	0.91	
Calenin	isogroup14367	RBH*	AT3G01570	g14367000C	92.9	2.00E-93	338	g14367000C	AT3G01570	92.9	2.00E-90	328	778	2	1.00	2	1.00	2	1.00	
Oil-Body Oleosin	At3g01570	isogroup14432	RBH	AT3G01570	g14432000C	95.56	3.00E-96	348	g14432000C	AT3G01570	95.56	6.00E-93	337	800	1	0.91	1	0.91	1	0.91
Oil-Body Oleosin	At4g25140	isogroup01873	RBH	AT4G25140	g01873000C	92.82	5.00E-84	307	g01873000C	AT4G25140	92.82	1.00E-89	326	962	3	0.97	3	0.97	3	0.97
Oil-Body Oleosin	At5g15210	isogroup06220	RBH	AT5G15210	g06220000C	94.96	7.00E-71	263	g06220000C	AT5G15210	94.96	3.00E-68	254	741	5	0.72	3	0.72	3	0.72
Oil-Body Oleosin	At5g40420	isogroup06227	RBH	AT5G40420	g06227000C	93	7.00E-92	334	g06227000C	AT5G40420	94.95	1.00E-102	369	810	4	0.73	4	0.73	4	0.73
Oil-Body Oleosin	At3g14870	isogroup02042	RBH	AT3G14870	g02042000C	91.62	1.00E-84	309	g02042000C	AT3G14870	91.62	6.00E-85	310	654	6	0.64	6	0.64	6	0.64
Oil-Body Oleosin	At1g48990	isogroup00875	RBH	AT1G48990	g00875000C	90.53	1.00E-76	283	g00875000C	AT1G48990	90.53	1.00E-84	310	1331	9	0.81	5	0.77	5	0.77
Oil-Body Oleosin	At2g25890	isogroup10280	RBH	AT2G25890	g10280000C	91.87	1.00E-53	206	g10280000C	AT2G25890	88.08	2.00E-70	261	649	2	0.90	2	0.90	2	0.90
Oil-Body Oleosin	isogroup14452	RBH*	AT2G25890	g14452000C	90.24	3.00E-53	204	g14452000C	AT2G25890	86.58	4.00E-67	250	715	1	0.93	1	0.93	1	0.93	
Phospholipid-Diacylglycerol_Acyltransferase	At5g13640	GDEH3V02JXKX	RBH*	AT5G13640	GDEH3V02	98.32	6.00E-66	250	GDEH3V02	AT5G13640	98.32	1.00E-66	247	374	na	na	na	na	na	na
Phospholipid-Diacylglycerol_Acyltransferase	isogroup08817	RBH	AT5G13640	g08817000C	87.66	0	808	g08817000C	AT5G13640	91.67	0	844	1071	109	0.77	3	0.58	3	0.58	
Phospholipid-Diacylglycerol_Acyltransferase	At3g44830	isogroup02243	RBH	AT3G44830	g02243000C	90.2	0	1080	g02243000C	AT3G44830	90.2	0	1100	1948	72	0.99	4	0.79	4	0.79
Triacylglycerol Lipase	At1g10740	GDNW3V01BGA2L	RBH*	AT1G10740	GDNW3V01	91.6	1.00E-68	245	GDNW3V01	AT1G10740	91.6	1.00E-70	236	460	na	na	na	na	na	na
Triacylglycerol Lipase	At5g18630	isogroup08480	RBH	AT5G18630	g08480000C	90	0	654	g08480000C	AT5G18630	90	0	642	1328	13	0.76	4	0.70	4	0.70
Triacylglycerol Lipase	At5g18640	isogroup08463	RBH	AT5G18640	g08463000C	93.35	0	682	g08463000C	AT5G18640	93.35	0	669	1460	71	0.75	2	0.40	2	0.40
Triacylglycerol Lipase	At2g15230	isogroup07883	RBH	AT2G15230	g07883000C	93.15	0	769	g07883000C	AT2G15230	93.15	0	759	1405	14	0.78	7	0.78	7	0.78
Monoacylglycerol Lipase	At1g11090	isogroup04279	RBH	AT1G11090	g04279000C	96.57	2.00E-178	622	g04279000C	AT1G11090	96.57	0	633	1071	5	0.92	3	0.92	3	0.92
Monoacylglycerol Lipase	isogroup18011	RBH	AT1G18360	g18011000C	78.25	4.00E-120	429	g18011000C	AT1G18360	79.3	6.00E-120	427	1060	1	1.00	1	1.00	1	1.00	
Monoacylglycerol Lipase	isogroup20006	RBH*	AT1G18360	g20006000C	78.01	2.00E-113	406	g20006000C	AT1G18360	78.72	4.00E-116	414	1029	1	1.00	1	1.00	1	1.00	
Monoacylglycerol Lipase	At1g18360	GDNW3V01BGA2L	RBH*	AT1G18360	GDNW3V01	90.62	1.00E-46	185	GDNW3V01	AT1G18360	90.62	3.00E-46	180	480	na	na	na	na	na	na
Monoacylglycerol Lipase	At1g52760	isogroup01398	RBH	AT1G52760	g01398000C	89.76	1.00E-175	613	g01398000C	AT1G52760	90.6									

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query Subject	% identity	E-Value		bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction	
		isogroup04279	co-ortholog	AT3G55190	g04279r000C	43.11	8.00E-63	238	g04279r000C	AT1G11090	95.83	1.00E-162	568	1071	2	0.50	1	0.28
		isogroup04816	co-ortholog	AT3G55190	g04816r000C	40.57	6.00E-61	233	g04816r000C	AT5G16120	88.52	0	654	1286	6	0.85	4	0.85
		isogroup05809	co-ortholog	AT3G55190	g05809r000C	39.45	1.00E-56	218	g05809r000C	AT1G77420	91.53	0	700	1391	3	0.62	2	0.62
		isogroup05937	co-ortholog	AT3G55190	g05937r000C	30.72	2.00E-28	124	g05937r000C	AT5G11650	92.17	0	724	1347	6	0.46	1	0.25
Monoacylglycerol Lipase	At3g55190	isogroup16494	co-ortholog	AT3G55190	g16494r000C	60.9	3.00E-82	178	g16494r000C	AT3G55180	89.63	4.00E-145	248	1779	0	0	0	0
		isogroup22171	co-ortholog	AT3G55190	g22171r000C	60.29	1.00E-72	271	g22171r000C	AT2G39420	92.12	4.00E-110	393	687	1	1.00	1	1.00
		isogroup05937	RBH	AT5G11650	g05937r000C	92.75	0	691	g05937r000C	AT5G11650	92.75	0	735	1347	9	0.71	1	0.12
Monoacylglycerol Lipase	At5g11650	isogroup04816	RBH	AT5G11650	g04816r000C	87.6	0	677	g04816r000C	AT5G11650	87.6	0	656	1280	5	0.92	3	0.92
Monoacylglycerol Lipase	At5g43280	isogroup06621	RBH	AT5G43280	g06621r000C	90.68	1.00E-147	520	g06621r000C	AT5G43280	90.68	5.00E-139	492	3145	26	0.89	5	0.88
Peroxisomal Enoyl-CoA Hydratase	At1g60550	isogroup05918	RBH	AT1G60550	g05918r000C	92.31	0	649	g05918r000C	AT1G60550	92.31	0	631	1222	4	0.75	2	0.75
Hydroxycytl-CoA Dehydrogenase	At3g15290	isogroup00259	RBH	AT3G15290	g00259r000C	91.53	3.00E-159	558	g00259r000C	AT3G15290	91.53	9.00E-151	529	2381	1	0.92	1	0.92
		isogroup06785	RBH*	AT3G15290	g06785r000C	88.33	1.00E-54	211	g06785r000C	AT3G15290	88.33	4.00E-53	203	2751	1	1.00	1	1.00
Ketoacyl-CoA Thiolase	At2g33150	isogroup21990	RBH	AT2G33150	g21990r000C	96.95	0	888	g21990r000C	AT2G33150	96.96	0	879	1586	108	0.77	1	0.14
Ketoacyl-CoA Thiolase	At5g48880	isogroup01570	RBH	AT5G48880	g01570r000C	92.56	0	851	g01570r000C	AT5G48880	93.44	0	836	2086	2916	0.94	2	0.56
Ketoacyl-CoA Thiolase	At1g04710	isogroup17018	RBH	AT1G04710	g17018r000C	94.39	0	593	g17018r000C	AT1G04710	94.39	0	572	1467	25	0.81	4	0.63
Enoyl-CoA Isomerase	At4g29010	GD75LUV03F1CPE	RBH*	AT4G29010	GD75LUV03F	97.14	2.00E-56	251	GD75LUV03F	AT4G29010	97.14	1.00E-77	270	469	na	na	na	na
		isogroup01276	RBH	AT4G29010	g01276r000C	94.61	0	1345	g01276r000C	AT4G29010	94.61	0	1321	2445	867	0.98	3	0.96
Enoyl-CoA Isomerase	At3g06860	isogroup01314	RBH	AT3G06860	g01314r000C	93.72	0	1358	g01314r000C	AT3G06860	93.72	0	1332	2223	33	0.94	2	0.92
Diacyl-CoA Reductase	At3g12800	isogroup05814	RBH	AT3G12800	g05814r000C	95.64	3.00E-154	542	g05814r000C	AT3G12800	95.64	1.00E-164	575	1095	9	0.73	4	0.66
Hydroxyisobutyryl-CoA Hydrolase	At5g65940	isogroup06541	RBH	AT5G65940	g06541r000C	91.34	0	715	g06541r000C	AT5G65940	91.34	0	682	1242	29	0.69	3	0.55
		isogroup20677	co-ortholog	AT2G30660	g20677r000C	44.26	2.00E-69	260	g20677r000C	AT1G60550	89.97	3.00E-160	560	1003	1	0.99	1	0.99
		GD75LUV03F1CPE	co-ortholog	AT2G30660	GD75LUV03F	56.14	2.00E-10	647	GD75LUV03F	AT3G60510	94.83	4.00E-35	111	387	na	na	na	na
		isogroup06621	co-ortholog	AT2G30660	g06621r000C	27.39	4.00E-12	705	g06621r000C	AT5G43280	89.89	5.00E-133	472	1122	16	0.93	3	0.92
		isogroup05918	co-ortholog	AT2G30660	g05918r000C	27.46	6.00E-08	565	g05918r000C	AT1G60550	91.72	1.00E-180	629	1242	4	0.77	4	0.77
Hydroxyisobutyryl-CoA Hydrolase	At2g30660	isogroup06541	co-ortholog	AT2G30660	g06541r000C	82.13	0	648	g06541r000C	AT3G65940	91.34	0	682	1242	29	0.69	3	0.55
		isogroup06566	co-ortholog	AT2G30660	g06566r000C	45.17	6.00E-92	335	g06566r000C	AT4G31810	91.44	0	766	1400	67	0.80	3	0.53
		isogroup22011	co-ortholog	AT2G30660	g22011r000C	53.07	4.00E-44	176	g22011r000C	AT3G60510	94.42	5.00E-115	409	682	0	0	0	0
		isogroup09804	co-ortholog	AT2G30660	g09804r000C	43.45	5.00E-80	296	g09804r000C	AT1G60550	90.12	7.00E-179	622	1165	5	0.95	3	0.95
		isogroup06038	co-ortholog	AT2G30660	g06038r000C	30.67	3.00E-13	733	g06038r000C	AT4G16210	97.36	5.00E-142	500	1014	5	0.50	2	0.32
		isogroup06624	co-ortholog	AT2G30660	g06624r000C	28.9	3.00E-12	712	g06624r000C	AT4G16800	90	5.00E-150	527	1232	103	0.88	2	0.49
		isogroup06998	co-ortholog	AT2G30660	g06998r000C	35.31	2.00E-52	204	g06998r000C	AT4G13360	92.14	0	757	1436	79	0.77	9	0.77
		isogroup18569	co-ortholog	AT2G30660	g18569r000C	44.2	2.00E-24	111	g18569r000C	AT3G24360	78.53	2.00E-76	281	568	1	1.00	1	1.00
		isogroup09804	co-ortholog	AT2G30660	g09804r000C	43.79	2.00E-80	297	g09804r000C	AT1G60550	90.46	5.00E-180	627	1165	2	0.95	2	0.95
		GD75LUV03F1CPE	co-ortholog	AT2G30660	GD75LUV03F	59.65	2.00E-11	682	GD75LUV03F	AT3G60510	94.83	4.00E-35	111	387	na	na	na	na
		isogroup06621	co-ortholog	AT2G30660	g06621r000C	29.13	3.00E-13	743	g06621r000C	AT5G43280	89.89	5.00E-133	472	1145	16	0.93	3	0.92
Hydroxyisobutyryl-CoA Hydrolase	At2g30660	isogroup06541	co-ortholog	AT2G30660	g06541r000C	78.93	1.00E-177	620	g06541r000C	AT5G65940	91.34	0	682	1242	29	0.69	3	0.55
		isogroup06566	co-ortholog	AT2G30660	g06566r000C	44.69	9.00E-90	328	g06566r000C	AT4G31810	91.44	0	766	1400	67	0.80	3	0.53
		isogroup20111	co-ortholog	AT2G30660	g20111r000C	53.51	2.00E-41	167	g20111r000C	AT3G60510	94.42	5.00E-115	409	682	0	0	0	0
		isogroup20677	co-ortholog	AT2G30660	g20677r000C	43.14	6.00E-69	259	g20677r000C	AT1G60550	89.97	3.00E-160	560	1003	1	0.99	1	0.99
		isogroup06038	co-ortholog	AT2G30660	g06038r000C	29.33	2.00E-10	651	g06038r000C	AT4G16210	97.36	3.00E-142	501	1014	4	0.90	3	0.90
		isogroup06624	co-ortholog	AT2G30660	g06624r000C	28.26	2.00E-11	682	g06624r000C	AT4G16800	90	5.00E-150	527	1232	103	0.88	2	0.49
		isogroup06998	co-ortholog	AT2G30660	g06998r000C	34.79	2.00E-48	191	g06998r000C	AT4G13360	92.14	0	757	1436	79	0.79	9	0.77
		isogroup18569	co-ortholog	AT2G30660	g18569r000C	42.11	2.00E-22	104	g18569r000C	AT3G24360	78.53	2.00E-76	281	568	1	1.00	1	1.00
Fatty Acid ω-Alcohol Oxidase		GDENH3V018X0KH	RBH*	AT3G23410	GDENH3V01	73.24	2.00E-18	928	GDENH3V01	AT3G23410	72.6	3.00E-21	963	316	na	na	na	na
	At3g23410	isogroup04042	RBH	AT3G23410	g04042r000C	85.88	0	139	g04042r000C	AT3G23410	85.86	0	1193	1627	232	0.82	2	0.65
		isogroup02239	RBH	AT4G19380	g02239r000C	84.69	0	723	g02239r000C	AT4G19380	84.69	0	744	1473	15	0.67	1	0.10
Fatty Acid ω-Alcohol Oxidase	At4g19380	isogroup19514	RBH*	AT4G19380	g19514r000C	85.71	1.00E-90	332	g19514r000C	AT4G19380	85.71	2.00E-89	324	547	1	1.00	1	1.00
Fatty Acid ω-Alcohol Oxidase	At4g28570	isogroup08222	RBH	AT4G28570	g08222r000C	88.82	0	1119	g08222r000C	AT4G28570	88.82	0	1119	2039	35	0.99	4	0.98
Fatty Acid ω-Alcohol Oxidase	At1g03990	isogroup21734	RBH	AT1G03990	g21734r000C	87	0	1154	g21734r000C	AT1G03990	87	0	1150	2622	4	1.00	2	1.00
Peroxisomal Long-Chain Acyl-CoA Synthetase	At5g27600	isogroup02710	RBH	AT5G27600	g02710r000C	89.5	0	1299	g02710r000C	AT5G27600	89.5	0	1269	32	0.98	3	0.93	
Peroxisomal Long-Chain Acyl-CoA Synthetase	At3g05970	GDENH3V0239314	RBH*	AT3G05970	GDENH3V02	97.92	1.00E-77	289	GDENH3V02	AT3G05970	91.19	2.00E-77	284	479	na	na	na	na
		isogroup1398	RBH	AT3G05970	g01398r000C	96.24	0	1284	g01398r000C	AT3G05970	96.24	0	1298	2065	232	0.82	2	0.65
		isogroup02239	RBH*	AT4G39850	GDENH3V02	84	3.00E-51	202	GDENH3V02	AT4G39850	84	5.00E-50	192	378	na	na	na	na
		isogroup10848	RBH*	AT4G39850	g10848r000C	95.12	6.00E-149	514	g10848r000C	AT4G39850	95.12	1.00E-155	533	1315	2	0.87	2	0.87
Peroxisomal Fatty Acid / Acyl-CoA Transporter	At4g39850	isogroup18385	RBH	AT4G39850	g18385r000C	98.96	7.00E-108	390	g18385r000C	AT4G39850	98.96	1.00E-104	374	581	1	1.00	1	1.00
		isogroup19643	RBH	AT4G39850	g19643r000C	95.3	0	1161	g19643r000C	AT4G39850	95.3	0	1112	1782	84	0.95	2	0.92
		isogroup19753																

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query Subject	% identity	E-Value		bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction	
Phosphatidylinositol-4-Kinase a	At1g51040	isogroup16387	co-ortholog	AT1G51040	g16387000C	88.25	7.0E-17	763	g16387000C	AT1G49340	98.57	0	979	1952	4	0.97	2	0.90
		isogroup16851	co-ortholog	AT1G51040	e16851000C	53.25	0.0E+00	87	e16851000C	AT5664070	95.65	2.00E-101	225	574	1	1.00	1	1.00
Phosphatidylinositol-4-Kinase b	At5g64070	isogroup16851	RH*	AT5G64070	GD75LV02Z	95.39	7.00E-82	304	GD75LV02Z	AT5G64070	96.03	6.00E-82	298	460	na	na	na	na
		isogroup16851	RH*	AT5G64070	g16851000C	95.65	4.00E-103	231	g16851000C	AT5G64070	95.65	2.00E-101	225	574	1	1.00	1	1.00
		isogroup10192	RH	AT5G64070	g10192000C	86.71	0	500	g10192000C	AT5G64070	87	0	508	1695	2	0.79	2	0.79
		isogroup00005	co-ortholog	AT1G664460	r00005c000C	40.23	5.00E-29	126	r00005c000C	AT1G62670	98.32	2.00E-100	360	1272	42	0.93	7	0.90
		isogroup00423	co-ortholog	AT1G664460	g00423r000C	65	1.00E-117	420	g00423r000C	AT2G46500	91.81	0	1054	2446	12	0.86	1	0.68
		isogroup04725	co-ortholog	AT1G664460	g04725r000C	41.92	4.00E-52	202	g04725r000C	AT1G13640	87.97	0	1021	2133	336	0.99	10	0.70
		isogroup09509	co-ortholog	AT1G664460	g09509r000C	64.65	3.00E-103	372	g09509r000C	AT5G24240	91.51	0	818	2138	20	1.00	5	0.97
		isogroup10661	co-ortholog	AT1G664460	e10661000C	40.86	9.00E-52	201	e10661000C	AT2G03890	95.88	0	1085	2217	6	0.98	4	0.98
		isogroup16375	co-ortholog	AT1G664460	g16375r000C	47.13	1.00E-12	71.6	g16375r000C	AT2G40850	87.39	4.00E-109	390	728	1	1.00	1	1.00
		isogroup18168	co-ortholog	AT1G664460	g18168r000C	91.91	2.00E-71	267	g18168r000C	AT2G46500	54.31	5.00E-99	357	1006	1	1.00	1	1.00
Phosphatidylinositol-4-Kinase g	At1g64460	isogroup17855	co-ortholog	AT1G64460	g17855r000C	34.51	3.00E-08	57	g17855r000C	AT3G43950	47.01	8.00E-25	107	478	1	1.00	1	1.00
		isogroup00005	RH	AT1G26270	r00005c000C	93.86	6.00E-153	539	r00005c000C	AT1G26270	93.86	6.00E-147	517	1272	1	0.97	1	0.97
Phosphatidylinositol-4-Kinase g	At1g26270	isogroup00005	co-ortholog	AT1G26270	GD75LV02Z	83.56	3.00E-67	255	GD75LV02Z	AT5G64070	96.03	6.00E-82	298	460	na	na	na	na
		isogroup10192	co-ortholog	AT5G09350	e10192r000C	75	2.00E-160	426	e10192r000C	AT5G64070	96.03	6.00E-82	298	460	na	na	na	na
		isogroup16308	co-ortholog	AT5G09350	e16308r000C	32.79	1.00E-06	53.9	e16308r000C	AT1G50030	96.8	0	728	1673	1	0.94	1	0.94
		isogroup16387	co-ortholog	AT5G09350	g16387r000C	41.57	2.00E-50	199	g16387r000C	AT1G49340	98.57	0	979	1932	4	0.97	2	0.90
		isogroup16851	co-ortholog	AT5G09350	e16851r000C	89.57	2.00E-98	217	e16851r000C	AT5G64070	95.65	2.00E-101	225	574	1	1.00	1	1.00
		isogroup00423	RH	AT2G46500	g00423r000C	92.83	0	1095	g00423r000C	AT2G46500	92.83	0	1063	2446	5	0.92	1	0.78
		isogroup18168	RH*	AT2G46500	g18168r000C	54.89	8.00E-99	359	g18168r000C	AT2G46500	54.31	5.00E-99	357	1006	1	1.00	1	1.00
		isogroup00373	co-ortholog	AT2G46500	g00373r000C	75.37	8.00E-59	180	g00373r000C	AT2G40850	76.12	1.00E-64	198	506	na	na	na	na
		isogroup16375	co-ortholog	AT2G46500	e16375r000C	87.39	2.00E-112	404	e16375r000C	AT2G40850	87.39	4.00E-109	390	728	1	1.00	1	1.00
		isogroup10661	co-ortholog	AT2G03890	g10661r000C	91.46	6.00E-37	153	g10661r000C	AT2G03890	95.88	0	150	3148	2	0.86	1	0.98
Phosphatidylinositol-4-Kinase g	At2g03890	isogroup10661	RH	AT2G03890	g10661r000C	95.88	0	1091	g10661r000C	AT2G03890	95.88	0	1085	2217	6	0.98	4	0.98
		isogroup00005	co-ortholog	AT3G56600	GD75LV03C	38.46	2.00E-17	72.4	GD75LV03C	AT2G40850	76.12	1.00E-64	198	506	na	na	na	na
		isogroup00005	co-ortholog	AT3G56600	r00005c000C	60.67	3.00E-58	224	r00005c000C	AT1G26270	98.32	2.00E-100	360	1272	42	0.93	7	0.90
		isogroup00423	co-ortholog	AT3G56600	g00423r000C	37.61	3.00E-51	201	g00423r000C	AT2G46500	91.81	0	1054	2446	12	0.86	1	0.68
		isogroup04725	co-ortholog	AT3G56600	g04725r000C	52.11	3.00E-103	374	g04725r000C	AT1G13640	88.83	0	1030	2133	365	1.00	10	0.84
		isogroup09509	co-ortholog	AT3G56600	g09509r000C	38.36	3.00E-51	201	g09509r000C	AT5G24240	91.51	0	818	2138	20	1.00	5	0.97
		isogroup10661	co-ortholog	AT3G56600	e10661r000C	51.96	3.00E-102	279	e10661r000C	AT2G03890	95.88	0	1085	2217	6	0.98	4	0.98
		isogroup16375	co-ortholog	AT3G56600	g16375r000C	72.48	2.00E-81	301	g16375r000C	AT2G40850	87.39	4.00E-109	390	728	1	1.00	1	1.00
		isogroup18168	co-ortholog	AT3G56600	g18168r000C	43.14	8.00E-23	106	g18168r000C	AT2G46500	54.31	5.00E-99	357	1006	1	1.00	1	1.00
		isogroup09509	RH	AT5G24240	g09509r000C	90.11	0	831	g09509r000C	AT5G24240	91.51	0	818	2138	20	1.00	5	0.97
Phosphatidylinositol-4-Kinase g	At5g24240	isogroup09509	RH	AT5G24240	g09509r000C	90.11	0	831	g09509r000C	AT5G24240	91.51	0	818	2138	20	1.00	5	0.97
		isogroup00373	co-ortholog	AT1G01460	GD75LV02Z	68.5	3.00E-52	183	GD75LV02Z	AT4G01190	85.04	1.00E-68	224	492	na	na	na	na
		isogroup00373	co-ortholog	AT1G01460	g00373r000C	35.61	6.00E-67	252	g00373r000C	AT1G60890	96.59	0	1532	2891	181	0.90	2	0.64
		isogroup0967	co-ortholog	AT1G01460	g0967r000C	42.21	9.00E-55	212	g0967r000C	AT1G21980	87.99	0	1374	2527	66	0.95	3	0.82
		isogroup1601	co-ortholog	AT1G01460	e1601r000C	35.68	3.00E-70	263	e1601r000C	AT1G77740	96.89	0	1105	2023	18	0.86	1	0.88
		isogroup17031	co-ortholog	AT1G01460	g17031r000C	31.21	3.00E-09	61.2	g17031r000C	AT1G71010	97.57	0	689	1088	1	1.00	1	1.00
		isogroup20500	co-ortholog	AT1G01460	e20500r000C	28.66	2.00E-07	55.5	e20500r000C	AT3G14270	95.24	2.00E-142	470	832	2	0.75	2	0.75
		isogroup1190	co-ortholog	AT1G01460	GD75LV02Z	85.04	9.00E-69	231	GD75LV02Z	AT4G01190	85.04	1.00E-68	224	492	na	na	na	na
		isogroup00967	RH	AT1G21980	g00967r000C	90.92	0	1347	g00967r000C	AT1G21980	88.25	0	1377	2527	36	0.83	1	0.40
		isogroup12162	RH	AT1G10900	g12162r000C	87.1	0	438	g12162r000C	AT1G10900	87.8	0	434	1166	2	0.87	2	0.87
Phosphatidylinositol-Phosphate Kinase type IB	At1g08390	isogroup00373	RH	AT1G08390	g00373r000C	96.47	0	1531	g00373r000C	AT1G60890	96.59	0	1532	2891	181	0.90	2	0.64
		isogroup1601	co-ortholog	AT1G08390	e1601r000C	35.68	3.00E-70	263	e1601r000C	AT1G77740	96.89	0	1105	2023	18	0.86	1	0.88
		isogroup17031	co-ortholog	AT1G08390	g17031r000C	31.21	3.00E-09	61.2	g17031r000C	AT1G71010	97.57	0	689	1088	1	1.00	1	1.00
		isogroup20500	co-ortholog	AT1G08390	e20500r000C	28.66	2.00E-07	55.5	e20500r000C	AT3G14270	95.24	2.00E-142	470	832	2	0.75	2	0.75
		isogroup1190	co-ortholog	AT1G08390	GD75LV02Z	85.04	9.00E-69	231	GD75LV02Z	AT4G01190	85.04	1.00E-68	224	492	na	na	na	na
		isogroup00967	RH	AT1G21980	g00967r000C	90.92	0	1347	g00967r000C	AT1G21980	88.25	0	1377	2527	36	0.83	1	0.40
		isogroup12162	RH	AT1G10900	g12162r000C	87.1	0	438	g12162r000C	AT1G10900	87.8	0	434	1166	2	0.87	2	0.87
		isogroup00373	RH	AT1G08390	g00373r000C	96.47	0	1531	g00373r000C	AT1G60890	96.59	0	1532	2891	181	0.90	2	0.64
		isogroup1601	co-ortholog	AT1G08390	e1601r000C	35.68	3.00E-70	263	e1601r000C	AT1G77740	96.89	0	1105	2023	18	0.86	1	0.88
		isogroup17031	co-ortholog	AT1G08390	g17031r000C	31.21	3.00E-09	61.2	g17031r000C	AT1G71010	97.57	0	689	1088	1	1.00	1	1.00
Phosphatidylinositol-Phosphate Kinase type IB	At2g26420	isogroup00373	RH	AT2G26420	g00373r000C	96.47	0	1531	g00373r000C	AT1G60890	96.59	0	1532	2891	181	0.90	2	0.64
		isogroup1601	co-ortholog	AT2G26420	e1601r000C	35.68	3.00E-70	263	e1601r000C	AT1G77740	96.89	0	1105	2023	18	0.86	1	0.88
		isogroup17031	co-ortholog	AT2G26420	g17031r000C	31.21	3.00E-09	61.2	g17031r000C	AT1G71010	97.57	0	689	1088	1	1.00	1	1.00
		isogroup20500	co-ortholog	AT2G26420	e20500r000C	28.66	2.00E-07	55.5	e20500r000C	AT3G14270	95.24	2.00E-142	470	832	2	0.75	2	0.75
		isogroup1190	co-ortholog	AT2G26420	GD75LV02Z	85.04	9.00E-69	231	GD75LV02Z	AT4G01190	85.04	1.00E-68	224	492	na	na	na	na
		isogroup00967	RH	AT1G21980	g00967r000C	90.92	0	1347	g00967r000C	AT1G21980								

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
Phosphoinositide-specific Phospholipase C	At3g08510	isogroup05616	RH	AT3G08510	g05616R000	94.14	0	568	g05616R000	AT3G08510	93.71	0	578	1893	17	1.00	3	0.96
		isogroup05615	co-ortholog	AT2G40116	g05615R000	75	3.00E-16	85	g05615R000	AT3G58690	96.15	3.00E-24	106	238	na	na	na	na
		isogroup01616	co-ortholog	AT2G40116	g01616R000	48.15	4.00E-155	546	g01616R000	AT3G58670	89.09	0	1040	1798	107	0.90	1	0.24
Phosphoinositide-specific Phospholipase C	At2g40116	isogroup05616	co-ortholog	AT2G40116	g05616R000	66.97	3.00E-90	330	g05616R000	AT3G08510	93.71	0	548	1893	41	0.98	2	0.78
		isogroup16978	co-ortholog	AT2G40116	g16978R000	67.86	6.00E-39	160	g16978R000	AT3G55940	90.44	7.00E-131	253	774	1	1.00	1	1.00
		isogroup20040	co-ortholog	AT2G40116	g20040R000	57.06	1.00E-155	363	g20040R000	AT3G58700	93.35	0	639	1553	5	0.71	4	0.71
Phosphoinositide-specific Phospholipase C	At3g47290	isogroup05616	co-ortholog	AT3G47290	g05616R000	56.6	6.00E-11	67	g05616R000	AT3G58690	96.15	3.00E-24	106	293	na	na	na	na
		isogroup16978	co-ortholog	AT3G47290	g16978R000	39.33	3.00E-98	357	g01616R000	AT3G58670	89.45	0	1044	1798	93	0.78	1	0.23
		isogroup20040	co-ortholog	AT3G47290	g20040R000	40.91	7.00E-44	176	g05616R000	AT3G58690	93.71	0	548	1893	41	0.98	2	0.78
Phosphoinositide-specific Phospholipase C	At3g47290	isogroup16978	co-ortholog	AT3G47290	g16978R000	41.73	1.00E-20	99.8	g16978R000	AT3G55940	90.44	7.00E-131	253	774	1	1.00	1	1.00
		isogroup20040	co-ortholog	AT3G47290	g20040R000	41.06	4.00E-64	243	g20040R000	AT3G58700	93.35	0	639	1553	5	0.71	4	0.71
		isogroup05616	RH	AT3G47290	g01616R000	89.77	0	1061	g01616R000	AT3G58670	89.8	0	1050	1798	96	0.81	1	0.16
Phosphoinositide-specific Phospholipase C	At5g58670	isogroup05616	co-ortholog	AT3G47290	g05616R000	56.6	1.00E-10	66.2	g05616R000	AT3G58690	96.15	3.00E-24	106	293	na	na	na	na
		isogroup16978	co-ortholog	AT3G47290	g16978R000	37.46	9.00E-89	325	g01616R000	AT3G58670	89.62	0	1049	1798	139	0.84	1	0.15
		isogroup05616	co-ortholog	AT3G47290	g05616R000	41.74	3.00E-42	171	g05616R000	AT3G08510	93.71	0	548	1893	41	0.98	2	0.78
Phosphoinositide-specific Phospholipase C	At3g47220	isogroup16978	co-ortholog	AT3G47220	g16978R000	43.55	3.00E-22	104	g16978R000	AT3G55940	90.44	7.00E-131	253	774	1	1.00	1	1.00
		isogroup20040	co-ortholog	AT3G47220	g20040R000	41.86	8.00E-59	226	g20040R000	AT3G58700	93.35	0	639	1553	5	0.71	4	0.71
		isogroup05616	RH	AT3G47220	g05616R000	93.35	0	649	g20040R000	AT3G58700	93.35	0	639	1553	5	0.71	4	0.71
Phosphoinositide-specific Phospholipase C	At3g55940	isogroup05616	RH*	AT3G55940	g05616R000	91.23	4.00E-57	220	g05616R000	AT3G55940	91.23	2.00E-56	214	459	na	na	na	na
		isogroup16978	RH	AT3G55940	g16978R000	89.15	1.00E-119	233	g16978R000	AT3G55940	90.44	7.00E-131	253	774	1	1.00	1	1.00
		isogroup05616	RH	AT3G55940	g05616R000	87.72	6.00E-47	112	g05616R000	AT3G55940	87.72	6.00E-50	113	449	na	na	na	na
Non specific Phospholipase C	At1g07230	isogroup05150	RH	AT1G07230	g05150R000	94.02	0	1041	g05150R000	AT1G07230	94.02	0	1025	1982	5	0.99	3	0.99
		isogroup21979	RH	AT2G26870	g21979R000	93.3	0	799	g21979R000	AT2G26870	93.75	0	810	1449	1	1.00	1	1.00
		isogroup20344	RH	AT3G03520	g20344R000	94.3	3.00E-178	624	g20344R000	AT3G03520	93.47	0	816	965	3	1.00	3	1.00
Non specific Phospholipase C	At3g03530	isogroup00651	RH	AT3G03530	g00651R000	93.47	0	959	g00651R000	AT3G03530	93.47	0	957	1578	4	0.55	2	0.55
		isogroup00651	co-ortholog	AT3G03540	g00651R000	86.91	0	894	g00651R000	AT3G03530	93.81	0	955	1578	10	0.94	2	0.92
		isogroup04645	co-ortholog	AT3G03540	g04645R000	53.31	2.00E-145	513	g04645R000	AT3G48610	94.64	0	1006	1814	15	0.92	5	0.85
Non specific Phospholipase C	At3g03540	isogroup05150	co-ortholog	AT3G03540	g05150R000	57.29	3.00E-157	553	g05150R000	AT1G07230	93.66	0	1018	1982	19	0.96	2	0.41
		isogroup20344	co-ortholog	AT3G03540	g20344R000	65.16	2.00E-121	434	g20344R000	AT3G03520	94.7	0	641	965	3	1.00	2	1.00
		isogroup21979	co-ortholog	AT3G03540	g21979R000	60.65	5.00E-145	491	g21979R000	AT2G26870	93.75	0	810	1449	1	1.00	1	1.00
Non specific Phospholipase C	At3g48610	isogroup04645	RH	AT3G48610	g04645R000	94.64	0	1027	g04645R000	AT3G48610	94.64	0	1006	1814	15	0.92	5	0.85
		isogroup14074	RH	AT4G34920	g14074R000	94.7	2.00E-105	380	g14074R000	AT4G34920	94.12	1.00E-111	398	648	1	0.47	1	0.47
		isogroup13060	co-ortholog	AT4G34930	g13060R000	67.17	4.00E-114	382	g13060R000	AT4G34930	96.25	8.00E-178	535	1112	3	1.00	2	1.00
Glycosylphosphatidylinositol-specific Phospholipase C	At4g34930	isogroup14074	co-ortholog	AT4G34930	g14074R000	73.93	2.00E-85	313	g14074R000	AT4G34920	94.12	1.00E-111	398	648	1	0.47	1	0.47
		isogroup13060	co-ortholog	AT4G34930	g13060R000	67.17	4.00E-114	382	g13060R000	AT4G34930	96.25	8.00E-178	535	1112	3	1.00	2	1.00
		isogroup14074	co-ortholog	AT4G34930	g14074R000	73.93	2.00E-85	313	g14074R000	AT4G34920	94.12	1.00E-111	398	648	1	0.47	1	0.47
Glycosylphosphatidylinositol-specific Phospholipase C	At4g38690	isogroup13060	RH*	AT4G38690	g13060R000	96.25	5.00E-178	536	g13060R000	AT4G38690	96.25	8.00E-178	535	1112	3	1.00	2	1.00
		isogroup00947	RH*	AT3G15730	g00947R000	93.02	1.00E-45	174	g00947R000	AT3G15730	93.02	1.00E-47	176	339	na	na	na	na
		isogroup00947	RH	AT3G15730	g00947R000	95.27	0	1015	g00947R000	AT3G15730	95.27	0	1008	2165	2112	0.90	4	0.59
Phospholipase D a	At1g52570	isogroup00947	co-ortholog	AT1G52570	g00947R000	88.02	0	947	g00947R000	AT3G15730	95.27	0	1008	2165	2112	0.90	4	0.59
		isogroup05440	co-ortholog	AT1G52570	g05440R000	51.66	1.00E-111	402	g05440R000	AT2G42010	98.67	0	775	1235	2	0.60	1	0.53
		isogroup12191	co-ortholog	AT1G52570	g12191R000	32.35	2.00E-21	102	g12191R000	AT3G05630	90.08	0	1544	3467	61	0.86	2	0.68
Phospholipase D a	At1g52570	isogroup15330	co-ortholog	AT1G52570	g15330R000	37.86	4.00E-07	55.1	g15330R000	AT3G16785	94.92	7.00E-94	227	565	1	1.00	1	1.00
		isogroup18369	co-ortholog	AT1G52570	g18369R000	45.67	1.00E-25	174	g18369R000	AT2G42010	98.71	0	657	1871	6	0.97	1	0.47
		isogroup18369	co-ortholog	AT1G52570	g18369R000	39.73	5.00E-103	374	g18369R000	AT4G35790	87.37	0	1075	2783	8	1.00	2	1.00
Phospholipase D a	At5g25370	isogroup20602	co-ortholog	AT1G52570	g20602R000	31.25	6.00E-16	84.3	g20602R000	AT3G16785	95.52	0	1165	2015	32	0.98	3	0.86
		isogroup00947	RH	AT5G25370	g00947R000	70.12	1.00E-56	219	g00947R000	AT5G25370	68.29	5.00E-56	213	494	na	na	na	na
		isogroup13060	RH	AT1G55180	g13060R000	89.05	2.00E-76	263	g13060R000	AT1G55180	89.05	9.00E-76	257	477	na	na	na	na
Phospholipase D b (PLD b)	At2g42010	isogroup05440	RH*	AT2G42010	g05440R000	99.09	7.00E-61	234	g05440R000	AT2G42010	99.09	6.00E-62	232	427	na	na	na	na
		isogroup15330	RH	AT2G42010	g15330R000	98.4	0	785	g05440R000	AT2G42010	98.67	0	775	1235	2	0.60	1	0.53
		isogroup15330	RH*	AT2G42010	g15330R000	81.13	2.00E-121	435	g15330R000	AT2G42010	85.71	0	657	1871	6	0.97	1	0.47
Phospholipase D b (PLD b)	At4g00240	isogroup00947	co-ortholog	AT4G00240	g00947R000	63.52	1.00E-53	209	g00947R000	AT4G11850	96.25	2.00E-85	310	483	na	na	na	na
		isogroup05440	co-ortholog	AT4G00240	g05440R000	48.44	2.00E-154	495	g00947R000	AT3G15730	94.87	0	1006	2165	3308	0.91	5	0.59
		isogroup12191	co-ortholog	AT4G00240	g12191R000	33.05	5.00E-20	98.2	g12191R000	AT3G05630	90.08	0	1544	3467	61	0.86	2	0.68
Phospholipase D b (PLD b)	At4g00240	isogroup15330	co-ortholog	AT4G00240	g15330R000	34.55	5.00E-07	55.1	g15330R000	AT3G16785	94.92	7.00E-94	227	565	1	1.00	1	1.00
		isogroup15330	co-ortholog	AT4G00240	g15330R000	85.02	2.00E-150	367	g15330R000	AT2G42010	85.71	0	657	1871	6	0.97	1	0.47
		isogroup15330	co-ortholog	AT4G00240	g15330R000	45.03	4.00E-143	507	g15330R000	AT4G35790	87.37	0	1075	2783	8	1.00	2	1.00
Phospholipase D g (PLD g)	At4g11830	isogroup20602	co-ortholog	AT4G00240	g20602R000	29.36	3.00E-13	75.9	g20602R000	AT3G16785	95.							

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis						
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads	Fraction	Minimum	Min Reads
Cytosolic Phospholipase A2	At1g61850	isogroup07095	RBH	At1G61850	g07095000C	95.29	0	1179	g07095000C	AT1G61850	95.29	0	1140	3792	240	0.98	1	0.40	
Lysophospholipase (LyoPLA)	At5g19290	isogroup01618	RBH	At5G19290	g01618000C	96.37	0	658	g01618000C	AT5G19290	96.37	0	660	1251	0	0	0	0	0
Lysophospholipase (LyoPLA)	At5g17780	isogroup18440	RBH	At5G17780	r18440000C	82.85	0	702	r18440000C	AT5G17780	82.85	0	711	1404	1	1.00	1	1.00	
Lysophospholipase (LyoPLA)	At5g14980	isogroup15706	RBH	At5G14980	r15706000C	93.6	0	637	r15706000C	AT5G14980	93.6	0	634	1132	1	1.00	1	1.00	
Lysophospholipase (LyoPLA)	At3g10840	isogroup18651	RBH	At3G10840	r18651000C	75.78	8.00E-131	465	r18651000C	AT3G10840	75.86	3.00E-124	441	1116	2	1.00	2	1.00	
Lysophospholipase (LyoPLA)	At1g64670	isogroup21278	RBH	At1G64670	r21278000C	89.38	0	740	r21278000C	AT1G64670	89.38	0	734	1214	7	0.97	2	0.97	
Lysophospholipase (LyoPLA)	At5g20660	isogroup14988	RBH	At5G20660	r14988000C	92.06	3.00E-137	485	r14988000C	AT5G20660	92.06	6.00E-138	486	1043	4	0.96	2	0.96	
Lysophospholipase (LyoPLA)	At4g22300	isogroup03293	RBH	At4G22300	g03293000C	88.37	5.00E-127	451	g03293000C	AT4G22300	89.77	5.00E-135	477	1095	19	0.62	2	0.48	
Lysophospholipase (LyoPLA)	At3g15650	isogroup03682	RBH	At3G15650	g03682000C	88.3	5.00E-126	449	g03682000C	AT3G15650	88.3	4.00E-133	471	1791	8	0.93	2	0.93	
Lysophospholipase (LyoPLA)	At1g52700	isogroup15828	RBH	At1G52700	r15828000C	94.89	2.00E-96	349	r15828000C	AT1G52700	94.89	3.00E-98	353	977	1	1.00	1	1.00	
DAD1-like Acylhydrolase	At1g06800	isogroup13234	RBH	At1G06800	g13234000C	93.23	1.00E-178	624	g13234000C	AT1G06800	93.23	1.00E-176	615	977	1	1.00	1	1.00	
.	.	GDENH3V02HCOTV	RBH	At1G06800	GDENH3V02	87.34	3.00E-36	151	GDENH3V02	AT1G06800	87.34	2.00E-38	153	325	na	na	na	na	
.	.	GDENH3V02GRJWR	co-ortholog	At1G51440	GDENH3V02	53.25	4.00E-35	147	GDENH3V02	AT2G31690	97.3	4.00E-79	289	454	na	na	na	na	
.	.	isogroup08120	co-ortholog	At1G51440	r08120000C	39.04	8.00E-62	236	r08120000C	AT2G31100	91.85	0	761	1270	5	0.48	1	0.38	
.	.	isogroup08463	co-ortholog	At1G51440	r08463000C	32.3	1.00E-11	63	r08463000C	AT5G18640	93.06	0	664	1460	41	0.81	2	0.65	
.	.	isogroup09480	co-ortholog	At1G51440	r09480000C	29.21	2.00E-09	62	r09480000C	AT5G18630	90.09	2.00E-178	389	1328	13	0.75	4	0.70	
.	.	isogroup08540	co-ortholog	At1G51440	r08540000C	57.35	2.00E-107	387	r08540000C	AT2G30550	88.75	0	718	1215	6	0.89	2	0.89	
.	.	isogroup09385	co-ortholog	At1G51440	r09385000C	41.05	2.00E-54	211	r09385000C	AT4G18550	92.6	4.00E-170	594	2201	1	0.92	1	0.92	
.	.	isogroup11478	co-ortholog	At1G51440	r11478000C	39.95	9.00E-71	265	r11478000C	AT1G06250	88.65	0	771	1407	22	0.98	3	0.95	
DAD1-like Acylhydrolase	isogroup13234	isogroup13234	co-ortholog	At1G51440	g13234000C	58.7	3.00E-105	380	g13234000C	AT1G06800	93.23	1.00E-176	615	977	1	1.00	1	1.00	
.	.	isogroup14332	co-ortholog	At1G51440	g14332000C	40	2.00E-75	281	g14332000C	AT4G18550	91.73	0	778	1357	2	0.95	2	0.95	
.	.	isogroup16295	co-ortholog	At1G51440	g16295000C	51.16	3.00E-07	547	g16295000C	AT4G16820	88.89	6.00E-78	288	534	1	1.00	1	1.00	
.	.	isogroup18429	co-ortholog	At1G51440	r18429000C	47.27	2.00E-34	145	r18429000C	AT1G05800	90.09	1.00E-108	389	764	1	1.00	1	1.00	
.	.	isogroup19634	co-ortholog	At1G51440	r19634000C	39.94	1.00E-64	212	r19634000C	AT2G44810	95.34	2.00E-178	621	1159	1	1.00	1	1.00	
DAD1-like Acylhydrolase	At4g16820	isogroup16295	RBH	AT4G16820	g16295000C	88.89	3.00E-78	290	g16295000C	AT4G16820	88.89	6.00E-78	286	534	1	1.00	1	1.00	
.	.	GD75ULV01BP4V7	RBH*	AT4G16820	GD75ULV01E	79.89	4.00E-65	247	GD75ULV01E	AT4G16820	79.89	8.00E-72	265	531	na	na	na	na	
DAD1-like Acylhydrolase	At2g42690	GD75ULV03FTGLC	RBH	AT2G42690	GD75ULV03F	90.68	4.00E-82	303	GD75ULV03F	AT2G42690	91.25	9.00E-82	298	483	na	na	na	na	
DAD1-like Acylhydrolase	At4g18550	isogroup09385	RBH*	AT4G18550	g09385000C	92.71	4.00E-161	565	g09385000C	AT4G18550	92.6	4.00E-170	594	2201	1	0.92	1	0.92	
.	.	isogroup14332	co-ortholog	At4G18550	g14332000C	91.73	0	774	g14332000C	AT4G18550	91.73	0	778	1357	2	0.95	2	0.95	
DAD1-like Acylhydrolase	At2g44810	isogroup19634	RBH	AT2G44810	r19634000C	95.34	5.00E-180	628	r19634000C	AT2G44810	95.34	2.00E-178	621	1159	1	1.00	1	1.00	
DAD1-like Acylhydrolase	At1g06250	isogroup11478	RBH	At1G06250	r11478000C	87.94	0	748	r11478000C	AT1G06250	88.65	0	771	1407	22	0.98	3	0.95	
DAD1-like Acylhydrolase	At1g05800	isogroup18429	RBH	At1G05800	g18429000C	90.09	8.00E-112	402	g18429000C	AT1G05800	90.09	1.00E-108	389	764	1	1.00	1	1.00	
DAD1-like Acylhydrolase	At2g30550	isogroup08540	RBH	At2G30550	g08540000C	88.51	0	699	g08540000C	AT2G30550	88.75	0	718	1215	6	0.89	2	0.89	
.	.	GDENH3V02GRJWR	co-ortholog	At1G30370	GDENH3V02	43.23	6.00E-28	123	GDENH3V02	AT2G31690	97.3	4.00E-79	289	454	na	na	na	na	
.	.	isogroup00001	co-ortholog	At1G30370	g00001c000C	29.73	9.00E-08	56.6	g00001c000C	AT3G14360	92.07	0	688	1456	1	0.87	1	0.87	
.	.	isogroup08120	co-ortholog	At1G30370	g08120000C	35.75	6.00E-62	236	r08120000C	AT2G31100	91.85	0	761	1270	2	0.91	2	0.91	
.	.	isogroup08463	co-ortholog	At1G30370	g08463000C	34.31	5.00E-10	63.9	r08463000C	AT5G18640	93.35	0	669	1460	71	0.75	2	0.40	
.	.	isogroup09480	co-ortholog	At1G30370	r09480000C	31.72	1.00E-09	62	r09480000C	AT5G18630	90	2.00E-178	389	1328	13	0.76	4	0.70	
.	.	isogroup08540	co-ortholog	At1G30370	g08540000C	44.65	4.00E-76	283	r08540000C	AT2G30550	88.75	0	718	1215	6	0.89	2	0.89	
.	.	isogroup09385	co-ortholog	At1G30370	r09385000C	40	1.00E-51	202	r09385000C	AT4G18550	92.6	4.00E-170	594	2201	1	0.92	1	0.92	
.	.	isogroup11478	co-ortholog	At1G30370	g11478000C	35.07	9.00E-68	256	g11478000C	AT1G06250	88.65	0	771	1407	22	0.98	3	0.95	
.	.	isogroup13234	co-ortholog	At1G30370	g13234000C	46.55	4.00E-75	280	g13234000C	AT1G06800	93.23	1.00E-176	615	977	1	1.00	1	1.00	
.	.	isogroup14332	co-ortholog	At1G30370	g14332000C	37.16	7.00E-66	249	g14332000C	AT4G18550	91.73	0	778	1357	2	0.95	2	0.95	
DAD1-like Acylhydrolase	isogroup14962	isogroup14962	co-ortholog	At1G30370	r14962000C	29.05	6.00E-07	53.9	r14962000C	AT3G14360	92.69	3.00E-122	433	676	1	1.00	1	1.00	
.	.	isogroup18429	co-ortholog	At1G30370	r18429000C	60	1.00E-29	287	r18429000C	AT4G16820	88.89	6.00E-78	286	534	1	1.00	1	1.00	
DAD1-like Acylhydrolase	isogroup18429	isogroup18429	co-ortholog	At1G30370	g18429000C	38.79	2.00E-23	108	g18429000C	AT1G05800	90.09	1.00E-108	389	764	1	1.00	1	1.00	
.	.	isogroup19634	co-ortholog	At1G30370	r19634000C	37.24	1.00E-55	215	r19634000C	AT2G44810	95.34	2.00E-178	621	1159	1	1.00	1	1.00	
DAD1-like Acylhydrolase	At2g31100	isogroup08120	RBH	AT2G31100	r08120000C	91.85	0	746	r08120000C	AT2G31100	91.85	0	761	1270	2	0.91	2	0.91	
DAD1-like Acylhydrolase	At2g31690	GDENH3V02GRJWR	RBH	AT2G31690	GDENH3V02	97.3	4.00E-81	300	GDENH3V02	AT2G31690	97.3	4.00E-79	289	454	na	na	na	na	
.	.	isogroup15643	RBH	AT3G22400	g15643000C	60.41	2.00E-59	229	g15643000C	AT3G22400	57.28	1.00E-60	288	568	1	0.43	1	0.43	
Cytosolic Lipoygenase	At3g22400	isogroup15713	RBH*	AT3G22400	r15713000C	94.5	5.00E-87	216	r15713000C	AT3G22400	94.5	4.00E-86	212	557	1	1.00	1	1.00	
Cytosolic Lipoygenase	At1g55020	isogroup07744	RBH	At1G55020	r07744000C	96.73	0	1207	r07744000C	At1G55020	94.73	0	1281	2526	10	0.83	4	0.83	
Plastidial Lipoygenase	At3g45140	isogroup02899	RBH	At3G45140	g02899000C	79.66	0	1257	g02899000C	AT3G45140	79.66	0	1273	2292	6	0.92	3	0.92	
Plastidial Lipoygenase	At1g17420	GD75ULV02EQYV7	RBH	At1G17420	GD75ULV02E	96.43	1.00E-93	342	GD75ULV02E	At1G17420	96.43	2.00E-93	337	504	na	na	na	na	
Plastidial Lipoygenase	At1g72520	isogroup09938	RBH	At1G72520	g09938000C	89.38	7.00E-144	509	g09938000C	AT1G72520	89.38	7.00E-141	496						



Supplementary Table 1. Camelina lipid metabolism genes

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis Query	Subject	% identity	E-Value	bit-score	BLASTX Analysis Query	Subject	% identity	E-Value	bit-score	Isotig Length	Variant Analysis Maximum	Max Reads	Fraction	Minimum	Min Reads	Fraction		
a-Dioxygenase-Peroxidase (involved in fatty acid $\alpha$ -oxidation)	At3g01420	isogroup04252	RH	AT3G01420	g04252000C	90.45	0	1197	g04252000C	AT3G01420	90.45	0	1199	2009	30	0.82	1	0.28	1	0.28		
a-Dioxygenase-Peroxidase (involved in fatty acid $\alpha$ -oxidation)	At1g73680	isogroup07131	RH	AT1G73680	e07131000C	91.41	0	1221	e07131000C	AT1G73680	91.41	0	1216	2033	28	0.91	0.68	2	0.52	1	0.52	
NAD+ Oxidoreductase (involved in fatty acid $\alpha$ -oxidation)	At1g54100	isogroup08197	RH*	AT1G73680	e15659000C	87.82	1.00E-98	359	e15659000C	AT1G73680	87.82	5.00E-100	359	581	1	1.00	1.00	1	1.00	1	1.00	
PTEN-like Phosphoinositide 3-Phosphatase	At5g39400	isogroup03493	co-ortholog	AT5G39400	g03493000C	42.78	1.00E-40	165	g03493000C	AT3G19420	92.59	0	1128	2211	60	0.95	5	0.89	1	0.89	1	0.89
PTEN-like Phosphoinositide 3-Phosphatase	At3g50110	isogroup17752	RH	AT3G50110	g17752000C	91.32	2.00E-153	481	g17752000C	AT3G50110	91.32	3.00E-165	477	935	1	1.00	1.00	1	1.00	1	1.00	
Myotubularin-like Phosphoinositide 3-Phosphatase	At5g04540	isogroup18754	RH	AT5G04540	g18754000C	90.72	4.00E-153	540	g18754000C	AT5G04540	90.72	8.00E-155	542	874	1	1.00	1.00	1	1.00	1	1.00	
Myotubularin-like Phosphoinositide 3-Phosphatase	At3g10550	isogroup01434	RH	AT3G10550	g01434000C	93.6	0	729	g01434000C	AT3G10550	93.6	0	713	2012	2	0.60	1	0.54	1	0.54	1	0.54
Type II Phosphoinositide 5-Phosphatase	At1g65580	isogroup12684	RH	AT1G65580	g12684000C	94.13	0	973	g12684000C	AT1G65580	94.13	0	962	2266	4	0.94	3	0.91	3	0.91	3	0.91
Type II Phosphoinositide 5-Phosphatase	At2g43900	isogroup20781	RH*	AT1G65580	e20781000C	89.94	4.00E-155	547	e20781000C	AT1G65580	90.25	5.00E-162	566	1035	2	0.40	1	0.29	1	0.29	1	0.29
Type II Phosphoinositide 5-Phosphatase	At1g05630	isogroup12772	RH*	AT1G05630	g12772000C	71.03	4.00E-45	149	g12772000C	AT1G05630	74.11	4.00E-49	159	531	1	1.00	1.00	1	1.00	1	1.00	
Type II Phosphoinositide 5-Phosphatase	At2g31830	isogroup08730	RH	AT2G31830	g08730000C	93.96	0	531	g08730000C	AT2G31830	93.96	0	531	1120	1	1.00	1.00	1	1.00	1	1.00	
Sac domain-containing Phosphoinositide Phosphatase	At3g51460	isogroup02114	co-ortholog	AT3G51460	g02114000C	28.57	1.00E-41	169	g02114000C	AT3G14205	92.23	0	1497	2918	152	0.92	2	0.81	1	0.81	1	0.81
Sac domain-containing Phosphoinositide Phosphatase	At5g66020	isogroup06479	co-ortholog	AT5G66020	g06479000C	85.83	0	1075	g06479000C	AT3G51460	94.3	0	1154	2074	88	0.97	4	0.72	1	0.72	1	0.72
Sac domain-containing Phosphoinositide Phosphatase	At1g17340	isogroup19480	RH*	AT1G17340	g1948000C	90.96	8.00E-93	318	g1948000C	AT1G17340	91.52	1.00E-90	307	845	2	0.90	2	0.90	2	0.90	2	0.90
Sac domain-containing Phosphoinositide Phosphatase	At1g26220	isogroup05964	RH	AT1G26220	g05964000C	96.43	0	1186	g05964000C	AT1G26220	96.43	0	1131	1945	42	0.73	1	0.18	1	0.18	1	0.18
Sac domain-containing Phosphoinositide Phosphatase	At3g59770	isogroup17997	RH*	AT3G59770	e17997000C	90.63	0	726	e17997000C	AT3G59770	90.63	0	703	1569	2	1.00	2	1.00	2	1.00	2	1.00
Sac domain-containing Phosphoinositide Phosphatase	At3g14205	isogroup02114	RH	AT3G14205	g02114000C	92.6	0	1521	g02114000C	AT3G14205	92.36	0	1498	2918	268	0.92	2	0.74	1	0.74	1	0.74
Sac domain-containing Phosphoinositide Phosphatase	At3g43220	isogroup02129	RH	AT3G43220	g02129000C	90.62	3.00E-171	600	g02129000C	AT3G43220	90.62	3.00E-167	585	1680	5	0.98	3	0.91	3	0.91	3	0.91
Sac domain-containing Phosphoinositide Phosphatase	At3g51830	isogroup17597	RH	AT3G51830	g17597000C	89.88	0	955	g17597000C	AT3G51830	89.88	0	928	1588	5	1.00	3	0.93	3	0.93	3	0.93
Sac domain-containing Phosphoinositide Phosphatase	At5g20840	isogroup16973	co-ortholog	AT5G20840	g16973000C	62.14	2.00E-30	131	g16973000C	AT4G37070	84.47	8.00E-46	176	498	1	1.00	1.00	1	1.00	1	1.00	
Patatin-like Acyl-Hydrolase	At2g26560	isogroup00590	co-ortholog	AT2G26560	e00590000C	55.94	5.00E-115	412	e00590000C	AT4G37050	85.94	0	721	1498	3	0.90	1	0.63	1	0.63	1	0.63
Patatin-like Acyl-Hydrolase	At4g37050	isogroup00590	RH	AT4G37050	g00590000C	89.12	0	733	g00590000C	AT4G37050	89.12	0	754	1498	47	0.85	1	0.35	1	0.35	1	0.35
Patatin-like Acyl-Hydrolase	At4g37060	isogroup15500	co-ortholog	AT4G37060	g15500000C	78.49	7.00E-151	531	g15500000C	AT4G37070	92	1.00E-173	605	1132	2	0.93	2	0.93	2	0.93	2	0.93
Patatin-like Acyl-Hydrolase	At4g37070	isogroup16973	co-ortholog	AT4G37070	g16973000C	59.35	6.00E-33	139	g16973000C	AT4G37070	84.47	8.00E-46	176	498	1	1.00	1.00	1	1.00	1	1.00	
Patatin-like Acyl-Hydrolase	At5g43590	isogroup16973	co-ortholog	AT5G43590	g16973000C	73.2	5.00E-34	143	g16973000C	AT4G37070	84.47	8.00E-46	176	498	1	1.00	1.00	1	1.00	1	1.00	
Patatin-like Acyl-Hydrolase	At3g63200	isogroup19739	RH	AT3G63200	g19739000C	88.4	4.00E-126	449	g19739000C	AT3G63200	88.4	1.00E-123	439	776	1	1.00	1.00	1	1.00	1	1.00	
Patatin-like Acyl-Hydrolase	At2g39220	isogroup03971	RH	AT2G39220	g03971000C	92.12	0	803	g03971000C	AT2G39220	92.34	0	791	1506	4	1.00	2	1.00	2	1.00	2	1.00
Patatin-like Acyl-Hydrolase	At3g49590	isogroup06881	RH	AT3G49590	g06881000C	84.95	0	773	g06881000C	AT3G49590	85.16	0	720	1583	3	0.77	3	0.77	3	0.77	3	0.77
Patatin-like Acyl-Hydrolase	At4g29800	isogroup20222	RH	AT4G29800	e20222000C	34.25	3.00E-28	124	e20222000C	AT4G29800	85.4	1.00E-116	415	648	1	1.00	1.00	1	1.00	1	1.00	
Patatin-like Acyl-Hydrolase	At5g04040	isogroup19739	co-ortholog	AT5G04040	g19739000C	31.37	8.00E-28	122	g19739000C	AT3G49590	87.8	0	706	1583	1	0.73	1	0.73	1	0.73	1	0.73
Patatin-like Acyl-Hydrolase	At3g71400	isogroup16363	RH*	AT3G71400	g16363000C	97.48	3.00E-127	241	g16363000C	AT3G71400	75.58	1.00E-127	242	915	2	1.00	2	1.00	2	1.00	2	1.00
Long Chain Base / Ceramide Kinase	At5g23450	isogroup00014	RH	AT5G23450	g00014000C	93.21	0	1450	g00014000C	AT5G23450	93.21	0	1467	2769	56	0.95	4	0.95	4	0.95	4	0.95
Long Chain Base / Ceramide Kinase	At4g21540	isogroup00014	RH	AT4G21540	g00014000C	83.33	2.00E-166	178	g00014000C	AT4G21540	69.23	6.00E-45	176	506	na	na	na	na	na	na	na	na
Long Chain Base 1-Phosphate Phosphatase	At1g27980	isogroup02867	RH	AT1G27980	g02867000C	95.49	0	967	g02867000C	AT1G27980	95.69	0	935	1645	16	0.57	1	0.23	1	0.23	1	0.23
Long Chain Base 1-Phosphate Phosphatase	At3g58490	isogroup17752	RH	AT3G58490	e05849000C	88.68	0	686	e05849000C	AT3G58490	89.01	0	495	648	4	0.78	2	0.78	2	0.78	2	0.78
Long Chain Base 1-Phosphate Phosphatase	At1g19640	isogroup17483	RH*	AT1G19640	e17483000C	85.55	1.00E-116	413	e17483000C	AT1G19640	86.72	3.00E-126	444	1009	1	1.00	1.00	1	1.00	1	1.00	
Jasmonic Acid Carboxyl Methyltransferase	At1g19640	isogroup17483	RH*	AT1G19640	e17483000C	87.8	3.00E-57	220	e17483000C	AT1G19640	87.8	9.00E-57	215	503	1	1.00	1.00	1	1.00	1	1.00	
Phospholipase A2 Activating Protein	At3g18860	isogroup10364	RH	AT3G18860	g10364000C	93.85	0	644	g10364000C	AT3G18860	93.85	0	632	2131	92	1.00	0.6	0.96	1	0.96	1	0.96
Ketoacyl-CoA Synthase (KCS)	At4g34520	isogroup03253	RH	AT4G34520	g03253000C	90.24	0	850	g03253000C	AT4G34520	89.63	0	820	1623	178	0.94	2	0.75	2	0.75	2	0.75
Ketoacyl-CoA Synthase (KCS)	At2g26250	isogroup01300	RH*	AT2G26250	g01300000C	98.26	8.00E-74	244	g01300000C	AT2G26250	99.12	7.00E-75	236	509	na	na	na	na	na	na	na	na
Ketoacyl-CoA Synthase (KCS)	At2g26250	isogroup19309	RH	AT2G26250	g19309000C	98.49	0	949	g19309000C	AT2G26250	98.49	0	910	1727	279	0.98	2	0.67	2	0.67	2	0.67
Ketoacyl-CoA Synthase (KCS)	At1g68530	isogroup19309	RH	AT1G68530	g19309000C	97.25	0	927	g19309000C	AT1G68530	97.87	0	927	1708	14	0.97	1	0.31	1	0.31	1	0.31

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship Arabidopsis	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
Ketoacyl-CoA Synthase (KCS)	At1g25450	isogroup08081	RBH	AT1G25450	g08081000C	94.27	0	897	g08081000C	AT1G25450	94.27	0	866	1399	5	0.88	4	0.88
Ketoacyl-CoA Synthase (KCS)	At1g11130	isogroup0265	RBH	AT1G11130	e12505000C	96.32	0	780	e12505000C	AT1G01120	96.02	0	760	1500	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At2g16280	isogroup05018	RBH	AT2G16280	g05018000C	97.53	0	734	g05018000C	AT2G16280	97.53	0	707	1638	16	0.80	1	0.32
Ketoacyl-CoA Synthase (KCS)	At2g26640	isogroup20829	RBH	AT2G26640	g20829000C	96.73	0	692	g20829000C	AT2G26640	96.73	0	966	1750	71	0.98	2	0.81
Ketoacyl-CoA Synthase (KCS)	At4g34510	isogroup09191	RBH	AT4G34510	g09191000C	89.17	0	848	g09191000C	AT4G34510	89.6	0	837	1521	4	0.96	4	0.96
Ketoacyl-CoA Synthase (KCS)	At4g35160	isogroup21241	RBH	AT4G35160	e21241000C	83.44	2.00E-162	521	e21241000C	AT3G52160	83.44	1.00E-160	521	1174	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At1g19440	isogroup04988	RBH	AT1G19440	g04988000C	97.72	0	986	g04988000C	AT1G19440	97.03	0	984	1525	13	0.87	4	0.75
Ketoacyl-CoA Synthase (KCS)	At4g24250	GDENH3V018RGO	RBH*	AT4G34250	g04988000C	96.3	2.00E-38	158	GDENH3V018RGO	AT4G34250	96.3	1.00E-38	154	247	na	na	na	na
.	.	isogroup20394	RBH	AT4G34250	g20394000C	93.09	3.00E-110	370	g20394000C	AT4G34250	93.09	6.00E-107	356	622	1	1.00	1	1.00
.	.	isogroup21996	RBH*	AT4G34250	e21996000C	81.93	8.00E-77	286	e21996000C	AT4G34250	81.93	9.00E-75	275	499	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At5g04530	isogroup17396	RBH	AT5G04530	g17396000C	94.5	0	791	g17396000C	AT5G04530	94.5	0	766	1201	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At1g07720	isogroup20099	RBH	AT1G07720	g20099000C	92.95	3.00E-133	473	g20099000C	AT1G07720	92.49	3.00E-135	477	782	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At5g43760	isogroup19972	RBH	AT5G43760	g19972000C	97.95	0	910	g19972000C	AT5G43760	97.95	0	962	1529	8	0.93	1	0.46
Ketoacyl-CoA Synthase (KCS)	At1g04220	isogroup04140	RBH	AT1G04220	r04140000C	94.69	0	799	r04140000C	AT1G04220	94.69	0	788	1532	2	0.50	1	0.42
.	.	GDENH3V01E05A	co-ortholog	AT2G64720	g04140000C	43.54	2.00E-33	141	GDENH3V01E05A	AT5G49070	90.07	7.00E-74	272	481	na	na	na	na
.	.	isogroup1300	co-ortholog	AT2G64720	g01300000C	45.78	1.00E-127	351	g01300000C	AT2G62520	97.85	0	904	1727	303	0.97	11	0.90
.	.	isogroup03253	co-ortholog	AT2G64720	g03253000C	52.26	8.00E-134	475	g03253000C	AT4G34520	89.85	0	820	1623	334	0.92	2	0.53
.	.	isogroup04140	co-ortholog	AT2G64720	g04140000C	60.4	7.00E-144	499	g04140000C	AT1G04220	94.69	0	788	1532	2	0.50	1	0.42
.	.	isogroup04988	co-ortholog	AT2G64720	r04988000C	59.16	5.00E-146	515	r04988000C	AT1G19440	97.03	0	984	1525	13	0.87	4	0.75
.	.	isogroup05018	co-ortholog	AT2G64720	g05018000C	52.08	2.00E-140	316	g05018000C	AT2G16280	97.53	0	707	1638	16	0.80	1	0.32
.	.	isogroup08081	co-ortholog	AT2G64720	g08081000C	55.94	4.00E-132	469	g08081000C	AT1G25450	94.05	0	865	1399	5	0.88	4	0.88
.	.	isogroup09191	co-ortholog	AT2G64720	g09191000C	56.14	1.00E-140	497	g09191000C	AT4G34510	89.6	0	837	1521	4	0.96	4	0.96
.	.	isogroup12505	co-ortholog	AT2G64720	e12505000C	60.87	2.00E-125	396	e12505000C	AT1G01120	96.02	0	760	1500	1	1.00	1	1.00
.	.	isogroup17396	co-ortholog	AT2G64720	e17396000C	42.82	4.00E-89	239	e17396000C	AT5G04530	94.5	0	766	1201	1	1.00	1	1.00
.	.	isogroup17435	co-ortholog	AT2G64720	e17435000C	41.69	2.00E-89	264	e17435000C	AT1G17160	91.82	0	593	1240	8	0.60	1	0.26
.	.	isogroup19309	co-ortholog	AT2G64720	g19309000C	55.07	6.00E-143	505	g19309000C	AT1G68530	97.87	0	927	1708	14	0.97	1	0.31
.	.	isogroup19972	co-ortholog	AT2G64720	r19972000C	57.11	7.00E-139	491	r19972000C	AT5G43760	97.95	0	962	1529	8	0.93	1	0.46
.	.	isogroup20099	co-ortholog	AT2G64720	g20099000C	34.76	7.00E-43	172	g20099000C	AT1G07720	92.49	3.00E-135	477	782	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At2g46720	isogroup20394	co-ortholog	AT2G64720	g20394000C	63.3	2.00E-74	258	g20394000C	AT4G34250	93.09	6.00E-107	356	622	1	1.00	1	1.00
.	.	isogroup20829	co-ortholog	AT2G64720	g20829000C	57.42	1.00E-156	551	g20829000C	AT2G26640	96.73	0	966	1750	71	0.98	2	0.81
.	.	isogroup21241	co-ortholog	AT2G64720	e21241000C	34	2.00E-61	239	e21241000C	AT3G52160	83.44	1.00E-160	521	1174	1	1.00	1	1.00
.	.	isogroup21996	co-ortholog	AT2G64720	e21996000C	35	4.00E-09	60.8	e21996000C	AT4G34250	81.93	9.00E-75	275	499	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At1g71160	isogroup17435	RBH	AT1G71160	g17435000C	91.82	0	620	g17435000C	AT1G71160	91.82	0	593	1240	8	0.60	1	0.26
Ketoacyl-CoA Synthase (KCS)	At5g49070	GD75ULV02CNTU	RBH	AT5G49070	GD75ULV02E	90.97	6.00E-79	293	GD75ULV02E	AT5G49070	90.97	2.00E-76	280	492	na	na	na	na
Ketoacyl-CoA Synthase (KCS)	At2g28630	GD75ULV01AT3A9	RBH	AT2G28630	GD75ULV01J	70.92	3.00E-55	181	GD75ULV01J	AT2G28630	70.92	4.00E-62	180	532	na	na	na	na
.	.	GDENH3V01E05A	co-ortholog	AT2G15090	g04140000C	44.16	7.00E-37	153	GDENH3V01E05A	AT5G49070	90.07	7.00E-74	272	481	na	na	na	na
.	.	isogroup1300	co-ortholog	AT2G15090	g01300000C	44.85	2.00E-126	342	g01300000C	AT2G62520	98.49	0	910	1727	356	0.98	2	0.62
.	.	isogroup03253	co-ortholog	AT2G15090	g03253000C	62.8	7.00E-169	598	g03253000C	AT4G34520	89.85	0	820	1623	178	0.94	2	0.75
.	.	isogroup04140	co-ortholog	AT2G15090	g04140000C	64.32	1.00E-141	479	g04140000C	AT1G04220	94.69	0	788	1532	2	0.50	1	0.42
.	.	isogroup04988	co-ortholog	AT2G15090	r04988000C	63.56	1.00E-173	607	r04988000C	AT1G19440	97.03	0	984	1525	13	0.87	4	0.75
.	.	isogroup05018	co-ortholog	AT2G15090	g05018000C	56.13	5.00E-173	377	g05018000C	AT2G16280	97.53	0	707	1638	16	0.80	1	0.32
.	.	isogroup08081	co-ortholog	AT2G15090	g08081000C	53.17	4.00E-138	489	g08081000C	AT1G25450	94.27	0	866	1399	5	0.88	4	0.88
.	.	isogroup09191	co-ortholog	AT2G15090	g09191000C	64.35	4.00E-164	566	g09191000C	AT4G34510	89.6	0	837	1521	4	0.96	4	0.96
.	.	isogroup12505	co-ortholog	AT2G15090	e12505000C	47.62	2.00E-110	347	e12505000C	AT1G01120	96.02	0	760	1500	1	1.00	1	1.00
.	.	isogroup17396	co-ortholog	AT2G15090	e17396000C	45.55	7.00E-87	231	e17396000C	AT5G04530	94.5	0	766	1201	1	1.00	1	1.00
.	.	isogroup17435	co-ortholog	AT2G15090	e17435000C	42.95	3.00E-93	271	e17435000C	AT1G17160	91.82	0	593	1240	8	0.60	1	0.26
.	.	isogroup19309	co-ortholog	AT2G15090	g19309000C	54.03	2.00E-153	540	g19309000C	AT1G68530	97.87	0	927	1708	14	0.97	1	0.31
.	.	isogroup19972	co-ortholog	AT2G15090	r19972000C	60.64	1.00E-137	488	r19972000C	AT5G43760	97.95	0	962	1529	8	0.93	1	0.46
.	.	isogroup20099	co-ortholog	AT2G15090	g20099000C	37.15	2.00E-40	164	g20099000C	AT1G07720	92.49	3.00E-135	477	782	1	1.00	1	1.00
Ketoacyl-CoA Synthase (KCS)	At2g15090	isogroup20394	co-ortholog	AT2G15090	g20394000C	82.98	2.00E-99	338	g20394000C	AT4G34250	93.09	6.00E-107	356	622	1	1.00	1	1.00
.	.	isogroup20829	co-ortholog	AT2G15090	g20829000C	56.38	1.00E-150	531	g20829000C	AT2G26640	96.73	0	966	1750	71	0.98	2	0.81
.	.	isogroup21241	co-ortholog	AT2G15090	e21241000C	36.78	6.00E-56	216	e21241000C	AT3G52160	83.44	1.00E-160	521	1174	1	1.00	1	1.00
.	.	isogroup21996	co-ortholog	AT2G15090	e21996000C	60.65	3.00E-49	194	e21996000C	AT4G34250	81.93	9.00E-75	275	499	1	1.00	1	1.00
Ketoacyl-CoA Reductase	At1g67730	isogroup10966	RBH*	AT1G67730	g10966000C	95.24	2.00E-180	629	g10966000C	AT1G67730	95.24	2.00E-174	608	1162	13	0.83	2	0.82
.	.	GD75ULV03GVNHX	RBH*	AT1G24470	GD75ULV03K	70	5.00E-34	142	GD75ULV03K	AT1G24470	70	1.00E-34	140	290	na	na	na	na
Ketoacyl-CoA Reductase	At1g24470	isogroup04564	RBH	AT1G24470	g04564000C	88	3.00E-156	308	g04564000C	AT1G24470	88	2.00E-154	304	1131	1	0.26	1	0.26
Enoyl-CoA Reductase	At3g55360	isogroup00784	RBH	AT3G55360	r00784000C	97.74	0	630	r00784000C	AT3G55360	97.74	0						

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis		BLASTX Analysis				Isotig Length	Variant Analysis							
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query Subject		% identity	E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction	
.	.	isogroup19850	co-ortholog	AT1G51420	g19850R00C	70.49	2.00E-31	84.7	g19850R00C	ATG565330	69.77	3.00E-54	125	527	1	0.44	1	0.44
.	.	isogroup10721	co-ortholog	AT1G51420	e11721I000C	44.13	4.00E-73	273	e11721I000C	ATG565370	81.87	3.00E-162	567	1078	1	0.82	1	0.82
Wax Synthase	.	isogroup20180	co-ortholog	AT1G51420	e20180R00C	43.97	5.00E-71	266	e20180R00C	ATG565370	83.93	1.00E-165	578	1044	1	1.00	1	1.00
.	.	isogroup09799	co-ortholog	AT1G51420	g09799R00C	52.86	5.00E-39	129	g09799R00C	ATG565340	50.53	2.00E-63	239	1562	4	0.80	2	0.80
.	.	isogroup17714	co-ortholog	AT1G51420	g17714R00C	36.59	8.00E-28	122	g17714R00C	ATG3651970	78.82	2.00E-93	308	683	1	0.83	1	0.83
.	.	isogroup21860	co-ortholog	AT1G51420	e21860R00C	47.13	7.00E-18	64.3	e21860R00C	ATG565360	85.25	3.00E-51	115	427	1	1.00	1	1.00
Wax Synthase	.	isogroup55320	co-ortholog	AT1G55320	GD75ULV03C	57.34	2.00E-37	154	GD75ULV03C	ATG565340	89.51	5.00E-71	262	436	na	na	na	na
.	.	isogroup19850	co-ortholog	AT1G55320	g19850R00C	45.35	1.00E-30	75.5	g19850R00C	ATG565350	69.77	3.00E-54	125	527	1	0.44	1	0.44
.	.	isogroup10721	co-ortholog	AT1G55320	e10721I000C	46.8	2.00E-79	293	e10721I000C	ATG565370	81.89	3.00E-162	567	1078	1	0.82	1	0.82
.	.	isogroup20180	co-ortholog	AT1G55320	e20180R00C	47.08	2.00E-77	286	e20180R00C	ATG565370	83.93	1.00E-165	578	1044	1	1.00	1	1.00
.	.	isogroup09799	co-ortholog	AT1G55320	g09799R00C	55.45	3.00E-65	146	g09799R00C	ATG565340	50.53	2.00E-63	239	1562	4	0.80	2	0.80
.	.	isogroup17714	co-ortholog	AT1G55320	g17714R00C	34.48	2.00E-25	107	g17714R00C	ATG3651970	78.82	2.00E-93	308	683	1	0.83	1	0.83
.	.	isogroup21860	co-ortholog	AT1G55320	e21860R00C	45	1.00E-23	80.9	e21860R00C	ATG565360	85.25	3.00E-51	115	427	1	1.00	1	1.00
Wax Synthase	.	isogroup34520	co-ortholog	AT1G34520	GD75ULV03C	62.94	9.00E-42	168	GD75ULV03C	ATG565340	89.51	5.00E-71	262	436	na	na	na	na
.	.	isogroup19850	co-ortholog	AT1G34520	g19850R00C	48.84	1.00E-31	84.7	g19850R00C	ATG565350	69.77	3.00E-54	125	527	1	0.44	1	0.44
.	.	isogroup10721	co-ortholog	AT1G34520	e10721I000C	50.44	2.00E-85	313	e10721I000C	ATG565370	81.89	3.00E-162	567	1078	1	0.82	1	0.82
.	.	isogroup20180	co-ortholog	AT1G34520	e20180R00C	49.85	9.00E-83	305	e20180R00C	ATG565370	83.93	1.00E-165	578	1044	1	1.00	1	1.00
.	.	isogroup09799	co-ortholog	AT1G34520	g09799R00C	40.8	1.00E-44	178	g09799R00C	ATG565340	50.53	2.00E-63	239	1562	4	0.80	2	0.80
.	.	isogroup17714	co-ortholog	AT1G34520	e17714R00C	41.38	3.00E-37	142	e17714R00C	ATG3651970	78.82	2.00E-93	308	683	1	0.83	1	0.83
.	.	isogroup21860	co-ortholog	AT1G34520	e21860R00C	60	3.00E-30	69.3	e21860R00C	ATG565360	85.25	3.00E-51	115	427	1	1.00	1	1.00
Aldehyde Decarboxylase	.	isogroup18251	RH	AT1G02205	g18251I000C	89.45	5.00E-131	466	g18251I000C	AT1G02205	89.45	2.00E-128	454	756	1	1.00	1	1.00
.	.	GDENH3V02HWI3G	RH*	AT1G02205	GDENH3V02I	92.74	1.00E-62	239	GDENH3V02I	ATG5657800	92.74	1.00E-61	231	404	na	na	na	na
Aldehyde Decarboxylase	.	isogroup17375	RH*	AT1G02205	e17375R00C	92.98	3.00E-92	337	e17375R00C	ATG5657800	92.98	6.00E-96	345	516	1	1.00	1	1.00
.	.	isogroup1671	RH*	AT1G02205	e1671R00C	84.21	5.00E-32	114	e1671R00C	ATG5657800	84.21	3.00E-35	144	216	1	1.00	1	1.00
Aldehyde Decarboxylase	.	isogroup21900	RH	AT1G02190	GD75ULV02I	92.11	2.00E-59	220	GD75ULV02I	AT1G02190	92.11	1.00E-60	217	422	na	na	na	na
Aldehyde Decarboxylase	.	isogroup21900	co-ortholog	AT1G02190	GD75ULV02I	92.11	2.00E-59	220	GD75ULV02I	AT1G02190	92.11	1.00E-60	217	422	na	na	na	na
.	.	isogroup17375	co-ortholog	AT2G37700	e17375R00C	38.27	8.00E-27	120	e17375R00C	ATG567800	92.98	6.00E-96	345	516	1	1.00	1	1.00
.	.	isogroup18251	co-ortholog	AT2G37700	g18251I000C	54.8	3.00E-71	267	g18251I000C	AT1G02205	89.45	2.00E-128	454	756	1	1.00	1	1.00
CER2 Protein	.	isogroup24510	RH	AT1G02451	GD75ULV02I	64.71	7.00E-16	83.2	GD75ULV02I	AT1G02451	64.71	2.00E-17	83.6	230	na	na	na	na
CER2 Protein	.	isogroup13840	RH	AT1G01384	g13840R00C	88.58	0	791	g13840R00C	AT1G01384	88.58	0	776	1485	4	0.96	4	0.96
CER2 Protein	.	isogroup23840	RH	AT1G02384	g23840R00C	81.1	5.00E-123	439	g23840R00C	AT1G02384	81.2	2.00E-121	431	752	1	1.00	1	1.00
.	.	GDENH3V02G28GL	RH*	AT1G02310	GDENH3V02I	81.69	5.00E-25	115	GDENH3V02I	ATG5602310	81.69	2.00E-27	116	215	na	na	na	na
.	.	isogroup09899	RH	AT1G02310	g09899R00C	85.78	0	725	g09899R00C	AT1G02310	85.78	0	731	1471	6	0.94	2	0.94
.	.	isogroup15740	RH*	AT1G02310	g15740R00C	84	2.00E-102	360	g15740R00C	AT1G02310	84.24	2.00E-104	365	666	1	1.00	1	1.00
CER3 Protein	.	isogroup15968	RH*	AT1G02310	g15968R00C	93.06	1.00E-180	632	g15968R00C	AT1G02310	93.06	2.00E-180	628	1060	1	0.85	1	0.85
.	.	isogroup18101	RH*	AT1G02310	g18101I000C	85.23	2.00E-107	390	g18101I000C	AT1G02310	85.23	1.00E-114	409	1102	1	1.00	1	1.00
.	.	isogroup18605	RH*	AT1G02310	g18605R00C	89.29	2.00E-87	323	g18605R00C	AT1G02310	89.29	2.00E-98	354	591	1	1.00	1	1.00
Fatty Acid w-Hydroxylase	.	isogroup1036558	RH*	AT1G01365	GD75ULV03C	97.55	2.00E-67	254	GD75ULV03C	AT1G01365	97.56	4.00E-67	250	464	na	na	na	na
Fatty Acid w-Hydroxylase	.	isogroup13159	RH	AT1G01315	g13159R00C	98.11	0	750	g13159R00C	AT1G01315	98.11	0	738	1168	4	0.96	2	0.96
Fatty Acid w-Hydroxylase	.	isogroup63450	RH*	AT1G01345	GD75ULV02I	83.75	5.00E-34	140	GD75ULV02I	AT1G01345	83.75	4.00E-35	140	244	na	na	na	na
Fatty Acid w-Hydroxylase	.	isogroup17445	RH	AT1G01345	g17445R00C	82.35	2.00E-118	424	g17445R00C	AT1G01345	87.6	1.00E-122	434	873	2	1.00	2	1.00
Fatty Acid w-Hydroxylase	.	isogroup101280	RH	AT1G01280	GD75ULV02I	94.33	4.00E-79	282	GD75ULV02I	AT1G01280	94.33	7.00E-77	282	553	na	na	na	na
Fatty Acid w-Hydroxylase	.	isogroup09970	RH	AT1G01280	g09970R00C	93.84	0	1021	g09970R00C	AT1G01280	93.84	0	1013	1938	48	0.97	3	0.96
.	.	isogroup18101	RH*	AT1G01365	GD75ULV03C	96.52	7.00E-73	228	GD75ULV03C	AT1G01365	96.52	1.00E-72	226	479	na	na	na	na
Fatty Acid w-Hydroxylase	.	isogroup00360	RH	AT1G01365	g00360R00C	93.96	0	1062	g00360R00C	AT1G01365	93.96	0	1046	2050	114	0.83	1	0.17
Fatty Acid w-Hydroxylase	.	isogroup163710	RH*	AT1G01637	GD75ULV01I	94.85	7.00E-75	268	GD75ULV01I	AT1G01637	94.85	6.00E-75	261	459	na	na	na	na
Fatty Acid w-Hydroxylase	.	isogroup12790	RH	AT1G01637	g12790R00C	95.11	1.00E-143	366	g12790R00C	AT1G01637	95.11	2.00E-142	360	835	1	1.00	1	1.00
Fatty Acid w-Hydroxylase	.	isogroup04681	RH	AT1G01637	g04681R00C	94.98	0	1055	g04681R00C	AT1G01637	94.98	0	1035	2474	17	0.95	3	0.91
.	.	isogroup09799	co-ortholog	AT1G01600	g09799R00C	28.82	7.00E-33	140	g09799R00C	AT1G01600	63.77	2.00E-123	439	1562	2	0.99	2	0.99
.	.	isogroup00001	co-ortholog	AT1G01600	g00001R00C	39	1.00E-85	315	g00001R00C	AT1G01600	90.89	0	896	1456	4	0.99	2	0.98
.	.	isogroup02819	co-ortholog	AT1G01600	e02819R00C	88.12	0	1001	e02819R00C	AT1G01600	93.96	0	1046	2050	114	0.83	1	0.17
.	.	isogroup04681	co-ortholog	AT1G01600	g04681R00C	76.88	0	865	g04681R00C	AT1G01600	94.98	0	1035	2474	17	0.95	3	0.91
.	.	isogroup04844	co-ortholog	AT1G01600	g04844R00C	23.58	2.00E-14	79	g04844R00C	AT1G01600	93.84	0	1013	1938	48	0.97	3	0.96
.	.	isogroup06283	co-ortholog	AT1G01600	g06283R00C	46.32	6.00E-88	323	g06283R00C	AT1G01600	79.08	0	687	1412	1	0.96	1	0.96
.	.	isogroup12790	co-ortholog	AT1G01600	g12790R00C	72.83	4.00E-108	291	g12790R00C	AT1G01600	95.11	2.00E-142	360	835	1	1.00	1	1.00
.	.	isogroup13159	co-ortholog	AT1G01600	e13159R00C	59.79	7.00E-126	449	e13159R00C	AT1G01600	98.11	0	738	1168	4	0.96	2	0.96
.	.	isogroup17445	co-ortholog	AT1G01600	g17445R00C	35.17	2.00E-31	135	g17445R00C	AT1G01600	87.6	1.00E-122	434	873	2	1.00	2	1.00
.	.	isogroup1805	co-ortholog	AT1G01600	g01805R00C	26.39	3.00E-11	68.2										

Supplementary Table 1. Camelina lipid metabolism genes

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship		TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis				
			Arabidopsis	Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity	E-Value		bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
.	.	isogroup05898	co-ortholog	AT1G01600	g05898r000c	21.89	1.00E-06	52.8	g05898r000c	AT4G19230	89.26	0	832	3081	3	0.84	2	0.84
.	.	isogroup06091	co-ortholog	AT1G01600	g06091r000c	28.73	4.00E-23	107	g06091r000c	AT5G52400	91.47	0	864	2183	26	0.90	7	0.89
.	.	isogroup06308	co-ortholog	AT1G01600	g06308r000c	23.86	6.00E-14	77.4	g06308r000c	AT3G26210	92.42	0	932	1628	5	0.99	3	0.99
.	.	isogroup06396	co-ortholog	AT1G01600	g06396r000c	25.65	1.00E-08	60.1	g06396r000c	AT3G50660	96.14	0	606	1608	61	0.96	4	0.70
.	.	isogroup07132	co-ortholog	AT1G01600	g07132r000c	25.24	1.00E-17	89.7	g07132r000c	AT1G75130	91.48	0	895	1622	3	0.90	2	0.90
.	.	isogroup07327	co-ortholog	AT1G01600	g07327r000c	37.41	1.00E-71	268	g07327r000c	AT4G39490	85.85	0	760	1521	7	1.00	2	1.00
.	.	isogroup07330	co-ortholog	AT1G01600	g07330r000c	28.57	8.00E-10	63.5	g07330r000c	AT1G16410	83.61	0	852	1544	25	0.88	2	0.83
.	.	isogroup07484	co-ortholog	AT1G01600	g07484r000c	26.06	3.00E-16	84.7	g07484r000c	AT4G37340	75.41	0	738	1517	1	0.78	1	0.78
.	.	isogroup08063	co-ortholog	AT1G01600	g08063r000c	24.67	3.00E-15	81.6	g08063r000c	AT5G25900	93.64	0	867	1385	36	0.97	3	0.75
.	.	isogroup08333	co-ortholog	AT1G01600	g08333r000c	36.53	1.00E-52	205	g08333r000c	AT2G23180	87.84	0	581	1353	2	0.71	2	0.71
.	.	isogroup08396	co-ortholog	AT1G01600	g08396r000c	45.58	1.00E-108	391	g08396r000c	AT5G23190	92.66	0	939	1926	34	0.99	1	0.53
.	.	isogroup08500	co-ortholog	AT1G01600	g08500r000c	36.88	3.00E-69	261	g08500r000c	AT3G26125	93.81	0	773	1451	4	0.73	1	0.43
.	.	isogroup08587	co-ortholog	AT1G01600	g08587r000c	23.83	2.00E-06	52	g08587r000c	AT5G05690	95.97	0	907	1695	97	0.91	1	0.22
.	.	isogroup09172	co-ortholog	AT1G01600	g09172r000c	41.31	1.00E-96	351	g09172r000c	AT1G69500	93.39	0	918	1596	18	0.80	1	0.19
.	.	isogroup09217	co-ortholog	AT1G01600	g09217r000c	23.76	6.00E-15	60.5	g09217r000c	AT5G10600	86.43	0	802	1375	4	0.76	1	0.31
.	.	isogroup09357	co-ortholog	AT1G01600	g09357r000c	24.38	2.00E-11	69.3	g09357r000c	AT5G52760	85.32	0	816	1676	4	0.97	2	0.97
.	.	isogroup10266	co-ortholog	AT1G01600	g10266r000c	23.88	9.00E-12	70.1	g10266r000c	AT3G26280	68.06	0	688	1713	2	0.64	1	0.28
.	.	isogroup10312	co-ortholog	AT1G01600	g10312r000c	22.37	2.00E-13	75.5	g10312r000c	AT2G46950	83.43	0	910	1672	6	0.92	3	0.91
.	.	isogroup10327	co-ortholog	AT1G01600	g10327r000c	22.22	3.00E-09	62	g10327r000c	AT4G12300	90.21	0	864	1622	10	0.89	1	0.30
.	.	isogroup10599	co-ortholog	AT1G01600	g10599r000c	22.07	1.00E-14	79.3	g10599r000c	AT2G46960	80.23	0	851	2302	6	0.70	5	0.70
.	.	isogroup11538	co-ortholog	AT1G01600	g11538r000c	26.07	1.00E-08	59.7	g11538r000c	AT3G30180	94.47	0	493	1663	68	0.97	5	0.88
.	.	isogroup11617	co-ortholog	AT1G01600	g11617r000c	22.74	2.00E-15	82.4	g11617r000c	AT1G13090	83.94	0	823	1620	1	0.96	1	0.96
.	.	isogroup13083	co-ortholog	AT1G01600	g13083r000c	27.44	3.00E-11	82.2	g13083r000c	AT4G12320	85.44	5.00E-77	282	477	1	1.00	1	1.00
.	.	isogroup14994	co-ortholog	AT1G01600	g14994r000c	26.67	2.00E-09	62.4	g14994r000c	AT4G37400	93.03	0	706	1168	1	1.00	1	1.00
.	.	isogroup15145	co-ortholog	AT1G01600	g15145r000c	21.21	2.00E-09	62.4	g15145r000c	AT5G04660	89.03	0	876	1537	1	1.00	1	1.00
.	.	isogroup15232	co-ortholog	AT1G01600	g15232r000c	27.4	5.00E-09	60.8	g15232r000c	AT1G64900	86.47	0	882	1546	1	0.78	1	0.78
.	.	isogroup15453	co-ortholog	AT1G01600	g15453r000c	24.52	1.00E-11	69.3	g15453r000c	AT2G12190	92.62	0	909	1501	1	1.00	1	1.00
.	.	isogroup15529	co-ortholog	AT1G01600	g15529r000c	42.45	2.00E-100	327	g15529r000c	AT3G56630	88.7	0	723	1617	1	1.00	1	1.00
.	.	isogroup15694	co-ortholog	AT1G01600	g15694r000c	25.82	1.00E-08	59.7	g15694r000c	AT1G13080	90.5	0	728	1211	4	0.58	1	0.46
.	.	isogroup16171	co-ortholog	AT1G01600	g16171r000c	24.4	5.00E-15	80.9	g16171r000c	AT4G37320	87.7	0	865	1585	1	1.00	1	1.00
.	.	isogroup16286	co-ortholog	AT1G01600	g16286r000c	23.28	2.00E-13	75.5	g16286r000c	AT1G13090	83.22	0	727	1351	1	0.98	1	0.98
.	.	isogroup16341	co-ortholog	AT1G01600	g16341r000c	20.32	5.00E-06	50.8	g16341r000c	AT5G04660	89.41	0	800	1353	1	1.00	1	1.00
.	.	isogroup16542	co-ortholog	AT1G01600	g16542r000c	34.98	5.00E-49	137	g16542r000c	AT1G24540	91.53	0	443	1141	1	1.00	1	1.00
.	.	isogroup16862	co-ortholog	AT1G01600	g16862r000c	26.87	3.00E-19	94.7	g16862r000c	AT4G13770	90.15	0	853	1511	8	1.00	2	0.88
.	.	isogroup17878	co-ortholog	AT1G01600	g17878r000c	28.15	3.00E-09	61.6	g17878r000c	AT2G46660	85.45	0	729	1292	1	0.67	1	0.67
.	.	isogroup18020	co-ortholog	AT1G01600	g18020r000c	29.41	7.00E-17	87	g18020r000c	AT3G48280	96.48	6.00E-149	355	857	1	1.00	1	1.00
.	.	isogroup18927	co-ortholog	AT1G01600	g18927r000c	24.93	8.00E-07	53.5	g18927r000c	AT4G37330	67.41	0	629	1355	1	1.00	1	1.00
.	.	isogroup20366	co-ortholog	AT1G01600	g20366r000c	31.09	3.00E-07	61.5	g20366r000c	AT4G37370	87.01	8.00E-86	312	544	1	1.00	1	1.00
.	.	isogroup22080	co-ortholog	AT1G01600	g22080r000c	20.55	2.00E-08	58.5	g22080r000c	AT5G04660	89.57	0	822	1404	1	1.00	1	1.00
ELO-like Elongase	At4g36830	isogroup09330	RH	AT4G36830	g09330r000c	92.31	3.00E-152	535	g09330r000c	AT4G36830	92.31	1.00E-155	545	1023	2	0.75	2	0.75
ELO-like Elongase	At1g75000	isogroup05517	RH	AT1G75000	g05517r000c	90.43	7.00E-140	494	g05517r000c	AT1G75000	90.43	2.00E-148	521	1077	4	0.70	2	0.70
Bifunctional Wax Ester Synthase / Diacylglycerol Acyltransferase	At5g53380	isogroup15035	RH	AT5G53380	g15035r000c	57.73	3.00E-63	241	g15035r000c	AT5G53380	57.99	2.00E-65	245	641	1	1.00	1	1.00
.	At2g38995	isogroup15035	co-ortholog	AT2G38995	g15035r000c	35.89	1.00E-31	135	g15035r000c	AT5G53380	57.99	2.00E-65	245	641	1	1.00	1	1.00
Bifunctional Wax Ester Synthase / Diacylglycerol Acyltransferase	At2g38995	GD75ULV02EACEN	co-ortholog	AT2G38995	GD75ULV02E	56.67	4.00E-43	173	GD75ULV02E	AT5G53390	88.96	3.00E-77	283	518	na	na	na	na
.	.	isogroup08603	co-ortholog	AT2G38995	g08603r000c	38.83	1.00E-30	149	g08603r000c	AT5G12420	74.63	5.00E-86	219	587	1	0.67	3	0.83
.	.	isogroup08603	co-ortholog	AT2G38995	g08603r000c	42.82	6.00E-93	399	g08603r000c	AT4G29410	85.26	0	788	1403	3	0.83	3	0.83
.	.	isogroup14505	co-ortholog	AT2G38995	g14505r000c	47.25	3.00E-17	87.8	g14505r000c	AT5G16350	77.32	1.00E-38	155	502	1	1.00	1	1.00
.	.	isogroup20795	co-ortholog	AT2G38995	g20795r000c	46.6	7.00E-46	182	g20795r000c	AT3G49190	83.64	1.00E-105	378	708	1	1.00	1	1.00
.	.	isogroup19325	co-ortholog	AT2G15050	g19325r000c	50.85	1.00E-23	105	g19325r000c	AT2G38540	69.75	4.00E-41	163	473	na	na	na	na
Lipid Transfer Protein type 1 (LTP1)	At2g15050	isogroup09354	co-ortholog	AT2G15050	g09354r000c	62.5	4.00E-34	140	g09354r000c	AT2G38540	87.29	4.00E-58	221	831	2	0.90	2	0.90
.	.	isogroup22170	co-ortholog	AT2G15050	g22170r000c	60	9.00E-34	139	g22170r000c	AT2G38540	87.29	8.00E-58	219	702	1	1.00	1	1.00
.	.	isogroup11166	co-ortholog	AT2G15050	g11166r000c	32.69	2.00E-06	48.5	g11166r000c	AT3G22600	85.88	1.00E-79	292	811	88	0.98	4	0.94
.	.	isogroup11712	co-ortholog	AT2G15050	g11712r000c	32.71	6.00E-11	63.9	g11712r000c	AT2G18370	93.97	1.00E-57	219	587	1	0.71	1	0.71
.	.	isogroup11844	co-ortholog	AT2G15050	g11844r000c	47.32	4.00E-20	94	g11844r000c	AT5G59310	92.86	7.00E-57	216	732	3	0.56	1	0.29
.	.	isogroup14566	co-ortholog	AT2G15050	g14566r000c	50.83	3.00E-24	108	g14566r000c	AT3G51600	94.07	2.00E-60	228	654	4	0.95	2	0.95
.	.	isogroup19325	co-ortholog	AT2G15050	g19325r000c	40.7	2.00E-11	65.1	g19325r000c	AT3G08770	71.17	1.00E-44	175	531	2	1.00	2	1.00
Lipid Transfer Protein type 1 (LTP1)	At2g18370	isogroup11712	RH	AT2G18370	g11712r000c	93.97	5.00E-57	216	g11712r000c	AT2G18370								

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
.	.	isogroup22170	co-ortholog	AT5G01870	e117120000	39.36	2.00E-14	75	e221700000	AT2G38540	87.29	8.00E-58	219	702	1	1.00	1	1.00
.	.	isogroup1171	co-ortholog	AT5G01870	e117120000	39.36	2.00E-14	75	e221700000	AT2G38540	87.29	8.00E-58	219	587	1	0.71	1	0.71
.	.	isogroup11844	co-ortholog	AT5G01870	g118440000	41.67	3.00E-18	87.8	g118440000	AT5G59310	92.86	7.00E-57	216	732	3	0.56	1	0.29
.	.	isogroup14566	co-ortholog	AT5G01870	g145660000	41.28	1.00E-17	86.3	g145660000	AT3G51600	94.07	2.00E-60	228	654	4	0.95	2	0.95
Lipid Transfer Protein type 1 (LTP1)	At5g01870	isogroup19325	co-ortholog	AT5G01870	g193250000	61.46	1.00E-30	129	g193250000	AT3G08770	71.17	1.00E-44	175	531	2	1.00	2	1.00
.	.	isogroup21927	co-ortholog	AT5G01870	e219270000	30.39	3.00E-06	48.1	e219270000	AT5G62065	90.83	4.00E-62	234	675	1	1.00	1	1.00
Lipid Transfer Protein type 1 (LTP1)	At5g59310	isogroup11844	RH	AT5G59310	g118440000	92.86	3.00E-54	207	g118440000	AT5G59310	92.86	5.00E-57	216	732	16	0.96	5	0.92
.	.	GDENH3V01CNXYR	co-ortholog	AT5G59320	GDENH3V01	45.69	8.00E-22	99.8	GDENH3V01	AT2G38540	69.75	4.00E-41	163	473	na	na	na	na
.	.	isogroup9354	co-ortholog	AT5G59320	g093540000	53.45	1.00E-29	125	g093540000	AT2G38540	87.29	1.00E-57	219	831	3	0.95	3	0.95
.	.	isogroup22170	co-ortholog	AT5G59320	e221700000	53.45	8.00E-30	126	e221700000	AT2G38540	87.29	8.00E-58	219	702	1	1.00	1	1.00
.	.	isogroup11712	co-ortholog	AT5G59320	e117120000	39.36	7.00E-13	70.1	e117120000	AT2G18370	93.97	1.00E-57	219	587	1	0.71	1	0.71
Lipid Transfer Protein type 1 (LTP1)	At5g59320	isogroup11844	co-ortholog	AT5G59320	g118440000	82.61	6.00E-48	186	g118440000	AT5G59310	92.86	5.00E-57	216	732	16	0.96	5	0.92
.	.	isogroup14566	co-ortholog	AT5G59320	g145660000	57.89	6.00E-27	117	g145660000	AT3G51600	94.07	2.00E-60	228	654	4	0.95	2	0.95
.	.	isogroup19325	co-ortholog	AT5G59320	e193250000	49.48	3.00E-20	94.7	e193250000	AT3G08770	71.17	1.00E-44	175	531	2	1.00	2	1.00
Lipid Transfer Protein type 1 (LTP1)	At2g15325	isogroup11844	co-ortholog	AT2G15325	g118440000	30.58	5.00E-07	50.8	g118440000	AT5G59310	92.86	7.00E-57	216	732	3	0.56	1	0.29
Lipid Transfer Protein type 2 (LTP2)	At1g56850	isogroup18354	RH	AT1G56850	e183540000	89.22	2.00E-49	184	e183540000	AT1G66850	89.22	2.00E-48	188	605	1	1.00	1	1.00
Lipid Transfer Protein type 2 (LTP2)	At1g48750	isogroup01492	RH	AT1G48750	g014920000	78.35	4.00E-32	134	g014920000	AT1G48750	78.35	3.00E-39	158	1735	1	0.93	1	0.93
Lipid Transfer Protein type 2 (LTP2)	At3g18280	GDENH3V02FX18M	RH	AT3G18280	GDENH3V02	92.86	7.00E-32	133	GDENH3V02	AT3G18280	86.52	1.00E-40	161	418	na	na	na	na
Lipid Transfer Protein type 2 (LTP2)	At5g38160	isogroup22272	RH	AT5G38160	e222720000	62.38	6.00E-31	130	e222720000	AT5G38160	62.38	4.00E-32	133	478	1	1.00	1	1.00
.	.	isogroup00027	co-ortholog	AT5G38180	g000270000	43.27	2.00E-16	82.4	g000270000	AT1G19835	92.07	0	1746	5100	0	0	0	0
.	.	isogroup01492	co-ortholog	AT5G38180	g014920000	42.86	7.00E-11	63.5	g014920000	AT1G48750	78.35	3.00E-39	158	1735	1	0.93	1	0.93
.	.	isogroup18354	co-ortholog	AT5G38180	g183540000	37.25	4.00E-15	77.4	g183540000	AT1G66850	89.22	2.00E-48	188	605	1	1.00	1	1.00
Lipid Transfer Protein type 2 (LTP2)	At5g38180	isogroup22272	co-ortholog	AT5G38180	e222720000	45.63	7.00E-18	87	e222720000	AT5G38160	62.38	4.00E-32	133	478	1	1.00	1	1.00
.	.	GDENH3V01DYSOG	co-ortholog	AT5G38180	GDENH3V01	34.83	1.00E-13	72.8	GDENH3V01	AT4G12825	63.74	1.00E-27	117	401	na	na	na	na
Lipid Transfer Protein type 2 (LTP2)	At5g38170	isogroup00027	co-ortholog	AT5G38170	g000270000	60.58	2.00E-30	128	g000270000	AT1G19835	92.07	0	1746	5100	0	0	0	0
.	.	isogroup01492	co-ortholog	AT5G38170	g014920000	44.12	2.00E-14	75.1	g014920000	AT1G48750	78.35	2.00E-39	158	1735	1	0.88	1	0.88
.	.	isogroup18354	co-ortholog	AT5G38170	g183540000	42.72	3.00E-18	88.2	g183540000	AT1G66850	89.22	2.00E-48	188	605	1	1.00	1	1.00
.	.	isogroup22272	co-ortholog	AT5G38170	e222720000	57.43	1.00E-25	112	e222720000	AT5G38160	62.38	4.00E-32	133	478	1	1.00	1	1.00
.	.	GDENH3V02GUZ09	co-ortholog	AT5G38170	GDENH3V02	44.32	1.00E-15	76.3	GDENH3V02	AT4G12825	74.39	1.00E-29	123	371	na	na	na	na
.	.	isogroup00027	co-ortholog	AT5G38170	g000270000	46.23	2.00E-18	89	g000270000	AT1G19835	92.07	0	1746	5100	0	0	0	0
.	.	isogroup01492	co-ortholog	AT5G38170	g014920000	34.62	1.00E-09	59.7	g014920000	AT1G48750	78.35	3.00E-39	158	1735	1	0.93	1	0.93
.	.	isogroup18354	co-ortholog	AT5G38170	g183540000	44.66	2.00E-18	89	g183540000	AT1G66850	89.22	2.00E-48	188	605	1	1.00	1	1.00
Lipid Transfer Protein type 2 (LTP2)	At3g57310	isogroup22272	co-ortholog	AT3G57310	e222720000	51.96	6.00E-20	93.6	e222720000	AT5G38160	62.38	4.00E-32	133	478	1	1.00	1	1.00
.	.	GDENH3V01DYSOG	co-ortholog	AT3G57310	GDENH3V01	44.44	4.00E-14	74.3	GDENH3V01	AT4G12825	63.74	1.00E-27	117	401	na	na	na	na
Lipid Transfer Protein type 2 (LTP2)	At1g73780	GDENH3V02FX18M	co-ortholog	AT1G73780	GDENH3V02	45.45	9.00E-14	73.2	GDENH3V02	AT3G18280	86.52	1.00E-40	161	418	na	na	na	na
.	.	isogroup00027	co-ortholog	AT1G73780	g000270000	45.45	4.00E-13	71.2	g000270000	AT1G19835	92.07	0	1746	5100	0	0	0	0
.	.	isogroup01492	co-ortholog	AT1G73780	g014920000	40.28	4.00E-13	70.9	g014920000	AT1G48750	78.35	2.00E-39	158	1735	1	0.88	1	0.88
.	.	isogroup18354	co-ortholog	AT1G73780	g183540000	43.94	9.00E-14	73.2	g183540000	AT1G66850	89.22	2.00E-48	188	605	1	1.00	1	1.00
.	.	isogroup22272	co-ortholog	AT1G73780	e222720000	44.44	2.00E-09	58.5	e222720000	AT5G38160	62.38	4.00E-32	133	478	1	1.00	1	1.00
Lipid Transfer Protein type 3 (LTP3)	At5g48485	isogroup22337	RH	AT5G48485	e223370000	85.56	9.00E-43	169	e223370000	AT5G48485	83.17	2.00E-46	180	420	2	1.00	2	1.00
Lipid Transfer Protein type 3 (LTP3)	At5g55410	isogroup10873	RH	AT5G55410	g108730000	84.55	5.00E-50	193	g108730000	AT5G55410	84.55	6.00E-51	197	609	1	0.52	1	0.52
Lipid Transfer Protein type 3 (LTP3)	At4g33550	isogroup16027	RH	AT4G33550	g160270000	95.74	5.00E-48	182	g160270000	AT4G33550	96.77	6.00E-49	188	581	2	0.53	1	0.26
Lipid Transfer Protein type 3 (LTP3)	At5g54550	GDENH3V01A6E44	RH	AT5G54550	GDENH3V01	70.1	9.00E-35	142	GDENH3V01	AT5G54550	70.83	2.00E-37	151	479	na	na	na	na
.	.	GDENH3V01A6E44	co-ortholog	AT5G54550	GDENH3V01	47.92	2.00E-21	98.6	GDENH3V01	AT5G54550	70.83	2.00E-37	151	479	na	na	na	na
Lipid Transfer Protein type 3 (LTP3)	At5g54600	isogroup0873	RH	AT5G54600	g08730000	54.13	1.00E-11	119	g08730000	AT5G54550	84.55	6.00E-51	197	609	1	1.00	1	1.00
.	.	isogroup22337	co-ortholog	AT5G54600	e223370000	31.82	1.00E-08	55.8	e223370000	AT5G48485	83.17	2.00E-46	180	420	2	1.00	2	1.00
.	.	GD75LV02ENSJ2	co-ortholog	AT1G32280	GD75LV02E	29.52	2.00E-08	55.1	GD75LV02E	AT2G13295	51.33	8.00E-30	125	473	na	na	na	na
Lipid Transfer Protein type 3 (LTP3)	At1g32280	isogroup14655	co-ortholog	AT1G32280	e146550000	60.98	5.00E-29	95.1	e146550000	AT5G56480	74.07	9.00E-41	119	495	1	1.00	1	1.00
.	.	isogroup16027	co-ortholog	AT1G32280	g160270000	39.73	4.00E-11	64.3	g160270000	AT4G33550	96.77	6.00E-49	188	581	2	0.53	1	0.26
.	.	isogroup20000	co-ortholog	AT1G32280	g200000000	44.83	3.00E-09	58.5	g200000000	AT4G30880	88.99	1.00E-51	199	592	1	1.00	1	1.00
Lipid Transfer Protein type 3 (LTP3)	At4g30880	isogroup20000	RH	AT4G30880	g200000000	88.99	2.00E-50	194	g200000000	AT4G30880	88.99	1.00E-51	199	592	1	1.00	1	1.00
Lipid Transfer Protein type 3 (LTP3)	At5g56480	isogroup14655	RH	AT5G56480	e146550000	73.42	2.00E-38	114	e146550000	AT5G56480	74.07	9.00E-41	119	495	1	1.00	1	1.00
.	.	GDENH3V01A6E44	co-ortholog	AT5G48490	GDENH3V01	35.05	5.00E-10	60.5	GDENH3V01	AT5G55450	70.83	2.00E-37	151	479	na	na	na	na
.	.	isogroup00621	co-ortholog	AT5G48490	g006210000	37.5	3.00E-09	58.5	g006210000	AT5G43280	90.68	3.00E-139	492	3145	11	0.88	4	0.88
Lipid Transfer Protein type 3 (LTP3)	At5g48490	isogroup10873	co-ortholog	AT5G48490	g108730000	30.61	7.00E-09	57	g108730000	AT5G55410	84.55	6.00E-51	197	609	1	0.52	1	0.52
Lipid Transfer Protein type 4 (LTP4)	At5g05960	GDENH3V01B58FR	RH	AT5G05960	GDENH3V01	87.07	7.00E-55	209</										

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
.	.	isogroup18563	co-ortholog	AT2644290	g18563000C	33.78	7.00E-09	58.5	g18563000C	AT1G73890	82.05	3.00E-64	240	498	1	1.00	1	1.00
.	.	isogroup19035	co-ortholog	AT2644290	e19035000C	37.1	5.00E-11	132	e19035000C	AT1G55260	82.29	4.00E-11	330	787	1	1.00	1	1.00
.	.	isogroup2223	co-ortholog	AT2644290	g2223000C	27.27	5.00E-07	52.4	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
.	.	isogroup01063	co-ortholog	AT2644290	g01063000C	34.15	7.00E-10	62	g01063000C	AT1G71720	86.13	0	785	2454	36	0.93	2	0.76
.	.	isogroup06577	co-ortholog	AT2644290	g06577000C	29.91	9.00E-08	54.7	g06577000C	AT1G05450	75.37	2.00E-83	305	940	2	0.74	2	0.74
Lipid Transfer Protein type 5 (LTP5)	At2g44300	isogroup17325	RBH	AT2G44300	e17325000C	89.13	1.00E-66	250	e17325000C	AT2G44300	89.13	6.00E-67	250	741	1	1.00	1	1.00
Lipid Transfer Protein type 5 (LTP5)	At2g48130	isogroup14385	RBH	AT2G48130	g14385000C	79.03	5.00E-73	271	g14385000C	AT2G48130	79.03	8.00E-77	283	722	1	0.81	1	0.81
Lipid Transfer Protein type 5 (LTP5)	At2g48140	isogroup05899	RBH	AT2G48140	g05899000C	82.26	9.00E-77	283	g05899000C	AT2G48140	82.59	2.00E-89	225	763	4	0.72	2	0.68
Lipid Transfer Protein type 5 (LTP5)	At3g22570	isogroup11166	co-ortholog	AT3G22570.1	g11166000C	42.72	6.00E-18	70.5	g11166000C	AT3G22600	84.12	2.00E-76	281	811	19	0.83	4	0.79
Lipid Transfer Protein type 5 (LTP5)	At3g22580	isogroup11166	co-ortholog	AT3G22580	g11166000C	50.91	3.00E-19	91.7	g11166000C	AT3G22600	84.12	2.00E-76	281	811	19	0.83	4	0.79
Lipid Transfer Protein type 5 (LTP5)	At3g22600	isogroup11166	RBH	AT3G22600	g11166000C	85.88	3.00E-70	261	g11166000C	AT3G22600	85.88	1.00E-79	292	811	18	0.98	4	0.94
Lipid Transfer Protein type 5 (LTP5)	At3g22620	isogroup05916	RBH	AT3G22620	g05916000C	94.58	2.00E-92	336	g05916000C	AT3G22620	94.58	7.00E-110	393	812	4	0.71	1	0.17
Lipid Transfer Protein type 5 (LTP5)	At3g43720	isogroup2223	RBH	AT3G43720	g2223000C	84.54	2.00E-83	305	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
Lipid Transfer Protein type 5 (LTP5)	At4g08670	isogroup20772	co-ortholog	AT4G08670	e20772000C	46.32	6.00E-17	85.1	e20772000C	AT4G05475	65.1	7.00E-90	328	1798	2	1.00	2	1.00
.	.	isogroup11166	co-ortholog	AT4G08670	g11166000C	33.33	1.00E-11	67.8	g11166000C	AT3G22600	84.12	2.00E-76	281	811	19	0.83	4	0.79
.	.	GD75ULV02E18UH	co-ortholog	AT4G08670	GD75ULV02E	40.18	3.00E-16	83.2	GD75ULV02E	AT2G13820	86.67	5.00E-64	239	432	na	na	na	na
.	.	isogroup14385	co-ortholog	AT4G08670	g14385000C	30.72	2.00E-10	63.2	g14385000C	AT2G48130	79.03	8.00E-77	283	722	1	0.81	1	0.81
.	.	isogroup2223	co-ortholog	AT4G08670	g2223000C	26.34	4.00E-10	62.4	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
.	.	isogroup2225	co-ortholog	AT4G08670	g2225000C	36.59	3.00E-09	59.7	g2225000C	AT2G27130	85.23	3.00E-81	297	631	5	0.97	3	0.97
.	.	isogroup20772	co-ortholog	AT4G14815	g20772000C	36.25	1.00E-09	60.1	g20772000C	AT4G05475	65.1	7.00E-90	328	1798	2	1.00	2	1.00
Lipid Transfer Protein type 5 (LTP5)	At4g14815	isogroup11166	co-ortholog	AT4G14815	g11166000C	58.02	3.00E-43	171	g11166000C	AT3G22600	85.88	1.00E-79	292	811	18	0.98	4	0.94
.	.	GD75ULV02E18UH	co-ortholog	AT4G14815	GD75ULV02E	36.45	5.00E-14	74.7	GD75ULV02E	AT2G13820	86.67	5.00E-64	239	432	na	na	na	na
.	.	isogroup3538	co-ortholog	AT4G14815	e03538000C	30.53	1.00E-08	56.6	e03538000C	AT1G62790	81.46	6.00E-64	242	808	1	1.00	1	1.00
.	.	isogroup14385	co-ortholog	AT4G14815	g14385000C	38.26	7.00E-10	94.7	g14385000C	AT2G48130	79.03	8.00E-77	283	722	1	0.81	1	0.81
.	.	isogroup17325	co-ortholog	AT4G14815	g17325000C	34.78	2.00E-09	59.3	g17325000C	AT2G44300	89.13	6.00E-67	250	741	1	1.00	1	1.00
.	.	isogroup18563	co-ortholog	AT4G14815	g18563000C	33.73	7.00E-07	50.8	g18563000C	AT1G73890	82.05	3.00E-64	240	498	1	1.00	1	1.00
.	.	isogroup19035	co-ortholog	AT4G14815	g19035000C	32.18	2.00E-10	63.2	g19035000C	AT1G55260	82.29	4.00E-91	330	787	1	1.00	1	1.00
.	.	isogroup2223	co-ortholog	AT4G14815	g2223000C	35.79	5.00E-09	58.2	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
.	.	isogroup2225	co-ortholog	AT4G14815	g2225000C	36.05	4.00E-06	48.5	g2225000C	AT2G27130	85.23	3.00E-81	297	631	5	0.97	3	0.97
Lipid Transfer Protein type 5 (LTP5)	At4g22640	isogroup18774	RBH	AT4G22640	g18774000C	76.32	6.00E-45	176	g18774000C	AT4G22640	76.32	6.00E-50	192	464	1	1.00	1	1.00
Lipid Transfer Protein type 5 (LTP5)	At5g09370	isogroup20772	co-ortholog	AT5G09370	e20772000C	44	3.00E-19	92.4	e20772000C	AT4G05475	65.1	7.00E-90	328	1798	2	1.00	2	1.00
.	.	isogroup11166	co-ortholog	AT5G09370	g11166000C	35.71	1.00E-11	66.6	g11166000C	AT3G22600	84.12	2.00E-76	281	811	19	0.83	4	0.79
.	.	GD75ULV02E18UH	co-ortholog	AT5G09370	GD75ULV02E	41.18	9.00E-18	87	GD75ULV02E	AT2G13820	86.67	5.00E-64	239	432	na	na	na	na
.	.	isogroup14385	co-ortholog	AT5G09370	g14385000C	32.82	2.00E-09	59.7	g14385000C	AT2G48130	79.03	8.00E-77	283	722	1	0.81	1	0.81
.	.	isogroup17325	co-ortholog	AT5G09370	g17325000C	28.1	2.00E-07	52.8	g17325000C	AT2G44300	89.13	6.00E-67	250	741	1	1.00	1	1.00
.	.	isogroup19035	co-ortholog	AT5G09370	g19035000C	32.98	5.00E-09	58.2	g19035000C	AT1G55260	82.29	4.00E-91	330	787	1	1.00	1	1.00
.	.	isogroup2223	co-ortholog	AT5G09370	g2223000C	31.75	1.00E-06	50.1	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
.	.	isogroup2225	co-ortholog	AT5G64080	g2225000C	40	3.00E-08	225	g2225000C	AT2G27130	85.23	3.00E-81	297	631	5	0.97	3	0.97
Lipid Transfer Protein type 5 (LTP5)	At5g64080	isogroup11166	co-ortholog	AT5G64080	g11166000C	30	6.00E-08	55.1	g11166000C	AT3G22600	84.12	2.00E-76	281	811	19	0.83	4	0.79
.	.	GD75ULV02E18UH	co-ortholog	AT5G64080	GD75ULV02E	58.21	6.00E-36	147	GD75ULV02E	AT2G13820	86.67	5.00E-64	239	432	na	na	na	na
.	.	isogroup14385	co-ortholog	AT5G64080	g14385000C	34.4	2.00E-10	63.5	g14385000C	AT2G48130	79.03	8.00E-77	283	722	1	0.81	1	0.81
.	.	isogroup17325	co-ortholog	AT5G64080	g17325000C	36.11	1.00E-06	50.4	g17325000C	AT2G44300	89.13	6.00E-67	250	741	1	1.00	1	1.00
.	.	isogroup19035	co-ortholog	AT5G64080	g19035000C	26.45	6.00E-07	51.6	g19035000C	AT1G55260	82.29	4.00E-91	330	787	1	1.00	1	1.00
.	.	isogroup2223	co-ortholog	AT5G64080	g2223000C	33.75	1.00E-13	73.9	g2223000C	AT3G43720	84.54	1.00E-92	335	914	7	0.98	4	0.98
.	.	isogroup2225	co-ortholog	AT5G64080	g2225000C	32.11	5.00E-08	42.7	g2225000C	AT2G27130	85.23	3.00E-81	297	631	5	0.97	3	0.97
Lipid Transfer Protein type 6 (LTP6)	At4g22490	isogroup18686	RBH	AT4G22490	g18686000C	82.35	1.00E-49	192	g18686000C	AT4G22490	82.35	3.00E-51	197	514	1	1.00	1	1.00
Lipid Transfer Protein type 6 (LTP6)	At4g22520	GDENH3V02GLDMV	RBH	AT4G22520	GDENH3V02	72.65	3.00E-42	167	GDENH3V02	AT4G22520	72.65	3.00E-45	176	404	na	na	na	na
Lipid Transfer Protein type 7 (LTP7)	At3g58550	GDENH3V01CHL52	RBH	AT3G58550	GDENH3V01	72.97	6.00E-39	157	GDENH3V01	AT3G58550	72.97	4.00E-39	155	346	na	na	na	na
Acyl-CoA Desaturase-like	At1g06080	isogroup09768	RBH	AT1G06080	g09768000C	98.31	6.00E-173	604	g09768000C	AT1G06080	98.31	2.00E-180	628	979	1	0.78	1	0.78
.	.	isogroup09768	co-ortholog	AT1G06120	g09768000C	61.67	9.00E-108	387	g09768000C	AT1G06080	98.31	2.00E-180	628	979	1	0.78	1	0.78
.	.	isogroup5024	co-ortholog	AT1G06120	g05024000C	59.34	1.00E-95	347	g05024000C	AT3G15850	93.1	0	734	1508	4	0.99	3	0.97
Acyl-CoA Desaturase-like	At1g06120	isogroup19939	co-ortholog	AT1G06120	e19939000C	69.23	7.00E-120	427	e19939000C	AT1G06360	92.31	4.00E-175	610	957	5	0.96	3	0.96
.	.	isogroup19799	co-ortholog	AT1G06120	e19799000C	59.86	1.00E-104	377	e19799000C	AT2G31360	95.78	2.00E-180	628	1084	8	0.85	3	0.85
ATP Citrate Lyase A subunit	At1g10670	isogroup01676	RBH	AT1G10670	g01676000C	93.45	0	838	g01676000C	AT1G10670	93.45	0	822	1801	8	0.55	1	0.22
.	.	isogroup01676	RBH	AT1G60810	g01676000C	97.87	0	852	g01676000C	AT1G60810	97.87	0	832	1801	22	0.94	7	0.91
ATP Citrate Lyase A subunit	At1g60810	isogroup21862	RBH*	AT1G60810	e21862000C	98.24	0	805	e21862000C									

Supplementary Table 1. Camelina lipid metabolism genes

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Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
.	.	isogroup14452	co-ortholog	AT16452000	g14452000C	39.77	2.00E-06	50.8	g14452000C	AT2625890	86.58	4.00E-67	250	715	1	0.93	1	0.93
.	.	isogroup14367	co-ortholog	AT16452000	g14367000C	48.21	8.00E-08	55.1	g14367000C	AT3601570	92.9	2.00E-90	328	778	2	1.00	2	1.00
.	.	isogroup14432	co-ortholog	AT16452000	g14432000C	48.21	7.00E-08	55.5	g14432000C	AT3601570	95.56	6.00E-93	337	800	1	0.91	1	0.91
.	.	isogroup06220	co-ortholog	AT16452000	g06220000C	60	4.00E-11	66.2	g06220000C	AT5651210	94.96	3.00E-68	254	741	5	0.72	3	0.72
.	.	isogroup08921	co-ortholog	AT16452000	g08921000C	46.03	1.00E-09	61.6	g08921000C	AT5661610	66.67	6.00E-100	360	921	2	0.94	2	0.94
.	.	isogroup01873	co-ortholog	AT16452000	g01873000C	57.45	3.00E-08	56.6	g01873000C	AT4625140	92.82	1.00E-89	326	962	174	0.97	3	0.61
.	.	isogroup21539	co-ortholog	AT16452000	g21539000C	51.35	9.00E-13	71.6	g21539000C	AT5607550	80.77	2.00E-41	164	553	1	1.00	1	1.00
Pollen-surface Oleosin	At5g61610	isogroup08921	RH	AT16452000	g08921000C	66.67	3.00E-100	362	g08921000C	AT5661610	66.67	6.00E-100	360	921	2	0.94	2	0.94
.	.	isogroup19756	RH*	AT16452000	g19756000C	72.34	4.00E-25	68.6	g19756000C	AT5661610	72.34	2.00E-26	705	484	0	0	0	0
Acyl-CoA Thioesterase	At5g48370	isogroup16311	RH	AT5648370	r16311000C	97.12	0	832	r16311000C	AT5648370	97.12	0	804	1291	7	1.00	2	0.94
Acyl-CoA Thioesterase	At1g01710	isogroup06515	RH	AT1601710	g06515000C	92.2	0	697	g06515000C	AT1601710	92.2	0	679	1534	10	0.70	2	0.58
.	.	isogroup11772	RH*	AT1601710	g11772000C	48.06	5.00E-19	93.6	g11772000C	AT1601710	50.77	1.00E-26	115	586	1	0.86	1	0.86
Acyl-CoA Thioesterase	At2g30720	isogroup07800	RH	AT2630720	g07800000C	86.9	0	439	g07800000C	AT2630720	84.42	4.00E-124	441	1567	28	0.46	1	0.30
Acyl-CoA Thioesterase	At4g00520	GD75ULV02EV3GF	RH	AT4600520	GD75ULV02E	83.17	1.00E-40	165	GD75ULV02E	AT4600520	83.17	7.00E-41	161	372	na	na	na	na
Malonyl-CoA Decarboxylase	At4g04320	GD75ULV01A1Q7W	RH*	AT4604320	GD75ULV01A	98.9	1.00E-48	192	GD75ULV01A	AT4604320	98.9	2.00E-47	184	452	na	na	na	na
.	.	isogroup18210	RH	AT4604320	g08210000C	92.95	0	734	g08210000C	AT4604320	92.95	0	707	1326	3	0.25	1	0.16
.	.	isogroup16426	RH	AT5604930	r16426000C	96.88	4.00E-128	457	r16426000C	AT5604930	96.88	6.00E-125	442	678	2	1.00	2	1.00
Translocase	At5g04930	isogroup16427	RH*	AT5604930	r16427000C	97.59	1.00E-68	171	r16427000C	AT5604930	98.78	3.00E-66	164	445	1	1.00	1	1.00
.	.	isogroup16956	RH*	AT5604930	r16956000C	96.41	7.00E-161	396	r16956000C	AT5604930	96.41	2.00E-160	398	878	1	1.00	1	1.00
.	.	GDENH3V01CN97I	RH*	AT5604930	GDENH3V01	100	2.00E-64	231	GDENH3V01	AT5604930	100	1.00E-62	221	396	na	na	na	na
Translocase	At1g72700	isogroup14035	RH	AT1672700	g14035000C	96.61	7.00E-99	360	g14035000C	AT1672700	96.61	4.00E-97	349	545	1	1.00	1	1.00
.	.	GDENH3V01B706	RH*	AT1672700	GDENH3V01	71.69	8.00E-59	227	GDENH3V01	AT1672700	71.69	3.00E-58	220	492	na	na	na	na
Translocase	At1g59820	isogroup01623	RH	AT1659820	r01623000C	97.4	0	1409	r01623000C	AT1659820	97.4	0	1357	2368	58	0.77	1	0.38
.	.	isogroup13566	RH*	AT1659820	r13566000C	96.73	3.00E-112	383	r13566000C	AT1659820	95.72	7.00E-111	376	616	1	1.00	1	1.00
.	.	isogroup14070	RH*	AT1659820	r14070000C	81.98	3.00E-46	185	r14070000C	AT1659820	81.98	1.00E-44	174	396	1	0.89	1	0.89
.	.	isogroup00449	RH	AT5644240	g00449000C	97.85	0	1103	g00449000C	AT5644240	97.85	0	1091	3785	12	0.98	2	0.80
Translocase	At5g44240	isogroup17603	RH*	AT5644240	r17603000C	98.04	0	849	r17603000C	AT5644240	98.04	0	835	1325	1	0.75	1	0.75
Translocase	At1g17500	GDENH3V01DKDCV	RH*	AT1617500	GDENH3V01	99.12	3.00E-88	240	GDENH3V01	AT1617500	100	2.00E-87	236	498	na	na	na	na
.	.	isogroup11371	RH	AT1617500	g11371000C	96.1	2.00E-116	319	g11371000C	AT1617500	96.1	1.00E-112	310	624	1	1.00	1	1.00
.	.	isogroup11364	RH*	AT1613210	g11364000C	56.23	7.00E-108	390	g11364000C	AT1613210	57.32	5.00E-104	374	1146	1	0.82	1	0.82
.	.	isogroup18611	RH	AT1613210	r18611000C	95.55	2.00E-172	604	r18611000C	AT1613210	96.55	6.00E-170	592	874	1	1.00	1	1.00
Translocase	At1g13210	isogroup22209	RH*	AT1613210	g22209000C	96.77	2.00E-103	376	g22209000C	AT1613210	96.77	2.00E-100	361	638	1	1.00	1	1.00
.	.	GDENH3V01CEUOM	RH*	AT1613210	GDENH3V01	95.56	4.00E-66	251	GDENH3V01	AT1613210	95.56	1.00E-66	248	405	na	na	na	na
Translocase	At3g13900	isogroup14029	RH	AT3613900	g14029000C	95.37	0	656	g14029000C	AT3613900	95.37	0	636	972	1	1.00	1	1.00
.	.	isogroup21144	RH*	AT3613900	g21144000C	92.98	5.00E-22	105	g21144000C	AT3613900	92.98	6.00E-28	118	308	1	1.00	1	1.00
.	.	GD75ULV02EVRQ	co-ortholog	AT1668710	GD75ULV02E	63.57	1.00E-50	200	GD75ULV02E	AT3627870	95.48	2.00E-81	296	467	na	na	na	na
.	.	isogroup00449	co-ortholog	AT1668710	g00449000C	35.2	4.00E-76	285	g00449000C	AT5644240	97.83	0	1081	3785	66	0.95	2	0.90
.	.	isogroup01623	co-ortholog	AT1668710	r01623000C	48.13	0	629	r01623000C	AT1659820	97.4	0	1357	2368	58	0.77	1	0.38
.	.	isogroup05678	co-ortholog	AT1668710	g05678000C	66.28	0	712	g05678000C	AT3627870	92.23	0	951	1731	3	1.00	3	1.00
Translocase	At1g68710	isogroup10758	co-ortholog	AT1668710	r10758000C	100	7.00E-17	882	r10758000C	AT5623535	99.37	5.00E-90	327	828	6	0.51	4	0.51
.	.	isogroup11364	co-ortholog	AT1668710	g11364000C	66.46	1.00E-106	233	g11364000C	AT1613210	89.44	6.00E-138	298	1146	1	0.91	1	0.91
.	.	isogroup11371	co-ortholog	AT1668710	g11371000C	57.14	4.00E-76	198	g11371000C	AT1617500	96.1	1.00E-112	310	624	1	1.00	1	1.00
.	.	isogroup13566	co-ortholog	AT1668710	g13566000C	26.06	3.00E-10	662	g13566000C	AT1659820	95.72	7.00E-111	376	626	1	1.00	1	1.00
.	.	isogroup14029	co-ortholog	AT1668710	g14029000C	60.06	3.00E-115	414	g14029000C	AT3613900	95.37	0	636	972	1	1.00	1	1.00
.	.	isogroup14070	co-ortholog	AT1668710	r14070000C	81.98	3.00E-42	173	r14070000C	AT1613210	96.61	4.00E-97	349	545	1	1.00	1	1.00
.	.	isogroup14070	co-ortholog	AT1668710	r14070000C	68.18	1.00E-32	128	r14070000C	AT1659820	81.98	1.00E-44	174	396	1	0.89	1	0.89
.	.	isogroup16426	co-ortholog	AT1668710	r16426000C	35.48	5.00E-31	135	r16426000C	AT5604930	96.88	6.00E-125	442	678	2	1.00	2	1.00
.	.	isogroup16427	co-ortholog	AT1668710	r16427000C	38.64	4.00E-20	67	r16427000C	AT5604930	98.78	3.00E-66	164	445	1	1.00	1	1.00
.	.	isogroup16956	co-ortholog	AT1668710	r16956000C	59.6	6.00E-26	118	r16956000C	AT5604930	96.41	2.00E-160	398	878	1	1.00	1	1.00
.	.	isogroup17603	co-ortholog	AT1668710	r17603000C	31.19	4.00E-49	195	r17603000C	AT5644240	98.04	0	835	1325	1	0.75	1	0.75
.	.	isogroup18246	co-ortholog	AT1668710	r18246000C	64.35	3.00E-163	374	r18246000C	AT3627870	94.13	0	885	1426	1	1.00	1	1.00
.	.	isogroup18611	co-ortholog	AT1668710	r18611000C	73.01	3.00E-130	464	r18611000C	AT1613210	96.55	6.00E-170	592	874	1	1.00	1	1.00
.	.	isogroup21146	co-ortholog	AT1668710	g21146000C	81.6	0	1069	g21146000C	AT1626130	94.16	0	1190	1977	2	0.64	1	0.52
.	.	isogroup22209	co-ortholog	AT1668710	g22209000C	70.1	5.00E-72	271	g22209000C	AT1613210	96.77	2.00E-100	361	638	1	1.00	1	1.00
.	.	isogroup00599	co-ortholog	AT1668710	g00599000C	24.79	1.00E-11	70.9	g00599000C	AT4629900	95.36	0	1000	3560	4	0.78	2	0.78
.	.	isogroup01865	co-ortholog	AT1668710	g01865000C	25.33	7.00E-07	55.1	g01865000C	AT5623630	94.31	0	2148	3604	4512	0.92	4	0.69
.	.	isogroup06379	co-ortholog	AT1668710	g06379000C	25.5	2.00E-15	83.6	g06379000C	AT5657110	94.69	0	2004	3391	240	0.95	3	0.92
Translocase	At1g26130	isogroup21146	RH	AT1626130	g21													

Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Arabidopsis Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads Fraction	Minimum	Min Reads Fraction
Translocase		isogroup05678	co-ortholog	AT1G54280	g05678r000c	52.65	1.00E-159	562	g05678r000c	AT3G27870	92.23	0	951	1731	3	1.00	3	1.00
		isogroup11364	co-ortholog	AT1G54280	e11364r000c	54.66	9.00E-83	179	g11364r000c	AT1G13210	89.44	6.00E-138	298	1146	1	0.91	1	0.91
		isogroup11371	co-ortholog	AT1G54280	g11371r000c	83.12	2.00E-107	289	g11371r000c	AT1G15700	96.1	1.00E-112	310	624	1	1.00	1	1.00
		isogroup11356	co-ortholog	AT1G54280	g13566r000c	30.06	1.00E-12	74.3	g13566r000c	AT1G59820	95.72	7.00E-111	376	626	1	1.00	1	1.00
		isogroup14029	co-ortholog	AT1G54280	g14029r000c	88.89	6.00E-176	616	g14029r000c	AT3G13900	95.37	0	636	972	1	1.00	1	1.00
		isogroup14035	co-ortholog	AT1G54280	e14035r000c	73.41	8.00E-66	251	e14035r000c	AT1G72700	96.61	4.00E-97	349	545	1	1.00	1	1.00
		isogroup14070	co-ortholog	AT1G54280	g14070r000c	67.39	2.00E-38	134	g14070r000c	AT1G59820	81.98	1.00E-44	174	396	1	0.89	1	0.89
		isogroup16426	co-ortholog	AT1G54280	e16426r000c	38.25	3.00E-36	152	e16426r000c	AT5G04930	96.88	6.00E-125	442	678	2	1.00	2	1.00
		isogroup16427	co-ortholog	AT1G54280	e16427r000c	38.64	4.00E-17	59.7	e16427r000c	AT5G04930	98.78	3.00E-66	164	445	1	1.00	1	1.00
		isogroup16956	co-ortholog	AT1G54280	e16956r000c	61.62	8.00E-28	124	e16956r000c	AT5G04930	96.41	2.00E-160	398	878	1	1.00	1	1.00
		isogroup17603	co-ortholog	AT1G54280	g17603r000c	35.28	1.00E-57	223	g17603r000c	AT5G44240	98.04	0	835	1325	1	0.75	1	0.75
		isogroup18246	co-ortholog	AT1G54280	g18246r000c	53.09	3.00E-143	508	g18246r000c	AT3G27870	94.13	0	885	1426	1	1.00	1	1.00
		isogroup18611	co-ortholog	AT1G54280	g18611r000c	46.58	4.00E-78	291	g18611r000c	AT1G13210	96.55	6.00E-170	592	874	1	1.00	1	1.00
		isogroup21144	co-ortholog	AT1G54280	e21144r000c	82.98	2.00E-19	96.7	e21144r000c	AT3G13900	92.98	6.00E-28	118	308	1	1.00	1	1.00
		isogroup21146	co-ortholog	AT1G54280	e21146r000c	54.5	0	696	e21146r000c	AT1G26130	94.16	0	1190	1977	2	0.64	1	0.52
	isogroup22209	co-ortholog	AT1G54280	e22209r000c	40.55	3.00E-79	195	e22209r000c	AT1G13210	96.77	2.00E-100	361	638	1	1.00	1	1.00	
	GDENH3V018918X	RH*	AT1G55840	GDENH3V01	90.32	2.00E-39	123	GDENH3V01	AT1G55840	90.32	3.00E-40	120	470	na	na	na	na	
Sec14-like Protein	At1g55840	isogroup06711	RH	AT1G55840	g06711r000c	96.67	7.00E-119	424	g06711r000c	AT1G55840	96.67	5.00E-115	410	1242	6	0.67	2	0.66
Sec14-like Protein	At5g47730	isogroup07891	RH	AT5G47730	e07891r000c	93.53	0	672	e07891r000c	AT5G47730	93.53	0	655	1295	24	0.92	3	0.85
Plastid Lipid-associated Protein	At2g35490	isogroup06869	RH	AT2G35490	g06869r000c	88.36	0	653	g06869r000c	AT2G35490	88.59	0	650	1327	13	0.92	1	0.10
Plastid Lipid-associated Protein	At4g22240	isogroup10153	RH	AT4G22240	g10153r000c	85.21	2.00E-149	526	g10153r000c	AT4G22240	85.21	9.00E-145	509	1109	2	0.60	1	0.29
Plastid Lipid-associated Protein	At4g04020	isogroup04330	RH	AT4G04020	g04330r000c	86.52	9.00E-156	547	g04330r000c	AT4G04020	86.52	1.00E-151	532	1172	17	0.89	2	0.85
Plastidial Long-Chain Acyl-CoA Synthetase	At4g14070	isogroup03785	RH	AT4G14070	g03785r000c	89.39	0	843	g03785r000c	AT4G14070	89.99	0	1310	2748	20	0.94	2	0.92
	GDENH3V0100A0C8	RH*	AT3G23790	GDENH3V01	54.74	1.00E-17	88.3	GDENH3V01	AT3G23790	54.74	7.00E-19	874	378	na	na	na	na	
	isogroup12733	RH	AT3G23790	g12733r000c	88.64	4.00E-157	553	g12733r000c	AT3G23790	90.26	3.00E-159	557	1008	2	0.73	2	0.73	
Plastidial Long-Chain Acyl-CoA Synthetase	At3g23790	isogroup12734	RH*	AT3G23790	g12734r000c	93.44	3.00E-98	357	g12734r000c	AT3G23790	93.44	7.00E-96	345	551	1	0.64	1	0.64
	GDENH3V029L1P	RH*	AT1G77590	GDENH3V02	93.04	5.00E-59	227	GDENH3V02	AT1G77590	93.04	4.00E-59	222	348	na	na	na	na	
Plastidial Long-Chain Acyl-CoA Synthetase	At1g77590	isogroup00142	RH	AT1G77590	g00142r000c	95.22	0	1361	g00142r000c	AT1G77590	95.22	0	1325	7802	0.80	0.80	0.80	
Long-Chain Acyl-CoA Synthetase	At4g23850	isogroup05645	RH	AT4G23850	g05645r000c	93.59	0	1150	g05645r000c	AT4G23850	93.59	0	1134	2289	233	0.96	3	0.88
	isogroup13002	RH*	AT4G23850	g13002r000c	93.09	9.00E-103	372	g13002r000c	AT4G23850	93.09	6.00E-103	655	1140	1	1.00	1	1.00	
Long-Chain Acyl-CoA Synthetase	At2g47240	isogroup02661	RH	AT2G47240	g02661r000c	95	0	1202	g02661r000c	AT2G47240	95	0	1186	2012	23	0.80	4	0.99
Long-Chain Acyl-CoA Synthetase	At2g04350	isogroup02661	RH	AT2G04350	g02661r000c	90.66	0	990	g02661r000c	AT2G04350	92.12	0	1016	2039	51	1.00	4	0.81
Long-Chain Acyl-CoA Synthetase	At1g49430	isogroup02997	RH	AT1G49430	g02997r000c	91.88	0	694	g02997r000c	AT1G49430	91.88	0	677	1887	154	0.94	2	0.61
Long-Chain Acyl-CoA Synthetase	At1g64400	isogroup07501	RH*	AT1G64400	g07501r000c	94.16	3.00E-79	273	g07501r000c	AT1G64400	94.16	3.00E-80	273	476	na	na	na	
	isogroup18049	RH	AT1G64400	g18049r000c	93.64	2.00E-93	341	g18049r000c	AT1G64400	93.64	8.00E-94	338	538	1	0.82	1	0.82	
Long-Chain Acyl-CoA Synthetase	At4g11030	isogroup07502	RH	AT4G11030	g07502r000c	94.3	5.00E-85	313	g07502r000c	AT4G11030	94.3	7.00E-85	308	504	na	na	na	
Plastidial ABC Ayl Transporter	At1g54350	isogroup03704	RH	AT1G54350	g03704r000c	90.73	0	1162	g03704r000c	AT1G54350	91.21	0	1143	2158	202	0.95	5	0.91
Epoide Hydroalase	At2g26740	isogroup11655	co-ortholog	AT2G26740	g11655r000c	54.38	4.00E-172	601	g11655r000c	AT2G26740	93.46	0	634	1176	14	0.70	1	0.17
	isogroup14303	co-ortholog	AT2G26750	e14303r000c	54.55	1.00E-75	281	e14303r000c	AT4G02340	93.7	4.00E-134	473	716	1	1.00	1	1.00	
	isogroup06700	co-ortholog	AT2G26750	g06700r000c	54.21	3.00E-105	379	g06700r000c	AT3G05600	88.52	3.00E-179	624	1223	2	0.64	2	0.64	
	isogroup11707	co-ortholog	AT2G26750	g11707r000c	54.33	2.00E-100	244	g11707r000c	AT4G15955	90	8.00E-154	320	1148	3	0.66	1	0.39	
	isogroup11791	co-ortholog	AT2G26750	g11791r000c	42.9	8.00E-70	261	g11791r000c	AT3G51000	92.26	1.00E-178	622	1141	2	1.00	2	1.00	
Epoide Hydroalase	At2g26750	isogroup20185	co-ortholog	AT2G26750	g20185r000c	89.41	2.00E-162	549	g20185r000c	AT2G26740	93.46	0	634	1175	14	0.70	1	0.17
	isogroup06550	co-ortholog	AT2G26750	g06550r000c	29.91	2.00E-06	56.3	g06550r000c	AT4G33180	88.67	2.00E-158	548	889	2	0.92	2	0.82	
	isogroup15894	co-ortholog	AT2G26750	g15894r000c	54.1	9.00E-99	358	g15894r000c	AT4G15960	85.03	2.00E-179	624	1165	3	1.00	3	1.00	
Epoide Hydroalase	At3g05600	isogroup06700	RH	AT3G05600	g06700r000c	88.52	1.00E-176	617	g06700r000c	AT3G05600	88.52	3.00E-179	624	1223	2	0.64	2	0.64
Epoide Hydroalase	At3g15960	GDENH3V02J121Y	RH	AT3G15960	GDENH3V02	56.45	1.00E-28	120	GDENH3V02	AT3G15960	56.45	3.00E-30	120	433	na	na	na	
Epoide Hydroalase	At4g02340	isogroup11655	RH	AT4G02340	g11655r000c	94.44	0	637	g11655r000c	AT4G02340	94.44	0	628	1160	3	0.96	2	0.96
	isogroup14303	RH*	AT4G02340	g14303r000c	93.7	4.00E-130	462	g14303r000c	AT4G02340	93.7	4.00E-134	473	716	1	1.00	1	1.00	
Epoide Hydroalase	At3g51000	isogroup11791	RH	AT3G51000	e11791r000c	92.26	5.00E-178	621	e11791r000c	AT3G51000	92.26	1.00E-178	622	1141	2	1.00	2	1.00
Cytosolic Holo-ACP Synthase	At2g02770	isogroup09124	RH*	AT2G02770	g09124r000c	33.7	1.00E-06	33.7	g09124r000c	AT2G02770	33.7	1.00E-07	52.4	452	1	1.00	1	1.00
	isogroup04059	RH*	AT1G36160	g04059r000c	89.76	2.00E-86	320	g04059r000c	AT1G36160	89.76	9.00E-86	311	522	na	na	na	na	
	isogroup07190	RH*	AT1G36160	g07190r000c	97.7	4.00E-154	453	g07190r000c	AT1G36160	97.71	2.00E-151	444	1456	1	0.79	1	0.79	
	isogroup19592	RH*	AT1G36160	e19592r000c	94.19	5.00E-83	308	e19592r000c	AT1G36160	94.19	8.00E-83	301	468	1	1.00	1	1.00	
	isogroup20684	RH	AT1G36160	g20684r000c	95	3.00E-176	283	g20684r000c	AT1G36160	95	5.00E-171	272	1038	1	0.81	1	0.81	
Cytosolic Homomeric Acetyl-CoA Carboxylase	At1g36160	isogroup00994	RH	AT1G36160	g00994r000c	98.25	0	701	g00994r000c	AT1G36160	94.94	0	678	1774	2	0.94	2	0.94
Sphingosine Transfer Protein	At2g34690	isogroup00994	RH	AT2G34690	g00994r000c	94.17	2.00E-113	405										



Supplementary Table 1. Camelina lipid metabolism genes

Function	AGI	Camelina Gene Candidate	Relationship Arabidopsis	TBLASTN Analysis				BLASTX Analysis				Isotig Length	Variant Analysis					
				Query	Subject	% identity	E-Value	bit-score	Query	Subject	% identity		E-Value	bit-score	Maximum	Max Reads	Fraction	Minimum
Lipid Acylhydrolase-like	At3g62590	isogroup1699	RBH	AT3G62590	g01699000C	86.14	0	895	g01699000C	AT3G62590	87	0	951	1880	26	0.92	2	0.62
Lipid Acylhydrolase-like	At4g00500	isogroup1811	RBH	AT4G00500	g001811000C	91.47	0	527	g001811000C	AT4G00500	96	0	525	2732	28	0.93	1	0.51
Lipid Acylhydrolase-like	At4g10950	isogroup18840	RBH	AT4G10950	g18840000C	91.46	0	587	g18840000C	AT4G10950	92.99	0	607	1263	3	1.00	3	1.00
Lipid Acylhydrolase-like	At4g13550	isogroup04260	RBH	AT4G13550	g04260000C	87.04	0	969	g04260000C	AT4G13550	87.04	0	985	2283	12	0.85	2	0.78
Lipid Acylhydrolase-like	At4g16070	isogroup17576	RBH	AT4G16070	g17576000C	93.95	0	947	g17576000C	AT4G16070	94.71	0	976	1612	20	0.95	3	0.92
Lipid Acylhydrolase-like	At5g24210	GD75ULV02D4OSV	RBH	AT5G24210	GD75ULV02I	76.54	1.00E-61	234	GD75ULV02I	AT5G24210	76.54	4.00E-68	253	474	na	na	na	na
.	.	GD75ULV02D4OSV	co-ortholog	AT5G24220	GD75ULV02I	45	7.00E-27	119	GD75ULV02I	AT5G24210	76.54	4.00E-68	253	474	na	na	na	na
.	.	isogroup00612	co-ortholog	AT5G24220	g00612000C	41.43	8.00E-74	275	g00612000C	AT5G24220	92.8	0	661	1455	23	0.86	3	0.82
Lipid Acylhydrolase-like	At5g24220	isogroup2208	co-ortholog	AT5G24220	g22208000C	55.11	4.00E-42	170	g22208000C	AT5G24230	94.3	2.00E-66	313	506	1	0.80	1	0.80
.	.	isogroup03644	co-ortholog	AT5G24220	g03644000C	39.24	7.00E-61	232	g03644000C	AT4G10955	91.67	6.00E-165	576	1023	14	0.83	1	0.26
.	.	isogroup07252	co-ortholog	AT5G24220	g07252000C	26.04	3.00E-29	127	g07252000C	AT5G50890	90.29	0	753	1507	34	0.94	5	0.70
Lipid Acylhydrolase-like	At5g37710	isogroup22382	RBH	AT5G37710	g22382000C	94.31	0	816	g22382000C	AT5G37710	94.31	0	842	1440	25	0.74	3	0.55
Lipid Acylhydrolase-like	At5g42930	GD75ULV02DM7K3	RBH*	AT5G42930	GD75ULV02I	88.31	1.00E-37	155	GD75ULV02I	AT5G42930	81.91	1.00E-45	177	284	na	na	na	na
.	.	isogroup18508	RBH	AT5G42930	g18508000C	87.72	8.00E-159	301	g18508000C	AT5G42930	87.72	1.00E-158	299	996	1	1.00	1	1.00
.	.	GD75ULV02DM7K3	co-ortholog	AT5G67050	GD75ULV02I	53.85	6.00E-17	87	GD75ULV02I	AT5G42930	81.91	1.00E-45	177	284	na	na	na	na
.	.	isogroup00001	co-ortholog	AT5G67050	g00001000C	43.06	4.00E-82	303	g00001000C	AT3G14360	92.07	0	688	1456	1	0.87	1	0.87
.	.	isogroup08463	co-ortholog	AT5G67050	g08463000C	28.31	2.00E-10	65.5	g08463000C	AT5G18640	93.35	0	669	1460	71	0.75	2	0.40
.	.	isogroup08480	co-ortholog	AT5G67050	g08480000C	23.94	1.00E-10	65.9	g08480000C	AT5G18630	90	0	642	1328	13	0.76	4	0.70
.	.	isogroup08540	co-ortholog	AT5G67050	g08540000C	23.74	4.00E-06	50.8	g08540000C	AT230550	88.75	0	718	1215	6	0.89	2	0.89
.	.	isogroup11478	co-ortholog	AT5G67050	g11478000C	28.49	1.00E-06	53.1	g11478000C	AT1G06250	88.65	0	771	1407	22	0.98	3	0.95
Lipid Acylhydrolase-like	At5g67050	isogroup12327	co-ortholog	AT5G67050	g12327000C	48.35	1.00E-85	315	g12327000C	AT1G45201	89.01	0	667	1178	1	0.59	1	0.59
.	.	isogroup14962	co-ortholog	AT5G67050	g14962000C	43.89	2.00E-49	195	g14962000C	AT3G14360	92.69	3.00E-122	433	676	1	1.00	1	1.00
.	.	isogroup18508	co-ortholog	AT5G67050	g18508000C	51.45	2.00E-63	147	g18508000C	AT5G42930	87.72	1.00E-158	299	996	1	1.00	1	1.00
Cyclopropane Fatty Acid Synthase	At3g23530	GD75ULV03HESLH	RBH	AT3G23530	GD75ULV03I	93.1	3.00E-80	174	GD75ULV03I	AT3G23530	94.19	3.00E-80	173	487	na	na	na	na
Cyclopropane Fatty Acid Synthase	At3g23510	isogroup19368	RBH	AT3G23510	g19368000C	79.86	0	687	g19368000C	AT3G23510	79.9	0	667	1342	4	0.88	3	0.88
.	.	isogroup07467	co-ortholog	AT3G23470	g07467000C	25.62	1.00E-17	89	g07467000C	AT4G33110	92.39	0	687	1261	4	0.51	1	0.45
Cyclopropane Fatty Acid Synthase	At3g23470	isogroup19368	co-ortholog	AT3G23470	g19368000C	73.14	9.00E-180	627	g19368000C	AT3G23510	79.9	0	667	1342	4	0.88	3	0.88
PPT1-like Thioesterase	At4g17470	isogroup18225	RBH	AT4G17470	g18225000C	75	2.00E-125	446	g18225000C	AT4G17470	75	2.00E-124	441	882	1	1.00	1	1.00
PPT1-like Thioesterase	At3g60340	isogroup04932	RBH	AT3G60340	g04932000C	92.01	0	637	g04932000C	AT3G60340	92.01	0	641	1385	39	0.91	2	0.79
.	.	isogroup05788	co-ortholog	AT5G47330	g05788000C	69.02	5.00E-120	428	g05788000C	AT4G17480	88.05	3.00E-151	531	1124	1	0.39	1	0.39
.	.	isogroup14019	co-ortholog	AT5G47330	g14019000C	65.16	4.00E-83	306	g14019000C	AT4G17483	84.16	9.00E-109	389	755	2	0.82	2	0.82
.	.	isogroup18225	co-ortholog	AT5G47330	g18225000C	63.99	2.00E-107	386	g18225000C	AT4G17470	75	2.00E-124	441	882	1	1.00	1	1.00
.	.	GDENH3V01833NZ	co-ortholog	AT5G47330	GDENH3V01I	67.9	1.00E-23	108	GDENH3V01I	AT5G47340	65.85	6.00E-24	105	397	na	na	na	na
.	.	isogroup04932	co-ortholog	AT5G47330	g04932000C	58	1.00E-106	384	g04932000C	AT3G60340	92.01	0	641	1385	39	0.91	2	0.79
PPT1-like Thioesterase	At5g47330	isogroup19291	co-ortholog	AT5G47330	g19291000C	75.95	9.00E-64	241	g19291000C	AT5G47340	76.25	5.00E-66	246	476	1	1.00	1	1.00
PPT1-like Thioesterase	At4g17480	isogroup05788	RBH	AT4G17480	g05788000C	88.74	3.00E-155	545	g05788000C	AT4G17480	88.74	5.00E-152	533	1124	1	0.22	1	0.22
PPT1-like Thioesterase	At4g17483	isogroup14019	RBH	AT4G17483	g14019000C	84.16	4.00E-111	399	g14019000C	AT4G17483	84.16	9.00E-109	389	755	2	0.82	2	0.82
.	.	isogroup05788	co-ortholog	AT5G47350	g05788000C	58.19	5.00E-97	352	g05788000C	AT4G17480	88.74	5.00E-152	533	1124	1	0.22	1	0.22
.	.	isogroup14019	co-ortholog	AT5G47350	g14019000C	55.11	3.00E-65	246	g14019000C	AT4G17483	84.16	9.00E-109	389	755	2	0.82	2	0.82
.	.	isogroup18225	co-ortholog	AT5G47350	g18225000C	55.86	5.00E-89	325	g18225000C	AT4G17470	75	2.00E-124	441	882	1	1.00	1	1.00
.	.	GDENH3V01833NZ	co-ortholog	AT5G47350	GDENH3V01I	59.76	4.00E-21	100	GDENH3V01I	AT5G47340	65.85	6.00E-24	105	397	na	na	na	na
.	.	isogroup04932	co-ortholog	AT5G47350	g04932000C	51.53	2.00E-91	333	g04932000C	AT3G60340	92.04	0	631	1385	18	0.98	4	0.78
PPT1-like Thioesterase	At5g47350	isogroup19291	co-ortholog	AT5G47350	g19291000C	62.5	5.00E-49	192	g19291000C	AT5G47340	76.25	5.00E-66	246	476	1	1.00	1	1.00
.	.	GDENH3V01833NZ	RBH*	AT5G47340	GDENH3V01I	65.85	7.00E-24	109	GDENH3V01I	AT5G47340	65.85	6.00E-24	105	397	na	na	na	na
PPT1-like Thioesterase	At5g47340	isogroup19291	RBH	AT5G47340	g19291000C	76.25	5.00E-66	249	g19291000C	AT5G47340	76.25	5.00E-66	246	476	1	1.00	1	1.00
Glycerophosphoryl Diester Phosphodiesterase	At5g08030	isogroup17866	RBH	AT5G08030	g17866000C	97.34	6.00E-101	365	g17866000C	AT5G08030	97.34	2.00E-104	374	600	1	1.00	1	1.00
Glycerophosphoryl Diester Phosphodiesterase	At1g74210	isogroup04780	RBH	AT1G74210	g04780000C	91.58	0	755	g04780000C	AT1G74210	91.58	0	751	1522	8	0.83	5	0.82
Phospholipid - Acyl acceptor Acyltransferase	At3g03310	isogroup04327	RBH	AT3G03310	g04327000C	93.32	0	843	g04327000C	AT3G03310	93.32	0	860	2212	19	0.95	4	0.92
Phospholipid - Acyl acceptor Acyltransferase	At1g04010	isogroup07784	RBH	AT1G04010	g07784000C	98.62	0	1042	g07784000C	AT1G04010	98.62	0	1061	1615	1	0.90	1	0.90
Phospholipid - Acyl acceptor Acyltransferase	At4g19860	isogroup01260	RBH	AT4G19860	g01260000C	93.47	0	870	g01260000C	AT4G19860	93.47	0	858	1732	188	0.84	5	0.78

**Supplementary Table 2** Primer sequences used to confirm SSP candidates

<b>Camelina SSP</b>	<b>Primer sequences</b>
CsSESA1	Forward primer TCGAGTTCGATGAAGACG Reverse primer TAGTAGTAAGAAGGGCCT
CsSESA2	Forward primer AAGAAATGGCAAACAAGC Reverse primer CCCAATCGTACTCGTCGC
CsSESA3	Forward primer CCGTGGTGATGACGAGTTT Reverse primer CGCCAACCTGCGGGATTC
CsSESA4	Forward primer CCGTGGTGATGACGAGTAC Reverse primer CGCCAACCTGCGGGATGT
CsSESA5	Forward primer AAGAAATGGCAAACAAGA Reverse primer CCCAATCGTACTCGTCACA
CsSESA6	Forward primer GTCGAGTTCGATGAAGAGA Reverse primer TTAGTAGTAAGAAGGGCCA
CsSESA7	Forward primer CGACGAAGATGACGCCACT Reverse primer AAACGCACTCTGGGTCTTG

## Supplementary Materials

### *Mass spectrometry analyses*

Mass spectrometry analyses were carried out by the Nebraska Center for Mass Spectrometry (NCMS) at the University of Nebraska-Lincoln. Protein spots were excised from Coomassie-stained 15% SDS-PAGE gels and digested as described (Shevchenko *et al.*, 1996), with slight modifications. The samples were washed with 100 mM ammonium bicarbonate, reduced with 10 mM DTT, alkylated with 55 mM iodoacetamide, washed twice with 100 mM ammonium bicarbonate, and digested *in situ* with 10 ng/μl trypsin (Promega, Madison, WI USA). Peptides were extracted with two 60 μl aliquots of 1:1 acetonitrile:water containing 1% formic acid and reduced in volume to approximately 25 μl by under vacuum. Peptide analysis by mass spectrometry was conducted as previously described (Schweitzer *et al.*, 2012). MS/MS data were processed using Masslynx software (Waters, Milford, MA USA) to produce peak lists that were searched against the NCBI non-redundant database, using the MASCOT (Matrix Science, Boston, MA USA) search engine. The following search parameters were used: mass accuracy 0.1 Daltons, enzyme specificity trypsin, fixed modification CAM, variable modification oxidized methionine. Protein identifications were based on random probability scores with a minimum value of 25.

### *Measuring protein content in SSP RNAi lines*

5 seeds of each line were pooled and weighed and ground to a fine powder in a microcentrifuge tube using liquid nitrogen. Total protein from each sample was extracted with 600 μl of buffer containing 0.1 M Tris, pH 8.8, 10 mM EDTA, 0.9 M Sucrose, and 0.4 % β-mercaptoethanol. Protein concentration was determined using a standard Bradford assay (Bradford, 1976).

*Preparation of RNAi suppression constructs for camelina SSP genes*

Partial sequences of camelina *CsSESA7* (nucleotide 120-360) and *CsSESCRU3* (nucleotide 866-1126) were amplified by PCR from a camelina seed cDNA for sense and antisense sequences for the 2S and 12S RNAi hairpin construct, respectively. To construct the 2S sense arm, a 240 base pair region of 2S *CsSESA7* was amplified with the oligonucleotide primers: 5'-GGGCTGCAGAAACGACGAAGATGACGCCACT-3' and 5'-GGGCTCGAGGCGGCCGCACGCACTCTGGGTCTTG-3' (added restriction sites are italicized). The *PstI/XhoI* cut fragment was used to replace the *KASII* sense arm in a modified version of a previously described plasmid utilizing a *FAD2* intron; pGEMT-KASIIHP-FAD2HP (Pidkowich *et al.*, 2007; Okuley *et al.*, 1994). The 2S antisense sequence used was PCR amplified from camelina developing seed cDNA using oligonucleotide primers with flanking *EcoRI/NotI* and *NheI* restriction sites: 5'-GGGGAATTCGCGGCCGCACGCACTCTGGGTCTTG-3' and 5'-GGGCTAGCGACGAAGATGACGCCACT-3'. The *EcoRI/NheI* cut fragment was used to replace the *KASII* antisense arm in the aforementioned plasmid to generate pGEMT-2SHP-FAD2HP.

The 12S hairpin was constructed similarly to the 2S hairpin structure above. A 269 base pair region for the 12S sense arm was PCR amplified from camelina cDNA with the following oligonucleotides, incorporating *SpeI* and *PstI* restriction sites: 5'-GGGACTAGTGGCTTCATGAGAATATTGAA-3' and 5'-GGGCTGCAGAAACCCTTGTCCTTGGCTCA-3'. The 12S antisense arm was amplified from cDNA using the following primers, with flanking *NheI* and *BglIII* restriction sites: 5'-GGGGCTAGCCCTTGTCCTTGGCTCA-3' and 5'-

GGGAGATCTGGCTTCATGAGAATATTGAA-3'. The sense and antisense 12S arms were used to replace the *FAD2* arms in the pGEMT-2SHP-FAD2HP plasmid, described above to generate pGEMT-2SHP-12SHP.

A cassette including the 2S hairpin, 12S hairpin and *FAD2* intron was cut from the pGEMT-2SHP-12SHP vector using *NotI* and cloned into the same site of pKMS3, downstream of a seed specific promoter from the soybean glycinin-1 gene, and upstream of the glycinin-1 3'UTR. This promoter-2S hairpin-12S hairpin cassette was then cloned into the *AscI* site of the pBinGlyRed2 binary vector that contains a DsRed fluorescent selectable marker.

#### *Preparation of FAD2 and FAE1 RNAi suppression constructs*

A *FAE1* RNAi suppression cassette was prepared by PCR amplification of a 251-bp portion of the camelina *FAE1* gene from a camelina cDNA developing seed cDNA using the oligonucleotides: 5'-TAATTCTAGACTCGAGGGGAATACTTCGTCTAGCTC-3' (*XbaI* and *XhoI* restriction sites italicized) and 5'-TATAAAGCTTACTAGTCCGACCGTTTTTTGACATGAGTC-3' (*HindIII* and *SpeI* restriction sites italicized). The PCR product was assembled sequentially in an inverted repeat orientation of either side of the *Flaveria trinervia* pyruvate orthophosphate dikinase (Pdk) intron (Wesley et al., 2001). The hairpin cassette was then cloned downstream of the seed-specific promoter for the *Glycine max* glycinin-1 gene and upstream of the 3'UTR for the glycinin-1 gene as a *NotI* fragment. The resulting vector contained *AscI* restriction sites that flanked the glycinin-1 promoter and 3'UTR. Using this restriction site the entire cassette containing promoter, RNAi hairpin and 3'UTR were assembled into the *MluI* site of the binary vector pBinGlyBar1 that contains a *bar* marker gene for Basta selection of transgenic plants to generate pBinGlyBar1+cFAE1 RNAi.

The *FAD2* RNAi hairpin cassette was prepared by PCR amplification of a 299-bp portion of the camelina *FAD2* gene from cDNA using the oligonucleotides: 5'-*TAATTCTAGACTCGAGCGTCTTGATCACTTACTTGCAG*-3' (added restriction sites are italicized) and 5'-*TATAAAGCTTACTAGTCTACATAGATACACTCCTTTGCC*-3'. The product was cloned sequentially in an inverted repeat orientation of either side of the *Flaveria trinervia* pyruvate orthophosphate dikinase (Pdk) intron (Wesley et al., 2001). The hairpin cassette was then cloned downstream of the seed-specific promoter for the *Brassica napus* oleosin gene and upstream of the oleosin 3'UTR as a *Not1* fragment. The resulting vector contained *AscI* restriction sites that flanked the oleosin promoter and 3'UTR. Using this restriction site the entire cassette containing promoter, RNAi hairpin and 3'UTR were assembled into the *MluI* site of pBinGlyBar1 and the *AscI* site of pBinGlyBar1+cFAE1 RNAi to make pBinGlyBar1+cFAD2 RNAi and pBinGlyBar1+cFAE1 RNAi+cFAD2 RNAi, respectively.

#### *Preparation of Arabidopsis FAD2 and FAE1 RNAi suppression constructs*

To facilitate the preparation of a construct for suppression of *FAD2* genes, an intron was amplified by PCR from the Arabidopsis *DIACYLGLYCEROL ACYLTRANSFERASE-1 (DGAT1)* gene with flanking restriction sites (*AscI* and *PacI* sites on 5' end and *SbfI* and *BsiWI* sites on 3' end) for cloning of inverted repeat sequences. Additional restriction sites (*NcoI* on 5' end and *KpnI* on 3' end) were added with PCR amplification using *Pfu* polymerase (Stratagene), genomic DNA from *A. thaliana* Col-0 as template, and the oligonucleotide primers: 5'-*TTCCATGGCGCGCCTTTTTAATTAAAAGCTATGGGCTTTTCTTGGGATTATG*-3' and 5'-*TTGGTACCTGCAGGTTTTTCGTACGTGAACCAGAAGATCATGTTCCCCACC*-3' (added restriction enzyme sites are shown in italics). The product was introduced into the pCR-Script Amp SK+ vector using a commercial cloning kit (Stratagene). A *FAD2* RNAi suppression

cassette was then prepared by PCR amplification of a 642-bp portion of the Arabidopsis *FAD2* gene from a corresponding cDNA clone using the oligonucleotides: 5'-  
TTCGTACGTTAATTAAGAACACCTTGTTCAAGATTCCGTAGTC-3' (*Bst*WI and *Pac*I restriction sites are italicized) and 5'-  
TTCCTGCAGGCGCGCCGCTGTGTCCTAACTGGTATCTGGGTCATAGC-3' (*Sbf*I and *Asc*I restriction sites are italicized). The PCR product was assembled sequentially in an inverted repeat orientation of either side of the *DGATI* intron. The hairpin cassette was then cloned downstream of the seed-specific promoter for the *Brassica napus* napin gene and upstream of the 3'UTR for the napin gene as an *Nco*I/*Kpn*I fragment. The resulting vector contained *Sal*I restriction sites that flanked the napin promoter and 3'UTR. Using this restriction site the entire cassette containing promoter, RNAi hairpin, and 3'UTR were assembled into the *Sal*I site of the previously described binary vector pEC92 that contains an *npt*III marker gene for kanamycin selection of transgenic plants. The resulting construct was designated pSH1. For preparation of a plant transformation construct containing seed-specific RNAi suppression cassettes for *FAD2* and *FAE1* genes, a *Sal*I fragment from pSH1 encompassing the complete *FAD2* suppression cassette was ligated into the *Xho*I site of the binary vector pBinGlyBar1-Mod to generate pBinGlyBar+AtFAD2. The pBinGlyBar1 vector contains a *bar* marker gene for Basta herbicide resistance screening of transgenic plants. The *FAE1* RNAi hairpin cassette was prepared by PCR amplification of a 426-bp portion of the Arabidopsis *FAE1* gene from a corresponding cDNA using Phusion polymerase. The oligonucleotide primers used for the PCR reaction were: 5'-TAATTCTAGACTCGAGGGTGTATTGCCATTGATTTGGC-3' (added *Xba*I and *Xho*I restriction sites are italicized) and 5'-  
TATAAAGCTTACTAGTGTTCCTTGGCGACGAAGGTAGC-3' (added *Hind*III and *Spe*I

restriction sites are italicized). The product was cloned sequentially into the previously described RNAi vector pHan-Intron (Schmidt and Herman, 2008) to generate a *FAE1* inverted repeat. The hairpin cassette was then recovered as a *NotI* fragment and ligated into the corresponding site of the vector pBetaConHyg. Flanking this cassette in pBetaConHyg was the seed-specific promoter for the  $\alpha'$  subunit of  $\beta$ -conglycinin gene from soybean and the 3'UTR of the phaseolin gene from *Phaseolus vulgaris*. The seed-specific expression cassette was then excised from pBetaConHyg as an *AscI* fragment, which was cloned into the *MluI* site of pBinGlyBar+AtFAD2 to create pBinGlyBar+AtFAD2+AtFAE1.

#### *Determination of total oil content in transgenic lines*

Total lipids were extracted from 30 mg of transgenic camelina seeds according to the Bligh and Dyer method (Bligh and Dyer, 1959). A triheptadecanoin internal standard (Nu-Chek Prep) was added prior to lipid extraction to allow for quantification of oil content. The lower organic layer from the extraction was transferred to a new tube and dried under nitrogen. Transesterification of the extracted total lipids was conducted by adding 1.5 ml of 2.5 % (v/v) sulfuric acid in methanol (with 0.01 % w/v BHT) and 250  $\mu$ l toluene to the dried lipids. The samples were then heated at 90°C for 1 h. After cooling, water (1 ml) and heptane (1 ml) were added to each tube. Heptane extracts containing fatty acid methyl esters were analyzed by gas chromatography as described (Cahoon *et al.*, 2006). Oil content was determined by comparison of the detector response from the seed lipid fatty acid methyl esters relative to methyl heptadecanoate from the triheptadecanoin internal standard.

#### *Statistical analyses*

The Microsoft Excel Student's *t*-Test function was used to determine significance. Paired tests with a two-tailed distribution were executed.



### *Estimation of transcript polymorphisms within assembled isotigs*

Read sequences contributing to each isotig from the assembly were extracted from the Newbler output file reads.placed, and mapped back to the isotig sequence using Newbler GS Reference Mapper (Roche, 2009). SNPs, including substitutions but excluding indels, among the fully mapped reads were recorded from 454AllDiffs.txt and only those with support from at least one read with a base quality score of 40 were retained. All possible variant transcripts that could be phased by SNP matching in overlaps were separated and scored as follows. Each read was weighted by the fraction of number of variants it is contributing to (a read shared among  $n$  transcript variants is counted  $1/n$ ), and then each variant was scored as the sum of the weights of contributing reads. Variants whose individual scores were less than 4% of the sum of scores of all the variants within an isotig were considered possible noise and discarded. We chose the 4% cutoff based on its ability to capture all known variants in *FAD2*.

### **References**

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